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Subject: Request for comments on proposed ST.26

In **Federal Register** Vol. 77, No. 94, Tuesday May 15, 2012, you requested comments on the proposed ST.26 standard for the presentation of nucleotide and amino acid sequences, where the standard is being revised to require the use of XML format, to update the standard, and to more closely align requirements of the standard with those of public sequence database providers.

Within the Intellectual Property & Science business of **Thomson Reuters**, in particular within the GENESEQ production team, there has been a very positive response to the proposed ST.26 standard.

In particular, with respect to '(3) Feature Keys and Qualifiers' and '(4) Definition of a Sequence for which a Sequence Listing is required':

- As far as we are concerned, the more information that can be presented in Feature Tables, the better, so we welcome the idea of more focused Feature Keys (only those relevant to patents) and a greater range of associated qualifiers.
- Broader selection of sequences is also welcomed, since the additional sequences available for inclusion (modified nucleotides, D-amino acids and variants) are already within the selection rules for our GENESEQ annotated sequence database product.

Since we are not involved in the patent application process, we can only really comment on the content issues and not the procedural or transitional issues associated with the new standard.

From an XML viewpoint, we welcome any initiative to standardise patent data to a global level (WIPO standard) so that Thomson Reuters development cost in processing the incoming data from various patent offices is minimal.

Regards,

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