

Sputnik_V18-V19 1 MSYSHSIKDCQEPD TVYDILIP--FKPNQD--GFS---PAIFQAQLTQPIVHN-PSEYFLSVVRFSPIONIPLTIPQIQYPNT 78
Mavirus_MV17 1 MK-----QY-IWLN~~ETIK~~SKNKQLAGPRGSYKRPVSVDFRSTTILDPKYNLLIVEEFLHKLIRL-----PL 61
Tlr_penton 1 MN-----Y-IFID-SSKINP--SCF-----YNFQQLN~~QKRV~~T---KYIKLIKAVIPYDDY-----LI 47
P_AP_PX 1 MH-----ES-ITLS--FTGNS-----TVLSANYF~~PSLNVY~~--GDSEIALLS~~QTFNSFP~~-----NII 47
P-1_NV_PX 1 MEN-----IVERA-VYIS--SRDREARGVSRP---DDFTTKMNP~~SLRLS~~NDARHE~~TAVDKISMTYSWH~~-----NIN 60
P-4_NV_PX 1 ME~~QLE~~--KIARNT~~EPKKS~~SYIL--VSDK-----STRIRTKFNP~~LLQD~~DKSKQYEMALV~~NETYYS~~FP-----NI 61
P-4_NVi_PX 1 ME-----DS-LTLS--LSGT-----SAVLEAQYF~~PPEL~~SANKSYV~~LGLV~~ELLTFNSIP-----NI 48
P-3_NVi_PX 1 MI-----ES-LTLS--LSGT-----SSVLETQYF~~PPIEL~~SDSKMYV~~LGLV~~ELLTFNSIP-----NV 48
P-6_NVi_PX 1 ME-----NS-LTIL--LSGS-----SSILEAQYF~~PPIEL~~SPHKQYV~~LGLV~~ELLTFNSIP-----NI 48
P-2_TC_PX 1 MQII-----SLVESKMLFV--LTGK-----SAILSADFN~~PPIDVSD~~-GVYELGV~~TNFEVY~~NSIP-----NI 53
P-1_CI_PX 1 MV-----ED-FYVT--LPSNAS-LE~~YFPNNTLTNYVTR~~LK~~EFHLQ~~-GTWV~~VGLTEVA~~F~~FPYSWY~~-----TI 56
P-2_CI_PX 1 MT-----QD-FYIT--LPSNAS-LNYF~~PNNTLTNYVTR~~LK~~SINLE~~-GTWV~~VGLSEVT~~F~~FPFSWY~~-----NVS 57
P-5_SP_PX 1 MA-----SH-FYVS--LPSNSS-M~~LYY~~PDNKT~~CKYT~~TKLHAP~~LSLH~~--DDYE~~VGLSEI~~Q~~CTWY~~-----NV 56
P-3_SP_PX 1 MG-----SH-FYMT--LPSNSS-M~~QYYP~~NKTK~~CF~~T~~TKLHT~~PLSLN--GDYE~~VALVEI~~Q~~FQCTWY~~-----NV 56
P-1_SP_PX 1 ME-----SEDQV~~VLT~~--LPSNSS-FD~~YFPNNTLTSF~~T~~TKLAT~~PLVLR--GEYE~~VALVDI~~I~~YPHSWT~~-----NV 58
P-2_SP_PX 1 ME-----SEDQV~~VLT~~--LPSNSS-FD~~YFPNNTLTSF~~T~~TKLAT~~PLVLR--GEYE~~VALVDI~~I~~YPHSWS~~-----NV 58
P-2_XT_PX 1 ME-----EEA-FYIT--LPSNAS-LST~~F~~QNEIS~~NYTVK~~L~~SKPVMLR~~--GEWE~~VGLTEI~~Q~~YPH~~T~~WN~~-----TF 57
P-1_XT_PX 1 MD-----EGS-FYMT--LPSNAS-SKI~~Y~~PD-----T~~TKLAK~~S~~VDLR~~--GPWE~~VALTEI~~Q~~YPHTWN~~-----TF 51
P-1_CPB_PX 1 MS-----DGG-FYIT--LPSNAS-SAV~~F~~PQNTIS~~NFTIR~~L~~IKPLDL~~P--GAWE~~VGLAEI~~Q~~YPHSWN~~-----TI 57
P-N1A_NV_PX 1 MF-----NTM-VVLH-AVFT-----GGEL~~T~~L~~F~~FE~~Q~~PIR-----RPRF~~VALRQC~~S~~L~~FN~~SWY~~-----NL 45
P-N1B_NV_PX 1 -----MVVLH--TVLT-----KGE~~Q~~T~~L~~FFER~~P~~IR-----RPRF~~VALRQC~~S~~L~~FN~~SWY~~-----NL 41

Consensus_aa: M.....p..hhls..h.ss.....s.hp~~h~~p..s.l.lp....b.l~~t~~.p~~h~~.h.s.....sh
Consensus_ss: e eeee e eeee eee eeeeeeee e

Sputnik_V18-V19 79 NVN--NTIYSVSIGYN---GYTSSQN~~FVQ~~FDPSLTPSPNIPAPNAPT~~VT~~SPNV~~EV~~TPY~~YYYI~~YD~~Y~~ST~~F~~LQ~~M~~INTALE~~NAFNEI~~SAPVGA 160
Mavirus_MV17 62 FKPA-GHDYQVGI~~FNR~~--STDEIM~~GVREVD~~FS---TFVDEDGY~~MYD~~YVD~~V~~GTAIN~~ETLAG~~CDG--IIGEE 124
Tlr_penton 48 NQY--NNTSQINSK---TYSI-----PIGI--YDV~~PSLIN~~Q~~IKSL~~VTP-----83
P_AP_PX 48 NPT--NNRLKIETIP~~PKR~~KDDY~~HVFE~~FCL---EDGC-~~YE~~IEDIN~~NYMA~~KEL~~SQV~~NN---DHG 101
P-1_NV_PX 61 PEYG-ND~~SVK~~YSPDG---GAT~~WT~~TVTF-----PSGM-YS~~YHDL~~N~~DFL~~H~~QDM~~KSN~~GHV~~GVG-VADGK 113
P-4_NV_PX 62 DST--NNNFRYSPDN--GAT~~WF~~NIDI---PEGS-~~YE~~ITD~~INDY~~V~~QRIM~~KDN~~GHY~~---DSAN 111
P-4_NVi_PX 49 DTG--NNKFYVGG---EVIIL-----PTGS-~~YE~~IEDI~~EKS~~LKEALTP-----84
P-3_NVi_PX 49 DFK--SNKFYVQG---EIIEL-----PTGS-~~YE~~IEDI~~ERTL~~Q~~EIL~~SL-----84
P-6_NVi_PX 49 DKG--NNKFYVGG---EEIVL-----PTGS-~~YKIQD~~IDS~~XLR~~EILTK-----84
P-2_TC_PX 54 DEE--NNKFFFGD---VEFII-----PTGC-~~YQLT~~D~~INNYL~~Q~~HVIE~~K~~QFS~~---N 93
P-1_CI_PX 57 PQQ--AV~~TM~~KIRRG~~P~~--DL~~VG~~EADI---SPGYNS~~PKEL~~IES~~IVK~~L~~F~~TDVGY---A 103
P-2_CI_PX 58 KKASRGLK~~VQ~~RVG---GITGIDI-----SPGYNS~~PRLL~~IN~~NIAS~~TL~~R~~GVN~~F~~---T 103
P-5_SP_PX 57 RKG--NNTLYIY---DRE~~TV~~TD~~SV~~PLLR---QIT~~VQEG~~Y~~YMN~~G~~VDF~~I~~HAINA~~LD~~VAT~~---R 107
P-3_SP_PX 57 REI--NNTITVF---NKMT-ED~~G~~VPLVR---NV~~T~~LPT~~GY~~Y~~Y~~Y~~Y~~GEELI~~ITM~~IN~~ASLD~~Q~~DW~~---R 106
P-1_SP_PX 59 NFT--NNKYSFSIG---DQ~~VIT~~GRV---PV~~GHY~~RDA~~Q~~S~~VCTA~~F~~NESL~~PANL---R 103
P-2_SP_PX 59 NFT--NNKYSLSIT---DQ~~VIT~~GRV---PE~~GHY~~REALS~~ICTAF~~N~~Q~~SL~~PPH~~L---R 103
P-2_XT_PX 58 ETD--EGLFYVGIH---GG~~PL~~KELN~~V~~---K~~GLYN~~SV~~KDL~~V~~KA~~IND~~KIE~~AYK---S 102
P-1_XT_PX 52 DPH--EGNFVVGKQ---DD~~LL~~KEYHI---K~~S~~GYNT~~INE~~V~~VKA~~INAR~~L~~DSLK---I 96
P-1_CPB_PX 58 NED--TPFEITFG---ATT~~WN~~-FIL---R~~RG~~Y~~ST~~I~~PEL~~LE~~H~~M~~SN~~VAR~~H~~PG---P 101
P-N1A_NV_PX 46 ERE--HQITTIASL---PPI~~V~~TL---PAGH-H~~T~~A~~ES~~V~~ET~~IN~~HVKS~~Q---83
P-N1B_NV_PX 42 ERE--HQITTI~~A~~AL---PPI~~A~~TAL---PAGH-H~~T~~A~~ES~~I~~V~~ETIN~~R~~A~~ES~~K---79

Consensus_aa: p...sp..h.h.....p.l.....Gh..ph.s.l.ph~~pp~~.h.....
Consensus_ss: eeeee eeeee hhhhhhhhhh

Sputnik_V18-V19 161 DAPFFFYDSNTEKISLIAQAAYDR~~TL~~TT~~PIE~~ICNVN~~L~~FT~~FF~~DSIKHIGLGYNTPTGRD~~IL~~FDV~~R~~FLGN~~NY~~YQDPETAPSY~~PE~~FFI 249
Mavirus_MV17 125 DIPV~~FS~~FNKHS~~KK~~FEIT~~T~~TEN~~FRN~~---GH~~F~~IM~~N~~DD~~MR~~V~~D~~F---NSF-----165
Tlr_penton 84 DLSS~~FLVQ~~FS~~SL~~TYRIT~~FS~~ASTN---FT~~MS~~F~~NQ~~SLANIL---GFQ-----Q~~TQ~~F~~Q~~SN~~SSY~~---T~~TTK~~---136
P_AP_PX 102 THL~~T~~FSIR~~MD~~PVD~~FRT~~YIK~~NGI~~---L~~R~~F~~N~~TS~~F~~SIAP~~V~~F---GYR-----K~~KD~~CG~~P~~F~~H~~E---E~~H~~R~~S~~D---154
P-1_NV_PX 114 DKFYIDIV~~V~~LT~~TYK~~V~~V~~VIV~~GDK~~YE---L~~D~~IR-G~~T~~K~~F~~GELI---G~~F~~D---P~~K~~V~~I~~S~~K~~TEY---G~~S~~K---165
P-4_NV_PX 112 DEYYITIE~~P~~NN~~TLK~~SV~~VDI~~SANYK---V~~D~~ST~~TANS~~IR~~T~~VL---G~~F~~N---S~~Q~~V~~Y~~SE~~GY~~N---161
P-4_NVi_PX 85 KGIT~~L~~KL~~K~~P~~NN~~TL~~R~~CM~~IK~~CN~~RS~~---I~~D~~F~~Q~~P~~DD~~S~~I~~G~~K~~L---G~~F~~T---S~~R~~V~~L~~SPN---T~~D~~Y---133
P-3_NVi_PX 85 KNIT~~L~~I~~K~~P~~NN~~TL~~R~~SVIT~~C~~SHE---V~~D~~FR~~PK~~DSIARLL---G~~F~~T---P~~R~~LL~~K~~PY---I~~T~~H---133
P-6_NVi_PX 85 KKIS~~I~~SI~~Q~~P~~NN~~TL~~R~~SI~~IK~~NRK---I~~D~~FR~~PQ~~DSI~~G~~ALL---G~~F~~T---Q~~R~~V~~L~~Q~~EN~~---X~~K~~H---133
P-2_TC_PX 94 DLL~~S~~ITAN~~NN~~TL~~H~~THIKAT~~KD~~---V~~D~~FT~~K~~P~~NT~~I~~G~~P~~V~~L---G~~F~~N---S~~Q~~I~~V~~PKN---I~~G~~K---140
P-1_CI_PX 104 NNIE~~V~~SYND~~L~~TG~~K~~VR~~V~~N~~V~~H~~K~~GW---Y~~L~~E~~F~~-S~~D~~V~~L~~S~~R~~M~~L~~---G~~Y~~D---K~~K~~R~~L~~R~~R~~G~~S~~H---E~~A~~E~~R~~---154
P-2_CI_PX 104 DYI~~Q~~IS~~Y~~IPIT~~G~~KAS~~V~~AV-ARGW---Y~~F~~E~~V~~-T~~E~~PL~~Q~~M~~L~~---G~~F~~R---K~~K~~R~~L~~G~~Y~~G~~Y~~H---E~~S~~D~~K~~---153
P-5_SP_PX 108 EK~~V~~N~~F~~S~~Y~~EAS~~R~~K~~CAI~~Q~~V~~Q~~P~~G~~I~~---I~~V~~L--P~~C~~S~~L~~A~~R~~M~~L~~---G~~F~~F---E~~K~~C~~N~~L~~T~~Q~~S~~T---E~~S~~P~~S~~---157
P-3_SP_PX 107 QR~~V~~GL~~F~~Y~~K~~K~~S~~SR~~K~~V~~V~~Q~~L~~RAD~~T~~G---L~~L~~I--P~~C~~N~~L~~A~~R~~M~~L~~---G~~F~~D---R~~E~~C~~H~~L~~L~~E~~S~~T---E~~S~~P~~M~~---156
P-1_SP_PX 104 NKAS~~F~~IN~~P~~ST~~L~~K~~V~~RAE~~I~~Q~~P~~DSG---V~~Y~~L--S~~E~~G~~L~~Q~~L~~F---G~~F~~P---E~~G~~T~~L~~C~~T~~N~~Q~~---E~~G~~K~~F~~---152
P-2_SP_PX 104 NKAC~~F~~TIN~~P~~ST~~L~~K~~V~~RATI~~Q~~P~~D~~TG---I~~Y~~L--S~~E~~G~~L~~Q~~L~~L---G~~F~~P---E~~G~~T~~L~~RAN~~Q~~---E~~A~~K~~F~~---152
P-2_XT_PX 103 P~~Y~~D~~V~~K~~L~~R~~Y~~D~~E~~L~~E~~RIV~~T~~V~~K~~G~~T~~HS---F~~L~~A--G~~N~~K~~L~~TH~~I~~L---G~~I~~D---S~~N~~N~~F~~N~~D~~SI---N~~G~~L~~Q~~---151
P-1_XT_PX 97 P~~H~~E~~I~~K~~L~~R~~Y~~D~~D~~L~~E~~RS~~V~~S~~V~~SE~~S~~PI---Y~~T~~F~~A~~P~~E~~K~~L~~A~~H~~I~~L~~---G~~M~~D---G~~Y~~I~~A~~P~~Y~~G~~T~~S~~L~~---P~~K~~V~~K~~K~~I~~---151
P-1_CPB_PX 102 P~~E~~V~~V~~M~~N~~YD~~P~~V~~G~~R~~K~~V~~R~~L~~K~~ST~~D~~F~~M~~Y---V~~F~~S--T~~D~~G~~E~~L~~A~~N~~I~~L---G~~L~~G---H~~K~~R~~N~~V~~Q~~---K~~E~~P~~F~~F---149
P-N1A_NV_PX 84 -I~~L~~T~~A~~K~~L~~D~~P~~L~~T~~G~~K~~I~~V~~L~~V~~ST~~G~~I---V~~F~~L--N~~A~~E~~L~~C~~A~~L~~F~~---G~~L~~E---A~~K~~D~~D~~Q~~M~~G~~E~~---R~~G~~L~~A~~---129
P-N1B_NV_PX 80 -I~~L~~T~~A~~E~~L~~D~~P~~L~~T~~G~~K~~I~~A~~L~~M~~S~~N~~G~~V~~---A~~F~~L--N~~A~~E~~L~~C~~A~~L~~F~~---G~~L~~E---A~~K~~D~~D~~Q~~L~~G~~E~~---R~~G~~L~~A~~---125

Consensus_aa: s...h.hp..s.ch.h.hp.....h.h.s.pl.hh.....Gh.....h.sp.....
Consensus_ss: eeeee eeeee e eee hhh

Sputnik_V18-V19	250	QMQQEYPT--LSNWNVAKTIQLVSNLLPI-----NKESIPSFNRNSVGIINAQGILADFPVLTNGPEARISIDFVATGP-	320
Mavirus_MV17	166	--EFD-----DIDEYSLVILNEDVETQDASTLEFLTPISHIVIESNDLPVSYELLPISISK-----NTTISDNTGVFL	231
Tlr_penton	137	--TPS-----INSPQTILINIKDIPD-----SQIIQAQNYD-VDFSFMLLNISNR-----GQNIQYENRSD-	189
P-AP_PX	155	--KAT-----NLNTINSIKVMCNIAH-----GSFNNQLQSHSIYEFPPSGRT-----GTKVVOQSPVNL-	205
P-1_NV_PX	166	--LPN-----ITNSIDTLHINTDLIT-----DSIVGGGRASNTLFLVITDND-----LS--RSYPPFSV	212
P-4_NV_PX	162	--ESEN---IVNILSVNSLRVTSVIA-----SSYNTGGTENIYSFFPVSVP-----GKIVQVEPLNL-	215
P-4_NVi_PX	134	--ESDL---PVTILKINALRVECNITS-----GAYINEHKVHTIHEFFPAVSP-----GKIIIEVPSPI-	187
P-3_NVi_PX	134	--NSDL---PVAALKVNALRVECNITS-----GAYINQNVQVHTIHEFFPAVPP-----GYKIIIEVPKQI-	187
P-6_NVi_PX	134	--SSDL---PVAALKVNALRVECNITS-----GAYINGQLAHTIHEFFPAVPP-----GYKIIIEVPSQV-	187
P-2_TC_PX	141	--DSDN---IADIMKLNISMIECNITI-----GSFKNGEPVHIIYQFFPNVPP-----GFKIVQSPDHV-	194
P-1_CI_PX	155	--VCD-----ISLDMSLLYFYSDIVQ-----GRSVDGDTLAPLLAIVPVKGRP-----REAVYQRFDYP-	205
P-2_CI_PX	154	--VCD-----VNLDLSTLYIYSDIVE-----GRAVGDTLAPLLGIVSVKGY-----GKAIYQRFDKP-	204
P-5_SP_PX	158	--PVD-----VHMYFHSFYVYSDILQ-----FRHVGDTSVPLLRRTIAVMPRSR-----QENIVNTYIAP-	209
P-3_SP_PX	157	--PVD-----PHVEFHTFMYSDIVQ-----YQHVGEVSVPLLRRTIATKARKD-----QNSVSTYNTPT-	208
P-1_SP_PX	153	--LPD-----LNGGLFAMYVYTDIIE-----NQRVGDISAPLLRIVAVDHQRA-----GEVVDSYQTP-	204
P-2_SP_PX	153	--LPD-----INGGLFAMYVYTDIIE-----NQRVGDTSAAPLLRIVAVDHQRA-----GEVVERTYQSP-	204
P-2_XT_PX	152	--CAD-----IKAGFYTLFVYTDIIR-----PQRIGEFYTPLLRRTVPIITGNS-----NEIVTQQFIKE-	202
P-1_XT_PX	152	--YAD-----IKAGFYTMFVYSDIIQ-----HQLVGDYSVQVLLRRTVEISGKN-----NEIITQRYTRP-	202
P-1_CPB_PX	150	--SAD-----ITGGFNSLYLYTDIVE-----HQFVGDVFSVPLLRRCVFRGRN-----NEFVTTITYDKP-	200
P-NIA_NV_PX	130	--LPLGDPPLKLVLPKIEAIIYFCDIVDR-----SQCLAFDEPSNVLAACLETRGRP-----HEKVYVGPDIIP-	189
P-N1B_NV_PX	126	--LPLGEPALKVALPKIEALYICCDIVDR-----TQCLSLGEPNSVLAACPETRGRP-----HEKVYVGPDPV-	185
Consensus_aa:		...ss.....h.s.l.l.ss.lhp.....h.....s...l..h.sps.....b.l.....	
Consensus_ss:	e.....e.....e.....e.....	
Sputnik_V18-V19	321	----WRLIDMFGSVP-----IYMVDLVYVWTDQGGQYLNII-PPGRILTCCKLVFIKKSLSKYLVSSEK	378
Mavirus_MV17	232	--TNKYKYLQNNQDYNLSILFRVENSNSNKYHNILQTNFNRFNLSFTIYDYDNEKHPLTLLPQTV-IQLKLLFESID-----	303
Tlr_penton	190	----ENTIEITG-----DIRQISVQLYKNDGQ---FFM-INSG-IQLSFQYE-----	227
P-AP_PX	206	----IYYRLNKT-----DINSITVQLVDQNNN--PIDN-FNET-LTVVLHVKRHGSDH-----	250
P-1_NV_PX	213	QPTRALFNNVAAN-----LISSMRFYVVDISGR--PINL-NGIE-WHMTLILRSIY-----	259
P-4_NV_PX	216	----IYLPITLG-----TISQMETKLVQNGK--LINL-RGEE-LSIRLHIREA-----	256
P-4_NVi_PX	188	----IYLPVTVK-----TINNQLHLIVDQDGH--LVNF-RGEV-ITIRLHLKSV-----	228
P-3_NVi_PX	188	----IYLPITVK-----IIDHLQIRIVDQDGD--LVNL-RGEV-ITIRLHLKNV-----	228
P-6_NVi_PX	188	----IYLPITVK-----SIDHLQIRIVDQDGH--LVNF-RNET-ITIRLHLKPT-----	228
P-2_TC_PX	195	----IYLPISVK-----TIRNITLKIIDQEK--LVNF-QQET-VTVGLHLQKKEENGY-----	240
P-1_CI_PX	206	----CYHPIQNK-----VFHTIEVDIRDSLGK--KILF-QRGR-VCVTLHFKRVNKA-----	249
P-2_CI_PX	205	----SYHPIQNK-----NFHTIEIDLRDSTGD--PILE-ERGR-VCVTLHFKRVNKI-----	248
P-5_SP_PX	210	----HYLPLKLF-----NFETIDIILTNETGE--VVPF-ERGK-VLVTLHFRRSSRLS-----	255
P-3_SP_PX	209	----HYVPLKLY-----NFETIDIILTNETGE--VVPF-ERGK-LIVKLFHFRERSPSL-----	253
P-1_SP_PX	205	----HYLVPKSK-----YIDTHIDIRSDFGD--KVPF-QNGK-VVLKLFHFRSRRSFFHL-----	252
P-2_SP_PX	205	----HYIPVKKR-----YIDSIHIDIRSDFGD--KVPF-QNGK-VVLKLFHFRSLRRPTFGF-----	252
P-2_XT_PX	203	----DYLVPVSKH-----HFDNITIEIKSDQNR--NVSF-KYK-AIVKLFHFRPRRAYY-----	247
P-1_XT_PX	203	----DYIPVCKQ-----HFDVAISIYSDQCK--PVKF-KYK-CLVRLHFRPRKELSY-----	248
P-1_CPB_PX	201	----HYVPVSKH-----HIDTITIEIKTDQNR--HVSF-RFGK-VIVKLFHFRPRERGF-----	246
P-NIA_NV_PX	190	----ICVAASS-----EFVSSIQIWRIRDDGR--RVDF-KDKP-VRLVLELT-----	229
P-N1B_NV_PX	186	----VCVAASS-----EFVSSIQIWRIRDDCGR--RVDF-KGKP-VRLVLELT-----	225
Consensus_aa:	hh.....hpslp.l.l.sp.sp...l.h.....l.lpLhLhpp.....	
Consensus_ss:	e.....e.....e.....e.....	

Figure S2. Multiple sequence alignment of virophage penton base proteins with the PX proteins from Polinton and Tlr elements. The last two lines in each block show consensus amino acid sequence (Consensus_aa) and consensus predicted secondary structures (Consensus_ss). Representative sequences have magenta names and they are colored according to predicted secondary structures (red: alpha-helix, blue: beta-strand). If the sequences are in aligned order, the sequences with black names directly under a representative sequence are in the same pre-aligned group. Consensus predicted secondary structure symbols: alpha-helix: h; beta-strand: e. Consensus amino acid symbols are: conserved amino acids are in uppercase letters; aliphatic (I, V, L): l; aromatic (Y, H, W, F): @; hydrophobic (W, F, Y, M, L, I, V, A, C, T, H): h; alcohol (S, T): o; polar residues (D, E, H, K, N, Q, R, S, T): p; tiny (A, G, C, S): t; small (A, G, C, S, V, N, D, T, P): s; bulky residues (E, F, I, K, L, M, Q, R, W, Y): b; positively charged (K, R, H): +; negatively charged (D, E): -; charged (D, E, K, R, H): c. The alignment was constructed with PROMALS3D (<http://prodata.swmed.edu/promals3d>). Abbreviations: AP, *Acyrtosiphon pisum*; NV, *Nematostella vectensis*; NVi, *Nasonia vitripennis*; TC, *Tribolium castaneum*; CI, *Ciona intestinalis*; SP, *Strongylocentrotus purpuratus*; XT, *Xenopus tropicalis*; CPB, *Chrysemys picta bellii*.