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UNITED STATES PATENT AND TRADEMARK OFFICE

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Trademark Trial and Appeal Board

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In re Paracel, Inc.

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Serial No. 78079533

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Jorge C. Barreno for Paracel, Inc.

Howard B. Levin, Trademark Examining Attorney, Law Office 115  
(Tomas V. Vlcek, Managing Attorney).

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Before Seeherman, Hanak and Walters, Administrative Trademark  
Judges.

Opinion by Hanak, Administrative Trademark Judge:

Paracel, Inc. (applicant) seeks to register in typed drawing form TRANSCRIPTASSEMBLER for "computer software used for collection, organization, analysis, integration and communication of scientific data in the field of biotechnology and life science." The intent-to-use application was filed on August 16, 2001.

Citing Section 2(e)(1) of the Trademark Act, the Examining Attorney refused registration on the basis that

applicant's mark is merely descriptive of applicant's computer software. When the refusal to register was made final, applicant appealed to this Board. Applicant and the Examining Attorney filed briefs. Applicant did not request an oral hearing.

A mark is merely descriptive pursuant to Section 2(e)(1) of the Trademark Act if it immediately conveys information about a significant quality or characteristic of the relevant goods or services. In re Gyulay, 820 F.2d 1216, 3 USPQ2d 1009 (Fed. Cir. 1987); In re Bed & Breakfast Registry, 791 F.2d 157, 229 USPQ 818, 819 (Fed. Cir. 1986). Of course, it need hardly be said that the mere descriptiveness of a mark is judged not in the abstract, but rather is judged in relationship to the goods or services for which the mark is sought to be registered. In re Abcor Development Corp., 588 F.2d 811, 200 USPQ 215, 216 (CCPA 1978). Finally, a mark need describe only one significant quality or characteristic of the relevant goods or services in order to be held merely descriptive. In re Gyulay, 3 USPQ2d at 1010.

At pages 3 to 5 of its brief, applicant has provided what it refers to as "a brief technology background." The Examining Attorney has not taken issue with the facts set forth in this background. Applicant notes that for many

years "scientists have been trying to understand the role of genes in the formation of diseases." Applicant states that there are "30,000 more or less known genes." Genes consist of strands of DNA which are "too long and complex to handle for researchers." Thus, "instead of studying an entire gene, researchers work on smaller pieces of each gene." According to applicant, one of the many ways to work on shorter portions of each gene is "to focus on 'transcripts.'" However, applicant states that often times a transcript is "still too long to study given current technology. Thus, researchers look at Expressed Sequence Tag (EST). EST is a small portion of a transcript."

Having provided the Board with the foregoing overview of the relevant technology, applicant commences at page 5 of its brief to explain how its computer software functions. According to applicant, its computer software "clusters and assembles millions of sequences of EST to find the sequences of transcripts." (Emphasis added). At page 6 of its brief, applicant acknowledges that "scientists, researchers, academicians, and other persons involved in life science and biotechnology commonly use the phrase 'transcript assembly.'" Continuing at page 6 of its brief, applicant further acknowledges that "the same scientists, researchers,

academicians, and other persons understand what a speaker or a writer means with the phrase 'transcript assembly,' i.e., the software clusters, organizes information about the sequence of EST to determine the information about the sequence of a piece of gene." At page 8 of its brief, applicant concedes that its "mark is highly suggestive," consisting simply of the "common words" TRANSCRIPT and ASSEMBLER.

Based just upon the foregoing information provided by applicant itself, we find that applicant's mark TRANSCRIPTASSEMBLER is merely descriptive of its computer software which, to use applicant's words, "assembles millions of sequences of EST to find the sequences of transcripts." (Applicant's brief page 5, emphasis added). Moreover, as previously noted, applicant has acknowledged that the phrase "transcript assembly" is commonly used and well understood by scientists and other in fields of life science and biotechnology. (Applicant's brief page 6).

In creating its "mark" TRANSCRIPTASSEMBLER, applicant has merely taken the commonly used and well understood phrase "transcript assembly"; condensed it; and changed the word "assembly" to the related word "assembler." Scientists and others who commonly use the term "transcript assembly" to

describe a particular type of computer software would likewise understand that applicant's "mark" TRANSCRIPTASSEMBLER is but a mere variation of "transcript assembly."

Indeed, while we have no doubt that highly educated scientists and others working in the fields of life science and biotechnology would have absolutely no trouble in readily understanding that the ASSEMBLER portion of applicant's "mark" is but a mere variation of the word "assembly," we also note that the Examining Attorney has made of record evidence showing that others have used the word "assembler" to describe the very type of computer software for which applicant seeks to register the "mark" TRANSCRIPTASSEMBLER. At its website, TIGR (The Institute of Genomic Research) has defined the word "assembler" as follows: "A tool for assembly of large sets of overlapping sequenced data such as ESTs, BACs or small genomes." Indeed, TIGR has produced its own assembler which was described in a publication entitled TIGR Assembler (1995).

Finally, if there is even the slightest doubt that applicant's "mark" TRANSCRIPTASSEMBLER is merely descriptive of computer software which organizes scientific data in the fields of biotechnology and life science, said doubt is

completely removed when one reviews applicant's own advertisement entitled "Paracel TranscriptAssembler™ ... A Complete Solution for Accurate EST Assembly." The first two sentences of this advertisement read as follows: "Paracel TranscriptAssembler™ is a complete, high-capacity solution for EST-based transcript reconstruction. It provides a comprehensive pipeline for all the steps required to accurately filter, mask, cluster and assemble transcripts."

Decision: The refusal to register is affirmed.