

Structure based alignment of picornaviral polymerases – FILE: 4-pico/sav/pico_v5.aln

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1
COXA_E.pdb GEIQWMSKSK ETGRLNINGP TRTKLEPSAF YDVFEGSKKP AVLTSKDPRL E--VDFEQAL FSKYVGNLTH EPD----EY
COXB_A.pdb GEIEFIESSK DAGFPVINTP SKTKLEPSVF HQVFEGNKEP AVLRSGDPRL K--ANFEEAI FSKYIGNVNT HVD----EY
EV68_A.pdb GEIVSNEKS- ---GVCINAP AKTKLQPSVF HQVFEGSKEP AVLNKSDPRL K--TDFEAEI FSKYTGKIM LMD----EY
EV71_A.pdb GEIQVWKPNK ETGRLSINGP TRTKLEPSVF HDVFEGNKEP AVLHSDPRL E--VDFEQAL FSKYVGNLTH EPD----EY
POLI_A.pdb GEIQWMRPSK EVGYPIINAP SKTKLEPSAF HYVFEGVKEP AVLTKNDPRL K--TDFEAEI FSKYVGNKIT EVD----EY
RHIN_A.pdb GQIQISKHVK DVGLPSIHTP TKTKLQPSVF YDIFPESKEP AVLTEKDPRL K--VDFDSAL FSKYKGNTEC SLN----EH
EMCV_A.pdb GALERLPDGL ---PRIHVP RKTALRPTVA RQVFQPAFAP AVLSKFDPRP D--ADVDEVA FSKHTSNQET LP----PV
FMDV_A.pdb GLIVDTRDVE ---ERVHVM RKTKLAPTVA HGVFNPEFGP AALSNDPRL NEGVVLDVEVI FSKHKGDTKM ---SABDKAL

81
COXA_E.pdb VTQAALHYAN QLKQLDINV- ----NKMMSM EEACYGTEYL EAI DLHTSAG YPYSALGVKK RDILDPI TRD TTKMKFYMDK
COXB_A.pdb MLEAVDHYAG QLATLDIST- ----EPMKL EDAVYGTGL EALDLTTSAG YPYVALGIKK RDILSKTKD LTKLKECMDK
EV68_A.pdb MEEAVDHYVG CLEPLDISV- ----DPIPL ESAMYGMDGL EALDLTTSAG FPYLLQGKK RDIFNRHTRD RIFNRMLEK
EV71_A.pdb IKEAALHYAN QLKOLEINT- ----SOMSM EEACYGTENL EAI DLHTSAG YPYSALGIKK RDILDPTTRD VSKMKFYMDK
POLI_A.pdb MKEAVDHYAG QLMSLDINT- ----EQMCL EDAMYGTDL EALDLSTSAG YPYVAMGKKK RDILNKQTRD TKEMQKLLD
RHIN_A.pdb IQVAVAHYSA QLATLDIDP- ----QPIAM EDSVFGMDGL EALDLNTSAG YPYVTLGIKK KDLINNKTKD ISKLLALDK
EMCV_A.pdb FRMVAREYAN RVFA----L LGRDNGRLSV KQALDGLGEM DPMDKNTSPG LPYTTLG---
FMDV_A.pdb FRRCAADYAS RLHS----V LGTANAPLSI YEATKGV DGL DAMEPDTAPG LPWALQG---

161
COXA_E.pdb YGLD----- ----LPYS TYVKDELRSI DKIRKKSRL IEASSLNSDV YLRMTFGHLY
COXB_A.pdb YGLN----- ----LPMV TYVKDELRSI EKVAKKSRL IEASSLNSDV AMRQTFGNLY
EV68_A.pdb YGVD----- ----LPFV TFVKDELRSK EKVEKKSRL IEASSLNSDV AMRVAFGNLY
EV71_A.pdb YGLD----- ----LPYS TYVKDELRSI DKIKKKSRL IEASSLNSDV YLRMAFGHLY
POLI_A.pdb YGIN----- ----LPLV TYVKDELRSK TKVEQKSRL IEASSLNSDV AMRMAFGNLY
RHIN_A.pdb YGVD----- ----LPMI TFLKDELRSK DKIAAGKTRV IEASSINDTI LFRTVYGNLF
EMCV_A.pdb ---MRRTDV VDWE TATLIP FAAERLEKMN NKDFS DIVYQ TFLKDELRSI EKVQAAKTRI VDVPPFEHCI LGRQLLGKFA
FMDV_A.pdb ---KRRGAL IDFENG TVGP EVEAAL KLME KREYK-FACQ TFLKDEIRPM EKVRAGKTRI VDVLPVEHIL YTRMMI GRFC

241
COXA_E.pdb ETFHANPGTV TGSAVGCNPD VFWSKLPILL PG----- SLFADFYSY DASLSPVWFR ALEVVLREIG Y---PEEAVS
COXB_A.pdb KTFHLNPGVV TGSAVGCDPD LFWSKIPVLM DG----- HLIADFYSY DASLSPVWFA CLKMILEKLG Y---THKETN
EV68_A.pdb ATFHSNPGTA TGSAVGCDPD TFWSKIPILL DG----- EIFAFDYTG DASLSPVWFA CLKKVLKLG Y---T-HQTS
EV71_A.pdb ETFHANPGTI TGSAVGCNPD TFWSKLPILL PG----- SLFADFYSY DASLSPVWFR ALELVLREIG Y---SEGALS
POLI_A.pdb AAFHNPGVI TGSAVGCDPD LFWSKIPVLM EE----- KLFADFYTGY DASLSPWFE ALKMVLEKIG F-GD---RVD
RHIN_A.pdb KTFHLNPGVV TGSAVGCDPE TFWSKIPMLM DG----- D CIMAFDYTN RVYDVVDSNF D-----NPT
EMCV_A.pdb SKFQTPGLE LGSAGCDPD VHWTAFA ---GVAMQGF RVYDVVDSNF D-----
FMDV_A.pdb AQMHSNNGPO IGSAVGCNPD VDWFORF ---GTHFAQYR NVWDVDSAF D-----

321
COXA_E.pdb LIEGI----- ----NH THHVYRNRTY CVLGGMPSGC SGT SIFNSMI NNIIIRTLLI
COXB_A.pdb YIDYL----- ----CN SHHLYRDKHY FVRGGMPSGC SGT SIFNSMI NNIIIRTLLM
EV68_A.pdb FIDYL----- ----CH SVHLYRDKRY LVNGGMPSGS SGT SIFNTMI NNIIIRTLLI
EV71_A.pdb LIEGI----- ----NH THHVYRNRTY CVLGGMPSGC SGT SIFNSMI NNIIIRALLI
POLI_A.pdb YIDYL----- ----NH SHHLYRNKTY CVKGGMPSGC SGT SIFNSMI NNIIIRTLLL
RHIN_A.pdb LINRL----- ----CN SKHIFKSTY EVEGGVPSC SGT SIFNSMI NNIIIRTLLV
EMCV_A.pdb ---STHSV AMFRLLAEF FSEENGFDPL VKDYLES LAI SKHAYEEKRY LITGGLPSGC AATSMNTIM NNIIIRAGLY
FMDV_A.pdb ---ANHCS DAMNIMFEEV FRTEFGFHPN AEWILKTLVN TEHAYENKRI TVEGGMPSGC SATSIINTIL NNIIYVLYALR

401
COXA_E.pdb KTFKIDLDLDE LHMVAYGDDV LASYPFPIDC LELAKTGKEY GLTMT- --KS PC---FN-E VTWENATFLK RGFLPDHQFP
COXB_A.pdb KVVYKIDLDQ FRMIAYGDDV TASYPWPIDA SLLAEAGKGY GLIMTPADKG EC---FN-E VTWNTVFLK RYFRADQYP
EV68_A.pdb RVYKIDLDQ FKMIAYGDDV TASYPHKIDP ALLAEAGKHY GLVMTPADKG TS---FV-D TNWENVFLK RYFRADQYP
EV71_A.pdb KTFKIDLDLDE LNMVAYGDDV LASYPFPIDC LELAKTGKEY GLTMTPADKS PC---FN-E VNWENATFLK RGFLPDEQFP
POLI_A.pdb KTYKIDLDLH LKMIAYGDDV TASYPHEVDA SLLAQSGKDY GLTMTPADKS AT---FE-T VTWENVFLK RYFRADQYP
RHIN_A.pdb DAYKHIDLDK LKIIAYGDDV IFSYKYKLM EAIAKEGQKY GLTI TPADKS SE---FK-E LDYGNVFLK RYFRADQYP
EMCV_A.pdb LTYKNFEFDD VKVLSYGDDL LVATNYQLNF DRVRTSLAKI GYKITPANKT ST---FPLE STLEDVFLK RKFKKE---G
FMDV_A.pdb RHYEGVELDT YTMISYGDDI VVASDYDLDF EALKPHFKSL GOTTIPADK- --SDKGFVLG HSDTDTVFLK RHFHMDYGTG

481
COXA_E.pdb FLIHPTMPMR EIHSIRWTK DARNTQDHRV SLCLLAWHNG KEEYEKFVST IRSVPIGR-A LAIPNYENLR RNWLELF---
COXB_A.pdb FLVHPVPMK DIHSIRWTK DPKNTQDHRV SLCLLAWHNG EHEYEFIRK IRSVPVGR-C LTLPAFSTLR RKWLSDF---
EV68_A.pdb FLIHPTMPMR EIHSIRWTK DPRNTQDHRV SLCYLAHNG EAYNEFCRKR IRSVPVGR-A LTLPAYSSLR RKWLSDF---
EV71_A.pdb FLIHPTMPMR EIHSIRWTK DARNTQDHRV SLCLLAWHNG KQEYKRVST IRSVPVGR-A LAIPNYENLR RNWLELF---
POLI_A.pdb FLIHPTMPMR EIHSIRWTK DPRNTQDHRV SLCLLAWHNG EEEYKFLAK IRSVPIGR-A LDLEPYSTLY DRWLSDF---
RHIN_A.pdb FLIHPTFPVE EIYESIRWTK KPSQMQEHVL SLCHLMWNG PEIYKDFETK IRSVSAGR-A LYIPPYELLR HEWYKFP---
EMCV_A.pdb PLYRPPMNR ALEAMLSYR P-GTLSEKLT SITMLAVHSG KQEYDRLFAP FREV-----G VIVPTFESVE YRWRSLFW--
FMDV_A.pdb -FYKPVMSK TLEAILSFAF R-GTIQEKLI SVAGLAVHSG PDEYRRLEFEP FQ-----GL FEIPSYRSLY LRWVNAVCGD

561
COXA_E.pdb -----
COXB_A.pdb -----
EV68_A.pdb -----
EV71_A.pdb -----
POLI_A.pdb -----
RHIN_A.pdb -----
EMCV_A.pdb -----
FMDV_A.pdb AAAL EHH

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Note that sequences are derived from the PDB coordinate files and reflect any mutations present in the reported structures.