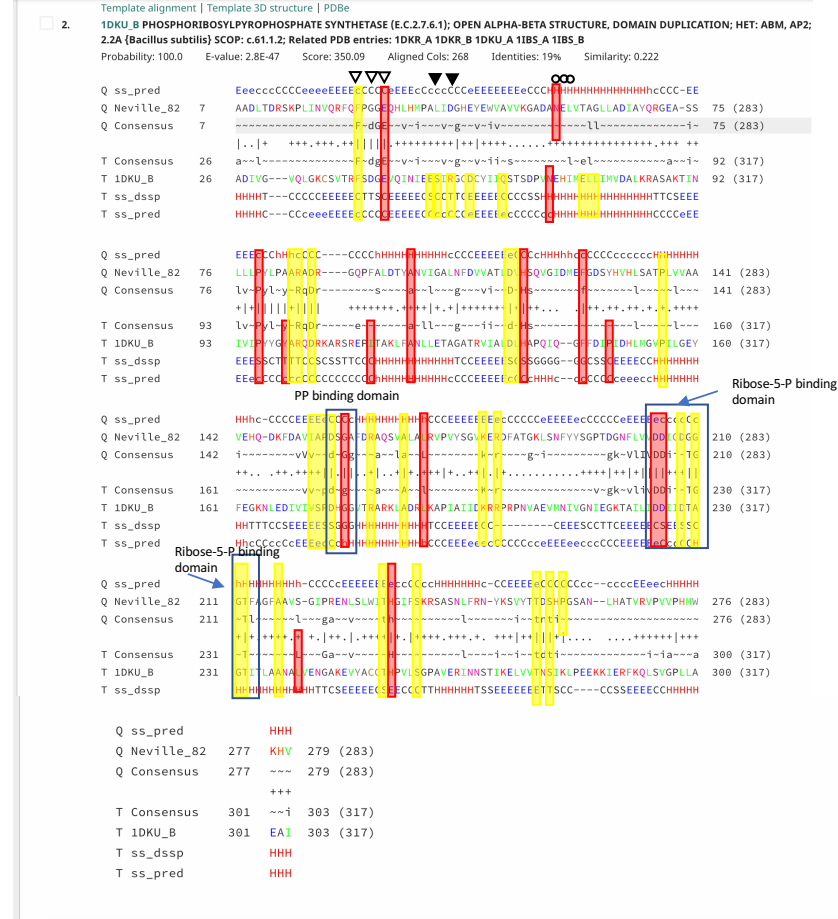


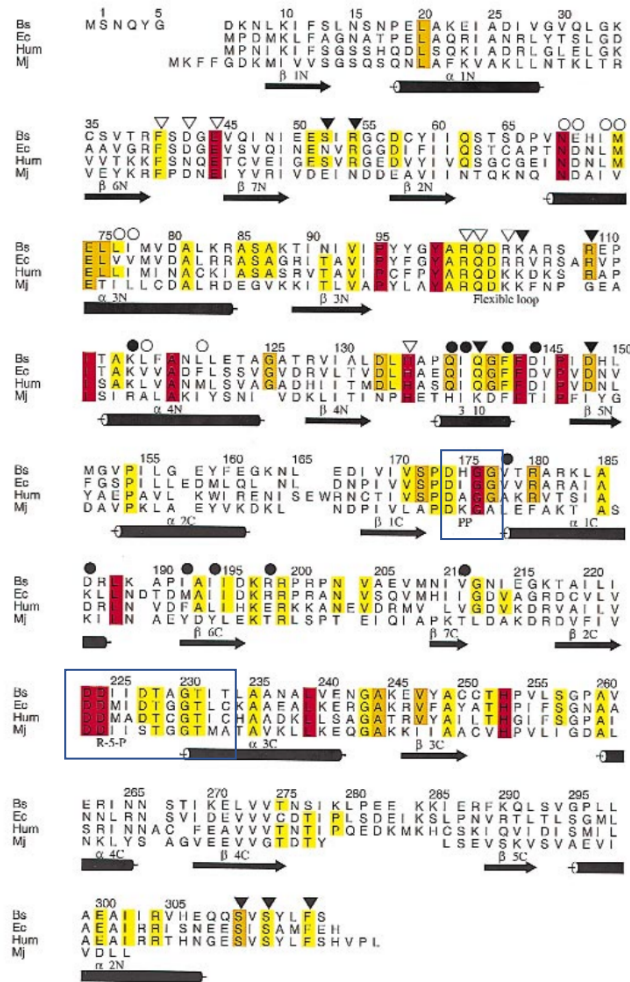
Alignment of Neville gp82 to Bacillus subtilis Phosphoribosylpyrophosphate synthetase



Structural basis for the function of *Bacillus subtilis* pyrophosphatase

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- Red indicates residues conserved in all PRPP synthetases. Orange and yellow are conserved in only some of the PRPP synthetases
- Solid Triangles indicate residues involved in mADP binding at the regulatory binding site
- Open triangles indicate residues involved in mADP binding at active (ATP) site