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## **Comparative Analysis of the Subunit Interfaces of a Morpheein for Different Species of Organisms**

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Poster Presentation P25

**COMPARATIVE ANALYSIS OF THE SUBUNIT INTERFACES OF A MORPHEEIN  
FOR DIFFERENT SPECIES OF ORGANISMS**

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A morpheein is a protein that has the ability to exist in multiple monomer conformations dictating structurally and functionally different quaternary structures. The presence of different quaternary structures has provided an explanation for allosteric regulation of protein activity (Jaffe, 2005). Porphobilinogen synthase (PBGS) is currently the only confirmed morpheein, but many other proteins found in the literature display similar characteristics. Further analysis of these putative morpheeins was undertaken using the crystal structures of the enzyme. Occasionally, information pertaining to the enzymatic characteristics of a putative morpheein from one species of organism is available, but the crystal structure is not. Therefore, this study was undertaken to analyze if the subunit interfaces of a putative morpheein existing in two different species of organism were similar enough to assume similar dissociation behavior. If the subunit interfaces between two species of an organism are highly conserved, it is hypothesized that water molecules, which aid in dissociation of the subunits, will accumulate similarly at the interfaces. Hence, dissociation behavior will be similar. The Protein Data Bank was used to attain protein crystal structures and NCBI FASTA sequences were used with the Jalview sequence alignment program to find the conserved sequences between species. Conserved sequences were labeled on the crystal structure using Swiss View PDB and those located at the subunit interfaces were recorded. The percentage of residues conserved at the interface was then calculated. 44.63% of interface residues were conserved for adenylosuccinate lyase, 57.80% were conserved for aristolochene synthase, and 47.69% were conserved for glutamate racemase. These results can be used to indicate the predictability of the dissociation patterns of protein subunits among different species for a particular putative morpheein.