

		*		*		*		
PtxC_KS1	ININTAC	C	STSLVAV	265	VEAHGTGTALG	401	NIGHLDT	442
PtxF_KS2	YAVQTAC	C	STSLVAV	265	VEAHGTATRLG	401	NVGH LDA	442
PtxF_KS3	LALDTMC	C	SSSLTAL	265	VEAHGTGTALG	401	NVGHLES	442
PtxF_KS4	VVVDTAC	C	SASLVAL	265	VEAHGTGTSLG	401	VIGHLEG	442
PtxB_KS5	LAVDTAC	C	SASLTAI	265	VEAHGTGTPLG	401	NIGHLES	442
PtxB_KS7	IAVDTAC	C	SGSLTAV	265	IEAHGTGTALG	401	NIGHLEA	442
PtxB_KS8	VALDTMC	C	SSSLVTI	265	LEAHGTGTALG	401	NIGHAES	442
PtxB_KS9	VVVDTAC	C	SSALVAM	265	VEANGSGSTVT	401	NIGHPLA	442
PtxH_KS10	MAVDTMC	C	SSSLTSI	265	LEAHGTGTSLG	401	NIGHTES	442
PtxH_KS11	LAVDSMCT	C	SSTMAI	265	VEAAANGTAFS	401	NLGHPEA	442
Consensus		DXXCSSXL			HGTGT		H	

S3 Fig. Sequence alignment of the conserved motifs in the KS domain core regions from *ptx* PKSs. The conserved catalytic triad of C-H-H is marked with an asterisk. The numbers indicate amino acid positions within each domain.