

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

Ex parte ARIE ABO and AMI ARONHEIM

Appeal 2008-3328
Application 10/330,372
Technology Center 1600

Decided: May 29, 2008

Before DEMETRA J. MILLS, ERIC GRIMES, and LORA M. GREEN,
Administrative Patent Judges.

GREEN, *Administrative Patent Judge.*

DECISION ON APPEAL

This is a decision on appeal under 35 U.S.C. § 134 from the Examiner's final rejection of claims 6, 45, 49, and 51.¹ We have jurisdiction under 35 U.S.C. § 6(b). Claim 6 is representative of the claims on appeal,

¹ Claims 1, 3-8, 45-49, 51, and 52 appear to be pending, with claims 2, 9-44, and 50 being cancelled, and claims 1, 3-5, 7, 8, 46-48, and 52 being indicated as being allowable (Br. 5).

and claim 6, along with claim 1, from which claim 6 depends, are reproduced below:

1. An isolated full-length Chp polypeptide, or a polypeptide fragment thereof, wherein (i) said Chp polypeptide or polypeptide fragment thereof has about 95% or greater identity to the amino acid sequence presented as SEQ ID NO: 2, and (ii) said Chp polypeptide or polypeptide fragment thereof has at least one biological activity selected from the group consisting of a PAK regulatory domain binding activity, a PAK kinase stimulatory activity, a JNK kinase stimulatory activity, a cytoskeletal-reorganizing activity, a Chp-specific immunogenic activity directed to SEQ ID NO:2 and combinations thereof.

6. The isolated Chp polypeptide or polypeptide fragment of claim 1, wherein said fragment consists essentially of a polypeptide having a sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:12, and SEQ ID NO:13.

Claims 6, 45, 49, and 51 stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that applicants regard as the invention.

The Examiner objects to the use of the transition phrase “consisting essentially of.” (Ans 4.) In making the rejection, the Examiner relies on an alignment of SEQ ID NO: 2 with SEQ ID NOs: 6, 7, 8, 9, 12, and 13 performed at the PTO using the Smith-Waterman algorithm.

The application was remanded to the Examiner on October 23, 2007, because the alignment relied upon was not in the record. In the remand (Remand 4), we cited page 9 of the Specification, which stated that “[t]he sum of the identical and homologous residues divided by the total number of residues in the sequence over which the Chp polypeptide is compared is

equal to the percent sequence similarity.” (Spec. 9:14-17.) We also noted that:

Both the Examiner and Appellant[s] appear to agree that is the definition by which sequence identity is to be determined (Br. 15-17; Answer 6). The disagreement appears to be how the language “by the total number of residues in the sequence over which the Chp polypeptide is compared,” *i.e.*, the denominator of the equation by which sequence identity is determined. According to the Examiner, that number is always 236 amino acids (*see, e.g.*, Answer 7), and according to Appellants that number is the number of residues of the overlap region (*see, e.g.*, Br. 19-20). Appellants present FASTA comparisons comparing SEQ ID NOs:2, 6, 7, 8, 9, 12, and 13 to SEQ ID NO:2, in which 100% sequence identity is obtained over the overlap region.

We think Appellants have the better argument. The FASTA comparisons submitted by Appellants demonstrate that it is not repugnant in the art to determine sequence identity based on the number of residues in the overlap region. In addition, as noted above, the Specification defines the denominator as “the total number of residues in the sequence over which the Chp polypeptide is compared.” The Examiner’s interpretation reads out the portion “over which the Chp polypeptide is compared.”

(Remand 4-5 (footnote omitted)).

In response to the Remand, the Examiner added the alignment of SEQ ID NO: 2 with SEQ ID NOs: 6, 7, 8, 9, 12, and 13 performed at the PTO using the Smith-Waterman algorithm to the record. In response to the comments of the panel, the Examiner asserts that the comparison is always to the 236 amino acids of SEQ ID NO:2 because that is required by claim 1, which requires “95% or greater identity to the amino acid sequence presented as SEQ ID NO: 2;” that is, according to the Examiner, the overlap region is the entire SEQ ID NO:2 (Response to Remand 2). Appellants

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respond that, as defined in the Specification, “when a Chp polypeptide fragment is compared to SEQ ID NO:2 to determine if it has 95% or greater identity the length of the sequence over which the Chp polypeptide is compared is the length of the Chp polypeptide fragment sequence.” (Reply Brief 5, dated January 2, 2008).

As we noted in the Remand,

“The test for definiteness is whether one skilled in the art would understand the bounds of the claim when read in light of the specification.” *Miles Laboratories, Inc. v. Shandon, Inc.*, 997 F.2d 870, 875, 27 USPQ2d 1123, 1126 (Fed. Cir. 1993). Claims are in compliance with 35 U.S.C. § 112, second paragraph, if “the claims, read in light of the specification, reasonably apprise those skilled in the art and are as precise as the subject matter permits.” *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1385, 231 USPQ 81, 94-95 (Fed. Cir. 1987). Moreover, it is axiomatic that Appellants may act as their own lexicographer. *See Merck & Co., v. TEVA Pharmaceuticals USA, Inc.*, 395 F.3d 1364, 1369-70, 73 USPQ2d 1641, 1646 (Fed. Cir. 2005).

(Remand 3-4.)

Again, we find that Appellants have the better argument, and that in light of the Specification, one would understand the metes and bounds of claim 6, as well as claims 45, 49, and 51. The rejection is thus reversed.

REVERSED

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