

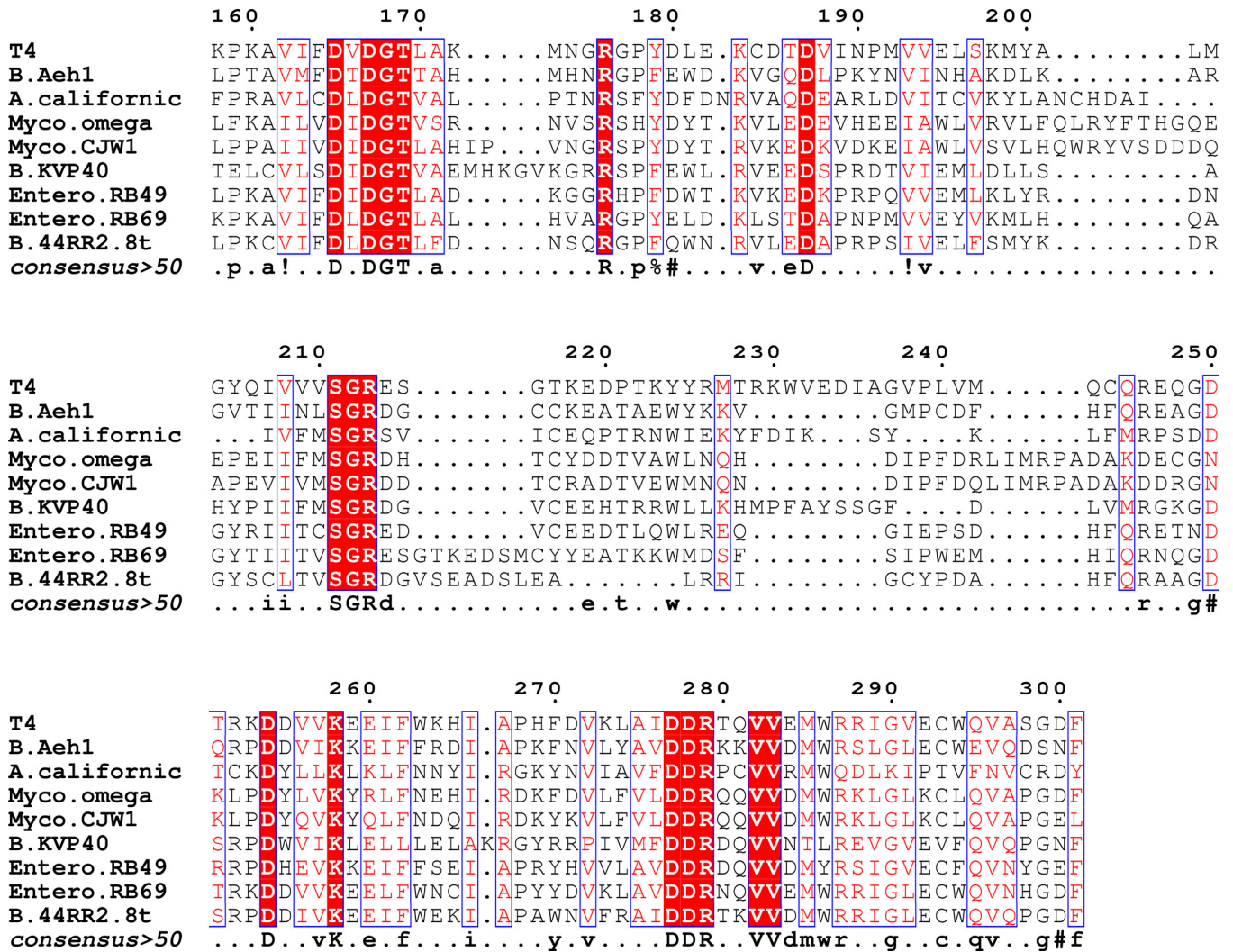
# The X-ray Crystal Structure of the Hypothetical Phosphotyrosine Phosphatase MDP-1 of the HAD Superfamily

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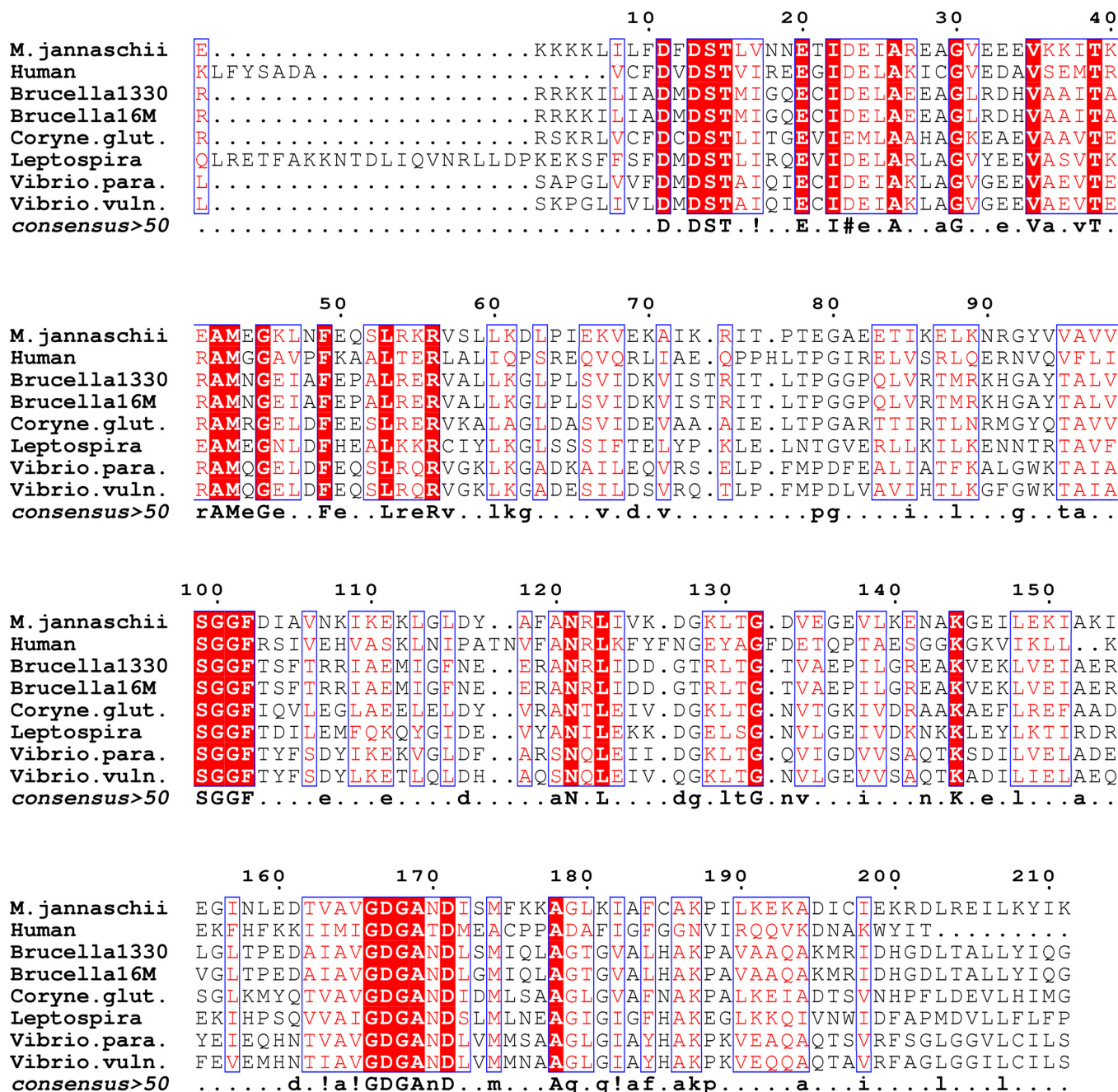
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## **SUPPORTING INFORMATION**

2 Figures of sequence alignments of polynucleotide 5'-hydroxy-kinase and 3'-phosphatases and phosphoserine phosphatases. 3 pages total.



**Figure 1S.** Sequence alignment of polynucleotide 5'-hydroxy-kinase and 3'-phosphatases. Only the sequences of the phosphatase domain are shown. Accession numbers for sequences: T4 KIPN\_BPT4; *Bacteriophage Aeh1* NP\_944160.1; *Autographa californica nucleopolyhedrovirus* NP\_054116.1; *Mycobacteriophage omega* NP\_818435.1; *Mycobacteriophage CJW1* NP\_817538.1; *Bacteriophage KVP40* NP\_899338.1; *Enterobacteria phage RB49* NP\_891791.1; *Enterobacteria phage RB69* NP\_861919.1; *Bacteriophage 44RR2.8t* NP\_932555.1.



**Figure 2S.** Sequence alignment of phosphoserine phosphatases. The N-terminal methionine is not shown. Accession numbers for sequences: *Methanocaldococcus jannaschii* AAB99612.1; Human SERB\_HUMAN; *Brucella suis* 1330 NP\_698389.1; *Brucella melitensis* 16M NP\_539532.1; *Cornebacterium glutamicum* CAF21185.1; *Leptospira interrogans* YP\_001727.1; *Vibrio parahaemolyticus* NP\_0798810.1; *Vibrio vulnificus* NP\_935467.1.