United States District Court,
N.D. California.

APPLERA CORPORATION-Applied Biosystems Group, a Delaware corporation,
Plaintiff.
v.
ILLUMINA, INC., a Delaware corporation, Solexa, Inc., a Delaware corporation, and Stephen C. MacEvicz, an individual,
Defendants.

No. C 07-02845 WHA

Feb. 21, 2008.

Anders Tingulstad Aannestad, David C. Doyle, Steven Emerson Comer, Brian Matthew Kramer, Morrison & Foerster LLP, San Diego, CA, Bryan Joseph Wilson, Eric Chingyun Pai, Morrison & Foerster LLP, Dara Tabesh, Attorney at Law, Palo Alto, CA, Kurtis David MacFerrin, Applera Corporation-Applied Biosystems, Foster City, CA, for Plaintiff.

Gregory E. Stanton, Attorney at Law, John Randolph Labbe, Thomas Irving Ross, Cullen Nelson Pendleton, Jeffrey H. Dean, Kevin Michael Flowers, Marshall, Gerstein & Borun LLP, Chicago, IL, Kimberly K. Dodd, Foley & Lardner LLP, Palo Alto, CA, for Defendants.

CLAIM CONSTRUCTION ORDER

WILLIAM ALSUP**, District Judge.**

INTRODUCTION

This is a claim construction order for United States Patent Nos. 5,750,341 and 6,306,597. This order addresses the six phrases selected for construction by the parties. A technology tutorial, as well as a full round of briefing and a hearing, preceded this order.

STATEMENT

Defendant Solexa, Inc., is the assignee of the '341 patent, '119 patent, and the '597 patent. The patents are directed towards methods of learning unknown sequences in DNA. DNA consists of a long polymer of simple units called nucleotides. Each nucleotide in human DNA consists of a deoxyribose sugar linked to both a phosphate group and one of four characteristic nitrogen "bases": adenine (A), cystosine (C), guanine (G), or thymine (T). The deoxyribose sugar has five carbons, numbered 1' to 5', respectively. It is the *sequence* of these bases that encodes information about the functioning of living organisms. The bases bond with one another, or "hybridize," to create a structure known as a double helix consisting of two intertwined strands of DNA. These two strands are perfectly complementary to one another, such that A bonds with its complement T and C bonds with its complement G.

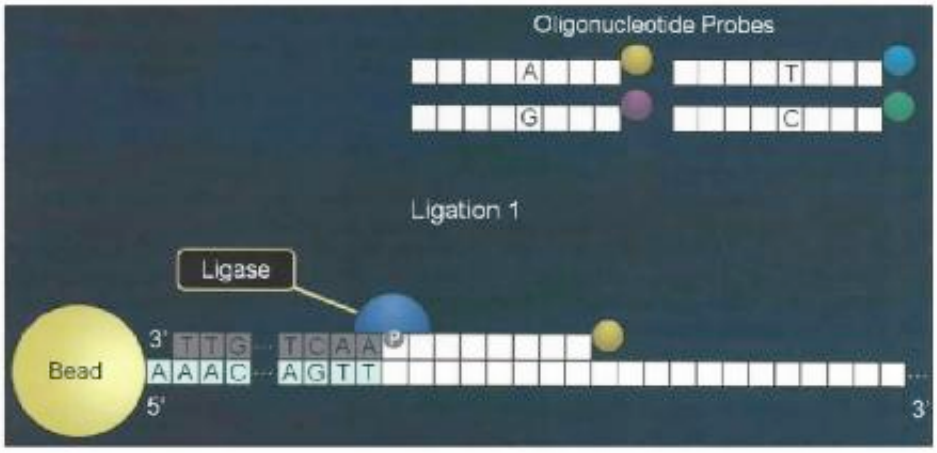
When a single strand of DNA exists in isolation, its sequence is unknown, *i.e.,* the exact lineup of the A, C, G, and T's is unknown. The patents teach a method whereby a target single strand of DNA may be sequenced, *i.e.,* the lineup of A, C, G, and T's may be exactly discovered.

A method used in the prior art for DNA sequencing was known as "Sanger sequencing." In a single DNA strand, adjacent nucleotides are chemically bonded. A dideoxynucleotide, or a ddNTP, is a type of nucleotide that lacks the hydroxyl group of a standard deoxynucleotide, or a dNTP. The lack of this hydroxyl group means that when a ddNTP is added to a sequence of DNA on a strand no further nucleotides, a ddNTP or a dNTP, may be added. The Sanger sequencing method made use of this chemical property. In Sanger sequencing, each base (*e.g.,* A, C, G, and T) was assigned a fluorescent color and the target DNA to be sequenced was bonded with a known DNA sequence. The known DNA sequence was then hybridized by an initializing primer, which added stability to the entire structure. Several strands of the target DNA were then brought into contact with single probe ddNTPs and dNTPs. The result was that several strands of the target DNA would hybridize to the different probes at various points on the DNA strand. Because ddNTPs halt further hybridization on any given single strand of the target DNA, many strands would have varying lengths depending on where the ddNTP hybridized. Some strands that hybridized with the target would be longer (*i.e.,* a ddNTP hybridized at a much later point in the sequence) and some would be shorter (*i.e.,* a ddNTP hybridized at a much earlier point in the sequence). These several strands that hybridized to the target DNA were then collected and placed in a capillary tube to form a group of strands of varying lengths. A magnetic field was then placed on the capillary tube causing the various strands to line up in order of length (*e.g.,* shortest to longest). Each individual strand would then be taken out of the tube and put through a light source which allowed the user to identify the fluorescent light associated with the ddNTP of that sequence. Because the varying strands were lined up according to their length, the user would go through strand by strand to decode each color, and hence base, associated with each nucleotide of the sequence in the correct order, thereby allowing the perfect complement to the target DNA sequence to be determined. In sum, the Sanger sequencing method allowed a target DNA strand to be sequenced by associating fluorescent labels with specific nucleotides that had hybridized with the target DNA sequence. Once the identities of the nucleotides that hybridized were determined, it was simply a matter of taking their complements to determine the sequence of the target DNA strand.

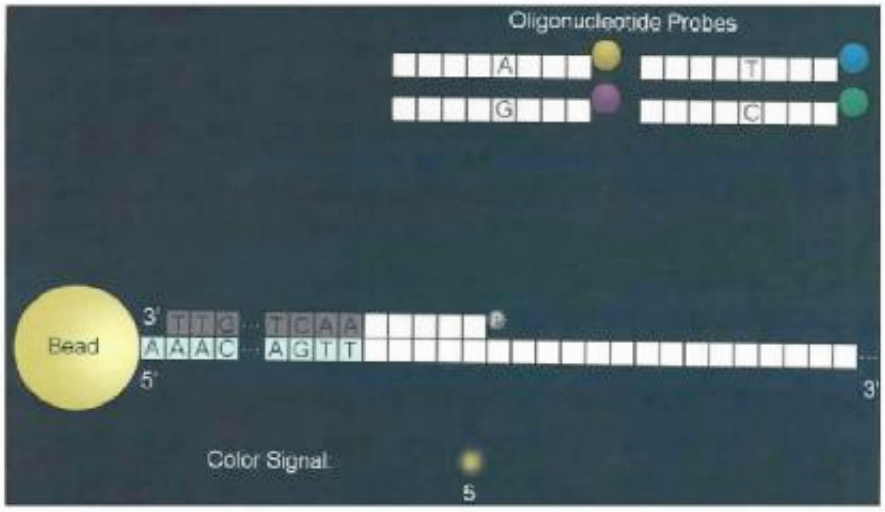
The patent specification teaches a method of DNA sequencing known as "sequencing by ligation" that builds upon the fluorescent-color identification scheme of Sanger sequencing. It begins by attaching the unknown target DNA sequence (along either the 5' to 3' carbon bonds or the 3' to 5' carbon bonds) to a binding region, whose sequence is known, that has already been hybridized by an "initializing oligonucleotide" (col.2:66-3:3) FN1. This collective structure is then attached to a solid support structure called a "bead." The unknown DNA sequence is then brought into a contact with a set of "oligonucleotide probes" that cover "all possible sequences of a predetermined length" (col.6:34-36). For example, if it is determined that the oligonucleotide probes should be eight bases long, then the set of oligonucleotide probes that are brought into contact with the first eight nucleotides of the target DNA sequence will contain all 65,536 (*i.e.,* 4 ^8) possible sequences. Out of these 65,536 possibilities, one will be the perfect complement for the first eight nucleotides of the target DNA sequence. In addition, each oligonucleotide probe in the set of probes is assigned a label corresponding to the identity of one of the bases located in the same position as the other probes (col.3:7-9). To illustrate with the same example, every probe in the set of 65,536 whose fifth nucleotide has a base of A may be assigned a fluorescent color (*e.g.,* yellow) as shown in the figure below. FN2

FN1. Unless otherwise stated, all citations to column and lines numbers in this order refer to the '341 patent.

FN2. Unless otherwise stated, all figures in this order were submitted by the parties as part of the claim construction briefing. The online version of this order is in color.

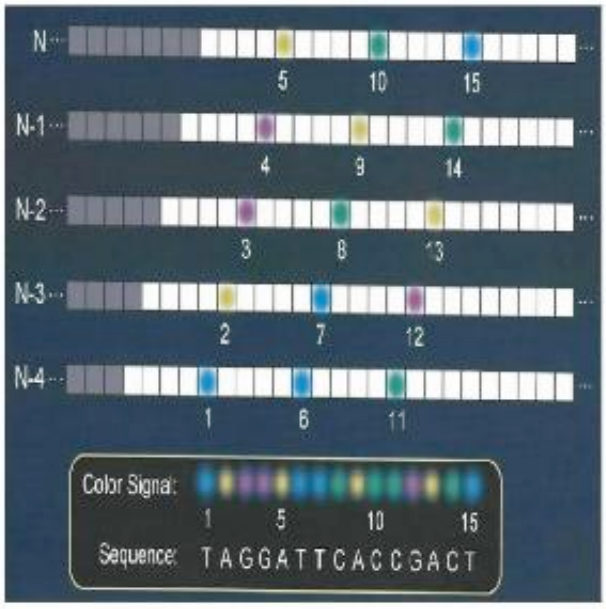


After the set of oligonucleotide probes are brought into contact with the DNA target sequence only the perfectly complementary oligonucleotide probe will hybridize with the DNA target sequence (col.11:49). The oligonucleotide probe which hybridizes with the target DNA sequence is then "ligated" (*i.e.*, glued) using an adhesive, ligase, to the adjacent probe (*e.g.*, the initializing oligonucleotide probe in the first iteration) forming a single longer probe that is more stably hybridized to the unknown DNA target sequence (col.3:3-7). Once the specific oligonucleotide probe has hybridized, the remaining uncomplementary probes can be washed away and the hybridized oligonucleotide probe may be cut at the nucleotide whose base has been designated with a color. The specific oligonucleotide probe that hybridized may then be identified by recording the label that had previously been assigned to it (*e.g.*, yellow) (col.5:10-12). Once the color for the probe is determined, the user then knows the specific identity of a nucleotide in the probe (*e.g.*, the fifth nucleotide is an A).



Repeating this process by ligating further oligonucleotide probes to the previously ligated probe allows additional nucleotide bases in the DNA target sequence to be identified. For instance, if every fifth nucleotide is assigned a color and the process is repeated, then the identity of every fifth nucleotide (*i.e.*, 5, 10, 15, 20, etc.) in the target DNA sequence could be determined.

The oligonucleotide probes can then be shifted one position over from the original starting point to interrogate different nucleotides in the target DNA sequence (*e.g.*, every fourth nucleotide). For example, if the first oligonucleotide probe began hybridizing at position N in the sequence, the next cycle may begin by hybridizing at position N-1. Repeating this process would then allow for identification of every fourth nucleotide (*i.e.*, 4, 9, 14, 19, etc.) in the target DNA sequence to be determined and then every third position for N-2 (*i.e.*, 3, 8, 13, 18, etc.).



Continuing this process ultimately allows for identification of every nucleotide in the target DNA sequence. This method allows a target DNA to be sequenced in much shorter time and with greater accuracy than the prior art.

* * *

This action was filed on May 31, 2007 by Applied Biosystems, alleging that the inventor of the patents had wrongfully assigned them to defendant Solexa who was later acquired by defendant Illumina. Illumina counterclaimed alleging plaintiff infringed the '341 patent, '119 patent, and the '597 patent. The '341 patent was the first out of the group to be filed and issued. The ' 119 patent was filed as a divisional application to the '341 patent. The ' 597 patent is a continuation of the ' 119 patent. Only terms from the ' 341 patent and '597 patent are presented for construction. A technology tutorial was held on January 30, 2008, and a hearing was held on February 13, 2008. Trial is set for September 29, 2008.

ANALYSIS

1. LEGAL STANDARD.

Claim construction is a matter of law to be decided by a judge, not a jury. Markman v. Westview Instruments, Inc., 517 U.S. 370, 388, 116 S.Ct. 1384, 134 L.Ed.2d 577 (1996). Courts must give words in the claims their ordinary and customary meaning, which "is the meaning that the term would have to a person of ordinary skill in the art in question at the time of the invention." Phillips v. AWH Corp., 415 F.3d 1303, 1312-13 (Fed.Cir.2005) (en banc).

Where this ordinary and customary meaning is not immediately clear, courts must primarily look to intrinsic evidence (*i.e.,* the claims, the specification, and the prosecution history) to determine the meaning. Id. at 1314. With respect to the specification, although a difficult task, a court must distinguish "between using the specification to interpret the meaning of a claim and importing limitations from the specification into the claim." Id. at 1323. The latter is not permissible.

Although courts have the discretion to consider extrinsic evidence, including expert and inventor testimony, dictionaries and scientific treatises, such evidence is "less significant than the intrinsic record in determining the legally operative meaning of claim language." Id. at 1317 (citation omitted). "The construction that stays true to the claim language and most naturally aligns with the patent's description of the invention will be, in the end, the correct construction." Id. at 1315. "Nonetheless, any articulated definition of a claim term ultimately must relate to the infringement questions it was intended to answer." E-Pass Tech., Inc. v. 3Com Corp., 473 F.3d 1213, 1219 (Fed.Cir.2007) (citing Wilson Sporting Goods Co. v. Hillerich & Bradsby Co., 442 F.3d 1322, 1326 (Fed.Cir.2006)).

2. DISPUTED CLAIM TERMS AND PHRASES.

AB and Solexa do not stipulate to any definitions prior to the hearing. The parties jointly selected six phrases for construction at this time. Those six phrases are: (1) "initializing oligonucleotide probe;" (2) "ligating an extension oligonucleotide probe to said extendable probe terminus;" (3) "extended oligonucleotide probe;" (4) "identifying;" (5) "just-ligated extension probe;" and (6) "repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined."

All of the disputed terms and phrases appear in claim 1 of the '341 patent. It recites (col.21:36-65):

1. A method for determining a sequence of nucleotides in a target polynucleotide, the method comprising the steps of:

(a) providing a probe-target duplex comprising an *initializing oligonucleotide probe* hybridized to a target polynucleotide, said probe having an extendable probe terminus;

(b) *ligating an extension oligonucleotide probe to said extendable probe terminus,* to form an extended duplex containing an *extended oligonucleotide probe;*

(c) *identifying,* in the extended duplex, at least one nucleotide in the target polynucleotide that is either (1) complementary to the *just-ligated extension probe* or (2) the nucleotide residue in the target polynucleotide which is immediately downstream of the extended oligonucleotide probe;

(d) generating an extendable probe terminus on the extended probe, if an extendable probe terminus is not already present, such that the terminus generated is different from the terminus to which the last extension probe was ligated; and

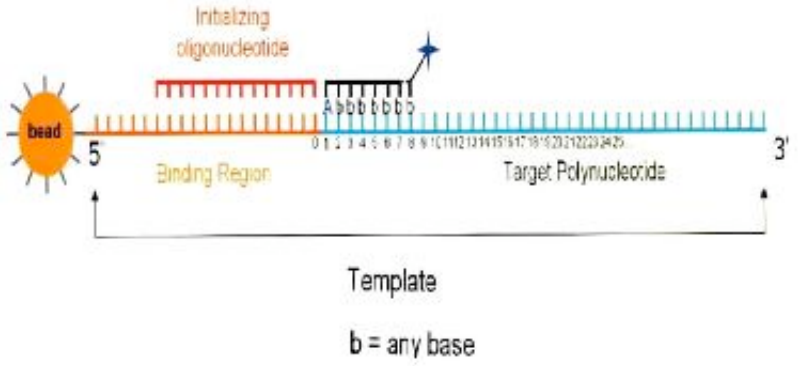
(e) *repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined.*

A. "Initializing Oligonucleotide Probe."

Solexa proposes that "initializing oligonucleotide probe" should mean "the oligonucleotide probe that hybridizes to a known sequence in a polynucleotide and establishes registration for extension." AB proposes that the term should mean "the oligonucleotide to which the first extension oligonucleotide probe will be ligated." The problem with Solexa's construction is that it is expressly proscribed by the language of the claim. To be sure, the specification teaches a different method than what is claimed, but the law is full of patents that claim less than taught in the specification (and, sadly, vice versa). The specification teaches (col.5:13-27):

Binding region (40) has a known sequence, but can vary greatly in length and composition. It must be sufficiently long to accommodate the hybridization of an initializing oligonucleotide .... Preferably, the binding region should be long enough to accommodate a set of different initializing oligonucleotides, each hybridizing to the template to produce a different starting point for subsequent ligation.

The specification further states, "[p]referably, a target polynucleotide is conjugated to a binding region to form a template, and the template is attached to a solid phase support ..." (col.8:8-10). The language makes clear that a binding region and the target polynucleotide are connected, and together form the template.



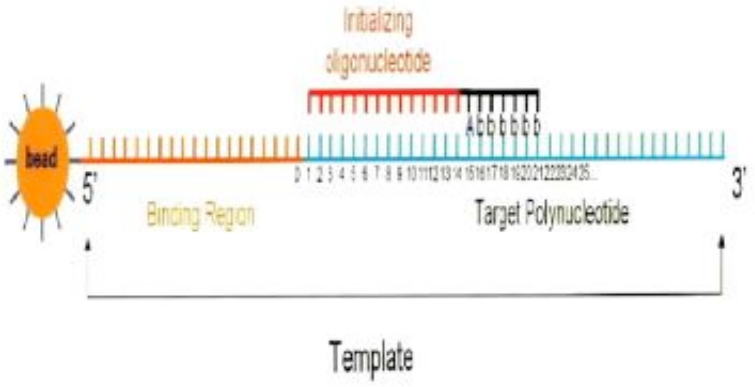
As Described in the '341 Specification

The binding region, target polynucleotide, and template are each distinct items. The initializing oligonucleotide then hybridizes with the binding region, a known sequence, and subsequent ligations are done.

Claim 1, however, states (col.21:38-41):

(a) providing a probe-target duplex comprising an initializing oligonucleotide probe *hybridized to a target polynucleotide*, said probe having an extendable probe terminus;

The claim language expressly provides that the initializing oligonucleotide probe hybridizes to a target polynucleotide, which is clearly not always a fully-known sequence.



As Described in Claim 1 of the '341 Patent

After much study of the specification, the undersigned judge is of the view that the inventor, patent counsel, and the examiner all made a drafting error. While it is tempting to just fix it up in the claim construction process, that temptation would be dangerous course, for it should be up to the PTO in the first instance to amend claims. As the Federal Circuit has held, "courts may not redraft claims, whether to make them operable or to sustain their validity." Chef America v. Lamb-Weston, Inc., 358 F.3d 1371, 1374 (Fed.Cir.2004). Even "a nonsensical result does not require the court to redraft the claims." Process Control Corp. v. Hydreclaim Corp., 190 F.3d 1350, 1357 (Fed.Cir.1999). It may be that, once redrafted, the examiner might recognize prior art problems that escaped attention before. The express language of the claim must govern. Solexa's construction must be rejected.

AB's construction also slightly misses the mark because it fails to take into account that the first extension oligonucleotide probe is ligated to the initializing probe *and* the second extension probe. As the specification teaches, "such extension starts from duplex formed between an initializing oligonucleotide and the template" (col.3:1-3). From there, subsequent ligations are made. The meaning for the term should thus take into account that the initializing oligonucleotide probe is the starting point for subsequent ligations.

Accordingly, the term "initializing oligonucleotide probe" is held to mean "the oligonucleotide to which the first extension oligonucleotide probe is first ligated."

B. "Ligating An Extension Oligonucleotide Probe To Said Extendable Probe Terminus."

The next battle is over the word "said," more particularly the phrase "said extendable probe terminus" in subparagraph (b). The issue comes down to whether the view of "said" is taken literally to refer only to the preceding subparagraph (a) or whether we take into account the iterative process called out by the claim whereby paragraphs (b) through (d) are repeated and the referent for "said" is viewed as in paragraph (d). The latter is correct and this time Solexa has the better argument.

Solexa proposes the term "ligating an extension oligonucleotide probe to said extendable probe terminus" should mean "forming a covalent bond between an extension oligonucleotide probe and the extendable probe terminus of either an initializing oligonucleotide or an extended oligonucleotide probe while hybridized to a target polynucleotide."

AB contends that Solexa's proposed construction is once again contradicted by the express language of the

claim. Specifically, the term refers to "*said* extendable probe terminus" (col.21:42-43) The only other preceding use of the term "extendable probe terminus" is in step (a) of the claim 1, which states, "providing a probe-target duplex comprising an initializing oligonucleotide probe hybridized to a target polynucleotide, said probe having *an extendable probe terminus*" (col.21:37-40). AB argues that Solexa's construction rewrites the claim term from "said extendable probe terminus" to "an extendable probe terminus" because step (a) of claim 1 expressly requires that the extendable probe terminus must be that of the initializing oligonucleotide probe. Accordingly, AB proposes that the term should mean "forming a covalent bond between a short oligonucleotide probe and the extendable probe terminus of the initializing oligonucleotide of step 1(a)"

The problem with AB's argument and construction is that they are inconsistent with the remaining steps of the claim and take steps (a) and (b) of claim 1 in isolation. "While certain terms may be at the center of the claim construction debate, the context of the surrounding words of the claim also must be considered in determining the ordinary and customary meaning of those terms." ACTV, Inc. v. Walt Disney Co., 346 F.3d 1082, 1088 (Fed.Cir.2003); *see also* Hockerson-Halberstadt, Inc. v. Converse Inc., 183 F.3d 1369, 1374 (Fed.Cir.1999) ("Proper claim construction, however, demands interpretation of the entire claim in context, not a single element in isolation"). Claim 1 goes on to state, "(e) repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined" (col.21:55-56). AB's construction would require that all extension probes be ligated only to the initializing oligonucleotide. But because ligations to the initializing oligonucleotide probe occur during the first iteration of steps (b)-(d), it would be impossible to repeat the process as directed by step (e), making step (e) entirely superfluous and the claim internally inconsistent at all times. It is significant that step (a) of claim 1 is only performed once, *i.e.,* step (e) of claim 1 does not refer to step (a).

Step (d) of claim 1 makes clear that the identity of the oligonucleotide with an extendable probe terminus to which extension oligonucleotide probes attach changes depending on which iteration is currently being processed. After identifying the probe that hyrbridized to the target sequence the claim proceeds to the next step of (col.21:50-54):

(d) generating an extendable probe terminus on the extended probe, if an extendable probe terminus is not already present, such that the terminus generated is different from the terminus to which the last extension probe was ligated;

A new extendable probe terminus is thus generated on each cycle as required by step (e), meaning the "*said* extendable probe terminus" of step (b) refers to whatever extendable probe terminus was generated on the previous cycle in step (d). Because step (e) does not require step (a) to be repeated, the "said" refers to the "extendable probe terminus" created in (d). The specification further provides, "[g]enerally, the oligonucleotide probes should be capable of being ligated to an initializing oligonucleotide or extended duplex to generate the extended duplex of the next extension cycle ..." (col.5:17-6:2). Solexa's proposed construction sufficiently captures this procedure.

This order holds "ligating an extension oligonucleotide probe to said extendable probe terminus" means "forming a covalent bond between an extension oligonucleotide probe and the extendable probe terminus of either an initializing oligonucleotide or an extended oligonucleotide probe while hybridized to a target polynucleotide."

C. "Extended Oligonucleotide Probe" And "Just-Ligated Extension Probe."

The parties' disagreement over the terms "extended oligonucleotide probe" and "just-ligated extension" centers around the same argument regarding the meaning of the term "ligating an extension oligonucleotide probe to said extendable probe terminus." The term "extended oligonucleotide probe" appeared in step (b) of claim 1. It recites, "ligating an extension oligonucleotide probe to said extendable probe terminus, to form an extended duplex containing an *extended oligonucleotide probe*" (col.21:42-44). AB argues under the same reasoning employed for its proposed construction for "ligating an extension oligonucleotide probe to said extendable probe terminus" that the "extended oligonucleotide probe" must always be the product of the extension oligonucleotide probe of step (b) ligating to the initializing oligonucleotide probe of step (a). Similarly, AB contends that the "just-ligated extension probe" means "the extension oligonucleotide probe of step (b) that was ligated within that cycle to the initializing oligonucleotide of step (a)" The parties essentially agree that the "just4igated extension probe" is the oligonucleotide probe that was just ligated within the current iteration, but they part company as to what it is ligated to. AB urges that because step (b) refers to "said extendable probe terminus" the "just4igated extension" must be ligated to the initializing oligonucleotide probe. Solexa argues that the "just4igated extension" may be ligated to either the initializing oligonucleotide probe or other extension probes that were ligated on previous cycles.

For the same reasons analyzed above, AB's construction must be rejected. Step (d) of claim 1 requires that the previous steps be repeated such that further extension probes are ligated to the current extended duplex to form the next extended duplex. The specification states, "the oligonucleotide probe probes should be capable of being ligated to an initializing oligonucleotide *or* extended duplex to generate the extended duplex of the next extension cycle ..." (col.5:66-6:2). Requiring all extension oligonucleotide probes to be ligated to the initializing probe would be inconsistent with this process.

Accordingly, this order holds that "extended oligonucleotide probe" means "an initializing oligonucleotide probe effectively extended by one or more nucleotides" and "just-ligated extension probe" means "the extension oligonucleotide probe ligated to either the initializing oligonucleotide probe or an extended oligonucleotide probe in the present cycle of the method."

D. "Identifying."

The parties spill much ink over how the term "identifying" should be construed. The term appears in claim 1 of the '341 patent and claim 1 of the '597 patent in the same context. Step (c) of claim 1 recites:

identifying, in the extended duplex, at least one nucleotide in the target polynucleotide that is either (1) complementary to the just-ligated extension probe or (2) the nucleotide residue in the target polynucleotide which is immediately downstream of the extended oligonucleotide probe;

The parties dispute is generally over how specific of an identification the claim requires. Solexa urges that "identifying" should mean "obtaining information sufficient to distinguish." AB proposes that "identifying" should mean "within each cycle determining the identity of a base, as either A, T, G, or C, in the target polynucleotide." AB's candidate, this order holds, is closer to the true mark.

For Solexa the word "identifying" can include merely gathering information that could eventually be used to distinguish between nucleotides even if insufficient to make a precise determination in the (b) to (e) cycle. Such a broad construction is not supported by the specification. The specification teaches (col.3:7-10):

During each cycle, the identity of one or more nucleotides in the template is determined by a label on, or

associated with, a successfully ligated oligonucleotide probe.

The specification further explains (col. 6:14-33 (emphasis added)):

Generally, the oligonucleotide probe need not form a perfectly matched duplex with the template, although such binding is preferred. In preferred embodiments in which *a single nucleotide in the template is identified* in each extension cycle, perfect base pairing is only required for identifying that particular nucleotide.... Likewise, in embodiments that rely on polymerase extension for *base identification,* the probe primarily serves as a spacer, so specific hybridization to the template is not critical, although it is desirable.

In his first office action with the USPTO, Inventor Stephen Macevicz overcame a prior art reference, Brennan, by arguing (Pai. Decl. Exh. D at 11):

Brennan et al. also teaches preparing long chains of labeled oligonucleotides which are digested by exonuclease to derive sequence information. Nowhere does this reference suggest iterative cycles of single-probe ligation and target nucleotide identification in a probe-target duplex, in accordance with the present invention.

Collectively, this language indicates that the very purpose of the identification process is to determine the base of specific nucleotides in the target polynucleotide during each iterative cycle. This process is then repeated as required by claim 1 until "the sequence of the target polynucleotide is determined" (col.18:16-17).

Solexa cites nothing in the specification that indicates identity should mean anything other than determining the base for a specific nucleotide. At the claim construction hearing, Solexa highlighted that the examples given in the specification employ the patented invention to sequence target DNA strands whose sequences are fully known. For instance, the specification shows how the patented method may be used to sequence pUC19, whose sequence was well known in the prior art (col.14:43). Solexa argues that these examples show that identifying does not mean base identification because the examples involve sequences whose bases are known. The examples, however, are shown in the specification to show how the patented invention works and to confirm its operation with a known DNA sequence. Logically, why would a user want to use the claimed method, whose express purpose is "determining the nucleotide sequence of a polynucleotide" (col.1:5-6), to sequence a target DNA strand that is already full known in the prior art? Solexa's argument is a far stretch.

Solexa next wrongly relies on the following excerpt from the specification (col.3:53-60):

As used herein 'sequence determination,' 'determining a nucleotide sequence,' 'sequencing,' and like terms, in reference to polynucleotides includes determination of partial as well as full sequence information of the polynucleotide. *That is, the term* includes sequence comparisons, fingerprinting, and like levels of information about a target polynucleotide, as well as the express identification and ordering of each nucleoside of the test polynucleotide.

Significantly, this express definition *does not* define the word "identifying." Solexa contends that this language shows that the term "identity," includes both "partial as well as full sequence information of the polynucleotide," thereby supporting their proposed construction because the terms "determining" and "identity" are used interchangeably in the patent. Solexa's argument is unsupported by the express language

of the definition. The definition indicates that "identification" was meant to be a more narrow term than the terms defined because it is included as a smaller subset to those terms. While the definition does include both partial and full sequence information, it only applies to the broader terms defined. In addition, even if the term "identifying" encompassed both partial and full sequence information, Solexa's construction would still be unsupported. Obtaining partial sequencing information does not mean "obtaining information sufficient to distinguish" as Solexa would have it. It simply means that only part of the sequence that is targeted for sequencing is identified, *i.e.,* only a portion of nucleotides in the sequence are identified by base. If identification beyond the bases of a nucleotide was meant to be claimed, the prosecutor could have readily claimed it by stating "sequencing" instead of "identifying" or by expressly saying information beyond base identification in the claim.

AB's proposed construction for "identifying," "within each cycle determining the identity of a base, as either A, T, G, or C, in the target polynucleotide," while generally in line with the specification, has a few minor problems. For clarity sake, the definition should make certain that more than one nucleotide may be identified during each cycle. This is expressly written in the claim, which states: "identifying ... *at least one* nucleotide in target polynucleotide ..." (col.21:45-46). AB's construction states "the identity of *a* base," which may be interpreted as only a single base being identified each cycle. In addition, as AB concedes, the definition should not be limited to the four bases of DNA because the specification also teaches that the invention may be used to sequence RNA, which has uracil as one its bases instead of thymine.

Accordingly, the term "identifying" is held to mean "within each cycle determining the identity of a base in the target polynucleotide."

E. "Repeating Steps (b), (c) And (d) Until A Sequence Of Nucleotides In The Target Polynucleotide Is Determined."

AB proposes that the term "repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined" should mean "completing, and then performing again, exactly what is described in steps (b), (c), and (d) until two or more nucleotides in the unknown sequence that is targeted for analysis are identified." Implicitly within this definition AB has defined "target polynucleotide" as necessarily containing a fully-unknown sequence. Such a limitation, however, cannot be read into the claim. AB primarily relies on one embodiment of the invention taught in the specification. The specification states, "[p]referably, a target polynucleotide is conjugated to a binding region to form a template ..." (col.8:8-10).

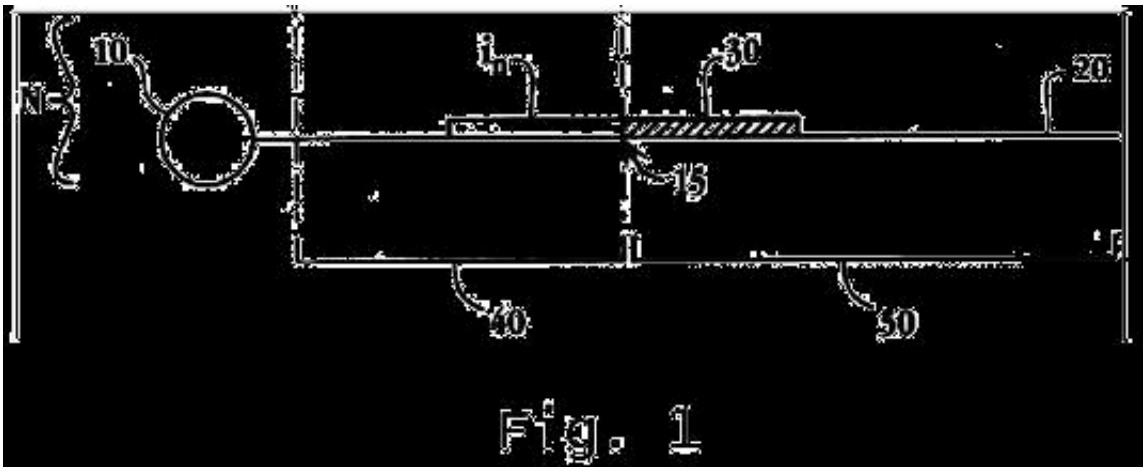


Fig. 1

In explaining Figure 1 above, the specification further teaches: "[t]emplate (20) comprising a *polynucleotide of unknown sequence* and binding region (40) is attached to solid support (10)" (col.4:46-48). AB urges that this description shows that the target polynucleotide must necessarily be a fully-unknown sequence. As the specification made clear, however, "the invention is not meant to be limited by the particular features of this embodiment" (col.4:45-46). Nowhere in the specification does it state that the target polynucleotide must always be a fully-unknown sequence. At times, the sequence may very well be a partially-known sequence that the user desires to be further sequenced. AB's construction does not comport with this possibility.

Solexa proposes the term should mean "repeating steps (b), (c), and (d) until partial or complete sequence information of the target polynucleotide is obtained, including, for example, sequence comparisons, fingerprinting, and like levels of information, as well as the express identification and ordering of nucleotides." Solexa's proposed construction is hopelessly long and complicated given the clear-cut language of the term being construed. This order finds that the term "repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined" requires no construction and may be sufficiently understood by a layperson without any guidance from this Court.

As such, the term "repeating steps (b), (c) and (d) until a sequence of nucleotides in the target polynucleotide is determined" shall have its ordinary and plain meaning.

CONCLUSION

This claim construction order will govern for the remainder of this action.

IT IS SO ORDERED.

N.D.Cal.,2008.
Applera Corp. v. Illumina, Inc.