

PtxE_PCPLoading	FDLGGDSLRL	52
PtxC_ACP1	FDLGLDSLVL	52
PtxF_ACP2	DRYGIDSLVI	52
PtxF_ACP3	DDYGLDSVLV	52
PtxF_ACP4	ENYGVDSLIV	52
PtxB_ACP5	ADYGFDSLGS	52
PtxB_PCP6	GEMGMNSVSL	52
PtxB_ACP7	DRYGVDSLIT	52
PtxB_ACP8	QDFGIDSIMV	52
PtxH_ACP9a	YELGLASADL	52
PtxH_ACP9b	AEEGFWDWAGL	52
PtxH_ACP10	ERYGMDSVLA	52
PtxH_ACP11	FSLGGNSLMA	52
PtxG_PCP12	FALGGHSLLI	52
PtxG_PCP13	FDLGGHSLLA	52
<b>Consensus</b>	<b>GX<sup>H</sup><sub>D</sub>S</b>	

**S4 Fig. Sequence alignment of the conserved motif in the ACP/PCP domain core regions from *ptx* PKSs and NRPSs.** The Ser residue functioning as the phosphopantetheine-binding site is marked with an asterisk. The numbers indicate amino acid positions within each domain.