

Online *DPI*: a web server to calculate the diffraction precision index for a protein structure. Addendum

K. S. Dinesh Kumar,^a M. Gurusaran,^a S. N. Satheesh,^a P. Radha,^a S. Pavithra,^a
K. P. S. Thulaa Tharshan,^a John R. Helliwell^{b*} and K. Sekar^{a*}

Received 30 July 2026

Accepted 3 August 2026

Keywords: estimated atomic coordinate errors; protein data bank entries.

^aSupercomputer Education and Research Centre, Laboratory for Structural Biology and Biocomputing, Indian Institute of Science, Bangalore 560 012, India, and ^bSchool of Chemistry, University of Manchester, Manchester M13 9PL, UK.

*Correspondence e-mail: john.helliwell@manchester.ac.uk, sekar@iisc.ac.in

From August 2026, the online computing server *Online_DPI* [Kumar *et al.* (2015). *J. Appl. Cryst.* **48**, 939–942] will be hosted by the International Union of Crystallography at <https://dpi.iucr.org/>.

Kumar *et al.* (2015) introduced the online computing server *Online_DPI* to calculate the Cruickshank diffraction precision index and atomic coordinate error for each of the atoms in a given three-dimensional macromolecular structure. The server allows the user to upload the atomic coordinates of a given structure [in Protein Data Bank (PDB) format] or provide the PDB accession code. Full details can be found in the original article.

As Professor Sekar is retiring on 31 July 2026, from August 2026 *Online_DPI* will be hosted by the International Union of Crystallography at <https://dpi.iucr.org/>.

References

Kumar, K. S. D., Gurusaran, M., Satheesh, S. N., Radha, P., Pavithra, S., Thulaa Tharshan, K. P. S., Helliwell, J. R. & Sekar, K. (2015). *J. Appl. Cryst.* **48**, 939–942.

