UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

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PARSE BIOSCIENCES INC., : Case Nos. IPR2023-00955

Petitioner, : and IPR2023-00958

v. : U.S. Patent Nos.

10X GENOMICS, INC., : 10,240,197 and

Patent Owner. : 10,697,013

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Deposition of GREGORY COOPER, Ph.D.

Conducted Virtually

Tuesday, September 3, 2024

10:07 a.m. EDT

Job No.: 551594

Pages 1 - 79

Reported by: Debra A. Whitehead

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Deposition of GREGORY COOPER, Ph.D., conducted virtually.

Pursuant to notice, before Debra Ann Whitehead, E-Notary Public in and for the Commonwealth of Virginia.

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A P P E A R A N C E S

ON BEHALF OF PETITIONER:

DEREK C. WALTER, ESQUIRE
WEIL, GOTSHAL & MANGES LLP
201 Redwood Shores Parkway
Redwood Shores, California 94065
(650) 802-3000

ON BEHALF OF PATENT OWNER:

MEGAN F. RAYMOND, ESQUIRE
GROOMBRIDGE, WU, BAUGHMAN & STONE LLP
801 17th Street NW
Suite 1050
Washington, DC 20006
(202) 505-5878

- and -

JOSHUA REICH, ESQUIRE
GROOMBRIDGE, WU, BAUGHMAN & STONE LLP
565 Fifth Avenue
Suite 2900
New York, New York 10017
(332) 269-0024

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A P P E A R A N C E S C O N T I N U E D

ALSO PRESENT:

JON THOMPSON, A/V Technician

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EXHIBITS MARKED IN TODAY'S SESSION

(None Marked)

EXHIBITS MARKED IN PRIOR SESSIONS

(Not Attached)

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P R O C E E D I N G S

GREGORY COOPER, Ph.D.,

having been duly sworn, testified as follows:

EXAMINATION BY COUNSEL FOR PATENT OWNER

BY MS. RAYMOND:

Q Good morning, Dr. Cooper.

A Good morning.

Q Is it your understanding that you're here to testify today about your reply declarations in IPR2023-00955 regarding the '197 patent and IPR2023-00958 regarding the '013 patent?

A Yes.

Q Okay. And for the record, those have previously been marked as Exhibit 1070 in the corresponding cases.

(Parse Exhibit 1070, previously marked, not attached.)

A 1070?

Q 1070, yes.

A Oh, there it is, yeah.

Q And today I am going to be asking you questions about both declarations. But if you

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have a response that's specific to one or the other, if you could please let me know. And if I'm asking you specifically about one case or the other, I'll let you know that as well.

Is that okay?

A Yes.

Q With respect to the two patents we're talking about today, is it your understanding that there is an implicit limitation that you have to be able to identify the sample polynucleotide sequence when you sequence it?

MR. WALTER: Objection. Vague.

A I'm not sure I understand the question.

Q Okay. Both patents have a sequencing step. Correct?

A Correct.

Q And when you sequence, is it your position that the claims have an implicit limitation that you have to be able to identify the sample polynucleotide sequence when you do that sequencing step?

MR. WALTER: Same objection.

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A So, yeah, I'm not -- I guess if you're focusing on a particular claim element, I'm happy to talk about that.

There is a sequencing step and there is using a first tag and a second tag and sequencing a sample sequence, but don't know -- I'm not sure I follow the nature of the question, whether there is an implicit requirement. It has a number of explicit elements.

MS. RAYMOND: Okay. If we could please then pull up what has now been marked as -- I'm trying to get the exhibit number. Exhibit 2101.

(10x Genomics Exhibit 2101, previously marked, not attached.)

Q Dr. Cooper, do you have access to that? Can you find that? And maybe we can drop it in the chat as well.

A This is a deposition transcript?

Q That's right. This is a deposition transcript of your deposition May 2nd, 2024, in IPR2023-00876.

A Okay. On the '981?

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Q Correct.
A Yes, I see it.
Q Could you please turn to Page 15 of that transcript.
A Using the page numbers at the top?
Q Yes. Correct.
A Yes. Okay.
Q And do you see a question there starting around Line 7, "In your opinion, how much of the tagged polynucleotide needs to be sequenced to meet this claim limitation?"
A Yes, I see that.
Q And is that talking about the sequencing claim limitation?
Do you agree with me on that?
A Yes, it looks like Claim 1g, yeah.
Q And then in your answer you say, So I suppose there is -- or excuse me. "So I suppose there's an implicit limitation there that you have to be able to identify the sequence," and then you go on.
Do you see that?

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A Yes.

Q Do you agree with your testimony there?

A Yes. I think the context of this question was whether there was some sort of minimum threshold. And I don't -- I think it's clear that the patent doesn't actually say what -- you know, the claims don't say it has to be X number of bases or X percentage.

But you certainly have to use the sample sequence, just like you use the first and second tag. So yes, I would agree with that.

Q And I apologize, we're going to be skipping around a bunch today.

But with respect to the Linnarsson reference, you recall testifying about the Linnarsson reference. Correct?

A Yes.

Q Okay. Do you agree that in Linnarsson the mRNA is indiscriminately released from each single cell?

A I don't know that that's true for all possible ways that one might do it. But I think

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there are many -- certainly part of Linnarsson has disclosures where you just crack open the cell and collect all the mRNA indiscriminately, yes.

Q Do you agree that Linnarsson's method begins with releasing mRNA from each single cell to provide a plurality of mRNA samples?

A Well, I suppose it depends on "begin." But you would need to obtain a sample first. But certainly extracting polynucleotides is a part of at least some of the disclosures of Linnarsson.

Q Do you agree that a POSA would understand that because the mRNA is indiscriminately released from each single cell and because Linnarsson does not describe any additional elimination or filtration, the released mRNA sample comprises substantially all mRNA molecules of said cell?

A I think that is certainly true about some disclosures. But I think we've gone over this before, about Linnarsson does talk about other techniques to target; for example, designing the RNA complementary sequence to be specific to one or more sample mRNAs.

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And I also don't think there's necessarily a requirement that one has to do it indiscriminately. If there were some other method for extracting polynucleotides, I think you could make that work with the Linnarsson disclosure.

But certainly some of the disclosure in Linnarsson encompasses cracking open the cell and indiscriminately collecting, you know, the RNA that comes out.

Q And you recall in your -- in performing your analysis regarding Linnarsson, you relied on both Figures 2 and Figures 11.

Do you recall that?

A I believe so. Among other figures, yes.

Q Okay. And in both Figures 2 and Figure 11 you relied on the poly-A tail functionality as part of generating the tag cDNA. Correct?

A I wouldn't say I relied only on the poly-A tail. That is, you know, Linnarsson describes the poly-A tail and the oligo(dT) primer as an exemplary RNA complementary sequence. It's not the only one, but it is certainly one of the

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examples that Linnarsson articulates and defines in their figures.

Q And it's an example you relied on. Correct?

A Correct. Among other portions of text and figures, yes.

Q And with respect to the reverse transcription in Linnarsson, do you agree that the CDS is an important part of that process?

MR. WALTER: Objection. Vague.

A So the CDS has -- Linnarsson describes the CDS as at least one mechanism to apply tags to the RNAs. It's not the only way. It talks about tags on the TSO as well. So it -- you know, Linnarsson has a process that includes a CDS and a TSO that are both part of reverse transcription and can be used in different ways, depending on the experimental design.

Q Does Linnarsson describe any way of initiating the reverse transcription process other than using a CDS?

A I don't believe so. I think this is the

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primary mechanism, that CDS includes an RNA complementary sequence which is used to prime the initial reverse transcription.

Q And does Linnarsson describe any way of continuing the reverse transcription process, other than using a TSO?

A I don't believe so, no; but I could be wrong. But I think that's correct.

Q And you agree that for a -- bacteria are prokaryotic. Correct?

A I'm sorry. Can you say that again?

Q You agree that bacteria are prokaryotic. Correct?

A Yes.

Q And do you agree that to the extent prokaryotic organisms have a poly-A tail, it's used in a different way or has different functionality than a poly-A tail in eukaryotic organisms?

A So I think there are examples of poly-A tails being added in prokaryotes. And I'm guessing, like all other biological questions, the

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answer to that is complicated. They're probably used in a variety of ways.

Certainly at a high level poly-A tail usage is different in bacteria or prokaryotes than compared to eukaryotic cells. But they could serve similar functions in some organisms and some contexts.

And so I'm not sure about the full scope of the mechanisms that poly-A tails contribute to, but there are certainly differences between bacteria and eukaryotes, yes.

Q Could we please turn to Page 64 of Exhibit 2101. This is your May deposition.

MR. WALTER: I'm sorry. Where is that in the -- is that in the files that were provided?

MS. RAYMOND: I believe so.

THE WITNESS: It's in the 955 bucket, the link that I downloaded.

MR. WALTER: Hold on one moment.

MS. RAYMOND: Sure.

(A discussion was held off the record.)

BY MS. RAYMOND:

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Q Dr. Cooper, if you could please turn to Page 64. That's the page at the top of this exhibit that we're looking at, your May 2024 transcript.

A Yes.

Q And at the bottom you were asked a question, "Do you agree that only eukaryotic organisms ordinarily have mRNA with a poly-A tail?"

Do you see that?

A Yes.

Q And you answered, "I don't think that's true. I think there are evidence of polyadenylation in some prokaryotic organisms. I don't think it's used in quite the same way or has the same -- same mess -- same functionality," and then you go on.

Do you see that?

A Yes.

Q Do you still agree with that statement?

A Yes.

Q Okay. Dr. Cooper and Counsel as well,

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are you able to find Exhibit 2103 in the folder link that was sent to you? It has not yet been used in this case.

(10x Genomics Exhibit 2103, previously marked, not attached.)

MR. WALTER: Yes, I have it.

A Yes.

Q Dr. Cooper, do you see that this is an article from the journal Cell?

A Yes, I see that.

Q And you were asked about this at your May 2024 deposition.

Do you recall that?

A Not specifically, but it's certainly possible.

Q Is Cell a reputable journal?

A Yes.

Q And if you could go to the page in this article with the number in the lower left corner 2728, and it's Table 1 in the article.

Do you see that?

A I do.

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Q And the fifth row down on the left it says, "Lack of polyadenylated mRNA."

Do you see that?

A I do see that.

Q And in the text on the middle of that row, the first sentence is, "Many eukaryotic-focusing scRNA-seq approaches rely on poly(T) primers to capture polyadenylated mRNAs. However, mRNA polyadenylation is absent in prokaryotic mRNAs except in transcripts bound for degradation."

Do you see that?

A I do see that.

Q And do you agree that mRNA polyadenylation is absent in prokaryotic mRNAs except in transcripts bound for degradation?

A No. I'd have to do more work on that. I don't -- I think that's a fairly strong statement. And so it's -- it's sort of not clear to me that that is a hard-and-fast rule and that there aren't other uses of poly-A tails in prokaryotes.

So that seems like an aggressive

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statement to me that I would have to do more work on.

Q Do you have any reason to doubt whether the statement in the article in Cell is true?

A I mean, generally absolutist kind of statements in biology are things that I shy away from. If you are making a hard-and-fast assertion that something can't be true or is exclusive or, you know, only, I think that's often a statement that can be difficult to back up. Biology is full of exceptions.

So, you know, so yeah, I think that is probably more aggressive than would be my understanding.

Q And could you see if you can find Exhibit 2102 in the folder.

(10X Genomics Exhibit 2102, previously marked, not attached.)

A Yes, I have it.

Q And that's a publication of BMC Genomics.

Do you agree?

A Yes.

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Q Have you seen this exhibit before?
A I don't know. It's possible.
Q Is it familiar from your last deposition, the May -- excuse me, the May 2024 deposition in the other IPR?
A It may be.
Q In your experience is BMC Genomics a reputable publication?
A Yes.
Q I am going to call your attention to a sequence -- or a sentence in the abstract on the first page. There's a heading that says, Background.
A I see that.
Q And then there's a second sentence that says, "However, unlike eukaryotic cells, mRNA sequencing of bacterial samples is more challenging due to the absence of a poly-A tail, but typically enables efficient capturing and enrichment of mRNA from the abundant rRNA molecules in a cell."
Do you see that?

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A I do see that.

Q And then calling your attention to the last paragraph on the same first page. The second sentence says, "First, unlike in eukaryotes, bacterial mRNA does not contain a poly-A tail at the 3 prime end that can be used to easily enrich for those molecules during reverse transcription."

Do you see that?

A I see that.

Q Okay. Were you -- do you agree with these statements?

A No. Again, I think these are overly assertive on what bacteria do or do not do. And, I mean, we -- we know just from the previous citation that you showed there are poly-A tails on some bacterial RNAs, in that author's opinion that's ones bound for degradation. So we know that statement isn't true. There are, in fact, examples of polyadenylated RNAs in bacteria.

So, no. It's -- again, this is one of those statements that asserts a degree of evidence and proof that really isn't there. And it

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certainly is true the bacteria used poly-A differently, but it's not fair to say that there's -- for example, they're saying there is no poly-A tail in bacteria. That's not true.

Q Do you agree that in bacteria there's typically not a large percentage of mRNA that's polyadenylated?

A I would say that in many studied bacteria the fraction of polyadenylated RNAs is smaller in bacteria than in eukaryotic cells. I don't know that that's necessarily true for every species of bacteria or every environmental context.

But yes, on average I would say the literature suggests that it is lower abundance in bacteria. But again, certainly not absent.

Q Could you please turn to Page 74 of your May 2024 transcript.

Are you there?

A Yes.

Q Okay. And around page -- around column -- try this again.

Around Line 4 you say, "But it is true to

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say that it is fundamentally different that -- whereas, in eukaryotes a large percentage of mRNAs are polyadenylated. In bacteria that's not true, it's typically there -- a large percentage are not polyadenylated."

Do you see that?

A Yes. And it goes on to talk about how I don't agree with extreme statements that it doesn't exist at all. And that's basically what I just said a few minutes ago.

Q Okay. So you agree with the statement still --

A Yes.

Q -- on Page 74?

A Yes.

Q And you agree that there's a qualitative difference in the nature of polyadenylation between prokaryotes and eukaryotes. Right?

A Yes, again from the -- from the literature that exists on looking at RNAs and prokaryotes and eukaryotes, yes.

Q And then could you turn to Page 75 of

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that transcript.

A Okay.

Q Starting on Line 5. "Do you agree that in general the rule for eukaryotes is that transcripts are polyadenylated. In general, the rule for bacteria is that they're not?"

A Right. And then I go on to say there is variability, that there are counter-examples and there are RNAs in eukaryotes that are not poly-A-tailed and there are RNAs in bacteria that are poly-A-tailed, so yes.

Q Then turning to Linnarsson. And that's Exhibit 1003, Dr. Cooper, just in case you want to pull it up and refer to it.

(Parse Exhibit 1003, previously marked, not attached.)

A Okay, I have it.

Q And, actually, if we could turn to Page 24. It says 1003.024 at the bottom.

A Okay, I'm there.

Q Okay. And you see the heading Example 1?

A I do.

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Q Okay. Do you recall how many examples there are in Linnarsson?

A I believe there are at least two. I can't remember, but two is my recollection at the moment.

Q And the second example you're thinking of, is that the one that's -- that starts at Page 1003.032?

A Yes, that looks right.

Q Okay. And at the moment you're not thinking of any other examples disclosed in Linnarsson. Correct?

A That's correct.

Q And would you agree that the mention of Figure 3 and Figure 4 is inside Example 1 in Linnarsson?

A Would I agree that they are mentioned in Example 1?

Q Correct. As a matter of organization of Linnarsson, would you agree that Figures 3 and Figures 4 are disclosed inside Example 1 in Linnarsson?

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A So they are certainly referenced in that, in Example 1, yes.

Q Do you know if they are referenced in connection with any -- with any other portion of Linnarsson?

A I don't know one way or another.

Q Okay.

A They're called out also in the top in the brief description of the drawings.

Q And in your opinion, are Figures 3 and 4 consistent with Example 1 of Linnarsson?

A I think that Figures 3 and 4 are intended to be examples, and they are certainly -- they are helpful to a skilled artisan to understand how to implement a method. I don't think there's an exclusivity. I think the information they're providing in Figure 3 is more general than just what's performed in Example 1.

Q In your opinion, is Figure 3 consistent with Example 1 of Linnarsson?

A I guess I'm more comfortable saying it's not inconsistent with Example 1.

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Q In your opinion, is Figure 4 consistent with Example 1 of Linnarsson?

A Just like for Figure 3, I think it's -- there it is general information that is not inconsistent with the example, but it's not exclusive to that example either.

Q And in your opinion, is Figure 2 consistent with Example 1 of Linnarsson?

A Sorry, I'm just trying to pull up Figure 2.

Again, so like Figures 3 and 4, Figure 2 is a very broad general overview that certainly helps a skilled artisan understand the work flow of Example 1. But again, Figure 2 is more general than that. So again it's the same answer, that it is not inconsistent with that example.

Q And you'd agree that Figures 3 and 4 are helpful in understanding the work flow of Example 1?

A Correct. Among other things, yes.

Q And you would agree that both Example 1 of Linnarsson and Example 2 of Linnarsson disclose

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fragmentation and capture. Correct?

A I'd have to refresh my memory on that on exactly what all is in the scope of those examples.

I'm not sure I'm seeing a fragmentation step in Example 2. But again, it's been a minute since I read through that in detail.

Oh, there it is. Yes. So yes, they reference cutting.

Q So do you agree that both Examples 1 and 2 of Linnarsson disclose fragmentation and capture?

A Yes, they are part of the experimental steps inside those examples. Yes.

Q And Examples 1 and 2 also both use biotin.

Correct?

A I'm not seeing biotin listed under Example 1, but maybe I just can't see that. Yeah, it looks like biotin is only mentioned under the text for Example 2.

Q Okay. So could you please turn to Page

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96 of your May 2024 declaration.

A Which exhibit number is that?

Q That is exhibit, I think it was Exhibit 2101.

A Oh, deposition you mean?

Q Yes. Sorry.

A Sorry, I thought you meant -- gotcha. I'm there.

Q And Page 96, Line 12.

A Okay.

Q You were asked, "And you'd agree that Example 1 of Linnarsson discloses what you called fragmentation and capture. Right?"

A Yes, I see that.

Q And you answered, "Yes, it looks like biotin is at least one component of the process, so that would imply that they're doing a solid-phase capture. Yes."

A Yes.

Q Do you agree with that testimony?

A Yes. I didn't see it at the first glance here, but yes, I'm guessing that's true.

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Q And you see in Linnarsson itself, if you go to 1003.024.

A Oh, there, I see it now. Yes.

Q You see a bio around Line 13, a CDS of a bio?

A Yes, I was looking for biotin rather than bio, so ...

Q Bio and biotin are the same. Correct?

A I believe in this text it is, yes.

Q You agree that Linnarsson discloses the creation of a cDNA library. Correct?

A Yes. Yes, generation of collection of cDNAs are part of Linnarsson, yes.

Q And there may be fragmentation involved in creating that cDNA library.

You agree with that?

A Yes. In some work flows, yes, you may use fragmentation, yes.

Q And if the cDNA library sequences are too long for further sequencing, you might need to do further fragmentation. Correct?

A That would depend on the sequencing

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technology you're using and the sample preparation. But yes, certainly in some circumstances you -- that fragmentation may be required to -- depending on your inputs and the sequencer and that sort of thing, yes, that can certainly be true.

Q And would you agree that Linnarsson discloses further fragmentation of the cDNA library, at least as an option?

A Yes, I think there is a dependent claim that specifically claims that, so yes.

Q Okay. Could you please turn to Linnarsson 1003.013.

A Okay.

Q And if we could go to Lines 4 through 8.

A I see that.

Q And you see it refers to, The term "cDNA library" refers to a collection of cloned complementary DNA, parenthesis, DNA fragments, which together constitute some portion of the transcriptome of a single cell or a plurality of single cells.

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Do you see that?

A Yeah. And it goes on as well. Yes.

Q What does the word "fragments" in Line 5 add, if anything, to the word "cDNA" or "DNA"?

A So I think it helps to read that, the sentence that immediately follows, which is that it says that cDNA is produced from fully transcribed mRNA found in a cell. And so I think what it's referring to is that the RNA, the expressed RNAs in the cell are fragments of RNA, and the cDNA fragments are the complementary DNA copies that are produced from those RNA fragments. So I think it's using that in a manner that says that, as opposed to say a whole chromosome or another large molecule that gene expression units are more fragment size, I think is the reason they're using that term there.

Q Would this statement mean anything different to you -- and "this statement" being the one about the cDNA labor that we're looking at.

A Yes.

Q Would it mean anything different to you

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if the word "fragments" was deleted and just said cDNA library refers to a collection of cloned complementary DNA, paren cDNA, which together constitutes some portion of the transcriptome?

A Well, it wouldn't read quite the same way, it would read a little funny. You would have to put something in its place. But you could imagine, for example, complementary cDNA molecules would be another thing they could use there. But it -- it would appear kind of unusual if they didn't have something in there to talk about, we're talking about discrete individual molecular units.

Q So in your view fragments here only means discrete individual molecular units?

A I wouldn't say only, but that would be my reading of it, yes. That's sort of my understanding that's why they're putting that word there, to help clarify they're not talking about cDNA as a hypothetical or something, we're talking about cloned molecules. Or not cloned. We're talking about generated molecules that are part of

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this process.

Q Do you recall in Linnarsson the disclosure of a BtsC1 cut site?

A I do.

Q Okay. And is it your position that a POSA reading Linnarsson would understand Linnarsson's method to use BtsC1 and only BtsC1 as a restriction enzyme cut site?

A So again, I think Linnarsson has a fairly broad disclosure. And the specific example they use is BtsC1.

So I think to the extent that they're looking at the specific examples and matching up the enzyme with the sequence that's inside the exemplary oligos that they're using, that that work flow is BtsC1.

But it is certainly possible one could imagine using a different enzyme, depending on the experimental context. But the only one called out by Linnarsson is BtsC1.

Q But a POSITA wouldn't understand Linnarsson to be limited to using BtsC1 as the

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restriction enzyme cut site for the performance method?

A I think a POSA could reasonably alter the design of their oligos to use a different enzyme, yes.

Q And it's your position that a POSITA would have to actually alter Linnarsson to use something other than BtsC1, as opposed to a POSITA understanding Linnarsson to broadly describe the use of a restriction enzyme cut site?

A Sorry, that was a lot to -- I guess my understanding would be that if a skilled artisan were building their own protocol, if they wanted to use a different enzyme because for whatever preference they would have to alter the sequence because different restriction enzymes target different cut sites. So one modification that they would need to make is to alter -- at the position of the cut site they'd have to alter that sequence in their oligo design. That is certainly within the competencies of a skilled artisan.

Q Your opinion is that Linnarsson is read

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broadly, is a broad disclosure? Correct?

A So I think Linnarsson -- so, for example, if you look at Figure 1, it provides a very general overview of a process.

And so Linnarsson certainly encompasses a range of protocols, some of which wouldn't use restriction enzymes at all, for example. But certainly changing a restriction enzyme is -- you know, maybe an analogy would be that they talk about Illumina or SOLiD sequencing. Right?

There are different kinds of molecular biology techniques that are within the scope of -- or within the competencies of a skilled artisan. And so yes, I think it is a fairly broad disclosure.

Q Does Linnarsson encompass the use of a restriction enzyme cut site other than BtsC1?

A Yes, I think that would be -- using different enzymes would be within scope of what Linnarsson discloses, yes. And as well as would be not using any restriction enzyme.

Q Okay. Before, with respect to

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Linnarsson, we were talking about Figures 3 and 4 and how they are relevant to Example 1.

Do you recall that?

A I do.

Q Okay. Could you tell me what aspects of Figure 3 are relevant to Example 1?

A Sorry. Give me a moment to pull up Figure 3.

So one aspect is obviously the template switching portion of the molecule, that is a part of however transcription is carried out. And to the extent that the examples involve reverse transcription, that is a key component of the molecule.

Another example is the -- what they refer to as the APS, the amplification primer I believe that's called. And so PCR is employed as part of the example. And so that sequence portion would be necessary for -- for priming that amplification step.

Q Anything else?

A So it's also disclosing a cell tag.

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Which obviously Linnarsson has a process whereby you can use a tag to track the cell of origin for a given polynucleotide. And so that is where it's -- an example of where they would embed the cell tag inside that oligo.

Q Anything else?

A That's all that emerges right this second.

Q And is there within Linnarsson a full description of its method using Figure 3, other than Example 1?

MR. WALTER: Objection. Vague.

A So I think that, you know, a skilled artisan again would read Linnarsson as a broad disclosure. So we can go back to Figures 1 and 2, for example, that describe high-level overviews of the process. And then if you look at Claim language, you would read, an artisan would read the claims and get the sort of step-by-step process of what's required for different versions of the protocol.

And I think Figures 3 and 4 are exemplary

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molecules, certainly not the only molecules that one might use as part of that. But, you know, I think, again, Linnarsson is fairly -- fairly general, fairly encompasses a wide range of protocols that would involve tracking polynucleotides to single cells.

Q Okay. That's a little bit different than what I was asking, which is whether Linnarsson includes a full description of using its method with Figure 3, other than what's described in Example 1.

A So I think if you look at Claim 1, for example, that is an example of a start-to-finish process that a POSA would read Figure 3 and understand as part of how to achieve Claim 1.

Q Anything else?

A There -- again, I -- connecting to Figure 1, because Figure 1 talks about, if I recall -- let me pull up Figure 1.

Yeah. So Figure 1, for example, provides a cartoon of the overview of the process. And to the extent, for example, it talks about tagging,

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it talks about reverse transcription, so it's outlining a high-level view of a protocol that a skilled artisan would read Figures 3 and 4 as contributing to in the context of Figure 1 because those are exemplary molecules for doing the tagging and the amplification and the reverse transcription that is described in Figure 1.

Q If I ask you the same question about Figure 3, would your answer be the same; that is, whether Linnarsson includes a full description of using its method with Figure 4, other than what's described in Example 1?

A Yes, my answer would be similar, that it's referring to things that are claimed in Claim 1, it is referring to Figure 1. And again, there are other places like Figure 2 is again showing components of the process. So I think a skilled artisan would use those figures in the context of the broad disclosure of Linnarsson.

Q And what aspects of Figure 4 are relevant to Example 1?

A So the -- certainly the, similar to

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Figure 3, there's the priming site, the APS portion of the molecule that's required for amplification priming.

And there's also the RCS portion of the molecule, the RNA complementary sequence, which is -- we talked about earlier is a region of the primer that initiates the reverse transcription. And that is also how you target your sample polynucleotides, depending on what your experiment is.

So this example it's an oligo(dT), so it's a series of thiamine residues. But it describes the RCS as being flexible and general, and you can use a range of different sequences depending on which sample mRNAs you would like to address.

So yeah, it has multiple portions.

Q We talked a little bit earlier about the biotin and I think the use of beads. Would you agree with me that if there is no biotin, you can't use the beads described in Examples 1 or 2?

A So I believe Examples 1 and 2 use

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streptavidin-coated beads, and biotin is the binding partner for that. But there are other solid substrates that one can use to purify polynucleotide mixtures.

So I'm not saying that's the only way one could do it, but streptavidin beads and biotin go hand in hand within a lot of protocols.

Q And you agree that Example 1 of Linnarsson used biotin and cut sites. Right?

A I believe that's true. I can go to Example 1 text. Oh, it was Page 30 -- 24.

Q Were you able to look at Example 1?

A Sorry, I'm looking right now, yep.

Q Sure.

A Yes, it is within Example 1. There is a BtsC1 digestion step.

Q And so you agree that Example 1 uses both biotin and a BtsC1 cut site. Right?

A Yes.

Q Could you pull up Exhibit 2015, please.

(10x Genomics Exhibit 2015, previously marked, not attached.)

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A This is G-U-A-N?
Q Correct.
A I see that.
Q Do you recognize this article?
A I believe so, yes.
Q And the authors here are from New England Biolabs.
Do you agree with that?
A Yes.
Q And New England Biolabs is well-known for selling restriction enzymes. Correct?
A That's right.
MS. RAYMOND: Why don't we take a short break, ten minutes, before we get into the next piece of this.
THE WITNESS: Okay.
(A recess was taken.)
BY MS. RAYMOND:
Q Could you, Dr. Cooper, please turn to Exhibit 1070. I'll be asking you about Exhibit 1070 in both proceedings, but perhaps we can focus on the '197 paragraph numbers.

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A '197, is that 955 or 958?
Q That is 955, yes.
A So this is patent owner's response?
Q What I'm looking for, what I'm going to ask you about, is Exhibit 1070, which is your reply declaration.
A Oh, gotcha, yes. I'm there.
Q Could you please turn to Paragraph 12.
A I see.
Q And you say, "Nowhere does the '197 patent disclose the simultaneous use of two tags, wherein a first tag is used to encode the cellular origin of a polynucleotide and the second tag distinguishes among polynucleotides in a cell."
Do you see that?
A Yes, I do.
Q And you recall saying the same thing about the '013 patent?
A Yeah, I'm sure I did. Yes.
Q Okay.
MS. RAYMOND: Could we pull up the '197 patent that is Exhibit 1001.

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(Parse Exhibit 1001, previously marked, not attached.)

MS. RAYMOND: And if we could go to Column 6, please.

A So this is 1001?

Q This is exhibit -- sorry, Exhibit 1001.

A Gotcha. Okay.

Q And I'm looking at the '197 patent. So this is in the 955 matter.

A Gotcha. Yeah, I'm there.

Q Okay. And I'm looking at the MID definition here.

Do you see that? Starting around Line 33?

A I see that.

Q And do you see the reference to a tag or combination of tags?

A I do.

Q And then the patent offers two types of tags, a source tag and UMI.

Do you see that?

A I don't see UMI in here.

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Q Sorry about that. I'm sorry, the words "UMI" are not present. But it says, "In certain embodiments, MIDS are employed to uniquely tag each individual polynucleotide in a sample"?

A I see that.

Q Do you see that?

And do you see the reference to a source tag?

A Well, the previous sentence talks about from a pool of polynucleotides derived from different sources, yes.

Q So do you agree with me that the '197 describes both a source tag and the tagging of a MID with a -- that provides a correlation between a polynucleotide and its source?

A Certainly this paragraph is talking about prior art uses of tags, which individually include tracking a source or using as a unique polynucleotide identifier. Yes, this is an overview of what's in the prior art.

Q And do you agree that it describes using a tag or a combination of tags such that it would

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be understood to refer to a combination of the two types of tags you just described?

A No, I don't think that's necessarily how one would read that. It talks about how a single MID can be composed of a combination of tags, which I think the simplest explanation of that would be, you know, much in the way that Linnarsson talks about using the TSO and the CDS tags to identify the source. So it's talking about sort of -- it doesn't necessarily imply dual functionality of tags. It just says that each function can be achieved with one or more polynucleotide tags.

Q But you agree that it describes using tags for multiple functions. Correct?

A Again, it describes prior art uses of tags that have been used in different individual ways. It certainly doesn't lay out an inventive combination here. It doesn't specifically say use this one and that one and combine them in this way, this is how you do that. It's -- again, this is a description of the universe of ways that

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people have used tags in the prior art up until this patent was published.

Q But you agree that it describes using tags for different functions. Correct?

A It describes different functions that have been used in the prior art in individual ways, yes.

Q And you agree that it says the MID uses a tag or combination of tags. Right?

A That is in the opening sentence of the paragraph, yes. That an individual MID can be comprised of a single or multiple tags, yes.

Q But it's your position that that -- that this wouldn't be read to -- wouldn't be read to describe using a combination of tags with different functions?

A It's not -- certainly that doesn't make that point clearly or explicitly. Again, this is just -- I think a skilled artisan would read this as a generic overview of what's in the prior art regarding use of tags.

Q Could you return to Paragraph 35 of your

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report.

A So we're back to Exhibit 1070.

Is that right?

Q Correct. And this is also Paragraph 33 in your '013 report.

A This is back to Linnarsson?

Q We're looking at your -- sorry, your declaration, Exhibit 1070. And yes, we're talking about Linnarsson.

A Yes. Okay.

Q And you say -- sorry. You say, "Thus Figure 11 is only one out of numerous figures and representative examples of Linnarsson's invention."

Do you see that?

A Yes.

Q How many Linnarsson figures do you rely on?

A I don't know the exact number, but certainly Figures 1, 2, 3, 4, 11, and perhaps others. I don't recall the entire -- they're all called out in the document, but I don't remember

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the full scope of all of them.

Q And then earlier we agreed that there are two examples in Linnarsson that you could recall.

Is that correct?

A So, well, yeah. The two examples that provide a protocol, sort of, and an example of a working protocol from start to finish, yes. I think in the more general use of examples, it talks about an example -- an exemplary CDS, an exemplary TSO. So it uses examples of individual components. There's a lot of other examples in there, where "example" is a more general term about describing individual components.

Q Okay. So when you say "representative examples" in Paragraph 35, what do you mean?

A Again, much in the same way that we just talked about, an exemplary TSO, an exemplary CDS, et cetera. So it's examples of -- of how one defines or builds or constructs parts of the protocol or parts of the work flow.

Q And with respect to Figure 11 in Linnarsson, you see there's a Step A? Is it fair

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for me to call it a step?

A You're talking about specifically of Figure 11?

Q Figure 11, yes. Figure 11 you see the A?

A Yes. Yes.

Q Is it fair for me it call that a step of Linnarsson?

A I think it is a step of Figure 11.

Q Okay. Sorry. And is it your position that Step A shown in Figure 11 is an optional step with respect to the Linnarsson method more generally?

A I think that there are certainly components here that are very optional. You know, at least the two examples would be the design of the RCS here, the RNA complementary sequence is oligo(dt), and we know that that's only one example of a sequence. The use of biotin here is also not required.

So again, I think the -- this is helping to understand the work flow a little bit better from that Example 1, that capital E Example 1.

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But certainly components of this are not required for Linnarsson's process more generally.

Q Beyond the design of the RCS and the use of biotin, in your opinion are there other elements shown in Figure 11 that are optional with respect to Linnarsson's method more generally?

A So the -- there's no cell tag on -- in the CDS that's highlighted here. And certainly Linnarsson makes clear that the CDS can include a cell tag. Doesn't have to. It talks about CDS and/or TSO. So that's another optional component of what's in Figure 11.

The primer -- the PR region, so it talks about the optionality of how you design the amplification sequences. And, you know, you might choose one set of primers for, you know, if you were eventually going to do Illumina versus SOLiD versus something else. So there are other aspects here that are also optional.

And I guess more generally too it's also the -- the input is described as generic, but we know that the nucleotides coming themselves can be

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samples of whatever you're interested in studying. So it might be human cells, it might be a mouse cell, it might be immune cells, it might be brain cells, it might be all kinds of things. Right? So that's -- it's intended to be -- that that, again, is another aspect that's modular and generic about this particular figure.

Q Okay. If you go to what's marked in Linnarsson as 1003.006, there is a description of Figure 11.

A Okay.

Q And you see it says Panel A shows a reverse transcription step?

A Yes.

Q Do you agree with me that some sort of reverse transcription step is required to perform Linnarsson's method?

A Generally speaking, yes, it is -- it is a method for doing gene expression, which often involves a reverse transcription step.

Q And would you agree with me that -- you see Panel B it says, Panel B shows a template

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switching step?

Do you see that?

A I see that.

Q And do you agree with me that some sort of template switching step is required to perform Linnarsson's method?

A Yes, as to the extent that that's part of how you build a cDNA, yes.

Q And that's part of how you build a cDNA library in Linnarsson. Correct?

A It is.

Q And do you see on the next page Linnarsson says, Panel C shows a single primer PCR step?

A I see that.

Q Do you agree with me that some sort of single primer PCR step is used to perform Linnarsson's method?

A So I think -- I don't necessarily think you always would necessarily amplify. But certainly amplification is part of many work flows. That would be. And I think for example in

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Claim 1 it does include an amplification step. But it wouldn't have to be a single primer, for example. It's just a primer to do some round of amplification.

Q Do you agree with me that a single primer PCR step is used in Linnarsson's method?

A I would say it's used in -- in Figure 11, but not necessarily all embodiments of Linnarsson.

Q Can you point me to an embodiment of Linnarsson where a single primer PCR step is not used?

A So I again would -- like we talked earlier about Figures 1 and 2 and Claim 1 being written to be broader than that. They -- you know, Claim 1, for example, encompasses amplification. So you would have to perform amplification. But you might choose to use different primers. You know, you can -- you can design PCR in lots of different ways.

Q And Panel D, Linnarsson goes on and says Panel D shows a fragmentation step?

A Yes.

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Q And do you agree that some sort of fragmentation step is used to perform Linnarsson's method?

A Only within Figure 11. There's -- you don't have to perform fragmentation in general.

Q Okay. And can you point me to a complete description of Linnarsson's method that doesn't use fragmentation?

A I would go back to my previous answer about Figure 1 providing an overview. Figure 2 talking about portions of it. Claim 1, for example, doesn't mention fragmentation, et cetera.

Q And I assume your answer would be the same with respect to Panel E showing an immobilization and end repair step?

A Correct. That's just one option for purifying a cDNA library. It's not necessary.

Q If you could turn to Paragraph 45 of your '197 declaration. Which is Paragraph 43 in your '013, in the '013 case.

A "The key point is," is that the paragraph?

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Q That's the paragraph. And if you could go towards the bottom of that paragraph you say, "While that may be true of Figure 11, it is not true of the embodiments based on Figure 4."

Do you see that?

A Yes.

Q What are "the embodiments based on Figure 4"?

A Well, any embodiment that doesn't use biotin, that actually puts a tag inside the CDS, for example. Because Figure 11 doesn't lend itself to sequencing the tag in CDS. So in work flows where you want to sequence -- you wouldn't put a cell tag in there if you didn't want to sequence it. So work flows that included the cell tag on the CDS, that would be different than what is carried out in Figure 11.

Q Where does Linnarsson describe work flows that include at the cell tag on the CDS?

A So Figure 1 is another example, you know, provides an overview of it. Claim 1 allows you to put -- and, in fact, I think there are dependent

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claims that specifically say put a tag on the TSO, put a tag on the CDS, et cetera.

Q Anywhere else in Linnarsson?

A I guess I'm not understanding the question.

Q I was asking you does -- where does Linnarsson describe work flows that include the cell tag on the CDS? And you pointed me to Figure 1 and the claims. And I was just wondering if there was anywhere else, in your view, that Linnarsson describes that?

A So I think basically all that -- you know, I would read it sort of the opposite. That the work -- it specifically talks about Figure 11 having optional steps. So by default I would say that would not be included. And that in general you would -- you know, Figure 4 would be an example of a CDS that can be used in a whole range of work flows. So it's giving you options at each step, or options at various steps, including the design of the CDS and the TSO.

Q Can you please turn to Paragraph 104 of

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your '197 report.

A Yeah, I see it.

Q Okay. And this goes back to our discussion about the cDNA library definition in Linnarsson. And you see here again that that description of the cDNA library is repeated.

Do you see that in Paragraph 104?

A Yes.

Q And in your opinion, is the only cDNA that is not a fragment an entire chromosome?

A No. The -- so the -- again, I think in this case the fragment is by definition it's connecting to -- you're converting fully transcribed mRNA into what is calling cDNA fragments. So they are providing the terms of that definition here, saying that the fragments of cDNA that come out are complementary DNA fragments driven by the fully transcribed mRNA. And so they're using that term there in that way. And that's -- they're giving that definition.

So I think the key point is that it doesn't imply or explicitly say fragmentation of

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some artificial sort. It's saying that the process of generating cDNA yields cDNA fragments.

Q And the cDNA fragment may be an entire reverse transcribed chromosome, in your opinion?

A No. Because there's no -- at least to my knowledge, there's no example of a gene that is expressed that would occupy the full length of the chromosome. So it's -- again, it's just a reflection of RNA in, cDNA out. The cDNA represents the RNA that was put in.

Q So in your opinion, a cDNA fragment may be an entire reverse transcribed gene?

A Well, an entire reversed transcribed mRNA.

Q Okay. Could you please turn to Paragraph 147 of your '197 report.

A Okay.

Q And you disagree with Dr. Quackenbush that ligation, as you proposed it, would add an additional step to Linnarsson's method?

A Yeah, that his language about adding an additional ligation step would increase complexity

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in the context of his argument, yes. I don't think that is a problem.

Q You don't think that's a problem. But is it -- is it your opinion that ligating would add a step to Linnarsson's disclosed process?

A Well, so ligating a -- well, the full context is important here. It's viewing Linnarsson in combination with McCloskey, where McCloskey is defining the nature of the unique molecular identifier tag. And how a skilled artisan would be motivated to do that because of the benefits of the unique molecule tag.

And that in that context a ligation step is -- you know, is a very routine, conventional, well-known step for adding tags to -- to cDNA molecules.

So in that context I don't think it's overburdensome or complicated. It's a very routine thing to do.

Q Can you turn to Paragraph 156 of your report, please.

A Okay.

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Q Actually, back to -- back to what we were previously talking about?

You do agree that ligating would add a step to Linnarsson. You say it's not overcomplicated, but you would agree it does add a step?

A I would say to the extent that you are adding this second functional tag. Again, Linnarsson discloses two tags, right, one on the CDS and one on the TSO, as an option.

But to the extent you're adding a tag that acts as a unique molecular identifier in the addition to the CDS and/or TSO, then, yes, it is an additional step to -- again to incorporate the benefit of McCloskey into the work flow of Linnarsson.

Q So if you're adding ligation to Linnarsson, that would add a step?

A Correct. To reap the benefit of the redundant molecule tracking, yes.

Q Got it. Okay. Sorry. Back to Paragraph 156. And you say "Linnarsson itself even

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discloses the process of ligating sequencing adapters to the cDNA molecules following both extension steps."

Right?

A Correct.

Q And that ligation occurs after amplification and after fragmentation?

Is that correct?

A No. It would be after you make that initial complementary DNA fragment but before amplification or any downstream processing.

Q And in Linnarsson, it's your view that that -- my question is about what Linnarsson discloses. And do you agree that Linnarsson discloses a process of ligating sequencing adapters to the cDNA molecules following both extension steps?

A Well, I think Linnarsson -- so Linnarsson certainly discloses that you have flexibility about the ends of the cDNA molecules in terms of the design and structure. And in other parts of the Linnarsson disclosure it talks about adding

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adapters for putting onto a sequencer, for example.

And so I think the point here again in the context of a skilled artisan being motivated to use the McCloskey unique molecular tag, you could easily add it after the second extension step that is written to Linnarsson, via ligation.

Q And with respect to Linnarsson's method, is it your opinion that all steps in Linnarsson require PCR of some type?

A All -- no, there are lots of steps that are not PCR.

Q Sorry. Is it your opinion that Linnarsson's method, or methods depending on your view, all require PCR of some type?

A I guess I've not done that analysis. I know, I believe amplification of some flavor is baked into Claim 1. So certainly to the extent that that's, you know, the main independent claim, I don't know if I'm comfortable saying that all conceivable embodiments would necessarily rely on amplification. There could be some. But

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certainly things that are called out by Claim 1 obviously need amplification. So, yeah, I guess I'm not -- I don't have a good answer for that question.

Q Okay. And if you could turn to Paragraph 159 of your '197 report.

A Okay.

Q Same bit as in your '013 report. But does the '197 patent disclose using Hug's method of ligation to add a sequence to the biotinylated end of a nucleic acid?

A I'm sorry. Which? Can you repeat that?

Q Does the '197 patent disclose using Hug's method of ligation to add a sequence to the biotinylated end of a nucleic acid?

A So I'm not sure that the '197 discloses use of biotin, for starters. And generally speaking, you don't ligate onto a biotinylated end. You know, a skilled artisan would understand that that's not something one would do.

I believe the '197 does refer to Hug, if I'm not mistaken. So I think it's cited in the

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'197 patent, but I could be wrong about that. But so I guess I'm not quite following the question because it's -- you wouldn't ligate to a biotinylated end.

Q And would your answer be the same if I asked you about the '013 patent disclosing using Hug's method of ligation to add a sequence to the biotinylated end of a nucleic acid?

A They share the same specification, so yes.

Q And in your -- in your report have you suggested using a restriction enzyme to create a sequence that permits the linker in Hug to -- well, let me ask it this way: Hug's method uses a restriction enzyme in order to -- to cut the polynucleotide to which the linker is attached.

Correct?

A I believe that is certainly one of the steps used in at least some of the portions of -- some of the methods in Hug, yes.

Q Okay. And in your report, either in this reply report or in your opening report -- and we

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can pull that up if necessary -- do you describe using a restriction enzyme to create that end that permits attachment of Hug's linker?

A I'm not sure if I specifically called out Hug's use of a restriction enzyme or not. The more general point was that Hug is just one example of how a skilled artisan might use ligation to add the McCloskey second tag. I'm not sure that I focused on whether -- whether or not and which enzyme one would use or not use from Hug.

MS. RAYMOND: If we could take a ten-minute break.

MR. WALTER: Great.

(A recess was taken.)

MS. RAYMOND: I have no further questions.

MR. WALTER: All right.

EXAMINATION BY COUNSEL FOR PETITIONER

BY MR. WALTER:

Q Professor Cooper, I have a few followup questions for you. Are you ready?

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A Yes.

Q All right. Do you recall on cross-examination you were asked some questions about Figures 3 and 4?

A Yes.

Q What is your understanding of whether Figures 3 and 4 in Linnarsson are depicting the type of TSO and CDS you could use with the approaches in Linnarsson where you used biotin and restriction enzyme to do fragmentation and capture?

A So Figures 3 and 4 don't include biotin. So the only aspects that would carry forward would be, for example, the use of an amplification primer site, et cetera. So again, they're part of the broader disclosure, but not tied to the digestion steps.

Q What's your understanding of whether Figures 3 and 4 include a restriction enzyme cut site for use with the fragmentation and capture approaches that are disclosed in Linnarsson?

A I don't believe they include that,

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because the portions of the molecule that are depicted in Figures 3 and 4 are all demarcated with whether it's part of the priming site, part of the cell tag, et cetera. So there's not an allocation to a cut site.

Q Now, you were shown an article, the Guan article, pertaining to restriction enzyme cut sites.

Do you recall that?

A I do.

Q And that was I believe an article that pertains to the Bts-1 restriction enzyme cut site?

A Yeah, that's in the title. Yes.

Q Let me just make sure that I've got the right article here.

What is your understanding of whether Linnarsson is contemplating use the Bts-1 restriction enzyme with any of its approaches?

MS. RAYMOND: Objection. Scope.

A It is -- Bts-1 isn't mentioned. That's a different enzyme than the one that is part of the example in Linnarsson.

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Q Now, you're aware there has been some suggestion in this case that some of the sequences that are disclosed in Linnarsson include the nucleotides that happen to correspond to Bts-1 restriction enzyme cut site.

Do you recall that?

A I do.

MS. RAYMOND: Objection. Form. Scope.

A I do recall.

Q Okay. What's your understanding of whether Linnarsson ever refers to those sequences of nucleotides that happen to correspond to the Bts-1 restriction enzyme cut site as a -- as a cut site for use with any of the approaches that are disclosed therein?

MS. RAYMOND: Objection. Form. Scope.

A Again, it doesn't refer to that enzyme. So any -- any use of it would be totally happenstance or coincidental that that sequence happened to appear in the examples of Figures 3 and 4.

Q Now, you were asked a lot of questions

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about Figures 3 and 4 appearing as part of Examples 1 and 2.

Do you recall that line of questioning?

A Yes.

Q What is your understanding as to whether the appearance of Figures 3 and 4 in the text related to Examples 1 and 2 means that Figures 3 and 4 must be used in an approach that uses every step that's disclosed in Figures 1 and 2, including fragmentation and capture?

MS. RAYMOND: Objection. Form. Scope.

A So I don't think Figure 1, for example, talks about fragmentation at all. Figure 1 is the broader --

Q I'm sorry, I meant -- sorry, let me ask the question again. I wasn't precise. Let me go again.

With regard to Figure 3 and 4, what is your understanding of the fact that Figures 3 and 4 discuss in connection with Examples 1 and 2 as to whether that means that Figures 3 and 4 must be used in an approach that uses every step in

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Examples 1 and 2, including fragmentation and capture?

MS. RAYMOND: Objection. Format. Scope.

A So I think it's clear that it's not really possible that they're intended to be understood that way.

For example, to the extent that the capital E Examples in Linnarsson talk about only sequencing one end of the molecule, that wouldn't make any sense to include a cell tag in the end of the molecule that you're not going to sequence.

So I think a skilled artisan would read that, and it would be very clear that Figures 3 and 4 are representative examples of things that are more -- more general than what is specifically outlined in the -- in, quote, the Example 1.

And I'd say that's also in keeping with the way it describes other portions about how the examples are not meant to be limiting, they include optional things, et cetera.

So I think it's not reasonable to expect a skilled artisan to look at Figures 3 and 4 and

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say they're only compatible with the work flow in Example 1.

MR. WALTER: No further questions from me.

MS. RAYMOND: Can we take a five-minute break.

(A recess was taken.)

EXAMINATION BY COUNSEL FOR PATENT OWNER

BY MS. RAYMOND:

Q Dr. Cooper, at the end of your counsel's questioning you said, "I think it's not reasonable to expect a skilled artisan to look at Figures 3 and 4 and say they are only compatible with the work flow in Example 1."

Do you remember that?

A Yes.

Q You would agree that it would be reasonable that a skilled artisan would look at Figures 3 and 4 and say they are compatible with the work flow in Example 1. Correct?

A Certainly some aspects are, absolutely.

Q So you think some aspects of Figures 3

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and 4 are not compatible with the work flow in Example 1?

A Well, the one example of -- maybe "compatibility" isn't the best word, but it's -- for example, where you put the cell tag, if you were never going to sequence that portion of the molecule, it wouldn't make sense to include that cell tag.

That said, I don't know that including the cell tag would necessarily break it; it just is not -- it wouldn't make sense to do that.

And, you know, another modification that you'd have to make is there's no biotin listed on Figures 3 and 4. So an artisan would have to understand that you would have to biotinylate to use, et cetera. So I think there are differences.

But it could be -- it's helpful to for a skilled artisan, but it's not an exclusive or one-to-one match.

MS. RAYMOND: Thank you. I have no more questions.

MR. WALTER: Okay. I have nothing else

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either, so I think we're done.

(Off the record at 12:08 p.m. EDT.)

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ACKNOWLEDGMENT OF DEPONENT

I, GREGORY COOPER, Ph.D., do hereby acknowledge that I have read and examined the foregoing testimony, and the same is a true, correct and complete transcription of the testimony given by me, and any corrections appear on the attached Errata sheet signed by me.

_____ _____

(DATE) (SIGNATURE)

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C E R T I F I C A T E

I, Debra Ann Whitehead, E-Notary Public in and for the Commonwealth of Virginia, do hereby certify:

That GREGORY COOPER, Ph.D., the witness whose deposition is hereinbefore set forth, was duly sworn by me before the commencement of such deposition and that such deposition was taken virtually and is a true record of the testimony given by such witness.

I further certify that the adverse party, PARSE BIOSCIENCES INC., was represented by counsel at the deposition.

I further certify that the deposition of GREGORY COOPER, Ph.D., occurred virtually, on Tuesday, September 3rd, 2024, from 10:07 a.m. to 12:08 p.m. EDT.

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I further certify that I am not related to any of the parties to this action by blood or marriage, I am not employed by or an attorney to any of the parties to this action, and that I am in no way interested, financially or otherwise, in the outcome of this matter.

IN WITNESS WHEREOF, I have hereunto set my hand this 4th day of September, 2024.

My commission expires:
October 31, 2027

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