

Reviewer Report

Title: 3D-Beacons: Decreasing the gap between protein sequences and structures through a federated network of protein structure data resources

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Reviewer Comments to Author:

This manuscript describes in detail the 3D-Beacons platform/initiative, which aims to facilitate access to 3D data as well as meta-information about experimentally determined and computationally predicted protein structure. This resource is very valuable for the broader scientific community in a time where the number of protein structure data available rapidly increases and many structures may be available for the same protein. A minor correction is required on page 7, where the authors describe 4 different types of protein structures: Experimentally determined, Template-based, Ab-initio and Conformational Ensembles. On many examples available on the website (e.g. <https://www.ebi.ac.uk/pdbe/pdbe-kb/3dbeacons/search/P15056>), there is one extra category which is structures derived from "Deep learning" methods. I am assuming this comprises a sub-set of Ab-initio structures, which the authors decided to keep as a separate category after submitting this study for publication. The main text should be updated to reflect this change as well as Figure 4.

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