From: Berger, Michael D (LDZX) [mailto:Michael.D.Berger@conocophillips.com]
Sent: Tuesday, September 29, 2009 1:15 PM
To: Fawcett, Susan
Subject: COMMENTS: Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures

Dear Susan K. Fawcett,

I appreciate the opportunity to comment and open dialog regarding the Sequence Listings Requirements.

These comments are my own personal comments and are not associated with ConocoPhillips in any way.

The USPTO has not posted this notice on it's official News & Notices pages or the Federal Register (FR) notices page.
http://www.uspto.gov/main/newsandnotices.htm
http://www.uspto.gov/web/menu/current.html

The notice is available here, but it hasn't been referenced or made easily accessible:
http://www.uspto.gov/web/offices/com/sol/notices/74fr40163.htm
http://edocket.access.gpo.gov/2009/pdf/E9-19179.pdf

Shouldn't that content be auto-generated for every USPTO FR Notice? Shouldn't there also be a consolidated page for this FR notice and comments?

Regarding the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures

(a) Whether the proposed collection of information is necessary for the proper performance of the functions of the agency, including whether the information shall have practical utility;
A CRF is required to ensure the Sequence Listing is correct and properly entered into the public sequence databases. Otherwise the public will not have access to the content of the patent.
(b) The accuracy of the agency's estimate of the burden (including hours and cost) of the proposed collection and information;
The agency underestimates the time required to prepare a sequence listing and the level of skill. It's like a translation, you can get an electronic translation but that would not be good enough to submit for a patent application. You can also get a paralegal to prepare a sequence listing, but a science background is required to understand the sequence, coding regions, protein motifs and the like. One single missed nucleotide can change the coding region, to correct that simple error might be considered "new matter" (and has been in many cases). The error often originates from the scientist and without proper sequence analysis might never be caught.
I usually estimate 10-15 minutes per sequence. More if its complicated, has variable characters, non-natural amino acids, or unique motifs.
(c) Ways to enhance the quality, utility, and clarity of the information to be collected; and
PatentIN and Checker are two utilities that the USPTO has really done well with. It may take time to manually enter the Sequence Listing, but once entered manipulating and generating the Sequence listing is fairly straight forward. They could improve the ability of PatentIN to import sequences from a FASTA or other standard format. Working with NCBI on Sequence Listing entry may be very helpful.
(d) Ways to minimize the burden of the collection of information on respondents.
CRFs are required, the applicant should be responsible for entering the CRF and the claims should be directed to the sequences as presented in the CRF. The current statements and

method of entry address that issue directly and with minimal paperwork. A CRF and statement are the minimum requirement.
If they are going to charge fees for sequence listings it should be based on the number of sequences, number of characters, or number of pages. An across the board fee punishes those with well drafted applications and lets those with larger sequence listings abuse the system.

Thank you for your time. Please call or email if you need additional information or have any questions.

Best regards,

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