

PtxF_KR2	VTGGAGGLGRAVADRLLS-RADARVLLGR	33	GVVHAAG--VLHDGFALT	KSEADFAAVLAPK	VAGLR	107
PtxF_KR3	VTGSGAIGRVLAEYLAR-TYRARLVLIGR	33	GVFHLAG--VADDGRATD	GDRERFAAVLAAK	TRGLV	116
PtxF_KR4	IIGGLGTVGRDTCRHLAQ-TYRAKLVVGR	33	GVVNAAM--VLVDQVVREL	PEAQLRSALDCK	TESTW	116
PtxB_KR5	LIGGTGGIARELSLDLAR-RHRARLVWFSR	33	GVVHAAM--VFDNHPLAEL	DETAFTAATR	VKIQAT	116
PtxB_KR7	ITGGTGALGLLVAEHIAA-VRRAAGLSGGG	33	GILHAAG--VLRDGLLLR	KDRADAEAVLAAK	VHGTV	117
PtxB_KR8	ITGGTRGIGLLTARHFVAEHGVRKLVLTGR	35	GVVHSAGFTDFENPAF	VVRKPKQSGMDRV	IGPKVFGVD	135
PtxH_KR10	LTGGAGGLGLIVAREIAASVRRATVVLTGR	34	GILHAAG--VIEDNFVLR	KSPEELERV	LAPKVAGLV	117

consensus GXGXXGXXXA

PtxF_KR2	ALDAATADDPLDFFVAFSSIAAHIGS--AGQTDYAYANAF	145
PtxF_KR3	HLDQLTRNDPLDLFVVFSSVSSLVGD--FGAASYATANRF	154
PtxF_KR4	SVLHAVRDESLDFVLFFSSGVAFEGN--HGQAGYAAGCTF	154
PtxB_KR5	ALAAVAEERLDFLAFSSAGSFGSF--AGNGAYICASAT	154
PtxB_KR7	LLDEATRDEPLDYFVAFSSAAAAFGN--AGQTDYAFANAF	155
PtxB_KR8	TLVEVFRDEPLRLFVLYSSVAATVPALAVGQSDYALANAY	175
PtxH_KR10	HLDEASRELPLEVFLCFSSLSGSFGN--PGQADYAAANAF	155

S5 Fig. Sequence alignment of the conserved motifs in the KR domain core regions from *ptx* PKSs. The conserved catalytic residues are marked with asterisks. The core region for the NADP(H)-binding motif is underlined. The numbers indicate amino acid positions within each domain. The “LDD” motif for B-type KR domains is shown in a box.