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(45) **Date of Patent:** **Jan. 1, 2013**(54) **LARGE-SCALE PRODUCTION OF SOLUBLE
HYALURONIDASE**(75) Inventors: **David Baker**, San Diego, CA (US);
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U.S.C. 154(b) by 0 days.(21) Appl. No.: **13/385,919**(22) Filed: **Mar. 13, 2012**(65) **Prior Publication Data**

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2009, now Pat. No. 8,187,855.(60) Provisional application No. 61/068,622, filed on Mar.
6, 2008.(51) **Int. Cl.****A61K 38/46** (2006.01)
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C07K 1/00 (2006.01)(52) **U.S. Cl.** **424/94.62**; 424/94.3; 435/69.1;
435/200; 435/201; 435/320.1; 435/325(58) **Field of Classification Search** 424/94.62;
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See application file for complete search history.(56) **References Cited****U.S. PATENT DOCUMENTS**5,292,509 A 3/1994 Hageman 424/94.61
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Primary Examiner — Herbert J Lilling(74) *Attorney, Agent, or Firm* — McKenna Long & Aldridge
LLP; Stephanie Seidman(57) **ABSTRACT**Provided are methods for preparing culture medium that con-
tains soluble hyaluronidases. The methods employ cells that
contain a plurality of active copies of nucleic acid encoding
the soluble hyaluronidase and a plurality of feedings and
temperature changes, whereby the encoded soluble hyalu-
ronidase is secreted into the cell culture medium.**18 Claims, No Drawings****Halozyne EX2093**
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LARGE-SCALE PRODUCTION OF SOLUBLE HYALURONIDASE

RELATED APPLICATIONS

This application is a divisional of allowed U.S. application Ser. No. 12/735,868, to David Baker and Louis Bookbinder, entitled "LARGE-SCALE PRODUCTION OF SOLUBLE HYALURONIDASE," filed Nov. 9, 2010, now U.S. Pat. No. 8,187,855 which is the national stage of International Application No. PCT/US09/001,455, to David Baker and Louis Bookbinder, entitled "LARGE-SCALE PRODUCTION OF SOLUBLE HYALURONIDASE," filed Mar. 6, 2009, which claims benefit of priority to U.S. Provisional Application Ser. No. 61/068,622, to David Baker and Louis Bookbinder, entitled "LARGE-SCALE PRODUCTION OF SOLUBLE HYALURONIDASE," filed Mar. 6, 2008.

This application is related to U.S. application Ser. No. 11/238,171 to Louis Bookbinder, Anirban Kundu, Gregory I. Frost, Michael F. Haller, Gilbert A. Keller, and Tyler M. Dylan, entitled SOLUBLE GLYCOSAMINOGLYCANS AND METHODS OF PREPARING AND USING SOLUBLE GLYCOSAMINOGLYCANS, filed Sep. 27, 2005 and published as U.S. Publication No. 20060104968, which is a continuation-in-part of U.S. application Ser. No. 11/065,716 to Louis Bookbinder, Anirban Kundu, Gregory I. Frost, Michael F. Haller, Gilbert A. Keller, and Tyler M. Dylan, entitled SOLUBLE GLYCOSAMINOGLYCANS AND METHODS OF PREPARING AND USING SOLUBLE GLYCOSAMINOGLYCANS, filed Feb. 23, 2005 and published as U.S. Publication No. 20050260186, which is a continuation-in-part of U.S. application Ser. No. 10/795,095 to Louis Bookbinder, Anirban Kundu and Gregory I. Frost, entitled SOLUBLE HYALURONIDASE GLYCOPROTEIN (SHASEGP), PROCESS FOR PREPARING THE SAME, USES AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEREOF, filed Mar. 5, 2004 and published as U.S. Publication No. 20040268425. The subject matter of each of the above-noted applications is incorporated by reference in its entirety.

FIELD OF THE INVENTION

Provided are methods for large-scale production of a recombinant human protein.

BACKGROUND

Hyaluronidases are a family of enzymes that degrade hyaluronic acid (also known as hyaluronan or hyaluronate), an essential component of the extracellular matrix and a major constituent of the interstitial barrier. By catalyzing the hydrolysis of hyaluronic acid, hyaluronidase lowers the viscosity of hyaluronic acid, thereby increasing tissue permeability. As such, hyaluronidases have been used, for example, as a spreading or dispersing agent in conjunction with other agents, drugs and proteins to enhance their dispersion and delivery. Hyaluronidases also have other therapeutic and cosmetic uses. Because of the increasing use of hyaluronidases for therapeutic and cosmetic uses, there is a need for large-scale quantities of purified hyaluronidase. Therefore, among the objects herein, it is an object to provide methods for the production and purification of hyaluronidases.

SUMMARY

Provided herein are methods for the production and purification of soluble hyaluronidases. In particular, provided

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herein are methods for the production and purification of soluble rHuPH20. Also provided herein are cell medium and harvested cell culture fluid that contain soluble rHuPH20. The methods provided herein can be used to produce and purify any quantity of soluble hyaluronidase, such as rHuPH20. For example, the methods and steps described herein are amendable for scale-up or scale-down, as would be apparent to one of skill in the art.

The methods provided herein can be used to produce and purify large-scale quantities of soluble rHuPH20. The methods provided herein for producing soluble rHuPH20 can include a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein cells contain between 150 and 300 copies of nucleic acid encoding soluble rHuPH20, the bioreactor contains at least 100 liters of cell culture and about 10^{10} - 10^{11} cells are inoculated per 100 liters cell culture and cells are cultured at a set temperature; b) feeding the cells with a first feed medium containing glucose, L-alanyl-L-glutamine, human insulin and yeast extract in amounts sufficient to increase cell growth and peak cell density, and to increase soluble rHuPH20 synthesis, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume; c) feeding the cells with a second feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and induce cell cycle arrest, wherein the amount of L-alanyl-L-glutamine is decreased compared to the amount of L-alanyl-L-glutamine in the second step, and the amount of yeast extract is increased compared to the amount of yeast extract in step b), and the feed medium is added to the culture at a volume of 4% of the cell culture volume and the temperature is lowered compared to the temperature in the step a) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase; d) feeding the cells with a third feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and increase cell cycle arrest, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume, the amount of L-alanyl-L-glutamine and glucose is decreased compared to the amount of L-alanyl-L-glutamine and glucose in step c), and the amount of yeast extract and sodium butyrate is increased compared to the amount of yeast extract and sodium butyrate in step c), and the temperature is lowered compared to the temperature in step c) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase; e) feeding the cells with a fourth feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and increase cell cycle arrest, wherein the amount of L-alanyl-L-glutamine and glucose is decreased compared to the amount of L-alanyl-L-glutamine and glucose in step d), the amount of sodium butyrate is decreased compared to the amount of sodium butyrate in step d), the temperature is lowered compared to the temperature in step d) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase and feed medium is added to the culture at a volume of 4% of the cell culture volume; f) culturing the cells until the viability drops below at least or about 50%; g) obtaining the harvest cell culture fluid; and h) the soluble rHuPH20 is purified from the harvest culture fluid.

The harvest cell culture fluid can be filtered prior to purification. In some examples, the temperature in step a) is 37° C., the temperature in step c) is 36.5° C., the temperature in

step d) is 36° C. and the temperature in step e) is 35.5° C. The soluble rHuPH20 purification can be effected by column chromatography, such as beaded crosslinked agarose column chromatography, beaded crosslinked phenyl-substituted agarose column chromatography, amino phenyl boronate column chromatography and hydroxyapatite column chromatography.

In one example, the method for producing soluble rHuPH20, includes steps of a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein the cells contain between 150 and 300 copies of nucleic acid encoding soluble rHuPH20, the bioreactor contains at least 100 liters of cell culture, the inoculation cell density is at or about 4×10^5 cells/mL and the cells are cultured at 37° C.; b) feeding the cells with a first feed medium containing at or about 33 g/L glucose, 32 mM L-alanyl-L-glutamine, 16.6 g/L yeast extract and 33 mg/L insulin, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume; c) feeding the cells with a second feed medium containing at or about 33 g/L glucose, 16 mM L-alanyl-L-glutamine, 33.4 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume and the temperature is lowered to 36.5° C.; d) feeding the cells with a third feed medium containing at or about 50 g/L glucose, 10 mM L-alanyl-L-glutamine, 50 g/L yeast extract and 1.8 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume and the temperature is lowered to 36° C.; e) feeding the cells with a fourth feed medium containing at or about 33 g/L glucose, 6.6 mM L-alanyl-L-glutamine, 50 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% of the cell culture volume and the temperature is lowered to 35.5° C.; f) continuing to culture the cells until viability drops below at least or about 50%; g) obtaining the harvest cell culture fluid; h) filtering the harvest cell culture fluid; and i) purifying the rHuPH20 from the harvest culture fluid using beaded crosslinked agarose column chromatography, beaded crosslinked phenyl-substituted agarose column chromatography, amino phenyl boronate column chromatography and hydroxyapatite column chromatography.

In another example, the method for producing soluble rHuPH20 includes the steps of a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein the cells comprise between 150 and 300 copies of nucleic acid encoding soluble rHuPH20; the bioreactor contains at least 100 liters of cell culture; the inoculation cell density is at or about 4×10^5 cells/mL; and the cells are cultured at or about 37° C.; b) feeding the cells with a first feed medium containing or containing about 33 g/L glucose, 32 mM L-alanyl-L-glutamine, 83.3 g/L yeast extract and 33 mg/L insulin, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; c) feeding the cells with a second feed medium containing or containing about 33 g/L glucose, 13 mM L-alanyl-L-glutamine, 166.7 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of at or about 4% of the cell culture volume and the temperature is lowered to 36.5° C.; d) feeding the cells with a third feed medium containing or containing about 50 g/L glucose, 10 mM L-alanyl-L-glutamine, 250 g/L yeast extract and 1.8 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume and the temperature is lowered to 36° C.; e) feeding the cells with a fourth feed medium containing or containing about 33 g/L glucose, 6.7 mM L-alanyl-

L-glutamine, 250 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume and the temperature is lowered to 35.5° C.; f) continuing to culture the cells until viability drops below at least or about 50%; g) obtaining the harvest cell culture fluid; h) filtering the harvest cell culture fluid; and i) purifying the rHuPH20 from the harvest culture fluid using beaded crosslinked agarose column chromatography, beaded crosslinked phenyl-substituted agarose column chromatography, amino phenyl boronate column chromatography and hydroxyapatite column chromatography.

In some examples, the volume of cell culture in the bioreactor is or is about 200, 300, 400, 500, 1000, 1500, 2000, 2500, 3000 or 3500 liters. In some examples, the amount of soluble rHuPH20 is produced per 100 L of cell culture using the methods provided herein at least or about 1, 5, 10, 15, 20, 25, 30, 35 or 40 grams of soluble rHuPH20. The specific activity of the soluble rHuPH20 can be at least or about 80000; 100000, 120000, 140000, 160000 or 180,000 units/mg. The cells that encode soluble rHuPH20 can, in some instances, be DG44 CHO cells. Further, the rHuPH20 can be encoded by nucleic acid set forth in SEQ ID NO:47.

Provided herein are cell culture media containing soluble rHuPH20 with an enzymatic activity of greater than 5000 units/mL, such as 10,000, 12,000, 14,000, 16,000, 18,000, 20,000, 22,000 or 24,000 units/mL. Also provided herein are harvested cell culture fluid containing soluble rHuPH20 with an enzymatic activity of greater than 5000 units/mL, such as 10,000, 12,000, 14,000, 16,000, 18,000, 20,000, 22,000 or 24,000 units/mL.

DETAILED DESCRIPTION

Outline

- A. Definitions
- B. Overview
- C. Hyaluronidase
 1. Structure and function
 2. PH20
 3. Therapeutic uses of hyaluronidases
 - a. Use as a spreading agent
 - b. Use in hypodermoclysis
 - c. Use in vitrectomy and ophthalmic disorders and conditions
 - d. Use in gene therapy
 - e. Cosmetic uses
 - f. Use in organ transplantation
 - g. Use in cancer treatment
 - h. Use in treatment of glycosaminoglycan accumulation in the brain
 - i. Use in treatment of glycosaminoglycan accumulation in cardiovascular disease
 - j. Use in pulmonary disease
 - k. Other uses
- D. Hyaluronidase-expressing cells
 - a. 3D35M cells
 - b. 2B2 cells
- E. Cell culture expansion
- F. Protein production
- G. Protein concentration and buffer exchange
- H. Purification
 1. Beaded crosslinked agarose column
 2. Beaded crosslinked phenyl-substituted agarose column
 3. Amino Phenyl Boronate column
 4. Hydroxyapatite column

6. Virus removal, protein concentration and buffer exchange
- I. Filling
- J. Monitoring and assays
 1. Monitoring conditions
 2. Monitoring soluble rHuPH20 production
- K. Examples

A. Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the invention(s) belong. All patents, patent applications, published applications and publications, Genbank sequences, databases, websites and other published materials referred to throughout the entire disclosure herein, unless noted otherwise, are incorporated by reference in their entirety. In the event that there are a plurality of definitions for terms herein, those in this section prevail. Where reference is made to a URL or other such identifier or address, it is understood that such identifiers can change and particular information on the internet can come and go, but equivalent information can be found by searching the internet. Reference thereto evidences the availability and public dissemination of such information.

As used herein, hyaluronidase refers to an enzyme that degrades hyaluronic acid. Hyaluronidases include bacterial hyaluronidases (EC 4.2.99.1), hyaluronidases from leeches, other parasites, and crustaceans (EC 3.2.1.36), and mammalian-type hyaluronidases (EC 3.2.1.35). Hyaluronidases also include any of non-human origin including, but not limited to, murine, canine, feline, leporine, avian, bovine, ovine, porcine, equine, piscine, ranine, bacterial, and any from leeches, other parasites, and crustaceans. Exemplary non-human hyaluronidases include, hyaluronidases from cows (SEQ ID NO:10), yellow jacket wasp (SEQ ID NOS:11 and 12), honey bee (SEQ ID NO:13), white-face hornet (SEQ ID NO:14), paper wasp (SEQ ID NO:15), mouse (SEQ ID NOS:16-18, 29), pig (SEQ ID NOS:19-20), rat (SEQ ID NOS:21-23, 28), rabbit (SEQ ID NO:24), sheep (SEQ ID NO:25), orangutan (SEQ ID NO:26), cynomolgus monkey (SEQ ID NO:27), guinea pig (SEQ ID NO:30), *Staphylococcus aureus* (SEQ ID NO:31), *Streptococcus pyogenes* (SEQ ID NO:32), and *Clostridium perfringens* (SEQ ID NO:33). Exemplary human hyaluronidases include HYAL1 (SEQ ID NO:34), HYAL2 (SEQ ID NO:35), HYAL3 (SEQ ID NO:36), HYAL4 (SEQ ID NO:37), and PH20 (SEQ ID NO:1). Also included amongst hyaluronidases are soluble human PH20 and soluble rHuPH20.

Reference to hyaluronidases includes precursor hyaluronidase polypeptides and mature hyaluronidase polypeptides (such as those in which a signal sequence has been removed), truncated forms thereof that have activity, and includes allelic variants and species variants, variants encoded by splice variants, and other variants, including polypeptides that have at least 40%, 45%, 50%, 55%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the precursor polypeptides set forth in SEQ ID NOS: 1 and 10-37, or the mature form thereof. For example, reference to hyaluronidase also includes the human PH20 precursor polypeptide variants set forth in SEQ ID NOS:48-49. Hyaluronidases also include those that contain chemical or posttranslational modifications and those that do not contain chemical or posttranslational modifications. Such modifications include, but are not limited to, pegylation, albu-

mination, glycosylation, farnesylation, carboxylation, hydroxylation, phosphorylation, and other polypeptide modifications known in the art.

As used herein, soluble human PH20 or sHuPH20 include mature polypeptides lacking all or a portion of the glycosylphosphatidyl inositol (GPI) attachment site at the C-terminus such that upon expression, the polypeptides are soluble. Exemplary sHuPH20 polypeptides include mature polypeptides having an amino acid sequence set forth in any one of SEQ ID NOS:4-9 and 45-46. The precursor polypeptides for such exemplary sHuPH20 polypeptides include a signal sequence. Exemplary of the precursors are those set forth in SEQ ID NOS:3 and 38-44, each of which contains a 35 amino acid signal sequence at amino acid positions 1-35. Soluble HuPH20 polypeptides also include those degraded during or after the production and purification methods described herein.

As used herein, soluble rHuPH20 refers to a soluble form of human PH20 that is recombinantly expressed in Chinese Hamster Ovary (CHO) cells. Soluble rHuPH20 is encoded by nucleic acid that includes the signal sequence and is set forth in SEQ ID NO:47. Also included are DNA molecules that are allelic variants thereof and other soluble variants. The nucleic acid encoding soluble rHuPH20 is expressed in CHO cells which secrete the mature polypeptide. As produced in the culture medium there is heterogeneity at the C-terminus so that the product includes a mixture of species that can include one or more of SEQ ID NOS. 4-9 in various abundance. Corresponding allelic variants and other variants also are included, including those corresponding to the precursor human PH20 polypeptides set forth in SEQ ID NOS:48-49. Other variants can have 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity with any of SEQ ID NOS. 4 as long they retain a hyaluronidase activity and are soluble.

As used herein, "soluble rHuPH20-expressing cells" refers to any CHO cell that expresses soluble rHuPH20. Exemplary soluble rHuPH20-expressing cells include 2B2 and 3D35M cells. Soluble rHuPH20-expressing cells are CHO cells into which nucleic acid that contains the sequence set forth in SEQ ID NO:55 has been introduced.

As used herein, hyaluronidase activity refers to any activity exhibited by a hyaluronidase polypeptide. Such activities can be tested in vitro and/or in vivo and include, but are not limited to, enzymatic activity, such as to effect cleavage of hyaluronic acid, ability to act as a dispersing or spreading agent and antigenicity. hyaluronidase activity refers to any activity exhibited by a hyaluronidase polypeptide.

As used herein, enzymatic activity refers to the activity of a hyaluronidase, as assessed in in vitro enzymatic assays, to cleave a substrate, such as hyaluronic acid. In vitro assays to determine the enzymatic activity of hyaluronidases, such as soluble rHuPH20, are known in the art and described herein. Exemplary assays include the microturbidity assay described below (see e.g. Example 9 and section I) that measures cleavage of hyaluronic acid by hyaluronidase indirectly by detecting the insoluble precipitate formed when the uncleaved hyaluronic acid binds with serum albumin.

As used herein, specific activity with reference to soluble rHuPH20 is the enzyme activity relative to the amount of soluble rHuPH20. Specific activity is calculated by dividing the enzymatic activity (units/mL) by the protein concentration (mg/mL).

As used herein, "exhibits at least one activity" or "retains at least one activity" refers to the activity exhibited by a variant soluble rHuPH20 as compared to any soluble rHuPH20 set forth in SEQ ID NOS:4-9 under the same conditions. Typi-

cally, a variant soluble rHuPH20 that retains or exhibits at least one activity of a soluble rHuPH20 set forth in SEQ ID NOS:4-9 retains at or about 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500% or more of the activity of a soluble rHuPH20 set forth in SEQ ID NOS:4-9. Exemplary activities include, but are not limited to, hyaluronidase activity and enzymatic activity.

As used herein, beaded crosslinked agarose column chromatography refers to chromatography using a column packed with beaded crosslinked agarose. Exemplary of beaded crosslinked agarose is Q Sepharose™.

As used herein, beaded crosslinked phenyl-substituted agarose column chromatography refers to chromatography using a column packed with beaded phenyl-substituted crosslinked agarose. Exemplary of beaded phenyl-substituted crosslinked agarose is Phenyl Sepharose™.

As used herein, amino phenyl boronate column chromatography refers to chromatography using a column packed with amino phenyl boronate agarose.

As used herein, hydroxyapatite column chromatography refers to chromatography using a column packed with hydroxyapatite.

As used herein, harvested cell culture fluid or harvest cell culture fluid (HCCF) refers to the fluid obtained following harvest of the cells from the bioreactor and separation of the cell culture medium from the cells, cell debris and other aggregates. The cell culture that is harvested from the bioreactor can be filtered to clarify the culture, removing the cells, cell debris and other aggregates to leave the harvested cell culture fluid.

As used herein, cell density refers to the number of cells in a given volume of medium.

As used herein, cell culture or culture refers to a cell population that is suspended in a medium under conditions suitable to maintain viability of the cells or grow the cells.

As used herein, medium, cell medium or cell culture medium refers to a solution containing nutrients sufficient to promote the growth of cells in a culture. Typically, these solutions contain essential and non-essential amino acids, vitamins, energy sources, lipids and/or trace elements. The medium also can contain additional supplements, such as hormones, growth factors and growth inhibitors. Reference to cell culture medium included

As used herein, the residues of naturally occurring α -amino acids are the residues of those 20 α -amino acids found in nature which are incorporated into protein by the specific recognition of the charged tRNA molecule with its cognate mRNA codon in humans.

As used herein, "in amounts sufficient to increase" when referring to a substance increasing parameters such as cell growth rate, peak cell density, protein synthesis or cell cycle arrest refers to the amount of a substance that effects an increase in one of these parameters compared to that observed in the absence of the substance. The parameters can be assessed in the presence and absence of a substance, and the amount of substance that increases the parameter (such as cell growth rate, peak cell density, protein synthesis or cell cycle arrest) compared to in the absence of the substance can be determined. The growth rate, peak cell density, protein synthesis or cell cycle arrest in the presence of the substance can be increased by at or about 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500% or more compared to the

growth rate, peak cell density, protein synthesis or cell cycle arrest in the absence of the substance.

As used herein, nucleic acids include DNA, RNA and analogs thereof, including peptide nucleic acids (PNA) and mixtures thereof. Nucleic acids can be single or double-stranded. When referring to probes or primers, which are optionally labeled, such as with a detectable label, such as a fluorescent or radiolabel, single-stranded molecules are contemplated. Such molecules are typically of a length such that their target is statistically unique or of low copy number (typically less than 5, generally less than 3) for probing or priming a library. Generally a probe or primer contains at least 14, 16 or 30 contiguous nucleotides of sequence complementary to or identical to a gene of interest. Probes and primers can be 10, 20, 30, 50, 100 or more nucleic acids long.

As used herein, a peptide refers to a polypeptide that is from 2 to 40 amino acids in length.

As used herein, the amino acids which occur in the various sequences of amino acids provided herein are identified according to their known, three-letter or one-letter abbreviations (Table 1). The nucleotides which occur in the various nucleic acid fragments are designated with the standard single-letter designations used routinely in the art.

As used herein, an "amino acid" is an organic compound containing an amino group and a carboxylic acid group. A polypeptide contains two or more amino acids. For purposes herein, amino acids include the twenty naturally-occurring amino acids, non-natural amino acids and amino acid analogs (i.e., amino acids wherein the α -carbon has a side chain).

As used herein, "amino acid residue" refers to an amino acid formed upon chemical digestion (hydrolysis) of a polypeptide at its peptide linkages. The amino acid residues described herein are presumed to be in the "L" isomeric form. Residues in the "D" isomeric form, which are so designated, can be substituted for any L-amino acid residue as long as the desired functional property is retained by the polypeptide. NH_2 refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxy group present at the carboxyl terminus of a polypeptide. In keeping with standard polypeptide nomenclature described in *J. Biol. Chem.*, 243: 3552-3559 (1969), and adopted 37 C.F.R. §§1.821-1.822, abbreviations for amino acid residues are shown in Table 1:

TABLE 1

Table of Correspondence			
SYMBOL			
1-Letter	3-Letter	AMINO ACID	
Y	Tyr	Tyrosine	
G	Gly	Glycine	
F	Phe	Phenylalanine	
M	Met	Methionine	
A	Ala	Alanine	
S	Ser	Serine	
I	Ile	Isoleucine	
L	Leu	Leucine	
T	Thr	Threonine	
V	Val	Valine	
P	Pro	Proline	
K	Lys	Lysine	
H	His	Histidine	
Q	Gln	Glutamine	
E	Glu	Glutamic acid	
Z	Glx	Glu and/or Gln	
W	Trp	Tryptophan	
R	Arg	Arginine	
D	Asp	Aspartic acid	

TABLE 1-continued

Table of Correspondence		
SYMBOL		
1-Letter	3-Letter	AMINO ACID
N	Asn	Asparagine
B	Asx	Asn and/or Asp
C	Cys	Cysteine
X	Xaa	Unknown or other

It should be noted that all amino acid residue sequences represented herein by formulae have a left to right orientation in the conventional direction of amino-terminus to carboxyl-terminus. In addition, the phrase "amino acid residue" is broadly defined to include the amino acids listed in the Table of Correspondence (Table 1) and modified and unusual amino acids, such as those referred to in 37 C.F.R. §§1.821-1.822, and incorporated herein by reference. Furthermore, it should be noted that a dash at the beginning or end of an amino acid residue sequence indicates a peptide bond to a further sequence of one or more amino acid residues, to an amino-terminal group such as NH₂ or to a carboxyl-terminal group such as COOH.

As used herein, "naturally occurring amino acids" refer to the 20 L-amino acids that occur in polypeptides.

As used herein, "non-natural amino acid" refers to an organic compound that has a structure similar to a natural amino acid but has been modified structurally to mimic the structure and reactivity of a natural amino acid. Non-naturally occurring amino acids thus include, for example, amino acids or analogs of amino acids other than the 20 naturally-occurring amino acids and include, but are not limited to, the D-isostereomers of amino acids. Exemplary non-natural amino acids are described herein and are known to those of skill in the art.

As used herein, a DNA construct is a single or double stranded, linear or circular DNA molecule that contains segments of DNA combined and juxtaposed in a manner not found in nature. DNA constructs exist as a result of human manipulation, and include clones and other copies of manipulated molecules.

As used herein, "similarity" between two proteins or nucleic acids refers to the relatedness between the sequence of amino acids of the proteins or the nucleotide sequences of the nucleic acids. Similarity can be based on the degree of identity and/or homology of sequences of residues and the residues contained therein. Methods for assessing the degree of similarity between proteins or nucleic acids are known to those of skill in the art. For example, in one method of assessing sequence similarity, two amino acid or nucleotide sequences are aligned in a manner that yields a maximal level of identity between the sequences. "Identity" refers to the extent to which the amino acid or nucleotide sequences are invariant. Alignment of amino acid sequences, and to some extent nucleotide sequences, also can take into account conservative differences and/or frequent substitutions in amino acids (or nucleotides). Conservative differences are those that preserve the physico-chemical properties of the residues involved. Alignments can be global (alignment of the compared sequences over the entire length of the sequences and including all residues) or local (the alignment of a portion of the sequences that includes only the most similar region or regions).

"Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: *Computa-*

tional Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). While there exists a number of methods to measure identity between two polynucleotide or polypeptides, the term "identity" is well known to skilled artisans (Carillo, H. & Lipton, D., *SIAM J Applied Math* 48:1073 (1988)).

As used herein, homologous (with respect to nucleic acid and/or amino acid sequences) means about greater than or equal to 25% sequence homology, typically greater than or equal to 25%, 40%, 50%, 60%, 70%, 80%, 85%, 90% or 95% sequence homology; the precise percentage can be specified if necessary. For purposes herein the terms "homology" and "identity" are often used interchangeably, unless otherwise indicated. In general, for determination of the percentage homology or identity, sequences are aligned so that the highest order match is obtained (see, e.g.: *Computational Molecular Biology*, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; Carillo et al. (1988) *SIAM J Applied Math* 48:1073). By sequence homology, the number of conserved amino acids is determined by standard alignment algorithms programs, and can be used with default gap penalties established by each supplier. Substantially homologous nucleic acid molecules would hybridize typically at moderate stringency or at high stringency all along the length of the nucleic acid of interest. Also contemplated are nucleic acid molecules that contain degenerate codons in place of codons in the hybridizing nucleic acid molecule.

Whether any two molecules have nucleotide sequences or amino acid sequences that are at least 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% "identical" or "homologous" can be determined using known computer algorithms such as the "FASTA" program, using for example, the default parameters as in Pearson et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:2444 (other programs include the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(I): 387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S. F., et al., *J Molec Biol* 215:403 (1990)); Guide to Huge Computers, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo et al. (1988) *SIAM J Applied Math* 48:1073). For example, the BLAST function of the National Center for Biotechnology Information database can be used to determine identity. Other commercially or publicly available programs include, DNASTar "MegAlign" program (Madison, Wis.) and the University of Wisconsin Genetics Computer Group (UWG) "Gap" program (Madison Wis.). Percent homology or identity of proteins and/or nucleic acid molecules can be determined, for example, by comparing sequence information using a GAP computer program (e.g., Needleman et al. (1970) *J. Mol. Biol.* 48:443, as revised by Smith and Waterman (1981) *Adv. Appl. Math.* 2:482). Briefly, the GAP program defines similarity as the number of aligned symbols (i.e., nucleotides or amino acids), which are similar, divided by the total number of symbols in the shorter of the

two sequences. Default parameters for the GAP program can include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) and the weighted comparison matrix of Gribskov et al. (1986) *Nucl. Acids Res.* 14:6745, as described by Schwartz and Dayhoff, eds., *ATLAS OF PROTEIN SEQUENCE AND STRUCTURE*, National Biomedical Research Foundation, pp. 353-358 (1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

Therefore, as used herein, the term "identity" or "homology" represents a comparison between a test and a reference polypeptide or polynucleotide. As used herein, the term at least "90% identical to" refers to percent identities from 90 to 99.99 relative to the reference nucleic acid or amino acid sequence of the polypeptide. Identity at a level of 90% or more is indicative of the fact that, assuming for exemplification purposes a test and reference polypeptide length of 100 amino acids are compared. No more than 10% (i.e., 10 out of 100) of the amino acids in the test polypeptide differs from that of the reference polypeptide. Similar comparisons can be made between test and reference polynucleotides. Such differences can be represented as point mutations randomly distributed over the entire length of a polypeptide or they can be clustered in one or more locations of varying length up to the maximum allowable, e.g. 10/100 amino acid difference (approximately 90% identity). Differences are defined as nucleic acid or amino acid substitutions, insertions or deletions. At the level of homologies or identities above about 85-90%, the result should be independent of the program and gap parameters set; such high levels of identity can be assessed readily, often by manual alignment without relying on software.

As used herein, an aligned sequence refers to the use of homology (similarity and/or identity) to align corresponding positions in a sequence of nucleotides or amino acids. Typically, two or more sequences that are related by 50% or more identity are aligned. An aligned set of sequences refers to 2 or more sequences that are aligned at corresponding positions and can include aligning sequences derived from RNAs, such as ESTs and other cDNAs, aligned with genomic DNA sequence.

As used herein, "primer" refers to a nucleic acid molecule that can act as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. It will be appreciated that a certain nucleic acid molecules can serve as a "probe" and as a "primer." A primer, however, has a 3' hydroxyl group for extension. A primer can be used in a variety of methods, including, for example, polymerase chain reaction (PCR), reverse-transcriptase (RT)-PCR, RNA PCR, LCR, multiplex PCR, panhandle PCR, capture PCR, expression PCR, 3' and 5' RACE, in situ PCR, ligation-mediated PCR and other amplification protocols.

As used herein, an allelic variant or allelic variation references any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and can result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or can encode polypeptides having altered amino acid sequence. The term "allelic variant" also is used herein to denote a protein encoded by an allelic variant of a gene. Typically the reference form of the gene encodes a wildtype form and/or predominant form of a polypeptide from a population or single reference member of a species. Typically, allelic variants,

which include variants between and among species typically have at least 80%, 90% or greater amino acid identity with a wildtype and/or predominant form from the same species; the degree of identity depends upon the gene and whether comparison is interspecies or intraspecies. Generally, intraspecies allelic variants have at least about 80%, 85%, 90% or 95% identity or greater with a wildtype and/or predominant form, including 96%, 97%, 98%, 99% or greater identity with a wildtype and/or predominant form of a polypeptide. Reference to an allelic variant herein generally refers to variations in proteins among members of the same species.

As used herein, "allele," which is used interchangeably herein with "allelic variant" refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for that gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide or several nucleotides, and can include substitutions, deletions and insertions of nucleotides. An allele of a gene also can be a form of a gene containing a mutation.

As used herein, species variants refer to variants in polypeptides among different species, including different mammalian species, such as mouse and human.

As used herein, a splice variant refers to a variant produced by differential processing of a primary transcript of genomic DNA that results in more than one type of mRNA.

As used herein, modification is in reference to modification of a sequence of amino acids of a polypeptide or a sequence of nucleotides in a nucleic acid molecule and includes deletions, insertions, and replacements of amino acids and nucleotides, respectively. Methods of modifying a polypeptide are routine to those of skill in the art, such as by using recombinant DNA methodologies.

As used herein, the term promoter means a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding region of genes.

As used herein, isolated or purified polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. Preparations can be determined to be substantially free if they appear free of readily detectable impurities as determined by standard methods of analysis, such as thin layer chromatography (TLC), gel electrophoresis and high performance liquid chromatography (HPLC), used by those of skill in the art to assess such purity, or sufficiently pure such that further purification would not detectably alter the physical and chemical properties, such as enzymatic and biological activities, of the substance. Methods for purification of the compounds to produce substantially chemically pure compounds are known to those of skill in the art. A substantially chemically pure compound, however, can be a mixture of stereoisomers. In such instances, further purification might increase the specific activity of the compound.

The term substantially free of cellular material includes preparations of proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the term substantially free of cellular material includes preparations of enzyme proteins having less than about 30% (by dry weight) of non-enzyme proteins (also referred to herein as a contami-

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nating protein), generally less than about 20% of non-enzyme proteins or 10% of non-enzyme proteins or less than about 5% of non-enzyme proteins. When the enzyme protein is recombinantly produced, it also is substantially free of culture medium, i.e., culture medium represents less than about or at 20%, 10% or 5% of the volume of the enzyme protein preparation.

As used herein, the term substantially free of chemical precursors or other chemicals includes preparations of enzyme proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. The term includes preparations of enzyme proteins having less than about 30% (by dry weight) 20%, 10%, 5% or less of chemical precursors or non-enzyme chemicals or components.

As used herein, synthetic, with reference to, for example, a synthetic nucleic acid molecule or a synthetic gene or a synthetic peptide refers to a nucleic acid molecule or polypeptide molecule that is produced by recombinant methods and/or by chemical synthesis methods.

As used herein, an expression vector includes vectors capable of expressing DNA that is operatively linked with regulatory sequences, such as promoter regions, that are capable of effecting expression of such DNA fragments. Such additional segments can include promoter and terminator sequences, and optionally can include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, and the like. Expression vectors are generally derived from plasmid or viral DNA, or can contain elements of both. Thus, an expression vector refers to a recombinant DNA or RNA construct, such as a plasmid, a phage, recombinant virus or other vector that, upon introduction into an appropriate host cell, results in expression of the cloned DNA. Appropriate expression vectors are well known to those of skill in the art and include those that are replicable in eukaryotic cells and/or prokaryotic cells and those that remain episomal or those which integrate into the host cell genome.

As used herein, vector also includes "virus vectors" or "viral vectors." Viral vectors are engineered viruses that are operatively linked to exogenous genes to transfer (as vehicles or shuttles) the exogenous genes into cells.

As used herein the term assessing is intended to include quantitative and qualitative determination in the sense of obtaining an absolute value for the activity of a protease, or a domain thereof, present in the sample, and also of obtaining an index, ratio, percentage, visual or other value indicative of the level of the activity. Assessment can be direct or indirect and the chemical species actually detected need not of course be the proteolysis product itself but can for example be a derivative thereof or some further substance. For example, detection of a cleavage product of a complement protein, such as by SDS-PAGE and protein staining with Coomassie blue.

As used herein, a composition refers to any mixture. It can be a solution, suspension, liquid, powder, paste, aqueous, non-aqueous or any combination thereof.

As used herein, a kit is a packaged combination that optionally includes other elements, such as additional reagents and instructions for use of the combination or elements thereof.

As used herein, "disease or disorder" refers to a pathological condition in an organism resulting from cause or condition including, but not limited to, infections, acquired conditions, genetic conditions, and characterized by identifiable symptoms.

As used herein, "treating" a subject with a disease or condition means that the subject's symptoms are partially or totally alleviated, or remain static following treatment. Hence

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treatment encompasses prophylaxis, therapy and/or cure. Prophylaxis refers to prevention of a potential disease and/or a prevention of worsening of symptoms or progression of a disease. Treatment also encompasses any pharmaceutical use of a modified interferon and compositions provided herein.

As used herein, a pharmaceutically effective agent, includes any therapeutic agent or bioactive agents, including, but not limited to, for example, anesthetics, vasoconstrictors, dispersing agents, conventional therapeutic drugs, including small molecule drugs and therapeutic proteins.

As used herein, treatment means any manner in which the symptoms of a condition, disorder or disease or other indication, are ameliorated or otherwise beneficially altered.

As used herein, a patient refers to a human subject.

As used herein, an effective amount is the quantity of a therapeutic agent necessary for preventing, curing, ameliorating, arresting or partially arresting a symptom of a disease or disorder.

As used herein, animal includes any animal, such as, but are not limited to primates including humans, gorillas and monkeys; rodents, such as mice and rats; fowl, such as chickens; ruminants, such as goats, cows, deer, sheep; ovine, such as pigs and other animals. Non-human animals exclude humans as the contemplated animal. The hyaluronidases provided herein are from any source, animal, plant, prokaryotic and fungal. Most enzymes are of animal origin, including mammalian origin.

As used herein, a control refers to a sample that is substantially identical to the test sample, except that it is not treated with a test parameter, or, if it is a plasma sample, it can be from a normal volunteer not affected with the condition of interest. A control also can be an internal control.

As used herein, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to a compound, comprising "an extracellular domain" includes compounds with one or a plurality of extracellular domains.

As used herein, ranges and amounts can be expressed as "about" a particular value or range. About also includes the exact amount. Hence "about 5 mM" means "about 5 mM" and also "5 mM."

As used herein, the abbreviations for any protective groups, amino acids and other compounds, are, unless indicated otherwise, in accord with their common usage, recognized abbreviations, or IUPAC-IUB Commission on Biochemical Nomenclature (see, (1972) *Biochem.* 11:1726).

B. Overview

Provided herein are methods for the large scale production of soluble hyaluronidases, such as soluble human hyaluronidases, including soluble human PH20 (sHuPH20), such as, for example, soluble rHuPH20. The methods typically utilize bioreactors to culture cells that produce the soluble hyaluronidase, such as CHO cells (e.g. DG44 CHO cells). Exemplary of such cells are 2B2 cells, which produce soluble rHuPH20. The volume of cell culture in the bioreactor can range from 1 L to 5000 L or more, but typically is or is about 200, 300, 400, 500, 1000, 1500, 2000, 2500, 3000 or 3500 liters. Prior to inoculation of the bioreactor, the cells are expanded through a series of increasing cell culture volumes to generate the required number of cells for seeding of the bioreactor. Typically, the cell culture in the bioreactor is seeded with 10^5 to 10^6 cells/mL, but can be seeded with more or less. The cells are then incubated in the bioreactor for 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or more days.

During this incubation, feed media is added to the cell culture to supply additional nutrients and supplements. Exemplary supplements or nutrients that can be included in the feed media include, but are not limited to, glucose, glutamine or glutamine-substitute, such as L-alanyl-L-glutamine, insulin, and sodium butyrate. The type and amount of supplement added can influence cell growth and protein production. For example, insulin and glutamine or glutamine-substitute can be incorporated into the first feed media added to the cell culture to increase cell growth and peak cell density. Subsequent feed media can be designed to promote protein production more than cell growth. Supplements such as insulin can be excluded or reduced in amount, as can glutamine or glutamine-substitute, such as L-alanyl-L-glutamine. In contrast, supplements such as yeast extract that enhance protein synthesis can be increased in amount. In addition, supplements that enhance cell cycle arrest and, therefore, increased protein production, also can be included. Exemplary of such supplements is sodium butyrate.

Following protein production in the bioreactor, the cells are harvested and the soluble hyaluronidase, such as soluble rHuPH20, that has been secreted into the cell culture media is concentrated prior to initiation of the purification process. The soluble hyaluronidase is then purified from the concentrated protein solution using a series of purification steps. Exemplary of purification methods that are used for the methods herein is a combination of ion-exchange chromatography, hydrophobic interaction chromatography and affinity chromatography. The purified protein is then concentrated and diafiltered.

Utilizing the methods described herein, between about 0.5-50 grams of soluble hyaluronidases, such as soluble rHuPH20, is produced per 100 L of cell culture. In some examples, the amount of soluble rHuPH20 produced per 100 L of culture is or is about 1, 2, 3, 4, 5, 10, 15, 20, 30, or 40 grams or more. In some examples, the yield of soluble hyaluronidase following purification can range from between or between about 10% to 50% of the amount produced before purification. For example, the yield following purification can be or be about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% of the amount produced before purification. Generally, the specific activity of soluble rHuPH20 produced using the methods herein is at least or about 80000, 100000, 120000, 140000, 160000 or 180,000 units/mg.

C. Hyaluronidases

Hyaluronidases are a family of enzymes that degrade hyaluronic acid (also known as hyaluronan or hyaluronate), an essential component of the extracellular matrix and a major constituent of the interstitial barrier. By catalyzing the hydrolysis of hyaluronic acid, hyaluronidase lowers the viscosity of hyaluronic acid, thereby increasing tissue permeability. As such, hyaluronidases have been used, for example, as a spreading or dispersing agent in conjunction with other agents, drugs and proteins to enhance their dispersion and delivery.

1. Structure and function of hyaluronidases

There are three general classes of hyaluronidases; mammalian hyaluronidase, bacterial hyaluronidase and hyaluronidase from leeches, other parasites and crustaceans. Mammalian-type hyaluronidases (EC 3.2.1.35) are endo- β -N-acetyl-hexosaminidases that hydrolyze the β 1 $\rightarrow$ 4 glycosidic bond of hyaluronic acid into various oligosaccharide lengths such as tetrasaccharides and hexasaccharides. They have both hydrolytic and transglycosidase activities and can degrade hyaluronic acid and chondroitin sulfates, such as C4-S and

C6-S. Hyaluronidases of this type include, but are not limited to, hyaluronidases from cows (SEQ ID NO:10), yellow jacket wasp (SEQ ID NOS:11 and 12), honey bee (SEQ ID NO:13), white-face hornet (SEQ ID NO:14), paper wasp (SEQ ID NO:15), mouse (SEQ ID NOS:16-18, 29), pig (SEQ ID NOS:19-20), rat (SEQ ID NOS:21-23, 228), rabbit (SEQ ID NO:24), sheep (SEQ ID NO:25), orangutan (SEQ ID NO:26), cynomolgus monkey (SEQ ID NO:27), guinea pig (SEQ ID NO:30) and human hyaluronidases.

There are six hyaluronidase-like genes in the human genome: HYAL1, HYAL2, HYAL3, HYAL4, HYALP1 and PH20/SPAM 1. HYALP1 is a pseudogene, and HYAL3 (SEQ ID NO:36) has not been shown to possess enzyme activity toward any known substrates. HYAL4 (precursor polypeptide set forth in SEQ ID NO:37) is a chondroitinase and exhibits little activity towards hyaluronic acid. HYAL1 (precursor polypeptide set forth in SEQ ID NO:34) is the prototypical acid-active enzyme and PH20 (precursor polypeptide set forth in SEQ ID NO:1) is the prototypical neutral-active enzyme. Acid-active hyaluronidases, such as HYAL1 and HYAL2 (precursor polypeptide set forth in SEQ ID NO:35) generally lack catalytic activity at neutral pH (i.e. pH 7). For example, HYAL1 has little catalytic activity in vitro over pH 4.5 (Frost et al. (1997) *Anal Biochemistry* 251:263-269). HYAL2 is an acid-active enzyme with a very low specific activity in vitro. The hyaluronidase-like enzymes also can be characterized by those which are generally locked to the plasma membrane via a glycosylphosphatidyl inositol anchor such as human HYAL2 and human PH20 (Danilkevitch-Miagkova, et al. (2003) *Proc Natl Acad Sci USA*. 100(8): 4580-5), and those which are generally soluble such as human HYAL1 (Frost et al, (1997) *Biochem Biophys Res Commun*. 236(1):10-5). By catalyzing the hydrolysis of hyaluronic acid, a major constituent of the interstitial barrier, hyaluronidase lowers the viscosity of hyaluronic acid, thereby increasing tissue permeability. It also has been shown to exhibit anti-cancer and anti-carcinogenic activities.

N-linked glycosylation of some hyaluronidases can be very important for their catalytic activity and stability. While altering the type of glycan modifying a glycoprotein can have dramatic effects on a protein's antigenicity, structural folding, solubility, and stability, many enzymes are not thought to require glycosylation for optimal enzyme activity. Hyaluronidases are, therefore, unique in this regard, in that removal of N-linked glycosylation can result in near complete inactivation of the hyaluronidase activity. For such hyaluronidases, the presence of N-linked glycans is critical for generating an active enzyme.

There are seven potential N-linked glycosylation sites at N82, N166, N235, N254, N368, N393, N490 of human PH20 exemplified in SEQ ID NO: 1. Disulfide bonds form between the cysteine residues C60 and C351 and between C224 and C238 to form the core hyaluronidase domain. However, additional cysteines are required in the carboxy terminus for neutral enzyme catalytic activity such that amino acids 36 to 464 of SEQ ID NO:1 contains the minimally active human PH20 hyaluronidase domain. Thus, N-linked glycosylation site N490 is not required for proper hyaluronidase activity.

N-linked oligosaccharides fall into several major types (oligomannose, complex, hybrid, sulfated), all of which have (Man) 3-GlcNAc-GlcNAc-cores attached via the amide nitrogen of Asn residues that fall within-Asn-Xaa-Thr/Ser-sequences (where Xaa is not Pro). Glycosylation at an-Asn-Xaa-Cys-site has been reported for coagulation protein C. In some instances, the hyaluronidase can contain both N-glycosidic and O-glycosidic linkages. For example, rHuPH20 (as

produced in the methods described herein) has O-linked oligosaccharides as well as N-linked oligosaccharides.

The methods described herein provide a process for the production and purification of large quantities of a soluble preparation of human PH20 hyaluronidase preparation.

2. PH20

Human PH20 (also known as sperm surface protein PH20), as noted above, is the prototypical neutral-active enzyme that is generally locked to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor. It is naturally involved in sperm-egg adhesion and aids penetration by sperm of the layer of cumulus cells by digesting hyaluronic acid. The PH20 mRNA transcript is normally translated to generate a 509 amino acid precursor protein containing a 35 amino acid signal sequence at the N-terminus (amino acid residue positions 1-35). The mature PH20 polypeptide is, therefore, a 474 amino acid polypeptide with an amino acid sequence set forth in SEQ ID NO:2.

Soluble forms of human PH20 (sHuPH20) can be produced and purified using the methods described herein. The generation of sHuPH20 are described in related U.S. patent application Ser. Nos. 10/795,095, 11/065,716 and 11/238,171 (also referred to in these applications as sHASEGP or rHuPH20), and in Examples 1 and 4, below. The soluble forms are produced by expressing nucleic acid encoding C-terminal truncations of the mature PH20 polypeptide that lack the GPI-attachment sites. Soluble forms of human PH20 include soluble rHuPH20, which is produced and purified using the methods provided herein.

3. Therapeutic Uses of Hyaluronidases

Various forms of hyaluronidases have been prepared and approved for therapeutic use in humans. For example, animal-derived hyaluronidase preparations include Vitrase® (ISTA Pharmaceuticals), a purified ovine testicular hyaluronidase, and Amphadase® (Amphastar Pharmaceuticals), a bovine testicular hyaluronidase. Hylenex® (Halozyme Therapeutics) is a human recombinant hyaluronidase produced by genetically engineered Chinese Hamster Ovary (CHO) cells containing nucleic acid encoding for soluble rHuPH20. Approved therapeutic uses for hyaluronidase include use as an adjuvant to increase the absorption and dispersion of other injected drugs, for hypodermoclysis (subcutaneous fluid administration), and as an adjunct in subcutaneous urography for improving resorption of radiopaque agents. In addition to these indications, hyaluronidases, including sHuPH20, can be used as a therapeutic or cosmetic agent for the treatment of additional diseases and conditions.

As noted above, hyaluronidase is a spreading or diffusing substance which modifies the permeability of connective tissue through the hydrolysis of hyaluronic acid, a polysaccharide found in the intercellular ground substance of connective tissue, and of certain specialized tissues, such as the umbilical cord and vitreous humor. When no spreading factor is present, materials injected subcutaneously, such as drugs, proteins, peptides and nucleic acid, spread very slowly. Co-injection with hyaluronidase, however, can cause rapid spreading. The rate of diffusion is proportional to the amount of enzyme, and the extent of diffusion is proportional to the volume of solution. Absorption and dispersion of injected drugs and agents can be enhanced by adding 10-1000 units hyaluronidase to the injection solution. In some examples, 150 U hyaluronidase is added. Hyaluronidases have multiple uses, including and in addition to their use as a spreading agent. Hyaluronidase is commonly used, for example, for peribulbar block in local anesthesia prior ophthalmic surgery. The presence of the enzyme prevents the need for additional blocks and speeds the time to the onset of akinesia (loss of eye move-

ment). Peribulbar and sub-Tenon's block are the most common applications of hyaluronidase for ophthalmic procedures. Hyaluronidase also can promote akinesia in cosmetic surgery, such as blepharoplasties and face lifts. Exemplary therapeutic and cosmetic uses for hyaluronidase are described below.

a. Use as a Spreading Agent

Hyaluronidases, such as soluble rHuPH20 produced using the methods described herein, can be used to promote or enhance the delivery agents and molecules to any of a variety of mammalian tissues in vivo. It can be used to facilitate the diffusion and, therefore, promote the delivery, of small molecule pharmacologic agents as well as larger molecule pharmacologic agents, such as proteins, nucleic acids and ribonucleic acids, and macromolecular compositions than can contain a combination of components including, but not limited to, nucleic acids, proteins, carbohydrates, lipids, lipid-based molecules and drugs. For example, molecules and macromolecular complexes ranging from about 10 nm to about 500 nm in diameter, can exhibit dramatic improvements in delivery through interstitial spaces when the interstitial space has been previously, or is coincidentally, exposed to hyaluronidase (see e.g. U.S. patent application Ser. Nos. 10/795,095, 11/065,716 and 11/238,171).

Examples of pharmaceutical, therapeutic and cosmetic agents and molecules that can be administered with hyaluronidase include, but are not limited to, anesthetics; anti-metabolites, anti-neoplastics and other anti-cancer agents; anti-virals; anti-infectives, including anti-bacterials and other antibiotics, anti-fungals and other anti-infectives; immunomodulatory agents; steroidal and non-steroidal anti-inflammatories; beta blockers; sympathomimetics; ducosanoids, prostaglandins and prostaglandin analogs; miotics, cholinergics and anti-cholinesterases; anti-allergens and decongestants; hormonal agents; growth factors; immunosuppressants; vaccines and toxoids; immune sera; antibodies; and any combination thereof. In one example, soluble rHuPH20 is administered with a cathepsin, such as cathepsin L.

b. Use in Hypodermoclysis

Hypodermoclysis, the infusion of fluids and electrolytes into the hypodermis of the skin, is a useful and simple hydration technique suitable for mildly to moderately dehydrated adult patients, especially the elderly. Although considered safe and effective, the most frequent adverse effect is mild subcutaneous edema that can be treated by local massage or systemic diuretics. Approximately 3 L can be given in a 24-hour period at two separate sites. Common infusion sites include the chest, abdomen, thighs and upper arms. Solutions used in hypodermoclysis include, for example, normal saline, half-normal saline, glucose with saline and 5% glucose. Potassium chloride also can be added to the solution. The addition of hyaluronidase to the solution can enhance fluid absorption and increase the overall rate of administration.

c. Use in Vitrectomy and Ophthalmic Disorders and Conditions

Hyaluronidase can be used to minimize the detachment or tearing of the retina during vitrectomy. This could cause, for example, the vitreous body to become uncoupled or "disinserted" from the retina, prior to removal of the vitreous body. Such disinsertion or uncoupling of the vitreous body can minimize the likelihood that further tearing or detachment of the retina will occur as the vitreous body is removed.

Hyaluronidase can be used for various ophthalmic applications, including the vitrectomy adjunct application described in U.S. Pat. No. 5,292,509. The use of a highly purified hyaluronidase, such as, for example, soluble rHuPH20 produced and purified by the methods described

herein, is preferable for intraocular procedures to minimize immunogenicity and toxicity. In some examples, a pegylated hyaluronidase can be used to prolong residence within the vitreous and prevent localized uptake.

Hyaluronidases can be used to treat and/or prevent ophthalmic disorders by, for example, preventing neovascularization and increasing the rate of clearance from the vitreous of materials toxic to the retina. Hyaluronidase can be administered in an amount effective to liquefy the vitreous humor of the eye without causing toxic damage to the eye. Liquefaction of the vitreous humor increases the rate of liquid exchange from the vitreal chamber. This increase in exchange removes the contaminating materials whose presence can cause ophthalmologic and retinal damage.

Hyaluronidase also can be used to reduce postoperative pressure. Hyaluronic acid has been used in eye primarily as a spacer during cataract and intraocular lens surgical procedures. It also is used in other ocular surgical procedures such as glaucoma, vitreous and retina surgery and in corneal transplantation. A common side effect occurring in postoperative cataract patients is a significant early, and occasionally prolonged, rise in intraocular pressure. Such a condition is sometimes serious, especially in patients with glaucomatous optic disc changes. Hyaluronidase can be co-administered with hyaluronic acid to the eye prior to surgery to reduce postoperative pressure in the eye. The hyaluronidase is administered in an amount effective to reduce the intraocular pressure to pre-operative levels by breaking down the hyaluronic acid without decreasing its effectiveness during surgery nor causing side effects in the patient (U.S. Pat. No. 6,745,776).

Hyaluronidase also can be administered to patients with glaucoma to remove glycosaminoglycans from the trabecular meshwork and reduce intraocular pressure, and can be applied to the vitreous to promote the resolution of vitreous hemorrhages (i.e. extravasation of blood into the vitreous), which can occur in connection with conditions such as diabetic retinopathy, retinal neovascularization, retinal vein occlusion, posterior vitreous detachment, retinal tears, ocular traumas and the like. The presence of vitreous hemorrhages, which are typically slow to resolve, can delay, complicate or prevent procedures that require the retina to be visualized through the vitreous for diagnosis and/or for treatment procedures such as laser photocoagulation and the like which are often primary treatments for conditions such as proliferative diabetic retinopathy.

d. Use in Gene Therapy

The efficacy of most gene delivery vehicles *in vivo* does not correspond to the efficacy found observed *in vitro*. Glycosaminoglycans can hinder the transfer and diffusion of DNA and viral vectors into many cell types. The levels such extracellular matrix material can hinder the process considerably. Administration of hyaluronidase can open channels in the extracellular matrix, thus enhancing delivery of gene therapy. For example, hyaluronidase can be administered with collagenase to facilitate transduction of DNA *in vivo* (Dubensky et al. (1984) *Proc Natl Acad Sci USA* 81(23): 7529-33). Hyaluronidase also can enhance gene therapy using adeno-associated virus (Favre et al. (2000) *Gene Therapy* 7(16):1417-20). The channels opened following administration of hyaluronidase are of a size that typically enhance diffusion of smaller molecules such as retroviruses, adenoviruses, adeno-associated viruses and DNA complexes (as well as other therapeutic and pharmacological agents of interest). The pores are not so large, however, as to promote the dislocation and movement of cells.

In some examples, viruses can be engineered to express hyaluronidase to facilitate their replication and spread within

a target tissue. The target tissue can be, for example, a cancerous tissue whereby the virus is capable of selective replication within the tumor. The virus also can be a non-lytic virus wherein the virus selectively replicates under a tissue specific promoter. As the viruses replicate, the co-expression of hyaluronidase with viral genes can facilitate the spread of the virus *in vivo*.

e. Cosmetic Uses

Hyaluronidases can be by administered to remove glycosaminoglycans involved in the accumulation of cellulite and to promote lymphatic flow. In some examples, human hyaluronidases, such as for example, soluble rHuPH20, are used for the treatment of cellulite. The hyaluronidase can be administered through repeated subcutaneous injections, through transdermal delivery in the form of ointments or creams or through the use of injectable slow release formulations to promote the continual degradation of glycosaminoglycans and prevent their return.

Hyaluronidase also can be used to treat conditions such as "pigskin" edema or "orange peel" edema. Hyaluronidases can effect depolymerization of the long mucopolysaccharide chains that can accumulate in the dermis and which are responsible for the retention of bound water and of the slowing, by capillary compression, of the diffusion of organic liquids, which eliminate metabolic wastes. Such retention of water and wastes associated with fat overloading of the lipocytes, constitutes classical "pigskin" edema or "orange peel" edema. Depolymerization can cut the long chains of mucopolysaccharides into shorter chains, resulting in the elimination of the bound water and wastes and restoration of the venous and lymphatic circulation, culminating in the disappearance of local edema.

f. Use in Organ Transplantation

The content of hyaluronic acid in an organ can increase with inflammation. An increased concentration of hyaluronic acid has been observed in tissue from different organs characterized by inflammatory-immunological injury such as alveolitis (Nettelbladt et al. (1991) *Am. Rev. Resp. Dis.* 139: 759-762) and myocardial infarction (Waldenström et al. (1991) *J. Clin. Invest.* 88(5): 1622-1628). Other examples include allograft rejection after a renal (Ha'Ilgren et al. (1990) *J. Exp. Med.* 171: 2063-2076; Wells et al. (1990) *Transplantation* 50: 240-243), small bowel (Wallander et al. (1993) *Transplant. Int.* 6: 133-137) or cardiac (Haellgren et al. (1990) *J Clin Invest* 185:668-673) transplantation; or a myocardial inflammation of viral origin (Waldenström et al. (1993) *Eur. J. Clin. Invest.* 23: 277-282). The occurrence of interstitial edemas in connection with the grafting of an organ constitutes a severe problem in the field of transplantation surgery. Grafts with interstitial edemas can swell to such a degree that the function is temporarily be lost. In some instances, the swelling can cause disruption of the kidney, resulting in a massive hemorrhage. Hyaluronidases can be used to degrade accumulated glycosaminoglycans in an organ transplant. Removal of such glycosaminoglycans promotes removal of water from the graft and thus enhances organ function.

g. Use in Cancer Treatment

Hyaluronidase has direct anticarcinogenic effects. Hyaluronidase prevents growth of tumors transplanted into mice (De Maeyer et al., (1992) *Int. J. Cancer* 51:657-660) and inhibits tumor formation upon exposure to carcinogens (Pawlowski et al. (1979) *Int. J. Cancer* 23:105-109). Hyaluronidase is effective as the sole therapeutic agent in the treatment of brain cancer (gliomas) (WO 198802261). In addition to these effects, hyaluronidases also can be used to enhance penetration of chemotherapeutic agents into solid tumors. They can be injected intratumorally with anti-cancer agents

or intravenously for disseminated cancers or hard to reach tumors. The anticancer agent can be a chemotherapeutic, an antibody, a peptide, or a gene therapy vector, virus or DNA. Additionally, hyaluronidase can be used to recruit tumor cells into the cycling pool for sensitization in previously chemorefractory tumors that have acquired multiple drug resistance (St Croix et al., (1998) *Cancer Lett* September 131(1): 35-44). Hyaluronidases, such as, for example soluble rHuPH20, also can enhance delivery of biologics such as monoclonal antibodies, cytokines and other drugs to tumors that accumulate glycosaminoglycans.

Hyaluronidases can also be used to increase the sensitivity of tumors that are resistant to conventional chemotherapy. For example, hyaluronidase, such as soluble rHuPH20, can be administered to a patient having a tumor associated with a HYAL1 defect in an amount effective to increase diffusion around the tumor site (e.g., to facilitate circulation and/or concentrations of chemotherapeutic agents in and around the tumor site), inhibit tumor cell motility, such as by hyaluronic acid degradation, and/or to lower the tumor cell apoptosis threshold. This can bring the tumor cell(s) to a state of anoikis, which renders the tumor cell more susceptible to the action of chemotherapeutic agents. Administration of hyaluronidase can induce responsiveness of previously chemotherapy-resistant tumors of the pancreas, stomach, colon, ovaries, and breast (Baumgartner et al. (1988) *Reg. Cancer Treat.* 1:55-58; Zanker et al. (1986) *Proc. Amer. Assoc. Cancer Res.* 27:390).

In one example, hyaluronidases are used in the treatment of metastatic and non-metastatic cancers, including those that have decreased endogenous hyaluronidase activity relative to non-cancerous cells. Hyaluronidases can be used as a chemotherapeutic agent alone or in combination with other chemotherapeutics. Exemplary cancers include, but are not limited to, small lung cell carcinoma, squamous lung cell carcinoma, and cancers of the breast, ovaries, head and neck, or any other cancer associated with depressed levels of hyaluronidase activity or decreased hyaluronic acid catabolism.

h. Use in Treatment of Glycosaminoglycan Accumulation in the Brain

Hyaluronic acid levels are elevated in a number of cerebrospinal pathologic conditions. Levels of cerebrospinal hyaluronic acid are normally less than 200 µg/L in adults (Laurent et al. (1996) *Acta Neurol Scand* September 94(3): 194-206), but can elevate to levels of over 8000 µg/L in diseases such as meningitis, spinal stenosis, head injury and cerebral infarction. Hyaluronidases, such as, for example, soluble rHuPH20, can be utilized to degrade critically elevated levels of substrate.

The lack of effective lymphatics in the brain also can lead to life threatening edema following head trauma. Hyaluronic acid accumulation is a result of increased synthesis by hyaluronic acid synthases and decreased degradation. Accumulation of hyaluronic acid can initially serve the beneficial purpose of increasing water content in the damaged tissue to facilitate leukocyte extravasation, but continued accumulation can be lethal. Administration of hyaluronidase, such as intrathecally or intravenously, to a patient suffering from head trauma can serve to remove tissue hyaluronic acid accumulation and the water associated with it.

Hyaluronidases also can be used in the treatment of edema associated with brain tumors, particularly that associated with glioblastoma multiform. The edema associated with brain tumors results from the accumulation of hyaluronic acid in the non-cancerous portions of the brain adjacent the tumor. Administration of hyaluronidase to the sites of hyaluronic acid accumulation (e.g., by intravenous injection or via a

shunt) can relieve the edema associated with such malignancies by degrading the excess hyaluronic acid at these sites.

i. Use in Treatment of Glycosaminoglycan Accumulation in Cardiovascular Disease

Hyaluronidase can be used in the treatment of some cardiovascular disease. Administration of hyaluronidase in animal models following experimental myocardial infarct can reduce infarct size (Maclean, et al (1976) *Science* 194(4261): 199-200). One proposed mechanism by which this can occur is by reducing hyaluronic acid accumulation that occurs following ischemia reperfusion. Reduction of infarct size is believed to occur from increased lymph drainage and increased tissue oxygenation and reduction of myocardial water content.

Hyaluronidases also can be used to limit coronary plaques from arteriosclerosis. Such plaques accumulate glycosaminoglycans and mediate macrophage and foam cell adhesion (Kolodgie et al. (2002) *Arterioscler Thromb Vasc Biol.* 22(10):1642-8).

j. Use in Pulmonary Disease

Levels of hyaluronic acid in bronchoalveolar lavages (BAL) from normal individuals are generally below 15 ng/ml. However, hyaluronic acid levels in BAL rise dramatically in conditions of respiratory distress (Bjermer et al. (1987) *Br Med J (Clin Res Ed)* 295(6602):803-6). The increased hyaluronic acid in the lung can prevent oxygen diffusion and gas exchange as well as activating neutrophil and macrophage responses. Purified preparations of soluble rHuPH20, such as those produced using the methods provided herein, can be delivered by either pulmonary or intravenous delivery to patients presenting with such conditions to reduce hyaluronan levels. Hyaluronidases also can be administered to patients suffering from other pulmonary complications that are associated with elevated glycosaminoglycans or to enhance the delivery of other co delivered molecules to the lung.

k. Other Uses

In further examples of its therapeutic use, hyaluronidase can be used for such purposes as an antidote to local necrosis from paravenous injection of necrotic substances such as vinka alkaloids (Few et al. (1987) *Amer. J. Matern. Child Nurs.* 12, 23-26), treatment of ganglion cysts (Paul et al. (1997) *J Hand Surg.* 22 (2): 219-21) and treatment of tissue necrosis due to venous insufficiency (Elder et al. (1980) *Lancet* 648-649). Hyaluronidases also can be used to treat ganglion cysts (also known as a wrist cyst, Bible cyst, or dorsal tendon cyst), which are the most common soft tissue mass of the hand and are fluid filled sacs that can be felt below the skin.

Hyaluronidases can be used in the treatment of spinal cord injury by degrading chondroitin sulfate proteoglycans (CSPGs). Following spinal cord injury, glial scars containing CSPGs are produced by astrocytes. CSPGs play a crucial role in the inhibition of axon growth. In addition, the expression of CSPG has been shown to increase following injury of the central nervous system (CNS). Hyaluronidases also can be utilized for the treatment of herniated disks in a process known as chemonucleolysis. Chondroitinase ABC, an enzyme cleaving similar substrates as hyaluronidase, can induce the reduction of intradiscal pressure in the lumbar spine. There are three types of disk injuries. A protruded disk is one that is intact but bulging. In an extruded disk, the fibrous wrapper has torn and the NP has oozed out, but is still connected to the disk. In a sequestered disk, a fragment of the NP has broken loose from the disk and is free in the spinal canal. Chemonucleolysis is typically effective on protruded and extruded disks, but not on sequestered disk injuries.

D. Soluble rHuPH20-Expressing Cells

The methods described herein can be used to generate and purify large quantities of soluble rHuPH20. Soluble rHuPH20 is expressed in CHO cells that are grown in large-scale cell culture. Expression is effected using an expression vector that contains the nucleotide sequence encoding the sequence of amino acids set forth in SEQ ID NO:3 (corresponding to amino acids 1 to 482 of the precursor human PH20 polypeptide set forth in SEQ ID NO:1). Following translation, the 35 amino acid signal sequence is cleaved and soluble rHuPH20 is secreted into the medium. The vector also contains an IRES downstream of the soluble rHuPH20 encoding region, a mouse dihydrofolate reductase gene and the SV40 pA sequence. The expression vector was introduced into DG44 cells, which are dihydrofolate reductase deficient (dhfr-) that have been adapted to grow in suspension culture in a chemically defined, animal product-free medium. The resulting soluble rHuPH20-expressing cells include those described in Examples 1 and 4, below, and include cells designated 3D35M, 2B2, 3E10B, 1B3, 5C1, 1G11 and 2G10 cells.

Other cells can be used to produce hyaluronidases similar to rHuPH20. Generally, protein expression systems suitable for the introduction of critical N-linked glycosylation residues on hyaluronidases are used. Such cells include, for example, yeast cells, fungal cells, plant cells, insect cells and mammalian cells. Many cell lines are available for mammalian expression including mouse, rat human, monkey, chicken and hamster cells. Exemplary cell lines include but are not limited to CHO (including DG44 cells and CHO-S cells), Balb/3T3, HeLa, MT2, mouse NSO (nonsecreting) and other myeloma cell lines, hybridoma and heterohybridoma cell lines, lymphocytes, fibroblasts, Sp2/0, COS, NIH3T3, HEK293, 293S, 2B8, and HKB cells. Cell lines also are available adapted to serum-free media, which facilitates purification of secreted proteins from the cell culture media.

a. 3D35M Cells

Exemplary of soluble rHuPH20-expressing cells are 3D35M cells, described in Example 1, below, and U.S. Patent Publication Nos. 20040268425, 20050260186 and 20060104968. 3D35M cells are dihydrofolate reductase deficient (dhfr-) DG44 CHO cells that express soluble rHuPH20. The cells were transformed with an HZ24 expression vector having the nucleotide sequence set forth in SEQ ID NO:50. This vector contains a CMV promoter driving expression of nucleic acid encoding a 482 amino acid (SEQ ID NO:3) polypeptide that corresponds to amino acid positions 1 to 482 of the full length human PH20 set forth in SEQ ID NO:1. This includes a 35 amino acid N-terminal signal sequence. The vector also contains an internal ribosome entry site (IRES) after the PH20-encoding sequence, followed by a mouse dihydrofolate reductase gene and the SV40 polyadenylation sequence. Following translation, the 482 amino acid polypeptide is processed to remove the 35 amino acid signal sequence, resulting in the secretion of soluble rHuPH20.

Characterization of 3D35M cells demonstrated that the nucleic acid region encoding soluble rHuPH20 is present in the cells at a copy number of approximately 318 copies/cells. Soluble rHuPH20 produced from 3D35M cells by the methods herein is a mixture of species that can include one or more of the polypeptides having sequences set forth in SEQ ID NOS:4-9. In an exemplary characterization of these species (described in Example 11), the species set forth in SEQ ID NO:4 was present at an abundance of 0.2%, the species set forth in SEQ ID NO:5 (corresponding to amino acids 1 to 446 of SEQ ID NO:4) was present at an abundance of 18.4%, the

species set forth in SEQ ID NO:6 (corresponding to amino acids 1 to 445 of SEQ ID NO:4) was present at an abundance of 11.8%, the species set forth in SEQ ID NO:7 (corresponding to amino acids 1 to 444 of SEQ ID NO:4) was present at an abundance of 56.1%; and the species set forth in SEQ ID NO:8 (corresponding to amino acids 1 to 443 of SEQ ID NO:4) was present at an abundance of 13.6%. Such heterogeneity in the soluble rHuPH20 preparation is likely a result of C-terminal cleavage by peptidases present during the production and purification methods provided herein.

The 3D35M cells can be grown in cell culture medium with or without methotrexate. Additional supplements, such as glutamine, also can be added. In some examples, the cells are grown in cell culture medium containing, for example, 50 nM, 100 nM, 500 nM, 1 or 2 μ M methotrexate and lacking hypoxanthine and thymidine. In one example, 3D35M cells are cultured at 37° C. in 5-7% CO₂ in culture medium (such as CD CHO Medium, Invitrogen) without hypoxanthine and thymidine and with 100 nM methotrexate and glutamine or a glutamine substitute, such as L-alanyl-L-glutamine, a stabilized, dipeptide form of L-glutamine. Other cell culture media appropriate for CHO cells can be used to culture 3D35M cells including, but not limited to, Dulbecco's modified Eagle's medium (DMEM), Eagle's Minimum essential medium (EMEM), Iscove's modified Eagle's medium (IMEM), F12 and RPMI. 3D35M cells grown under such conditions in shaking flasks can produce in excess of 1000 units/mL hyaluronidase activity. When cultured in a bioreactor, such as described in Example 3, below, 3D35M cells can produce soluble rHuPH20 with enzymatic activity in excess of 2000 units/mL.

b. 2B2 Cells

Exemplary of soluble rHuPH20-expressing cells for production of rHuPH20 in the methods provided herein are described in Example 4 and designated 2B2 cells. 2B2 cells were generated by adapting 3D35M cells to higher methotrexate levels (i.e. 20 μ M) and selecting clones that grew in the higher methotrexate concentration. This adaptation increased the hyaluronidase activity produced by the cells. DG44 cells are dihydrofolate reductase-deficient (dhfr-) and, therefore, cannot make nucleosides. The expression vector present in 3D35M and 2B2 cells contains, in addition to the PH20 gene, the coding sequence for mouse dihydrofolate reductase. Methotrexate is a strong competitive dihydrofolate reductase inhibitor. Therefore, by increasing the concentration of methotrexate in the culture media, the hyaluronidase-expressing cells are forced to produce more mouse dihydrofolate reductase to remain viable. This can be effected by, for example, gene amplification or rearrangement of the integrated DNA to a more stable and productive arrangement. Thus, forcing an increase in the production of mouse dihydrofolate reductase also can result in an increase in the production of sHuPH20. A comparison of enzymatic activity of soluble rHuPH20 produced by 2B2 cells and 3D35M cells demonstrated that activity was typically between 80% and 100% higher in 2B2 cells (see e.g. Example 5, below) compared to 3D35M cells.

2B2 cells were selected from amongst the cell clones that were isolated following selection with 20 μ M methotrexate as the cell line that produced soluble rHuPH20 having the greatest enzymatic activity (see, e.g. Example 4). When characterized, it was observed that the nucleic acid region encoding soluble rHuPH20 was present in 2B2 cells at a copy number of approximately 206 copies/cell. Southern blot analysis of Spe I-, Xba I- and BamH I/Hind III-digested genomic 2B2 cell DNA using a probe specific for the nucleic acid region encoding soluble rHuPH20 revealed the following restriction digest profile: one major hybridizing band of ~7.7 kb and four

minor hybridizing bands (~13.9, ~6.6, ~5.7 and ~4.6 kb) with DNA digested with Spe I; one major hybridizing band of ~5.0 kb and two minor hybridizing bands (~13.9 and ~6.5 kb) with DNA digested with Xba I; and one single hybridizing band of ~1.4 kb observed using 2B2 DNA digested with BamH I and

UHind III. 2B2 cells can be grown in cell culture medium with or without methotrexate. Additional supplements, such as glutamine, insulin and yeast extract also can be added. In some examples, the cells are grown in cell culture medium containing, for example, 50 nM, 100 nM, 500 nM, 1 μ M, 2 μ M, 10 μ M, 20 μ M or more methotrexate and lacking hypoxanthine and thymidine. In one example, 2B2 cells are cultured at 37° C. in 5-7% CO₂ in culture medium (such as CD CHO Medium, Invitrogen) without hypoxanthine and thymidine and with 20 μ M methotrexate and glutamine or L-alanyl-L-glutamine, a stabilized, dipeptide form of L-glutamine. Other cell culture media appropriate for CHO cells can be used to culture 2B2 cells, including, but not limited to, Dulbecco's modified Eagle's medium (DMEM), Eagle's Minimum essential medium (EMEM), Iscove's modified Eagle's medium (IMEM), F12 and RPMI. 2B2 cells grown under such conditions in shaking flasks can produce in excess of 3000 units/mL hyaluronidase activity. When cultured in a bioreactor, such as described in Example 8, below, 2B2 cells can produce soluble rHuPH20 having enzymatic activity in excess of 17000 units/mL hyaluronidase activity.

Soluble rHuPH20 produced from 2B2 cells by the methods herein is a mixture of species of polypeptides having sequences set forth in SEQ ID NOS:4-9. In an exemplary characterization the soluble rHuPH20 product produced by 2B2 cells (described in Example 11), the species set forth in SEQ ID NO:4 was present at an abundance of 1.9%, the species set forth in SEQ ID NO:5 (corresponding to amino acids 1 to 446 of SEQ ID NO:4) was present at an abundance of 46.7%, the species set forth in SEQ ID NO:6 (corresponding to amino acids 1 to 445 of SEQ ID NO:4) was present at an abundance of 16.7%, the species set forth in SEQ ID NO:7 (corresponding to amino acids 1 to 444 of SEQ ID NO:4) was present at an abundance of 27.8%; and the species set forth in SEQ ID NO:8 (corresponding to amino acids 1 to 443 of SEQ ID NO:4) was present at an abundance of 6.9%. As noted for soluble rHuPH20 produced from 3D35M cells, the heterogeneity in the soluble rHuPH20 preparation from 2B2 cells is likely a result of C-terminal cleavage by peptidases present during the production and purification methods provided herein.

E. Cell Culture Expansion

The methods described herein employ bioreactors to grow large volumes of cell culture to produce large quantities of soluble rHuPH20. As described in detail below, these methods include a cell expansion phase, a protein production phase, a protein concentration and buffer exchange phase, and a purification phase. The soluble rHuPH20-expressing cells, such as 2B2 cells, are initially expanded from an original inoculum, such as an aliquot of cells from a working cell bank (WCB) or master cell bank (MCB), to a larger volume prior to culture in the bioreactor for the production phase. The final culture volume in the expansion phase is directly proportional to the volume of the bioreactor used in the following production phase. Typically, a larger bioreactor is inoculated using a larger final culture volume from the expansion phase than is a smaller bioreactor.

The soluble rHuPH20-expressing cells are expanded through a series of cultures, each increasing in volume from

the previous one, and each being used as the inoculum for the subsequent culture. Exemplary of such cells are 2B2 cells. The original inoculum is typically one in which the purity and identity of the cells and the cell number are defined. These cells can be stored frozen, such as at -20° C., -70° C. or -80° C., or can be maintained in liquid media at, for example, 4° C., or maintained in culture at, for example, 37° C. In some instances, the original inoculum is a master cell bank or working cell bank aliquot that has been stored frozen. In such cases, the inoculum is thawed, such as in a 37° C. waterbath. The original cell inoculum is typically centrifuged and the cells are resuspended in an appropriate cell culture media. For example, 2B2 cells can be resuspended in, and subsequently cultured in, basal media, such as CD CHO media (Invitrogen), or reconstituted powdered CD CHO AGT™ media (Invitrogen), supplemented with 8 mM glutamine or L-alanyl-L-glutamine and 20 μ M methotrexate. In another example, cells can be grown in basal media supplemented with 8 mM glutamine or L-alanyl-L-glutamine and 100 mM methotrexate. Any other suitable cell culture media also can be used to expand hyaluronidase-expressing cells. For example, cells can be cultured in Dulbecco's modified Eagle's medium (DMEM), Eagle's Minimum essential medium (EMEM), Iscove's modified Eagle's medium (IMEM), F12, RPMI, or other chemically-defined or undefined media, with or without additional supplements. Typically, the cells are grown in serum-free media, but also can be grown in media containing serum. One of skill in the art could prepare cell culture media using other basal cell culture media to which various nutrients can be supplemented to make the cell culture media in which soluble rHuPH20-expressing cells are cultured.

The cell inoculum is added to the first of a series of increasing volumes of cell culture media, thus expanding the cell culture. Following the initial inoculation, the cells are expanded in a humidified incubator or bioreactor at an appropriate temperature with an appropriate amount of CO₂. Typically, the amount of CO₂ is between 4% and 9%, typically between 6.0% and 8.0%, such as 7.0% and the temperature is between 35° C. and 39° C., typically between 36° C. and 38° C., such as 37° C. For example, 2B2 and 3D35M cells can be grown in a 37° C. humidified incubator with 7% CO₂. The culture can be agitated, such as at 90-130 rpm, during this process. When the cells reach the desired density, such as, for example, greater than 1.0×10⁶ cells/mL (e.g. between 1.5×10⁶ cells/mL and 2.5×10⁶ cells/mL), the cell culture is used to inoculate a larger volume of fresh cell culture media. For example, cells can be inoculated into the next culture at a density of 4×10⁴ to 4×10⁶ cells/mL, typically 2×10⁵ to 6×10⁵ cells/mL, such as 4×10⁵ cells/mL. The process is repeated until the cells have been expanded to the desired volume and cell density for seeding of, for example, 4×10⁴ to 4×10⁶ cells/mL into the bioreactor.

In one example, soluble rHuPH20-expressing cells, such as 2B2 cells, are initially added to approximately 20 mL of fresh cell culture media in a 125 mL shaker flask, resulting in a culture volume of 20-30 mL, typically 25 mL. Following incubation at 37° C., 7% CO₂ and expansion of the cells to a density of greater than 1.5×10⁶ cells/mL, fresh media is added to the flask to expand the cell culture to 40 mL. The cells are incubated again until a density of greater than 1.5×10⁶ cells/mL is attained, after which the entire cell culture (approximately 40 mL) is added to fresh media to make 100 mL culture volume in a 125 mL spinner flask. This process is repeated by transferring the entire cell culture (approximately 100 mL) to a 250 mL spinner flask containing sufficient fresh media to make a final culture volume of 200 mL, then a 1 L spinner flask containing sufficient fresh media to make a final

culture volume of 800 mL, then a 6 L spinner flask containing sufficient fresh media to make a final culture volume a final volume of 5 L, and finally to a 36 L spinner flask containing sufficient fresh media to make a final culture volume of 32 L. Between each transfer, the cells are incubated until the culture reached a density of greater than 1.5×10^6 cells/mL. In some examples, a higher cell density is attained following incubation of the final 36 L spinner flask. For example, cells in the 36 L spinner flask can be expanded to a cell density of 3.55×10^6 cells/mL to 6.05×10^6 cells/mL. This process can be used to expand soluble rHuPH20-expressing cells before introduction to a 400 L bioreactor (300 L culture volume) for the protein production phase (see, e.g. Example 8). Smaller volumes of cell culture and different cell densities can be used for smaller bioreactors. For example, cells can be expanded to a volume of approximately 20 L with a cell density of between 1.8×10^6 cells/mL and 2.5×10^6 cells/mL prior to introduction to a 125 L bioreactor. In another example, soluble rHuPH20-expressing cells are expanded to a volume of approximately 800 mL with a cell density of between 1.5×10^6 cells/mL and 2.5×10^6 cells/mL prior to introduction to a 5 L bioreactor.

This process, like any of the processes described herein, also can be scaled-up by one of skill in the art for introduction of the cells into a bioreactor with a culture volume larger than 300 L. For example, the process can be scaled up for introduction of the cells into a bioreactor with a 2500 L culture volume, such as described in Example 12. Thus, in one example of the methods provided herein, following thawing, the cells are serially expanded through a 125 mL shaker flask (working volume of 20-30 mL, such as 25 mL), a 250 mL shaker flask (working volume of 45-55 mL, such as 50 mL), a 1 L shaker flask (working volume of 190-210 mL, such as 200 mL), two 2 L shaker flasks (working volume of 350-450 mL per flask, such as 400 mL per flask), six 2 L shaker flasks (working volume of 350-450 mL per flask, such as 400 mL per flask), a 25 L wave bioreactor (working volume of 14-16 L, such as 15 L), a 100 L wave bioreactor (working volume of 75-85 L, such as 80 L), and a 600 L seed bioreactor (working volume of 440-520 L, such as 480 L).

F. Protein Production

Following cell expansion, the soluble rHuPH20-expressing cells are transferred to a bioreactor for the production phase, during which large quantities of soluble rHuPH20 are secreted into the cell media. This phase typically is designed such that the cells growth is maximized in the first half of the bioreactor run, and soluble rHuPH20 production is maximized in the second half of the bioreactor run. The cells are provided with a series of feed media at particular time points throughout the production to regulate this process. The bioreactor conditions also are typically monitored to ensure optimal conditions are maintained throughout the process. The methods described herein for protein can be scaled up or down by one of skill in the art. Further, modifications to, for example, cell media, incubation times, feeding protocols. One of skill in the art can empirically determine the appropriate conditions for protein production for any given bioreactor and cell type.

Bioreactors of different sizes and designs can be utilized in the methods herein. Bioreactors with working volumes of between 1 L and 5000 L or more can be used in the methods herein. In some examples, a 5 L, 36 L, 125 L, 400 L or 3500 L bioreactor is used in the methods herein to culture cells in volumes of approximately 4 L, 23 L, 100 L, 300 L and 2500 L, respectively. Typically, the bioreactor is sterilized prior to the addition of cell culture media or cells. Sterilization can be

effected by autoclaving or otherwise treating with steam for some bioreactors, or by treatment with a sterilizing solution, such as dilute sodium hydroxide, dilute nitric acid or sodium hypochlorite. In some examples, the bioreactor is sterilized by steam at 121° C., 20 PSI for 30 minutes. Following sterilization, cell culture media can be added to the bioreactor and then assessed for contamination, such by microbial contamination, after a period of time to ensure that the sterilization process was effective.

The cell culture from the expansion phase, described above, is added to the sterilized bioreactor containing fresh cell culture media. Generally, the soluble rHuPH20-expressing cells are inoculated into the fresh cell culture media at a cell density of 10^4 to 10^7 cells/mL, such as 10^5 to 10^6 cells/mL. For example, cells can be inoculated at a density of 1×10^4 , 5×10^4 , 1×10^5 , 5×10^5 , 1×10^6 , 4×10^6 , or 1×10^7 cells/mL. In one example, soluble rHuPH20-expressing cells are inoculated at a cell density of 4×10^5 cells/mL. The total cell count following inoculation can be, therefore, between 10^7 and 10^{14} , depending on the size of the bioreactor and the cell density. For example, a cell culture volume of 100 L can have a cell density following inoculation of approximately 10^9 , 10^{10} , 10^{11} or 10^{12} cells. In another example, a cell culture volume of 2500 L can have a cell density following inoculation of approximately 10^{10} , 10^{11} , 10^{12} or 10^{13} cells.

The volumes of inoculating cell culture and fresh culture media used are dependent upon the size of the bioreactor and the cell density of the inoculum. For example, approximately 30 L of soluble rHuPH20-expressing cells, such as 2B2 cells, can be added to a 400 L bioreactor containing 230 L fresh cell culture media, for a total volume of approximately 260 L and an inoculation cell density of 4×10^5 cells/mL (total cell count of approximately 10^{11} cells). This can be scaled up or down as necessary, depending on the bioreactor. For example, approximately 20 L of soluble rHuPH20-expressing cells, such as 3D35M cells, can be added to a 125 L bioreactor containing 65 L fresh cell culture media, for a total volume of approximately 85 L and an inoculation cell density of 4×10^5 cells/mL (total cell count of approximately 3.4×10^{10} cells). In another example, for production in a 3500 L bioreactor, 2B2 cells are added to fresh cell culture media for a total cell culture volume of 1900-2300 L, such as 2100 L.

The fresh cell culture media contains the appropriate supplements to provide the necessary nutrients to the cells to promote cell growth. Supplements that can be added to the basal cell medium include, but are not limited to, glucose, insulin, sodium butyrate, yeast extract and glutamine or a glutamine substitute, such as L-alanyl-L-glutamine. In some instances, the basal medium contains sufficient glucose that no further glucose needs to be added. In other instances, glucose is added to the media later in the production process, such as in a subsequent feed media. The addition of insulin to the medium can promote cell growth and increase peak cell density. Glutamine or glutamine-substitutes, such as or L-alanyl-L-glutamine, can support cell cycle progression and also enhance cell growth. One of skill in the art can empirically determine the amount and quality of the nutrients that can be supplemented to the basal medium. In some examples, glutamine or glutamine-substitute is added to the basal cell culture medium at 1 mM, 2 mM, 3 mM, 4 mM, 5 mM, 6 mM, 7 mM, 8 mM, 9 mM, 10 mM, 15 mM or 20 mM. Insulin can be added to the cell culture medium at, for example, 0.5 mg/L to 50 mg/L, such as 1 mg/L to 40 mg/L, 2 mg to 30 mg/L, or 5 mg/L to 20 mg/L. For example, basal cell culture medium supplemented with 5 mg/L insulin and 8 mM L-alanyl-L-glutamine can be used as the fresh cell culture media into which the soluble rHuPH20-expressing cells are inoculated.

Additional supplements, such as antibiotics, anti-fungals, indicators, salts, vitamins, amino acids and growth factors also can be added.

The individual parameters of the bioreactor can be set to maintain optimal conditions throughout the protein production process. The specific parameters that can be set depend on the bioreactor used, and can include, but are not limited to, temperature, pH, dissolved oxygen, impeller speed, vessel pressure, air sparge and air overlay. In one example, the conditions of a 125 L bioreactor containing 100 L cell culture of 3D35M cells are set to; temperature: 37° C.; dissolved oxygen: 25%±10%; impeller speed: 50 RPM; vessel pressure: 3 psi; air sparge: 1 L/minute; air overlay: 1 L/minute, pH:7.2 In another example, the conditions of a 400 L bioreactor containing an initial cell culture volume of 260 L are set to; temperature: 37° C.; impeller speed 40-55 RPM; vessel pressure: 3 psi; air sparge: 0.5-1.5 L/minute; air overlay: 1 L/minute. In a further example, the conditions of a 3000 L bioreactor containing an initial culture volume of 2100 L are set to; temperature: 37° C. (or between 36.5° C. and 37.5° C.; impeller speed: 35 RPM (or 70-80 RPM); vessel pressure: 5 psi (or 3-7 psi); air sparge: 12 L/minute (or 11-13 L/minute); dissolved oxygen: 25%, or >25%; pH pre inoculation: 7.2 (or pH 7.1-7.3); pH post inoculation: ≤7.2 (or ≤7.3). One of skill in the art can empirically determine the appropriate conditions for growth of a particular soluble rHuPH20-expressing cell in a particular bioreactor.

The soluble rHuPH20-expressing cells are typically cultured in the bioreactor for between 10 and 25 days. In some examples, the soluble rHuPH20-expressing cells are cultured in the bioreactor for 12, 13, 14, 15 or 16 days before harvesting. In other examples, the cells are harvested when the viable cell count (VCC) falls to a particular level, such as, for example, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60% or 70%. In one example, the cells are harvested when the VCC is between 30% and 35%. In another example, the cells are harvested within 24 hours of the VCC dropping below 50%.

During the bioreactor culture, the cells can be grown as batch cultures, in which the culture is grown to completion without the addition of further nutrients. In other examples, the cells are grown as fed-batch cultures and provided with a series of feed media at particular time points to supplement nutrients and glucose throughout. In some instances, the nutrients provided in the cell culture medium into which the cells were inoculated have depleted by 3, 4, 5, 6, 7 days or more post-inoculation. Thus, providing additional nutrients or supplements can produce higher yields of protein than batch cultures. In one example, cells are provided with feed media on days 6, 9 and 11 post-inoculation. In another example, cells are provided with feed media on days 7, 9 and 11 post-inoculation. In a further example, cells are provided with feed media on days 5, 7, 9 and 11 post-inoculation. The volume of feed media added to the bioreactor culture can range between, for example, 0.5% and 20%, such as 1-20%, 2-15%, 3-10% or 4-5% of the cell culture volume. In some instances, the feed media is added at a volume equivalent to 4% of the cell culture volume.

The addition of various supplements to the feed media also can be used to regulate the growth and/or cell cycle of the cells. Exemplary nutrients and supplements that can be included in the feed media include, but are not limited to, glutamine or glutamine-substitute, such as L-alanyl-L-glutamine, insulin, yeast extract, glucose and sodium butyrate or sodium butyrate. Furthermore, the basal media used in the feed media also can be concentrated, thus providing additional nutrients, such as essential amino acids, that may have been depleted during cell culture. The basal media in the feed

media can be 2×, 3×, 4×, 5×, 6× or more concentrated. In other examples, the basal media is less concentrated, or the same concentration as the cell culture media in the bioreactor.

The supplements included in the feed media can be used to regulate cell growth and protein production. For example, the first feed media added to the cell culture can include nutrients that enhance cell cycle progression, cell growth and peak cell density. Subsequent feed medias can promote cell growth arrest and/or protein synthesis. The amount of each supplement in each feed media can vary, such as by increasing or decreasing from one feed media to the next, or can be the same from one feed media to the next. In some examples, the amount of a supplement is increased from one feed media to the next, such as by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, 200%, 300%, 400% or more. In other examples, the amount of a supplement is decreased from one feed media to the next, such as by 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more. In one example, a supplement is omitted from a feed media. In other examples, the amount of a supplement in the feed media stays the same. One of skill in the art can empirically determine the optimum amount of each supplement for each feed media to promote the desired amount of cell growth and protein production.

Exemplary supplements or nutrients that can be included in the feed media include, but are not limited to, glucose, glutamine or glutamine-substitute, such as L-alanyl-L-glutamine, insulin, and sodium butyrate. The type and amount of supplement added can influence cell growth and protein production. For example, insulin and glutamine or glutamine-substitute can be incorporated into the first feed media added to the cell culture to increase cell growth and peak cell density. Subsequent feed media can be designed to promote protein production more than cell growth. Supplements such as insulin can be excluded or reduced in amount, as can glutamine or glutamine-substitute, such as L-alanyl-L-glutamine. In contrast, supplements such as yeast extract that enhance protein synthesis can be increased in amount. In addition, supplements that enhance cell cycle arrest and, therefore, increased protein production, also can be included. Exemplary of such supplements is sodium butyrate.

In one example, insulin is added to one or more feed media. The addition of insulin can increase peak cell density by, for example, 2%, 5%, 10%, 15%, 20%, 25%, 30% or more. Although insulin can be incorporated into any feed media, typically, insulin is added to early feed media, such as the first feed media, or the first and second feed media, to promote maximal cell growth in the initial phase of the bioreactor run. For example, a feed media, such as the first feed media, can contain amount of insulin at or about 5 mg/L, 10 mg/L, 15 mg/L, 20 mg/L, 25 mg/L, 30 mg/L, 35 mg/L, 40 mg/L, 45 mg/L, 50 mg/L, 55 mg/L, 60 mg/L or more. In contrast, the amount of insulin added to later feed media can be reduced or can be completely omitted.

Glutamine or glutamine-substitute, such as L-alanyl-L-glutamine, also can be added to the feed media. In some instances, the amount of glutamine or glutamine-substitute added to the first feed media is more than the amount of glutamine or glutamine-substitute added to subsequent feed media. In particular examples, the amount of glutamine or glutamine-substitute added to each subsequent feed media is reduced compared to the amount added in the prior feed media. The optimal amount added to each feed media can be determined empirically by one of skill in the art, and can include, for example, concentrations of glutamine or

glutamine-substitute at or about 1 mM, 5 mM, 10 mM, 15 mM, 20 mM, 25 mM, 30 mM, 35 mM, 40 mM, 45 mM, 50 mM or more.

Typically, the basal media used in the feed media also is supplemented with glucose. The amount of glucose added to each feed media can be increased or decreased relative to the previous feed media, or can stay approximately constant. In some examples, the amount of glucose added to the feed media is or is about 10 g/L, 15 g/L, 20 g/L, 25 g/L, 30 g/L, 35 g/L, 40 g/L, 45 g/L, 50 g/L, 55 g/L, 60 g/L, 75 g/L, 80 g/L or more.

In addition, supplements that promote protein synthesis also can be included. Such nutrients include, for example, yeast extract. In some instances, the amount of yeast extract included in the feed media is increased during the bioreactor run. For example, the amount of yeast extract in the third feed media can be increased compared to the amount in the second feed media, which can be increased compared to the amount in the second feed media. In some examples, the amount of yeast extract added to the feed media is between 5 and 1000 g/L, such as or as about 10 g/L, 20 g/L, 30 g/L, 40 g/L, 50 g/L, 75 g/L, 100 g/L, 125 g/L, 150 g/L, 175 g/L, 200 g/L, 250 g/L, 300 g/L, 350 g/L, 400 g/L or more.

Supplements that enhance cell cycle arrest and, therefore, increase protein production, also can be included. Typically, such supplements are included in feed media that are added to the bioreactor later in the run and not included in the first feed media. For example, supplements that enhance cell cycle arrest can be added to the second feed media and subsequent feed media. Exemplary of such supplements is sodium butyrate. In some examples, the amount of sodium butyrate added to the feed media is between 0.1 g/L and 10 g/L, such as or as about 0.2 g/L, 0.3 g/L, 0.4 g/L, 0.5 g/L, 0.6 g/L, 0.7 g/L, 0.8 g/L, 0.9 g/L, 1.0 g/L, 1.1 g/L, 1.2 g/L, 1.3 g/L, 1.4 g/L, 1.5 g/L, 1.6 g/L, 1.7 g/L, 1.8 g/L, 1.9 g/L, 2.0 g/L, 2.5 g/L, 3.0 g/L, 3.5 g/L, or more.

Further, any one or more of the bioreactor conditions can be altered during the production phase to optimize protein production. In one example, the temperature is lowered. This can serve to promote cell cycle arrest, prolong cell viability (thereby increasing total protein production), and help stabilize the hyaluronidase that has been secreted. For example, the temperature of the bioreactor can be reduced at each feeding, such as from 37° C. to 36.5° C. on the second feeding, to 36° C. on the third feeding and to 35.5° C. on the fourth feeding. One of skill in the art can empirically determine the appropriate feed media and the time at which to provide the feed, as well as the appropriate conditions in the bioreactor.

In one example, cells are provided with feed media on days 6, 9 and 11 post-inoculation. In another example, cells are provided with feed media on days 7, 9 and 11 post-inoculation. In a further example, cells are provided with feed media on days 5, 7, 9 and 11 post-inoculation. The feed media provided at each time-point can be the same or different, and can include supplements such as, but not limited to, glucose, sodium butyrate, insulin, glutamine or a glutamine substitute and yeast extract. For example, 2B2 cells growing in a 260 L culture in a 400 L bioreactor can be provided with a first feed at day 5 containing 10.4 L of 4× basal media (e.g. CD CHO media) with 33 g/L Glucose, 32 mM L-alanyl-L-glutamine, 16.6 g/L Yeast extract and 33 mg/L Insulin, a second feed at day 7 containing 10.8 L of 2× basal media (e.g. CD CHO media), 33 g/L Glucose, 16 mM L-alanyl-L-glutamine, 33.4 g/L Yeast extract and 0.92 g/L Sodium Butyrate, a third feed at day 9 containing 10.8 L 1× basal media (e.g. CD CHO media), 50 g/L Glucose, 10 mM L-alanyl-L-glutamine, 50 g/L Yeast extract and 1.80 g/L Sodium Butyrate, and a fourth feed

at day 11 containing 1× basal media (e.g. CD CHO media), 33 g/L Glucose, 6.6 mM L-alanyl-L-glutamine, 50 g/L Yeast extract and 0.92 g/L Sodium Butyrate. This can be scaled up or down by one of skill in the art for production of rHuPH20 in larger or smaller bioreactors, respectively. Further, one of skill in the art can alter the amount of type of one more supplements added to the media to enhance cell growth and/or protein production.

In another example, the following feed media are provided to cells on days 5, 7, 9 and 11: Feed #1 Medium: basal media+33 g/L Glucose+26.6 mM L-alanyl-L-glutamine+83.3 g/L Yeastolate+33 mg/L rHuInsulin; Feed #2: basal media+33 g/L Glucose+13.4 mM L-alanyl-L-glutamine+166.7 g/L Yeastolate+0.92 g/L Sodium Butyrate; Feed #3: basal media+50 g/L Glucose+10 mM L-alanyl-L-glutamine+250 g/L Yeastolate+1.8 g/L Sodium Butyrate; Feed #4: basal media+33.3 g/L Glucose+6.7 mM L-alanyl-L-glutamine+250 g/L Yeastolate+0.92 g/L Sodium butyrate.

G. Cell Culture Harvest, Protein Concentration and Buffer Exchange

Following the protein production phase, the cells are harvested and the soluble rHuPH20 that has been secreted into the cell culture media is concentrated prior to initiation of the purification process. In addition to concentrating the protein, the cell culture media can be exchanged with an appropriate buffer at this time. Multiple systems and processes to effect protein concentration and buffer exchange are known in the art and can be used in the methods herein. Described below are exemplary methods of such, and one of skill in the art will recognize that these methods can be modified or substituted with other effective methods to achieve a satisfactory level of protein concentration and buffer exchange.

The cells are harvested from the bioreactor and processed through a cell removal and clarification system to separate the cell culture fluid containing the hyaluronidase from cells and cell debris. An example of such a system is one that contains a series of filters that allow only the protein to pass through and be collected. Any filter or series of filters capable of separating the hyaluronidase from cells and cell debris can be used. For example, the cell culture harvest can be passed through a series of capsule filters, such as polyethersulfone filters. These can have decreasing pore sizes to incrementally remove, for example, cells, cell debris and smaller particles, such as viruses. In some examples, a series of four filters with pore sizes of 8.0 μm, 0.65 μm, 0.22 μm and 0.22 μm is used to clarify the cell culture to obtain the harvested cell culture fluid (HCCF). Another example of a cell removal and clarification system that can be used in the methods herein is a series of filters that in the first stage contains four modules in parallel, each containing a layer of diatomaceous earth graded to 4-8 μm and a layer of diatomaceous earth graded to 1.4-1.1 μm, followed by a cellulose membrane. The second stage contains a single module containing a layer of diatomaceous earth graded to 0.1-0.11 μm and a layer of diatomaceous earth graded to <0.1 μm followed by a cellulose membrane, and the third stage is a 0.22 μm polyethersulfone capsule filter.

Once the cells and debris have been separated from the HCCF, the protein in the HCCF typically is concentrated and the cell culture media exchanged with an appropriate buffer. The protein can be concentrated by 2×, 3×, 4×, 5×, 6×, 7×, 8×, 9×, 10×, 11×, 12×, 13× or more. In some examples, the protein is concentrated 10×. In other examples, the protein is concentrated 6×. Any method of protein concentration known in the art can be utilized. Exemplary of such methods include concentration using tangential flow filtration (TFF) systems

with molecular weight cut off (MWCO) filters. For example, the clarified HCCF can be passed through a series of two 30 kDa MWCO spiral polyethersulfone filters to concentrate the protein 10x. In another example, the HCCF is passed through a series of four 30 kDa MWCO filters. For large-scale production of hyaluronidase, such as, for example, 100 L and 300 L cultures, filters with surface areas of between 0.5 and 5 square meters are typically employed for this purpose. In some examples, filters with a surface area of 1.2 square meters or 2.8 square meters are used.

A buffer exchange is performed following protein concentration. One of skill in the art can empirically determine an appropriate buffer. Exemplary of suitable buffers is a 10 mM Hepes, 25 mM NaCl, pH 7.0 buffer, or a 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 buffer. Following harvesting, concentration and buffer exchange, the concentrated protein solution is typically passed through another filter, such as a 0.22 µm capsule filter, before being stored in a sterile storage bag.

In some examples, the concentrated protein solution is treated to inactivate any residual virus contamination. Virus inactivation can be effected by any method known in the art. For example, the concentrated protein solution can be mixed with a 10% Triton X-100, 3% tri (n-butyl) phosphate (TNBP), to a final concentration of 1% Triton X-100, 0.3% TNBP, at room temperature for between 15 and 75 minutes. In some examples, the protein is exposed to the viral inactivation solution for 30-45 minutes.

H. Purification

The soluble rHuPH20 is purified from the concentrated protein solution using a series of purification steps. Many purification techniques are known in the art and can be utilized in the methods herein. Such methods can include, but are not limited to, chromatographic methods such as ion-exchange chromatography, size-exclusion chromatography, affinity chromatography (AC), high performance liquid chromatography (HPLC), reversed phase chromatography (RPC) and hydrophobic interaction chromatography (HIC), and gel filtration methods, or any combination thereof.

Exemplary of purification methods that are used for the methods herein is a combination of ion-exchange chromatography, hydrophobic interaction chromatography and affinity chromatography. In ion-exchange chromatography, the proteins can be separated from a complex solution or mixture based on electrostatic forces between charged functional groups of the proteins and charged functional groups of the chromatography-column matrix. Cation-exchange resins have negatively charged functional groups that attract positively charged functional groups of proteins, and anion-exchange resins have positively charged functional groups that attract negatively charged functional groups of proteins. Proteins bound through electrostatic forces to the matrix can be eluted by increasing the ionic strength of the buffer solution within the chromatography column over time. In hydrophobic interaction chromatography, a protein can be separated from a complex solution or mixture based on its hydrophobicity. A complex solution containing the protein is applied to a chromatography column equilibrated with a high salt buffer that facilitates binding of the protein to the resin. A salt-gradient mobile phase with decreasing ionic strength is then introduced into the chromatography column to release bound proteins from the matrix. Alternatively, hydrophobic interaction chromatography may separate a monomeric protein from a complex solution or mixture by binding hydrophobic impurities, including inactive dimers and aggregates of the protein, while permitting the monomeric protein to flow through the

chromatography column relatively unimpeded. In affinity chromatography, a proteins can be separated from a complex solution based on the affinity of the protein for a ligand or ligand-binding entity that is covalently bound to the matrix. Other proteins in the complex solution or mixture with weak affinity, or lacking affinity, for the ligand or ligand-binding entity flow through the chromatography column unimpeded, leaving the protein of interest bound to the matrix. The protein can then be eluted from the chromatography column by altering buffer conditions to decrease the affinity for the ligand or ligand-binding entity.

In one example, the soluble rHuPH20 is purified from the concentrated protein solution by sequential purification through a beaded crosslinked agarose column, such as a Q Sepharose™ column (ion-exchange chromatography), beaded crosslinked phenyl-substituted agarose column, such as a Phenyl Sepharose™ column (hydrophobic interaction chromatography), an Amino Phenyl Boronate column (affinity chromatography) and finally through a Hydroxyapatite column (ion-exchange chromatography). Each of these columns exhibit different binding properties with regards to hyaluronidase, such that the beaded crosslinked agarose column (e.g. Q Sepharose™ column) is a capture step (i.e. soluble rHuPH20 is bound to the resin while some other proteins flow through), the beaded crosslinked phenyl-substituted agarose (e.g. Phenyl Sepharose™ column) is a flow through step (i.e. soluble rHuPH20 flows through the column while some other proteins are captured), the Amino Phenyl Boronate column is another capture step, and the Hydroxyapatite column is a polishing step to further purify the soluble rHuPH20.

Prior to use, the columns are typically sterilized and the equilibrated. Sterilization can be effected by any method known in the art, including, but not limited to, sterilization with 1.0 M NaOH. Equilibration can be effected by the addition of an appropriate buffer to the column, such as a buffer similar to or the same as the buffer used to subsequently wash the column or the buffer in which the protein is contained in prior to loading. One of skill in the art can readily determine buffers suitable for use in equilibrating each column. Exemplary buffers are provided below. Between each chromatography step, the eluted protein can be filtered, such as through a 0.22 µm filter, to remove any contaminating microorganism or large aggregates. In some examples, the filtered eluate is stored, such as in sterile storage bags, prior to use in the next step. Following column chromatography, the purified hyaluronidase can subsequently be subjected to a virus removal step, followed by protein concentration and buffer exchange for final formulation. Exemplary purification methods are described in more detail below.

1. Beaded Crosslinked Agarose Column

The concentrated protein obtained from the of harvested cell culture fluid (HCCF) can be loaded onto a beaded crosslinked agarose column, such as, for example, a Q Sepharose™ column, which is a strong anion exchanger and captures soluble rHuPH20 while allowing other proteins to flow through. The bound soluble rHuPH20 can then be eluted using an appropriate buffer. The dimensions of the column used is typically dependent on the volume of concentrated protein obtained from the HCCF. For example, concentrated protein obtained from culture of hyaluronidase-expressing cells in a 100 L bioreactor culture can be loaded onto a column that is 20 cm high, 14 cm in diameter and contains 3 L resin. In another example, concentrated protein obtained from culture of soluble rHuPH20-expressing cells in a 300 L bioreactor culture can be loaded onto a column that is 29 cm high, 20 cm in diameter and contains 9 L resin. This can be

scaled up or down as necessary, depending on the volume of the concentrated protein solution and the expected amount of protein. For example, concentrated protein obtained from culture of soluble rHuPH20-expressing cells in a 20 L bioreactor culture can be loaded onto a Q Sepharose™ column that is 28 cm high, 7 cm in diameter and contains 1.1 L resin, and concentrated protein obtained from culture of soluble rHuPH20-expressing cells in a 2500 L bioreactor culture can be loaded onto a Q Sepharose™ column that is 26 cm high, 63 cm in diameter and contains 81 L resin.

Prior to loading with the protein, the column is typically equilibrated. Equilibration can be effected by passing through 1, 2, 3, 4, 5, 6, 7, 8, 9 or more column volumes of buffer. In some examples, 5 column volumes of buffer is passed through the column for equilibration. Buffers suitable for equilibration include those similar to the buffers that will be used to wash the column after the protein had been loaded. For example, a beaded crosslinked agarose column, such as a Q Sepharose™ column can be equilibrated with 10 mM Hepes, 25 mM NaCl, pH 7.5. Other neutral pH buffers can be used, as will be recognized by one of skill in the art.

After loading the protein concentrate, the column is washed and the protein eluted. Suitable buffers for washing such columns containing bound soluble rHuPH20 include, for example, 10 mM Hepes, 25 mM NaCl, pH 7.0; 10 mM Hepes, 50 mM NaCl, pH 7.0; and 10 mM Tris, 20 mM Na₂SO₄, pH 7.5. The column can be washed with one or more types of buffer. For example, the column can be washed with 20 mM Na₂SO₄, pH 7.5 and 10 mM Hepes, 50 mM NaCl, pH 7.0. Typically, washing is effected by passing through 1, 2, 3, 4, 5, 6, 7, 8, 9 or more column volumes of buffer. In some examples, 5 column volumes of buffer is used to wash the column. The soluble rHuPH20 is then eluted using a buffer with a higher salt concentration, such as for example, 10 mM Hepes, 400 mM NaCl, pH 7.0. In some examples, the absorbance at A₂₈₀ is monitored to determine when to collect the eluate, as any absorbance during this process generally indicates the presence of soluble rHuPH20. Thus, in one example, the eluate is collected when the absorbance begins reading is 0.025. Typically, the eluate is filtered through an appropriate filter, such as a 0.22 µm filter, before being stored, such as in a sterile storage bag.

2. Beaded Crosslinked Phenyl-substituted Agarose Column

Following purification through a beaded crosslinked agarose column, the protein solution can be subjected to hydrophobic interaction chromatography using a beaded crosslinked phenyl-substituted agarose column, such as a Phenyl Sepharose™ column, in which the soluble rHuPH20 flows through the column while other contaminating proteins are captured. The column used in the methods herein can range in size, depending on the volume and amount of protein being purified through it. Exemplary sizes include columns that are 29 cm high, 20 cm in diameter with 9 L resin for use in the purification of soluble rHuPH20 from cells grown in a 100 L bioreactor culture, columns that are 29 cm high, 30 cm in diameter with 19-21 L resin for use in the purification of hyaluronidase from cells grown in a 300 L bioreactor culture, and columns that are 35 cm high, 80 cm in diameter with 176 L resin for use in the purification of soluble rHuPH20 from cells grown in a 2500 L bioreactor culture. One of skill in the art can scale up or down as appropriate.

The sterilized beaded crosslinked phenyl-substituted agarose column, such as a Phenyl Sepharose™ column, can be equilibrated prior to loading of the protein with an appropriate buffer, such as, for example, 5 mM potassium phosphate, 0.5 M ammonium sulfate, 0.1 mM CaCl₂, pH 7.0. The protein

eluate from the Q Sepharose column purification also is supplemented with ammonium sulfate, potassium phosphate and CaCl₂. These can be supplemented to the protein to final concentrations of, for example, about 5 mM potassium phosphate, 0.5 M ammonium sulfate and 0.1 mM CaCl₂, pH 7.0. Following loading of the protein, 5 mM potassium phosphate, 0.5 M ammonium sulfate and 0.1 mM CaCl₂, pH 7.0 also is added to the column and the flow through filtered is collected, such as in a sterile bag.

3. Amino Phenyl Boronate Column

Following hydrophobic interaction chromatography, the column-purified protein can be loaded onto an Amino Phenyl Boronate column for further purification. Amino Phenyl boronate ligand-mediated chromatography differs from many other ligands used for affinity chromatography. Whereas most ligands bind to a particular binding site on a protein by a mixture of noncovalent interactions, phenyl boronate interacts predominantly by forming a temporary covalent bond with 1,2-cis-diol groups. The boronate ligand will bind to any molecule containing the appropriate group, including soluble rHuPH20, which is highly glycosylated.

The Amino Phenyl Boronate column used in the methods herein can range in size, depending on the volume and amount of protein being purified through it. Exemplary sizes include columns that are 29 cm high, 20 cm in diameter with 6.3 L resin for use in the purification of hyaluronidase from cells grown in a 100 L bioreactor culture, columns that are 29 cm high, 30 cm in diameter with 19-21 L resin for use in the purification of hyaluronidase from cells grown in a 300 L bioreactor culture, and, and columns that are 35 cm high, 80 cm in diameter with 176 L resin for use in the purification of hyaluronidase from cells grown in a 2500 L bioreactor culture. One of skill in the art can scale up or down as appropriate. Buffers suitable for equilibrating the Amino Phenyl Boronate column include, for example, buffers containing 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0.

Following loading of the Phenyl Sepharose column-purified protein onto the Amino Phenyl Boronate column, the column is washed with suitable wash buffers. Exemplary wash buffers include, but are not limited to, 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0, and 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0 and 20 mM bicine, 100 mM NaCl, pH 9.0. In one example, the Amino Phenyl Boronate column with the bound hyaluronidase is washed first with 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0, then with 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0 and finally with 20 mM bicine, 100 mM NaCl, pH 9.0. The bound hyaluronidase can then be eluted, such as with 50 mM Hepes, 100 mM NaCl, pH 7.0. One of skill in the art can modify one or more of the buffers to similarly effect purification. Typically, the eluted soluble rHuPH20 also is filtered to remove any microbial contamination or large aggregates.

4. Hydroxyapatite Column

Following Phenyl Boronate column chromatography, the protein solution containing the soluble rHuPH20 can be loaded onto a Hydroxyapatite column in a final polishing step. Hydroxyapatite is a crystalline form of calcium phosphate with the molecular formula Ca₁₀(PO₄)₆(OH)₂. It can be used as a polishing step to separate closely copurifying proteins, operating by mixed-mode ion exchange due to its inclusion of both positively and negatively charged moieties. Various hydroxyapatite chromatographic media are available commercially, and any available form of the material can be used in the methods herein. Examples of hydroxyapatites include, but are not limited to, those that are agglomerated to form particles and sintered at high temperatures into a stable

porous ceramic mass. The particle size can vary, such as ranging from about 1 μm to about 1,000 μm in diameter. The porosity also can vary, such as from about 100 Å to about 10,000 Å.

The Hydroxyapatite column used in the methods herein can range in size, depending on the volume and amount of protein being purified through it. Exemplary sizes include columns that are 20 cm high, 30 cm in diameter with 13 L resin for use in the purification of hyaluronidase from cells grown in a 300 L bioreactor culture, and columns that are 23 cm high, 80 cm in diameter with 116 L resin for use in the purification of hyaluronidase from cells grown in a 2500 L bioreactor culture. One of skill in the art can scale up or down as appropriate.

For the methods described herein, the Hydroxyapatite column can be equilibrated with 5 mM potassium phosphate, 200 mM NaCl or 5 mM potassium phosphate, 200 mM NaCl, 0.1 mM CaCl_2 , pH 7.0. Equilibration using solutions such as these make the column compatible with the partially-purified hyaluronidase, which itself is supplemented with potassium phosphate and CaCl_2 to final concentrations of 5 mM and 0.1 mM, respectively. Following loading of the protein onto the column, the column can be washed with, for example, 10 mM potassium phosphate, 100 mM NaCl, 0.1 mM CaCl_2 , pH 7.0, to remove any unbound contaminating proteins. The bound soluble rHuPH20 can then be eluted with an appropriate elution buffer. For example, elution can be effected by the addition of 70 mM potassium phosphate, pH 7.0. In some examples, the eluate is filtered, such as through a 0.22 μm filter.

6. Virus Removal, Protein Concentration and Buffer Exchange

The soluble rHuPH20 obtained flowing column chromatography can be subjected to post-purification steps that serve to formulate the protein in the desired buffer at the desired concentration. The protein also can be subjected to a viral removal step to ensure it is free from contamination and suitable for use as a therapeutic. Viral removal is typically effected with the use of a filter that allows only the soluble protein to pass through while trapping any viruses (and other contaminants that are equal to in size or larger than viruses). Such filters are available commercially, and any can be used in the methods herein. Pores sizes of filters useful for viral removal include, but are not limited to, 10 nm, 15 nm, 20 nm, 25 nm, 30 nm, 40 nm, 50 nm, 60 nm, 75 nm and 100 nm. In one example, the purified hyaluronidase is filtered through a filter containing 20 nm pores. The protein can be pumped into the filter by, for example, peristaltic pump or by use of a pressure tank.

Following viral removal, the soluble rHuPH20 can be concentrated and subjected to buffer exchange. The soluble rHuPH20 can be concentrated by 2 $\times$, 3 $\times$, 4 $\times$, 5 $\times$, 6 $\times$, 7 $\times$, 8 $\times$, 9 $\times$, 10 $\times$, 11 $\times$, 12 $\times$, 13 $\times$ or more. In some examples, the protein is concentrated approximately 6 $\times$. This can result in, for example, a concentration of between 0.1 mg/mL and 50 mg/mL. In some examples, the purified hyaluronidase is concentrated to approximately 1 mg/mL. In other examples, the purified hyaluronidase is concentrated to approximately 10 mg/mL. Any method of protein concentration known in the art can be utilized. Exemplary of such methods include concentration using tangential flow filtration (TFF) systems with molecular weight cut off (MWCO) filters. For example, the purified hyaluronidase can be passed through a 10 kDa MWCO spiral polyethersulfone filters to concentrate the protein 10 $\times$. In another example, the protein is passed through a series of four 30 kDa MWCO filters. For large-scale production of hyaluronidase, such as, for example, 100 L and 300 L

cultures, filters with surface areas of between 0.5 and 5 square meters are typically employed for this purpose. In some examples, filters with a surface area of 1.2 square meters or 2.8 square meters are used.

A buffer exchange is generally performed following protein concentration to formulate the protein in the desired buffer for subsequent use, for example, as a therapeutic. One of skill in the art can empirically determine an appropriate buffer. Exemplary of suitable buffers are saline buffers, including, but not limited to, 10 mM Hepes, 130 mM NaCl, pH 7.0, and 10 mM Histidine, 130 mM NaCl, pH 6.0. The purified hyaluronidase can, in some example, be passed through another filter, such as a 0.22 μm capsule filter, before being stored in a sterile environment.

I. Filling

The methods described herein for the production and purification of soluble rHuPH20 also can include a filling step, in which the purified protein is aseptically filled into smaller containers for long-term storage and use. The soluble rHuPH20 can be filled into the containers as a liquid formulation, or as a powder, such as following lyophilization. For large-scale production, automated filling systems that include, for example, pumps to transfer the protein to the containers and weighing stations to measure the fill volume are typically used and are widely available. Manual or a combination of automated and manual filling of containers also can be performed, however. Suitable containers include, but are not limited to, glass or plastic vials, blister packs, bottles, tubes, inhalers, pumps, bags, syringes, bottles, or any other suitable container. Suitable closures or caps also can be used to seal the container. The filling process can include first passing the soluble rHuPH20 through a filter prior to filling to remove microbial contaminant and larger aggregates or sediment. For example, the protein can be filtered through a 0.22 μm filter before being aliquoted into suitable containers. One of skill in the art can determine the appropriate fill volume and can include, for example, volumes ranging from 0.1 mL to 100 mL. In some examples, vials are aseptically filled with 1 mL, 5 mL or 20 mL soluble rHuPH20. Following capping or closure of the containers, the containers can be stored at an appropriate temperature. In some examples, the containers are flash frozen and stored at between -15°C . and -35°C . In other examples, the containers are refrigerated, such as at between 3°C . and 15°C . Typically, long-term storage of liquids is at lower temperatures to minimize degradation. Soluble rHuPH20 in powder form can be stored for long periods at room temperature without significant degradation.

J. Monitoring and Assays

The methods described herein can be monitored at one or more steps, measuring one or more conditions, parameters or products at each point. This can ensure that optimal conditions are maintained throughout, and also can be used to assess efficiency and productivity of the process. Monitoring can occur, for example, one or more times during the cell expansion phase, protein production phase (i.e. in the bioreactor), and/or the protein purification stage, as well as any time between, before or after, such as during concentration/buffer exchange procedures or filling. Monitoring can include, but is not limited to, measuring pH, temperature, volumes, contamination, purity, protein concentration, enzyme activity, cell viability and cell number. In addition to monitoring conditions, parameters or products throughout the process, the purified soluble rHuPH20 produced as the

end product also can be assessed and characterized with respect to, for example, protein concentration, enzyme activity, impurities, contamination, osmolality, degradation, post-translational modifications and monosaccharide content.

1. Monitoring the Conditions

The conditions during one or more of the steps in the methods provided herein can be monitored to ensure optimal conditions are maintained throughout the process. If the monitoring demonstrates that the conditions are not within an optimal range, then the conditions can be altered. Conditions that can be monitored vary for each process. For example, during the cell culture phases (i.e. cell expansion and protein production in the bioreactor), conditions to be monitored include, but are not limited to, temperature, cell culture pH, cell culture nutrients (e.g. glucose), CO₂ levels and O₂ levels. Typically, the conditions are monitored automatically using in-built systems in, for example the incubator or bioreactor.

During the protein purification stage, conditions that can be monitored include, but are not limited to, pH, conductivity and flow rate. These conditions can be monitored before, during and/or after one or more column chromatography steps. For example, the buffers used to equilibrate, wash or elute the column can be monitored. This can be performed before the buffer is loaded or after the buffer has run through the column.

2. Monitoring Soluble rHuPH20 Production

Soluble rHuPH20 production, and parameters associated with soluble rHuPH20 production, also can be monitored throughout the process. These include, but are not limited to, cell number, cell viability, contamination, protein concentration, enzyme activity, purity, osmolality, post-translational modifications. Any method to assess these parameters can be used. For example, mammalian cell viability can be assessed by taking a small aliquot of the cell culture and staining with trypan blue, which permeates only damaged cell membranes, thus staining only dead cells. The cells can be visualized under microscope and counted using, for example, a hemocytometer. Other methods include assessing cell viability by measuring metabolic activity. For example, an aliquot of the cell culture can be incubated with a tetrazolium salt (e.g. MTT, XTT or WST-1) that is cleaved into a colored formazan product by metabolically active cells.

Soluble rHuPH20 concentration in a particular sample can be assessed by methods well-known in the art, including but not limited to, enzyme-linked immunosorbent assays (ELISA); SDS-PAGE; Bradford, Lowry, and/or BCA methods; UV absorbance, and other quantifiable protein labeling methods, such as, but not limited to, immunological, radioactive and fluorescent methods and related methods. Additionally, the presence and extent of degradation can be measured by standard techniques such as sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), Western blotting of electrophoresed hyaluronidase-containing samples and chromatography, such as, for example, RP-HPLC. The purity of a hyaluronidase-containing sample can be assessed by, for example, SDS-PAGE, RP-HPLC, size-exclusion chromatography, anion-exchange chromatography and isoelectric focusing (IEF). Soluble rHuPH20-containing samples, such as samples containing purified hyaluronidase, can be further characterized by assessing the sialic acid and monosaccharide content. This can be accomplished by, for example, hydrolyzing the sample with 40% trifluoroacetic acid, fluorescently labeling the released monosaccharides and separating them using RP-HPLC (see Example 10).

Soluble rHuPH20 produced and purified using the methods provided herein also can be assessed for the presence of post-translational modifications. Such assays are known in

the art and include assays to measure glycosylation, hydroxylation, and carboxylation. In an exemplary assay for glycosylation, carbohydrate analysis can be performed, for example, with SDS page analysis of soluble rHuPH20 exposed to hydrazinolysis or endoglycosidase treatment. Hydrazinolysis releases N- and O-linked glycans from glycoproteins by incubation with anhydrous hydrazine, while endoglycosidase release involves PNGase F, which releases most N-glycans from glycoproteins. Hydrazinolysis or endoglycosidase treatment of soluble rHuPH20 polypeptides generates a reducing terminus that can be tagged with a fluorophore or chromophore label. Labeled soluble rHuPH20 polypeptides can be analyzed by fluorophore-assisted carbohydrate electrophoresis (FACE). The fluorescent tag for glycans also can be used for monosaccharide analysis, profiling or fingerprinting of complex glycosylation patterns by HPLC. Exemplary HPLC methods include hydrophilic interaction chromatography, electronic interaction, ion-exchange, hydrophobic interaction, and size-exclusion chromatography. Exemplary glycan probes include, but are not limited to, 3-(acetylamino)-6-aminoacridine (AA-Ac) and 2-aminobenzoic acid (2-AA). Carbohydrate moieties can also be detected through use of specific antibodies that recognize the glycosylated hyaluronidase polypeptide.

An exemplary assay to measure β -hydroxylation comprises reverse phase HPLC analysis of soluble rHuPH20 polypeptides that have been subjected to alkaline hydrolysis (Przysiecki et al. (1987) PNAS 84:7856-7860). Carboxylation and γ -carboxylation of hyaluronidase polypeptides can be assessed using mass spectrometry with matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) analysis, as described in the art (see, e.g. Harvey et al. J Biol Chem 278:8363-8369, Maum et al. Prot Sci 14:1171-1180).

The enzymatic activity of soluble rHuPH20 in a sample can be assessed at any point during the methods described herein. In one example, activity is measured using a microturbidity assay (see e.g. Example 10). This is based on the formation of an insoluble precipitate when hyaluronic acid binds with serum albumin. The activity is measured by incubating soluble rHuPH20 with sodium hyaluronate (hyaluronic acid) for a set period of time (e.g. 10 minutes) and then precipitating the undigested sodium hyaluronate with the addition of acidified serum albumin. The turbidity of the resulting sample is measured at 640 nm after an additional development period. The decrease in turbidity resulting from enzyme activity on the sodium hyaluronate substrate is a measure of the soluble rHuPH20 enzymatic activity. In another example, enzymatic activity is measured using a microtiter assay in which residual biotinylated hyaluronic acid is measured following incubation with the sample containing soluble rHuPH20 (see e.g. Frost and Stern (1997) Anal. Biochem. 251:263-269, U.S. Patent Publication No. 20050260186). The free carboxyl groups on the glucuronic acid residues of hyaluronic acid are biotinylated, and the biotinylated hyaluronic acid substrate is covalently couple to a microtiter plate. Following incubation with the sample containing soluble rHuPH20, the residual biotinylated hyaluronic acid substrate is detected using an avidin-peroxidase reaction, and compared to that obtained following reaction with hyaluronidase standards of known activity. Other assays to measure enzymatic activity also are known in the art and can be used in the methods herein (see e.g. Delpech et al., (1995) Anal. Biochem. 229:35-41; Takahashi et al., (2003) Anal. Biochem. 322:257-263).

The presence of any contamination also can be monitored. Contamination can include, but is not limited to, microbial contamination (e.g. viruses, bacteria and mycoplasma),

microbial products contamination (e.g. endotoxin), or other process-related impurities. Any suitable method or assay can be used. For example, viruses and bacteria can be cultured using methods well known in the art to determine whether they are present or not in a sample, and if so, in what quantities. Microscopy also can be used to detect microbial contamination. For example, a sample can be assessed for the presence of viruses or bacteria using transmission electron microscopy (TEM). *Mycoplasma* detection can be effected using, for example, biochemical or molecular techniques, including, but not limited to, PCR to amplify mycoplasma-specific nucleic acid, biochemical tests to detect mycoplasma-specific enzymes and cell-based fluorescence to detect mycoplasma antigens or nucleic acid.

The presence of microbial products, such as bacterial endotoxins, also can be monitored. An example of a suitable assay for detecting the presence of endotoxin is the *Limulus Amebocyte* Lysate (LAL) assay. Two types of LAL assays can be used: gel clot and photometric (chromogenic and turbidimetric). LAL is an aqueous extract of blood cells (amebocytes) from the horse shoe crab. Endotoxin triggers a cascade of enzymatic reactions, which result in activated clotting enzyme. In the presence of bacterial endotoxins, at an elevated temperature, the LAL reagent will clot after addition of reagent. The formation of the gel clot is proportional to the concentration of the endotoxin. In the kinetic assay, the proenzyme in the LAL is activated when in contact with endotoxins produced by gram negative bacteria. The rate of activation is directly proportional with the concentration of the endotoxin present. The level of activation can be measured through a subsequent substrate reaction which is measured spectrophotometrically.

K. EXAMPLES

The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

Example 1

Generation of a Soluble rHuPH20-Expressing Cell Line

The HZ24 plasmid (set forth in SEQ ID NO:50) was used to transfect Chinese Hamster Ovary (CHO cells) (see e.g. related application Nos. 10,795,095, 11/065,716 and 11/238,171). The HZ24 plasmid vector for expression of soluble rHuPH20 contains a pCI vector backbone (Promega), DNA encoding amino acids 1-482 of human PH20 hyaluronidase (SEQ ID NO:47), an internal ribosomal entry site (IRES) from the ECMV virus (Clontech), and the mouse dihydrofolate reductase (DHFR) gene. The pCI vector backbone also includes DNA encoding the Beta-lactamase resistance gene (AmpR), an f1 origin of replication, a Cytomegalovirus immediate-early enhancer/promoter region (CMV), a chimeric intron, and an SV40 late polyadenylation signal (SV40). The DNA encoding the soluble rHuPH20 construct contains an NheI site and a Kozak consensus sequence prior to the DNA encoding the methionine at amino acid position 1 of the native 35 amino acid signal sequence of human PH20, and a stop codon following the DNA encoding the tyrosine corresponding to amino acid position 482 of the human PH20 hyaluronidase set forth in SEQ ID NO:1), followed by a BamHI restriction site. The construct pCI-PH20-IRES-DHFR-SV40pa (HZ24), therefore, results in a single mRNA species driven by the CMV promoter that encodes amino

acids 1-482 of human PH20 (set forth in SEQ ID NO:3) and amino acids 1-186 of mouse dihydrofolate reductase (set forth in SEQ ID NO:51), separated by the internal ribosomal entry site (IRES).

Non-transfected DG44 CHO cells growing in GIBCO Modified CD-CHO media for DHFR(-) cells, supplemented with 4 mM Glutamine and 18 ml/L Plurionic F68/L (Gibco), were seeded at 0.5×10^6 cells/ml in a shaker flask in preparation for transfection. Cells were grown at 37° C. in 5% CO₂ in a humidified incubator, shaking at 120 rpm. Exponentially growing non-transfected DG44 CHO cells were tested for viability prior to transfection.

Sixty million viable cells of the non-transfected DG44 CHO cell culture were pelleted and resuspended to a density of 2×10^7 cells in 0.7 mL of 2× transfection buffer (2×HeBS: 40 mM Hepes, pH 7.0, 274 mM NaCl, 10 mM KCl, 1.4 mM Na₂HPO₄, 12 mM dextrose). To each aliquot of resuspended cells, 0.09 mL (250 µg) of the linear HZ24 plasmid (linearized by overnight digestion with Cla I (New England Biolabs) was added, and the cell/DNA solutions were transferred into 0.4 cm gap BTX (Gentronics) electroporation cuvettes at room temperature. A negative control electroporation was performed with no plasmid DNA mixed with the cells. The cell/plasmid mixes were electroporated with a capacitor discharge of 330 V and 960 µF or at 350 V and 960 µF.

The cells were removed from the cuvettes after electroporation and transferred into 5 mL of Modified CD-CHO media for DHFR(-) cells, supplemented with 4 mM Glutamine and 18 ml/L Plurionic F68/L (Gibco), and allowed to grow in a well of a E-well tissue culture plate without selection for 2 days at 37° C. in 5% CO₂ in a humidified incubator.

Two days post-electroporation, 0.5 mL of tissue culture media was removed from each well and tested for the presence of hyaluronidase activity, using the microturbidity assay described in Example 9.

TABLE 1

Initial Hyaluronidase Activity of HZ24 Transfected DG44 CHO cells at 40 hours post-transfection		
	Dilution	Activity Units/ml
Transfection 1 330 V	1 to 10	0.25
Transfection 2 350 V	1 to 10	0.52
Negative Control	1 to 10	0.015

Cells from Transfection 2 (350V) were collected from the tissue culture well, counted and diluted to 1×10^4 to 2×10^4 viable cells per mL. A 0.1 mL aliquot of the cell suspension was transferred to each well of five, 96 well round bottom tissue culture plates. One hundred microliters of CD-CHO media (GIBCO) containing 4 mM GlutaMAX™-I supplement (GIBCO™, Invitrogen Corporation) and without hypoxanthine and thymidine supplements were added to the wells containing cells (final volume 0.2 mL).

Ten clones were identified from the 5 plates grown without methotrexate.

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TABLE 2

Hyaluronidase activity of identified clones	
Plate/Well ID	Relative Hyaluronidase
1C3	261
2C2	261
3D3	261
3E5	243
3C6	174
2G8	103
1B9	304
2D9	273
4D10	302

Six HZ24 clones were expanded in culture and transferred into shaker flasks as single cell suspensions. Clones 3D3, 3E5, 2G8, 2D9, 1E11, and 4D10 were plated into 96-well round bottom tissue culture plates using a two-dimensional infinite dilution strategy in which cells were diluted 1:2 down the plate, and 1:3 across the plate, starting at 5000 cells in the top left hand well. Diluted clones were grown in a background of 500 non-transfected DG44 CHO cells per well, to provide necessary growth factors for the initial days in culture. Ten plates were made per subclone, with 5 plates containing 50 nM methotrexate and 5 plates without methotrexate.

Clone 3D3 produced 24 visual subclones (13 from the no methotrexate treatment, and 11 from the 50 nM methotrexate treatment. Significant hyaluronidase activity was measured in the supernatants from 8 of the 24 subclones (>50 Units/mL), and these 8 subclones were expanded into T-25 tissue culture flasks. Clones isolated from the methotrexate treatment protocol were expanded in the presence of 50 nM methotrexate. Clone 3D35M was further expanded in 500 nM methotrexate giving rise to clones producing in excess of 1,000 Units/ml in shaker flasks (clone 3D35M; or Gen1 3D35M). A master cell bank (MCB) of the 3D35M cells was then prepared.

Example 2

Determination of the Copy Number of the Nucleic Acid Region Encoding Soluble rHuPH20 in 3D35M Cells

The copy number of the nucleic acid region encoding soluble rHuPH20 in 3D35M cells was determined by quantitative PCR. Total genomic DNA was extracted from 3D35M cells from the MCB. Six independent dilutions of the DNA were prepared for analysis in duplicate, each of which contained approximately 6.6 ng DNA (equivalent to approximately 100 cells). Negative controls containing no template also were prepared, as were positive controls containing the plasmid and the DNA equivalent of 1000 CHO cells (6.6 ng). The reactions were assembled according to the TaqMan Universal PCR Master Mix Protocol (Applied Biosystems) and run in duplicate. A standard curve was generated using eight dilutions of the HZ24 plasmid, representing a range of approximately 5×10^6 to 49 copies of plasmid DNA. The standard was diluted in CHO control genomic DNA (equivalent of 100 cells). The reactions were assembled according to the TaqMan™ Universal PCR Master Mix Protocol (Applied Biosystems) using the HZM3.P1 forward primer and the HZM3.P2 reverse primer (set forth in SEQ ID NOS:52 and 53, respectively) and the HZM3 probe (SEQ ID NO:54), which contained the fluorescent dyes 6FAM (6-carboxyfluorescein) and TAMRA (6-carboxytetramethylrhodamine). The reactions were run in duplicate using the following cycling

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conditions: 50° C. for 2 minutes, 95° C. for 10 minutes, followed by 40 cycles of 95° C. for 15 seconds and 60° C. for 1 minute. A standard quantitative PCR reaction to assay GAPDH copies for each DNA sample also was performed. Data was collected by the ABI Prism 7700™ Sequence Detection System software version 1.9 (Applied Biosystems).

The target gene copy numbers per cell were calculated as the ratio of target copies (soluble rHuPH20) to normalized copies (GAPDH) for the six dilutions of 3D35M genomic DNA. The Dixon Q Outlier statistics test was applied to the data set. The copy number of the sHuPH20 region in 3D35M cells was found to be 317.87 ± 11.64 .

Example 3

Production and Purification of Gen1 Soluble rHuPH20

A. 5 L Bioreactor Process

A vial of 3D35M was thawed and expanded from T-25 flasks through 1 L spinner flasks in CD CHO (Invitrogen, Carlsbad Calif.) supplemented with 100 nM Methotrexate and 40 mL/L GlutaMAX™-I (Invitrogen; 200 mM stock solution). Cells were transferred from spinner flasks to a 5 L bioreactor (Braun) at an inoculation density of 4×10^5 viable cells per ml in 5 L media. Parameters were temperature Setpoint 37° C., pH 7.2 (starting Setpoint), with Dissolved Oxygen Setpoint 25% and an air overlay of 0-100 cc/min. At 168 hrs, 250 ml of Feed #1 Medium (CD CHO with 50 g/L Glucose) was added. At 216 hours, 250 ml of Feed #2 Medium (CD CHO with 50 g/L Glucose and 10 mM Sodium Butyrate) was added, and at 264 hours 250 ml of Feed #2 Medium was added. This process resulted in a final productivity of 1600 Units per ml with a maximal cell density of 6×10^6 cells/ml. The addition of sodium butyrate was to enhance the production of soluble rHuPH20 in the final stages of production.

Conditioned media from the 3D35M clone was clarified by depth filtration and tangential flow diafiltration into 10 mM Hepes pH 7.0. Soluble rHuPH20 was then purified by sequential chromatography on Q Sepharose (Pharmacia) ion exchange, Phenyl Sepharose (Pharmacia) hydrophobic interaction chromatography, Amino phenyl boronate (ProMetrics) and Hydroxyapatite Chromatography (Biorad, Richmond, Calif.).

Soluble rHuPH20 bound to Q Sepharose and eluted at 400 mM NaCl in the same buffer. The eluate was diluted with 2M ammonium sulfate to a final concentration of 500 mM ammonium sulfate and passed through a Phenyl Sepharose (low sub) column, followed by binding under the same conditions to a phenyl boronate resin. The soluble rHuPH20 was eluted from the Phenyl Sepharose resin in Hepes pH 6.9 after washing at pH 9.0 in 50 mM bicine without ammonium sulfate. The eluate was loaded onto a ceramic hydroxyapatite resin at pH 6.9 in 5 mM potassium phosphate and 1 mM CaCl_2 and eluted with 80 mM potassium phosphate, pH 7.4 with 0.1 mM CaCl_2 .

The resultant soluble rHuPH20 possessed a specific activity in excess of 65,000 Units/mg protein by way of the microturbidity assay (see Example 9). Purified soluble rHuPH20 eluted as a single peak from 24 to 26 minutes from a Pharmacia 5RPC styrene divinylbenzene column with a gradient between 0.1% TFA/ H_2O and 0.1% TFA/90% acetonitrile/10% H_2O and resolved as a single broad 61 kDa band by SDS electrophoresis that reduced to a sharp 51 kDa band upon

treatment with PNGASE-F. N-terminal amino acid sequencing revealed that the leader peptide had been efficiently removed.

B. Upstream Cell Culture Expansion Process into 100 L Bioreactor Cell Culture

A scaled-up process was used to separately purify soluble rHuPH20 from four different vials of 3D35M cell to produce 4 separate batches of sHuPH20; HUA0406C, HUA0410C, HUA0415C and HUA0420C. Each vial was separately expanded and cultured through a 125 L bioreactor, then purified using column chromatography. Samples were taken throughout the process to assess such parameters as enzyme yield. The description of the process provided below sets forth representative specifications for such things as bioreactor starting and feed media volumes, transfer cell densities, and wash and elution volumes. The exact numbers vary slightly with each batch, and are detailed in Tables 3 to 10.

Four vials of 3D35M cells were thawed in a 37° C. water bath, CD CHO containing 100 nM methotrexate and 40 mL/L GlutaMAX™-I was added and the cells were centrifuged. The cells were re-suspended in a 125 mL shake flask with 20 mL of fresh media and placed in a 37° C., 7% CO₂ incubator. The cells were expanded up to 40 mL in the 125 mL shake flask. When the cell density reached 1.5-2.5×10⁶ cells/mL, the culture was expanded into a 125 mL spinner flask in a 100 mL culture volume. The flask was incubated at 37° C., 7% CO₂. When the cell density reached 1.5-2.5×10⁶ cells/mL, the culture was expanded into a 250 mL spinner flask in 200 mL culture volume, and the flask was incubated at 37° C., 7% CO₂. When the cell density reached 1.5-2.5×10⁶ cells/mL, the culture was expanded into a 1 L spinner flask in 800 mL culture volume and incubated at 37° C., 7% CO₂. When the cell density reached 1.5-2.5×10⁶ cells/mL, the culture was expanded into a 6 L spinner flask in 5 L culture volume and incubated at 37° C., 7% CO₂. When the cell density reached 1.5-2.5×10⁶ cells/mL, the culture was expanded into a 36 L spinner flask in 20 L culture volume and incubated at 37° C., 7% CO₂.

A 125 L reactor was sterilized with steam at 121° C., 20 PSI and 65 L of CD CHO media was added. Before use, the

reactor was checked for contamination. When the cell density in the 36 L spinner flasks reached 1.8-2.5×10⁶ cells/mL, 20 L cell culture were transferred from the 36 L spinner flasks to the 125 L bioreactor (Braun), resulting a final volume of 85 L and a seeding density of approximately 4×10⁵ cells/mL. Parameters were temperature setpoint, 37° C.; pH: 7.2; Dissolved oxygen: 25%±10%; Impeller Speed 50 rpm; Vessel Pressure 3 psi; Air Sparge 1 L/min.; Air Overlay: 1 L/min. The reactor was sampled daily for cell counts, pH verification, media analysis, protein production and retention. Nutrient feeds were added during the run. At Day 6, 3.4 L of Feed #1 Medium (CD CHO+50 g/L Glucose+40 mL/L GlutaMAX™-I) was added, and culture temperature was changed to 36.5° C. At day 9, 3.5 L of Feed #2 (CD CHO+50 g/L Glucose+40 mL/L GlutaMAX™-I+1.1 g/L Sodium Butyrate) was added, and culture temperature was changed to 36° C. At day 11, 3.7 L of Feed #3 (CD CHO+50 g/L Glucose+40 mL/L GlutaMAX™-I+1.1 g/L Sodium Butyrate) was added, and the culture temperature was changed to 35.5° C. The reactor was harvested at 14 days or when the viability of the cells dropped below 50%. The process resulted in production of soluble rHuPH20 with an enzymatic activity of 1600 Units/ml with a maximal cell density of 8 million cells/mL. At harvest, the culture was sampled for mycoplasma, bioburden, endotoxin, and virus in vitro and in vivo, transmission electron microscopy (TEM) for viral particles, and enzyme activity.

The one hundred liter bioreactor cell culture harvest was filtered through a series of disposable capsule filters having a polyethersulfone medium (Sartorius): first through a 8.0 µm depth capsule, a 0.65 µm depth capsule, a 0.22 µm capsule, and finally through a 0.22 µm Sartopore 2000 cm² filter and into a 100 L sterile storage bag. The culture was concentrated 10× using two TFF with Spiral Polyethersulfone 30 kDa MWCO filters (Millipore), followed by a 6× buffer exchange with 10 mM HEPES, 25 mM Na₂SO₄, pH 7.0 into a 0.22 µm final filter into a 20 L sterile storage bag. Table 3 provides monitoring data related to the cell culture, harvest, concentration and buffer exchange steps.

TABLE 3

Monitoring data for cell culture, harvest, concentration and buffer exchange steps.				
Parameter	HUA0406C	HUA04010C	HUA0415C	HUA0420C
Time from thaw to inoculate 100 L bioreactor (days)	21	19	17	18
100 L inoculation density (×10 ⁶ cells/mL)	0.45	0.33	0.44	0.46
Doubling time in logarithmic growth (hr)	29.8	27.3	29.2	23.5
Max. cell density (×10 ⁶ cells/mL)	5.65	8.70	6.07	9.70
Harvest viability (%)	41	48	41	41
Harvest titer (U/ml)	1964	1670	991	1319
Time in 100-L bioreactor (days)	13	13	12	13
Clarified harvest volume (mL)	81800	93300	91800	89100
Clarified harvest enzyme assay (U/mL)	2385	1768	1039	1425
Concentrate enzyme assay (U/mL)	22954	17091	8561	17785
Buffer exchanged concentrate enzyme assay (U/mL)	15829	11649	9915	8679
Filtered buffer exchanged concentrate enzyme assay (U/mL)	21550	10882	9471	8527
Buffer exchanged concentrate volume(mL)	10699	13578	12727	20500
Ratio enzyme units concentration/harvest	0.87	0.96	1.32	1.4

A Q Sepharose (Pharmacia) ion exchange column (3 L resin, Height=20 cm, Diameter=14 cm) was prepared. Wash samples were collected for a determination of pH, conductivity and endotoxin (LAL) assay. The column was equilibrated with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5. The concentrated, diafiltered harvest was loaded onto the Q column at a flow rate of 100 cm/hr. The column was washed with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 and 10 mM Hepes, 50 mM NaCl, pH 7.0. The protein was eluted with 10 mM Hepes, 400 mM NaCl, pH 7.0 and filtered through a 0.22 µm final filter into a sterile bag.

Phenyl-Sepharose (Pharmacia) hydrophobic interaction chromatography was next performed. A Phenyl-Sepharose (PS) column (9.1 L resin, Height=29 cm, Diameter=20 cm) was prepared. The column was equilibrated with 5 column volumes of 5 mM potassium phosphate, 0.5 M ammonium sulfate, 0.1 mM CaCl₂, pH 7.0. The protein eluate from above was supplemented with 2M ammonium sulfate, 1 M potassium phosphate and 1 M CaCl₂ stock solutions to final concentrations of 5 mM, 0.5 M and 0.1 mM, respectively. The protein was loaded onto the PS column at a flow rate of 100 cm/hr. 5 mM potassium phosphate, 0.5 M ammonium sulfate and 0.1 mM CaCl₂ pH 7.0 was added at 100 cm/hr. The flow through was passed through a 0.22 µm final filter into a sterile bag.

The PS-purified protein was loaded onto an aminophenyl boronate column (ProMedics) (6.3 L resin, Height=20 cm, Diameter=20 cm) that had been equilibrated with 5 column volumes of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The protein was passed through the column at a flow rate of 100 cm/hr, and the column was washed with 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0. The column was then washed with 20 mM bicine, 100 mM NaCl, pH 9.0 and the protein eluted with 50 mM Hepes, 100 mM NaCl pH 6.9 through a sterile filter and into a 20 L sterile bag. The eluate was tested for bioburden, protein concentration and enzyme activity.

A hydroxyapatite (HAP) column (BioRad) (1.6 L resin, Height=10 cm, Diameter=14 cm) was equilibrated with 5 mM potassium phosphate, 100 mM NaCl, 0.1 mM CaCl₂ pH 7.0. Wash samples were collected and tested for pH, conductivity and endotoxin (LAL assay). The aminophenyl boronate purified protein was supplemented with potassium phosphate and CaCl₂ to yield final concentrations of 5 mM potassium phosphate and 0.1 mM CaCl₂ and loaded onto the HAP column at a flow rate of 100 cm/hr. The column was washed with 5 mM potassium phosphate pH 7.0, 100 mM NaCl, 0.1 mM CaCl₂, then 10 mM potassium phosphate pH 7.0, 100 mM NaCl, 0.1 mM CaCl₂ pH. The protein was eluted with 70 mM

potassium phosphate pH 7.0 and filtered through a 0.22 µm filter into a 5 L sterile storage bag. The eluate was tested for bioburden, protein concentration and enzyme activity.

The HAP-purified protein was then pumped through a 20 nM viral removal filter via a pressure tank. The protein was added to the DV20 pressure tank and filter (Pall Corporation), passing through an Ultipor DV20 Filter with 20 nm pores (Pall Corporation) into a sterile 20 L storage bag. The filtrate was tested for protein concentration, enzyme activity, oligosaccharide, monosaccharide and sialic acid profiling, and process-related impurities. The protein in the filtrate was then concentrated to 1 mg/mL using a 10 kD molecular weight cut off (MWCO) Sartocoon Slice tangential flow filtration (TFF) system (Sartorius). The filter was first prepared by washing with a Hepes/saline solution (10 mM Hepes, 130 mM NaCl, pH 7.0) and the permeate was sampled for pH and conductivity. Following concentration, the concentrated protein was sampled and tested for protein concentration and enzyme activity. A 6x buffer exchange was performed on the concentrated protein into the final buffer: 10 mM Hepes, 130 mM NaCl, pH 7.0. The concentrated protein was passed through a 0.22 µm filter into a 20 L sterile storage bag. The protein was sampled and tested for protein concentration, enzyme activity, free sulfhydryl groups, oligosaccharide profiling and osmolality.

Tables 4 to 10 provide monitoring data related to each of the purification steps described above, for each 3D35M cell lot.

TABLE 4

Q sepharose column data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Load volume (mL)	10647	13524	12852	20418
Load Volume/Resin Volume ratio	3.1	4.9	4.5	7.3
Column Volume (mL)	2770	3840	2850	2880
Eluate volume (mL)	6108	5923	5759	6284
Protein Conc. of Eluate (mg/mL)	2.8	3.05	2.80	2.86
Eluate Enzyme Assay (U/mL)	24493	26683	18321	21052
Enzyme Yield (%)	65	107	87	76

TABLE 5

Phenyl Sepharose column data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Volume Before Stock Solution Addition (mL)	5670	5015	5694	6251
Load Volume (mL)	7599	6693	7631	8360
Column Volume (mL)	9106	9420	9340	9420
Load Volume/Resin Volume ratio	0.8	0.71	0.82	0.89
Eluate volume (mL)	16144	18010	16960	17328
Protein Cone of Eluate (mg/mL)	0.4	0.33	0.33	0.38
Eluate Enzyme Assay (U/mL)	8806	6585	4472	7509
Protein Yield (%)	41	40	36	37
Enzyme Yield (%)	102	88	82	96

TABLE 6

Amino Phenyl Boronate column data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Load Volume (mL)	16136	17958	16931	17884
Load Volume/Resin	2.99	3.15	3.08	2.98
Volume ratio				
Column Volume (mL)	5400	5700	5500	5300
Eluate volume (mL)	17595	22084	20686	19145
Protein Conc. of Eluate (mg/mL)	0.0	0.03	0.03	0.04
Protein Conc. of Filtered Eluate (mg/mL)	not tested	0.03	0.00	0.04
Eluate Enzyme Assay (U/mL)	4050	2410	1523	4721
Protein Yield (%)	0	11	11	12
Enzyme Yield (%)	not determined	41	40	69

TABLE 7

Hydroxyapatite column data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Volume Before Stock Solution Addition (mL)	16345	20799	20640	19103
Load Volume/Resin	10.95	13.58	14.19	12.81
Volume ratio				
Column Volume (mL)	1500	1540	1462	1500
Load volume (mL)	16429	20917	20746	19213
Eluate volume (mL)	4100	2415	1936	2419
Protein Conc. of Eluate (mg/mL)	not tested	0.24	0.17	0.23
Protein Conc. of Filtered Eluate (mg/mL)	NA	NA	0.17	NA
Eluate Enzyme Assay (U/mL)	14051	29089	20424	29826
Protein Yield (%)	Not tested	93	53	73
Enzyme Yield (%)	87	118	140	104

TABLE 8

DV20 filtration data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Start volume (mL)	4077	2233	1917	2419
Filtrate Volume (mL)	4602	3334	2963	3504
Protein Conc. of Filtrate (mg/mL)	0.1	NA	0.09	NA
Protein Conc. of Filtered Eluate (mg/mL)	NA	0.15	0.09	0.16
Protein Yield (%)	not tested	93	82	101

TABLE 9

Final concentration data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Start volume (mL)	4575	3298	2963	3492
Concentrate Volume (mL)	562	407	237	316

TABLE 9-continued

Final concentration data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Protein Conc. of Concentrate (mg/mL)	0.9	1.24	1.16	1.73
Protein Yield (%)	111	102	103	98

TABLE 10

Buffer Exchange into Final Formulation data				
Parameter	HUA0406C	HUA0410C	HUA0415C	HUA0420C
Start Volume (mL)	562	407	237	316
Final Volume Buffer	594	516	310	554
Exchanged Concentrate (mL)				
Protein Conc. of Concentrate (mg/mL)	1.00	0.97	0.98	1.00
Protein Conc. of Filtered Concentrate (mg/mL)	0.95	0.92	0.95	1.02
Protein Yield (%)	118	99	110	101

The purified and concentrated soluble rHuPH20 protein was aseptically filled into sterile vials with 5 mL and 1 mL fill volumes. The protein was passed through a 0.22 µm filter to an operator controlled pump that was used to fill the vials using a gravimetric readout. The vials were closed with stoppers and secured with crimped caps. The closed vials were visually inspected for foreign particles and then labeled.

Following labeling, the vials were flash-frozen by submersion in liquid nitrogen for no longer than 1 minute and stored at $\leq -15^{\circ}\text{C}$. ($-20\pm 5^{\circ}\text{C}$). Production and purification of soluble rHuPH20 using this method yielded approximately 400-700 mg soluble rHuPH20 with a specific activity of 96,000 units/mg to 144,000 units/mg.

Example 4

Production of Gen2 Soluble rHuPH20

The Gen1 3D35M cell line described above was adapted to higher methotrexate levels to produce Gen2 clones. 3D35M cells were seeded from established methotrexate-containing cultures into CD CHO medium containing 8 mM GlutaMAX™-I and 1.0 µM methotrexate. The cells were adapted to a higher methotrexate level by growing and passaging them 9 times over a period of 46 days in a 37° C., 7% CO₂ humidified incubator. The amplified population of cells was cloned out by limiting dilution in 96-well tissue culture plates containing medium with 2.0 µM methotrexate. After approximately 4 weeks, clones were identified and clone 3E10B was selected for expansion. 3E10B cells were grown in CD CHO medium containing 8 mM GlutaMAX™-I and 2.0 µM methotrexate for 20 passages, with testing for cell viability by trypan blue staining and counting with a hemocytometer, and enzyme activity by the microturbidity assay (described below in Example 9). A master cell bank (MCB) of the 3E10B cell line was created and frozen and used for subsequent studies.

Amplification of the cell line continued by culturing 3E10B cells in CD CHO medium containing 8 mM GlutaMAX™-I and 4.0 µM methotrexate. After the 12th passage, cells were frozen in vials as a research cell bank (RCB). One vial of the RCB was thawed and cultured in medium containing 8.0 µM methotrexate. After 5 days, the methotrexate concentration in the medium was increased to 16.0 µM, then 20.0 µM 18 days later. Cells from the 8th passage in medium containing 20.0 µM methotrexate were cloned out by limiting dilution in 96-well tissue culture plates containing CD CHO medium containing 4 mM GlutaMAX™-I and 20.0 µM methotrexate. Clones 1B3, 2B2 and 5C1 were identified 5-6 weeks later. Cells from the 9th passage of 3D35M also were cloned out by limiting dilution in 96-well tissue culture plates with CD CHO medium containing 8 mM

GlutaMAX™-I and 20.0 µM methotrexate, and clones 1G11, 2E10 and 2G10 were identified.

Cells cultures of each of 1B3, 2B2, 5C1, 1G11, 2E10 and 2G10 were seeded at a density of 4×10^5 cells/mL in a volume of 50 mL in 250 mL shaker flasks. The cultures were allowed to grow and decline without additional feeds for 10-14 days to determine the growth rate and productivity of the cells. Samples were taken periodically and assayed for hyaluronidase activity (Tables 11 and 12).

TABLE 11

Hyaluronidase activity of 1B3, 2B2 and 5C1 cells			
Hours post inoculation	Soluble rHuPH20 Enzyme activity in cell culture (units)		
	1B3	2B2	5C1
74			382
95		942	
101			582
142		2287	
144	955		
169	1200		
195			
238	1611		
242			2139
265		3070	
336	2252		

TABLE 12

Hyaluronidase activity of 1B3, 2B2 and 2E10 cells			
Hours post inoculation	Soluble rHuPH20 Enzyme activity in cell culture (units)		
	1B3	2B2	2E10
98	470		
123			1179
143		2228	
216			2814
290	2860		
291			2542
337		2992	

Four cell lines (2B2, 2G10, 1G11 and 2E10) were compared in a study in which all were seeded at a density of 4×10^5 cells/mL in a volume of 50 mL in 250 mL shaker flask. All received 10% (v/v) feeds on day 8 and 5% feeds with feed media containing CD CHO medium supplemented with 50 g/L glucose, 40 g/L yeast extract and 1.1 g/L sodium butyrate. The cells were harvested on day 15. Samples were taken periodically and assayed for soluble rHuPH20 enzymatic activity (Table 13).

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TABLE 13

Hyaluronidase activity of 2E10, 1G11, 2G10 and 2B2 cells				
Hours post inoculation	Soluble rHuPH20 Enzyme activity in cell culture (units)			
	2E10	1G11	2G10	2B2
122	991	87	1688	
124				878
194	2151	1387	2430	
196				2642
285	6231	3831	7952	
287				8822
364	5880	2955	11064	
366				15684

In both the batch and fed-batch conditions, culture of 2B2 cells exhibited higher enzymatic activity, although other cells (e.g. 2G10 cells) also exhibited good enzyme productivity the 2B2 cell line was, therefore, selected for expansion in medium containing 20.0 μ M methotrexate. After the 11th passage, 2B2 cells were frozen in vials as a research cell bank (RCB).

Example 5

Enzymatic Activity of Soluble rHuPH20 Produced in 3E10B and 2B2 Cells

Soluble rHuPH20 produced by 3E10B and 2B2 cells was assayed for enzymatic activity using the Microturbidity assay (Example 9). Frozen vials of 3E10B and 2B2 cells banks were thawed and the cells were cultured separately for two passages in growth medium (CD CHO medium with 8 mM GlutaMAXTM-I and either 2.0 μ M methotrexate for 3E10B cells, or 20.0 μ M methotrexate for 2B2 cells) in 37° C., 6% CO₂ in a humidified incubator. Cells were inoculated into 20 mL growth medium in 125 mL Erlenmeyer flasks (Corning) at 5×10^5 cells/mL, and grown for 8 days in 37° C., 6% CO₂ in a humidified incubator with a shaker platform rotating at approximately 100 rpm. On days 8 and 10, the cultures received 5% v/v of feed medium containing CD CHO medium supplemented with 50 g/L glucose, 50 g/L Yeast extract, and 2.2 g/L (20 mM) sodium butyrate to initiate the production phase. The cultures were sampled during the production phase on day 8 (190 hours), day 10 (240 hours), day 14 (332 hours), day 15 (258 hours), day 16 (382 hours) and day 18 (427 hours), and the viability was allowed to decline to zero. The samples were then analyzed for hyaluronidase activity.

Tables 14 and 15 set forth the viability (viable cell density (VCD) and percentage viability) and activity (units/flask) of the 3E10B and 2B2 cells at each time point. The enzyme activity of soluble rHuPH20 produced by 2B2 cells was consistently higher than that produced by 3E10B cells. For example, on day 8, the enzyme activity of soluble rHuPH20 produced by 2B2 cells was 69% higher than that of produced by 3E10B cells (2484 units/mL compared to 1469 units/mL). A similar trend was observed throughout the production phase. The viability of the cell cultures declined at a similar rate. When the production rate of the cells was calculated, it was observed that 3E10B cells produced 0.23 picograms soluble rHuPH20 per cell per day (pcd) on day 8 and 0.38 pcd on day 15. In comparison, 2B2 cells produced 0.46 picograms soluble rHuPH20 pcd on day 8 and 0.69 pcd on day 15, which was 100% and 82% higher than production by 3E10B on days

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8 and 15, respectively. A master cell bank (MCB) of 2B2 cells was then prepared for subsequent studies.

TABLE 14

Viability and activity of Clone 3E10B				
Hours post inoculation	VCD	% viability	Activity (Units/mL)	Volume (mL)
0	5	99	0	20
190	79.8	96	1469	20
240	61.6	76	2388	20
332	16.8	22	5396	20
358	16.4	17	5628	20
382	8.4	10	6772	20
427	0	0	6476	20

Total Activity (units) per flask (U/mL times volume (mL)): 129520

TABLE 15

Viability and activity of Clone 2B2				
Hours post inoculation	VCD	% viability	Activity (Units/flask)	Volume (mL)
0	5	99	0	20
190	68	94	2484	20
240	77.6	89	3532	20
332	32	38	8196	20
358	15.8	17	9680	20
382	9.8	13	10788	20
427	0	0	10044	20

Total Activity (units) per flask (U/mL times volume (mL)): 200880

Example 6

Genetic Stability Testing of 2B2 Cells

A. Determination of Copy Number of the Nucleic Acid Region Encoding Soluble rHuPH20 in 2B2 Cells

The copy number of the nucleic acid region encoding soluble rHuPH20 in 2B2 cells was determined by PCR. Total genomic DNA was extracted from 2×10^7 2B2 cells from the MCB using a QIAamp DNeasy kit (Qiagen). Genomic DNA also was extracted from DG-44 CHO cells as a negative control. The purity of the extracted DNA was verified by agarose gel electrophoresis and UV spectrophotometry. To generate fragments of DNA (versus high molecular weight DNA), the genomic DNA was sheared by sonication. This ensured more accurate pipetting and template accessibility. Six independent dilutions of the genomic DNA (to amounts dilutions equivalent to approximately 1000 cells/ μ L) from 2B2 and DG-44 cells were prepared and analyzed in duplicate in two assays; a target assay, which targeted and amplified a sequence specific to the nucleic acid region encoding soluble rHuPH20 plasmid DNA, and an endogenous control, which targeted and amplified GAPDH sequence. The endogenous control was used as a normalizing the results. The target assay included a standard curve generated from a serial dilution of known amounts of the HZ24 plasmid mixed into DG-44 CHO genomic DNA. The endogenous control included a standard curve generated from serial dilutions of DG-44 CHO genomic DNA mixed with HZ24 plasmid DNA. The mammalian genome size was assumed to be 3×10^9 base pairs. Each assay included a negative control (no template) and a positive control (HZ24 plasmid DNA for the target assay and host cell DNA for the endogenous control normalizing assay). The reactions were prepared using the HZM3.P1 for-

ward primer and the HZM3.P2 reverse primer (set forth in SEQ ID NOS:52 and 53, respectively) and the HZM3 probe (SEQ ID NO:54), which contained the fluorescent dyes 6FAM (6-carboxyfluorescein) and TAMRA (6-carboxytetramethylrhodamine). The samples were amplified using the Applied Biosystems Prism® 7900 Sequence Detection System with standard cycling conditions (50° C. for 2 minutes, 95° C. 10 min, 95° C. 15 seconds and 60° C. for 1 min for 40 cycles).

The target gene copy numbers per cell were calculated as the ratio of target copies to normalized copies (GAPDH) for the six dilutions of 2B2 genomic DNA. The Dixon Q Outlier statistics test was applied to the data set. The copy number of the nucleic acid region encoding soluble rHuPH20 plasmid in 2132 cells was found to be 206.61±8.35.

B. mRNA Sequence Analysis

The sequence of the PH20 mRNA generated from the HZ24 plasmid in 2B2 cells was determined. RNA was extracted from 2×10⁷ 2B2 cells from the MCB using a RNeasy Mini Kit (Qiagen). The sample was treated with DNase I to remove contaminating DNA, and the purity of the RNA was verified by agarose gel electrophoresis and UV spectrophotometry. A reverse transcription reaction using SuperScript™ Reverse Transcriptase (Invitrogen) and a control reaction lacking reverse transcriptase was performed using the extracted RNA and oligo d(t) and random primers. The resulting cDNA products were then used as templates in PCR amplifications. Two different sets of primer pairs were used; AP01/AP03 and AP10/AP12. AP01/AP03 was designed to amplify 1719 base pair region, while primer pair AP10/AP12 was designed to amplify a larger region (1811 base pairs) to obtain the reverse strand sequence of the 3' end. Table 5 sets forth the sequences of the primers. Each PCR reaction included single primer controls, a negative control using the no reverse transcriptase control (described above) as template, and a positive control with control primers and control template. The amplification products were visualized by agarose gel electrophoresis and confirmed to be of the expected size, then purified to remove excess primers and dNTPs by gel extraction or EXOSAP (USB).

The purified products were sequenced using the BigDye® Terminator v1.1 Cycle Sequencing Kit (Applied Biosystems) and the primers set forth in Table 16. The sequence data were assembled and the derived consensus sequence (SEQ ID NO:55) compared to the reference sequence using Sequencher software version 4.1.2 (Gene Code Corporation). A total of 1449 base pairs of sequence data were generated. The sequence was found to be identical to the reference sequence (SEQ ID NO:47) except for one base pair difference at position 1131, which was observed to be a thymidine (T) instead of the expected cytosine I. This is a silent mutation, with no effect on the amino acid sequence.

TABLE 16

Primers for PCR amplification and sequencing		
Primer name	Sequence	SEQ ID NO.
AP01	TTCTCTCCACAGGTGTC	56
AP02	AAGATTTCCTTACAAGAC	57
AP03	TGGCGAGAGGGGAAGAC	58
AP04	CCATTATTGTAACACTC	59
AP06	CCGAACGATTGCGCAC	60

TABLE 16-continued

Primers for PCR amplification and sequencing		
Primer name	Sequence	SEQ ID NO.
AP07	AGCCATTCCCAATTGTC	61
AP08	CTCCAGTTCAATTACAG	62
AP09	CGTTAGCTATGGATCCTC	63
AP10	CGAGACAGAGAAGACTCTTGCG	64
AP12	CATTCAACAGACCTTGCAATTC	65

C. Southern Blot Analysis of 2B2 Cells

A Southern Blot analysis was performed on 2B2 cells to obtain a structure map. Total DNA was extracted from 1×10⁷ 2B2 cells and 1×10⁷ control DG-44 cells using a Maxwell 16® system (Promega). The extracted DNA and a HZ24 plasmid control construct were evaluated for purity by agarose gel electrophoresis.

DNA from 2B2 cells, DG-44 cells and the HZ24 plasmid control were digested with Spe I, Xba I, and a double digest using BamH I/Hind III. Another BamH I/Hind digest was performed on the HZ24 plasmid control and the approximately 1.4 kb was purified by gel extraction and radioactively labeled with α-³²P to generate a labeled probe. Approximately 10 µg each of digested 2B2 DNA and DG-44 DNA, and 10 µg DG-44 DNA with 250 µg HZ24 plasmid DNA, was electrophoresed on an agarose gel. An image was taken on the gel following electrophoresis, then a Southern blot transfer was performed. The nylon membrane was hybridized with the labeled probe then washed at room temperature for 30 minutes then twice at 55° C. for 30 minutes. An initial autoradiograph was exposed for 24 hours and visually inspected. It was determined that a longer exposure was needed, so a second autoradiograph was exposed for 3 days for a darker exposure of the hybridized bands. After developing the film, the bands were sized using an Alphamager® (Alpha Innotech).

No hybridizing bands were observed for the DG-44 negative control digest and single hybridizing bands of expected sizes were observed in the HZ24 digests (BamH I/Hind III digest: ~1.4 kb; Spe I digest: ~6.6 kb; Xba I digest: ~6.5 kb). There was one major hybridizing band of ~7.7 kb and four minor hybridizing bands (~13.9, ~6.6, ~5.7 and ~4.6 kb) observed using 2B2 DNA digested with Spe I, one major hybridizing band of ~5.0 kb and two minor hybridizing bands (~13.9 and ~6.5 kb) observed using 2B2 DNA digested with Xba I, and one single hybridizing band of ~1.4 kb observed using 2B2 DNA digested with BamH I/Hind III. The presence of the single ~1.4 kb hybridizing band in the BamH I/Hind III indicated that there were no large sequence insertions or deletions within the probed region. The results from the single Xba I and Spe I digests indicate that there are multiple integration sites of the HZ24 plasmid in the genome of the 2B2 cells.

Example 7

Production of Gen2 Soluble rHuPH20 in 30 L Bioreactor Cell Culture

Soluble rHuPH20 was produced and purified from 2B2 cells using a 36 L bioreactor (30 L culture volume) to determine optimal processes for scale-up to a 400 L bioreactor

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(300 L culture volume). Four separate 36 L bioreactor runs are detailed below in sections A to D.

A. Production and Characterization of Soluble rHuPH2O Lots 056-099 and 056-100

A vial of 2B2 (1×10^7 cells) was thawed and cultured at 37° C., 7% CO₂ for 8 passages in CD CHO (Invitrogen, Carlsbad, Calif.) supplemented with 20 μ M methotrexate and 40 mL/L GlutaMAX™-I (Invitrogen), after which it was expanded to 600 mL. One week later, the culture was expanded to 5 L in CD CHO medium supplemented with 40 mL/L GlutaMAX™-I and no methotrexate. A 36 L bioreactor containing 25 L CD CHO medium supplemented with 1 L GlutaMAX™-I and 30 mL gentamicin sulfate was inoculated with the 5 L culture at an initial seeding density of 3.6×10^5 cell/mL. The agitation set point of the bioreactor was set to 75 RPM; temperature: 37° C.; pH: 7.15; dissolved oxygen: 30%. The bioreactor received filtered air overlay and an air/oxygen/CO₂ sparge, as controlled by an Applikon controller.

The culture was fed 7 times throughout the bioreactor run, at 161, 184, 237, 256, 280, 304 and 328 hours post inoculation. The feed media were filtered into the bioreactor via peristaltic pump. The content of each feed media and the bioreactor feed parameters throughout the run are provided in Tables 17 and 18, respectively.

TABLE 17

Feed Media formulations							
Component	Feed #1	Feed #2	Feed #3	Feed #4	Feed #5	Feed #6	Feed #7
CD CHO liquid medium	1 L	1 L	1 L	1 L	1 L	1 L	1 L
GlutaMAX™-I	120 mL	80 mL	40 mL	40 mL	40 mL	30 mL	30 mL
CD CHO AGT powder	48.6 g	24.3 g	0	0	0	0	0
Yeastolate	150 mL	300 mL	300 mL	150 mL	150 mL	0	0
Ultrafiltrate (200 g/L)							
Sodium butyrate	1.65 g	2.35 g	1.65 g	1.65 g	1.65 g	1.65 g	1.65 g

TABLE 18

Bioreactor Parameters							
Hours	VCD	% viability	pH	Hyaluronidase Units	Vol (L)	Glucose	Feed
0	3.6	97	7.28	0	31	6000	—
15	6.2	94	7.45	117	31	5780	—
44	11.3	97	7.15	290	31	5320	—
88	25.6	97	6.85	517	31	3430	—
115	42.6	95	6.75	1132	31	2920	—
139	56.4	96	6.74	1320	31	2220	—
161	71.9	97	6.82	2296	31	520	Feed #1
184	83.9	96	6.81	2748	32	610	Feed #2
213	82.7	96	6.87	3396	33	1190	—
237	80.5	89	7.21	4450	33	200	Feed #3
256	62.3	71	7.03	4750	34	240	Feed #4
280	52.7	66	7.01	5030	35	600	Feed #5
304	44.6	59	7.00	5970	36	560	Feed #6
328	33.3	47	7.00	7240	37	570	Feed #7
351	26.1	34	7.00	7360	37	250	—

The bioreactor was harvested and filtered through a system that contained a series of capsule filters (Sartorius) with pore sizes of 8 μ m, 0.65 μ m, 0.45 μ m and 0.22 μ m, respectively. The harvest was performed using a peristaltic pump and completed in approximately 5 hours, yielding approximately

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32 L of harvested cell culture fluid (HCCF). The HCCF was supplemented with EDTA and Tris to final concentrations of 10 mM each, pH 7.6. The HCCF was then stored at 2-8° C. before being concentrated and subjected to a buffer exchange.

To concentrate the protein, a 2.5 ft² Millipore spiral wound cartridge with a 30 kDa MWCO was first equilibrated in 150 mM NaCl, 10 mM Hepes, 10 mM EDTA, pH 7.5. Fifteen L of HCCF was concentrated 15 $\times$ to 1 L. The concentrate was 10 $\times$ buffer exchanged with the 150 mM NaCl, 10 mM Hepes, 10 mM EDTA, pH 7.5 buffer, and the retentate was filtered through a 0.2 μ m capsule into a 2 L storage bag, for a final volume of 1.1 L. The retentate was then stored at 2-8° C.

The concentrated and buffer exchanged protein solution was then purified using column chromatography through a Q Sepharose column, a phenyl Sepharose column, an Amino Phenyl column and a Hydroxyapatite column. The hyaluronidase units in the protein solution before and after each chromatography step were assessed and used to determine the yield for each step.

Briefly, a Q sepharose column with a 1.1 L column bed was sanitized with 2.8 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then cleaned with 2.5 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, rinsed in 4.1 L sterile water for injection (SWFI) and equilibrated with 2.5 L of 10 mM

Hepes, 25 mM NaCl, pH 7.0. The buffer exchanged protein (1 L at 170,160 units/mL) was loaded onto the column. The flowthrough was 1.0 L at 479 units/mL, indicating that nearly all of the product bound the resin. The column was washed with 4 L of 10 mM Hepes, 25 mM NaCl, pH 7.0, and 4.2 L of 10 mM Hepes, 50 mM NaCl, pH 7.0. The product was then eluted in 3.0 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, yielding 3 L at 49,940 units/mL, and filtered through a 0.2 μ m filter.

A Phenyl Sepharose column with a 2.1 L column bed was sanitized with 4.8 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then rinsed with 5.0 L SWFI and cleaned with 4.6 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate and rinsed again with 6.8 L SWFI. The column was then equilibrated in 5.5 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate. To the eluate from the Q Sepharose column, 10.3 mL of 1 M potassium phosphate monobasic, 10.3 mL 1 M potassium phosphate dibasic and 0.42 mL 1 mL CaCl₂ was added. This was then loaded onto the column and the flow through and chase (1 L of 5 mM potassium phosphate, 0.5 mM ammonium sulfate) were collected, yielding 7.4 L at 20,030 units/mL. The product was filtered through a 0.2 μ m filter.

An Amino Phenyl Boronate column with a 1.8 L column bed was sanitized with 4.5 L 1.0 N NaOH and stored in 0.1 N

NaOH prior to use. It was then rinsed with 3.9 L SWFI, cleaned with 4.2 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate and rinsed again with 4.0 L SWFI. The column was then equilibrated with 7.5 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The flow through material from the Phenyl Sepharose column was loaded onto the Amino Phenyl Boronate column after being supplemented with ammonium sulfate to a final concentration of 0.5 M. The column was washed with 6.5 L of 5 mM potassium phosphate pH 7.0, then with 7.8 L of 20 mM bicine, pH 9.0 then with 9.0 L of 20 mM bicine, 100 mM NaCl, pH 9.0. The product was eluted with 4.8 L 50 mM Hepes, 100 mM NaCl, pH 7.0, resulting in 4.8 L at 22,940 units/mL, and filtered through a 0.2 μ m filter.

An Hydroxyapatite column with a 0.8 L column bed was sanitized with 2.7 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. The column was neutralized with 2.1 L of 200 mM potassium phosphate, pH 7.0 then equilibrated in 2.2 L of 5 mM potassium phosphate, 100 mM NaCl. To the eluate from the Amino Phenyl Boronate column, 9.1 mL of 1 M potassium phosphate monobasic, 9.1 mL 1 M potassium phosphate dibasic and 0.452 mL 1 M CaCl_2 was added. This was then loaded onto the column and the flow through was 4.5 L at 10 units/mL, indicating good binding of the soluble HuPH20. The column was washed with 3.3 L of 5 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0, then with 2.9 L of 10 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0. The product was eluted with 1.0 L of 70 mM potassium phosphate, pH 7.0, resulting in 1 L at 130,000 units/mL, and filtered through a 0.2 μ m filter.

The purified product was concentrated using a 2.5 ft^2 Millipore 30 kDa MWCO cartridge that had been equilibrated in 130 mM NaCl, 10 mM Hepes, pH 7.0. The product was concentrated 74 mL, and buffer exchanged 10 $\times$ with the 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer then filtered through a 0.2 μ m filter. A_{280} measurements were performed and indicated that the protein concentration was 11.3 mg/mL. An additional 9.6 mL of 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer was added to bring the protein concentration to 10 mg/mL (Lot 056-99). Ten mL of the 10 mg/mL protein solution was diluted in the buffer to yield a 1 mg/mL solution (Lot 056-100. Both solutions were filtered through a 0.2 μ m filter.

The formulated product was filled into 10 mL and 1 mL glass vials, the combined total of which yielded 761 mg soluble rHuPH20. The vials were frozen at -80°C . then transferred to -20°C . for storage. Lot 056-99 and 056-100 were then characterized with respect to activity and purity. Lots 056-99 and 056-100 exhibited 1,350,786 units/mL and 129,982 units/mL enzyme activity, and 130,00 units/mg and

124,00 units/mg specific activity (calculated from enzyme activity and protein concentration). The purity of the soluble rHuPH20 samples was determined by SDS-PAGE, IsoElectric Focusing (IEF), reverse phase high pressure liquid chromatography (RP-HPLC), size-exclusion chromatography (SEC) and anion-exchange chromatography. As determined by RP-HPLC, purity of the two Lots was observed to be approximately 95%. As determined by SEC, purity of the two Lots was observed to be approximately 99%. Endotoxin levels were shown to be <0.5 EU/mL and 0.1 EU/mL for lots 056-99 and 056-100, respectively. Osmolarity was measured to be 271 mOsm/kg and 291 mOsm/kg for lots 056-99 and 056-100, respectively.

B. Modifications to Increase Soluble rHuPH20 Production: Bioreactor Batch 2B2-20K.5

Modifications were made to the method described above in section A. These modifications were intended to increase the product yield and improve the efficiency and scalability of manufacturing. The manufacturing steps described below include thaw of frozen cells from the research cell bank, expansion of cells in continuous culture, operation of fed-batch bioreactor system, harvest and clarification of cell culture fluid, and concentration and buffer exchange of bulk product. The modifications include, for example, the addition of recombinant human insulin to the bioreactor medium to increase the growth rate and product expression levels of the cells. Also, the number of feeds has been reduced from 7 to 5. Other modifications of the methods described above also were made.

A vial of 2B2 (1×10^7 cells) was thawed and cultured in CD CHO (Invitrogen, Carlsbad, Calif.) supplemented with 20 μM methotrexate and 40 mL/L GlutaMAXTM-I (Invitrogen), after which it was expanded to 100 mL, 450 mL then to 4.5 L in CD CHO medium supplemented with 40 mL/L GlutaMAXTM-I and no methotrexate. A 36 L bioreactor containing 20 L CD CHO medium supplemented with 800 L GlutaMAXTM-I, 30 mL gentamicin sulfate and 100 mg recombinant human insulin was inoculated with 3.6 L 2B2 culture at an initial seeding density of 4.3×10^5 cell/mL. The agitation set point of the bioreactor was set to 80 RPM; temperature: 37°C .; pH: 7.15; dissolved oxygen: 25%. The bioreactor received filtered air overlay and an air/oxygen/ CO_2 sparge, as controlled by an Applikon controller.

The culture was fed 5 times throughout the 13 day bioreactor run, at 117, 143, 196, 235, and 283 hours post inoculation. The feed media were filtered into the bioreactor via peristaltic pump. The content of each feed media and the bioreactor feed parameters throughout the run are provided in Tables 19 and 20, respectively.

TABLE 19

Feed Media formulations						
Component	Initial bioreactor medium	Feed #1	Feed #2	Feed #3	Feed #4	Feed #5
CD CHO liquid medium	12 L	0	0	0	0	0
GlutaMAX TM -I	800 mL	120 mL	80 mL	40 mL	40 mL	40 mL
CD CHO	194.4 g	97.2 g	48.6 g	24.3 g	24.3 g	24.3 g
AGT powder						
SWFI	8 L	800 mL	900 mL	700 mL	700 mL	700 mL
Yeastolate	0	0	0	200 mL	200 mL	200 mL
Ultrafiltrate (200 g/L)						
Dextrose	0	30 g	60 g	40 g	40 g	40 g

TABLE 19-continued

Feed Media formulations						
Component	Initial bioreactor medium	Feed #1	Feed #2	Feed #3	Feed #4	Feed #5
Gentamicin	30 mL	0	0	0	0	0
rHuInsulin	25 mL	0	0	0	0	0
Sodium butyrate	0	0	0	2.2 g	1.1 g	1.1 g

TABLE 20

Bioreactor Parameters							
Hours	VCD	% viability	pH	Hyalu-ronidase Units	Vol (L)	Glucose	Feed
0	4.3	98	7.28	0	25	8820	—
55	17.1	99	7.07	580	25	4950	—
94	40.6	99	6.77	1059	25	3800	—
117	57.5	99	6.76	1720	25	2310	Feed #1
143	88.8	99	6.75	3168	26	2770	Feed #2
167	93.7	99	6.80	6982	27	3830	—
196	96.2	97	6.89	4560	27	2060	Feed #3
222	78.9	85	6.83	4920	28	2720	—
235	80	76	6.81	5670	28	1870	Feed #4
260	54.3	65	6.76	5865	29	2930	—
283	38.7	44	6.73	6540	29	1880	Feed #5
308	37.3	39	6.78	8460	29	2400	—
313	33.7	34	6.78	8190	29	2300	—

The bioreactor was harvested and filtered through a system that contained a series of Millipore Pod filters DOHC (0.5 m²) and A1HC stacks, which contain layers of graded-pore-size diatomaceous earth, followed by final filtration through capsule filter (Sartorius Sartobran 300) into a 50 L storage bag. The harvest was performed using a peristaltic pump and completed in approximately 2 hours, yielding approximately 30 L of harvested cell culture fluid (HCCF). Twenty-eight L HCCF was supplemented with EDTA and Tris to final concentrations of 10 mM each, and a pH 7.5. The remaining 2 L HCCF was left without Tris/EDTA, to assess the effect of adding Tris/EDTA on the concentration/buffer exchange step. The HCCF was then stored at 2-8° C. before being concentrated and subjected to a buffer exchange.

To concentrate the protein, a 0.1 m² Millipore Pellicon 2 biomax A screen cassette with a 30 kDa MWCO was first equilibrated in 20 mM Na₂SO₄, 10 mM Tris, pH 7.5. 2 L of HCCF with and without Tris/EDTA was concentrated 10× and buffer exchanged 10× with the 20 mM Na₂SO₄, 10 mM Tris, pH 7.5 buffer. The protein levels were measured by absorbance at A₂₆₀. The remaining HCCF (approximately 26.5 L) was then concentrated and subjected to buffer exchange. Two 0.1 m² Millipore Pellicon 2 biomax A screen cassettes with a 30 kDa MWCO were assembled in the TFF system and equilibrated in 20 mM Na₂SO₄, 10 mM Tris, pH

7.5. The HCCF was concentrated approximately 10× to 2.5 L, and buffer exchanged 10× with 20 mM Na₂SO₄, 10 mM Tris, pH 7.5. The retentate was filtered through a 0.2 µm vacuum filter into 1 L and 500 mL storage bags, for a final volume of 2.6 L. The retentate was then stored at 2-8° C. Samples taken during the concentration and buffer exchange process were analyzed by RP-HPLC to determine the effect of the addition of Tris/EDTA to the sample. It was observed that the addition of Tris/EDTA facilitated a more efficient processing step.

C. Production and Characterization of Soluble rHuPH20
Lots 056-122 and 056-123 (Bioreactor Batch 2B2-20K.6).

Modifications described above in section C were incorporated into the manufacturing steps to produce and purify two lots of soluble rHuPH20; Lots 056-122 and 056-123. The process described below include thaw of frozen cells from the research cell bank HZ24-2B2; expansion of cells in continuous culture; operation of 36 L fed-batch bioreactor system at the 30 L scale; cell removal, clarification, and buffer exchange of bulk product; 4-step column chromatography; and formulation, fill, and finish operations.

A vial of 2B2 (1×10⁷ cells) was thawed and cultured at 37° C., 7% CO₂ in CD CHO (Invitrogen, Carlsbad, Calif.) supplemented with 20 µM methotrexate and 40 mL/L GlutaMAX™-I (Invitrogen), after which it was expanded to 400 mL then 4.4 L in CD CHO medium supplemented with 40 mL/L GlutaMAX™-I and no methotrexate. A 36 L bioreactor (Bellco 1964 series) containing 20 L CD CHO medium supplemented with 800 L GlutaMAX™-I, 100 mg recombinant human insulin and 30 mL gentamicin sulfate was inoculated with the 4 L culture at an initial seeding density of 4.9×10⁵ cell/mL. The agitation set point of the bioreactor was set to 80 RPM; temperature: 37° C.; pH: 7.15; dissolved oxygen: 25%. The bioreactor received filtered air overlay and an air/oxygen/CO₂ sparge, as controlled by an Applikon ADI 1030 controller.

The culture was fed 4 times throughout the 13 day bioreactor run, at 127, 163, 208 and hours post inoculation. The feed media were filtered into the bioreactor via peristaltic pump. The temperature setpoint of the bioreactor was reduced from 37° C. to 36.5° C. on day 7, to 36.0° C. on day 9 and finally to 35.5° C. on day 11. The content of each feed media and the bioreactor feed parameters throughout the run are provided in Tables 21 and 22, respectively.

TABLE 21

Feed Media formulations					
Component	Initial bioreactor medium	Feed #1	Feed #2	Feed #3	Feed #4
CD CHO AGT powder (Invitrogen; part #: 10743-029; lot # 1366333)	0	97.2 g	48.6 g	24.3 g	24.3 g

TABLE 21-continued

Feed Media formulations					
Component	Initial bioreactor medium	Feed #1	Feed #2	Feed #3	Feed #4
CD CHO AGT powder (Invitrogen; part #: 10743-029; lot # 1320613)	267.3 g	0	0	0	0
CD CHO AGT powder (Invitrogen; part #: 12490-017; lot # 1300803)	218.7 g	0	0	0	0
SWFI	20 L	700 mL	700 mL	600 mL	600 mL
GlutaMAX™-I (Invitrogen)	800 mL	160 mL	80 mL	60 mL	40 mL
Yeastolate Ultrafiltrate (Invitrogen; 200 g/L)	0	100 mL	200 mL	300 mL	300 mL
Dextrose (D-glucose)	0	40 g	40 g	60 g	40 g
Gentamicin	30 mL	0	0	0	0
rHuInsulin	100 mg	40 mg	0	0	0
Sodium butyrate	0	0	1.1 g	2.2 g	1.1 g

TABLE 22

Bioreactor Parameters							
Hours	Viable cell density (×10 ⁵ cells/mL)	% viability	pH	Hyaluronidase Units	Vol (L)	Glucose	Feed
0	4.9	92	7.26	79	25	7780	—
24	9.2	95	7.21	141	25	6060	—
48	17.3	97	7.13	243	25	5280	—
72	33	99	6.82	407	25	3910	—
98	49.3	99	6.77	658	25	3200	—
127	67	98	6.83	1296	25	1610	Feed #1
144	88.1	98	6.78	1886	26	2860	—
163	92.4	99	6.89	2439	26	1680	Feed #2
192	91	97	6.85	3140	27	1480	—
208	92.7	96	6.91	3188	27	230	Feed #3
235	70	76	6.86	5118	28	1940	—
261	63	61	6.84	5862	28	280	Feed #4
291	36.4	45	6.76	7072	29	1570	—
307	29.3	32	6.81	8160	29	1250	Harvest

The bioreactor was harvested and filtered through a system that contained a series of Millipore Pod filters DOHC (0.5 m²) and A1HC stacks (0.1 m²), which contain layers of graded-pore-size diatomaceous earth, followed by final filtration through capsule filter (Sartorius Sartobran 300) into 20 L storage bags. The harvest was performed using a peristaltic pump and completed in approximately 1 hour, yielding approximately 34 L of harvested cell culture fluid (HCCF). This includes the 29 L bioreactor volume plus approximately 5 L PBS chase. The HCCF was supplemented with EDTA and Tris to final concentrations of 10 mM each, and a final pH of 7.5. The HCCF was then stored at 2-8° C. before being concentrated and subjected to a buffer exchange.

To concentrate the protein, a 7.0 ft² Sartorius Sartocoon 2 crossflow cassette with a 30 kDa MWCO was first equilibrated in 20 mM Na₂SO₄, 10 mM Tris, pH 7.5. 34 L of HCCF was concentrated 10× to 3 L and buffer exchanged 10× with the 20 mM Na₂SO₄, 10 mM Tris, pH 7.5 buffer. The retentate was filtered through a 0.2 μm capsule filter into a 5 L storage bags for a final volume of 3.0 L. The retentate was then stored at 2-8° C.

The concentrated and buffer exchanged protein solution was then purified using column chromatography through a Q

Sepharose column, a phenyl Sepharose column, an Amino Phenyl column and a Hydroxyapatite column. The hyaluronidase units in the protein solution before and after each chromatography step were assessed and used to determine the yield for each step.

Briefly, a Q sepharose column with a 1.1 L column bed, diameter 7 cm, height 28 cm was sanitized with 2.1 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then cleaned with 2.5 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, rinsed in 4.5 L sterile water for injection (SWFI) and equilibrated with 4.3 L of 10 mM Hepes, 25 mM NaCl, pH 7.0. The buffer exchanged protein (3 L at 94,960 hyaluronidase units/mL) was loaded onto the column. The flowthrough and first wash was 5830 mL at 75 hyaluronidase units/mL, indicating that nearly all of the product (99.8%) bound the resin. The column was washed with 4.2 L of 10 mM Hepes, 25 mM NaCl, pH 7.0, and 4.6 L of 10 mM Hepes, 50 mM NaCl, pH 7.0. The product was then eluted in 2.9 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, yielding 2880 mL at 96,080 units/mL, and filtered through a 0.2 μm filter.

A Phenyl Sepharose column with a 2.2 L column bed (height 28 cm, diameter 10 cm) was sanitized with 5.0 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then rinsed with 4.5 L SWFI and cleaned with 4.6 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate and rinsed again with 6.8 L SWFI. The column was then equilibrated in 4.6 L of 5 mM potassium phosphate, 0.5 mM ammonium sulfate. To the eluate from the Q Sepharose column, 9.6 mL of 1 M potassium phosphate monobasic, 9.6 mL 1 M potassium phosphate dibasic and 0.4 mL 1 M CaCl₂ was added. This was then loaded onto the column and the flow through and chase (5 mM potassium phosphate, 0.5 mM ammonium sulfate) were collected, yielding 6905 mL at 36,280 units/mL. The product was filtered through a 0.2 μm filter.

An Amino Phenyl Boronate column with a 2.2 L column bed (height 29 cm, diameter 10 cm) was sanitized with 3.8 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then rinsed with 5.0 L SWFI, cleaned with 5.0 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate and rinsed again with 5.0 L SWFI. The column was then equilibrated with 5.0 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The flow through material from the Phenyl Sepharose column was loaded onto the Amino Phenyl Boronate column. The column was washed with 9.9 L of 5 mM potassium

phosphate, 0.5M ammonium sulfate, pH 7.0, then with 9.7 L of 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0 then with 9.9 L of 20 mM bicine, 100 mM NaCl, pH 9.0. The product was eluted with 5.0 L 50 mM Hepes, 100 mM NaCl, pH 7.0, resulting in 4460 mL at 48,400 units/mL, and filtered through a 0.2 μ m filter.

A Hydroxyapatite column with a 1.1 L column bed (diameter 7 cm, height 28 cm) was sanitized with 2.7 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. The column was neutralized with 2.1 L of 200 mM potassium phosphate, pH 7.0, then equilibrated in 2.2 L of 5 mM potassium phosphate, 100 mM NaCl. To the eluate from the Amino Phenyl Boronate column, 11.2 mL of 1 M potassium phosphate monobasic, 11.2 mL 1 M potassium phosphate dibasic and 0.45 mL 1 mL CaCl_2 was added. This was then loaded onto the column and subsequently washed with 3.5 L of 5 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0, then with 3.5 L of 10 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0. The product was eluted with 1.4 L of 70 mM potassium phosphate, pH 7.0, resulting in 1260 mL at 152,560 units/mL, and filtered through a 0.2 μ m filter.

The purified product was concentrated using a 0.05 ft² Millipore 30 kDa MWCO cartridge that had been equilibrated in 130 mM NaCl, 10 mM Hepes, pH 7.0. The product was concentrated from 1250 mL at 1.04/mg/mL to 120 mL and buffer exchanged 10 $\times$ with the 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer then filtered through a 0.2 μ m filter. A₂₈₀ measurements were performed and indicated that the soluble rHuPH20 concentration of the remaining 118 ml was 11.45 mg/mL. An additional 17 mL of 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer was added to bring the protein concentration to 10 mg/mL (Lot 056-122). Ten mL of the 10 mg/mL protein solution was diluted in the buffer to yield a 1 mg/mL solution (Lot 056-123). Both solutions were filtered through a 0.2 μ m filter.

The formulated product was filled into 10 mL and 1 mL glass vials, the combined total of which yielded 1308 mg soluble rHuPH20. The vials were frozen at -80° C. then transferred to -20° C. for storage. Lot 056-122 and 056-123 were then characterized with respect to activity and purity. Lots 056-122 and 056-123 exhibited 1,376,992 units/mL and 129,412 units/mL enzyme activity, and 136,900 units/mg and

124,400 units/mg specific activity (calculated from enzyme activity and protein concentration). The purity of the soluble rHuPH20 samples was determined by SDS-PAGE, IsoElectric Focusing (IEF), reverse phase high pressure liquid chromatography (RP-HPLC), size-exclusion chromatography (SEC) and anion-exchange chromatography. As determined by RP-HPLC, purity of the two Lots was observed to be approximately 96.2%. As determined by SEC, purity of the two Lots was observed to be greater than 99%. Endotoxin levels were shown to be <0.8 EU/mL and 0.09 EU/mL for lots 056-122 and 056-123, respectively. Osmolarity was measured to be 265 mOsm/kg and 256 mOsm/kg for lots 056-122 and 056-123, respectively. The pH of each was 7.2.

D. Reproducibility of the Production Process of Gen 2 Soluble rHuPH20 in 30 L Bioreactor Cell Culture

The process described above for Batch 2B2-20K.6 was used for a subsequent batch to demonstrate the reproducibility of the process. The process was modified slightly by the incorporation of a viral inactivation step immediately prior to the column chromatography steps.

A vial of 2B2 cells (1×10^7 cells) was thawed and cultured at 37° C., 7% CO₂ for 7 passages in CD CHO (Invitrogen, Carlsbad, Calif.) supplemented with 20 μ M methotrexate and 40 mL/L GlutaMAX™-I (Invitrogen), after which it was expanded to 400 mL then 4.4 L in CD CHO medium supplemented with 40 mL/L GlutaMAX™-I and no methotrexate. A 36 L bioreactor (Bellco 1964 series) containing 20 L CD CHO medium supplemented with 800 mL GlutaMAX™-I, 100 mg recombinant human insulin and 300 mg gentamicin sulfate was inoculated with 3 L culture at an initial seeding density of 4.7×10^5 cell/mL. The agitation set point of the bioreactor was set to 80 RPM; temperature: 37° C.; pH: 7.15; dissolved oxygen: 25%. The bioreactor received filtered air overlay and an air/oxygen/CO₂ sparge, as controlled by an Applikon ADI 1030 controller.

The culture was fed 4 times throughout the 13 day bioreactor run, at 127, 163, 208 and hours post inoculation. The feed media were filtered into the bioreactor via peristaltic pump. The temperature setpoint of the bioreactor was reduced from 37° C. to 36.5° C. on day 7, to 36.0° C. on day 9 and finally to 35.5° C. on day 11. The content of each feed media and the bioreactor feed parameters throughout the run are provided in Tables 23 and 24, respectively.

TABLE 23

Feed Media formulations					
Component	Initial bioreactor medium	Feed #1	Feed #2	Feed #3	Feed #4
CD CHO liquid medium (Invitrogen)	20 L	0	0	0	0
CD CHO AGT powder	0 g	97.2 g	48.6 g	24.3 g	24.3 g
SWFI	0	700 mL	700 mL	600 mL	600 mL
GlutaMAX™-I (Invitrogen)	800 mL	160 mL	80 mL	60 mL	40 mL
Yeastolate Ultrafiltrate (Invitrogen; 200 g/L)	0	100 mL	200 mL	300 mL	300 mL
Dextrose (D-glucose)	0	40 g	40 g	60 g	50 g
Gentamicin	300 mg	0	0	0	0
rHuInsulin	100 mg	40 mg	0	0	0
Sodium butyrate	0	0	1.1 g	2.2 g	1.1 g

TABLE 24

Bioreactor Parameters							
Hours	Viable cell density ($\times 10^5$ cells/mL)	% viability	pH	Hyaluronidase Units	Vol (L)	Glucose	Feed
0	4.7	98	7.28	113	24	8200	—
24	8.9	98	7.23	202	24	6160	—
50	19.3	97	7.15	332	24	5480	—
76	36.7	99	6.85	680	24	3620	—
120	73.6	99	6.76	1619	24	2100	Feed #1
145	84.3	99	6.75	2842	25	2660	—
165	98.8	99	6.87	3756	25	840	Feed #2
190	95.3	99	6.85	4773	26	1330	—
201	105	97	6.90	5484	26	270	Feed #3
214	95.9	93	6.82	6344	27	2590	—
242	81.2	81	6.75	7890	27	1350	Feed #4
268	51.9	48	6.65	10398	28	2500	—
287	38.4	41	6.70	11864	28	2170	—
308	31.6	31	6.66	12864	28	1850	Harvest

The bioreactor was harvested and filtered through a system that contained a series of Millipore Pod filters DOHC (0.5 m²) and A 1 HC stacks (0.1 m²), which contain layers of graded-pore-size diatomaceous earth, followed by final filtration through capsule filter (Sartorius Sartobran 300) into 20 L storage bags. The harvest was performed using aperistaltic pump and completed in approximately 75 minutes, yielding approximately 30 L of harvested cell culture fluid (HCCF). This includes the 28 L bioreactor volume plus approximately 2 L PBS chase. The HCCF was supplemented with EDTA and Tris to final concentrations of 10 mM each, and a final pH of 7.5. The HCCF was then stored at 2-8° C. before being concentrated and subjected to a buffer exchange.

To concentrate the protein, a Sartorius Slice system with 3x1.0 ft² Sartocoil Slice crossflow cassettes (30 kDa MWCO) was first equilibrated in 20 mM Na₂SO₄, mM Tris, pH 7.5. Thirty liters of HCCF was concentrated 10x to 3 L and buffer exchanged 10x with the 20 mM Na₂SO₄, 10 mM Tris, pH 7.5 buffer. The average flux rate during the concentration was 115 mL/minute and the average transmembrane pressure was 16 psig. The average flux rate during the diafiltration was 150 mL/minute and the average transmembrane pressure was 15 psig. The retentate was filtered through a 0.2 µm vacuum filter systems into a 5 L storage bags for a final volume of 3.0 L. The retentate was then stored at 2-8° C.

Viral inactivation was performed by mixing 235 mL of a filtered solution of 10% w/w Triton X-100, 35 w/w Tri-butyl phosphate in SWFI with 2.15 L of room-temperature concentrated and buffer exchanged protein in a glass spinner flask stirring at 30-40 rpm. After 45 minutes, the protein solution was loaded onto the Q sepharose column (as described below). The loading took 24 minutes, which resulted in a total exposure time to the detergent solution of 69 minutes.

The Q sepharose column with a 1.1 L column bed, diameter 7 cm, height 28 cm was sanitized with 2.1 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then cleaned with 2.5 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, rinsed in 4.5 L sterile water for injection (SWFI) and equilibrated with 4.5 L of 10 mM Hepes, 25 mM NaCl, pH 7.0. The buffer exchanged, viral inactivated protein (2385 mL at 133,040 hyaluronidase units/mL) was loaded onto the column. The column was washed with 4.5 L of 10 mM Hepes, 25 mM NaCl, pH 7.0, and 4.5 L of 10 mM Hepes, 50 mM NaCl, pH 7.0. The product was then eluted in 2.5 L of 10 mM Hepes, 400 mM NaCl, pH 7.0, yielding 2500 mL at 133,680 units/mL, and filtered through a 0.2 µm filter.

A Phenyl Sepharose column with a 2.2 L column bed (height 28 cm, diameter 10 cm) was sanitized with 5.0 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then rinsed with 6.0 L SWFI and equilibrated in 4.6 L of 5 mM potassium phosphate, 0.5 mM ammonium sulfate. To elute the column, 9.6 mL of 1 M potassium phosphate monobasic, 9.6 mL 1 M potassium phosphate dibasic and 0.4 mL 1 mL CaCl₂ was added. This was then loaded onto the column and the flow through and chase (5 mM potassium phosphate, 0.5 mM ammonium sulfate) were collected, yielding 6450 mL at 43,840 units/mL. The product was filtered through a 0.2 µm filter.

An Amino Phenyl Boronate column with a 2.2 L column bed (height 29 cm, diameter 10 cm) was sanitized with 3.5 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. It was then rinsed with 5.0 L SWFI and equilibrated with 9.0 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The flow through material from the Phenyl Sepharose column was loaded onto the Amino Phenyl Boronate column. The column was washed with 9.9 L of 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0, then with 9.9 L of 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0. The product was eluted with 4.4 L 50 mM Hepes, 100 mM NaCl, pH 7.0, yielding 4389 mL at 33,840 units/mL, and filtered through a 0.2 µm filter.

A Hydroxyapatite column with a 1.1 L column bed (diameter 7 cm, height 28 cm) was sanitized with 2.1 L 1.0 N NaOH and stored in 0.1 N NaOH prior to use. The column was neutralized with 3.6 L of 200 mM potassium phosphate, pH 7.0, then equilibrated in 3.2 L of 5 mM potassium phosphate, 100 mM NaCl. To the eluate from the Amino Phenyl Boronate column, 11 mL of 1 M potassium phosphate monobasic, 11 mL 1 M potassium phosphate dibasic and 0.44 mL 1 mL CaCl₂ was added. This was then loaded onto the column and subsequently washed with 4.8 L of 5 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0, then with 3.8 L of 10 mM potassium phosphate, 100 mM NaCl, 0.5 M ammonium sulfate, pH 7.0. The product was eluted with 1.5 L of 70 mM potassium phosphate, pH 7.0, resulting in 1500 mL at 114,320 units/mL, and filtered through a 0.2 µm filter.

The purified product was concentrated using a 0.05 ft² Millipore 30 kDa MWCO cartridge that had been equilibrated in 130 mM NaCl, 10 mM Hepes, pH 7.0. The product was concentrated from 1500 mL at 0.961 mg/mL to 125 mL and buffer exchanged 10x with the 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer then filtered through a 0.2 µm filter. A₂₈₀ measurements were performed and indicated that the protein concentration of the remaining 122 mL was 11.431 mg/mL. An additional 17.5 mL of 130 mM NaCl, 10 mM Hepes, pH 7.0 buffer was added to bring the protein concentration to 10 mg/mL (Lot 056-135). Ten mL of the 10 mg/mL protein solution was diluted in the buffer to yield a 1 mg/mL solution (Lot 056-136). Both solutions were filtered through a 0.2 µm filter.

The formulated product was filled into 5 mL and 1 mL glass vials, the combined total of which yielded 1324 mg soluble rHuPH20. The vials were frozen at -80° C. then transferred to -20° C. for storage. Lot 056-135 and 056-136 were then characterized with respect to activity and purity. Lots 056-135 and 056-136 exhibited 1,301,010 units/mL and 127,661 units/mL enzyme activity, and 121,600 units/mg and 127,700 units/mg specific activity (calculated from enzyme activity and protein concentration). The purity of the soluble rHuPH20 samples was determined by SDS-PAGE, IsoElectric Focusing (IEF), reverse phase high pressure liquid chromatography (RP-HPLC), size-exclusion chromatography

(SEC) and anion-exchange chromatography. As determined by RP-HPLC, purity of the two Lots was observed to be between 93.5% and 93.7%. As determined by SEC, purity of the two Lots was observed to be greater than 99%. Endotoxin levels were shown to be <0.84 EU/mL and 0.09 EU/mL for lots 056-135 and 056-136, respectively. Osmolarity was measured to be 255 mOsm/kg and 260 mOsm/kg for lots 056-135 and 056-136, respectively. The pH of each was 7.2.

Example 8

A. Production of Gen2 Soluble rHuPH20 in 300 L Bioreactor Cell Culture

The production and purification methods detailed in Example 7, above, were scaled-up for production using a 400 L bioreactor. A vial of 2B2 cells (1×10^7 cells) was thawed and expanded from shaker flasks through 36 L spinner flasks in CD CHO (Invitrogen, Carlsbad, Calif.) supplemented with 20 μ M methotrexate and 8 mM GlutaMAX™-I (Invitrogen). Briefly, the a vial of cells was thawed in a 37° C. water bath, media was added and the cells were centrifuged. The cells were re-suspended in a 125 mL shake flask with 20 mL of fresh media and placed in a 37° C., 7% CO₂ incubator. The cells were expanded up to 40 mL in the 125 mL shake flask. When the cell density reached greater than 1.5×10^6 cells/mL, the culture was expanded into a 125 mL spinner flask in a 100 mL culture volume. The flask was incubated at 37° C., 7% CO₂. When the cell density reached greater than 1.5×10^6 cells/mL, the culture was expanded into a 250 mL spinner flask in 200 mL culture volume, and the flask was incubated at 37° C., 7% CO₂. When the cell density reached greater than 1.5×10^6 cells/mL, the culture was expanded into a 1 L spinner flask in 800 mL culture volume and incubated at 37° C., 7% CO₂. When the cell density reached greater than 1.5×10^6 cells/mL, the culture was expanded into a 6 L spinner flask in 5000 mL culture volume and incubated at 37° C., 7% CO₂. When the cell density reached greater than 1.5×10^6 cells/mL the culture was expanded into a 36 L spinner flask in 32 L culture volume and incubated at 37° C., 7% CO₂.

A 400 L reactor was sterilized by steam at 121° C. for 30 minutes and 230 mL of CD CHO media supplemented with 8 mM GlutaMAX™-I and 5 mg/L rHuInsulin was added. Before use, the reactor was checked for contamination. Approximately 30 L cells were transferred from the 36 L spinner flasks to the 400 L bioreactor (Braun) at an inoculation density of 4.0×10^5 viable cells per ml and a total volume of 260 L. Parameters were temperature setpoint, 37° C.; Impeller Speed 40-55 RPM; Vessel Pressure: 3 psi; Air Sparge 0.5-1.5 L/Min.; Air Overlay: 3 L/min. The reactor was sampled daily for cell counts, pH verification, media analysis, protein production and retention. Also, during the run nutrient feeds were added. At 120 hrs (day 5), 10.4 L of Feed #1 Medium (4×CD CHO+33 g/L Glucose+160 mL/L GlutaMAX™-I+16.6 g/L Yeastolate+33 mg/L rHuInsulin) was added. At 168 hours (day 7), 10.8 L of Feed #2 (2×CD CHO+33 g/L Glucose+80 mL/L GlutaMAX™-I+33.4 g/L Yeastolate+0.92 g/L Sodium Butyrate) was added, and culture temperature was changed to 36.5° C. At 216 hours (day 9), 10.8 L of Feed #3 (1×CD CHO+50 g/L Glucose+50 mL/L GlutaMAX™-I+50 g/L Yeastolate+1.80 g/L Sodium Butyrate) was added, and culture temperature was changed to 36° C. At 264 hours (day 11), 10.8 L of Feed #4 (1× CD CHO+33 g/L Glucose+33 mL/L GlutaMAX™-I+50 g/L Yeastolate+0.92 g/L Sodium Butyrate) was added, and culture temperature was changed to 35.5° C. The addition of the feed media was observed to dramatically enhance the production of soluble rHuPH20 in the final stages of production. The

reactor was harvested at 14 days or when the viability of the cells dropped below 40%. The process resulted in a final productivity of 17,000 Units per ml with a maximal cell density of 12 million cells/mL. At harvest, the culture was sampled for mycoplasma, bioburden, endotoxin and viral in vitro and in vivo, TEM for viral particles and enzyme activity.

The culture was pumped by a peristaltic pump through four Millistak filtration system modules (Millipore) in parallel, each containing a layer of diatomaceous earth graded to 4-8 μ m and a layer of diatomaceous earth graded to 1.4-1.1 μ m, followed by a cellulose membrane, then through a second single Millistak filtration system (Millipore) containing a layer of diatomaceous earth graded to 0.4-0.1 μ m and a layer of diatomaceous earth graded to <0.1 μ m, followed by a cellulose membrane, and then through a 0.22 μ m final filter into a sterile single use flexible bag with a 350 L capacity. The harvested cell culture fluid was supplemented with 10 mM EDTA and 10 mM Tris to a pH of 7.5. The culture was concentrated 10× with a model tangential flow filtration (TFF) apparatus using four Sartoslice TFF 30 kDa molecular weight cut-off (MWCO) polyether sulfone (PES) filters (Sartorius), followed by a 10× buffer exchange with 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 into a 0.22 μ m final filter into a 50 L sterile storage bag.

The concentrated, diafiltered harvest was inactivated for virus. Prior to viral inactivation, a solution of 10% Triton X-100, 3% tri (n-butyl) phosphate (TNBP) was prepared. The concentrated, diafiltered harvest was exposed to 1% Triton X-100, 0.3% TNBP for 1 hour in a 36 L glass reaction vessel immediately prior to purification on the Q column.

B. Purification of Gen2 sHuPH20

A Q Sepharose (Pharmacia) ion exchange column (9 L resin, H=29 cm, D=20 cm) was prepared. Wash samples were collected for a determination of pH, conductivity and endotoxin (LAL) assay. The column was equilibrated with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5. Following viral inactivation, the concentrated, diafiltered harvest was loaded onto the Q column at a flow rate of 100 cm/hr. The column was washed with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 and 10 mM Hepes, 50 mM NaCl, pH 7.0. The protein was eluted with 10 mM Hepes, 400 mM NaCl, pH 7.0 into a 0.22 μ m final filter into sterile bag. The eluate sample was tested for bioburden, protein concentration and enzyme activity. A₂₈₀ absorbance readings were taken at the beginning and end of the exchange.

Phenyl-Sepharose (Pharmacia) hydrophobic interaction chromatography was next performed. A Phenyl-Sepharose (PS) column (19-21 L resin, H=29 cm, D=30 cm) was prepared. The wash was collected and sampled for pH, conductivity and endotoxin (LAL assay). The column was equilibrated with 5 column volumes of 5 mM potassium phosphate, 0.5 M ammonium sulfate, 0.1 mM CaCl₂, pH 7.0. The protein eluate from above was supplemented with 2M ammonium sulfate, 1 M potassium phosphate and 1 M CaCl₂ stock solutions to yield final concentrations of 5 mM, 0.5 M and 0.1 mM, respectively. The protein was loaded onto the PS column at a flow rate of 100 cm/hr. 5 mM potassium phosphate, 0.5 M ammonium sulfate and 0.1 mM CaCl₂ pH 7.0 was added at 100 cm/hr. The flow through was passed through a 0.22 μ m final filter into a sterile bag. The flow through was sampled for bioburden, protein concentration and enzyme activity.

An aminophenyl boronate column (ProMedics; 21 L resin, H=29 cm, D=30 cm) was prepared. The wash was collected and sampled for pH, conductivity and endotoxin (LAL assay). The column was equilibrated with 5 column volumes of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The PS purified protein was loaded onto the aminophenyl bor-

onate column at a flow rate of 100 cm/hr. The column was washed with 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0. The column was washed with 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0. The column was washed with 20 mM bicine, 100 mM sodium chloride, pH 9.0. The protein was eluted with 50 mM Hepes, 100 mM NaCl, pH 6.9 and passed through a sterile filter into a sterile bag. The eluted sample was tested for bioburden, protein concentration and enzyme activity.

The hydroxyapatite (HAP) column (BioRad; 13 L resin, H=20 cm, D=30 cm) was prepared. The wash was collected and test for pH, conductivity and endotoxin (LAL assay). The column was equilibrated with 5 mM potassium phosphate, 100 mM NaCl, 0.1 mM CaCl₂, pH 7.0. The aminophenyl boronate purified protein was supplemented to final concentrations of 5 mM potassium phosphate and 0.1 mM CaCl₂ and loaded onto the HAP column at a flow rate of 100 cm/hr. The column was washed with 5 mM potassium phosphate, pH 7, 100 mM NaCl, 0.1 mM CaCl₂. The column was next washed with 10 mM potassium phosphate, pH 7, 100 mM NaCl, 0.1 mM CaCl₂. The protein was eluted with 70 mM potassium phosphate, pH 7.0 and passed through a 0.22 µm sterile filter into a sterile bag. The eluted sample was tested for bioburden, protein concentration and enzyme activity.

The HAP purified protein was then passed through a viral removal filter. The sterilized Virosart filter (Sartorius) was first prepared by washing with 2 L of 70 mM potassium phosphate, pH 7.0. Before use, the filtered buffer was sampled for pH and conductivity. The HAP purified protein was pumped via a peristaltic pump through the 20 nM viral removal filter. The filtered protein in 70 mM potassium phosphate, pH 7.0 was passed through a 0.22 µm final filter into a sterile bag. The viral filtered sample was tested for protein

concentration, enzyme activity, oligosaccharide, monosaccharide and sialic acid profiling (as described in Examples 9 to 10, below).

The protein in the filtrate was then concentrated to 10 mg/mL using a 10 kD molecular weight cut off (MWCO) Sartoon Slice tangential flow filtration (TFF) system (Sartorius). The filter was first prepared by washing with 10 mM histidine, 130 mM NaCl, pH 6.0 and the permeate was sampled for pH and conductivity. Following concentration, the concentrated protein was sampled and tested for protein concentration and enzyme activity. A 6× buffer exchange was performed on the concentrated protein into the final buffer: 10 mM histidine, 130 mM NaCl, pH 6.0. Following buffer exchange, the concentrated protein was passed through a 0.22 µm filter into a 20 L sterile storage bag. The protein was sampled and tested for protein concentration, enzyme activity, free sulfhydryl groups, oligosaccharide profiling and osmolarity (as described in Examples 9 to 10, below).

The sterile filtered bulk protein was then aseptically dispensed at 20 mL into 30 mL sterile Teflon vials (Nalgene). The vials were then flash frozen and stored at -20±5° C. Production and purification of soluble rHuPH20 using this method yielded approximately 11 and 15 grams, with specific activity of 95,000 units/mg to 120,000 units/mg.

C. Comparison of Production and Purification of Gen1 and Gen2 sHuPH20

The production and purification of Gen2 soluble rHuPH20 in a 300 L bioreactor cell culture contained some changes in the protocols compared to the production and purification of Gen1 soluble rHuPH20 in a 100 L bioreactor cell culture (described in Example 4). Table 25 sets forth exemplary differences, in addition to simple scale up changes, between the methods.

TABLE 25

Exemplary differences between Gen1 and Gen2 soluble rHuPH20 production and purification using the 100 L and 300 L bioreactor cell culture methods		
Process Difference	Gen1 soluble rHuPH20	Gen2 soluble rHuPH20
Cell line	3D35M	2B2
Media used to expand cell inoculum	Contains 0.10 µM methotrexate (0.045 mg/L)	Contains 20 µM methotrexate (9 mg/L)
Media in 6 L cultures onwards	Contains 0.10 µM methotrexate	Contains no methotrexate
36 L spinner flask	No instrumentation 20 L operating volume.	Equipped with instrumentation that monitors and controls pH, dissolved oxygen, sparge and overlay gas flow rate. 32 L operating volume
Final operating volume in bioreactor	Approx. 100 L in a 125 L bioreactor (initial culture volume + 65 L)	Approx. 300 L in a 400 L bioreactor (initial culture volume + 260 L)
Culture media in final bioreactor	No rHuInsulin	5.0 mg/L rHuInsulin
Media feed volume	Scaled at 4% of the bioreactor cell culture volume i.e. 3.4, 3.5 and 3.7 L, resulting in a target bioreactor volume of ~92 L.	Scaled at 4% of the bioreactor cell culture volume i.e. 10.4, 10.8, 11.2 and 11.7 L, resulting in a target bioreactor volume of ~303 L.
Media feed	Feed #1 Medium: CD CHO + 50 g/L Glucose + 8 mM GlutaMAX™-I Feed #2 (CD CHO + 50 g/L Glucose + 8 mM GlutaMAX™-I + 1.1 g/L Sodium Butyrate Feed #3: CD CHO + 50 g/L Glucose + 8 mM	Feed #1 Medium: 4x CD CHO + 33 g/L Glucose + 32 mM GlutaMAX™-I + 16.6 g/L Yeastolate + 33 mg/L rHuInsulin Feed #2: 2x CD CHO + 33 g/L Glucose + 16 mM GlutaMAX™-I + 33.4 g/L Yeastolate + 0.92 g/L

TABLE 25-continued

Exemplary differences between Gen1 and Gen2 soluble rHuPH20 production and purification using the 100 L and 300 L bioreactor cell culture methods		
Process Difference	Gen1 soluble rHuPH20	Gen2 soluble rHuPH20
	GlutaMAX TM -I + 1.1 g/L Sodium Butyrate	Sodium Butyrate Feed #3: 1x CD CHO + 50 g/L Glucose + 10 mM GlutaMAX TM -I + 50 g/L Yeastolate + 1.80 g/L Sodium Butyrate Feed #4: 1x CD CHO + 33 g/L Glucose + 6.6 mM GlutaMAX TM -I + 50 g/L Yeastolate + 0.92 g/L Sodium Butyrate
Filtration of bioreactor cell culture	Four polyethersulfone filters (8.0 µm, 0.65 µm, 0.22 µm and 0.22 µm) in series 100 L storage bag	1 st stage - Four modules in parallel, each with a layer of diatomaceous earth graded to 4-8 µm and a layer of diatomaceous earth graded to 1.4-1.1 µm, followed by a cellulose membrane. 2 nd stage -single module containing a layer of diatomaceous earth graded to 0.4-0.11 µm and a layer of diatomaceous earth graded to <0.1 µm, followed by a cellulose membrane. 3 rd stage - 0.22 µm polyethersulfone filter 300 L storage bag Harvested cell culture is supplemented with 10 mM EDTA, 10 mM Tris to a pH of 7.5.
Concentration and buffer exchange prior to chromatography	Concentrate with 2 TFF with Millipore Spiral Polyethersulfone 30K MWCO Filter Buffer Exchange the Concentrate 6x with 10 mM Hepes, 25 mM NaCl, pH 7.0 20 L sterile storage bag	Concentrate using four Sartorius Sartoslice TFF 30K MWCO Filter Buffer Exchange the Concentrate 10x with 10 mM Tris, 20 mM Na2SO4, pH 7.5 50 L sterile storage bag
Viral inactivation prior to chromatography	None	Viral inactivation performed with the addition of a 1% Triton X-100, 0.3% Tributyl Phosphate, pH 7.5, A280 measurements at the beginning and end Sartorius Virosart filter (20 nm)
1 st purification step (Q sepharose)	No absorbance reading	
Viral filtration after chromatography	Pall DV-20 filter (20 nm)	
Concentration and buffer exchange after chromatography	Hepes/saline pH 7.0 buffer Protein concentrated to 1 mg/ml	Histidine/saline, pH 6.0 buffer Protein concentrated to 10 mg/ml
Vial filling	5 mL and 1 mL fill volumes Stored at -≤30° C. Glass/rubber stopper	20 mL fill volumes Stored at ≤20° C. Teflon/screw cap
Soluble rHuPH20 yield	Approx. 400-700 mg	Approx. 11-25 g

Example 9

Determination of Enzymatic Activity of Soluble rHuPH20

Enzymatic activity of soluble rHuPH20 in samples such as cell cultures, purification fractions and purified solutions was determined using a turbidometric assay, which based on the formation of an insoluble precipitate when hyaluronic acid binds with serum albumin. The activity is measured by incu-

bating soluble rHuPH20 with sodium hyaluronate (hyaluronic acid) for a set period of time (10 minutes) and then precipitating the undigested sodium hyaluronate with the addition of acidified serum albumin. The turbidity of the resulting sample is measured at 640 nm after a 30 minute development period. The decrease in turbidity resulting from enzyme activity on the sodium hyaluronate substrate is a measure of the soluble rHuPH20 enzymatic activity. The method is run using a calibration curve generated with dilutions of a soluble rHuPH20 assay working reference standard,

and sample activity measurements are made relative to this calibration curve.

Dilutions of the sample were prepared in Enzyme Diluent Solutions. The Enzyme Diluent Solution was prepared by dissolving 33.0 ± 0.05 mg of hydrolyzed gelatin in 25.0 mL of the 50 mM PIPES Reaction Buffer (140 mM NaCl, 50 mM PIPES, pH 5.5) and 25.0 mL of SWFI, and diluting 0.2 mL of 25% Buminate solution into the mixture and vortexing for 30 seconds. This was performed within 2 hours of use and stored on ice until needed. The samples were diluted to an estimated 1-2 U/mL. Generally, the maximum dilution per step did not exceed 1:100 and the initial sample size for the first dilution was not be less than 20 μ L. The minimum sample volumes needed to perform the assay were: In-process Samples, FPLC Fractions: 80 μ L; Tissue Culture Supernatants: 1 mL; Concentrated Material 80 μ L; Purified or Final Step Material: 80 μ L. The dilutions were made in triplicate in a Low Protein Binding 96-well plate, and 30 μ L of each dilution was transferred to Optilux black/clear bottom plates (BD Biosciences).

Dilutions of known soluble rHuPH20 with a concentration of 2.5 U/mL were prepared in Enzyme Diluent Solution to generate a standard curve and added to the Optilux plate in triplicate. The dilutions included 0 U/mL, 0.25 U/mL, 0.5 U/mL, 1.0 U/mL, 1.5 U/mL, 2.0 U/mL, and 2.5 U/mL. "Reagent blank" wells that contained 60 μ L of Enzyme Diluent Solution were included in the plate as a negative control. The plate was then covered and warmed on a heat block for 5 minutes at 37° C. The cover was removed and the plate was shaken for 10 seconds. After shaking, the plate was returned to the plate to the heat block and the MULTIDROP 384 Liquid Handling Device was primed with the warm 0.25 mg/mL sodium hyaluronate solution (prepared by dissolving 100 mg of sodium hyaluronate (LifeCore Biomedical) in 20.0 mL of SWFI. This was mixed by gently rotating and/or rocking at 2-8° C. for 2-4 hours, or until completely dissolved). The reaction plate was transferred to the MULTIDROP 384 and the reaction was initiated by pressing the start key to dispense 30 μ L sodium hyaluronate into each well. The plate was then removed from the MULTIDROP 384 and shaken for 10 seconds before being transferred to a heat block with the plate cover replaced. The plate was incubated at 37° C. for 10 minutes

The MULTIDROP 384 was prepared to stop the reaction by priming the machine with Serum Working Solution and changing the volume setting to 240 μ L. (25 mL of Serum Stock Solution [1 volume of Horse Serum (Sigma) was diluted with 9 volumes of 500 mM Acetate Buffer Solution and the pH was adjusted to 3.1 with hydrochloric acid] in 75 mL of 500 mM Acetate Buffer Solution). The plate was removed from the heat block and placed onto the MULTIDROP 384 and 240 μ L of serum Working Solutions was dispensed into the wells. The plate was removed and shaken on a plate reader for 10 seconds. After a further 15 minutes, the turbidity of the samples was measured at 640 nm and the enzyme activity (in U/mL) of each sample was determined by fitting to the standard curve.

Specific activity (Units/mg) was calculated by dividing the enzyme activity (U/ml) by the protein concentration (mg/mL).

Example 10

Determination of Sialic Acid and Monosaccharide Content

The sialic acid and monosaccharide content of soluble rHuPH20 can be assessed by reverse phase liquid chromatog-

raphy (RPLC) following hydrolysis with trifluoroacetic acid. In one example, the sialic acid and monosaccharide content of purified hyaluronidase lot # HUB0701E (1.2 mg/mL; produced and purified essentially as described in Example 8) was determined. Briefly, 100 μ g sample was hydrolyzed with 40% (v/v) trifluoroacetic acid at 100° C. for 4 hours in duplicate.

Following hydrolysis, the samples were dried down and resuspended in 300 μ L water. A 45 μ L aliquot from each re-suspended sample was transferred to a new tube and dried down, and 10 μ L of a 10 mg/mL sodium acetate solution was added to each. The released monosaccharides were fluorescently labeled by the addition of 50 μ L of a solution containing 30 mg/mL 2-aminobenzoic acid, 20 mg/mL sodium cyanoborohydride, approximately 40 mg/mL sodium acetate and 20 mg/mL boric acid in methanol. The mixture was incubated for 30 minutes at 80° C. in the dark. The derivitization reaction was quenched by the addition of 440 μ L of mobile phase A (0.2% (v/v) n-butylamine, 0.5% (v/v) phosphoric acid, 1% (v/v) tetrahydrofuran). A matrix blank of water also was hydrolyzed and derivitized as described for the hyaluronidase sample as a negative control. The released monosaccharides were separated by RPLC using an Octadecyl (C_{18}) reverse phase column (4.6x250 mm, 5 μ m particle size; J. T. Baker) and monitored by fluorescence detection (360 nm excitation, 425 nm emission). Quantitation of the monosaccharide content was made by comparison of the chromatograms from the hyaluronidase sample with chromatograms of monosaccharide standards including N-D-glucosamine (GlcN), N-D-galactosamine (GalN), galactose, fucose and mannose. Table 26 presents the molar ratio of each monosaccharide per hyaluronidase molecule.

TABLE 26

Monosaccharide content of soluble rHuPH20						
Lot	Replicate	GlcN	GalN	Galactose	Mannose	Fucose
HUB0701E	1	14.28	0.07*	6.19	25.28	2.69
	2	13.66	0.08*	6.00	24.34	2.61
	Average	13.97	0.08*	6.10	24.81	2.65

*GalN results were below the limit of detection

Example 11

C-terminal Heterogeneity of Soluble rHuPH20 from 3D35M and 2B2 Cells

C-terminal sequencing was performed on two lots of sHuPH20 produced and purified from 3D35M cells in a 100 L bioreactor volume (Lot HUA0505MA) and 2B2 cells in a 300 L bioreactor volume (Lot HUB0701EB). The lots were separately digested with endoproteinase Asp-N, which specifically cleaves peptide bonds N-terminally at aspartic and cysteic acid. This releases the C-terminal portion of the soluble rHuPH20 at the aspartic acid at position 431 of SEQ ID NO:4. The C-terminal fragments were separated and characterized to determine the sequence and abundance of each population in Lot HUA0505MA and Lot HUB0701EB.

It was observed that the soluble rHuPH20 preparations from 3D35M cells and 2B2 cells displayed heterogeneity, and contained polypeptides that differed from one another in their C-terminal sequence (Tables 27 and 28). This heterogeneity is likely the result of C-terminal cleavage of the expressed 447 amino acid polypeptide (SEQ ID NO:4) by peptidases present in the cell culture medium or other solutions during the production and purification process. The polypeptides in the

soluble rHuPH20 preparations have amino acid sequences corresponding to amino acids 1-447, 1-446, 1-445, 1-444 and 1-443 of the soluble rHuPH20 sequence set forth SEQ ID NO:4. The full amino acid sequence of each of these polypeptides is forth in SEQ ID NOS: 4 to 8, respectively. As noted in tables 27 and 28, the abundance of each polypeptide in the soluble rHuPH20 preparations from 3D35M cells and 2B2 cells differs.

TABLE 27

Analysis of C-terminal fragments from Lot HUA0505MA							
Frag- ment	Amino acid position (relative to SEQ ID NO: 4)	Sequence	Theor. Mass	Exp. Mass	Error	Elution time	Abundance
D28a	431-447	DAFKLPPMETEEPQIFY (SEQ ID NO: 66)	2053.97	2054.42	0.45	99.87	0.2%
D28b	431-446	DAFKLPPMETEEPQIF (SEQ ID NO: 67)	1890.91	1891.28	0.37	97.02	18.4%
D28c	431-445	DAFKLPPMETEEPQI (SEQ ID NO: 68)	1743.84	1744.17	0.33	86.4	11.8%
D28d	431-444	DAFKLPPMETEEPQ (SEQ ID NO: 69)	1630.70	1631.07	0.32	74.15	56.1%
D28e	431-443	DAFKLPPMETEEP (SEQ ID NO: 70)	1502.70	1502.98	0.28	77.36	13.6%
D28f	431-442	DAFKLPPMETEE (SEQ ID NO: 71)	1405.64	ND	N/A	N/A	0.0%

TABLE 28

Analysis of C-terminal fragments from Lot HUB0701EB							
Frag- ment	Amino acid position (relative to SEQ ID NO: 4)	Sequence	Theor. Mass	Exp. Mass	Error	Elution time	Abundance
D28a	431-477	DAFKLPPMETEEPQIFY (SEQ ID NO: 66)	2053.97	2054.42	0.45	99.89	1.9%
D28b	431-446	DAFKLPPMETEEPQIF (SEQ ID NO: 67)	1890.91	1891.36	0.45	96.92	46.7%
D28c	431-445	DAFKLPPMETEEPQI (SEQ ID NO: 68)	1743.84	1744.24	0.40	85.98	16.7%
D28d	431-444	DAFKLPPMETEEPQ (SEQ ID NO: 69)	1630.70	1631.14	0.39	73.9	27.8%
D28e	431-443	DAFKLPPMETEEP (SEQ ID NO: 70)	1502.70	1503.03	0.33	77.02	6.9%
D28f	431-442	DAFKLPPMETEE (SEQ ID NO: 71)	1405.64	ND	N/A	N/A	0.0%

Example 12

Production and Purification of Soluble rHuPH20 in 2500 L Bioreactor Cell Culture

The production and purification of soluble rHuPH20 can be scaled up from a 300 L batch-fed bioreactor process (de-

scribed in Example 8) to a 2500 L batch-fed bioreactor process. Like production of rHuPH20 in a 300 L bioreactor cell culture, the production of rHuPH20 in a 2500 L bioreactor cell culture is performed by first thawing and expanding a vial of 2B2 cells, culturing in a bioreactor, harvesting and clarifying the culture, concentrating and buffer-exchanging the harvest, followed by viral inactivation. The rHuPH20 is then purified from the concentrate using a series of purification

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steps that utilize Q sepharose, Phenyl sepharose, aminophenyl boronate and hydroxyapatite boronate, followed by viral filtration.

1. Cell Culture Expansion

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To generate higher cell numbers required for seeding the 2500 L bioreactor cell culture compared to the 300 L culture, the cell culture is serially expanded through a 125 mL shaker

flask, a 250 mL shaker, a 1 L shaker flask, two 2 L shaker flasks, six 2 L shaker flasks, a 25 L WAVE Bioreactor™ (GE Healthcare Life Sciences), a 100 L WAVE Bioreactor™, and a 600 L stirred tank seed bioreactor (ABEC, Inc. Bethlehem, Pa.; Stainless Technology division). At each expansion, the target seeding density is 4×10^5 cells/mL. The temperature throughout the expansion is 37° C. (or between 36° C. and 38° C.) with 7% CO₂ (or between 6-8% CO₂). The flasks are agitated at approximately 110 RPM (or 90-130 RPM), the 25 L and 100 L WAVE Bioreactor™ are rocked at 20 RPM (or 15-25 or 18-22 RPM, respectively) and the 600 L seed bioreactor is agitated at 90 RPM (or 85-95 RPM).

First, a vial of 2B2 cells (1×10^7 cells) from the working cell bank is thawed in a 37° C. water bath for approximately 2 minutes (preferably no more than 5 minutes) before media is added and the cells are centrifuged. The cells are re-suspended to approximately 25 mL (or between 20-30 mL) with fresh media (CD CHO AGT™ with 40 mL/L (8 mM) GlutaMAX™-I and 20 μM methotrexate in a 125 mL shaker flask and placed in a 37° C., 7% CO₂ incubator. When the cell density reaches approximately 8×10^5 cells/mL, the culture is transferred into a 250 mL shake flask in a 50 mL culture volume (or 45-55 mL). Following incubation, when the cell density reaches approximately 1.6×10^6 cells/mL, the culture is expanded into a 1 L flask in 200 mL culture volume (or 190-210 mL) and incubated. When the cell density in the 1 L flask reaches approximately 1.6×10^6 cells/mL, the culture is expanded into 2x2 L flasks, each with a total culture volume of approximately 400 mL (or between 350-450 mL per flask), and incubated. When the cell density in the 2 L flasks reaches approximately 1.2×10^6 cells/mL, the culture is expanded into 6x2 L flasks, each with a total culture volume of approximately 400 mL (or between 350-450 mL per flask), and incubated. When the cell density in the 2 L flasks reaches approximately 2.5×10^6 cells/mL, the culture is expanded into a 25 L WAVE Bioreactor™, with a total culture volume of approximately 15 L (or between 14-16 L) and incubated with an air flow of 1.5 L/minute.

When the cell density in the 25 L WAVE Bioreactor™ reaches approximately 2.2×10^6 cells/mL, the culture is expanded into a 100 L WAVE Bioreactor™, with a total culture volume of approximately 80 L (or between 75-85 L), using CD-CHO AGT™ media that is supplemented with 3.6 g/L methotrexate, 40 mL/L GlutaMAX™-I and 1 mL/L 1N NaOH, and incubated with an air flow of 1.5 L/minute. When the cell density in the 100 L WAVE Bioreactor™ reaches approximately 2.6×10^6 cells/mL, the culture is expanded into a 600 L seed bioreactor ABEC, Inc. Bethlehem, Pa.; Stainless Technology division) with a total culture volume of approximately 480 L (or between 440-520 L) using CD-CHO AGT™ media that is supplemented with 40 mL/L GlutaMAX™-I and incubated until the cell density in the 600 L bioreactor reaches approximately 1.6×10^6 cells/mL.

2. rHuPH20 Production

A 3500 L bioreactor with a total volume of 3523 L and a working volume of 500-2500 L (ABEC, Inc. Bethlehem, Pa.) is used for high yield production of rHuPH20. Following sterilization, approximately 1800-2000 L CD-CHO AGT™ media containing 24.3 g/L powdered CD-CHO AGT™, supplemented with 40 mL/L GlutaMAX™-I and 5 mg/L rHuInsulin is added to the bioreactor. Parameters are set to: temperature setpoint, 37° C.; Impeller Speed 75 RPM; Vessel Pressure: 5 psi; Air Sparge 18 L/min; dissolved oxygen: 25%; pH ≤ 7.2 . Before use, the reactor is checked for contamination. Approximately between 300-500 L of cells (depending on cell count) from the 600 L seed bioreactor culture are inoculated into the cell culture medium in the 3500 L biore-

actor at an inoculation density of 4.0×10^5 viable cells per mL, to reach a total volume of 2100 L. During the 14 day cell incubation, the bioreactor is sampled daily for cell viability, cell density, pH verification, and enzymatic activity. Temperature and dissolved oxygen also are monitored closely.

Nutrient feeds are added during the 14 day bioreactor run, each at approximately 4% v/v. At day 5, approximately 84 L (or 4% v/v) of Feed #1 Medium (81 g/L powdered CD-CHO AGT™+33 g/L Glucose+13.3 mL/L GlutaMAX™-I+83.3 g/L Yeastolate+33 mg/L rHuInsulin) is added. At day 7, approximately 87 L (or 4% v/v) of Feed #2 (40.5 g/L powdered CD-CHO AGT™+33 g/L Glucose+66.7 mL/L GlutaMAX™-I+166.7 g/L Yeastolate+0.92 g/L Sodium butyrate) is added, and culture temperature is changed to 36.5° C. At day 9, approximately 91 L (or 4% v/v) of Feed #3 (20.3 g/L powdered CD-CHO AGT™+50 g/L Glucose+50 mL/L GlutaMAX™-I+250 g/L Yeastolate+1.8 g/L Sodium butyrate) is added, and culture temperature is changed to 36° C. At day 11, approximately 94 L (or 4% v/v) of Feed #4 (20.3 g/L powdered CD-CHO AGT™+33.3 g/L Glucose+33.3 mL/L GlutaMAX™-I+250 g/L Yeastolate+0.92 g/L Sodium butyrate) is added, and culture temperature is changed to 35.5° C. The reactor is harvested at 14 days, yielding 2400-2600 L harvest (typically approximately 2500 L).

The culture is pressure transferred through 20 Millistak filtration system modules (Millipore) in parallel, each containing a layer of diatomaceous earth graded to 4-8 μm and a layer of diatomaceous earth graded to 1.4-1.1 μm, followed by a cellulose membrane, then through a second Millistak filtration system (Millipore) containing 10 modules, each with a layer of diatomaceous earth graded to 0.4-0.11 μm and a layer of diatomaceous earth graded to <0.1 μm, followed by a cellulose membrane, and then through a 0.22 μm final filter into a sterile single use flexible bag with a 350 L capacity. The harvested cell culture fluid is supplemented with 10 mM EDTA and 10 mM Tris, pH 8.4, to a target pH of 7.5. The culture is concentrated 10x with a tangential flow filtration (TFF) apparatus (Pall) using 18-21 m² of Sartoslice TFF 30 kDa molecular weight cut-off (MWCO) polyether sulfone (PES) filters (Sartorius), followed by a 10x buffer exchange with 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 into a 0.22 μm final filter into a 350 L sterile storage bag.

The concentrated, diafiltered harvest is inactivated for virus. Prior to viral inactivation, a solution of 10% Triton X-100, 3% tri (n-butyl) phosphate (TNBP) was prepared. The concentrated, diafiltered harvest was exposed to 1% Triton X-100, 0.3% TNBP up to 2 hours in 500 L stainless steel reaction vessels immediately prior to purification on the Q column.

B. Purification of Gen2 rHuPH20

A Q Sepharose (Pharmacia) ion exchange column (81 L resin, H=26 cm, D=63 cm) is prepared. The column is equilibrated with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5. Following viral inactivation, the concentrated, diafiltered, viral-inactivated harvest of approximately 250 L is loaded onto the Q column at a flow rate of 150 cm/hr. The column is washed with 5 column volumes of 10 mM Tris, 20 mM Na₂SO₄, pH 7.5 and 10 mM Hepes, 50 mM NaCl, pH 7.0. The protein is eluted with 10 mM Hepes, 400 mM NaCl, pH 7.0 into a 0.22 μm final filter into sterile bag. The eluate sample is tested for bioburden, protein concentration and enzyme activity. A₂₈₀ absorbance reading were taken at the beginning and end of the exchange.

Phenyl-Sepharose (Pharmacia) hydrophobic interaction chromatography is next performed. A Phenyl-Sepharose (PS) column (176 L resin, H=35 cm, D=80 cm) is prepared. The column is equilibrated with 5 column volumes of 5 mM

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potassium phosphate, 0.5 M ammonium sulfate, 0.1 mM CaCl_2 , pH 7.0. The protein eluate from above is supplemented with 2M ammonium sulfate, 1 M potassium phosphate and 1 M CaCl_2 stock solutions to yield final concentrations of 5 mM, 0.5 M and 0.1 mM, respectively. The protein is loaded onto the PS column at a flow rate of 100 cm/hr. 5 mM potassium phosphate, 0.5 M ammonium sulfate and 0.1 mM CaCl_2 pH 7.0 was added at 100 cm/hr. The flow through is passed through a 0.22 μm final filter into a sterile bag. The flow through is sampled for bioburden, protein concentration and enzyme activity.

An aminophenyl boronate column (ProMedics; 176 L resin, H=35 cm, D=80 cm) is then prepared. The column is equilibrated with 5 column volumes of 5 mM potassium phosphate, 0.5 M ammonium sulfate. The PS-purified protein is loaded onto the aminophenyl boronate column at a flow rate of 50 cm/hr. The flow rate was increased to 100 cm/hr for the remainder of the process. The column was first washed with 5 mM potassium phosphate, 0.5 M ammonium sulfate, pH 7.0, then 20 mM bicine, 0.5 M ammonium sulfate, pH 9.0, and then with 20 mM bicine, 100 mM sodium chloride, pH 9.0. The protein is eluted with 50 mM Hepes, 100 mM NaCl, pH 6.9 and passed through a sterile filter into a sterile bag. The eluted sample is tested for bioburden, protein concentration and enzyme activity.

The hydroxyapatite (HAP) column (BioRad; 116 L resin, H=23 cm, D=80 cm) is prepared. The column is equilibrated with 5 mM potassium phosphate, 100 mM NaCl, 0.1 mM CaCl_2 , pH 7.0. The aminophenyl boronate purified protein is supplemented to final concentrations of 5 mM potassium phosphate and 0.1 mM CaCl_2 and loaded onto the HAP column at a flow rate of 100 cm/hr. The column is first washed with 5 mM potassium phosphate, pH 7, 100 mM NaCl, 0.1 mM CaCl_2 , then 10 mM potassium phosphate, pH 7; 100 mM NaCl, 0.1 mM CaCl_2 . The protein is eluted with 70 mM

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potassium phosphate, pH 7.0 and passed through a 0.22 μm sterile filter into a sterile bag. The eluted sample is tested for bioburden, protein concentration and enzyme activity.

The HAP purified protein is then passed through a viral removal filter. The sterilized Viosart filter (Sartorius) is first prepared by washing with 2 L of 70 mM potassium phosphate, pH 7.0. The HAP purified protein is pumped via a peristaltic pump through the 20 nM viral removal filter. The filtered protein in 70 mM potassium phosphate, pH 7.0 is then passed through a 0.22 μm final filter into a sterile bag. The viral filtered sample is tested for protein concentration, enzyme activity, oligosaccharide, monosaccharide and sialic acid profiling (as described in Examples 9 to 10, below).

The protein in the filtrate was then concentrated 8-12 $\times$ using three 10 kD molecular weight cut off (MWCO) Sartcon PES cassettes, each with a filter surface area of 0.7 m², for a total surface area of 2.1 m². Following concentration, the concentrated protein was sampled and tested for protein concentration and enzyme activity. A 10 $\times$ diafiltration is then performed on the concentrated protein. This can be performed one of two ways: 1) using a 20 mM histidine, 130 mM NaCl, pH 6.5 buffer and 1% polysorbate 80; or 2) using a 10 mM histidine, 130 mM NaCl, pH 6.5 buffer. The concentrated, diafiltered bulk protein is at a concentration of approximately 10 mg/mL. Following buffer exchange, the concentrated protein is passed through a 0.22 μm filter into a 20 L sterile storage bag.

The sterile filtered bulk protein is then aseptically dispensed at 400 mL into 1 L sterile PFA Nalgene bottles. The bottles are then flash frozen in a liquid nitrogen bath and stored at less than -20° C. for the bulk protein that does not contain the polysorbate 80, and less than -70° C. for the bulk protein that does contain the polysorbate 80.

Table 29 sets forth some exemplary differences between production of rHuPH20 in a 300 L and 2500 L bioreactor culture

TABLE 29

Exemplary differences between production of rHuPH20 in a 300 L and 2500 L bioreactor culture		
Process Difference	300 L cell culture	2500 L cell culture
Cell line	2B2	2B2
Media used to expand cell inoculum	Contains 20 μM methotrexate (9 mg/L)	Contains 20 μM methotrexate (9 mg/L)
Cell expansion	Expanded through 125 mL flask, 250 mL flask, 1 L flask, 6 L flask and 36 L flask.	Expanded through 125 mL flask, 250 mL flask, 1 L flask, 2 $\times$ 2 L shaker flasks, 6 $\times$ 2 L shaker flasks, 25 L WAVE Bioreactor™, 100 L WAVE Bioreactor™, and a 600 L stirred tank seed bioreactor
Final operating volume in bioreactor	Approx. 300 L in a 400 L bioreactor	Approx. 2500 L in a 3500 L bioreactor
Culture media in at bioreactor inoculation	CD CHO with 5.0 mg/L rHuInsulin	CD CHO AGT™ with 5.0 mg/L rHuInsulin
	40 mL/L (8 mM)	40 mL/L (8 mM)
	GlutaMAX™-I	GlutaMAX™-I
Media feed volume	Scaled at 4% of the bioreactor cell culture volume i.e. approximately 10.4, 10.8, 11.2 and 11.7 L, resulting in a target bioreactor volume of ~300 L.	Scaled at 4% of the bioreactor cell culture volume i.e. approximately 84, 87, 91, and 94 L, resulting in a target bioreactor volume of ~2500 L.
Media feed	Feed #1 Medium: 4x CD CHO + 33 g/L Glucose + 32 mM GlutaMAX™-I + 16.6 g/L Yeastolate + 33 mg/L rHuInsulin	Feed #1 Medium: 81 g/L powdered CD-CHO AGT™ + 33 g/L Glucose + 26.6 mM GlutaMAX™-I + 83.3 g/L Yeastolate + 33 mg/L

TABLE 29-continued

Exemplary differences between production of rHuPH20 in a 300 L and 2500 L bioreactor culture		
Process Difference	300 L cell culture	2500 L cell culture
	Feed #2: 2x CD CHO + 33 g/L Glucose + 16 mM GlutaMAX™-I + 33.4 g/L Yeastolate + 0.92 g/L Sodium Butyrate Feed #3: 1x CD CHO + 50 g/L Glucose + 10 mM GlutaMAX™-I + 50 g/L Yeastolate + 1.80 g/L Sodium Butyrate Feed #4: 1x CD CHO + 33 g/L Glucose + 6.7 mM GlutaMAX™-I + 50 g/L Yeastolate + 0.92 g/L Sodium Butyrate	rHuInsulin Feed #2: 40.5 g/L powdered CD-CHO AGT™ + 33 g/L Glucose + 13.4 mM GlutaMAX™-I + 166.7 g/L Yeastolate + 0.92 g/L Sodium butyrate Feed #3: 20.3 g/L powdered CD-CHO AGT™ + 50 g/L Glucose + 10 mM GlutaMAX™-I + 250 g/L Yeastolate + 1.8 g/L Sodium butyrate Feed #4: 20.3 g/L powdered CD-CHO AGT™ + 33.3 g/L Glucose + 6.7 mM GlutaMAX™-I + 250 g/L Yeastolate + 0.92 g/L Sodium butyrate
Filtration of bioreactor cell culture	1 st stage - 4 modules in parallel, each with a layer of diatomaceous earth graded to 4-8 µm and a layer of diatomaceous earth graded to 1.4-1.1 µm, followed by a cellulose membrane. 2 nd stage -single module containing a layer of diatomaceous earth graded to 0.4-0.11 µm and a layer of diatomaceous earth graded to <0.1 µm, followed by a cellulose membrane. 3 rd stage - 0.22 µm polyethersulfone filter 300 L storage bag	1 t stage - 20 modules in parallel, each with a layer of diatomaceous earth graded to 4-8 µm and a layer of diatomaceous earth graded to 1.4-1.1 µm, followed by a cellulose membrane. 2 nd stage -10 modules containing a layer of diatomaceous earth graded to 0.4-0.11 µm and a layer of diatomaceous earth graded to <0.1 µm, followed by a cellulose membrane. 3 rd stage - 0.22 µm polyethersulfone filter 350 L storage bag
Concentration and buffer exchange prior to chromatography	Concentrate using four Sartorius Sartoslice TFF 30K MWCO Filter Buffer Exchange the Concentrate 10x with 10 mM Tris, 20 mM Na2SO4, pH 7.5 50 L sterile storage bag	Concentrate with 2 TFF with Millipore Spiral Polyethersulfone 30K MWCO Filter Buffer Exchange the Concentrate 6x with 10 mM Hepes, 25 mM NaCl, pH 7.0 20 L sterile storage bag
Q sepharose column	9 L resin, H = 29 cm, D = 20 cm	81 L resin, H = 26 cm, D = 63 cm
A Phenyl-Sepharose (PS) column	19-21 L resin, H = 29 cm, D = 30 cm	176 L resin, H = 35 cm, D = 80 cm
aminophenyl boronate column	21 L resin, H = 29 cm, D = 30 cm	176 L resin, H = 35 cm, D = 80 cm
hydroxyapatite (HAP) column	13 L resin, H = 20 cm, D = 30 cm	116 L resin, H = 23 cm, D = 80 cm
Protein Concentration	Single 10 kD MWCO Sartocon Slice tangential flow filtration (TFF) 6x buffer exchange with 10 mM histidine, 130 mM NaCl, pH 6.0	Three 10 kD molecular weight cut off (MWCO) Sartocon PES cassettes 10x diafiltration with: 1) 20 mM histidine, 130 mM NaCl, pH 6.5 buffer and 1% polysorbate 80; or 2) 10 mM histidine, 130 mM NaCl, pH 6.5 buffer.
Vial filling	20 mL fill volumes Stored at ≤20° C.	400 mL fill volumes Stored at ≤20° C. if protein does not polysorbate 80, or ≤70° C. if protein does contain polysorbate 80

Since modifications will be apparent to those of skill in this art, it is intended that this invention be limited only by the scope of the appended claims.

 SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 71

<210> SEQ ID NO 1

<211> LENGTH: 509

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: precursor human PH20

<400> SEQUENCE: 1

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Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1              5              10              15

Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20              25              30

Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35              40              45

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50              55              60

Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65              70              75              80

Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85              90              95

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100              105              110

Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115              120              125

Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130              135              140

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145              150              155              160

Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165              170              175

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180              185              190

Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195              200              205

Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210              215              220

Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225              230              235              240

Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245              250              255

Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260              265              270

Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275              280              285

Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290              295              300

Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305              310              315              320

Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile

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325                               330                               335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340                               345                               350

Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355                               360                               365

Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370                               375                               380

Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385                               390                               395                               400

Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405                               410                               415

Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420                               425                               430

Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435                               440                               445

Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450                               455                               460

Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465                               470                               475                               480

Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
485                               490                               495

Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
500                               505

<210> SEQ ID NO 2
<211> LENGTH: 474
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: Mature PH20

<400> SEQUENCE: 2

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
1      5      10      15

Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
20     25     30

Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
35     40     45

Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
50     55     60

Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
65     70     75     80

Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
85     90     95

Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
100    105    110

Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
115    120    125

Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
130    135    140

Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
145    150    155    160

Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
165    170    175

Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
180    185    190

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His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445
 Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu
 450 455 460
 Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 465 470

<210> SEQ ID NO 3

<211> LENGTH: 482

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: precursor soluble rHuPH20

<400> SEQUENCE: 3

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80

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Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
				85					90					95	
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100					105					110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
		115					120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
	130					135						140			
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
		195					200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225				230						235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245					250						255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
		260						265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305				310						315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
			325						330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340						345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
		355					360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385				390					395						400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
			405						410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420					425					430		
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
	435						440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
465					470					475					480
Phe	Tyr														

<210> SEQ ID NO 4

<211> LENGTH: 447

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: soluble rHuPH20 1-447

<400> SEQUENCE: 4
Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1             5             10             15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
          20             25             30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35             40             45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50             55             60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65             70             75             80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
          85             90             95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
          100             105             110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
          115             120             125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
          130             135             140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
          145             150             155             160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
          165             170             175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
          180             185             190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
          195             200             205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
          210             215             220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
          225             230             235             240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
          245             250             255
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
          260             265             270
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
          275             280             285
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
          290             295             300
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
          305             310             315             320
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
          325             330             335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
          340             345             350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
          355             360             365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
          370             375             380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys

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385	390	395	400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp	405	410	415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala	420	425	430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr	435	440	445

<210> SEQ ID NO 5
 <211> LENGTH: 446
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: soluble rHuPH20 1-446

<400> SEQUENCE: 5

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp	1	5	10	15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro	20	25	30	
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala	35	40	45	
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr	50	55	60	
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro	65	70	75	80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile	85	90	95	
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp	100	105	110	
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val	115	120	125	
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu	130	135	140	
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala	145	150	155	160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg	165	170	175	
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His	180	185	190	
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile	195	200	205	
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu	210	215	220	
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr	225	230	235	240
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile	245	250	255	
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val	260	265	270	
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr	275	280	285	
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp	290	295	300	
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp	305	310	315	320

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Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
      325                      330                      335
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
      340                      345                      350
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
      355                      360                      365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
      370                      375                      380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
      385                      390                      395                      400
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
      405                      410                      415
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
      420                      425                      430
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
      435                      440                      445

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<210> SEQ ID NO 6
<211> LENGTH: 445
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: soluble rHuPH20 1-445

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<400> SEQUENCE: 6

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Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
  1              5              10              15
Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
      20              25              30
Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
      35              40              45
Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
      50              55              60
Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
      65              70              75              80
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
      85              90              95
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
      100             105             110
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
      115             120             125
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
      130             135             140
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
      145             150             155             160
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
      165             170             175
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
      180             185             190
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
      195             200             205
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
      210             215             220
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
      225             230             235             240

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Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile	
				245					250					255		
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val	
				260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr	
				275					280					285		
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp	
				290					295					300		
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp	
305					310					315					320	
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu	
				325					330					335		
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys	
				340					345					350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp	
				355					360					365		
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly	
				370					375					380		
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys	
385					390					395					400	
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp	
				405					410					415		
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala	
				420					425					430		
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile				
				435					440					445		

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<210> SEQ ID NO 7
<211> LENGTH: 444
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: soluble rHuHP20 1-444
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<400> SEQUENCE: 7

Leu	Asn	Phe		Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50				55						60				
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75				80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130				135						140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg

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165										170										175									
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His														
			180						185						190														
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile														
		195						200					205																
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu														
		210				215					220																		
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr														
		225			230				235					240															
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile														
			245					250						255															
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val														
		260					265						270																
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr														
		275					280					285																	
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp														
		290				295					300																		
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp														
		305			310				315					320															
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu														
			325					330						335															
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys														
		340					345					350																	
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp														
		355				360						365																	
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly														
		370			375				380																				
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys														
		385			390			395						400															
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp														
			405					410					415																
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala														
		420				425						430																	
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln																		
		435				440																							

<210> SEQ ID NO 8

<211> LENGTH: 443

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: soluble rHuPH20 1-443

<400> SEQUENCE: 8

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5				10						15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
		20					25					30			
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35				40					45				
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
		50			55				60						
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
		65			70			75						80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85					90						95	

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Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro
 435 440

<210> SEQ ID NO 9
 <211> LENGTH: 442
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: soluble rHuPH20 1-442

<400> SEQUENCE: 9

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15

Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
	35						40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55					60				
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75					80
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
				165					170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
				245					250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
		290				295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305				310						315					320
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
				325					330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
			340						345				350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp
		355					360					365			
Asn	Phe	Ala	Ile												

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<210> SEQ ID NO 10
<211> LENGTH: 450
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<220> FEATURE:
<223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 10
Met Arg Pro Phe Ser Leu Glu Val Ser Leu His Leu Pro Trp Ala Met
 1             5             10             15
Ala Ala His Leu Leu Pro Val Cys Thr Leu Phe Leu Asn Leu Leu Ser
 20             25             30
Met Thr Gln Gly Ser Arg Asp Pro Val Val Pro Asn Gln Pro Phe Thr
 35             40             45
Thr Ile Trp Asn Ala Asn Thr Glu Trp Cys Met Lys His Gly Val
 50             55             60
Asp Val Asp Ile Ser Ile Phe Asp Val Val Thr Asn Pro Gly Gln Thr
 65             70             75             80
Phe Arg Gly Pro Asn Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly Thr
 85             90             95
Tyr Pro Tyr Tyr Thr Ser Ala Gly Glu Pro Val Phe Gly Gly Leu Pro
100            105            110
Gln Asn Ala Ser Leu Asn Ala His Leu Ala Arg Thr Phe Gln Asp Ile
115            120            125
Leu Ala Ala Met Pro Glu Pro Arg Phe Ser Gly Leu Ala Val Ile Asp
130            135            140
Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys Asp
145            150            155            160
Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Lys Gln His Pro Asp
165            170            175
Trp Leu Ala Pro Arg Val Glu Ala Ala Ala Gln Asp Gln Phe Glu Gly
180            185            190
Ala Ala Glu Glu Trp Met Ala Gly Thr Leu Lys Leu Gly Gln Ala Leu
195            200            205
Arg Pro Gln Gly Leu Trp Gly Phe Tyr Asn Phe Pro Glu Cys Tyr Asn
210            215            220
Tyr Asp Phe Lys Ser Pro Asn Tyr Thr Gly Arg Cys Pro Leu Asn Ile
225            230            235            240
Cys Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg Ala
245            250            255
Leu Tyr Pro Ser Ile Tyr Leu Pro Ala Ala Leu Glu Gly Thr Lys Lys
260            265            270
Thr Gln Met Phe Val Gln His Arg Val Ala Glu Ala Phe Arg Val Ala
275            280            285
Ala Gly Ala Gly Asp Pro Lys Leu Pro Val Leu Pro Tyr Met Gln Leu
290            295            300
Phe Tyr Asp Met Thr Asn His Phe Leu Pro Ala Glu Glu Leu Glu His
305            310            315            320
Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu Trp
325            330            335
Val Ser Trp Leu Ser Thr Ser Thr Lys Glu Ser Cys Gln Ala Ile Lys
340            345            350
Glu Tyr Val Asp Thr Thr Leu Gly Pro Ser Ile Leu Asn Val Thr Ser
355            360            365

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Gly Ala Arg Leu Cys Ser Gln Val Leu Cys Ser Gly His Gly Arg Cys
 370 375 380

Ala Arg Arg Pro Ser Tyr Pro Lys Ala Arg Leu Ile Leu Asn Ser Thr
 385 390 395 400

Ser Phe Ser Ile Lys Pro Thr Pro Gly Gly Gly Pro Leu Thr Leu Gln
 405 410 415

Gly Ala Leu Ser Leu Glu Asp Arg Leu Arg Met Ala Val Glu Phe Glu
 420 425 430

Cys Arg Cys Tyr Arg Gly Trp Arg Gly Thr Arg Cys Glu Gln Trp Gly
 435 440 445

Met Trp
 450

<210> SEQ ID NO 11
 <211> LENGTH: 331
 <212> TYPE: PRT
 <213> ORGANISM: *Vespula vulgaris*
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase A

<400> SEQUENCE: 11

Ser Glu Arg Pro Lys Arg Val Phe Asn Ile Tyr Trp Asn Val Pro Thr
 1 5 10 15

Phe Met Cys His Gln Tyr Asp Leu Tyr Phe Asp Glu Val Thr Asn Phe
 20 25 30

Asn Ile Lys Arg Asn Ser Lys Asp Asp Phe Gln Gly Asp Lys Ile Ala
 35 40 45

Ile Phe Tyr Asp Pro Gly Glu Phe Pro Ala Leu Leu Ser Leu Lys Asp
 50 55 60

Gly Lys Tyr Lys Lys Arg Asn Gly Gly Val Pro Gln Glu Gly Asn Ile
 65 70 75 80

Thr Ile His Leu Gln Lys Phe Ile Glu Asn Leu Asp Lys Ile Tyr Pro
 85 90 95

Asn Arg Asn Phe Ser Gly Ile Gly Val Ile Asp Phe Glu Arg Trp Arg
 100 105 110

Pro Ile Phe Arg Gln Asn Trp Gly Asn Met Lys Ile His Lys Asn Phe
 115 120 125

Ser Ile Asp Leu Val Arg Asn Glu His Pro Thr Trp Asn Lys Lys Met
 130 135 140

Ile Glu Leu Glu Ala Ser Lys Arg Phe Glu Lys Tyr Ala Arg Phe Phe
 145 150 155 160

Met Glu Glu Thr Leu Lys Leu Ala Lys Lys Thr Arg Lys Gln Ala Asp
 165 170 175

Trp Gly Tyr Tyr Gly Tyr Pro Tyr Cys Phe Asn Met Ser Pro Asn Asn
 180 185 190

Leu Val Pro Glu Cys Asp Val Thr Ala Met His Glu Asn Asp Lys Met
 195 200 205

Ser Trp Leu Phe Asn Asn Gln Asn Val Leu Leu Pro Ser Val Tyr Val
 210 215 220

Arg Gln Glu Leu Thr Pro Asp Gln Arg Ile Gly Leu Val Gln Gly Arg
 225 230 235 240

Val Lys Glu Ala Val Arg Ile Ser Asn Asn Leu Lys His Ser Pro Lys
 245 250 255

Val Leu Ser Tyr Trp Trp Tyr Val Tyr Gln Asp Glu Thr Asn Thr Phe
 260 265 270

Leu Thr Glu Thr Asp Val Lys Lys Thr Phe Gln Glu Ile Val Ile Asn

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275	280	285
Gly Gly Asp Gly Ile Ile Ile Trp Gly Ser Ser Ser Asp Val Asn Ser		
290	295	300
Leu Ser Lys Cys Lys Arg Leu Gln Asp Tyr Leu Leu Thr Val Leu Gly		
305	310	315
Pro Ile Ala Ile Asn Val Thr Glu Ala Val Asn		
325	330	

<210> SEQ ID NO 12
 <211> LENGTH: 340
 <212> TYPE: PRT
 <213> ORGANISM: *Vespula vulgaris*
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase B

 <400> SEQUENCE: 12

Asp Arg Thr Ile Trp Pro Lys Lys Gly Phe Ser Ile Tyr Trp Asn Ile		
1	5	10
Pro Thr His Phe Cys His Asn Phe Gly Val Tyr Phe Lys Glu Leu Lys		
20	25	30
Gln Phe Asn Ile Lys Tyr Asn Ser Met Asn Asn Phe Arg Gly Glu Thr		
35	40	45
Ile Ser Leu Phe Tyr Asp Pro Gly Asn Phe Pro Ser Met Val Leu Leu		
50	55	60
Lys Asn Gly Thr Tyr Glu Ile Arg Asn Glu Gly Val Pro Gln Lys Gly		
65	70	75
Asn Leu Thr Ile His Leu Glu Gln Phe Thr Lys Glu Leu Asp Glu Ile		
85	90	95
Tyr Pro Lys Lys Ile Ala Gly Gly Ile Gly Val Ile His Phe His Asn		
100	105	110
Trp Arg Pro Ile Phe Arg Arg Asn Val Asp Asn Leu Lys Ile Asn Lys		
115	120	125
Asp Ile Ser Ile Asp Leu Val Arg Lys Glu His Pro Lys Trp Asp Lys		
130	135	140
Ser Met Ile Glu Lys Glu Ala Ser Asn Arg Phe Glu Thr Ser Ala Lys		
145	150	155
Ile Phe Met Glu Lys Thr Leu Lys Leu Ala Lys Glu Ile Arg Lys Lys		
165	170	175
Thr Glu Trp Gly Tyr His Gly Tyr Pro His Cys Leu Ser Gly Ser Thr		
180	185	190
Asp Lys Pro Ser Phe Asp Cys Asp Ala Leu Ser Met Ser Glu Asn Asp		
195	200	205
Lys Met Ser Trp Leu Phe Asn Asn Gln Asn Val Leu Leu Pro Ser Ile		
210	215	220
Tyr Leu Lys Asn Val Leu Lys Pro Asp Glu Lys Ile His Leu Val Gln		
225	230	235
Glu Arg Leu Lys Glu Ala Ile Arg Ile Ser Lys Asn Phe Lys His Leu		
245	250	255
Pro Lys Val Leu Pro Tyr Trp Trp Tyr Thr Tyr Gln Asp Lys Glu Ser		
260	265	270
Ile Phe Leu Thr Glu Ala Asp Val Lys Asn Thr Phe Lys Glu Ile Leu		
275	280	285
Thr Asn Gly Ala Asp Gly Ile Ile Ile Trp Gly Val Ser Tyr Glu Leu		
290	295	300
Thr Asp Arg Lys Arg Cys Glu Lys Leu Lys Glu Tyr Leu Met Lys Ile		
305	310	315
		320

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Leu Gly Pro Ile Ala Phe Lys Val Thr Lys Ala Val Lys Glu Asn Thr
 325 330 335

Pro Leu Asn Phe
 340

<210> SEQ ID NO 13
 <211> LENGTH: 382
 <212> TYPE: PRT
 <213> ORGANISM: Apis mellifera
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 13

Met Ser Arg Pro Leu Val Ile Thr Glu Gly Met Met Ile Gly Val Leu
 1 5 10 15

Leu Met Leu Ala Pro Ile Asn Ala Leu Leu Gly Phe Val Gln Ser
 20 25 30

Thr Pro Asp Asn Asn Lys Thr Val Arg Glu Phe Asn Val Tyr Trp Asn
 35 40 45

Val Pro Thr Phe Met Cys His Lys Tyr Gly Leu Arg Phe Glu Glu Val
 50 55 60

Ser Glu Lys Tyr Gly Ile Leu Gln Asn Trp Met Asp Lys Phe Arg Gly
 65 70 75 80

Glu Glu Ile Ala Ile Leu Tyr Asp Pro Gly Met Phe Pro Ala Leu Leu
 85 90 95

Lys Asp Pro Asn Gly Asn Val Val Ala Arg Asn Gly Gly Val Pro Gln
 100 105 110

Leu Gly Asn Leu Thr Lys His Leu Gln Val Phe Arg Asp His Leu Ile
 115 120 125

Asn Gln Ile Pro Asp Lys Ser Phe Pro Gly Val Gly Val Ile Asp Phe
 130 135 140

Glu Ser Trp Arg Pro Ile Phe Arg Gln Asn Trp Ala Ser Leu Gln Pro
 145 150 155 160

Tyr Lys Lys Leu Ser Val Glu Val Val Arg Glu His Pro Phe Trp
 165 170 175

Asp Asp Gln Arg Val Glu Gln Glu Ala Lys Arg Arg Phe Glu Lys Tyr
 180 185 190

Gly Gln Leu Phe Met Glu Glu Thr Leu Lys Ala Ala Lys Arg Met Arg
 195 200 205

Pro Ala Ala Asn Trp Gly Tyr Tyr Ala Tyr Pro Tyr Cys Tyr Asn Leu
 210 215 220

Thr Pro Asn Gln Pro Ser Ala Gln Cys Glu Ala Thr Thr Met Gln Glu
 225 230 235 240

Asn Asp Lys Met Ser Trp Leu Phe Glu Ser Glu Asp Val Leu Leu Pro
 245 250 255

Ser Val Tyr Leu Arg Trp Asn Leu Thr Ser Gly Glu Arg Val Gly Leu
 260 265 270

Val Gly Gly Arg Val Lys Glu Ala Leu Arg Ile Ala Arg Gln Met Thr
 275 280 285

Thr Ser Arg Lys Lys Val Leu Pro Tyr Tyr Trp Tyr Lys Tyr Gln Asp
 290 295 300

Arg Arg Asp Thr Asp Leu Ser Arg Ala Asp Leu Glu Ala Thr Leu Arg
 305 310 315 320

Lys Ile Thr Asp Leu Gly Ala Asp Gly Phe Ile Ile Trp Gly Ser Ser
 325 330 335

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Asp Asp Ile Asn Thr Lys Ala Lys Cys Leu Gln Phe Arg Glu Tyr Leu
340 345 350

Asn Asn Glu Leu Gly Pro Ala Val Lys Arg Ile Ala Leu Asn Asn Asn
355 360 365

Ala Asn Asp Arg Leu Thr Val Asp Val Ser Val Asp Gln Val
370 375 380

<210> SEQ ID NO 14

<211> LENGTH: 331

<212> TYPE: PRT

<213> ORGANISM: Dolichovespula maculata

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 14

Ser Glu Arg Pro Lys Arg Val Phe Asn Ile Tyr Trp Asn Val Pro Thr
1 5 10 15

Phe Met Cys His Gln Tyr Gly Leu Tyr Phe Asp Glu Val Thr Asn Phe
20 25 30

Asn Ile Lys His Asn Ser Lys Asp Asp Phe Gln Gly Asp Lys Ile Ser
35 40 45

Ile Phe Tyr Asp Pro Gly Glu Phe Pro Ala Leu Leu Pro Leu Lys Glu
50 55 60

Gly Asn Tyr Lys Ile Arg Asn Gly Gly Val Pro Gln Glu Gly Asn Ile
65 70 75 80

Thr Ile His Leu Gln Arg Phe Ile Glu Asn Leu Asp Lys Thr Tyr Pro
85 90 95

Asn Arg Asn Phe Asn Gly Ile Gly Val Ile Asp Phe Glu Arg Trp Arg
100 105 110

Pro Ile Phe Arg Gln Asn Trp Gly Asn Met Met Ile His Lys Lys Phe
115 120 125

Ser Ile Asp Leu Val Arg Asn Glu His Pro Phe Trp Asp Lys Lys Met
130 135 140

Ile Glu Leu Glu Ala Ser Lys Arg Phe Glu Lys Tyr Ala Arg Leu Phe
145 150 155 160

Met Glu Glu Thr Leu Lys Leu Ala Lys Lys Thr Arg Lys Gln Ala Asp
165 170 175

Trp Gly Tyr Tyr Gly Tyr Pro Tyr Cys Phe Asn Met Ser Pro Asn Asn
180 185 190

Leu Val Pro Asp Cys Asp Ala Thr Ala Met Leu Glu Asn Asp Lys Met
195 200 205

Ser Trp Leu Phe Asn Asn Gln Asn Val Leu Leu Pro Ser Val Tyr Ile
210 215 220

Arg His Glu Leu Thr Pro Asp Gln Arg Val Gly Leu Val Gln Gly Arg
225 230 235 240

Val Lys Glu Ala Val Arg Ile Ser Asn Asn Leu Lys His Ser Pro Lys
245 250 255

Val Leu Ser Tyr Trp Trp Tyr Val Tyr Gln Asp Asp Thr Asn Thr Phe
260 265 270

Leu Thr Glu Thr Asp Val Lys Lys Thr Phe Gln Glu Ile Ala Ile Asn
275 280 285

Gly Gly Asp Gly Ile Ile Ile Trp Gly Ser Ser Ser Asp Val Asn Ser
290 295 300

Leu Ser Lys Cys Lys Arg Leu Arg Glu Tyr Leu Leu Thr Val Leu Gly
305 310 315 320

Pro Ile Thr Val Asn Val Thr Glu Thr Val Asn

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325 330

<210> SEQ ID NO 15
 <211> LENGTH: 367
 <212> TYPE: PRT
 <213> ORGANISM: Polistes annularis
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 15

Tyr Val Ser Leu Ser Pro Asp Ser Val Phe Asn Ile Ile Thr Asp Asp
 1 5 10 15

Ile Ser His Gln Ile Leu Ser Arg Ser Asn Cys Glu Arg Ser Lys Arg
 20 25 30

Pro Lys Arg Val Phe Ser Ile Tyr Trp Asn Val Pro Thr Phe Met Cys
 35 40 45

His Gln Tyr Gly Met Asn Phe Asp Glu Val Thr Asp Phe Asn Ile Lys
 50 55 60

His Asn Ser Lys Asp Asn Phe Arg Gly Glu Thr Ile Ser Ile Tyr Tyr
 65 70 75 80

Asp Pro Gly Lys Phe Pro Ala Leu Met Pro Leu Lys Asn Gly Asn Tyr
 85 90 95

Glu Glu Arg Asn Gly Gly Val Pro Gln Arg Gly Asn Ile Thr Ile His
 100 105 110

Leu Gln Gln Phe Asn Glu Asp Leu Asp Lys Met Thr Pro Asp Lys Asn
 115 120 125

Phe Gly Gly Ile Gly Val Ile Asp Phe Glu Arg Trp Lys Pro Ile Phe
 130 135 140

Arg Gln Asn Trp Gly Asn Thr Glu Ile His Lys Lys Tyr Ser Ile Glu
 145 150 155 160

Leu Val Arg Lys Glu His Pro Lys Trp Ser Glu Ser Met Ile Glu Ala
 165 170 175

Glu Ala Thr Lys Lys Phe Glu Lys Tyr Ala Arg Tyr Phe Met Glu Glu
 180 185 190

Thr Leu Lys Leu Ala Lys Lys Thr Arg Lys Arg Ala Lys Trp Gly Tyr
 195 200 205

Tyr Gly Phe Pro Tyr Cys Tyr Asn Val Thr Pro Asn Asn Pro Gly Pro
 210 215 220

Asp Cys Asp Ala Lys Ala Thr Ile Glu Asn Asp Arg Leu Ser Trp Met
 225 230 235 240

Tyr Asn Asn Gln Glu Ile Leu Phe Pro Ser Val Tyr Val Arg His Glu
 245 250 255

Gln Lys Pro Glu Glu Arg Val Tyr Leu Val Gln Gly Arg Ile Lys Glu
 260 265 270

Ala Val Arg Ile Ser Asn Asn Leu Glu His Ser Pro Ser Val Leu Ala
 275 280 285

Tyr Trp Trp Tyr Val Tyr Gln Asp Lys Met Asp Ile Tyr Leu Ser Glu
 290 295 300

Thr Asp Val Glu Lys Thr Phe Gln Glu Ile Val Thr Asn Gly Gly Asp
 305 310 315 320

Gly Ile Ile Ile Trp Gly Ser Ser Ser Asp Val Asn Ser Leu Ser Lys
 325 330 335

Cys Lys Arg Leu Arg Glu Tyr Leu Leu Asn Thr Leu Gly Pro Phe Ala
 340 345 350

Val Asn Val Thr Glu Thr Val Asn Gly Arg Ser Ser Leu Asn Phe
 355 360 365

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<210> SEQ ID NO 16
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<220> FEATURE:
<223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 16
Met Leu Gly Leu Thr Gln His Ala Gln Lys Val Trp Arg Met Lys Pro
 1             5             10             15
Phe Ser Pro Glu Val Ser Pro Gly Ser Ser Pro Ala Thr Ala Gly His
 20             25             30
Leu Leu Arg Ile Ser Thr Leu Phe Leu Thr Leu Leu Glu Leu Ala Gln
 35             40             45
Val Cys Arg Gly Ser Val Val Ser Asn Arg Pro Phe Ile Thr Val Trp
 50             55             60
Asn Gly Asp Thr His Trp Cys Leu Thr Glu Tyr Gly Val Asp Val Asp
 65             70             75             80
Val Ser Val Phe Asp Val Val Ala Asn Lys Glu Gln Ser Phe Gln Gly
 85             90             95
Ser Asn Met Thr Ile Phe Tyr Arg Glu Glu Leu Gly Thr Tyr Pro Tyr
 100            105            110
Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu Pro Gln Asn Ala
 115            120            125
Ser Leu Val Thr His Leu Ala His Thr Phe Gln Asp Ile Lys Ala Ala
 130            135            140
Met Pro Glu Pro Asp Phe Ser Gly Leu Ala Val Ile Asp Trp Glu Ala
 145            150            155            160
Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Ser Lys Asp Ile Tyr Arg
 165            170            175
Gln Arg Ser Met Glu Leu Val Gln Ala Glu His Pro Asp Trp Pro Glu
 180            185            190
Thr Leu Val Glu Ala Ala Ala Lys Asn Gln Phe Gln Glu Ala Ala Glu
 195            200            205
Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Gln Val Leu Arg Pro Arg
 210            215            220
Gly Leu Trp Gly Tyr Tyr Gly Phe Pro Asp Cys Tyr Asn Asn Asp Phe
 225            230            235            240
Leu Ser Leu Asn Tyr Thr Gly Gln Cys Pro Val Phe Val Arg Asp Gln
 245            250            255
Asn Asp Gln Leu Gly Trp Leu Trp Asn Gln Ser Tyr Ala Leu Tyr Pro
 260            265            270
Ser Ile Tyr Leu Pro Ala Ala Leu Met Gly Thr Gly Lys Ser Gln Met
 275            280            285
Tyr Val Arg His Arg Val Gln Glu Ala Leu Arg Val Ala Ile Val Ser
 290            295            300
Arg Asp Pro His Val Pro Val Met Pro Tyr Val Gln Ile Phe Tyr Glu
 305            310            315            320
Met Thr Asp Tyr Leu Leu Pro Leu Glu Glu Leu Glu His Ser Leu Gly
 325            330            335
Glu Ser Ala Ala Gln Gly Val Ala Gly Ala Val Leu Trp Leu Ser Ser
 340            345            350
Asp Lys Thr Ser Thr Lys Glu Ser Cys Gln Ala Ile Lys Ala Tyr Met
 355            360            365

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Asp Ser Thr Leu Gly Pro Phe Ile Val Asn Val Thr Ser Ala Ala Leu
 370 375 380
 Leu Cys Ser Glu Ala Leu Cys Ser Gly His Gly Arg Cys Val Arg His
 385 390 395 400
 Pro Ser Tyr Pro Glu Ala Leu Leu Thr Leu Asn Pro Ala Ser Phe Ser
 405 410 415
 Ile Glu Leu Thr His Asp Gly Arg Pro Pro Ser Leu Lys Gly Thr Leu
 420 425 430
 Ser Leu Lys Asp Arg Ala Gln Met Ala Met Lys Phe Arg Cys Arg Cys
 435 440 445
 Tyr Arg Gly Trp Arg Gly Lys Trp Cys Asp Lys Arg Gly Met
 450 455 460

<210> SEQ ID NO 17
 <211> LENGTH: 473
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <223> OTHER INFORMATION: Hyaluronidase 2

<400> SEQUENCE: 17

Met Arg Ala Gly Leu Gly Pro Ile Ile Thr Leu Ala Leu Val Leu Glu
 1 5 10 15
 Val Ala Trp Ala Gly Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr
 20 25 30
 Gly Arg Pro Phe Val Val Ala Trp Asn Val Pro Thr Gln Glu Cys Ala
 35 40 45
 Pro Arg His Lys Val Pro Leu Asp Leu Arg Ala Phe Asp Val Lys Ala
 50 55 60
 Thr Pro Asn Glu Gly Phe Phe Asn Gln Asn Ile Thr Thr Phe Tyr Tyr
 65 70 75 80
 Asp Arg Leu Gly Leu Tyr Pro Arg Phe Asp Ala Ala Gly Thr Ser Val
 85 90 95
 His Gly Gly Val Pro Gln Asn Gly Ser Leu Cys Ala His Leu Pro Met
 100 105 110
 Leu Lys Glu Ser Val Glu Arg Tyr Ile Gln Thr Gln Glu Pro Gly Gly
 115 120 125
 Leu Ala Val Ile Asp Trp Glu Glu Trp Arg Pro Val Trp Val Arg Asn
 130 135 140
 Trp Gln Glu Lys Asp Val Tyr Arg Gln Ser Ser Arg Gln Leu Val Ala
 145 150 155 160
 Ser Arg His Pro Asp Trp Pro Ser Asp Arg Val Met Lys Gln Ala Gln
 165 170 175
 Tyr Glu Phe Glu Phe Ala Ala Arg Gln Phe Met Leu Asn Thr Leu Arg
 180 185 190
 Tyr Val Lys Ala Val Arg Pro Gln His Leu Trp Gly Phe Tyr Leu Phe
 195 200 205
 Pro Asp Cys Tyr Asn His Asp Tyr Val Gln Asn Trp Glu Ser Tyr Thr
 210 215 220
 Gly Arg Cys Pro Asp Val Glu Val Ala Arg Asn Asp Gln Leu Ala Trp
 225 230 235 240
 Leu Trp Ala Glu Ser Thr Ala Leu Phe Pro Ser Val Tyr Leu Asp Glu
 245 250 255
 Thr Leu Ala Ser Ser Val His Ser Arg Asn Phe Val Ser Phe Arg Val
 260 265 270
 Arg Glu Ala Leu Arg Val Ala His Thr His His Ala Asn His Ala Leu

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275					280					285						
Pro	Val	Tyr	Val	Phe	Thr	Arg	Pro	Thr	Tyr	Thr	Arg	Gly	Leu	Thr	Gly	
290					295					300						
Leu	Ser	Gln	Val	Asp	Leu	Ile	Ser	Thr	Ile	Gly	Glu	Ser	Ala	Ala	Leu	
305					310					315					320	
Gly	Ser	Ala	Gly	Val	Ile	Phe	Trp	Gly	Asp	Ser	Glu	Asp	Ala	Ser	Ser	
325					330					335						
Met	Glu	Thr	Cys	Gln	Tyr	Leu	Lys	Asn	Tyr	Leu	Thr	Gln	Leu	Leu	Val	
340					345					350						
Pro	Tyr	Ile	Val	Asn	Val	Ser	Trp	Ala	Thr	Gln	Tyr	Cys	Ser	Trp	Thr	
355					360					365						
Gln	Cys	His	Gly	His	Gly	Arg	Cys	Val	Arg	Arg	Asn	Pro	Ser	Ala	Asn	
370					375					380						
Thr	Phe	Leu	His	Leu	Asn	Ala	Ser	Ser	Phe	Arg	Leu	Val	Pro	Gly	His	
385					390					395					400	
Thr	Pro	Ser	Glu	Pro	Gln	Leu	Arg	Pro	Glu	Gly	Gln	Leu	Ser	Glu	Ala	
405					410					415						
Asp	Leu	Asn	Tyr	Leu	Gln	Lys	His	Phe	Arg	Cys	Gln	Cys	Tyr	Leu	Gly	
420					425					430						
Trp	Gly	Gly	Glu	Gln	Cys	Gln	Arg	Asn	Tyr	Lys	Gly	Ala	Ala	Gly	Asn	
435					440					445						
Ala	Ser	Arg	Ala	Trp	Ala	Gly	Ser	His	Leu	Thr	Ser	Leu	Leu	Gly	Leu	
450					455					460						
Val	Ala	Val	Ala	Leu	Thr	Trp	Thr	Leu								
465					470											

<210> SEQ ID NO 18

<211> LENGTH: 412

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 3

<400> SEQUENCE: 18

Met	Ile	Met	His	Leu	Gly	Leu	Met	Met	Val	Val	Gly	Leu	Thr	Leu	Cys
1				5					10					15	
Leu	Met	His	Gly	Gln	Ala	Leu	Leu	Gln	Val	Pro	Glu	His	Pro	Phe	Ser
			20					25					30		
Val	Val	Trp	Asn	Val	Pro	Ser	Ala	Arg	Cys	Lys	Ala	His	Phe	Gly	Val
		35					40					45			
His	Leu	Pro	Leu	Asp	Ala	Leu	Gly	Ile	Val	Ala	Asn	His	Gly	Gln	His
	50					55					60				
Phe	His	Gly	Gln	Asn	Ile	Ser	Ile	Phe	Tyr	Lys	Asn	Gln	Phe	Gly	Leu
65				70					75					80	
Tyr	Pro	Tyr	Phe	Gly	Pro	Arg	Gly	Thr	Ala	His	Asn	Gly	Gly	Ile	Pro
			85					90					95		
Gln	Ala	Val	Ser	Leu	Asp	His	His	Leu	Ala	Arg	Ala	Ala	His	Gln	Ile
			100					105					110		
Leu	His	Ser	Leu	Gly	Ser	Ser	Phe	Ala	Gly	Leu	Ala	Val	Leu	Asp	Trp
			115				120					125			
Glu	Glu	Trp	Tyr	Pro	Leu	Trp	Ala	Gly	Asn	Trp	Gly	Pro	His	Arg	Gln
		130				135					140				
Val	Tyr	Leu	Ala	Ala	Ser	Trp	Val	Trp	Thr	Gln	Gln	Met	Phe	Pro	Gly
145					150					155					160
Leu	Asp	Pro	Gln	Glu	Gln	Leu	His	Lys	Ala	His	Thr	Ser	Phe	Glu	Gln
				165					170						175

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Ala Ala Arg Ala Leu Met Glu Tyr Thr Leu Gln Leu Gly Arg Thr Leu
180 185 190

Arg Pro Ser Gly Leu Trp Gly Phe Tyr Arg Tyr Pro Ala Cys Gly Asn
195 200 205

Gly Trp His Lys Met Ala Ser Asn Tyr Thr Gly His Cys His Ala Ala
210 215 220

Ile Thr Thr Gln Asn Thr Gln Leu Arg Trp Leu Trp Ala Ala Ser Ser
225 230 235 240

Ala Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Leu Ala Tyr
245 250 255

Arg Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala
260 265 270

Leu Leu Glu His Ser His Pro Leu Pro Val Leu Ala Tyr Ser Arg Leu
275 280 285

Thr His Arg Ser Ser Gly Arg Phe Leu Ser Leu Asp Asp Leu Met Gln
290 295 300

Thr Ile Gly Val Ser Ala Ala Leu Gly Thr Ala Gly Val Val Leu Trp
305 310 315 320

Gly Asp Leu Ser Phe Ser Ser Ser Glu Glu Lys Cys Trp Arg Leu His
325 330 335

Asp Tyr Leu Val Gly Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Lys
340 345 350

Ala Asp Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys
355 360 365

Ala Arg Lys Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Gln Pro
370 375 380

Asp Asp Ser Leu Gly Ala Trp Asn Ser Phe Arg Cys His Cys Tyr Ser
385 390 395 400

Gly Trp Ala Gly Pro Thr Cys Leu Glu Pro Lys Pro
405 410

<210> SEQ ID NO 19
<211> LENGTH: 435
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 19

Met Ala Ala His Leu Leu Pro Ile Cys Thr Leu Phe Leu Asn Leu Leu
1 5 10 15

Ser Val Ala Gln Gly Ser Arg Asp Pro Val Val Leu Asn Arg Pro Phe
20 25 30

Thr Thr Ile Trp Asn Ala Asn Thr Gln Trp Cys Leu Lys Arg His Gly
35 40 45

Val Asp Val Asp Val Ser Val Phe Glu Val Val Val Asn Pro Gly Gln
50 55 60

Thr Phe Arg Gly Pro Asn Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
65 70 75 80

Thr Tyr Pro Tyr Tyr Thr Ser Ala Gly Glu Pro Val Phe Gly Gly Leu
85 90 95

Pro Gln Asn Ala Ser Leu Asp Val His Leu Asn Arg Thr Phe Lys Asp
100 105 110

Ile Leu Ala Ala Met Pro Glu Ser Asn Phe Ser Gly Leu Ala Val Ile
115 120 125

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Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Ala Lys
 130                      135                      140

Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Lys Gln His Pro
 145                      150                      155                      160

Asp Trp Pro Ala Pro Trp Val Glu Ala Ala Ala Gln Asp Gln Phe Gln
                      165                      170                      175

Glu Ala Ala Gln Thr Trp Met Ala Gly Thr Leu Lys Leu Gly Gln Thr
 180                      185                      190

Leu Arg Pro His Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
 195                      200                      205

Asn Tyr Asp Phe Gln Ser Ser Asn Tyr Thr Gly Gln Cys Pro Pro Gly
 210                      215                      220

Val Ser Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
 225                      230                      235                      240

Ala Leu Tyr Pro Ser Ile Tyr Leu Pro Ser Ala Leu Glu Gly Thr Asn
                      245                      250                      255

Lys Thr Gln Leu Tyr Val Gln His Arg Val Asn Glu Ala Phe Arg Val
                      260                      265                      270

Ala Ala Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Ala Gln
 275                      280                      285

Ile Phe His Asp Met Thr Asn Arg Leu Leu Ser Arg Glu Glu Leu Glu
 290                      295                      300

His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
 305                      310                      315                      320

Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ser Ile
 325                      330                      335

Lys Glu Tyr Val Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
 340                      345                      350

Ser Gly Ala Leu Leu Cys Ser Gln Ala Val Cys Ser Gly His Gly Arg
 355                      360                      365

Cys Val Arg Arg Pro Ser His Thr Glu Ala Leu Pro Ile Leu Asn Pro
 370                      375                      380

Ser Ser Phe Ser Ile Lys Pro Thr Pro Gly Gly Gly Pro Leu Thr Leu
 385                      390                      395                      400

Gln Gly Ala Leu Ser Leu Lys Asp Arg Val Gln Met Ala Glu Glu Phe
 405                      410                      415

Gln Cys Arg Cys Tyr Pro Gly Trp Arg Gly Thr Trp Cys Glu Gln Gln
 420                      425                      430

Gly Thr Arg
 435

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<210> SEQ ID NO 20
<211> LENGTH: 419
<212> TYPE: PRT
<213> ORGANISM: Sus scrofa
<220> FEATURE:
<223> OTHER INFORMATION: hyaluronidase 3

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<400> SEQUENCE: 20

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Met Thr Met Gln Leu Gly Leu Ala Leu Val Leu Gly Val Ala Met Cys
 1                      5                      10                      15

Leu Gly Cys Gly Gln Pro Leu Leu Arg Ala Pro Glu Arg Pro Phe Cys
                      20                      25                      30

Val Leu Trp Asn Val Pro Ser Ala Arg Cys Lys Ala Arg Phe Gly Val
 35                      40                      45

His Leu Pro Leu Glu Ala Leu Gly Ile Thr Ala Asn His Gly Gln Arg

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50	55	60
Phe His Gly Gln Asn Ile Thr Ile Phe Tyr Lys Ser Gln Leu Gly Leu		
65	70	75 80
Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro		
	85	90 95
Gln Ala Val Ser Leu Asp His His Leu Ala Arg Ala Ala Tyr Gln Ile		
	100	105 110
His Arg Ser Leu Arg Pro Gly Phe Thr Gly Leu Ala Val Leu Asp Trp		
	115	120 125
Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Gln Ala		
	130	135 140
Tyr Gln Ala Ala Ser Cys Ala Trp Ala Gln Arg Val Tyr Pro Asn Leu		
	145	150 155 160
Asp Pro Gln Glu Gln Leu Cys Lys Ala Arg Ala Gly Phe Glu Glu Ala		
	165	170 175
Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Leu Gly Arg Met Leu Arg		
	180	185 190
Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly		
	195	200 205
Trp His Gly Thr Ala Ser Asn Tyr Thr Gly His Cys His Ala Ala Ala		
	210	215 220
Leu Ala Arg Asn Thr Gln Leu Tyr Trp Leu Trp Ala Ala Ser Ser Ala		
	225	230 235 240
Leu Phe Pro Ser Ile Tyr Leu Pro Pro Gly Leu Pro Pro Ala Tyr His		
	245	250 255
Gln Ala Phe Val Arg Tyr Arg Leu Glu Glu Ala Phe Arg Val Ala Leu		
	260	265 270
Val Gly His Pro His Pro Leu Pro Val Leu Ala Tyr Ala Arg Leu Thr		
	275	280 285
His Arg Asn Ser Gly Arg Phe Leu Ser Gln Asp Glu Leu Val Gln Thr		
	290	295 300
Ile Gly Val Ser Ala Ala Leu Gly Ala Ser Gly Val Val Leu Trp Gly		
	305	310 315 320
Asp Leu Ser Phe Ser Ser Ser Glu Glu Glu Cys Trp His Leu Arg Gly		
	325	330 335
Tyr Leu Val Gly Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala		
	340	345 350
Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala		
	355	360 365
Trp Gln Asp Pro Gly Gln Leu Lys Val Phe Leu His Leu His Pro Gly		
	370	375 380
Gly Ser Pro Gly Ala Trp Glu Ser Phe Ser Cys Arg Cys Tyr Trp Gly		
	385	390 395 400
Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Glu Leu Gly Pro Glu		
	405	410 415
Glu Ala Thr		

<210> SEQ ID NO 21

<211> LENGTH: 449

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 1

<400> SEQUENCE: 21

-continued

Met	Lys	Pro	Phe	Ser	Pro	Glu	Val	Ser	Pro	Asp	Pro	Cys	Pro	Ala	Thr
1				5					10					15	
Ala	Ala	His	Leu	Leu	Arg	Thr	Tyr	Thr	Leu	Phe	Leu	Thr	Leu	Leu	Glu
			20					25					30		
Leu	Ala	Gln	Gly	Cys	Arg	Gly	Ser	Met	Val	Ser	Asn	Arg	Pro	Phe	Ile
		35					40					45			
Thr	Val	Trp	Asn	Ala	Asp	Thr	His	Trp	Cys	Leu	Lys	Asp	His	Gly	Val
	50					55					60				
Asp	Val	Asp	Val	Ser	Val	Phe	Asp	Val	Val	Ala	Asn	Lys	Glu	Gln	Asn
65					70					75					80
Phe	Gln	Gly	Pro	Asn	Met	Thr	Ile	Phe	Tyr	Arg	Glu	Glu	Leu	Gly	Thr
				85					90					95	
Tyr	Pro	Tyr	Tyr	Thr	Pro	Thr	Gly	Glu	Pro	Val	Phe	Gly	Gly	Leu	Pro
			100					105					110		
Gln	Asn	Ala	Ser	Leu	Val	Thr	His	Leu	Ala	His	Ala	Phe	Gln	Asp	Ile
		115					120					125			
Lys	Ala	Ala	Met	Pro	Glu	Pro	Asp	Phe	Ser	Gly	Leu	Ala	Val	Ile	Asp
	130					135					140				
Trp	Glu	Ala	Trp	Arg	Pro	Arg	Trp	Ala	Phe	Asn	Trp	Asp	Ser	Lys	Asp
145					150					155					160
Ile	Tyr	Gln	Gln	Arg	Ser	Met	Glu	Leu	Val	Arg	Ala	Glu	His	Pro	Asp
				165					170					175	
Trp	Pro	Glu	Thr	Leu	Val	Glu	Ala	Glu	Ala	Gln	Gly	Gln	Phe	Gln	Glu
			180					185					190		
Ala	Ala	Glu	Ala	Trp	Met	Ala	Gly	Thr	Leu	Gln	Leu	Gly	Gln	Val	Leu
		195					200					205			
Arg	Pro	Arg	Gly	Leu	Trp	Gly	Tyr	Tyr	Gly	Phe	Pro	Asp	Cys	Tyr	Asn
	210					215					220				
Tyr	Asp	Phe	Leu	Ser	Pro	Asn	Tyr	Thr	Gly	Gln	Cys	Ser	Leu	Ser	Ile
225					230					235					240
His	Asp	Gln	Asn	Asp	Gln	Leu	Gly	Trp	Leu	Trp	Asn	Gln	Ser	Tyr	Ala
			245					250						255	
Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Pro	Ala	Ala	Leu	Met	Gly	Thr	Gly	Lys
			260					265					270		
Ser	Gln	Met	Tyr	Val	Arg	Tyr	Arg	Val	Gln	Glu	Ala	Phe	Arg	Leu	Ala
		275					280					285			
Leu	Val	Ser	Arg	Asp	Pro	His	Val	Pro	Ile	Met	Pro	Tyr	Val	Gln	Ile
	290					295					300				
Phe	Tyr	Glu	Lys	Thr	Asp	Tyr	Leu	Leu	Pro	Leu	Glu	Glu	Leu	Glu	His
305				310					315					320	
Ser	Leu	Gly	Glu	Ser	Ala	Ala	Gln	Gly	Ala	Ala	Gly	Ala	Val	Leu	Trp
			325					330						335	
Ile	Ser	Ser	Glu	Lys	Thr	Ser	Thr	Lys	Glu	Ser	Cys	Gln	Ala	Ile	Lys
			340					345					350		
Ala	Tyr	Met	Asp	Ser	Thr	Leu	Gly	Pro	Phe	Ile	Leu	Asn	Val	Thr	Ser
	355						360					365			
Ala	Ala	Leu	Leu	Cys	Ser	Glu	Ala	Leu	Cys	Ser	Gly	Arg	Gly	Arg	Cys
	370					375					380				
Val	Arg	His	Pro	Ser	Tyr	Pro	Glu	Ala	Leu	Leu	Thr	Leu	Ser	Pro	Ala
385					390					395					400
Ser	Phe	Ser	Ile	Glu	Pro	Thr	His	Asp	Gly	Arg	Pro	Leu	Ser	Leu	Lys
			405						410					415	
Gly	Thr	Leu	Ser	Leu	Lys	Asp	Arg	Ala	Gln	Met	Ala	Met	Lys	Phe	Lys
			420					425					430		

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Cys Arg Cys Tyr Arg Gly Trp Ser Gly Glu Trp Cys Lys Lys Gln Asp
 435 440 445

Met

<210> SEQ ID NO 22

<211> LENGTH: 473

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 2

<400> SEQUENCE: 22

Met Arg Ala Gly Leu Gly Pro Ile Ile Thr Leu Ala Leu Val Leu Glu
 1 5 10 15

Val Ala Trp Ala Ser Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr
 20 25 30

Gly Arg Pro Phe Val Val Ala Trp Asn Val Pro Thr Gln Glu Cys Ala
 35 40 45

Pro Arg His Lys Val Pro Leu Asp Leu Arg Ala Phe Asp Val Glu Ala
 50 55 60

Thr Pro Asn Glu Gly Phe Phe Asn Gln Asn Ile Thr Thr Phe Tyr Tyr
 65 70 75 80

Asp Arg Leu Gly Leu Tyr Pro Arg Phe Asp Ala Ala Gly Met Ser Val
 85 90 95

His Gly Gly Val Pro Gln Asn Gly Ser Leu Cys Ala His Leu Pro Met
 100 105 110

Leu Lys Glu Ala Val Glu Arg Tyr Ile Gln Thr Gln Glu Pro Ala Gly
 115 120 125

Leu Ala Val Ile Asp Trp Glu Glu Trp Arg Pro Val Trp Val Arg Asn
 130 135 140

Trp Gln Glu Lys Asp Val Tyr Arg Gln Ser Ser Arg Gln Leu Val Ala
 145 150 155 160

Ser Arg His Pro Asp Trp Pro Ser Asp Arg Ile Val Lys Gln Ala Gln
 165 170 175

Tyr Glu Phe Glu Phe Ala Ala Arg Gln Phe Met Leu Asn Thr Leu Arg
 180 185 190

Tyr Val Lys Ala Val Arg Pro Gln His Leu Trp Gly Phe Tyr Leu Phe
 195 200 205

Pro Asp Cys Tyr Asn His Asp Tyr Val Gln Asn Trp Asp Ser Tyr Thr
 210 215 220

Gly Arg Cys Pro Asp Val Glu Val Ala Gln Asn Asp Gln Leu Ala Trp
 225 230 235 240

Leu Trp Ala Glu Asn Thr Ala Leu Phe Pro Ser Val Tyr Leu Asp Lys
 245 250 255

Thr Leu Ala Ser Ser Lys His Ser Arg Asn Phe Val Ser Phe Arg Val
 260 265 270

Gln Glu Ala Leu Arg Val Ala His Thr His His Ala Asn His Ala Leu
 275 280 285

Pro Val Tyr Val Phe Thr Arg Pro Thr Tyr Thr Arg Arg Leu Thr Glu
 290 295 300

Leu Asn Gln Met Asp Leu Ile Ser Thr Ile Gly Glu Ser Ala Ala Leu
 305 310 315 320

Gly Ser Ala Gly Val Ile Phe Trp Gly Asp Ser Val Tyr Ala Ser Ser
 325 330 335

Met Glu Asn Cys Gln Asn Leu Lys Lys Tyr Leu Thr Gln Thr Leu Val

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Pro	Tyr	Ile	Val	Asn	Val	Ser	Trp	Ala	Thr	Gln	Tyr	Cys	Ser	Trp	Thr
	355						360					365			
Gln	Cys	His	Gly	His	Gly	Arg	Cys	Val	Arg	Arg	Asn	Pro	Ser	Ala	Ser
	370					375					380				
Thr	Phe	Leu	His	Leu	Ser	Pro	Ser	Ser	Phe	Arg	Leu	Val	Pro	Gly	Arg
	385				390					395				400	
Thr	Pro	Ser	Glu	Pro	Gln	Leu	Arg	Pro	Glu	Gly	Glu	Leu	Ser	Glu	Asp
			405						410					415	
Asp	Leu	Ser	Tyr	Leu	Gln	Met	His	Phe	Arg	Cys	His	Cys	Tyr	Leu	Gly
			420					425					430		
Trp	Gly	Gly	Glu	Gln	Cys	Gln	Trp	Asn	His	Lys	Arg	Ala	Ala	Gly	Asp
	435						440					445			
Ala	Ser	Arg	Ala	Trp	Ala	Gly	Ala	His	Leu	Ala	Ser	Leu	Leu	Gly	Leu
	450					455					460				
Val	Ala	Met	Thr	Leu	Thr	Trp	Thr	Leu							
	465				470										

<210> SEQ ID NO 23

<211> LENGTH: 412

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 3

<400> SEQUENCE: 23

Met	Ile	Thr	Gln	Leu	Gly	Leu	Thr	Leu	Val	Val	Gly	Leu	Thr	Leu	Cys
1				5				10						15	
Leu	Val	His	Val	Gln	Ala	Leu	Leu	Gln	Val	Pro	Glu	Phe	Pro	Phe	Ser
			20				25					30			
Val	Leu	Trp	Asn	Val	Pro	Ser	Ala	Arg	Cys	Lys	Thr	Arg	Phe	Gly	Val
	35						40					45			
His	Leu	Pro	Leu	Asp	Ala	Leu	Gly	Ile	Ile	Ala	Asn	His	Gly	Gln	Arg
	50					55					60				
Phe	His	Gly	Gln	Asn	Ile	Thr	Ile	Phe	Tyr	Lys	Asn	Gln	Phe	Gly	Leu
	65			70					75					80	
Tyr	Pro	Tyr	Phe	Gly	Pro	Arg	Gly	Thr	Ala	His	Asn	Gly	Gly	Ile	Pro
			85					90						95	
Gln	Ala	Val	Ser	Leu	Asp	His	His	Leu	Ala	Gln	Ala	Ala	His	Gln	Ile
			100					105					110		
Leu	His	Asn	Leu	Gly	Ser	Ser	Phe	Ala	Gly	Leu	Ala	Val	Leu	Asp	Trp
		115					120					125			
Glu	Glu	Trp	Tyr	Pro	Leu	Trp	Ala	Gly	Asn	Trp	Gly	Thr	His	Arg	Gln
	130					135					140				
Val	Tyr	Gln	Ala	Ala	Ser	Trp	Ala	Trp	Ala	Gln	Gln	Met	Phe	Pro	Asp
	145				150					155				160	
Leu	Asn	Pro	Gln	Glu	Gln	Leu	His	Lys	Ala	Gln	Thr	Gly	Phe	Glu	Gln
			165					170					175		
Ala	Ala	Arg	Ala	Leu	Met	Glu	His	Thr	Leu	Arg	Leu	Gly	Gln	Met	Leu
			180					185					190		
Arg	Pro	His	Gly	Leu	Trp	Gly	Phe	Tyr	Arg	Tyr	Pro	Val	Cys	Gly	Asn
		195					200					205			
Gly	Trp	His	Asn	Met	Ala	Ser	Asn	Tyr	Thr	Gly	His	Cys	His	Pro	Ala
	210					215					220				
Ile	Ile	Thr	Arg	Asn	Thr	Gln	Leu	Arg	Trp	Leu	Trp	Ala	Ala	Ser	Ser
	225				230					235				240	

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Ala Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala Tyr
245 250 255

His Gln Thr Phe Val Arg His Arg Leu Glu Ala Phe Arg Val Ala
260 265 270

Leu Thr Gly His Ala His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu
275 280 285

Thr His Arg Ser Ser Gly Arg Phe Leu Ser Leu Asp Asp Leu Met Gln
290 295 300

Thr Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp
305 310 315 320

Gly Asp Leu Ser Val Ser Ser Ser Glu Glu Glu Cys Trp Arg Leu His
325 330 335

Asp Tyr Leu Val Gly Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Lys
340 345 350

Ala Ala Thr Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys
355 360 365

Ser Trp Lys Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Gln Pro
370 375 380

Asp Asp Asn Leu Gly Ala Trp Lys Ser Phe Arg Cys Arg Cys Tyr Leu
385 390 395 400

Gly Trp Ser Gly Pro Thr Cys Leu Glu Pro Lys Pro
405 410

<210> SEQ ID NO 24
<211> LENGTH: 545
<212> TYPE: PRT
<213> ORGANISM: Oryctolagus cuniculus
<220> FEATURE:
<223> OTHER INFORMATION: PH20

<400> SEQUENCE: 24

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Gly Ser Ala Val Glu
1 5 10 15

Leu Ser Gly Val Phe Gln Ile Val Phe Ile Phe Leu Leu Ile Pro Cys
20 25 30

Cys Leu Thr Ala Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
35 40 45

Phe Leu Trp Ala Trp Asn Ala Pro Thr Glu Phe Cys Leu Gly Lys Ser
50 55 60

Gly Glu Pro Leu Asp Met Ser Leu Phe Ser Leu Phe Gly Ser Pro Arg
65 70 75 80

Lys Asn Lys Thr Gly Gln Gly Ile Thr Ile Phe Tyr Val Asp Arg Leu
85 90 95

Gly Tyr Tyr Pro Tyr Ile Asp Pro His Thr Gly Ala Ile Val His Gly
100 105 110

Arg Ile Pro Gln Leu Gly Pro Leu Gln Gln His Leu Thr Lys Leu Arg
115 120 125

Gln Glu Ile Leu Tyr Tyr Met Pro Lys Asp Asn Val Gly Leu Ala Val
130 135 140

Ile Asp Trp Glu Glu Trp Leu Pro Thr Trp Leu Arg Asn Trp Lys Pro
145 150 155 160

Lys Asp Ile Tyr Arg Ile Lys Ser Ile Glu Leu Val Lys Ser Gln His
165 170 175

Pro Gln Tyr Asn His Ser Tyr Ala Thr Glu Lys Ala Lys Arg Asp Phe
180 185 190

-continued

Glu Lys Ala Gly Lys Asp Phe Met Glu Glu Thr Leu Lys Leu Gly Arg
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Asp Lys Pro Asn Leu Tyr Lys Gly Ser Cys Phe
 225 230 235 240
 Asp Ile Glu Lys Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Lys Glu
 245 250 255
 Ser Thr Ala Leu Phe Pro Ser Val Tyr Leu Thr Ser Arg Ala Arg Ser
 260 265 270
 Ala Thr Ala Leu Ser Lys Leu Tyr Val Val Arg Asn Arg Val His Glu
 275 280 285
 Ala Ile Arg Val Ser Lys Ile Pro Asp Asp Lys Ser Pro Leu Pro Asn
 290 295 300
 Phe Val Tyr Thr Arg Leu Val Phe Thr Asp Gln Ile Phe Gln Phe Leu
 305 310 315 320
 Ser His His Asp Leu Val Tyr Thr Ile Gly Glu Ile Val Ala Leu Gly
 325 330 335
 Ala Ser Gly Ile Val Val Trp Gly Ser Gln Ser Leu Ala Arg Ser Met
 340 345 350
 Lys Ser Cys Leu His Leu Asp Asn Tyr Met Lys Thr Ile Leu Asn Pro
 355 360 365
 Tyr Leu Ile Asn Val Thr Leu Ala Ala Lys Met Cys Asn Gln Val Leu
 370 375 380
 Cys Gln Glu Gln Gly Val Cys Thr Arg Lys Asn Trp Asn Pro Asn Asp
 385 390 395 400
 Tyr Leu His Leu Asn Pro Gly Asn Phe Ala Ile Gln Leu Gly Ser Asn
 405 410 415
 Gly Thr Tyr Lys Val Asp Gly Lys Pro Thr Leu Thr Asp Leu Glu Gln
 420 425 430
 Phe Ser Lys Asn Phe Gln Cys Ser Cys Tyr Thr Asn Leu Asn Cys Lys
 435 440 445
 Glu Arg Thr Asp Met Asn Asn Val Arg Thr Val Asn Val Cys Ala Val
 450 455 460
 Glu Asn Val Cys Ile Asp Thr Asn Val Gly Pro Gln Ala Val Thr Tyr
 465 470 475 480
 Ala Pro Lys Glu Lys Lys Asp Val Ala His Ile Leu Ser Asn Thr Thr
 485 490 495
 Ser Ile Asn Ser Ser Thr Thr Met Ser Leu Pro Phe Pro Arg Lys His
 500 505 510
 Val Ser Gly Cys Leu Leu Val Leu Cys Met Tyr Ser Gln Tyr Leu Asn
 515 520 525
 Ile Cys Tyr Arg Leu Val Ala Ile Gly Ile Gln His Gly Tyr Tyr Leu
 530 535 540
 Lys
 545

<210> SEQ ID NO 25

<211> LENGTH: 476

<212> TYPE: PRT

<213> ORGANISM: Ovis aries

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 2

<400> SEQUENCE: 25

Met Trp Thr Gly Leu Gly Pro Ala Val Thr Leu Ala Leu Val Leu Val

-continued

1	5	10	15
Val Ala Trp	Ala Thr Glu Leu Lys	Pro Thr Ala Pro	Pro Ile Phe Thr
	20	25	30
Gly Arg Pro	Phe Val Val Ala Trp	Asp Val Pro Thr	Gln Asp Cys Gly
	35	40	45
Pro Arg His	Lys Met Pro Leu Asp	Pro Lys Asp Met	Lys Ala Phe Asp
	50	55	60
Val Gln Ala	Ser Pro Asn Glu Gly	Phe Val Asn Gln	Asn Ile Thr Ile
	65	70	75
Phe Tyr Arg	Asp Arg Leu Gly	Met Tyr Pro His	Phe Asn Ser Val Gly
	85	90	95
Arg Ser Val	His Gly Gly Val	Pro Gln Asn Gly	Ser Leu Trp Val His
	100	105	110
Leu Glu Met	Leu Lys Gly His	Val Glu His Tyr	Ile Arg Thr Gln Glu
	115	120	125
Pro Ala Gly	Leu Ala Val Ile	Asp Trp Glu Asp	Trp Arg Pro Val Trp
	130	135	140
Val Arg Asn	Trp Gln Asp Lys	Asp Val Tyr Arg	Arg Arg Leu Ser Arg Gln
	145	150	155
Leu Val Ala	Ser His His Pro	Asp Trp Pro Pro	Glu Arg Ile Val Lys
	165	170	175
Glu Ala Gln	Tyr Glu Phe Glu	Phe Ala Ala Arg	Gln Phe Met Leu Glu
	180	185	190
Thr Leu Arg	Phe Val Lys Ala	Phe Arg Pro Arg	His Leu Trp Gly Phe
	195	200	205
Tyr Leu Phe	Pro Asp Cys Tyr	Asn His Asp Tyr	Val Gln Asn Trp Glu
	210	215	220
Thr Tyr Thr	Gly Arg Cys Pro	Asp Val Glu Val	Ser Arg Asn Asp Gln
	225	230	235
Leu Ser Trp	Leu Trp Ala Glu	Ser Thr Ala Leu	Phe Pro Ser Val Tyr
	245	250	255
Leu Glu Glu	Thr Leu Ala Ser	Ser Thr His Gly	Arg Asn Phe Val Ser
	260	265	270
Phe Arg Val	Gln Glu Ala Leu	Arg Val Ala Asp	Val His His Ala Asn
	275	280	285
His Ala Leu	Pro Val Tyr Val	Phe Thr Arg Pro	Thr Tyr Ser Arg Gly
	290	295	300
Leu Thr Gly	Leu Ser Glu Met	Asp Leu Ile Ser	Thr Ile Gly Glu Ser
	305	310	315
Ala Ala Leu	Gly Ala Ala Gly	Val Ile Leu Trp	Gly Asp Ala Gly Phe
	325	330	335
Thr Thr Ser	Asn Glu Thr Cys	Arg Arg Leu Lys	Asp Tyr Leu Thr Arg
	340	345	350
Ser Leu Val	Pro Tyr Val Val	Asn Val Ser Trp	Ala Ala Gln Tyr Cys
	355	360	365
Ser Trp Ala	Gln Cys His Gly	His Gly Arg Cys	Val Arg Arg Asp Pro
	370	375	380
Asn Ala His	Thr Phe Leu His	Leu Ser Ala Ser	Ser Phe Arg Leu Val
	385	390	395
Pro Ser His	Ala Pro Asp Glu	Pro Arg Leu Arg	Pro Glu Gly Glu Leu
	405	410	415
Ser Trp Ala	Asp Arg Asn His	Leu Gln Thr His	Phe Arg Cys Gln Cys
	420	425	430

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Tyr Leu Gly Trp Gly Gly Glu Gln Cys Gln Trp Asp Arg Arg Arg Ala
435 440 445

Ala Gly Gly Ala Ser Gly Ala Trp Ala Gly Ser His Leu Thr Gly Leu
450 455 460

Leu Ala Val Ala Val Leu Ala Phe Thr Trp Thr Ser
465 470 475

<210> SEQ ID NO 26

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Pongo pygmaeus

<220> FEATURE:

<223> OTHER INFORMATION: hyaluronidase 3

<400> SEQUENCE: 26

Met Thr Thr Arg Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
1 5 10 15

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
20 25 30

Val Leu Trp Asn Val Pro Ser Ala His Cys Lys Ser Arg Phe Gly Val
35 40 45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
50 55 60

Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65 70 75 80

Tyr Pro Tyr Phe Gly Pro Lys Gly Thr Ala His Asn Gly Gly Ile Pro
85 90 95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
100 105 110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
115 120 125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
130 135 140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145 150 155 160

Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
165 170 175

Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
180 185 190

Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
195 200 205

Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
210 215 220

Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
225 230 235 240

Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
245 250 255

Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
260 265 270

Val Gly His Leu Pro Val Leu Ala Tyr Val Arg Leu Thr His Arg Arg
275 280 285

Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Thr Ile Gly Val
290 295 300

Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly Asp Leu Ser
305 310 315 320

Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp Tyr Leu Val

-continued

325	330	335
Asp Thr Leu Gly Pro Tyr Gly Ile Asn Val Thr Arg Ala Ala Met Ala		
340	345	350
Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala Arg Arg Asp		
355	360	365
Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp Gly Ser Leu		
370	375	380
Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly Trp Ala Gly		
385	390	395
Pro Thr Cys Gln Glu Pro Arg Leu Gly Pro Lys Glu Ala Val		
405	410	

<210> SEQ ID NO 27

<211> LENGTH: 510

<212> TYPE: PRT

<213> ORGANISM: Macaca fascicularis

<220> FEATURE:

<223> OTHER INFORMATION: PH20

<400> SEQUENCE: 27

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys		
1	5	10
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys		
20	25	30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Ile Ile Pro Asn Val Pro		
35	40	45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe		
50	55	60
Asn Glu Pro Leu Asp Met Ser Leu Phe Thr Leu Met Gly Ser Pro Arg		
65	70	75
Ile Asn Val Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu		
85	90	95
Gly Tyr Tyr Pro Tyr Ile Asp Leu Thr Thr Gly Val Thr Val His Gly		
100	105	110
Gly Ile Pro Gln Lys Val Ser Leu Gln Asp His Leu Asp Lys Ser Lys		
115	120	125
Gln Asp Ile Leu Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val		
130	135	140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro		
145	150	155
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn		
165	170	175
Val Gln Leu Ser Leu Pro Gln Ala Thr Asp Lys Ala Lys Gln Glu Phe		
180	185	190
Glu Lys Ala Gly Lys Asp Phe Met Leu Glu Thr Ile Lys Leu Gly Arg		
195	200	205
Ser Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys		
210	215	220
Tyr Asn His His Tyr Arg Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asp		
225	230	235
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser		
245	250	255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Val Val		
260	265	270
Val Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val		
275	280	285

-continued

Ser Lys Ile Pro Asp Ala Lys Asn Pro Leu Pro Val Phe Val Tyr Ala
 290 295 300
 Arg Leu Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Arg Glu Glu
 305 310 315 320
 Leu Val Ser Thr Leu Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Ser Leu Ser Ile Thr Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Thr Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asp Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Asp Ile Arg Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val His Gly Lys Pro Thr Val Glu Asp Leu Glu Glu Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Thr Asn Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Ser Leu Lys Pro Pro Val Glu Thr Glu Gly Ser Pro Pro
 465 470 475 480
 Ile Phe Tyr Asn Thr Ser Ser Ser Thr Val Ser Thr Thr Met Phe Ile
 485 490 495
 Val Asn Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 500 505 510

<210> SEQ ID NO 28
 <211> LENGTH: 529
 <212> TYPE: PRT
 <213> ORGANISM: Cavia porcellus
 <220> FEATURE:
 <223> OTHER INFORMATION: PH20

<400> SEQUENCE: 28

Met Gly Ala Phe Thr Phe Lys His Ser Phe Phe Gly Ser Phe Val Glu
 1 5 10 15
 Cys Ser Gly Val Leu Gln Thr Val Phe Ile Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Ala Asp Lys Arg Ala Pro Pro Leu Ile Pro Asn Val Pro Leu
 35 40 45
 Leu Trp Val Trp Asn Ala Pro Thr Glu Phe Cys Ile Gly Gly Thr Asn
 50 55 60
 Gln Pro Leu Asp Met Ser Phe Phe Ser Ile Val Gly Thr Pro Arg Lys
 65 70 75 80
 Asn Ile Thr Gly Gln Ser Ile Thr Leu Tyr Tyr Val Asp Arg Leu Gly
 85 90 95
 Tyr Tyr Pro Tyr Ile Asp Pro His Thr Gly Ala Ile Val His Gly Gly
 100 105 110
 Leu Pro Gln Leu Met Asn Leu Gln Gln His Leu Arg Lys Ser Arg Gln
 115 120 125
 Asp Ile Leu Phe Tyr Met Pro Thr Asp Ser Val Gly Leu Ala Val Ile
 130 135 140

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Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Thr	Arg	Asn	Trp	Arg	Pro	Lys
145					150					155					160
Asp	Ile	Tyr	Arg	Asn	Lys	Ser	Ile	Glu	Leu	Val	Lys	Ser	Gln	His	Pro
				165					170					175	
Gln	Tyr	Asn	His	Ser	Tyr	Ala	Val	Ala	Val	Ala	Lys	Arg	Asp	Phe	Glu
			180						185					190	
Arg	Thr	Gly	Lys	Ala	Phe	Met	Leu	Glu	Thr	Leu	Lys	Leu	Gly	Lys	Ser
		195					200					205			
Leu	Arg	Pro	Ser	Ser	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr
	210					215						220			
Asn	Thr	His	Phe	Thr	Lys	Pro	Asn	Tyr	Asp	Gly	His	Cys	Pro	Pro	Ile
225					230					235					240
Glu	Leu	Gln	Arg	Asn	Asn	Asp	Leu	Gln	Trp	Leu	Trp	Asn	Asp	Ser	Thr
				245					250					255	
Ala	Leu	Tyr	Pro	Ser	Val	Tyr	Leu	Thr	Ser	Arg	Val	Arg	Ser	Ser	Gln
			260					265						270	
Asn	Gly	Ala	Leu	Tyr	Val	Arg	Asn	Arg	Val	His	Glu	Ser	Ile	Arg	Val
		275					280						285		
Ser	Lys	Leu	Met	Asp	Asp	Lys	Asn	Pro	Leu	Pro	Ile	Tyr	Val	Tyr	Ile
	290					295					300				
Arg	Leu	Val	Phe	Thr	Asp	Gln	Thr	Thr	Thr	Phe	Leu	Glu	Leu	Asp	Asp
305					310					315					320
Leu	Val	His	Ser	Val	Gly	Glu	Ile	Val	Pro	Leu	Gly	Val	Ser	Gly	Ile
				325					330					335	
Ile	Ile	Trp	Gly	Ser	Leu	Ser	Leu	Thr	Arg	Ser	Leu	Val	Ser	Cys	Ile
		340						345					350		
Gly	Leu	Glu	Asn	Tyr	Met	Lys	Gly	Thr	Leu	Leu	Pro	Tyr	Leu	Ile	Asn
	355						360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Gly	Gln	Val	Leu	Cys	Lys	Asn	Gln
	370					375					380				
Gly	Ile	Cys	Thr	Arg	Lys	Asp	Trp	Asn	Thr	Asn	Thr	Tyr	Leu	His	Leu
385					390					395					400
Asn	Ala	Thr	Asn	Phe	Asp	Ile	Glu	Leu	Gln	Gln	Asn	Gly	Lys	Phe	Val
			405						410					415	
Val	His	Gly	Lys	Pro	Ser	Leu	Glu	Asp	Leu	Gln	Glu	Phe	Ser	Lys	Asn
			420					425					430		
Phe	His	Cys	Ser	Cys	Tyr	Thr	Asn	Val	Ala	Cys	Lys	Asp	Arg	Leu	Asp
		435					440					445			
Val	His	Asn	Val	Arg	Ser	Val	Asn	Val	Cys	Thr	Ala	Asn	Asn	Ile	Cys
	450					455					460				
Ile	Asp	Ala	Val	Leu	Asn	Phe	Pro	Ser	Leu	Asp	Asp	Asp	Asp	Glu	Pro
465				470						475					480
Pro	Ile	Thr	Asp	Asp	Thr	Ser	Gln	Asn	Gln	Asp	Ser	Ile	Ser	Asp	Ile
			485						490					495	
Thr	Ser	Ser	Ala	Pro	Pro	Ser	Ser	His	Ile	Leu	Pro	Lys	Asp	Leu	Ser
			500					505					510		
Trp	Cys	Leu	Phe	Leu	Leu	Ser	Ile	Phe	Ser	Gln	His	Trp	Lys	Tyr	Leu
		515					520					525			

Leu

<210> SEQ ID NO 29

<211> LENGTH: 512

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<220> FEATURE:

-continued

<223> OTHER INFORMATION: PH20

<400> SEQUENCE: 29

Met Gly Glu Leu Gln Phe Lys Trp Leu Phe Trp Arg Ser Phe Ala Glu
 1 5 10 15
 Ser Gly Gly Thr Phe Gln Thr Val Leu Ile Phe Leu Phe Ile Pro Tyr
 20 25 30
 Ser Leu Thr Val Asp Tyr Arg Ala Thr Pro Val Leu Ser Asp Thr Thr
 35 40 45
 Phe Val Trp Val Trp Asn Val Pro Thr Glu Ala Cys Val Glu Asn Val
 50 55 60
 Thr Glu Pro Ile Asp Leu Ser Phe Phe Ser Leu Ile Gly Ser Pro Arg
 65 70 75 80
 Lys Thr Ala Ile Gly Gln Pro Val Thr Leu Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Asn Tyr Pro His Ile Asp Ala Gln Gln Thr Glu His His Gly Gly
 100 105 110
 Ile Pro Gln Lys Gly Asp Leu Thr Thr His Leu Val Lys Ala Lys Glu
 115 120 125
 Asp Val Glu Arg Tyr Ile Pro Thr Asp Lys Leu Gly Leu Ala Ile Ile
 130 135 140
 Asp Trp Glu Glu Trp Arg Pro Thr Trp Met Arg Asn Trp Thr Pro Lys
 145 150 155 160
 Asp Ile Tyr Arg Asn Lys Ser Ile Glu Leu Val Gln Ala Ala Asp Pro
 165 170 175
 Ala Ile Asn Ile Thr Glu Ala Thr Val Arg Ala Lys Ala Gln Phe Glu
 180 185 190
 Gly Ala Ala Lys Glu Phe Met Glu Gly Thr Leu Lys Leu Gly Lys His
 195 200 205
 Ile Arg Pro Lys His Leu Trp Gly Phe Tyr Leu Phe Pro Asp Cys Tyr
 210 215 220
 Asn Asn Lys Phe Gln Val Asp Asn Tyr Asp Gly Gln Cys Pro Asp Val
 225 230 235 240
 Glu Lys Lys Arg Asn Asp Asp Leu Asp Trp Leu Trp Lys Glu Ser Thr
 245 250 255
 Gly Leu Tyr Pro Ser Val Tyr Leu Lys Lys Asp Leu Lys Ser Ser Arg
 260 265 270
 Lys Ala Thr Leu Tyr Val Arg Tyr Arg Val Leu Glu Ser Ile Arg Val
 275 280 285
 Ser Lys Val Ser Asp Glu Ser Asn Pro Val Pro Ile Phe Val Tyr Ile
 290 295 300
 Arg Leu Val Phe Thr Asp His Val Ser Glu Tyr Leu Leu Glu Asp Asp
 305 310 315 320
 Leu Val Asn Thr Ile Gly Glu Ile Val Ala Gln Gly Thr Ser Gly Ile
 325 330 335
 Ile Ile Trp Asp Ala Met Ser Leu Ala Gln Arg Ser Ala Gly Cys Pro
 340 345 350
 Ile Leu Arg Gln Tyr Met Lys Thr Thr Leu Asn Pro Tyr Ile Val Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Thr Leu Cys Lys Glu Lys
 370 375 380
 Gly Met Cys Ser Arg Lys Thr Glu Ser Ser Asp Ala Tyr Leu His Leu
 385 390 395 400
 Asp Pro Ser Ser Phe Ser Ile Asn Val Thr Glu Ala Gly Lys Tyr Glu

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Val	Leu	Gly	Lys	Pro	Glu	Val	Lys	Asp	Leu	Glu	Tyr	Phe	Ser	Glu	His
			420					425					430		
Phe	Lys	Cys	Ser	Cys	Phe	Ser	Lys	Met	Thr	Cys	Glu	Glu	Thr	Ser	Asp
		435					440					445			
Met	Arg	Ser	Ile	Gln	Asp	Val	Asn	Val	Cys	Met	Gly	Asp	Asn	Val	Cys
	450					455					460				
Ile	Lys	Ala	Thr	Leu	Gly	Pro	Asn	Ser	Ala	Phe	His	Leu	Leu	Pro	Gly
465				470					475					480	
Lys	Gly	Leu	Leu	Leu	Met	Thr	Thr	Leu	Ala	His	Ile	Leu	His	His	Leu
		485						490					495		
Pro	His	Asp	Ile	Phe	Val	Phe	Pro	Trp	Lys	Met	Leu	Val	Ser	Thr	Pro
		500						505					510		

<210> SEQ ID NO 30
 <211> LENGTH: 512
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <223> OTHER INFORMATION: PH20
 <400> SEQUENCE: 30

Met	Gly	Glu	Leu	Arg	Phe	Lys	His	Leu	Phe	Trp	Gly	Ser	Phe	Val	Glu
1				5					10					15	
Ser	Gly	Gly	Thr	Phe	Gln	Thr	Val	Leu	Ile	Phe	Leu	Leu	Ile	Pro	Cys
			20				25						30		
Ser	Leu	Thr	Val	Asp	Tyr	Arg	Ala	Ala	Pro	Ile	Leu	Ser	Asn	Thr	Thr
		35				40						45			
Phe	Leu	Trp	Ile	Trp	Asn	Val	Pro	Thr	Glu	Arg	Cys	Val	Gly	Asn	Val
	50				55					60					
Asn	Asp	Pro	Ile	Asp	Leu	Ser	Phe	Phe	Ser	Leu	Ile	Gly	Ser	Pro	Arg
65				70					75					80	
Lys	Thr	Ala	Thr	Gly	Gln	Pro	Val	Thr	Leu	Phe	Tyr	Val	Asp	Arg	Leu
			85					90					95		
Gly	Leu	Tyr	Pro	His	Ile	Asp	Ala	Asn	Gln	Ala	Glu	His	Tyr	Gly	Gly
		100					105						110		
Ile	Pro	Gln	Arg	Gly	Asp	Tyr	Gln	Ala	His	Leu	Arg	Lys	Ala	Lys	Thr
		115				120						125			
Asp	Ile	Glu	His	Tyr	Ile	Pro	Asp	Asp	Lys	Leu	Gly	Leu	Ala	Ile	Ile
	130					135					140				
Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Leu	Arg	Asn	Trp	Lys	Pro	Lys
145				150					155					160	
Asp	Asn	Tyr	Arg	Asn	Lys	Ser	Ile	Glu	Leu	Val	Gln	Ser	Thr	Asn	Pro
		165						170					175		
Gly	Leu	Ser	Ile	Thr	Glu	Ala	Thr	Gln	Lys	Ala	Ile	Gln	Gln	Phe	Glu
		180					185					190			
Glu	Ala	Gly	Arg	Lys	Phe	Met	Glu	Gly	Thr	Leu	His	Leu	Gly	Lys	Phe
	195					200					205				
Leu	Arg	Pro	Asn	Gln	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr
	210				215					220					
Asn	Asn	Lys	Phe	Gln	Asp	Pro	Lys	Tyr	Asp	Gly	Gln	Cys	Pro	Ala	Val
225				230					235					240	
Glu	Lys	Lys	Arg	Asn	Asp	Asn	Leu	Lys	Trp	Leu	Trp	Lys	Ala	Ser	Thr
		245					250						255		
Gly	Leu	Tyr	Pro	Ser	Val	Tyr	Leu	Lys	Lys	Asp	Leu	Lys	Ser	Asn	Arg
		260					265					270			

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Gln Ala Thr Leu Tyr Val Arg Tyr Arg Val Val Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Val Gly Asn Ala Ser Asp Pro Val Pro Ile Phe Val Tyr Ile
 290 295 300
 Arg Leu Val Phe Thr Asp Arg Thr Ser Glu Tyr Leu Leu Glu Asp Asp
 305 310 315 320
 Leu Val Asn Thr Ile Gly Glu Ile Val Ala Leu Gly Thr Ser Gly Ile
 325 330 335
 Ile Ile Trp Asp Ala Met Ser Leu Ala Gln Arg Ala Ala Gly Cys Pro
 340 345 350
 Ile Leu His Lys Tyr Met Gln Thr Thr Leu Asn Pro Tyr Ile Val Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Thr Leu Cys Asn Glu Lys
 370 375 380
 Gly Met Cys Ser Arg Arg Lys Glu Ser Ser Asp Val Tyr Leu His Leu
 385 390 395 400
 Asn Pro Ser His Phe Asp Ile Met Leu Thr Glu Thr Gly Lys Tyr Glu
 405 410 415
 Val Leu Gly Asn Pro Arg Val Gly Asp Leu Glu Tyr Phe Ser Glu His
 420 425 430
 Phe Lys Cys Ser Cys Phe Ser Arg Met Thr Cys Lys Glu Thr Ser Asp
 435 440 445
 Val Lys Asn Val Gln Asp Val Asn Val Cys Val Gly Asp Asn Val Cys
 450 455 460
 Ile Lys Ala Lys Val Glu Pro Asn Pro Ala Phe Tyr Leu Leu Pro Gly
 465 470 475 480
 Lys Ser Leu Leu Phe Met Thr Thr Leu Gly His Val Leu Tyr His Leu
 485 490 495
 Pro Gln Asp Ile Phe Val Phe Pro Arg Lys Thr Leu Val Ser Thr Pro
 500 505 510

<210> SEQ ID NO 31
 <211> LENGTH: 807
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 31

Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
 1 5 10 15
 Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Val
 20 25 30
 Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
 35 40 45
 Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
 50 55 60
 Lys Tyr Asp Glu Asn Asn Pro Asp Met Lys Lys Lys Phe Asp Ala Thr
 65 70 75 80
 Glu Lys Glu Ala Thr Asn Leu Leu Lys Glu Met Lys Thr Glu Ser Gly
 85 90 95
 Arg Lys Tyr Leu Trp Ser Gly Ala Glu Thr Leu Glu Thr Asn Ser Ser
 100 105 110
 His Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
 115 120 125

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Arg	Asn	Pro	Lys	Thr	Thr	Leu	Asn	Thr	Asp	Glu	Asn	Lys	Lys	Lys	Val
130						135					140				
Lys	Asp	Ala	Leu	Glu	Trp	Leu	His	Lys	Asn	Ala	Tyr	Gly	Lys	Glu	Pro
145				150						155					160
Asp	Lys	Lys	Val	Lys	Glu	Leu	Ser	Glu	Asn	Phe	Thr	Lys	Thr	Thr	Gly
			165						170						175
Lys	Asn	Thr	Asn	Leu	Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Pro	Lys
	180							185					190		
Ser	Leu	Thr	Asn	Thr	Leu	Ile	Leu	Leu	Asn	Asp	Gln	Phe	Ser	Asn	Glu
	195						200					205			
Glu	Lys	Lys	Lys	Phe	Thr	Ala	Pro	Ile	Lys	Thr	Phe	Ala	Pro	Asp	Ser
	210					215					220				
Asp	Lys	Ile	Leu	Ser	Ser	Val	Gly	Lys	Ala	Glu	Leu	Ala	Lys	Gly	Gly
225					230					235					240
Asn	Leu	Val	Asp	Ile	Ser	Lys	Val	Lys	Leu	Leu	Glu	Cys	Ile	Ile	Glu
			245						250						255
Glu	Asp	Lys	Asp	Met	Met	Lys	Lys	Ser	Ile	Asp	Ser	Phe	Asn	Lys	Val
			260					265					270		
Phe	Thr	Tyr	Val	Gln	Asp	Ser	Ala	Thr	Gly	Lys	Glu	Arg	Asn	Gly	Phe
	275						280					285			
Tyr	Lys	Asp	Gly	Ser	Tyr	Ile	Asp	His	Gln	Asp	Val	Pro	Tyr	Thr	Gly
	290					295					300				
Ala	Tyr	Gly	Val	Val	Leu	Leu	Glu	Gly	Ile	Ser	Gln	Met	Met	Pro	Met
305					310					315					320
Ile	Lys	Glu	Thr	Pro	Phe	Asn	Asp	Lys	Thr	Gln	Asn	Asp	Thr	Thr	Leu
			325						330					335	
Lys	Ser	Trp	Ile	Asp	Asp	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly	Glu
		340						345					350		
Met	Met	Asp	Leu	Ser	Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu	Thr
		355					360					365			
Ser	His	Ser	Ala	Ser	Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu	Ser
	370					375					380				
Asp	Ala	Met	Asp	Asp	Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Lys	Ile	Val	Lys
385					390					395					400
Ser	Ser	Val	Glu	Ser	Asp	Ser	Ser	Tyr	Lys	Gln	Asn	Asp	Tyr	Leu	Asn
			405						410					415	
Ser	Tyr	Ser	Asp	Ile	Asp	Lys	Met	Lys	Ser	Leu	Met	Thr	Asp	Asn	Ser
			420					425					430		
Ile	Ser	Lys	Asn	Gly	Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp	Met
		435					440					445			
Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly	Leu
	450					455					460				
Ser	Met	Thr	Ser	Lys	Asn	Val	Ala	Arg	Tyr	Glu	Ser	Ile	Asn	Gly	Glu
465					470					475					480
Asn	Leu	Lys	Gly	Trp	His	Thr	Gly	Ala	Gly	Met	Ser	Tyr	Leu	Tyr	Asn
			485						490					495	
Ser	Asp	Val	Lys	His	Tyr	His	Asp	Asn	Phe	Trp	Val	Thr	Ala	Asp	Met
			500					505					510		
Lys	Arg	Leu	Ser	Gly	Thr	Thr	Thr	Leu	Asp	Asn	Glu	Ile	Leu	Lys	Asp
		515						520					525		
Thr	Asp	Asp	Lys	Lys	Ser	Ser	Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys	Val
					535						540				
Asp	Asp	Gln	His	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	Lys
545					550					555					560

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Thr Leu Thr Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val
 565 570 575
 Phe Leu Gly Thr Gly Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val
 580 585 590
 Thr Thr Ile Glu Asn Arg Lys Ala Asn Gly Tyr Thr Leu Tyr Thr Asp
 595 600 605
 Asp Lys Gln Thr Thr Asn Ser Asp Asn Gln Glu Asn Asn Ser Val Phe
 610 615 620
 Leu Glu Ser Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn
 625 630 635 640
 Lys Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Lys
 645 650 655
 Glu Ile Asn Lys Ser Gln Lys Asp Thr Gln Lys Thr Asp Glu Tyr Tyr
 660 665 670
 Glu Val Thr Gln Lys His Ser Asn Ser Asp Asn Lys Tyr Gly Tyr Val
 675 680 685
 Leu Tyr Pro Gly Leu Ser Lys Asp Val Phe Lys Thr Lys Lys Asp Glu
 690 695 700
 Val Thr Val Val Lys Gln Glu Asp Asp Phe His Val Val Lys Asp Asn
 705 710 715 720
 Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe
 725 730 735
 Asp Ile Asn Asn Thr Lys Val Glu Val Lys Ala Lys Gly Met Phe Ile
 740 745 750
 Leu Lys Lys Lys Asp Asp Asn Thr Tyr Glu Cys Ser Phe Tyr Asn Pro
 755 760 765
 Glu Ser Thr Asn Ser Ala Ser Asp Ile Glu Ser Lys Ile Ser Met Thr
 770 775 780
 Gly Tyr Ser Ile Thr Asn Lys Asn Thr Ser Thr Ser Asn Glu Ser Gly
 785 790 795 800
 Val His Phe Glu Leu Thr Lys
 805

<210> SEQ ID NO 32
 <211> LENGTH: 371
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus pyogenes bacteriophage H4489A
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 32

Met Thr Glu Asn Ile Pro Leu Arg Val Gln Phe Lys Arg Met Ser Ala
 1 5 10 15
 Asp Glu Trp Ala Arg Ser Asp Val Ile Leu Leu Glu Gly Glu Ile Gly
 20 25 30
 Phe Glu Thr Asp Thr Gly Phe Ala Lys Phe Gly Asp Gly Gln Asn Thr
 35 40 45
 Phe Ser Lys Leu Lys Tyr Leu Thr Gly Pro Lys Gly Pro Lys Gly Asp
 50 55 60
 Thr Gly Leu Gln Gly Lys Thr Gly Gly Thr Gly Pro Arg Gly Pro Ala
 65 70 75 80
 Gly Lys Pro Gly Thr Thr Asp Tyr Asp Gln Leu Gln Asn Lys Pro Asp
 85 90 95
 Leu Gly Ala Phe Ala Gln Lys Glu Glu Thr Asn Ser Lys Ile Thr Lys
 100 105 110

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Leu Glu Ser Ser Lys Ala Asp Lys Ser Ala Val Tyr Ser Lys Ala Glu
 115 120 125
 Ser Lys Ile Glu Leu Asp Lys Lys Leu Ser Leu Thr Gly Gly Ile Val
 130 135 140
 Thr Gly Gln Leu Gln Phe Lys Pro Asn Lys Ser Gly Ile Lys Pro Ser
 145 150 155 160
 Ser Ser Val Gly Gly Ala Ile Asn Ile Asp Met Ser Lys Ser Glu Gly
 165 170 175
 Ala Ala Met Val Met Tyr Thr Asn Lys Asp Thr Thr Asp Gly Pro Leu
 180 185 190
 Met Ile Leu Arg Ser Asp Lys Asp Thr Phe Asp Gln Ser Ala Gln Phe
 195 200 205
 Val Asp Tyr Ser Gly Lys Thr Asn Ala Val Asn Ile Val Met Arg Gln
 210 215 220
 Pro Ser Ala Pro Asn Phe Ser Ser Ala Leu Asn Ile Thr Ser Ala Asn
 225 230 235 240
 Glu Gly Gly Ser Ala Met Gln Ile Arg Gly Val Glu Lys Ala Leu Gly
 245 250 255
 Thr Leu Lys Ile Thr His Glu Asn Pro Asn Val Glu Ala Lys Tyr Asp
 260 265 270
 Glu Asn Ala Ala Ala Leu Ser Ile Asp Ile Val Lys Lys Gln Lys Gly
 275 280 285
 Gly Lys Gly Thr Ala Ala Gln Gly Ile Tyr Ile Asn Ser Thr Ser Gly
 290 295 300
 Thr Ala Gly Lys Met Leu Arg Ile Arg Asn Lys Asn Glu Asp Lys Phe
 305 310 315 320
 Tyr Val Gly Pro Asp Gly Gly Phe His Ser Gly Ala Asn Ser Thr Val
 325 330 335
 Ala Gly Asn Leu Thr Val Lys Asp Pro Thr Ser Gly Lys His Ala Ala
 340 345 350
 Thr Lys Asp Tyr Val Asp Glu Lys Ile Ala Glu Leu Lys Lys Leu Ile
 355 360 365
 Leu Lys Lys
 370

<210> SEQ ID NO 33
 <211> LENGTH: 1628
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium perfringens
 <220> FEATURE:
 <223> OTHER INFORMATION: hyaluronidase

<400> SEQUENCE: 33

Met Asn Lys Asn Ile Arg Lys Ile Ile Thr Ser Thr Val Leu Ala Ala
 1 5 10 15
 Met Thr Ile Ser Val Leu Pro Ser Asn Leu Val Val Phe Ala Thr Asp
 20 25 30
 Gly Ile Thr Glu Asn Phe Tyr Glu Ile Tyr Pro Lys Pro Gln Glu Ile
 35 40 45
 Ser Tyr Ser Gly Gly Glu Phe Gln Ile Ser Asp Glu Ile Asn Ile Val
 50 55 60
 Tyr Asp Asp Gly Ile Asp Thr Tyr Thr Lys Lys Arg Val Asp Glu Val
 65 70 75 80
 Leu Glu Ala Ser Asn Leu Glu Ala Thr Val Ser Asn Glu Ile Val Pro
 85 90 95
 Gly Lys Thr Asn Phe Leu Val Gly Ile Asn Glu Ser Gly Gly Val Val

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100						105						110					
Asp	Asn	Tyr	Phe	Asn	Lys	Asn	Ile	Pro	His	Asp	Glu	Ser	Phe	Phe	Asp		
115						120						125					
Glu	Lys	Met	Asp	Ala	Asn	Ile	Val	Ser	Val	Lys	Asp	Gly	Val	Ile	Gly		
130						135						140					
Val	Ile	Gly	Glu	Asp	Thr	Asp	Ser	Ala	Phe	Tyr	Gly	Val	Thr	Thr	Leu		
145						150						155					
Lys	His	Val	Phe	Asn	Gln	Leu	Glu	Glu	Gly	Asn	Lys	Ile	Gln	Ser	Phe		
			165						170			175					
Arg	Ala	Asp	Asp	Tyr	Ala	Glu	Val	Ala	His	Arg	Gly	Phe	Ile	Glu	Gly		
			180						185			190					
Tyr	Tyr	Gly	Asn	Pro	Trp	Ser	Asn	Glu	Asp	Arg	Ala	Glu	Leu	Met	Lys		
195						200						205					
Phe	Gly	Gly	Asp	Tyr	Lys	Leu	Asn	Gln	Tyr	Val	Phe	Ala	Pro	Lys	Asp		
210						215						220					
Asp	Pro	Tyr	His	Asn	Ser	Lys	Trp	Arg	Asp	Leu	Tyr	Pro	Glu	Glu	Lys		
225						230						235					
Leu	Ser	Glu	Ile	Lys	Lys	Leu	Ala	Gln	Val	Gly	Asn	Glu	Thr	Lys	Asn		
			245						250			255					
Arg	Tyr	Val	Tyr	Ala	Leu	His	Pro	Phe	Met	Asn	Asn	Pro	Val	Arg	Phe		
			260						265			270					
Asp	Thr	Glu	Glu	Asn	Tyr	Gln	Asn	Asp	Leu	Gly	Val	Ile	Lys	Ala	Lys		
275						280						285					
Phe	Thr	Gln	Leu	Leu	Glu	Asn	Asp	Val	Arg	Gln	Phe	Ala	Ile	Leu	Ala		
290						295						300					
Asp	Asp	Ala	Ser	Ala	Pro	Ala	Gln	Gly	Ala	Ser	Met	Tyr	Val	Lys	Leu		
305						310						315					
Leu	Thr	Asp	Leu	Thr	Arg	Trp	Leu	Glu	Glu	Gln	Gln	Ser	Thr	Tyr	Pro		
			325						330			335					
Asp	Leu	Lys	Thr	Asp	Leu	Met	Phe	Cys	Pro	Ser	Asp	Tyr	Tyr	Gly	Asn		
			340						345			350					
Gly	Ser	Ser	Ala	Gln	Leu	Lys	Glu	Leu	Asn	Lys	Ala	Glu	Asp	Asn	Val		
355						360						365					
Ser	Ile	Val	Met	Thr	Gly	Gly	Arg	Ile	Trp	Gly	Glu	Val	Asp	Glu	Asn		
370						375						380					
Phe	Ala	Asn	Asn	Phe	Met	Asn	Asn	Ile	Ser	Thr	Glu	Gly	His	Pro	Gly		
385						390						395					
Arg	Ala	Pro	Phe	Phe	Trp	Ile	Asn	Trp	Pro	Cys	Ser	Asp	Asn	Ser	Lys		
			405						410			415					
Gln	His	Leu	Ile	Met	Gly	Gly	Asn	Asp	Thr	Phe	Leu	His	Pro	Gly	Val		
			420						425			430					
Asp	Pro	Ser	Lys	Ile	Asp	Gly	Ile	Val	Leu	Asn	Pro	Met	Gln	Gln	Ala		
435						440						445					
Glu	Ala	Asn	Lys	Ser	Ala	Leu	Phe	Ala	Ile	Ala	Asp	Tyr	Ala	Trp	Asn		
450						455						460					
Ile	Trp	Asp	Asn	Lys	Glu	Glu	Ala	Asp	Glu	Asn	Trp	Asn	Asp	Ser	Phe		
465						470						475					
Lys	Tyr	Met	Asp	His	Gly	Thr	Ala	Glu	Glu	Thr	Asn	Ser	Ser	Leu	Ala		
			485						490			495					
Leu	Arg	Glu	Ile	Ser	Lys	His	Met	Ile	Asn	Gln	Asn	Met	Asp	Gly	Arg		
			500						505			510					
Val	Arg	Pro	Leu	Gln	Glu	Ser	Val	Glu	Leu	Ala	Pro	Lys	Leu	Glu	Ala		
515						520						525					

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Phe	Lys	Gln	Lys	Tyr	Asp	Ser	Gly	Ala	Ser	Ile	Lys	Glu	Asp	Ala	Leu
530						535					540				
Glu	Leu	Ile	Ala	Glu	Phe	Thr	Asn	Leu	Gln	Lys	Ala	Ala	Asp	Tyr	Tyr
545					550					555					560
Lys	Asn	Asn	Pro	Gly	Asn	Glu	Arg	Thr	Arg	Asp	Gln	Ile	Ile	Tyr	Trp
				565					570					575	
Leu	Asn	Cys	Trp	Glu	Asp	Thr	Met	Asp	Ala	Ala	Ile	Gly	Tyr	Leu	Lys
			580					585					590		
Ser	Ala	Ile	Ala	Ile	Glu	Glu	Gly	Asp	Asp	Glu	Ala	Ala	Trp	Ala	Asn
			595				600					605			
Tyr	Ser	Glu	Ala	Gln	Gly	Ala	Phe	Glu	Lys	Ser	Lys	Thr	Tyr	Gly	Phe
	610					615						620			
His	Tyr	Val	Asp	His	Thr	Glu	Tyr	Ala	Glu	Val	Gly	Val	Gln	His	Ile
625					630					635					640
Val	Pro	Phe	Ile	Lys	Ser	Met	Gly	Gln	Asn	Leu	Ser	Val	Val	Ile	Gly
				645					650					655	
Ser	Ile	Val	Asp	Pro	Asn	Arg	Ile	Ile	Ala	Thr	Tyr	Ile	Ser	Asn	Arg
			660				665						670		
Gln	Asp	Ala	Pro	Thr	Gly	Asn	Pro	Asp	Asn	Ile	Phe	Asp	Asn	Asn	Ala
		675				680						685			
Ser	Thr	Glu	Leu	Val	Tyr	Lys	Asn	Pro	Asn	Arg	Ile	Asp	Val	Gly	Thr
	690					695					700				
Tyr	Val	Gly	Val	Lys	Tyr	Ser	Asn	Pro	Ile	Thr	Leu	Asn	Asn	Val	Glu
705				710						715					720
Phe	Leu	Met	Gly	Ala	Asn	Ser	Asn	Pro	Asn	Asp	Thr	Met	Gln	Lys	Ala
			725					730					735		
Lys	Ile	Gln	Tyr	Thr	Val	Asp	Gly	Arg	Glu	Trp	Ile	Asp	Leu	Glu	Glu
			740				745					750			
Gly	Val	Glu	Tyr	Thr	Met	Pro	Gly	Ala	Ile	Lys	Val	Glu	Asn	Leu	Asp
		755				760						765			
Leu	Lys	Val	Arg	Gly	Val	Arg	Leu	Ile	Ala	Thr	Glu	Ala	Arg	Glu	Asn
	770				775						780				
Thr	Trp	Leu	Gly	Val	Arg	Asp	Ile	Asn	Val	Asn	Lys	Lys	Glu	Asp	Ser
785					790					795					800
Asn	Ser	Gly	Val	Glu	Phe	Asn	Pro	Ser	Leu	Ile	Arg	Ser	Glu	Ser	Trp
			805						810					815	
Gln	Val	Tyr	Glu	Gly	Asn	Glu	Ala	Asn	Leu	Leu	Asp	Gly	Asp	Asp	Asn
			820				825					830			
Thr	Gly	Val	Trp	Tyr	Lys	Thr	Leu	Asn	Gly	Asp	Thr	Ser	Leu	Ala	Gly
		835				840						845			
Glu	Phe	Ile	Gly	Leu	Asp	Leu	Gly	Lys	Glu	Ile	Lys	Leu	Asp	Gly	Ile
	850				855					860					
Arg	Phe	Val	Ile	Gly	Lys	Asn	Gly	Gly	Gly	Ser	Ser	Asp	Lys	Trp	Asn
865					870					875					880
Lys	Phe	Lys	Leu	Glu	Tyr	Ser	Leu	Asp	Asn	Glu	Ser	Trp	Thr	Thr	Ile
			885					890					895		
Lys	Glu	Tyr	Asp	Lys	Thr	Gly	Ala	Pro	Ala	Gly	Lys	Asp	Val	Ile	Glu
			900				905						910		
Glu	Ser	Phe	Glu	Thr	Pro	Ile	Ser	Ala	Lys	Tyr	Ile	Arg	Leu	Thr	Asn
		915					920					925			
Met	Glu	Asn	Ile	Asn	Lys	Trp	Leu	Thr	Phe	Ser	Glu	Phe	Ala	Ile	Ile
	930					935					940				
Ser	Asp	Glu	Leu	Glu	Asn	Ala	Gly	Asn	Lys	Glu	Asn	Val	Tyr	Thr	Asn
945					950					955					960

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Thr Glu Leu Asp Leu Leu Ser Leu Ala Lys Glu Asp Val Thr Lys Leu
 965 970 975
 Ile Pro Thr Asp Asp Ile Ser Leu Asn His Gly Glu Tyr Ile Gly Val
 980 985 990
 Lys Leu Asn Arg Ile Lys Asp Leu Ser Asn Ile Asn Leu Glu Ile Ser
 995 1000 1005
 Asn Asp Thr Gly Leu Lys Leu Gln Ser Ser Met Asn Gly Val Glu Trp
 1010 1015 1020
 Thr Glu Ile Thr Asp Lys Asn Thr Leu Glu Asp Gly Arg Tyr Val Arg
 1025 1030 1035 1040
 Leu Ile Asn Thr Ser Asn Glu Ala Val Asn Phe Asn Leu Thr Lys Phe
 1045 1050 1055
 Glu Val Asn Ser Asn Glu Val Tyr Glu Pro Ser Leu Val Asp Ala Tyr
 1060 1065 1070
 Val Gly Asp Asp Gly Ala Lys Lys Ala Val Asp Gly Asp Leu Lys Thr
 1075 1080 1085
 Arg Val Lys Phe Leu Gly Ala Pro Ser Thr Gly Asp Thr Ile Val Tyr
 1090 1095 1100
 Asp Leu Gly Gln Glu Ile Leu Val Asp Asn Leu Lys Tyr Val Val Leu
 1105 1110 1115 1120
 Asp Thr Glu Val Asp His Val Arg Asp Gly Lys Ile Gln Leu Ser Leu
 1125 1130 1135
 Asp Gly Glu Thr Trp Thr Asp Ala Ile Thr Ile Gly Asp Gly Val Glu
 1140 1145 1150
 Asn Gly Val Asp Asp Met Phe Ser Thr Pro Leu Lys Asn Gly Tyr Lys
 1155 1160 1165
 His Gly Asn Gln Ser Gly Gly Ile Val Pro Ile Asp Ser Ala Tyr Val
 1170 1175 1180
 Glu Gly Asp Asn Leu Asn Gln Lys Ala Arg Tyr Val Arg Ile Leu Phe
 1185 1190 1195 1200
 Thr Ala Pro Tyr Arg His Arg Trp Thr Val Ile Asn Glu Leu Met Ile
 1205 1210 1215
 Asn Asn Gly Glu Tyr Ile Ser Thr Val Asn Asp Pro Thr Tyr Ile Ser
 1220 1225 1230
 Asn Pro Ile Glu Glu Arg Gly Phe Ala Pro Ser Asn Leu Arg Asp Gly
 1235 1240 1245
 Asn Leu Thr Thr Ser Tyr Lys Pro Asn Thr Asn Asn Gly Glu Ile Ser
 1250 1255 1260
 Glu Gly Ser Ile Thr Tyr Arg Leu Ser Glu Lys Thr Asp Val Arg Lys
 1265 1270 1275 1280
 Val Thr Ile Val Gln Ser Gly Ser Ser Ile Ser Asn Ala Lys Val Met
 1285 1290 1295
 Ala Arg Val Gly Asp Gly Ser Glu Asn Val Thr Asp Gln Trp Val Gln
 1300 1305 1310
 Leu Gly Thr Leu Ser Asn Ser Leu Asn Glu Phe Ile Asn Arg Asp Tyr
 1315 1320 1325
 Asn Asn Ile Tyr Glu Ile Lys Ile Glu Trp Thr Asp Val Ala Pro Asn
 1330 1335 1340
 Ile Tyr Glu Ile Ile Thr Leu Asn Gln Glu Phe Glu Phe Pro Val Asn
 1345 1350 1355 1360
 Asp Ser Leu Lys Ala Lys Tyr Asp Glu Leu Ile Asn Leu Ser Gly Asp
 1365 1370 1375
 Glu Tyr Thr Leu Ser Ser Phe Glu Thr Leu Lys Glu Ala Leu Asn Glu

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1380	1385	1390
Ala Lys Ser Ile Leu Asp Asp 1395	Ser Asn Ser Ser Gln 1400	Lys Lys Ile Asp 1405
Lys Ala Leu Glu Lys Leu Asn Lys 1410	Ala Glu Glu Arg 1415	Leu Asp Leu Arg 1420
Ala Thr Asp Phe Glu Asp Phe Asn Lys 1425	Val Leu Thr 1430	Leu Gly Asn Ser 1435 1440
Leu Val Glu Glu Glu Tyr Thr 1445	Ala Glu Ser Trp 1450	Ala Leu Phe Ser Glu 1455
Val Leu Glu Ala Ala Asn Glu 1460	Ala Asn Lys Asn Lys 1465	Ala Asp Tyr Thr 1470
Gln Asp Gln Ile Asn Gln Ile 1475	Val Ile Asp 1480	Leu Asp Ala Ser Ile Lys 1485
Ala Leu Val Lys Glu Thr 1490	Pro Glu Val Asp Lys 1495	Thr Asn Leu Gly Glu 1500
Leu Ile Asn Gln Gly Lys Ser Leu 1505	Leu Asp Glu Ser Val 1510	Glu Gly Phe 1515 1520
Asn Val Gly Glu Tyr His Lys 1525	Gly Ala Lys Asp 1530	Gly Leu Thr Val Glu 1535
Ile Asn Lys Ala Glu Glu Val 1540	Phe Asn Lys Glu Asp 1545	Ala Thr Glu Glu 1550
Glu Ile Asn Leu Ala Lys Glu 1555	Ser Leu Glu Gly 1560	Ala Ile Ala Arg Phe 1565
Asn Ser Leu Leu Ile Glu Glu 1570	Ser Thr Gly Asp 1575	Phe Asn Gly Asn Gly 1580
Lys Ile Asp Ile Gly Asp Leu 1585	Ala Met Val Ser Lys 1590	Asn Ile Gly Ser 1595 1600
Thr Thr Asn Thr Ser Leu Asp 1605	Leu Asn Lys Asp 1610	Gly Ser Ile Asp Glu 1615
Tyr Glu Ile Ser Phe Ile Asn 1620	His Arg Ile Leu Asn 1625	

<210> SEQ ID NO 34

<211> LENGTH: 435

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: Hyaluronidase-1 [Precursor]

<400> SEQUENCE: 34

Met	Ala	Ala	His	Leu	Leu	Pro	Ile	Cys	Ala	Leu	Phe	Leu	Thr	Leu	Leu
1				5					10					15	
Asp	Met	Ala	Gln	Gly	Phe	Arg	Gly	Pro	Leu	Leu	Pro	Asn	Arg	Pro	Phe
		20					25						30		
Thr	Thr	Val	Trp	Asn	Ala	Asn	Thr	Gln	Trp	Cys	Leu	Glu	Arg	His	Gly
		35					40					45			
Val	Asp	Val	Asp	Val	Ser	Val	Phe	Asp	Val	Val	Ala	Asn	Pro	Gly	Gln
	50				55						60				
Thr	Phe	Arg	Gly	Pro	Asp	Met	Thr	Ile	Phe	Tyr	Ser	Ser	Gln	Leu	Gly
	65			70					75					80	
Thr	Tyr	Pro	Tyr	Tyr	Thr	Pro	Thr	Gly	Glu	Pro	Val	Phe	Gly	Gly	Leu
			85					90						95	
Pro	Gln	Asn	Ala	Ser	Leu	Ile	Ala	His	Leu	Ala	Arg	Thr	Phe	Gln	Asp
			100				105						110		
Ile	Leu	Ala	Ala	Ile	Pro	Ala	Pro	Asp	Phe	Ser	Gly	Leu	Ala	Val	Ile
		115					120					125			

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Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys
 130          135          140

Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro
 145          150          155          160

Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln
          165          170          175

Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala
          180          185          190

Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
          195          200          205

Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly
          210          215          220

Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
          225          230          235          240

Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly
          245          250          255

Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val
          260          265          270

Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln
          275          280          285

Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu
          290          295          300

His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
          305          310          315          320

Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile
          325          330          335

Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
          340          345          350

Ser Gly Ala Leu Leu Cys Ser Gln Ala Leu Cys Ser Gly His Gly Arg
          355          360          365

Cys Val Arg Arg Thr Ser His Pro Lys Ala Leu Leu Leu Leu Asn Pro
          370          375          380

Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Gly Pro Leu Ser Leu
          385          390          395          400

Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe
          405          410          415

Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys
          420          425          430

Ser Met Trp
          435

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<210> SEQ ID NO 35
<211> LENGTH: 473
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: Hyaluronidase-2 [Precursor]

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<400> SEQUENCE: 35

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Met Arg Ala Gly Pro Gly Pro Thr Val Thr Leu Ala Leu Val Leu Ala
 1          5          10          15

Val Ala Trp Ala Met Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr
          20          25          30

Gly Arg Pro Phe Val Val Ala Trp Asp Val Pro Thr Gln Asp Cys Gly
          35          40          45

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Pro	Arg	Leu	Lys	Val	Pro	Leu	Asp	Leu	Asn	Ala	Phe	Asp	Val	Gln	Ala
50						55					60				
Ser	Pro	Asn	Glu	Gly	Phe	Val	Asn	Gln	Asn	Ile	Thr	Ile	Phe	Tyr	Arg
65					70					75					80
Asp	Arg	Leu	Gly	Leu	Tyr	Pro	Arg	Phe	Asp	Ser	Ala	Gly	Arg	Ser	Val
			85						90					95	
His	Gly	Gly	Val	Pro	Gln	Asn	Val	Ser	Leu	Trp	Ala	His	Arg	Lys	Met
			100					105						110	
Leu	Gln	Lys	Arg	Val	Glu	His	Tyr	Ile	Arg	Thr	Gln	Glu	Ser	Ala	Gly
			115					120						125	
Leu	Ala	Val	Ile	Asp	Trp	Glu	Asp	Trp	Arg	Pro	Val	Trp	Val	Arg	Asn
			130					135				140			
Trp	Gln	Asp	Lys	Asp	Val	Tyr	Arg	Arg	Leu	Ser	Arg	Gln	Leu	Val	Ala
145					150					155					160
Ser	Arg	His	Pro	Asp	Trp	Pro	Pro	Asp	Arg	Ile	Val	Lys	Gln	Ala	Gln
				165					170						175
Tyr	Glu	Phe	Glu	Phe	Ala	Ala	Gln	Gln	Phe	Met	Leu	Glu	Thr	Leu	Arg
			180						185					190	
Tyr	Val	Lys	Ala	Val	Arg	Pro	Arg	His	Leu	Trp	Gly	Phe	Tyr	Leu	Phe
			195					200					205		
Pro	Asp	Cys	Tyr	Asn	His	Asp	Tyr	Val	Gln	Asn	Trp	Glu	Ser	Tyr	Thr
			210					215				220			
Gly	Arg	Cys	Pro	Asp	Val	Glu	Val	Ala	Arg	Asn	Asp	Gln	Leu	Ala	Trp
225					230					235					240
Leu	Trp	Ala	Glu	Ser	Thr	Ala	Leu	Phe	Pro	Ser	Val	Tyr	Leu	Asp	Glu
			245						250					255	
Thr	Leu	Ala	Ser	Ser	Arg	His	Gly	Arg	Asn	Phe	Val	Ser	Phe	Arg	Val
			260						265					270	
Gln	Glu	Ala	Leu	Arg	Val	Ala	Arg	Thr	His	His	Ala	Asn	His	Ala	Leu
			275					280						285	
Pro	Val	Tyr	Val	Phe	Thr	Arg	Pro	Thr	Tyr	Ser	Arg	Arg	Leu	Thr	Gly
			290					295				300			
Leu	Ser	Glu	Met	Asp	Leu	Ile	Ser	Thr	Ile	Gly	Glu	Ser	Ala	Ala	Leu
305					310					315					320
Gly	Ala	Ala	Gly	Val	Ile	Leu	Trp	Gly	Asp	Ala	Gly	Tyr	Thr	Thr	Ser
			325						330					335	
Thr	Glu	Thr	Cys	Gln	Tyr	Leu	Lys	Asp	Tyr	Leu	Thr	Arg	Leu	Leu	Val
			340						345				350		
Pro	Tyr	Val	Val	Asn	Val	Ser	Trp	Ala	Thr	Gln	Tyr	Cys	Ser	Arg	Ala
			355					360					365		
Gln	Cys	His	Gly	His	Gly	Arg	Cys	Val	Arg	Arg	Asn	Pro	Ser	Ala	Ser
			370					375							
Thr	Phe	Leu	His	Leu	Ser	Thr	Asn	Ser	Phe	Arg	Leu	Val	Pro	Gly	His
385					390					395					400
Ala	Pro	Gly	Glu	Pro	Gln	Leu	Arg	Pro	Val	Gly	Glu	Leu	Ser	Trp	Ala
			405						410					415	
Asp	Ile	Asp	His	Leu	Gln	Thr	His	Phe	Arg	Cys	Gln	Cys	Tyr	Leu	Gly
			420						425					430	
Trp	Ser	Gly	Glu	Gln	Cys	Gln	Trp	Asp	His	Arg	Gln	Ala	Ala	Gly	Gly
			435					440					445		
Ala	Ser	Glu	Ala	Trp	Ala	Gly	Ser	His	Leu	Thr	Ser	Leu	Leu	Ala	Leu
			450					455				460			
Ala	Ala	Leu	Ala	Phe	Thr	Trp	Thr	Leu							
465								470							

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<210> SEQ ID NO 36
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: Hyaluronidase-3 [Precursor]

<400> SEQUENCE: 36
Met Thr Thr Gln Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
 1             5             10             15
Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
 20             25             30
Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
 35             40             45
His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
 50             55             60
Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
 65             70             75             80
Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
 85             90             95
Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
 100            105            110
His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
 115            120            125
Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
 130            135            140
Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
 145            150            155            160
Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
 165            170            175
Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
 180            185            190
Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
 195            200            205
Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
 210            215            220
Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
 225            230            235            240
Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
 245            250            255
Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
 260            265            270
Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
 275            280            285
His Arg Arg Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Ser
 290            295            300
Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly
 305            310            315            320
Asp Leu Ser Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp
 325            330            335
Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
 340            345            350
Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
 355            360            365

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Arg	Arg	Asp	Pro	Gly	Gln	Met	Glu	Ala	Phe	Leu	His	Leu	Trp	Pro	Asp
370						375					380				
Gly	Ser	Leu	Gly	Asp	Trp	Lys	Ser	Phe	Ser	Cys	His	Cys	Tyr	Trp	Gly
385					390					395					400
Trp	Ala	Gly	Pro	Thr	Cys	Gln	Glu	Pro	Arg	Pro	Gly	Pro	Lys	Glu	Ala
				405					410					415	

Val

<210> SEQ ID NO 37
 <211> LENGTH: 481
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: Hyaluronidase-4

<400> SEQUENCE: 37

Met	Lys	Val	Leu	Ser	Glu	Gly	Gln	Leu	Lys	Leu	Cys	Val	Val	Gln	Pro
1				5					10					15	
Val	His	Leu	Thr	Ser	Trp	Leu	Leu	Ile	Phe	Phe	Ile	Leu	Lys	Ser	Ile
			20					25					30		
Ser	Cys	Leu	Lys	Pro	Ala	Arg	Leu	Pro	Ile	Tyr	Gln	Arg	Lys	Pro	Phe
		35					40					45			
Ile	Ala	Ala	Trp	Asn	Ala	Pro	Thr	Asp	Gln	Cys	Leu	Ile	Lys	Tyr	Asn
		50				55					60				
Leu	Arg	Leu	Asn	Leu	Lys	Met	Phe	Pro	Val	Ile	Gly	Ser	Pro	Leu	Ala
65				70						75					80
Lys	Ala	Arg	Gly	Gln	Asn	Val	Thr	Ile	Phe	Tyr	Val	Asn	Arg	Leu	Gly
			85						90					95	
Tyr	Tyr	Pro	Trp	Tyr	Thr	Ser	Gln	Gly	Val	Pro	Ile	Asn	Gly	Gly	Leu
		100					105						110		
Pro	Gln	Asn	Ile	Ser	Leu	Gln	Val	His	Leu	Glu	Lys	Ala	Asp	Gln	Asp
		115				120						125			
Ile	Asn	Tyr	Tyr	Ile	Pro	Ala	Glu	Asp	Phe	Ser	Gly	Leu	Ala	Val	Ile
	130					135					140				
Asp	Trp	Glu	Tyr	Trp	Arg	Pro	Gln	Trp	Ala	Arg	Asn	Trp	Asn	Ser	Lys
145					150					155					160
Asp	Val	Tyr	Arg	Gln	Lys	Ser	Arg	Lys	Leu	Ile	Ser	Asp	Met	Gly	Lys
			165						170					175	
Asn	Val	Ser	Ala	Thr	Asp	Ile	Glu	Tyr	Leu	Ala	Lys	Val	Thr	Phe	Glu
			180					185					190		
Glu	Ser	Ala	Lys	Ala	Phe	Met	Lys	Glu	Thr	Ile	Lys	Leu	Gly	Ile	Lys
		195					200					205			
Ser	Arg	Pro	Lys	Gly	Leu	Trp	Gly	Tyr	Tyr	Leu	Tyr	Pro	Asp	Cys	His
	210					215					220				
Asn	Tyr	Asn	Val	Tyr	Ala	Pro	Asn	Tyr	Ser	Gly	Ser	Cys	Pro	Glu	Asp
225				230						235					240
Glu	Val	Leu	Arg	Asn	Asn	Glu	Leu	Ser	Trp	Leu	Trp	Asn	Ser	Ser	Ala
			245						250					255	
Ala	Leu	Tyr	Pro	Ser	Ile	Gly	Val	Trp	Lys	Ser	Leu	Gly	Asp	Ser	Glu
		260					265						270		
Asn	Ile	Leu	Arg	Phe	Ser	Lys	Phe	Arg	Val	His	Glu	Ser	Met	Arg	Ile
	275						280					285			
Ser	Thr	Met	Thr	Ser	His	Asp	Tyr	Ala	Leu	Pro	Val	Phe	Val	Tyr	Thr
	290					295					300				
Arg	Leu	Gly	Tyr	Arg	Asp	Glu	Pro	Leu	Phe	Phe	Leu	Ser	Lys	Gln	Asp
305					310					315					320

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Leu Val Ser Thr Ile Gly Glu Ser Ala Ala Leu Gly Ala Ala Gly Ile
 325 330 335
 Val Ile Trp Gly Asp Met Asn Leu Thr Ala Ser Lys Ala Asn Cys Thr
 340 345 350
 Lys Val Lys Gln Phe Val Ser Ser Asp Leu Gly Ser Tyr Ile Ala Asn
 355 360 365
 Val Thr Arg Ala Ala Glu Val Cys Ser Leu His Leu Cys Arg Asn Asn
 370 375 380
 Gly Arg Cys Ile Arg Lys Met Trp Asn Ala Pro Ser Tyr Leu His Leu
 385 390 395 400
 Asn Pro Ala Ser Tyr His Ile Glu Ala Ser Glu Asp Gly Glu Phe Thr
 405 410 415
 Val Lys Gly Lys Ala Ser Asp Thr Asp Leu Ala Val Met Ala Asp Thr
 420 425 430
 Phe Ser Cys His Cys Tyr Gln Gly Tyr Glu Gly Ala Asp Cys Arg Glu
 435 440 445
 Ile Lys Thr Ala Asp Gly Cys Ser Gly Val Ser Pro Ser Pro Gly Ser
 450 455 460
 Leu Met Thr Leu Cys Leu Leu Leu Leu Ala Ser Tyr Arg Ser Ile Gln
 465 470 475 480
 Leu

<210> SEQ ID NO 38
 <211> LENGTH: 467
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: sHuPH20 precursor 1-467

<400> SEQUENCE: 38

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys

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195	200	205
Leu Leu Arg Pro Asn His 210	Leu Trp Gly Tyr Tyr 215	Leu Phe Pro Asp Cys 220
Tyr Asn His His Tyr Lys Lys 225	Pro Gly Tyr Asn Gly Ser Cys Phe Asn 230	235 240
Val Glu Ile Lys Arg Asn Asp 245	Asp Leu Ser Trp Leu Trp Asn Glu Ser 250	255
Thr Ala Leu Tyr Pro Ser Ile 260	Tyr Leu Asn Thr Gln Gln Ser Pro Val 265	270
Ala Ala Thr Leu Tyr Val Arg 275	Asn Arg Val Arg Glu Ala Ile Arg Val 280	285
Ser Lys Ile Pro Asp Ala Lys 290	Ser Pro Leu Pro Val Phe Ala Tyr Thr 295	300
Arg Ile Val Phe Thr Asp Gln Val 305	Leu Lys Phe Leu Ser Gln Asp Glu 310	315 320
Leu Val Tyr Thr Phe Gly Glu Thr 325	Val Ala Leu Gly Ala Ser Gly Ile 330	335
Val Ile Trp Gly Thr Leu Ser 340	Ile Met Arg Ser Met Lys Ser Cys Leu 345	350
Leu Leu Asp Asn Tyr Met Glu 355	Thr Ile Leu Asn Pro Tyr Ile Ile Asn 360	365
Val Thr Leu Ala Ala Lys Met 370	Cys Ser Gln Val Leu Cys Gln Glu Gln 375	380
Gly Val Cys Ile Arg Lys Asn Trp 385	Asn Ser Ser Asp Tyr Leu His Leu 390	395 400
Asn Pro Asp Asn Phe Ala Ile 405	Gln Leu Glu Lys Gly Gly Lys Phe Thr 410	415
Val Arg Gly Lys Pro Thr Leu 420	Glu Asp Leu Glu Gln Phe Ser Glu Lys 425	430
Phe Tyr Cys Ser Cys Tyr Ser 435	Thr Leu Ser Cys Lys Glu Lys Ala Asp 440	445
Val Lys Asp Thr Asp Ala Val 450	Asp Val Cys Ile Ala Asp Gly Val Cys 455	460
Ile Asp Ala 465		

<210> SEQ ID NO 39

<211> LENGTH: 477

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: sHuPH20 precursor 1-477

<400> SEQUENCE: 39

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys 1 5 10 15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys 20 25 30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro 35 40 45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe 50 55 60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg 65 70 75 80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu 85 90 95

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Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu
 465 470 475

<210> SEQ ID NO 40
 <211> LENGTH: 478
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: sHuPH20 precursor 1-478

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<400> SEQUENCE: 40

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Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1           5           10           15

Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20           25           30

Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35           40           45

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50           55           60

Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65           70           75           80

Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85           90           95

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100           105           110

Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115           120           125

Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130           135           140

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145           150           155           160

Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165           170           175

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180           185           190

Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195           200           205

Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210           215           220

Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225           230           235           240

Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245           250           255

Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260           265           270

Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275           280           285

Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290           295           300

Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305           310           315           320

Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325           330           335

Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340           345           350

Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355           360           365

Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370           375           380

Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385           390           395           400

Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405           410           415

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Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430

Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445

Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460

Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro
 465 470 475

<210> SEQ ID NO 41
 <211> LENGTH: 479
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: sHuPH20 precursor 1-479

<400> SEQUENCE: 41

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15

Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30

Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60

Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80

Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110

Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125

Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140

Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160

Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175

Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190

Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205

Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220

Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240

Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255

Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270

Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285

Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300

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Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln
 465 470 475

<210> SEQ ID NO 42
 <211> LENGTH: 480
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: sHuPH20 precursor 1-480

<400> SEQUENCE: 42

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys

-continued

195					200					205					
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
210						215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
				245					250					255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
			260					265					270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
			275				280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
290						295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
				325					330					335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
			340					345					350		
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
		355					360					365			
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
		370				375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395					400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
				405					410					415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420					425					430		
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
		435					440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
		450				455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
465					470					475					480

<210> SEQ ID NO 43

<211> LENGTH: 481

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: sHuPH20 precursor 1-481

<400> SEQUENCE: 43

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
		35					40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
		50				55					60				
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65					70					75					80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
				85					90						95

-continued

Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 115 120 125
 Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 130 135 140
 Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 145 150 155 160
 Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 165 170 175
 Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 180 185 190
 Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 195 200 205
 Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 210 215 220
 Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 225 230 235 240
 Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 245 250 255
 Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe

<210> SEQ ID NO 44

<211> LENGTH: 483

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

-continued

<220> FEATURE:

<223> OTHER INFORMATION: sHuPH20 precursor 1-483

<400> SEQUENCE: 44

```

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1           5           10           15
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
          20           25           30
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35           40           45
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50           55           60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65           70           75           80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
          85           90           95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
          100          105          110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
          115          120          125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
          130          135          140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
          145          150          155          160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
          165          170          175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
          180          185          190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
          195          200          205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
          210          215          220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
          225          230          235          240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
          245          250          255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
          260          265          270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
          275          280          285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
          290          295          300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
          305          310          315          320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
          325          330          335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
          340          345          350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
          355          360          365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
          370          375          380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
          385          390          395          400

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[illegible]

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<210> SEQ ID NO 45
<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: sHuPH20 mature 36-467
```

<400> SEQUENCE: 45

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
			5						10			15			
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20						25			30			
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
			35						40			45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
			50						55			60			
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
			65						70			75			
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85						90			95			
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100						105			110			
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
			115						120			125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
			130						135			140			
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
			145						150			155			
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
			165						170			175			
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180						185			190			
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
			195						200			205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
			210						215			220			
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
			225						230			235			
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
			245						250			255			
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260						265			270			
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
			275						280			285			

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Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430

<210> SEQ ID NO 46
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: sHuPH20 mature 36-483

<400> SEQUENCE: 46

Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220

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Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala
 420 425 430
 Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn
 435 440 445

<210> SEQ ID NO 47

<211> LENGTH: 1446

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: DNA encoding soluble rHuPH20 "precursor"

<400> SEQUENCE: 47

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atgggagtgct taaaattcaa gcacatcttt ttcagaagct ttgttaaadc aagtggagta    60
tcccagatag ttttcacctt ccttctgatt ccatgttgct tgactctgaa tttcagagca    120
cctcctgtta ttccaaatgt gcctttctct tgggcctgga atgccccaaag tgaattttgt    180
cttggaatat ttgatgagcc actagatatg agcctcttct ctttcatagg aagccccga    240
ataaacgccca ccgggcaagg tggtacaata ttttatgttg atagacttgg ctactatcct    300
tacatagatt caatcacagg agtaactgtg aatggaggaa tccccagaa gatttcctta    360
caagaccatc tggacaaagc taagaaagac attacatttt atatgccagt agacaatttg    420
ggaatggctg ttattgactg ggaagaatgg agaccactt gggcaagaaa ctggaaacct    480
aaagatgttt acaagaatag gtctattgaa ttggttcagc aacaaaatgt acaacttagt    540
ctcacagagg ccatgagaaa agcaaaacaa gaatttgaaa aggcaggaaa ggatttcctg    600
gtagagacta taaaattggg aaaattactt cgcccaaatc acttgtgggg ttattatctt    660
tttccggatt gttacaacca tcactataag aaaccgggtt acaatggaag ttgcttcaat    720
gtagaataaa aaagaaatga tgatctcagc tgggtgtgga atgaaagcac tgctctttac    780
ccatccattt atttgaacac tcagcagctc cctgtagctg ctacactcta tgtgcgcaat    840

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cgagttcggg aagccatcag agtttccaaa atacctgatg caaaaagtc accctcgggt	900
tttgcataata cccgcatagt ttttactgat caagttttga aattcctttc tcaagatgaa	960
cttgtgtata catttggcga aactgttgct ctgggtgctt ctggaattgt aatatgggga	1020
accctcagta taatgcaag tatgaaatct tgcttgctcc tagacaatta catggagact	1080
atactgaatc cttacataat caacgtcaca ctacgagcca aaatgtgtag ccaagtgtt	1140
tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtacta tcttcacctc	1200
aaccagata attttgctat tcaacttgag aaaggtggaa agttcacagt acgtggaaaa	1260
ccgacacttg aagacctgga gcaattttct gaaaaatttt attgcagctg ttatagcacc	1320
ttgagttgta aggagaaagc tgatgtaaaa gacactgatg ctgttgatgt gtgtattgct	1380
gatggtgtct gtatagatgc ttttctaaaa cctcccatgg agacagaaga acctcaaatt	1440
ttctac	1446

<210> SEQ ID NO 48

<211> LENGTH: 509

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<223> OTHER INFORMATION: PH20 variant P48A

<400> SEQUENCE: 48

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
1				5					10					15	
Ser	Ser	Gly	Val	Ser	Gln	Ile	Val	Phe	Thr	Phe	Leu	Leu	Ile	Pro	Cys
			20					25					30		
Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Ala
			35				40					45			
Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
			50			55					60				
Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg
65				70					75					80	
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu
			85					90					95		
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly
			100				105						110		
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys
			115				120					125			
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
			130			135						140			
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155				160	
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
			165					170						175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
			195				200					205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
210					215						220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235				240	
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245					250						255	

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Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 260 265 270
 Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 275 280 285
 Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 290 295 300
 Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 305 310 315 320
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
 485 490 495
 Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
 500 505

<210> SEQ ID NO 49
 <211> LENGTH: 509
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: precursor PH20 variant L499W

<400> SEQUENCE: 49

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 100 105 110
 Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys

-continued

115					120					125					
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val
130						135					140				
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro
145					150					155					160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn
				165					170					175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe
			180					185					190		
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys
	195					200						205			
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys
	210					215					220				
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn
225					230					235					240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser
			245					250					255		
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val
			260				265						270		
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val
		275					280					285			
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr
	290					295					300				
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu
305					310					315					320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile
			325					330					335		
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu
		340					345					350			
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn
	355					360					365				
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln
	370					375					380				
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu
385					390					395					400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr
			405					410					415		
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys
			420				425					430			
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp
	435						440					445			
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys
	450					455					460				
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile
465					470					475					480
Phe	Tyr	Asn	Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val
			485					490					495		
Ser	Ile	Trp	Phe	Leu	Ile	Ile	Ser	Ser	Val	Ala	Ser	Leu			
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<210> SEQ ID NO 50

<211> LENGTH: 6630

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: HZ24 vector

<400> SEQUENCE: 50

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aatatgaccg ccattgttggc attgattatt gactagtatt taatagtaat caattacggg	180
gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc	240
gcctggctga ccgcccacg acccccgcgc attgacgtca ataatgacgt atgttcccat	300
agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc	360
ccacttggca gtacatcaag tgtatcatat gccaaagtccg cccctattg acgtcaatga	420
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gcagtacatc tacgtattag tcatcgctat taccatgggtg atgcgggtttt ggcagtacac	540
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caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaataaccc	660
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agaatggaga cccacttggg caagaaactg gaaacctaaa gatgtttaca agaataggtc	1560
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gaaatcttgc ttgctcctag acaattacat ggagactata ctgaatcctt acataatcaa	2160
cgtcacacta gcagccaaaa tgtgtagcca agtgccttgc caggagcaag gagtgtgtat	2220
aaggaaaaac tggaattcaa gtgactatct tcacctcaac ccagataatt ttgctattca	2280

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acttgagaaa ggtggaaagt tcacagtacg tggaaaaccg acacttgaag acctggagca	2340
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<210> SEQ ID NO 51
 <211> LENGTH: 186
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <223> OTHER INFORMATION: dihydrofolate reductase

<400> SEQUENCE: 51

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1				5				10						15	

Gly	Lys	Asn	Gly	Asp	Leu	Pro	Trp	Pro	Pro	Leu	Arg	Asn	Glu	Phe	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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20	25	30	
Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln Asn			
35	40	45	
Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys Asn			
50	55	60	
Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu Lys			
65	70	75	80
Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp Ala			
85	90	95	
Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met Val			
100	105	110	
Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln Pro			
115	120	125	
Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu Ser			
130	135	140	
Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu Pro			
145	150	155	160
Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile Lys			
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Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp			
180	185		
<210> SEQ ID NO 52			
<211> LENGTH: 23			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: HZM3.P1 forward primer			
<400> SEQUENCE: 52			
tttgaacact cagcagtcctc ctg			23
<210> SEQ ID NO 53			
<211> LENGTH: 20			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: HZM3.P2 reverse primer			
<400> SEQUENCE: 53			
aactctgatg gcttcccgaa			20
<210> SEQ ID NO 54			
<211> LENGTH: 28			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: HZM3 probe			
<400> SEQUENCE: 54			
agctgctaca ctctatgtgc gcaatcga			28
<210> SEQ ID NO 55			
<211> LENGTH: 1449			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
<220> FEATURE:			
<223> OTHER INFORMATION: PH20 mRNA sequence from 3D35M cells			
<400> SEQUENCE: 55			
atgggagtg ctaaaattcaa gcacatcttt ttcagaagct ttgttaaadc aagtggagta			60

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tcccagatag ttttcacctt ccttctgatt ccatgttgct tgactctgaa tttcagagca	120
cctcctgtta ttccaaatgt gcctttcctc tgggcctgga atgccccaaag tgaattttgt	180
cttggaanaa ttgatgagcc actagatatg agcctcttct ctttcatatg aagccccga	240
ataaacgccca cggggcaagg tgttacaata ttttatgttg atagacttgg ctactatcct	300
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ctcacagagg ccatgagaa agcaaaacaa gaatttgaaa aggcagggaa ggatttcctg	600
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tttgcatata cccgcatagt ttttactgat caagttttga aattcctttc tcaagatgaa	960
cttggtgata catttggcga aactgttgct ctgggtgctt ctggaattgt aatatgggga	1020
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ttctactga	1449

<210> SEQ ID NO 56
 <211> LENGTH: 17
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: AP01

<400> SEQUENCE: 56

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<210> SEQ ID NO 57
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: AP02

<400> SEQUENCE: 57

aagatttcct tacaagac	18
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<210> SEQ ID NO 58
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: AP03

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<400> SEQUENCE: 58

tggcgagagg ggaaagac

18

<210> SEQ ID NO 59

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP04

<400> SEQUENCE: 59

ccatttattt gaacactc

18

<210> SEQ ID NO 60

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP06

<400> SEQUENCE: 60

ccgaactcga ttgcgcac

18

<210> SEQ ID NO 61

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP07

<400> SEQUENCE: 61

agccattccc aaattgtc

18

<210> SEQ ID NO 62

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP08

<400> SEQUENCE: 62

ctcccagttc aattacag

18

<210> SEQ ID NO 63

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP09

<400> SEQUENCE: 63

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<210> SEQ ID NO 64

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AP10

<400> SEQUENCE: 64

cgagacagag aagactcttg cg

22

<210> SEQ ID NO 65

<211> LENGTH: 22

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: AP12

<400> SEQUENCE: 65

cattcaacag accttgccatt cc

22

<210> SEQ ID NO 66
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal peptide cleaved from soluble
rHuPH20 aa 431-447

<400> SEQUENCE: 66

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
1 5 10 15

Tyr

<210> SEQ ID NO 67
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal peptide cleaved from soluble
rHuPH20 aa 431-446

<400> SEQUENCE: 67

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe
1 5 10 15

<210> SEQ ID NO 68
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal peptide cleaved from soluble
rHuPH20 aa 431-445

<400> SEQUENCE: 68

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
1 5 10 15

<210> SEQ ID NO 69
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal peptide cleaved from soluble rHuPH20
aa 431-444

<400> SEQUENCE: 69

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro Gln
1 5 10

<210> SEQ ID NO 70
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal peptide cleaved from soluble rHuPH20
aa 431-443

<400> SEQUENCE: 70

Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu Pro
1 5 10

-continued

<210> SEQ ID NO 71
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal peptide cleaved from soluble rHuPH20
 aa 431-442

 <400> SEQUENCE: 71

 Asp Ala Phe Lys Leu Pro Pro Met Glu Thr Glu Glu
 1 5 10

The invention claimed is:

1. A harvested cell culture fluid, comprising soluble rHuPH20 with an enzymatic activity that is greater than 5000 units/mL.

2. The harvested cell culture fluid of claim 1, wherein the enzymatic activity is or is about 10,000, 12,000, 14,000, 16,000, 18,000, 20,000, 22,000 or 24,000 units/mL.

3. The harvested cell culture fluid of claim 1, wherein the culture medium is produced by a method comprising:

a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein:

the cells comprise between 150 and 300 copies of nucleic acid encoding soluble rHuPH20;

the bioreactor contains at least 100 liters of cell culture; and about 10^{10} - 10^{11} cells are inoculated per 100 liters cell culture; and

the cells are cultured at a set temperature;

b) feeding the cells with a first feed medium containing glucose, L-alanyl-L-glutamine, human insulin and yeast extract in amounts sufficient to increase cell growth and peak cell density, and to increase soluble PH20 synthesis, wherein the feed medium is added to the culture at a volume of 0.5% or about 0.5% to 20% or about 20% of the cell culture volume;

c) feeding the cells with a second feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and induce cell cycle arrest; and lowering the temperature compared to the temperature in step a) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase; wherein:

the amount of L-alanyl-L-glutamine is decreased compared to the amount of L-alanyl-L-glutamine in step b);

the amount of yeast extract is increased compared to the amount of yeast extract in step b); and

the feed medium is added to the culture at a volume of 0.5% or about 0.5% to 20% or about 20% of the cell culture volume;

d) feeding the cells with a third feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and increase cell cycle arrest, and lowering the temperature compared to the temperature in step c) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase; wherein:

the amount of L-alanyl-L-glutamine is decreased compared to the amount of L-alanyl-L-glutamine in step c);

the amounts of yeast extract, glucose and sodium butyrate are increased compared to the amounts of yeast extract, glucose and sodium butyrate in step c); and

the feed medium is added to the culture at a volume of 0.5% or about 0.5% to 20% or about 20% of the cell culture volume;

e) feeding the cells with a fourth feed medium containing glucose, L-alanyl-L-glutamine, yeast extract and sodium butyrate in amounts sufficient to increase soluble rHuPH20 synthesis and increase cell cycle arrest, and lowering the temperature compared to the temperature in step d) to a temperature sufficient to increase cell cycle arrest, increase cell viability and stabilize the soluble hyaluronidase; wherein:

the amount of L-alanyl-L-glutamine and glucose is decreased compared to the amount of L-alanyl-L-glutamine and glucose in step d);

the amount of sodium butyrate is decreased compared to the amount of sodium butyrate in step d); and

the feed medium is added to the culture at a volume of 0.5% or about 0.5% to 20% or about 20% of the cell culture volume;

f) continuing to culture the cells until viability drops below at least or about 50%; and

g) harvesting the cell culture fluid.

4. The harvested cell culture fluid of claim 3, wherein the temperature in step a) is or is about 37° C.

5. The harvested cell culture fluid of claim 3, wherein the temperature in step c) is or is about 36.5° C.

6. The harvested cell culture fluid of claim 3, wherein the temperature in step d) is 36° C.

7. The harvested cell culture fluid of claim 3, wherein the temperature in step e) is 35.5° C.

8. The harvested cell culture fluid of claim 3, wherein the harvest cell culture fluid is filtered.

9. The harvested cell culture fluid of claim 3, wherein a feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume.

10. The harvested cell culture fluid of claim 1, wherein the cell culture medium is produced by a method, comprising:

a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein:

the cells comprise between 150 and 300 copies of nucleic acid encoding soluble rHuPH20;

the bioreactor contains at least 100 liters of cell culture; the inoculation cell density is at or about 4×10^5 cells/mL; and

the cells are cultured at or at about 37° C.;

b) feeding the cells with a first feed medium containing or containing about 33 g/L glucose, 32 mM L-alanyl-L-glutamine, 16.6 g/L yeast extract and 33 mg/L insulin,

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- wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume;
- c) feeding the cells with a second feed medium containing or containing about 33 g/L glucose, 16 mM L-alanyl-L-glutamine, 33.4 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 36.5° C.;
- d) feeding the cells with a third feed medium containing or containing about 50 g/L glucose, 10 mM L-alanyl-L-glutamine, 50 g/L yeast extract and 1.8 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 36° C.;
- e) feeding the cells with a fourth feed medium containing or containing about 33 g/L glucose, 6.6 mM L-alanyl-L-glutamine, 50 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 35.5° C.;
- f) continuing to culture the cells until viability drops below at least or about 50%;
- g) harvesting the cell culture fluid; and
- h) filtering the harvested cell culture fluid.
- 11.** The harvested cell culture fluid of claim 1, wherein the cell culture medium is produced by a method, comprising:
- a) inoculating cell medium in a bioreactor with an inoculum of cells that encode soluble rHuPH20 to produce a cell culture, wherein:
- the cells comprise between 150 and 300 copies of nucleic acid encoding soluble rHuPH20;
- the bioreactor contains at least 100 liters of cell culture;
- the inoculation cell density is at or about 4×10^5 cells/mL; and
- the cells are cultured at or at about 37° C.;
- b) feeding the cells with a first feed medium containing or containing about 33 g/L glucose, 32 mM L-alanyl-L-glutamine, 83.3 g/L yeast extract and 33 mg/L insulin, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume;

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- c) feeding the cells with a second feed medium containing or containing about 33 g/L glucose, 13 mM L-alanyl-L-glutamine, 166.7 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 36.5° C.;
- d) feeding the cells with a third feed medium containing or containing about 50 g/L glucose, 10 mM L-alanyl-L-glutamine, 250 g/L yeast extract and 1.8 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 36° C.;
- e) feeding the cells with a fourth feed medium containing or containing about 33 g/L glucose, 6.7 mM L-alanyl-L-glutamine, 250 g/L yeast extract and 0.92 g/L sodium butyrate, wherein the feed medium is added to the culture at a volume of 4% or about 4% of the cell culture volume; and
- the temperature is lowered to 35.5° C.;
- f) continuing to culture the cells until viability drops below at least or about 50%;
- g) harvesting the cell culture fluid; and
- h) filtering the harvested cell culture fluid.
- 12.** The harvested cell culture fluid of claim 1, wherein the volume of cell culture in the bioreactor is or is about 200, 300, 400, 500, 1000, 1500, 2000, 2500, 3000 or 3500 liters.
- 13.** The harvested cell culture fluid of claim 3, wherein the cells that encode soluble rHuPH20 are DG44 CHO cells.
- 14.** The harvested cell culture fluid of claim 10, wherein the cells that encode soluble rHuPH20 are DG44 CHO cells.
- 15.** The harvested cell culture fluid of claim 11, wherein the cells that encode soluble rHuPH20 are DG44 CHO cells.
- 16.** The harvested cell culture fluid of claim 3, wherein the rHuPH20 is encoded by nucleic acid set forth in SEQ ID NO:47.
- 17.** The harvested cell culture fluid of claim 10, wherein the rHuPH20 is encoded by nucleic acid set forth in SEQ ID NO:47.
- 18.** The harvested cell culture fluid of claim 11, wherein the rHuPH20 is encoded by nucleic acid set forth in SEQ ID NO:47.

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