IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

SCALE BIOSCIENCES, INC. and ROCHE SEQUENCING SOLUTIONS, INC.,	)	
Plaintiffs,	)	
v.	)	Civil Action No. 22-1597-CJB
PARSE BIOSCIENCES, INC.,	)	
Defendant.	)	

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MEMORANDUM OPINION

August 4, 2026
Wilmington, Delaware

Christopher J. Burke

BURKE, United States Magistrate Judge

In this action, Plaintiff Scale Biosciences, Inc. ("Scale") and Plaintiff Roche Sequencing Solutions, Inc. ("Roche") alleged that Defendant Parse Biosciences, Inc. (hereafter, "Parse") infringes various claims of United States Patent Nos. 10,626,442 ("the '442 patent"), 10,982,256 ("the '256 patent"), 11,512,341 ("the '341 patent"), and 11,634,752 ("'752 patent"). (D.I. 70 at ¶ 1) Presently before the Court[1] is Parse's "Motion for Summary Judgment #3: Parse Does Not Literally Infringe the '442, '256, or '752 Patents[,]" filed pursuant to Federal Rule of Civil Procedure 56 ("Motion"). (D.I. 318) For the reasons set forth below, the Motion is DENIED.

I. BACKGROUND

The Court incorporates by reference its discussion of the factual and procedural background of this case found in its Memorandum Opinion dated October 8, 2025 ("October 8 MO"), to the extent it is relevant to the instant Motion. (D.I. 466 at 2-5) Below the Court includes additional background information also relevant to the Motion.

A. Procedural Background

Parse filed the instant Motion on February 24, 2025—the same date that the parties each filed various other summary judgment and *Daubert* motions. (D.I. 318) The Motion was fully briefed as of April 17, 2025. (D.I. 395)

After the parties filed and briefed their various summary judgment motions, the Court heard extensive argument on and resolved certain of those motions. For example, in its October 8 MO, the Court granted Parse's motion for summary judgment of invalidity of all of the

[1] The parties have jointly consented to the Court's jurisdiction to conduct all proceedings in this case, including trial, the entry of final judgment, and all post-trial proceedings. (D.I. 12)

asserted claims of the '752 patent for lack of written description and enablement. (October 8 MO at 28) And on June 30, 2026, the Court denied Scale's motion for reargument under Local Rule 7.1.5 with regard to the decision set out in the October 8 MO. (D.I. 552) In light of those rulings, the instant Motion is moot with respect to the '752 patent. Thus, below the Court will address the Motion only as it relates to Parse's arguments regarding non-infringement of claim 11 of the '442 patent and claims 1, 2, 5, and 6 of the '256 patent ("the asserted claims" and "the asserted patents" respectively). (D.I. 318; D.I. 439 at 1)

B. Factual Background

The inventions of the '442 patent and '256 patent relate "generally to the field of detection, identification, and quantification of target molecules in a sample . . . [and] in part to the detection, identification, and quantification of individual target molecules in single cells of a complex cell population while retaining cell specific information regarding that target molecule." ('442 patent, col. 1:51-57; '256 patent, col. 1:52-57) In relation to these concepts, the patents discuss and use the terms "target molecules" and "nucleic acid targets." As will be explained further below, here the parties agree that the meaning of those two terms goes to the heart of their dispute regarding the Motion. Therefore, below the Court will provide some further context for those terms and their use in the relevant asserted claims.

The Court starts by setting out asserted claim 11 of the '442 patent (and non-asserted claim 1 of that patent, from which claim 11 depends),[2] as well as asserted claim 1 of the '256 patent (upon which the remaining asserted claims of that patent depend), with the key terms italicized:

[2] As will be seen below, claim 11 also depends on non-asserted claim 9, but the Court omits that claim here, as it is not particularly relevant to the disputes implicated by the Motion.

1. A method of uniquely labeling *target molecules* within a plurality of cells, the method comprising:

(a) coupling a common linker sequence to *target molecules* within the plurality of cells;

(b) dividing the plurality of cells into at least two primary reaction volumes, the at least two primary reaction volumes comprising a first primary reaction volume and a second primary reaction volume;

(c) providing primary nucleic acid tags to the at least two primary reaction volumes, wherein the primary nucleic acid tags provided to the first reaction volume are different from the primary nucleic acid tags provided to a second reaction volume;

(d) coupling the common linker sequences within each of the at least two primary reaction volumes with the provided primary nucleic acid tags;

(e) pooling the at least two primary reaction volumes;

(f) splitting the combined primary reaction volumes into at least two secondary reaction volumes, the at least two secondary reaction volumes comprising a first secondary reaction volume and a second secondary reaction volume;

(g) providing secondary nucleic acid tags to each of the at least two secondary reaction volumes, wherein the secondary nucleic acid tags provided to the first secondary reaction volume are different from the secondary nucleic acid tags provided to the second reaction volume; and

(h) coupling the *target molecules* within each of the at least two secondary reaction volumes with the provided secondary nucleic acid tags. . . .

11. The method of claim **9**, wherein the *target molecules* are RNA and wherein step (a) comprises hybridizing the common linker to the RNA.

('442 patent, cols. 57:62-58:25, 58:62-64 (emphasis added))

1. A method for identifying whether a plurality of *nucleic acid targets* is present in a plurality of cells comprising:

> a) binding to the *nucleic acid targets* in the plurality of cells a plurality of unique binding agent (UBA) nucleic acid tags;
>
> b) extending the UBAs bound to the targets, and
>
> c) assembling cell originating barcodes (COB) on the extended UBAs by subsequently adding multiple assayable polymer subunit (APS) oligonucleotides to each of the extended UBAs in the plurality of cells in an ordered manner during successive rounds of split pool synthesis wherein the APS oligonucleotides in each round anneal to the APS from a previous round and are covalently linked to the adjacently annealed APS to create unique codes that represent the identities of individual cells in which the tags are bound, and wherein the method does not include a step of isolating each cell in the plurality of cells.

('256 patent, col. 58:11-28 (emphasis added))

The term "target molecules" can encompass a wide swath of different types of molecules of interest, such as "proteins, nucleic acids, lipids, carbohydrates, small molecules, organic monomers, or drugs." ('442 patent, col. 33:42-45; '256 patent, col. 33:55-57) Thus, nucleic acid target molecules are one type of target molecule. And while (as seen above) asserted claim 11 of the '442 patent recites a method for attaching tags to "target molecules[,]" the asserted claims of the '256 patent implicate attaching such tags only to "nucleic acid targets." In the briefing on this Motion, the parties tended to focus on the term "target molecules" when they were making their respective arguments. (D.I. 325 at 23-24; D.I. 366 at 22) Indeed, Parse asserted (and Scale did not disagree) that the term "nucleic acid targets" as used in the '256 patent should be construed similarly to "target molecules" as used in the '442 patent. (D.I. 325 at 23 & n.4) In light of this, in resolving the Motion, the Court will focus largely on the term "target molecules"

as set out in the asserted claim of the '442 patent—knowing that the parties' arguments on the Motion rise and fall with the decision as to that term.[3]

Earlier in the case, the Court issued a partial constriction of the term "target molecules." The Court concluded that the term meant (as both parties agreed that it did): "molecules of interest . . . that are being detected or quantified." (D.I. 119) However, at the time, the Court declined to address an additional dispute that the parties appeared to be having about whether a "target molecule" must also be one of a "known individual identity[,]" since the record as to that dispute was significantly underdeveloped. (*Id.*) That dispute is now joined in the briefing regarding the instant Motion and will be addressed herein.

Additionally, the Court here sets out some facts about the accused products and the process of tagging (or labeling) target molecules, which will provide further context for the Motion.

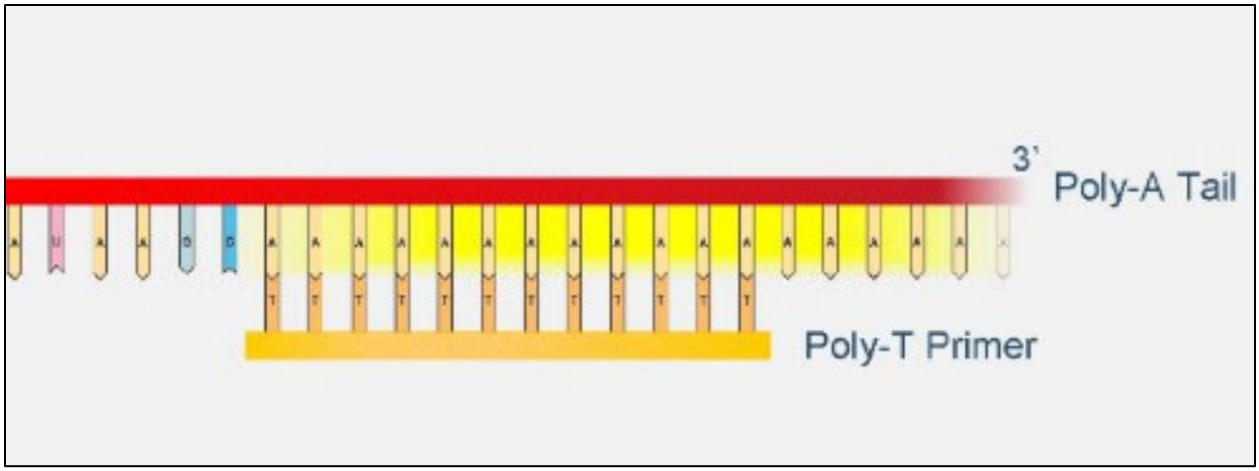
In this case, Scale has identified several lines of products offered by Parse that allegedly infringe the asserted claims, including the following: Evercode WT Products, Evercode TCR Products, Evercode Fixation Products, BCR kits, Gene Capture kits, CRISPR Detect kits, etc. (the "Accused Products"). (D.I. 70 at ¶¶ 15-26; *see also* D.I. 320 at ¶ 3 (citing D.I. 328, ex. 10 at ¶ 76)) Both parties agree that these Parse Accused Products can be used for what is known as "whole transcriptome" barcoding. (D.I. 320 at ¶¶ 3-4; D.I. 363 at ¶¶ 3-4) A "transcriptome" is the collection of all transcribed mRNA molecules found in a given cell (with each individual mRNA molecule being known as a "transcript"). (D.I. 320 at ¶ 1; D.I. 328, ex. 10 at ¶ 20) This

[3] Relatedly, and because the '442 patent and the '256 patent share a common specification, (D.I. 395 at 14; D.I. 366 at 26), hereafter the Court will mainly cite to the '442 patent.

means that use of the Parse Accused Products can and does result in the labeling of all of those transcribed mRNA molecules contained within the cell for purposes of later sequencing and analysis. (D.I. 320 at ¶ 4; D.I. 328, ex. 10 at ¶ 109; *see also* D.I. 366 at 29-30 ("The molecules of interest detected or quantified by the Parse Accused Products include the mRNA molecules in the transcriptome of a cell or nucleus."))

The tagging/labeling process that allows for the whole transcriptome sequencing described above is facilitated by the use of primers and a procedure known as "reverse transcription." More specifically, reverse transcription is the process for synthesizing a (more stable) cDNA molecule that is complimentary to the (less stable) mRNA molecule that is produced in the cell. (D.I. 547 at 6 (citing D.I. 313, ex. 23 at ¶¶ 59-60; D.I. 327 at ¶ 21)) Primers are important for facilitating the process of reverse transcription. This is because they bind in a complementary fashion to the mRNA molecules and provide a starting point for nucleotides to then be added to the growing cDNA molecule. (D.I. 327, ex. 30 at ¶¶ 52-55)

The types of primers used in the reverse transcription process (and the means by which they target certain molecules) will also have some relevance here. It is undisputed that the Parse Accused Products use two types of primers: (1) poly-T primers (also referred to as poly-dT primers); and (2) random hexamer primers. (D.I. 320 at ¶ 5; D.I. 366 at 30 (citing D.I. 368, ex. A at ¶ 110)) Poly-T primers have a series of nucleotides containing Thymine ("T") that are complimentary to what is known as a poly-A sequence (or "poly-A tail"), which is a series of nucleotides containing Adenine ("A") found in almost all mRNA molecules; a poly-T primer will bind to a poly-A sequence in the mRNA molecule as shown below:



(D.I. 320 at ¶ 6; D.I. 328, ex. 12 at ¶ 59; *see also* D.I. 325 at 32-33) Random hexamer primers contain a random sequence of six nucleotide base pairs (i.e., As, Ts, Cs (for Cytosine) and Gs (for Guanine)) and bind all single-stranded nucleic acid molecules that contain a complementary sequence in a similar fashion. (D.I. 320 at ¶ 7; D.I. 328, ex. 10 at ¶ 110; *see also* D.I. 325 at 33)

Additional facts relevant to the resolution of the instant Motion will be discussed in Section III.

II. STANDARD OF REVIEW

The Court incorporates by reference its discussion of the legal standards relating to summary judgment motions, patent infringement, and claim construction, which were set out in its October 8 MO, (D.I. 466 at 5-6), and in its Memorandum Opinion dated November 4, 2025 ("November 4 MO"), (D.I. 499 at 6-7).

III. DISCUSSION

With the Motion, Parse argues that, as a matter of undisputed fact, its Accused Products do not infringe the asserted claims. (D.I. 325 at 23) Here, the infringement inquiry turns on the resolution of the parties' claim construction dispute over the term "target molecules" (and, relatedly, over the term "nucleic acid targets") as used in the asserted claims. Parse argues that the plain and ordinary meaning of "target molecules" requires that the "target molecules are

specific molecules of interest with a *known individual identity* sufficient to distinguish the molecules being detected or quantified[.]" (*Id.* at 25 (emphasis added)) Under that construction, Parse argues that its Accused Products "do not infringe because they take a completely untargeted approach to label *all RNA*—hundreds of thousands of RNA molecules per cell in bulk—with no means to discriminate between them or even know what they have labeled[.]" (*Id.* at 23)

For its part, Scale believes that the construction of "target molecules" should remain simply as "molecules of interest that are being detected or quantified[.]" (D.I. 366 at 23-24 (citing '442 patent, col. 16:15-18 (*cited in* D.I. 119))) To the extent that this prior construction even needs further clarification, Scale argues that such further construction should note that target molecules "need not be specific molecules with a known individual identity." (D.I. 366 at 23-24) Were this proposed construction adopted, Scale asserts that there is a dispute of fact as to whether the Parse Accused Products infringe the asserted claims by tagging "target molecules." (*Id.* at 22)

In order to resolve this Motion (i.e., one raising non-infringement at the summary judgment stage), the Court must engage in the familiar two-step analysis for analyzing patent infringement. *See Markman v. Westview Instruments, Inc.*, 52 F.3d 967, 976 (Fed. Cir. 1995); (D.I. 499 at 6-7). The Court does so below, explaining why: (1) Scale's proposed construction of the disputed claim term is the correct one; and (2) this decision results in denial of the Motion, as there is a genuine and material dispute of fact regarding infringement.

A. Step One: Claim Construction

The Court begins with the first step of the infringement inquiry: i.e., it again assesses the appropriate construction of "target molecules."

To do so, the Court begins with the language of the asserted claims. On that front, in the Court's view, there is nothing inherent about the term "target molecules" itself that necessarily indicates whether such a molecule must be a "specific" molecule of interest with "a known individual identity" (as Parse suggests). Put differently, the plain and ordinary meaning of the word "target"—as that word is used to modify "molecules" in the disputed term—seems simply to require that the molecule at issue be a "target" (or be "targeted") in *some* way. But that doesn't necessarily evoke a requirement that the structure, sequence, or individual identity of that molecule must be *known in advance* at the start of the cell labeling process.

Thus, the Court next turns to the specification. Here, the intrinsic evidence (as at times amplified by some extrinsic evidence offered by the parties) supports Scale's position. There are at least four reasons why this is so.

First, the specification contains a definition of "target molecules"—one that does not support the narrowing limitation that Parse seeks to shoehorn into the construction at issue. This definition, found at lines 15-18 of column 16 of the '442 patent, had informed the Court's prior construction of the term at the earlier *Markman* stage of the case. (D.I. 119) Here the patent states only that "[t]he term 'epitope'[4] and 'target molecule' are used interchangeably herein to refer to the *molecule of interest* (parts of it or the whole molecule) being detected and/or quantified by the methods described herein." ('442 patent, col. 16:15-18 (emphasis added)) As Scale notes, this definition bolsters its position—in the sense that when the patentee defined the term at issue, it made no mention of any requirement that a "target molecule" *must* have an "individual identity" that is "known" in advance. (D.I. 366 at 23 ("When a patentee explicitly

[4] In light of this definition, the Court will understand "epitope" to have the same meaning as "target molecule" with regard to those terms' use in the asserted patents.

defines a claim term in the patent specification, the patentee's definition controls.") (quoting *Martek Bioscience Corp. v. Nutrinova, Inc*., 579 F.3d 1363, 1380 (Fed. Cir. 2009))

Parse disagrees. In its view, relying solely on the words of this definition would render the word "target" meaningless. (D.I. 325 at 26, 28) But the Court does not necessarily see why that is so. As the patent suggests, in order to be a "target" molecule, the molecule must be "of interest" to those engaging in the claimed method. A molecule can surely be "of interest" in this way, even if its *individual* identity (e.g., enough of its sequence to distinguish it from other molecules) is not known in advance.[5]

Second, Scale's argument is bolstered by another portion of the specification, which explicitly states that a "target molecule can have either a known *or unknown* structure or sequence." ('442 patent, col. 33:66-67 (emphasis added) (*cited in* D.I. 366 at 25)) This statement seems particularly problematic for Parse, because it appears to directly contradict its proposed construction. That is, this excerpt suggests that the structure or sequence of a target molecule could be "unknown"—perhaps partly unknown, largely unknown, or even entirely unknown—in advance to those using the claimed method, *not* that such a molecule *must always* have a "known individual identity."[6]

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[5] In its opening brief, Parse additionally criticized Scale's position by pointing to aspects of a particular (and lengthy) construction for "target molecules" that it claimed Scale was putting forward. (D.I. 325 at 26, 28) However, in its answering brief, Scale confirmed that it was not promoting that particular construction. (D.I. 366 at 23) As a result, the Court need not further address this proposal herein.

[6] In addressing this portion of the specification, Parse responds (citing to two paragraphs in its expert Dr. Lior Pachter's rebuttal report) by stating that: (1) it "does not suggest that the *identity*, or *entire* structure or sequence, is completely unknown"; (2) the specification's reference to a target molecule having an "unknown structure or sequence" is referring to situations where there are simply "slight variations between different forms of the same 'target molecule'"; and that (3) this part of the specification cannot be suggesting that "the *entire* sequence or structure of a target was unknown" because in such a circumstance, "it would

Third, another portion of the '442 patent's specification appears to provide an important clue indicating that Scale's claim construction position is correct. On lines 46-51 of column 41, the specification explains how certain complexes "can be used to . . . detect a *novel transcript* in order to diagnose or condition, i.e. fetal abnormality or cancer." ('442 patent, col. 41:46-51 (emphasis added) (*cited in* D.I. 366 at 27)) Scale's infringement expert Dr. Peter A. Sims then goes on to explain that:

> [A] "novel transcript" is one that is not known before using the methods of the Asserted . . . Patents to detect it. It can be targeted for any of the reasons noted above—e.g., it shares some sequence with other transcripts. But the novel transcript itself and the rest of its sequence would be unknown.

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be impossible to design a [unique binding agent, or] UBA to bind [to that molecule, as the '442 patent requires]." (D.I. 325 at 28-29 (citing D.I. 328, ex. 14 at ¶¶ 84, 139) (emphasis added)) Scale responds by asserting that the two cited paragraphs from Dr. Pachter's report "do not support this proposition, which is flatly wrong." (D.I. 366 at 29 (citing D.I. 328, ex. 14 at ¶¶ 84, 139)) In support of *that* assertion, Scale cites to a declaration from its expert, Dr. Peter A. Sims, in which Dr. Sims references evidence indicating that it has been possible for scientists since the 1980s to design an antibody to bind to a target antigen whose entire identity, structure, and sequence were unknown (and gives an example of how this process led to the discovery of the PSMA antigen). (D.I. 368 at ¶¶ 67-68 (*cited in* D.I. 366 at 29)) And then in response to *that*, Parse pushes back by citing to a further declaration from Dr. Pachter, who disagrees that the discovery of PSMA grew out of a circumstance where the *entire* structure or sequence of that molecule was unknown in advance. (D.I. 399 at ¶¶ 76-78 (*cited in* D.I. 395 at 17))

In the end here, the evidence cited does not convince the Court that it is impossible for a target molecule's structure or sequence to be entirely unknown in advance of the tagging process. Dr. Sims flatly says that this is possible, and he provides a cited example. And in his response to that example, Dr. Pachter never directly says that such a situation could not happen. (D.I. 399 at ¶¶ 76-78) And indeed, even when discussing the PSMA example, Dr. Pachter seems to equivocate at times about whether, in fact, the entirety of that antigen was unknown before it was obtained. (*Id*. at ¶ 78 ("Even if the identity of PSMA was not known at the time the 7E11-C5 antibody was obtained . . . .")) And so even after assessing this extrinsic evidence, the Court ends where it began: i.e., with the conclusion that the specification's reference to a target molecule potentially having an "unknown structure or sequence" seems to support Scale's position.

(D.I. 326, ex. 14 at ¶ 49; *see also* D.I. 329, ex. 18 at ¶ 135)[7]

Indeed, Scale persuasively points to further intrinsic evidence (as augmented by some additional submitted extrinsic evidence) that it says helps demonstrate how, in the claimed invention, a "unique binding agent" (or "UBA") may detect a "novel transcript" with an identity and a sequence that is not known in advance. (D.I. 366 at 27-29) Here, Scale begins by noting that the patent explains that UBAs can bind to a target molecule in a "sequence-specific" manner. (*Id*. at 27 (citing '442 patent, col. 17:47-48)) From there, Scale, citing to Dr. Sims' testimony, asserts that "[i]n the context of nucleic acid UBAs and nucleic acid targets . . . 'sequence-specific' binding means that each nucleic acid UBA will bind specifically to any target molecules that contain the complementary sequence[, and such] binding is specific to the sequence in the target molecule, even if multiple target molecules include that sequence[.]" (D.I. 366 at 27 (citing D.I. 326, ex. 14 at ¶ 30)) Dr. Sims then, *inter alia*, identifies gene fusion as a type of event wherein "the identity and sequence of a novel RNA transcript arising from [such a process] are unknown until the novel transcript is detected and sequenced." (D.I. 326, ex. 14 at ¶ 34 (*cited in* D.I. 366 at 27))

Scale also identifies examples in the specification of a phenomenon known as "cross-reactivity," where the same UBA can bind to and thus be used to target more than one molecule. (D.I. 366 at 28-29) Here, Scale points to the patent specification's disclosure of the Stat3 epitope, ('442 patent, col. 36:5-8), and to a referenced prophetic example about ERK proteins,

[7] Parse takes issue with how Dr. Sims interprets "novel transcript" here—alleging that he "misinterprets" the term. (D.I. 325 at 29) But in support, Parse cites to the same portions of Dr. Pachter's report that it referenced when addressing the "known or unknown structure or sequence" portion of the specification, discussed above. (D.I. 325 at 29 (citing D.I. 328, ex. 14 at ¶¶ 84, 139)) These paragraphs of Dr. Pachter's report don't specifically speak to the "novel transcript" portion of the specification. And otherwise, for the reasons cited above, Scale's proffered expert evidence was more persuasive on this point.

(*id.* at col. 57:20-59), as demonstrating that the patentee understood such cross-reactivity to be possible in practicing the asserted claims. (D.I. 366 at 28-29) In both scenarios, a single UBA is found to bind to the same epitope found on the various different Stat3 and ERK molecular entities (that each have different sequences despite belonging to the same family of proteins). (D.I. 366 at 28-29; *see also* D.I. 326, ex. 14 at ¶ 38; D.I. 368 at ¶¶ 69-70) The implication of this evidence seems to be that if the specification discloses examples of UBAs that can bind to multiple different target molecules via the process of cross-reactivity, then it must be possible that such target molecules are ones that do not necessarily have an individual identity "known in advance."

Parse's response to this argument seemed weak. Parse asserts, citing to its expert Dr. Lior Pachter's testimony, only that such cross-reactivity is "undesirable" and "should be avoided." (D.I. 395 at 17 (citing D.I. 399 at ¶¶ 79-81)) But Parse and Dr. Pachter never say that Dr. Sims is wrong to conclude that the specification discloses examples of cross-reactivity, or that he is wrong to conclude that in such examples, a UBA ends up targeting multiple target molecules.

Therefore, this mix of intrinsic and extrinsic evidence regarding sequence-specific binding and cross-reactivity also appears helpful to Scale in demonstrating that the detection of a "novel transcript" is a process wherein the individual identity of such a transcript is not known in advance.

Fourth, the intrinsic evidence that was cited most heavily by Parse simply did not do the work that Parse needed it to do. In this regard, Parse prominently focuses on portions of the specification that describe target molecules as "the molecules detected or measured by binding of a UBA whose *target-specific* region(s) recognize thereto." ('442 patent, col. 33:40-42 (*cited in*

D.I. 325 at 26) (emphasis added); *see also* D.I. 395 at 13) From there, Parse makes the following arguments about how the way that UBAs are described should impact the proper construction of "target molecules":

- Parse notes that the patents say that "[e]ach UBA in the population is *specific* for a target molecule" thus providing for "the *specificity* for the target molecule recognized in a cell[,]" ('442 patent, col. 16:44-47 (emphasis added) (*cited in* D.I. 325 at 26));

- Because each UBA must specifically bind *only* to a target molecule in order to determine whether that particular molecule is present in the cell, someone practicing the claimed method must know the individual identity of the target molecule *a priori*, in order to be able to design/select an appropriate UBA that is capable of binding to a *specific* target molecule, (D.I. 328, ex. 14 at ¶¶ 84, 139 (*cited in* D.I. 325 at 26-27));

- Therefore, it follows that the "target molecules" that the UBAs bind to in the asserted claim *must* be "specific molecules with a known individual identity"—so that one knows how to construct a UBA that will bind to that molecule, (D.I. 325 at 27).

To further bolster this argument, Parse states that the "specification is replete with disclosures consistent with" its proposed construction of "target molecules." (D.I. 325 at 27; D.I. 395 at 15-16) Parse cites supportively here to various places throughout the specification where target molecules are again described as being "uniquely" labeled or bound to "target molecule-specific [UBAs.]" (D.I. 325 at 27-28 (citing '442 patent, cols. 2:59-60, 3:6-7, 4:31-32, 4:39-41, 4:48-49, 10:29-30, 10:51-52, 34:56-57, 56:63-57:18, 57:20-59); *see also* D.I. 395 at 15-16)

Yet in the Court's view, these disclosures about UBAs and how they function don't limit "target molecules" to only being molecules whose individual identity was known in advance. That is because:

- To the extent that Parse's argument in its opening brief was that a UBA is "targeted" in such a way that it will bind to only *one* specific molecule—and that references to their being only one, "specific" target supports the conclusion that a target

molecule must be something that is known in advance[8]—the Court has already rejected such a position in this case. That is, the Court previously construed the term "unique binding agent" to mean "a molecule or assembly that is designed to bind with *at least* one target molecule, at least one target molecule surrogate, or both[.]" (D.I. 118 (emphasis added); *see also* D.I. 366 at 24-25)

- Even though the specification describes embodiments of the invention (like the ones Parse points to, listed above), and even if the language used in those descriptions is helpful to Parse, those are simply embodiments, nothing more. Indeed, nearly all of the portions of the specification cited by Parse repeatedly note that they are only describing the features of "some embodiments" of the invention—not necessarily what is *absolutely required* of the claimed invention in all cases. (*See, e.g.*, '442 patent, cols. 2:58, 4:25, 4:33, 4:42, 16:41-47; *see also* D.I. 366 at 24-25) As the United States Court of Appeals for the Federal Circuit has repeatedly noted, "one of the cardinal sins of patent law[is] reading a limitation from the written description into the claims." *Phillips v. AWH Corp.*, 415 F.3d 1303, 1319-20 (Fed. Cir. 2005) (en banc); *see also Specialty Composites v. Cabot Corp.*, 845 F.2d 981, 987 (Fed. Cir. 1988) ("[P]articular embodiments appearing in the specification will not generally be read into the claims."). The Court does not intend to commit that "cardinal sin" here.

- As the Court has previously noted above, in addition to the particular embodiments that Parse focuses on, the specification *also* includes descriptions of a target molecule in which the identity and structure of the molecule is said to be "unknown" or "novel." *See supra* at 11-14. Those specification excerpts would, of course, simply underscore the point that the patent doesn't *require* that a target molecule's individual identity be known in advance.

[8] In its reply brief, Parse seems to have backed away from the idea that it was making this type of suggestion—asserting there that even if a UBA (as the Court has ruled) can bind to more than one target molecule, it could still be the case that each of those (multiple) target molecules had an individual identity known in advance. (D.I. 395 at 14-15 (citing '442 patent, col. 18:5-26)) Of course, even if it could be the case that there are circumstances where a UBA is known to bind to more than one target molecule that each have a known individual identity, that doesn't mean that in *all instances*, a UBA must be known in advance to do so.

Having now discussed the parties' references to the intrinsic evidence, the Court concludes by taking note of some further extrinsic evidence cited by Parse. Here, Parse most prominently relied on a patent application submitted to the United States Patent and Trademark Office by the inventor of the asserted patents, Dr. Gary P. Nolan (U.S. Patent Application No. 2023/0049314, or "Nolan 2014"); Nolan 2014 was submitted shortly after the patent applications that led to the '442 and '256 patents, and it states that it is an extension of the methods set out in those applications. (D.I. 329, ex. 26 at [0068])[9] For the reasons set forth below, the Court concludes that Nolan 2014 does not demonstrate that Parse's claim construction position is correct.

Parse argues that Nolan 2014 "consistently use[s the term] 'target molecule' as requiring knowledge of its individual identity." (D.I. 325 at 29-30) As an initial matter, however, Nolan 2014 defines "target molecules" in a manner consistent with how that term is defined in the specification of the '442 and '256 patents (again, a definition that says nothing about such molecules being required to have a specific individual identity that must be known in advance)—a fact that would seem to cut against Parse's argument here. (D.I. 329, ex. 26 at [0072] ("the terms 'epitope' and 'target molecule' are used interchangeably herein to refer to the molecule of interest (or a portion thereof) that is being detected or quantified by the methods described herein")) But Parse asserts that: (1) when Nolan 2014 discusses targeted labeling, it discloses

[9] While "reliance on patent applications from unrelated inventions is [often] unpersuasive[,]" *Traveler Innovations Ltd. v. Evenflo Co., Inc.*, Civil Action No. 24-1204-RGA, 2026 WL 161354, at *14 (D. Del. Jan. 21, 2026), the patentee's own explanation of the technology at issue contained in a contemporaneous patent application can sometimes be useful in assessing the meaning of a disputed claim term, *see Rsch. Frontiers, Inc. v. E Ink Corp.*, Civil Action No. 13-1231-LPS, 2016 WL 1169580, at *12 n.18 (D. Del. Mar. 24, 2016), *report and recommendation adopted*, 2016 WL 7217217 (D. Del. Dec. 13, 2016), *aff'd*, 706 F. App'x 685 (Fed. Cir. 2017).

that "[e]ach UBA is capable of binding or hybridizing to a *single species* of target molecule [and that] this specificity of binding or hybridization [] enables detection of the target molecule in a given individual cell[,]" (D.I. 325 at 29 (emphasis in original) (quoting D.I. 329, ex. 26 at [0071])); but (2) when Nolan 2014 describes an *untargeted* labeling process, it quits referring to "target molecules" and "UBAs" and "instead discloses using a '*non-specific* binding agent comprising a poly-[T primer] for *non-specific hybridization with mRNA molecules*[,]'" (D.I. 325 at 29-30 (citing D.I. 329, ex. 26 at [0020]) (certain emphasis added)).

Yet in the Court's view, the disclosures in Nolan 2014 do not unequivocally support Parse's position. For example, Scale identifies a portion of Nolan 2014 that describes the use of a UBA utilizing a poly-dT primer in turn "hybridiz[ing] with *target RNA sequences* in fixed, permeabilized cells" in order to identify cells with "one or more *target RNA molecules of interest*." (D.I. 366 at 26 (citing D.I. 329, ex. 26 at [0065]); *see also* D.I. 329, ex. 26 at FIG. 29) This directly contradicts Parse's assertion that Nolan 2014's discussion of a "targeted" approach is consistent with Parse's position here—because the example above is one where a poly-dT primer binds to a group or class of molecules (i.e., a group or class without an *individual* identity known in advance) and where this is described in Nolan 2014 as a way to tag "*target* RNA molecules[.]"[10]

[10] In its opening brief, Parse also made reference to two other pieces of extrinsic evidence: (1) a 2020 article, authored by a number of researchers including Dr. Nolan, entitled "Ultra-high throughput single-cell analysis of proteins and RNAs by split-pool synthesis" ("O'Huallachain"); and (2) certain testimony of Dr. Thomas Albert, a Roche scientist. (D.I. 325 at 30-31) That said, after Scale criticized Parse's use of these resources, (D.I. 366 at 26), by the time of its reply brief, Parse did not further mention either of them, (*see generally* D.I. 395). So it may be that even Parse acknowledges these pieces of evidence are not particularly useful here.

In any event, the Court agrees with Scale that this extrinsic evidence is not terribly elucidating. O'Huallachain is a scientific article authored by Dr. Nolan and other researchers in 2020, several years after the filing of the application that led to the '442 patent. (D.I. 325 at 30;

Therefore, having exhausted all of the parties' claim construction arguments, the Court concludes that Scale's proposed construction is more appropriate. As such, the Court finds that the term "target molecules" (and the related term "nucleic acid targets") should be construed to mean "[nucleic acid] molecules of interest that are being detected or quantified and that need not be specific molecules with a known individual identity." (*See* D.I. 366 at 24)

B. Step Two: Comparing the Properly Construed Claims to the Allegedly Infringing Products

With the proper construction of "target molecules" determined, the Court now turns to the parties' infringement-related arguments. While matters of claim construction, even when raised in the context of analyzing infringement, are questions of law for the Court to decide, the ultimate question of whether or not the Accused Products infringe is a question of fact. *Innovention Toys, LLC v. MGA Ent., Inc.*, 637 F.3d 1314, 1318-19 (Fed. Cir. 2011). Therefore, the Court must determine whether Parse has succeeded in showing that, as a matter of undisputed fact, its Accused Products do not infringe the asserted claims.

In general, Parse's non-infringement arguments are premised on that idea that "whole transcriptome" sequencing (which is undisputedly what the Parse Accused Products do) is an *untargeted* approach to labeling "target molecules" (or "nucleic acid targets"). (D.I. 325 at 23) Put another way, Parse's position is as follows:

D.I. 366 at 26) Whatever teaching this article provides is simply too far afield from our inquiry here, which is about what is the meaning of the term "target molecules" as described in the asserted patents' specifications. *See Cont'l Cirs. LLC v. Intel Corp.*, 915 F.3d 788, 799 (Fed. Cir. 2019) (noting that such a source is generally "not reliable enough to be dispositive"); (D.I. 366 at 26 ("The non-patent publication co-authored by Dr. Nolan is likewise irrelevant to the way that 'target molecules' is defined in the common specification of the [asserted patents.]")). The same applies to Dr. Albert's testimony, as the testimony of a non-inventor scientist is not particularly relevant to how the specification of the asserted patents defines "target molecules." (D.I. 366 at 26)

- By using the terms "target molecules" and "nucleic acid targets," the asserted claims require the "specific molecule of interest" to have "a known individual identity[.]" (D.I. 325 at 32)

- The Parse Accused Products are used to label all RNA molecules found within a given cell by binding poly-T and random hexamer primers to each RNA. (*Id.*; D.I. 320 at ¶ 3-5)

- Poly-T or random hexamer primers will simply bind to any and all RNA molecules that at any point in their structure contain a single strand of nucleotides with a complementary sequence to the poly-T or random hexamer primer. (D.I. 320 at ¶¶ 6-7; D.I. 328, ex. 12 at ¶ 59; D.I. 328, ex. 10 at ¶ 110)

- Therefore, the whole transcriptome approach to labeling in the Accused Products does not practice the asserted claims because the individual identity (i.e., some distinguishing sequence) of the RNA molecules being targeted is not known *a priori*. (D.I. 325 at 33)

However, such an argument unravels here because the Court has disagreed with Parse's proposed construction of "target molecules" and "nucleic acid targets." So the relevant inquiry is whether there is a dispute of fact as to whether the Parse Accused Products meet each and every limitation of the asserted claims *under the proper construction* of those terms—i.e., "[nucleic acid] molecules of interest that are being detected or quantified [and] need not be specific molecules with a known individual identity."

Scale argues that it is improper to say that the Accused Products do not label "target molecules" or "nucleic acid targets" under its proposed construction adopted by the Court herein. (D.I. 366 at 29) The "molecules of interest that are being detected or quantified" by the Accused Products can readily be defined as all mRNA molecules within the cell. (*Id.* at 29-30; D.I. 326, ex. 14 at ¶ 141) By using various types of primers composed of nucleic acid sequences (i.e., poly-T primers and random hexamer primers), the Accused Products can be said to only "target" the mRNA molecules present in the cell, as these primers are incapable of binding to the proteins, lipids, or double-stranded DNA also contained therein. (D.I. 366 at 30; D.I. 326, ex. 14

at ¶¶ 141-43; D.I. 376, ex. C at 174) Thus, as Parse seems to concede, under the meaning of the claim terms adopted by the Court, there is at least a material dispute of fact as to whether "the transcriptome of a cell [can] be considered 'target molecules.'" (D.I. 395 at 19)

Therefore, the Court finds that there is a dispute of fact as to that particular question—i.e., whether the Accused Products perform the labeling of "target molecules" or "nucleic acid targets" as directed by the asserted claims. And this prevents Parse from prevailing on its Motion.

IV. CONCLUSION

For the foregoing reasons, the Court DENIES Parse's Motion. An appropriate Order will issue.