PTO-1390 (05-13)
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TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A SUBMISSION UNDER 35 U.S.C. 371		Attorney Docket No. Q0052.70018US01 U.S. Application No. (if known, see 37 CFR 1.5)
International Application No. PCT/US2012/033343	International Filing Date 12 April 2012	Priority Date Claimed 12 April 2011
Title of Invention	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY	
First Named Inventor	David Wilson et al.	

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information.

1. ☐ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). NOTE: The express request under 35 U.S.C. 371(f) will not be effective unless the requirements under 35 U.S.C. 371(c)(1), (2), and (4) for payment of the basic national fee, copy of the International Application and English translation thereof (if required), and the oath or declaration of the inventor(s) have been received.

2. ☐ A copy of the International Application (35 U.S.C. 371(c)(2)) is attached hereto (not required if the International Application was previously communicated by the International Bureau or was filed in the United States Receiving Office (RO/US)).

3. ☐ An English language translation of the International Application (35 U.S.C. 371(c)(2)).
   a. ☐ is attached hereto.
   b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4).

4. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
   a. ☐ is attached.
   b. ☐ was previously filed in the international phase under PCT Rule 4.17(iv).

Items 5 to 8 below concern amendments made in the international phase.

PCT Article 19 and 34 amendments

5. ☐ Amendments to the claims under PCT Article 19 are attached (not required if communicated by the International Bureau) (35 U.S.C. 371(c)(3)).

6. ☐ English translation of the PCT Article 19 amendment is attached (35 U.S.C. 371(c)(3)).

7. ☐ English translation of annexes (Article 19 and/or 34 amendments only) of the International Preliminary Examination Report is attached (35 U.S.C. 371(c)(5)).

Cancellation of amendments made in the international phase

8a. ☐ Do not enter the amendment made in the international phase under PCT Article 19.

8b. ☐ Do not enter the amendment made in the international phase under PCT Article 34.

NOTE: A proper amendment made in English under Article 19 or 34 will be entered in the U.S. national phase application absent a clear instruction from applicant not to enter the amendment(s).

The following items 9 to 17 concern a document(s) or information included.

9. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.

10. ☒ A preliminary amendment.

11. ☒ An Application Data Sheet under 37 CFR 1.76.

12. ☐ A substitute specification. NOTE: A substitute specification cannot include claims. See 37 CFR 1.125(b).

13. ☐ A power of attorney and/or change of address letter.

14. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13*ter*.3 and 37 CFR 1.821–1.825.

15. ☐ Assignment papers *(cover sheet and document(s))*. Name of Assignee:

16. ☐ 37 CFR 3.73(c) Statement *(when there is an Assignee)*.

3276648.1

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U.S. APPLN. No. (if known - see 37 CFR 1.5)	INTERNATIONAL APPLICATION No.	ATTORNEY DOCKET No.
	PCT/US2012/033343	Q0052.70018US01

17. [X] Other items or information: PCT Form IB/304, International Search Report, Published International Application

The following fees have been submitted.	CALCULATIONS	PTO USE ONLY
18. [X] Basic national fee (37 CFR 1.492(a)) **$280**	$ 280.00	
19. [X] Examination fee (37 CFR 1.492(c)) If the written opinion prepared by ISA/US or the international preliminary examination report prepared by IPEA/US indicates all claims satisfy provisions of PCT Article 33(1)-(4) ..... **$0** All other situations **$720**	$ 720.00	
20. [X] Search fee (37 CFR 1.492(b)) If the written opinion prepared by ISA/US or the international preliminary examination report prepared by IPEA/US indicates all claims satisfy provisions of PCT Article 33(1)-(4) ..... **$0** Search fee (37 CFR 1.445(a)(2)) has been paid on the international application to the USPTO as an International Searching Authority ..... **$120** International Search Report prepared by an ISA other than the US and provided to the Office or previously communicated to the US by the IB ..... **$480** All other situations **$600**	$ 480.00	
TOTAL OF 18, 19, and 20 =	$ 1,480.00	
[ ] Additional fee for specification and drawings filed in paper over 100 sheets (excluding sequence listing in compliance with 37 CFR 1.821(c) or (e) in an electronic medium or computer program listing in an electronic medium) (37 CFR 1.492(j)). Fee for each additional 50 sheets of paper or fraction thereof **$400**		
Total Sheets: 71 - 100 =	Extra Sheets: /50 =	Number of each addition 50 or fraction thereof (round **up** to a whole number):	RATE: **x $400**	$
Surcharge of **$140.00** for furnishing any of the search fee, examination fee, or the oath or declaration after the date of commencement of the national stage (37 CFR 1.492(h)).				$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	20 - 20 =	0	x **$80**	$ 0	
Independent claims	3 - 3 =	0	x **$420**	$ 0	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ **$780**	$	
Processing fee of **$140.00** for furnishing the English translation later than 30 months from the earliest claimed priority date (37 CFR 1.492(i)). +				$	
TOTAL OF ABOVE CALCULATIONS =				$ 1,480.00	
[ ] **Applicant asserts small entity status.** See 37 CFR 1.27. Fees above are reduced by ½.					
[ ] **Applicant certifies micro entity status.** See 37 CFR 1.29. Fees above are reduced by ¾. Applicant must attach form PTO/SB/15A or B or equivalent.					
TOTAL NATIONAL FEE =				$ 1,480.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). **$40.00** per property. +				$	
				$	
TOTAL FEES ENCLOSED =				$ 1,480.00	
				Amount to be refunded:	$
				Amount to be charged:	$

a. ☐ A check in the amount of $ _____ to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. 23/2825 in the amount of $ _____ to cover the above fees.

c. ☒ The Director is hereby authorized to charge additional fees which may be required, or credit any overpayment, to Deposit Account No. 23/2825 as follows:

i. ☒ any required fee.

ii. ☐ any required fee except for excess claims fees required under 37 CFR 1.492(d) and (e) and multiple dependent claim fee required under 37 CFR 1.492(f).

d. ☒ Fees are to be charged to a credit card. **WARNING:** Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038. The PTO-2038 should only be mailed or faxed to the USPTO. However, when paying the basic national fee, the PTO-2038 may NOT be faxed to the USPTO.

ADVISORY: If filing by EFS-Web, do **NOT** attach the PTO-2038 form as a PDF along with your EFS-Web submission. Please be advised that this is **not** recommended and by doing so your **credit card information may be displayed via PAIR**. To protect your information, it is recommended to pay fees online by using the electronic payment method.

NOTE: Where an appropriate time limit under 37 CFR 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the International Application to pending status.

Correspondence Address

☒ The address associated with Customer Number: 23628 **OR** ☐ Correspondence address below

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Address					
City		State		Zip Code	
Country			Telephone		
Email					

Signature	/Andrea J. Gabert/	Date	October 11, 2013
Name (Print/Type)	Andrea J. Gabert, Ph.D.	Registration No. (Attorney/Agent)	68,904

Application Data Sheet

Application Information

Application Type::	Regular
Subject Matter::	Utility
Suggested Group Art Unit::	N/A
CD-ROM or CD-R?::	None
Sequence submission?::	None
Computer Readable Form (CRF)?::	No
Title::	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY
Attorney Docket Number::	Q0052.70018US01
Request for Early Publication?::	No
Request for Non-Publication?::	No
Small Entity?::	No
Petition included?::	No
Secrecy Order in Parent Appl.?::	No

Applicant Information

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Status::	Full Capacity

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Initial 10/11/2013

State or Province of mailing address:: MA

Postal or Zip Code of mailing address:: 02021

Correspondence Information

Correspondence Customer Number:: 23628

Representative Information

Representative Customer Number:: 23628

Domestic Priority Information

Application::	Continuity Type::	Parent Application::	Parent Filing Date::
This Application	National Stage of	PCT/US2012/033343	04/12/12
PCT/US2012/033343	An application claiming the benefit under 35 USC 119(e)	61/474315	04/12/11
PCT/US2012/033343	An application claiming the benefit under 35 USC 119(e)	61/524693	08/17/11

Foreign Priority Information

Assignee Information

Assignee name:: Quanterix Corporation

Street of mailing address:: 113 Hartwell Avenue

City of mailing address:: Lexington

State or Province of mailing address:: MA

Postal or Zip Code of mailing address:: 02421-3125

Signature:

A signature of the applicant or representative is required in accordance with 37 CFR 1.33 and 10.18. Please see 37 CFR 1.4(d) for the form of the signature.			
Signature	/Andrea J. Gabert/	Date	October 11, 2013
Name (Print/Type)	Andrea J. Gabert, Ph.D.	Registration No. (Attorney/Agent)	68,904

460261

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE

United States Patent and Trademark Office

April 19, 2012

THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE.

APPLICATION NUMBER: *61/474,315*
FILING DATE: *April 12, 2011*
RELATED PCT APPLICATION NUMBER: *PCT/US12/33343*

THE COUNTRY CODE AND NUMBER OF YOUR PRIORITY APPLICATION, TO BE USED FOR FILING ABROAD UNDER THE PARIS CONVENTION, IS *US61/474,315*

Certified by

David J. Kappos

Under Secretary of Commerce
for Intellectual Property
and Director of the United States
Patent and Trademark Office

PTO/SB/16 (12-08)
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PROVISIONAL APPLICATION FOR PATENT COVER SHEET – Page 1 of 2

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

VIA EFS-WEB

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)

Additional inventors are being named on the _____ *separately numbered sheets attached hereto.*

TITLE OF THE INVENTION (500 characters max):

METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT

Direct all correspondence to: **CORRESPONDENCE ADDRESS**

[X] The address corresponding to Customer Number: 23628

OR

[ ] Firm or Individual Name

Address

City	State	Zip
Country	Telephone	Email

ENCLOSED APPLICATION PARTS (*check all that apply*)

[X] Application Data Sheet. See 37 CFR 1.76
[ ] CD(s), Number of CDs _____
[X] Drawing(s) *Number of Sheets* 6
[X] Other (specify) Appendix A
[X] Specification (e.g. description of the invention) *Number of Pages* 70

Fees Due: Filing Fee of $220 ($110 for small entity). If the specification and drawings exceed 100 sheets of paper, an application size fee is also due, which is $270 ($135 for small entity) for each additional 50 sheets or fraction thereof. See 35 U.S.C. 41(a)(1)(G) and 37 CFR 1.16(s).

METHOD OF PAYMENT OF THE FILING FEE AND APPLICATION SIZE FEE FOR THIS PROVISIONAL APPLICATION FOR PATENT

[X] Applicant claims small entity status. See 37 CFR 1.27.

[ ] A check or money order made payable to the *Director of the United States Patent and Trademark Office* is enclosed to cover the filing fee and application size fee (if applicable).

[ ] Payment by credit card. Form PTO-2038 is attached.

TOTAL FEE AMOUNT ($)

[ ] The Director is hereby authorized to charge the filing fee and application size fee (if applicable) or credit any overpayment to Deposit Account Number: _____ .

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

2299366.1

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The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

[X] No.

[ ] Yes, the name of the U.S. Government agency and the Government contract number are:

_____

WARNING:

Petitioner/applicant is cautioned to avoid submitting personal information in documents filed in a patent application that may contribute to identity theft. Personal information such as social security numbers, bank account numbers, or credit card numbers (other than a check or credit card authorization form PTO-2038 submitted for payment purposes) is never required by the USPTO to support a petition or an application. If this type of personal information is included in documents submitted to the USPTO, petitioners/applicants should consider redacting such personal information from the documents before submitting them to the USPTO. Petitioner/applicant is advised that the record of a patent application is available to the public after publication of the application (unless a non-publication request in compliance with 37 CFR 1.213(a) is made in the application) or issuance of a patent. Furthermore, the record from an abandoned application may also be available to the public if the application is referenced in a published application or an issued patent (see 37 CFR 1.14). Checks and credit card authorization forms PTO-2038 submitted for payment purposes are not retained in the application file and therefore are not publicly available.

SIGNATURE	/Michael J. Pomianek/	Date	April 12, 2011
TYPED or PRINTED NAME	Michael J. Pomianek, Ph.D.	REGISTRATION NO. *(if appropriate)*	46,190
TELEPHONE	617.646.8000	Docket Number:	Q0052.70017US00

Application Data Sheet

Application Information

Application Type::	Provisional
Subject Matter::	Utility
Suggested Group Art Unit::	N/A
CD-ROM or CD-R?::	None
Sequence submission?::	None
Computer Readable Form (CRF)?::	No
Title::	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT
Attorney Docket Number::	Q0052.70017US00
Request for Early Publication?::	No
Request for Non-Publication?::	No
Small Entity?::	Yes
Petition included?::	No
Secrecy Order in Parent Appl.?::	No

Applicant Information

Correspondence Information

Correspondence Customer Number::	23628

Representative Information

Representative Customer Number::	23628

Fujirebio Diagnostics, Inc. v. Quanterix Corp.
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Domestic Priority Information

Foreign Priority Information

Assignee Information

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METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT

Field of the Invention

The present invention generally relates, in some embodiments, to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide.

Background of the Invention

Hypoxia generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Oxygen deprivation to the brain results in neuronal damage and death, which is in turn related to the extent of long term brain dysfunction. The concentration of certain biomarkers may become elevated under hypoxic conditions. For example, certain such biomarkers have been found to become elevated in the brain and central nervous system under hypoxic condition. However, since such biomarkers must diffuse across the blood brain barrier, they may be present in the blood in proportion in extremely low concentrations that are not reliably measurable by typical conventional immunoassays. While the concentration of some biomarkers in the brain and central nervous system are known to increase with hypoxic events, the increased concentration has not been correlated with specific diagnostic indications and/or methods of treatment. In addition, while some methods exist for determining a cerebral hypoxic event in a patient and/or determining a course of treatment following a hypoxic event, many of the known methods are costly (e.g., magnetic resonance imaging) and/or provide unclear results and/or predictors. Accordingly, improved methods are needed.

Summary of the Invention

In some embodiments, a method for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide comprises performing an assay to determine a measure of the

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concentration of beta-amyloid peptide in the sample, wherein the limit of detection of beta-amyloid peptide of the assay is less than about 0.2 pg/mL.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on a measured concentration of at least one biomarker measured in each sample by an assay performed on a plurality of samples obtained from the patient following the event to determine the measure of the concentration of the at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprises performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises determining a measure of the concentration of a biomarker in each of a plurality of sample obtained from the patient

following the event, wherein the assay has a limit of quantification of less than about 10 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of a first biomarker in the plurality of samples, wherein the measured concentration has been determined by performing an assay to measure the concentration of only the first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises determining a measure of the concentration of only a first biomarker in each of a plurality of sample obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 100 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of beta-amyloid peptide present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay

has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a measure of the concentration of beta-amyloid in each of a plurality of samples obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 500 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and (c) determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined in step (b).

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined, which has been determined by: (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples have been obtained from the

patient over a period of time of at least about 48 hours and (b) determining the baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time.

In some embodiments, a method for performing an assay and providing data for determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and (c) providing data derived in steps (a) and (b) to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time

Brief Description of the Drawings

Figure 1a is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 1b is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 2 shows plots of a measure of the concentration of beta-amyloid (1-42) versus time for patients having (a-c) a good outcome and (d-f) a bad outcome;

Figure 3 shows a plot of a measure of the concentration of beta-amyloid (1-42) versus time including various parameters that may be correlated with a prognostic indication and/or a method of treatment;

Figure 4 shows an exemplary calibration dose-response of an assay method for determining a measure of the concentration of beta-amyloid (1-42) up to 250 pg/mL;

Figure 5 provides a plot showing day-to-day reproducibility for determining a

measure of the concentration of beta-amyloid (1-42), according to some embodiments of the present invention;

Figure 6 shows plots of a measure of the concentration of beta-amyloid (1-42) in plasma and CSF samples from Alzheimer's, MCI, and normal control subjects; and

Figure 7 shows a plot of a measure of the concentration of beta-amyloid (1-42) versus time for an exemplary patient

Other aspects, embodiments, and features of the invention will become apparent from the following detailed description when considered in conjunction with the accompanying drawings. The accompanying figures are schematic and are not intended to be drawn to scale. For purposes of clarity, not every component is labeled in every figure, nor is every component of each embodiment of the invention shown where illustration is not necessary to allow those of ordinary skill in the art to understand the invention. All patent applications and patents incorporated herein by reference are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Detailed Description

The present invention generally relates to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide. In some cases, the beta-amyloid peptide is beta-amyloid (1-42). The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles.

In some embodiments, a method of the present invention comprises determining a measure of the concentration of at least one biomarker in one or more samples obtained from a patient following a hypoxic event (or a suspected hypoxic event). A prognostic indication of the patient's recovery and/or determining a course of treatment may be based at least in part on the measure of the concentration of the at least one biomarker present in the one or more samples. It should be understood, that while much of the discussion below is directed to methods involving the analysis of more than one sample, this is by way of example only, and similar methods may be employed wherein only a single sample is employed.

As will be known to those of ordinary skill in the art, the term "hypoxia" generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Hypoxia at a cellular level develops when delivery of oxygen to cell mitochondria slows as the partial pressure gradient from capillaries to tissues decreases. As the delivery of oxygen decreases, aerobic metabolism stops and less efficient anaerobic pathways of glycolysis become responsible for the production of cellular energy. The end result is an increase in cellular concentrations of sodium, calcium, and hydrogen ions which may lead to cell death.

Oxygen deprivation to the brain results in neuronal damage and death. The extent of neuronal damage and death in turn relates to the extent of long term brain dysfunction, as can be assessed using standard criteria (such as Cerebral Performance Category, CPC rating, or like criteria). Severe hypoxia can result in a patient's death and/or an irreversible brain injury (e.g., resulting in the patient being in a vegetative state). Hypoxic events may be global (e.g., due to low oxygen content in the blood) or focused (e.g., affecting only an area of the brain). Causes of hypoxia include, but are not limited to, local asphyxia (e.g., caused by smoke inhalation), carbon monoxide poisoning and/or toxicity, cardiac arrest, choking, drowning, high altitudes, strangulation, an ischemic event, thrombosis, arterial embolism, hemorrhage, swelling of the brain, stroke, physical trauma and/or physical injury (e.g., blunt trauma to the head), arteriosclerosis, and/or atherosclerosis. In some cases, the event may be myocardial infarction, myocardial ischemia, and/or transient ischemic attack.

Hypoxic conditions can lead to the production and/or change in the concentration of certain biomarkers. That is, the concentration of certain biomarkers increase or decrease following the hypoxic event. For example, the production of the proteolytic products of β-amyloid precursor protein has been found to become elevated in the brain and central nervous system under hypoxic condition. The increased concentration is theorized to be due to a hypoxia-inducible factor (HIF-1) that promotes the production of beta-amyloid peptides from amyloid precursor protein, a membrane protein concentrated in neuronal synapses. A cascade of beta-amyloid peptides, including beta-amyloid (1-42), is generated in the brain in proportion to the extent of hypoxia. Beta-amyloid peptides could in turn diffuse across the blood brain barrier and into the blood in proportion to the extent of hypoxia, and may be generally found in low abundance. The ability to determine a change in the concentration of a biomarker in a plurality of samples (or a single sample) obtained from a patient following a hypoxic event can, in

some embodiments, be correlated with a prognostic indication of the patient's recovery from a brain injury and/or used to determine a method of treatment. In some cases, sample(s) of the patient's cerebrospinal fluid (CSF) may be obtained and analyzed to determine the concentration and/or a change in the concentration of the biomarker. In some cases, however, it is advantageous to determine the level of a biomarker in the blood of a patient as compared to CSF, as blood sampling is generally less invasive and may result in fewer complications as compared to CSF sampling. However, many of the biomarkers that are present in the CSF have a slow rate of transmission across and/or a high barrier of transportation across the blood-brain barrier (BBB) and thus, the concentration of the biomarker in the patient's blood may be sufficient lowered as compared to the concentration in CSF to make it difficult or impossible to accurately determine using typically employed conventional immunoassays. Accordingly, assay methods which have very low limits of quantification (LOQ) and/or limits of detection (LOD) are generally necessary to determine a measure of the concentration of a biomarker in the patient's blood to provide statistically significant and/or meaningful results. In some embodiments, the methods of the present invention make use of methods having very low LODs and/or LOQs (e.g., in the low pg/mL range) to determine a measure of the concentration of a biomarker in a sample(s) obtained from a patient following a hypoxic event. Various parameters related to the changes in the concentration of the biomarker in the samples (e.g., blood samples) may be correlated with a prognostic indication and/or a method of treatment following a hypoxic event. Correlations (e.g., between the concentration and prognostic indication(s) and/or between the concentration and method(s) of treatment) have been discovered and/or are now discoverable due to recent advancements in technology which allow for the determination of the low concentrations of biomarkers in bodily fluids with sufficient accuracy and precision, thus allowing for the variations in concentration to be statistically significant and therefore, diagnostic.

In embodiments where a plurality of samples are obtained from a patient, the samples may be obtained from a patient over any suitable period of time. Generally, the period of time may be selected such that the concentration of a biomarker in the samples becomes statistically significant and/or a trend is observable (e.g., an increase and/or decrease in the concentration). For biomarkers which are analyzed in blood samples, the period of time over which a plurality of samples are obtained from the patient may account for any lag time required for the biomarker to cross the BBB. Non-limiting

examples of suitable periods of time in which the samples may be obtained from the patient include 1 hour, 2 hours, 3 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 18 hours, 24 hours, 36 hours, 48 hours, 60 hours, 72 hours, 4 days, 5 days, 6 days, 7 days, or more. In some cases, the duration of time of sample collection time is at least 60 hours, or at least 72 hours. In some cases, the duration of time of sample collection is between 12 hours and 7 days, or between 24 hours and 4 days, or between 2 days and 4 days, or between 3 days and 4 days. The first sample may be obtained from the patient without a short timeframe following the hypoxic event. For example, the first sample may be obtained from the patient within 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 8 hours, 10 hours, or 12 hours of the hypoxic event. In some cases, the first sample is obtained within 6 hours of the hypoxic event. In some embodiments, a first sample is obtained from the patient within 6 hours of the suspected hypoxic event, and at about 1, about 2, about 6, about 12, about 24, about 48, and about 72 hours, following the first sampling. In some embodiments, additional samples are obtained at about 96 and/or at about 108 hours following the first sampling.

Any number of samples (e.g., one or more) may be obtained from the patient over the time period of sample collection. Generally, the minimum number of samples obtained is such that a trend (e.g., an increase or decrease) in the concentration of the biomarker is observable. Non-limiting examples of the number of samples that are obtained from the patient (e.g., during the prescribed collection time) is at least about bout 1, about 2, at least about 3, at least about 4, at least abut 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 12, at least about 15 or more. In some cases, the number of samples obtained from the patient is between 2 and 20, between 5 and 15, or between 5 and 10.

The sample(s) obtained from the patient may be from any suitable bodily source. In some cases, the samples are CSF samples. In some cases, the samples are blood or blood products (e.g., whole blood, plasma, serum, etc.). In other cases, the samples may be urine or saliva samples. In some embodiments, the samples may be analyzed directly (e.g., without the need for extraction of the biomarker from the fluid sample) and/or with dilution (e.g., addition of a buffer or agent to the sample). Generally, each of the samples obtained from the patient is collected using substantially similar procedures (e.g., to ensure minimal variation between samples based on sample collection methods). Those of ordinary skill in the art will be aware of suitable systems and methods for obtaining a sample from a patient.

Each of or substantially all of the samples may be analyzed using an assay method (e.g., as described herein) to determine a measure of the concentration of at least one biomarker in each, a subset of or substantially all of the samples. In some cases, the methods comprise determining a measure of the concentration of a single biomarker in the samples. In other cases, a method comprises determining a measure of the concentration of more than one biomarker in each, a subset of or substantially all of the samples. For example, a measure of the concentration of 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, biomarkers may be determined in the samples.

In some embodiments, the methods of the present invention comprise determining a prognostic indication based at least in part on the measured concentration of the at least one biomarker in the samples. In some cases, the prognostic indication may be correlated with standard criteria employed to define long-term brain dysfunction and/or injury. Those of ordinary skill in the art will be aware of such criteria, for example, cerebral performance category ratings ("CPC rating"), or more specifically, Glasgow-Pittsburgh cerebral performance category ratings (or scale) (e.g., see Teasdale G, Jennett B (1974); *Assessment of coma and impaired consciousness*; Lancet 2 (7872): 81–84). The CPC scale ranges from 1 to 5, with 1 representing a slight possibility of neurological deficit and 5 representing severe deficit and/or death. In some methods of the present invention, the prognostic indication of the patient's recovery from the brain injury is classified as either "good" (e.g., correlating to a CPC score of 1 or 2) corresponding to a high likelihood of recovery and/or returning to independent living, or "poor" (e.g., correlating to a CPC score of 3, 4, or 5) corresponding to little possibility of a full recovery and resulting in assisted living and/or death.

In the CPC scale, a rating of 1 is generally classified as good cerebral performance. The patient is conscious and alert, is able to work, but may have mild neurological or psychological deficit. A rating of 2 is generally classified as having moderate cerebral disability. The patient is conscious and has sufficient cerebral function for independent activities of daily life, and is generally able to work in sheltered environment. A rating of 3 corresponds to severe cerebral disability. While the patient is conscious, they generally depend on others for daily support because of impaired brain function. The patient may have abilities ranging from ambulatory state to severe dementia or paralysis. A rating of 4 corresponds to a coma or vegetative state. The patient is generally unaware, even if they appear awake (e.g., the patient is in a vegetative state) without interaction with environment and is cerebral unresponsive. A

rating of 5 refers to brain death, associated with apnea, areflexia, and/or EEG silence. The CPC scale is summarized in Table 1.

Table 1: CPC Scale Summary

CPC Score	Description
1	Conscious and alert with normal function or only slight disability
2	Conscious and alert with moderate disability
3	Conscious with severe disability
4	Comatose or persistent vegetative state
5	Brain dead or death from other causes

Other non-limiting examples of suitable criteria include the "scale g" criteria (e.g., see Dekaban AS, Robinson CE.; Application of a new rating scale of brain dysfunction to monitoring rehabilitation in 65 patients with severe head injury, Bull Clin Neurosci., 1984; 49, 82-92), the "Rancho Los Amigos Scale," and the "Disabilities Rating Scale."

In addition to the biomarkers specifically mentioned herein, those of ordinary skill will be aware of other suitable biomarkers to use in connection with the methods described herein. As described herein, the biomarker generally undergoes a change in concentration as a result of a hypoxic event. For example, the concentration of the biomarker may increase or decrease as a result of the hypoxic event. Non-limiting examples of biomarkers include neuron specific neuronal enolase (NSE), β-site aPP-cleaving enzyme 1 (BACe1), S100B, myelin basic protein (MBP), growth associated protein 43, glutamine synthetase, glial fibrillary acid protein (GFAP), glycine transporter (e.g., GLYT1, GLYT2), neuron specific glycoprotein (e.g., GP50), calpain, neurofibrillary protein, heat shock protein 72, beta-amyloid precursor proteins, calbindin D-28K, proteolipid protein, myeline associated glycoprotein, neurofilament H, creatine kinase protein (e.g., CK-BB), tau proteins (including phosphorylated taus such as p-tau-81 or p-tau-231), and endothelium membrane proteins (e.g., thrombomodulin).

In some cases, the biomarker may be a beta-amyloid peptide. Beta-amyloid peptides are known to those of ordinary skill in the art (e.g., see Blennow et al., Nature Reviews, Neurology, 6, 2010, 131; Portelius et al., Neurobiology of Aging, 2009, Corrected Proof in Press, doi:10.1016/j.neurobiolaging.2009.06.002). Beta-amyloid peptides are formed by sequential cleavage of the amyloid precursor protein (APP). APP can be processed by alpha-, beta-, and gamma-secretases, wherein the beta-amyloid peptide is generated by successive actions of the beta and gamma secretases. Various

forms of beta-amyloid peptides may be contemplated for use as a target with the methods described herein, include isoforms and short isoforms (e.g., ranging from beta-amyloid (1–14) up to beta-amyloid (1–43)). Beta-amyloid isoforms can have varying lengths of amino acids, with beta-amyloid (1-40) and beta-amyloid (1-42) being the most common. Non-limiting examples of isoforms of beta-amyloid peptides include beta-amyloid (1–40), beta-amyloid (1–42), beta-amyloid (1–37), beta-amyloid (1–38) and beta-amyloid (1–39). Non-limiting examples of short beta-amyloid isoforms include beta-amyloid (1–14), beta-amyloid (1–15) and beta-amyloid (1–16). In some embodiments, the biomarker is beta-amyloid (1-42).

As will be know, mild ischemia due to arteriolosclerosis is common in the elderly, and more common in Alzheimer's patients, an arteriolosclerosis could result in chronic upregulation of beta amyloid (1-42), which could lead to plaque deposits in the brain. In certain embodiments, the methods of the invention are performed on subjects not diagnosed with or suspected of suffering from Alzheimer's disease and the prognosis determined/provided by the methods disclosed herein does not relate to Alzheimer's disease. In other embodiments, the methods of the invention and the prognosis determined/provided by the methods disclosed herein may be used in the context of Alzheimer's disease.

The plurality of samples obtained from the patient may be analyzed (e.g., using an assay method as described herein) to determine a measure of the concentration of the at least one biomarker in each of the samples (or a single sample). A prognostic indication and/or a method of treatment may be determined based at least in part on the measure of the concentration of the biomarker in each of the plurality of samples. The data may be analyzed using a variety of techniques, as described herein, and a prognostic indication for recovery from a brain injury (e.g., a "good" outcome or a "poor" outcome), or a specific method of treatment may be determined based on the results.

In some embodiments, the measure of the concentration of the at least one biomarker for each of the plurality of samples obtained from the patient may be plotted on a graph of concentration versus time (e.g., in hours), and one or more parameters can be obtained from the graph and used to determine the method of treatment and/or the prognostic indication. Non-limiting examples of parameters that may be determined and/or employed include baseline biomarker concentration, increase in biomarker concentration, duration of rise of biomarker concentration, maximum slope of increasing biomarker concentration, rate of change of biomarker concentration, area under the curve

and/or magnitude of the fold increase of biomarker concentration. Each of the parameters and their determination will now be described in detail, followed by a description of possible data analysis and methods useful or potentially useful to determine suitable correlations between the measure of the concentration determined in the samples and a treatment/prognostic indication. The measure of the concentration of the biomarker may be determined/displayed in any suitable unit. In some cases, the measure of the concentration is determined/displayed in pg/mL.

The term "baseline biomarker concentration" refers to the concentration of the biomarker generally present in a fluid sample from a normal patient (e.g., prior to or unexposed to a hypoxic event). The baseline biomarker concentration can be determined using a variety of methods which will be commonly known and understood by those of ordinary skill in the art. In some cases, the baseline biomarker concentration can be determined by averaging the value of a biomarker present in a population of control patients (e.g., patients who have not experienced a hypoxic event). This may be useful in embodiments where the baseline concentration of the biomarker is substantially the same for a given population of individuals (e.g., based on age, gender, medical condition, etc). However, many of the methods described herein require accurate determination of extremely low concentrations of the at least one biomarker in samples obtained from a patient, and accordingly, a general baseline concentration of a biomarker (e.g., based on a sampling of a population) may not provide enough accuracy and/or precision to give useful results. Accordingly, a measure of the baseline biomarker concentration, in some embodiments, may be determined for each individual patient.

In some cases, the baseline biomarker concentration for each individual is equal to the measure of the concentration of the biomarker in the first sample obtained from the patient following the hypoxic event. In other cases, if available, a baseline biomarker concentration is the measure of the concentration of the biomarker present in a sample obtained from the patient prior to the hypoxic event. In yet other cases, the baseline biomarker concentration is the average concentration of the biomarker determined in a plurality of samples taken from the patient immediately or substantially immediately following the hypoxic event (e.g., prior to the concentration of the biomarker increasing due to the hypoxic event). That is, the concentration of the biomarker in the plurality of samples obtained from the patient in a selected time period following the hypoxic event may be averaged to determine the baseline biomarker concentration for that patient. As will be understood by those of ordinary skill in the art, in such cases, any sample which

has a concentration level that significantly differs from the other concentration levels during that period of time (e.g., a data point/outlier having a concentration which deviates significantly from the other concentrations measured during the time frame) may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by greater than about 50% from the calculated average, that sample may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by more than about 0.5 pg/mL, 1 pg/mL, 2 pg/mL, 5 pg/mL, or 10 pg/mL from the calculated average, that sample may be excluded from the averaging calculation. An anomalous data point may be observed and/or caused by administration of drugs to the patient. The baseline biomarker concentration may be determined by averaging the concentration of the biomarker in the samples obtained from the patient between the first sample (e.g., obtained within 6 hours of the hypoxic event) and 24 hours following the first collection of a sample, or between the first sample and 18 hours following the first collection of a sample, or between the first sample, and 12 hours following the first collection of a sample, or between the first sample, and 6 hours following the first collection of a sample (e.g., not including any outliers).

The term "change in biomarker concentration" refers to the change (e.g., increase or decrease) in concentration of the biomarker over the time period in which the samples are collected. An increase in biomarker concentration may be calculated by subtracting the baseline biomarker concentration (e.g., as described herein) from the maximum biomarker concentration. The "maximum biomarker concentration" is the maximum measured concentration of the biomarker measured in a single sample collected over the duration of the sample collection. For example, if the duration of the sample collection is 72 hours, the maximum concentration is equal to the maximum measured concentration in a single sample which was obtained from the patient in the 72 hour period. A decrease in biomarker concentration may be calculated by subtracting an elevated biomarker concentration (e.g., as described herein) from the minimum biomarker concentration.

The term "magnitude of the fold increase of biomarker concentration" refers to the magnitude of the fold-increase in concentration over the duration of sample collection, and may be calculated by dividing the maximum biomarker concentration (e.g., as described herein) by the baseline biomarker concentration (e.g., as described herein).

The term "duration of rise of biomarker concentration" refers to the time over which the concentration of the biomarker is increasing during the time period over which the samples are collected. In some cases, the duration of rise of biomarker concentration can be determined by subtracting the time at which the last sample was collected at approximately the baseline biomarker concentration (e.g., starting time of the rise) from the time at which the maximum biomarker concentration was observed (e.g., ending time of the rise). That is, the duration of the rise may be equal to the ending time of the rise minus the starting time of the rise. The duration of rise is generally provided in hours.

The term "maximum slope of increasing biomarker concentration" refers to the slope at which the maximum increase in concentration occurred over the time period in which the samples were collected. Those of ordinary skill will be aware of methods to calculate this value using common graphical analysis methods. For example, a plot may be prepared showing concentration versus time, and the maximum slope may be calculated based on this plot. In some cases, the maximum slope is equal to the slope between two data points, whereas in other cases, the maximum slope may be determined based on the average slope between a plurality of data points.

The term "area under the curve," (or AUC) is a common parameter used to analyze data, and such calculations will be well known and understood by those of ordinary skill in the art. In context with the methods of this disclosure, the AUC refers to the area under the biomarker concentration versus time curve. Generally the calculation takes into account the baseline biomarker concentration.

The above parameters, alone or in combination, may be correlated to a prognostic indication and/or a method of treatment for a patient following a hypoxic event. Following determination of a correlation between biomarker concentrations and a prognostic indication and/or a method of treatment (e.g., using a plurality of samples obtained from a plurality of test patients with known outcomes), the correlation can be used in connection with methods to determine prognosis (e.g., prognostic indications) and/or methods of treatment for patients with unknown outcomes. That is, an algorithm can be developed relating changes in a biomarker concentration and specific methods of treatment and/or prognostic indications using samples from test patients having been subject to known methods of treatment and/or having a known prognosis. Once the algorithm has been developed, it can be used to determine methods of treatment and/or prognostic indications for patients with unknown outcomes.

To determine a correlation between a biomarker and a prognostic indication and/or a method of treatment (e.g., to develop an algorithm relating the measured biomarker concentration to preferred methods of treatment and/or prognostic indications), a plurality of samples from a plurality of test patients may be obtained. A "test patient" is a patient who has a known outcome (e.g., a good or a poor CPC score) and/or has received a certain treatment. The plurality of the samples obtained from each of the test patients may be analyzed to determine the measure of the concentration of at least one biomarker in the each of the samples. Some or all of the parameters described herein may be determined for each patient, and the data may be analyzed to determine correlations between the parameters and the patient outcomes and/or treatments, which can in turn be used to develop an algorithm. The algorithm may then be applied to the concentration of the at least one biomarker in samples obtained from a patient having an unknown outcome to determine a method of treatment and/or a prognostic indication for that patient. A specific example of such an analysis is described below, and further details are provided in Example 1.

Similar analysis and methods may be used to correlate suitable methods of treatment based upon the measured concentration(s) of a biomarker in a plurality of samples obtained from a patient. In some cases, the method of treatment may comprise administering at least one therapeutic agent to the patient. For example, the therapeutic agent may be a neuroprotective drug. Other non-limiting methods of treatment include administration of anti-oxidants, hypothermia, blood thinning, and administration of steroids (e.g., to help reduce brain swelling) (e.g., see T. S. Richmond, Cerebral Resuscitation After Global Brain Ischemia: Linking Research to Practice, American Association of Critical-Care Nurses Journal, May 1997, Volume 8, Number 2).

A therapeutic agent is generally administered in an amount effective to provide a medically desirable result. The effective amount will vary with the particular condition being treated, the age and physical condition of the subject being treated, the severity of the condition, the duration of the treatment, the nature of the concurrent therapy (if any), the specific route of administration and the like factors within the knowledge and expertise of the health care practitioner. In some cases, a therapeutic agent may reduce brain injuries resulting from the hypoxic event. In some cases, the method of treatment may involve a change in treatment, such as an increase or decrease in the dose of a therapeutic agent, a switch from one therapeutic agent to another therapeutic agent, an addition of another therapeutic agent to the existing therapeutic agent, or a combination

thereof. A switch from one therapeutic agent to another may involve a switch to a therapeutic agent with a high risk profile but where the likelihood of expected benefit is increased.

In one embodiment, a method of the present invention for determining a treatment protocol for and/or a prognostic indication of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a plurality of samples to determine a measure of the concentration of beta-amyloid peptide in each sample and determining a prognostic indication of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measure of the concentration of beta-amyloid peptide present in the samples. In some embodiments, the beta-amyloid peptide is beta-amyloid (1-42). The sample, in some embodiments, is a blood sample from the patient and/or plasma and/or serum derived from the blood sample. In some cases, the concentration of the beta-amyloid in the samples is less than about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL, or less. In some cases, the assay has a limit of quantification of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL or less. In some cases, the assay has a limit of detection of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less.

In one embodiment, a correlation was determined between certain parameters (e.g., maximum beta-amyloid peptide concentration, duration of increase of beta-amyloid concentration, and the magnitude of the fold increase of beta-amyloid concentration) and a good (e.g., CPC rating 1 or 2) and a poor (e.g., CPC rating of 3, 4, or 5) prognostic indication. To determine the correlation, an assay was carried out on each of the samples obtained from a plurality of test patients having undergone a hypoxic event (e.g., patients having a known outcome and/or having undergone a certain method of treatment following a hypoxic event). The first sample was taken within 6 hours of the hypoxic event, and additional samples were generally obtained at about 1, 2, 6, 12, 24, 48, and 72 hours following the first sample (and optionally, at 96 and/or 108 hours). Each of the test patients had a known prognostic outcome according to the CPC scale. For each test

patient, a plot of the measured concentration of beta-amyloid in pg/mL versus time in hours was prepared. The data was analyzed and the sum of the increase in beta-amyloid concentration (in pg/mL), the duration of the increase of beta-amyloid concentration (in hours), and the magnitude of the fold increase of beta-amyloid concentration was determined to correlate with a "good" or "poor" prognosis for the patients. In particular, a sum of greater than 50 correlated with a poor prognosis (e.g., a CPC score of 3, 4, or 5) and a score of less than about 50 correlated with a good prognosis (e.g., a CPC score of 1 or 2). Accordingly, a correlation/algorithm was established between the varying parameters relating to concentration and a prognostic indication.

The developed correlation/algorithm can be applied to patients with unknown outcomes. That is, samples may be obtained from a patient and the concentration of beta-amyloid in each of the samples can be determined. The data may be analyzed to determine the increase in beta-amyloid concentration (in pg/mL), the duration of the increase of beta-amyloid concentration (in hours), and the magnitude of the fold increase of beta-amyloid concentration. If the sum of the three parameters is greater than 50, the prognostic indication for that patient is "poor," and if the sum is less than 50, the prognostic indication is "good." Using similar techniques, a variety of correlations may be determined for this beta-amyloid (e.g., analysis of the area under the curve) and/or other biomarkers.

Exemplary Assay Methods and Systems

Those of ordinary skill in the art will be aware of a variety of assay methods and systems that may be used in connection with the methods of the present invention. Generally, the methods employed have low limits of detection and/or limits of quantification as compared to bulk analysis techniques (e.g., ELISA methods). The use of assay methods that have low limits of detection and/or limits of quantification allows for correlations to be made between the various parameters discussed above and a method of treatment and/or diagnostic indication that may otherwise not be determinable and/or apparent. For example, in the method described above which correlates the sum of three parameters relating to beta-amyloid concentration to a prognostic indication of brain injury, the limits of detection, and/or limits of quantification needs to be substantially lower than the LOD and/or LOQ provided by common ELISA techniques.

The terms "limit of detection" (or LOD) and "limit of quantification" (or LOQ) are given their ordinary meaning in the art. The LOD refers to the lowest analyte

concentration likely to be reliably distinguished from background noise and at which detection is feasible. The LOD as used herein is defined as three standard deviations (SD) above background noise. The LOQ refers to the lowest concentration at which the analyte can not only be reliably detected but at which some predefined goals for bias and imprecision are met. Generally, as is used herein, the LOQ refers to the lowest concentration above the LOD wherein the coefficient of variation (CV) of the measured concentrations less than about 20%.

In some cases, an assay method employed has a limit of detection and/or a limit of quantification of less than about 500 pg/mL, 250 pg/mL, 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less. In some cases, an assay method employed has a limit of quantification and/or a limit of detection between about 100 pg/mL and about 0.01 pg/mL, between about 50 pg/mL and about 0.02 pg/mL, between about 25 pg/mL and about 0.02 pg/mL, between about 10 pg/mL and about 0.02 pg/mL. As will be understood by those of ordinary skill the art, the LOQ and/or LOD may differ for each assay method and/or each biomarker determined with the same assay. In some embodiments, the LOD of an assay employed for detecting of beta-amyloid (e.g., beta-amyloid (1-42)) is about equal to or less than 0.02 pg/mL. In some embodiments, the LOQ for an assay employed for detecting beta-amyloid (e.g., beta-amyloid (1-42)) is equal to or less than 0.04 pg/mL

In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is less than about 5000 fM, less than about 3000 fM, less than about 2000 fM, less than about 1000 fM, less than about 500 fM, less than about 300 fM, less than about 200 fM, less than about 100 fM, less than about 50 fM, less than about 25 fM, less than about 10 fM, less than about 5 fM, less than about 2 fM, less than about 1 fM, less than about 0.5 fM, less than about 0.1 fM, or less. In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is between about 5000 fM and about 0.1 fM, between about 3000 fM and about 0.1 fM, between about 1000 fM and about 0.1 fM, between about 1000 fM and about 1 fM, between about 100 fM and about 1 fM, between about 100 fM and about 0.1 fM, or the like. The concentration of analyte molecules or particles in a fluid sample may be considered to be substantially accurately determined if the measured concentration of the biomarker molecules in the fluid sample

is within about 10% of the actual (e.g., true) concentration of the biomarker molecules in the fluid sample. In certain embodiments, the measured concentration of the biomarker molecules in the fluid sample may be within about 5%, within about 4%, within about 3%, within about 2%, within about 1%, within about 0.5%, within about 0.4%, within about 0.3%, within about 0.2% or within about 0.1%, of the actual concentration of the biomarker molecules in the fluid sample. In some cases, the measure of the concentration determined differs from the true (e.g., actual) concentration by no greater than about 20%, no greater than about 15%, no greater than 10%, no greater than 5%, no greater than 4%, no greater than 3%, no greater than 2%, no greater than 1%, or no greater than 0.5%. The accuracy of the assay method may be determined, in some embodiments, by determining the concentration of biomarker molecules in a fluid sample of a known concentration using the selected assay method.

In some embodiments, an assay method employs a step of spatially segregating biomarker molecules into a plurality of locations to facilitate detection/quantification, such that each location comprises/contains either zero or one or more biomarker molecules. Additionally, in some embodiments, the locations may be configured in a manner such that each location can be individually addressed. In some embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be determined by detecting biomarker molecules immobilized with respect to a binding surface having affinity for at least one type of biomarker molecule. In certain embodiments the binding surface may form (e.g., a surface of a well/reaction vessel on a substrate) or be contained within (e.g., a surface of a capture object, such as a bead, contained within a well) one of a plurality of locations (e.g., a plurality of wells/reaction vessels) on a substrate (e.g., plate, dish, chip, optical fiber end, etc). At least a portion of the locations may be addressed and a measure indicative of the number/percentage/fraction of the locations containing at least one biomarker molecule may be made. In some cases, based upon the number/percentage/fraction, a measure of the concentration of biomarker molecules in the fluid sample may be determined. The measure of the concentration of biomarker molecules in the fluid sample may be determined by a digital analysis method/system optionally employing Poisson distribution adjustment and/or based at least in part on a measured intensity of a signal, as will be known to those of ordinary skill in the art. In some cases, the assay methods and/or systems may be automated.

Certain methods and systems which employ spatially segregating analyte molecules (e.g., biomarkers) are known in the art, and are described in U.S. Patent Application Publication No. US-2007-0259448 (Serial No. 11/707,385), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF TARGET ANALYTE CONCENTRATION IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259385 (Serial No. 11/707,383), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR DETECTING CELLS AND CELLULAR COMPONENTS IN SMALL DEFINED VOLUMES," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259381 (Serial No. 11/707,384), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF REACTION COMPONENTS THAT AFFECT A REACTION," by Walt et al.; International Patent Publication No. WO 2009/029073 (International Patent Application No. PCT/US2007/019184), filed August 30, 2007, entitled "METHODS OF DETERMINING THE CONCENTRATION OF AN ANALYTE IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al.; U.S. Patent Application Publication No. US-2010-00754072 (Serial No. 12/236,486), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES ON SINGLE MOLECULE ARRAYS," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075439 (Serial No. 12/236488), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES BY CAPTURE-AND-RELEASE USING REDUCING AGENTS FOLLOWED BY QUANTIFICATION," by Duffy et al.; International Patent Publication No. WO2010/039179 (International Patent Application No. PCT/US2009/005248), filed September 22, 2009, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR ENZYMES," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075355 (Serial No. 12/236490), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF ENZYMES BY CAPTURE-AND-RELEASE FOLLOWED BY QUANTIFICATION," by Duffy et al.; U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No.

PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

Additional details of exemplary, non-limiting assay methods which comprise one or more steps of spatially segregating biomarker molecules will now be described. In certain embodiments, a method for detection and/or quantifying biomarker molecules in a sample comprises immobilizing a plurality of biomarker molecules with respect to a plurality of capture objects (e.g., beads) that each include a binding surface having affinity for at least one type of biomarker. For example, the capture objects may comprise a plurality of beads comprising a plurality of capture components (e.g., an antibody having specific affinity for a biomarker of interest, etc.). At least some of the capture objects (e.g., at least some associated with at least one biomarker molecule) may be spatially separated/segregated into a plurality of locations, and at least some of the locations may be addressed/interrogated (e.g., using an imaging system). A measure of the concentration of biomarker molecules in the fluid sample may be determined based on the information received when addressing the locations (e.g., using the information

received from the imaging system and/or processed using a computer implemented control system). In some cases, a measure of the concentration may be based at least in part on the number of locations determined to contain a capture object that is or was associated with at least one biomarker molecule. In other cases and/or under differing conditions, a measure of the concentration may be based at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarker molecules and/or capture objects associated with a biomarker molecule at one or more of the addressed locations.

In some embodiments, the number/percentage/fraction of locations containing a capture object but not containing a biomarker molecule may also be determined and/or the number/percentage/fraction of locations not containing any capture object may also be determined. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the total number of locations determined to contain a capture object not associated with a biomarker molecule and/or a measure of the concentration of biomarker molecule in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the number of locations determined to not contain any capture objects. In yet other embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object and a biomarker molecule to the total number of locations addressed and/or analyzed.

In certain embodiments, at least some of the plurality of capture objects (e.g., at least some associated with at least one biomarker molecule) are spatially separated into a plurality of locations, for example, a plurality of reaction vessels in an array format. The plurality of reaction vessels may be formed in, on and/or of any suitable material, and in some cases, the reaction vessels can be sealed or may be formed upon the mating of a substrate with a sealing component, as discussed in more detail below. In certain embodiments, especially where quantization of the capture objects associated with at least one biomarker molecule is desired, the partitioning of the capture objects can be performed such that at least some (e.g., a statistically significant fraction; e.g., as described in International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR

PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al (see Appendix A)) of the reaction vessels comprise at least one or, in certain cases, only one capture object associated with at least one biomarker molecule and at least some (e.g., a statistically significant fraction) of the reaction vessels comprise an capture object not associated with any biomarker molecules. The capture objects associated with at least one biomarker molecule may be quantified in certain embodiments, thereby allowing for the detection and/or quantification of biomarker molecules in the fluid sample by techniques described in more detail herein.

An exemplary assay method may proceed as follows. A sample fluid containing or suspected of containing biomarker molecules is provided. An assay consumable comprising a plurality of assay sites is exposed to the sample fluid. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the assay sites contain a single biomarker molecule and a statistically significant fraction of the assay sites do not contain any biomarker molecules. The assay sites may optionally be exposed to a variety of reagents (e.g., using a reagent loader) and or rinsed. The assay sites may then optionally be sealed and imaged (see, for example, U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.). The images are then analyzed (e.g., using a computer implemented control system) such that a measure of the concentration of the biomarker molecules in the fluid sample may be obtained, based at least in part, by determination of the number/fraction/percentage of assay sites which contain a biomarker molecule and/or the number/fraction/percentage of sites which do not contain any biomarkers molecules. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that at least some assay sites comprise more than one biomarker molecule. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be obtained at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarkers molecules at one or more of the assay sites

In some cases, the methods optionally comprise exposing the fluid sample to a plurality of capture objects, for example, beads. At least some of the biomarker molecules are immobilized with respect to a bead. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a

statistically significant fraction of the beads do not associate with any biomarker molecules. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may then be spatially separated/segregated into a plurality of assay sites (e.g., of an assay consumable). The assay sites may optionally be exposed to a variety of reagents and/or rinsed. At least some of the assay sites may then be addressed to determine the number of assay sites containing a biomarker molecule. In some cases, the number of assay sites containing a bead not associated with a biomarker molecule, the number of assay sites not containing a bead and/or the total number of assay sites addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample. In some cases, more than one biomarker molecule may associate with a bead and/or more than one bead may be present in an assay site. In some cases, the plurality biomarker molecules may be exposed to at least one additional reaction component prior to, concurrent with, and/or following spatially separating at least some of the biomarker molecules into a plurality of locations.

The biomarker molecules may be directly detected or indirectly detected. In the case of direct detection, a biomarker molecule may comprise a molecule or moiety that may be directly interrogated and/or detected (e.g., a fluorescent entity). In the case of indirect detection, an additional component is used for determining the presence of the biomarker molecule. For example, the biomarker molecules (e.g., optionally associated with a bead) may be exposed to at least one type of binding ligand. A "binding ligand," is any molecule, particle, or the like which specifically binds to or otherwise specifically associates with a biomarker molecule to aid in the detection of the biomarker molecule. In certain embodiments, a binding ligand may be adapted to be directly detected (e.g., the binding ligand comprises a detectable molecule or moiety) or may be adapted to be indirectly detected (e.g., including a component that can convert a precursor labeling agent into a labeling agent). A component of a binding ligand may be adapted to be directly detected in embodiments where the component comprises a measurable property (e.g., a fluorescence emission, a color, etc.). A component of a binding ligand may facilitate indirect detection, for example, by converting a precursor labeling agent into a labeling agent (e.g., an agent that is detected in an assay). A "precursor labeling agent" is any molecule, particle, or the like, that can be converted to a labeling agent upon exposure to a suitable converting agent (e.g., an enzymatic component). A "labeling

agent" is any molecule, particle, or the like, that facilitates detection, by acting as the detected entity, using a chosen detection technique. In some embodiments, the binding ligand may comprise an enzymatic component (e.g., horseradish peroxidase, beta-galactosidase, alkaline phosphatase, etc). A first type of binding ligand may or may not be used in conjunction with additional binding ligands (e.g., second type, etc.).

More than one type of binding may be employed in any given assay method, for example, a first type of binding ligand and a second type of binding ligand. In one example, the first type of binding ligand is able to associate with a first type of biomarker molecule and the second type of binding ligand is able to associate with the first binding ligand. In another example, both a first type of binding ligand and a second type of binding ligand may associate with the same or different epitopes of a single biomarker molecule, as described herein. In some embodiments, at least one binding ligand comprises an enzymatic component.

In some embodiments, a binding ligand and/or a biomarker may comprise an enzymatic component. The enzymatic component may convert a precursor labeling agent (e.g., an enzymatic substrate) into a labeling agent (e.g., a detectable product). A measure of the concentration of biomarker molecules in the fluid sample can then be determined based at least in part by determining the number of locations containing a labeling agent (e.g., by relating the number of locations containing a labeling agent to the number of locations containing a biomarker molecule (or number of capture objects associated with at least one biomarker molecule to total number of capture objects)). Non-limiting examples of enzymes or enzymatic components include horseradish peroxidase, beta-galactosidase, and alkaline phosphatase. Other non-limiting examples of systems or methods for detection include embodiments where nucleic acid precursors are replicated into multiple copies or converted to a nucleic acid that can be detected readily, such as the polymerase chain reaction (PCR), rolling circle amplification (RCA), ligation, Loop-Mediated Isothermal Amplification (LAMP), etc. Such systems and methods will be known to those of ordinary skill in the art, for example, as described in "DNA Amplification: Current Technologies and Applications," Vadim Demidov et al., 2004.

Another exemplary embodiment of indirect detection is as follows. In some cases, the biomarker molecules may be exposed to a precursor labeling agent (e.g., enzymatic substrate) and the enzymatic substrate may be converted to a detectable product (e.g., fluorescent molecule) upon exposure to a biomarker molecule.

The assay methods and systems may employ a variety of different components, steps, and/or other aspects that will be known and understood by those of ordinary skill in the art. For example, a method may further comprise determining at least one background signal determination (e.g., and further comprising subtracting the background signal from other determinations), wash steps, and the like. In some cases, the assays or systems may include the use of at least one binding ligand, as described herein. In some cases, the measure of the concentration of biomarker molecules in a fluid sample is based at least in part on comparison of a measured parameter to a calibration curve. In some instances, the calibration curve is formed at least in part by determination at least one calibration factor, as described above.

In certain embodiments, solubilized, or suspended precursor labeling agents may be employed, wherein the precursor labeling agents are converted to labeling agents which are insoluble in the liquid and/or which become immobilized within/near the location (e.g., within the reaction vessel in which the labeling agent is formed). Such precursor labeling agents and labeling agents and their use is described in commonly owned U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al., incorporated herein by reference.

An exemplary embodiment of an assay method that may be used in certain embodiments of the invention is illustrated in Figure 1a. A plurality of capture objects 2, are provided (step (A)). In this particular example, the plurality of capture objects comprises a plurality of beads. The beads are exposed to a fluid sample containing a plurality of biomarker molecules 3 (e.g., beads 2 are incubated with biomarker molecules 3). At least some of the biomarker molecules are immobilized with respect to a bead. In this example, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a statistically significant fraction of the beads do not associate with any biomarker molecules. For example, as shown in step (B), biomarker molecule 4 is immobilized with respect to bead 5, thereby forming complex 6, whereas some beads 7 are not associated with any biomarker molecules. It should be understood, in some embodiments, more than one biomarker molecule may associate with at least some of the beads, as described herein. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may

then be spatially separated/segregated into a plurality of locations. As shown in step (C), the plurality of locations is illustrated as substrate 8 comprising a plurality of wells/reaction vessels 9. In this example, each reaction vessel comprises either zero or one beads. At least some of the reaction vessels may then be addressed (e.g., optically or via other detection means) to determine the number of locations containing a biomarker molecule. For example, as shown in step (D), the plurality of reaction vessels are interrogated optically using light source 15, wherein each reaction vessel is exposed to electromagnetic radiation (represented by arrows 10) from light source 15. The light emitted (represented by arrows 11) from each reaction vessel is determined (and/or recorded) by detector 15 (in this example, housed in the same system as light source 15). The number of reaction vessels containing a biomarker molecule (e.g., reaction vessels 12) is determined based on the light detected from the reaction vessels. In some cases, the number of reaction vessels containing a bead not associated with a biomarker molecule (e.g., reaction vessel 13), the number of wells not containing a bead (e.g., reaction vessel 14) and/or the total number of wells addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

A non-limiting example of an embodiment where a capture object is associated with more than one biomarker molecule is illustrated in Figure 1b. A plurality of capture objects 20 are provided (step (A)). In this example, the plurality of capture objects comprises a plurality of beads. The plurality of beads is exposed to a fluid sample containing plurality of biomarker molecules 21 (e.g., beads 20 are incubated with biomarker molecules 21). At least some of the biomarker molecules are immobilized with respect to a bead. For example, as shown in step (B), biomarker molecule 22 is immobilized with respect to bead 24, thereby forming complex 26. Also illustrated is complex 30 comprising a bead immobilized with respect to three biomarker molecules and complex 32 comprising a bead immobilized with respect to two biomarker molecules. Additionally, in some cases, some of the beads may not associate with any biomarker molecules (e.g., bead 28). The plurality of beads from step (B) is exposed to a plurality of binding ligands 31. As shown in step (C), a binding ligand associates with some of the biomarker molecules immobilized with respect to a bead. For example, complex 40 comprises bead 34, biomarker molecule 36, and binding ligand 38. The binding ligands are provided in a manner such that a statistically significant fraction of the beads comprising at least one biomarker molecule become associated with at least

one binding ligand (e.g., one, two, three, etc.) and a statistically significant fraction of the beads comprising at least one biomarker molecule do not become associated with any binding ligands. At least a portion of the plurality of beads from step (C) are then spatially separated into a plurality of locations. As shown in step (D), in this example, the locations comprise a plurality of reaction vessels 41 on a substrate 42. The plurality of reaction vessels may be exposed to the plurality of beads from step (C) such at each reaction vessel contains zero or one beads. The substrate may then be analyzed to determine the number of reaction vessels containing a binding ligand (e.g., reaction vessels 43), wherein in the number may be related to a measure of the concentration of biomarker molecules in the fluid sample. In some cases, the number of reaction vessels containing a bead and not containing a binding ligand (e.g., reaction vessel 44), the number of reaction vessels not containing a bead (e.g., reaction vessel 45), and/or the total number of reaction vessels addressed/analyzed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

In some embodiments, a plurality of locations may be addressed and/or a plurality of capture objects and/or species/molecules/particles of interest may be detected substantially simultaneously. "Substantially simultaneously" when used in this context, refers to addressing/detection of the locations/capture objects/species/molecules/particles of interest at approximately the same time such that the time periods during which at least two locations/capture objects/species/molecules/particles of interest are addressed/detected overlap, as opposed to being sequentially addressed/detected, where they would not. Simultaneous addressing/detection can be accomplished by using various techniques, including optical techniques (e.g., CCD detector). Spatially segregating capture objects/species/molecules/particles into a plurality of discrete, resolvable locations, according to some embodiments facilitates substantially simultaneous detection by allowing multiple locations to be addressed substantially simultaneously. For example, for embodiments where individual species/molecules/particles are associated with capture objects that are spatially segregated with respect to the other capture objects into a plurality of discrete, separately resolvable locations during detection, substantially simultaneously addressing the plurality of discrete, separately resolvable locations permits individual capture objects, and thus individual species/molecules/particles (e.g., biomarker molecules) to be resolved. For example, in certain embodiments, individual molecules/particles of a

plurality of molecules/particles are partitioned across a plurality of reaction vessels such that each reaction vessel contains zero or only one species/molecule/particle. In some cases, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5% of all species/molecules/particles are spatially separated with respect to other species/molecules/particles during detection. A plurality of species/molecules/particles may be detected substantially simultaneously within a time period of less than about 1 second, less than about 500 milliseconds, less than about 100 milliseconds, less than about 50 milliseconds, less than about 10 milliseconds, less than about 1 millisecond, less than about 500 microseconds, less than about 100 microseconds, less than about 50 microseconds, less than about 10 microseconds, less than about 1 microsecond, less than about 0.5 microseconds, less than about 0.1 microseconds, or less than about 0.01 microseconds, less than about 0.001 microseconds, or less. In some embodiments, the plurality of species/molecules/particles may be detected substantially simultaneously within a time period of between about 100 microseconds and about 0.001 microseconds, between about 10 microseconds and about 0.01 microseconds, or less.

In some embodiments, the locations are optically interrogated. The locations exhibiting changes in their optical signature may be identified by a conventional optical train and optical detection system. Depending on the detected species (e.g., type of fluorescence entity, etc.) and the operative wavelengths, optical filters designed for a particular wavelength may be employed for optical interrogation of the locations. In embodiments where optical interrogation is used, the system may comprise more than one light source and/or a plurality of filters to adjust the wavelength and/or intensity of the light source. In some embodiments, the optical signal from a plurality of locations is captured using a CCD camera.

In some embodiments of the present invention, the plurality of reaction vessels may be sealed (e.g., after the introduction of the biomarker molecules, binding ligands, and/or precursor labeling agent), for example, through the mating of the second substrate and a sealing component. The sealing of the reaction vessels may be such that the contents of each reaction vessel cannot escape the reaction vessel during the remainder of the assay. In some cases, the reaction vessels may be sealed after the addition of the biomarker molecules and, optionally, at least one type of precursor labeling agent to facilitate detection of the biomarker molecules. For embodiments employing precursor labeling agents, by sealing the contents in some or each reaction vessel, a reaction to

produce the detectable labeling agents can proceed within the sealed reaction vessels, thereby producing a detectable amount of labeling agents that is retained in the reaction vessel for detection purposes.

The plurality of locations may be formed may be formed using a variety of methods and/or materials. In some embodiments, the plurality of locations comprises a plurality of reaction vessels/wells on a substrate. In some cases, the plurality of reaction vessels is formed as an array of depressions on a first surface. In other cases, however, the plurality of reaction vessels may be formed by mating a sealing component comprising a plurality of depressions with a substrate that may either have a featureless surface or include depressions aligned with those on the sealing component. Any of the device components, for example, the substrate or sealing component, may be fabricated from a compliant material, e.g., an elastomeric polymer material, to aid in sealing. The surfaces may be or made to be hydrophobic or contain hydrophobic regions to minimize leakage of aqueous samples from the microwells. The reactions vessels, in certain embodiments, may be configured to receive and contain only a single capture object.

In some embodiments, the reaction vessels may all have approximately the same volume. In other embodiments, the reaction vessels may have differing volumes. The volume of each individual reaction vessel may be selected to be appropriate to facilitate any particular assay protocol. For example, in one set of embodiments where it is desirable to limit the number of capture objects used for biomarker capture contained in each vessel to a small number, the volume of the reaction vessels may range from attoliters or smaller to nanoliters or larger depending upon the nature of the capture objects, the detection technique and equipment employed, the number and density of the wells on the substrate and the expected concentration of capture objects in the fluid applied to the substrate containing the wells. In one embodiment, the size of the reaction vessel may be selected such only a single capture object used for biomarker capture can be fully contained within the reaction vessel (see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS ," by Duffy et al. (see Appendix A), each herein incorporated by reference). .

In some embodiments, the reaction vessels may have a volume between about 1 femtoliter and about 1 picoliter, between about 1 femtoliters and about 100 femtoliters, between about 10 attoliters and about 100 picoliters, between about 1 picoliter and about 100 picoliters, between about 1 femtoliter and about 1 picoliter, or between about 30 femtoliters and about 60 femtoliters. In some cases, the reaction vessels have a volume of less than about 1 picoliter, less than about 500 femtoliters, less than about 100 femtoliters, less than about 50 femtoliters, or less than about 1 femtoliter. In some cases, the reaction vessels have a volume of about 10 femtoliters, about 20 femtoliters, about 30 femtoliters, about 40 femtoliters, about 50 femtoliters, about 60 femtoliters, about 70 femtoliters, about 80 femtoliters, about 90 femtoliters, or about 100 femtoliters.

The total number of locations and/or density of the locations employed in an assay (e.g., the number/density of reaction vessels in an array) can depend on the composition and end use of the array. For example, the number of reaction vessels employed may depend on the number of types of biomarker molecule and/or binding ligand employed, the suspected concentration range of the assay, the method of detection, the size of the capture objects, the type of detection entity (e.g., free labeling agent in solution, precipitating labeling agent, etc.). Arrays containing from about 2 to many billions of reaction vessels (or total number of reaction vessels) can be made by utilizing a variety of techniques and materials. Increasing the number of reaction vessels in the array can be used to increase the dynamic range of an assay or to allow multiple samples or multiple types of biomarker molecules to be assayed in parallel. The array may comprise between one thousand and one million reaction vessels per sample to be analyzed. In some cases, the array comprises greater than one million reaction vessels. In some embodiments, the array comprises between about 1,000 and about 50,000, between about 1,000 and about 1,000,000, between about 1,000 and about 10,000, between about 10,000 and about 100,000, between about 100,000 and about 1,000,000, between about 100,000 and about 500,000, between about 1,000 and about 100,000, between about 50,000 and about 100,000, between about 20,000 and about 80,000, between about 30,000 and about 70,000, between about 40,000 and about 60,000 reaction vessels. In some embodiments, the array comprises about 10,000, about 20,000, about 50,000, about 100,000, about 150,000, about 200,000, about 300,000, about 500,000, about 1,000,000, or more, reaction vessels.

The array of reaction vessels may be arranged on a substantially planar surface or in a non-planar three-dimensional arrangement. The reaction vessels may be arrayed in a

regular pattern or may be randomly distributed. In a specific embodiment, the array is a regular pattern of sites on a substantially planar surface permitting the sites to be addressed in the X-Y coordinate plane.

In some embodiments, the reaction vessels are formed in a solid material. As will be appreciated by those in the art, the number of potentially suitable materials in which the reaction vessels can be formed is very large, and includes, but is not limited to, glass (including modified and/or functionalized glass), plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, cyclic olefin copolymer (COC), cyclic olefin polymer (COP), Teflon®, polysaccharides, nylon or nitrocellulose, etc.), elastomers (such as poly(dimethyl siloxane) and poly urethanes), composite materials, ceramics, silica or silica-based materials (including silicon and modified silicon), carbon, metals, optical fiber bundles, or the like. In general, the substrate material may be selected to allow for optical detection without appreciable autofluorescence. In certain embodiments, the reaction vessels may be formed in a flexible material.

A reaction vessel in a surface (e.g., substrate or sealing component) may be formed using a variety of techniques known in the art, including, but not limited to, photolithography, stamping techniques, molding techniques, etching techniques, or the like. As will be appreciated by those of the ordinary skill in the art, the technique used can depend on the composition and shape of the supporting material and the size and number of reaction vessels.

In a particular embodiment, an array of reaction vessels is formed by creating microwells on one end of a fiber optic bundle and utilizing a planar compliant surface as a sealing component. In certain such embodiments, an array of reaction vessels in the end of a fiber optic bundle may be formed as follows. First, an array of microwells is etched into the end of a polished fiber optic bundle. Techniques and materials for forming and etching a fiber optic bundle are known to those of ordinary skill in the art. For example, the diameter of the optical fibers, the presence, size and composition of core and cladding regions of the fiber, and the depth and specificity of the etch may be varied by the etching technique chosen so that microwells of the desired volume may be formed. In certain embodiments, the etching process creates microwells by preferentially etching the core material of the individual glass fibers in the bundle such that each well is approximately aligned with a single fiber and isolated from adjacent wells by the cladding material. Potential advantages of the fiber optic array format is

that it can produce thousands to millions of reaction vessels without complicated microfabrication procedures and that it can provide the ability to observe and optically address many reaction vessels simultaneously.

Each microwell may be aligned with an optical fiber in the bundle so that the fiber optic bundle can carry both excitation and emission light to and from the wells, enabling remote interrogation of the well contents. Further, an array of optical fibers may provide the capability for simultaneous or non-simultaneous excitation of molecules in adjacent vessels, without signal "cross-talk" between fibers. That is, excitation light transmitted in one fiber does not escape to a neighboring fiber.

Alternatively, the equivalent structures of a plurality of reaction vessels may be fabricated using other methods and materials that do not utilize the ends of an optical fiber bundle as a substrate. For example, the array may be a spotted, printed or photolithographically fabricated substrate produced by techniques known in the art; see for example WO95/25116; WO95/35505; PCT US98/09163; U.S. Patent Nos. 5,700,637, 5,807,522, 5,445,934, 6,406,845, and 6,482,593. In some cases, the array may be produced using molding, embossing, and/or etching techniques as will be known to those of ordinary skill in the art.

In some embodiments, the plurality of locations may not comprise a plurality of reaction vessels/wells. For example, in embodiments where capture objects are employed, a patterned substantially planar surface may be employed and the patterned areas form a plurality of locations. In some cases, the patterned areas may comprise substantially hydrophilic surfaces which are substantially surrounded by substantially hydrophobic surfaces. In certain embodiments, a plurality of capture objects (e.g., beads) may be substantially surrounded by a substantially hydrophilic medium (e.g., comprising water), and the beads may be exposed to the patterned surface such that the beads associate in the patterned areas (e.g., the hydrophilic locations on the surface), thereby spatially segregating the plurality of beads. For example, in one such embodiment, a substrate may be or include a gel or other material able to provide a sufficient barrier to mass transport (e.g., convective and/or diffusional barrier) to prevent capture objects used for biomarker capture and/or precursor labeling agent and/or labeling agent from moving from one location on or in the material to another location so as to cause interference or cross-talk between spatial locations containing different capture objects during the time frame required to address the locations and complete the assay. For example, in one embodiment, a plurality of capture objects is spatially

separated by dispersing the capture objects on and/or in a hydrogel material. In some cases, a precursor labeling agent may be already present in the hydrogel, thereby facilitating development of a local concentration of the labeling agent (e.g., upon exposure to a binding ligand or biomarker molecule carrying an enzymatic component). As still yet another embodiment, the capture objects may be confined in one or more capillaries. In some cases, the plurality of capture objects may be absorbed or localized on a porous or fibrous substrate, for example, filter paper. In some embodiments, the capture objects may be spatially segregated on a uniform surface (e.g., a planar surface), and the capture objects may be detected using precursor labeling agents which are converted to substantially insoluble or precipitating labeling agents that remain localized at or near the location of where the corresponding capture object is localized. The use of such substantially insoluble or precipitating labeling agents is described herein. In some cases, single biomarker molecules may be spatially segregated into a plurality of droplets. That is, single biomarker molecules may be substantially contained in a droplet containing a first fluid. The droplet may be substantially surrounded by a second fluid, wherein the second fluid is substantially immiscible with the first fluid.

In some embodiments, during the assay, at least one washing step may be carried out. In certain embodiments, the wash solution is selected so that it does not cause appreciable change to the configuration of the capture objects and/or biomarker molecules and/or does not disrupt any specific binding interaction between at least two components of the assay (e.g., a capture component and a biomarker molecule). In other cases, the wash solution may be a solution that is selected to chemically interact with one or more assay components. As will be understood by those of ordinary skill in the art, a wash step may be performed at any appropriate time point during the inventive methods. For example, a plurality of capture objects may be washed after exposing the capture objects to one or more solutions comprising biomarker molecules, binding ligands, precursor labeling agents, or the like. As another example, following immobilization of the biomarker molecules with respect to a plurality of capture objects, the plurality of capture objects may be subjected to a washing step thereby removing any biomarker molecules not specifically immobilized with respect to a capture object.

Other assay methods in addition to those described herein are known in the art and may be used in connection with the inventive methods. For example, various analyzers are commercially available for the determination of the concentration of

biomarkers. The assay methods employed should meet the algorithm requirements for LOD and LOQ.

The following examples are included to demonstrate various features of the invention. Those of ordinary skill in the art should, in light of the present disclosure, will appreciate that many changes can be made in the specific embodiments which are disclosed while still obtaining a like or similar result without departing from the scope of the invention as defined by the appended claims. Accordingly, the following examples are intended only to illustrate certain features of the present invention, but do not necessarily exemplify the full scope of the invention.

Example 1

The following example provides experimental details relating to prognostication of neurological outcome in comatose survivors of oxygen deprivation.

26 unconscious patients were resuscitated with restoration of spontaneous circulation (ROSC). All included patients were >18 years old, had systolic blood pressure >80 mmHg for more than 5 min after ROSC, and were unconscious (prior to the use of sedatives/hypnotics) with a Glasgow Coma Scale (GCS) ≤7. Patients with a terminal disease or a primary coagulopathy were excluded, as were patients admitted more than 6 h after cardiac arrest. Serial blood samples were collected within 6h after cardiac arrest, and continued at intervals from 1-108 h. Inclusion criteria included age >18 years old, systolic BP >80mmHg after ROSC, and a Glasgow Coma Scale ≤7.

Upon admission, hypothermia treatment was started immediately after resuscitation. Ventilation was administered during the coma period, with a target PaO_2 of ≥12 kPa (90 mmHg) and $PaCO_2$ between 5.0 and 5.5 kPa (38–41 mmHg). Targeted mean arterial pressure was 65–100 mmHg, with application of inotropic/vasopressor support, if required, using dobutamine as the first line medication, followed by noradrenaline (norepinephrine) or adrenaline (epinephrine), if necessary. If the patient was considered euvolaemic but had a diuresis of less than 0.5 ml/kg/h, furosemide was administered. Furosemide was also given if the intensive care physician considered that the patient had a fluid overload. All patients received an arterial line in the radial or femoral artery for blood sampling.

Patient outcome was assessed in accordance with the Glasgow-Pittsburgh cerebral performance category (CPC) scale at discharge from the intensive care unit and 6 months later. The CPC scale ranges from 1 to 5, with 1 representing mildest possible

neurological deficit (patient is able to return to work), and 4-5 representing the most severe deficit (vegetative) and death. A CPC of 1 or 2 was considered a "good" outcome and a CPC score of 3–5 a "poor" outcome. For patients who died after ICU discharge, the better of the two scores was used, as recommended by the Utstein templates.

Serial blood samples were collected for each sample, starting as soon as possible in the emergency phase (within 6 h after cardiac arrest), and continuing at 1, 2, 6, 12, 24, 48, 72, 96, and 108 h after cardiac arrest. Serum aliquots were frozen until assayed. Samples were measured in triplicate using the assay method described in Example 2. The assay had a dynamic range to 250 pg/mL, with limit of quantification of less than 0.04 pg/mL, enabling measurement of low abundance serum Aβ42 (i.e., beta-amyloid (1-42)) in all samples. Applicant notes the measurements carried out in this study would not be possible with most current Aβ42 assay methods due to insufficient sensitivity. All patients exhibited a significant time-dependent elevation of Aβ42. After a lag period of about 10 or more hours, significant Aβ42 elevations were observed. Elevations ranged from approximately 50% to over 30-fold, with most elevations in the range of 3-10-fold (average approximately 7-fold).

Figure 2 depicts representative exemplary time course profiles for patients with (a-c) "good" and (d-f) "poor" 6-month outcomes. Serum Aβ42 measurements followed resuscitation from cardiac arrest. CPC scores depicted are after discharge from the ICU and 6 months later. In particular, Figure 2 (a) depicts data from the patient exhibiting the highest baseline Aβ42 and smallest relative increase in Aβ42 among all patients (two sets of data points run on different days are shown); (d) depicts data from the patient exhibiting the largest relative increase from baseline (35-fold), with Aβ42 rising 60+ hours; (c and f) depict comparative data from two patients with a CPC score of 3 upon discharge from the ICU. The patient exhibiting the more modest increase in Aβ42 (c) recovered good brain function (CPC 1), while the patient exhibiting the greater increase in Aβ42 (f) did not recover.

Quantitative differences in the appearance of the Aβ42 profiles were examined to determine a correlation with patient outcome. Profile parameters examined were: increase in beta-amyloid concentration (e.g., the magnitude of the rise), the fold increase of beta-amyloid concentration (e.g., the ratio of the peak Aβ42 to the baseline value), the maximum slope of the Aβ42 rise, and the duration of increase of beta-amyloid concentration (e.g., duration of over which the Aβ42 exhibited increasing values) (see

Figure 2 for an exemplary graph including these parameters). Table 2 shows the CPC assessment for the patients by their attending neurologists. Table 3 shows the correlation of Aβ42 profile parameters (Figure 3) with overall six-month outcome (0 = "good," 1 = "poor"). For each Aβ42 profile parameter, patients were sorted in either "good" or "poor" columns. Average values of each parameter for good outcomes were compared with average values for poor outcomes. Student t-test results for significance between good vs. poor were then calculated, as summarized in Table 3. In addition, an Aβ42 Score was calculated by summing the Aβ42 profile parameters of magnitude, rise ratio, and duration of rise (the three parameters that demonstrated statistical significance). Aβ42 Score was also evaluated for statistical significance between good and poor outcomes, and its significance was found to be enhanced relative to the individual Aβ42 profile parameters ($P = 0.00009$). Table 4 summarizes the statistical significance of Aβ42 profile parameters and Aβ42 Score. A P of 0.00009 indicates a high degree of statistical significance that Aβ42 Score is different between good and poor outcomes. 100% of patients with an Aβ42 Score > 50 had poor six month outcomes. 90% of patients with an Aβ42 Score < 50 had good six month outcomes.

These results indicate that blood tests for Aβ42 in the initial days following hypoxic insult can predict six-month patient outcome with a high degree of accuracy.

Table 2.

Study nr		CPC ICU discharge	CPC 6 months	Best over outcome (0=good response)
1	DA 820724	4	3	0
2	BL 810228	2	1	0
3	AL 871028	1	1	0
4	BR 270918	4	4	0
5	GR 510506	3	1	0
6	MA 230226	5	5	1
7	AA 260646	4	3	1
8	SK 300828	4	4	0
9	AO 301128	5	5	1
10	LS 860912	2	1	0
11	HT 480413	4	3	1
12	BK 321215	5	5	1
13	BF 470824	3	3	0
14	LM 380618	4	4	1
15	PN 330609	2	5	0
16	ES 370113	4	5	1
17	SF 440126	3	1	0
18	AJ 320418	4	4	0
19	DF 450604	3	2	0
20	BJ 430820	4	4	0
21	KM 461001	2	2	0
22	MK 371130	5	5	1
23	SW 480701	3	2	0
24	HW 460322	4	4	0
25	POL 290502	5	5	1
26	LB 470807	5	4	1
27	GJ 430318	4	3	1
28	ZD 290527	5	5	1
29	EG 500929	5	5	1
30	LS 221008	4	4	1
31	NL 470826	5	5	1

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Table 3.

Patient	Magnitude of increase (pg/mL)		Duration of rise (hr)		Rise ratios (fold increase)		Slope (pg/ml/hr)		Abeta score	
	Good	Poor	Good	Poor	Good	Poor	Good	Poor	Good	Poor
MA 290226		16				6		0.61		
AA 803606		6.8		60		35		0.155		101.6
OL 810648	12		31		5		0.316		48	
LS 660312	12.4		56		5		0.617		41.4	
HT 450415		4.6		63		5.6		0.242		70.2
BK 321275		6.6		71		3.5		0.067		89.2
BE 370824	5.05		30		6.3		0.168		41.36	
PM 430609	7.8		10		3.5		0.5		21.4	
EB 370511		14		90		8		0.35		82
SP 310126	6.2		12		1.65		0.456		31.83	
UE 450804	7.2		25		8.75		0.266		46.96	
BJ 430420	11		56.5		6.5		0.202		72	
RM 461001	4		10		2.1		0.4		36.3	
JDK 371020		14				2.3		0.83		
SW 460701	7.1		1		3.95		0.546		14.06	
HW 450122	6.6		12		2.6		0.256		21	
PCL 280805		8.1				3.46		0.758		
LP 470607		12.3		51		6.7		0.265		72
GJ 430818		8.8		84		16.8		0.174		118.3
RD 310427		6.6				14.8		0.358		
EG 300828		16.4		30		7		0.45		51.4
D 2 22 1008		7.8		68		4.8		0.206		80.4
NL 470826		9.2		96		15.4		0.141		78.6
AVG	8.12	10.25	20.95	80.33	4.56	10.52	0.39	0.37	33.63	82.68
t-test (P)	0.081455564		0.000014		0.023243907		0.399662724		0.000009	

Table 4.

t-test "Good" vs "Poor" 6 Mo Outcome	P
1. Max slope of Ab42 rise	0.400
2. Magnitude of Ab42 rise	0.0815
3. Ab42 rise ratio	0.0232
4. Duration of Ab42 rise	0.000014
5. Overall Ab42 Score (sum of 2-4)	0.000009

		6 Mo Outcome	
		Poor	Good
Ab42 score	<50	0	9
	>50	9	1

Sensitivity for calling poor outcome: 9/9 (100%)
Specificity for calling good outcome: 9/10 (90%)

Example 2

The following example describes a beta-amyloid (1-42) (i.e., Aβ42) ultra-sensitive digital immunoassay for plasma amyloid β42 using single molecule arrays.

Summary: Aβ42 has gained attention in the last 15 years as a biomarker correlating with Alzheimer's disease (AD) onset, mild cognitive impairment, vascular dementia, and other cognitive disorders. Substantial clinical data has validated the disease relevance of cerebral spinal fluid (CSF) levels of Aβ42, and there has been significant interest in measuring blood levels of the biomarker. However, the concentrations of Aβ42 in plasma are close to or below the limits of detection of most current immunoassay methods, making their precise determination challenging. A single

molecule capable assay technology was utilized in this example to develop and validate an ultra-sensitive assay for measuring Aβ42 in plasma.

Reagents were developed for a paramagnetic bead-based ELISA. Aβ42 molecules in plasma were captured on antibody-coated paramagnetic capture beads and labeled with an enzyme conjugate. The beads were loaded into arrays of 50,000, 50-femtoliter reaction wells etched into bundles of optical fibers. Single capture beads trapped in each well were sealed in the presence of enzyme substrate and imaged using a fluorescence microscope fitted with a CCD camera. At low concentrations, the images were analyzed for the presence or absence of single immunocomplexes of labeled Aβ42, resulting in a digital signal. At high concentrations, the analog intensity of the beads was normalized to the digital signals, extending the dynamic range of the assay to over four logs. Analytical performance of the assay was evaluated, and plasma and CSF samples from Alzheimer's disease patients and normal control subjects were tested for Aβ42.

The assay described in this example has a detection limit (i.e., LOD) of 0.02 pg/mL and was linear to 250 pg/mL Aβ42 ($R2 > 0.999$). Recovery of Aβ42 spikes in plasma averaged 103% of expected. The assay exhibited no cross reactivity to shorter peptide variants Aβ38 and Aβ40, and 11-16% cross reactivity to the longer variant Aβ43. Intra-assay coefficients of variation (CV) were less than 10% down to 0.5 pg/mL. Total CVs (intra-assay and inter-assay) across six days of testing were 6.1%, 5.7%, and 10.0% for Aβ42 levels of 0.5, 1.0, and 5.0 pg/mL, respectively. The limit of quantification was estimated by testing ultra low panels of depleted plasma on multiple days. The total CVs were less than 20% for all ultra low panels tested (lowest panel 0.072 pg/mL), yielding an estimated limit of quantification (LOQ) of 0.042 pg/mL (0.189 fmol/L) using a criterion of 20%. Results using CSF samples from AD patients and age-matched normal control subjects showed excellent discrimination between the two populations, but results with plasma samples obtained from these same individuals showed no discrimination.

Further Description: Beta-amyloid peptides are 36-43 amino acid proteolytic products from the amyloid precursor protein that have gained considerable attention in the last 15 years as a biomarker correlating with Alzheimer's disease onset, mild cognitive impairment, vascular dementia, and other cognitive disorders Clinical validation has now been developed around disease relevance of cerebral spinal fluid levels of Aβ42, and there follows a significant interest in measuring blood levels of this biomarker. The interest originates in part from extensive pharmacologic efforts aimed at

blocking production of beat-amyloid through inhibition of β-secretase and γ-secretase activating protein, and use of plasma measurements of amyloid β peptides as outcome indicators. Concentrations of Aβ42 in plasma are, however, over 100-fold lower than in cerebrospinal fluid. Recently reported was a blinded proficiency survey of several laboratories assaying plasma Aβ42 with different ELISA protocols. The survey showed high inter-lab variability in measured Aβ42 values and a broad range of intra-assay CVs; inter-assay CVs were not evaluated. A high-sensitivity ELISA for measurement of plasma Aβ42 has been reported, but potential therapeutic strategies aimed at lowering Aβ42 may put robust measurement of the peptide in blood beyond the reach of all current ELISA methods. To address this, a solid-phase extraction was recently developed and reverse-phase HPLC pre-treatment aimed at concentrating plasma levels of Aβ42 for improved immunoassay quantification. Enrichment of plasma Aβ42 by these procedures was found to lower the limit of detection to approximately 1 pg/mL, allowing quantification of the peptide in normal plasma at levels previously below the detection limit of even the high-sensitivity ELISA.

This example described the development and validation of a novel digital immunoassay using single molecule array technology that is capable of measuring Aβ42 in both normal and highly depleted plasma without biomarker enrichment or sample pretreatment procedures. The assay exhibits over 1000-fold greater sensitivity than validated commercially available ELISAs, and more than 50-fold greater sensitivity than what have been attainable using sample enrichment procedures described to date. The assay can be used for directly measuring and monitoring plasma Aβ42 in therapeutic trials aimed at altering and lowering levels of this peptide, down to sub-femtomolar levels.

The single molecule array technology employed two primary steps: a standard ELISA conducted with paramagnetic beads, followed by isolation of individual beads in arrays of femtoliter-sized reaction wells for digital imaging. Isolation of the individual beads in microwells permits the buildup of fluorescent product from the enzyme label such that signal from a single immunocomplex is readily detected using a CCD camera. This approach permits counting of single molecules when Aβ42 concentrations are low enough that the ratio of bound labeled peptide per bead is much less than one. In this concentration realm, Poisson statistics predict that bead-containing microwells in the array will contain either a single labeled Aβ42 molecule or no labeled Aβ42 molecules, resulting in a binary signal. Due to the amplified sensitivity for detecting label

molecules afforded by confining fluorescent product buildup to the microwells, concentrations of label (detector anti-Aβ42 antibody and enzyme label) can be reduced relative to standard ELISAs. Lowered concentrations of labeling reagents reduces their interaction with capture beads, resulting in reduced nonspecific binding enabling high signal to background ratios, even at extremely low concentrations of biomarker. For higher biomarker concentrations where all beads contain one or more labeled immunocomplexes, digital signals from the Poisson realm are used to calibrate analog intensity measurements, extending the dynamic range to over four logs.

Three reagents were developed for this Aβ42 immunoassay: capture beads, biotinylated detector, and a conjugate of streptavidin:beta-galactosidase. The capture bead reagent comprised of a commercially available monoclonal anti Aβ42 antibody (Covance) directed to a N-terminus epitope (amino acids 3-8). The antibody was covalently attached by standard coupling chemistry to 2.7 μm carboxy paramagnetic microbeads (Varian). Because individual beads were captured in array wells 4.5 μm wide x 3.25 μm deep, it was important that the capture beads remain monomeric. The antibody-coated beads were diluted to a working concentration of 5 x 10^6 beads/mL in Tris buffer with a surfactant and BSA. The biotinylated detector reagent was comprised of a commercially available monoclonal anti Aβ42 antibody (Invitrogen) directed to the C-terminus of the peptide. The antibody was biotinylated using standard methods (Solulink), and the biotinylation level was confirmed spectrophotometrically per manufacturer's instructions. The monomeric state of the detector antibody before and after biotinylation was confirmed by size exclusion HPLC. The biotinylated detector antibody was diluted to a concentration of 0.1 μg/ml for assay in a PBS diluent containing a surfactant and newborn calf serum, NCS (PBS/NCS). The enzyme conjugate—streptavidin:β-galactosidase (SβG)—was prepared by covalent conjugation of purified streptavidin (Thermo Scientific) and β-galactosidase (Sigma) using standard coupling chemistry (1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride, Thermo Scientific). Aliquots of a concentrated stock solution of SβG were prepared in PBS with 50% glycerol and transferred to -20°C for storage. Prior to assay, an aliquot was thawed and diluted to 25 pM in PBS/NCS with $MgCl_2$. Purified Aβ42 antigen for calibrators and peptide variants Aβ38, Aβ40, and Aβ43 for specificity testing were from Merck.

Assay calibrators and controls were prepared by dilution of Aβ42 stock in PBS diluent containing a surfactant and BSA (PBS/BSA). In some cases, a stock solution

prepared by dilution to 3.5 ng/mL in PBS/Tween-20. For dynamic range/linearity characterization, a series of calibrators were prepared by serial 3-fold dilution to give a calibration range of 0 – 250 pg/mL. To evaluate assay day-to-day reproducibility at low concentrations, three low controls were prepared at 0.5, 1.0, and 5.0 pg/mL in PBS/BSA. To estimate the limit of quantification (LOQ), three ultra-low plasma controls were prepared using a pool of immunodepleted normal human EDTA plasma. Immunodepletion was accomplished by incubation overnight at 2-8 °C with shaking of 5 mL of plasma with 1 x 10^9 Aβ42 capture beads prepared as described above. The immunodepleted plasma was used as an ultra low plasma control, along with two additional ultra-low controls of immunodepleted plasma spiked with trace amounts of Aβ42.

50,000 well optical fiber microarrays were prepared as previously described. In brief, optical fiber bundles (Schott North America) were cut into 5 cm lengths and sequentially polished with 30, 9, and 1 um-sized diamond lapping films. One end of each bundle was etched in a 0.025 N HCl solution for 2 minutes and then submerged into water. The differential etch rate of the core and cladding glass of the fiber bundles caused an array of 4.5 um diameter wells to be formed in the core fibers.

Bead-plasma incubations and labeling of immunocomplexes in conical 96 well plates (Axygen) were conducted using a robotic liquid handling system (Tecan EVO 150). Conical wells are used to facilitate magnetic attraction of the beads to the sides of the wells for efficient removal of reaction mixtures and bead washing. For magnetic attraction, a microplate bar magnet (Invitrogen) was used. Incubation periods were conducted with shaking on a microplate shaker (VWR) to keep beads suspended in the wells. The assays were initiated by mixing 100 uL of sample with 500,000 capture beads, and the mixtures were incubated with shaking for two hours. Plasma samples were pre-diluted 1:4 prior to assay with PBS/BSA as a precaution for sample quality and interference effects. Following incubation, the beads were washed 3 times with a wash buffer of 5-fold concentrated PBS with a surfactant (5xPBS). 100 uL of biotinylated detector antibody was then added and incubated with the beads for 45 minutes. After a second sequence of three washes with 5xPBS, 100 µL of streptavidin-β-galactosidase was incubated with the beads for 30 minutes to form the final enzyme-labeled immunocomplex. The beads were then washed six times per above, and concentrated to 2 x 10^7 beads/ml with the addition of a reduced volume (25 µL) of array loading buffer comprised of PBS with a surfactant. Beads were then loaded onto the arrays. 10 µL of

the concentrated bead solution (2 x 10^6 beads) were pipetted onto the arrays and the arrays were centrifuged at 1,300 g for 10 minutes. Excess beads were removed by a PBS rinse and swabbing with deionized water. With this technique, array filling by the beads was generally 50-60%, which was adequate for minimizing contributions to imprecision from Poisson noise. Wells containing labeled Aβ42-labeled beads were detected utilizing β-galactosidase catalyzed hydrolysis of resorufin β-D-galactopyranoside (RGP, Invitrogen) into fluorescent product (resorufin, excitation 558nm, emission 577nm). To introduce RGP substrate to the array wells, droplets of substrate were placed on a silicone gasket and introduced into the array wells with a mechanical platform. This step resulted in an array of sealed femtoliter wells in which enzyme-containing beads developed a concentrated fluorescence signal.

Imaging was accomplished via a custom-built fluorescence imaging system containing a light source, objectives, filter cubes and a CCD camera. For each sample, five fluorescent images of one second each were acquired (to identify wells containing an enzyme) and one white light image was acquired (to identify wells containing a bead). Background fluorescence and any contaminating artifacts were discriminated from true 'positive' wells by analyzing for signal growth over the multiple images. These images were analyzed to determine the average number of enzymes per bead (AEB) across the concentration range. In some cases, at <50% active beads, the system was determined to be in the digital realm, so AEB was be determined from the fraction of beads that contain at least one enzyme and the Poisson distribution; and at >50% active beads, the average fluorescence intensity of the beads was normalized to the average fluorescence intensity of beads containing a single enzyme to yield AEB. In other cases, at <70% active beads relative to total beads, AEB was determined as a count of active beads corrected for a low statistical probability of multiple enzymes per bead; and at >70% active beads, the probability of multiple enzymes/bead increases such that all wells contain multiple enzymes and all are growing in signal and in this realm, the signal is was no longer digital, and average fluorescence intensities of the wells were converted to AEB based on the average intensities of wells containing single enzymes as determined at lower Aβ42 concentrations. The AEB unit worked continuously across the digital and analog realms.

For description of various details associate with this assay, see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No.

PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

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Figure 4 shows a representative calibration dose-response of the Aβ42 assay up to 250 pg/mL. The assay demonstrated a highly linear response, with a linear regression R^2 of 0.9993. The inset highlights the low background at very low Aβ42 concentrations. In a study of calibration curves obtained on six different days, the mean signal to noise ratio at 1.0 pg/mL was 15.7 (SD 2.2). Limits of detection (3SD method) across the six days ranged from 0.014 to 0.032 pg/mL, with an average of 0.020 pg/mL (0.09 fmol/L), representing greater than four logs of assay range. In particular, Figure 4 shows a representative dose-response of the digital Aβ42 immunoassay. Y-axis refers to the average number of label enzymes per individual microbead captured in the microwells of the optical fiber array. The inset highlights the low background obtained with single-molecule counting and digital quantification of extremely low analyte levels. Analysis

of six separate calibration curves gave a mean signal to noise ratio at 1.0 pg/mL of 15.7 (SD 2.2).

Linearity in the extreme low end of the assay range was further evaluated by a series of four-fold dilutions (to 256-fold) of depleted plasma that had been spiked with 4 pg/mL Aβ42. The average recovery across the dilutions was within 0.02 pg/mL of the expected values. At the final 256-fold dilution, the assay measured an Aβ42 value of 0.118 pg/mL as compared with an expected value 0.099 pg/mL.

Recovery was evaluated by spiking 25 pg/mL Aβ42 into four normal plasma samples as well as the depleted plasma pool. Recoveries ranged from 91.5 – 113.4%, with an average of 103.6%.

Specificity of the assay for Aβ42 was evaluated by assaying 0.5, 1.0, 5.0, 10 and 50 pg/mL of the peptide variants Aβ38, Aβ40, and Aβ43 in PBS/BSA. No detectable cross reactivity was noted for the shorter Aβ38 and Aβ40 peptides, while the longer Aβ43 variant exhibited a cross reactivity of 11-16%.

Limits of detection (LOD) were estimated as three standard deviations above the zero calibrator across calibration curves on six separate days (n = 3 replicates per curve). LODs ranged from 0.014 to 0.032 pg/mL, with an average of 0.020 pg/mL (0.09 fmol/L).

Limit of quantification (LOQ) was estimated with guidance from NCCLS EP17-A [20]. Total CVs from low panel members assayed on multiple days (Table 5) were plotted vs. their respective measured value (Figure 5). The analyte concentration at which the assay's total measurement variation crossed 20% CV was taken to represent an estimated LOQ. Because none of the total CVs exceeded 20%, the 20% threshold was extrapolated from the equation of a non-linear power fit of the data ($R^2 = 0.703$, KaleidaGraph). A LOQ of 0.032 pg/mL (0.144 fmol/L) was estimated at the 20% threshold.

Table 5.

Study 1: Within-run Imprecision

	pg/mL Aβ42								
Panel	result 1	result 2	result 3	result 4	result 5	result 6	AVG	SD	CV
L1	0.41	0.4	0.35	0.36	0.37	0.37	0.38	0.026	6.8%
L2	0.83	0.74	0.69	0.75	0.69	0.70	0.73	0.056	7.7%
L3	3.82	4.04	3.81	3.45	3.38	4.18	3.78	0.316	8.4%

Study 2: Total Imprecision

	pg/mL Aβ42								
Panel	day 1	day 2	day 3	day 4	day 5	day 6	AVG	SD_{tot}	CV_{tot}
L1	0.46	0.51	0.52	0.45	0.45	0.48	0.48	0.025	6.1%
L2	0.94	0.97	0.98	0.92	1.04	0.89	0.95	0.054	5.7%
L3	3.99	5.22	5.25	4.54	5.00	4.70	4.78	0.478	10.0%

Study 3: Total Imprecision - Ultra Low Plasma

	pg/mL Aβ42								
Panel	day 1	day 2	day 3	day 4	day 5	day 6	AVG	SD_{tot}	CV_{tot}
Depleted	0.069	0.056	0.069	0.079	0.087	ND	0.072	0.012	16.3%
L2	0.151	0.128	0.123	0.110	0.118	ND	0.126	0.015	12.3%
L3	0.409	0.333	0.459	0.471	0.434	ND	0.421	0.055	13.0%

To further validate the assay, a pilot study of matched EDTA plasma and CSF samples from eight patients diagnosed with AD and nine normal individuals were assayed with the Aβ42 test (Figure 6). Normal and disease specimens were matched with respect to age, gender, and collection dates. Patients were diagnosed with AD according to clinical criteria. The clinical work-up also included imaging and MMSE cognitive scoring criteria. Normal age matched individuals also received MMSE testing to ensure high cognitive functioning. All samples were collected under IRB approval and obtained from PrecisionMed SAMPLE (Serial Alzheimer's Disease and MCI Prospective Longitudinal Evaluation) repository. The results were consistent with previous data reported for both sample types. With CSF samples, excellent discrimination (P=0.000015) was observed between AD subjects and normal subjects. Results for the AD CSF specimens ranged from 192.1-333.6 pg/mL, and normal CSF specimens ranged from 509.9 to 1127.8 pg/ml. On the other hand, results from the plasma specimens lacked discrimination between AD and normal subjects (P=0.69). Aβ42 levels in AD plasma ranged from 12.6 to 25.8 pg/mL, while results for the normal plasma specimens ranged from 8.8 to 22.1 pg/mL, in agreement with reported ELISA values following solid phase extraction and HPLC enrichment.

To test the assay performance in another clinical context, serial serum samples from a 41-year old man who was resuscitated after cardiac arrest with restoration of

spontaneous circulation were analyzed. Samples were measured in triplicate in the Aβ42 assay. Figure 7 depicts the profile of the serum Aβ42 change and shows a dramatic increase after the first 24 hours. Data from this study are the first to directly link hypoxic stress to Aβ elevation in humans. The Aβ42 concentrations measured in this study, particularly during the first 24 hours, were below the measurement capability of commercially available immunoassays, illustrating the potential utility of SiMoA technology as a new tool for precise measurement of low-abundance Aβ42 and other protein biomarkers.

Discussion. The data presented here indicate that the Aβ42 assay represents a capability for extremely sensitive and reproducible Aβ42 measurement in serum and plasma. The assay allows highly sensitive (limit of quantification 0.032 pg/mL) and precise quantification of Aβ42 in biological fluids.

Current immunoassays for measurement of Aβ42 in plasma are based on the ELISA or the Luminex techniques. In addition to lower analytical sensitivity, these immunoassays are hampered by low recovery of spiked Aβ42 into plasma or serum and as a result the measured concentration of Aβ42 increases when the plasma sample is diluted. These phenomena are likely due to matrix effects, probably by interaction and binding of Aβ42 to plasma proteins. This means that unrelated plasma proteins contribute to the concentration interpreted to come from Aβ42 in this type of assay. The immunoassay presented here showed highly linear dilution characteristics, together with a recovery of around 100%, suggesting that it gives a very accurate measure of the Aβ42 concentration. This is likely because the interference from plasma proteins is lost when samples are pre-diluted 1:4 prior to measurement. Because the assay has such high sensitivity, pre-diluting the samples does not compromise the capability of the method to precisely measure low abundance Aβ42.

Conflicting results have been reported regarding the association of plasma levels of Aβ42 with AD. For example, one report reported a statistically significant decrease in plasma Aβ42 in a cohort of 149 AD patients relative to 89 age-matched controls (mean 38 and 52 pg/mL respectively, $p < 0.01$), although there was large overlap between the two populations. In another case, no discernable difference in plasma Aβ42 between sporadic AD patients (n= 78) and age-matched controls (n = 61) was reported. Use of different ELISAs and analytical noise could have contributed to lack of agreement. It is also clear that most previously available assays measure Aβ42 close to the limit of

quantification, which may contribute to variation and inconsistent results between studies. If there is a decline in plasma Aβ42 with AD, it appears to be modest, requiring statistically powered studies to discern. Because depression of measurable Aβ42 in CSF relative to controls is a well established hallmark of AD (also seen here), the apparent disconnect between CSF and plasma results can led to the suggestion that the normal equilibrium between CSF and plasma may be disrupted with the initiation of amyloid deposition in the brain. The study reported here was intended to confirm expected performance of the Aβ42 assay with plasma and CSF clinical samples. The data were consistent with expected results from both sample types.

The Aβ42 assay described here was able to precisely monitor serum Aβ42 changes in a survivor of oxygen deprivation. Cerebral ischemia is believed to play a role in AD pathogenesis. The finding of a significant increase in serum Aβ42 following oxygen deprivation is the first direct demonstration of a link between hypoxic stress and Aβ elevation in humans. Nevertheless, the kinetic profile depicted in Figure 7could reflect proteolysis of amyloid precursor protein by β-secretase (BACE1), in which BACE1 is upregulated by the transcription factor hypoxia-inducible factor-1. Animal models have helped elucidate this pathway, and detecting hypoxia-driven amyloid cascade in humans could have significance for further understanding this process and its role in AD pathogenesis.

While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the present invention. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the teachings of the present invention is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, the invention may be practiced otherwise than as specifically

described and claimed. The present invention is directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the scope of the present invention.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, i.e., elements that are conjunctively present in some cases and disjunctively present in other cases. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified unless clearly indicated to the contrary. Thus, as a non-limiting example, a reference to "A and/or B," when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A without B (optionally including elements other than B); in another embodiment, to B without A (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in a list, "or" or "and/or" shall be interpreted as being inclusive, i.e., the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as "only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of exactly one element of a number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (i.e. "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or "exactly one of." "Consisting essentially of," when used in the claims, shall have its ordinary meaning as used in the field of patent law.

As used herein in the specification and in the claims, the phrase "at least one," in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements.

This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase "at least one" refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, "at least one of A and B" (or, equivalently, "at least one of A or B," or, equivalently "at least one of A and/or B") can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

In the claims, as well as in the specification above, all transitional phrases such as "comprising," "including," "carrying," "having," "containing," "involving," "holding," and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

What is claimed:

Claims

1. A method for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide, comprising:

performing an assay to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the limit of detection of beta-amyloid peptide of the assay is less than about 0.2 pg/mL.

2. The method of claim 1, wherein the beta-amyloid peptide is beta-amyloid (1-42).

3. The method of claim 1, wherein the patient has had a hypoxic event or a suspected hypoxic event.

4. The method of claim 1, wherein the sample is a bodily fluid.

5. The method of claim 4, wherein the bodily fluid is blood or a blood component.

6. The method of claim 4, wherein the bodily fluid is CSF.

7. The method of claim 5, wherein the blood component is plasma or serum.

8. The method of claim 1, wherein the measure of the concentration of beta-amyloid peptide is determined in a plurality of samples taken from the patient over a period of time.

9. The method of claim 8, wherein the plurality of samples are collected within 96 hours after the patient has experienced a hypoxic event or suspected hypoxic event.

10. A method of determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event, wherein the prognosis and/or the course of treatment is based at least in part on the measure of the concentration of beta-amyloid peptide determined in the patient sample according to the method of any one of claims 1-9.

11. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

12. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on a measured concentration of at least one biomarker measured in each sample by an assay performed on a plurality of samples obtained from the patient following the event to determine the measure of the concentration of the at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

13. A method for performing an assay and providing data for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

14. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

determining a measure of the concentration of a biomarker in each of a plurality of sample obtained from the patient following the event, wherein the assay has a limit of quantification of less than about 10 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; ; and

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

15. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

16. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of a first biomarker in the plurality of samples, wherein the measured concentration has been determined by performing an assay to measure the concentration of only the first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

17. A method for performing an assay and providing data for determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

18. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

determining a measure of the concentration of only a first biomarker in each of a plurality of sample obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 100 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

19. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

20. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of beta-amyloid peptide present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

21. A method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

22. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

determining a measure of the concentration of beta-amyloid in each of a plurality of samples obtained from the patient following the event wherein the concentration of beta-amyloid peptide in the samples is less than about 500 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and

determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

23. The method of any one of claims 11-22, wherein the biomarker is a beta-amyloid peptide.

24. The method of any one of claims 11-22, wherein the beta-amyloid peptide is beta-amyloid (1-42).

25. The method of any one of claims 11-22, wherein the hypoxic event is caused by cardiac arrest.

26. The method of any one of claims 11-22, wherein the hypoxic event is caused by stroke.

27. The method of any one of claims 11-22, wherein the hypoxic event is caused by an ischemic event.

28. The method of any one of claims 11-22, wherein the hypoxic event is caused by a thrombosis.

29. The method of any one of claims 11-22, wherein the hypoxic event is caused by arterial embolism.

30. The method of any one of claims 11-22, wherein the hypoxic event is caused by a hemorrhage.

31. The method of any one of claims 11-22, wherein the hypoxic event is caused by a high altitude.

32. The method of any one of claims 11-22, wherein the hypoxic event is caused by asphyxia.

33. The method of any one of claims 11-22, wherein the hypoxic event is caused by an asthmatic event.

34. The method of any one of claims 11-22, wherein the hypoxic event is caused by swelling of the brain.

35. The method of any one of claims 11-22, wherein the hypoxic event is caused by physical trauma and/or physical injury.

36. The method of any one of claims 11-22, wherein the hypoxic event is caused by arteriosclerosis or atherosclerosis.

37. The method of any one of claims 11-22, wherein the patient's prognosis is correlated with a Cerebral Performance Category (CPC) score.

38. The method of claim 37, wherein the CPC score includes classifications of good or poor.

39. The method of claim 38, wherein a good CPC score indicates a prognosis of the patient being conscious and alert with normal function or only slight disability or conscious and alert with moderate disability after a selected period of time.

40. The method of claim 38, wherein a poor CPC score indicates a prognosis of the patient being conscious with the patient having a severe disability, being comatose or in a persistent vegetative state, or being brain dead or suffering death from other causes after a selected period of time.

41. The method of claim 38 or 39, wherein the selected period of time is about 1 week, or about 2 weeks, or about 4 weeks, or about 2 months, or about 3 months, or about 4 months, or about 5 months, or about 6 months, or about 9 months, or about 1 year, or about 1.5 years, or about 2 years.

42. The method of any one of claims 11-22, wherein the plurality of samples are obtained from the patient within 2 days, 2.5 days, 3 days, 3.5 days, 4 days, 5 days, 6 days, or 7 days following the event.

43. The method of any one of claims 11-22, wherein 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more, samples are obtained from the patient.

44. The method of any one of claims 11-22, wherein the limit of quantification is less than about 9 pg/mL, 8 pg/mL, 7 pg/mL, 6 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.5 pg/mL, 0.1 pg/mL, or 0.05 pg/mL.

45. The method of any one of claims 11-22, wherein the measure of the concentration of biomarker or beta-amyloid peptide in the sample is less than about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL.

46. The method of any one of claims 11-22, wherein the limit of detection for the assay is less than about 10 pg/mL, 9 pg/mL, 8 pg/mL, 7 pg/mL, 6 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.5 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.02 pg/mL.

47. The method of any one of claims 11-22, wherein a change in the concentration of the biomarker or beta-amyloid peptide in the plurality of samples is determined as a function of time.

48. The method of claim 47, wherein the concentration of the biomarker or beta-amyloid peptide in the plurality of samples is plotted on a graph as concentration versus time.

49. The method of claim 47, wherein the prognosis and/or course or treatment is based at least in part on the area under the curve plotted on the graph.

50. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on whether the change in concentration with time reflects an increase in biomarker concentration or beta-amyloid peptide concentration.

51. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the duration of rise of biomarker concentration or beta-amyloid peptide concentration.

52. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the magnitude of the fold increase of biomarker concentration or beta-amyloid peptide concentration.

53. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the sum of the increase in biomarker concentration or beta-amyloid peptide concentration, the duration of rise of biomarker concentration or beta-amyloid peptide concentration, and the magnitude of the fold increase of biomarker concentration or beta-amyloid peptide concentration.

54. The method of claim 53, wherein the prognosis is good for the recovery from the brain injury if the sum is less than about 50.

55. The method of claim 53, wherein the prognosis is poor for the recovery from the brain injury if the sum is greater than about 50.

56. The method of any one of claims 11-22, wherein the biomarker is neuron specific neuronal enolase (NSE), β-site aPP-cleaving enzyme 1 (BACe1), S100B, myelin basic protein (MBP), growth associate protein 43, glutamine synthetase, glial fibrillary acid protein (GFAP), a glycine transporter, a neuron specific glycoprotein, calpain, neurofibrillary protein, heat shock protein 72, a beta-amyloid precursor protein, calbindin D-28K, proteolipid protein, myeline associated glycoprotein, neurofilament H, creatine kinase protein (e.g., CK-BB), a tau protein, an endotheliam membrane protein, or combinations thereof.

57. The method of any one of claims 11-22, wherein the brain injuries have not been correlated solely with Alzheimer's disease.

58. The method of any one of claims 11-22, wherein the biomarker or beta-amyloid peptide is measured in bodily fluid.

59. The method of claim 58, wherein the bodily fluid is blood or CSF.

60. The method of claim 58, wherein the bodily fluid is plasma and/or serum derived from a blood sample.

61. The method of any one of claims 11-22, wherein the concentration of only a single biomarker is determined.

62. A method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

(a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours;

(b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and

(c) determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined in step (b).

63. A method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined, which has been determined by:

(a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples have been obtained from the patient over a period of time of at least about 48 hours; and

(b) determining the baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in

which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time.

64. A method for performing an assay and providing data for determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

(a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours;

(b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and

(c) providing data derived in steps (a) and (b) to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time.

65. The method of any one of claims 62-64, wherein the prognosis and/or method of treatment is based at least in part on the difference between the baseline concentration and the maximum concentration, the magnitude of the fold increase between the baseline concentration and the maximum concentration, and/or the duration of time.

66. The method of claim 65, wherein the prognosis and/or method of treatment is based at least in part on the sum of the difference between the baseline concentration and the maximum concentration, the magnitude of the fold increase between the baseline concentration and the maximum concentration, and/or the duration of time.

67. The method of claim 66, wherein when the sum is less than about 50, the prognosis is good based on the CPC scale.

68. The method of claim 67, wherein when the sum is greater than about 50, the prognosis is poor based on the CPC scale.

69. The method of any one of claims 62-64, wherein the baseline concentration is equal to the concentration of beta-amyloid peptide present in the first sample obtained from the patient.

70. The method of any one of claims 62-64, wherein the baseline concentration is equal to the average concentration of beta-amyloid peptide present in the samples obtained from the patient with the first 24 hours of the event, provided that any sample which has a beta-amyloid peptide concentration greater than about 1 pg/mL than the average is removed from the calculation of the average.

71. The method of claim 70, wherein the maximum concentration is equal to the highest concentration of beta-amyloid peptide measured in a single sample obtained from the patient over the period of time.

72. The method of any one of claims 62-64, wherein the duration of the rise is the time period in which the concentration of beta-amyloid is increasing between the last sample having a concentration at the about the baseline value and the time at which the sample having the maximum concentration of beta-amyloid was obtained.

73. The method of any preceding claim, wherein the duration of the rise is determined in hours.

74. The method of any preceding claim, wherein the concentration is determined in pg/mL.

75. The method of any preceding claim, wherein the assay comprises:

spatially segregating at least a portion of the biomarkers into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

76. The method of claim 75, further comprising exposing the plurality of biomarker molecules to a plurality of binding ligands such that at least some of the biomarker molecules associate with a single binding ligand and a statistically significant fraction of the biomarker molecules do not associate with any binding ligand;

77. The method of any preceding claim, wherein the assay comprises:

immobilizing biomarker molecules with respect to a plurality of capture objects such that at least some of the capture objects associate with at least one biomarker molecule and a statistically significant fraction of the capture objects do not associate with any biomarker molecules;

spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

78. The method of any preceding claim, wherein the assay comprises:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one biomarker, to a solution containing or suspected of containing the at least one type of biomarker;

immobilizing biomarker molecules with respect to the plurality of capture objects such that at least some of the capture objects associate with at least one biomarker molecule and a statistically significant fraction of the capture objects do not associate with any biomarker molecules;

spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

79. A method of any preceding claim, wherein the assay comprises:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of biomarker, to a solution containing or suspected of containing the at least one type of biomarker to form capture objects comprising at least one immobilized biomarker molecule;

mixing the capture objects prepared in the exposing step to a plurality of binding ligands such that at least some of the capture objects associate with a single binding ligand and a statistically significant fraction of the capture objects do not associate with any binding ligand;

spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of locations containing a binding ligand; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a binding ligand.

80. The method of any preceding claim, wherein in the addressing step, the number of said locations containing a capture object that includes a binding surface having affinity for at least one type of biomarker not containing a biomarker molecule or a binding ligand is determined.

81. The method of claim 80, wherein the measure of the concentration of biomarker in the sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker containing a biomarker molecule or a binding ligand, to the total number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker.

82. The method of any preceding claim, wherein the measure of the concentration of biomarker molecules in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker molecules containing a biomarker molecule or a binding ligand, to the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker molecule but not to contain any capture objects that include a binding surface having affinity for at least one type of biomarker containing a biomarker molecule or a binding ligand.

83. The method of any preceding claim, wherein the plurality of capture objects that include a binding surface having affinity for at least one type of biomarker comprises a plurality of beads.

84. The method of any preceding claim, wherein the plurality of locations comprises a plurality of reaction vessels.

85. The method of any preceding claim, wherein the binding ligand comprises an enzymatic component.

86. The method of any preceding claim, wherein the measure of the concentration of biomarker molecules in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standard.

87. The method of any preceding claim, wherein following the spatially segregating step, the locations are exposed to precursor labeling agent.

88. The method of claim 87, wherein the precursor labeling agent is converted to a labeling agent upon exposure to a binding ligand.

89. The method of 88, wherein the number of locations containing a capture object containing a biomarker molecule or a labeling agent is determined by determining the number of locations comprising a labeling agent.

90. The method of any preceding claim, wherein the average volume of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters, or between about 1 femtoliter and about 1 picoliter.

91. The method of any preceding claim, wherein the average diameter of the plurality of beads is between about 0.1 micrometer and about 100 micrometers, or between about 1 micrometer and about 10 micrometers.

92. The method of any preceding claim, further comprising performing at least one wash step.

93. The method of any preceding claim, further comprising sealing the plurality of reaction vessels.

94. The method of any preceding claim, wherein the plurality of locations is addressed using optical techniques.

95. The method of any preceding claim, wherein the binding surface comprises a plurality of capture components.

Abstract

The present invention, in some embodiments, generally relates to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide.

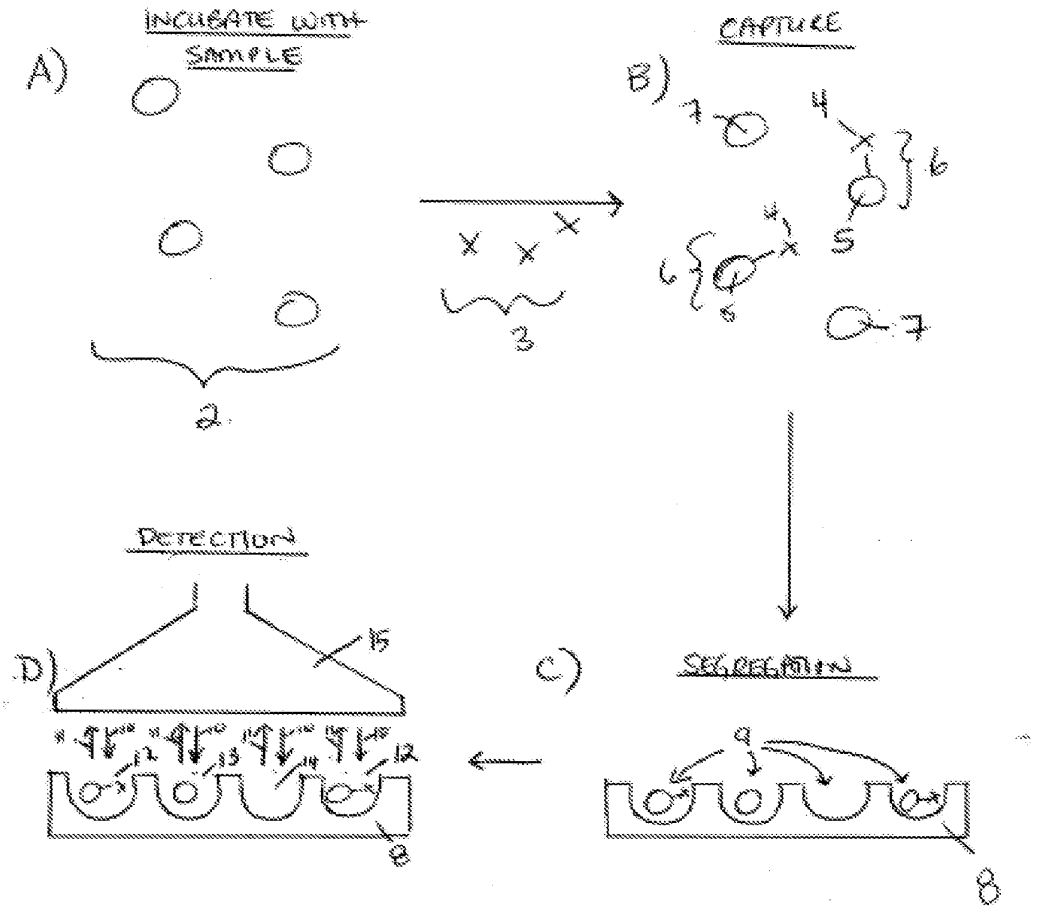

INCUBATE WITH SAMPLE
A)
2
CAPTURE
B)
1
3
4
5
6
7
8
SELECTION
C)
9
8
DETECTION
D)
15
12
8

Figure 1a

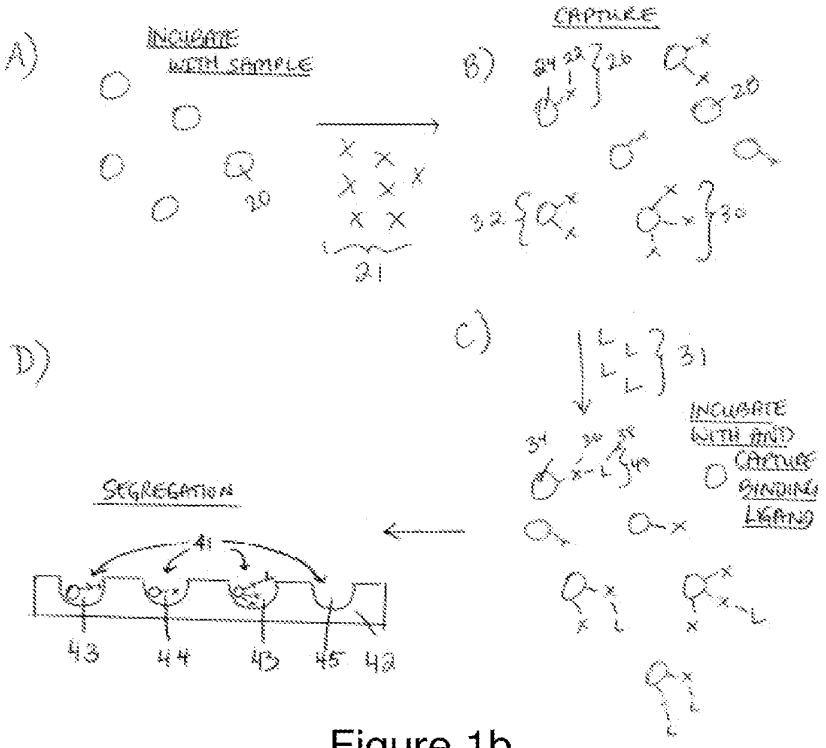

A)
INCUBATE WITH SAMPLE
20
21
B)
CAPTURE
20
30
32
C)
31
INCUBATE WITH AND CAPTURE BINDING LIGAND
D)
SEGREGATION
41
43
44
45
42

Figure 1b

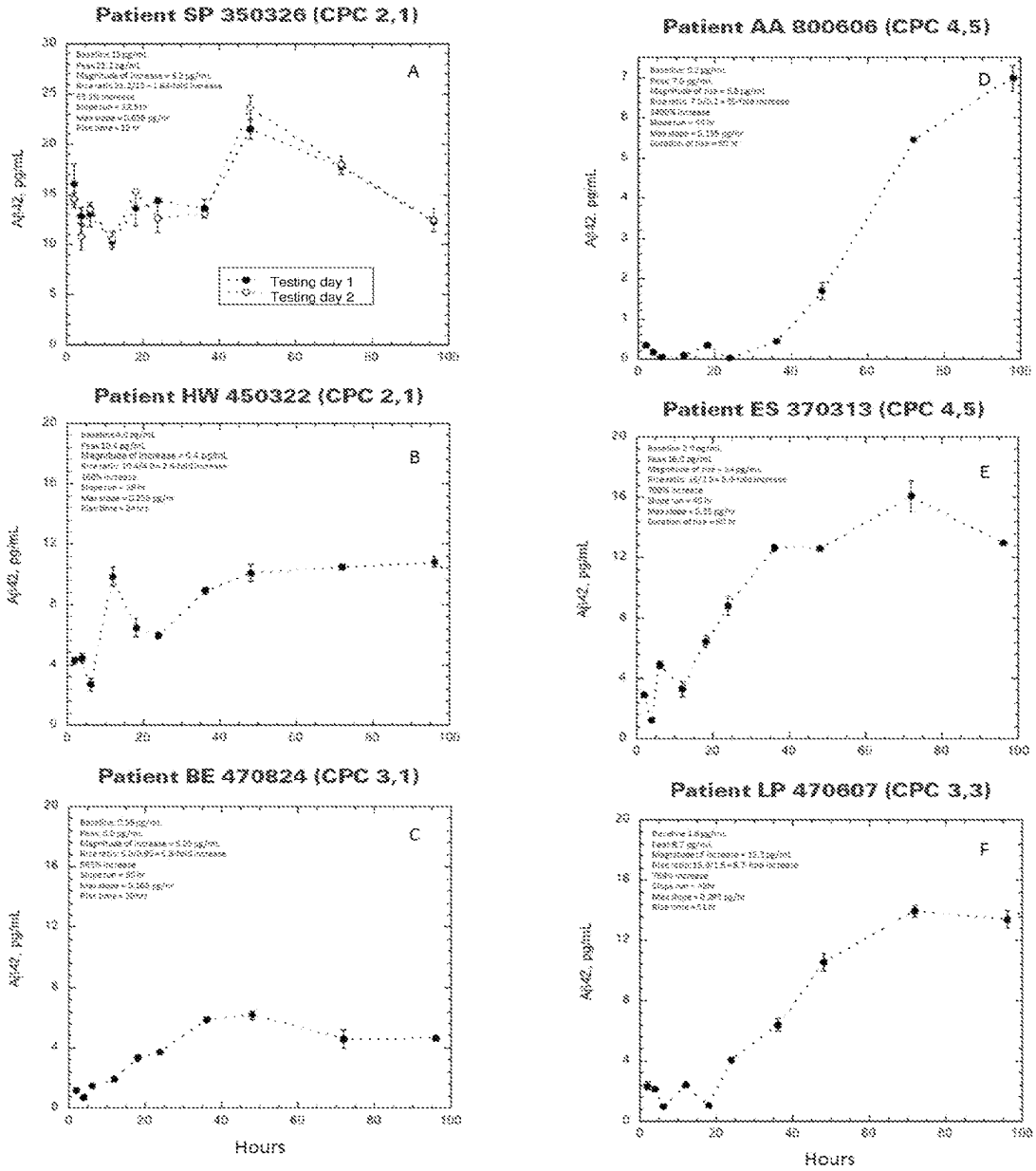

Patient SP 350326 (CPC 2,1)
A
Aβ42, pg/mL
Testing day 1
Testing day 2
Patient AA 800606 (CPC 4,5)
D
Aβ42, pg/mL
Patient HW 450322 (CPC 2,1)
B
Aβ42, pg/mL
Patient ES 370313 (CPC 4,5)
E
Aβ42, pg/mL
Patient BE 470824 (CPC 3,1)
C
Aβ42, pg/mL
Hours
Patient LP 470607 (CPC 3,3)
F
Aβ42, pg/mL
Hours

Figure 2

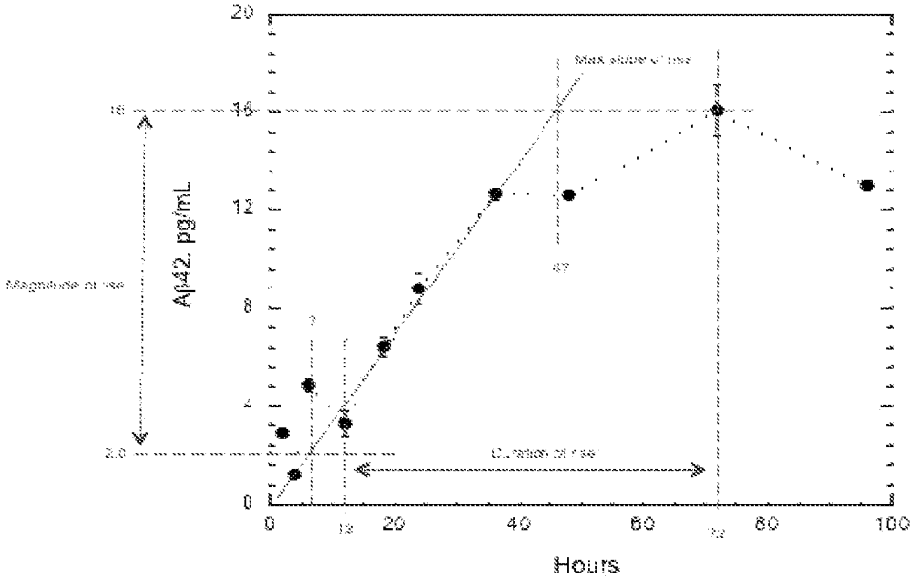


Figure 3

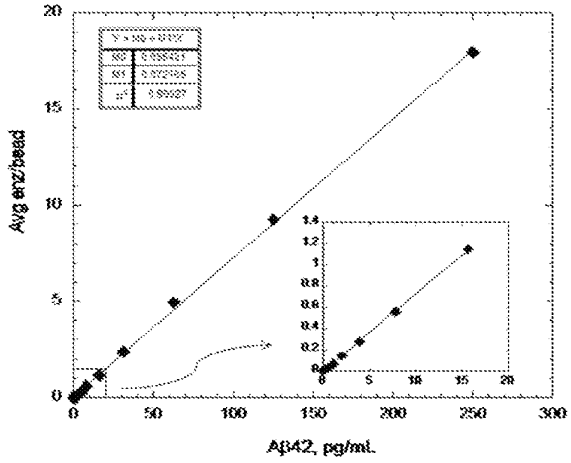


Figure 4

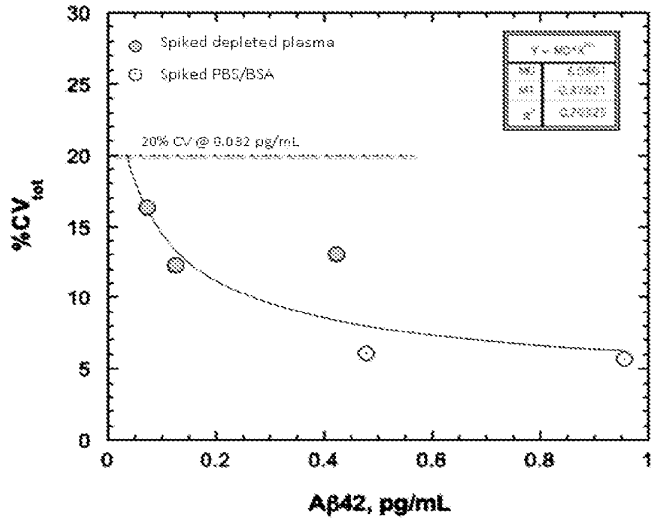


Figure 5

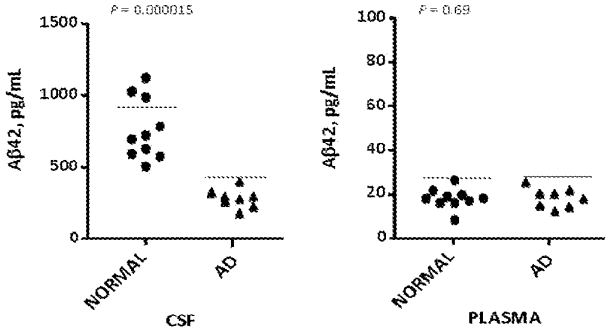


Figure 6

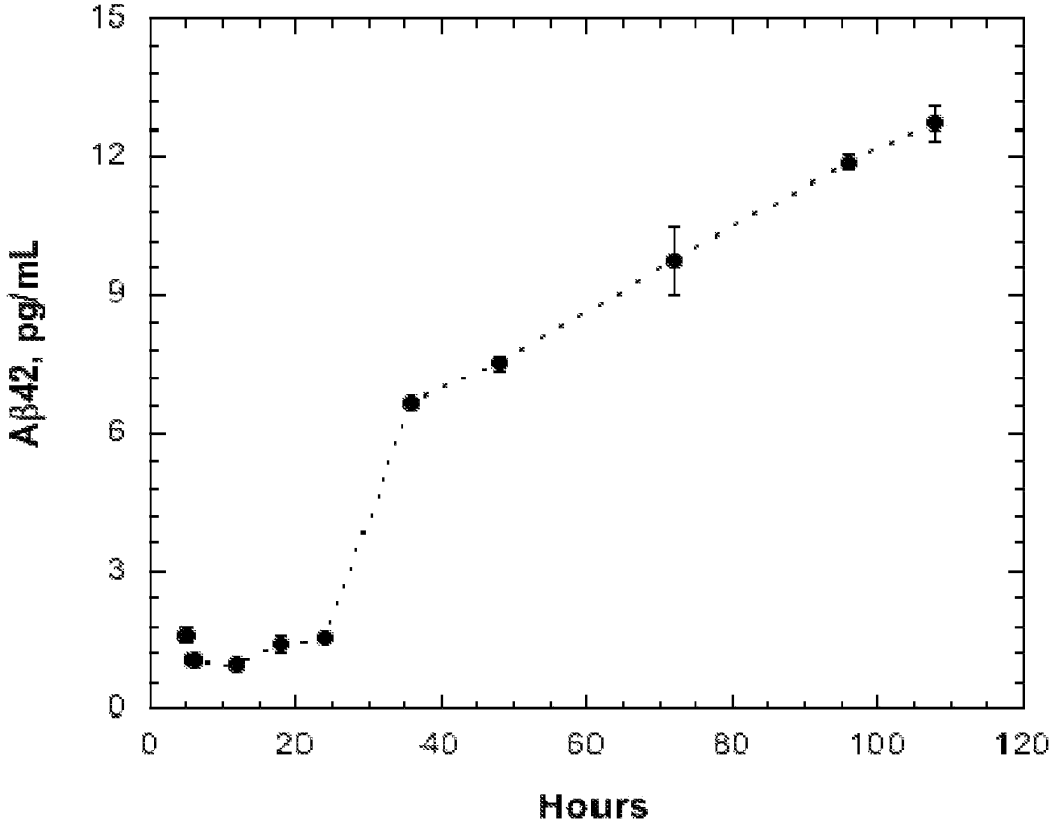


Figure 7

APPENDIX A

ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS

Field of the Invention

Described are systems and methods for detecting analyte molecules or particles in a fluid sample and in some cases, determining a measure of the concentration of the molecules or particles in the fluid sample.

Related Applications

This application is a continuation-in-part of U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "Ultra-Sensitive Detection of Molecules or Particles Using Beads or Other Capture Objects," by Duffy et al.., which claims the benefit of U.S. Provisional Patent Application Serial No. 61/309,141, filed March 1, 2010, entitled "Ultra-Sensitive Detection of Molecules or Particles Using Beads or Other Capture Objects," by Duffy et al. Each of the above-indicated applications is incorporated herein by reference.

Background of the Invention

Methods and systems that are able to quickly and accurately detect and, in certain cases, quantify a target analyte molecule in a sample are the cornerstones of modern analytical measurements. Such systems and/or methods are employed in many areas such as academic and industrial research, environmental assessment, food safety, medical diagnosis, and detection of chemical, biological, and/or radiological warfare agents. Advantageous features of such techniques may include specificity, speed, and sensitivity.

Most current techniques for quantifying low levels of analyte molecules in a sample use amplification procedures to increase the number of reporter molecules in order to be able to provide a measurable signal. For example, these known processes include enzyme-linked immunosorbent assays (ELISA) for amplifying the signal in antibody-based assays, as well as the polymerase chain reaction (PCR) for amplifying target DNA strands in DNA-based assays. A more sensitive but indirect protein target amplification technique, called immunoPCR *(see* Sano, T.; Smith, C. L.; Cantor, *C. R. Science* 1992, *258,* 120-122), makes use of oligonucleotide markers, which can subsequently be amplified using PCR and detected using a DNA hybridization assay

(*see* Nam, J. M.; Thaxton, C. S.; Mirkin, C. A. *Science* 2003; *301,* 1884-1886; Niemeyer, C. M.; Adler, M.; Pignataro, B.; Lenhert, S.; Gao, S.; Chi, L. F.; Fuchs, H.; Blohm, *D. Nucleic Acids Research* 1999, *27,*4553-4561; and Zhou, H.; Fisher, R. J.; Papas, T. S. *Nucleic Acids Research* 1993, *21,* 6038-6039). While the immuno-PCR method permits ultra low-level protein detection, it is a complex assay procedure, and can be prone to false-positive signal generation (*see* Niemeyer, C. M.; Adler, M.; Wacker, R. *Trends in Biotechnology* 2005, 23,208-216).

One feature of typical known methods and/or systems for detecting or quantifying low concentrations of a particular analyte in solution is that they are based on ensemble responses in which many analyte molecules give rise to a measured signal. Most detection schemes require that a large number of molecules are present in the ensemble for the aggregate signal to be above the detection threshold. This requirement limits the sensitivity of most detection techniques and the dynamic range (i.e., the range of concentrations that can be detected). Many of the known methods and techniques are further plagued with problems of non-specific binding, which is the binding of analyte molecules or particles to be detected or reporter species non-specifically to sites other than those expected. This leads to an increase in the background signal, and therefore limits the lowest concentration that may be accurately or reproducibly detected.

Accordingly, improved methods for detecting and, optionally, quantifying analyte molecules or particles in a fluid sample are needed, especially in samples where such molecules or particles are present at very low concentration.

Summary of the Invention

Described herein are systems and methods for detecting analyte molecules or particles in a fluid sample and in some cases, determining a measure of the concentration of the molecules or particles in the fluid sample. The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at

least one type of analyte molecules or particles, immobilizing analyte molecules or particles with respect to the plurality of capture objects such that at least some of the capture objects associate with a single analyte molecule or particle and a statistically significant fraction of the capture objects do not associate with any analyte molecule or particle, spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations, addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing an analyte molecule or particle, and determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of locations determined to contain an analyte molecule or particle.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at least one type of analyte molecules or particles to form capture objects comprising at least one immobilized analyte molecule or particle, mixing the capture objects prepared in the exposing step to a plurality of binding ligands such that at least some of the capture objects associate with a single binding ligand and a statistically significant fraction of the capture objects do not associate with any binding ligand, spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of locations, addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of locations containing a binding ligand, and determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of locations determined to contain a binding ligand.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises providing a substrate comprising a plurality of locations, at least a portion of which locations contain a bead, wherein with respect to the total number of beads present on the substrate, the ratio of beads comprising at least one analyte molecule or particle to beads comprising no analyte molecules or particles is between about 8:1 and about 1:10,000,000, addressing at least a portion of the plurality of locations, wherein during the addressing step at least two of the plurality of locations is addressed at least partially concurrently, detecting at

each addressed location the presence or absence of a bead and whether, if present, the bead comprises any analyte molecules or particles, and determining a measure of the concentration of analyte molecules or particles in the fluid sample at least in part by determining the number of locations addressed containing a bead comprising at least one analyte molecule or particle.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises providing a substrate comprising a plurality of locations, at least a portion of which contain a bead, wherein with respect to the total number of beads present on the substrate, the ratio of beads comprising at least one analyte molecule or particle associated with a binding ligand to beads comprising no analyte molecules or particles associated with a binding ligand is between about 8:1 and about 1:10,000,000, addressing at least a portion of the plurality of locations, wherein during the addressing step at least two of the plurality of locations is addressed at least partially concurrently, detecting at each addressed location the presence or absence of a bead and whether, if present, the bead comprises any analyte molecules or particles associated with a binding ligand, and determining a measure of the concentration of analyte molecules or particles in the fluid sample at least in part by determining the number of locations addressed containing a bead comprising at least one analyte molecule or particle associated with a binding ligand.

In some embodiments, an article or kit comprises a plurality of beads having an average diameter between about 0.1 micrometer and about 100 micrometers, and a substrate comprising a plurality of reaction vessels, wherein the average depth of the reaction vessels is between about 1.0 times and about 1.5 times the average diameter of the beads and the average diameter of the reactions vessels is between about 1.0 times and about 1.9 times the average diameter of the beads.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at least one type of analyte molecules or particles, wherein at least some of the capture objects become associated with at least one analyte molecule or particle, mixing the plurality of capture objects prepared in the exposing step to a plurality of binding ligands comprising an enzymatic component such that a statistically significant fraction of the capture objects associated with at least one analyte molecule or particle associate with a

single binding ligand, spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of separate locations, determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part by addressing at least a portion of the plurality of locations subjected to the spatially segregating step to determine the presence of the enzymatic component or a product of a reaction involving the enzymatic component.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises immobilizing a plurality of analyte molecules or particles with respect to a plurality of beads, spatially segregating at least a portion of the plurality of beads into a plurality of separate locations, and addressing at least some of the plurality of locations and determining the number of locations containing a bead, and further determining the number of said locations containing a bead and an analyte molecule or particle, and determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the ratio of the number of locations containing a bead and an analyte molecule and particle, to the number of locations containing a bead.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises immobilizing a plurality of analyte molecules or particles with respect to a plurality of beads, spatially segregating at least a portion of the plurality of beads into a plurality of separate locations, addressing at least some of the plurality of locations and determining the number of locations containing a bead, further determining the number of said locations containing a bead and an analyte molecule or particle, and determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the ratio of the number of locations containing a bead and an analyte molecule and particle, to the number of locations containing a bead but not containing any analyte molecules or particles.

In some embodiments, a method for determining a measure of the concentration of analyte molecules or particles in a fluid sample comprises providing a plurality of capture objects that each are associated with either a single analyte molecule or particle or are free of any analyte molecules or particles, individually addressing at least a portion of the capture objects and determining the number of said capture objects associated with an analyte molecule or particle, and determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of

capture objects subjected to the addressing step determined to be associated with an analyte molecule or particle.

Brief Description of the Drawings

Other aspects, embodiments, and features of the invention will become apparent from the following detailed description when considered in conjunction with the accompanying drawings. The accompanying figures are schematic and are not intended to be drawn to scale. For purposes of clarity, not every component is labeled in every figure, nor is every component of each embodiment of the invention shown where illustration is not necessary to allow those of ordinary skill in the art to understand the invention. All patent applications and patents mentioned in the text are incorporated by reference in their entirety. In case of conflict between the description contained in the present specification and a document incorporated by reference, the present specification, including definitions, will control.

FIG. 1 is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

FIG. 2 is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

FIG. 3 is a schematic diagram depicting one embodiment of a portion of a method of the present invention;

FIG. 4A is a schematic flow diagram depicting one embodiment of steps (A-C) for performing an exemplary method of the present invention;

FIG. 4B is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

FIG. 4C is a schematic diagram depicting one embodiment for performing an exemplary method of the present invention;

FIG. 5 is a schematic flow diagram depicting one embodiment of steps (A-C) for performing an exemplary method of the present invention;

FIG. 6 is a schematic flow diagram depicting an embodiment of a method (steps A-D) for the formation of a plurality of reaction vessels through mating of a substrate and a sealing component and depicting examples of the size (E, F) of a sealing component relative to a substrate;

FIG. 7 depicts an experimental set-up for detection using light, according to one embodiment of the present invention;

FIG. 8 shows a fiber optic array that has been sealed with a sealing component, according to one embodiment;

FIG. 9A shows a schematic diagram depicting a method of indirectly detecting an analyte molecule associated with a capture object, according to some embodiments;

FIG. 9B shows a schematic diagram depicting a method of indirectly detecting an analyte molecule immobilized with respect to a capture object using a binding ligand, according to some embodiments;

FIGS. 10A and 10B show schematic diagrams depicting some embodiments of steps for crosslinking a binding ligand and an analyte molecule, according to some methods of the present invention;

FIGS. 11A and 11B show non-limiting examples of a system employing an optical detection system of the present invention according to some embodiments;

FIG. 12 is a schematic block diagram showing a system employing a fiber optic assembly with an optical detection system according to an embodiment of the invention;

FIG. 13 shows a graph of a schematic calibration curve that may be used to determine the concentration of analyte molecules or particles in a fluid sample, according to some embodiments of the present invention;

FIG. 14 show plots of the fraction of capture objects determined to be associated with an analyte molecule comprising A) PSA, B) TNF-alpha, or C) DNA, versus the concentration of analyte molecules in a fluid sample, according to an exemplary embodiment;

FIG. 15 shows a plot of the log of the fraction of capture objects determined to be associated with an analyte molecule versus the log of the concentration of analyte molecules in a fluid sample, according to an exemplary embodiment;

FIG. 16 shows a graph of the number of reaction vessels comprising a bead versus the total number of beads provided to the reaction vessels, according to a non-limiting embodiment;

FIGS. 17A-17C show non-limiting images of beads contained in arrays comprising a plurality of reaction vessels;

FIG. 18A shows a non-limiting fluorescence image of an array containing beads,

FIG. 18B shows an enlargement of the image from FIG. 18A;

FIGS. 19A and 19B show graphs of the number of reaction vessels determined to contain an analyte molecule versus the concentration of analyte molecules in a fluid sample, according to certain embodiments;

FIG. 19C shows a graph of the total fluorescence read-out versus the concentration of analyte molecules in a fluid sample, according to an exemplary embodiment;

FIG. 20 shows a plot of the %Poisson Noise against the experimental variance over three measurements from the experimental data shown in FIG. 19B.

FIG. 21 shows a plot of the fraction of capture objects determined to be associated with an analyte molecule versus the concentration of binding ligand provided, at two concentrations of analyte molecules, according to an exemplary embodiment;

FIG. 22 shows a plot of the fraction of capture objects determined to be associated with an analyte molecule versus the concentration of binding ligand per capture object provided, at two concentrations of analyte molecules, according to an exemplary embodiment;

FIG. 23 shows a plot of the fraction of capture objects determined to be associated with an analyte molecule versus the concentration of binding ligand provided, at two concentrations of analyte molecules, according to an exemplary embodiment;

FIG. 24 shows a plot of the total chemiluminescence versus the concentration of binding ligand provided, according to an exemplary embodiment;

FIG. 25A and 25B show schematic diagrams depicting one embodiment of steps for performing one method of the present invention;

FIG. 25C shows an image of beads contained in a plurality of reaction vessels, according to an exemplary embodiment;

FIG. 25D shows a fluorescence image of an array comprising a plurality of beads, some of which are associated with an analyte molecule following carrying out a method of the present invention, according to an exemplary embodiment.

FIG. 26 shows a plot of the optical density versus the concentration of TNF-alpha, according to an exemplary embodiment;

FIG. 27 shows a plot of the concentration of PSA determined for a plurality of human subjects;

FIG. 28 shows a histogram of the average fluorescence intensity of reaction vessels in an assay method, according to one embodiment of the present invention;

FIG. 29A shows a fluorescence image taken at a first wavelength of a portion of an array of reaction vessels containing beads;

FIG. 29B is a fluorescence image taken at the first wavelength of a portion of an array of reaction vessels containing beads, wherein the beads are associated with fluorescent entities;

FIG. 29C is a fluorescence image of a portion of the array from FIG. 29B taken at a second wavelength;

FIG. 29D shows a plot of (i) beads and (ii) beads associated with fluorescent entities, at varying concentrations of analyte molecules;

FIGS. 30A and 30B shows plots of dissociation of immunocomplexes over time, according to some embodiments;

FIG. 31 shows plot of average analyte molecules per bead versus concentration of analyte molecules, according to some embodiments.

Detailed Description

Described herein are systems and methods that may in certain embodiments be employed for the detection and/or quantification of analyte molecules, particles (such as, for example, cells, cell organelles and other biological or non-biological particulates), and the like, in a sample. The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles. It should be understood, that while much of the discussion below is directed to analyte molecules, this is by way of example only, and other materials may be detected and/or quantified, for example, analytes in particulate form. Some exemplary analyte molecules and particles are described herein.

The systems and methods of the present invention in certain instances may help reduce the negative effects of non-specific binding on detection sensitivity when compared to typical conventional systems and methods for performing similar assays. Non-specific binding is the binding or association in a non-specific fashion of one component of an assay with another component of the assay with which it is not desirable that it interact. For example, association, binding, or immobilization of a binding ligand with a substrate or assay material as opposed to with an analyte molecule or particle to which it has binding specificity. Non-specific binding may lead to false positive signals. Non-specific binding may not only affect the accuracy of the assay measurement, but may also limit the lowest level of detection. Therefore, certain methods and/or systems of the present invention that provide improvements in the level

of non-specific binding, may allow for the detection and/or quantification of analyte molecules in a sample at a lower detection limit as compared to typical conventional technologies. In addition, certain embodiments of the methods and/or systems of the present invention may also allow for the detection and/or quantification of analyte molecules in certain samples in which such analyte molecules have previously been undetected and/or unquantifiable because of the very low concentration in which they are present.

Certain methods of the present invention may be useful for characterizing analyte molecules in a sample. In some cases, the methods may be useful for detecting and/or quantifying analyte molecules in a fluid sample which is suspected of containing at least one type of analyte molecule, since, as explained in more detail below, the inventive assays may be designed such that the number (or equivalently fraction) of interrogated locations (e.g., wells, reaction sites, areas on a surface, etc.) which contain a capture object (e.g., bead, surface, etc. providing a capture surface) comprising an analyte molecule - or, more generally, the number or fraction of interrogated capture objects of a total interrogated population comprising an analyte molecule - can be correlated to the concentration of analyte molecules in the fluid sample. Certain embodiments of present invention thus can provide a measure of the concentration of analyte molecules in a fluid sample based at least in part on the number or fraction of locations, e.g., on a substrate, which contain a capture object associated with an analyte molecule. In some cases, this number/fraction may be related to the total number of locations comprising a capture object (e.g., with or without an associated analyte molecule or labeling agent) and/or to the total number of locations interrogated. Specific methods and calculations of how to quantify analyte molecules in a fluid sample using embodiments of the invention are discussed more below.

In certain embodiments, a method for detection and/or quantifying analyte molecules (or particles) in a sample comprises immobilizing a plurality of analyte molecules with respect to a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule (or particle). For example, the capture objects may comprise a plurality of beads comprising a plurality of capture components (e.g., an antibody having specific affinity for an analyte molecule of interest, etc.). At least some of the capture objects (e.g., at least some associated with at least one analyte molecule) may be spatially separated/segregated into a plurality of locations, and at least some of the locations may be addressed/interrogated. A measure

of the concentration of analyte molecules in the fluid sample may be determined based on the information received when addressing the locations. In some cases, a measure of the concentration may be based at least in part on the number of locations determined to contain a capture object that is or was associated with at least one analyte molecule. In other cases and/or under differing conditions, a measure of the concentration may be based at least in part on an intensity level of at least one signal indicative of the presence of a plurality of analyte molecules and/or capture objects associated with an analyte molecule at one or more of the addressed locations.

In some embodiments, the number/fraction of locations containing a capture object but not containing an analyte molecule may also be determined and/or the number/fraction of locations not containing any capture object may also be determined. In such embodiments, a measure of the concentration of analyte molecule in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with an analyte molecule to the total number of locations determined to contain a capture object not associated with an analyte molecule and/or a measure of the concentration of analyte molecule in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with an analyte molecule to the number of locations determined to not contain any capture objects. In yet other embodiments, a measure of the concentration of analyte molecules in a fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object and an analyte molecule to the total number of locations addressed and/or analyzed.

In certain embodiments, at least some of the plurality of capture objects (e.g., at least some associated with at least one analyte molecule) are spatially separated into a plurality of locations, for example, a plurality of reaction vessels in an array format. The plurality of reaction vessels may be formed in, on and/or of any suitable material, and in some cases, the reaction vessels can be sealed or may be formed upon the mating of a substrate with a sealing component, as discussed in more detail below. In certain embodiments, especially where quantization of the capture objects associated with at least one analyte molecule is desired, the partitioning of the capture objects can be performed such that at least some (e.g., a statistically significant fraction) of the reaction vessels comprise at least one or, in certain cases, only one capture object associated with at least one analyte molecule and at least some (e.g., a statistically significant fraction) of the reaction vessels comprise an capture object not associated with any analyte

molecules. The capture objects associated with at least one analyte molecule may be quantified in certain embodiments, thereby allowing for the detection and/or quantification of analyte molecules in the fluid sample by techniques described in more detail herein.

An exemplary embodiment of an inventive assay method is illustrated in FIG. 1. A plurality of capture objects 2, are provided (step (A)). In this particular example, the plurality of capture objects comprises a plurality of beads. The beads are exposed to a fluid sample containing a plurality of analyte molecules 3 (e.g., beads 2 are incubated with analyte molecules 3). At least some of the analyte molecules are immobilized with respect to a bead. In this example, the analyte molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single analyte molecule and a statistically significant fraction of the beads do not associate with any analyte molecules. For example, as shown in step (B), analyte molecule 4 is immobilized with respect to bead 5, thereby forming complex 6, whereas some beads 7 are not associated with any analyte molecules. It should be understood, in some embodiments, more than one analyte molecule may associate with at least some of the beads, as described herein. At least some of the plurality of beads (e.g., those associated with a single analyte molecule or not associated with any analyte molecules) may then be spatially separated/segregated into a plurality of locations. As shown in step (C), the plurality of locations is illustrated as substrate 8 comprising a plurality of wells/reaction vessels 9. In this example, each reaction vessel comprises either zero or one beads. At least some of the reaction vessels may then be addressed (e.g., optically or via other detection means) to determine the number of locations containing an analyte molecule. For example, as shown in step (D), the plurality of reaction vessels are interrogated optically using light source 15, wherein each reaction vessel is exposed to electromagnetic radiation (represented by arrows 10) from light source 15. The light emitted (represented by arrows 11) from each reaction vessel is determined (and/or recorded) by detector 15 (in this example, housed in the same system as light source 15). The number of reaction vessels containing an analyte molecule (e.g., reaction vessels 12) is determined based on the light detected from the reaction vessels. In some cases, the number of reaction vessels containing a bead not associated with an analyte molecule (e.g., reaction vessel 13), the number of wells not containing a bead (e.g., reaction vessel 14) and/or the total number of wells addressed may also be determined. Such

determination(s) may then be used to determine a measure of the concentration of analyte molecules in the fluid sample.

A statistically significant fraction of capture objects that contain at least one analyte molecule (or no analyte molecules) will typically be able to be reproducibly detected and quantified using a particular system of detection and will typically be above the background noise (e.g., non-specific binding) that is determined when carrying out the assay with a sample that does not contain any analyte molecules, divided by the total number of objects (or locations) addressed. A "statistically significant fraction" as used herein for the present embodiments, may be estimated according to the Equation 1:

$$n \geq 3\sqrt{n} \qquad \text{(Eq. 1)}$$

wherein n is the number of determined events for a selected category of events. That is, a statistically significant fraction occurs when the number of events is greater than three times square root of the number of events. For example, to determine a statistically significant fraction of the capture objects not associated with any analyte molecules or particles, n is the number of capture objects detected that are not associated with any analyte molecules or particles. As another example, to determine a statistically significant fraction of the capture objects associated with at least one analyte molecule, n is the number of capture objects detected that are determined to be associated with an analyte molecule.

In some embodiments, the statistically significant fraction of capture objects (e.g., beads) associated with at least one analyte molecule (or a single analyte molecule in some cases where the ratio of mixing capture objects to analyte molecules would lead, statistically, to only zero or one analyte molecule associate with each capture object) to the total number of capture objects (e.g., beads) is less than about 1:2, less than about 1:3, less than about 1:4. is less than about 2:5, less than about 1:5, less than about 1:10, less than about 1:20, less than about 1:100, less than about 1:200, or less than about 1:500. Therefore, in such embodiments, the fraction of capture objects (e.g., beads) not associated with any analyte molecules to the total number of capture objects (e.g., beads) is at least about 1:100, about 1:50, about 1:20, about 1:10, about 1:5, about 1:4, about 1:3, about 1:2, about 1:1, about 2:1, about 3:1, about 4:1, about 5:1, about 10:1, about 20:1, about 50:1, about 100:1, or the like.

In some embodiments, the percentage of capture objects (e.g., beads) associated with at least one analyte molecule (or a single analyte molecule in some cases where the ratio of mixing capture objects to analyte molecules would lead, statistically, to only zero

or one analyte molecule associate with each capture objects) is less than about 50%, less than about 40%, less than about 30%, less than about 20%, less than about 10%, less than about 5%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.01%, or the like, the total number of capture objects. In some embodiments, the percentage of capture objects (e.g., beads) not associated with an analyte molecule to the total number of capture objects (e.g., beads) is at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or the like, the total number of capture objects.

In some embodiments, prior to spatially separating the plurality of capture objects, the capture objects may be exposed to a plurality of binding ligands which have an affinity for at least one type of analyte molecule (or particle). A "binding ligand," as used herein, is any molecule, particle, or the like which specifically binds to or otherwise specifically associates with an analyte molecule to aid in the detection of the analyte molecule. Binding ligands may be particularly useful in embodiments where at least some of the capture objects are associated with respect to more than one analyte molecule (e.g., two, three, four, five, or more, analyte molecules). In some cases, the binding ligand may be provided in a manner (e.g., at a concentration level) such that a statistically significant fraction of the capture objects comprising at least one analyte molecule associate with at least one binding ligand (or in some cases, a single binding ligand) and a statistically significant fraction of the capture objects (e.g., capture objects either associated with at least one analyte molecule or not associated with any analyte molecules) do not associate with any binding ligand.

A statistically significant fraction of the locations that contain a capture object (e.g., bead) associated with at least one analyte molecule and a single binding ligand is greater than or equal to the minimum number of locations that can be reproducibly determined to contain an capture object (e.g., bead) associated with a single binding ligand with a particular system of detection (i.e., substantially similar results are obtained for multiple essentially identical fluid samples comprising the capture objects associated with an analyte molecule and/or binding ligand) and that is above the background noise (e.g., non-specific binding) that is determined when carrying out the assay with a sample that does not contain any analyte molecules and/or binding ligands, divided by the total number of locations. The statistically significant fraction of locations that contain a capture object associated with at least one analyte molecule and a single binding ligand

can be determined according to Equation 1. The ratio of the number of capture objects to analyte molecules and/or binding ligands which may be provided such that substantially all of the capture objects are associated with zero or a single analyte molecule may be calculated using a Poisson distribution adjustment, as described herein.

In some embodiments, the statistically significant fraction of capture objects (e.g., beads) associated with at least one analyte molecule and at least one binding ligand to the total number of capture objects (e.g., beads) is less than about 1:2, less than about 1:3, less than about 1:4. is less than about 2:5, less than about 1:5, less than about 1:10, less than about 1:20, less than about 1:100, less than about 1:200, or less than about 1:500. In some cases, the statistically significant fraction of capture objects (e.g., beads) associated not associated with any binding ligand to the total number of capture objects at least about 1:100, about 1:50, about 1:20, about 1:10, about 1:5, about 1:4, about 1:3, about 1:2, about 1:1, about 2:1, about 3:1, about 4:1, about 5:1, about 10:1, about 20:1, about 50:1, about 100:1, or the like.

In some embodiments, the percentage of capture objects (e.g., beads) associated with at least one analyte molecule and at least one binding ligand to the total number of capture objects (e.g., beads) is less than about 50%, less than about 40%, less than about 30%, less than about 20%, less than about 10%, less than about 5%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.01%, or less. In some embodiments, the percentage of capture objects (e.g., beads) not associated with any binding ligand to the total number of capture objects is at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or greater.

A non-limiting example of an embodiment where a capture object is associated with more than one analyte molecule is illustrated in FIG. 2. A plurality of capture objects 20 are provided (step (A)). In this example, the plurality of capture objects comprises a plurality of beads. The plurality of beads is exposed to a fluid sample containing plurality of analyte molecules 21 (e.g., beads 20 are incubated with analyte molecules 21). At least some of the analyte molecules are immobilized with respect to a bead. For example, as shown in step (B), analyte molecule 22 is immobilized with respect to bead 24, thereby forming complex 26. Also illustrated is complex 30 comprising a bead immobilized with respect to three analyte molecules and complex 32 comprising a bead immobilized with respect to two analyte molecules. Additionally, in some cases, some of the beads may not associate with any analyte molecules (e.g., bead

28). The plurality of beads from step (B) is exposed to a plurality of binding ligands 31. As shown in step (C), a binding ligand associates with some of the analyte molecules immobilized with respect to a bead. For example, complex 40 comprises bead 34, analyte molecule 36, and binding ligand 38. The binding ligands are provided in a manner such that a statistically significant fraction of the beads comprising at least one analyte molecule become associated with at least one binding ligand (e.g., one, two, three, etc.) and a statistically significant fraction (i.e. as determined by Equation 1 above) of the beads comprising at least one analyte molecule do not become associated with any binding ligands. At least a portion of the plurality of beads from step (C) are then spatially separated into a plurality of locations. As shown in step (D), in this example, the locations comprise a plurality of reaction vessels 41 on a substrate 42. The plurality of reaction vessels may be exposed to the plurality of beads from step (C) such at each reaction vessel contains zero or one beads. The substrate may then be analyzed to determine the number of reaction vessels containing a binding ligand (e.g., reaction vessels 43), wherein in the number may be related to a measure of the concentration of analyte molecules in the fluid sample. In some cases, the number of reaction vessels containing a bead and not containing a binding ligand (e.g., reaction vessel 44), the number of reaction vessels not containing a bead (e.g., reaction vessel 45), and/or the total number of reaction vessels addressed/analyzed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of analyte molecules in the fluid sample.

The foregoing exemplary methods may be performed using a number of different assay formats, different reaction conditions, and/or detection systems in different embodiments of the invention, several examples of which are described below. Additional components and/or method steps may be utilized as a substitute for and/or in combination with the exemplary methods and components described herein within the scope of the invention. It should be understood, while certain of the discussion herein focuses on a plurality of locations comprising a plurality of wells/reaction vessels in a substrate, this is by no means limiting and other materials may be used to segregate capture objects/molecules into a plurality of spatially distinct locations (e.g., regions in/on a hydrogel, points/regions on the surface of a planar substrate, etc.). As another example, while much of the discussion herein focuses on a plurality of capture objects comprising a plurality of beads, this is by no means limiting

and in other embodiments the capture objects may take other physical forms (e.g., nanotubes, disks, rings, microfluidic droplets, etc.).

Exemplary Assay Formats

The inventive assays may be carried our according to a very wide variety of basic protocols and formats. The particular format chosen can be based on the nature of the analyte molecules, the nature of the fluid sample containing the analyte molecules, and the availability and properties of binding partners of the analyte as well as other factors. Several exemplary basic formats were discussed previously in the context of the discussion of FIGS. 1-2. As would be apparent to those skilled in the art with the benefit of the teachings provided by the present disclosure, the invention may alternatively be performed according to protocols/formats not specifically described in the specific, exemplary embodiments illustrated in this detailed description, but which do not require undue burden or experimentation to practice.

As described above, an exemplary basic assay format/protocol comprises exposing a plurality of capture objects (e.g., beads) configured to capture an analyte molecule or particle to a sample containing or suspected of containing such analyte molecules (or particles). At least some of the analyte molecules may become immobilized with respect to a capture object. The plurality of capture objects may each include a binding surface having affinity for at least one type of analyte molecule. At least a portion of the capture objects may then be spatially segregated into a plurality of locations (e.g., reaction vessels/wells). Based at least in part on a determination of the number of locations comprising a capture object comprising at least one analyte molecule, a measure of the concentration of analyte molecules may be determined. Various other aspects of this basic assay format will now be discussed, including numerous considerations regarding the materials, concentrations, solutions, steps, and the like.

In certain embodiments, a plurality of capture objects is exposed to a sample containing or suspected of containing at least one type of analyte molecules, wherein the plurality of capture objects comprises a binding surface having an affinity for the at least one type of analyte molecule. In some cases, the binding surface may comprise a plurality of capture components. A "capture component", as used herein, is any molecule, other chemical/biological entity, or solid support modification disposed upon a solid support that can be used to specifically attach, bind or otherwise capture a target

molecule or particle (e.g., an analyte molecule), such that the target molecule/particle becomes immobilized with respect to the capture component and the support. The immobilization, as described herein, may be caused by the association of an analyte molecule with a capture component on the surface of the capture object. As used herein, "immobilized" means captured, attached, bound, or affixed so as to prevent dissociation or loss of the target molecule/particle, but does not require absolute immobility with respect to either the capture component or the object.

The number of analyte molecules which are immobilized with respect to a capture object may depend on the ratio of the total number of analyte molecules in the sample versus at least one of the total number, size, and/or surface density of capture components of capture objects provided. In some embodiments, the number of molecules or particles immobilized with respect to a single capture object may follow a standard Poisson distribution. In some cases, a statistically significant number of the capture objects associate with a single analyte molecule and a statistically significant number of capture objects do not associate with any analyte molecules. The total number of capture objects provided may be between about 10,000 and about 10,000,000, between about 50,000 and about 5,000,000, or between about 100,000 and about 1,000,000. In some cases, the total number of capture objects provided is at least about 10,000, at least about 50,000, at least about 100,000, at least about 1,000,000, at least about 5,000,000, or at least about 10,000,000. In some cases, the ratio of the number of analyte molecules in the fluid sample to capture objects provided is between about 10:1 and about 1:10,000,000, between about 8:1 and about 1:10,000,000, between about 10:1 and about 2:1, between about 2:1 and about 1:10, or less than about 1:10 (e.g., about 1:20, about 1:30, etc.). The ratio of analyte molecules in the fluid sample to capture objects provided may affect the assay steps and/or analysis carried out to determine a measure of the concentration of analyte molecules in the fluid sample, as described herein in the Quantification section.

In some cases, substantially all of the analyte molecules provided in the sample may become immobilized with respect to a capture object. That is, greater than about 90%, greater than about 95%, greater than about 97%, greater than about 98%, or greater than about 99% of the analyte molecules in the sample may become immobilized with respect to a capture object. In some cases, however, only a fraction of the analyte molecules in the sample may become immobilized with respect to a capture object. That is, in some cases, between about 1% and about 90%, between about 10% and about 90%,

between about 20% and about 80%, or between about 30% and about 70% of the analyte molecules provided in the sample are immobilized with respect to a capture object. In some embodiments, at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, or about 90%, or about 95% of the analyte molecules are immobilized with respect to a capture object.

In some formats of the assay, following immobilization, the plurality of capture objects (e.g., at least some of which are associated with at least one analyte molecule) may be exposed to a plurality of binding ligands. At least some of the analyte molecules immobilized with respect to a capture object may associate with a binding ligand. The number of binding ligands which associate with a capture object (e.g., via an analyte molecule) may depend on the ratio of the total number of analyte molecules immobilized with respect to a single capture object versus the total number of binding ligands exposed to the capture objects. For example, in embodiments where substantially all of the capture objects are associated with either zero or one analyte molecules, conditions may be selected such that substantially all of the analyte molecules associate with a single binding ligand, therefore each capture object associated with a single analyte molecule becomes associated with a single binding ligand (e.g., via the analyte molecule). Thus, the number of locations (e.g., reaction vessels) which contain a single analyte molecule may be determined by determining the number of locations (e.g., reaction vessels) which comprise a binding ligand. In such embodiments (e.g., where zero or at least one analyte molecules are associated with each capture object), the ratio of binding ligands provided (e.g., in a mixing step) to the total number of analyte molecules immobilized with respect to a capture object may be about 20:1, about 10:1, about 5:1, about 2:1, or about 1:1.

In some embodiments, however, a single capture object may be associated with zero, one, or more than one (e.g., two, three, four, etc.) analyte molecules. In such embodiments, the binding ligand may be provided at a concentration such that a statistically significant fraction of the capture objects comprising at least one analyte molecule associate with only a single binding ligand and a statistically significant fraction of the capture objects comprising at least one analyte molecule do not associate with any binding ligand. In other embodiments, however, the binding ligands may be provided at a concentration such that a statistically significant fraction of the capture objects comprising at least one analyte molecule associate with at least one binding ligand (e.g., one, two, three, etc.) and a statistically significant fraction of the

capture objects comprising at least one analyte molecule do not associate with any binding ligand. The concentration of analyte molecules in the fluid sample may then be determined, either with an analysis based at least in part of the number of locations containing a capture object associated with a binding ligand (e.g., by relating the concentration of analyte molecules in the fluid sample to the number of locations comprising a binding ligand), and/or an analysis based at least in part on an intensity reading of a signal indicative of the number of binding ligands at the addressed locations (e.g., in embodiments where at least some of the capture objects comprise more than one analyte molecule and/or more than one binding ligand, as described herein). In such embodiments (e.g., wherein more than one analyte molecule may be immobilized with respect to each capture object), the ratio of the number of binding ligands provided in solution to the number of analyte molecules immobilized with respect to a capture object may be about 1:50, about 1:40, about 1:30, about 1:20, about 1:10, about 1:5, about 1:3, about 1:2, about 1:1, or the like. In some cases, the ratio of the number of binding ligands provided in solution may be calculated based on the number of capture objects provided. In some cases, the ratio of binding ligands provided to the number of capture objects is about 1:50, about 1:40, about 1:30, about 1:20, about 1:10, about 1:5, about 1:3, about 1:2, about 1:1, or the like. In other cases, the ratio the number of capture objects to the number of binding ligands provided is about 1:50, about 1:40, about 1:30, about 1:20, about 1:10, about 1:5, about 1:3, about 1:2, or the like. In some embodiments, the quantification determination may comprise a Poisson distribution adjustment, as described herein.

In some embodiments, the concentration of binding ligand used in an assay may be selected as to minimize certain events which may occur when an excess of binding ligand is present, for example, non-specific binding of the binding ligand. In some cases, if the concentration of binding ligand is too high, an increase in background readings may occur due to non-specific interactions (e.g., with the capture objects, reaction vessels, etc.). In some cases, the concentration of binding ligand may be selected (or estimated, in the case of an unknown concentration of analyte molecule) such that a only a fraction of the analyte molecules immobilized with respect to a capture object associate with a binding ligand (e.g., about 0.1%, about 1%, about 2%, about 3%, about 4%, about 5%, about 10%, about 20%, about 30%, about 40%, about 50%, or more). This may be especially useful in embodiments where the percentage of capture objects which associate with at least one analyte molecule is relatively high (e.g., greater than about

20%, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90%, or more). By providing the binding ligand at a lower concentration, in some cases, not every analyte molecule immobilized with respect to a capture object will associate with a binding ligand, which can be advantageous for quantification, for example when the presence of a binding ligand is required for detection, and especially when using a digital/binary read-out technique. For example, if the percentage of capture objects associated with an analyte molecule is about 50% or greater, a reduced number of binding ligands may be provided such that less than all of the immobilized analyte molecules associate with a binding ligand. In other cases, the percentage of binding ligands that associate with an analyte molecule may be reduced by decreasing the incubation time with the analyte molecule (e.g., limit the time of exposure such that only a fraction of the immobilized analyte molecules associate with an analyte molecule).

The total number of analyte molecules/binding ligands/capture objects/etc. in a solution may be determined using calculations with knowledge of the concentration of the analyte molecules/binding ligands/capture objects/etc. in solution. For example, the total number of binding ligands in a solution may be determined according to Equation 2:

$$\#of \quad binding \quad ligands = N_A \times [binding \quad ligand] \times volume \qquad \text{(Eq. 2)}$$

wherein N_A is Avogadro's number (6.022×10^{23} mol^{-1}), [binding ligand] is the concentration of the binding ligand in solution in moles per liter, and volume is the total volume of solution in liters employed. Similar calculations may be carried out for other components (e.g., analyte molecules (e.g., in a calibration sample), capture objects, etc.).

Following immobilization of a plurality of analyte molecules with respect to a plurality of capture objects and, in some cases, association of a binding ligand to at least some the immobilized analyte molecules, at least a portion of the capture objects may be spatially segregated into a plurality of locations. The percentage of capture objects which are spatially segregated into the plurality of locations may vary depending on numerous factors including, but not limited to, the ratio of the number of capture objects versus the total number of locations, the method of spatially segregating the capture objects, and/or the length of the time the capture objects are exposed to the locations. In some cases, at least about 0.5%, at least about 1%, at least about 2%, at least about 5%,

at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least above 90%, or more, of the capture objects are spatially segregated into the plurality of locations. In some cases, between about 0.1% and about 50%, between about 0.1% and about 30%, between about 0.5% and about 20%, between about 0.5% and about 10%, between about 0.5% and about 5%, between about 1% and about 10%, or about 0.5%, about 1%, about 2%, about 4%, about 5%, about 10%, about 20%, about 30%, about 50%, about 70%, or about 90% of the capture objects are spatially segregated into the plurality of locations. Following spatially segregating at least a portion of the capture objects into a plurality of locations, at least a portion of the locations may be addressed. The number of locations addressed may be about 0.5%, about 1%, about 2%, about 3%, about 5%, about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, or more, of the total number of locations.

The portion of locations may be addressed to determine the number of locations containing an analyte molecule, or in some cases, a binding ligand. In some cases, the number of locations containing a capture object not associated with an analyte molecule (or a binding ligand), the number of locations containing and/or not containing a capture object, and/or the total number of locations analyzed/determined may also be determined. A measure of the concentration of analyte molecules in the fluid sample may be determined at least in part on the number of locations determined to contain an analyte molecule (or binding ligand). In some cases the measure of the concentration of analyte molecules in the fluid sample may be based at least in part on the ratio of the number of locations containing a capture object associated with an analyte molecule to the total number of locations addressed or the total number of locations addressed that contain a capture object. In other cases, a measure of the concentration of analyte molecules in the fluid sample may be based at least in part on the ratio of the number of locations containing a capture object associated with an analyte molecule to the number of locations containing a capture object not associated with an analyte molecule. Specific methods and calculations which may be used to determine the measure of the concentration of analyte molecules in the fluid sample are discussed in more detail below.

The ratios, percentages, and other parameters described herein with respect to the amount/quantity/ratio of a first component to a second component (for example, analyte molecules/capture objects, binding ligands/capture objects, binding ligands/analyte

molecules, capture objects/locations, precursor labeling agents/binding ligands, etc.) may be adjusted as desired to yield a desired ratio of analyte molecules/binding ligands captured per capture object, and/or may be controlled or determined using no more than routine experimentation, calculations (in some cases, including accounting for Poisson distributions), screening tests, etc., given the teaching and guidance provided by the present specification. For example, if the number of capture objects provided is known (e.g., as determined using a similar formula as given in Equation 1), the number of binding ligands that need to be provided may be determined based on the desired ratio of capture objects to binding ligands, and hence, the amount of moles of binding ligand that should be provided may be determined. As another example, in the case of an unknown concentration of analyte molecules, if a first assay method indicates that a significant number of capture objects comprise more than one analyte molecule (e.g., all or a significant number of locations are determined to contain an analyte molecule or there is less than a statistically significant number of beads determined to be free of analyte molecules), the fluid sample may be diluted and/or the number of capture objects may be increased such that the number of capture objects comprising at least one analyte molecule may be decreased.

Other aspects of the assay will now be discussed in detail. It should be understood, that none, a portion of, or all of the following steps may be performed at least once during the certain exemplary assay formats described herein. Non-limiting examples of additional steps not described which may be performed include, but are not limited to, washing and/or exposure to additional binding ligands, precursor labeling agents, and/or labeling agents, etc.

In some embodiments, the plurality of capture objects (e.g., at least some of which are associated with at least one analyte molecule) may be exposed to at least one additional reaction component prior to, concurrent with, and/or following spatially separating at least some of the plurality of capture objects into a plurality of locations. In some cases, the capture objects may be exposed to a plurality of binding ligands. In certain embodiments, a binding ligand may be adapted to be directly detected (e.g., the binding ligand comprises a detectable molecule or moiety) or may be adapted to be indirectly detected (e.g., including a component that can convert a precursor labeling agent into a labeling agent), as discussed more below. More than one type of binding may be employed in any given assay method, for example, a first type of binding ligand and a second type of binding ligand. In one example, the first type of binding ligand is

able to associate with a first type of analyte molecule and the second type of binding ligand is able to associate with the first binding ligand. In another example, both a first type of binding ligand and a second type of binding ligand may associate with the same or different epitopes of a single analyte molecule, as described below.

Certain binding ligands can comprise a component that is able to facilitate detection, either directly or indirectly. A component may be adapted to be directly detected in embodiments where the component comprises a measurable property (e.g., a fluorescence emission, a color, etc.). A component may facilitate indirect detection, for example, by converting a precursor labeling agent into a labeling agent (e.g., an agent that is detected in an assay). A "precursor labeling agent" is any molecule, particle, or the like, that can be converted to a labeling agent upon exposure to a suitable converting agent (e.g., an enzymatic component). A "labeling agent" is any molecule, particle, or the like, that facilitates detection, by acting as the detected entity, using a chosen detection technique.

In some embodiments, at least one binding ligand comprises an enzymatic component. In some embodiments, the analyte molecule may comprise an enzymatic component. The enzymatic component may convert a precursor labeling agent (e.g., an enzymatic substrate) into a labeling agent (e.g., a detectable product). A measure of the concentration of analyte molecules in the fluid sample can then be determined based at least in part by determining the number of locations containing a labeling agent (e.g., by relating the number of locations containing a labeling agent to the number of locations containing an analyte molecule). Non-limiting examples of enzymes or enzymatic components include horseradish peroxidase, beta-galactosidase, and alkaline phosphatase. Other non-limiting examples of systems or methods for detection include embodiments where nucleic acid precursors are replicated into multiple copies or converted to a nucleic acid that can be detected readily, such as the polymerase chain reaction (PCR), rolling circle amplification (RCA), ligation, Loop-Mediated Isothermal Amplification (LAMP), etc. Such systems and methods will be known to those of ordinary skill in the art, for example, as described in "DNA Amplification: Current Technologies and Applications," Vadim Demidov et al., 2004.

As an example of an assay method which comprises the use of a precursor labeling agent, as shown in FIG. 3, substrate 100 comprising a plurality of locations is provided, wherein the locations comprise reaction vessels. In reaction vessel 101 (e.g., location), analyte molecule 102 is immobilized with respect to bead 103 (e.g., capture

object). Binding ligand 104 is associated with analyte molecule 102. Binding ligand 104 comprises an enzymatic component (not shown). Precursor labeling agent 106 is converted to labeling agent 108 (upon exposure to the enzymatic component). Labeling agent 108 is detected using methods described herein. In contrast, reaction vessel 111 contains analyte molecule 112 immobilized with respect to bead 110. In this reaction vessel, analyte molecule 112 is not associated with a binding ligand comprising an enzymatic component. Therefore, precursor labeling agent 114 is not converted to a labeling agent in the reaction vessel. Thus this reaction vessel would give a different signal as compared to reaction vessel 101 where the precursor labeling agent was converted to a labeling agent. In some cases, there may also be reaction vessels which contain a bead not associated with an analyte molecule, for example, reaction vessel 121 contains bead 116. Additionally, some of the reaction vessels may not comprise any bead, for example, reaction vessel 123. Reaction vessels 121 and 123 may give different signals as compared to reaction vessel 101 as there would be no labeling agent present. However, reaction vessels 121 and 123 may contain precursor labeling agent 117. More than one precursor labeling agent may be present in any given reaction vessel.

In certain embodiments, solubilized, or suspended precursor labeling agents may be employed, wherein the precursor labeling agents are converted to labeling agents which are insoluble in the liquid and/or which become immobilized within/near the location (e.g., within the reaction vessel in which the labeling agent is formed). Such precursor labeling agents and labeling agents and their use is described in commonly owned U.S. Patent Application Serial No. 12/236,484, entitled "High Sensitivity Determination of the Concentration of Analyte molecules in a Fluid Sample," by Duffy, et al., filed September 23, 2008, incorporated herein by reference.

In some embodiments, during the assay, at least one washing step may be carried out. In one instance, a plurality of capture objects may be washed after exposing the capture objects to one or more solutions comprising analyte molecules, binding ligands, precursor labeling agents, or the like. For example, following immobilization of the analyte molecules with respect to a plurality of capture objects, the plurality of capture objects may be subjected to a washing step thereby removing any analyte molecules not specifically immobilized with respect to a capture object. In certain embodiments, the wash solution is selected so that it does not cause appreciable change to the configuration of the capture objects and/or analyte molecules and/or does not disrupt any specific binding interaction between at least two components of the assay (e.g., a capture

component and an analyte molecule). In other cases, the wash solution may be a solution that is selected to chemically interact with one or more assay components. As will be understood by those of ordinary skill in the art, a wash step may be performed at any appropriate time point during the inventive methods.

In some embodiments, assay methods may be carried out that do not comprise the use of a plurality of capture objects comprising a binding surface for at least one type of analyte molecule and/or a plurality of locations to which the capture objects may be spatially separated. For example, an assay according to the invention in certain embodiments may use any suitable method which is capable of isolating single analyte molecules and/or capture objects associated with one or more analyte molecules such that they can be individually addressed for detection. For example, an assay method may comprise providing a plurality of capture objects which are each associated with either a single analyte molecule or are free of any analyte molecules. At least a portion of the capture objects may be individually addressed to determine the number of the capture objects associated with an analyte molecule or particle. Based at least in part on the number of capture objects determined to be associated with an analyte molecule, a measure of the concentration of analyte molecules or particles in a fluid sample may be determined.

FIG. 4A illustrates a non-limiting embodiment where single analyte molecules are spatially segregating into a plurality of droplets. In FIG. 4A, plurality of analyte molecules 70 are provided, as shown in step (A). In this example, analyte molecules 70 are capable of being optically detected (e.g., the analyte molecules may be directly detected using optical interrogation). At least some of the plurality of analyte molecules 70 are contained within liquid droplets 72 (e.g., using microfluidic techniques) which comprise fluid 71, as shown in step (B). Additionally, some droplets may be present which do not contain any analyte molecules (e.g., droplets 74 comprising fluid 71). Plurality of droplets 75 are substantially surrounded by fluid 73 which is substantially immiscible with fluid 71. Plurality of droplets 75 can be optically interrogated by feeding droplets into column 74 such that each droplet passes by an optical detection system (e.g., comprising light source 76 and detector 78) single file, as shown in step (C). Each droplet may be determined to contain an analyte molecule when there is a change in the optical single (e.g., a change in optical signal due to the presence of an analyte molecule in the droplet).

As another example, as illustrated in FIG. 4B, plurality of analyte molecules 80 are provided, as shown in step (A). In this example, analyte molecules 70 are not capable of being optically detected, and must be indirectly detection (as described herein). Plurality of analyte molecules 80 are exposed to a plurality of binding ligands 82, such that at least one binding ligand associates with a significant portion of the analyte molecules, as shown in step (B), to form complex 83, as shown in step (B). In this example, each binding ligand 82 comprises enzymatic component 84. At least a portion of complexes 83 may be contained in droplets 85 (e.g., using microfluidic techniques), as shown in step (C), which comprise liquid 79. Additionally, some droplets may be present which do not contain any complexes (e.g., droplets 86 comprising fluid 79). Plurality of droplets 91 are substantially surrounded by fluid 87 which is substantially immiscible with fluid 79. Droplets 85 and 86 may additionally comprise precursor labeling agent 86, which is converted to labeling agent 88 upon exposure to enzymatic component 84, as indicated by arrow 87. Plurality of droplets 91 can be optically interrogated by feeding the plurality of droplets into column 89 such that each droplet passes by an optical detection system (e.g., comprising light source 90 and detector 92) single file, as shown in step (D). Each droplet may be determined to contain an analyte molecule when there is a change in the optical single (e.g., a change in optical signal due to the presence of a labeling agent in the droplet).

As yet another example, FIG. 4C illustrates and embodiment where single analyte molecules 282 are associated with respect to objects 280 via capture components 274. Additionally, in this example, the immobilized analyte molecules are associated with binding ligand 284. The droplets can be optically interrogated by feeding droplets into column 287 such that each droplet passed by the optical detection system (e.g., comprising light source 286 and detector 288) single file. Each droplet may be determined to contain a binding ligand when there is a change in the optical single (e.g., a change in optical signal due to the presence of a binding ligand in the droplet).

The following sections provide additional information regarding method steps, materials, and parameters that may be used to practice the assay methods described above.

Capture Objects and Spatial Locations for Capture Object Segregation

In some embodiments, the method and systems of the present invention utilize a plurality of capture objects that each includes a binding surface having affinity for at

least one type of analyte molecule. The plurality of capture objects may be configured to be able to be spatially segregated from each other, that is, the capture objects may be provided in a form such that the capture objects are capable of being spatially separated into a plurality of locations. For example, the plurality of capture objects may comprise a plurality of beads (which can be of any shape, e.g., sphere-like, disks, rings, cube-like, etc.), a dispersion or suspension of particulates (e.g., a plurality of particles in suspension in a fluid), nanotubes, or the like. In some embodiments, the plurality of capture objects is insoluble or substantially insoluble in the solvent(s) or solution(s) utilized in the assay. In some cases, the capture objects are solid or substantially solid (e.g., is essentially free of pores), however, in some cases, the plurality of capture objects may be porous or substantially porous, hollow, partially hollow, etc. The plurality of capture objects may be non-absorbent, substantially non-absorbent, substantially absorbent, or absorbent. In some cases, the capture objects may comprise a magnetic material, which as described herein, may facilitate certain aspect of the assay (e.g., washing step). In some cases, a capture object surface may also comprise a protective or passivating layer that can reduce or minimize non-specific binding events (e.g., analyte molecules, binding ligands, etc.).

In some embodiments, the capture objects each include a binding surface having affinity for at least one type of analyte molecule of interest. The portion of the capture object which comprises a binding surface may be selected or configured based upon the physical shape/characteristics and properties of the capture objects (e.g., size, shape), and the format of the assay. In some embodiments, substantially all of the outer surfaces of the capture objects form the binding surfaces. A binding surface having an affinity for at least one type of analyte molecule may be formed via the association of a plurality of capture components with a capture object. In some cases, an analyte molecule may associate with a capture component (e.g., become immobilized with respect to) via formation of at least one chemical bond and/or physical adsorption, or combination thereof. Non-limiting examples of types of chemical bonds include ionic bonds, covalent bonds (e.g., carbon-carbon, carbon-oxygen, oxygen-silicon, sulfur-sulfur, phosphorus-nitrogen, carbon-nitrogen, metal-oxygen, or other covalent bonds), hydrogen bonds (e.g., between hydroxyl, amine, carboxyl, thiol, and/or similar functional groups), dative bonds (e.g., complexation or chelation between metal ions and monodentate or multidentate ligands), Van der Waals interactions, or the like. Capture components which are useful or potentially useful for practicing certain aspects and embodiments of

the invention are discussed in more detail below. At least some of the analyte molecules, upon exposure to the plurality of capture objects comprising a plurality of capture components, become immobilized with respect to a capture component. In certain embodiments, substantially all of the plurality of analyte molecules in the fluid sample tested may become immobilized with respect to the capture components (and hence, the capture objects).

Without wishing to be bound by any theory, the use in certain embodiments of the invention of a capture step in which a plurality of capture objects having a large surface area for binding are exposed to a fluid sample containing the analyte molecules or particles such that the analyte molecules/particles become immobilized with respect to the capture objects may facilitate an increase in the speed and/or efficiency of the assay for detection and quantification of concentration of the analyte in the sample compared to assays where the analyte molecules themselves are segregated for detection without being exposed to and immobilized with respect to a capture object. This increase in binding speed and efficiency may be further enhanced if the solution in which the plurality of analyte molecules and capture objects are incubated for capture is agitated (e.g., stirred) to increase the collision frequency and mass transfer rate between the plurality of capture objects (e.g., plurality of beads) and the analyte molecules (e.g., as contrasted with a substrate comprising a stationary surface (e.g., a microtiter plate)).

The plurality of capture objects for analyte capture may be of any suitable size or shape. Non-limiting examples of suitable shapes include spheres, cubes, ellipsoids, tubes, sheets, and the like. In certain embodiments, the average diameter (if substantially spherical) or average maximum cross-sectional dimension (for other shapes) of a capture object may be greater than about 0.1 um (micrometer), greater than about 1 um, greater than about 10 um, greater than about 100 um, greater than about 1 mm, or the like. In other embodiments, the average diameter of a capture object or the maximum dimension of a capture object in one dimension may be between about 0.1 um and about 100 um, between about 1 um and about 100 um, between about 10 um and about 100 um, between about 0.1 um and about 1 mm, between about 1 um and about 10 mm, between about 0.1 um and about 10 um, or the like. The "average diameter" or "average maximum cross-sectional dimension" of a plurality of capture objects, as used herein, is the arithmetic average of the diameters/maximum cross-sectional dimensions of the capture objects. Those of ordinary skill in the art will be able to determine the average diameter/maximum cross-sectional dimension of a population of capture objects, for

example, using laser light scattering, microscopy, sieve analysis, or other known techniques. For example, in some cases, a Coulter counter may be used to determine the average diameter of a plurality of beads.

The capture objects for analyte capture may be fabricated from one or more suitable materials, for example, plastics or synthetic polymers (e.g., polyethylene, polypropylene, polystyrene, polyamide, polyurethane, phenolic polymers, or nitrocellulose etc.), naturally derived polymers (latex rubber, polysaccharides, polypeptides, etc), composite materials, ceramics, silica or silica-based materials, carbon, metals or metal compounds (e.g., comprising gold, silver, steel, aluminum, copper, etc.), inorganic glasses, silica, and a variety of other suitable materials. Non-limiting examples of potentially suitable configurations include beads (e.g., magnetic beads), tubes (e.g., nanotubes), plates, disks, dipsticks, or the like.

In some cases, the capture objects may be selected such that the capture object itself is detectable by the system. This may be useful in embodiments where the fraction or percentage of capture objects associated with an analyte molecule is to be determined (e.g., when the total number of capture objects interrogated and detected is used to determine the fraction of capture objects associated with an analyte molecule). For example, a capture object may be characterized as having an emission or absorption spectrum that can be exploited for detection so that capture objects may be interrogated to determine which spatial location contains a capture object. The properties of the emission spectrum (e.g., wavelength(s), intensity, etc.), may be selected such that the emission produced by the capture objects does not substantially alter and/or interfere with any other emission from components used in the assay (e.g., the emission of any labels used to determine the presence or absence of an analyte molecule). In some cases, dye molecules may be associated with a capture object using the binding ligands present on the surface of the capture object (e.g., a dye molecule may associate via a bond or interaction with a capture component). In some cases, between about 1 and about 50,000, or between about 1000 and about 50.000, or between about 1000 and about 20.000, or between about 10,000 and about 20,000, or between about 1,000 and about 10,000, or between about 10,000 and about 30,000, or between about 1 and about 10,000 dye molecules (e.g., fluorescent dye molecules) are associated with each capture object. See, for example, Example 21. In some cases, dye molecules might first be associated with the capture object, before the binding ligands are attached to the capture object. This approach reduces the chances that the affinity of the binding ligands are reduced by

attachment of dye molecules. In some cases, dye molecules are attached to an inert, "blocking" protein (e.g., bovine serum albumin) and the dye-labeled inert protein is used to block the beads after binding ligands are attached to the capture object. It should be understood, that in some cases, the capture objects may be detected and quantified using white light (e.g., as described herein, for example using bright field, dark field and/or phase contrast imaging).

In some embodiments, more than one type of capture object for analyte capture may be employed. In some cases, each type of capture object may include a surface with differing binding specificity. In these embodiments, more than one type of analyte molecule may be quantified and/or detected in a single, multiplexed assay method. For example, the plurality of capture objects for analyte capture may comprise a plurality of a first type of capture object comprising a binding surface having an affinity for a first type of analyte molecule and a plurality of a second type of capture objects comprising a binding surface having an affinity for a second type of analyte molecule. Upon exposure to a sample containing the first type of analyte molecule and the second type of analyte molecule, the first type of analyte molecule becomes immobilized with respect to the first type of capture object and the second type of analyte molecule becomes immobilized with respect to the second type of capture object. The first type of capture object and the second type of capture object may be encoded to be distinguishable from each other (e.g., to facilitate differentiation upon detection) by including a differing detectable property. For example, each type of capture object may have a differing fluorescence emission, a spectral reflectivity, shape, a spectral absorption, or an FTIR emission or absorption. In a particular embodiment, each type of capture object may comprise one or more dye compounds (e.g., fluorescent dyes) but at varying concentration levels, such that each type of capture object has a distinctive signal (e.g., based on the intensity of the fluorescent emission). Upon spatially segregating the capture objects after the capture step into a plurality of locations for detection, a location comprising a first type of capture object associated with a first type of analyte molecule may be distinguished from a location comprising a second type of capture object associated with a second type of analyte molecule via detection of the differing property. The number of locations comprising each type of capture object and/or the number of capture objects associated with an analyte molecule may be determined, enabling a determination of a measure of the concentration of both the first type of analyte molecule

and the second type of analyte molecules in the fluid sample based at least in part on these numbers.

For example, as illustrated in FIG. 5, step (A) a plurality of a first type of capture object 132 comprising a first type of capture component 134 and a plurality of a second type of capture object 136 comprising a second type of capture component 138 are provided. The plurality of capture objects is exposed to a fluid sample comprising a plurality of a first type of analyte molecule 140 and a second type of analyte molecule 142. As shown in step (B), at least some of the first type of analyte molecule 140 may associate with a capture object of the first type 132 via capture component 134 and at least some of the second type of analyte molecule 142 may associate with a capture object of the second type 136 via capture component 138. Some of the first type of capture objects and second type of capture objects may not associate with any first type of or second type of analyte molecules. At least some of the plurality of capture objects from step (B) may be spatially segregated into a plurality of locations (represented by reaction vessels 142 formed in substrate 146, as shown in step (C). Some of the reaction vessels may not comprise any capture objects. The plurality of reaction vessels may then be analyzed (e.g., for example, as illustrated in FIG. 1, step (D)) to determine the number of reaction vessels containing a first type of capture object associated with a first type of analyte molecule (e.g., reaction vessel 144) and the number of reaction vessels containing a second type of capture object associated with a second type of analyte molecule (e.g., reaction vessel 145). Additionally, the number of locations containing a first type of capture object or a second type of capture object not associated with any analyte molecules may also be determined. A measure of the concentration of the first type (or second type) of analyte molecule may be determined at least in part based on the number of the first type (or second type) of analyte molecule detected. Alternatively, a measure of the concentration of either first type (or second type) of analyte molecule in the fluid sample may be based on the ratio of the number of reaction vessels comprising the first type (or second type) of capture object associated with a first type (or second type) of analyte molecule to the number of reactions vessels comprising the first type (or second type) of capture objects not associated with any analyte molecules. Additional methods for determining the concentration of the first and/or second types of analyte molecules in the fluid sample may be carried out using methods similar to those described herein for samples comprising a single type of analyte molecule. Using optical detection, the first type of capture object may have a maximum wavelength of emission

at a first wavelength and the second type of capture object may maximum wavelength of emission at a second wavelength, and therefore, allow for the reaction vessels which contain a first type of capture object to be distinguished from the reaction vessels which contain a second type of capture object.

Alternatively, or in combination, with use of coded capture objects for multiplexing, as described above, in some multiplexed assays, similar capture object types may be employed that may, in certain cases, each include capture components specific for multiple types of analytes. In certain such assays, a first type of binding ligand, e.g., having affinity for a first analyte molecule type, and a second, third, etc. type of binding ligand having affinity for a second, third, etc., respectively type of analyte molecule type and configured to be detectably distinguishable from each other (e.g., through use of differing detectable markers, enzymatic components and/or labeling agents, etc.) may be used in conjunction with the assay, and the detection/quantification of the different types of binding ligands may be correlated to the presence/concentration of different types of analyte molecules in the fluid sample.

In a particular embodiment, the plurality of capture objects for analyte capture comprises a plurality of beads. The beads may each comprise a plurality of capture components via which a plurality of analyte molecules may be immobilized. The plurality of capture components may be present on the surface of the beads. In some embodiments, the beads may be magnetic beads. The magnetic property of the beads may help in separating the beads from a solution (e.g., comprising a plurality of unbound analyte molecules) and/or during washing step(s) (e.g., to remove excess fluid sample, labeling agents, etc.). Potentially suitable beads, including magnetic beads, are available from a number of commercial suppliers. As noted above, there are many other examples of potentially suitable capture objects for analyte capture including nanotubes (e.g., carbon nanotubes), microfluidic droplets (e.g., droplets of a first fluid substantially surrounded by a second fluid), etc.

Those of ordinary skill in the art will be aware of methods and techniques for exposing a plurality of capture objects to a fluid sample containing or suspected of containing an analyte molecule or particle for initial analyte capture. For example, the plurality of capture objects may be added (e.g., as a solid, as a solution) directly to a fluid sample. As another example, the fluid sample may be added to the plurality of capture objects (e.g., in solution, as a solid). In some instances, the solutions may be agitated (e.g., stirred, shaken, etc.).

Following immobilization of the analyte molecules with respect to a plurality of capture objects, the capture objects may be subjected to at least one wash step. The wash step may aid in the removal of any unbound molecules (e.g., analyte molecules, or other reaction components) from the solution. For example, referring to FIG. 1, following immobilization of analyte molecules 4 with beads 6, as shown in step (B), a wash step may be performed to remove any unbound analyte molecules not immobilized with respect to an analyte molecule. As another example, referring to FIG. 2, following association of binding ligands 31 with analyte molecules 36, as shown in step (C), a wash step may be performed to remove any unbound binding ligands. The wash step may be performed using any suitable technique known to those of ordinary skill in the art, for example, by incubation of the capture objects with a wash solution followed by centrifuging the solution comprising the capture objects and decanting off the liquid, or by using filtration techniques. In embodiments where the plurality of capture objects comprises a plurality of magnetic beads, the beads may be isolated from the bulk solution with aid of a magnet.

The plurality of capture objects subsequent to the capture step (e.g., at least some associated with at least one analyte molecule) may be exposed to one or more additional reagents, prior to spatially segregating the plurality of capture objects into a plurality of locations for detection. For example, as noted previously, the capture objects may be exposed a plurality of binding ligands, at least some of which may associate with an immobilized analyte molecule. The capture objects may be exposed to more than one type of binding ligand (e.g., a first type of binding ligand and a second, third, etc. type of a binding ligand), as noted above. The association of a binding ligand with an immobilized analyte molecule may aid in the detection of the analyte molecules, as described herein.

In some embodiments, in addition to a plurality of capture objects for analyte capture, a plurality of control objects may also be provided and/or employed. A control object(s) may be useful for a variety of purposes including, but not limited to, identification of the orientation of the plurality of locations (e.g., in the case where the plurality of locations is formed as an array of reaction sites, reaction vessels, etc.), to help determine the quality of the assay, and/or to help calibrate the detection system (e.g., optical interrogation system), as described below. It should be understood, that more than one type of control object may be present in any assay format (e.g., a first type of control object to determine quality of the assay and a second type of control object to

act as a location marker), or a single type of control object may have more than one of the above-described functions.

In some cases, the control objects used to identify the orientation of the plurality of locations (e.g., reaction vessels, sites, etc.) on an array (e.g., function as location marker(s) for an array). For example, a control object may be randomly or specifically distributed on an array, and may provide one or more reference locations for determining the orientation/position of the array. Such a feature may be useful when comparing multiple images of a portion of the array at different time intervals. That is, the positions of control objects in the array may be used to register the images. In some cases, the control objects may be use to provide reference locations in embodiments where a plurality of images of small overlapping regions are being combined to form a larger image.

The presence of control objects in an assay may provide information regarding the quality of the assay. For example, if a location is found to contain a control object comprising an enzymatic component but no labeling agent is present (e.g., the product of which would be present upon exposure of a control object comprising an enzymatic component to a precursor labeling agent), this gives an indication that some aspect of the assay may not be functioning properly. For example, the quality of the reagents may be compromised (e.g., concentration of precursor labeling agent is too low, decomposition of the precursor labeling agent, etc.), and/or perhaps not all of the locations were exposed to the precursor labeling agent.

In some embodiments, the control objects may be used to calibration the detection system. For example, the control objects may output an optical signal which may be used to calibration an optical detection system. In some embodiments, the control objects can be characterized and doped with a particular characteristic (e.g., fluorescence, color, absorbance, etc.) which can act as a quality control check for the detection system performance.

In some cases, the control objects may be used to standardize or normalize the system to account for variations of the performance and/or characteristics of different system components in different assays, over the course of time, etc. (e.g., detection system, arrays, reagents, etc.) between different potion of an array used in a test, and/or between two different arrays. For example, experimental set-up, parameters and/or variations may lead to changes the intensity of a signal (e.g., fluorescence signal) produced from a single array at different time points, or between at least two arrays at

simultaneous or different time points. In addition, in a single array, different portions of the array may produce different background signals. Such variations may lead to changes in calibration signals (e.g., determination of an average bead signal) between arrays, portions of and array or at multiple times, which can lead to inaccurate determinations in some cases. Non-limiting examples of parameters that may cause variation include labeling agent concentration, temperature, focus, intensity of detection light, depth and/or size of the locations in an array, etc. To account for the effects of some or all of such variations, in some embodiments, a plurality of control objects may be utilized. In certain instances, such control objects are essentially free of association with analyte molecules or particles. In certain embodiments, less than about 20%, about 10%, about 5%, about 1%, etc. of the control objects are associated with analyte molecules or particles. The control objects may be distinguishable from the capture objects (e.g., each may produce a distinguishable signal) and the system may be configured such that any analyte molecules associated with a control object are not accounted for in the concentration determination of the analyte molecules. The signals from the control objects may be used to normalize the interrogation values between different arrays, or in areas of a single array. For example, because the signals from the control objects should be approximately equal between arrays and/or about a single array, the control object signals may be normalized to an appropriate value and the signals of the non-control objects (e.g., the capture objects associated with an analyte molecule) may be adjusted accordingly.

The control object may be provided with the plurality of capture objects for analyte capture prior to exposure to a fluid sample containing analyte molecules, or may be added at another point in the assay (e.g., following exposure to the plurality of analyte molecules and/or binding ligands, and/or prior to spatially segregating the plurality of capture objects into a plurality of locations). The control objects may be distinguishable from the capture objects using techniques known to those of ordinary skill in the art. For example, in some embodiments, the control objects may comprise a unique property (e.g., are encoded) as compare to the capture objects comprising a binding surface for the analyte molecules. For example, the control object may have a different fluorescence emission, a spectral reflectivity, shape, a spectral absorption, or an FTIR emission or absorption, as compared to the capture objects. The percentage of control objects to total number of objects (e.g., capture objects and control objects) in the assay may be about

0.0001%, about 0.0005%, about 0.001%, about 0.005%, about 0.01%, about 0.05%, about 0.1%, about 0.5%, about 1%, about 5%, or the like.

In some embodiments, the control objects are configured as negative binding controls and may be of a similar shape and size as the capture objects used for immobilizing analyte molecules, however, the control objects may lack a binding surface for the analyte molecules (e.g., a plurality of capture components). For example, the control objects may comprise a plurality of beads, and the capture objects for immobilizing the analyte molecules may comprise the same or similar beads, additionally comprising at least one surface comprising a plurality of capture components.

In one embodiment, the control objects may comprise a positive control and include an enzymatic component. A precursor labeling agent may be converted to a labeling agent upon exposure to the enzymatic component. In some cases, the enzymatic component may be the same as the enzymatic component being used to detect the analyte molecules in a fluid sample (e.g., comprised in another component of the assay, for example, an enzymatic component comprised in a binding ligand, an analyte molecule, etc.). In such embodiments, the control object may be distinguishable from the capture objects such that the reaction vessels having a positive signal may be analyzed to determine whether the reaction vessel comprises a control object (e.g., having a first detectable signal) or a capture object (e.g., having a second detectable signal distinguishable from the first detectable signal). In other cases, the enzymatic component may be the different than an enzymatic component being used to detect the analyte molecules in a fluid sample (e.g., comprised in another component of the assay, for example, an enzymatic component comprised in a binding ligand, an analyte molecule, etc.). In this embodiment, the control object may or may not be distinguishable from the capture objects. Both a first type and a second type of precursor labeling agent may be provided to the reaction vessels, and the first type of precursor labeling agent may be converted to a first type of labeling agent upon exposure to the enzymatic component associated with the control beads and the second type of precursor labeling agent may be converted to a second type of labeling agent upon exposure to the other enzymatic component (e.g., comprised in the binding ligand/analyte molecule/etc.). The reaction vessels containing the first type of labeling agent correspond to the reaction vessels containing a control object and reaction vessels containing a second type of labeling agent correspond to the reaction vessels which contain a binding ligand/analyte

molecule/etc. The plurality of locations containing a control bead may be observed to analyze, for example, the effectiveness of the enzymatic conversion reaction

A variety of methods may be used to prepare the controls objects, for example, similar methods described herein for the capture objects (e.g., beads comprising a plurality of capture components). In some cases, some of the control objects may comprise an enzymatic component. The control objects may be prepared such that 1) the majority of control objects each comprise at least one enzymatic component (e.g., one, two, three, four, etc.) or 2) some of the control objects comprise a single enzymatic component and the remainder of the control objects do not comprise any enzymatic component. In the first case, during formation of the control objects, the ratio of enzymatic components provided in solution to objects may be greater than 1:1, greater than about 2:1, greater than about 5:1, greater than about 10:1, or the like. In such cases, it would be expected that after partitioning the control objects on a substrate, each location comprising a control object would give a positive signal on exposure to a precursor labeling agent. In the second case, during formation of the control objects, the ratio of enzymatic components provided in solution to objects may be less than about 1:5, less than about 1:10, less than about 1:20, less than about 1:50, or the like. In such cases, it would be expected that ratio of the number of locations comprising a control object and giving a positive signal to the number of locations comprising a control object not giving a positive signal would be approximately similar to the ratio of enzymatic components to objects during formation of the control objects and/or may follow a Poisson distribution.

As described above, following immobilization of a plurality of analyte molecules with respect to the plurality of capture objects in the analyte capture step, at least a portion of the capture objects may be spatially segregated into a plurality of locations, for example on a substrate. For example, each of capture objects of the portion of capture objects which are spatially segregated may be positioned in and/or associated with a location (e.g., a spot, region, well, etc. on the surface and/or in the body of a substrate) that spatially distinct from the locations in which each of the other capture objects are located, such that the capture objects and locations can be individually resolved by an analytical detection system employed to address the locations. As an example, each of a potion of the capture objects may be spatially segregated into an array of reaction vessels on a substrate, such that statistically only zero or one capture objects are located in at least some of the reaction vessels and in certain cases in essentially each reaction vessel.

Each location may be individually addressable relative to the other locations. Additionally, the locations may be arranged such that a plurality of locations may be addressed substantially simultaneously, as described herein, while still permitting the ability to resolve individual locations and capture objects.

It should be understood, that while much of the discussion herein focusing on locations containing a single capture object, this is by no means limiting, and in some embodiments, more than one capture object may be contained at a single location. In such embodiments, the ratio of capture objects to analyte molecules may be such that following spatial segregation of the plurality of capture objects into the plurality of locations, a statistically significant fraction of the locations contain no analyte molecules and a statistically significant fraction of locations contain at least one analyte molecule. That is, while a single location may contain a plurality of capture objects, in some cases, none of the capture objects are associated with any analyte molecules and only a single one of the capture objects in an addressed location is associated with at least one analyte molecule.

As noted above, in some embodiments, the plurality of locations comprises a plurality of reaction vessels/wells on a substrate. The reactions vessels, in certain embodiments, may be configured to receive and contain only a single capture object used for analyte capture. The plurality of capture objects can be partitioned across a plurality of such reaction vessels (e.g., configured as an array of reaction vessels on a substrate), in some cases, to facilitate determination of a measure of the concentration of analyte molecules in a fluid sample by means discussed in further detail below and in the examples.

In some embodiments of the present invention, the plurality of reaction vessels may be sealed e.g., after the introduction of the capture objects used for analyte capture, for example, through the mating of the second substrate and a sealing component. The sealing of the reaction vessels may be such that the contents of each reaction vessel cannot escape the reaction vessel during the remainder of the assay. In some cases, the reaction vessels may be sealed after the addition of the capture objects and, optionally, a precursor labeling agent to facilitate detection of the analyte molecules. For embodiments employing precursor labeling agents, by sealing the contents in some or each reaction vessel, a reaction to produce the detectable labeling agents can proceed within the sealed reaction vessels, thereby producing a detectable amount of labeling agents that is retained in the reaction vessel for detection purposes.

The plurality of locations comprising a plurality of reaction vessels may be formed using a variety of methods and/or materials. In some cases, the plurality of reaction vessels is formed as an array of depressions on a first surface. In other cases, however, the plurality of reaction vessels may be formed by mating a sealing component comprising a plurality of depressions with a substrate that may either have a featureless surface or include depressions aligned with those on the sealing component. Any of the device components, for example, the substrate or sealing component, may be fabricated from a compliant material, e.g., an elastomeric polymer material, to aid in sealing. The surfaces may be or made to be hydrophobic or contain hydrophobic regions to minimize leakage of aqueous samples from the microwells.

In some cases, the sealing component may be capable of contacting the exterior surface of an array of microwells (e.g., the cladding of a fiber optic bundle as described in more detail below) such that each reaction vessel becomes sealed or isolated such that the contents of each reaction vessel cannot escape the reaction vessel. According to one embodiment, the sealing component may be a silicone elastomer gasket that may be placed against an array of microwells with application of substantially uniform pressure across the entire substrate. In some cases, the reaction vessels may be sealed after the addition of the plurality of capture objects used for analyte capture and, optionally, any precursor labeling agent molecule that may be used to facilitate detection of the analyte molecule.

A non-limiting example of the formation of a plurality of reaction vessels containing assay solution on/in a substrate is depicted in FIG. 6. FIG. 6, panel (A) shows a surface comprising a plurality of microwells 139, which have been exposed to an assay solution 141 (e.g., a solution containing the capture objects used for analyte capture and/or control objects obtained after performance of the analyte capture step(s) and any washing step(s)), and a sealing component 143. Sealing component 143 in this example comprises a substantially planar bottom surface. Mating of substrate 139 with sealing component 143 forms a plurality of sealed reaction vessels 145. The areas between the reaction vessels 148 may be modified to aid in the formation of a tight seal between the reaction vessels.

A second embodiment is shown in FIG. 6, panel (B), in which sealing component 162 comprising a plurality of microwells 163 is mated with a substantially planar surface 158 which has been exposed to assay solution 162, thereby forming a plurality of reaction vessels 164.

In a third embodiment, as shown in FIG. 6, panel (C), substrate surface 166 comprising a plurality of microwells 167 is mated with sealing component 170 also comprising a plurality of microwells 171. In this embodiment, the microwells in the substrate and the microwells in the sealing components are substantially aligned so each reaction vessel 172 formed comprises a portion of the microwell from the sealing component and a portion of a microwell from the substrate. In FIG. 6, panel (D), the microwells are not aligned such that each reaction vessel comprises either a microwell from the sealing component 173 or a microwell from the substrate 175.

The sealing component may be essentially the same size as the substrate or may be different in size. In some cases, the sealing component is approximately the same size as the substrate and mates with substantially the entire surface of the substrate. In other cases, as depicted in FIG. 6, panel (E), the sealing component 176 is smaller than the substrate 174 and the sealing component only mates with a portion 178 of the substrate. In yet another embodiment, as depicted in FIG. 6, panel (F), the sealing component 182 is larger than the substrate 180, and only a portion 184 of the sealing component mates with the substrate 180.

In some embodiments, the reaction vessels may all have approximately the same volume. In other embodiments, the reaction vessels may have differing volumes. The volume of each individual reaction vessel may be selected to be appropriate to facilitate any particular assay protocol. For example, in one set of embodiments where it is desirable to limit the number of capture objects used for analyte capture contained in each vessel to a small number, the volume of the reaction vessels may range from attoliters or smaller to nanoliters or larger depending upon the nature of the capture objects, the detection technique and equipment employed, the number and density of the wells on the substrate and the expected concentration of capture objects in the fluid applied to the substrate containing the wells. In one embodiment, the size of the reaction vessel may be selected such only a single capture object used for analyte capture can be fully contained within the reaction vessel. In accordance with one embodiment of the present invention, the reaction vessels may have a volume between about 1 femtoliter and about 1 picoliter, between about 1 femtoliters and about 100 femtoliters, between about 10 attoliters and about 100 picoliters, between about 1 picoliter and about 100 picoliters, between about 1 femtoliter and about 1 picoliter, or between about 30 femtoliters and about 60 femtoliters. In some cases, the reaction vessels have a volume of less than about 1 picoliter, less than about 500 femtoliters, less than about 100

femtoliters, less than about 50 femtoliters, or less than about 1 femtoliter. In some cases, the reaction vessels have a volume of about 10 femtoliters, about 20 femtoliters, about 30 femtoliters, about 40 femtoliters, about 50 femtoliters, about 60 femtoliters, about 70 femtoliters, about 80 femtoliters, about 90 femtoliters, or about 100 femtoliters.

In embodiments where the plurality of capture objects used for analyte capture comprise a plurality of beads and the plurality of locations comprise a plurality of reaction vessels having a shape that is essentially that of a circular cylinder, the size of the reaction vessels may be based upon the size of the beads and may be designed so as to ensure that the number of wells containing more than a single bead is minimal. In some cases, the maximum permissible well diameter may be calculated according to Equation 3:

$$2 * BeadRadius + \sqrt{\left(3 * BeadRadius^2 - WellDepth^2 + 2 * WellDepth * BeadRadius\right)} \quad \text{(Eq. 3)}$$

and/or the maximum permissible well depth may be calculated according to Equation 4:

$$BeadRadius + \sqrt{\left(4 * BeadRadius * WellDiameter - WellDiameter^2\right)} \quad \text{(Eq. 4)}$$

The minimum permissible well depth and the minimum permissible well diameter to assure that a single bead can be contained in the well, in most embodiments, will not be less than the average diameter of the bead. Having a properly sized reaction vessel which allows for no more than a single bead to be present in a reaction vessel may provide better ability to resolve individual beads allowing for more accuracy with regard to determining a measure of the concentration of analyte molecules in a fluid sample by the means described in more detail below and in the Examples. For example, if the reaction vessels are too large, more than one bead may be able to fit in the reaction vessel, which may lead to an increase in the number of reaction vessels containing multiple analyte molecules, which may introduce inaccuracy in a concentration determination using an algorithm/statistical model based on single molecule detection (see below). In some cases, however, it may be desirable to have more than one bead fit in a reaction vessel. On the other hand, in the reaction vessel is too small, a bead may not be able to fit in the reaction vessel, thereby preventing proper sealing of the reaction vessel (e.g., in embodiments where the reaction vessel is sealed) and/or may lead to difficulties in addressing individual locations (e.g., in embodiments where a labeling agent is produced for detection, the labeling agent may disperse away from the reaction vessel it is produced in). In such cases, there may be false positives (e.g., a reaction vessel which does not contain an analyte molecule may be determined to contain an analyte molecule based on the labeling agent which has diffused away from the location

in which it was produced) which may lead to imprecise determination of a measure of the concentration of analyte molecules in a fluid sample.

In some embodiments, the average depth of the reaction vessels is between about 1.0 and about 1.7 times, between about 1.0 times and about 1.5 times, between about 1.0 times and about 1.3 times, or between about 1.1 times and about 1.4 times the average diameter of the beads. In some embodiments, the average diameter of the reactions vessels is between about 1.0 times and about 1.9 times, between about 1.2 times and about 1.7 times, between about 1.0 times and about 1.5 times, or between about 1.3 times and about 1.6 times the average diameter of the beads. In a particular embodiment, the average depth of the reaction vessels is between about 1.0 times and about 1.5 times the average diameter of the beads and the average diameter of the reactions vessels is between about 1.0 times and about 1.9 times the average diameter of the beads.

The total number of locations and/or density of the locations employed in an assay (e.g., the number/density of reaction vessels in an array) can depend on the composition and end use of the array. For example, the number of reaction vessels employed may depend on the number of capture objects employed, the suspected concentration range of the assay, the method of detection, the size of the capture objects, the type of detection entity (e.g., free labeling agent in solution, precipitating labeling agent, etc.). Arrays containing from about 2 to many billions of reaction vessels (or total number of reaction vessels) can be made by utilizing a variety of techniques and materials. Increasing the number of reaction vessels in the array can be used to increase the dynamic range of an assay or to allow multiple samples or multiple types of analyte molecules to be assayed in parallel. The array may comprise between one thousand and one million reaction vessels per sample to be analyzed. In some cases, the array comprises greater than one million reaction vessels. In some embodiments, the array comprises between about 1,000 and about 50,000, between about 1,000 and about 1,000,000, between about 1,000 and about 10,000, between about 10,000 and about 100,000, between about 100,000 and about 1,000,000, between about 100,000 and about 500,000, between about 1,000 and about 100,000, between about 50,000 and about 100,000, between about 20,000 and about 80,000, between about 30,000 and about 70,000, between about 40,000 and about 60,000, or the like, reaction vessels. In some embodiments, the array comprises about 10,000, about 20,000, about 50,000, about 100,000, about 150,000, about 200,000, about 300,000, about 500,000, about 1,000,000, or more, reaction vessels.

The array of reaction vessels may be arranged on a substantially planar surface or in a non-planar three-dimensional arrangement. The reaction vessels may be arrayed in a regular pattern or may be randomly distributed. In a specific embodiment, the array is a regular pattern of sites on a substantially planar surface permitting the sites to be addressed in the X-Y coordinate plane.

In some embodiments, the reaction vessels are formed in a solid material. As will be appreciated by those in the art, the number of potentially suitable materials in which the reaction vessels can be formed is very large, and includes, but is not limited to, glass (including modified and/or functionalized glass), plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, cyclic olefin copolymer (COC), cyclic olefin polymer (COP), Teflon®, polysaccharides, nylon or nitrocellulose, etc.), elastomers (such as poly(dimethyl siloxane) and poly urethanes), composite materials, ceramics, silica or silica-based materials (including silicon and modified silicon), carbon, metals, optical fiber bundles, or the like. In general, the substrate material may be selected to allow for optical detection without appreciable autofluorescence. In certain embodiments, the reaction vessels may be formed in a flexible material.

A reaction vessel in a surface (e.g., substrate or sealing component) may be formed using a variety of techniques known in the art, including, but not limited to, photolithography, stamping techniques, molding techniques, etching techniques, or the like. As will be appreciated by those of the ordinary skill in the art, the technique used can depend on the composition and shape of the supporting material and the size and number of reaction vessels.

In a particular embodiment, an array of reaction vessels is formed by creating microwells on one end of a fiber optic bundle and utilizing a planar compliant surface as a sealing component. In certain such embodiments, an array of reaction vessels in the end of a fiber optic bundle may be formed as follows. First, an array of microwells is etched into the end of a polished fiber optic bundle. Techniques and materials for forming and etching a fiber optic bundle are known to those of ordinary skill in the art. For example, the diameter of the optical fibers, the presence, size and composition of core and cladding regions of the fiber, and the depth and specificity of the etch may be varied by the etching technique chosen so that microwells of the desired volume may be formed. In certain embodiments, the etching process creates microwells by preferentially etching the core material of the individual glass fibers in the bundle such

that each well is approximately aligned with a single fiber and isolated from adjacent wells by the cladding material. Potential advantages of the fiber optic array format is that it can produce thousands to millions of reaction vessels without complicated microfabrication procedures and that it can provide the ability to observe and optically address many reaction vessels simultaneously.

Each microwell may be aligned with an optical fiber in the bundle so that the fiber optic bundle can carry both excitation and emission light to and from the wells, enabling remote interrogation of the well contents. Further, an array of optical fibers may provide the capability for simultaneous or non-simultaneous excitation of molecules in adjacent vessels, without signal "cross-talk" between fibers. That is, excitation light transmitted in one fiber does not escape to a neighboring fiber.

Alternatively, the equivalent structures of a plurality of reaction vessels may be fabricated using other methods and materials that do not utilize the ends of an optical fiber bundle as a substrate. For example, the array may be a spotted, printed or photolithographically fabricated substrate produced by techniques known in the art; see for example WO95/25116; WO95/35505; PCT US98/09163; U.S. Patent Nos. 5,700,637, 5,807,522, 5,445,934, 6,406,845, and 6,482,593. In some cases, the array may be produced using molding, embossing, and/or etching techniques as will be known to those of ordinary skill in the art.

In certain embodiments, the present invention provides a system equipped with a mechanical platform that applies a sealing component to a substrate. The platform may be positioned beneath a stage on the system. After the chosen reaction components have been added to an array of reaction vessels, the sealing component may be mated with the array. For example, the sealing component may be sandwiched between a flat surface (such as, for example, a microscope slide) and the array of reaction vessels using uniform pressure applied by the mechanical platform.

A non-limiting embodiment is illustrated in FIG. 7. A sealing component 300 is placed on top of mechanical platform 302. The assay solution 304 is placed on top of the sealing component 300. The mechanical platform is moved upwards towards the array 306 (e.g., fiber optic array) such that uniform pressure is applied. As shown in FIG. 8, the sealing component 300 forms a tight seal with the array 306. In other instances, varying pressure may be applied to the sealing component to form a tight seal between the sealing component and the array. The system may also comprise additional

components 312 that may be utilized to analyze the array (e.g., microscope, computer, etc.) as discussed more herein.

The plurality of capture objects used for analyte capture may be spatially separated into the plurality of reaction vessels using any of a wide variety of techniques known to those of ordinary skill in the art. In some cases, the plurality of reaction vessels may be exposed to a solution containing the plurality of capture objects. In some cases, force may be applied to the solution and/or capture objects, thereby aiding in the spatial separation of the capture objects from the fluid phase and/or the deposition of the capture objects in the vessels. For example, after application of an assay solution containing the capture objects to a substrate containing the reaction vessels, the substrate and solution may be centrifuged to assist in depositing the capture objects in the reaction vessels. In embodiments where the capture objects (e.g., beads) are magnetic, a magnet may be used to aid in containing the capture objects in the reaction vessels. In some cases, when the plurality of reaction vessels is formed on the end of a fiber optic bundle (or another planar surface), a material (e.g., tubing) may be placed around the edges of the surface of the array comprising the plurality of reaction vessel to form a container to hold the solution in place while the capture objects settle in the reaction vessels or are placed into the reaction vessels (e.g., while centrifuging). Following placement of the capture objects into at least some of the reaction vessels, the surrounding material may be removed and the surface of the array may be washed and/or swabbed to remove any excess solution/capture objects.

In some embodiments, the substrate does not include wells or reaction vessels forming the plurality of reaction vessels but uses/provides other means to spatially segregate the plurality of capture objects used for analyte capture. In some cases, a patterned substantially planar surface may be employed, wherein the patterned areas form a plurality of locations. In some cases, the patterned areas may comprise substantially hydrophilic surfaces which are substantially surrounded by substantially hydrophobic surfaces. A plurality of capture objects (e.g., beads) may be substantially surround by a substantially hydrophilic medium (e.g., comprising water), and the beads may be exposed to the pattern surface such that the beads associate in the patterned areas (e.g., the locations), thereby spatially segregating the plurality of beads. For example, in one such embodiment, a substrate may be or include a gel or other material able to provide a sufficient barrier to mass transport (e.g., convective and/or diffusional barrier) to prevent capture objects used for analyte capture and/or precursor labeling agent and/or

labeling agent from moving from one location on or in the material to another location so as to cause interference or cross-talk between spatial locations containing different capture objects during the time frame required to address the locations and complete the assay. For example, in one embodiment, a plurality of capture objects is spatially separated by dispersing the capture objects on and/or in a hydrogel material. In some cases, a precursor labeling agent may be already present in the hydrogel, thereby facilitating development of a local concentration of the labeling agent (e.g., upon exposure to a binding ligand or analyte molecule carrying an enzymatic component). As still yet another embodiment, the capture objects may be confined in one or more capillaries. In some cases, the plurality of capture objects may be absorbed or localized on a porous or fibrous substrate, for example, filter paper. In some embodiments, the capture objects may be spatially segregated on a uniform surface (e.g., a planar surface), and the capture objects may be detected using precursor labeling agents which are converted to substantially insoluble or precipitating labeling agents that remain localized at or near the location of where the corresponding capture object is localized. The use of such substantially insoluble or precipitating labeling agents is described herein.

Articles and Kits

In some embodiments of the present invention, an article or kit for determining a measure of the concentration of analyte molecules or particles in a fluid sample is provided. The article or kit may comprise a plurality of beads and a substrate comprising a plurality of reaction vessels. The reaction vessels may be configured to receive and contain the capture objects. The plurality of beads in certain embodiment have an average diameter between about 0.1 micrometer and about 100 micrometers and the size of the reaction vessels may be selected such that only either zero or one beads is able to be contained in single reaction vessels. In some cases, the average depth of the reaction vessels is between about 1.0 times and about 1.5 times the average diameter of the beads and the average diameter of the reactions vessels is between about 1.0 times and about 1.9 times the average diameter of the beads. In certain embodiments, the beads may have an average diameter between about between about 1 micrometer and about 10 micrometers, between about 1 micrometer and about 5 micrometers, or any range of sizes described herein.

The plurality of beads provided may have a variety of properties and parameters, as described herein. For example, the beads may be magnetic. The plurality of beads

may comprise a binding surface (e.g., a plurality of capture components) having an affinity for at least one type of analyte molecule or particle.

The plurality of reaction vessels may be formed in any suitable substrate, as described herein. In a particular embodiment, the plurality of reaction vessels is formed on the end of a fiber optic bundle. The fiber optic bundle may be prepared (e.g., etched) according to methods known to those of ordinary skill in the art and/or methods described herein. In other embodiments, the plurality of reactions vessels is formed in a plate or similar substantially planar material (e.g., using lithography or other known techniques). Exemplary suitable materials are described herein.

The average depth of the plurality of reaction vessels may be between about 1.0 and about 1.5 times, or between about 1.1 and about 1.3 times the average diameter of the beads, or any range described herein. The average diameter of the plurality of reaction vessels may be between about 1.0 times and about 1.9 times, or between about 1.3 times and about 1.8 times the average diameter of the beads, or any range described herein. The average depth and/or the average diameter of the plurality of reaction vessels may be chosen such that no more than one bead is able to be contained in a reaction vessels. Methods for calculating maximum depths and maximum diameters to facilitate single bead loading are described herein. The average volume of the plurality of reaction vessels may be between about 10 attoliters and about 100 picoliters, between about 1 femtoliter and about 1 picoliter, or any desired range. The substrate may comprise any number of reaction vessels, for example, between about 1,000 and about 1,000,000 reaction vessels, between about 10,000 and about 100,000 reaction vessels, or between about 100,000 and about 300,000 reaction vessels, or any other desired range.

The article or kit may comprise any number of additional components, some of which are described in detail herein. In some cases, the article or kit may further comprise a sealing component configured for sealing the plurality of reaction vessels. In certain embodiments, the plurality of reaction vessels may be formed upon the mating of at least a portion of a sealing component and at least a portion of the second substrate, as shown in FIGS. 7A-7F and as discussed in more detail herein. As another example, the kit may also provide solutions for carrying out an assay method as described herein. Non-limiting example of solutions include solutions containing one or more types of binding ligands and precursor labeling agents. In some cases, the article or kit may comprise at least one type of control bead.

In some embodiments, the kit may optionally include instructions for use of the plurality of beads and the plurality or reaction vessels (and any additional components provided). That is, the kit can include a description of use of the beads and reaction vessels, for example, for use with a system to determine a measure of the concentration of analyte molecules (or particles) in a fluid sample. As used herein, "instructions" can define a component of instruction and/or promotion, and typically involve written instructions on or associated with packaging of the invention. Instructions also can include any oral or electronic instructions provided in any manner such that a user of the kit will clearly recognize that the instructions are to be associated with the kit. Additionally, the kit may include other components depending on the specific application, as described herein. As used herein, "promoted" includes all methods of doing business including methods of education, hospital and other clinical instruction, scientific inquiry, drug discovery or development, academic research, pharmaceutical industry activity including pharmaceutical sales, and any advertising or other promotional activity including written, oral and electronic communication of any form, associated with the invention.

Capture Components

In some embodiments of the present invention, the surface of the capture objects may provide a binding surface having an affinity for at least one type of analyte molecule or particle. In some embodiments, the binding surface may comprise at least one type of capture component. Generally, the capture component allows the attachment of a molecule, particle, or complex to a solid support (that is, a surface of a capture object) for the purposes of immobilization, detection, quantification, and/or other analysis of the molecule, particle, or complex. A capture component is used in the present invention, in some cases, to immobilize an analyte molecule with respect to a capture object (e.g., a bead).

As will be appreciated by those in the art, the composition of the capture component will depend on the composition of the analyte molecule. Capture components for a wide variety of target molecules are known or can be readily found or developed using known techniques. For example, when the target molecule is a protein, the capture components may comprise proteins, particularly antibodies or fragments thereof (e.g., antigen-binding fragments (Fabs), Fab' fragments, pepsin fragments, $F(ab')_2$ fragments, full-length polyclonal or monoclonal antibodies, antibody-like fragments,

etc.), other proteins, such as receptor proteins, Protein A, Protein C, etc., or small molecules. In some cases, capture components for proteins comprise peptides. For example, when the target molecule is an enzyme, suitable capture components may include enzyme substrates and/or enzyme inhibitors. In some cases, when the target analyte is a phosphorylated species, the capture component may comprise a phosphate-binding agent. For example, the phosphate-binding agent may comprise metal-ion affinity media such as those describe in U.S. Patent No. 7,070,921 and U.S. Patent Application No. 20060121544. In addition, when the target molecule is a single-stranded nucleic acid, the capture component may be a complementary nucleic acid. Similarly, the target molecule may be a nucleic acid binding protein and the capture component may be a single-stranded or double-stranded nucleic acid; alternatively, the capture component may be a nucleic acid-binding protein when the target molecule is a single or double stranded nucleic acid. Alternatively, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, nucleic acid "aptamers" may be developed for capturing virtually any target molecule. Also, for example, when the target molecule is a carbohydrate, potentially suitable capture components include, for example, antibodies, lectins, and selectins. As will be appreciated by those of ordinary skill in the art, any molecule that can specifically associate with a target molecule of interest may potentially be used as a capture component.

For certain embodiments, suitable target analyte molecule/capture component pairs can include, but are not limited to, antibodies/antigens, receptors/ligands, proteins/nucleic acid, nucleic acids/nucleic acids, enzymes/substrates and/or inhibitors, carbohydrates (including glycoproteins and glycolipids)/lectins and/or selectins, proteins/proteins, proteins/small molecules; small molecules/small molecules, etc. According to one embodiment, the capture components are portions (particularly the extracellular portions) of cell surface receptors that are known to multimerize, such as the growth hormone receptor, glucose transporters (particularly GLUT 4 receptor), and T-cell receptors and the target analyte molecules are one or more receptor target ligands.

In a particular embodiment, the capture component may be attached to the surface of a capture object via a linkage, which may comprise any moiety, functionalization, or modification of the binding surface and/or capture component that facilitates the attachment of the capture component to the surface. The linkage between the capture component and the surface may comprise one or more chemical or physical

(e.g., non-specific attachment via van der Waals forces, hydrogen bonding, electrostatic interactions, hydrophobic/hydrophilic interactions; etc.) bonds and/or chemical linkers providing such bond(s). In certain embodiments, the capture component comprises a capture extender component. In such embodiments, the capture component comprises a first portion that binds the analyte molecule and a second portion that can be used for attachment to the binding surface.

In certain embodiments, a capture object surface may also comprise a protective or passivating layer that can reduce or minimize non-specific attachment of non-capture components (e.g., analyte molecules, binding ligands) to the binding surface during the assay which may lead to false positive signals during detection or to loss of signal. Examples of materials that may be utilized in certain embodiments to form passivating layers include, but are not limited to: polymers, such as poly(ethylene glycol), that repel the non-specific binding of proteins; naturally occurring proteins with this property, such as serum albumin and casein; surfactants, e.g., zwitterionic surfactants, such as sulfobetaines; naturally occurring long-chain lipids; and nucleic acids, such as salmon sperm DNA.

The method of attachment of the capture component to a capture object surface depends of the type of linkage employed and may potentially be accomplished by a wide variety of suitable coupling chemistries/techniques known to those of ordinary skill in the art. The particular means of attachment selected will depend on the material characteristics of the capture object surface and the nature of the capture component. In certain embodiments, the capture components may be attached to the capture object surface through the use of reactive functional groups on each. According to one embodiment, the functional groups are chemical functionalities. That is, the binding surface may be derivatized such that a chemical functionality is presented at the binding surface which can react with a chemical functionality on the capture component resulting in attachment. Examples of functional groups for attachment that may be useful include, but are not limited to, amino groups, carboxy groups, epoxide groups, maleimide groups, oxo groups, and thiol groups. Functional groups can be attached, either directly or through the use of a linker, the combination of which is sometimes referred to herein as a "crosslinker." Crosslinkers are known in the art; for example, homo-or hetero-bifunctional crosslinkers as are well known (e.g., see 1994 Pierce Chemical Company catalog, technical section on crosslinkers, pages 155-200, or "Bioconjugate Techniques" by Greg T. Hermanson, Academic Press, 1996). Non-limiting example of crosslinkers

include alkyl groups (including substituted alkyl groups and alkyl groups containing heteroatom moieties), esters, amide, amine, epoxy groups and ethylene glycol and derivatives. A crosslinker may also comprise a sulfone group, forming a sulfonamide.

According to one embodiment, the functional group is a light-activated functional group. That is, the functional group can be activated by light to attach the capture component to the capture object surface. One example is PhotoLink™ technology available from SurModics, Inc. in Eden Prairie, MN.

In some cases, the capture object may comprise streptavidin-coated surfaces and the capture component may be biotinylated. Exposure of the capture component to the streptavidin-coated surfaces can cause association of the capture component with the surface by interaction between the biotin component and streptavidin.

In certain embodiments, attachment of the capture component to the binding surface may be effected without covalently modifying the binding surface of a capture object. For example, the attachment functionality can be added to the binding surface by using a linker that has both a functional group reactive with the capture component and a group that has binding affinity for the binding surface. In certain embodiments, a linker comprises a protein capable of binding or sticking to the binding surface; for example, in one such embodiment, the linker is serum albumin with free amine groups on its surface. A second linker (crosslinker) can then be added to attach the amine groups of the albumin to the capture component (e.g., to carboxy groups).

According to one embodiment in which a chemical crosslinker is used to attach the capture components to the capture object, the analyte molecule may be captured on the binding surface of a capture object using a capture component attached via chemical crosslinking in the following manner. First, the binding surface is derivatized with a functional group, such as, an amine group. Next, a crosslinker and the capture component are placed in contact with the binding surface such that one end of the crosslinker attaches to the amine group and the capture component attaches to the other end of the crosslinker. In this way, capture components comprising proteins, lectins, nucleic acids, small organic molecules, carbohydrates can be attached.

One embodiment utilizes proteinaceous capture components. As is known in the art, any number of techniques may be used to attach a proteinaceous capture component to a wide variety of solid surfaces. "Protein" or "proteinaceous" in this context includes proteins, polypeptides, peptides, including, for example, enzymes, and antibodies. A wide variety of techniques are known to add reactive moieties to proteins, for example,

the method outlined in U.S. Patent No. 5,620,850. The attachment of proteins to surfaces is known, for example, see Heller, Acc. Chem. Res. 23:128 (1990), and many other similar references.

In some embodiments, the capture component (or binding ligand) may comprise Fab' fragments. The use of Fab' fragments as opposed to whole antibodies may help reduce non-specific binding between the capture component and the binding ligand. In some cases, the Fc region of a capture component (or binding ligand) may be removed (e.g., proteolytically). In some cases, an enzyme may be used to remove the Fc region (e.g., pepsin, which may produce $F(ab')_2$ fragments and papain, which may produce Fab fragments). In some instances, the capture component may be attached to a binding surface using amines or may be modified with biotin (e.g., using NHS-biotin) to facilitate binding to an avidin or streptavidin coated capture object surface. $F(ab')_2$ fragments may be subjected to a chemical reduction treatment (e.g., by exposure to 2-mercaptoethylamine) to, in some cases, form two thiol-bearing Fab' fragments. These thiol-bearing fragments can then be attached via reaction with a Michael acceptor such as maleimide. For example, the Fab' fragments may then be treated with a reagent (e.g., maleimide-biotin) to attach at least one biotin moiety (i.e., biotinylated) to facilitate attachment to streptavidin-coated surfaces as described above.

Certain embodiments utilize nucleic acids as the capture component, for example for when the analyte molecule is a nucleic acid or a nucleic acid binding protein, or when the it is desired that the capture component serve as an aptamer for binding a protein, as is well known in the art.

According to one embodiment, each binding surface of a capture object comprises a plurality of capture components. The plurality of capture components, in some cases, may be distributed randomly on the binding surface like a "lawn." Alternatively, the capture components may be spatially segregated into distinct region(s) and distributed in any desired fashion.

Binding between the capture component and the analyte molecule, in certain embodiments, is specific, e.g., as when the capture component and the analyte molecule are complementary parts of a binding pair. In certain such embodiments, the capture component binds both specifically and directly to the analyte molecule. By "specifically bind" or "binding specificity," it is meant that the capture component binds the analyte molecule with specificity sufficient to differentiate between the analyte molecule and other components or contaminants of the test sample. For example, the capture

component, according to one embodiment, may be an antibody that binds specifically to some portion of an analyte molecule (e.g., an antigen). The antibody, according to one embodiment, can be any antibody capable of binding specifically to an analyte molecule of interest. For example, appropriate antibodies include, but are not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to as antibody mimetics), chimeric antibodies, humanized antibodies, antibody fusions (sometimes referred to as "antibody conjugates"), and fragments of each, respectively. As another example, the analyte molecule may be an antibody and the capture component may be an antigen.

According to one embodiment in which an analyte particle is a biological cell (e.g., mammalian, avian, reptilian, other vertebrate, insect, yeast, bacterial, cell, etc.), the capture component may be a ligand having specific affinity for a cell surface antigen (e.g., a cell surface receptor). In one embodiment, the capture component is an adhesion molecule receptor or portion thereof, which has binding specificity for a cell adhesion molecule expressed on the surface of a target cell type. In use, the adhesion molecule receptor binds with an adhesion molecule on the extracellular surface of the target cell, thereby immobilizing or capturing the cell. In one embodiment in which the analyte particle is a cell, the capture component is fibronectin, which has specificity for, for example, analyte particles comprising neural cells.

In some embodiments, as will be appreciated by those of ordinary skill in the art, it is possible to detect analyte molecules using capture components for which binding to analyte molecules is not highly specific. For example, such systems/methods may use different capture components such as, for example, a panel of different binding ligands, and detection of any particular analyte molecule is determined via a "signature" of binding to this panel of binding ligands, similar to the manner in which "electronic noses" work. This may find particular utility in the detection of certain small molecule analytes. In some embodiments, the binding affinity between analyte molecules and capture components should be sufficient to remain bound under the conditions of the assay, including wash steps to remove molecules or particles that are non-specifically bound. In some cases, for example in the detection of certain biomolecules, the binding constant of the analyte molecule to its complementary capture component may be between at least about 10^4 and about 10^6 M^{-1}, at least about 10^5 and about 10^9 M^{-1}, at least about 10^7 and about 10^9 M^{-1}, greater than about 10^9 M^{-1}, or the like. For example,

typical affinities for IgG antibodies for their antigens are in the range 10^5-10^{10} M^{-1}. The affinity of biotin for streptavidin is 10^{15} M^{-1}.

In certain embodiments, the capture component is chosen to be able to bind to a corresponding binding partner associated with or attached to the analyte molecule. For example, the capture component according to one embodiment is a chemical crosslinker as described above able to bind to proteins generally. According to one embodiment, every protein molecule in a fluid sample comprises an analyte molecule that attaches to such a chemical crosslinker. In another example, the capture component comprises streptavidin, which binds with high affinity to biotin, and thus captures any analyte molecules to which biotin has been attached. Alternatively, the capture component may be biotin, and streptavidin may be attached to or associated with the analyte molecules such that the analyte molecules can be captured by the biotin.

According to one embodiment, the binding surfaces of a capture object may be functionalized with capture components in the following manner. First, the surface of a capture object is prepared for attachment of the capture component(s) by being modified to form or directly bind to the capture components, or a linker may be added to the binding surface of the capture object such that the capture component(s) attaches to the binding surface of the capture object via the linker. In one embodiment, the binding surfaces of the capture object are derivatized with a chemical functionality as described above. Next, the capture component may be added, which binds to and is immobilized by the chemical functionality.

Exemplary Target Analytes

As will be appreciated by those in the art, a large number of analyte molecules and particles may be detected and, optionally, quantified using methods and systems of the present invention; basically, any analyte molecule that is able to be made to become immobilized with respect to a capture object (e.g., via a binding surface comprising a plurality of capture components) can be potentially investigated using the invention. Certain more specific targets of potential interest that may comprise an analyte molecule are mentioned below. The list below is exemplary and non-limiting.

In some embodiments, the analyte molecule may be an enzyme. Non-limiting examples of enzymes include, an oxidoreductase, transferase, kinase, hydrolase, lyase, isomerase, ligase, and the like. Additional examples of enzymes include, but are not limited to, polymerases, cathepsins, calpains, amino-transferases such as, for example,

AST and ALT, proteases such as, for example, caspases, nucleotide cyclases, transferases, lipases, enzymes associated with heart attacks, and the like. When a system/method of the present invention is used to detect the presence of viral or bacterial agents, appropriate target enzymes include viral or bacterial polymerases and other such enzymes, including viral or bacterial proteases, or the like.

In other embodiments, the analyte molecule may comprise an enzymatic component. For example, the analyte particle can be a cell having an enzyme or enzymatic component present on its extracellular surface. Alternatively, the analyte particle is a cell having no enzymatic component on its surface. Such a cell is typically identified using an indirect assaying method described below. Non-limiting example of enzymatic components are horseradish peroxidase, beta-galactosidase, and alkaline phosphatase.

In yet other embodiments, the analyte molecule may be a biomolecule. Non-limiting examples of biomolecules include hormones, antibodies, cytokines, proteins, nucleic acids, lipids, carbohydrates, lipids cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, or combinations thereof. Non-limiting embodiments of proteins include peptides, polypeptides, protein fragments, protein complexes, fusion proteins, recombinant proteins, phosphoproteins, glycoproteins, lipoproteins, or the like. As will be appreciated by those in the art, there are a large number of possible proteinaceous analyte molecules that may be detected or evaluated for binding partners using the present invention. In addition to enzymes as discussed above, suitable protein analyte molecules include, but are not limited to, immunoglobulins, hormones, growth factors, cytokines (many of which serve as ligands for cellular receptors), cancer markers, etc. Non-limiting examples of biomolecules include PSA and TNF-alpha.

In certain embodiments, the analyte molecule may be a host-translationally modified protein (e.g., phosphorylation, methylation, glycosylation) and the capture component may be an antibody specific to a post-translational modification. Modified proteins may be captured with capture components comprising a multiplicity of specific antibodies and then the captured proteins may be further bound to a binding ligand comprising a secondary antibody with specificity to a post-translational modification. Alternatively, modified proteins may be captured with capture components comprising an antibody specific for a post-translational modification and then the captured proteins

may be further bound to binding ligands comprising antibodies specific to each modified protein.

In another embodiment, the analyte molecule is a nucleic acid. A nucleic acid may be captured with a complementary nucleic acid fragment (e.g., an oligonucleotide) and then optionally subsequently labeled with a binding ligand comprising a different complementary oligonucleotide.

Suitable analyte molecules and particles include, but are not limited to small molecules (including organic compounds and inorganic compounds), environmental pollutants (including pesticides, insecticides, toxins, etc.), therapeutic molecules (including therapeutic and abused drugs, antibiotics, etc.), biomolecules (including hormones, cytokines, proteins, nucleic acids, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc), whole cells (including prokaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells), viruses (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.), spores, etc.

The fluid sample containing or suspected of containing an analyte molecule may be derived from any suitable source. In some cases, the sample may comprise a liquid, fluent particulate solid, fluid suspension of solid particles, supercritical fluid, and/or gas. In some cases, the analyte molecule may be separated or purified from its source prior to determination; however, in certain embodiments, an untreated sample containing the analyte molecule may be tested directly. The source of the analyte molecule may be synthetic (e.g., produced in a laboratory), the environment (e.g., air, soil, etc.), a mammal, an animal, a plant, or any combination thereof. In a particular example, the source of an analyte molecule is a human bodily substance (e.g., blood, serum, plasma, urine, saliva, tissue, organ, or the like). The volume of the fluid sample analyzed may potentially be any amount within a wide range of volumes, depending on a number of factors such as, for example, the number of capture objects used/available, the number of locations us/available, etc. In a few particular exemplary embodiments, the sample volume may be about 0.01 ul, about 0.1 uL, about 1 uL, about 5 uL, about 10 uL, about 100 uL, about 1 mL, about 5 mL, about 10 mL, or the like. In some cases, the volume of the fluid sample is between about 0.01 uL and about 10 mL, between about 0.01 uL and about 1 mL, between about 0.01 uL and about 100 uL, or between about 0.1 uL and about 10 uL.

In some cases, the fluid sample may be diluted prior to use in an assay. For example, in embodiments where the source of an analyte molecule is a human body fluid (e.g., blood, serum), the fluid may be diluted with an appropriate solvent (e.g., a buffer such as PBS buffer). A fluid sample may be diluted about 1-fold, about 2-fold, about 3-fold, about 4-fold, about 5-fold, about 6-fold, about 10-fold, or greater, prior to use. The sample may be added to a solution comprising the plurality of capture objects, or the plurality of capture objects may be added directly to or as a solution to the sample.

Binding Ligands and Precursor Labeling Agents/Labeling Agent

Binding ligands may be selected from any suitable molecule, particle, or the like, as discussed more below, able to associate with an analyte molecule and/or to associate with another binding ligand. Certain binding ligands can comprise an entity that is able to facilitate detection, either directly (e.g., via a detectable moiety) or indirectly. A component may facilitate indirect detection, for example, by converting a precursor labeling agent molecule into a labeling agent molecule (e.g., an agent that is detected in an assay). In some embodiments, the binding ligand may comprise an enzymatic component (e.g., horseradish peroxidase, beta-galactosidase, alkaline phosphatase, etc). A first type of binding ligand may or may not be used in conjunction with additional binding ligands (e.g., second type, etc.), as discussed herein.

In some embodiments, the plurality of capture objects, at least some of which comprise at least one analyte molecule, may be exposed to a plurality of binding ligands such that a binding ligand associates with at least some of the plurality of analyte molecules. In embodiments where a statistically significant fraction of the capture objects are associated with a single analyte molecule and a statistically significant fraction of the capture objects are not associated with any analyte molecules (e.g., where the number of analyte molecules is less than the total number of capture objects), a binding ligand may associate with substantially all of the analyte molecules immobilized with respect to a capture object. In some cases, greater than about 80%, greater than about 85%, greater than about 90%, greater than about 95%, greater than about 97%, greater than about 98%, greater than about 99%, or more, analyte molecules may become associated with a binding ligand.

In other embodiments where substantially all of the capture objects comprise at least one analyte molecule (e.g., in embodiments where the number of analyte molecules is about equal to or greater than the number of capture objects provided), the capture

objects may be exposed to the binding ligand such that a statistically significant fraction of the capture objects associate with at least one binding ligand (or in certain embodiments substantially only a single binding ligand) and a statistically significant fraction of the capture objects do not associate with any binding ligand. In some cases, the capture objects may be exposed to the binding ligands such that at least some of the capture objects associate with at least one binding ligand and a statistically significant fraction of the capture objects do not associate with any binding ligand. A screening test to determine an appropriate amount of binding ligand to use for a desired degree of binding ligand loading (e.g. to facilitate selection of an appropriate quantity of binding ligand to use for a particular situation) may be performed with calibration standards containing a known concentration of analyte molecule and varying quantities of binding ligand using a Poisson analysis. In certain embodiments, it is determined whether the analyte is essentially fully labeled or only partially labeled with binding ligand. The percentage active analyte molecules (i.e. those associated with binding ligand) detected can be converted to the percentage analyte molecules associated with zero, one, two etc. binding ligands using Poisson distribution adjustment as described elsewhere herein.

In some embodiments, more than one type of binding ligand may be used. In some embodiments, a first type of binding ligand and a second type of binding ligand may be provided. In some instances, at least two, at least three, at least four, at least five, at least eight, at least ten, or more, types of binding ligands may be provided. When a plurality of capture objects, some of which are associated with at least one analyte molecule, are exposed to a plurality of types of binding ligand, at least some of the plurality of immobilized analyte molecules may associate with at least one of each type of binding ligand. The binding ligands may be selected such that they interact with each other in a variety of different manners. In a first example, the first type of binding ligand may be able to associate with an analyte molecule and the second type of binding ligand may be able to associate with the first type of binding ligand. In such embodiments, the first type of binding ligand may comprise a first component which aids in association of the analyte molecule and a second component which aids in association of the second type of binding ligand with the first type of binding ligand. In a particular embodiment, the second component is biotin and the second type of binding ligand comprises an enzyme or an enzymatic component which associates with the biotin.

As another example, both the first type of binding ligand and the second type of binding ligand may associate directly with an analyte molecule. Without being bound by

theory or any particular mechanism, the association of both the first type and the second type of binding ligand may provide additional specificity and reliability in performing an assay, by identifying only locations which are determined to contain both the first type of binding ligand and/or the second type of binding ligand (e.g., either through direct or indirect detection) as containing an analyte molecule. Such assay methods may reduce the number of false positives caused by non-specific binding as locations that are found to only have a single type of binding ligand (e.g., only the first type of labeling agent or the second type of labeling agent) would be not be considered or counted as a location comprising an analyte molecule. The first type of binding ligand may comprise a first type of enzymatic component and the second type of binding ligand may comprise a second type of enzymatic component which differs from the first type of enzymatic component. A capture object comprising an analyte molecule, the first type of binding ligand, and the second type of binding ligand may be exposed to a first type of precursor labeling agent which is converted to a first type of labeling agent (e.g., comprising a first measurable property) upon exposure to the first type of enzymatic component and a second type of precursor labeling agent which is converted to a second type of labeling agent (e.g., comprising a measurable property which is distinguishable from the first measurable property) upon exposure to the second type of enzymatic component. Therefore, only locations which are determined to contain the first type of labeling agent and the second type of labeling agent are determined to contain an analyte molecule. As another example, the first type of binding ligand and the second type of binding ligand may each incorporate a component (e.g., such as a DNA label) and a third type of binding ligand may comprise two components complimentary to the components of the first type and second type of binding ligands (e.g., two types of complimentary DNA labels), wherein the third type of binding ligand also comprises an molecule or moiety for direct or indirect detection (e.g., the presence of the third type of binding ligand in a reaction vessel is required to determine the presence or absence of an analyte molecule in a location). When both the first type of binding ligands and the second types of binding ligands are present in substantially close proximity to each other (e.g., via association with an analyte molecule) association of the third type of binding ligand may occur, thus allowing detection of the analyte molecule. More information regarding the use of more than one type of binding ligand in a manner which may reduce certain negative affects associated with non-specific binding, are described in commonly owned U.S. Patent Application Serial No. 12/731,135, entitled "Ultra-Sensitive Detection of Molecules

using Dual Detection Methods" by Duffy et al., filed March 24, 2010, and International Patent Application No. (not yet determined), entitled "Ultra-Sensitive Detection of Molecules using Dual Detection Methods" by Duffy et al., filed March 1, 2011 (Attorney Docket No. Q0052.70012WO00), herein incorporated by reference.

Detection

The plurality of capture objects, some of which comprise at least one analyte molecule and/or at least one binding ligand can be detected and/or quantified, and the detection and/or quantification can be related to the presence and, optionally, the quantity and/or concentration of analyte molecules/particles in the sample being tested. In some embodiments, the plurality of capture objects may be detected and/or quantified by spatially segregating the plurality of capture objects into a plurality of locations. In some embodiments, the plurality of locations comprises a plurality of reaction vessels (e.g., in an array). In some cases, a detector may be configured to detect the capture objects in or at a plurality of locations (e.g., an array of reaction vessels). In some embodiments, the capture objects may be able to produce or be made to produce a detectable signal, for example, fluorescence emission, which may aid in the detection of the capture objects. In some cases, the capture objects may be detected using scattering techniques, as described herein.

In some embodiments, the number of capture objects spatially segregated may be substantially equal to the number of capture objects exposed to a fluid sample containing or suspected of containing analyte molecules. In some embodiments, however, the number of capture objects spatially segregated into a plurality of locations may be substantially less than the number of capture objects exposed to a fluid sample containing or suspected of containing analyte molecules. In some cases, about 1%, about 2%, about 3%, about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, or more, of the capture objects exposed to a fluid sample are spatially segregated into a plurality of locations. In some instances, between about 1% and about 99%, between about 10% and about 90%, between about 20% and about 80%, between about 30% and about 70%, between about 50% and about 90%, between about 1% and about 50%, between about 5% and about 40%, or between about 10% and about 30% of the capture objects exposed to a fluid sample are spatially segregated into a plurality of locations.

The analyte molecules (or binding ligands) which are spatially segregated may be detected and/or quantified directly or indirectly. In the case of direct detection, the analyte molecules may comprise a molecule or moiety that may be directly interrogated and/or detected, for example, a fluorescent entity (e.g., a fluorescent moiety, fluorescent bead, fluorescent antibody, etc.), a metal nanoparticle or nanocluster (e.g., a gold nanocluster or nanoparticle, silver nanocluster or nanoparticle), a quantum dot (e.g., CdSe quantum dot, CdTe quantum dot, etc.), and radioactive isotopes. In embodiments where the assay comprises the use of one or more types of binding ligands, the binding ligands may comprise a molecule(s) or moiety(ies) that may be directly interrogated and/or detected. A location that comprises such an analyte molecule or binding ligand which comprises a moiety that may be directly interrogated and/or detected can be made to emit a signal upon interrogation of the location.

In some embodiments, non-enzymatic detection methods may be employed. Non-enzymatic detection methods will be known to those of ordinary skill in the art. Non-limiting examples include Raman scattering, electromagnetic radiation resonance methods (e.g., whispering gallery modes), spectroscopy (e.g., infrared, atomic spectroscopies), absorbance, piezoelectric transduction (e.g., quartz crystal microbalance (QCM)), circular dichroism, electron microscopies (e.g., scanning electron microscopy (SEM), x-ray photoelectron microscopy (XPS)), scanning probe microscopies (e.g., atomic force microscopy (AFM), scanning tunneling microscopy (STM)), light scattering; surface plasmon resonance (SPR), evanescent wave detection, optical interferometry and other methods based on measuring changes in refractive index, electrical transduction methods, such as conduction and capacitance; magnetic transduction effects (e.g., magnetoresistive effect), calorimetry (e.g., differential scanning calorimetry (DSC)), diffraction; nuclear magnetic resonance (NMR), electron paramagnetic resonance (EPR), mass spectroscopy (e.g., matrix assisted laser desorption and ionization (MALDI)), fluorescence technologies (e.g., fluorescence resonance energy transfer (FRET), time-resolved fluorescence (TRF), fluorescence polarization (FP)), and luminescent oxygen channeling (LOCI).

In some embodiments, the plurality of analyte molecules (or binding ligands) are indirectly detected. The indirect approach can include, for example, exposing an analyte molecule, or a binding ligand associated with an analyte molecule, to a precursor labeling agent, wherein the precursor labeling agent is converted into a labeling agent upon exposure to the analyte molecule or the binding ligand associated with an analyte

molecule. The labeling agent may comprise a molecule or moiety that can be interrogated and/or detected. The presence or absence of an analyte molecule or binding ligand at a location may then be determined by determining the presence or absence of a labeling agent at/in the location. For example, the analyte molecule may comprise an enzymatic component and the precursor labeling agent molecule may be a chromogenic, fluorogenic, or chemiluminescent enzymatic precursor labeling agent molecule which is converted to a chromogenic, fluorogenic, or chemiluminescent product (each an example of a labeling agent) upon exposure to the converting agent. In this instance, the precursor labeling agent may be an enzymatic label, for example, a chromogenic, fluorogenic, or chemiluminescent enzymatic precursor labeling agent, that upon contact with the enzymatic component, is converted into a labeling agent, which is detectable. In some cases, the chromogenic, fluorogenic, or chemiluminescent enzymatic precursor labeling agent is provided in an amount sufficient to contact every location. In some embodiments, an electrochemiluminescent precursor labeling agent is converted to an electrochemiluminescent labeling agent. In some cases, the enzymatic component may comprise beta-galactosidase, horseradish peroxidase, or alkaline phosphatase.

As will be understood by those of ordinary skill in the art, a variety of appropriate chromogenic, fluorogenic, or chemiluminescent enzymatic precursor labeling agents may be selected for conversion by many different enzymes. Thus, any known chromogenic, fluorogenic, or chemiluminescent enzyme precursor labeling agent capable of producing a labeling agent in a reaction with a particular enzyme can potentially be used in the present invention as the precursor labeling agent in embodiments where the analyte molecule or a binding ligand associated with an analyte molecule comprises an enzymatic component. For example, many chromogenic, fluorogenic, or chemiluminescent precursor labeling agent suitable for use an enzymatic precursor labeling agent molecule are disclosed in *The Handbook -A Guide to Fluorescent Probes and Labeling Technologies,* Tenth Ed., Chapter 10.

In another embodiment, the analyte molecule may be a protein and the binding ligand may comprise a component which is capable of binding both to the analyte molecule and an enzymatic component. Exposure of the precursor labeling agent molecule to the enzymatic component bound to the binding ligand may convert the precursor labeling agent molecule to a chromogenic, fluorogenic, of chemiluminescent labeling agent molecule that may be detected.

Two non-limiting examples of indirect detection of an analyte molecule are illustrated in FIGS. 9A and 9B. In FIG. 9A, a location 150 (in this embodiment, represented by a reaction vessel) is provided which comprises capture object 152 (in this embodiment, represented by a bead). Analyte molecule 154 is immobilized with respect to capture object 152 via capture component 156. The reaction vessel is exposed to precursor labeling agent 158, which upon exposure to analyte molecule 154, is converted to labeling agent molecule 160, as indicated by arrow 159. As another example, in FIG. 9B, location 170 (in this embodiment, represented by a reaction vessel) is provided which comprises capture object 172 (in this embodiment, represented by a bead). Analyte molecule 174 is immobilized with respect to capture object 172 via capture component 176, and binding ligand 177 is associated with analyte molecule 174. The reaction vessel is exposed to precursor labeling agent 158, which upon exposure to binding ligand 177, is converted to a labeling agent molecule 180, as indicated by arrow 179.

In some embodiments, a plurality of locations may be addressed and/or a plurality of capture objects and/or species/molecules/particles of interest may be detected substantially simultaneously. "Substantially simultaneously" when used in this context, refers to addressing/detection of the locations/capture objects/species/molecules/particles of interest at approximately the same time such that the time periods during which at least two locations/capture objects/species/molecules/particles of interest are addressed/detected overlap, as opposed to being sequentially addressed/detected, where they would not. Simultaneous addressing/detection can be accomplished by using various techniques, including optical techniques (e.g., CCD detector). Spatially segregating capture objects/species/molecules/particles into a plurality of discrete, resolvable locations, according to some embodiments facilitates substantially simultaneous detection by allowing multiple locations to be addressed substantially simultaneously. For example, for embodiments where individual species/molecules/particles are associated with capture objects that are spatially segregated with respect to the other capture objects into a plurality of discrete, separately resolvable locations during detection, substantially simultaneously addressing the plurality of discrete, separately resolvable locations permits individual capture objects, and thus individual species/molecules/particles (e.g., analyte molecules) to be resolved. For example, in certain embodiments, individual molecules/particles of a plurality of molecules/particles are partitioned across a plurality of reaction vessels such that each

reaction vessel contains zero or only one species/molecule/particle. In some cases, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5% of all species/molecules/particles are spatially separated with respect to other species/molecules/particles during detection. A plurality of species/molecules/particles may be detected substantially simultaneously within a time period of less than about 1 second, less than about 500 milliseconds, less than about 100 milliseconds, less than about 50 milliseconds, less than about 10 milliseconds, less than about 1 millisecond, less than about 500 microseconds, less than about 100 microseconds, less than about 50 microseconds, less than about 10 microseconds, less than about 1 microsecond, less than about 0.5 microseconds, less than about 0.1 microseconds, or less than about 0.01 microseconds, less than about 0.001 microseconds, or less. In some embodiments, the plurality of species/molecules/particles may be detected substantially simultaneously within a time period of between about 100 microseconds and about 0.001 microseconds, between about 10 microseconds and about 0.01 microseconds, or less.

In some embodiments, techniques may be used to prevent or reduce dissociation of an analyte molecule from a capture component and/or capture object, and/or to prevent or reduce dissociation of a binding ligand from an analyte molecule and/or another binding ligand. As will be known to those of ordinary skill in the art, some reversible affinity interactions between selected analyte molecules, capture components, and/or binding ligands (e.g., between an antibody and an antigen) are governed by thermodynamics. Accordingly, at some point during certain assay methods, some dissociation may occur between an analyte molecule and a capture component and/or a binding ligand, and/or between a binding ligand and an analyte molecule and/or another binding ligand. This may result in a reduced number of analyte molecules (e.g., immunocomplexes) being detected than are actually present. The dissociation constant of a particular pair of components (e.g., antibody-antigen pair), washing and/or fluid exposure, time between exposure and interrogation, and/or other factors, may affect the degree to which a dissociation event alters determination of analyte molecules and/or particles. Accordingly, certain techniques may be used to reduce the effects of dissociation processes.

In a first embodiment, dissociation may be reduced or eliminated by removing fluids from the assay locations (e.g., wells) following spatial segregation of a plurality of analyte molecules (e.g., associated with a capture object via a capture component and/or

associated with at least one binding ligand) into a plurality of such locations. That is, all or substantially all of the fluid surrounding or substantially contained in or at the locations may be removed. For example. the fluid may be removed by air and/or vacuum drying. Removal of the fluid may reduce or eliminate dissociation. Immediately prior to interrogation of the locations, a fluid may be added to the locations thereby rehydrating the complexes to facilitate interrogation using a detector.

In a specific example, a plurality of analyte molecules is associated (e.g., via a capture object) with beads (one embodiment of capture objects). The beads, and thus the analyte molecules, are optionally associated with at least one binding ligand and/or exposed to a material (e.g., a buffer) to keep the analyte molecules and/or binding ligands hydrated (e.g., immunocomplexes may be exposed to a buffer containing a certain carbohydrate). Following loading of the beads into a plurality of wells (e.g., locations), excess solution (e.g., buffers) is removed by air and/or vacuum drying. In this embodiment, by eliminating the contact of the beads with bulk solution, the dissociation of the analyte molecules and/or binding ligands is essentially eliminated or substantially reduced as compared to a similar system where the fluid is not removed. In this case, the wells comprising the beads may be stored (e.g., for 1 min, 2 min, 5 min, 10 min, 20 min, 30 min, 1 hour, 2 hours, 3 hours, 4 hours, 6 hours, 12 hours, or more) with none or substantially none (e.g., less than about 20%, less than about 15%, less than about 10%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.3%, less than about 0.1%, less than about 0.01%, or less) of the analyte molecules (and/or binding ligands) dissociating. Immediately prior to or close in time to the time when interrogations of the wells are performed (e.g., about 1 second, about 5 seconds, about 10 seconds, about 30 seconds, about 1 minute, about 2 minutes, or about 5 minutes prior), a solution may be provided to the wells, optionally followed by sealing (e.g., prior to interrogation). See, for example, Example 22.

In a second embodiment, dissociation may be reduced or eliminated by crosslinking an analyte molecule with a capture component, and/or crosslinking a binding ligand with an analyte molecule and/or a second binding ligand. For example, an analyte molecule comprising an antigen may be crosslinked with a binding ligand and/or capture component comprising an antibody. Crosslinking methods and techniques that may be employed are known to those of ordinary skill in the art. In some cases, following association of an analyte molecule with a capture component (e.g.,

associated with a capture object) and/or association of a binding ligand with the analyte molecule and/or a second binding ligand, the complex may be exposed to a crosslinking reagent (e.g., 1-ethyl-3-[3-dimethylaminopropyl]carbodiimide (i.e., EDC), glutaraldehyde, etc.), thereby promoting the desired crosslinking reaction. The crosslinking reagent may be selected according to the properties of the reagents used for assay, and various factors may be considered including the length of the crosslinking reagent and/or the necessary functional groups when selecting a crosslinking agent, as would be understood by those skilled in the art. Excess crosslinking reagent may optionally be removed and/or unreacted crosslinking groups may be quenched prior to interrogation and/or prior exposure to a labeling agent precursor or other reagent. The assay may be then carried out according to the methods as described herein. See, for example, Example 23.

A non-limiting example of a crosslinking reaction is shown in FIG. 10A. In this figure, bead 502 comprising capture component 504 (e.g., capture antibodies) is associated with analyte molecule 506. Analyte molecule 506 is also associated with binding ligand 508. Complex 507 is exposed to crosslinking reagent 510 and a reaction occurs as indicated by arrow 511. First crosslinking reagent 512 forms a crosslink between analyte molecule 506 and capture component 504 and crosslinking reagent 514 forms a crosslink between analyte molecule 506 and binding ligand 508.

As another example, the binding ligand may comprise a crosslinking component capable of forming a crosslink between two components (e.g., an analyte molecule and a binding ligand, or a capture component and an analyte molecule, or a first binding ligand and a second binding ligand), as shown in FIG. 10B. In this figure, bead 522 comprising capture component 524 (e.g., capture antibody) is associated with analyte molecule 526. Analyte molecule 526 is also associated with binding ligand 528 comprising crosslinking component 530. Upon exposure to an external stimulus (e.g., UV-light, chemical stimulus, etc.), as indicated by arrow 531, crosslink 532 forms between analyte molecule 526 and binding ligand 524. Non-limiting examples of crosslinking components useful for this purpose include N-succinimidyl-6-[4'-azido-2'-nitrophenylamino]) hexanoate (i.e., SANPAH) and succinimidyl 6-(4,4'-azipentanamido)hexanoate (i.e., LC-SDA).

During the step of the method where the locations into which the capture objects/analyte molecules have been segregated are addressed, any of a variety of parameters may be determined. In some embodiments, the number of locations which comprise a capture object and an analyte molecule (or binding ligand) is determined.

The number of locations which comprise a capture object but do not comprise an analyte molecule (or binding ligand) may also be determined. In some cases, the number of locations which are addressed which do not contain a capture object may also be determined. In still yet other cases, the total number of locations addressed may also be determined. A single interrogation or multiple interrogations of any subset or all of the locations ultimately addressed may be made at any given time to facilitate one or all of the above described determinations. For example, a first determination may be completed under a first range of wavelengths (e.g., white light) to determine the number of locations comprising a capture object, wherein the locations are not distinguished as to whether an analyte molecule (or binding ligand) is associated with the capture object, and a second determination of the same or some subset of the locations may be completed under a second range of wavelengths (e.g., fluorescence) to determine the number of locations which comprise a capture object associated with an analyte molecule (or binding ligand). Exemplary detection methods are described below.

Detection Methods

In some embodiments, in the systems/methods in which the species to be detected are partitioned across a plurality of locations, the locations can be interrogated using a variety of techniques, including techniques known to those of ordinary skill in the art.

In a specific embodiment of the present invention, the locations are optically interrogated. The locations exhibiting changes in their optical signature may be identified by a conventional optical train and optical detection system. Depending on the detected species (e.g., labeling agent molecules, particles, etc.) and the operative wavelengths, optical filters designed for a particular wavelength may be employed for optical interrogation of the locations.

In embodiments where optical interrogation is used, the system may comprise more than one light source and/or a plurality of filters to adjust the wavelength and/or intensity of the light source. For example, in some cases, a first interrogation of the locations may be conducted using light of a first range of wavelengths (e.g., white light in embodiments where the capture objects are not fluorescent, or a wavelength range where the capture objects fluoresce), whereas a second interrogation is conducted using light of a second, differing range of wavelengths, such that the plurality of detectable molecules fluoresce. An exemplary system configuration is provided below (see FIG. 11).

In some embodiments, the optical signal from a plurality of locations is captured using a CCD camera Other non-limiting examples of camera imaging types that can be used to capture images include charge injection devices (CIDs), complimentary metal oxide semiconductors (CMOSs) devices, scientific CMOS (sCMOS) devices, and time delay integration (TDI) devices, as will be known to those of ordinary skill in the art. The camera may be obtained from a commercial source. CIDs are solid state, two dimensional multi pixel imaging devices similar to CCDs, but differ in how the image is captured and read. For examples of CIDs, see U.S. Patent No. 3,521,244 and U.S. Patent No. 4,016,550. CMOS devices are also two dimensional, solid state imaging devices but differ from standard CCD arrays in how the charge is collected and read out. The pixels are built into a semiconductor technology platform that manufactures CMOS transistors thus allowing a significant gain in signal from substantial readout electronics and significant correction electronics built onto the device. For example, see U.S. Patent No. 5,883,830. sCMOS devices comprise CMOS imaging technology with certain technological improvements that allows excellent sensitivity and dynamic range. TDI devices employs a CCD device that allows columns of pixels to be shifted into and adjacent column and allowed to continue gathering light. This type of device is typically used in such a manner that the shifting of the column of pixels is synchronous with the motion of the image being gathered such that a moving image can be integrated for a significant amount of time and is not blurred by the relative motion of the image on the camera. In some embodiments, a scanning mirror system coupled with a photodiode or photomultiplier tube (PMT) could be used to for imaging.

In one embodiment, the plurality of locations is formed directly as a plurality of reaction vessels in an end of a fiber optic bundle. According to one embodiment, the array of reaction vessels for the present invention can be used in conjunction with an optical detection system such as the system described in U.S. Publication No. 2003/0027126. For example, according to one embodiment, the array of reaction vessels of the present invention is formed in one end of a fiber optic assembly comprising a fiber optic bundle constructed of clad fibers so that light does not mix between fibers.

FIGS. 11A and 11B show non-limiting examples of a system of the present invention according to some embodiments. The system comprises a light source 452, excitation filter 454, dichromatic mirror 458, emission filter 460, objective 470, and array 472. Light 453 given off from light source 452 is passed through excitation filter 454. The light reflects off dichromatic mirror 458, passes through objective 470 and

shines on array 472. In some cases, stray light 464 may be reduced by a stray light reducing function 468, such as an iris or aperture. Light 471 emitted from the array passes through objective 470 and emission filter 460. Light 462 is observed. The system may comprise additional components (e.g., additional filters, mirrors, magnification devices, etc.) as needed for particular applications, as would be understood by those of ordinary skill in the art.

The system shown in FIG. 11A may additionally comprise components which aid in the determination of the number of reaction vessels which contain a capture object (e.g., using white light). Alternatively, the additional components may be used to determine the total number of locations and/or provide spatially information regarding the position of the locations (e.g., containing or not containing a capture object), which may help corroborate signals observed under different light regimes (e.g., fluorescence, white light) corresponding with the position of a location (e.g., a mask may be created).

In FIGS. 11A and 11B, excitation light is emitted from source 452 and collimated into a beam 453. The excitation filter 454 may be configured to transmit only the wavelength band that excites the fluorophore (e.g., 575 nm +/- 10 nm for resorufin). The excitation light is reflected downward by the dichroic filter 458 and excites the substrate 472 containing the sample through the objective lens 470. The image light is collected by the objective lens 470, collimated into a beam 471 and transmitted through the dichroic filter 458. Only the image light corresponding to the fluorescence wavelength band (e.g., 670 nm +/- 30 nm for resorufin) is transmitted through the emission filter 460. The remaining collimated beam 462 contains only the emitted fluorescence wavelengths which will subsequently be imaged through the camera system.

The same system may be used to determine the positioning of the locations containing sample (e.g., reaction vessels). The array comprising the reaction vessels containing capture objects may be illuminated with a "bright field" white light illumination. The array may be illuminated (e.g., using light source 475 shown in FIG. 11A) by directing a pseudo-collimated white light (e.g., white light LED) onto the array surface from an angle (e.g., θ_1 in FIG. 11A may be about 20 degrees, about 25 degrees, about 30 degrees, about 35 degrees, about 40 degrees, or greater) just outside the numerical aperture of the collection objective. Light that hits the surface of the array 472 (e.g., light 476) is reflected (and scattered) off the surface, collimated 471, and collected

by the objective lens (470). The collimated beam is subsequently imaged through the camera system.

The same system may also be used to determine which locations contain a capture object (e.g., bead). Any particular bead may or may not be associated with an analyte molecule and/or binding ligand. The array may be illuminated (e.g., using light source 473 as shown in FIG. 11A) with a "dark field" white light illumination. The array may be illuminated by aiming a pseudo-collimated white light (e.g., white light LED 473) onto the array surface from an angle (e.g., θ_2 in FIG. 11A is about 65 degrees, about 70 degrees, about 75 degrees, about 80 degrees, about 85 degrees) substantially outside the numerical aperture of the collection objective. Light that hits the surface of the array 472 (e.g., light 474) is reflected (and scattered) off the surface, collimated 471, and collected by the objective lens 470. The collimated beam is subsequently imaged by the camera system.

In some embodiments, an optical detection system may be employed, for example, as described in U.S. Publication No. 2003/0027126. In an exemplary system, light returning from an array of reaction vessels formed at the distal end of a fiber optic bundle is altered via use of a magnification changer to enable adjustment of the image size of the fiber's proximal or distal end. The magnified image is then shuttered and filtered by a shutter wheel. The image is then captured by charge coupled device (CCD) camera. A computer may be provided that includes and executes imaging processing software to process the information from the CCD camera and also optionally may be configured to control shutter and filter wheels. As depicted in U.S. Publication No. 20030027126, the proximal end of the bundle is received by a z-translation stage and x-y micropositioner.

For example, FIG. 12 shows a schematic block diagram of a system employing a fiber optic assembly 400 with an optical detection system. The fiber optic assembly 400 that comprises a fiber optic bundle or array 402 that is constructed from clad fibers so that light does not mix between fibers. An array of reaction vessels 401 is formed at/attached to the bundle's distal end 412, with the proximal end 414 being operatively connected with a *z*-translation stage 416 and x-y micropositioner 418. These two components act in concert to properly position the proximal end 414 of the bundle 402 for a microscope objective lens 420. Light collected by the objective lens 420 is passed to a reflected light fluorescence attachment with three pointer cube slider 422. The attachment 422 allows directs light from a 75 watt Xe lamp 424 through the objective

lens 420 to be coupled into the fiber bundle 402. The light from source 424 is condensed by condensing lens 426, then filtered and/or shuttered by filter and shutter wheel 428, and subsequently passes through a ND filter slide 430. Light returning from the distal end 412 of the bundle 402 passes through the attachment 422 to a magnification changer 432 which enables adjustment of the image size of the fiber's proximal or distal end. Light passing through the magnification changer 432 is then shuttered and filtered by a second wheel 434. The light is collected by a charge coupled device (CCD) camera 436. A computer 438 executes imaging processing software to process the information from the CCD camera 436 and also optionally controls other components of the system, including but not limited to the first and second shutter and filter wheels 428, 434.

An array of reaction vessels used to practice some embodiments of the present invention may be integral with or attached to the distal end of the fiber optic bundle using a variety of compatible processes. In some cases, microwells are formed at the center of each individual fiber of the fiber optic bundle and the microwells may or may not be sealed. Each optical fiber of the fiber optic bundle may convey light from the single microwell formed at the center of the fiber's distal end. This feature enables the interrogation of the optical signature of individual reaction vessels to identify reactions/contents in each microwell. Consequently, by collecting the image of the end of the bundle with the CCD array, the optical signatures of the reaction vessels may be individually interrogated and/or imaged substantially simultaneously.

Quantification

According to some embodiments of the present invention, the methods, systems, and/or devices are used to determine the presence and/or a measure of the concentration of analyte molecules (or particles) in a fluid sample based at least in part on detecting and/or quantifying at least some of a plurality of capture objects used to capture the analyte molecules (and optionally at least one binding ligand). In certain embodiments where concentration is determined, a correlation and/or calibration relating the number (or fraction/percentage) of locations containing a capture object comprising at least one analyte molecule (and/or at least one binding ligand) to the quantity/concentration of analyte molecules in the fluid sample is employed. In some cases, the concentration of the analyte molecules in a fluid sample may be linearly proportional to the number/fraction of locations containing a capture object comprising at least one analyte molecule (and/or at least one binding ligand). In other cases, the measure of

concentration of the analyte molecules in a fluid sample may be related to the number/fraction of locations containing a capture object associated with at least one analyte molecule (and/or at least one binding ligand) by a non-linear relationship. In some embodiments, a measure of the concentration of analyte molecules in a fluid sample may be determined at least in part using a calibration curve developed using samples containing known concentrations of target analyte molecules. Methods to determine a measure of the concentration of analyte molecules in a fluid sample are discussed more below.

Certain embodiments of present invention are distinguished by the ability to detect and/or quantify low numbers/concentrations of capture objects comprising at least one analyte molecule (and/or at least one binding ligand) and may be well suited to determine a measure of the concentration of analyte molecules in a fluid sample containing very low concentrations of the analyte molecule. This capability may be facilitated, in certain embodiments, at least in part by spatially isolating individual capture objects, including at least some comprising at least one analyte molecule (and/or at least one binding ligand), for example, by partitioning a plurality of such capture objects across an array of locations (e.g., reaction vessels), and then detecting their presence in the reaction vessels. The presence of a capture object comprising at least one analyte molecule (and/or at least one binding ligand) in a reaction vessel, in some embodiments, can be determined and the number of such reaction vessels counted in a binary fashion. That is, in embodiments where a location (e.g., a reaction vessel) is found to contain at least one capture object associated with at least one analyte molecule (and/or binding ligand), the location is counted as one. In embodiments where a location (e.g., a reaction vessel) is found to contain a capture object, the location is counted as zero. For example, wells that are counted as "ones" may be determined by detecting the presence of a detectable molecule or particle in a reaction vessel that, as described above, indicates the presence of a capture object comprising at least one analyte molecule (and/or at least one binding ligand) in the well.

In embodiments where a fluid sample containing or suspected of containing is contacted with a plurality of capture objects such that any analyte molecules present in the sample are immobilized with respect to the plurality of capture objects such that a statistically significant fraction (e.g., as described above) of the capture objects associate with a single analyte molecule and a statistically significant fraction of the capture objects do not associate with any analyte molecules (e.g., as shown in FIG. 1, step (B)), a

determination of a measure of the concentration of analyte molecules in the fluid sample may be carried out as follows. First, at least a portion of the capture objects (at least some of which have a single analyte molecule immobilized) are spatially segregated into a plurality of locations (e.g., as shown in FIG. 1, step (C)). The number of locations that contain an analyte molecule immobilized with respect to a capture object is determined, either directly (e.g., by detection of the analyte molecule itself (e.g., see FIG. 1, step (D)) or indirectly (e.g., by detection of a binding ligand associated with the analyte molecule, by detection of a labeling agent (e.g., formed via conversion of a precursor labeling agent upon exposure to an analyte molecule see FIG. 4A), etc.). In some embodiments, a measure of the concentration of analyte molecules in a fluid sample is determined at least in part on the determination of the number of the plurality of locations that contain an analyte molecule (e.g., reaction vessels 12 in FIG. 1, step (D)). In certain such embodiments, a measure of the concentration of analyte molecules in the fluid sample is determined at least in part by comparison of this measured parameter to a calibration standard and/or by using a Poisson and/or Gaussian distribution analysis of the number of locations that would be expected to contain an analyte molecule.

In some embodiments the number of locations which comprise a capture object not associated with an analyte molecule may also be determined (e.g., reaction vessel 13 in FIG. 1, step (D)). In such cases, a measure of the concentration of analyte molecules in a fluid sample may be determined based at least in part on the ratio of locations comprising an analyte molecule immobilized with respect to a capture object, to the number of locations comprising a capture object not associated with an analyte molecule. In some cases, the number of locations which do not comprise a capture object may also be determined (e.g., reaction vessel 14 in FIG. 1, step (D)). In such cases, a measure of the concentration of analyte molecules in a fluid sample may be determined based at least in part on the ratio of locations comprising an analyte molecule immobilized with respect to a capture object to the number of locations not comprising a capture object and/or the number of locations not comprising an analyte molecule – whether or not such location contains a capture object (in either case above or elsewhere, the denominator for the ratio/fraction may or may not include the positive ("on" or "one") locations added to the nil ("off" or "zero") locations depending upon preference). In yet other cases, the total number of locations addressed/analyzed may be determined (e.g., reaction vessels 12, 13, and 14 in FIG. 1, step (D)) and a measure of the concentration of analyte molecules in a fluid sample may be based on the ratio of the locations comprising an

analyte molecule immobilized with respect to a capture object to the total number of locations addressed/analyzed.

It should be understood, that in some assay methods, a measure of the concentration of analyte molecules in a fluid sample may be carried out using more than one type of analysis (e.g., a first analysis based on the number of locations comprising an analyte molecule immobilized with respect to a capture object, and a second analysis based on the ratio of the ratio/fraction of locations comprising an analyte molecule immobilized with respect to a capture component, to the total number of locations comprising a capture object, etc.). In such embodiments, the second analysis may be used as a quality control measure (e.g., to confirm that the first analysis provided a reasonable result) and/or the two analysis results may be averaged.

In some embodiments, the determination of a measure of the concentration of analyte molecules in a fluid sample being tested may be carried out using a similar analysis as described above, but by determining the number of reaction vessels which comprise a binding ligand as opposed to the number of reaction vessels which comprise an analyte molecule immobilized with respect to a capture object. As described herein, in some cases, following immobilization of a plurality of analyte molecules to a plurality of capture objects, the plurality of capture objects may be exposed to at least one type of binding ligand such that at least some of the immobilized analyte molecules associate with at least one binding ligand (e.g., see FIG. 2, step (B). This assay method may be especially useful in embodiments where more than one analyte molecule is expected to become associated with each capture object, but binary quantification may still be desired. In some cases, the binding ligand may be provided at a concentration such that at least some of the capture objects containing at least one analyte molecule do not associate with any binding ligands (e.g., see FIG. 2, step (C). In such embodiments, the number of locations containing a capture object associated with a binding ligand (e.g., via an analyte molecule) can replace the number of locations containing a capture object associated with an analyte molecule in the analysis and methods described above.

A measure of the concentration of analyte molecules or particles in a fluid sample may be determined using a variety of calibration techniques, and the particular technique resulting in the most accuracy and reliability can depend on the relative number/concentration of analyte molecules in the sample to the number/concentration of capture objects exposed to the sample (and or, for embodiments using binding ligands, the relative number/concentration of binding ligands to the number/concentration of

capture objects exposed to each other during/after capture of the analyte molecules by the capture objects). Non-limiting examples of concentration determination methods that may be useful in particular analyte concentration regimes include the above described binary read-out methods, and/or methods in which the relative positive signal intensity measured for the locations ("intensity read-out methods") is employed. Either or both of the above methods – or alternative methods – may further employ a comparison of the measured parameter with a calibration curve.

It is currently believed that the most accurate method of determination may depend at least in part on the concentration of analyte molecules contained in the fluid sample. For example, in embodiments in which the concentration of the analyte molecules in the sample being tested results in a statistically significant fraction of locations to which that capture objects are partitioned comprising a single analyte molecule or binding ligand and a statistically significant fraction of locations not comprising any analyte molecules or binding ligands (e.g., at or approaching a regime where essentially no locations comprise more than one analyte molecule or binding ligand), a binary read-out method may be particularly useful, and in some cases, may be used in conjunction with a calibration curve. In other embodiments, where a larger number of locations comprise more than one analyte molecule and/or more than one binding ligand, a determination based at least in part on an intensity read-out may provide a more accurate measure of the concentration of analyte molecules in a fluid sample. Such a determination may also be used in conjunction with a calibration curve.

In certain embodiments, the fraction of locations (e.g., the statistically significant fraction) which comprises at least one capture object associated with an analyte molecule and/or binding ligand is less than about 50%, less than about 40%, less than about 25%, less than about 10%, less than about 5%, less than about 1%, less than about 0.5%, or less than about 0.1% of the total number of locations containing a capture object. In such embodiments, a measure of the concentration of analyte molecules in the fluid sample may be determined using a binary read-out method. In some cases, the percentage of locations which do not contain a capture object associated with an analyte molecule and/or binding ligand is at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 90%, or at least about 95%, at least about 99%, at least about 99.5%, at least about 99.9%, or greater, of the total number of locations.

While the discussion below focuses primarily on the use of a binary read-out system (e.g., based on counting the number of "on" and "off" locations) for ultra low level detection capability, this is by no means limiting, and the inventive methods and assays may also in certain embodiments employ instead of or in addition to a binary quantification protocol , one based in measurement of intensity (i.e. an intensity read-out method) (e.g., to extend dynamic range). As noted, in some cases, the detection systems and quantification methods may be configured so that the system can use either or both of a binary read-out determination and an intensity read-out determination, depending on the assay format and/or the concentration of analyte molecules in the fluid sample. For example, the method and/or system may be able to determine a base parameter from a first measurement and decide to use either a binary read-out determination or an intensity read-out determination depending on the result of the first determination, as described in more detail below and as is described in commonly owned U.S. Patent Application Serial No. 12/731,136, entitled "Methods and systems for extending dynamic range in assays for the detection of molecules or particles" by Rissin et al., filed March 24, 2010, and International Patent Application No. (not yet determined), entitled "Methods and systems for extending dynamic range in assays for the detection of molecules or particles" by Rissin et al., filed March 1, 2011 (Attorney Docket No. Q0052.70013WO00), each herein incorporated by reference.

According to one embodiment, the quantification method of the present invention can be performed as follows. A fluid sample containing or suspected of containing an analyte molecule of interest is contacted with a plurality of capture objects and, optionally, one or more binding ligands and the capture objects are partitioned across an array of locations, such as reaction vessels/wells (as described previously). In some embodiments, where a binary read-out method is desired to be used for determination, in the step of contacting the fluid sample with the capture objects, the relative amounts/concentrations of fluid sample and capture object containing solution are selected (e.g., based on a known or estimated/suspected approximate concentration range of analyte molecules in the sample) so that the ratio of analyte molecules in the fluid sample to total number of capture objects provided to the solution will be less than about 1:5, less than about 1:10, less than about 1:12, less than about 1:15, less than about 1:20, less than about 1:50, less than about 1:100, or less. With such ratios, at least some of the capture objects statistically will be expected associate with a single analyte molecule and the majority of the remainder of the capture objects will not associate with

any analyte molecules. The number of capture objects associating with multiple analyte molecules under such conditions may be low enough to be neglected, such that capture object determined to comprise an analyte molecule can be assumed to comprise a single analyte molecule. Under such conditions, an analysis system configured to perform a binary read out quantification may be used to determine the number of locations which comprise a capture object associated with an analyte molecule by any detection method as described herein. The number of locations which comprise a capture object associated with an analyte molecule is then counted (e.g., FIG. 1, step (D), the total number of reaction vessels comprising an analyte molecules is two, e.g., reaction vessels 12) and, in some cases, the fraction of the total number of locations containing a capture object which contain a capture object associated with an analyte molecule is calculated (e.g., in FIG. 1, total number of reaction vessels comprising a capture object is three, reactions vessels 12 and 13; thus, fraction of the total number of locations comprising a capture object associated with an analyte molecule is 2:3). Utilization of a zero (no analyte molecule detected) or one (an analyte molecule detected) response, in conjunction with using an array with a large number of locations can permit a determination of bulk concentrations of analyte molecules in the sample by counting the actual number of molecules contained in the volume of sample partitioned across and contained in the locations. In some cases, the analyte molecule may be detected indirectly (e.g., the read-out is accomplished by counting the number of locations containing at least one labeling agent molecule, wherein the labeling agent has been converted from a precursor labeling agent upon exposure to an analyte molecule). In instances where a large number of locations (e.g., at least about 10,000 locations) are substantially simultaneously interrogated, the ratio of locations comprising an analyte molecule associated with a capture object to total number of locations determined (e.g., in some cases, the locations which contain a capture object associate with or not associated with any analyte molecules) may be at least about 1:100, at least about 1:1000, at least about 1:10,000 or less. Utilizing an array with a large number of locations (e.g., at least about 10,000, at least about 50,000, at least about 100,000, at least about 500,000, etc.) may provide a statistically significant signal even at this low ratio.

In some assays, a Poisson distribution adjustment may be applied to numbers and/or ratios determined by a binary read-out method to facilitate and/or improve accuracy of determining a concentration of analyte molecules in a fluid sample. For example, in embodiments where the ratio of analyte molecules in the fluid sample to the

total number of capture objects contacted with the fluid sample is greater than about 1:10, greater than about 1:5, greater than about 1:4, greater than about 1:3, or greater than about 1:2, or between about 1:10 and about 1:2, between about 1:5 and about 1:2, the number of analyte molecules immobilized per capture may be zero or one, with a greater proportion containing more than one than for the regime described in the paragraph above. In some such cases, performance and accuracy of the concentration determinations may be improved over use of an assumption that all positive locations contain only a single analyte molecule (as described in the paragraph above) by employing a Poisson distribution adjustment to predict the number of locations expected to contain 0, 1, 2, 3, 4, etc., analyte molecules per capture object.

A Poisson distribution describes the likelihood of a number of events occurring if the average number of events is known. If the expected number of occurrences is μ, then the probability ($P_\mu(\nu)$) that there are exactly ν occurrences (ν being a non-negative integer, $\nu = 0, 1, 2, ...$) may be determined by Equation 5:

$$P_\mu(\nu) = e^{-\mu}\left(\frac{\mu^\nu}{\nu!}\right) \qquad \text{(Eq. 5)}$$

In some embodiment of the present invention, μ is equal to the fraction of the number of locations determined to contain an analyte molecule associated with an analyte to the total number of capture objects detected (e.g., either associated with or not associated with any analyte molecules), and ν is the number of capture objects associated with a certain number of analyte molecules (e.g., the number of capture objects associated with either 0, 1, 2, 3, etc. analyte molecule). By determining μ from interrogating the array of locations during an assay, the concentration of analyte molecules in the sample can be determined using a Poisson distribution adjustment. For example, in an assay using the binary mode of measurements where capture objects associated with 1, 2, 3, 4, etc. analyte molecules are not distinguished from each other (e.g., where $\nu = 1, 2, 3, 4$ are not differentiated from each other) and the wells (e.g., locations, reaction vessels) are simply characterized as "on" wells, then occurrences of $\nu = 0$ can by determined definitively as the number of "off" wells. ($P_\mu(0)$) may be calculated according to Equation 6:

$$P_\mu(0) = e^{-\mu}\left(\frac{\mu^0}{0!}\right) = e^{-\mu} \qquad \text{(Eq. 6)}$$

and the number of expected occurrences, μ, may be determined based on a rearrangement of Equation 5, as given in Equation 7:

$$\mu = -\ln[P_\mu(0)] \quad \text{(Eq. 7).}$$

The number of occurrences of capture objects associated with no analyte molecules (or binding ligands), $P_\mu(0)$, is equal to 1 minus the total number of capture objects with all other occurrences (e.g., capture objects associated at least one analyte molecule or binding ligand) then μ is given by Equation 8:

$$\mu = \frac{Number\ of\ Analyte\ molecules}{Number\ of\ Capture\ objects} = -\ln(1 - fraction\ of\ "on"\ wells) \quad \text{(Eq. 8).}$$

Rearranging Equation 8, the total number of analyte molecules in the fluid sample contained in the locations interrogated containing a capture object can be determined using Equation (9):

$$Number\ of\ Analyte\ molecules = -\ln(1 - fraction\ of\ "on"\ wells) \times Number\ of\ Capture\ objects \quad \text{(Eq. 9).}$$

Therefore, the total number of molecules can be determined from the fraction of "on" wells for a given number of wells containing capture objects, and a measure of the concentration of analyte molecules in the fluid sample may be based at least in part on this number (as well as, e.g., any dilutions of the sample during the assay, the number and volume of the wells containing capture objects interrogated, etc.). The number of capture objects with 1, 2, 3, 4 etc. associated analyte molecules can also be determined by calculating $P_\mu(1)$, $P_\mu(2)$, $P_\mu(3)$ etc. from the μ determined and Equation 5.

As a non-limiting example of use of a Poisson distribution adjustment, in an assay where 26% of 50,000 capture objects interrogated were "on" (i.e., contained one or more analyte molecules and/or binding ligands) then the total number of analyte molecules present is calculated as $-\ln(1-0.26)\times 50{,}000 = 15{,}056$ molecules. Of these 15,056 molecules, using $\mu = -\ln(1-0.26) = 0.3011$ in the Eq. 5 for $\nu = 1$, 11,141 capture objects are calculated to have 1 analyte molecule, 1,677 capture objects 2 analyte molecules, 168 capture objects 3 analyte molecules, 13 capture objects 4 analyte molecules, and 1 capture object 5 analyte molecules. A similar analysis may be applied to embodiments where a statistically significant fraction of the spatially separated capture objects are associated with at least one binding ligand and a statistically significant fraction of spatially separated capture objects are not associated with any binding ligands.

In some embodiments, wherein the ratio of locations comprising a capture object associated with at least one analyte molecule and/or a binding ligand to locations containing a capture object free of any analyte molecule/binding ligand is high (e.g., greater than about 1:2, greater than about 1:1, greater than about 2:1, greater than about

4:1, greater than about 8:1, or greater), the determination of the concentration of analyte molecules in the fluid sample may be based at least in part on an intensity read-out determination. In such an embodiment, the total intensity of the array (e.g., total fluorescence) may be determined and a measure of the concentration of analyte molecules in the fluid sample is based at least in part on this determination.

In some embodiments, a measure of the concentration of analyte molecules or particles in the fluid sample may be determined at least in part by comparison of a measured parameter to a calibration standard. In some cases, a calibration curve may be used, similar to as described herein, wherein the total intensity is determined for a plurality of samples comprising the analyte molecule at a known concentration using a substantially similar assay format. For example, the number and/or fraction of locations that comprise a capture object associated with an analyte molecule (e.g., based on a binary read-out), or alternatively, the total intensity of the array, may be compared to a calibration curve to determine a measure of the concentration of the analyte molecule in the fluid sample. The calibration curve may be produced by completing the assay with a plurality of standardized samples of known concentration under similar conditions used to analyze test samples with unknown concentrations. A calibration curve may relate the fraction of the capture objects determined to be associated with an analyte molecule and/or binding ligand with a known concentration of the analyte molecule. The assay may then be completed on a sample containing the analyte molecule in an unknown concentration, and number/fraction of capture objects determined to be associated with an analyte molecule and/or binding ligand may be compared to the calibration curve, (or a mathematical equation fitting same) to determine a measure of the concentration of the analyte molecule in the fluid sample.

In one exemplary embodiment for performing a calibration, four standardized fluid samples comprising an analyte molecule in varying concentration (w, x, y, and z) are used. An assay (e.g., immobilizing the analyte molecules with respect to a plurality of capture objects, optionally exposing the capture objects to at least one type of binding ligand, partitioning at least a portion of the capture objects into a plurality of discrete, separately addressable locations, detecting at least a portion of the capture objects, etc.) is carried out for each calibration sample, and the number/fraction of capture objects comprising an analyte molecule and/or binding ligand (b, c, d, and e) is determined. A plot/equation/look-up table, etc. is produced relating the values b, c, d, and e to concentrations w, x, y, and z, respectively, as depicted in FIG. 13. The assay may be

then be carried out under substantially identical conditions on a fluid sample containing an analyte molecule of unknown concentration, wherein the resulting value of number/fraction of capture objects comprising an analyte molecule and/or binding ligand determined to detection of the capture objects is f. This value (f) may be plotted on the graph and a measure of the unknown concentration of the target analyte in the fluid sample (t) may be determined. In some cases, the calibration curve may have a limit of detection, wherein the limit of detection is the lowest concentration of analyte molecules in a fluid sample that may be accurately determined. In some cases, the r^2 value of the calibration curve may be greater than about 0.5, greater than about 0.75, greater than about 0.8, greater than about 0.9, greater than about 0.95, greater than about 0.97, greater than about 0.98, greater than about 0.99, greater than about 0.9999, or about 1. Values b, c, d, and e may be based on the absolute number of measured locations/capture objects associated with an analyte molecule (or binding ligand), or a ratio of the number of locations containing a capture object associated with an analyte molecule (or binding ligand) to the number of locations containing a capture object not associated with any analyte molecules or a ratio of the number of locations containing a capture object associated with an analyte molecule (or binding ligand) to the number of locations containing a capture object or a ratio of the number of locations containing a capture object associated with an analyte molecule (or binding ligand) to the total number of locations addressed, etc. Any number of calibration standards may be used to develop the calibration curve (e.g., about 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, calibration standards).

In some embodiments, the concentration of analyte molecules in the fluid sample may be determined through use of a calibration curve using an assay system employing a computer. The computer may execute software that may use the data collected to produce the calibration curve and/or to determine a measure of the concentration of analyte molecules in a test fluid sample from such calibration curve. For example, a fluorescence image of an array comprising the plurality of capture objects partitioned across the array may be collected and analyzed using image analysis software (e.g., IP Lab, BD Biosciences). The analysis software may automatically calculate the number of locations that have fluorescence intensity over the background intensity (e.g., a number that correlates to the number of locations which comprise an analyte molecule). The number of locations which comprise fluorescence intensity over the background intensity may be divided by the total number of locations addressed, for example, to determine the fraction of locations which comprise an analyte molecule. The active location fraction

may be compared to a calibration curve to determine a measure of the concentration of analyte molecules in the fluid sample.

In certain embodiments, it may be possible to increase both the dynamic range and the sensitivity of the assay by expanding the number of locations into which the capture objects are partitioned and/or by adjusting the ratio of capture objects (e.g. beads) to analyte molecules in the initial capture step. In certain cases, decreasing or increasing the analyte-to bead ratio may result in more dynamic range. In some cases, as the volume of a sample increases, detecting small numbers of analyte molecule with accuracy, may, in some cases, become more challenging for example, due to limitations of equipment, time constraints, etc. For example, to achieve the same efficiencies in larger volume sample (e.g., 1 mL, 10 mL) as achieved with a smaller volume sample (e.g., 100 μL), more beads (e.g., 10 and 100 times more beads, respectively) may be necessary, and thus, the beads may need to be spatially segregated into larger number of locations, wherein the larger number of locations may require an increased imaging area.

For the capture step, the choice of bead concentration may depend on several competing factors. For example, it can be advantageous if sufficient beads are present to capture most of the target analyte from thermodynamic and kinetic perspectives. As an exemplary illustration, thermodynamically, 200,000 beads in 100 μL that each have about 80,000 capture components (e.g. antibodies) bound to correlates to an antibody concentration of about 0.3 nM, and the antibody-protein equilibrium at that concentration may give rise to a relatively high capture efficiency of target analyte molecules in certain cases (e.g. >70%). Kinetically, for 200,000 beads dispersed in 100 μL, the average distance between beads can be estimated to be about 80 μm. Proteins the size of TNF-α and PSA (17.3 and 30 kDa, respectively), as exemplary analyte molecules, for example, will typically tend to diffuse 80 μm in less than 1 min, such that, over a 2 hour incubation, capture of such analyte molecules will tend not to be limited kinetically. In addition, it can also be advantageous to provide sufficient beads loaded onto the arrays to limit Poisson noise to a desired or acceptable amount. Considering as an example a situation where 200,000 beads in a in 10 μL volume are loaded onto an array, typically about 20,000–30,000 beads may become trapped in femtoliter sized wells of the array. For a typical background signal (e.g. due to non specific binding, etc.) of 1% active beads, this loading would be expected to result in a background signal of 200–300 active beads detected, corresponding to a coefficient of variation (CV) from Poisson noise of 6–7%, which may be acceptable in typical embodiments. However, bead concentrations

above certain concentrations may be undesirable in certain cases in that they may lead to: a) increases in non-specific binding that may reduce signal-to-background; and/or b) undesirably low ratios of analyte-to-bead such that the fraction of active beads is too low, resulting in high CVs from Poisson noise. In certain embodiments, considering a balance of factors such as those discussed above, providing about 200,000 to 1,000,000 beads per 100 µL of test sample may be desirable or, in certain cases optimal, for performing certain assays of the invention.

For embodiments of the inventive assay employing one or more binding ligand(s) to label the captured analyte molecules, it may be advantageous to, in certain instances, adjust the concentrations used to yield desirable or optimal performance. For example, considering an embodiment involving an analyte molecule that is a protein (captured protein) and employing a first binding ligand comprising a detection antibody and a second binding ligand comprising an enzyme conjugate (e.g. SβG), the concentrations of detection antibody and enzyme conjugate (SβG) used to label the captured protein may in some cases be limited or minimized to yield an acceptable background signal (e.g. 1% or less) and Poisson noise. The choice of the concentrations of detection antibody and enzyme conjugate (SβG) used to label the captured protein can be factors in improving the performance of or optimizing certain of the inventive assay methods. In certain cases, it may be desirable for only a fraction of the capture proteins to be labeled so as to avoid saturating signals produced by the assay. For example, for a particular assay where background levels observed are equivalent to ~1–2 fM of target protein, such that the ratio of analyte to bead may be about 0.3–0.6, the number of active beads may be in the range of about 25–40% if every protein was labeled with an enzyme, which may be higher than desirable in some cases. To produce background signals that may be closer to a lower end of the dynamic range for a digital detection assay— considering e.g. that in certain cases 1% active beads may provide a reasonable noise floor for background in digital detection assays of the invention—appropriate labeling of the captured protein can potentially be achieved by kinetic control of the labeling steps, either by limiting or minimizing the concentrations of both labeling reagents or by using shorter incubation times. For example, in an embodiment where label concentrations are minimized, use of a standard ELISA incubation time may provide acceptable results; e.g. using a total assay time of ~6 h. This length of time may be acceptable for testing that tolerates a daily turnaround time for samples. For shorter turnaround times of, for example, <1 hour

(e.g., for point-of-care applications), the assay could be performed with shorter incubations with higher concentrations of labels.

In some embodiments, accuracy of a particular method of determining concentration with the inventive assays may be compromised, i.e. both above and below the thresholds of the dynamic range for the particular method. For example, as the concentration of the capture objects associated with an analyte molecule goes down, eventually, when below the lower limit of the dynamic range, the number of capture objects associated an analyte molecule may be too low to observe a sufficient number of occupied locations to obtain a reliable and reproducible measurement. In such a situation, the number of locations could be decreased in order to make sure that at least some (e.g., a statistically significant number) of them are occupied by a capture object associated with an analyte molecule, and/or the sample tested could be concentrated and/or the number of capture objects incubated with the sample could be decreased, etc. to increase the number/fraction of positive capture objects detected. On the other hand, a binary read-out system/method may be above its upper threshold of accuracy and/or utility when, for example, loading approaches saturation with "on" capture objects such that substantially 100% of the locations contain at least one capture object associated with an analyte molecule. At this limit, discrimination between two samples with concentrations falling in this range may not be feasible using a binary read-out system/method. In such a situation, to provide a more accurate result, a greater number of locations could be used, the concentration of the sample could be reduced, for example, through serial dilutions, the number of capture objects incubated with the sample could be increased, etc. to decrease the number/fraction of positive capture objects detected, and/or an intensity read-out system/method could be employed.

In some embodiments, the concentration of analyte molecules or particles in the fluid sample that may be substantially accurately determined is less than about 5000 fM, less than about 3000 fM, less than about 2000 fM, less than about 1000 fM, less than about 500 fM, less than about 300 fM, less than about 200 fM, less than about 100 fM, less than about 50 fM, less than about 25 fM, less than about 10 fM, less than about 5 fM, less than about 2 fM, less than about 1 fM, less than about 500 aM (attomolar), less than about 100 aM, less than about 10 aM, less than about 5 aM, less than about 1 aM, less than about 0.1 aM, less than about 500 zM (zeptomolar), less than about 100 zM, less than about 10 zM, less than about 5 zM, less than about 1 zM, less than about 0.1 zM, or less. In some cases, the limit of detection (e.g., the lowest concentration of an

analyte molecule which may be determined in solution substantially accurately) is about 100 fM, about 50 fM, about 25 fM, about 10 fM, about 5 fM, about 2 fM, about 1 fM, about 500 aM (attomolar), about 100 aM, about 50 aM, about 10 aM, about 5 aM, about 1 aM, about 0.1 aM, about 500 zM (zeptomolar), about 100 zM, about 50 zM, about 10 zM, about 5 zM, about 1 zM, about 0.1 zM, or less. In some embodiments, the concentration of analyte molecules or particles in the fluid sample that may be substantially accurately determined is between about 5000 fM and about 0.1 fM, between about 3000 fM and about 0.1 fM, between about 1000 fM and about 0.1 fM, between about 1000 fM and about 0.1 zM, between about 100 fM and about 1 zM, between about 100 aM and about 0.1 zM. The concentration of analyte molecules or particles in a fluid sample may be considered to be substantially accurately determined if the measured concentration of the analyte molecules or particles in the fluid sample is within about 10% of the actual (e.g., true) concentration of the analyte molecules or particles in the fluid sample. In certain embodiments, the measured concentration of the analyte molecules or particles in the fluid sample may be within about 5%, within about 4%, within about 3%, within about 2%, within about 1%, within about 0.5%, within about 0.4%, within about 0.3%, within about 0.2% or within about 0.1%, of the actual concentration of the analyte molecules or particles in the fluid sample. In some cases, the measure of the concentration determined differs from the true (e.g., actual) concentration by no greater than about 20%, no greater than about 15%, no greater than 10%, no greater than 5%, no greater than 4%, no greater than 3%, no greater than 2%, no greater than 1%, or no greater than 0.5%. The accuracy of the assay method may be determined, in some embodiments, by determining the concentration of analyte molecules in a fluid sample of a known concentration using the selected assay method.

In some embodiments, more than one of the above described types of analysis and quantification methods may be employed with the same system and in a single assay. For example, in embodiments where the analyte molecules are present at lower concentration ranges, single analyte molecules can be detected, and the data may be analyzed using a digital analysis method (binary quantification). In some cases using binary quantification, as previously described, the data may be processed using a Poisson distribution adjustment. At higher concentration ranges (e.g., where it may become challenging or inaccurate to perform binary quantification), the data may be analyzed using an analog analysis method, based, for example on measured relative signal intensities (intensity read-out determination). In certain embodiments, the results of the

two analysis methods (digital and analog) may both be utilized by a single assay system/protocol of the invention by linking the two methods using a single calibration curve. For example, in some embodiments, at low concentration levels (e.g., in the digital/binary concentration range), a measure of the concentration of analyte molecules in a fluid sample may be determined at least in part by counting beads as either "on" (e.g., by determining if the reaction vessel contains a bead associated with an analyte molecule) or "off" (e.g., by determining if the reaction vessel contains a bead not associated with any analyte molecule). At low ratios of analyte molecules to beads (e.g., less than about 1:5, less than about 1:10, less than about 1:20, etc.), substantially all of the beads are associated with either zero or a single analyte molecule. In this range, the percentage of active beads (e.g., "on" reaction vessels) increases linearly with increasing analyte concentration, and a digital analysis method may be most suitable.

As the analyte concentration increases, however, more of the beads will associate with more than one analyte molecule. Therefore, as the analyte concentration increases (but still in the digital range), the percentage of active beads in a population generally will not be linearly related to the bulk analyte concentration as some of the beads may associate with more than one analyte molecule. In these concentration ranges, the data may be advantageously analyzed using a digital analysis method with the above described Poisson distribution adjustment. The above described non-linear effect can be accounted for using Poisson distribution adjustment across substantially the concentration range in which there remains a statistically significant fraction of beads not associated with any analyte molecules or particles in the sample. For example, ranges of percentage of active beads (i.e. "on" beads divided by total beads multiplied by 100%) for which a digital analysis method may be able to accurately determine a measure of the concentration, include up to about 20% active beads, up to about 30% active beads, up to about 35% active beads, up to about 40% active beads, up to about 45% active beads, up to about 50% active beads, up to about 60% active beads, up to about 70% active beads, up to about 80% active beads, or more. In many cases when operating in the ranges above, using a Poisson distribution adjustment will improve accuracy.

Above a certain active bead percentage (i.e., where there is no longer a statistically significant fraction of beads present in the population that are not associated with any of analyte molecules or particles, or, potentially advantageously for situations where there may be a statistically significant fraction of beads present in the population that are not associated with any of analyte molecules or particles but that result in active

bead percentages above a certain level – e.g., greater than or substantially greater than about 40%) (or active location percentage, in embodiments where beads are not employed)) improvements in accuracy and/or reliability in the determination of analyte molecule concentration may potentially be realized by employing an intensity measurement based analog determination and analysis rather than or supplementary to a digital/binary counting/Poisson distribution adjustment as previously described. At higher active bead percentages, the probability of an active bead (e.g., positive reaction vessel) being surrounded by other active beads (e.g., positive reaction vessels) is higher and may in certain assay set ups create certain practical challenges to exclusively using the digital/binary determination method. For example, in certain embodiments, leakage of a detectable component into a reaction vessel from an adjacent reaction vessel may occur to some extent. Use of an analog, intensity level based technique in such situations can potentially yield more favorable performance. In an intensity measurement based analog determination and analysis, the association of multiple analyte molecules at relatively high concentrations with single beads is quantified. The intensity of at least one signal from the plurality of reaction vessels which contain at least one analyte molecule may be determined. In some cases, the intensity is determined as the total overall intensity for the reaction vessels containing at least one analyte molecule (e.g., the intensity of the reaction vessels in determined as a whole). In other cases, the intensity of each reaction vessel with a signal may be determined and averaged, giving rise to an average bead signal (ABS).

According to certain embodiments, an inventive assay system may include a link between the results/parameters of the two analysis methods/systems (i.e. digital and analog), for example, with the aid of a calibration curve, so that the system is able to operate in multiple modes of quantification depending on the signal relating to the number/fraction of "on" beads detected. Such systems can have substantially expanded dynamic ranges in certain cases. Further description of such systems which can combine and use more than one quantification method for a single assay is provided in commonly owned U.S. Patent Application Serial No. 12/731,136, entitled "Methods and systems for extending dynamic range in assays for the detection of molecules or particles" by Rissin et al., filed March 24, 2010, and International Patent Application No. (not yet determined), entitled "Methods and systems for extending dynamic range in assays for the detection of molecules or particles" by Rissin et al., filed March 1, 2011 (Attorney Docket No. Q0052.70013WO00), each herein incorporated by reference.

The following examples are included to demonstrate various features of the invention. Those of ordinary skill in the art should, in light of the present disclosure, will appreciate that many changes can be made in the specific embodiments which are disclosed while still obtaining a like or similar result without departing from the scope of the invention as defined by the appended claims. Accordingly, the following examples are intended only to illustrate certain features of the present invention, but do not necessarily exemplify the full scope of the invention.

Example 1

This following example describes materials used in Examples 2-19. Optical fiber bundles were purchased from Schott North America (Southbridge, MA). Non-reinforced gloss silicone sheeting was obtained from Specialty Manufacturing (Saginaw, MI). Hydrochloric acid, anhydrous ethanol, and molecular biology grade Tween-20 were purchased from Sigma-Aldrich (Saint Louis, MO). 2.8-um (micrometer)-diameter tosyl-activated magnetic beads were purchased from Invitrogen (Carlsbad, CA). 2.7-um-diameter carboxy-terminated magnetic beads were purchased from Varian, Inc. (Lake Forest, CA). Monoclonal anti-human TNF-α capture antibody, polyclonal anti-human TNF-α detection antibody, and recombinant human TNF-α were purchased from R&D systems (Minneapolis, MN). Monoclonal anti-PSA capture antibody and monoclonal detection antibody were purchased from BiosPacific (Emeryville, CA); the detection antibody was biotinylated using standard methods. 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC), N-hydroxysulfosuccinimide (NHS), and SuperBlock® T-20 Blocking Buffer were purchased from Thermo Scientific (Rockford, IL). DNA was purchased from Integrated DNA Technologies (Coralville, IA) and/or purified DNA was ordered from Integrated DNA Technologies (Coralville, IA). Streptavidin-β-galactosidase (SβG) was purchased from Invitrogen or conjugated in house using standard protocols. Resorufin-β-D-galactopyranoside (RGP) was purchased from Invitrogen (Carlsbad, CA). The fiber polisher and polishing consumables were purchased from Allied High Tech Products (Rancho Dominguez, CA).

Example 2

The following describes a non-limiting example of the preparation of 2.8-um-diameter magnetic beads functionalized with protein capture antibody. 600 uL (microliter) of 2.8-um-diameter tosyl-activated magnetic bead stock (1.2×10^9 beads)

was washed three times in 0.1 M sodium borate coating buffer pH 9.5. 1000 ug (microgram) of capture antibody was dissolved in 600 uL of sodium borate coating buffer. 300 uL of 3M ammonium sulfate was added to the antibody solution. The 600 uL of bead solution was pelleted using a magnetic separator and the supernatant was removed. The antibody solution was added to the beads and the solution was allowed to mix at 37°C for 24 hours. After incubation, the supernatant was removed and 1000 uL of PBS buffer containing 0.5% bovine serum and 0.05% Tween-20 was added to the beads. The beads were blocked overnight (~8 hours) at 37°C. The functionalized and blocked beads were washed three times with 1 ml PBS buffer containing 0.1% bovine serum and 0.05% Tween-20. Finally, 1 mL of PBS containing 0.1% bovine serum, 0.05% Tween-20, and 0.02% sodium azide was added to the functionalized and blocked beads. 50 uL aliquots were stored at 4°C for later use.

Example 3

The following describes a non-limiting example of the preparation of 2.7-um-diameter magnetic beads functionalized with protein capture antibody. 500 uL of 2.7-um-diameter carboxy-terminated magnetic beads stock (1.15×10^9 beads) was washed twice in 0.01 M sodium hydroxide, followed by three washes in deionized water. Following the final wash, the bead solution was pelleted and the wash solution was removed. 500 uL of a freshly prepared 50 mg/mL solution of NHS in 25 mM MES, pH 6.0, was added to the bead pellet and mixed. Immediately, a 500 uL of a freshly prepared 50 mg/mL solution of EDC in 25 mM MES, pH 6.0, was added to the bead solution and mixed. The solution was then allowed to mix for 30 min at room temperature. After activation, the beads were washed twice with 25 mM MES at pH 5.0. Meanwhile, 1000 uL of 25 mM MES at pH 5.0 was used to dissolve 1000 ug of capture antibody. The antibody solution was then added to the activated beads and the coupling reaction was allowed to proceed for 3 hours at room temperature. After incubation, the supernatant was removed using the magnetic separator, and 1000 uL of 100 mM Tris-HCl (pH 7.4) was added and allowed to mix at room temperature for one hour to block any remaining reactive sites. Finally, the functionalized beads were stored in 1 mL of SuperBlock blocking buffer, and 0.02% sodium azide was added to the functionalized and blocked beads. 50 uL aliquots were stored at 4°C for later use.

Example 4

The following describes a non-limiting example of the preparation of 2.7-um-diameter magnetic beads functionalized with DNA. 120 µL of 2.7-um-diameter carboxy-terminated magnetic beads was washed three times with 0.01 M NaOH, followed by deionized water for another three times. 500 uL of freshly prepared 50 mg/mL NHS in cold 25 mM MES (pH 6) was added to the pellet of beads after the final wash, and the beads were re-suspended by vortexing briefly. 500 uL of freshly prepared 50 mg/mL EDC solution in cold 25 mM MES (pH 6) was immediately added to this bead suspension and mixed for 30 min. After activation, the beads were washed three times with cold 25 mM MES (pH 5). DNA capture probe with amine modification at 5' end (5'-NH2/C12-GTT GTC AAG ATG CTA CCG TTC AGA G-3' (SEQ ID NO. 1)) was dissolved in nuclease-free water to make a 2.6 mM stock solution. 60 µL of the DNA stock was added to 600 uL of the coupling buffer that contains 0.1 M sodium phosphate and 0.5 M NaCl, pH 8. The resulting DNA solution was added to the washed beads and mixed for 3 hours at room temperature. The bead suspension was vortexed every 30 min during the reaction. After incubation, the DNA supernatant was removed and 1 mL of 100 mM Tris-HCL (pH 7.4) was added to the pellet and mixed for 1 hour to inactivate the remaining binding sites on the beads. Finally, the beads were washed in Tris-EDTA (TE) buffer and 0.05% Tween-20 for three times, and stored in TE buffer containing 0.05% Tween-20 and 0.02% sodium azide at 4 °C.

Example 5

The following describes a non-limiting example of the capture of proteins on magnetic beads and formation of enzyme-labeled immunocomplex. Test solutions containing the protein of interest were incubated with suspensions of magnetic beads functionalized with capture antibody (e.g., see Example 2) for 1 h at 37 °C. The beads were then separated and washed three times in PBS. The beads were resuspended and incubated with solutions containing detection antibodies for 30 min at 37 °C. The beads were then separated and washed three times in PBS. The beads were incubated with solutions containing SβG (e.g., target analyte) for 30 min at 37 °C, separated, and washed six times in PBS and 0.1% Tween-20. The beads were then resuspended in 10 uL of PBS in order to load into the wells of the fiber bundle arrays.

Example 6

The following describes a non-limiting example of the capture of DNA on magnetic beads and formation of enzyme-labeled complex (FIG. 14). Beads functionalized with DNA capture probe (e.g., see Example 4) that is specific to the complementary target DNA of interest were incubated with solutions containing the target DNA (5'-TT GAC GGC GAA GAC CTG GAT GTA TTG CTC C TCT GAA CGG TAG CAT CTT GAC AAC-3' (SEQ ID NO. 2)) (e.g., target analyte) for 2 hrs. After incubation, the DNA target solution was removed and the beads were washed three times in 0.2× SSC buffer containing 0.1% Tween-20. The beads were then resuspended and mixed with 10 nM biotinylated signal probe (5'-TAC ATC CAG GTC TTC GCC GTC AA/Biotin/-3' (SEQ ID NO. 3)) (e.g., first type of binding ligand) that is also specific to the target DNA for 1 hr. The beads were then washed three times in 0.2× SSC buffer containing 0.1% Tween-20 after removing the signal probe. A solution 10 pM containing SβG (e.g., second type of binding ligand comprising an enzymatic component) was then added to the bead pellet, resuspended, and mixed for 1 hr. The beads were then separated and washed six times in 5× PBS buffer containing 0.1% Tween-20. The beads were then resuspended in 10 µL of PBS and loaded onto a femtoliter well array.

Example 7

The following example describes the capture of biotin-labeled DNA on magnetic beads and formation of enzyme-labeled complex, according to a non-limiting embodiment (see FIG. 15). Beads functionalized with DNA capture probe that is specific to DNA of interest were incubated with 1 uM target DNA-biotin (5'-biotin-C TCT GAA CGG TAG CAT CTT GAC AAC-3' (SEQ ID NO. 4)) overnight (16 hrs) in TE buffer containing 0.5M NaCl and 0.01% Tween-20. After incubation, the DNA target solution was removed and the beads were washed three times in PBS buffer containing 0.1% Tween-20. The bead stock was distributed into a microtiter plate giving 400,000 beads per well in 100 uL. The buffer was aspirated from the microtiter plate wells, the beads were resuspended and incubated with various concentrations of SβG in Superblock containing 0.05% Tween-20 for 5 hr. In some cases, the beads were resuspended every 30 min during the incubation. The beads were then separated and washed six times with 5x PBS buffer containing 0.1% Tween-20. Finally, the beads were resuspended in 10 uL of PBS containing 0.1% Tween-20. In some embodiments,

the beads were then separated and washed six times with 5× PBS buffer containing 0.1% Tween-20. For detection of enzyme, the beads were either: a) resuspended in 20 µL of PBS containing 0.1% Tween-20, and 10 µL aliquots were loaded onto two femtoliter well arrays for detection, or; b) resuspended in 100 µL of 100 µM RGP in PBS, incubated for 1 h at room temperature, and read on a fluorescence plate reader (Infinite M200, Tecan).

Example 8

The following describes a non-limiting example of the preparation of microwells arrays. Optical fiber bundles approximately 5-cm long were sequentially polished on a polishing machine using 30-, 9-, and 1-micron-sized diamond lapping films. The polished fiber bundles were chemically etched in a 0.025 M HCl solution for 130 seconds, and then immediately submerged into water to quench the reaction. To remove impurities from etching, the etched fibers were sonicated for 5 s and washed in water for 5 min. The fibers were then dried under vacuum and exposed to air plasma for 5 min to clean and activate the glass surface. The arrays were silanized for 30 minutes in a 2% solution of silane to make the surfaces hydrophobic.

Example 9

The following describes a non-limiting example of the loading of beads into microwells. To apply the solution of beads to the etched wells in a fiber bundle, clear PVC tubing (1/16" I.D. 1/8" O.D.) and clear heat shrink (3/16" ID) were cut into approximately 1 cm long. A piece of PVC tubing was first put onto the etched and functionalized end of a fiber bundle to create a reservoir to hold the bead solution, followed by the application of heat shrink around the interface between the PVC tubing and fiber bundle to provide a tight seal. 10 uL of the concentrated bead solution was pipetted into the reservoir created by the PVC tubing. The fiber bundle was then centrifuged at 3000 rpm (~1333 g) for 10 minutes to force the beads into the etched wells. The PVC tubing/heat shrink assembly was removed after centrifugation. The distal end of the fiber bundle was dipped in PBS solution to wash off excess bead solution, followed by swabbing the surface with deionized water.

Example 10

The following describes a non-limiting example of the detection of beads and enzyme-labeled beads in microwell arrays. A custom-built imaging system containing a mercury light source, filter cubes, objectives, and a CCD camera was used for acquiring fluorescence images. Fiber bundle arrays were mounted on the microscope stage using a custom fixture. A droplet of β-galactosidase substrate (100 μM RPG) was placed on the silicone gasket material, and put into contact with the distal end of the fiber array. The precision mechanical platform moved the silicone sheet into contact with the distal end of the etched optical fiber array, creating an array of isolated femtoliter reaction vessels. Fluorescence images were acquired at 577 nm with an exposure time 1011 ms. Five frames (at 30 seconds per frame) were taken for each fiber bundle array. The fluorescent images were analyzed using image analysis software to determine the presence or absence of enzymatic activity within each well of the microwell array. The data was analyzed using a developed image processing software using MathWorks MATLAB and MathWorks Image Processing toolbox. The software aligned acquired image frames, identified reaction vessel positions, located reaction vessels with beads and measured the change in reaction vessel intensity over a predefined time period. Reaction vessels containing beads with sufficient intensity growth over all data frames were counted and the final number of active reaction vessels wes reported as a percentage of all identified reaction vessels.

As well as fluorescence, the arrays were imaged with white light to identify those wells that contain beads. After acquiring the fluorescence images, the distal (sealed) end of the fiber bundle arrays were illuminated with white light and imaged on the CCD camera. Due to scattering of light by the beads, those wells that contained a bead appeared brighter in the image than wells without beads. Beaded wells were identified using this method by software.

Example 11

The following describes a non-limiting example of the loading of beads into an array of microwells (FIG. 16). Arrays of 50,000 microwells were prepared as described above. 2.8 um beads were prepared as described above. 10-uL solutions containing different numbers of beads (from 80,000 to 2 million beads) were prepared as described above. Beads were loaded into the arrays of microwells as described above. The array loaded with a solution comprising 2 million beads was imaged using scanning electron

microscopy (SEM). SEM showed that >99% of the 50,000 wells contained a bead, and each of these well only contained a single bead. The arrays loaded with 80,000 to 200,000 beads were imaged using white-light microscopy and image analysis was used to identify wells that contained a bead. The number of beads per array was determined over three arrays and plotted as a function of number of beads in solution (FIG. 16B). From FIG. 16B, in this embodiment, the number of beads loaded is a fraction of those provided in solution and not every well contains a bead at these assay-relevant bead loading concentrations. In some cases, the presence of a bead in a well (using white light images) may be correlated to those wells that contain enzymatic activity. In such cases, the read-out may be ratiometric (%active beads) and normalized for variation in bead loading.

Example 12

The following describes a non-limiting example of bead filling as a function of well depth (FIG. 17). In some embodiments, a single bead containing single analyte molecules can be delivered into a microwell so that they can be spatially isolated and sealed. To achieve this situation, the well depth and width may be carefully controlled to parameters optimized for a given bead diameter. FIGS. 17A-17C show SEM images of beads loaded as described above into arrays of microwells where the well depth was controlled by etching for different times. On average, the wells etch at a rate of approximately 1.5 to 1.7 μm per minute. Therefore, wells of 3.25 um depth are produced in about 115 to 130 s. For a well depth of 2.5 um (FIG. 17A), very few beads are retained in the microwells as they are too shallow and detection of single analytes may be poor. At 3-um depth (FIG. 17B), SEM images show good filling of single beads into single wells, and a low occurrence of two beads in one well; this array may seal well and allow large numbers of single beads to be interrogated for the presence of a single analyte. For 3.5-um deep wells (FIG. 17C), many of the wells contain two beads as well as those that contain one. The presence of a second bead above the plane of the array may deteriorate the sealing of the array as described above and may denigrate the quality of single bead isolation. These experiments indicated that an optimal well depth for 2.8-um diameter beads, in this embodiment, is between about 3 and about 3.25 um. While this range is optimal, it is also possible to perform the inventive measurements using well depths of 3.6 um, i.e., the upper limit as indicated by Eq.(4).

Example 13

The following example describes the comparison of a non-limiting method of the present invention versus a conventional plate reader for detecting enzyme (see FIGS. 18A, 18B, and 19). Biotin-DNA beads were prepared as described above. These beads were then incubated with a low concentration of SβG such that beads statistically contained either zero or one enzymes. These beads were loaded into microwells, sealed, and imaged as described above; FIG. 18A and 18B show representative images. In some cases, an increase in sensitivity to enzyme label that comes from isolating single beads is observed as compared to traditional bulk measurements. Beads coated with DNA were prepared, incubated with biotinylated DNA, and then incubated with various concentrations of SβG (from 350 aM to 320 fM) as described above. Enzymes on these beads were then measured in two ways. First, the beads were loaded into microwell arrays, sealed and imaged as described above. The fraction of active wells was determined as described above and is plotted as a function of the concentration of SβG in FIGS. 19A, the lower range expanded in FIG. 19B. Second, the beads were incubated with 100 uL of RPG in a microtiter plate for one hour and read on a fluorescence plate reader. The fluorescence signal as a function of the concentration of SβG is plotted in FIG. 19C. The lower limit of detection (LOD) of the inventive method (defined as the concentration at which the signal rises above three standard deviations over the background) in this experiment was 384 zM. The LOD of the bulk measurement on the plate reader was 14.5 fM. The single molecule array approach of the present invention, therefore, provided an increase of 37,760-fold in sensitivity to enzyme label over the plate reader. It should be noted that at the concentrations tested statistically only zero or single analytes should be detected on beads; for example, the ratio of enzymes to beads at 350 aM was 21,070/400,000 = 0.053.

Example 14

The following example illustrates the precision of detection in a method as described herein, in a non-limiting embodiment. Detection of single molecules may allow for high precision. In theory, the lowest variance in the measurement is the Poisson noise associated with counting small numbers of events. In this non-limiting example, the %Poisson Noise is given by $\sqrt{N}/N$, where N is the number of active (enzyme-associated) beads. FIG. 20 shows a plot of the %Poisson Noise against the experimental variance over three measurements (%CV) from the experimental data in

FIG. 19B. As can be seen, the imprecision of the measurement (%CV) tracks closely with the Poisson Noise, suggesting that the Poisson noise may limit the precision of the methods in some cases.

Example 15

The following non-limiting example describes the detection of PSA in serum (FIG. 21). 2.8-um-diameter beads coated in anti-PSA antibody were prepared as described above. These beads were incubated with 25% bovine serum or 25% bovine serum spiked with 50 fM PSA. The beads were then labeled with anti-PSA detection antibody and three different concentrations of SβG (1, 10, or 100 pM). The beads were then loaded into microwell arrays, sealed and imaged as described above. Image analysis was used to determine the fraction of beads that contained an enzyme. These data show that the invention can be used to detect low concentrations of proteins in serum by performing ELISAs on single beads and detecting single enzyme labels. Because of the high efficiency of the capture of analyte using beads in this invention, the concentration of enzyme label used can be varied to only label a fraction of the analytes captured on the beads in order to optimize the signal-to-background and dynamic range of the measurement. In this data set, 1 pM of enzyme label gave an optimal signal-to-background ratio.

Example 16

The following non-limiting example describes the detection of TNF-α (FIG. 22). 2.8-um-diameter beads coated in anti-TNF-α antibody were prepared as described above. These beads were incubated with 25% bovine serum or 25% bovine serum spiked with 100 fM TNF-α. The beads were then labeled with anti-TNF-α detection antibody (e.g., first binding ligand) and two different concentrations of SβG (1 or 100 pM) (e.g., second binding ligand comprising an enzymatic component). The beads were then loaded into microwell arrays, sealed and imaged as described above. Image analysis was used to determine the fraction of beads that contained an enzyme. These data show that the invention can be used to detect low concentrations of TNF-α in serum by performing ELISAs on single beads and detecting single enzyme labels. As in the previous example, the amount of enzyme label can be varied to ensure that the measurement detects only single enzyme labels on the beads and optimize the signal-to-background ratio. In this

particular example, the backgrounds are very low so the signal-to-background ratio is optimal at an enzyme label concentration of 1 pM and 100,000 beads.

Example 17

The following non-limiting example describes the detection of DNA in buffer (FIG. 23). 2.7-um-diameter beads functionalized with a capture sequence of DNA were prepared as described as above. These beads were then incubated with various concentrations of target DNA and then labeled with a biotinylated signal probe DNA sequence as described above. The beads were then labeled by incubating with various concentrations of SβG (1, 10, or 100 pM). The beads were then loaded into microwell arrays, sealed and imaged as described above. Image analysis was used to determine the fraction of beads contained an enzyme. These data show that the invention can be used to detect low concentrations of DNA by forming sandwich-like complexes on single beads and detecting single enzyme labels. As in the case of protein detection, the amount of enzyme label can be varied to ensure that there are statistically one or zero enzymes per bead even in the case where there are more than one target DNA molecules captured. This allows the dynamic range and signal-to-background of the single molecule measurement to be optimized. In this case, 10 pM of SβG gave the optimal signal-to-background.

Comparative Example 18

The following non-limiting example describes a method using detection comprising chemiluminscence from alkaline phosphatase (FIG. 24). Different concentrations of 10 uL of alkaline phosphatase were mixed with 90 uL of a solution containing the most sensitive chemiluminescent substrate available (APS-5; Lumigen Inc.) in a microtiter plate and incubated for 5 mins. The microtiter plate was then read in chemiluminescence mode of a plate reader. FIG. 24 shows a plot of chemiluminescence as a function of concentration of alkaline phosphatase. The lowest concentration of enzyme that could be detected above background was 100 aM and the calculated limit of detection was 50 aM, close to the reported value of 30 aM. Single molecule detection of β-galactosidase on beads in this invention (LOD = 220 zM) is, therefore, more than 100 times more sensitive than chemiluminscent detection of alkaline phosphatase, the most sensitive enzyme label system that is commercially available.

Example 19

The clinical use of protein biomarkers for the differentiation of healthy and disease states, and for monitoring disease progression, requires the measurement of low concentrations of proteins in complex samples. Certain current immunoassays can measure proteins at concentrations above 10^{-12} M, whereas the concentration of the majority of proteins important in cancer, neurological disorders, and the early stages of infection are thought to circulate in the range from 10^{-16} to 10^{-12} M. For example: a 1 mm^3 tumor composed of a million cells that each secrete 5000 proteins into 5 L of circulating blood translates to ~2×10^{-15} M (or 2 femtomolar, fM); early HIV infection with sera containing 2–3000 virions equates to concentrations of p24 antigen ranging from 60×10^{-18} M (60 attomolar, aM) to 15×10^{-15} M (15 femtomolar). Attempts to develop protein-based detection methods capable of detecting these concentrations have focused on the replication of nucleic acid labels on proteins, or on measuring the bulk, ensemble properties of labeled protein molecules. Sensitive methods for detecting proteins have, however, lagged behind those for nucleic acids, such as the polymerase chain reaction (PCR), limiting the number of proteins in the proteome that have been detected in blood. The isolation and detection of single protein molecules provides the most direct method for measuring extremely low concentrations of proteins, although the sensitive and precise detection of single protein molecules has proven challenging. The following describes a non-limiting exemplary method for detecting thousands of single protein molecules simultaneously using the same reagents as the gold standard for detecting proteins, namely, the enzyme-linked immunosorbent assay (ELISA). The method can detect proteins in serum at attomolar concentrations and may enable the measurement of a single molecule in blood.

The method makes use of arrays of femtoliter-sized reaction chambers (FIG. 25) that can isolate and detect single enzyme molecules. In the first step, a sandwich antibody complex is formed on microscopic beads, and the bound complexes are labeled with an enzyme reporter molecule, as in a conventional bead-based ELISA. When assaying samples containing extremely low concentrations of protein, the ratio of protein molecules (and the resulting enzyme label complex) to beads is small (typically less than 1:1) and, as such, the percentage of beads that contain a labeled immunocomplex follows a Poisson distribution, leading to single immunocomplexes on individual beads. For example, if 50 aM of a protein in 0.1 mL (3000 molecules) was captured on 200,000 beads, then 1.5% of the beads would have one protein molecule and 98.5% would have

zero protein molecules (FIG. 25B). It is typically not possible to detect these low numbers of proteins using conventional detection technology (e.g., a plate reader), because the fluorophores generated by each enzyme diffuse into a large assay volume (typically 0.1–1 mL), and it takes hundreds of thousands of enzyme labels to generate a fluorescence signal above background (FIG. 15A). The method of this Example enables the detection of very low concentrations of enzyme labels by confining the fluorophores generated by individual enzymes to extremely small volumes (~50 fL), leading to a high local concentration of fluorescent product molecules. To achieve this localization in an immunoassay, in the second step of the method the immunoassay beads are loaded into an array of femtoliter-sized wells (FIG. 25B). The loaded array is then sealed against a rubber gasket in the presence of a droplet of fluorogenic enzyme substrate, isolating each bead in a femtoliter reaction chamber. Beads possessing a single enzyme-labeled immunocomplex generate a locally high concentration of fluorescent product in the 50-fL reaction chambers. By using standard fluorescence imaging on a microscope, it is possible to detect single enzyme molecules, and to image tens to hundreds of thousands of immunocomplexes substantially simultaneously. By isolating the enzymes associated with each immunocomplex, each complex can give rise to a high measurable signal which can result in substantially improved sensitivity over bulk measurements. The protein concentration in the test sample, in some cases, is determined by simply counting the number of wells containing both a bead and fluorescent product relative to the total number of wells containing beads (FIG. 25D). The concentration is then determined digitally rather than by using the total analog signal.

FIG. 25A shows the capturing and labeling single protein molecules on beads using standard ELISA reagents. FIG. 25B shows the loading of beads into femtoliter microwell arrays for isolation and detection of single molecules. FIG. 25C shows an SEM image of a small section of a femtoliter well array after bead loading. 2.7-μm-diameter beads were loaded into an array of wells with diameters of 4.5 μm and depths of 3.25 μm. FIG. 25D shows a fluorescence image of a small section of the femtoliter well array after signals from single molecules are generated. While the majority of femtoliter chambers contain a bead from the assay, only a fraction of those beads possess catalytic enzyme activity, indicative of a single, bound protein. The concentration of protein in bulk solution may be correlated to the percentage or number of beads that have bound a protein molecule. The exemplary assay was capable of providing linearity over ~4.5 logs for 50,000 beads.

FIG. 15 shows the digitization of enzyme-linked complexes can increase sensitivity substantially compared to bulk, ensemble measurements. FIG. 15 shows a log-log plot of signal output (% active beads for assay comprising the use of capture objects; Relative Fluorescence Units (r.f.u.) for plate reader) as a function of the concentration of SβG. SβG concentrations for the ensemble readout ranged from 3 fM to 300 fM, with a detection limit of 15×10^{-15} M (15 fM; line (i)). For the exemplary assay according to the current invention, SβG concentrations ranged from 350 zM to 7 fM, demonstrating a linear response over 4.5 logs, with a detection limit of 220×10^{-21} M (220 zM; line (ii)). Error bars are based on the standard deviation over three replicates for both technologies. LODs were determined from the signal at three standard deviations above background. Table 1 provides information regarding the imprecision of this exemplary assay according to the current invention relating to Poisson noise of counting single events. The intrinsic variation (Poisson noise) of counting single active beads is given by $\sqrt{n}$. Comparing the Poisson noise associated coefficient of variation (%CV) with the %CV for this exemplary assay according to the current invention over three measurements shows that the imprecision of the assay is determined only by counting error. This observation suggests that this assays according to the current invention, in some cases, may have imprecision <20% as long as at least 25 active beads are detected, equating to an enzyme concentration of 4.5 aM.

Table 1.

[SbG] (aM)	Average # single complexes	Average % active	Measurement %CV	Poisson %CV
0	1	0.0016%	87%	122%
0.35	3	0.0086%	75%	55%
0.7	5	0.0099%	63%	46%
3.5	22	0.0413%	10%	21%
7	38	0.0713%	15%	16%
35	237	0.4461%	1%	7%
70	385	0.8183%	5%	5%
350	1787	3.3802%	2%	2%
700	4036	7.5865%	5%	2%
3500	15634	30.6479%	3%	1%
7000	24836	44.5296%	1%	1%

To quantify the potential sensitivity that may be achieved by singulating enzyme-labeled molecules compared to conventional ensemble measurements, a model sandwich assay was developed to capture enzyme molecules on beads; the population of beads were either singulated and read using methods of the current invention, or read as an

ensemble population on a conventional plate reader. Beads were functionalized with DNA capture molecules, and subsequently saturated with biotinylated complementary DNA target molecules in a one-step hybridization (see Methods section below). These beads were used to capture various concentrations of an enzyme conjugate, streptavidin-β-galactosidase (SβG), commonly used as a label in ELISA. While the exemplary assay according to the current invention and conventional assay incubations were performed under the substantially similar conditions, in these example the assays diverged at the bead readout step. For the comparative conventional assay, beads were read out in 100 uL on a fluorescence plate reader after 1 h incubation with 100 μM resorufin-β-D-galactopyranoside (RGP), a fluorogenic substrate for β-galactosidase. The detection limit of the capture assay on the microtiter plate reader was 15 fM of SβG (FIG. 15). For single molecule detection according to the present invention, the beads were loaded into the femtoliter arrays and, after sealing a solution of RGP into the wells of the array, signal generated from single enzymes accumulated in the reaction chambers for 2.5 min, with fluorescent images acquired every 30 s. A white light image of the array was acquired at the end of the experiment. These images were analyzed to identify wells that contained beads (from the white light image) and determine which of those beads had an associated enzyme molecule bound (from time-lapsed fluorescent images). FIG. 15 shows a log-log plot of the percentage of beads that contained an enzyme as a function of bulk SβG concentration. The limit of detection (LOD) for the assay according to the invention was 220 zeptomolar (13 molecules in 100 μL, or 22 yoctomoles), corresponding to an improvement in sensitivity over the plate reader of a factor of 68,000, showing that singulation can result in a dramatic increase in sensitivity over conventional ensemble measurements. The concentration of SβG detected using the assay of the present invention was a factor of 140 lower than chemiluminescence detection of alkaline phosphatase (30 aM), the current most sensitive ELISA system. The high thermodynamic and kinetic efficiency that may be achieved for the present process (Table 2) can enable the detection of very low numbers of enzyme labels and indicates that the measurement of a single labeled molecule from blood is a possibility.

Table 2. Calculations of the capture efficiency of enzyme label from 0.35 aM to 7000 aM for the assay performed according to the invention (FIG. 15).

	Column A	Column B	Column C	Column D	Column E	Column F
[SβG] (aM)	Average % active beads observed (Figure 2)	Enzyme/bead ratio from Poisson distribution	Total # of enzymes on 400,000 beads	Background corrected # of enzymes on beads	Calculated # of enzymes in 100-µL sample	Capture Efficiency
0	0.0016%	0.000016	7	---	---	---
0.35	0.0086%	0.000086	34	28	21	132%
0.7	0.0099%	0.000099	40	33	42	79%
3.5	0.0413%	0.000413	165	159	211	75%
7	0.0713%	0.000713	285	279	421	66%
35	0.4461%	0.004471	1789	1782	2107	85%
70	0.8183%	0.008217	3287	3280	4214	78%
350	3.3802%	0.034387	13755	13748	21070	65%
700	7.5865%	0.078897	31559	31552	42140	75%
3500	30.6479%	0.365974	146390	146383	210700	69%
7000	44.5296%	0.589320	235728	235722	421400	56%

In Table 2, for the experiments, on average 50,000 beads (~12.5%) were interrogated out of the 400,000 incubated with the solutions of enzyme. The low fraction of beads detected was limited by the number of reaction vessels used in this example (50,000 wells). By accounting for bead loss, the number of active beads observed experimentally (Column A) can be used to estimate the total number of active beads out of the 400,000 used (Column B). After background subtraction (Column C) and applying a Poisson distribution adjustment based on the distribution of 0, 1, 2, 3, 4, etc., enzyme molecules per bead, the total number of molecules captured on beads can be determined (Column D). The ratio of this number to the total number of enzymes in 100 uL at the start of the experiment (Column E; volume × concentration × Avogadro's number) yields a capture efficiency (Column F). The overall efficiency of capture and detection of enzyme using the present assay is high (65-85%) and in some embodiments, may be minimally limited in this experiment by the slow diffusion of the large SβG conjugate (MW ~ 515 kDa).

A sandwich-based assay was developed for two clinically-relevant protein biomarkers, namely prostate specific antigen (PSA) and tumor necrosis factor-α (TNF-α). These assays show that the high enzyme label sensitivity of the assay of this Example translates to highly sensitive (<1 fM) assays suitable for detecting proteins in blood. An assay for DNA was also developed to show that the assay of this Example can be used to directly detect single nucleic acid molecules without requiring replication of the target. All assays were performed as outlined in FIG. 25A and FIG. 25B, apart from the DNA assay where a capture sequence and a biotinylated signal sequence were used in place of capture and detection antibodies, respectively. FIGS. 14A-14C show data from

the assays for A) PSA, B) TNF-α, and C) DNA. The human forms of the proteins were spiked into 25% bovine serum to be representative of clinical test samples; a four-fold dilution factor was used which may reduce matrix effects in immunoassays. DNA was detected in buffer to be representative of purified nucleic acid preparation techniques. Using digital detection to detect PSA in 25% serum, an LOD of 46 aM (1.5 fg/mL) was attained, equating to 184 aM in whole serum. A leading commercial PSA assay (ADVIA Centaur, Siemens) reports an LOD of 3 pM (0.1 ng/mL) in human serum, and ultra-sensitive assays have been reported with LODs in the range of 10–30 fM. The single molecule assay of the present Example was, therefore, more sensitive than the commercial assay by a factor of 15,000, and more sensitive than other ultra-sensitive methods by a factor of at least 50. The detection limit in the TNF-α determination was 148 aM (2.5 fg/mL), corresponding to 590 aM in whole serum. The highest sensitivity commercially-available ELISA for TNF-α has an LOD of 21 fM (0.34 pg/mL) in serum (Table 1). The assay of the present Example, therefore, imparted an improvement over the most sensitive TNF-α assay of a factor of 35. The LOD of the digital DNA sandwich assay was 135 aM, corresponding to about 8000 copies. The ability of certain assays of the present invention to potentially measure much lower concentrations of proteins compared to conventional techniques arises from the extremely low background signals that may be achieved by digitizing the detection of proteins.

FIGS. 14A-14C shows the attomolar detection of proteins in serum and DNA in buffer using digital detection. Plots of % active beads against analyte concentration for: (FIG. 14A) human PSA spiked into 25% serum, (FIG. 14B) human TNF-α spiked into 25% serum, and (FIG. 14C) DNA in buffer. The bottom row of plots shows the low-end of the concentration range. Assays were performed by sequentially incubating specific capture beads with target solution, biotinylated detector, and SβG conjugate. After completion of the assay, beads were loaded into femtoliter well arrays and interrogated for the presence of single immunocomplexes.

Background in the inventive digital detection immunoassays may arise, at least in part from non-specific binding (NSB) of detection antibody and enzyme conjugate to the capture bead surface (Table 3). Because the inventive assays can provide improved label sensitivity over conventional assays (FIG. 15), significantly less detection antibody (~1 nM) and enzyme conjugate (1–50 pM) can be used to detect binding events compared to conventional assays (labeling reagent concentrations ~10 nM). The decreased label concentration may result in substantially reduced NSB to the capture

surface, resulting in much lower background signals and lower LODs. For example, in the TNF-α and PSA determinations as described above, the NSB levels were equivalent to the signal produced by 1.8 fM and 1.2 fM of target protein, respectively. The highest sensitivity commercial TNF-α assay has an NSB level equivalent to 85 fM of TNF-α (FIG. 26), a factor of 50 higher. The ability to reduce backgrounds in certain assays of the present invention by lowering the concentration of labeling reagents can translate to immunoassays with improved sensitivity over conventional assays.

Table 3. NSB dropout data.

NSB Dropout Experiment (SiMoA PSA assay)					
	Average	SD	CV	% NSB	
No dAb; No PSA	0.110%	0.162%	147%	from SbG	20%
No SbG; No PSA	0.000%	0.000%	---	from dAb	80%
NSB	0.541%	0.194%	36%	Total NSB	100%

In Table 3, a dropout experiment isolating the sources of NSB in the PSA digital assay. By comparing 'no detection antibody NSB' (No dAb) and 'no SβG NSB' (No SβG) to total NSB (NSB), the contribution of detection antibody and SβG to the NSB of the assay was determined.

To demonstrate the unique diagnostic measurements that could be afforded by detecting single molecules of a protein in human clinical samples, PSA was measured in serum samples from patients who had undergone radical prostatectomy (RP). PSA is a serum biomarker for prostate cancer used as both a screening tool and to monitor for the biochemical recurrence of patients who have undergone radical prostatectomy. After radical prostatectomy, the vast majority of PSA is eliminated, and levels fall below the detection limit of standard commercial assays (3 pM or 0.1 ng/mL). Regular monitoring of these patients for return of PSA can detect recurrence of prostate cancer, but several years may pass post-surgery for biochemical recurrence to be detected by current immunoanalyzers. The ability to accurately quantify PSA levels in post-prostatectomy patients at very low concentrations (<3 fM or 100 fg/mL) may provide early indication of recurrence should PSA levels increase. FIG. 27 shows PSA levels measured using the assay of this Example in the serum of thirty patients (age 60–89) who had undergone radical prostatectomy and whose blood was collected at least 6 weeks post-surgery. The PSA levels in the sera of all 30 patients were below the detection limit of commercial assays. Here, whole serum samples were diluted 1:4 in buffer and measured using the

PSA digital assay of this Example (FIG. 14A). PSA was successfully detected in all 30 patients using the present assay. Nine of the thirty samples fell below the LOD of the previously highest sensitivity PSA assay. These data demonstrate a potential clinical utility of certain inventive assays for measuring proteins in serum at concentrations well below the capability of current technology. Table 4 summarizes the patient results.

FIG. 27 shows digital detection of PSA in serum samples of patients who had undergone radical prostatectomy. The concentrations of PSA were determined using the assay of the present Example in serum samples from RP patients (circles (iv)), healthy control samples (circles (ii)), and Bio-Rad PSA control samples (circles (i)). RP patient samples were obtained from SeraCare Life Sciences (Milford, MA) and all had undetectable PSA levels as measured by a leading clinical diagnostic assay (ADVIA Centaur); line (iv) represents the detection limit of the ADVIA Centaur PSA assay (100 pg/mL or 3 pM). All 30 patient samples were above the detection limit of the inventive PSA digital assay, shown by the line (v) (0.00584 pg/mL or 184 aM), with the lowest patient PSA concentrations measured at 0.014 pg/mL (420 aM) using the present assay. Patient samples with the lowest PSA levels were detectable, but approached the LOD of the assay resulting in a high dose %CV. The present assay was validated for specificity to PSA using control standards (Bio-Rad) and serum from healthy individuals (ProMedDx) that had been assayed using the ADVIA Centaur PSA assay (See Table 5).

Table 4. Summary of Patient Results

Patient ID	[PSA] (pg/mL)	Dose %CV	Patient ID	[PSA] (pg/mL)	Dose %CV	Patient ID	[PSA] (pg/mL)	Dose %CV
S600	9.39	6%	S590	0.22	22%	S580	0.30	4%
S599	0.75	10%	S589	0.85	17%	S579	1.22	15%
S598	2.71	12%	S588	2.33	3%	S578	0.090	91%
S597	1.79	12%	S587	1.06	13%	S577	1.92	6%
S596	2.46	17%	S586	1.29	22%	S576	0.014	286%
S595	0.32	21%	S585	0.49	84%	S575	0.79	63%
S594	1.63	15%	S584	0.056	136%	S574	1.62	20%
S593	1.15	12%	S583	1.33	26%	S573	0.22	32%
S592	3.46	9%	S582	4.76	9%	S572	1.04	20%
S591	0.21	25%	S581	1.57	31%	S571	0.24	21%

Table 5.

	Centaur (ng/mL)	Assay Method of the present invention (ng/mL)
Bio-Rad Control 1	0.838	1.06 ± 0.21
Bio-Rad Control 2	2.47	2.66 ± 0.36
Normals		
ProMedDx S376	2.1	1.60
ProMedDx S378	2.3	1.70
ProMedDx S381	2.9	2.14
ProMedDx S388	4.1	3.95
ProMedDx S395	0.93	0.63
ProMedDx S396	0.9	0.77
ProMedDx S397	1.2	0.66

Table 5 shows the specificity of the present assay was confirmed using PSA samples from Bio-Rad (controls) and ProMedDx (serum from healthy individuals) that had previously been tested on a commercial immunoanalyzer (ADVIA Centaur, Siemens). The PSA concentrations of the healthy serum samples determined using the exemplary method were (24±12)% lower than those originally determined on the ADVIA Centaur. There are two possible explanations for this systematic bias between the two technologies. First, the ADVIA Centaur values were obtained on fresh serum, whereas values for the present assay were obtained after the sera had been frozen for extended periods of time and had experienced a freeze-thaw cycle. Second, there may be differences between the PSA calibrators used to generate the calibration curves that would result in differences in PSA concentrations determined. Complex PSA from the World Health Organization (WHO) was used as calibrators; the ADVIA Centaur calibration PSA is unknown.

By isolating and detecting single immunocomplexes formed in ELISA, certain assays of the invention can impart sensitivity, precision, and dynamic range improvements over standard readout methods and other known ultra-sensitive approaches. While certain of the inventive assays can provide sensitivity below the detectable limit of standard and ultra-sensitive readout formats in serum, potentially two more logs of sensitivity may be available based on the enzyme label LOD (FIG. 15). The ability to isolate and interrogate single molecules on individual beads according to certain embodiments of the invention may facilitate distinguishing true antibody-antigen binding events from non-specifically bound complexes. Identifying and differentiating these two populations may permit the detection of a single biomarker molecule in a human serum sample.

Capture of proteins on magnetic beads and formation of enzyme-labeled immunocomplex (FIG. 14 and 27). Beads functionalized with an antibody to the target protein were prepared according to the manufacturer's instructions. Test solutions containing the protein of interest were incubated with suspensions of 200,000 magnetic beads for 2 h at room temperature. The beads were then separated and washed three times in PBS and 0.1% Tween-20. The beads were resuspended and incubated with solutions containing detection antibody (typically, 1–3 nM) for 45 min at room temperature. The beads were then separated and washed three times in PBS and 0.1% Tween-20. The beads were incubated with solutions containing SβG (1–50 pM) for 30 min at room temperature, separated, and washed six times in PBS and 0.1% Tween-20. The beads were then resuspended in 10 μL of PBS and loaded onto a femtoliter well array.

Example 20

FIG. 28 shows a histogram of the average fluorescence intensity of reaction vessels in an experiment of the present invention. A representative set of images from the experiment were analyzed to determine populations of reaction vessels that: (i) contained no beads; (ii) contained a bead (from white light scatter) but no enzyme (no increase in fluorescence intensity); and, (iii) contained a bead (from white light scatter) and an enzyme (increasing fluorescence intensity over four consecutive images, and an overall increase in fluorescence of at least 20%). Specifically, line (i) represents data from empty reaction vessels, line (ii) represents reaction vessels with a bead but no enzyme ("off" beads), and line (iii) represents reaction vessels with both a bead and enzymatic activity ("on" beads).

Example 21

The following example describes determination of assay locations comprising a capture object using capture objects (e.g., beads) which are fluorescent.

In some cases, it may be advantageous to determine the presence or absence of beads in a location (e.g., well in this example) using methods other than dark field detection methods. In some cases, dark field detection methods may not be ideal because 1) the scattering light source may send a non-uniform field of light to the beaded array surface and thus, the intensity distribution of scattered light produced by wells comprising beads may be broad and beaded wells that are in the extreme high or extreme

low intensity region of the distribution may not be accurately determined to contain a bead.; 2) small differences in scatter from beaded and empty wells may result in detection algorithms based on local, well-to-well differences in scattering lacking desired accuracy at high bead occupancy because the well-to-well differences are to small to be consistently detected; and 3) the use of dark field scatter to detect beads may eliminate using different bead types on the same array for multiplexing purposes

Microspheres of many different colors and fluorescent emission wavelengths are commercially available and some were employed in an assay as described herein. Emission wavelengths were chosen so there was no spectral overlap with readout wavelengths for detecting resorufin dye produced by single enzyme molecule catalysis (570/590 excitation/emission) which were used in this example as the detected entity,. In experiments investigating commercially available fluorescent beads (e.g., FITC labeled and Qdot 525 labeled beads), the amount of fluorescent dye loaded into the beads, in some cases, was so high that the bead fluorescence bled into the resorufin channel (570/590). It is important in some embodiments to have low background fluorescence over the wavelengths of detection of the analyte molecules because the amount of fluorescence product in the wells (e.g., from the analyte molecules) may be relatively small.

Accordingly, in this example, beads were loaded (e.g., as described below) with varying quantities of dyes so that the beads could be easily counted by the imaging system, while keeping the amount of dye low enough so it did not interfere with the current background level of the system. In this example, each bead surface comprised about 100,000 antibody molecules (e.g., capture components), and only a very small fraction of these antibodies are then used to associate an analyte molecule or particle. For example, if about 10 analyte molecules associate with a bead on average, only 10 capture antibody molecules (0.01 % of capture components) have bound a target molecule which are then detected by the system. Due to the large fraction of unused antibodies available on the bead surface, the dye labeling approach in this example employed covalent attachment of dye molecules directly to the antibodies on the bead surface.

Alexa Fluor® 488 sulfodichlorophenol ester (AF-488 SDP ester) is an amine reactive dye molecule purchased from Invitrogen that was used in this example. Antibody coated beads were incubated with various molar ratios of the AF-488 SDP ester. Antibody:AF-488 SDP ester molar ratios from 1:27 to 1:800 were tested, all of

which gave bright signal in the Alexa 488 channel. FIG. 29A shows the antibody beads modified at a 1:27 ratio. The beads were seen in the Alexa 488 channel, while the background resorufin channel fluorescence of the AF-488 modified beads appears to be comparable to the standard unmodified antibody beads. Specifically, FIG. 29A shows an image of a portion of the standard array using the resorufin channel; FIG. 29B an image of a portion of the Alexa 488 modified 1:27 molar ratio beads using the resorufin channel; and FIG. 29C an image of a portion of the Alexa 488 modified 1:27 molar ratio beads using the Alexa 488 channel.

Table 6 shows the relative intensities of both the Alexa 488 modified beads and the standard unmodified beads in both fluorescent channels. The standard beads give a similar background fluorescence in both channels, and the Alexa 488 beads give a bright signal in the Alexa channel (~400 counts) while maintaining a resorufin background signal that is comparable to the standard beads.

Table. 6

Upright Imager Results			
standard beads			
	average	stdev	%cv
Alexa intensity beaded	98.37	8.13	8%
Alexa intensity empty	52.14	8.22	16%
Net signal	46.23		
	average	stdev	%cv
Resorufin intensity beaded	134.16	16.28	12%
Resorufin intensity empty	97.09	3.86	4%
Net signal	37.08		
Alexa488 labeled beads			
	average	stdev	%cv
Alexa intensity beaded	469.85	89.04	19%
Alexa intensity empty	64.53	1.44	2%
Net signal	405.32		
Resorufin intensity beaded	114.93	5.45	5%
Resorufin intensity empty	85.06	3.79	4%
Net signal	29.86		

By comparing the intensity of the modified beads to an Alexa-488 calibration curve, each bead was calculated to have approximately 5,000 Alexa-488 dye molecules

bound. With such a low number of dye molecules on the bead surface, experiments were performed to assess if the Alexa-488 labeling procedure negatively impacted the antibody beads in a protein detection assay. The antibody beads that were labeled with Alexa-488 dye specifically bind Tau protein, for a protein relevant to Alzheimer's disease. Control beads and Alexa-488 beads with Tau specific capture antibody were compared in an assay similar to those described in Examples 3, 5, 8, 9, and 10 above but with anti-Tau antibodies The results shown in FIG. 29D suggest that the Alexa-488 conjugation has little or no negative impact on bead performance in the assay. Specifically, FIG. 29D shows results comparing signal from control beads and Alexa-488 labeled beads for the Tau assay.

While the initial assay results show that the Alexa-488 conjugation has little or no negative impact on the performance of the antibody beads used in the assay, it was also determined whether the Alexa-488 labeling resulted in a bead counting advantage over unlabeled assay beads. The results of this determination are summarized in Table 7. The results were determined using two modes of analysis of a single strip using Alexa-488 conjugated beads in the Tau assay. This strip was analyzed using the standard dark field method, and also the Alexa-488 detection method. Results comparing the dark field method to the fluorescence detection method for counting beads reveal an improvement in the Alexa-488 detection method over the dark field method. Across the arrays, anywhere from 1300 to 6500 beads were not counted using dark field imaging.

Table 7.

Strip 242, beads counted using dark field imaging					
Conc.	T. Pos. PreMorph	Beads	% Active		
0.00 pg/mL	586	25806	2.271		
0.00 pg/mL	532	28584	1.861		
0.00 pg/mL	685	31899	2.147		
6.25 pg/mL	14969	28625	52.293		
6.25 pg/mL	15988	26330	60.722		
6.25 pg/mL	17456	30850	56.583		
25.00 pg/mL	32482	32741	99.209		
25.00 pg/mL	28028	28155	99.549		
Strip 242, beads counted using Alexa channel					
Conc.	T. Pos. PreMorph	Beads	% Active	bead increase	% increase
0.00 pg/mL	735	31890	2.305	6084	23.58%
0.00 pg/mL	553	29954	1.846	1370	4.79%
0.00 pg/mL	756	35299	2.142	3400	10.66%
6.25 pg/mL	17277	33045	52.283	4420	15.44%
6.25 pg/mL	19735	32528	60.671	6198	23.54%
6.25 pg/mL	21086	37385	56.402	6535	21.18%
25.00 pg/mL	36222	36497	99.247	3756	11.47%
25.00 pg/mL	33144	33245	99.696	5090	18.08%

Example 22

In the certain embodiments of assay methods of the present invention, there may be a variation in the elapsed time between addition of detector antibody and interrogation of certain arrays or regions of arrays versus interrogation of other arrays or regions. In certain cases, dissociation that may occur over such time intervals may result in inaccuracies in later made versus earlier made determinations of analyte molecule concentrations. This example investigated the effect of measures to reduce dissociation on the time variant accuracy of assay determinations. In this example, the assay comprised the following steps:

1. Immunocomplexes of enzyme-labeled PSA molecules (capture anti-PSA, PSA in serum, biotinylated detection anti-PSA, and SβG) were formed on magnetic beads and washed using methods similar to those described in Examples 3 and 5. Magnetic beads presenting immunocomplexes were exchanged into buffer containing a certain carbohydrate (e.g., sucrose, tehalose, etc.), or any other molecular species that can help maintain hydration state of proteins.
2. After loading beads into the microwells of fiber bundle arrays using methods similar to those described in Example 9, excess of buffer was removed by air/vacuum drying.
3. The fiber bundle with beads loaded were stored for various periods of time.
4. Right before signal generating/array read out, the dried fiber bundles were dipped in PBS buffer, wiped with a swab, dipped in PBS buffer again, and then dipped in a solution containing 100 μM RGP. The arrays were then sealed and read out using methods similar to those described above in Example 10.

Dissociation of the biotinylated detection antibody from the captured analyte molecule, in particular, can cause a continual signal drop over time. In certain cases, dissociation can account for more than a 50% signal drop over the course of interrogation of an array or series of arrays during conduct of an assay (e.g., see FIG. 30A). FIG. 30A shows data from the similar experiments carried out over four different days. In these experiments, immunocomplexes of enzyme-labeled PSA were prepared simultaneously on beads in 64 wells of a 96-well plate that were arranged in 8-well columns. The beads from each column were then tested on a strip of 8 arrays using single molecule detection (Example 10) at increasing times (shown on the x-axis). Each data point is the average concentration of PSA determined from a column of 8 wells by comparison to a calibration curve that was obtained before the first column was tested. .

This signal drop over time (which is manifested as a drop in the concentration of PSA that is determined) may be more pronounced in assays using proteins as reagents/targets than in assays involving nucleic acids (e.g. DNA). The decrease of signal fits to a dissociation model in certain cases.

By carrying out drying of the wells in the present Example, the dissociation effects was eliminated and/or reduced by up to 90% (e.g., see FIG. 30B).

Those of ordinary skill in the art will be aware that while traditional immunoassays (e.g., ELISA) can suffer from signal loss due to dissociation of detection entities, in general, they do not require special treatment for the dissociation of immunocomplex because the plates are read out very quickly. For example, within a minute or so, a microplate reader can generate signal for a full 96-well plate. The difference in dissociation between well 1 and well 96 within this time frame is negligible. However, for assays like the methods described herein wherein interrogation of the assay sites may in certain cases take a longer time period, dissociation may affect the precision and/or accuracy of the methods. Accordingly, the process of drying the assay sites can prevent loss of an analyte molecule and/or binding ligand and reduce effects of dissociation.

In some embodiments, additional components may be provided which maintain the native configuration and/or biological activity of analyte molecules (e.g., proteins) in the microwells and which can protect the immunocomplexes and/or labeling agent(s) (e.g. enzyme(s)) during the drying/rehydration process. For example, routine screening tests may be used to identify agents that can keep an antibody/antigen/enzyme complex intact and/or maintain enzyme activity after drying/rehydration. Without such agents, drying may denature and/or deactivate enzymes or other components of the assay. For example, screening of known nonionic kosmotropes revealed that carbohydrates help keep 90-100% of the immunocomplex signal after drying/rehydration treatment. Carbohydrates and other molecules may be used to maintain antibody active during dehydration in protein array assay and/or may be used to keep protein activity during dehydration/lyophilization.

Example 23

The following example describes the crosslinking of a binding ligand to an analyte molecule to aid in the prevention of disassociation of the binding ligand from the analyte molecule. In this assay, enzyme labeled PSA immunocomplexes were formed on

beads using methods similar to those described in Example 3, 5, and 22, using concentrations of PSA of 0, 0.1, and 1 pg/mL spiked into serum. One set of beads were reacted with 10 mg/mL of EDC for 10 minutes to cross-link the detection antibody to other proteins associated with the beads, e.g., PSA, capture antibody and blocking proteins. Control beads were not reacted with EDC. Control bead were then read using methods similar to those described above in Example 10 at t = 0 and then 2 hours later. The cross-linked beads were also read using methods similar to as described in Example 10 at about 2 hours after crosslinking The result showed that after 2 hours the average number of enzymes per bead on the control beads was reduced because of dissociation of the detection antibody. The crosslinked beads, however, maintained the high AEB even after 2 hours. These data suggest that crosslinking the detection antibody to proteins irreversibly associated with the beads substantially eliminated the dissociation effects. In addition, crosslinking boosted the signal, also as shown in FIG. 31 (EDAC-treated; (ii)) relative to the 0 hour wait (i) presumably because of the extra dissociation time the control beads experienced before being read.

While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the present invention. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the teachings of the present invention is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, the invention may be practiced otherwise than as specifically described and claimed. The present invention is directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or

methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the scope of the present invention.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

In the claims, as well as in the specification above, all transitional phrases such as "comprising," "including," "carrying," "having," "containing," "involving," "holding," and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively.

What is claimed:

Claims

1. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at least one type of analyte molecules or particles;

immobilizing analyte molecules or particles with respect to the plurality of capture objects such that at least some of the capture objects associate with at least one analyte molecule or particle and a statistically significant fraction of the capture objects do not associate with any analyte molecule or particle;

spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing an analyte molecule or particle; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of locations determined to contain an analyte molecule or particle.

2. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at least one type of analyte molecules or particles to form capture objects comprising at least one immobilized analyte molecule or particle;

mixing the capture objects prepared in the exposing step to a plurality of binding ligands such that at least some of the capture objects associate with a single binding ligand and a statistically significant fraction of the capture objects do not associate with any binding ligand;

spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of locations containing a binding ligand; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of locations determined to contain a binding ligand.

3. The method of claim 1 or 2, wherein the percentage of capture objects which associate with at least one analyte molecule and/or binding ligand is less than about 50%, less than about 40%, less than about 30%, less than about 20%, less than about 10%, or less than about 5%, or less than about 1%, or less than about 0.5%, or less than about 0.1% or the total number of capture objects.

4. The method of claim 1 or 2, wherein the percentage of capture objects which do not associated with any analyte molecules and/or binding ligands is at least about 20%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95%, or at least about 99%, or at least about 99.5%, or at least about 99.9%, of the total number of capture objects.

5. The method of claim 1 or 2, wherein in the addressing step, the number of said locations containing a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle not containing an analyte molecule or particle or a binding ligand is determined.

6. The method of claim 5, wherein the measure of the concentration of analyte molecule or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle containing an analyte molecule or particle or a binding ligand, to the total number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle.

7. The method of claim 5, wherein the measure of the concentration of analyte molecule or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle containing an analyte molecule or particle or a binding ligand, to the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle but not to contain any capture objects that include a binding surface having affinity for at least one type of analyte molecule or particle containing an analyte molecule or particle or a binding ligand.

8. The method of claim 1 or 2, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle containing an analyte molecule or particle or binding ligand, to the number of locations addressed in the addressing step that do not contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle.

9. The method of claim 1 or 2, wherein the plurality of capture objects that include a binding surface having affinity for at least one type of analyte molecule or particle comprises a plurality of beads.

10. The method of claim 1 or 2, wherein the plurality of locations comprises a plurality of reaction vessels.

11. The method of claim 10, wherein the plurality of reaction vessels is formed on the end of a fiber optic bundle.

12. The method of claim 1, wherein at least a portion of the analyte molecules or particles are associated with at least one binding ligand.

13. The method of claim 1, wherein the analyte molecules or particles comprise an enzymatic component.

14. The method of claim 2 or 12, wherein the binding ligand comprises an enzymatic component.

15 The method of claim 1 or 2, wherein the concentration of analyte molecules or particles in the fluid sample is less than about 50×10^{-15} M, or less than about 40×10^{-15} M, or less than about 30×10^{-15} M, or less than about 20×10^{-15} M, or less than about 10×10^{-15} M, or less than about 5×10^{-15} M, or less than about 1×10^{-15} M.

16. The method of claim 1 or 2, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standard.

17. The method of claim 1, wherein during the immobilizing step, at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90%, or at least about 95% of the analyte molecules or particles are immobilized with respect to a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle.

18. The method of claim 2, wherein during the mixing step, at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% of the immobilized analyte molecules or particles associate with a binding ligand.

19. The method of claim 1 or 2, wherein during the spatially segregating step, at least about 5%, or at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% of the capture objects subjected to the immobilizing steps are spatially separated into the plurality of locations.

20. The method of claim 10, wherein the number of reaction vessels addressed in the addressing step is at least about 5%, or at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% of the total number of reaction vessels.

21. The method of claim 1 or 2, wherein the portion of the capture objects that include a binding surface having affinity for at least one type of analyte molecule or particle are spatially separated by exposing the plurality of locations to a solution comprising the plurality of capture objects.

22. The method of claim 2 or claim 12, wherein following the spatially segregating step, the locations are exposed to precursor labeling agent.

23. The method of claim 22, wherein the precursor labeling agent is converted to a labeling agent upon exposure to a binding ligand.

24. The method of claim 23, wherein the number of locations containing a capture object containing an analyte molecule or particle or a labeling agent is determined by determining the number of locations comprising a labeling agent.

25. The method of claim 23, wherein the labeling agent is a chromogenic, fluorescent, or chemiluminescent.

26. The method of claim 1 or 2, wherein the analyte molecules or particles are proteins.

27. The method of claim 1 or 2, wherein the analyte molecules or particles are nucleic acids.

28. The method of claim 10, wherein the plurality of reaction vessels are formed upon the mating of at least a portion of a sealing component and at least a portion of a substrate.

29. The method of claim 10, wherein the plurality of reaction vessels are formed in a planar substrate.

30. The method of claim 10, wherein the average volume of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters.

31. The method of claim 10, wherein the average volume of the plurality of reaction vessels is between about 1 femtoliter and about 1 picoliter.

32. The method of claim 9, wherein the average diameter of the plurality of beads is between about 0.1 micrometer and about 100 micrometers.

33. The method of claim 9, wherein the average diameter of the plurality of beads is between about 1 micrometer and about 10 micrometers.

34. The method of claim 1 or 2, further comprising performing at least one wash step.

35. The method of claim 10, further comprising sealing the plurality of reaction vessels.

36. The method of claim 1 or 2, wherein the plurality of locations is addressed using optical techniques.

37. The method of claim 1 or 2, wherein the binding surface comprises a plurality of capture components.

38. The method of claim 1, wherein the percentage of locations addressed in the addressing step determined to contain an analyte molecule or particle is less than about 10%, or less than about 5%, or less than about 1%, or less than about 0.1% of the total number of locations addressed.

39. The method of claim 2, wherein the percentage of locations addressed in the addressing step determined to contain a binding ligand is less than about 10%, or less

than about 5%, or less than about 1%, or less than about 0.1% of the total number of locations addressed.

40. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

providing a substrate comprising a plurality of locations, at least a portion of which locations contain a bead, wherein with respect to the total number of beads present on the substrate, the ratio of beads comprising at least one analyte molecule or particle to beads comprising no analyte molecules or particles is between about 8:1 and about 1:10,000,000;

addressing at least a portion of the plurality of locations, wherein during the addressing step at least two of the plurality of locations is addressed at least partially concurrently;

detecting at each addressed location the presence or absence of a bead and whether, if present, the bead comprises any analyte molecules or particles; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample at least in part by determining the number of locations addressed containing a bead comprising at least one analyte molecule or particle.

41. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

providing a substrate comprising a plurality of locations, at least a portion of which contain a bead, wherein with respect to the total number of beads present on the substrate, the ratio of beads comprising at least one analyte molecule or particle associated with a binding ligand to beads comprising no analyte molecules or particles associated with a binding ligand is between about 8:1 and about 1:10,000,000;

addressing at least a portion of the plurality of locations, wherein during the addressing step at least two of the plurality of locations is addressed at least partially concurrently;

detecting at each addressed location the presence or absence of a bead and whether, if present, the bead comprises any analyte molecules or particles associated with a binding ligand; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample at least in part by determining the number of locations addressed

containing a bead comprising at least one analyte molecule or particle associated with a binding ligand.

42. The method of claim 40 or 41, wherein the ratio is between about 2:1 and about 1:1,000,000.

43. The method of claim 40 or 41, wherein the ratio is between about 1:10 and about 1:100,000.

44. The method of claim 40 or 41, wherein the ratio is between about 2:1 and about 1:10.

45. The method of claim 40 or 41, wherein in the addressing step, the number of said locations containing a bead but not containing any beads comprising an analyte molecule or particle or a binding ligand is determined.

46. The method of claim 40 or 41, wherein in the addressing step, the number of said locations containing a bead is determined.

47. The method of claim 46, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a bead comprising an analyte molecule or particle or binding ligand, to the number of locations addressed in the addressing step determined to contain a bead.

48. The method of claim 45, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a bead comprising an analyte molecule or particle or binding ligand, to the number of locations addressed in the addressing step determined to contain a bead but not to contain any beads comprising an analyte molecule or particle or a binding ligand.

49. The method of claim 40 or 41, wherein the measure of the concentration of analyte molecule or particles in the fluid sample is based at least in part on the ratio of

the number of locations addressed in the addressing step determined to contain a bead comprising an analyte molecule or particle or binding ligand, to the total number of locations addressed.

50. The method of claim 40 or 41, wherein the plurality of locations comprise a plurality of reaction vessels.

51. The method of claim 50, wherein the plurality of reaction vessels is formed on the end of a fiber optic bundle.

52. The method of claim 3 or 4, wherein the percent of locations comprising at least one bead is greater than about 50%, or greater than about 60%, or greater than about 70%, or greater than about 80%, or greater than about 90%, or greater than about 95%.

53. The method of claim 40 or 41, wherein the analyte molecules or particles are proteins or nucleic acids.

54. The method of claim 40, wherein at least a portion of the analyte molecules or particles are associated with at least one binding ligand.

55. The method of claim 41 or 54, wherein the binding ligand comprises an enzymatic component.

56 The method of claim 40 or 41, wherein the concentration of analyte molecules or particles in the fluid sample is less than about 50×10^{-15} M.

57. The method of claim 40 or 41, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standard.

58. The method of claim 40 or 41, wherein each of the capture objects comprising at least one analyte molecule comprise one, two, three, four, or five analyte molecules.

59. The method of claim 41 or 54, wherein following the providing step, the locations are exposed to precursor labeling agent.

60. The method of claim 59, wherein the precursor binding ligand is converted to a labeling agent upon exposure to a binding ligand.

61. The method of claim 60, wherein the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle containing an analyte molecule or particle or a labeling agent is determined by determining the number of locations addressed comprising a labeling agent.

62. The method of claim 59, wherein the labeling agent is a chromogenic, fluorescent, or chemiluminescent.

63. The method of claim 50, wherein the plurality of reaction vessels is formed upon the mating of at least a portion of a sealing component and at least a portion of a second substrate.

64. The method of claim 50, wherein the volume of each of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters.

65. The method of claim 40 or 41, wherein the average diameter of the beads is between about 0.1 micrometer and about 100 micrometers.

66. The method of claim 40 or 41, wherein the average diameter of the beads is between about 1 micrometer and about 10 micrometers.

67. The method of claim 40 or 41, further comprising performing at least one wash step.

68. The method of claim 40 or 41, wherein the plurality of locations is addressed using optical detection.

69. The method of claim 40 or 41, wherein the bead comprises a plurality of capture components.

70. The method of claim 50, wherein the number of reaction vessels addressed is at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% of the total number of reaction vessels.

71. An article or kit, comprising:

a plurality of beads having an average diameter between about 0.1 micrometer and about 100 micrometers; and

a substrate comprising a plurality of reaction vessels, wherein the average depth of the reaction vessels is between about 1.0 times and about 1.5 times the average diameter of the beads and the average diameter of the reactions vessels is between about 1.0 times and about 1.9 times the average diameter of the beads.

72. The article or kit of claim 71, wherein the average diameter of the plurality of beads is between about 1 micrometer and about 10 micrometers.

73. The article or kit of claim 71, wherein the average diameter of the plurality beads is between about 1 micrometer and about 5 micrometers.

74. The article or kit claim 71, wherein the plurality of reaction vessels is formed on the end of a fiber optic bundle.

75. The article or kit claim 71, wherein the article further comprises a sealing component.

76. The article or kit claim 71, wherein the average depth of the plurality of reaction vessels is between about 1.1 and about 1.3 times the average diameter of the beads.

77. The article or kit claim 71, wherein the average diameter of the plurality of reaction vessels is between about 1.3 and about 1.8 times the average diameter of the beads.

78. The article or kit of claim 71, wherein the average volume of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters.

79. The article or kit of claim 71, wherein the average volume of the plurality of reaction vessels is between about 1 femtoliter and about 1 picoliter.

80. The article or kit of claim 71, wherein the plurality of beads comprise binding surfaces having an affinity for at least one type of analyte molecule or particle.

81. The article or kit of claim 80, wherein the binding surfaces comprise a plurality of capture components.

82. The article or kit of claim 71, wherein the substrate comprises between about 1,000 and about 1,000,000 reaction vessels.

83. The article or kit of claim 71, wherein the substrate comprises between about 10,000 and about 100,000 reaction vessels.

84. The article or kit of claim 71, further comprising a plurality of control beads.

85. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of analyte molecule or particle, to a solution containing or suspected of containing the at least one type of analyte molecules or particles, wherein at least some of the capture objects become associated with at least one analyte molecule or particle;

mixing the plurality of capture objects prepared in the exposing step to a plurality of binding ligands comprising an enzymatic component such that a statistically significant fraction of the capture objects associated with at least one analyte molecule or particle associate with a single binding ligand;

spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of separate locations; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part by addressing at least a portion of the plurality of locations subjected to the spatially segregating step to determine the presence of the enzymatic component or a product of a reaction involving the enzymatic component.

86. The method of claim 85, wherein the analyte molecule or particle is a protein.

87. The method of claim 85, wherein the binding surface comprises a plurality of capture components.

88. The method of claim 85, wherein the reaction involving the enzymatic component comprises exposing the enzymatic component to a precursor labeling agent.

89. The method of claim 88, wherein the precursor labeling agent is converted to a labeling agent upon exposure to the enzymatic component.

90. The method of claim 89, wherein the labeling agent is chromogenic, fluorescent, or chemiluminescent.

91. The method of claim 85, wherein the enzymatic component comprises horseradish peroxidase, beta-galactosidase, or alkaline phosphatase.

92. The method of claim 85, wherein the plurality of locations comprise a plurality of reaction vessels.

93. The method of claim 92, wherein the plurality of reaction vessels is formed on the end of a fiber optic bundle.

94. The method of claim 85, further comprising determining the number of locations addressed in the determining step determined to contain an enzymatic component or a product of a reaction involving the enzymatic component.

95. The method of claim 94, further comprising determining the number of locations addressed in the determining step determined to contain a capture object that includes a

binding surface having affinity for at least one type of analyte molecule or particle but determined not to contain an enzymatic component or a product of a reaction involving the enzymatic component.

96. The method of claim 94, further comprising determining the number of locations addressed in the determining step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle.

97. The method of claim 94, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the number of locations addressed in the determining step determined to contain an enzymatic component or a product of a reaction involving the enzymatic component.

98. The method of claim 96, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the determining step determined to contain an enzymatic component or a product of a reaction involving the enzymatic component, to the number of locations addressed in the determining step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle.

99. The method of claim 95, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is based at least in part on the ratio of the number of locations addressed in the determining step determined to contain an enzymatic component or a product of a reaction involving the enzymatic component, to the number of locations addressed in the determining step determined to contain a capture object that includes a binding surface having affinity for at least one type of analyte molecule or particle but determined not to contain an enzymatic component or a product of a reaction involving the enzymatic component.

100. The method of claim 94, wherein the measure of the concentration of analyte molecules or particle in a fluid sample is based at least in part on the ratio of the number of locations addressed in the determining step determined to contain an enzymatic

component or a product of a reaction involving the enzymatic component to the total number of locations addressed.

101. The method of claim 85, wherein the locations are addressed optically.

102. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

immobilizing a plurality of analyte molecules or particles with respect to a plurality of beads;

spatially segregating at least a portion of the plurality of beads into a plurality of separate locations;

addressing at least some of the plurality of locations and determining the number of locations containing a bead;

further determining the number of said locations containing a bead and an analyte molecule or particle; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the ratio of the number of locations containing a bead and an analyte molecule and particle, to the number of locations containing a bead.

103. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

immobilizing a plurality of analyte molecules or particles with respect to a plurality of beads;

spatially segregating at least a portion of the plurality of beads into a plurality of separate locations;

addressing at least some of the plurality of locations and determining the number of locations containing a bead;

further determining the number of said locations containing a bead and an analyte molecule or particle; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the ratio of the number of locations containing a bead and an analyte molecule and particle, to the number of locations containing a bead but not containing any analyte molecules or particles.

104. The method of claim 102 or 103, wherein the number of said locations containing a bead is determined using optical techniques.

105. The method of claim 104, wherein the number of said locations containing a bead is determined using white light.

106. The method of claim 104, wherein the number of said locations containing a bead and an analyte molecule or particle is determined using fluorescence.

107. The method of claim 104, wherein the optical techniques comprises the use of a CCD detector.

108. The method of claim 104, wherein the optical techniques comprises the use of a CID, CMOS, sCMOS, or TDI device.

109. The method of claim 102 or 103, wherein the plurality of locations comprises a plurality of reaction vessels.

110. The method of claim 109, wherein the plurality of reaction vessels is formed on the end of a fiber optic bundle.

111. The method of claim 102 or 103, wherein at least a portion of the analyte molecules or particles are associated with at least one binding ligand.

112. The method of claim 102 or 103, wherein the analyte molecules or particles comprise an enzymatic component.

113. The method of claim 112, wherein the binding ligand comprises an enzymatic component.

114 The method of claim 102 or 103, wherein the concentration of analyte molecules or particles in the fluid sample is less than about 50×10^{-15} M, or less than about 40×10^{-15} M, or less than about 30×10^{-15} M, or less than about 20×10^{-15} M, or less than about 10×10^{-15} M, or less than about, or less than about 1×10^{-15} M.

115. The method of claim 102 or 103, wherein the measure of the concentration of analyte molecules or particles in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standard.

116. The method of claim 102 or 103, wherein during the spatially segregating step, at least about 5%, or at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% of the capture objects subjected to the immobilizing steps are spatially separated into the plurality of locations.

117. The method of claim 102 or 103, wherein the number of locations addressed in the addressing step is at least about 5%, or at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% of the total number of location.

118. The method of claim 102 or 103, wherein the plurality of beads each include a binding surface having affinity for at least one type of analyte molecule or particle.

119. The method of claim 102 or 103, wherein following the spatially segregating step, the locations are exposed to precursor labeling agent.

120. The method of claim 119, wherein the precursor binding ligand is converted to a labeling agent upon exposure to a binding ligand.

121. The method of claim 120, wherein the number of locations containing a capture object containing an analyte molecule or particle or a labeling agent is determined by determining the number of locations comprising a labeling agent.

122. The method of claim 120 wherein the labeling agent is a chromogenic, fluorescent, or chemiluminescent.

123. The method of claim 102 or 103, wherein the analyte molecules or particles are proteins.

124. The method of claim 102 or 103, wherein the analyte molecules or particles are nucleic acids.

125. The method of claim 109, wherein the average volume of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters.

126. The method of claim 109, wherein the average volume of the plurality of reaction vessels is between about 1 femtoliter and about 1 picoliter.

127. The method of claim 102 or 103, wherein the average diameter of the plurality of beads is between about 0.1 micrometer and about 100 micrometers.

128. The method of claim 102 or 103, wherein the average diameter of the plurality of beads is between about 1 micrometer and about 10 micrometers.

129. The method of claim 102 or 103, further comprising performing at least one wash step.

130. The method of claim 109, further comprising sealing the plurality of reaction vessels.

131. A method for determining a measure of the concentration of analyte molecules or particles in a fluid sample, comprising:

providing a plurality of capture objects that each are associated with either a single analyte molecule or particle or are free of any analyte molecules or particles;

individually addressing at least a portion of the capture objects and determining the number of said capture objects associated with an analyte molecule or particle; and

determining a measure of the concentration of analyte molecules or particles in the fluid sample based at least in part on the number of capture objects subjected to the addressing step determined to be associated with an analyte molecule or particle.

132. The method of claim 131, wherein the capture objects each include a binding surface having affinity for at least one type of analyte molecule or particle and the forming step comprises exposing the plurality of capture objects to a solution containing or suspected of containing the at least one type of analyte molecules or particles.

133. The method of claim 132, comprising a step of immobilizing analyte molecules or particles with respect to the plurality of capture objects such that a statistically significant fraction of the capture objects associate with a single analyte molecule or particle and a statistically significant fraction of the capture objects are free of any analyte molecule or particle.

134. The method of claim 133, comprising a step of individually isolating at least a portion of the capture objects subjected to the immobilizing step from the remainder of said portion of the capture objects.

135. The method of claim 134, wherein the capture objects comprise or are each contained within a liquid droplet that is immiscible within a fluid in which the droplet is suspended during at least the addressing step.

136. The method of claim 131, wherein at least a portion of the analyte molecules or particles are associated with at least one binding ligand.

137. The method of claim 131, wherein the analyte molecules or particles comprise an enzymatic component.

138. The method of claim 136, wherein the binding ligand comprises an enzymatic component.

139. The method of claim 131, wherein the concentration of analyte molecules or particles in the fluid sample is less than about 50×10^{-15} M, or less than about 40×10^{-15} M, or less than about 30×10^{-15} M, or less than about 20×10^{-15} M, or less than about 10×10^{-15} M, or less than about 5×10^{-15} M, or less than about 1×10^{-15} M.

140. The method of claim 131wherein the measure of the concentration of analyte molecules or particles in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standards.

141. The method of claim 131, wherein the plurality of locations is addressed using optical techniques.

Abstract

The present invention relates to systems and methods for detecting analyte molecules or particles in a fluid sample and in some cases, determining a measure of the concentration of the molecules or particles in the fluid sample. Methods of the present invention may comprise immobilizing a plurality of analyte molecules or particles with respect to a plurality of capture objects. At least a portion of the plurality of capture objects may be spatially separated into a plurality of locations. A measure of the concentration of analyte molecules in a fluid sample may be determined, at least in part, on the number of reaction vessels comprising an analyte molecule immobilized with respect to a capture object. In some cases, the assay may additionally comprise steps including binding ligands, precursor labeling agents, and/or enzymatic components.

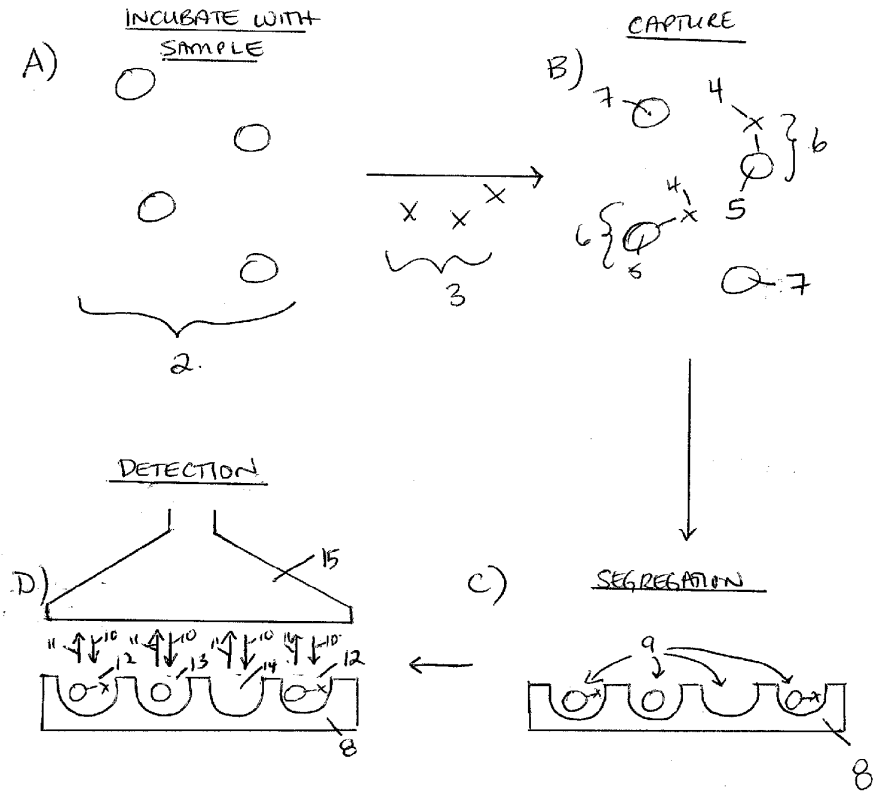

INCUBATE WITH SAMPLE
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SEGREGATION
C)
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DETECTION
D)
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FIG. 1

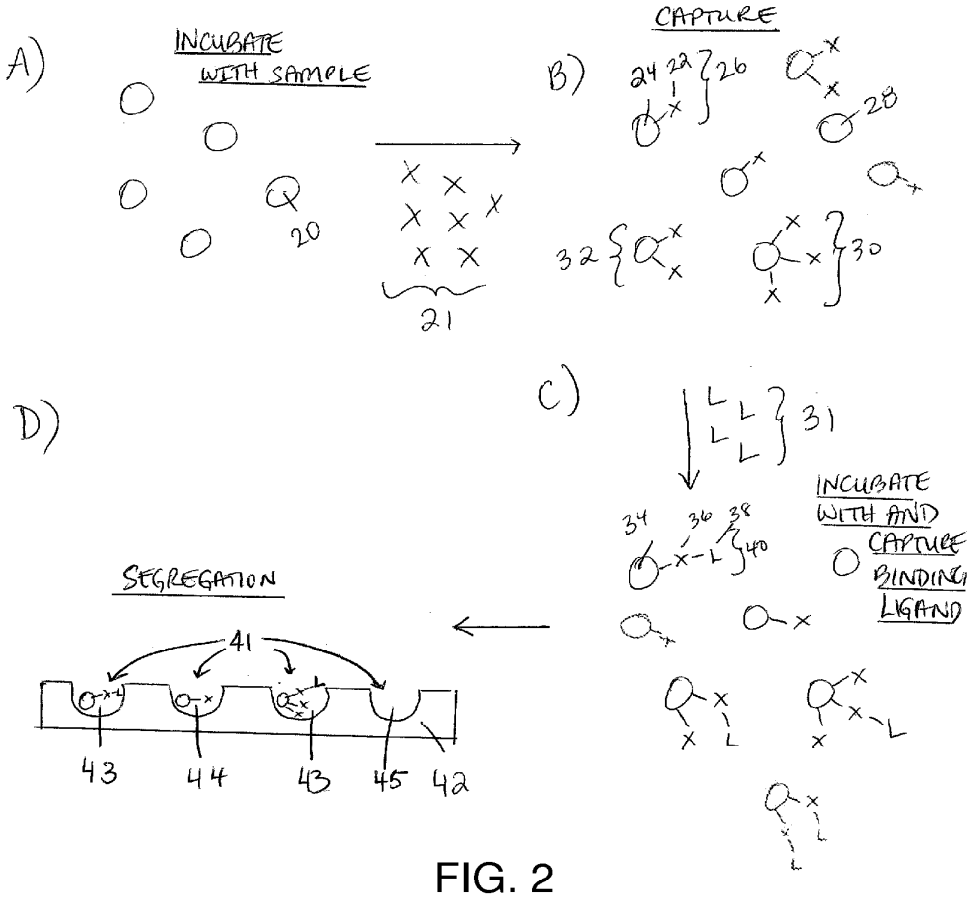

A)
INCUBATE WITH SAMPLE
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CAPTURE
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C)
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INCUBATE WITH AND CAPTURE BINDING LIGAND
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D)
SEGREGATION
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FIG. 2

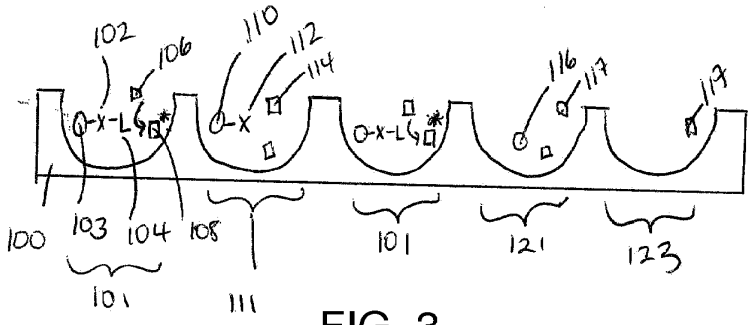

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FIG. 3

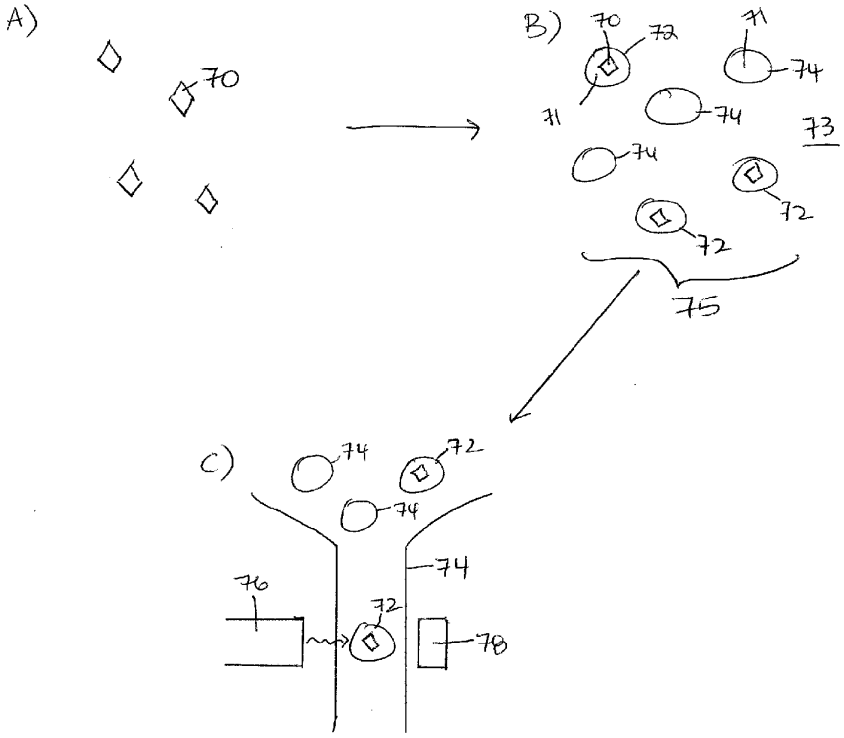

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C)
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FIG. 4A

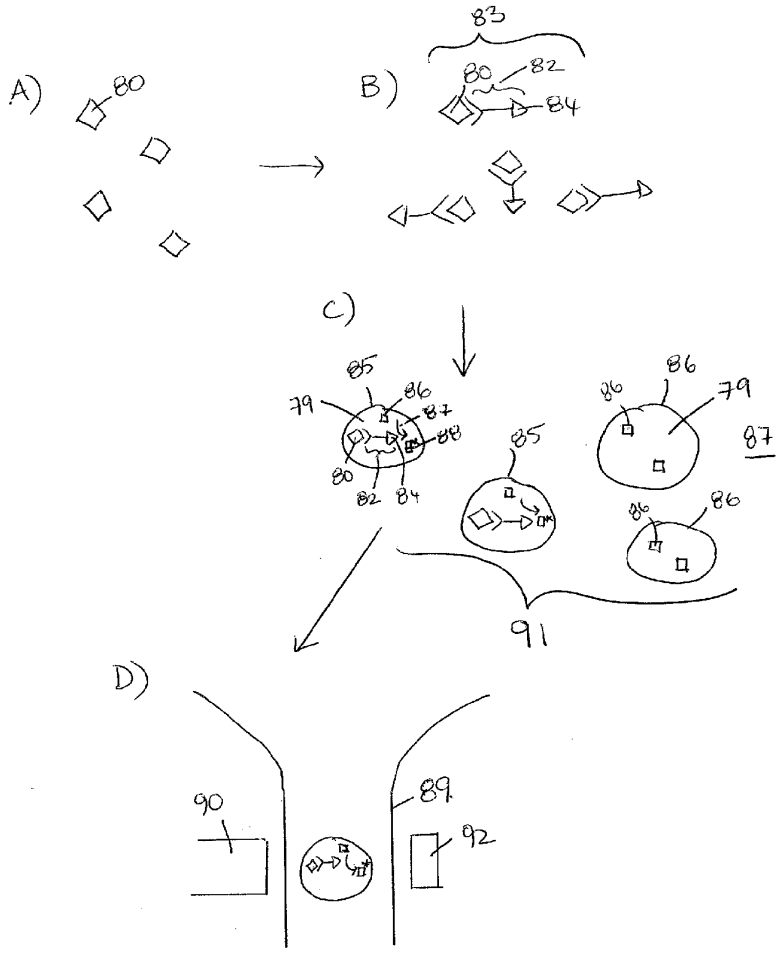

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FIG. 4B

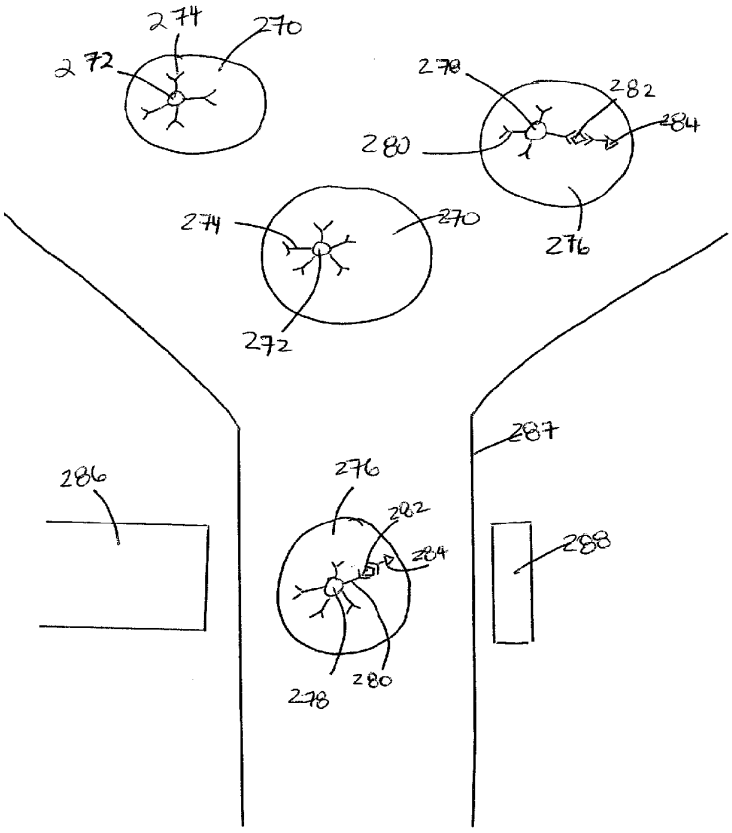

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FIG. 4C

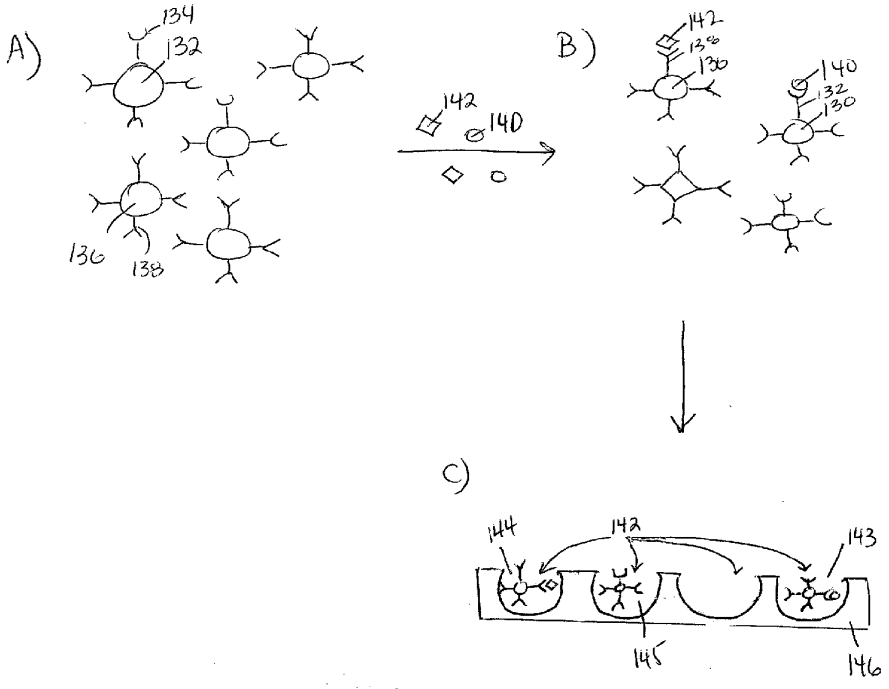

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B)
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C)
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FIG. 5

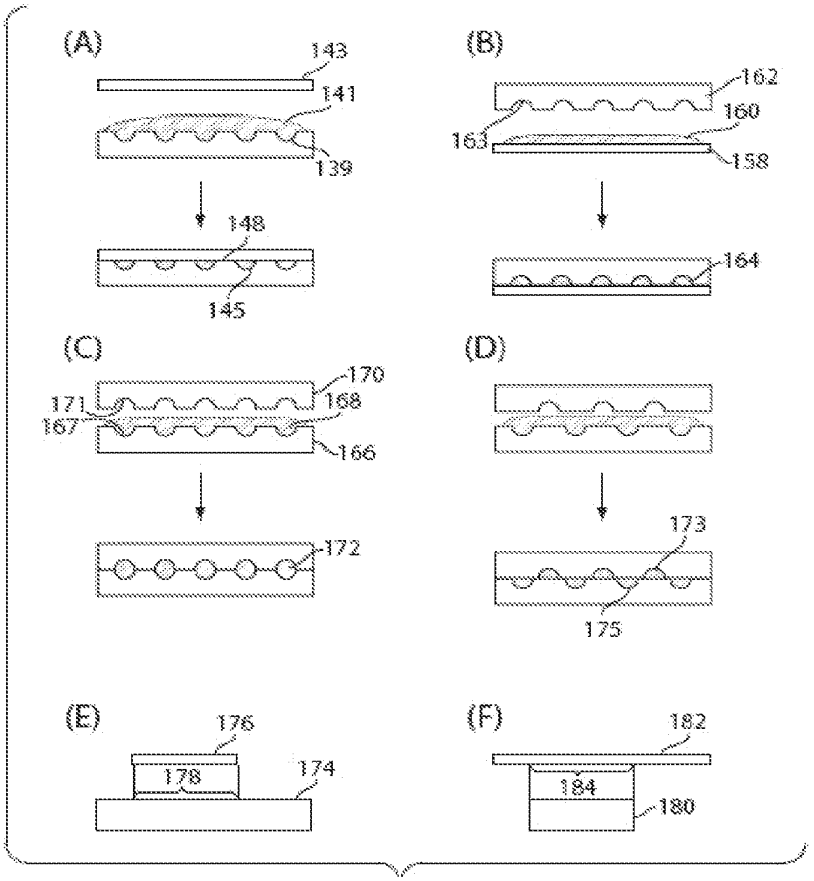

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(B)
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(C)
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(D)
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(F)
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180

FIG. 6

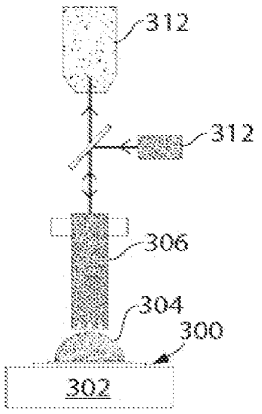


FIG. 7

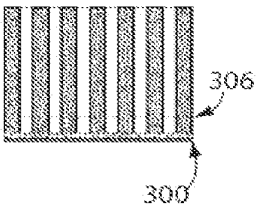


FIG. 8

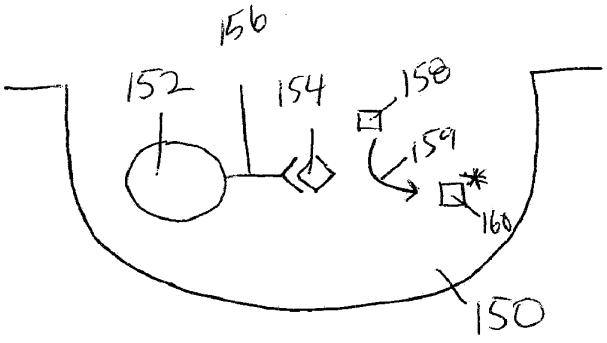


FIG. 9A

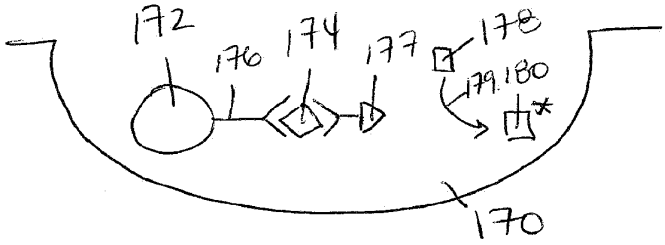


FIG. 9B

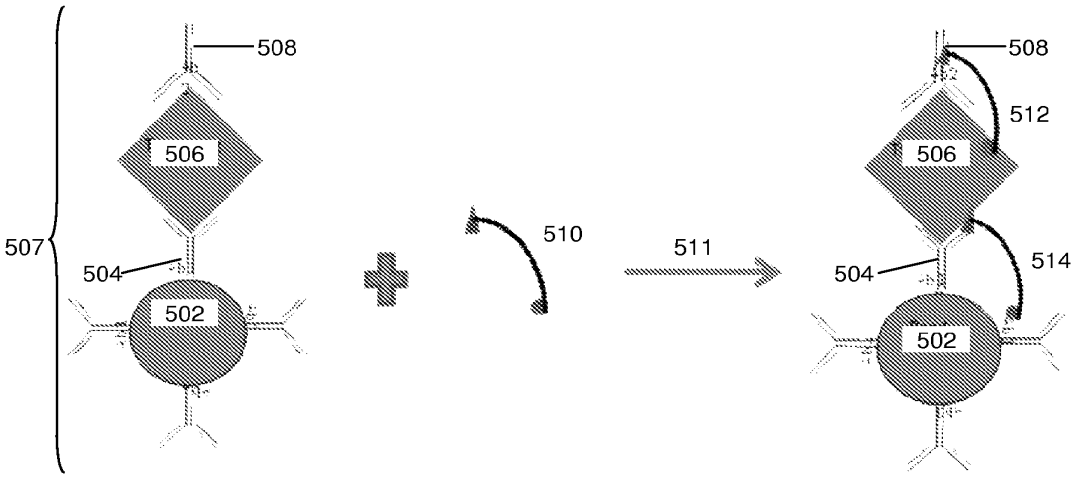


FIG. 10A

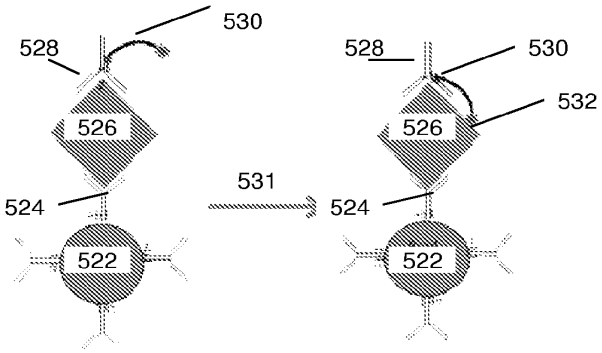


FIG. 10B

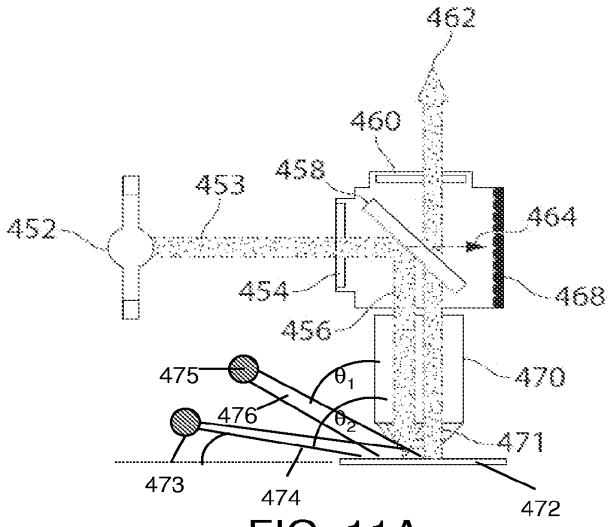


FIG. 11A

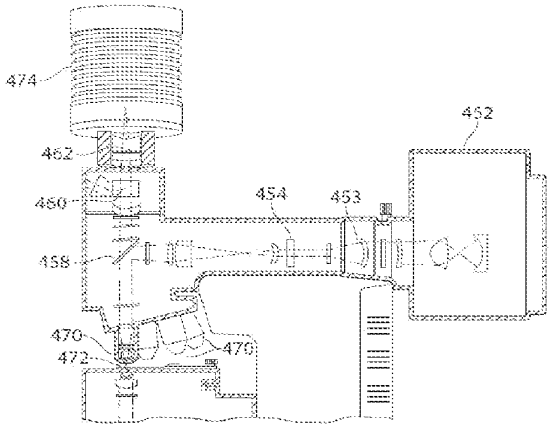


FIG. 11B

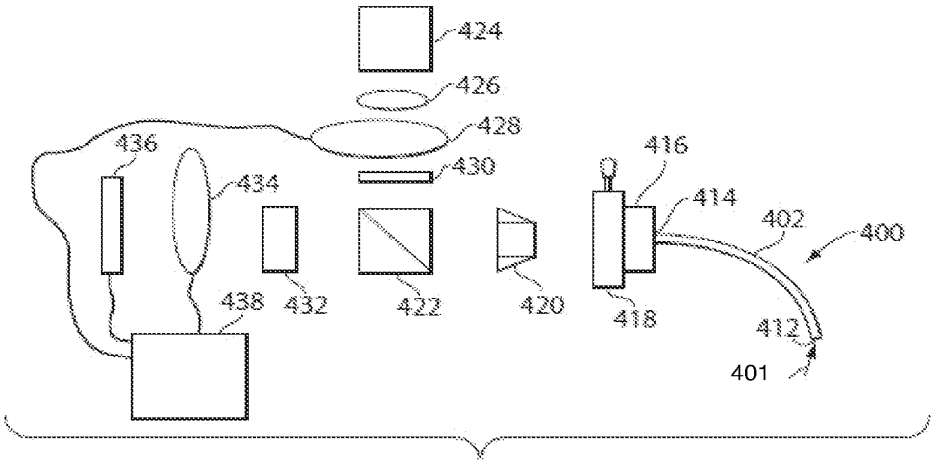

424
426
428
430
436
434
416
414
402
400
438
432
422
420
418
412
401

FIG. 12

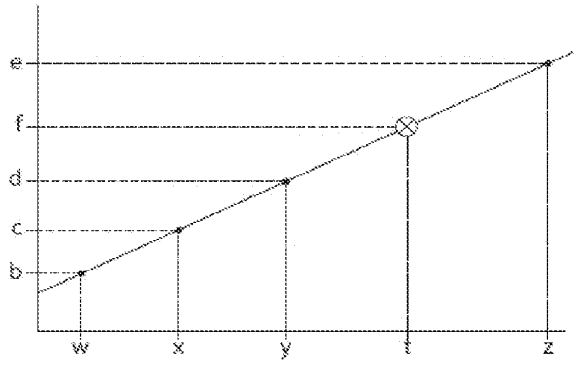

e
f
d
c
b
w
x
y
z

FIG. 13

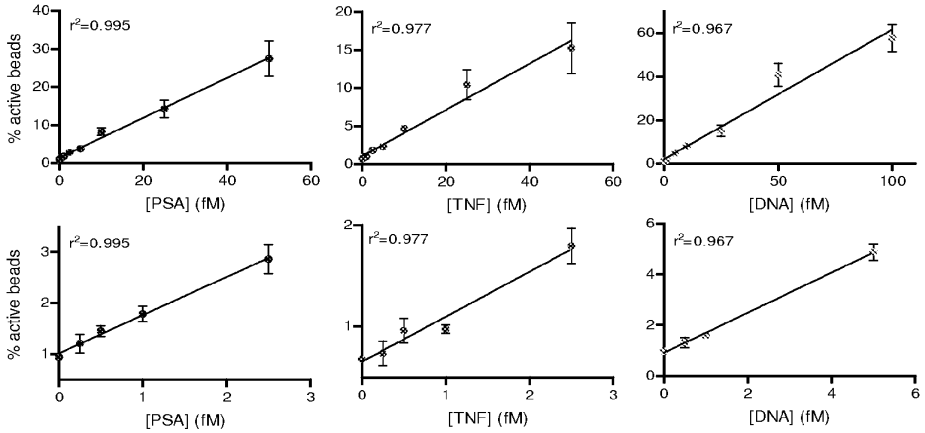


FIG. 14A FIG. 14B FIG. 14C

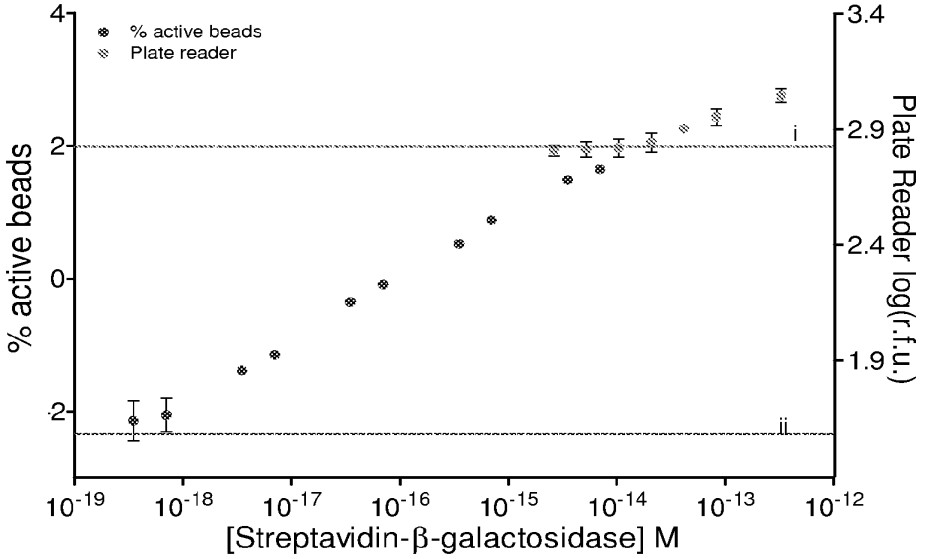


FIG. 15

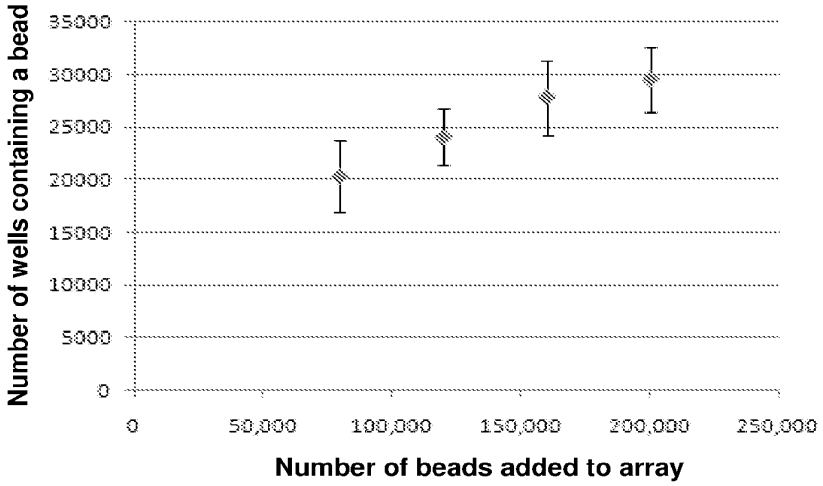

Number of wells containing a bead
35000
30000
25000
20000
15000
10000
5000
0
0
50,000
100,000
150,000
200,000
250,000
Number of beads added to array

FIG. 16

FIG. 17A

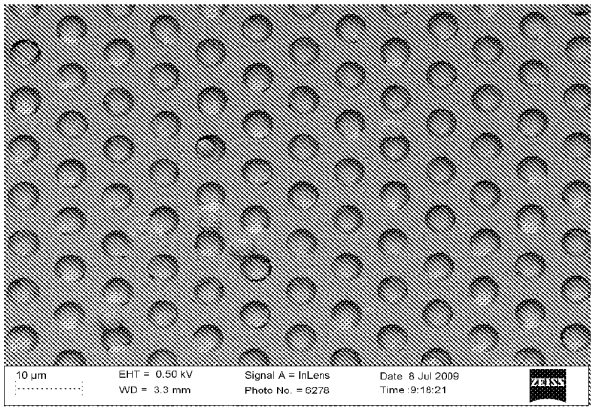


FIG. 17B

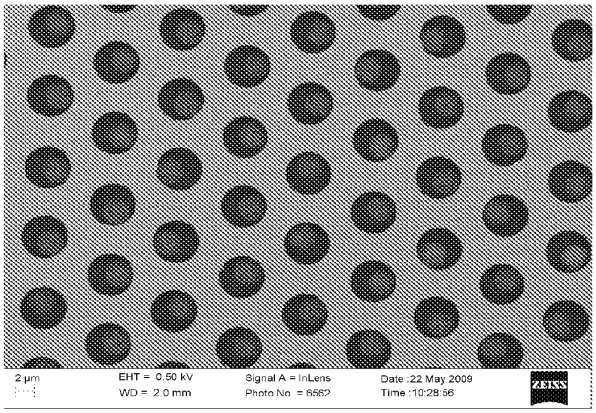


FIG. 17C

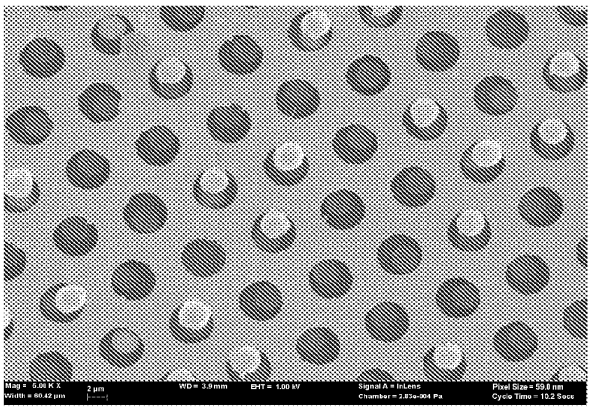


FIG. 18A

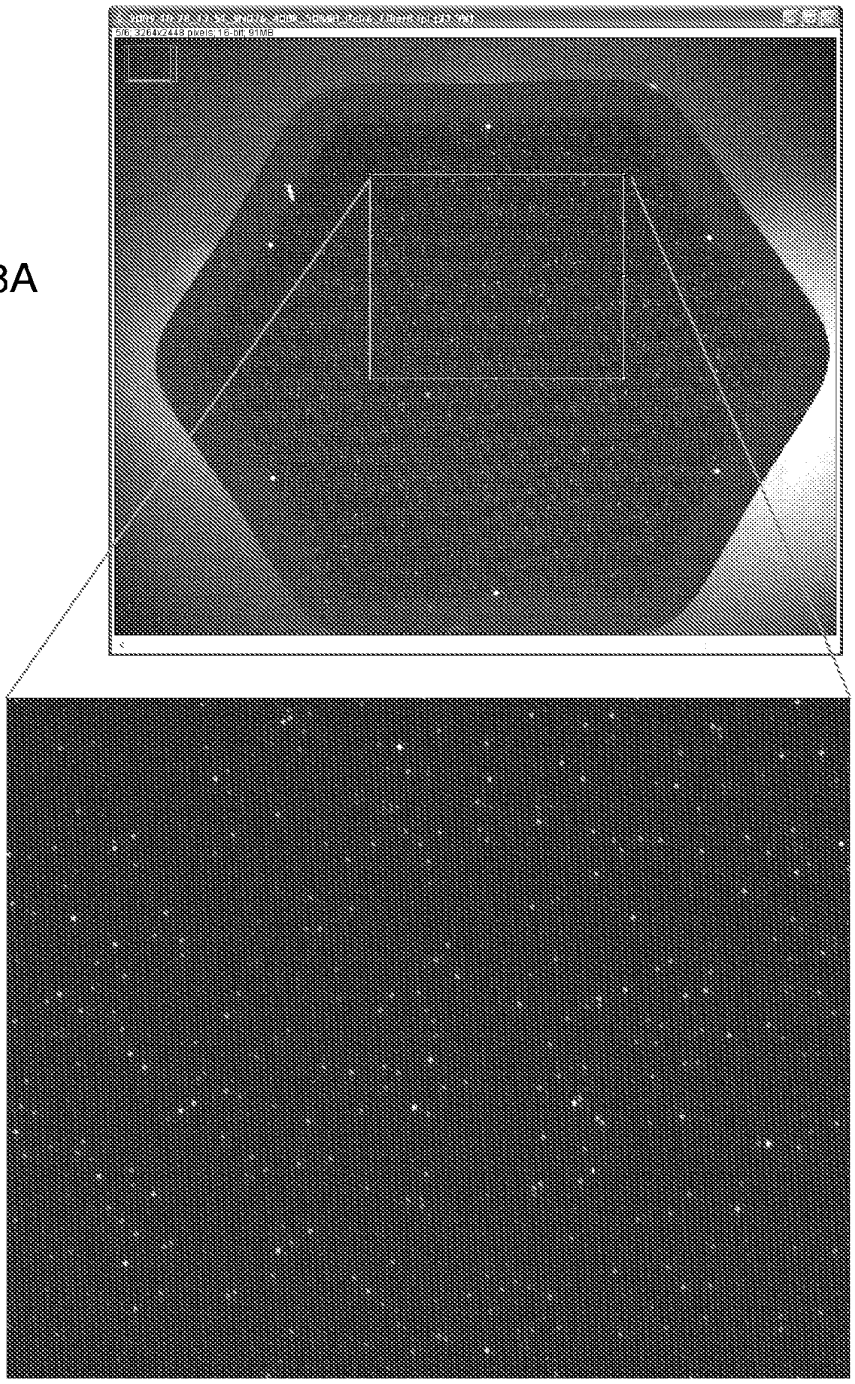


FIG. 18B

FIG. 19A

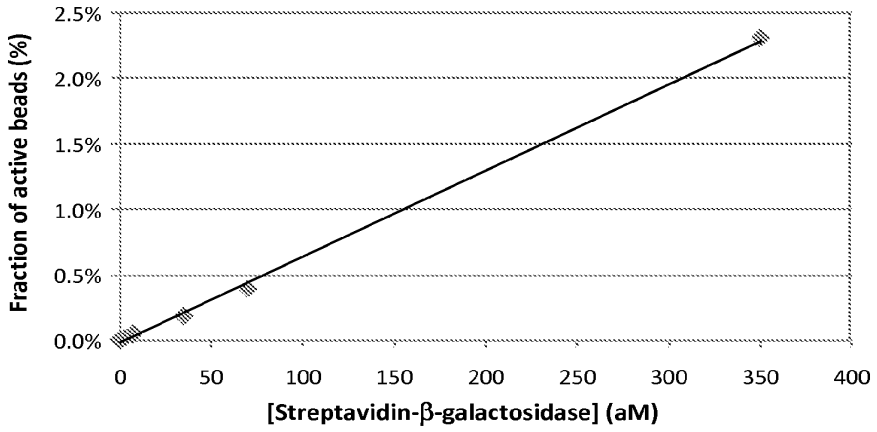


FIG. 19B

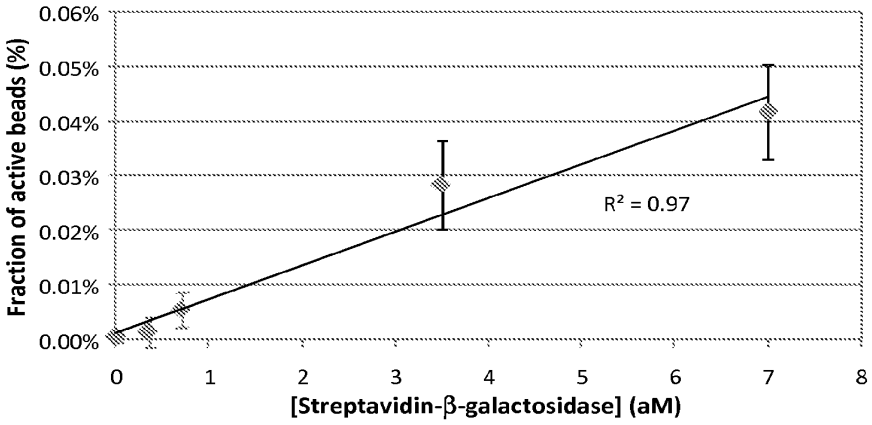
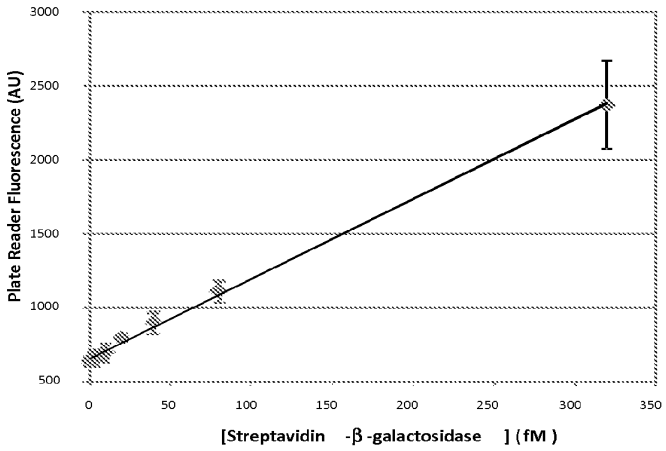


FIG. 19C



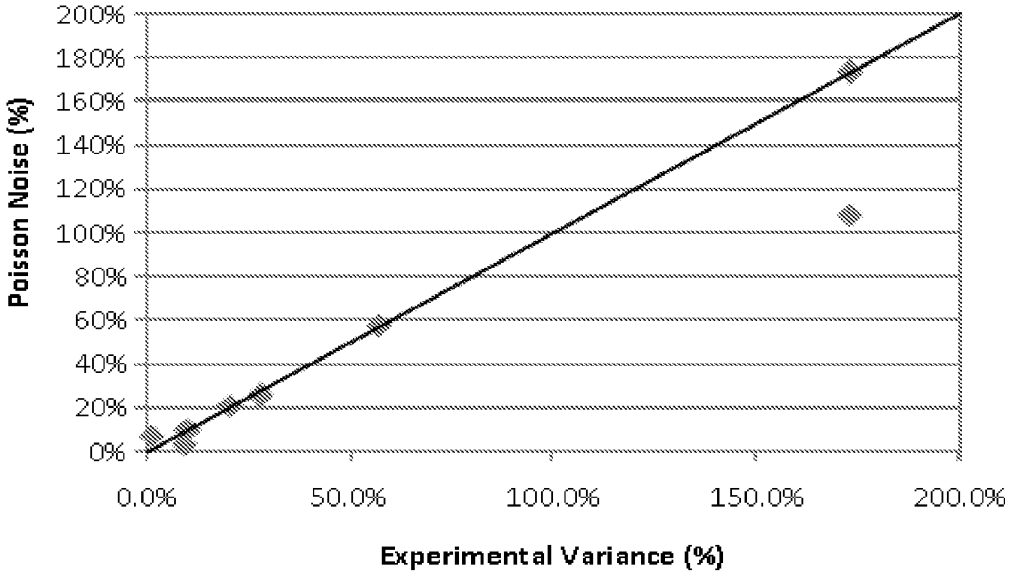

200%
180%
160%
140%
120%
100%
80%
60%
40%
20%
0%
Poisson Noise (%)
0.0%
50.0%
100.0%
150.0%
200.0%
Experimental Variance (%)

FIG. 20

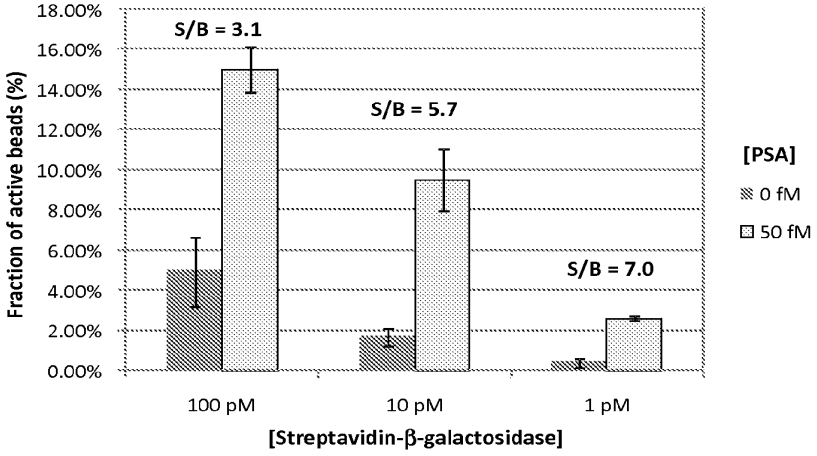

18.00%
16.00%
14.00%
12.00%
10.00%
8.00%
6.00%
4.00%
2.00%
0.00%
Fraction of active beads (%)
S/B = 3.1
S/B = 5.7
S/B = 7.0
100 pM
10 pM
1 pM
[Streptavidin-β-galactosidase]
[PSA]
0 fM
50 fM

FIG. 21

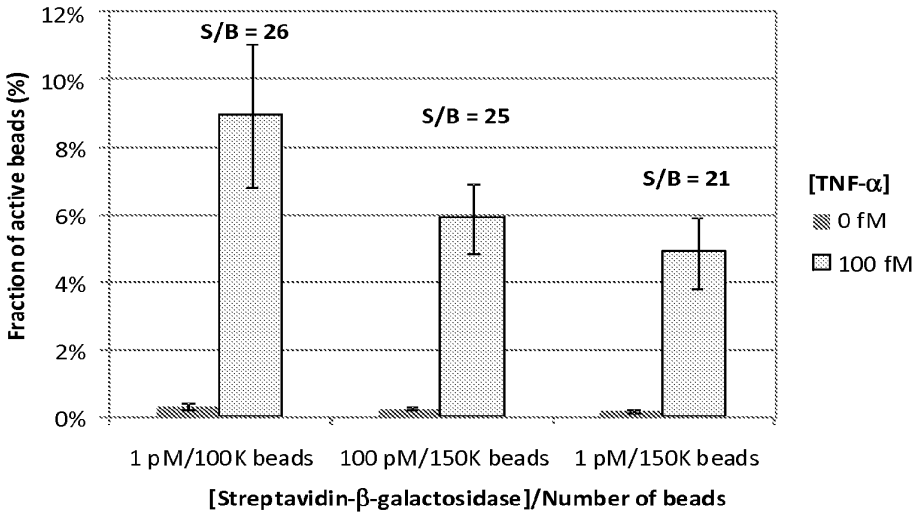

12%
10%
8%
6%
4%
2%
0%
Fraction of active beads (%)
S/B = 26
S/B = 25
S/B = 21
[TNF-α]
0 fM
100 fM
1 pM/100K beads
100 pM/150K beads
1 pM/150K beads
[Streptavidin-β-galactosidase]/Number of beads

FIG. 22

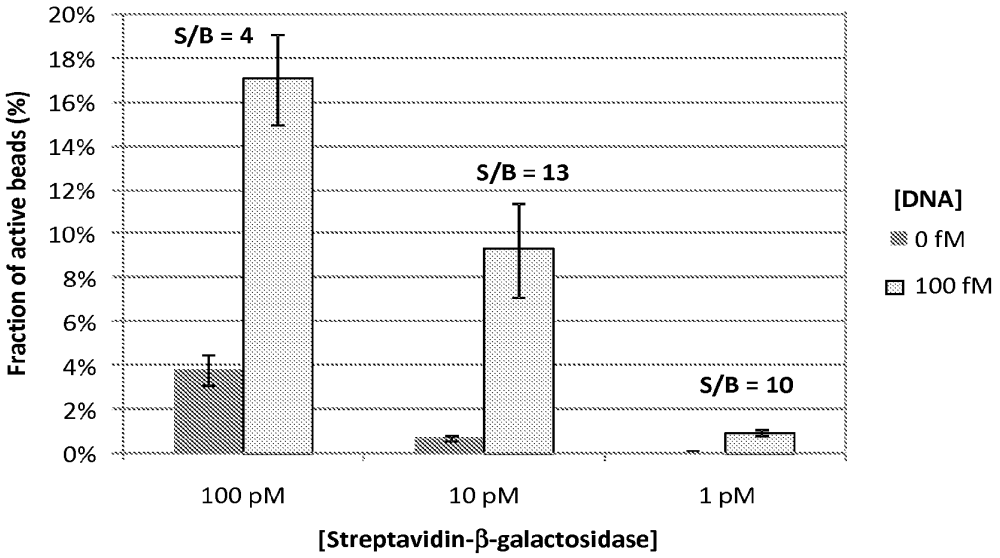

20%
18%
16%
14%
12%
10%
8%
6%
4%
2%
0%
Fraction of active beads (%)
S/B = 4
S/B = 13
S/B = 10
[DNA]
0 fM
100 fM
100 pM
10 pM
1 pM
[Streptavidin-β-galactosidase]

FIG. 23

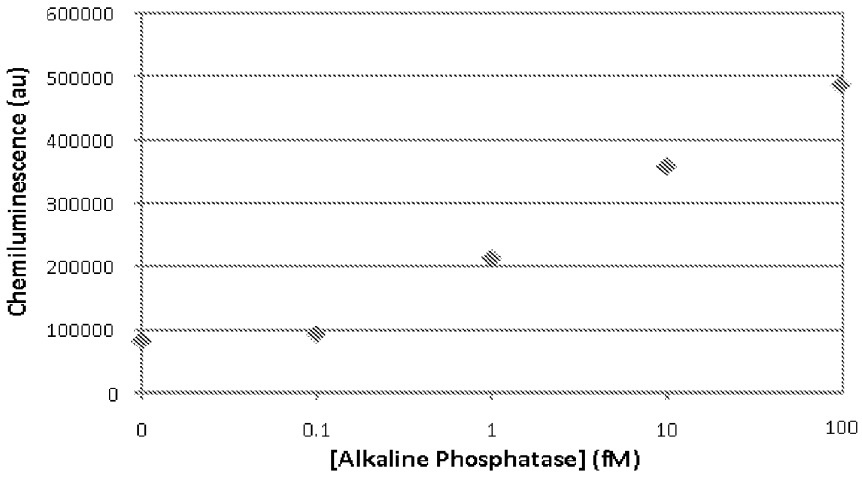

600000
500000
400000
300000
200000
100000
0
Chemiluminescence (au)
0
0.1
1
10
100
[Alkaline Phosphatase] (fM)

FIG. 24

FIG. 25A

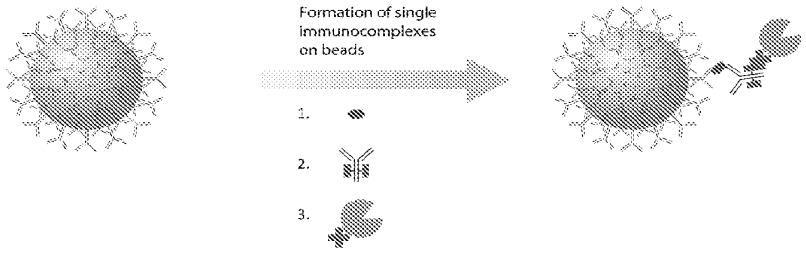
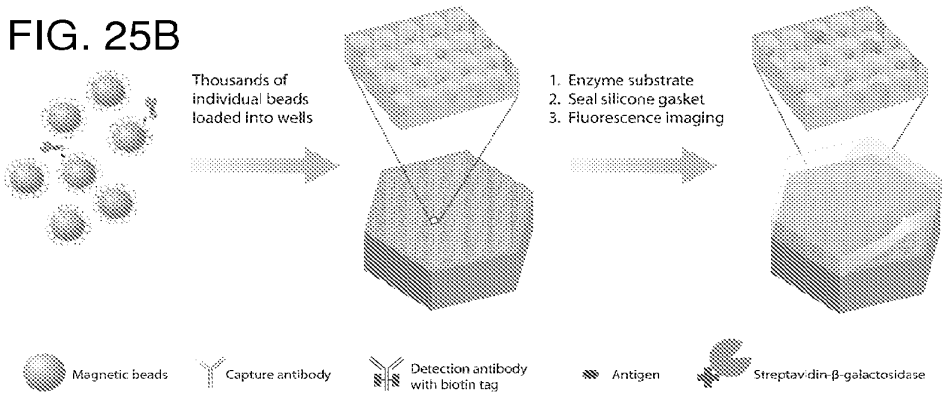


FIG. 25B



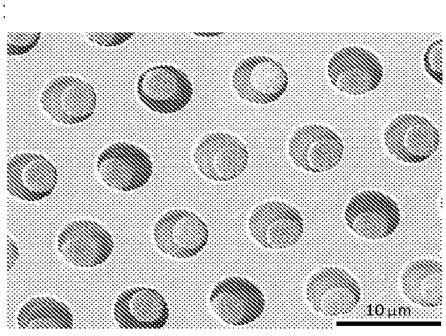


FIG. 25C

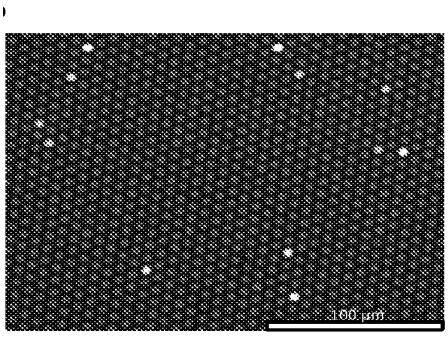


FIG. 25D

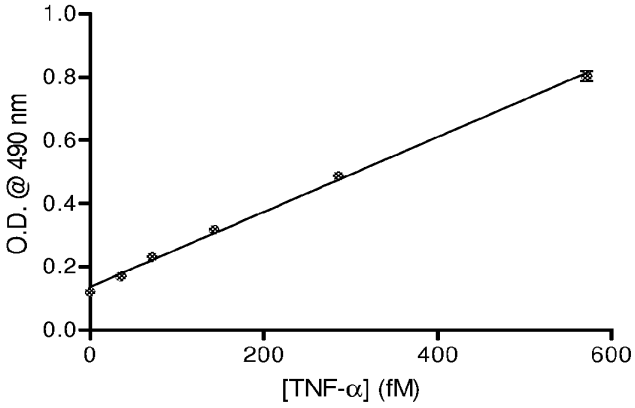

1.0
0.8
0.6
0.4
0.2
0.0
O.D. @ 490 nm
0
200
400
600
[TNF-α] (fM)

FIG. 26

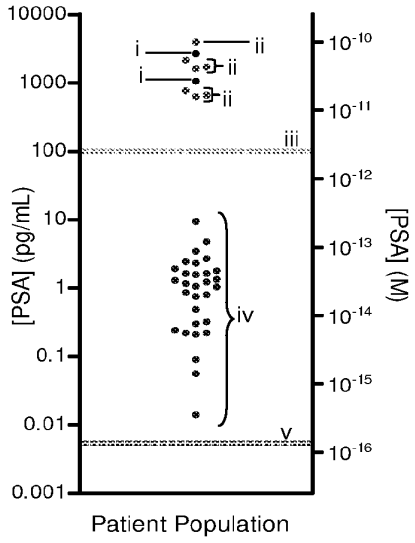

10000
1000
100
10
1
0.1
0.01
0.001
[PSA] (pg/mL)
i
ii
i
ii
ii
iii
iv
v
10^{-10}
10^{-11}
10^{-12}
10^{-13}
10^{-14}
10^{-15}
10^{-16}
[PSA] (M)
Patient Population

FIG. 27

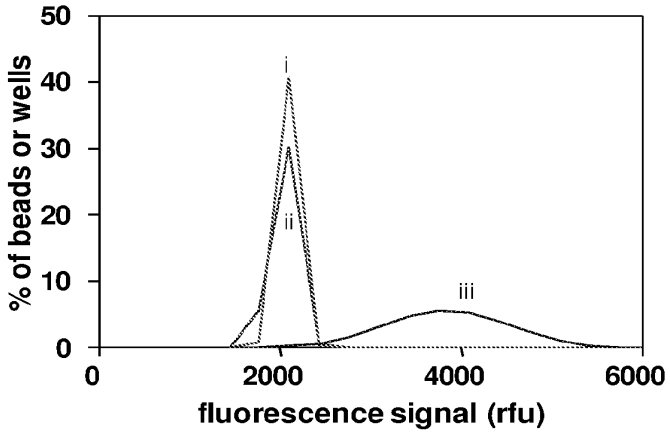


FIG. 28

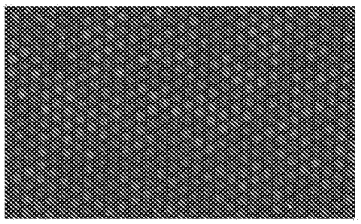


FIG. 29A

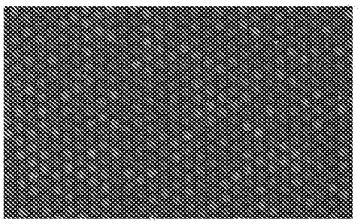


FIG. 29B

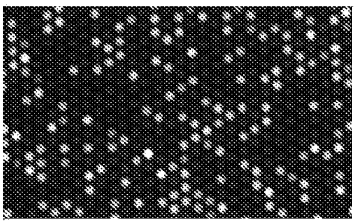


FIG. 29C

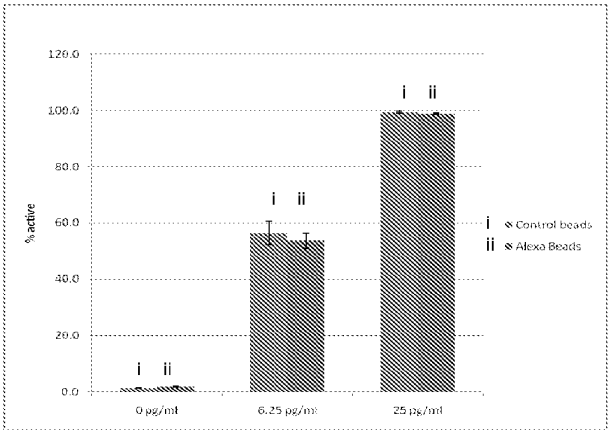


FIG. 29D

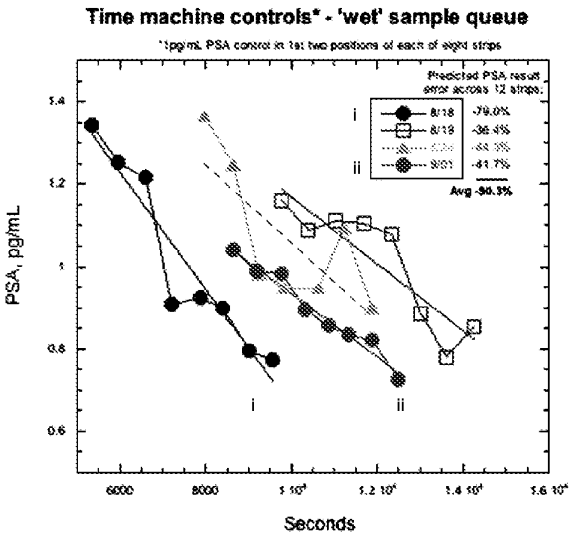


FIG. 30A

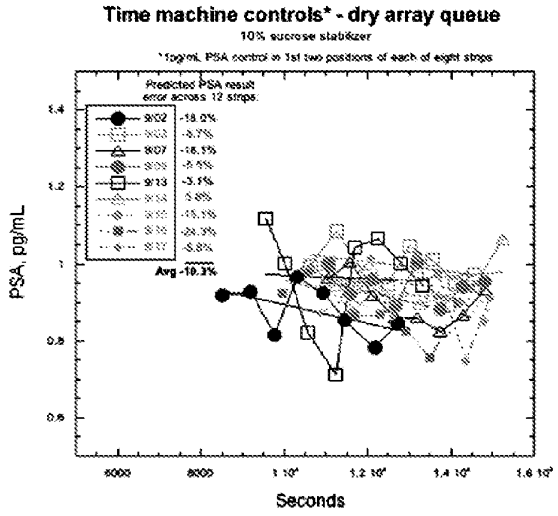


FIG. 30B

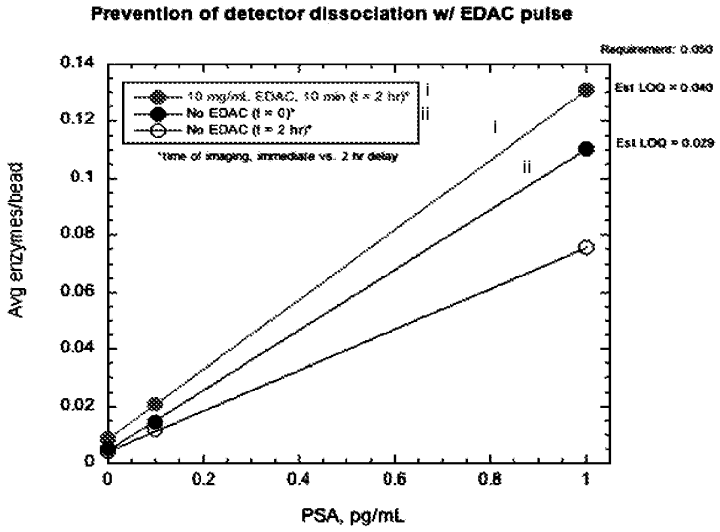


FIG. 31

Electronic Acknowledgement Receipt

EFS ID:	9858180
Application Number:	61474315
International Application Number:	
Confirmation Number:	1448
Title of Invention:	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT
First Named Inventor/Applicant Name:	. .
Customer Number:	23628
Filer:	Michael Pomianek/Joan Meagher
Filer Authorized By:	Michael Pomianek
Attorney Docket Number:	Q0052.70017US00
Receipt Date:	12-APR-2011
Filing Date:	
Time Stamp:	10:09:38
Application Type:	Provisional

Payment information:

Submitted with Payment	no

File Listing:

Document Number	Document Description	File Name	File Size(Bytes)/ Message Digest	Multi Part /.zip	Pages (if appl.)
1	Provisional Cover Sheet (SB16)	Q005270017US00-PROCVR-MJP.pdf	44140 0624627afd163e07d7abc0f6e6d0bd46165d3b8b	no	2

Warnings:

This is not a USPTO supplied Provisional Cover Sheet SB16 form.

Information:					
2	Application Data Sheet	Q005270017US00-ADS-MJP.pdf	15037 03d64b70f7deb24c5f8f5e3ecb2dca90d5f8658c	no	2
Warnings:					
Information:					
This is not an USPTO supplied ADS fillable form					
3		Q005270017US00-PROAPL-MJP.pdf	659580 79fb78b82c10d69501035af7d1ac6696fbc33754	yes	70
	Multipart Description/PDF files in .zip description				
	Document Description		**Start**	**End**	
	Specification		1	53	
	Claims		54	69	
	Abstract		70	70	
Warnings:					
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4	Drawings-other than black and white line drawings	Q005270017US00-DRW-MJP.pdf	2395611 40de9830889dd1b30065389a61bda0d30e7583e9	no	6
Warnings:					
Information:					
5	Appendix to the Specification	Q005270017US00-APPENDIX-MJP.pdf	9772298 99cb7de59f1950e8307aca18ecfaf0007c67dc98	no	162
Warnings:					
Information:					
		Total Files Size (in bytes):	12886666		

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New Applications Under 35 U.S.C. 111
If a new application is being filed and the application includes the necessary components for a filing date (see 37 CFR 1.53(b)-(d) and MPEP 506), a Filing Receipt (37 CFR 1.54) will be issued in due course and the date shown on this Acknowledgement Receipt will establish the filing date of the application.

National Stage of an International Application under 35 U.S.C. 371
If a timely submission to enter the national stage of an international application is compliant with the conditions of 35 U.S.C. 371 and other applicable requirements a Form PCT/DO/EO/903 indicating acceptance of the application as a national stage submission under 35 U.S.C. 371 will be issued in addition to the Filing Receipt, in due course.

New International Application Filed with the USPTO as a Receiving Office
If a new international application is being filed and the international application includes the necessary components for an international filing date (see PCT Article 11 and MPEP 1810), a Notification of the International Application Number and of the International Filing Date (Form PCT/RO/105) will be issued in due course, subject to prescriptions concerning national security, and the date shown on this Acknowledgement Receipt will establish the international filing date of the application.

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DOCUMENT MADE AVAILABLE UNDER THE PATENT COOPERATION TREATY (PCT)

International application number:		**PCT/US2012/033343**
International filing date:		**12 April 2012 (12.04.2012)**
Document type:		**Certified copy of priority document**
Document details:	Country/Office:	**US**
	Number:	**61/474,315**
	Filing date:	**12 April 2011 (12.04.2011)**
Date of receipt at the International Bureau:		**20 April 2012 (20.04.2012)**

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a),(b) or (b-*bis*)

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1211 Geneva 20, Switzerland
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460262

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE

United States Patent and Trademark Office

April 19, 2012

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APPLICATION NUMBER: *61/524,693*
FILING DATE: *August 17, 2011*
RELATED PCT APPLICATION NUMBER: *PCT/US12/33343*

THE COUNTRY CODE AND NUMBER OF YOUR PRIORITY APPLICATION, TO BE USED FOR FILING ABROAD UNDER THE PARIS CONVENTION, IS *US61/524,693*

Certified by

David J. Kappos

Under Secretary of Commerce
for Intellectual Property
and Director of the United States
Patent and Trademark Office

PTO/SB/16 (12-08)
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PROVISIONAL APPLICATION FOR PATENT COVER SHEET – Page 1 of 2

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)

Additional inventors are being named on the _____ separately numbered sheets attached hereto.

TITLE OF THE INVENTION (500 characters max):

METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY

Direct all correspondence to: **CORRESPONDENCE ADDRESS**

[X] The address corresponding to Customer Number: 23628

OR

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ENCLOSED APPLICATION PARTS (*check all that apply*)

[X] Application Data Sheet. See 37 CFR 1.76 [ ] CD(s), Number of CDs _____

[X] Drawing(s) *Number of Sheets* 4 [ ] Other (specify) _____

[X] Specification (e.g. description of the invention) *Number of Pages* 67

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SIGNATURE	/Michael J. Pomianek/	Date	August 17, 2011
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Application Data Sheet

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METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY

Field of the Invention

The present invention generally relates, in some embodiments, to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury. In some embodiments, the brain injury results from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of tau protein in a patient sample containing or suspected of containing tau protein.

Background of the Invention

A brain injury in a human may be caused by any number of events or conditions. In some cases, a brain injury may be caused by external mechanical force, such as rapid acceleration or deceleration, impact, blast waves, or penetration by a projectile. This type of acquired brain injury is generally known as traumatic brain injury. Another type of acquired brain injury involves biochemical forces, such as oxygen deprivation (hypoxia). Hypoxia generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Oxygen deprivation to the brain results in neuronal damage and death, which is in turn related to the extent of long term brain dysfunction. The concentration of certain biomarkers may become elevated as a result of neuronal damage and death. For example, tau proteins are associated with microtubules and localized in the axonal compartment of neurons. Tau is known to be elevated in the cerebrospinal fluid (CSF) of patients with neurodegenerative disease and head injuries. However, since such biomarkers must diffuse across the blood brain barrier, they may be present in the blood in proportion in extremely low concentrations that are not reliably measurable by typical conventional immunoassays. While the concentration of some biomarkers in the brain and central nervous system are known to increase with hypoxic events, the increased concentration has not been correlated with specific diagnostic indications and/or methods of treatment. In addition, while some methods exist for determining a brain injury in a patient and/or determining a course of treatment following a brain injury, many of the known methods are costly (e.g.,

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magnetic resonance imaging) and/or provide unclear results and/or predictors. Accordingly, improved methods are needed.

Summary of the Invention

In some embodiments, a method for determining a measure of the concentration of tau protein in a patient sample containing or suspected of containing tau protein is provided comprising performing an assay to determine a measure of the concentration of tau protein in the sample, wherein the limit of detection of tau protein of the assay is less than about 0.2 pg/mL.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury is provided comprising performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of tau protein in the sample; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of tau protein present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury is provided comprising determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of tau protein present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of tau protein in the sample.

In some embodiments, a method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury is provided comprising performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of tau protein in the sample; and providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury

and/or a method of treatment based at least in part on the measured concentration of tau protein present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury is provided comprising determining a measure of the concentration of tau protein in each of a plurality of samples obtained from the patient following the brain injury; and determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration tau protein present in the sample.

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury is provided comprising (a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area is determined for the entire time period and/or for a second peak in the tau protein concentration; and (c) determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the area under the curve for the entire time period and/or the second peak in the tau protein concentration determined in step (b).

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury is provided comprising determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area is determined for the entire time period and/or for a second peak in the tau protein concentration, which has been determined by (a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples have been obtained from the patient over a period of time of at least about 48 hours; and (b) determining the

area under the curve of a graph of the tau protein concentration in the plurality of samples versus time for the entire time period and/or for a second peak in the tau protein.

In some embodiments, a method for performing an assay and providing data for determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury is provided comprising (a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area under the curve is determined for the entire time period and/or for a second peak in the tau protein concentration; and (c) providing data derived in steps (a) and (b) to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the area under the curve determined for the entire time period and/or for a second peak in the tau protein concentration.

Brief Description of the Drawings

Figure 1a is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 1b is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 2 show plots of serum tau concentrations for numerous patients following resuscitation from cardiac arrest having a-c) a poor outcome and d) a good outcome;

Figure 3 shows plots of receiver operating characteristics (ROC) curves and areas under the curve values of tau protein concentration versus time for a) the first 24 hours, b) all serial samplings, and c) the secondary tau peak only;

Figure 4 illustrates six naturally occurring isoforms of tau proteins.

Other aspects, embodiments, and features of the invention will become apparent from the following detailed description when considered in conjunction with the accompanying drawings. The accompanying figures are schematic and are not intended to be drawn to scale. For purposes of clarity, not every component is labeled in every

figure, nor is every component of each embodiment of the invention shown where illustration is not necessary to allow those of ordinary skill in the art to understand the invention. All patent applications and patents incorporated herein by reference are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Detailed Description

The present invention generally relates to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury. In some embodiments, the brain injury may result from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of tau protein in a patient sample containing or suspected of containing tau protein. The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles.

In some embodiments, a method of the present invention comprises determining a measure of the concentration of at least one biomarker in one or more samples obtained from a patient following a brain injury. In some embodiments, a method of the present invention comprises determining a measure of the concentration of at least one biomarker in one or more samples obtained from a patient following the brain injury (e.g., optionally resulting from a hypoxic event). A prognostic indication of the patient's recovery and/or determining a course of treatment (e.g., from the brain injury, optionally resulting from a hypoxic event) may be based at least in part on the measure of the concentration of the at least one biomarker present in the one or more samples. It should be understood, that while much of the discussion below is directed to methods involving the analysis of more than one sample, this is by way of example only, and similar methods may be employed wherein only a single sample is employed.

As will be known to those of ordinary skill in the art, the term "hypoxia" generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Hypoxia at a cellular level develops when delivery of oxygen to cell mitochondria slows as the partial pressure

gradient from capillaries to tissues decreases. As the delivery of oxygen decreases, aerobic metabolism stops and less efficient anaerobic pathways of glycolysis become responsible for the production of cellular energy. The end result is an increase in cellular concentrations of sodium, calcium, and hydrogen ions which may lead to cell death.

Oxygen deprivation to the brain results in neuronal damage and death. The extent of neuronal damage and death in turn relates to the extent of long term brain dysfunction, as can be assessed using standard criteria (such as Cerebral Performance Category, CPC rating, or like criteria). Severe hypoxia can result in a patient's death and/or an irreversible brain injury (e.g., resulting in the patient being in a vegetative state). Hypoxic events may be global (e.g., due to low oxygen content in the blood) or focused (e.g., affecting only an area of the brain). Causes of hypoxia include, but are not limited to, local asphyxia (e.g., caused by smoke inhalation), carbon monoxide poisoning and/or toxicity, cardiac arrest, choking, drowning, high altitudes, strangulation, an ischemic event, thrombosis, arterial embolism, hemorrhage, swelling of the brain, stroke, physical trauma and/or physical injury (e.g., blunt trauma to the head), arteriosclerosis, and/or atherosclerosis. In some cases, the event may be myocardial infarction, myocardial ischemia, and/or transient ischemic attack.

Hypoxic conditions can lead to the production and/or change in the concentration of certain biomarkers. That is, the concentration of certain biomarkers increases or decreases following the hypoxic event. For example, the production of the proteolytic products of β-amyloid precursor protein has been found to become elevated in the brain and central nervous system under hypoxic condition. The increased concentration is theorized to be due to a hypoxia-inducible factor (HIF-1) that promotes the production of beta-amyloid peptides from amyloid precursor protein, a membrane protein concentrated in neuronal synapses. A cascade of biomarkers, such as tau proteins, is generated in the brain in proportion to the extent of hypoxia. Such biomarkers could in turn diffuse across the blood brain barrier and into the blood in proportion to the extent of hypoxia, and may be generally found in low abundance. The ability to determine a change in the concentration of a biomarker in a plurality of samples (or a single sample) obtained from a patient following a hypoxic event can, in some embodiments, be correlated with a prognostic indication of the patient's recovery from a brain injury and/or used to

determine a method of treatment. In some cases, sample(s) of the patient's cerebrospinal fluid (CSF) may be obtained and analyzed to determine the concentration and/or a change in the concentration of the biomarker. In some cases, however, it is advantageous to determine the level of a biomarker in the blood of a patient as compared to CSF, as blood sampling is generally less invasive and may result in fewer complications as compared to CSF sampling. However, many of the biomarkers that are present in the CSF have a slow rate of transmission across and/or a high barrier of transportation across the blood-brain barrier (BBB) and thus, the concentration of the biomarker in the patient's blood may be sufficient lowered as compared to the concentration in CSF to make it difficult or impossible to accurately determine using typically employed conventional immunoassays. Accordingly, assay methods which have very low limits of quantification (LOQ) and/or limits of detection (LOD) are generally necessary to determine a measure of the concentration of a biomarker in the patient's blood to provide statistically significant and/or meaningful results. In some embodiments, the methods of the present invention make use of methods having very low LODs and/or LOQs (e.g., in the low pg/mL range) to determine a measure of the concentration of a biomarker in a sample(s) obtained from a patient following a hypoxic event. Various parameters related to the changes in the concentration of the biomarker in the samples (e.g., blood samples) may be correlated with a prognostic indication and/or a method of treatment following a hypoxic event. Correlations (e.g., between the concentration and prognostic indication(s) and/or between the concentration and method(s) of treatment) have been discovered and/or are now discoverable due to recent advancements in technology which allow for the determination of the low concentrations of biomarkers in bodily fluids with sufficient accuracy and precision, thus allowing for the variations in concentration to be statistically significant and therefore, diagnostic.

It should be noted, that while many of the embodiments described herein focus on brain injuries caused by hypoxic events, this is by no way limiting, and in some embodiments, the brain injury may be caused by other events, for example, traumatic brain injuries wherein the force is such that the skull fractures causing mechanical damage to the brain. In some cases, a traumatic brain injury may be caused by external

mechanical force, such as rapid acceleration or deceleration, impact, blast waves, or penetration by a projectile.

In embodiments where a plurality of samples are obtained from a patient, the samples may be obtained from a patient over any suitable period of time. Generally, the period of time may be selected such that the concentration of a biomarker in the samples becomes statistically significant and/or a trend is observable (e.g., an increase and/or decrease in the concentration). For biomarkers which are analyzed in blood samples, the period of time over which a plurality of samples are obtained from the patient may account for any lag time required for the biomarker to cross the BBB. Non-limiting examples of suitable periods of time in which the samples may be obtained from the patient include 1 hour, 2 hours, 3 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 18 hours, 24 hours, 36 hours, 48 hours, 60 hours, 72 hours, 4 days, 5 days, 6 days, 7 days, or more. In some cases, the duration of time of sample collection time is at least 60 hours, or at least 72 hours. In some cases, the duration of time of sample collection is between 12 hours and 7 days, or between 24 hours and 4 days, or between 2 days and 4 days, or between 3 days and 4 days. The first sample may be obtained from the patient without a short timeframe following the brain injury. For example, the first sample may be obtained from the patient within 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 8 hours, 10 hours, or 12 hours of the brain injury . In some cases, the first sample is obtained within 6 hours of the brain injury. In some embodiments, a first sample is obtained from the patient within 6 hours of the suspected brain injury, and at about 1, about 2, about 6, about 12, about 24, about 48, and about 72 hours, following the first sampling. In some embodiments, additional samples are obtained at about 96 and/or at about 108 hours following the first sampling.

Any number of samples (e.g., one or more) may be obtained from the patient over the time period of sample collection. Generally, the minimum number of samples obtained is such that a trend (e.g., an increase or decrease) in the concentration of the biomarker is observable. Non-limiting examples of the number of samples that are obtained from the patient (e.g., during the prescribed collection time) is at least about bout 1, about 2, at least about 3, at least about 4, at least abut 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 12, at least about

15 or more. In some cases, the number of samples obtained from the patient is between 2 and 20, between 5 and 15, or between 5 and 10.

The sample(s) obtained from the patient may be from any suitable bodily source. In some cases, the samples are CSF fluid samples. In some cases, the samples are not CSF fluid samples. In some cases, the samples are blood or blood products (e.g., whole blood, plasma, serum, etc.). In other cases, the samples may be urine or saliva samples. In some embodiments, the samples may be analyzed directly (e.g., without the need for extraction of the biomarker from the fluid sample) and/or with dilution (e.g., addition of a buffer or agent to the sample). Generally, each of the samples obtained from the patient is collected using substantially similar procedures (e.g., to ensure minimal variation between samples based on sample collection methods). Those of ordinary skill in the art will be aware of suitable systems and methods for obtaining a sample from a patient.

Each of or substantially all of the samples may be analyzed using an assay method (e.g., as described herein) to determine a measure of the concentration of at least one biomarker in each, a subset of or substantially all of the samples. In some cases, the methods comprise determining a measure of the concentration of a single biomarker in the samples. In other cases, a method comprises determining a measure of the concentration of more than one biomarker in each, a subset of or substantially all of the samples. For example, a measure of the concentration of 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, biomarkers may be determined in the samples.

In some embodiments, the methods of the present invention comprise determining a prognostic indication based at least in part on the measured concentration of the at least one biomarker in the samples. In some cases, the prognostic indication may be correlated with standard criteria employed to define long-term brain dysfunction and/or injury. Those of ordinary skill in the art will be aware of such criteria, for example, cerebral performance category ratings ("CPC rating"), or more specifically, Glasgow-Pittsburgh cerebral performance category ratings (or scale) (e.g., see Teasdale G, Jennett B (1974); *Assessment of coma and impaired consciousness*; Lancet 2 (7872): 81–84). The CPC scale ranges from 1 to 5, with 1 representing a slight possibility of neurological deficit and 5 representing severe deficit and/or death. In some methods of the present invention, the prognostic indication of the patient's recovery from the brain injury is classified as

either "good" (e.g., correlating to a CPC score of 1 or 2) corresponding to a high likelihood of recovery and/or returning to independent living, or "poor" (e.g., correlating to a CPC score of 3, 4, or 5) corresponding to little possibility of a full recovery and resulting in assisted living and/or death.

In the CPC scale, a rating of 1 is generally classified as good cerebral performance. The patient is conscious and alert, is able to work, but may have mild neurological or psychological deficit. A rating of 2 is generally classified as having moderate cerebral disability. The patient is conscious and has sufficient cerebral function for independent activities of daily life, and is generally able to work in sheltered environment. A rating of 3 corresponds to severe cerebral disability. While the patient is conscious, they generally depend on others for daily support because of impaired brain function. The patient may have abilities ranging from ambulatory state to severe dementia or paralysis. A rating of 4 corresponds to a coma or vegetative state. The patient is generally unaware, even if they appear awake (e.g., the patient is in a vegetative state) without interaction with environment and is cerebral unresponsive. A rating of 5 refers to brain death, associated with apnea, areflexia, and/or EEG silence. The CPC scale is summarized in Table 1.

Table 1: CPC Scale Summary

CPC Score	Description
1	Conscious and alert with normal function or only slight disability
2	Conscious and alert with moderate disability
3	Conscious with severe disability
4	Comatose or persistent vegetative state
5	Brain dead or death from other causes

Other non-limiting examples of suitable criteria include the "scale g" criteria (e.g., see Dekaban AS, Robinson CE.; Application of a new rating scale of brain dysfunction to monitoring rehabilitation in 65 patients with severe head injury, Bull Clin Neurosci., 1984; 49, 82-92), the "Rancho Los Amigos Scale," and the "Disabilities Rating Scale."

In addition to the biomarkers specifically mentioned herein, those of ordinary skill will be aware of other suitable biomarkers to use in connection with the methods described herein. As described herein, the biomarker generally undergoes a change in

concentration as a result of a hypoxic event. For example, the concentration of the biomarker may increase or decrease as a result of the brain injury. Non-limiting examples of biomarkers include neuron specific neuronal enolase (NSE), β-site aPP-cleaving enzyme 1 (BACe1), S100B, myelin basic protein (MBP), growth associated protein 43, glutamine synthetase, glial fibrillary acid protein (GFAP), glycine transporter (e.g., GLYT1, GLYT2), neuron specific glycoprotein (e.g., GP50), calpain, neurofibrillary protein, heat shock protein 72, beta-amyloid precursor proteins, calbindin D-28K, proteolipid protein, myeline associated glycoprotein, neurofilament H, creatine kinase protein (e.g., CK-BB), tau proteins (including phosphorylated taus such as p-tau-81 or p-tau-231), and endothelium membrane proteins (e.g., thrombomodulin).

In some cases, the biomarker is a tau protein. Various forms and/or combinations of tau proteins may be contemplated for use as a target biomarker with the methods described herein, include isoforms and short isoforms, for example, ranging from tau 23 (352a.a, "0N3R", wherein R indicates the number of repeats and N indicates the number or amino terminal inserts, as will be understood by those of ordinary skill in the art) to tau 40 (441a.a,"2N4R"). There are six known naturally-occurring tau proteins, the sequences of which are well known in the art. The six tau proteins include tau 23 (352, 0N3R), tau 24 (383, 0N4R), tau 37 (381, 1N3R), tau 34 (412, 1N4R), tau 39 (410, 2N3R), tau 40 (441, 2N4R), and/or combinations thereof (e.g., see FIG. 4). In some cases, at least some of the tau proteins may be phosphorylated.

Those of ordinary skill in the art will understand that determination of a biomarker in a sample may comprise determining the concentration a single isoform of a biomarker, or alternatively, may comprise determining the concentration of a plurality of isoforms of the biomarker. For example, with respect to tau proteins, in some cases, the concentration of tau protein employed in the algorithms and methods described herein may be the concentration of a single isoform of tau protein in the sample, or alternatively, the concentration of tau protein employed in the algorithms and methods described herein may be the concentration of a plurality of forms of tau proteins in the sample.

The plurality of samples obtained from the patient may be analyzed (e.g., using an assay method as described herein) to determine a measure of the concentration of the at least one biomarker in each of the samples (or a single sample). A prognostic indication

and/or a method of treatment may be determined based at least in part on the measure of the concentration of the biomarker in each of the plurality of samples. The data may be analyzed using a variety of techniques, as described herein, and a prognostic indication for recovery from a brain injury (e.g., a "good" outcome or a "poor" outcome), or a specific method of treatment may be determined based on the results.

In some embodiments, the measure of the concentration of the at least one biomarker for each of the plurality of samples obtained from the patient may be plotted on a graph of concentration versus time (e.g., in hours), and one or more parameters can be obtained from the graph and used to determine the method of treatment and/or the prognostic indication. Non-limiting examples of parameters that may be determined and/or employed include baseline biomarker concentration, increase in biomarker concentration, duration of rise of biomarker concentration, maximum slope of increasing biomarker concentration, rate of change of biomarker concentration, area under the curve and/or magnitude of the fold increase of biomarker concentration. Each of the parameters and their determination will now be described in detail, followed by a description of possible data analysis and methods useful or potentially useful to determine suitable correlations between the measure of the concentration determined in the samples and a treatment/prognostic indication. The measure of the concentration of the biomarker may be determined/displayed in any suitable unit. In some cases, the measure of the concentration is determined/displayed in pg/mL.

The term "baseline biomarker concentration" refers to the concentration of the biomarker generally present in a fluid sample from a normal patient (e.g., prior to or unexposed to a hypoxic event). The baseline biomarker concentration can be determined using a variety of methods which will be commonly known and understood by those of ordinary skill in the art. In some cases, the baseline biomarker concentration can be determined by averaging the value of a biomarker present in a population of control patients (e.g., patients who have not experienced a hypoxic event). This may be useful in embodiments where the baseline concentration of the biomarker is substantially the same for a given population of individuals (e.g., based on age, gender, medical condition, etc.). However, many of the methods described herein require accurate determination of extremely low concentrations of the at least one biomarker in samples obtained from a

patient, and accordingly, a general baseline concentration of a biomarker (e.g., based on a sampling of a population) may not provide enough accuracy and/or precision to give useful results. Accordingly, a measure of the baseline biomarker concentration, in some embodiments, may be determined for each individual patient. In some embodiments, the baseline biomarker concentration may be set to zero, e.g., in embodiments where the concentration of the biomarker is zero or essentially zero in normal patients.

In some cases, the baseline biomarker concentration for each individual is equal to the measure of the concentration of the biomarker in the first sample obtained from the patient following the hypoxic event. In other cases, if available, a baseline biomarker concentration is the measure of the concentration of the biomarker present in a sample obtained from the patient prior to the hypoxic event. In yet other cases, the baseline biomarker concentration is the average concentration of the biomarker determined in a plurality of samples taken from the patient immediately or substantially immediately following the hypoxic event (e.g., prior to the concentration of the biomarker increasing due to the hypoxic event). That is, the concentration of the biomarker in the plurality of samples obtained from the patient in a selected time period following the hypoxic event may be averaged to determine the baseline biomarker concentration for that patient. As will be understood by those of ordinary skill in the art, in such cases, any sample which has a concentration level that significantly differs from the other concentration levels during that period of time (e.g., a data point/outlier having a concentration which deviates significantly from the other concentrations measured during the time frame) may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by greater than about 50% from the calculated average, that sample may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by more than about 0.5 pg/mL, 1 pg/mL, 2 pg/mL, 5 pg/mL, or 10 pg/mL from the calculated average, that sample may be excluded from the averaging calculation. An anomalous data point may be observed and/or caused by administration of drugs to the patient. The baseline biomarker concentration may be determined by averaging the concentration of the biomarker in the samples obtained from the patient between the first sample (e.g., obtained within 6 hours of the hypoxic event) and 24 hours following the first collection of a sample, or between the first sample and 18 hours following the first

collection of a sample, or between the first sample, and 12 hours following the first collection of a sample, or between the first sample, and 6 hours following the first collection of a sample (e.g., not including any outliers).

The term "area under the curve," (or AUC) is a common parameter used to analyze data, and such calculations will be well known and understood by those of ordinary skill in the art. In context with the methods of this disclosure, the AUC refers to the area under the biomarker concentration versus time curve. Generally the calculation takes into account the baseline biomarker concentration. Those of ordinary skill it the art will be aware of suitable algorithms and/or computer programs capable of determining the area under the curve for a selected set of data. In some cases, the area under the curve may be determined for more than one portion of the data. For example, a first area under the curve value may be determined for a first range of data, and a second area under the curve value may be determined for a second range of data. The first and the second ranges of data may or may not be overlapping (e.g., may comprise some overlapping data points or may comprise different data points). It should be understood, that determining the area under the curve can be accomplished using a variety of techniques which will be known to those of ordinary skill in the art, including but not limited to, plotting the concentration versus time on a graph and determining the area under the line/curve (e.g., optionally with use of a computer program) and/or determining a functional relationship between the concentration and time and integrating the data without requiring physically plotting or drawing of a graph. As used herein, the phrase "determining the area under the curve of a graph of a biomarker concentration versus time" covers all of the above techniques and others applicable for determining the area or equivalent, and is not limited to physically or electronically plotting the concentration versus time on a graph and determining the area under the line/curve.

The term "change in biomarker concentration" refers to the change (e.g., increase or decrease) in concentration of the biomarker over the time period in which the samples are collected. An increase in biomarker concentration may be calculated by subtracting the baseline biomarker concentration (e.g., as described herein) from the maximum biomarker concentration. The "maximum biomarker concentration" is the maximum measured concentration of the biomarker measured in a single sample collected over the

duration of the sample collection. For example, if the duration of the sample collection is 72 hours, the maximum concentration is equal to the maximum measured concentration in a single sample which was obtained from the patient in the 72 hour period. A decrease in biomarker concentration may be calculated by subtracting an elevated biomarker concentration (e.g., as described herein) from the minimum biomarker concentration.

The term "magnitude of the fold increase of biomarker concentration" refers to the magnitude of the fold-increase in concentration over the duration of sample collection, and may be calculated by dividing the maximum biomarker concentration (e.g., as described herein) by the baseline biomarker concentration (e.g., as described herein).

The term "duration of rise of biomarker concentration" refers to the time over which the concentration of the biomarker is increasing during the time period over which the samples are collected. In some cases, the duration of rise of biomarker concentration can be determined by subtracting the time at which the last sample was collected at approximately the baseline biomarker concentration (e.g., starting time of the rise) from the time at which the maximum biomarker concentration was observed (e.g., ending time of the rise). That is, the duration of the rise may be equal to the ending time of the rise minus the starting time of the rise. The duration of rise is generally provided in hours.

The term "maximum slope of increasing biomarker concentration" refers to the slope at which the maximum increase in concentration occurred over the time period in which the samples were collected. Those of ordinary skill will be aware of methods to calculate this value using common graphical analysis methods. For example, a plot may be prepared showing concentration versus time, and the maximum slope may be calculated based on this plot. In some cases, the maximum slope is equal to the slope between two data points, whereas in other cases, the maximum slope may be determined based on the average slope between a plurality of data points.

The above parameters, alone or in combination, may be correlated to a prognostic indication and/or a method of treatment for a patient following a brain injury (e.g., caused by a hypoxic event). Following determination of a correlation between biomarker concentrations and a prognostic indication and/or a method of treatment (e.g., using a

plurality of samples obtained from a plurality of test patients with known outcomes), the correlation can be used in connection with methods to determine prognosis (e.g., prognostic indications) and/or methods of treatment for patients with unknown outcomes. That is, an algorithm can be developed relating changes in a biomarker concentration and specific methods of treatment and/or prognostic indications using samples from test patients having been subject to known methods of treatment and/or having a known prognosis. Once the algorithm has been developed, it can be used to determine methods of treatment and/or prognostic indications for patients with unknown outcomes.

To determine a correlation between a biomarker and a prognostic indication and/or a method of treatment (e.g., to develop an algorithm relating the measured biomarker concentration to preferred methods of treatment and/or prognostic indications), a plurality of samples from a plurality of test patients may be obtained. A "test patient" is a patient who has a known outcome (e.g., a good or a poor CPC score) and/or has received a certain treatment. The plurality of the samples obtained from each of the test patients may be analyzed to determine the measure of the concentration of at least one biomarker in the each of the samples. Some or all of the parameters described herein may be determined for each patient, and the data may be analyzed to determine correlations between the parameters and the patient outcomes and/or treatments, which can in turn be used to develop an algorithm. The algorithm may then be applied to the concentration of the at least one biomarker in samples obtained from a patient having an unknown outcome to determine a method of treatment and/or a prognostic indication for that patient. A specific example of such an analysis is described below, and further details are provided in Example 1.

Similar analysis and methods may be used to correlate suitable methods of treatment based upon the measured concentration(s) of a biomarker in a plurality of samples obtained from a patient. In some cases, the method of treatment may comprise administering at least one therapeutic agent to the patient. For example, the therapeutic agent may be a neuroprotective drug. Other non-limiting methods of treatment include administration of anti-oxidants, hypothermia, blood thinning, and administration of steroids (e.g., to help reduce brain swelling) (e.g., see T. S. Richmond, Cerebral

Resuscitation After Global Brain Ischemia: Linking Research to Practice, American Association of Critical-Care Nurses Journal, May 1997, Volume 8, Number 2).

A therapeutic agent is generally administered in an amount effective to provide a medically desirable result. The effective amount will vary with the particular condition being treated, the age and physical condition of the subject being treated, the severity of the condition, the duration of the treatment, the nature of the concurrent therapy (if any), the specific route of administration and the like factors within the knowledge and expertise of the health care practitioner. In some cases, a therapeutic agent may reduce brain injuries resulting from the hypoxic event. In some cases, the method of treatment may involve a change in treatment, such as an increase or decrease in the dose of a therapeutic agent, a switch from one therapeutic agent to another therapeutic agent, an addition of another therapeutic agent to the existing therapeutic agent, or a combination thereof. A switch from one therapeutic agent to another may involve a switch to a therapeutic agent with a high risk profile but where the likelihood of expected benefit is increased.

In one embodiment, a method of the present invention for determining a treatment protocol for and/or a prognostic indication of a patient's recovery from a brain injury (e.g., resulting from a hypoxic event) comprises performing an assay on a plurality of samples to determine a measure of the concentration of tau protein in each sample and determining a prognostic indication of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measure of the concentration of tau protein present in the samples. The sample, in some embodiments, is a blood sample from the patient and/or plasma and/or serum derived from the blood sample. In some cases, the concentration of the tau protein in the samples is less than about 1000 pg/mL, about 900 pg/mL, about 800 pg/mL, about 700 pg/mL, about 600 pg/mL, about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL, or less. In some cases, the assay has a limit of quantification of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL or less. In some cases, the assay has a limit

of detection of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less.

In one embodiment, a correlation was determined between certain parameters (e.g., area under the curve of a plot of tau protein concentration versus time) and a good (e.g., CPC rating 1 or 2) or a poor (e.g., CPC rating of 3, 4, or 5) prognostic indication. To determine the correlation, an assay was carried out on each of the samples obtained from a plurality of test patients having undergone a brain injury (e.g., resulting from a hypoxic event) (e.g., patients having a known outcome and/or having undergone a certain method of treatment following a brain injury). The first sample was taken within 6 hours of the brain injury (e.g., resulting from a hypoxic event), and additional samples were generally obtained at about 1, 2, 6, 12, 24, 48, and 72 hours following the first sample (and optionally, at 96 and/or 108 hours). Each of the test patients had a known prognostic outcome according to the CPC scale. For each test patient, a plot of the measured concentration of tau protein in pg/mL time in hours was prepared. The data was analyzed and the area under the curve of the tau protein concentration (in pg/mL) versus time (in hours) was determined for a variety of time ranges, and was determined to correlate with a "good" or "poor" prognosis for the patients. In some embodiments, the plot of the concentration of the tau protein versus time showed two peaks, one occurring mostly in the first 24 hours following the hypoxic event, and one occurring at some point following the first 24 hours following the hypoxic event. Thus, the area under the curve was determined for each patient for three ranges of time: 1) for the entire duration of the data collection, 2) for the first 24 hours, and 3) for the second peak in tau protein concentration (if present). Generally, the baseline used to determine the area under the curve for 1) and 2) was set to zero, whereas the baseline used to determine the area under the curve for 3) was set as the concentration of tau protein determined at the beginning of the rise of the second peak. For the total area under the curve, a value of greater than about 800 correlated with a poor prognosis (e.g., a CPC score of 3, 4, or 5) and a value of less than about 800 correlated with a good prognosis (e.g., a CPC score of 1 or 2). For the area under the curve of the second peak, a value of greater than about 500 correlated

with a poor prognosis (e.g., a CPC score of 3, 4, or 5) and a value of less than about 500 correlated with a good prognosis (e.g., a CPC score of 1 or 2). Accordingly, a correlation/algorithm was established between the varying parameters relating to concentration and a prognostic indication.

The developed correlation/algorithm can be applied to patients with unknown outcomes. That is, samples may be obtained from a patient and the concentration of tau protein in each of the samples can be determined. The data may be analyzed to determine the total area under the curve and/or the area under the curve of the second tau protein peak. If the sum of the total area under the curve and/or the area under the curve of the second peak is greater than 800 or 500, respectively, the prognostic indication for that patient is "poor," and if the sum is less than 800 or 500, respectively, the prognostic indication is "good." Using similar techniques, a variety of correlations may be determined for this tau protein (e.g., increase in tau protein concentration, duration of the increase of tau protein concentration, and/or the magnitude of the fold increase of tau protein) and/or other biomarkers.

Exemplary Assay Methods and Systems

Those of ordinary skill in the art will be aware of a variety of assay methods and systems that may be used in connection with the methods of the present invention. Generally, the methods employed have low limits of detection and/or limits of quantification as compared to bulk analysis techniques (e.g., ELISA methods). The use of assay methods that have low limits of detection and/or limits of quantification allows for correlations to be made between the various parameters discussed above and a method of treatment and/or diagnostic indication that may otherwise not be determinable and/or apparent. For example, in the method described above which correlates the total area under the curve and/or the area under the curve of a second peak of tau protein concentration to a prognostic indication of brain injury, the limits of detection, and/or limits of quantification needs to be substantially lower than the LOD and/or LOQ provided by common ELISA techniques.

The terms "limit of detection" (or LOD) and "limit of quantification" (or LOQ) are given their ordinary meaning in the art. The LOD refers to the lowest analyte

concentration likely to be reliably distinguished from background noise and at which detection is feasible. The LOD as used herein is defined as three standard deviations (SD) above background noise. The LOQ refers to the lowest concentration at which the analyte can not only be reliably detected but at which some predefined goals for bias and imprecision are met. Generally, as is used herein, the LOQ refers to the lowest concentration above the LOD wherein the coefficient of variation (CV) of the measured concentrations less than about 20%.

In some cases, an assay method employed has a limit of detection and/or a limit of quantification of less than about 500 pg/mL, 250 pg/mL, 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less. In some cases, an assay method employed has a limit of quantification and/or a limit of detection between about 100 pg/mL and about 0.01 pg/mL, between about 50 pg/mL and about 0.02 pg/mL, between about 25 pg/mL and about 0.02 pg/mL, between about 10 pg/mL and about 0.02 pg/mL. As will be understood by those of ordinary skill the art, the LOQ and/or LOD may differ for each assay method and/or each biomarker determined with the same assay. In some embodiments, the LOD of an assay employed for detecting tau protein is about equal to or less than 0.02 pg/mL. In some embodiments, the LOQ for an assay employed for detecting tau protein is equal to or less than 0.04 pg/mL

In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is less than about 5000 fM, less than about 3000 fM, less than about 2000 fM, less than about 1000 fM, less than about 500 fM, less than about 300 fM, less than about 200 fM, less than about 100 fM, less than about 50 fM, less than about 25 fM, less than about 10 fM, less than about 5 fM, less than about 2 fM, less than about 1 fM, less than about 0.5 fM, less than about 0.1 fM, or less. In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is between about 5000 fM and about 0.1 fM, between about 3000 fM and about 0.1 fM, between about 1000 fM and about 0.1 fM, between about 1000 fM and about 1 fM, between about 100 fM and about 1 fM, between about 100 fM and about 0.1 fM, or the like. The concentration of analyte molecules or

particles in a fluid sample may be considered to be substantially accurately determined if the measured concentration of the biomarker molecules in the fluid sample is within about 10% of the actual (e.g., true) concentration of the biomarker molecules in the fluid sample. In certain embodiments, the measured concentration of the biomarker molecules in the fluid sample may be within about 5%, within about 4%, within about 3%, within about 2%, within about 1%, within about 0.5%, within about 0.4%, within about 0.3%, within about 0.2% or within about 0.1%, of the actual concentration of the biomarker molecules in the fluid sample. In some cases, the measure of the concentration determined differs from the true (e.g., actual) concentration by no greater than about 20%, no greater than about 15%, no greater than 10%, no greater than 5%, no greater than 4%, no greater than 3%, no greater than 2%, no greater than 1%, or no greater than 0.5%. The accuracy of the assay method may be determined, in some embodiments, by determining the concentration of biomarker molecules in a fluid sample of a known concentration using the selected assay method.

In some embodiments, an assay method employs a step of spatially segregating biomarker molecules into a plurality of locations to facilitate detection/quantification, such that each location comprises/contains either zero or one or more biomarker molecules. Additionally, in some embodiments, the locations may be configured in a manner such that each location can be individually addressed. In some embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be determined by detecting biomarker molecules immobilized with respect to a binding surface having affinity for at least one type of biomarker molecule. In certain embodiments the binding surface may form (e.g., a surface of a well/reaction vessel on a substrate) or be contained within (e.g., a surface of a capture object, such as a bead, contained within a well) one of a plurality of locations (e.g., a plurality of wells/reaction vessels) on a substrate (e.g., plate, dish, chip, optical fiber end, etc.). At least a portion of the locations may be addressed and a measure indicative of the number/percentage/fraction of the locations containing at least one biomarker molecule may be made. In some cases, based upon the number/percentage/fraction, a measure of the concentration of biomarker molecules in the fluid sample may be determined. The measure of the concentration of biomarker molecules in the fluid sample may be

determined by a digital analysis method/system optionally employing Poisson distribution adjustment and/or based at least in part on a measured intensity of a signal, as will be known to those of ordinary skill in the art. In some cases, the assay methods and/or systems may be automated.

Certain methods and systems which employ spatially segregating analyte molecules (e.g., biomarkers) are known in the art, and are described in U.S. Patent Application Publication No. US-2007-0259448 (Serial No. 11/707,385), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF TARGET ANALYTE CONCENTRATION IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259385 (Serial No. 11/707,383), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR DETECTING CELLS AND CELLULAR COMPONENTS IN SMALL DEFINED VOLUMES," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259381 (Serial No. 11/707,384), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF REACTION COMPONENTS THAT AFFECT A REACTION," by Walt et al.; International Patent Publication No. WO 2009/029073 (International Patent Application No. PCT/US2007/019184), filed August 30, 2007, entitled "METHODS OF DETERMINING THE CONCENTRATION OF AN ANALYTE IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al.; U.S. Patent Application Publication No. US-2010-00754072 (Serial No. 12/236,486), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES ON SINGLE MOLECULE ARRAYS," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075439 (Serial No. 12/236488), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES BY CAPTURE-AND-RELEASE USING REDUCING AGENTS FOLLOWED BY QUANTIFICATION," by Duffy et al.; International Patent Publication No. WO2010/039179 (International Patent Application No. PCT/US2009/005248), filed September 22, 2009, entitled "ULTRA-SENSITIVE

DETECTION OF MOLECULES OR ENZYMES," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075355 (Serial No. 12/236490), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF ENZYMES BY CAPTURE-AND-RELEASE FOLLOWED BY QUANTIFICATION," by Duffy et al.; U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

Additional details of exemplary, non-limiting assay methods which comprise one or more steps of spatially segregating biomarker molecules will now be described. In certain embodiments, a method for detection and/or quantifying biomarker molecules in a sample comprises immobilizing a plurality of biomarker molecules with respect to a

plurality of capture objects (e.g., beads) that each include a binding surface having affinity for at least one type of biomarker. For example, the capture objects may comprise a plurality of beads comprising a plurality of capture components (e.g., an antibody having specific affinity for a biomarker of interest, etc.). At least some of the capture objects (e.g., at least some associated with at least one biomarker molecule) may be spatially separated/segregated into a plurality of locations, and at least some of the locations may be addressed/interrogated (e.g., using an imaging system). A measure of the concentration of biomarker molecules in the fluid sample may be determined based on the information received when addressing the locations (e.g., using the information received from the imaging system and/or processed using a computer implemented control system). In some cases, a measure of the concentration may be based at least in part on the number of locations determined to contain a capture object that is or was associated with at least one biomarker molecule. In other cases and/or under differing conditions, a measure of the concentration may be based at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarker molecules and/or capture objects associated with a biomarker molecule at one or more of the addressed locations.

In some embodiments, the number/percentage/fraction of locations containing a capture object but not containing a biomarker molecule may also be determined and/or the number/percentage/fraction of locations not containing any capture object may also be determined. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the total number of locations determined to contain a capture object not associated with a biomarker molecule and/or a measure of the concentration of biomarker molecule in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the number of locations determined to not contain any capture objects. In yet other embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be based at least in part on the ratio of the number of locations determined to contain

a capture object and a biomarker molecule to the total number of locations addressed and/or analyzed.

In certain embodiments, at least some of the plurality of capture objects (e.g., at least some associated with at least one biomarker molecule) are spatially separated into a plurality of locations, for example, a plurality of reaction vessels in an array format. The plurality of reaction vessels may be formed in, on and/or of any suitable material, and in some cases, the reaction vessels can be sealed or may be formed upon the mating of a substrate with a sealing component, as discussed in more detail below. In certain embodiments, especially where quantization of the capture objects associated with at least one biomarker molecule is desired, the partitioning of the capture objects can be performed such that at least some (e.g., a statistically significant fraction; e.g., as described in International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al (see Appendix A)) of the reaction vessels comprise at least one or, in certain cases, only one capture object associated with at least one biomarker molecule and at least some (e.g., a statistically significant fraction) of the reaction vessels comprise an capture object not associated with any biomarker molecules. The capture objects associated with at least one biomarker molecule may be quantified in certain embodiments, thereby allowing for the detection and/or quantification of biomarker molecules in the fluid sample by techniques described in more detail herein.

An exemplary assay method may proceed as follows. A sample fluid containing or suspected of containing biomarker molecules is provided. An assay consumable comprising a plurality of assay sites is exposed to the sample fluid. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the assay sites contain a single biomarker molecule and a statistically significant fraction of the assay sites do not contain any biomarker molecules. The assay sites may optionally be exposed to a variety of reagents (e.g., using a reagent loader) and or rinsed. The assay sites may then optionally be sealed and imaged (see, for example, U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE

DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.). The images are then analyzed (e.g., using a computer implemented control system) such that a measure of the concentration of the biomarker molecules in the fluid sample may be obtained, based at least in part, by determination of the number/fraction/percentage of assay sites which contain a biomarker molecule and/or the number/fraction/percentage of sites which do not contain any biomarkers molecules. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that at least some assay sites comprise more than one biomarker molecule. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be obtained at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarkers molecules at one or more of the assay sites

In some cases, the methods optionally comprise exposing the fluid sample to a plurality of capture objects, for example, beads. At least some of the biomarker molecules are immobilized with respect to a bead. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a statistically significant fraction of the beads do not associate with any biomarker molecules. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may then be spatially separated/segregated into a plurality of assay sites (e.g., of an assay consumable). The assay sites may optionally be exposed to a variety of reagents and/or rinsed. At least some of the assay sites may then be addressed to determine the number of assay sites containing a biomarker molecule. In some cases, the number of assay sites containing a bead not associated with a biomarker molecule, the number of assay sites not containing a bead and/or the total number of assay sites addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample. In some cases, more than one biomarker molecule may associate with a bead and/or more than one bead may be present in an assay site. In some cases, the plurality biomarker molecules may be exposed to at least one additional reaction component prior to, concurrent with, and/or following spatially separating at least some of the biomarker molecules into a plurality of locations.

The biomarker molecules may be directly detected or indirectly detected. In the case of direct detection, a biomarker molecule may comprise a molecule or moiety that may be directly interrogated and/or detected (e.g., a fluorescent entity). In the case of indirect detection, an additional component is used for determining the presence of the biomarker molecule. For example, the biomarker molecules (e.g., optionally associated with a bead) may be exposed to at least one type of binding ligand. A "binding ligand," is any molecule, particle, or the like which specifically binds to or otherwise specifically associates with a biomarker molecule to aid in the detection of the biomarker molecule. In certain embodiments, a binding ligand may be adapted to be directly detected (e.g., the binding ligand comprises a detectable molecule or moiety) or may be adapted to be indirectly detected (e.g., including a component that can convert a precursor labeling agent into a labeling agent). A component of a binding ligand may be adapted to be directly detected in embodiments where the component comprises a measurable property (e.g., a fluorescence emission, a color, etc.). A component of a binding ligand may facilitate indirect detection, for example, by converting a precursor labeling agent into a labeling agent (e.g., an agent that is detected in an assay). A "precursor labeling agent" is any molecule, particle, or the like, that can be converted to a labeling agent upon exposure to a suitable converting agent (e.g., an enzymatic component). A "labeling agent" is any molecule, particle, or the like, that facilitates detection, by acting as the detected entity, using a chosen detection technique. In some embodiments, the binding ligand may comprise an enzymatic component (e.g., horseradish peroxidase, beta-galactosidase, alkaline phosphatase, etc.). A first type of binding ligand may or may not be used in conjunction with additional binding ligands (e.g., second type, etc.).

More than one type of binding may be employed in any given assay method, for example, a first type of binding ligand and a second type of binding ligand. In one example, the first type of binding ligand is able to associate with a first type of biomarker molecule and the second type of binding ligand is able to associate with the first binding ligand. In another example, both a first type of binding ligand and a second type of binding ligand may associate with the same or different epitopes of a single biomarker molecule, as described herein. In some embodiments, at least one binding ligand comprises an enzymatic component.

In some embodiments, a binding ligand and/or a biomarker may comprise an enzymatic component. The enzymatic component may convert a precursor labeling agent (e.g., an enzymatic substrate) into a labeling agent (e.g., a detectable product). A measure of the concentration of biomarker molecules in the fluid sample can then be determined based at least in part by determining the number of locations containing a labeling agent (e.g., by relating the number of locations containing a labeling agent to the number of locations containing a biomarker molecule (or number of capture objects associated with at least one biomarker molecule to total number of capture objects)). Non-limiting examples of enzymes or enzymatic components include horseradish peroxidase, beta-galactosidase, and alkaline phosphatase. Other non-limiting examples of systems or methods for detection include embodiments where nucleic acid precursors are replicated into multiple copies or converted to a nucleic acid that can be detected readily, such as the polymerase chain reaction (PCR), rolling circle amplification (RCA), ligation, Loop-Mediated Isothermal Amplification (LAMP), etc. Such systems and methods will be known to those of ordinary skill in the art, for example, as described in "DNA Amplification: Current Technologies and Applications," Vadim Demidov et al., 2004.

Another exemplary embodiment of indirect detection is as follows. In some cases, the biomarker molecules may be exposed to a precursor labeling agent (e.g., enzymatic substrate) and the enzymatic substrate may be converted to a detectable product (e.g., fluorescent molecule) upon exposure to a biomarker molecule.

The assay methods and systems may employ a variety of different components, steps, and/or other aspects that will be known and understood by those of ordinary skill in the art. For example, a method may further comprise determining at least one background signal determination (e.g., and further comprising subtracting the background signal from other determinations), wash steps, and the like. In some cases, the assays or systems may include the use of at least one binding ligand, as described herein. In some cases, the measure of the concentration of biomarker molecules in a fluid sample is based at least in part on comparison of a measured parameter to a calibration curve. In some instances, the calibration curve is formed at least in part by determination at least one calibration factor, as described above.

As will be understood by those of ordinary skill in the art, a system and/or method may be calibrated using natural and/or synthetic forms of the target biomarker, and/or analogues thereof. In embodiments where the target analyte is a tau protein, the system and/or method may be calibrated using one or more natural and/or synthetic isoforms of tau protein. Naturally occurring tau proteins are described herein. Synthetic isoforms of tau proteins include two nearest neighbor antibody epitope synthetic peptides (<20 amino acids) to long synthetic peptides (80-100 amino acids in length. In some cases, short isoforms of the naturally occurring tau proteins may be employed. For example, tau protein isoforms can have varying lengths of amino acids selected from the tau 441 sequence. Non-limiting examples of short forms of tau proteins include tau 50-mers (e.g., comprising residues 187-237, 190-240, or 155-205 of tau 441) and tau 64-mers (e.g., comprising residues 155-235 of tau 441, RGAAP PGQKG QTPPA PKpTPP SSKSG DRSGY SSPGS PGTSR TPSLP TPPTR EPKKV AVVRT PPKS-NH_2 (SEQ ID NO.: 1)). In some cases, at least a portion of the tau protein(s) used may be phosphorylated (e.g., RGAAP PGQKG QTPPA PKpTPP SSKSG DRSGY SSPGS PGTSR TPSLP TPPTR EPKKV AVVRpT PPKS-NH2 (SEQ ID NO.: 2)).

In certain embodiments, solubilized, or suspended precursor labeling agents may be employed, wherein the precursor labeling agents are converted to labeling agents which are insoluble in the liquid and/or which become immobilized within/near the location (e.g., within the reaction vessel in which the labeling agent is formed). Such precursor labeling agents and labeling agents and their use is described in commonly owned U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al., incorporated herein by reference.

An exemplary embodiment of an assay method that may be used in certain embodiments of the invention is illustrated in Figure 1a. A plurality of capture objects 2, are provided (step (A)). In this particular example, the plurality of capture objects comprises a plurality of beads. The beads are exposed to a fluid sample containing a plurality of biomarker molecules 3 (e.g., beads 2 are incubated with biomarker molecules 3). At least some of the biomarker molecules are immobilized with respect to a bead. In

this example, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a statistically significant fraction of the beads do not associate with any biomarker molecules. For example, as shown in step (B), biomarker molecule 4 is immobilized with respect to bead 5, thereby forming complex 6, whereas some beads 7 are not associated with any biomarker molecules. It should be understood, in some embodiments, more than one biomarker molecule may associate with at least some of the beads, as described herein. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may then be spatially separated/segregated into a plurality of locations. As shown in step (C), the plurality of locations is illustrated as substrate 8 comprising a plurality of wells/reaction vessels 9. In this example, each reaction vessel comprises either zero or one beads. At least some of the reaction vessels may then be addressed (e.g., optically or via other detection means) to determine the number of locations containing a biomarker molecule. For example, as shown in step (D), the plurality of reaction vessels are interrogated optically using light source 15, wherein each reaction vessel is exposed to electromagnetic radiation (represented by arrows 10) from light source 15. The light emitted (represented by arrows 11) from each reaction vessel is determined (and/or recorded) by detector 15 (in this example, housed in the same system as light source 15). The number of reaction vessels containing a biomarker molecule (e.g., reaction vessels 12) is determined based on the light detected from the reaction vessels. In some cases, the number of reaction vessels containing a bead not associated with a biomarker molecule (e.g., reaction vessel 13), the number of wells not containing a bead (e.g., reaction vessel 14) and/or the total number of wells addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

A non-limiting example of an embodiment where a capture object is associated with more than one biomarker molecule is illustrated in Figure 1b. A plurality of capture objects 20 are provided (step (A)). In this example, the plurality of capture objects comprises a plurality of beads. The plurality of beads is exposed to a fluid sample containing plurality of biomarker molecules 21 (e.g., beads 20 are incubated with

biomarker molecules 21). At least some of the biomarker molecules are immobilized with respect to a bead. For example, as shown in step (B), biomarker molecule 22 is immobilized with respect to bead 24, thereby forming complex 26. Also illustrated is complex 30 comprising a bead immobilized with respect to three biomarker molecules and complex 32 comprising a bead immobilized with respect to two biomarker molecules. Additionally, in some cases, some of the beads may not associate with any biomarker molecules (e.g., bead 28). The plurality of beads from step (B) is exposed to a plurality of binding ligands 31. As shown in step (C), a binding ligand associates with some of the biomarker molecules immobilized with respect to a bead. For example, complex 40 comprises bead 34, biomarker molecule 36, and binding ligand 38. The binding ligands are provided in a manner such that a statistically significant fraction of the beads comprising at least one biomarker molecule become associated with at least one binding ligand (e.g., one, two, three, etc.) and a statistically significant fraction of the beads comprising at least one biomarker molecule do not become associated with any binding ligands. At least a portion of the plurality of beads from step (C) are then spatially separated into a plurality of locations. As shown in step (D), in this example, the locations comprise a plurality of reaction vessels 41 on a substrate 42. The plurality of reaction vessels may be exposed to the plurality of beads from step (C) such at each reaction vessel contains zero or one beads. The substrate may then be analyzed to determine the number of reaction vessels containing a binding ligand (e.g., reaction vessels 43), wherein in the number may be related to a measure of the concentration of biomarker molecules in the fluid sample. In some cases, the number of reaction vessels containing a bead and not containing a binding ligand (e.g., reaction vessel 44), the number of reaction vessels not containing a bead (e.g., reaction vessel 45), and/or the total number of reaction vessels addressed/analyzed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

In some embodiments, a plurality of locations may be addressed and/or a plurality of capture objects and/or species/molecules/particles of interest may be detected substantially simultaneously. "Substantially simultaneously" when used in this context, refers to addressing/detection of the locations/capture objects/species/molecules/particles

of interest at approximately the same time such that the time periods during which at least two locations/capture objects/species/molecules/particles of interest are addressed/detected overlap, as opposed to being sequentially addressed/detected, where they would not. Simultaneous addressing/detection can be accomplished by using various techniques, including optical techniques (e.g., CCD detector). Spatially segregating capture objects/species/molecules/particles into a plurality of discrete, resolvable locations, according to some embodiments facilitates substantially simultaneous detection by allowing multiple locations to be addressed substantially simultaneously. For example, for embodiments where individual species/molecules/particles are associated with capture objects that are spatially segregated with respect to the other capture objects into a plurality of discrete, separately resolvable locations during detection, substantially simultaneously addressing the plurality of discrete, separately resolvable locations permits individual capture objects, and thus individual species/molecules/particles (e.g., biomarker molecules) to be resolved. For example, in certain embodiments, individual molecules/particles of a plurality of molecules/particles are partitioned across a plurality of reaction vessels such that each reaction vessel contains zero or only one species/molecule/particle. In some cases, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5% of all species/molecules/particles are spatially separated with respect to other species/molecules/particles during detection. A plurality of species/molecules/particles may be detected substantially simultaneously within a time period of less than about 1 second, less than about 500 milliseconds, less than about 100 milliseconds, less than about 50 milliseconds, less than about 10 milliseconds, less than about 1 millisecond, less than about 500 microseconds, less than about 100 microseconds, less than about 50 microseconds, less than about 10 microseconds, less than about 1 microsecond, less than about 0.5 microseconds, less than about 0.1 microseconds, or less than about 0.01 microseconds, less than about 0.001 microseconds, or less. In some embodiments, the plurality of species/molecules/particles may be detected substantially simultaneously within a time period of between about 100 microseconds and about 0.001 microseconds, between about 10 microseconds and about 0.01 microseconds, or less.

In some embodiments, the locations are optically interrogated. The locations exhibiting changes in their optical signature may be identified by a conventional optical train and optical detection system. Depending on the detected species (e.g., type of fluorescence entity, etc.) and the operative wavelengths, optical filters designed for a particular wavelength may be employed for optical interrogation of the locations. In embodiments where optical interrogation is used, the system may comprise more than one light source and/or a plurality of filters to adjust the wavelength and/or intensity of the light source. In some embodiments, the optical signal from a plurality of locations is captured using a CCD camera.

In some embodiments of the present invention, the plurality of reaction vessels may be sealed (e.g., after the introduction of the biomarker molecules, binding ligands, and/or precursor labeling agent), for example, through the mating of the second substrate and a sealing component. The sealing of the reaction vessels may be such that the contents of each reaction vessel cannot escape the reaction vessel during the remainder of the assay. In some cases, the reaction vessels may be sealed after the addition of the biomarker molecules and, optionally, at least one type of precursor labeling agent to facilitate detection of the biomarker molecules. For embodiments employing precursor labeling agents, by sealing the contents in some or each reaction vessel, a reaction to produce the detectable labeling agents can proceed within the sealed reaction vessels, thereby producing a detectable amount of labeling agents that is retained in the reaction vessel for detection purposes.

The plurality of locations may be formed may be formed using a variety of methods and/or materials. In some embodiments, the plurality of locations comprises a plurality of reaction vessels/wells on a substrate. In some cases, the plurality of reaction vessels is formed as an array of depressions on a first surface. In other cases, however, the plurality of reaction vessels may be formed by mating a sealing component comprising a plurality of depressions with a substrate that may either have a featureless surface or include depressions aligned with those on the sealing component. Any of the device components, for example, the substrate or sealing component, may be fabricated from a compliant material, e.g., an elastomeric polymer material, to aid in sealing. The surfaces may be or made to be hydrophobic or contain hydrophobic regions to minimize

leakage of aqueous samples from the microwells. The reactions vessels, in certain embodiments, may be configured to receive and contain only a single capture object.

In some embodiments, the reaction vessels may all have approximately the same volume. In other embodiments, the reaction vessels may have differing volumes. The volume of each individual reaction vessel may be selected to be appropriate to facilitate any particular assay protocol. For example, in one set of embodiments where it is desirable to limit the number of capture objects used for biomarker capture contained in each vessel to a small number, the volume of the reaction vessels may range from attoliters or smaller to nanoliters or larger depending upon the nature of the capture objects, the detection technique and equipment employed, the number and density of the wells on the substrate and the expected concentration of capture objects in the fluid applied to the substrate containing the wells. In one embodiment, the size of the reaction vessel may be selected such only a single capture object used for biomarker capture can be fully contained within the reaction vessel (see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS ," by Duffy et al. (see Appendix A), each herein incorporated by reference).

In some embodiments, the reaction vessels may have a volume between about 1 femtoliter and about 1 picoliter, between about 1 femtoliters and about 100 femtoliters, between about 10 attoliters and about 100 picoliters, between about 1 picoliter and about 100 picoliters, between about 1 femtoliter and about 1 picoliter, or between about 30 femtoliters and about 60 femtoliters. In some cases, the reaction vessels have a volume of less than about 1 picoliter, less than about 500 femtoliters, less than about 100 femtoliters, less than about 50 femtoliters, or less than about 1 femtoliter. In some cases, the reaction vessels have a volume of about 10 femtoliters, about 20 femtoliters, about 30 femtoliters, about 40 femtoliters, about 50 femtoliters, about 60 femtoliters, about 70 femtoliters, about 80 femtoliters, about 90 femtoliters, or about 100 femtoliters.

The total number of locations and/or density of the locations employed in an assay (e.g., the number/density of reaction vessels in an array) can depend on the composition and end use of the array. For example, the number of reaction vessels employed may depend on the number of types of biomarker molecule and/or binding ligand employed, the suspected concentration range of the assay, the method of detection, the size of the capture objects, the type of detection entity (e.g., free labeling agent in solution, precipitating labeling agent, etc.). Arrays containing from about 2 to many billions of reaction vessels (or total number of reaction vessels) can be made by utilizing a variety of techniques and materials. Increasing the number of reaction vessels in the array can be used to increase the dynamic range of an assay or to allow multiple samples or multiple types of biomarker molecules to be assayed in parallel. The array may comprise between one thousand and one million reaction vessels per sample to be analyzed. In some cases, the array comprises greater than one million reaction vessels. In some embodiments, the array comprises between about 1,000 and about 50,000, between about 1,000 and about 1,000,000, between about 1,000 and about 10,000, between about 10,000 and about 100,000, between about 100,000 and about 1,000,000, between about 100,000 and about 500,000, between about 1,000 and about 100,000, between about 50,000 and about 100,000, between about 20,000 and about 80,000, between about 30,000 and about 70,000, between about 40,000 and about 60,000 reaction vessels. In some embodiments, the array comprises about 10,000, about 20,000, about 50,000, about 100,000, about 150,000, about 200,000, about 300,000, about 500,000, about 1,000,000, or more, reaction vessels.

The array of reaction vessels may be arranged on a substantially planar surface or in a non-planar three-dimensional arrangement. The reaction vessels may be arrayed in a regular pattern or may be randomly distributed. In a specific embodiment, the array is a regular pattern of sites on a substantially planar surface permitting the sites to be addressed in the X-Y coordinate plane.

In some embodiments, the reaction vessels are formed in a solid material. As will be appreciated by those in the art, the number of potentially suitable materials in which the reaction vessels can be formed is very large, and includes, but is not limited to, glass (including modified and/or functionalized glass), plastics (including acrylics, polystyrene

and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, cyclic olefin copolymer (COC), cyclic olefin polymer (COP), Teflon®, polysaccharides, nylon or nitrocellulose, etc.), elastomers (such as poly(dimethyl siloxane) and poly urethanes), composite materials, ceramics, silica or silica-based materials (including silicon and modified silicon), carbon, metals, optical fiber bundles, or the like. In general, the substrate material may be selected to allow for optical detection without appreciable autofluorescence. In certain embodiments, the reaction vessels may be formed in a flexible material.

A reaction vessel in a surface (e.g., substrate or sealing component) may be formed using a variety of techniques known in the art, including, but not limited to, photolithography, stamping techniques, molding techniques, etching techniques, or the like. As will be appreciated by those of the ordinary skill in the art, the technique used can depend on the composition and shape of the supporting material and the size and number of reaction vessels.

In a particular embodiment, an array of reaction vessels is formed by creating microwells on one end of a fiber optic bundle and utilizing a planar compliant surface as a sealing component. In certain such embodiments, an array of reaction vessels in the end of a fiber optic bundle may be formed as follows. First, an array of microwells is etched into the end of a polished fiber optic bundle. Techniques and materials for forming and etching a fiber optic bundle are known to those of ordinary skill in the art. For example, the diameter of the optical fibers, the presence, size and composition of core and cladding regions of the fiber, and the depth and specificity of the etch may be varied by the etching technique chosen so that microwells of the desired volume may be formed. In certain embodiments, the etching process creates microwells by preferentially etching the core material of the individual glass fibers in the bundle such that each well is approximately aligned with a single fiber and isolated from adjacent wells by the cladding material. Potential advantages of the fiber optic array format is that it can produce thousands to millions of reaction vessels without complicated microfabrication procedures and that it can provide the ability to observe and optically address many reaction vessels simultaneously.

Each microwell may be aligned with an optical fiber in the bundle so that the fiber optic bundle can carry both excitation and emission light to and from the wells, enabling remote interrogation of the well contents. Further, an array of optical fibers may provide the capability for simultaneous or non-simultaneous excitation of molecules in adjacent vessels, without signal "cross-talk" between fibers. That is, excitation light transmitted in one fiber does not escape to a neighboring fiber.

Alternatively, the equivalent structures of a plurality of reaction vessels may be fabricated using other methods and materials that do not utilize the ends of an optical fiber bundle as a substrate. For example, the array may be a spotted, printed or photolithographically fabricated substrate produced by techniques known in the art; see for example WO95/25116; WO95/35505; PCT US98/09163; U.S. Patent Nos. 5,700,637, 5,807,522, 5,445,934, 6,406,845, and 6,482,593. In some cases, the array may be produced using molding, embossing, and/or etching techniques as will be known to those of ordinary skill in the art.

In some embodiments, the plurality of locations may not comprise a plurality of reaction vessels/wells. For example, in embodiments where capture objects are employed, a patterned substantially planar surface may be employed and the patterned areas form a plurality of locations. In some cases, the patterned areas may comprise substantially hydrophilic surfaces which are substantially surrounded by substantially hydrophobic surfaces. In certain embodiments, a plurality of capture objects (e.g., beads) may be substantially surrounded by a substantially hydrophilic medium (e.g., comprising water), and the beads may be exposed to the patterned surface such that the beads associate in the patterned areas (e.g., the hydrophilic locations on the surface), thereby spatially segregating the plurality of beads. For example, in one such embodiment, a substrate may be or include a gel or other material able to provide a sufficient barrier to mass transport (e.g., convective and/or diffusional barrier) to prevent capture objects used for biomarker capture and/or precursor labeling agent and/or labeling agent from moving from one location on or in the material to another location so as to cause interference or cross-talk between spatial locations containing different capture objects during the time frame required to address the locations and complete the assay. For example, in one embodiment, a plurality of capture objects is spatially separated by dispersing the capture

objects on and/or in a hydrogel material. In some cases, a precursor labeling agent may be already present in the hydrogel, thereby facilitating development of a local concentration of the labeling agent (e.g., upon exposure to a binding ligand or biomarker molecule carrying an enzymatic component). As still yet another embodiment, the capture objects may be confined in one or more capillaries. In some cases, the plurality of capture objects may be absorbed or localized on a porous or fibrous substrate, for example, filter paper. In some embodiments, the capture objects may be spatially segregated on a uniform surface (e.g., a planar surface), and the capture objects may be detected using precursor labeling agents which are converted to substantially insoluble or precipitating labeling agents that remain localized at or near the location of where the corresponding capture object is localized. The use of such substantially insoluble or precipitating labeling agents is described herein. In some cases, single biomarker molecules may be spatially segregated into a plurality of droplets. That is, single biomarker molecules may be substantially contained in a droplet containing a first fluid. The droplet may be substantially surrounded by a second fluid, wherein the second fluid is substantially immiscible with the first fluid.

In some embodiments, during the assay, at least one washing step may be carried out. In certain embodiments, the wash solution is selected so that it does not cause appreciable change to the configuration of the capture objects and/or biomarker molecules and/or does not disrupt any specific binding interaction between at least two components of the assay (e.g., a capture component and a biomarker molecule). In other cases, the wash solution may be a solution that is selected to chemically interact with one or more assay components. As will be understood by those of ordinary skill in the art, a wash step may be performed at any appropriate time point during the inventive methods. For example, a plurality of capture objects may be washed after exposing the capture objects to one or more solutions comprising biomarker molecules, binding ligands, precursor labeling agents, or the like. As another example, following immobilization of the biomarker molecules with respect to a plurality of capture objects, the plurality of capture objects may be subjected to a washing step thereby removing any biomarker molecules not specifically immobilized with respect to a capture object.

Other assay methods in addition to those described herein are known in the art and may be used in connection with the inventive methods. For example, various analyzers are commercially available for the determination of the concentration of biomarkers. The assay methods employed should meet the algorithm requirements for LOD and LOQ.

The following examples are included to demonstrate various features of the invention. Those of ordinary skill in the art should, in light of the present disclosure, will appreciate that many changes can be made in the specific embodiments which are disclosed while still obtaining a like or similar result without departing from the scope of the invention as defined by the appended claims. Accordingly, the following examples are intended only to illustrate certain features of the present invention, but do not necessarily exemplify the full scope of the invention.

Example 1

The following example provides experimental details relating to prognostication of neurological outcome in comatose survivors of oxygen deprivation, using tau proteins

Objective: Use of peripheral tau protein measurements as an indicator of the presence of brain injury has remained elusive, in large part due to the lack of adequate sensitivity for reliable measurement of the protein in serum or plasma using common technologies. Additionally, little was known about the time-dependence of tau protein release from the central nervous system into peripheral circulation. Using methods described herein, which, in certain embodiments are capable of ultra sensitive tau protein measurement, serial serum samples from 25 resuscitated cardiac arrest patients were analyzed to longitudinally study tau protein release into serum and determine prognostic significance of tau protein elevation for prediction of long-term cognitive impairment from hypoxic insult.

Summary of Methods: 25 unconscious patients with cardiac arrest were resuscitated with restoration of spontaneous circulation and admitted to a hospital intensive care unit (ICU). Patients were treated with hypothermia and repeated blood samplings were obtained during the first five days in the ICU. Serum levels of total tau protein were measured with a digital immunoassay described in Example 2. Cognitive

assessments were made using Cerebral Performance Categorization (CPC) at discharge from the ICU and six months later. Tau protein data were analyzed in the context of six-month cognitive outcome.

Summary of Results: Tau protein elevations ranged from modest to very high, and exhibited unexpected bi-modal kinetic profiles in many patients. Total area-under-the-curve (AUC) was highly prognostic for six-month cognitive outcome. AUC of the secondary tau protein peak exhibited 100% sensitivity and 91% specificity for predicting 6-month outcome.

Summary of Conclusions: The data indicate that sufficiently sensitive peripheral tau protein measurements in conjunction with an understanding of tau protein release kinetics have clinical utility for brain injury assessment and prognostication of cognitive outcome.

Additional Background: Tau proteins, with a molecular mass of 48 to 67 kd depending on isoform, are associated with microtubules and localized in the axonal compartment of neurons. Tau proteins plays a structural role in the assembly of tubulin monomers into axonal microtubule bundles, which are important for maintaining the cytoskeleton and axonal transport. Tau protein is generally elevated in the cerebrospinal fluid (CSF) of patients with neurodegenerative disease and severe head injuries, making it a candidate for peripheral measurement as a biomarker of acquired or traumatic brain injury (ABI, TBI). However, studies on peripheral tau protein have been hampered by its low abundance in serum and plasma (typically low pg/mL), making its measurement difficult.

While CSF tau protein elevation is known to correlate with 1-year outcome in severe TBI patients, no such correlation has been made to serum tau protein, in part because most common assays cannot accurately detect the low levels of tau protein in serum. In addition, the clinical value of serum tau protein for assessment of minor head injury has been questioned. A previous studiy looked at serum tau protein elevation measured in 24 ischemic stroke patients studied using an immunoassay with a limit of detection of 60 pg/mL, but no correlation was made or found between tau protein appearance to stroke severity. A recent rat TBI model indicated serum tau protein elevation peaked rapidly and declined after six hours, with no significant additional tau

protein elevation over 7 days. Little else has been reported about the kinetics of tau protein movement across the blood brain barrier (BBB), nor the potential prognostic significance of peripheral tau protein appearance with ABI or TBI.

Methods: This example employed the protocol described in Example 2 below, which is capable in certain embodiments of three logs greater sensitivity than typical conventional methods. The assay was utilized to examine serial serum samples from 25 resuscitated cardiac arrest patients to longitudinally study tau protein release into serum and probe for prognostic significance of tau protein elevation for prediction of long-term cognitive impairment due to hypoxic insult.

The study was performed at the general intensive care unit at Uppsala University Hospital, Sweden, and approved by the Human Ethics Committee of Uppsala, Sweden. Twenty-five unconscious patients with cardiac arrest were resuscitated with restoration of spontaneous circulation (ROSC). Patients were >18 yrs old, exhibited systolic blood pressure >80mmHg after ROSC, and a Glasgow Coma Scale ≤7.

Upon admission, hypothermia treatment was started immediately after resuscitation. Ventilation was administered during the coma period, with a target PaO_2 of ≥12 kPa (90 mmHg) and $PaCO_2$ between 5.0 and 5.5 kPa (38–41 mmHg). Targeted mean arterial pressure was 65–100 mmHg, with application of inotropic/vasopressor support, if required, using dobutamine as the first line medication, followed by noradrenaline (norepinephrine) or adrenaline (epinephrine), if necessary. If the patient was considered euvolaemic but had a diuresis of less than 0.5 ml/kg/h, furosemide was administered. Furosemide was also given if the intensive care physician considered that the patient had a fluid overload. All patients received an arterial line in the radial or femoral artery for blood sampling. Serial blood samples were collected, starting as soon as possible in the emergency phase (within 6 h after cardiac arrest), and continuing at 1, 2, 6, 12, 24, 48, 72, 96, and 108 h after cardiac arrest. Serum aliquots were frozen at -70°C until analysis.

Patient outcome was assessed in accordance with the Glasgow-Pittsburgh cerebral performance category (CPC) scale at discharge from the intensive care unit and 6 months later. The CPC scale ranges from 1 to 5, with 1 representing mildest possible neurological deficit (patient is able to return to work), and 4-5 representing the most

severe deficit (vegetative) and death. A CPC of 1 or 2 was considered a "good" outcome and a CPC score of 3–5 a "poor" outcome. For patients who died after ICU discharge, the better of the two scores was used, as recommended by the Utstein templates.

Patient serum samples were measured in triplicate by a single molecule digital immunoassay for tau protein (see Example 2 for more details). The technique involves performing a paramagnetic bead-based ELISA using beta-galactosidase as a reporter, followed by isolation of individual capture beads within femtoliter-sized reaction wells in a microarray. Isolation of individual beads permits the buildup of fluorescent substrate in the presence of tau protein, such that wells containing a single immunocomplex can be detected. The limit of detection of the assay is 0.02 pg/mL, making it approximately 1000-fold more sensitive than typical conventional immunoassays. The assay was calibrated from 0 pg/mL to 100 pg/mL total tau protein and was able to precisely measure serum tau protein in the patient samples. The extreme sensitivity of the method permits pre-dilution of the samples prior to assay, reducing potential endogenous interferences. All samples were pre-diluted 1:4 with a PBS-tween diluent prior to assay.

Tau protein elevation profiles were analyzed for area-under-the-curve (AUC) with GraphPad Prism 5.0d (GraphPad Software, La Jolla, CA). Four of the 25 patients died 24-48 hours after admission, and these patients were excluded from AUC analysis. AUC was evaluated during the first 24-hour period as well as over the full time course of samples (to 108 hours) using a baseline of zero. In addition, the AUC of secondary tau protein elevation peaks were estimated assuming a baseline corresponding to the tau protein concentration measured at the initial time point of the secondary peak. Statistical significance between 'good' and 'poor' 6-month outcome was determined by student t-test, with significance taken as $p < 0.05$.

Results: Representative elevation profiles for patients with good and poor 6-month outcomes are depicted in Figure 2**.** Figure 2 shows serum tau following resuscitation from cardiac arrest. CPC scores are listing for each patient in the legends. The first two numbers correspond to the CPC assessments upon discharge from the ICU and six months later. The third number represents overall 6-month outcome assessment (1=poor, 0=good). Figures 2a-2c depict representative groupings of patients exhibiting different profiles of tau elevations: a) initial 24-hour peaks; b) delayed peaks, and c) both

initial 24-hour and delayed peaks. Figure 2d depicts representative profiles from patients with good outcomes. Note the difference in scales. Error bars depict SD of triplicate measurements.

Tau protein expression ranged from almost undetectable to large elevations approaching 700 pg/mL. There was a strong general association between tau protein elevation and patient outcome: the more tau protein expressed, the greater the likelihood for poor 6-month outcome. Tau protein elevation also showed clear bi-modal tendencies, with the appearance of one or both peaks varying with patient. The initial peak was generally fully expressed during the first 24 hours following cardiac arrest, while the secondary peak generally expressed after 24-48 hours. Some patients exhibited only the first peak (Figure 2a), some exhibited only the second peak (Figure 2b), and some exhibited both peaks (Figure 2c).

Table 2.

Patient	AUC </= 24 hr		AUC all		AUC 2nd peak only	
	Good	Poor	Good	Poor	Good	Poor
2		1590		4759		1450
3	708.9		2145		0	
4	748.1		2861		154.2	
5		625.2		3207		1890
6		179.9		1232		897.5
7	4.72		92.86		64.6	
8		11.18		1646		1545
9	59		1141		0	
10		109.7		9336		8296
11	14.63		64.56		0	
12		52.15		649.2		597.8
13	26.01		288.5		215.8	
14	12.91		431.5		393	
15	12.31		184.4		168.2	
17	0.02		30.66		30.9	
18	15.78		46.62		0	
20		334.6		8527		8511
21		580.8		19875		18051
23		1039		26150		23935
24		12.92		72.9		35.94
25		9.37		8987		8842
AVG	160.26	413.17	730.61	7521.83	101.66	6447.39
t-test (p)	0.090609467		0.011726946		0.01197362	

To compare the significance of the primary and secondary elevation profiles for 6-month outcome, AUCs were calculated for the first 24 hours (referred to as the "first peak"), the full time course, and the secondary peak only. Table 2 exhibits AUCs for each patient, which are plotted in Figure 3. More specifically, Table 2 tabulates

characteristics of serum tau elevation profiles from resuscitated survivors of cardiac arrest during the first 96-108 hours following admission to the ICD. Parameters were sorted on the basis of good or poor 6-month cerebral outcome and compared by student t-test. Four patients (all with good outcome) exhibited no discernable secondary peaks. Figure 3 plots AUC results a) across the first 24 hours, b) for all serial samplings, and c) the secondary tau peak only. Error bars depict standard error of the means.

Weak correlation was observed between the initial 24 hours and 6-month outcome ($p > 0.05$). Notably, there was a strong correlation between the secondary peak and 6-month outcome ($p = 0.01$). The weak correlation between initial tau protein appearance and outcome reflects inter-patient differences in primary peak expression rather than lack of significance between tau protein elevation and outcome. Calculation of overall AUC gave similar statistical significance with outcome as the AUC of the second peak only. Patients with good outcome generally had very low serum tau protein, and secondary peaks where either absent or weak (Figure 2d).

The appearance and magnitude of the secondary tau protein peak was highly prognostic for 6-month outcome. Bifurcating the data with an AUC cut point of 500 resulted in 100% sensitivity (10/10 patients) and 91% specificity (10/11 patients) for predicting good and poor 6-month outcomes respectively.

Discussion: These data represent a high-resolution longitudinal examination of serum tau protein elevation following an acute ABI event. The bimodal profile elevation kinetics are consistent with two modes of neuronal damage: initially upon acute oxygen deprivation, followed by delayed cell death due to apoptosis and/or cerebral swelling. With ROSC as an inclusion criterion, the elevation kinetics should be unrelated to reperfusion differences between patients. Patients were all treated with hypothermia, and were not treated with drugs known to significantly affect BBB permeability. It seems likely the bimodal profiles are related to neuronal damage rather than BBB or reperfusion variables.

Inter-patient differences in expression one or both elevation peaks could be related to the extent and duration of the hypoxia. Global cerebral ischemia could trigger rapid necrosis in addition to longer-term apoptosis cascades. Sub lethal hypoxic encephalopathy can set a series of toxic reactions in motion that finish off injured neurons

and kill additional ones over hours or days following the insult. While early tau protein peaks were less prognostics for 6-month outcome than the secondary elevation, they are nonetheless deadly when high levels of tau protein are measured. Among the four patients who did not survive the first 48 hours, two patients had prominent initial tau protein peaks of well over 200 pg/mL that had dropped 10-fold by 24 hours (not shown). In these patients, it may have been that the acute initial necrosis was sufficiently lethal, and it might be anticipated that survival would have witnessed prominent secondary peaks.

It is noted that the serial sampling in this study was concluded at 108 hours. It may be that additional tau protein elevation occurs beyond 108 hours. Studies of tau protein elevation in CSF following severe TBI have revealed temporal elevations well beyond five days. It is possible that patients in the present study exhibiting tau protein peaks in the first 24 hours with minimal secondary elevation could go on to express significant additional tau protein beyond 108 hours.

Since the magnitude of cognitive impairment should reflect the magnitude of hypoxia, correlation of serum tau protein elevation with cognitive outcome indicates released tau protein reflects the extent of hypoxia and associated neuronal damage. Serum tau protein appearance as measured by digital immunoassay exhibited considerable prognostic significance for 6-month cognitive outcome, with a sensitivity and specificity of 100% using an AUC cut point of 500. This example demonstrates that serial blood measurements of tau protein in the ICU following resuscitation from cardiac arrest has a clinical value for stratifying likely cognitive outcome.

Example 2

The following example describes the tau protein ultra-sensitive digital immunoassay for plasma tau using single molecule arrays that was employed in Example 1.

Reagents were developed for a paramagnetic bead-based ELISA. Tau protein molecules in plasma were captured on antibody-coated paramagnetic capture beads and labeled with an enzyme conjugate. The beads were loaded into arrays of 50,000, 50-femtoliter reaction wells etched into bundles of optical fibers. Single capture beads

trapped in each well were sealed in the presence of enzyme substrate and imaged using a fluorescence microscope fitted with a CCD camera. At low concentrations, the images were analyzed for the presence or absence of single immunocomplexes of labeled tau protein, resulting in a digital signal. At high concentrations, the analog intensity of the beads was normalized to the digital signals, extending the dynamic range of the assay to over four logs. Analytical performance of the assay was evaluated, and serum samples from hypoxia patients were tested for tau protein.

The assay described in this example has a detection limit (i.e., LOD) of 0.02 pg/mL and was linear to 100 pg/mL tau protein ($R2 > 0.996$, Patient LJ cal curve). Results using serum samples from hypoxia patients showed a bi-phasic response across the time course post hypoxic insult.

Concentrations of tau protein in serum and plasma are believed to be over 100-fold lower than in cerebrospinal fluid.

This example describes the development and validation of a digital immunoassay using single molecule array technology that is capable of measuring tau protein in hypoxia induced serum without biomarker enrichment or sample pretreatment procedures. The assay exhibits over 1000-fold greater sensitivity than validated commercially available ELISAs. The assay can be used for directly measuring and monitoring serum tau protein in therapeutic trials aimed at altering and lowering levels of this protein, down to sub-femtomolar levels.

The single molecule array technology employed two primary steps: an initial analyte capture step conducted with paramagnetic beads, followed by isolation of individual beads in arrays of femtoliter-sized reaction wells for digital imaging. Isolation of the individual beads in microwells permits the buildup of fluorescent product from the enzyme label such that signal from a single immunocomplex is readily detected using a CCD camera. This approach permits counting of single molecules when tau protein concentrations are low enough that the ratio of bound labeled peptide per bead is much less than one. In this concentration realm, Poisson statistics predict that bead-containing microwells in the array will contain either a single labeled tau protein molecule or no labeled tau protein molecules, resulting in a binary signal. Due to the amplified sensitivity for detecting label molecules afforded by confining fluorescent product

buildup to the microwells, concentrations of label (detector anti-Tau antibody and enzyme label) can be reduced relative to standard ELISAs. Lowered concentrations of labeling reagents reduces their interaction with capture beads, resulting in reduced nonspecific binding enabling high signal to background ratios, even at extremely low concentrations of biomarker. For higher biomarker concentrations where all beads contain one or more labeled immunocomplexes, digital signals from the Poisson realm are used to calibrate analog intensity measurements, extending the dynamic range to over four logs.

Three reagents were developed for this tau protein immunoassay: capture beads, biotinylated detector, and a conjugate of streptavidin:beta-galactosidase The capture bead reagent comprised of a commercially available monoclonal anti-tau antibody (Covance) directed to an epitope (amino acids 210-230). The antibody was covalently attached by standard coupling chemistry to 2.7 μm carboxy paramagnetic microbeads (Varian). Because individual beads were captured in array wells 4.5 μm wide x 3.25 μm deep, it was advantageous that the capture beads remain monomeric. The antibody-coated beads were diluted to a working concentration of 6 x 106 beads/mL in Tris buffer with a surfactant and BSA. The biotinylated detector reagent was comprised of two commercially available monoclonal anti-tau antibodys (Pierce) directed to the N-terminus of the Capture Detector (amino acids 159-163 and 194-198). The antibodies were biotinylated using standard methods (Solulink), and the biotinylation level was confirmed spectrophotometrically per manufacturer's instructions. The monomeric state of the detector antibody before and after biotinylation was confirmed by size exclusion HPLC. The biotinylated detector antibodies were diluted to individual concentration of 0.2 μg/ml for assay in a PBS diluent containing a surfactant and newborn calf serum, NCS (PBS/NCS). The enzyme conjugate—streptavidin: β-galactosidase (SβG)—was prepared by covalent conjugation of purified streptavidin (Thermo Scientific) and β-galactosidase (Sigma) using standard coupling chemistry (1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride, Thermo Scientific). Aliquots of a concentrated stock solution of SβG were prepared in PBS with 50% glycerol and transferred to -20°C for storage. Prior to assay, an aliquot was thawed and diluted to 25 pM in PBS/NCS with

MgCl2. Purified Tau 381 antigen for calibrators and for specificity testing were from Millipore.

Assay calibrators and controls were prepared by dilution of Tau 381 stock in PBS diluent containing a surfactant and BSA (PBS/BSA). In some cases, a stock solution prepared by dilution to 1000 ng/mL in PBS/10G. For dynamic range/linearity characterization, a series of calibrators were prepared by serial 3-fold dilution to give a calibration range of 0 – 100 pg/mL. To evaluate assay day-to-day reproducibility at low concentrations, three low controls were prepared at 0.1, 5.0, and 50.0 pg/mL in PBS/BSA.

50,000 well optical fiber microarrays were prepared as previously described. In brief, optical fiber bundles (Schott North America) were cut into 5 cm lengths and sequentially polished with 30, 9, and 1 um-sized diamond lapping films. One end of each bundle was etched in a 0.025 N HCl solution for 2 minutes and then submerged into water. The differential etch rate of the core and cladding glass of the fiber bundles caused an array of 4.5 um diameter wells to be formed in the core fibers.

Bead-plasma incubations and labeling of immunocomplexes in conical 96 well plates (Axygen) were conducted using a robotic liquid handling system (Tecan EVO 150). Conical wells are used to facilitate magnetic attraction of the beads to the sides of the wells for efficient removal of reaction mixtures and bead washing. For magnetic attraction, a microplate bar magnet (Invitrogen) was used. Incubation periods were conducted with shaking on a microplate shaker (VWR) to keep beads suspended in the wells. The assays were initiated by mixing 100 uL of sample with 600,000 capture beads, and the mixtures were incubated with shaking for two hours. Serum samples were pre-diluted 1:4 prior to assay with PBS/BSA as a precaution for sample quality and interference effects. Following serum incubation in the presence of biotinylated detector antibody, the beads were washed 3 times with a wash buffer of 5-fold concentrated PBS with a surfactant (5xPBS). After a the wash step, 100 µL of streptavidin-β-galactosidase was incubated with the beads for 30 minutes to form the final enzyme-labeled immunocomplex. The beads were then washed eight times per above, and concentrated to 2 x 107 beads/ml with the addition of a reduced volume (30 µL) of array loading buffer comprised of PBS with a surfactant. Beads were then loaded onto the arrays. 10

μL of the concentrated bead solution (2 x 106 beads) were pipetted onto the arrays and the arrays were centrifuged at 1,300 g for 10 minutes. Excess beads were removed by a PBS rinse and swabbing with deionized water. With this technique, array filling by the beads was generally 50-60%, which was adequate for minimizing contributions to imprecision from Poisson noise. Wells containing tau protein-labeled beads were detected utilizing beta-galactosidase catalyzed hydrolysis of resorufin β-D-galactopyranoside (RGP, Invitrogen) into fluorescent product (resorufin, excitation 558nm, emission 577nm). To introduce RGP substrate to the array wells, droplets of substrate were placed on a silicone gasket and introduced into the array wells with a mechanical platform. This step resulted in an array of sealed femtoliter wells in which enzyme-containing beads developed a concentrated fluorescence signal.

Imaging was accomplished via a custom-built fluorescence imaging system containing a light source, objectives, filter cubes and a CCD camera. For each sample, five fluorescent images of one second each were acquired (to identify wells containing an enzyme) and one white light image was acquired (to identify wells containing a bead). Background fluorescence and any contaminating artifacts were discriminated from true 'positive' wells by analyzing for signal growth over the multiple images. These images were analyzed to determine the average number of enzymes per bead (AEB) across the concentration range. In some cases, at <50% active beads, the system was determined to be in the digital realm, so AEB was be determined from the fraction of beads that contain at least one enzyme and the Poisson distribution; and at >50% active beads, the average fluorescence intensity of the beads was normalized to the average fluorescence intensity of beads containing a single enzyme to yield AEB. In other cases, at <70% active beads relative to total beads, AEB was determined as a count of active beads corrected for a low statistical probability of multiple enzymes per bead; and at >70% active beads, the probability of multiple enzymes/bead increases such that all wells contain multiple enzymes and all are growing in signal and in this realm, the signal is was no longer digital, and average fluorescence intensities of the wells were converted to AEB based on the average intensities of wells containing single enzymes as determined at lower Aβ42 concentrations. The AEB unit worked continuously across the digital and analog realms.

For description of various details associate with this assay, see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the present invention. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials,

and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the teachings of the present invention is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, the invention may be practiced otherwise than as specifically described and claimed. The present invention is directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the scope of the present invention.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, i.e., elements that are conjunctively present in some cases and disjunctively present in other cases. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified unless clearly indicated to the contrary. Thus, as a non-limiting example, a reference to "A and/or B," when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A without B (optionally including elements other than B); in another embodiment, to B without A (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in a list, "or" or "and/or" shall be interpreted as being inclusive, i.e., the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as

"only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of exactly one element of a number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (i.e. "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or "exactly one of." "Consisting essentially of," when used in the claims, shall have its ordinary meaning as used in the field of patent law.

As used herein in the specification and in the claims, the phrase "at least one," in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements. This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase "at least one" refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, "at least one of A and B" (or, equivalently, "at least one of A or B," or, equivalently "at least one of A and/or B") can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

In the claims, as well as in the specification above, all transitional phrases such as "comprising," "including," "carrying," "having," "containing," "involving," "holding," and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

What is claimed:

Claims

1. A method for determining a measure of the concentration of tau protein in a patient sample containing or suspected of containing tau protein, comprising:

performing an assay to determine a measure of the concentration of tau protein in the sample, wherein the limit of detection of tau protein of the assay is less than about 0.2 pg/mL.

2. The method of claim 1, wherein the tau protein is tau 23 (352, 0N3R), tau 24 (383, 0N4R), tau 37 (381, 1N3R), tau 34 (412, 1N4R), tau 39 (410, 2N3R), and/or tau 40 (441, 2N4R), optionally phosphorylated.

3. The method of claim 1, wherein the patient is suspected to have a brain injury, optionally resulting from a hypoxic event.

4. The method of claim 1, wherein the sample is a bodily fluid.

5. The method of claim 4, wherein the bodily fluid is blood or a blood component.

6. The method of claim 4, wherein the bodily fluid is CSF.

7. The method of claim 5, wherein the blood component is plasma or serum.

8. The method of claim 1, wherein the measure of the concentration of tau protein is determined in a plurality of samples taken from the patient over a period of time.

9. The method of claim 8, wherein the plurality of samples are collected within 96 hours after the patient has experienced the brain injury or suspected brain injury, optionally resulting from a hypoxic event.

10. A method of determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury, wherein the prognosis and/or the course of treatment is based at least in part on the measure of the concentration of tau protein determined in the patient sample according to the method of any one of claims 1-9.

11. The method of claim 10, wherein the brain injury results from a hypoxic event.

12. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of tau protein in the sample; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of tau protein present in the sample.

13. The method of claim 12, wherein the brain injury results from a hypoxic event.

14. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of tau protein present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of tau protein in the sample.

15. The method of claim 14, wherein the brain injury results from a hypoxic event.

16. A method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury, comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of tau protein in the sample; and

providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of tau protein present in the sample.

17. The method of claim 16, wherein the brain injury results from a hypoxic event.

18. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury, comprising:

determining a measure of the concentration of tau protein in each of a plurality of samples obtained from the patient following the brain injury; and

determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration tau protein present in the sample.

19. The method of claim 18, wherein the brain injury results from a hypoxic event.

20. The method of any one of claims 12-19, wherein the tau protein is tau 23 (352, 0N3R), tau 24 (383, 0N4R), tau 37 (381, 1N3R), tau 34 (412, 1N4R), tau 39 (410, 2N3R), and/or tau 40 (441, 2N4R), optionally phosphorylated.

21. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by cardiac arrest.

22. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by stroke.

23. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by an ischemic event.

24. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by a thrombosis.

25. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by arterial embolism.

26. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by a hemorrhage.

27. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by a high altitude.

28. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by asphyxia.

29. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by an asthmatic event.

30. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by swelling of the brain.

31. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by physical trauma and/or physical injury.

32. The method of any one of claims 12-19, wherein the brain injury comprises a hypoxic event caused by arteriosclerosis or atherosclerosis.

33. The method of any one of claims 12-19, wherein the patient's prognosis is correlated with a Cerebral Performance Category (CPC) score.

34. The method of claim 33, wherein the CPC score includes classifications of good or poor.

35. The method of claim 34, wherein a good CPC score indicates a prognosis of the patient being conscious and alert with normal function or only slight disability or conscious and alert with moderate disability after a selected period of time.

36. The method of claim 34, wherein a poor CPC score indicates a prognosis of the patient being conscious with the patient having a severe disability, being comatose or in a persistent vegetative state, or being brain dead or suffering death from other causes after a selected period of time.

37. The method of claim 34 or 35, wherein the selected period of time is about 1 week, or about 2 weeks, or about 4 weeks, or about 2 months, or about 3 months, or about 4 months, or about 5 months, or about 6 months, or about 9 months, or about 1 year, or about 1.5 years, or about 2 years.

38. The method of any one of claims 12-19, wherein the plurality of samples are obtained from the patient within 2 days, 2.5 days, 3 days, 3.5 days, 4 days, 5 days, 6 days, or 7 days following the brain injury.

39. The method of any one of claims 12-19, wherein 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more, samples are obtained from the patient.

40. The method of any one of claims 12-19, wherein the measure of tau protein concentration in the sample is less than about 1000 pg/mL, or less than about 900 pg/mL, or less than about 800 pg/mL, or less than about 700 pg/mL, or less than about 600

pg/mL, or less than about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL.

41. The method of any one of claims 12-19, wherein the limit of detection for the assay is less than about 10 pg/mL, 9 pg/mL, 8 pg/mL, 7 pg/mL, 6 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.5 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.02 pg/mL.

42. The method of any one of claims 12-19, wherein a change in the concentration of tau protein in the plurality of samples is determined as a function of time.

43. The method of claim 42, wherein the concentration of tau protein in the plurality of samples is plotted on a graph as concentration versus time.

44. The method of claim 42, wherein the prognosis and/or course or treatment is based at least in part on at least a portion of the area under the curve plotted on the graph.

45. The method of claim 44, wherein the prognosis and/or course or treatment is based at least in part on the area under the curve plotted on the graph for samples obtained in the first 2 days, 2.5 days, 3 days, 3.5 days, 4 days, 5 days, 6 days, or 7 days following the brain injury.

46. The method of claim 42, wherein the prognosis and/or course of treatment is based at least in part on the area under the curve plotted on the graph for a second peak of tau protein concentration.

47. The method of claim 45, wherein the prognosis is good for the recovery from the brain injury if the area under the curve is less than about 800.

48. The method of claim 45, wherein the prognosis is poor for the recovery from the brain injury if the area under the curve is greater than about 800.

49. The method of claim 46, wherein the prognosis is good for the recovery from the brain injury if the area under the curve is less than about 500.

50. The method of claim 46, wherein the prognosis is poor for the recovery from the brain injury if the area under the curve is greater than about 500.

51. The method of any one of claims 12-19, wherein the biomarker or tau protein is measured in bodily fluid.

52. The method of claim 51, wherein the bodily fluid is blood.

53. The method of claim 51, wherein the bodily fluid is plasma and/or serum derived from a blood sample.

54. The method of any one of claims 12-19, wherein the concentration of only a single biomarker is determined.

55. A method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury, comprising:

(a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours;

(b) determining the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area is determined for the entire time period and/or for a second peak in the tau protein concentration; and

(c) determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the area under the curve for the entire time period and/or the second peak in the tau protein concentration determined in step (b).

56. The method of claim 55, wherein the brain injury results from a hypoxic event.

57. A method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area is determined for the entire time period and/or for a second peak in the tau protein concentration, which has been determined by:

(a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples have been obtained from the patient over a period of time of at least about 48 hours; and

(b) determining the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time for the entire time period and/or for a second peak in the tau protein.

58. The method of claim 57, wherein the brain injury results from a hypoxic event.

59. A method for performing an assay and providing data for determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury, comprising:

(a) performing an assay on each of a plurality of samples obtained from the patient following the brain injury to determine the measured concentration of tau protein in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours;

(b) determining the area under the curve of a graph of the tau protein concentration in the plurality of samples versus time, wherein the area under the curve is determined for the entire time period and/or for a second peak in the tau protein concentration; and

(c) providing data derived in steps (a) and (b) to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least

in part on the area under the curve determined for the entire time period and/or for a second peak in the tau protein concentration.

60. The method of any one of claims 55-59, wherein when the area under the curve for the entire time period is less than about 800, the prognosis is good based on the CPC scale.

61. The method of any one of claims 55-59, wherein when the area under the curve for the entire time period is greater than about 800, the prognosis is poor based on the CPC scale.

62. The method of any one of claims 55-59, wherein when the area under the curve for the second peak in the tau protein concentration is less than about 500, the prognosis is good based on the CPC scale.

63. The method of any one of claim 55-59, wherein when the area under the curve for the second peak in the tau protein concentration is greater than about 500, the prognosis is poor based on the CPC scale.

64. The method of any one of claims 55-59, wherein the baseline concentration for determining the area under the curve for the entire time period is equal to zero.

65. The method of any one of claims 55-59, wherein the baseline concentration for determining the area under the curve of the second peak of tau protein concentration is equal to the concentration of tau protein present in the sample obtained from the patient substantially immediately prior to a second increase in tau protein concentration.

66. The method of any preceding claim, wherein the tau protein is tau 23 (352, 0N3R), tau 24 (383, 0N4R), tau 37 (381, 1N3R), tau 34 (412, 1N4R), tau 39 (410, 2N3R), and/or tau 40 (441, 2N4R), optionally phosphorylated.

67. The method of any preceding claim, wherein tau protein is measured in bodily fluid.

68. The method of claim 67, wherein the bodily fluid is blood.

69. The method of claim 67, wherein the bodily fluid is not CSF.

70. The method of any preceding claim, wherein the assay comprises:

spatially segregating at least a portion of the biomarkers into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

71. The method of claim 70, further comprising exposing the plurality of biomarker molecules to a plurality of binding ligands such that at least some of the biomarker molecules associate with a single binding ligand and a statistically significant fraction of the biomarker molecules do not associate with any binding ligand;

72. The method of any preceding claim, wherein the assay comprises:

immobilizing biomarker molecules with respect to a plurality of capture objects such that at least some of the capture objects associate with at least one biomarker molecule and a statistically significant fraction of the capture objects do not associate with any biomarker molecules;

spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

73. The method of any preceding claim, wherein the assay comprises:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one biomarker, to a solution containing or suspected of containing the at least one type of biomarker;

immobilizing biomarker molecules with respect to the plurality of capture objects such that at least some of the capture objects associate with at least one biomarker molecule and a statistically significant fraction of the capture objects do not associate with any biomarker molecules;

spatially segregating at least a portion of the capture objects subjected to the immobilizing step into a plurality of separate locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of said locations containing a biomarker molecule; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a biomarker molecule.

74. A method of any preceding claim, wherein the assay comprises:

exposing a plurality of capture objects that each include a binding surface having affinity for at least one type of biomarker, to a solution containing or suspected of containing the at least one type of biomarker to form capture objects comprising at least one immobilized biomarker molecule;

mixing the capture objects prepared in the exposing step to a plurality of binding ligands such that at least some of the capture objects associate with a single binding ligand and a statistically significant fraction of the capture objects do not associate with any binding ligand;

spatially segregating at least a portion of the capture objects subjected to the mixing step into a plurality of locations;

addressing at least a portion of the plurality of locations subjected to the spatially segregating step and determining the number of locations containing a binding ligand; and

determining a measure of the concentration of biomarker in the sample based at least in part on the number of locations determined to contain a binding ligand.

75. The method of any preceding claim, wherein in the addressing step, the number of said locations containing a capture object that includes a binding surface having affinity for at least one type of biomarker not containing a biomarker molecule or a binding ligand is determined.

76. The method of claim 75, wherein the measure of the concentration of biomarker in the sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker containing a biomarker molecule or a binding ligand, to the total number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker.

77. The method of any preceding claim, wherein the measure of the concentration of biomarker molecules in the fluid sample is based at least in part on the ratio of the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker molecules containing a biomarker molecule or a binding ligand, to the number of locations addressed in the addressing step determined to contain a capture object that includes a binding surface having affinity for at least one type of biomarker molecule but not to contain any capture objects that include a binding surface having affinity for at least one type of biomarker containing a biomarker molecule or a binding ligand.

78. The method of any preceding claim, wherein the plurality of capture objects that include a binding surface having affinity for at least one type of biomarker comprises a plurality of beads.

79. The method of any preceding claim, wherein the plurality of locations comprises a plurality of reaction vessels.

80. The method of any preceding claim, wherein the binding ligand comprises an enzymatic component.

81. The method of any preceding claim, wherein the measure of the concentration of biomarker molecules in the fluid sample is determined at least in part by comparison of a measured parameter to a calibration standard.

82. The method of any preceding claim, wherein following the spatially segregating step, the locations are exposed to precursor labeling agent.

83. The method of claim 82, wherein the precursor labeling agent is converted to a labeling agent upon exposure to a binding ligand.

84. The method of claim 83, wherein the number of locations containing a capture object containing a biomarker molecule or a labeling agent is determined by determining the number of locations comprising a labeling agent.

85. The method of any preceding claim, wherein the average volume of the plurality of reaction vessels is between about 10 attoliters and about 100 picoliters, or between about 1 femtoliter and about 1 picoliter.

86. The method of any preceding claim, wherein the average diameter of the plurality of beads is between about 0.1 micrometer and about 100 micrometers, or between about 1 micrometer and about 10 micrometers.

87. The method of any preceding claim, further comprising performing at least one wash step.

88. The method of any preceding claim, further comprising sealing the plurality of reaction vessels.

89. The method of any preceding claim, wherein the plurality of locations is addressed using optical techniques.

90. The method of any preceding claim, wherein the binding surface comprises a plurality of capture components.

Abstract

The present invention, in some embodiments, generally relates to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury. In some embodiments, the brain injury results from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of tau protein in a patient sample containing or suspected of containing tau protein.

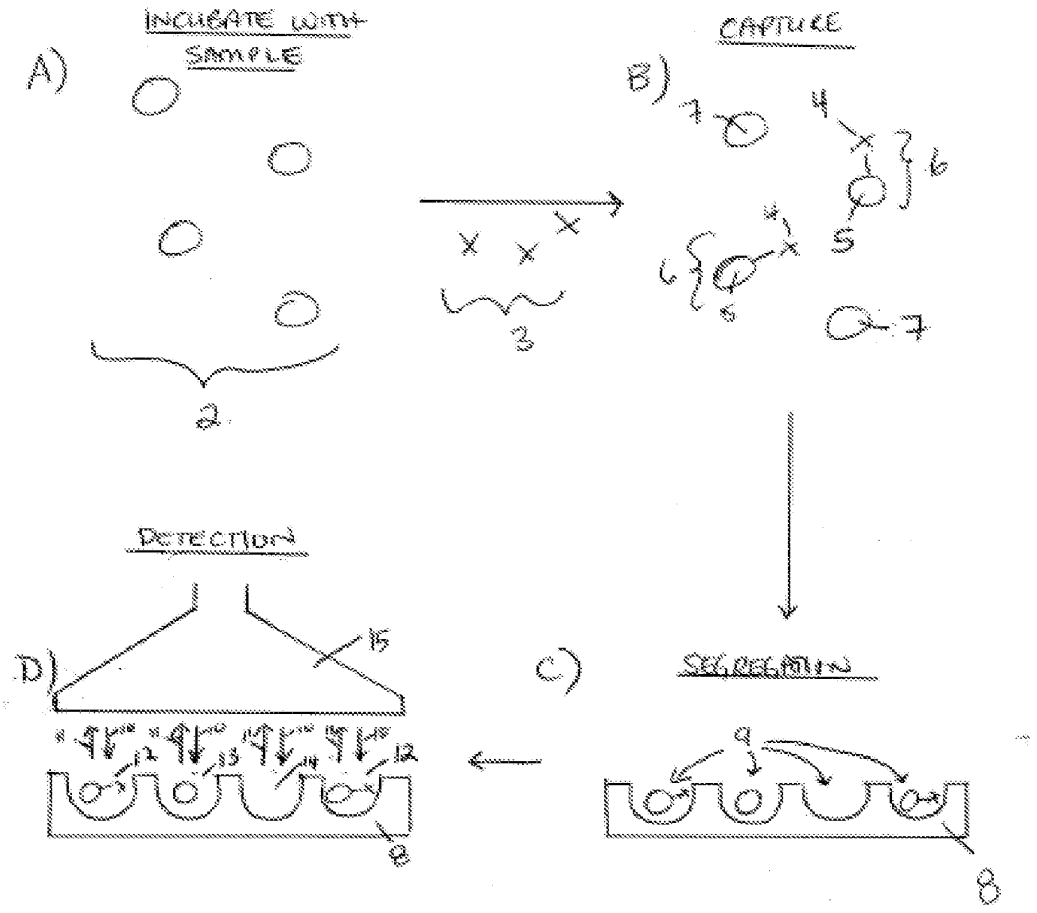


Figure 1a

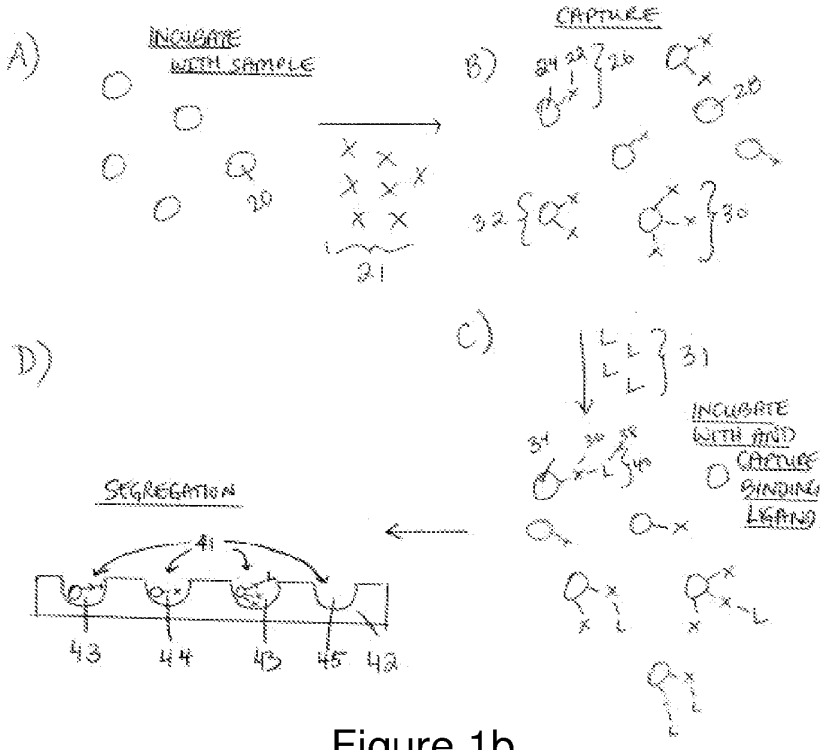

A)
INCUBATE WITH SAMPLE
B)
CAPTURE
C)
INCUBATE WITH AND CHELATE BINDING LIGHTS
D)
SEGREGATION
41
43
44
45
42

Figure 1b

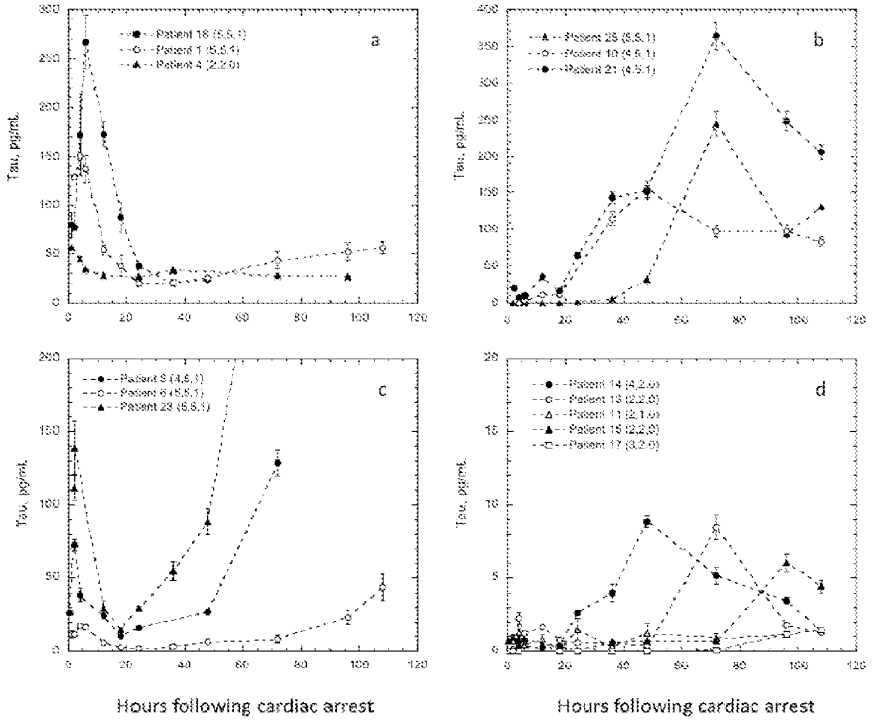


Figure 2

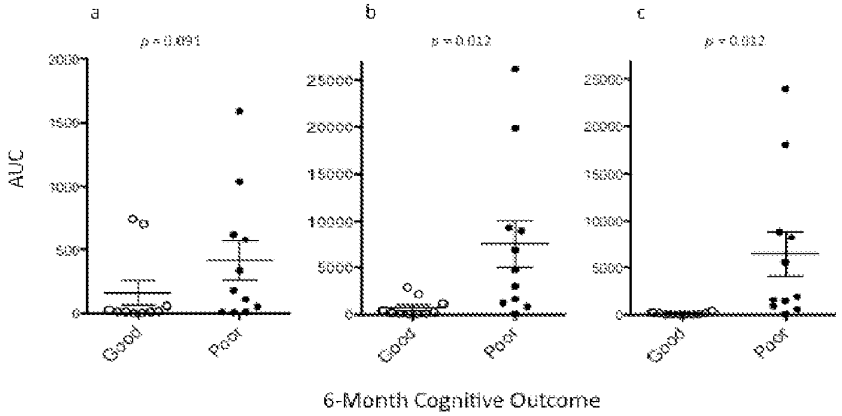


Figure 3

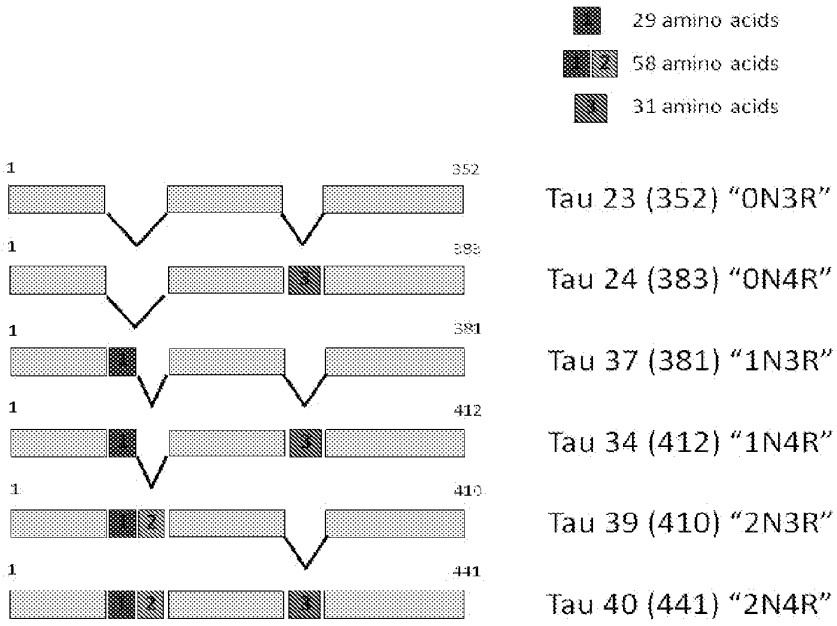

29 amino acids
58 amino acids
31 amino acids
1
352
Tau 23 (352) "0N3R"
1
383
Tau 24 (383) "0N4R"
1
381
Tau 37 (381) "1N3R"
1
412
Tau 34 (412) "1N4R"
1
410
Tau 39 (410) "2N3R"
1
441
Tau 40 (441) "2N4R"

Figure 4

Electronic Acknowledgement Receipt

EFS ID:	10760632
Application Number:	61524693
International Application Number:	
Confirmation Number:	5500
Title of Invention:	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY
First Named Inventor/Applicant Name:	to be added
Customer Number:	23628
Filer:	Michael Pomianek/Judy Daley
Filer Authorized By:	Michael Pomianek
Attorney Docket Number:	Q0052.70018US00
Receipt Date:	17-AUG-2011
Filing Date:	
Time Stamp:	19:00:39
Application Type:	Provisional

Payment information:

Submitted with Payment	no

File Listing:

Document Number	Document Description	File Name	File Size(Bytes)/ Message Digest	Multi Part /.zip	Pages (if appl.)
1	Provisional Cover Sheet (SB16)	Q005270018US00-PROCVR-MJP.pdf	38800 7336d216b0571c1b4995c5da73f40da3372 5d139	no	2

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2	Application Data Sheet	Q005270018US00-ADS-MJP.pdf	10964 deb7dac2d18125172b2afca332464e5e3771b0f2	no	1
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Multipart Description/PDF files in .zip description		
Document Description	**Start**	**End**
Specification	1	52
Claims	53	66
Abstract	67	67

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4	Drawings-other than black and white line drawings	Q005270018US00-DRW-MJP.pdf	275759 f523a70096550e10349c438cddd024d2b72d799f	no	4
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DOCUMENT MADE AVAILABLE UNDER THE PATENT COOPERATION TREATY (PCT)

International application number:		**PCT/US2012/033343**
International filing date:		**12 April 2012 (12.04.2012)**
Document type:		**Certified copy of priority document**
Document details:	Country/Office:	**US**
	Number:	**61/524,693**
	Filing date:	**17 August 2011 (17.08.2011)**
Date of receipt at the International Bureau:		**20 April 2012 (20.04.2012)**

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a),(b) or (b-*bis*)

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April 19, 2012

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APPLICATION NUMBER: *61/474,315*
FILING DATE: *April 12, 2011*
RELATED PCT APPLICATION NUMBER: *PCT/US12/33343*

THE COUNTRY CODE AND NUMBER OF YOUR PRIORITY APPLICATION, TO BE USED FOR FILING ABROAD UNDER THE PARIS CONVENTION, IS *US61/474,315*

Certified by

David J. Kappos

Under Secretary of Commerce
for Intellectual Property
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PTO/SB/16 (12-08)
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PROVISIONAL APPLICATION FOR PATENT COVER SHEET – Page 1 of 2

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

VIA EFS-WEB

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)

Additional inventors are being named on the _____ *separately numbered sheets attached hereto.*

TITLE OF THE INVENTION (500 characters max):

METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT

Direct all correspondence to: **CORRESPONDENCE ADDRESS**

[X] The address corresponding to Customer Number: 23628

OR

[ ] Firm or Individual Name

Address

City	State	Zip
Country	Telephone	Email

ENCLOSED APPLICATION PARTS (*check all that apply*)

[X] Application Data Sheet. See 37 CFR 1.76
[ ] CD(s), Number of CDs _____
[X] Drawing(s) *Number of Sheets* 6
[X] Other (specify) Appendix A
[X] Specification (e.g. description of the invention) *Number of Pages* 70

Fees Due: Filing Fee of $220 ($110 for small entity). If the specification and drawings exceed 100 sheets of paper, an application size fee is also due, which is $270 ($135 for small entity) for each additional 50 sheets or fraction thereof. See 35 U.S.C. 41(a)(1)(G) and 37 CFR 1.16(s).

METHOD OF PAYMENT OF THE FILING FEE AND APPLICATION SIZE FEE FOR THIS PROVISIONAL APPLICATION FOR PATENT

[X] Applicant claims small entity status. See 37 CFR 1.27.

[ ] A check or money order made payable to the *Director of the United States Patent and Trademark Office* is enclosed to cover the filing fee and application size fee (if applicable).

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SIGNATURE	/Michael J. Pomianek/	Date	April 12, 2011
TYPED or PRINTED NAME	Michael J. Pomianek, Ph.D.	REGISTRATION NO. *(if appropriate)*	46,190
TELEPHONE	617.646.8000	Docket Number:	Q0052.70017US00

Application Data Sheet

Application Information

Application Type::	Provisional
Subject Matter::	Utility
Suggested Group Art Unit::	N/A
CD-ROM or CD-R?::	None
Sequence submission?::	None
Computer Readable Form (CRF)?::	No
Title::	METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT
Attorney Docket Number::	Q0052.70017US00
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Request for Non-Publication?::	No
Small Entity?::	Yes
Petition included?::	No
Secrecy Order in Parent Appl.?::	No

Applicant Information

Correspondence Information

Correspondence Customer Number::	23628

Representative Information

Representative Customer Number::	23628

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Domestic Priority Information

Foreign Priority Information

Assignee Information

Quanterix Corporation
One Kendall Square
Building 1400, 2nd Floor
Cambridge, MA 02139

Fujirebio Diagnostics, Inc. v. Quanterix Corp.
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METHODS OF DETERMINING A TREATMENT PROTOCOL FOR AND/OR A PROGNOSIS OF A PATIENT'S RECOVERY FROM A BRAIN INJURY RESULTING FROM A HYPOXIC EVENT

Field of the Invention

The present invention generally relates, in some embodiments, to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide.

Background of the Invention

Hypoxia generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Oxygen deprivation to the brain results in neuronal damage and death, which is in turn related to the extent of long term brain dysfunction. The concentration of certain biomarkers may become elevated under hypoxic conditions. For example, certain such biomarkers have been found to become elevated in the brain and central nervous system under hypoxic condition. However, since such biomarkers must diffuse across the blood brain barrier, they may be present in the blood in proportion in extremely low concentrations that are not reliably measurable by typical conventional immunoassays. While the concentration of some biomarkers in the brain and central nervous system are known to increase with hypoxic events, the increased concentration has not been correlated with specific diagnostic indications and/or methods of treatment. In addition, while some methods exist for determining a cerebral hypoxic event in a patient and/or determining a course of treatment following a hypoxic event, many of the known methods are costly (e.g., magnetic resonance imaging) and/or provide unclear results and/or predictors. Accordingly, improved methods are needed.

Summary of the Invention

In some embodiments, a method for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide comprises performing an assay to determine a measure of the

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concentration of beta-amyloid peptide in the sample, wherein the limit of detection of beta-amyloid peptide of the assay is less than about 0.2 pg/mL.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on a measured concentration of at least one biomarker measured in each sample by an assay performed on a plurality of samples obtained from the patient following the event to determine the measure of the concentration of the at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprises performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event comprises determining a measure of the concentration of a biomarker in each of a plurality of sample obtained from the patient

following the event, wherein the assay has a limit of quantification of less than about 10 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of a first biomarker in the plurality of samples, wherein the measured concentration has been determined by performing an assay to measure the concentration of only the first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event comprises determining a measure of the concentration of only a first biomarker in each of a plurality of sample obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 100 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of beta-amyloid peptide present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

In some embodiments, a method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay

has a limit of quantification of less than about 10 pg/mL; and providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a measure of the concentration of beta-amyloid in each of a plurality of samples obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 500 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and (c) determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined in step (b).

In some embodiments, a method of determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time determined, which has been determined by: (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples have been obtained from the

patient over a period of time of at least about 48 hours and (b) determining the baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time.

In some embodiments, a method for performing an assay and providing data for determining a method of treatment for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event comprises (a) performing an assay on each of a plurality of samples obtained from the patient following the event to determine the measured concentration of beta-amyloid peptide in each of the samples, wherein the plurality of samples are obtained from the patient over a period of time of at least about 48 hours; (b) determining a baseline concentration of beta-amyloid peptide for the patient, the maximum concentration of beta-amyloid peptide concentration in a single sample obtained during the period of time, and the duration of time in which the concentration of beta-amyloid peptide is increasing in the samples obtained from the patient during the period of time; and (c) providing data derived in steps (a) and (b) to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the baseline concentration, the maximum concentration, and/or the duration of time

Brief Description of the Drawings

Figure 1a is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 1b is a schematic flow diagram depicting one embodiment of steps (A-D) for performing an exemplary method of the present invention;

Figure 2 shows plots of a measure of the concentration of beta-amyloid (1-42) versus time for patients having (a-c) a good outcome and (d-f) a bad outcome;

Figure 3 shows a plot of a measure of the concentration of beta-amyloid (1-42) versus time including various parameters that may be correlated with a prognostic indication and/or a method of treatment;

Figure 4 shows an exemplary calibration dose-response of an assay method for determining a measure of the concentration of beta-amyloid (1-42) up to 250 pg/mL;

Figure 5 provides a plot showing day-to-day reproducibility for determining a

measure of the concentration of beta-amyloid (1-42), according to some embodiments of the present invention;

Figure 6 shows plots of a measure of the concentration of beta-amyloid (1-42) in plasma and CSF samples from Alzheimer's, MCI, and normal control subjects; and

Figure 7 shows a plot of a measure of the concentration of beta-amyloid (1-42) versus time for an exemplary patient

Other aspects, embodiments, and features of the invention will become apparent from the following detailed description when considered in conjunction with the accompanying drawings. The accompanying figures are schematic and are not intended to be drawn to scale. For purposes of clarity, not every component is labeled in every figure, nor is every component of each embodiment of the invention shown where illustration is not necessary to allow those of ordinary skill in the art to understand the invention. All patent applications and patents incorporated herein by reference are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Detailed Description

The present invention generally relates to methods of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event. In some embodiments, methods are provided for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide. In some cases, the beta-amyloid peptide is beta-amyloid (1-42). The subject matter of the present invention involves, in some cases, interrelated products, alternative solutions to a particular problem, and/or a plurality of different uses of one or more systems and/or articles.

In some embodiments, a method of the present invention comprises determining a measure of the concentration of at least one biomarker in one or more samples obtained from a patient following a hypoxic event (or a suspected hypoxic event). A prognostic indication of the patient's recovery and/or determining a course of treatment may be based at least in part on the measure of the concentration of the at least one biomarker present in the one or more samples. It should be understood, that while much of the discussion below is directed to methods involving the analysis of more than one sample, this is by way of example only, and similar methods may be employed wherein only a single sample is employed.

As will be known to those of ordinary skill in the art, the term "hypoxia" generally refers to a deficiency in the amount of oxygen reaching body tissues or a condition of insufficient levels of oxygen in tissue or blood. Hypoxia at a cellular level develops when delivery of oxygen to cell mitochondria slows as the partial pressure gradient from capillaries to tissues decreases. As the delivery of oxygen decreases, aerobic metabolism stops and less efficient anaerobic pathways of glycolysis become responsible for the production of cellular energy. The end result is an increase in cellular concentrations of sodium, calcium, and hydrogen ions which may lead to cell death.

Oxygen deprivation to the brain results in neuronal damage and death. The extent of neuronal damage and death in turn relates to the extent of long term brain dysfunction, as can be assessed using standard criteria (such as Cerebral Performance Category, CPC rating, or like criteria). Severe hypoxia can result in a patient's death and/or an irreversible brain injury (e.g., resulting in the patient being in a vegetative state). Hypoxic events may be global (e.g., due to low oxygen content in the blood) or focused (e.g., affecting only an area of the brain). Causes of hypoxia include, but are not limited to, local asphyxia (e.g., caused by smoke inhalation), carbon monoxide poisoning and/or toxicity, cardiac arrest, choking, drowning, high altitudes, strangulation, an ischemic event, thrombosis, arterial embolism, hemorrhage, swelling of the brain, stroke, physical trauma and/or physical injury (e.g., blunt trauma to the head), arteriosclerosis, and/or atherosclerosis. In some cases, the event may be myocardial infarction, myocardial ischemia, and/or transient ischemic attack.

Hypoxic conditions can lead to the production and/or change in the concentration of certain biomarkers. That is, the concentration of certain biomarkers increase or decrease following the hypoxic event. For example, the production of the proteolytic products of β-amyloid precursor protein has been found to become elevated in the brain and central nervous system under hypoxic condition. The increased concentration is theorized to be due to a hypoxia-inducible factor (HIF-1) that promotes the production of beta-amyloid peptides from amyloid precursor protein, a membrane protein concentrated in neuronal synapses. A cascade of beta-amyloid peptides, including beta-amyloid (1-42), is generated in the brain in proportion to the extent of hypoxia. Beta-amyloid peptides could in turn diffuse across the blood brain barrier and into the blood in proportion to the extent of hypoxia, and may be generally found in low abundance. The ability to determine a change in the concentration of a biomarker in a plurality of samples (or a single sample) obtained from a patient following a hypoxic event can, in

some embodiments, be correlated with a prognostic indication of the patient's recovery from a brain injury and/or used to determine a method of treatment. In some cases, sample(s) of the patient's cerebrospinal fluid (CSF) may be obtained and analyzed to determine the concentration and/or a change in the concentration of the biomarker. In some cases, however, it is advantageous to determine the level of a biomarker in the blood of a patient as compared to CSF, as blood sampling is generally less invasive and may result in fewer complications as compared to CSF sampling. However, many of the biomarkers that are present in the CSF have a slow rate of transmission across and/or a high barrier of transportation across the blood-brain barrier (BBB) and thus, the concentration of the biomarker in the patient's blood may be sufficient lowered as compared to the concentration in CSF to make it difficult or impossible to accurately determine using typically employed conventional immunoassays. Accordingly, assay methods which have very low limits of quantification (LOQ) and/or limits of detection (LOD) are generally necessary to determine a measure of the concentration of a biomarker in the patient's blood to provide statistically significant and/or meaningful results. In some embodiments, the methods of the present invention make use of methods having very low LODs and/or LOQs (e.g., in the low pg/mL range) to determine a measure of the concentration of a biomarker in a sample(s) obtained from a patient following a hypoxic event. Various parameters related to the changes in the concentration of the biomarker in the samples (e.g., blood samples) may be correlated with a prognostic indication and/or a method of treatment following a hypoxic event. Correlations (e.g., between the concentration and prognostic indication(s) and/or between the concentration and method(s) of treatment) have been discovered and/or are now discoverable due to recent advancements in technology which allow for the determination of the low concentrations of biomarkers in bodily fluids with sufficient accuracy and precision, thus allowing for the variations in concentration to be statistically significant and therefore, diagnostic.

In embodiments where a plurality of samples are obtained from a patient, the samples may be obtained from a patient over any suitable period of time. Generally, the period of time may be selected such that the concentration of a biomarker in the samples becomes statistically significant and/or a trend is observable (e.g., an increase and/or decrease in the concentration). For biomarkers which are analyzed in blood samples, the period of time over which a plurality of samples are obtained from the patient may account for any lag time required for the biomarker to cross the BBB. Non-limiting

examples of suitable periods of time in which the samples may be obtained from the patient include 1 hour, 2 hours, 3 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 18 hours, 24 hours, 36 hours, 48 hours, 60 hours, 72 hours, 4 days, 5 days, 6 days, 7 days, or more. In some cases, the duration of time of sample collection time is at least 60 hours, or at least 72 hours. In some cases, the duration of time of sample collection is between 12 hours and 7 days, or between 24 hours and 4 days, or between 2 days and 4 days, or between 3 days and 4 days. The first sample may be obtained from the patient without a short timeframe following the hypoxic event. For example, the first sample may be obtained from the patient within 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 8 hours, 10 hours, or 12 hours of the hypoxic event. In some cases, the first sample is obtained within 6 hours of the hypoxic event. In some embodiments, a first sample is obtained from the patient within 6 hours of the suspected hypoxic event, and at about 1, about 2, about 6, about 12, about 24, about 48, and about 72 hours, following the first sampling. In some embodiments, additional samples are obtained at about 96 and/or at about 108 hours following the first sampling.

Any number of samples (e.g., one or more) may be obtained from the patient over the time period of sample collection. Generally, the minimum number of samples obtained is such that a trend (e.g., an increase or decrease) in the concentration of the biomarker is observable. Non-limiting examples of the number of samples that are obtained from the patient (e.g., during the prescribed collection time) is at least about bout 1, about 2, at least about 3, at least about 4, at least abut 5, at least about 6, at least about 7, at least about 8, at least about 9, at least about 10, at least about 12, at least about 15 or more. In some cases, the number of samples obtained from the patient is between 2 and 20, between 5 and 15, or between 5 and 10.

The sample(s) obtained from the patient may be from any suitable bodily source. In some cases, the samples are CSF samples. In some cases, the samples are blood or blood products (e.g., whole blood, plasma, serum, etc.). In other cases, the samples may be urine or saliva samples. In some embodiments, the samples may be analyzed directly (e.g., without the need for extraction of the biomarker from the fluid sample) and/or with dilution (e.g., addition of a buffer or agent to the sample). Generally, each of the samples obtained from the patient is collected using substantially similar procedures (e.g., to ensure minimal variation between samples based on sample collection methods). Those of ordinary skill in the art will be aware of suitable systems and methods for obtaining a sample from a patient.

Each of or substantially all of the samples may be analyzed using an assay method (e.g., as described herein) to determine a measure of the concentration of at least one biomarker in each, a subset of or substantially all of the samples. In some cases, the methods comprise determining a measure of the concentration of a single biomarker in the samples. In other cases, a method comprises determining a measure of the concentration of more than one biomarker in each, a subset of or substantially all of the samples. For example, a measure of the concentration of 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, biomarkers may be determined in the samples.

In some embodiments, the methods of the present invention comprise determining a prognostic indication based at least in part on the measured concentration of the at least one biomarker in the samples. In some cases, the prognostic indication may be correlated with standard criteria employed to define long-term brain dysfunction and/or injury. Those of ordinary skill in the art will be aware of such criteria, for example, cerebral performance category ratings ("CPC rating"), or more specifically, Glasgow-Pittsburgh cerebral performance category ratings (or scale) (e.g., see Teasdale G, Jennett B (1974); *Assessment of coma and impaired consciousness*; Lancet 2 (7872): 81–84). The CPC scale ranges from 1 to 5, with 1 representing a slight possibility of neurological deficit and 5 representing severe deficit and/or death. In some methods of the present invention, the prognostic indication of the patient's recovery from the brain injury is classified as either "good" (e.g., correlating to a CPC score of 1 or 2) corresponding to a high likelihood of recovery and/or returning to independent living, or "poor" (e.g., correlating to a CPC score of 3, 4, or 5) corresponding to little possibility of a full recovery and resulting in assisted living and/or death.

In the CPC scale, a rating of 1 is generally classified as good cerebral performance. The patient is conscious and alert, is able to work, but may have mild neurological or psychological deficit. A rating of 2 is generally classified as having moderate cerebral disability. The patient is conscious and has sufficient cerebral function for independent activities of daily life, and is generally able to work in sheltered environment. A rating of 3 corresponds to severe cerebral disability. While the patient is conscious, they generally depend on others for daily support because of impaired brain function. The patient may have abilities ranging from ambulatory state to severe dementia or paralysis. A rating of 4 corresponds to a coma or vegetative state. The patient is generally unaware, even if they appear awake (e.g., the patient is in a vegetative state) without interaction with environment and is cerebral unresponsive. A

rating of 5 refers to brain death, associated with apnea, areflexia, and/or EEG silence. The CPC scale is summarized in Table 1.

Table 1: CPC Scale Summary

CPC Score	Description
1	Conscious and alert with normal function or only slight disability
2	Conscious and alert with moderate disability
3	Conscious with severe disability
4	Comatose or persistent vegetative state
5	Brain dead or death from other causes

Other non-limiting examples of suitable criteria include the "scale g" criteria (e.g., see Dekaban AS, Robinson CE.; Application of a new rating scale of brain dysfunction to monitoring rehabilitation in 65 patients with severe head injury, Bull Clin Neurosci., 1984; 49, 82-92), the "Rancho Los Amigos Scale," and the "Disabilities Rating Scale."

In addition to the biomarkers specifically mentioned herein, those of ordinary skill will be aware of other suitable biomarkers to use in connection with the methods described herein. As described herein, the biomarker generally undergoes a change in concentration as a result of a hypoxic event. For example, the concentration of the biomarker may increase or decrease as a result of the hypoxic event. Non-limiting examples of biomarkers include neuron specific neuronal enolase (NSE), β-site aPP-cleaving enzyme 1 (BACe1), S100B, myelin basic protein (MBP), growth associated protein 43, glutamine synthetase, glial fibrillary acid protein (GFAP), glycine transporter (e.g., GLYT1, GLYT2), neuron specific glycoprotein (e.g., GP50), calpain, neurofibrillary protein, heat shock protein 72, beta-amyloid precursor proteins, calbindin D-28K, proteolipid protein, myeline associated glycoprotein, neurofilament H, creatine kinase protein (e.g., CK-BB), tau proteins (including phosphorylated taus such as p-tau-81 or p-tau-231), and endothelium membrane proteins (e.g., thrombomodulin).

In some cases, the biomarker may be a beta-amyloid peptide. Beta-amyloid peptides are known to those of ordinary skill in the art (e.g., see Blennow et al., Nature Reviews, Neurology, 6, 2010, 131; Portelius et al., Neurobiology of Aging, 2009, Corrected Proof in Press, doi:10.1016/j.neurobiolaging.2009.06.002). Beta-amyloid peptides are formed by sequential cleavage of the amyloid precursor protein (APP). APP can be processed by alpha-, beta-, and gamma-secretases, wherein the beta-amyloid peptide is generated by successive actions of the beta and gamma secretases. Various

forms of beta-amyloid peptides may be contemplated for use as a target with the methods described herein, include isoforms and short isoforms (e.g., ranging from beta-amyloid (1–14) up to beta-amyloid (1–43)). Beta-amyloid isoforms can have varying lengths of amino acids, with beta-amyloid (1-40) and beta-amyloid (1-42) being the most common. Non-limiting examples of isoforms of beta-amyloid peptides include beta-amyloid (1–40), beta-amyloid (1–42), beta-amyloid (1–37), beta-amyloid (1–38) and beta-amyloid (1–39). Non-limiting examples of short beta-amyloid isoforms include beta-amyloid (1–14), beta-amyloid (1–15) and beta-amyloid (1–16). In some embodiments, the biomarker is beta-amyloid (1-42).

As will be know, mild ischemia due to arteriolosclerosis is common in the elderly, and more common in Alzheimer's patients, an arteriolosclerosis could result in chronic upregulation of beta amyloid (1-42), which could lead to plaque deposits in the brain. In certain embodiments, the methods of the invention are performed on subjects not diagnosed with or suspected of suffering from Alzheimer's disease and the prognosis determined/provided by the methods disclosed herein does not relate to Alzheimer's disease. In other embodiments, the methods of the invention and the prognosis determined/provided by the methods disclosed herein may be used in the context of Alzheimer's disease.

The plurality of samples obtained from the patient may be analyzed (e.g., using an assay method as described herein) to determine a measure of the concentration of the at least one biomarker in each of the samples (or a single sample). A prognostic indication and/or a method of treatment may be determined based at least in part on the measure of the concentration of the biomarker in each of the plurality of samples. The data may be analyzed using a variety of techniques, as described herein, and a prognostic indication for recovery from a brain injury (e.g., a "good" outcome or a "poor" outcome), or a specific method of treatment may be determined based on the results.

In some embodiments, the measure of the concentration of the at least one biomarker for each of the plurality of samples obtained from the patient may be plotted on a graph of concentration versus time (e.g., in hours), and one or more parameters can be obtained from the graph and used to determine the method of treatment and/or the prognostic indication. Non-limiting examples of parameters that may be determined and/or employed include baseline biomarker concentration, increase in biomarker concentration, duration of rise of biomarker concentration, maximum slope of increasing biomarker concentration, rate of change of biomarker concentration, area under the curve

and/or magnitude of the fold increase of biomarker concentration. Each of the parameters and their determination will now be described in detail, followed by a description of possible data analysis and methods useful or potentially useful to determine suitable correlations between the measure of the concentration determined in the samples and a treatment/prognostic indication. The measure of the concentration of the biomarker may be determined/displayed in any suitable unit. In some cases, the measure of the concentration is determined/displayed in pg/mL.

The term "baseline biomarker concentration" refers to the concentration of the biomarker generally present in a fluid sample from a normal patient (e.g., prior to or unexposed to a hypoxic event). The baseline biomarker concentration can be determined using a variety of methods which will be commonly known and understood by those of ordinary skill in the art. In some cases, the baseline biomarker concentration can be determined by averaging the value of a biomarker present in a population of control patients (e.g., patients who have not experienced a hypoxic event). This may be useful in embodiments where the baseline concentration of the biomarker is substantially the same for a given population of individuals (e.g., based on age, gender, medical condition, etc). However, many of the methods described herein require accurate determination of extremely low concentrations of the at least one biomarker in samples obtained from a patient, and accordingly, a general baseline concentration of a biomarker (e.g., based on a sampling of a population) may not provide enough accuracy and/or precision to give useful results. Accordingly, a measure of the baseline biomarker concentration, in some embodiments, may be determined for each individual patient.

In some cases, the baseline biomarker concentration for each individual is equal to the measure of the concentration of the biomarker in the first sample obtained from the patient following the hypoxic event. In other cases, if available, a baseline biomarker concentration is the measure of the concentration of the biomarker present in a sample obtained from the patient prior to the hypoxic event. In yet other cases, the baseline biomarker concentration is the average concentration of the biomarker determined in a plurality of samples taken from the patient immediately or substantially immediately following the hypoxic event (e.g., prior to the concentration of the biomarker increasing due to the hypoxic event). That is, the concentration of the biomarker in the plurality of samples obtained from the patient in a selected time period following the hypoxic event may be averaged to determine the baseline biomarker concentration for that patient. As will be understood by those of ordinary skill in the art, in such cases, any sample which

has a concentration level that significantly differs from the other concentration levels during that period of time (e.g., a data point/outlier having a concentration which deviates significantly from the other concentrations measured during the time frame) may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by greater than about 50% from the calculated average, that sample may be excluded from the averaging calculation. In some cases, if a sample has a concentration which differs by more than about 0.5 pg/mL, 1 pg/mL, 2 pg/mL, 5 pg/mL, or 10 pg/mL from the calculated average, that sample may be excluded from the averaging calculation. An anomalous data point may be observed and/or caused by administration of drugs to the patient. The baseline biomarker concentration may be determined by averaging the concentration of the biomarker in the samples obtained from the patient between the first sample (e.g., obtained within 6 hours of the hypoxic event) and 24 hours following the first collection of a sample, or between the first sample and 18 hours following the first collection of a sample, or between the first sample, and 12 hours following the first collection of a sample, or between the first sample, and 6 hours following the first collection of a sample (e.g., not including any outliers).

The term "change in biomarker concentration" refers to the change (e.g., increase or decrease) in concentration of the biomarker over the time period in which the samples are collected. An increase in biomarker concentration may be calculated by subtracting the baseline biomarker concentration (e.g., as described herein) from the maximum biomarker concentration. The "maximum biomarker concentration" is the maximum measured concentration of the biomarker measured in a single sample collected over the duration of the sample collection. For example, if the duration of the sample collection is 72 hours, the maximum concentration is equal to the maximum measured concentration in a single sample which was obtained from the patient in the 72 hour period. A decrease in biomarker concentration may be calculated by subtracting an elevated biomarker concentration (e.g., as described herein) from the minimum biomarker concentration.

The term "magnitude of the fold increase of biomarker concentration" refers to the magnitude of the fold-increase in concentration over the duration of sample collection, and may be calculated by dividing the maximum biomarker concentration (e.g., as described herein) by the baseline biomarker concentration (e.g., as described herein).

The term "duration of rise of biomarker concentration" refers to the time over which the concentration of the biomarker is increasing during the time period over which the samples are collected. In some cases, the duration of rise of biomarker concentration can be determined by subtracting the time at which the last sample was collected at approximately the baseline biomarker concentration (e.g., starting time of the rise) from the time at which the maximum biomarker concentration was observed (e.g., ending time of the rise). That is, the duration of the rise may be equal to the ending time of the rise minus the starting time of the rise. The duration of rise is generally provided in hours.

The term "maximum slope of increasing biomarker concentration" refers to the slope at which the maximum increase in concentration occurred over the time period in which the samples were collected. Those of ordinary skill will be aware of methods to calculate this value using common graphical analysis methods. For example, a plot may be prepared showing concentration versus time, and the maximum slope may be calculated based on this plot. In some cases, the maximum slope is equal to the slope between two data points, whereas in other cases, the maximum slope may be determined based on the average slope between a plurality of data points.

The term "area under the curve," (or AUC) is a common parameter used to analyze data, and such calculations will be well known and understood by those of ordinary skill in the art. In context with the methods of this disclosure, the AUC refers to the area under the biomarker concentration versus time curve. Generally the calculation takes into account the baseline biomarker concentration.

The above parameters, alone or in combination, may be correlated to a prognostic indication and/or a method of treatment for a patient following a hypoxic event. Following determination of a correlation between biomarker concentrations and a prognostic indication and/or a method of treatment (e.g., using a plurality of samples obtained from a plurality of test patients with known outcomes), the correlation can be used in connection with methods to determine prognosis (e.g., prognostic indications) and/or methods of treatment for patients with unknown outcomes. That is, an algorithm can be developed relating changes in a biomarker concentration and specific methods of treatment and/or prognostic indications using samples from test patients having been subject to known methods of treatment and/or having a known prognosis. Once the algorithm has been developed, it can be used to determine methods of treatment and/or prognostic indications for patients with unknown outcomes.

To determine a correlation between a biomarker and a prognostic indication and/or a method of treatment (e.g., to develop an algorithm relating the measured biomarker concentration to preferred methods of treatment and/or prognostic indications), a plurality of samples from a plurality of test patients may be obtained. A "test patient" is a patient who has a known outcome (e.g., a good or a poor CPC score) and/or has received a certain treatment. The plurality of the samples obtained from each of the test patients may be analyzed to determine the measure of the concentration of at least one biomarker in the each of the samples. Some or all of the parameters described herein may be determined for each patient, and the data may be analyzed to determine correlations between the parameters and the patient outcomes and/or treatments, which can in turn be used to develop an algorithm. The algorithm may then be applied to the concentration of the at least one biomarker in samples obtained from a patient having an unknown outcome to determine a method of treatment and/or a prognostic indication for that patient. A specific example of such an analysis is described below, and further details are provided in Example 1.

Similar analysis and methods may be used to correlate suitable methods of treatment based upon the measured concentration(s) of a biomarker in a plurality of samples obtained from a patient. In some cases, the method of treatment may comprise administering at least one therapeutic agent to the patient. For example, the therapeutic agent may be a neuroprotective drug. Other non-limiting methods of treatment include administration of anti-oxidants, hypothermia, blood thinning, and administration of steroids (e.g., to help reduce brain swelling) (e.g., see T. S. Richmond, Cerebral Resuscitation After Global Brain Ischemia: Linking Research to Practice, American Association of Critical-Care Nurses Journal, May 1997, Volume 8, Number 2).

A therapeutic agent is generally administered in an amount effective to provide a medically desirable result. The effective amount will vary with the particular condition being treated, the age and physical condition of the subject being treated, the severity of the condition, the duration of the treatment, the nature of the concurrent therapy (if any), the specific route of administration and the like factors within the knowledge and expertise of the health care practitioner. In some cases, a therapeutic agent may reduce brain injuries resulting from the hypoxic event. In some cases, the method of treatment may involve a change in treatment, such as an increase or decrease in the dose of a therapeutic agent, a switch from one therapeutic agent to another therapeutic agent, an addition of another therapeutic agent to the existing therapeutic agent, or a combination

thereof. A switch from one therapeutic agent to another may involve a switch to a therapeutic agent with a high risk profile but where the likelihood of expected benefit is increased.

In one embodiment, a method of the present invention for determining a treatment protocol for and/or a prognostic indication of a patient's recovery from a brain injury resulting from a hypoxic event comprises performing an assay on a plurality of samples to determine a measure of the concentration of beta-amyloid peptide in each sample and determining a prognostic indication of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measure of the concentration of beta-amyloid peptide present in the samples. In some embodiments, the beta-amyloid peptide is beta-amyloid (1-42). The sample, in some embodiments, is a blood sample from the patient and/or plasma and/or serum derived from the blood sample. In some cases, the concentration of the beta-amyloid in the samples is less than about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL, or less. In some cases, the assay has a limit of quantification of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL or less. In some cases, the assay has a limit of detection of less than about 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less.

In one embodiment, a correlation was determined between certain parameters (e.g., maximum beta-amyloid peptide concentration, duration of increase of beta-amyloid concentration, and the magnitude of the fold increase of beta-amyloid concentration) and a good (e.g., CPC rating 1 or 2) and a poor (e.g., CPC rating of 3, 4, or 5) prognostic indication. To determine the correlation, an assay was carried out on each of the samples obtained from a plurality of test patients having undergone a hypoxic event (e.g., patients having a known outcome and/or having undergone a certain method of treatment following a hypoxic event). The first sample was taken within 6 hours of the hypoxic event, and additional samples were generally obtained at about 1, 2, 6, 12, 24, 48, and 72 hours following the first sample (and optionally, at 96 and/or 108 hours). Each of the test patients had a known prognostic outcome according to the CPC scale. For each test

patient, a plot of the measured concentration of beta-amyloid in pg/mL versus time in hours was prepared. The data was analyzed and the sum of the increase in beta-amyloid concentration (in pg/mL), the duration of the increase of beta-amyloid concentration (in hours), and the magnitude of the fold increase of beta-amyloid concentration was determined to correlate with a "good" or "poor" prognosis for the patients. In particular, a sum of greater than 50 correlated with a poor prognosis (e.g., a CPC score of 3, 4, or 5) and a score of less than about 50 correlated with a good prognosis (e.g., a CPC score of 1 or 2). Accordingly, a correlation/algorithm was established between the varying parameters relating to concentration and a prognostic indication.

The developed correlation/algorithm can be applied to patients with unknown outcomes. That is, samples may be obtained from a patient and the concentration of beta-amyloid in each of the samples can be determined. The data may be analyzed to determine the increase in beta-amyloid concentration (in pg/mL), the duration of the increase of beta-amyloid concentration (in hours), and the magnitude of the fold increase of beta-amyloid concentration. If the sum of the three parameters is greater than 50, the prognostic indication for that patient is "poor," and if the sum is less than 50, the prognostic indication is "good." Using similar techniques, a variety of correlations may be determined for this beta-amyloid (e.g., analysis of the area under the curve) and/or other biomarkers.

Exemplary Assay Methods and Systems

Those of ordinary skill in the art will be aware of a variety of assay methods and systems that may be used in connection with the methods of the present invention. Generally, the methods employed have low limits of detection and/or limits of quantification as compared to bulk analysis techniques (e.g., ELISA methods). The use of assay methods that have low limits of detection and/or limits of quantification allows for correlations to be made between the various parameters discussed above and a method of treatment and/or diagnostic indication that may otherwise not be determinable and/or apparent. For example, in the method described above which correlates the sum of three parameters relating to beta-amyloid concentration to a prognostic indication of brain injury, the limits of detection, and/or limits of quantification needs to be substantially lower than the LOD and/or LOQ provided by common ELISA techniques.

The terms "limit of detection" (or LOD) and "limit of quantification" (or LOQ) are given their ordinary meaning in the art. The LOD refers to the lowest analyte

concentration likely to be reliably distinguished from background noise and at which detection is feasible. The LOD as used herein is defined as three standard deviations (SD) above background noise. The LOQ refers to the lowest concentration at which the analyte can not only be reliably detected but at which some predefined goals for bias and imprecision are met. Generally, as is used herein, the LOQ refers to the lowest concentration above the LOD wherein the coefficient of variation (CV) of the measured concentrations less than about 20%.

In some cases, an assay method employed has a limit of detection and/or a limit of quantification of less than about 500 pg/mL, 250 pg/mL, 100 pg/mL, 50 pg/mL, 40 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.8 pg/mL, 0.7 pg/mL, 0.6 pg/mL, 0.5 pg/mL, 0.4 pg/mL, 0.3 pg/mL, 0.2 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.04 pg/mL, 0.02 pg/mL, 0.01 pg/mL, or less. In some cases, an assay method employed has a limit of quantification and/or a limit of detection between about 100 pg/mL and about 0.01 pg/mL, between about 50 pg/mL and about 0.02 pg/mL, between about 25 pg/mL and about 0.02 pg/mL, between about 10 pg/mL and about 0.02 pg/mL. As will be understood by those of ordinary skill the art, the LOQ and/or LOD may differ for each assay method and/or each biomarker determined with the same assay. In some embodiments, the LOD of an assay employed for detecting of beta-amyloid (e.g., beta-amyloid (1-42)) is about equal to or less than 0.02 pg/mL. In some embodiments, the LOQ for an assay employed for detecting beta-amyloid (e.g., beta-amyloid (1-42)) is equal to or less than 0.04 pg/mL

In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is less than about 5000 fM, less than about 3000 fM, less than about 2000 fM, less than about 1000 fM, less than about 500 fM, less than about 300 fM, less than about 200 fM, less than about 100 fM, less than about 50 fM, less than about 25 fM, less than about 10 fM, less than about 5 fM, less than about 2 fM, less than about 1 fM, less than about 0.5 fM, less than about 0.1 fM, or less. In some embodiments, the concentration of biomarker molecules in the fluid sample that may be substantially accurately determined is between about 5000 fM and about 0.1 fM, between about 3000 fM and about 0.1 fM, between about 1000 fM and about 0.1 fM, between about 1000 fM and about 1 fM, between about 100 fM and about 1 fM, between about 100 fM and about 0.1 fM, or the like. The concentration of analyte molecules or particles in a fluid sample may be considered to be substantially accurately determined if the measured concentration of the biomarker molecules in the fluid sample

is within about 10% of the actual (e.g., true) concentration of the biomarker molecules in the fluid sample. In certain embodiments, the measured concentration of the biomarker molecules in the fluid sample may be within about 5%, within about 4%, within about 3%, within about 2%, within about 1%, within about 0.5%, within about 0.4%, within about 0.3%, within about 0.2% or within about 0.1%, of the actual concentration of the biomarker molecules in the fluid sample. In some cases, the measure of the concentration determined differs from the true (e.g., actual) concentration by no greater than about 20%, no greater than about 15%, no greater than 10%, no greater than 5%, no greater than 4%, no greater than 3%, no greater than 2%, no greater than 1%, or no greater than 0.5%. The accuracy of the assay method may be determined, in some embodiments, by determining the concentration of biomarker molecules in a fluid sample of a known concentration using the selected assay method.

In some embodiments, an assay method employs a step of spatially segregating biomarker molecules into a plurality of locations to facilitate detection/quantification, such that each location comprises/contains either zero or one or more biomarker molecules. Additionally, in some embodiments, the locations may be configured in a manner such that each location can be individually addressed. In some embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be determined by detecting biomarker molecules immobilized with respect to a binding surface having affinity for at least one type of biomarker molecule. In certain embodiments the binding surface may form (e.g., a surface of a well/reaction vessel on a substrate) or be contained within (e.g., a surface of a capture object, such as a bead, contained within a well) one of a plurality of locations (e.g., a plurality of wells/reaction vessels) on a substrate (e.g., plate, dish, chip, optical fiber end, etc). At least a portion of the locations may be addressed and a measure indicative of the number/percentage/fraction of the locations containing at least one biomarker molecule may be made. In some cases, based upon the number/percentage/fraction, a measure of the concentration of biomarker molecules in the fluid sample may be determined. The measure of the concentration of biomarker molecules in the fluid sample may be determined by a digital analysis method/system optionally employing Poisson distribution adjustment and/or based at least in part on a measured intensity of a signal, as will be known to those of ordinary skill in the art. In some cases, the assay methods and/or systems may be automated.

Certain methods and systems which employ spatially segregating analyte molecules (e.g., biomarkers) are known in the art, and are described in U.S. Patent Application Publication No. US-2007-0259448 (Serial No. 11/707,385), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF TARGET ANALYTE CONCENTRATION IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259385 (Serial No. 11/707,383), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR DETECTING CELLS AND CELLULAR COMPONENTS IN SMALL DEFINED VOLUMES," by Walt et al.; U.S. Patent Application Publication No. US-2007-0259381 (Serial No. 11/707,384), filed February 16, 2007, entitled "METHODS AND ARRAYS FOR TARGET ANALYTE DETECTION AND DETERMINATION OF REACTION COMPONENTS THAT AFFECT A REACTION," by Walt et al.; International Patent Publication No. WO 2009/029073 (International Patent Application No. PCT/US2007/019184), filed August 30, 2007, entitled "METHODS OF DETERMINING THE CONCENTRATION OF AN ANALYTE IN SOLUTION," by Walt et al.; U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al.; U.S. Patent Application Publication No. US-2010-00754072 (Serial No. 12/236,486), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES ON SINGLE MOLECULE ARRAYS," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075439 (Serial No. 12/236488), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES BY CAPTURE-AND-RELEASE USING REDUCING AGENTS FOLLOWED BY QUANTIFICATION," by Duffy et al.; International Patent Publication No. WO2010/039179 (International Patent Application No. PCT/US2009/005248), filed September 22, 2009, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR ENZYMES," by Duffy et al.; U.S. Patent Application Publication No. US-2010-0075355 (Serial No. 12/236490), filed September 23, 2008, entitled "ULTRA-SENSITIVE DETECTION OF ENZYMES BY CAPTURE-AND-RELEASE FOLLOWED BY QUANTIFICATION," by Duffy et al.; U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No.

PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

Additional details of exemplary, non-limiting assay methods which comprise one or more steps of spatially segregating biomarker molecules will now be described. In certain embodiments, a method for detection and/or quantifying biomarker molecules in a sample comprises immobilizing a plurality of biomarker molecules with respect to a plurality of capture objects (e.g., beads) that each include a binding surface having affinity for at least one type of biomarker. For example, the capture objects may comprise a plurality of beads comprising a plurality of capture components (e.g., an antibody having specific affinity for a biomarker of interest, etc.). At least some of the capture objects (e.g., at least some associated with at least one biomarker molecule) may be spatially separated/segregated into a plurality of locations, and at least some of the locations may be addressed/interrogated (e.g., using an imaging system). A measure of the concentration of biomarker molecules in the fluid sample may be determined based on the information received when addressing the locations (e.g., using the information

received from the imaging system and/or processed using a computer implemented control system). In some cases, a measure of the concentration may be based at least in part on the number of locations determined to contain a capture object that is or was associated with at least one biomarker molecule. In other cases and/or under differing conditions, a measure of the concentration may be based at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarker molecules and/or capture objects associated with a biomarker molecule at one or more of the addressed locations.

In some embodiments, the number/percentage/fraction of locations containing a capture object but not containing a biomarker molecule may also be determined and/or the number/percentage/fraction of locations not containing any capture object may also be determined. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the total number of locations determined to contain a capture object not associated with a biomarker molecule and/or a measure of the concentration of biomarker molecule in the fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object associated with a biomarker molecule to the number of locations determined to not contain any capture objects. In yet other embodiments, a measure of the concentration of biomarker molecules in a fluid sample may be based at least in part on the ratio of the number of locations determined to contain a capture object and a biomarker molecule to the total number of locations addressed and/or analyzed.

In certain embodiments, at least some of the plurality of capture objects (e.g., at least some associated with at least one biomarker molecule) are spatially separated into a plurality of locations, for example, a plurality of reaction vessels in an array format. The plurality of reaction vessels may be formed in, on and/or of any suitable material, and in some cases, the reaction vessels can be sealed or may be formed upon the mating of a substrate with a sealing component, as discussed in more detail below. In certain embodiments, especially where quantization of the capture objects associated with at least one biomarker molecule is desired, the partitioning of the capture objects can be performed such that at least some (e.g., a statistically significant fraction; e.g., as described in International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR

PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al (see Appendix A)) of the reaction vessels comprise at least one or, in certain cases, only one capture object associated with at least one biomarker molecule and at least some (e.g., a statistically significant fraction) of the reaction vessels comprise an capture object not associated with any biomarker molecules. The capture objects associated with at least one biomarker molecule may be quantified in certain embodiments, thereby allowing for the detection and/or quantification of biomarker molecules in the fluid sample by techniques described in more detail herein.

An exemplary assay method may proceed as follows. A sample fluid containing or suspected of containing biomarker molecules is provided. An assay consumable comprising a plurality of assay sites is exposed to the sample fluid. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the assay sites contain a single biomarker molecule and a statistically significant fraction of the assay sites do not contain any biomarker molecules. The assay sites may optionally be exposed to a variety of reagents (e.g., using a reagent loader) and or rinsed. The assay sites may then optionally be sealed and imaged (see, for example, U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.). The images are then analyzed (e.g., using a computer implemented control system) such that a measure of the concentration of the biomarker molecules in the fluid sample may be obtained, based at least in part, by determination of the number/fraction/percentage of assay sites which contain a biomarker molecule and/or the number/fraction/percentage of sites which do not contain any biomarkers molecules. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that at least some assay sites comprise more than one biomarker molecule. In such embodiments, a measure of the concentration of biomarker molecules in the fluid sample may be obtained at least in part on an intensity level of at least one signal indicative of the presence of a plurality of biomarkers molecules at one or more of the assay sites

In some cases, the methods optionally comprise exposing the fluid sample to a plurality of capture objects, for example, beads. At least some of the biomarker molecules are immobilized with respect to a bead. In some cases, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a

statistically significant fraction of the beads do not associate with any biomarker molecules. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may then be spatially separated/segregated into a plurality of assay sites (e.g., of an assay consumable). The assay sites may optionally be exposed to a variety of reagents and/or rinsed. At least some of the assay sites may then be addressed to determine the number of assay sites containing a biomarker molecule. In some cases, the number of assay sites containing a bead not associated with a biomarker molecule, the number of assay sites not containing a bead and/or the total number of assay sites addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample. In some cases, more than one biomarker molecule may associate with a bead and/or more than one bead may be present in an assay site. In some cases, the plurality biomarker molecules may be exposed to at least one additional reaction component prior to, concurrent with, and/or following spatially separating at least some of the biomarker molecules into a plurality of locations.

The biomarker molecules may be directly detected or indirectly detected. In the case of direct detection, a biomarker molecule may comprise a molecule or moiety that may be directly interrogated and/or detected (e.g., a fluorescent entity). In the case of indirect detection, an additional component is used for determining the presence of the biomarker molecule. For example, the biomarker molecules (e.g., optionally associated with a bead) may be exposed to at least one type of binding ligand. A "binding ligand," is any molecule, particle, or the like which specifically binds to or otherwise specifically associates with a biomarker molecule to aid in the detection of the biomarker molecule. In certain embodiments, a binding ligand may be adapted to be directly detected (e.g., the binding ligand comprises a detectable molecule or moiety) or may be adapted to be indirectly detected (e.g., including a component that can convert a precursor labeling agent into a labeling agent). A component of a binding ligand may be adapted to be directly detected in embodiments where the component comprises a measurable property (e.g., a fluorescence emission, a color, etc.). A component of a binding ligand may facilitate indirect detection, for example, by converting a precursor labeling agent into a labeling agent (e.g., an agent that is detected in an assay). A "precursor labeling agent" is any molecule, particle, or the like, that can be converted to a labeling agent upon exposure to a suitable converting agent (e.g., an enzymatic component). A "labeling

agent" is any molecule, particle, or the like, that facilitates detection, by acting as the detected entity, using a chosen detection technique. In some embodiments, the binding ligand may comprise an enzymatic component (e.g., horseradish peroxidase, beta-galactosidase, alkaline phosphatase, etc). A first type of binding ligand may or may not be used in conjunction with additional binding ligands (e.g., second type, etc.).

More than one type of binding may be employed in any given assay method, for example, a first type of binding ligand and a second type of binding ligand. In one example, the first type of binding ligand is able to associate with a first type of biomarker molecule and the second type of binding ligand is able to associate with the first binding ligand. In another example, both a first type of binding ligand and a second type of binding ligand may associate with the same or different epitopes of a single biomarker molecule, as described herein. In some embodiments, at least one binding ligand comprises an enzymatic component.

In some embodiments, a binding ligand and/or a biomarker may comprise an enzymatic component. The enzymatic component may convert a precursor labeling agent (e.g., an enzymatic substrate) into a labeling agent (e.g., a detectable product). A measure of the concentration of biomarker molecules in the fluid sample can then be determined based at least in part by determining the number of locations containing a labeling agent (e.g., by relating the number of locations containing a labeling agent to the number of locations containing a biomarker molecule (or number of capture objects associated with at least one biomarker molecule to total number of capture objects)). Non-limiting examples of enzymes or enzymatic components include horseradish peroxidase, beta-galactosidase, and alkaline phosphatase. Other non-limiting examples of systems or methods for detection include embodiments where nucleic acid precursors are replicated into multiple copies or converted to a nucleic acid that can be detected readily, such as the polymerase chain reaction (PCR), rolling circle amplification (RCA), ligation, Loop-Mediated Isothermal Amplification (LAMP), etc. Such systems and methods will be known to those of ordinary skill in the art, for example, as described in "DNA Amplification: Current Technologies and Applications," Vadim Demidov et al., 2004.

Another exemplary embodiment of indirect detection is as follows. In some cases, the biomarker molecules may be exposed to a precursor labeling agent (e.g., enzymatic substrate) and the enzymatic substrate may be converted to a detectable product (e.g., fluorescent molecule) upon exposure to a biomarker molecule.

The assay methods and systems may employ a variety of different components, steps, and/or other aspects that will be known and understood by those of ordinary skill in the art. For example, a method may further comprise determining at least one background signal determination (e.g., and further comprising subtracting the background signal from other determinations), wash steps, and the like. In some cases, the assays or systems may include the use of at least one binding ligand, as described herein. In some cases, the measure of the concentration of biomarker molecules in a fluid sample is based at least in part on comparison of a measured parameter to a calibration curve. In some instances, the calibration curve is formed at least in part by determination at least one calibration factor, as described above.

In certain embodiments, solubilized, or suspended precursor labeling agents may be employed, wherein the precursor labeling agents are converted to labeling agents which are insoluble in the liquid and/or which become immobilized within/near the location (e.g., within the reaction vessel in which the labeling agent is formed). Such precursor labeling agents and labeling agents and their use is described in commonly owned U.S. Patent Application Publication No. US-2010-0075862 (Serial No. 12/236484), filed September 23, 2008, entitled "HIGH SENSITIVITY DETERMINATION OF THE CONCENTRATION OF ANALYTE MOLECULES OR PARTICLES IN A FLUID SAMPLE," by Duffy et al., incorporated herein by reference.

An exemplary embodiment of an assay method that may be used in certain embodiments of the invention is illustrated in Figure 1a. A plurality of capture objects 2, are provided (step (A)). In this particular example, the plurality of capture objects comprises a plurality of beads. The beads are exposed to a fluid sample containing a plurality of biomarker molecules 3 (e.g., beads 2 are incubated with biomarker molecules 3). At least some of the biomarker molecules are immobilized with respect to a bead. In this example, the biomarker molecules are provided in a manner (e.g., at a concentration) such that a statistically significant fraction of the beads associate with a single biomarker molecule and a statistically significant fraction of the beads do not associate with any biomarker molecules. For example, as shown in step (B), biomarker molecule 4 is immobilized with respect to bead 5, thereby forming complex 6, whereas some beads 7 are not associated with any biomarker molecules. It should be understood, in some embodiments, more than one biomarker molecule may associate with at least some of the beads, as described herein. At least some of the plurality of beads (e.g., those associated with a single biomarker molecule or not associated with any biomarker molecules) may

then be spatially separated/segregated into a plurality of locations. As shown in step (C), the plurality of locations is illustrated as substrate 8 comprising a plurality of wells/reaction vessels 9. In this example, each reaction vessel comprises either zero or one beads. At least some of the reaction vessels may then be addressed (e.g., optically or via other detection means) to determine the number of locations containing a biomarker molecule. For example, as shown in step (D), the plurality of reaction vessels are interrogated optically using light source 15, wherein each reaction vessel is exposed to electromagnetic radiation (represented by arrows 10) from light source 15. The light emitted (represented by arrows 11) from each reaction vessel is determined (and/or recorded) by detector 15 (in this example, housed in the same system as light source 15). The number of reaction vessels containing a biomarker molecule (e.g., reaction vessels 12) is determined based on the light detected from the reaction vessels. In some cases, the number of reaction vessels containing a bead not associated with a biomarker molecule (e.g., reaction vessel 13), the number of wells not containing a bead (e.g., reaction vessel 14) and/or the total number of wells addressed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

A non-limiting example of an embodiment where a capture object is associated with more than one biomarker molecule is illustrated in Figure 1b. A plurality of capture objects 20 are provided (step (A)). In this example, the plurality of capture objects comprises a plurality of beads. The plurality of beads is exposed to a fluid sample containing plurality of biomarker molecules 21 (e.g., beads 20 are incubated with biomarker molecules 21). At least some of the biomarker molecules are immobilized with respect to a bead. For example, as shown in step (B), biomarker molecule 22 is immobilized with respect to bead 24, thereby forming complex 26. Also illustrated is complex 30 comprising a bead immobilized with respect to three biomarker molecules and complex 32 comprising a bead immobilized with respect to two biomarker molecules. Additionally, in some cases, some of the beads may not associate with any biomarker molecules (e.g., bead 28). The plurality of beads from step (B) is exposed to a plurality of binding ligands 31. As shown in step (C), a binding ligand associates with some of the biomarker molecules immobilized with respect to a bead. For example, complex 40 comprises bead 34, biomarker molecule 36, and binding ligand 38. The binding ligands are provided in a manner such that a statistically significant fraction of the beads comprising at least one biomarker molecule become associated with at least

one binding ligand (e.g., one, two, three, etc.) and a statistically significant fraction of the beads comprising at least one biomarker molecule do not become associated with any binding ligands. At least a portion of the plurality of beads from step (C) are then spatially separated into a plurality of locations. As shown in step (D), in this example, the locations comprise a plurality of reaction vessels 41 on a substrate 42. The plurality of reaction vessels may be exposed to the plurality of beads from step (C) such at each reaction vessel contains zero or one beads. The substrate may then be analyzed to determine the number of reaction vessels containing a binding ligand (e.g., reaction vessels 43), wherein in the number may be related to a measure of the concentration of biomarker molecules in the fluid sample. In some cases, the number of reaction vessels containing a bead and not containing a binding ligand (e.g., reaction vessel 44), the number of reaction vessels not containing a bead (e.g., reaction vessel 45), and/or the total number of reaction vessels addressed/analyzed may also be determined. Such determination(s) may then be used to determine a measure of the concentration of biomarker molecules in the fluid sample.

In some embodiments, a plurality of locations may be addressed and/or a plurality of capture objects and/or species/molecules/particles of interest may be detected substantially simultaneously. "Substantially simultaneously" when used in this context, refers to addressing/detection of the locations/capture objects/species/molecules/particles of interest at approximately the same time such that the time periods during which at least two locations/capture objects/species/molecules/particles of interest are addressed/detected overlap, as opposed to being sequentially addressed/detected, where they would not. Simultaneous addressing/detection can be accomplished by using various techniques, including optical techniques (e.g., CCD detector). Spatially segregating capture objects/species/molecules/particles into a plurality of discrete, resolvable locations, according to some embodiments facilitates substantially simultaneous detection by allowing multiple locations to be addressed substantially simultaneously. For example, for embodiments where individual species/molecules/particles are associated with capture objects that are spatially segregated with respect to the other capture objects into a plurality of discrete, separately resolvable locations during detection, substantially simultaneously addressing the plurality of discrete, separately resolvable locations permits individual capture objects, and thus individual species/molecules/particles (e.g., biomarker molecules) to be resolved. For example, in certain embodiments, individual molecules/particles of a

plurality of molecules/particles are partitioned across a plurality of reaction vessels such that each reaction vessel contains zero or only one species/molecule/particle. In some cases, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5% of all species/molecules/particles are spatially separated with respect to other species/molecules/particles during detection. A plurality of species/molecules/particles may be detected substantially simultaneously within a time period of less than about 1 second, less than about 500 milliseconds, less than about 100 milliseconds, less than about 50 milliseconds, less than about 10 milliseconds, less than about 1 millisecond, less than about 500 microseconds, less than about 100 microseconds, less than about 50 microseconds, less than about 10 microseconds, less than about 1 microsecond, less than about 0.5 microseconds, less than about 0.1 microseconds, or less than about 0.01 microseconds, less than about 0.001 microseconds, or less. In some embodiments, the plurality of species/molecules/particles may be detected substantially simultaneously within a time period of between about 100 microseconds and about 0.001 microseconds, between about 10 microseconds and about 0.01 microseconds, or less.

In some embodiments, the locations are optically interrogated. The locations exhibiting changes in their optical signature may be identified by a conventional optical train and optical detection system. Depending on the detected species (e.g., type of fluorescence entity, etc.) and the operative wavelengths, optical filters designed for a particular wavelength may be employed for optical interrogation of the locations. In embodiments where optical interrogation is used, the system may comprise more than one light source and/or a plurality of filters to adjust the wavelength and/or intensity of the light source. In some embodiments, the optical signal from a plurality of locations is captured using a CCD camera.

In some embodiments of the present invention, the plurality of reaction vessels may be sealed (e.g., after the introduction of the biomarker molecules, binding ligands, and/or precursor labeling agent), for example, through the mating of the second substrate and a sealing component. The sealing of the reaction vessels may be such that the contents of each reaction vessel cannot escape the reaction vessel during the remainder of the assay. In some cases, the reaction vessels may be sealed after the addition of the biomarker molecules and, optionally, at least one type of precursor labeling agent to facilitate detection of the biomarker molecules. For embodiments employing precursor labeling agents, by sealing the contents in some or each reaction vessel, a reaction to

produce the detectable labeling agents can proceed within the sealed reaction vessels, thereby producing a detectable amount of labeling agents that is retained in the reaction vessel for detection purposes.

The plurality of locations may be formed may be formed using a variety of methods and/or materials. In some embodiments, the plurality of locations comprises a plurality of reaction vessels/wells on a substrate. In some cases, the plurality of reaction vessels is formed as an array of depressions on a first surface. In other cases, however, the plurality of reaction vessels may be formed by mating a sealing component comprising a plurality of depressions with a substrate that may either have a featureless surface or include depressions aligned with those on the sealing component. Any of the device components, for example, the substrate or sealing component, may be fabricated from a compliant material, e.g., an elastomeric polymer material, to aid in sealing. The surfaces may be or made to be hydrophobic or contain hydrophobic regions to minimize leakage of aqueous samples from the microwells. The reactions vessels, in certain embodiments, may be configured to receive and contain only a single capture object.

In some embodiments, the reaction vessels may all have approximately the same volume. In other embodiments, the reaction vessels may have differing volumes. The volume of each individual reaction vessel may be selected to be appropriate to facilitate any particular assay protocol. For example, in one set of embodiments where it is desirable to limit the number of capture objects used for biomarker capture contained in each vessel to a small number, the volume of the reaction vessels may range from attoliters or smaller to nanoliters or larger depending upon the nature of the capture objects, the detection technique and equipment employed, the number and density of the wells on the substrate and the expected concentration of capture objects in the fluid applied to the substrate containing the wells. In one embodiment, the size of the reaction vessel may be selected such only a single capture object used for biomarker capture can be fully contained within the reaction vessel (see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No. PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS ," by Duffy et al. (see Appendix A), each herein incorporated by reference). .

In some embodiments, the reaction vessels may have a volume between about 1 femtoliter and about 1 picoliter, between about 1 femtoliters and about 100 femtoliters, between about 10 attoliters and about 100 picoliters, between about 1 picoliter and about 100 picoliters, between about 1 femtoliter and about 1 picoliter, or between about 30 femtoliters and about 60 femtoliters. In some cases, the reaction vessels have a volume of less than about 1 picoliter, less than about 500 femtoliters, less than about 100 femtoliters, less than about 50 femtoliters, or less than about 1 femtoliter. In some cases, the reaction vessels have a volume of about 10 femtoliters, about 20 femtoliters, about 30 femtoliters, about 40 femtoliters, about 50 femtoliters, about 60 femtoliters, about 70 femtoliters, about 80 femtoliters, about 90 femtoliters, or about 100 femtoliters.

The total number of locations and/or density of the locations employed in an assay (e.g., the number/density of reaction vessels in an array) can depend on the composition and end use of the array. For example, the number of reaction vessels employed may depend on the number of types of biomarker molecule and/or binding ligand employed, the suspected concentration range of the assay, the method of detection, the size of the capture objects, the type of detection entity (e.g., free labeling agent in solution, precipitating labeling agent, etc.). Arrays containing from about 2 to many billions of reaction vessels (or total number of reaction vessels) can be made by utilizing a variety of techniques and materials. Increasing the number of reaction vessels in the array can be used to increase the dynamic range of an assay or to allow multiple samples or multiple types of biomarker molecules to be assayed in parallel. The array may comprise between one thousand and one million reaction vessels per sample to be analyzed. In some cases, the array comprises greater than one million reaction vessels. In some embodiments, the array comprises between about 1,000 and about 50,000, between about 1,000 and about 1,000,000, between about 1,000 and about 10,000, between about 10,000 and about 100,000, between about 100,000 and about 1,000,000, between about 100,000 and about 500,000, between about 1,000 and about 100,000, between about 50,000 and about 100,000, between about 20,000 and about 80,000, between about 30,000 and about 70,000, between about 40,000 and about 60,000 reaction vessels. In some embodiments, the array comprises about 10,000, about 20,000, about 50,000, about 100,000, about 150,000, about 200,000, about 300,000, about 500,000, about 1,000,000, or more, reaction vessels.

The array of reaction vessels may be arranged on a substantially planar surface or in a non-planar three-dimensional arrangement. The reaction vessels may be arrayed in a

regular pattern or may be randomly distributed. In a specific embodiment, the array is a regular pattern of sites on a substantially planar surface permitting the sites to be addressed in the X-Y coordinate plane.

In some embodiments, the reaction vessels are formed in a solid material. As will be appreciated by those in the art, the number of potentially suitable materials in which the reaction vessels can be formed is very large, and includes, but is not limited to, glass (including modified and/or functionalized glass), plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, cyclic olefin copolymer (COC), cyclic olefin polymer (COP), Teflon®, polysaccharides, nylon or nitrocellulose, etc.), elastomers (such as poly(dimethyl siloxane) and poly urethanes), composite materials, ceramics, silica or silica-based materials (including silicon and modified silicon), carbon, metals, optical fiber bundles, or the like. In general, the substrate material may be selected to allow for optical detection without appreciable autofluorescence. In certain embodiments, the reaction vessels may be formed in a flexible material.

A reaction vessel in a surface (e.g., substrate or sealing component) may be formed using a variety of techniques known in the art, including, but not limited to, photolithography, stamping techniques, molding techniques, etching techniques, or the like. As will be appreciated by those of the ordinary skill in the art, the technique used can depend on the composition and shape of the supporting material and the size and number of reaction vessels.

In a particular embodiment, an array of reaction vessels is formed by creating microwells on one end of a fiber optic bundle and utilizing a planar compliant surface as a sealing component. In certain such embodiments, an array of reaction vessels in the end of a fiber optic bundle may be formed as follows. First, an array of microwells is etched into the end of a polished fiber optic bundle. Techniques and materials for forming and etching a fiber optic bundle are known to those of ordinary skill in the art. For example, the diameter of the optical fibers, the presence, size and composition of core and cladding regions of the fiber, and the depth and specificity of the etch may be varied by the etching technique chosen so that microwells of the desired volume may be formed. In certain embodiments, the etching process creates microwells by preferentially etching the core material of the individual glass fibers in the bundle such that each well is approximately aligned with a single fiber and isolated from adjacent wells by the cladding material. Potential advantages of the fiber optic array format is

that it can produce thousands to millions of reaction vessels without complicated microfabrication procedures and that it can provide the ability to observe and optically address many reaction vessels simultaneously.

Each microwell may be aligned with an optical fiber in the bundle so that the fiber optic bundle can carry both excitation and emission light to and from the wells, enabling remote interrogation of the well contents. Further, an array of optical fibers may provide the capability for simultaneous or non-simultaneous excitation of molecules in adjacent vessels, without signal "cross-talk" between fibers. That is, excitation light transmitted in one fiber does not escape to a neighboring fiber.

Alternatively, the equivalent structures of a plurality of reaction vessels may be fabricated using other methods and materials that do not utilize the ends of an optical fiber bundle as a substrate. For example, the array may be a spotted, printed or photolithographically fabricated substrate produced by techniques known in the art; see for example WO95/25116; WO95/35505; PCT US98/09163; U.S. Patent Nos. 5,700,637, 5,807,522, 5,445,934, 6,406,845, and 6,482,593. In some cases, the array may be produced using molding, embossing, and/or etching techniques as will be known to those of ordinary skill in the art.

In some embodiments, the plurality of locations may not comprise a plurality of reaction vessels/wells. For example, in embodiments where capture objects are employed, a patterned substantially planar surface may be employed and the patterned areas form a plurality of locations. In some cases, the patterned areas may comprise substantially hydrophilic surfaces which are substantially surrounded by substantially hydrophobic surfaces. In certain embodiments, a plurality of capture objects (e.g., beads) may be substantially surrounded by a substantially hydrophilic medium (e.g., comprising water), and the beads may be exposed to the patterned surface such that the beads associate in the patterned areas (e.g., the hydrophilic locations on the surface), thereby spatially segregating the plurality of beads. For example, in one such embodiment, a substrate may be or include a gel or other material able to provide a sufficient barrier to mass transport (e.g., convective and/or diffusional barrier) to prevent capture objects used for biomarker capture and/or precursor labeling agent and/or labeling agent from moving from one location on or in the material to another location so as to cause interference or cross-talk between spatial locations containing different capture objects during the time frame required to address the locations and complete the assay. For example, in one embodiment, a plurality of capture objects is spatially

separated by dispersing the capture objects on and/or in a hydrogel material. In some cases, a precursor labeling agent may be already present in the hydrogel, thereby facilitating development of a local concentration of the labeling agent (e.g., upon exposure to a binding ligand or biomarker molecule carrying an enzymatic component). As still yet another embodiment, the capture objects may be confined in one or more capillaries. In some cases, the plurality of capture objects may be absorbed or localized on a porous or fibrous substrate, for example, filter paper. In some embodiments, the capture objects may be spatially segregated on a uniform surface (e.g., a planar surface), and the capture objects may be detected using precursor labeling agents which are converted to substantially insoluble or precipitating labeling agents that remain localized at or near the location of where the corresponding capture object is localized. The use of such substantially insoluble or precipitating labeling agents is described herein. In some cases, single biomarker molecules may be spatially segregated into a plurality of droplets. That is, single biomarker molecules may be substantially contained in a droplet containing a first fluid. The droplet may be substantially surrounded by a second fluid, wherein the second fluid is substantially immiscible with the first fluid.

In some embodiments, during the assay, at least one washing step may be carried out. In certain embodiments, the wash solution is selected so that it does not cause appreciable change to the configuration of the capture objects and/or biomarker molecules and/or does not disrupt any specific binding interaction between at least two components of the assay (e.g., a capture component and a biomarker molecule). In other cases, the wash solution may be a solution that is selected to chemically interact with one or more assay components. As will be understood by those of ordinary skill in the art, a wash step may be performed at any appropriate time point during the inventive methods. For example, a plurality of capture objects may be washed after exposing the capture objects to one or more solutions comprising biomarker molecules, binding ligands, precursor labeling agents, or the like. As another example, following immobilization of the biomarker molecules with respect to a plurality of capture objects, the plurality of capture objects may be subjected to a washing step thereby removing any biomarker molecules not specifically immobilized with respect to a capture object.

Other assay methods in addition to those described herein are known in the art and may be used in connection with the inventive methods. For example, various analyzers are commercially available for the determination of the concentration of

biomarkers. The assay methods employed should meet the algorithm requirements for LOD and LOQ.

The following examples are included to demonstrate various features of the invention. Those of ordinary skill in the art should, in light of the present disclosure, will appreciate that many changes can be made in the specific embodiments which are disclosed while still obtaining a like or similar result without departing from the scope of the invention as defined by the appended claims. Accordingly, the following examples are intended only to illustrate certain features of the present invention, but do not necessarily exemplify the full scope of the invention.

Example 1

The following example provides experimental details relating to prognostication of neurological outcome in comatose survivors of oxygen deprivation.

26 unconscious patients were resuscitated with restoration of spontaneous circulation (ROSC). All included patients were >18 years old, had systolic blood pressure >80 mmHg for more than 5 min after ROSC, and were unconscious (prior to the use of sedatives/hypnotics) with a Glasgow Coma Scale (GCS) ≤7. Patients with a terminal disease or a primary coagulopathy were excluded, as were patients admitted more than 6 h after cardiac arrest. Serial blood samples were collected within 6h after cardiac arrest, and continued at intervals from 1-108 h. Inclusion criteria included age >18 years old, systolic BP >80mmHg after ROSC, and a Glasgow Coma Scale ≤7.

Upon admission, hypothermia treatment was started immediately after resuscitation. Ventilation was administered during the coma period, with a target PaO_2 of ≥12 kPa (90 mmHg) and $PaCO_2$ between 5.0 and 5.5 kPa (38–41 mmHg). Targeted mean arterial pressure was 65–100 mmHg, with application of inotropic/vasopressor support, if required, using dobutamine as the first line medication, followed by noradrenaline (norepinephrine) or adrenaline (epinephrine), if necessary. If the patient was considered euvolaemic but had a diuresis of less than 0.5 ml/kg/h, furosemide was administered. Furosemide was also given if the intensive care physician considered that the patient had a fluid overload. All patients received an arterial line in the radial or femoral artery for blood sampling.

Patient outcome was assessed in accordance with the Glasgow-Pittsburgh cerebral performance category (CPC) scale at discharge from the intensive care unit and 6 months later. The CPC scale ranges from 1 to 5, with 1 representing mildest possible

neurological deficit (patient is able to return to work), and 4-5 representing the most severe deficit (vegetative) and death. A CPC of 1 or 2 was considered a "good" outcome and a CPC score of 3–5 a "poor" outcome. For patients who died after ICU discharge, the better of the two scores was used, as recommended by the Utstein templates.

Serial blood samples were collected for each sample, starting as soon as possible in the emergency phase (within 6 h after cardiac arrest), and continuing at 1, 2, 6, 12, 24, 48, 72, 96, and 108 h after cardiac arrest. Serum aliquots were frozen until assayed. Samples were measured in triplicate using the assay method described in Example 2. The assay had a dynamic range to 250 pg/mL, with limit of quantification of less than 0.04 pg/mL, enabling measurement of low abundance serum Aβ42 (i.e., beta-amyloid (1-42)) in all samples. Applicant notes the measurements carried out in this study would not be possible with most current Aβ42 assay methods due to insufficient sensitivity. All patients exhibited a significant time-dependent elevation of Aβ42. After a lag period of about 10 or more hours, significant Aβ42 elevations were observed. Elevations ranged from approximately 50% to over 30-fold, with most elevations in the range of 3-10-fold (average approximately 7-fold).

Figure 2 depicts representative exemplary time course profiles for patients with (a-c) "good" and (d-f) "poor" 6-month outcomes. Serum Aβ42 measurements followed resuscitation from cardiac arrest. CPC scores depicted are after discharge from the ICU and 6 months later. In particular, Figure 2 (a) depicts data from the patient exhibiting the highest baseline Aβ42 and smallest relative increase in Aβ42 among all patients (two sets of data points run on different days are shown); (d) depicts data from the patient exhibiting the largest relative increase from baseline (35-fold), with Aβ42 rising 60+ hours; (c and f) depict comparative data from two patients with a CPC score of 3 upon discharge from the ICU. The patient exhibiting the more modest increase in Aβ42 (c) recovered good brain function (CPC 1), while the patient exhibiting the greater increase in Aβ42 (f) did not recover.

Quantitative differences in the appearance of the Aβ42 profiles were examined to determine a correlation with patient outcome. Profile parameters examined were: increase in beta-amyloid concentration (e.g., the magnitude of the rise), the fold increase of beta-amyloid concentration (e.g., the ratio of the peak Aβ42 to the baseline value), the maximum slope of the Aβ42 rise, and the duration of increase of beta-amyloid concentration (e.g., duration of over which the Aβ42 exhibited increasing values) (see

Figure 2 for an exemplary graph including these parameters). Table 2 shows the CPC assessment for the patients by their attending neurologists. Table 3 shows the correlation of Aβ42 profile parameters (Figure 3) with overall six-month outcome (0 = "good," 1 = "poor"). For each Aβ42 profile parameter, patients were sorted in either "good" or "poor" columns. Average values of each parameter for good outcomes were compared with average values for poor outcomes. Student t-test results for significance between good vs. poor were then calculated, as summarized in Table 3. In addition, an Aβ42 Score was calculated by summing the Aβ42 profile parameters of magnitude, rise ratio, and duration of rise (the three parameters that demonstrated statistical significance). Aβ42 Score was also evaluated for statistical significance between good and poor outcomes, and its significance was found to be enhanced relative to the individual Aβ42 profile parameters ($P = 0.00009$). Table 4 summarizes the statistical significance of Aβ42 profile parameters and Aβ42 Score. A P of 0.00009 indicates a high degree of statistical significance that Aβ42 Score is different between good and poor outcomes. 100% of patients with an Aβ42 Score > 50 had poor six month outcomes. 90% of patients with an Aβ42 Score < 50 had good six month outcomes.

These results indicate that blood tests for Aβ42 in the initial days following hypoxic insult can predict six-month patient outcome with a high degree of accuracy.

Table 2.

Study nr		CPC ICU discharge	CPC 6 months	Best over outcome (0=good 1=poor)
1	DA 820724	4	3	0
2	BL 810228	2	1	0
3	AL 871028	1	1	0
4	BR 270910	1	1	0
5	GR 510506	3	1	0
6	MA 230226	5	5	1
7	AA 260646	4	3	1
8	SL 300828	4	3	0
9	AO 301128	5	5	1
10	LS 860912	2	1	0
11	HT 480413	4	5	1
12	BK 321215	5	5	1
13	BF 470824	3	3	0
14	LM 380618	4	5	1
15	PN 330609	2	5	0
16	EO 370113	4	5	1
17	SF 440126	3	1	0
18	AJ 320418	4	5	1
19	DF 450604	3	2	0
20	BJ 430820	4	2	0
21	KM 461001	2	2	0
22	MK 371130	5	5	1
23	SW 480701	3	2	0
24	HW 460322	2	1	0
25	POL 290502	5	5	1
26	LB 470807	5	5	1
27	GJ 430318	4	5	1
28	ZD 330527	5	5	1
29	EO 500929	5	5	1
30	LS 221008	5	5	1
31	NL 470826	5	5	1

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Table 3.

Patient	Magnitude of increase (pg/mL)		Duration of rise (hr)		Rise ratios (fold increase)		Slope (pg/ml/hr)		Abeta score	
	Good	Poor	Good	Poor	Good	Poor	Good	Poor	Good	Poor
MA 290226		16				6		0.61		
AA 803606		6.8		60		35		0.155		101.6
OL 810648	12		31		5		0.316		48	
LS 660312	12.4		56		5		0.617		41.4	
HT 450415		4.6		63		5.6		0.242		70.2
BK 321275		6.6		71		3.5		0.087		80.2
BE 370824	5.05		30		6.3		0.168		41.35	
PM 540609	7.8		10		3.5		0.5		21.4	
EB 370511		14		90		8		0.35		82
SP 310126	6.2		12		1.65		0.456		31.83	
UE 450804	7.2		25		8.75		0.266		46.96	
BJ 430420	11		56.5		6.5		0.202		74	
RM 461001	4		10		2.1		0.4		36.3	
JDK 371020		14				2.3		0.83		
SW 460701	7.1		1		3.95		0.546		14.08	
HW 450102	6.6		12		2.6		0.256		21	
PCL 280805		8.1				3.45		0.758		
LP 470607		12.3		81		6.7		0.265		72
GJ 430818		8.8		84		16.8		0.174		118.3
RD 310427		6.6				14.8		0.358		
EG 300828		16.4		30		7		0.45		51.4
DJ 221008		7.8		68		4.8		0.206		80.4
KL 470826		9.2		96		15.4		0.141		78.6
AVG	8.12	10.25	20.95	80.33	4.58	10.52	0.39	0.37	33.63	82.68
t-test (P)	0.081455564		0.000014		0.023243907		0.399662724		0.000009	

Table 4.

t-test "Good" vs "Poor" 6 Mo Outcome	P
1. Max slope of Ab42 rise	0.400
2. Magnitude of Ab42 rise	0.0815
3. Ab42 rise ratio	0.0232
4. Duration of Ab42 rise	0.000014
5. Overall Ab42 Score (sum of 2-4)	0.000009

		6 Mo Outcome	
		Poor	Good
Ab42 score	<50	0	9
	>50	9	1

Sensitivity for calling poor outcome: 9/9 (100%)
Specificity for calling good outcome: 9/10 (90%)

Example 2

The following example describes a beta-amyloid (1-42) (i.e., Aβ42) ultra-sensitive digital immunoassay for plasma amyloid β42 using single molecule arrays.

Summary: Aβ42 has gained attention in the last 15 years as a biomarker correlating with Alzheimer's disease (AD) onset, mild cognitive impairment, vascular dementia, and other cognitive disorders. Substantial clinical data has validated the disease relevance of cerebral spinal fluid (CSF) levels of Aβ42, and there has been significant interest in measuring blood levels of the biomarker. However, the concentrations of Aβ42 in plasma are close to or below the limits of detection of most current immunoassay methods, making their precise determination challenging. A single

molecule capable assay technology was utilized in this example to develop and validate an ultra-sensitive assay for measuring Aβ42 in plasma.

Reagents were developed for a paramagnetic bead-based ELISA. Aβ42 molecules in plasma were captured on antibody-coated paramagnetic capture beads and labeled with an enzyme conjugate. The beads were loaded into arrays of 50,000, 50-femtoliter reaction wells etched into bundles of optical fibers. Single capture beads trapped in each well were sealed in the presence of enzyme substrate and imaged using a fluorescence microscope fitted with a CCD camera. At low concentrations, the images were analyzed for the presence or absence of single immunocomplexes of labeled Aβ42, resulting in a digital signal. At high concentrations, the analog intensity of the beads was normalized to the digital signals, extending the dynamic range of the assay to over four logs. Analytical performance of the assay was evaluated, and plasma and CSF samples from Alzheimer's disease patients and normal control subjects were tested for Aβ42.

The assay described in this example has a detection limit (i.e., LOD) of 0.02 pg/mL and was linear to 250 pg/mL Aβ42 ($R2 > 0.999$). Recovery of Aβ42 spikes in plasma averaged 103% of expected. The assay exhibited no cross reactivity to shorter peptide variants Aβ38 and Aβ40, and 11-16% cross reactivity to the longer variant Aβ43. Intra-assay coefficients of variation (CV) were less than 10% down to 0.5 pg/mL. Total CVs (intra-assay and inter-assay) across six days of testing were 6.1%, 5.7%, and 10.0% for Aβ42 levels of 0.5, 1.0, and 5.0 pg/mL, respectively. The limit of quantification was estimated by testing ultra low panels of depleted plasma on multiple days. The total CVs were less than 20% for all ultra low panels tested (lowest panel 0.072 pg/mL), yielding an estimated limit of quantification (LOQ) of 0.042 pg/mL (0.189 fmol/L) using a criterion of 20%. Results using CSF samples from AD patients and age-matched normal control subjects showed excellent discrimination between the two populations, but results with plasma samples obtained from these same individuals showed no discrimination.

Further Description: Beta-amyloid peptides are 36-43 amino acid proteolytic products from the amyloid precursor protein that have gained considerable attention in the last 15 years as a biomarker correlating with Alzheimer's disease onset, mild cognitive impairment, vascular dementia, and other cognitive disorders Clinical validation has now been developed around disease relevance of cerebral spinal fluid levels of Aβ42, and there follows a significant interest in measuring blood levels of this biomarker. The interest originates in part from extensive pharmacologic efforts aimed at

blocking production of beat-amyloid through inhibition of β-secretase and γ-secretase activating protein, and use of plasma measurements of amyloid β peptides as outcome indicators. Concentrations of Aβ42 in plasma are, however, over 100-fold lower than in cerebrospinal fluid. Recently reported was a blinded proficiency survey of several laboratories assaying plasma Aβ42 with different ELISA protocols. The survey showed high inter-lab variability in measured Aβ42 values and a broad range of intra-assay CVs; inter-assay CVs were not evaluated. A high-sensitivity ELISA for measurement of plasma Aβ42 has been reported, but potential therapeutic strategies aimed at lowering Aβ42 may put robust measurement of the peptide in blood beyond the reach of all current ELISA methods. To address this, a solid-phase extraction was recently developed and reverse-phase HPLC pre-treatment aimed at concentrating plasma levels of Aβ42 for improved immunoassay quantification. Enrichment of plasma Aβ42 by these procedures was found to lower the limit of detection to approximately 1 pg/mL, allowing quantification of the peptide in normal plasma at levels previously below the detection limit of even the high-sensitivity ELISA.

This example described the development and validation of a novel digital immunoassay using single molecule array technology that is capable of measuring Aβ42 in both normal and highly depleted plasma without biomarker enrichment or sample pretreatment procedures. The assay exhibits over 1000-fold greater sensitivity than validated commercially available ELISAs, and more than 50-fold greater sensitivity than what have been attainable using sample enrichment procedures described to date. The assay can be used for directly measuring and monitoring plasma Aβ42 in therapeutic trials aimed at altering and lowering levels of this peptide, down to sub-femtomolar levels.

The single molecule array technology employed two primary steps: a standard ELISA conducted with paramagnetic beads, followed by isolation of individual beads in arrays of femtoliter-sized reaction wells for digital imaging. Isolation of the individual beads in microwells permits the buildup of fluorescent product from the enzyme label such that signal from a single immunocomplex is readily detected using a CCD camera. This approach permits counting of single molecules when Aβ42 concentrations are low enough that the ratio of bound labeled peptide per bead is much less than one. In this concentration realm, Poisson statistics predict that bead-containing microwells in the array will contain either a single labeled Aβ42 molecule or no labeled Aβ42 molecules, resulting in a binary signal. Due to the amplified sensitivity for detecting label

molecules afforded by confining fluorescent product buildup to the microwells, concentrations of label (detector anti-Aβ42 antibody and enzyme label) can be reduced relative to standard ELISAs. Lowered concentrations of labeling reagents reduces their interaction with capture beads, resulting in reduced nonspecific binding enabling high signal to background ratios, even at extremely low concentrations of biomarker. For higher biomarker concentrations where all beads contain one or more labeled immunocomplexes, digital signals from the Poisson realm are used to calibrate analog intensity measurements, extending the dynamic range to over four logs.

Three reagents were developed for this Aβ42 immunoassay: capture beads, biotinylated detector, and a conjugate of streptavidin:beta-galactosidase. The capture bead reagent comprised of a commercially available monoclonal anti Aβ42 antibody (Covance) directed to a N-terminus epitope (amino acids 3-8). The antibody was covalently attached by standard coupling chemistry to 2.7 μm carboxy paramagnetic microbeads (Varian). Because individual beads were captured in array wells 4.5 μm wide x 3.25 μm deep, it was important that the capture beads remain monomeric. The antibody-coated beads were diluted to a working concentration of 5 x 10^6 beads/mL in Tris buffer with a surfactant and BSA. The biotinylated detector reagent was comprised of a commercially available monoclonal anti Aβ42 antibody (Invitrogen) directed to the C-terminus of the peptide. The antibody was biotinylated using standard methods (Solulink), and the biotinylation level was confirmed spectrophotometrically per manufacturer's instructions. The monomeric state of the detector antibody before and after biotinylation was confirmed by size exclusion HPLC. The biotinylated detector antibody was diluted to a concentration of 0.1 μg/ml for assay in a PBS diluent containing a surfactant and newborn calf serum, NCS (PBS/NCS). The enzyme conjugate—streptavidin:β-galactosidase (SβG)—was prepared by covalent conjugation of purified streptavidin (Thermo Scientific) and β-galactosidase (Sigma) using standard coupling chemistry (1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride, Thermo Scientific). Aliquots of a concentrated stock solution of SβG were prepared in PBS with 50% glycerol and transferred to -20°C for storage. Prior to assay, an aliquot was thawed and diluted to 25 pM in PBS/NCS with $MgCl_2$. Purified Aβ42 antigen for calibrators and peptide variants Aβ38, Aβ40, and Aβ43 for specificity testing were from Merck.

Assay calibrators and controls were prepared by dilution of Aβ42 stock in PBS diluent containing a surfactant and BSA (PBS/BSA). In some cases, a stock solution

prepared by dilution to 3.5 ng/mL in PBS/Tween-20. For dynamic range/linearity characterization, a series of calibrators were prepared by serial 3-fold dilution to give a calibration range of 0 – 250 pg/mL. To evaluate assay day-to-day reproducibility at low concentrations, three low controls were prepared at 0.5, 1.0, and 5.0 pg/mL in PBS/BSA. To estimate the limit of quantification (LOQ), three ultra-low plasma controls were prepared using a pool of immunodepleted normal human EDTA plasma. Immunodepletion was accomplished by incubation overnight at 2-8 °C with shaking of 5 mL of plasma with 1 x 10^9 Aβ42 capture beads prepared as described above. The immunodepleted plasma was used as an ultra low plasma control, along with two additional ultra-low controls of immunodepleted plasma spiked with trace amounts of Aβ42.

50,000 well optical fiber microarrays were prepared as previously described. In brief, optical fiber bundles (Schott North America) were cut into 5 cm lengths and sequentially polished with 30, 9, and 1 um-sized diamond lapping films. One end of each bundle was etched in a 0.025 N HCl solution for 2 minutes and then submerged into water. The differential etch rate of the core and cladding glass of the fiber bundles caused an array of 4.5 um diameter wells to be formed in the core fibers.

Bead-plasma incubations and labeling of immunocomplexes in conical 96 well plates (Axygen) were conducted using a robotic liquid handling system (Tecan EVO 150). Conical wells are used to facilitate magnetic attraction of the beads to the sides of the wells for efficient removal of reaction mixtures and bead washing. For magnetic attraction, a microplate bar magnet (Invitrogen) was used. Incubation periods were conducted with shaking on a microplate shaker (VWR) to keep beads suspended in the wells. The assays were initiated by mixing 100 uL of sample with 500,000 capture beads, and the mixtures were incubated with shaking for two hours. Plasma samples were pre-diluted 1:4 prior to assay with PBS/BSA as a precaution for sample quality and interference effects. Following incubation, the beads were washed 3 times with a wash buffer of 5-fold concentrated PBS with a surfactant (5xPBS). 100 uL of biotinylated detector antibody was then added and incubated with the beads for 45 minutes. After a second sequence of three washes with 5xPBS, 100 µL of streptavidin-β-galactosidase was incubated with the beads for 30 minutes to form the final enzyme-labeled immunocomplex. The beads were then washed six times per above, and concentrated to 2 x 10^7 beads/ml with the addition of a reduced volume (25 µL) of array loading buffer comprised of PBS with a surfactant. Beads were then loaded onto the arrays. 10 µL of

the concentrated bead solution (2 x 10^6 beads) were pipetted onto the arrays and the arrays were centrifuged at 1,300 g for 10 minutes. Excess beads were removed by a PBS rinse and swabbing with deionized water. With this technique, array filling by the beads was generally 50-60%, which was adequate for minimizing contributions to imprecision from Poisson noise. Wells containing labeled Aβ42-labeled beads were detected utilizing β-galactosidase catalyzed hydrolysis of resorufin β-D-galactopyranoside (RGP, Invitrogen) into fluorescent product (resorufin, excitation 558nm, emission 577nm). To introduce RGP substrate to the array wells, droplets of substrate were placed on a silicone gasket and introduced into the array wells with a mechanical platform. This step resulted in an array of sealed femtoliter wells in which enzyme-containing beads developed a concentrated fluorescence signal.

Imaging was accomplished via a custom-built fluorescence imaging system containing a light source, objectives, filter cubes and a CCD camera. For each sample, five fluorescent images of one second each were acquired (to identify wells containing an enzyme) and one white light image was acquired (to identify wells containing a bead). Background fluorescence and any contaminating artifacts were discriminated from true 'positive' wells by analyzing for signal growth over the multiple images. These images were analyzed to determine the average number of enzymes per bead (AEB) across the concentration range. In some cases, at <50% active beads, the system was determined to be in the digital realm, so AEB was be determined from the fraction of beads that contain at least one enzyme and the Poisson distribution; and at >50% active beads, the average fluorescence intensity of the beads was normalized to the average fluorescence intensity of beads containing a single enzyme to yield AEB. In other cases, at <70% active beads relative to total beads, AEB was determined as a count of active beads corrected for a low statistical probability of multiple enzymes per bead; and at >70% active beads, the probability of multiple enzymes/bead increases such that all wells contain multiple enzymes and all are growing in signal and in this realm, the signal is was no longer digital, and average fluorescence intensities of the wells were converted to AEB based on the average intensities of wells containing single enzymes as determined at lower Aβ42 concentrations. The AEB unit worked continuously across the digital and analog realms.

For description of various details associate with this assay, see, for example, U.S. Patent Application Serial No. 12/731,130, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al.; International Patent Application No.

PCT/US2011/026645, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES USING BEADS OR OTHER CAPTURE OBJECTS," by Duffy et al. (e.g., see Appendix A); International Patent Application No. PCT/US2011/026657, filed March 1, 2011, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; U.S. Patent Application Serial No. 12/731135, filed March 24, 2010, entitled "ULTRA-SENSITIVE DETECTION OF MOLECULES USING DUAL DETECTION METHODS," by Duffy et al.; International Patent Application No. PCT/US2011/026665, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; U.S. Patent Application Serial No. 12/731136, filed March 24, 2010, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Duffy et al.; U.S. Patent Application Serial No. 13/035,472, filed February 25, 2011, entitled "SYSTEMS, DEVICES, AND METHODS FOR ULTRA-SENSITIVE DETECTION OF MOLECULES OR PARTICLES," by Fournier et al.; U.S. Patent Application Serial No. 13/037,987, filed March 1, 2011, entitled "METHODS AND SYSTEMS FOR EXTENDING DYNAMIC RANGE IN ASSAYS FOR THE DETECTION OF MOLECULES OR PARTICLES," by Rissin et al.; each herein incorporated by reference.

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Figure 4 shows a representative calibration dose-response of the Aβ42 assay up to 250 pg/mL. The assay demonstrated a highly linear response, with a linear regression R^2 of 0.9993. The inset highlights the low background at very low Aβ42 concentrations. In a study of calibration curves obtained on six different days, the mean signal to noise ratio at 1.0 pg/mL was 15.7 (SD 2.2). Limits of detection (3SD method) across the six days ranged from 0.014 to 0.032 pg/mL, with an average of 0.020 pg/mL (0.09 fmol/L), representing greater than four logs of assay range. In particular, Figure 4 shows a representative dose-response of the digital Aβ42 immunoassay. Y-axis refers to the average number of label enzymes per individual microbead captured in the microwells of the optical fiber array. The inset highlights the low background obtained with single-molecule counting and digital quantification of extremely low analyte levels. Analysis

of six separate calibration curves gave a mean signal to noise ratio at 1.0 pg/mL of 15.7 (SD 2.2).

Linearity in the extreme low end of the assay range was further evaluated by a series of four-fold dilutions (to 256-fold) of depleted plasma that had been spiked with 4 pg/mL Aβ42. The average recovery across the dilutions was within 0.02 pg/mL of the expected values. At the final 256-fold dilution, the assay measured an Aβ42 value of 0.118 pg/mL as compared with an expected value 0.099 pg/mL.

Recovery was evaluated by spiking 25 pg/mL Aβ42 into four normal plasma samples as well as the depleted plasma pool. Recoveries ranged from 91.5 – 113.4%, with an average of 103.6%.

Specificity of the assay for Aβ42 was evaluated by assaying 0.5, 1.0, 5.0, 10 and 50 pg/mL of the peptide variants Aβ38, Aβ40, and Aβ43 in PBS/BSA. No detectable cross reactivity was noted for the shorter Aβ38 and Aβ40 peptides, while the longer Aβ43 variant exhibited a cross reactivity of 11-16%.

Limits of detection (LOD) were estimated as three standard deviations above the zero calibrator across calibration curves on six separate days (n = 3 replicates per curve). LODs ranged from 0.014 to 0.032 pg/mL, with an average of 0.020 pg/mL (0.09 fmol/L).

Limit of quantification (LOQ) was estimated with guidance from NCCLS EP17-A [20]. Total CVs from low panel members assayed on multiple days (Table 5) were plotted vs. their respective measured value (Figure 5). The analyte concentration at which the assay's total measurement variation crossed 20% CV was taken to represent an estimated LOQ. Because none of the total CVs exceeded 20%, the 20% threshold was extrapolated from the equation of a non-linear power fit of the data ($R^2 = 0.703$, KaleidaGraph). A LOQ of 0.032 pg/mL (0.144 fmol/L) was estimated at the 20% threshold.

Table 5.

Study 1: Within-run Imprecision

	pg/mL Aβ42								
Panel	result 1	result 2	result 3	result 4	result 5	result 6	AVG	SD	CV
L1	0.41	0.4	0.35	0.36	0.37	0.37	0.38	0.026	6.8%
L2	0.83	0.74	0.69	0.75	0.69	0.70	0.73	0.056	7.7%
L3	3.82	4.04	3.81	3.45	3.38	4.18	3.78	0.316	8.4%

Study 2: Total Imprecision

	pg/mL Aβ42								
Panel	day 1	day 2	day 3	day 4	day 5	day 6	AVG	SD_{tot}	CV_{tot}
L1	0.46	0.51	0.52	0.45	0.45	0.48	0.48	0.025	6.1%
L2	0.94	0.97	0.98	0.92	1.04	0.89	0.95	0.054	5.7%
L3	3.99	5.22	5.25	4.54	5.00	4.70	4.78	0.478	10.0%

Study 3: Total Imprecision - Ultra Low Plasma

	pg/mL Aβ42								
Panel	day 1	day 2	day 3	day 4	day 5	day 6	AVG	SD_{tot}	CV_{tot}
Depleted	0.069	0.056	0.069	0.079	0.087	ND	0.072	0.012	16.3%
L2	0.151	0.128	0.123	0.110	0.118	ND	0.126	0.015	12.3%
L3	0.409	0.333	0.459	0.471	0.434	ND	0.421	0.055	13.0%

To further validate the assay, a pilot study of matched EDTA plasma and CSF samples from eight patients diagnosed with AD and nine normal individuals were assayed with the Aβ42 test (Figure 6). Normal and disease specimens were matched with respect to age, gender, and collection dates. Patients were diagnosed with AD according to clinical criteria. The clinical work-up also included imaging and MMSE cognitive scoring criteria. Normal age matched individuals also received MMSE testing to ensure high cognitive functioning. All samples were collected under IRB approval and obtained from PrecisionMed SAMPLE (Serial Alzheimer's Disease and MCI Prospective Longitudinal Evaluation) repository. The results were consistent with previous data reported for both sample types. With CSF samples, excellent discrimination (P=0.000015) was observed between AD subjects and normal subjects. Results for the AD CSF specimens ranged from 192.1-333.6 pg/mL, and normal CSF specimens ranged from 509.9 to 1127.8 pg/ml. On the other hand, results from the plasma specimens lacked discrimination between AD and normal subjects (P=0.69). Aβ42 levels in AD plasma ranged from 12.6 to 25.8 pg/mL, while results for the normal plasma specimens ranged from 8.8 to 22.1 pg/mL, in agreement with reported ELISA values following solid phase extraction and HPLC enrichment.

To test the assay performance in another clinical context, serial serum samples from a 41-year old man who was resuscitated after cardiac arrest with restoration of

spontaneous circulation were analyzed. Samples were measured in triplicate in the Aβ42 assay. Figure 7 depicts the profile of the serum Aβ42 change and shows a dramatic increase after the first 24 hours. Data from this study are the first to directly link hypoxic stress to Aβ elevation in humans. The Aβ42 concentrations measured in this study, particularly during the first 24 hours, were below the measurement capability of commercially available immunoassays, illustrating the potential utility of SiMoA technology as a new tool for precise measurement of low-abundance Aβ42 and other protein biomarkers.

Discussion. The data presented here indicate that the Aβ42 assay represents a capability for extremely sensitive and reproducible Aβ42 measurement in serum and plasma. The assay allows highly sensitive (limit of quantification 0.032 pg/mL) and precise quantification of Aβ42 in biological fluids.

Current immunoassays for measurement of Aβ42 in plasma are based on the ELISA or the Luminex techniques. In addition to lower analytical sensitivity, these immunoassays are hampered by low recovery of spiked Aβ42 into plasma or serum and as a result the measured concentration of Aβ42 increases when the plasma sample is diluted. These phenomena are likely due to matrix effects, probably by interaction and binding of Aβ42 to plasma proteins. This means that unrelated plasma proteins contribute to the concentration interpreted to come from Aβ42 in this type of assay. The immunoassay presented here showed highly linear dilution characteristics, together with a recovery of around 100%, suggesting that it gives a very accurate measure of the Aβ42 concentration. This is likely because the interference from plasma proteins is lost when samples are pre-diluted 1:4 prior to measurement. Because the assay has such high sensitivity, pre-diluting the samples does not compromise the capability of the method to precisely measure low abundance Aβ42.

Conflicting results have been reported regarding the association of plasma levels of Aβ42 with AD. For example, one report reported a statistically significant decrease in plasma Aβ42 in a cohort of 149 AD patients relative to 89 age-matched controls (mean 38 and 52 pg/mL respectively, $p < 0.01$), although there was large overlap between the two populations. In another case, no discernable difference in plasma Aβ42 between sporadic AD patients (n= 78) and age-matched controls (n = 61) was reported. Use of different ELISAs and analytical noise could have contributed to lack of agreement. It is also clear that most previously available assays measure Aβ42 close to the limit of

quantification, which may contribute to variation and inconsistent results between studies. If there is a decline in plasma Aβ42 with AD, it appears to be modest, requiring statistically powered studies to discern. Because depression of measurable Aβ42 in CSF relative to controls is a well established hallmark of AD (also seen here), the apparent disconnect between CSF and plasma results can led to the suggestion that the normal equilibrium between CSF and plasma may be disrupted with the initiation of amyloid deposition in the brain. The study reported here was intended to confirm expected performance of the Aβ42 assay with plasma and CSF clinical samples. The data were consistent with expected results from both sample types.

The Aβ42 assay described here was able to precisely monitor serum Aβ42 changes in a survivor of oxygen deprivation. Cerebral ischemia is believed to play a role in AD pathogenesis. The finding of a significant increase in serum Aβ42 following oxygen deprivation is the first direct demonstration of a link between hypoxic stress and Aβ elevation in humans. Nevertheless, the kinetic profile depicted in Figure 7could reflect proteolysis of amyloid precursor protein by β-secretase (BACE1), in which BACE1 is upregulated by the transcription factor hypoxia-inducible factor-1. Animal models have helped elucidate this pathway, and detecting hypoxia-driven amyloid cascade in humans could have significance for further understanding this process and its role in AD pathogenesis.

While several embodiments of the present invention have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the functions and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the present invention. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the teachings of the present invention is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents thereto, the invention may be practiced otherwise than as specifically

described and claimed. The present invention is directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features, systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the scope of the present invention.

The indefinite articles "a" and "an," as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean "at least one."

The phrase "and/or," as used herein in the specification and in the claims, should be understood to mean "either or both" of the elements so conjoined, i.e., elements that are conjunctively present in some cases and disjunctively present in other cases. Other elements may optionally be present other than the elements specifically identified by the "and/or" clause, whether related or unrelated to those elements specifically identified unless clearly indicated to the contrary. Thus, as a non-limiting example, a reference to "A and/or B," when used in conjunction with open-ended language such as "comprising" can refer, in one embodiment, to A without B (optionally including elements other than B); in another embodiment, to B without A (optionally including elements other than A); in yet another embodiment, to both A and B (optionally including other elements); etc.

As used herein in the specification and in the claims, "or" should be understood to have the same meaning as "and/or" as defined above. For example, when separating items in a list, "or" or "and/or" shall be interpreted as being inclusive, i.e., the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted items. Only terms clearly indicated to the contrary, such as "only one of" or "exactly one of," or, when used in the claims, "consisting of," will refer to the inclusion of exactly one element of a number or list of elements. In general, the term "or" as used herein shall only be interpreted as indicating exclusive alternatives (i.e. "one or the other but not both") when preceded by terms of exclusivity, such as "either," "one of," "only one of," or "exactly one of." "Consisting essentially of," when used in the claims, shall have its ordinary meaning as used in the field of patent law.

As used herein in the specification and in the claims, the phrase "at least one," in reference to a list of one or more elements, should be understood to mean at least one element selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements.

This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase "at least one" refers, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, "at least one of A and B" (or, equivalently, "at least one of A or B," or, equivalently "at least one of A and/or B") can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A); in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

In the claims, as well as in the specification above, all transitional phrases such as "comprising," "including," "carrying," "having," "containing," "involving," "holding," and the like are to be understood to be open-ended, i.e., to mean including but not limited to. Only the transitional phrases "consisting of" and "consisting essentially of" shall be closed or semi-closed transitional phrases, respectively, as set forth in the United States Patent Office Manual of Patent Examining Procedures, Section 2111.03.

What is claimed:

Claims

1. A method for determining a measure of the concentration of beta-amyloid peptide in a patient sample containing or suspected of containing beta-amyloid peptide, comprising:

performing an assay to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the limit of detection of beta-amyloid peptide of the assay is less than about 0.2 pg/mL.

2. The method of claim 1, wherein the beta-amyloid peptide is beta-amyloid (1-42).

3. The method of claim 1, wherein the patient has had a hypoxic event or a suspected hypoxic event.

4. The method of claim 1, wherein the sample is a bodily fluid.

5. The method of claim 4, wherein the bodily fluid is blood or a blood component.

6. The method of claim 4, wherein the bodily fluid is CSF.

7. The method of claim 5, wherein the blood component is plasma or serum.

8. The method of claim 1, wherein the measure of the concentration of beta-amyloid peptide is determined in a plurality of samples taken from the patient over a period of time.

9. The method of claim 8, wherein the plurality of samples are collected within 96 hours after the patient has experienced a hypoxic event or suspected hypoxic event.

10. A method of determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event, wherein the prognosis and/or the course of treatment is based at least in part on the measure of the concentration of beta-amyloid peptide determined in the patient sample according to the method of any one of claims 1-9.

11. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

12. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on a measured concentration of at least one biomarker measured in each sample by an assay performed on a plurality of samples obtained from the patient following the event to determine the measure of the concentration of the at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

13. A method for performing an assay and providing data for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

performing an assay on a plurality of samples obtained from the patient following the event to determine a measure of the concentration of at least one biomarker in each sample, wherein the concentration of the biomarker in each sample is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

14. A method for determining a patient's prognosis for recovery from, and/or determining a course of treatment for, a brain injury following a hypoxic event or suspected hypoxic event, comprising:

determining a measure of the concentration of a biomarker in each of a plurality of sample obtained from the patient following the event, wherein the assay has a limit of quantification of less than about 10 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; ; and

determining a prognosis of the patient's recovery and/or determining a course of treatment based at least in part on the measured concentration of the at least one biomarker measured in each sample.

15. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

16. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of a first biomarker in the plurality of samples, wherein the measured concentration has been determined by performing an assay to measure the concentration of only the first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

17. A method for performing an assay and providing data for determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

performing an assay to determine a measure of the concentration of only a first biomarker present in a plurality of samples obtained from the patient following the event, wherein the concentration of the first biomarker is less than about 100 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

18. A method of determining a treatment protocol for, and/or a prognosis of a patient's recovery from, a brain injury resulting from a hypoxic event, comprising:

determining a measure of the concentration of only a first biomarker in each of a plurality of sample obtained from the patient following the event wherein the concentration of the first biomarker in the samples is less than about 100 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of the first biomarker in the plurality of samples.

19. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

20. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on a measured concentration of beta-amyloid peptide present in a patient sample, wherein the measured concentration has been determined by performing an assay on the patient sample, which comprises a blood sample from the patient and/or plasma and/or serum derived from the blood sample, to determine the measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL.

21. A method for performing an assay and providing data for determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

performing an assay on a blood sample from the patient and/or plasma and/or serum derived from the blood sample to determine a measure of the concentration of beta-amyloid peptide in the sample, wherein the concentration of the biomarker is less than about 500 pg/mL, and wherein the assay has a limit of quantification of less than about 10 pg/mL; and

providing data from the assay to enable determining a prognosis of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

22. A method of determining a treatment protocol for and/or a prognosis of a patient's recovery from a brain injury resulting from a hypoxic event, comprising:

determining a measure of the concentration of beta-amyloid in each of a plurality of samples obtained from the patient following the event wherein the concentration of beta-amyloid peptide in the samples is less than about 500 pg/mL, and wherein the limit of quantification of the assay used to determine the measure of concentration is less than about 10 pg/mL; and

determining a prognostic of the patient's recovery from the brain injury and/or a method of treatment based at least in part on the measured concentration of beta-amyloid peptide present in the sample.

23. The method of any one of claims 11-22, wherein the biomarker is a beta-amyloid peptide.

24. The method of any one of claims 11-22, wherein the beta-amyloid peptide is beta-amyloid (1-42).

25. The method of any one of claims 11-22, wherein the hypoxic event is caused by cardiac arrest.

26. The method of any one of claims 11-22, wherein the hypoxic event is caused by stroke.

27. The method of any one of claims 11-22, wherein the hypoxic event is caused by an ischemic event.

28. The method of any one of claims 11-22, wherein the hypoxic event is caused by a thrombosis.

29. The method of any one of claims 11-22, wherein the hypoxic event is caused by arterial embolism.

30. The method of any one of claims 11-22, wherein the hypoxic event is caused by a hemorrhage.

31. The method of any one of claims 11-22, wherein the hypoxic event is caused by a high altitude.

32. The method of any one of claims 11-22, wherein the hypoxic event is caused by asphyxia.

33. The method of any one of claims 11-22, wherein the hypoxic event is caused by an asthmatic event.

34. The method of any one of claims 11-22, wherein the hypoxic event is caused by swelling of the brain.

35. The method of any one of claims 11-22, wherein the hypoxic event is caused by physical trauma and/or physical injury.

36. The method of any one of claims 11-22, wherein the hypoxic event is caused by arteriosclerosis or atherosclerosis.

37. The method of any one of claims 11-22, wherein the patient's prognosis is correlated with a Cerebral Performance Category (CPC) score.

38. The method of claim 37, wherein the CPC score includes classifications of good or poor.

39. The method of claim 38, wherein a good CPC score indicates a prognosis of the patient being conscious and alert with normal function or only slight disability or conscious and alert with moderate disability after a selected period of time.

40. The method of claim 38, wherein a poor CPC score indicates a prognosis of the patient being conscious with the patient having a severe disability, being comatose or in a persistent vegetative state, or being brain dead or suffering death from other causes after a selected period of time.

41. The method of claim 38 or 39, wherein the selected period of time is about 1 week, or about 2 weeks, or about 4 weeks, or about 2 months, or about 3 months, or about 4 months, or about 5 months, or about 6 months, or about 9 months, or about 1 year, or about 1.5 years, or about 2 years.

42. The method of any one of claims 11-22, wherein the plurality of samples are obtained from the patient within 2 days, 2.5 days, 3 days, 3.5 days, 4 days, 5 days, 6 days, or 7 days following the event.

43. The method of any one of claims 11-22, wherein 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more, samples are obtained from the patient.

44. The method of any one of claims 11-22, wherein the limit of quantification is less than about 9 pg/mL, 8 pg/mL, 7 pg/mL, 6 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.5 pg/mL, 0.1 pg/mL, or 0.05 pg/mL.

45. The method of any one of claims 11-22, wherein the measure of the concentration of biomarker or beta-amyloid peptide in the sample is less than about 500 pg/mL, about 400 pg/mL, about 300 pg/mL, 200 pg/mL, 100 pg/mL, 50 pg/mL, 30 pg/mL, 20 pg/mL, 10 pg/mL, 5 pg/mL or 1 pg/mL.

46. The method of any one of claims 11-22, wherein the limit of detection for the assay is less than about 10 pg/mL, 9 pg/mL, 8 pg/mL, 7 pg/mL, 6 pg/mL, 5 pg/mL, 4 pg/mL, 3 pg/mL, 2 pg/mL, 1 pg/mL, 0.5 pg/mL, 0.1 pg/mL, 0.05 pg/mL, 0.02 pg/mL.

47. The method of any one of claims 11-22, wherein a change in the concentration of the biomarker or beta-amyloid peptide in the plurality of samples is determined as a function of time.

48. The method of claim 47, wherein the concentration of the biomarker or beta-amyloid peptide in the plurality of samples is plotted on a graph as concentration versus time.

49. The method of claim 47, wherein the prognosis and/or course or treatment is based at least in part on the area under the curve plotted on the graph.

50. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on whether the change in concentration with time reflects an increase in biomarker concentration or beta-amyloid peptide concentration.

51. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the duration of rise of biomarker concentration or beta-amyloid peptide concentration.

52. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the magnitude of the fold increase of biomarker concentration or beta-amyloid peptide concentration.

53. The method of claim 47, wherein the prognosis and/or course of treatment is based at least in part on the sum of the increase in biomarker concentration or beta-amyloid peptide concentration, the duration of rise of biomarker concentration or beta-amyloid peptide concentration, and the magnitude of the fold increase of biomarker concentration or beta-amyloid peptide concentration.

54. The method of claim 53, wherein the prognosis is good for the recovery from the brain injury if the sum is less than about 50.

55. The method of claim 53, wherein the prognosis is poor for the recovery from the brain injury if the sum is greater than about 50.

56. The method of any one of claims 11-22, wherein the biomarker is neuron specific neuronal enolase (NSE), β-site aPP-cleaving enzyme 1 (BACe1), S100B, myelin basic protein (MBP), growth associate protein 43, glutamine synthetase, glial fibrillary acid protein (GFAP), a glycine transporter, a neuron specific glycoprotein, calpain, neurofibrillary protein, heat shock protein 72, a beta-amyloid precursor protein, calbindin D-28K, proteolipid protein, myeline associated glycoprotein, neurofilament H, creatine kinase protein (e.g., CK-BB), a tau protein, an endotheliam membrane protein, or combinations thereof.

57. The method of any one of claims 11-22, wherein the brain injuries have not been correlated solely with Alzheimer's disease.

58. The method of any one of claims 11-22, wherein the biomarker or beta-amyloid peptide is measured in bodily fluid.

59. The method of claim 58, wherein the bodily fluid is blood or CSF.