

Figure S1. The possible functional domains predicted for SvX-homologues by NCBI Conserved Domain Search, HMMER and Phyre2 servers.

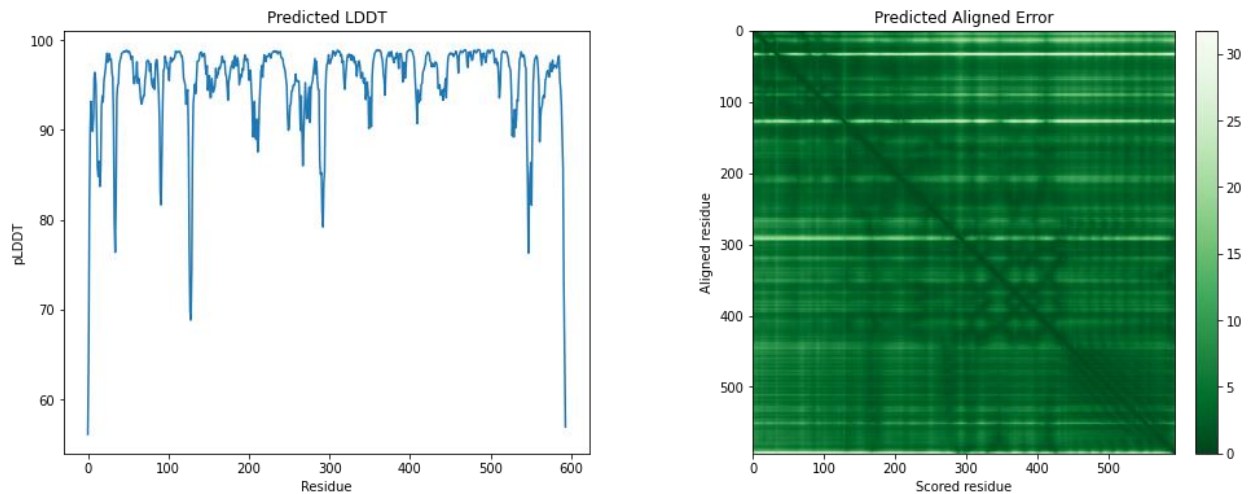


Figure S2. The results of the predicted local-distance difference test for each residue position of the Svx protein of the *Pectobacterium atrosepticum* model built by AlphaFold 2. The model confidence is high, with LDDT above 70% for the majority of the residues. The region of low confidence (slightly below 70%) is located on the loop.

WP_011092533.1	X118	-----AGGG--SMGM-----WIGPASLKDNWGLAHEFTHALQGQ---
ZP_06941093.1	X1274	VNDVAISIGAA--HSGY-PVMNASFNATS---KSLNTAPLNSWLLWHEVGHNAAEA---
WP_001034562.1	X1264	TNDVQISIGDA--HSGY-PVMNSSFSTNS---TTLPTTPLNDWLIWHEVGHNAAE---
NP_001123498.2	X611	VADVQISAGWM--HSGY-PIMCHLESVKEII--NEMDMRSRGVWGPVHELGHNQQRH---
WP_012420550.1	X454	VVDRQISAGAG--HSGY-PAMATKDWNTNSIA---TGSIIHSGSWGLWHELGHNHQSP---
ZP_04093101.1	X254	T-SPFMYANNY--LTGY-----AEDSIEFVL---DIEKFTKDGWGPWHEVGHVHHQV---
WP_015834470.1	X204	----YMFATNG--HMGF-----NGDAALQRL-----LTTNNGWGIWHEVGHVHHQV---
WP_011590734.1	X723	SGGAFMNAGNG--VIGIRPG-----NQDAILAANKGWGVAHELGHVHFDTG---
WP_008764444.1	X536	--GSYMWASDY--QIGF-----VYTYLGNILLEDNVMAAEDNAGWPAHEIGHVHQAA---
XP_001330197.1	X317	NFDSYVPAGAFAVVGANFIQAPFSWSTAMI---NYEGAKWGWGWNVHEVGHVHHQV---
XP_654508.1	X343	NFDQRVDAGAFAVVGWRFVTQNPSPDWAACV--GKDGLINYGNWGLPHEMNHMQGTYLK

WP_011092533.1	--TGGFQGAGGDDYVGIWESHANMTHQMDEF--GTSAHCEMQVNYSHIYLGST--RNR	X205
ZP_06941093.1	--PFNVGAT-----EVVNNLALYMQDCHLGKMARVEQ-----DIRIAP-----	X1361
WP_001034562.1	--PLNVPAT-----EVANNLALYMQDRYLGMNVRVAD-----DITVAP-----	X1351
NP_001123498.2	--GWEFPHT-----TEATCNLSVYVHETV-LGIPRAQA-----HEALSP--PER	X703
WP_012420550.1	--PFTMEGQT-----EVSNIIFSMVCEVMG-TGKDFESCW-----GGMGMP--YGM	X545
ZP_04093101.1	--PWLSEGMG-----ETTNNIYSLAVQLAF-GNKSME-----V-DGR	X333
WP_015834470.1	--PYTWSGGTG-----MTETVNNLYSLAVQEGF--HDRASF-----DKY	X279
WP_011590734.1	-----GRT-----IVEVTNNMPLFFESKY-KTKTRIT-----DQNIWE--NNT	X801
WP_008764444.1	----INWASST-----ESSNNLFSNFIIYKLGKYKSR-----GNGLGSVATAR	X622
XP_001330197.1	---WGISGTG-----ETTNNVINFITYAML-TEIDATR-----QITLGG--SFN	X409
XP_654508.1	GGNWGISNPG-----EETNNVMTSINYILY-TNIAGHR-----NQGLSG-----	X438

Figure S3. The alignment of the amino acid sequence of the Svx protein of *Pectobacterium atrosepticum* (*Pba*) (NCBI ID WP\_011092533.1) with M60 family metalloproteinases of *Vibrio cholerae*: (NCBI ID ZP\_06941093.1), *Escherichia coli* (NCBI ID WP\_001034562.1); *Bacillus thuringiensis* (NCBI ID ZP\_04093101.1), *Photobacterium damela* (NCBI ID WP\_015834470.1), *Bacteroides thetaiotaomicron* (NCBI ID WP\_008764444.1), *Trichomonas vaginalis* (NCBI ID XP\_001330197.1), *Entamoeba histolytica* (NCBI ID XP\_654508.1), *Homo sapiens* (NCBI ID NP\_001123498.2), *Akkermansia muciniphila* (NCBI ID WP\_012420550.1), *Clostridium perfringens* (NCBI ID WP\_011590734.1) (Nakjang et al., 2012). The conservative zinc-binding motif HEXXH(8,28)E is colored in red and carbohydrate binding residues are coloured in green. The alignment was built using the MAFFT algorithm and the BLOSUM62 substitution matrix.