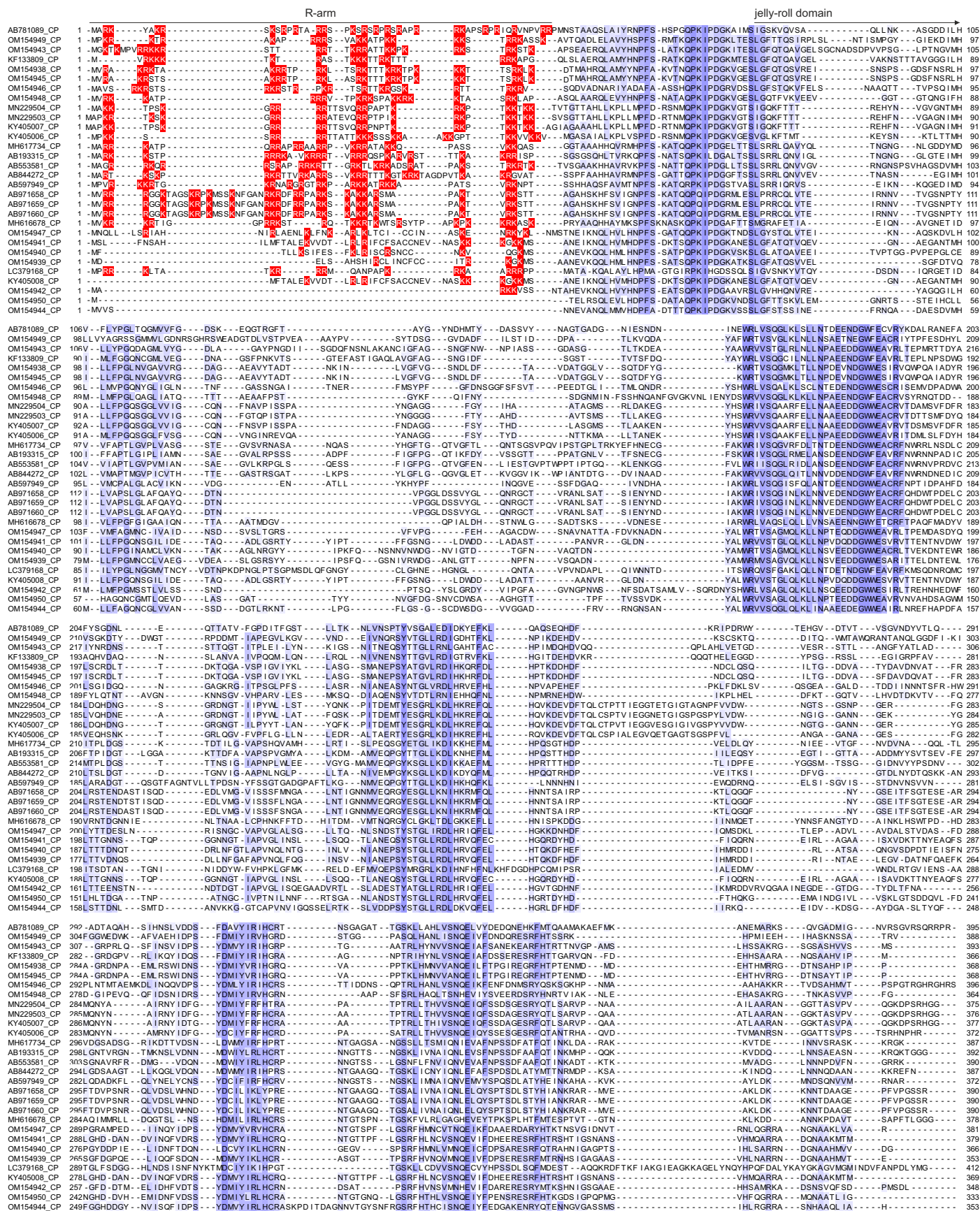
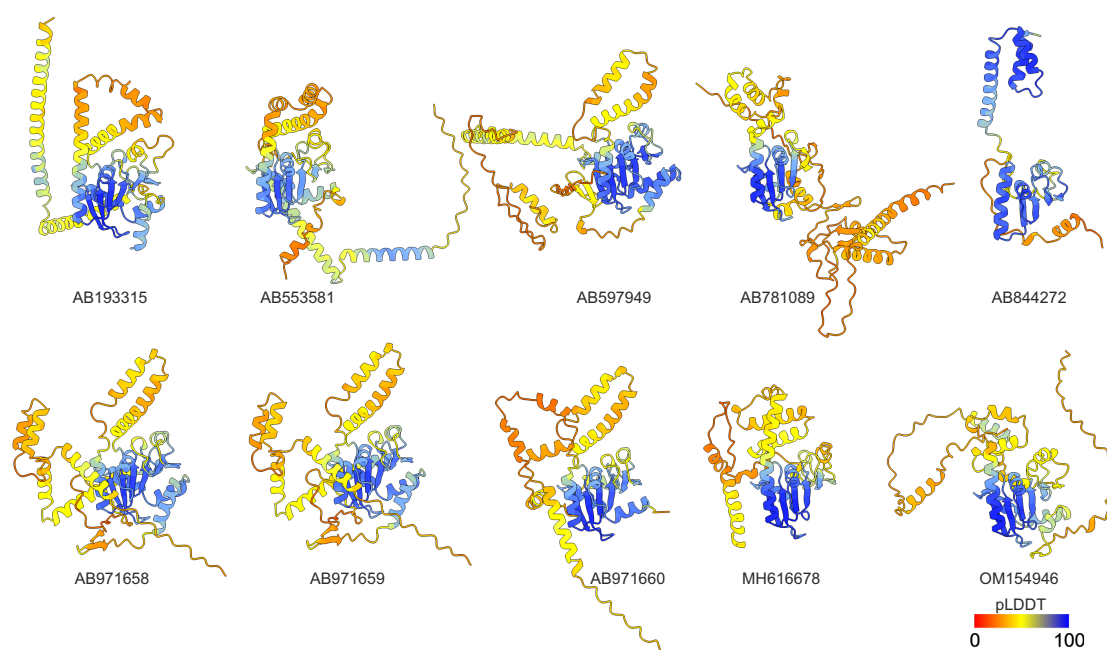




Supplementary Figure 1: The multiple sequence alignment of the bacillalysin capsid proteins. The sequences were aligned using PROMALS3D [24]. The alignment is colored according to conservation (Blosum62 matrix) and visualized with Jalview [25]. Arg and Lys residues in the R-arm are highlighted in red background. The beginning of the jelly-roll domain is indicated above the alignment.



Supplementary Figure 2: Structural models of the putative PLA1 homologs encoded by bacilladnaviruses. The models are colored according to their pLDDT values, with the color key provided at the bottom right corner.

5xk2_A 1 I PTTQLLEDFKFWQYAAATCPNNYVAKDGEKLNCSVGNCPDVEAAGSTVKLSFSDDTITDTAGFVAVDNTNKAIIVVAFRRS-----YSIRN-----WVTDATFP-----QTD-----PG 100

1d13_A 2 VSDQLFNQFNLFADQYSAAYCGKNNDAPAGTNITCTGNACPEVEKADATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGS-----RSIEN-----WIGNLNFD-----LKE-----IND-----102

3g7n_B 5 --AAAFPDLHRAAKLSAAATGCI-----GKA-----FVDTIVKRIYDL-VTDTNNGFVGYSTKEKTIIVIMRGS-----TTITD-----FVNDIDIA-----LIT-PELSGVT-----88

OM154946_1 61 EVVRHHFRETDFEQFAKDAYESPD-----T-----YAIRTNP-----QTGEKEMFVAGT-----QMRKKDMIAGQWQNVADL-----GLKGLDNHFE-----133

MH616678_1 7 2 -----KKSXLDOGLFDAYQDDP-----L-----FVLRKNK-----WTGKTEMIAGT PDWKTWRGAGQ-----WQNVAE-----VGKASSG-----VVL 66

AB781089_1 157 QLMAQEFGDKSFGAFADAYASER-----G-----YAIRTNP-----HTGNKEMFVAGT-----RNGWD-----WASNALE-----VTGASHILNNPV 224

AB844272_1 81 KYFKSYMKESELSDLWAAAYASPA-----G-----MAKRVPN-----LTGKKELFIAGT-----RNDVN-----WQNFVAGT-----GHTKVTQFGDA-----IEE 151

AB971658_1 77 KYFKSYMKESELSDLWAAAYASPA-----G-----MAKRVPN-----LTGKKELFIAGT-----RNDVN-----WQNFVAGT-----GHTKVTQFGDA-----IEE 142

AB971659_1 72 KYFKSYMKESELSDLWAAAYASPA-----G-----MAKRVPN-----LTGKKELFIAGT-----RNDVN-----WQNFVAGT-----GHTKVTQFGDA-----IEE 142

AB971660_1 8 KYFKSYMKESELSDLWAAAYASPA-----G-----MAKRVPN-----LTGKKELFIAGT-----RNDVN-----WQNFVAGT-----GHTKVTQFGDA-----IEE 78

AB597949_1 79 SYFTDYAEKSHLGEFSAAAYSAPS-----G-----VAIRVNP-----HTGLKEAFIAGT-----RGPLD-----WGRNIIEGADSIVSAGLHKVTNI-----MPK 153

AB553581_1 33 RYWGNYIDTSNVSGFQEQAAYVNKD-----G-----LAIRINP-----TTGYKELFIAGT-----RSPLE-----WQNVVAGT-----IGITATENEEL-----LHA 103

AB193315_1 21 GYWSEYLDQADIIETFHQQAAYANAD-----G-----LAIRINP-----VTGYKELVYSGS-----RGVRD-----HIQNLAEGL-----LSRGIDDDYDEW-----LEA 91

5xk2_A 101 LCDGC-----KAE-----LGF-----WFAWKVV-----RDRIKTLDELKPEHSDYKIVVVGHSLGAAIASLAAADLRTKN-----YDAIILYAYAAPRVANKPLAEFITNQ 186

1d13_A 103 ICSGC-----RGH-----DGF-----TSSWRSV-----ADTLRQKVEDAVRHPDYRVVFTGHS LGGALATVAGADLRGNG-----YDIDVFSYGAPRVGNRAFAEFLTVO 188

3g7n_B 89 FPSDV-----KIM-----RGV-----HRPWSAV-----HDTIITEVKALIAKYPDYTLEAVGHSLGGALTSIAHVLAQNFPDKSLYSNALNAFPIGNQAWADFGTQA 176

OM154946_1 134 -----KKNLPESMHYHP-----FMKADVA-----RSNAVKMKQAKADND-----D-VEVVYGHSRGAAIVSDMK-----LPDS TKKVGLD-----AMVIAHD 204

MH616678_1 67 EVGTAAAGVGVAATSWLGPESVVP-----AAA-----FVELKTAEEVAGLNTAGM- ISGHFRGEYVDYLEQVAIDN-D-VEVYIGHSRGAAIMNMQ-----VPTSTIKIGLD-----ATALDAG 169

AB781089_1 225 HSGV-RAGEVGMYATGN-----PVP-----PEY-----LGLAEK-VADT IETPNGR IATPWRAKAQEFYSQVVDE-E-VDVVYGHSRGAAIVADMQ-----LPAAVTKIGLD-----AMILADN 322

AB844272_1 152 HVPMDADKG-----AKLLKGFMTQV-----FFPGGISKQLSAAEG-----VEINQMI LDE-D-IDVVYGHSRGASYFSFID-----DSVTKIGLD-----AEVLTSD 232

AB971658_1 143 HVPMDADKG-----AKLLKGFMTQV-----FFPGGISKQLSAAEG-----VEINQMI LDE-D-IDVVYGHSRGASYFSFID-----DSVTKIGLD-----AEVLTSD 223

AB971659_1 143 HVPMDADKG-----AKLLKGFMTQV-----FFPGGISKQLSAAEG-----VEINQMI LDE-D-IDVVYGHSRGASYFSFID-----DSVTKIGLD-----AEVLTSD 223

AB971660_1 79 HVPMDADKG-----AKLLKGFMTQV-----FFPGGISKQLSAAEG-----VEINQMI LDE-D-IDVVYGHSRGASYFSFID-----DSVTKIGLD-----AEVLTSD 159

AB597949_1 154 GELRNKAE-----AAANVLENVSPVGRISKILTRSEGE-----ELAEETFREE-G-VQVYIGHSRGAAI LQYFPE-----EEFTTIALD-----ANIVGHD 232

AB553581_1 104 VGGAEKAKLAYQAK-----YASALDPLGAIA-----LSGVKNI SGISVDA-----RDEWADYDKLVEAE-G-IEVVYGHSRGSAIMSAME-----SEVKYISLD-----AMIAHP 194

AB193315_1 92 YGAGKKAETLWTFETGWGKARAADPMDDQA-----FEWAKTALSGSELA-----RDYWTQYDVTVEAE-G-VEVVYGHSRGAATISGLK-----SNVKKIGLD-----AMYIAKE 185

5xk2_A 187 G--NNYRFT-HNDDPVPKLP-----LLT-MGVVHISPEYYITAPDNTTIVTDNQ-----VTVL DGYV-----NFKGNTG-----TSG--GLPDLLAFHSHVWF-----263

1d13_A 189 TGGTLYRIT-HTNDIVPRLP-----PRE-FGYSHSSPEYWLKSGTLVPVTRND-----IVKIEGID-DATGGNNQ-----PNIP--DIPAHLWFF-----262

3g7n_B 177 A-GTFNRGN-NVL DGVPNMY-----SSPLVNFKHVYTEYYS-----GTEAS-----TVKCEGQR-----DKSCSAG-----NGMYA-VTPGHIASF-----245

OM154946_1 205 P--DMLNLIQ-SGS-----PFDKGLSLGNRKNRNT-IRWKOD--G-GWL ANAIGWTYAP-----KKKK-----PSSK-HFKEAKKKRGGSSNDFAI VKPPSA-----283

MH616678_1 170 Q-SNLYNLV-DGS-----DLDHMTLTGSKHA-----QVIT--G-GRSK-----HVTRSAS--DP-----AITTR--DPE--SLMTHRSRL-----DPNRW-----234

AB781089_1 323 K--GMINFYQGGRGFDPGHP IAWFKSOVDMALGS-TGENN--IHLEVE--G-MHT--ELWNHDS-----EDYMLEP-----384

AB844272_1 233 D-TDYVNLQ-SED-----WFTKGI GK-KGGHH--VRIK--G-TSQ--FVVGTKA--DKKRMRRDRPI IKGKLLKIDKK--AERAKFSKK-----GISIAKGRK-----312

AB971658_1 224 D-TDYVNLQ-SED-----WFTKGI GK-KGGHH--VRIK--G-TSQ--FVVGTKA--DKKRMRRDRPI IKGKLLKIDKK--AERAKFSKK-----GISIAKGRK-----303

AB971659_1 224 D-TDYVNLQ-SED-----WFTKGI GK-KGGHH--VRIK--G-TSQ--FVVGTKA--DKKRMRRDRPI IKGKLLKIDKK--AERAKFSKK-----GISIAKGRK-----303

AB971660_1 160 D-TDYVNLQ-SED-----WFTKGI GK-KGGHH--VRIK--G-TSQ--FVVGTKA--DKKRMRRDRPI IKGKLLKIDKK--AERAKFSKK-----GISIAKGRK-----239

AB597949_1 233 P-MSAPNFS-SDD-----IFSRTIGI-GRKRK--VELP--G-RSF--KAWETKA--KKAK--ADKK--AEDRKKSKL-----GVPLAELKKEFYEQADK 306

AB553581_1 195 K-SEFLNLQ-SGR-----GGVDLALAP-NYKNN--LVIE--D-RAF--NVSRRPVHTRKKKAK-----ASKE--AVTRHKQSRQKRDERSRHQKT-----267

AB193315_1 186 D-TEFTNLA-NANLLIPLQP-----GVVDYATSG-GYKHN--VYLP--N-RAF--DVARGKDV-EKKPK-----PTGE--ASAA--QRKKQRRQRPAQKS-----262

5xk2_A 264 -----IHADACKG-----271

1d13_A 263 -----GLIGTCL-----269

3g7n_B 246 -----GVVMLTAGCGYL-----257

OM154946_1 284 -----RSKRKG-----LS-IRKPEGSA-----AAKK-QRKRDDTWLDIK-----RPK-----KGPR-----YMSDSD 328

MH616678_1 235 -----KKRVIA--GGTSL-LGL-----SET-AEV-----VYG-----ESKFREK--KKKAHKRKS--HKKHKRR-----280

AB781089_1 -----395

AB844272_1 313 -----FKDRAKL-TGKTGLRVGIGT-----IASKVDQAVNM-TDVGEAVKKTVG-----VKDSSAEL-----LAKG-----KKRDR--LKARQFQRRPPKKRAKKSDDSVSL-----395

AB971658_1 304 -----FKDRAKL-TGKTGLRVGIGT-----IASKVDQAVNM-TDVGEAVKKTVG-----VKDSSAEL-----LAKG-----KKRDR--LKARQFQRRPPKKRAKKSDDSVSL-----386

AB971659_1 304 -----FKDRAKL-TGKTGLRVGIGT-----IASKVDQAVNM-TDVGEAVKKTVG-----VKDSSAEL-----LAKG-----KKRDR--LKARQFQRRPPKKRAKKSDDSVSL-----386

AB971660_1 240 -----FKDRAKL-TGKTGLRVGIGT-----IASKVDQAVNM-TDVGEAVKKTVG-----VKDSSAEL-----LAKG-----KKRDR--LKARQFQRRPPKKRAKKSDDSVSL-----322

AB597949_1 307 ATRRQHMKLVERAKTK-----IGKK-----FAANLAKYIAK-QSAETAIKALPGGSYLP I GQASAPVAAYPPLPRLVEGLDRSGTGVVPYTKRNRK--KKMTSARK--SKYARLNDLPHMGDID 415

AB553581_1 268 -----SDRIKV-----LDKL-LGRKRPRDQKVIMEKAIKK-QKVKKQLTLLKE-----RPKKRPPKKRKHKKRKG-----RPFQRS-----331

AB193315_1 263 -----RERVKE-----LDKL-LGRKTDQKKAQYLRNRRKYFKWKHHYKDAKR-----LGKIVYSEYKKHQLKKS-----GVYRRRR-----328

Supplementary Figure 3: Multiple sequence alignment of the PLA1 homologs from bacilladnaviruses and cellular organisms. The top three sequences represent cellular PLA1 homologs with available 3D structures and are identified with the corresponding PDB accession numbers. The alignment is colored according to conservation (Blosum62 matrix) and visualized with Jalview [25]. The catalytic triad is highlighted with red background.

Supplementary table 1. Results of the HHsearch analysis of the previously unannotated bacilladnavirus proteins.

Virus protein	Annotation	HHsearch profile	HHsearch probability
AB193315_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	96.42
AB553581_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	95.48
AB597949_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	93.68
AB781089_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	95.51
AB844272_1	Phospholipase A1	7OTS_A Monoacylglycerol lipase ABHD6; alpha/beta-Hydrolase domain containing 6 2-arachidonoylglycerol hydrolase monoacylglycerol lipase ABHD6 endocannabinoid system 2-AG; HET: OLA, SO4, BOG, GOL; 1.792A [Homo sapiens]	98.97
AB971658_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	94.94
AB971659_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	94.94
AB971660_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	95.3
MH616678_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	95.07
OM154946_1	Phospholipase A1	7X0D_B Phospholipase A1; Phospholipase A1, HYDROLASE; HET: SO4; 2.3972515576A [Capsicum annuum]	95.83
MH617734_1	Phospholipase A1 (inactivated ortholog of AB781089_1)	P0DOK3 VP1_CDDV1 Viral protein 1 OS=Chaetoceros diatodnavirus 1 OX=2169869 PE=4 SV=1	96.89

Supplementary table 2. Results of the DALI searches queried with the bacilladnavirus PLA1 homologs against the PDB database.

Virus protein	pLDDT	DALI hit in PDB	Z-score
AB193315_1	73.1	5xk2-A mono- and diacylglycerol lipase from <i>Aspergillus oryzae</i>	8.2
AB553581_1	68.2	7xey-B lipase-like protein PAD4	8
AB597949_1	67.9	7xey-B lipase-like protein PAD4	7.4
AB781089_1	55.7	2qua-A lipase LipA from <i>Serratia marcescens</i>	7.5
AB844272_1	79.6	4fle-A esterase YqiA from <i>Yersinia enterocolitica</i>	7.2
AB971658_1	67.2	7x0d-A phospholipase A1 from <i>Capsicum annuum</i>	7.8
AB971659_1	67.1	7x0d-A phospholipase A1 from <i>Capsicum annuum</i>	7.9
AB971660_1	66.3	6nkc-B lipase Lip_vut1 from goat rumen metagenome	7.9
MH616678_1	68	1uwc-A feruloyl esterase from <i>Aspergillus niger</i>	8
OM154946_1	66.6	1dt3-A lipase from <i>Thermomyces lanuginosa</i>	7.8