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PBCV1_VP54      1  MAGGLSQLVAYGAQDVYLTGNPQITFFKTVYRRYT---NFAIE-SIQQTI--NGSVGFNGKVVSTQISRN  63
P3_NV           1  MAQAISEKI-----NP-----NRIPREPFGLKAESSLNRTTFNPSSASPGETLYINIPKL      50
PgVV_00012     1  M-----MDRIS---GFSTN-SYRLQVLGSSSSASANQIVRFELPSN  36
Consensus_aa:  .....pRhs...sh.hp.Shp..h..stSht.sp.l.hpIsp.
Consensus_ss:      hh h                      eeeeee          eeee

PBCV1_VP54     64  GD----LITDIVVEFVLTKGG--NGGTTYPAEELLQDVELEIGGQRIDK-HYNDW--FRTYDALFRMND  124
P3_NV          51  AENVVIVPGSVSLLFDLNVTHANNFLVNNVGRNLVSRKILFGGETLQDTQRVDL--FQTYHDLYLQAE  118
PgVV_00012    37  S---IVDIRKFAMAFKLAVTG--DDHARLSDVNNIVERVSITVGGTELESS-GFSKYNVLKQIKKCLM---  97
Consensus_aa:  t.....pshh.F.Ls.sG..ss.h...ssp1lpc1pl.hGGp1pp...ch..hpphc.hh...
Consensus_ss:      eee eeeeeeeeee          hhhhhhhheeeeeee          hhh hhhhhhhh

PBCV1_VP54     125  DRY-----NYRRTDWNNELVG-----AQKRFYVPLIF-----FNQTPGL  161
P3_NV          119  DREDRIKQGISSENMRKLR TNAGDKATSDAKEVALAAVHNTKYCIPLDHP-----ILGEHV  175
PgVV_00012    98  -----ADE-GCVLTE-HPEIARTKSYNTGVAYNLNGGEPADYRIDEWMGF---LGE  144
Consensus_aa:  .....s..ss.hh.....hpp.hhhsL.....h...G.
Consensus_ss:      hh          hhhhh          eeee          h

PBCV1_VP54     162  ALPLIA--LQY-HEVKLYFTLASQVQGVNYNGSSAIAG-----AAQPTMSVWVDYIFLD-----  212
P3_NV          176  FYP----KALPHPLIFEITLAPVSDVVYADTVKTP-----TYTITNLELEYACIS-----  222
PgVV_00012    145  CEPRVIDTSKF-PPIQISITLAAAQAVVVQGS LAGTPAQFVTEGSTNGDYSLTDIYATVPVLAFNDGLYD  213
Consensus_aa:  hbP.....h...lbh.hTLAs...sVsbss.s.hs.....sbsHhslbph.hls.....
Consensus_ss:      e e          eeeeee          eeeeee          eeeeeeeeeeee

PBCV1_VP54     213  -TQ--ERTRFA--QLPHEYLIEQLQFTGSETATPSATTQASQNI RLNFNHPTKYLAWNFNNPTNYGQYTA  277
P3_NV          223  -SEYLAREALSAYQVGRGFFYENVIL-----HKTFTISKPN-DGVTINE  263
PgVV_00012    214  GMT--EAILQK--QGFLELPYKNIYIN-----FQNVGNSVVRWN CSSASIDRIWTA  258
Consensus_aa:  ..p.....b...Q...h.hcp.....@shspss...hs.
Consensus_ss:      hh hhhhhh          ee eeeee          eeeee          eehh

PBCV1_VP54     278  LANIPGACSGAGTAAATVTTDPDYGNTG-----TYNEQ--LAVLDS-AKIQLNGQDR  325
P3_NV          264  HINLPRRSMT---GILCLFTESYTGGA-----RDSKQFVNPSITS-ININVDGMPN  310
PgVV_00012    259  TRDLTHNSKK---APVLVEGYNGDYGKMFNYADEKYSRYMNFPSPPSS---AGITSQHRINSSLLPQ  320
Consensus_aa:  h.s.l.s.t.....hs1hh.sYss.....p.spp...ss1sS.hpIp.s.bsp
Consensus_ss:      h          eeeeee          eee eeee          h

PBCV1_VP54     326  FA-----TRKGSYFNK--VQPYQS-IGGV---TPA---GVLYSFALKPAGRQPSGT-----CNFS  372
P3_NV          311  RLYSKGMTPPDL---WESVKKRFG-REGVKQ--KDFYANNKFALWVDLRA---HPDNSIHGGGLVLNNT  370
PgVV_00012    321  FA---MSPMDSALLTRQSVPKHYQKKHGLKTMTSNF---NASCVRNLNLEG---SEQLR-----IASG  373
Consensus_aa:  .h.....s.c.....b..V...b...GL...psh...s..hh.hsLcs...p.p.p.....hs.s
Consensus_ss:      hh          hhh          hh          hhhh h          eeeeeee          e

PBCV1_VP54     373  RID--NATLSLT YKTC SIDATSPA AVLGNTEVTVTANTATLLTALNIYAKNYNVLRIMS-GMGLLAYAN  437
P3_NV          371  R-D--GVKLEMKRKVGGT--GNITCYMF-VVA---DAL-----MEVMNSNLRAIMY--  412
PgVV_00012    374  L-DSRSIALQGHFDLNLGDSNDTPI DVF-VET---TSVLRVGRNL-----MIEVVA-----  419
Consensus_aa:  ..D..sh.l.p.chsth..ss.sh.h..h.h...sth.....hclhs.....
Consensus_ss:      eeeeeee          eee ee          hhh          ee          eeeee          hhh

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**Figure S3.** Multiple sequence alignment of the major capsid proteins of PBCV-1 and Polinton 3 of *Nematostella vectensis* (P3\_NV) with the protein 00012 of the virophage PgVV. The last two lines in each block show consensus amino acid sequence (Consensus\_aa) and consensus predicted secondary structures (Consensus\_ss). The protein sequences are colored according to predicted secondary structures (red: alpha-helix, blue: beta-strand). Consensus amino acid symbols: 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>).