Trying To Deduce Function From Structural Variability And Conservation

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A comparative case is presented for two similar proteins from *Shigella flexneri* and *Bacillus cereus* which are homologs of the *E. coli* protein ybjQ. These two proteins are members of the COG0393, a widely conserved family of proteins in bacteria and archaea that are functionally uncharacterized. All members of the sequence family are about 100 residues. The two examples presented are both homopentamers and have 54% sequence identity. Despite the high sequence identity, the *B. cereus* protein contains regions of structural variation. A sequence alignment of the protein family reveals a pair of

conserved glycines at residues 44 and 45. These conserved glycines are located in a loop that it is a region of structural variation in the *B. cereus* protein. This area of structural variation has been predicted as a region of disorder from the DisEMBL server which may be important to the function of these proteins.



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