

22 January 2019

Dear PSI Editors,

We are pleased to resubmit the proposal for a PSI standard: the PSI Extended FASTA Format (PEFF). We have addressed all the comments from the Steering Group review and many outstanding issues identified during the last spring workshop and in other conversations since. We feel that this proposal is much stronger than the previous one. We include a document that provides a response to all points made by the steering group, and we also provide the new specification draft, both a clean version and a marked up version that shows all changes since the previous submission. With the growing interest in proteogenomics, PEFF neatly addresses in a standardized manner the growing problem challenge of how to encode and use not just the protein sequences, but also the many known annotations on those protein sequences.

With this submission, we provide the following files:

- CoverLetter.docx (this cover letter)
- ResponseToSteeringGroupReview_v1.docx (point-by-point response)
- PEFF_SpecDoc_1.0.draft32.docx (the full specification document)
- PEFF_SpecDoc_1.0.draft32_wMarkup.docx (same document with tracked changes)
- PEFF_Tiny_Valid.peff (updated example file)
- SmallTestDB-PEFF1.0.peff (updated example file)
- PEFF_AnnotID_Insulin_Valid.peff (updated example file)

All these materials and more are available in the PEFF GitHub repository:

<https://github.com/HUPO-PSI/PEFF>

Furthermore, although not included in this submission bundle, PEFF 1.0 files (according to the current draft specification) can already be downloaded from the neXtProt knowledge base, e.g.:

ftp://ftp.nextprot.org/pub/current_release/peff/

or through the web interface:

https://www.nextprot.org/entry/NX_P00738/ (then select download link in upper right and choose PEFF)

https://api.nextprot.org/export/entry/NX_P00738.peff

Furthermore, software supporting PEFF is already being developed. The widely used Comet search engine supports the current draft of PEFF as described here:

http://comet-ms.sourceforge.net/release/release_201701/

(search on page for PEFF)

We hope that you will find these materials suitable for re-entry into the PSI Document Process.

Sincerely,

Pierre-Alain Binz, Centre Hospitalier Universitaire Vaudois

Jim Shofstahl, Thermo Fisher Scientific

Juan Antonio Vizcaíno, EMBL-EBI

Harald Barsnes, Proteomics Unit, University of Bergen

Robert Chalkley, University California San Francisco

Gerben Menschaert, Ghent University, Ghent, Belgium

Karl Clauser, Broad Institute, Cambridge MA, USA

Lydie Lane, Swiss Institute of Bioinformatics

Sean L. Seymour, Seymour Data Science, LLC

Eugene A. Kapp, Walter & Eliza Hall Institute of Medical Research and the University of Melbourne

Eric W. Deutsch, Institute for Systems Biology