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PtxF_DH2	LADH	RVGAEPVMPAVG 45
PtxF_DH3	LRDH	VIGGRAMLAGAA 45
PtxF_DH4	LRDH	VVAGRPILPGVG 45
PtxB_DH7	LRDH	VVGGEVLPGVA 45
PtxH_DH9	LHGH	VVYGRSLLPGVG 45
PtxH_DH10	LRDH	QVRGYRILPGVA 45
consensus	HXXXGXXXXP	

S6 Fig. Sequence alignment of the conserved motif in the DH domain core regions from *ptx* PKSs. The proposed active catalytic His residue is marked with an asterisk. The numbers indicate amino acid positions within each domain.