Announcement of the BioSync web site

We are pleased to announce the BioSync Web resource at *http://biosync.sdsc.edu*. Developed on behalf of the Structural Biology Synchrotron Users Organization (BioSync), this resource serves as a structural biologist's guide to synchrotron facilities. The BioSync organization has collaborated with the San Diego Supercomputer Center to create a comprehensive synchrotron portal and informational web site using modern information practices. Users of the web site can investigate the different technical capabilities of each beamline and find out logistical information such as scheduling and travel arrangements. Synchrotron personnel update the web site regularly to provide current information to the user community and to help guide projects to the appropriate facility. In addition, BioSync is working with the Protein Data Bank (PDB; *http://www.rcsb.org/pdb*) to automatically include beamline specific information with structure depositions. The BioSync web resource strives to provide timely, accurate, and complete information on synchrotron resources to the community of structural biologists. This resource is a part of the National Biomedical Computation Resource, an NIH National Center for Research Resources hosted at the San Diego Supercomputer Center.

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Questions about the structure of the botulinum neurotoxin B light chain in complex with a target peptide

Hanson and Stevens[1] recently reported the cocrystal structure of the botulinum neurotoxin B light chain in complex with a 38-residue target peptide of synaptobrevin II. Based on a careful examination of the published data, we have serious concerns about the strength of experimental evidence supporting the presence of the target peptide, and consequently the validity of inferences about substrate binding made in the report.

The experimental B-factors (PDB entry 1f83) are excessively high for the substrate atoms. Their average B-factor is 128 Å^2, approximately four times the average B-factor for the protease atoms. While B-factors alone do not provide a definitive measure of quality for model features, excessive B-factors for the peptide substrate in this case raise warning signs.

In addition to having excessive B-factors the substrate model does not conform to expected stereochemical restraints. Conformational analysis of the peptide reveals only a few of the 36 modeled peptide residues in most favored regions of the Ramachandran plot while seven peptide residues fall in disallowed regions. While the enzyme may induce a strained peptide conformation, there are scarcely few strong contacts between substrate and enzyme to stabilize such a high-energy conformation. Furthermore, there are few

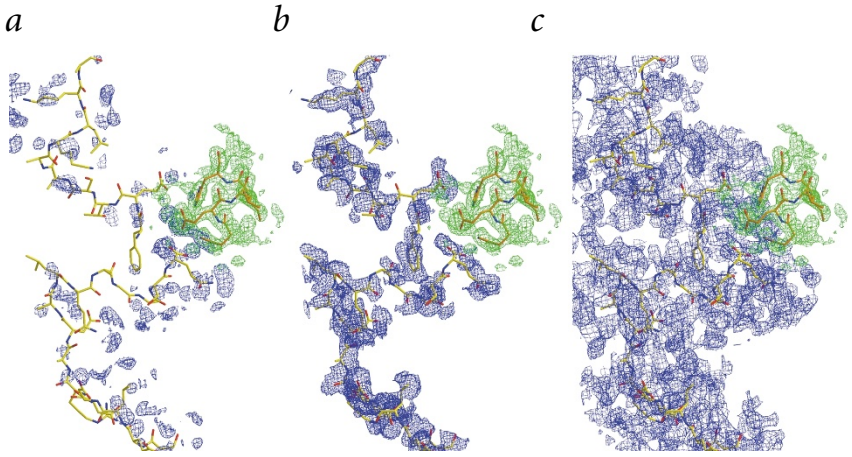

Fig. 1 Electron density for modeled substrate synaptobrevin II and BotB light chain. Orientation of the model fragments, map contour levels and colors approximate Fig. 2 of Hanson and Stevens[1]. ***a***, Electron density of a wARP[3] map. Displayed in blue (1.2 σ level) and within 4 Å (using the 'blob' contouring feature in XtalView[6]) is electron density of the modeled substrate. Shown in green, electron density of the zinc binding HEXXH motif of the botulinum B light chain, but contoured at 2.0 σ and within 3 Å of the binding motif. The wARP[3] map reveals strong and clear electron density that agrees with the enzyme model (green contours) whereas very little electron density for the substrate (blue contours) appears even at the lower contour level. No connectivity from which the features of the modeled substrate could be confirmed is evident. ***b***, CNS[5] σ_A[4] weighted $F_o - F_c$ omit electron density map superimposed on the modeled substrate, with display parameters chosen to generate a view of electron density apparently confirming the presence of the modeled substrate. This electron density map was made by selecting a high grid density for smoothness, a relatively low contour level for connectivity (matching the reported[1] contour level of 1.2 σ), and with a small cutoff radius (1.6 Å) using the 'blob' feature in XtalView[6] to force conformity of the map with the model. ***c***, Same CNS σ_A weighted $F_o - F_c$ omit map as in (*b*), same contour level as reported[1], but with a larger volume displayed. The 'blob' cutoff radius is now set to 4 Å and the electron density map reveals many features not related to the modeled substrate and poor connectivity. At this contour level, the map shows many large positive features even in the core of the protein, indicating that the map is in fact contoured at noise level. From inspection of panels (*a*) and (*c*) we do not believe that it is possible to discern details of the interaction between substrate and enzyme such as are shown in Fig. 3 of Hanson and Stevens[1].