

HMPV_L

β1

α1

1 10 20 30

HMPV_L MDP.LNE.STVN**V**Y**L**P**D**S**Y****K**G**V**I**S**F**S**E**T**N**A**I**G**

RSV_L MDPIING.NSAN**V**Y**L**T**D**S**Y****K**G**V**I**S**F**S**E**C**N**A**L**G**

hPIV3_L MI.INQQS.DNRQKGNIKNLGAKRARNMDTESNNGTVSD**I**L**Y**P**E**C**H****L**N**S**P**I**V**K**G**R**I**A**Q**L**H

MUMPS_L MAGLNE**I**L**L**P**E**V**H****L**N**S**P**I**V**R**Y**K**L**F**Y**I**

MEASLES_L MDSLSVNO**I**L**Y**P**E**V**H****D**S**P**I**V**T**N**K**I**V**A**I**L**

NIPAH_L MADELSISD**I**I**Y**P**E**C**H****D**S**P**I**V**S**G**K**L**I**S**A**I**

EBOLA_L MATQHTQ**Y**P**D**A**R****S**S**P**I**V**L**D**Q**C**D**L**V**T**

MARBURG_L MQHP**T**Q**Y**P**D**A**R****S**S**P**I**I**L**D**Q**C**D**L**L**A**

VSV_L .MEVHDFETDEFNDFNEDDYATREFLN**P**D**E**R**M**T. Y**L**N**H**A**D**Y**N****N**S**P**L**I**S**D**D**I**D**N**L**I**

RABIES_L MLD**P**G**E**V**Y**D**D**P**I**D**V**E**S**D. A**E**P**R**G**A**P**S**V**P**N. **I**L**R**N**S****D**Y**N****N**S**P**L**I**E**D**P**V**R**L**M**L**

HMPV_L

α2 α3

40 50 60 70

HMPV_L .SCL**L**K**R**P**Y**L**K**N**D**N**T**A**K**V**A**I**E**N**P****V**I**E**. H. V**R****L**K**N**A**V**N**S**K**M**K**T**S.

RSV_L .SY**I**F**N**G**P**Y**L**K**N****D**Y**T**N**L**I**S**R**Q**N**P****L**I**E**. H. I**N****L**K**K**L**N**I**T**Q**S**L**M**S**K**Y. H**K**

hPIV3_L T**I**M**S****L**P**Q**P**Y**D**M**D**D**S**I**L**V**I**T**R**Q**K**I**R**L**N**K**L**D**K**R**Q**R**S. I**R**. R**L**K**L**I**L**T**E**K. V**S**D**L**G

MUMPS_L L**H**Q**L**P**N**D**L**E**P**D**D**L**G**P**L**A**N**Q**N**W**K**A**I**R. S**E**E**S**Q**V**H**A**R**L**K**Q**I**R**V**E**L**I**A**R**I**P**S**L**R**W**T**R**S**Q**R

MEASLES_L E**Y**A**R****V**P**H**A**Y**S**L**E**D**P**T**L**C**Q**N**I**K**H**R**L**K**N. G**F**S**N**Q**M**I. I**N**N**V**.E**V**G**N**V**I**K**S**K. L**R**S**Y**P

NIPAH_L E**Y**A**Q**L**R**H**N**Q**P**S**D**D**K**R**L**S**E**N**I**R**L**N**L**H**G**. K**R**K**S**L**Y**I. L**R**Q**S**.K**Q**G**D**Y**I**R**N**N. I**K**N**L**K

EBOLA_L R**A**C**G**L**Y**S**S**Y**S**L**N**P**Q**. L**R**N**C**K**L**P**K**H. I**Y**R**L**K**Y**D**V**T**V**T**K**F**L**S**D**. V**P**V**A**T

MARBURG_L R**S**L**G**L**Y**S**H**Y**S**H**N**P**K**. L**R**N**C**R**I**P**H**H. I**Y**R**L**R**N**S**T**A**L**K**T**F**L**O**N**. C**S**I**L**T

VSV_L R**K**F**N**S**L**P**I**P**S**M**W**D**S**. K**N**W**D**G**V**. L**E**M**L**T. L**E**M**L**T.

RABIES_L E**W**L**K**T**G**N**R**P**C**R**M**T**L**T**D**N**C**S**R**S**Y**K**V**L. L**E**M**L**T. L**E**M**L**T. K**D**Y**E**K.

HMPV_L

α4 α5 α6

80 90 100 110

HMPV_L .D**Y**K**V**V**E**P**V**N**M**Q**H**E**I**M**K**N**V**H**S**. C**E**L**T**L**L**K**Q**F**L**T**R**S**K**N**I**S**T**L**K**L**N**.

RSV_L G**E**I**K**I**E**P**T**Y**F**Q**S**L**L**M**T**Y**K**S**M**T**S**L. E**Q**I**T**T**N**L**L**K**K**I**I**R**R**A**I**E**I**S**D**V**K**V**Y**.

hPIV3_L K**Y**T**F**I**R****P**E**M**S**K**E**M**F. K**L**H**I**P**G**I**N**S**K**V**T**E**L**L**L**K**A**D**R**T**Y**S**Q**M**T**D**G**L**R**D**L**W

MUMPS_L E**I**A**I**L**I**W**P**R**I**L**P**I**L**Q. A**Y**D**L**R**Q**S**M**Q**L**P**T**V**W**E**K**L**T**Q**S**T**V**N**L**I**S**D**G**L**E**R**V**V

MEASLES_L A**H**S**H**I**P**Y**P**E**C**N**N**I**L**F. N**I**E**D**K**E**S**T**R**K**I**R**E**L**L**K**G**N**S**L**Y**S**K**S**V**S**D**K**V**F**Q**C**L

NIPAH_L E**F**M**H**I**A****P**E**C**N**N**I**L**F. S**I**T**S**Q**G**M**T**S**K**L**D**N**I**M**K**K**S**F**K**A**Y**N**I**I**S**K**R**V**I**G**M**L

EBOLA_L L**P**I**D**F**I**V**P**V**L**L**K**A**L**S. G**N**G**F**C**P**V**E**P**R**C**Q**Q**F**L**D**E**I**I**K**Y**T**M**Q**D**A**L**F**L**K**Y**L**K**N**V**G**A**Q**E**D**C

MARBURG_L V**P**F**H**S**I**W**D**H**I**L**T**S**I**Q. Y**D**A**I**N**H**V**D**D**F**K**Y**L**L**P**S**E**L**V**K**Y**A**N**W**D**N**E**F**L**K**A**Y**L**N**K**I**L**G**D**H**V

VSV_L S**C**Q**A**. N**P**I**S**T**S**Q**M**H**K**.

RABIES_L K**V**D**L**D**S**L**K****V**G**T**A**A**Q**S**.

HMPV_L

α7

120

HMPV_L .M**I**T**C**D**W**L**Q**L**K**S. T**S**D.

RSV_L .A**I**L**N**K**L**G**L**K**E**K**D**K**I**K**S**N**N**G**Q**E**D**N. S**V**I**T**I**I**K**D**D**I**L**A**V**K**D**N**Q**S**H**L**K**A**V**K**N**H**S**T**K**Q**K

hPIV3_L I**N**V**L**S**K**L**A**S. K**N**D**G**S**N**Y.

MUMPS_L L**H**I**S**N**Q**L**T**G**K**P**N**L**F**T**R**S**R**A**G**Q**D**. A**K**

MEASLES_L R**D**T**N**S**R**L**G**L. G**S**E**L**.

NIPAH_L Q**N**I**T**R**N**L**I**T. Q**D**R**R**D**E**I. I**N**

EBOLA_L V**D**E**H**F**Q**E**K**.

MARBURG_L F**S**A**S**A**R**S**Q**C.

VSV_L .W**M**G**S**W**L**M**S**D**N**H**D**A**S**Q**G**Y**S**F**L**H**E**V**D**K**E**A**E**I**T**F**D**V**V**E. **T**F**I**. R**G**W**G**N**K**P**I**.

RABIES_L .M**I**T**S**L**W**L**Y**G**A**H**S**E**S**N**R**S**R**R**C**I**T**D**L**A**H**F**Y**S**K**S**S**P**I**E**K**.L**L**N. C**T**L**G**N**R**G**L**K.

HMPV_L

TT α7

130 140 150 160

HMPV_L D. T**S**I. L**S**F**I**D**V**E**F**I**P**S**W**. V**S**N**W**F**S**N**W**Y**N****L**N**K**L**I**L**E**F**R**.R**E**E.

RSV_L D**T**I**K**T**T**L**L**K**L**M**C**S**M**Q**H**P**P**S**W**. L**I**H**W**F**N**L**Y**T**K**L**N**I**L**T**Q**Y**R**.S**S**E.

hPIV3_L N**E**E**I**N**N**I**S**K**V**H**T**. Y**K**L**D**K**W**Y**N**. P**F**K**T****W**F**T**I**K**Y**D****M**R**R**L**L**Q**K**A**R**N. **E**V**T**.

MUMPS_L D**S**S**I**P**S**T**R**E**L**S**Q**I. W**F**N**N**E**W**S**G**. S**V**K**T****W**L**M**I**K**Y**R****M**R**L**I**T**N**Q**.T**G**E.

MEASLES_L E**D**I**K**E**K**V**I**N**L**G**V**Y. M**H**S**S**Q**W**F**E**. P**F**L**F****W**F**T**V**K**T**E****M**R**S**V**I**K**S**Q**T**.H**T**C.

NIPAH_L I**H**E**C**R**R**L**G**D**L**G**K**N. M**S**Q**S**W**Y**E. C**F**L**F****W**F**T**I**K**T**E****M**R**A**V**I**K**N**S**Q**.K**P**K.

EBOLA_L I**L**S**S**. I**Q**G**N**E**F**L**H**. Q**M**F**F****W**Y**D**L**A**I**L**T**R**R**G**R**L**N**R**G. **N**S**R**S**T**

MARBURG_L E**D**F**S**. P**K**E**N**P**Y**Y**W**. G**M**L**L**V**H**L**S**Q**L**A**R**R**I**K**G**Q**R**G. **S**L**R**S**N**

VSV_L E**Y**I**K**K**E**R**W**T**D**S**F**K. **I**L**A**Y**L**C**Q**K**F**L**D**L**H**K**L**T**L**I**L**N**A**V**S**E**V**E**L**L**N**I**A**R**T**

RABIES_L I**P**P**E**G**V**L**S**C**L**E**K**V**D****Y**D**K**A**F**G**R**Y**L**A**N**T**Y**S**S**Y**L**F**H**V**I**I**L**Y**M**N**A**L**D**R**D**E**E**K**T**I**L**A**L**

HMPV_L

β2 TT β3 β4

170 180 190

HMPV_L V**I**R**T**G**S**I**C**. R**S**L**G**K**L**V**F**I. V. S**S**Y**G**C**I**V**K**.

RSV_L V**K**N**H**G**F**I**L**I**D**N**H**T**L**N**G**F**Q**F**I**. L. N**Q**Y**G**C**I**V**Y**.

hPIV3_L F**N**M**G**K**D**Y. N**L**L**E**D**Q**K**N**L**L**L**I**. H**P**E**L**V**L**I**D**.

MUMPS_L L**T**. D**L**V. T**I**V**D**T**R**S**T**L**C**I. T**P**E**L**V**A**L**Y**S.

MEASLES_L H**R**R**R**H**T**P. V**F**F**T**G**S**S**V**E**L**L**I**. S**R**D**L**V**A**I**S**.

NIPAH_L F**R**S**D**S**C**I. I**H**M**R**D**K**S**T**E**I**L. N**P**N**L**C**I**F**Q**S.

EBOLA_L W**F**V**H**D**D**L**I**. D**I**L**G**Y**G**D**V**V**F**W**K**I**P**S**M**L**P**L**N**T**Q**G**I**. P**H**A**M**D**W**Y**Q**S**V**F**K**E**A**V

MARBURG_L W**K**F**I**G**T**D**L**. E**L**F**G**I**A**D**F**V**I**F**K**V**P**V**K**T**I**I**R**N**A**V**S**L**Q**A**S**K**P**G**L**R**I**W**Y**R**D**Q**N**L**T**P**Y**L

VSV_L F**K**G**K**V**R**R**S**S**H**G**T**N**I**. C**R**I**R**V**P**S**L**G**P**T**F**I**S**E. G**W**A**Y**.

RABIES_L W**K**.D**L**T**S**V**D**I**G**K**D**L. V**K**F**K**D**Q**I**W**G**L**L**I**V**T**K. D**F**V**Y**.

β5 α8

HMPV_L 200 210 220 230 240 250

HMPV_L SNKSKRVSFTRYNQLTWKDVMLSRFANFCIWVSNLSLNEQEGGLRSNLQGMLETNKLTY

RSV_L HKELKRITVTFTYNOFLTWKNISLSRLNVCLITWISNCLNLTNLKSLGLRCGFNNVITLQLF

hPIV3_L .KQNYNGYLI TPEL VLMYCDVIEGRWNISACAKLDPKL QS MYQKGNLW

MUMPS_L .NEHKALTYLTFEMVLMVTDMLEGRNLVSSLTASHYL SP LKKRTEILL

MEASLES_L .KESQHVYYLT FEFVLMYCDVIEGRMLTETAMTIDARY TE LLGVRVYMW

NIPAH_L DKTGKCCYYLTPEMVLMYCDVLEGRMMMETTVKSDIKY QP LISRSNALW

EBOLA_L QGHTHIVSVSTADVLMICKDLITCFNNTTLSKIAFIEDPVCSDYP NFKIIVSMLY

MARBURG_L CDDEFIVSVASYECFIMIKDVFIERNTWEICARAWLEDSDGADYP PLDVLGELY

VSV_L . . FKLLDILMDRNFLLMVKDVIIGRMQTVLSMVCRI DNLFSQDIFSLNLY

RABIES_L . . SQSSNCLFDRNY TMLKDLFLSRFNSLMILLSP EPLYSDDLIAQLCQLY

α9 α10 α11

HMPV_L 260 270 280 290 300

HMPV_L ETVDYMLSLCCNEGFLVKFEFEGFIMSEILRITE.HAQF . . STRFRNTLLNGLYITDQLTK

RSV_L LYGDCLIKLIFHNVEGFYIIEKEVEGFIMSLILNTE.EDQF . . RKRFRNYSMLNNITDANK

hPIV3_L EVIDKLFPIIMGEKTFDVIILLPALLSLIQTHDP.VKQL . . RGAFLNHHVLSMELIFES

MUMPS_L TLVDDLALMGDKVYGVVSSLSFVYVYQYGDV.VVDI . . KGT FYGFICNEILLDLTE

MEASLES_L KLIDGFFPALGNPTQYIVAMLEPLSLAYLQLRDI . TVEL . . RGAFLNHCFTETIHDVLDO

NIPAH_L GLIDPLFFVWGNRIYNIIVSMIEPLVLLALQLKDE.ARIL . . RGAFLHHCICEKMHQLSE

EBOLA_L QSGDYLLSILGSDGYKLIKFLPELCLAKIQLCSK.YTER . . KGRFLTQMHLVAHNTLEE

MARBURG_L NQGDIIAMYLEDDGFKLIKHLPELVCVSCIQTHGI.FTPR . . KYWFFQSQMLKSYVDELHD

VSV_L RIGDKIVERQGNFSDYDLIKMVPEICNKLMLKLARESRPLVPQFPFHENHIKT SVDE

RABIES_L IAGDQVLSMCGNSGYEVIKILEPYYVNSLVRRAEKFRPLIHLGDPVFFIKD KVSQ

α12 α13

HMPV_L 310 320 330 340 350 360

HMPV_L LKNKNRLRVHSTVLENN . . DYPMYEVVLKLLGDITL.RCIKLLINKNLNAAYELYEIFRIF

RSV_L AQKNLLSRVCHTLLDKTVDNIINGRWIILLKSKFL.KLIKLAGDNNLNLSELYFLFRIF

hPIV3_L RESIKEFL SVDYIDKILDIIDKSTIDEIAEIFSFRTF

MUMPS_L DNIFTEEE ANKVLLDLTSQFDNLSPDLTAELLCIMRLW

MEASLES_L NGFSDGFT YHELTEALDYIFITDIDLHGTETIYISFFFRSF

NIPAH_L CGFTDQKI RSMFIDDLISILNIDNHLLEFFSFRTF

EBOLA_L ITEMRALKPSQA QKIREFHR . TLIRLEMTPQQCLELFSIQKHW

MARBURG_L LNLKLQISDNKA ECAQNFIK . TIVQAKLTPQQYCSLQKHW

VSV_L . . GAK IDRGIRFLHD . QIMSVKTVDLTLVIYGSFRHW

RABIES_L LEGTF GPSAKRF.F.K . VLDDQFNIHDLVFFVYGCYRHW

α14 β6 α15

HMPV_L 370 380 390 400 410 420 TT

HMPV_L GHPMVDERDAMD AVKLNNEITKILRLESLETLRGAFILRITIKGFVDNN.KRWPKIKNLKV

RSV_L GHPMVDERQAMD AVKNCNETKFYLLSSLMLRGAFAIYRITIKGFVNNY.NRWPTLRNAIV

hPIV3_L GHPPLIASIAAEKVRKYMYIEKQLKFDITINKCHAFICTIINGYRERHGGOWPPTLPDH

MUMPS_L GLPPLTASQAASKVRKESMCAVKVLDQFTIMKTAFFFHALINGYRSHNGIWPPPTLHGN

MEASLES_L GHPPLA VTAENVRKYMNQPKVIIVYETLMKGHAIFCGIINGYRDRHGGWPPPTLPLN

NIPAH_L GHPPILEAKVAEKVREHMLADK VLEYAPIMKAHAFICGTIINGYRDRHGGWPPPTLPLPAH

EBOLA_L GHPPLVHSETAIQKVKKHAQSTKILKPKVMFETFCVFKFIVAKNHYHSQ.GSWSYVTSDRN

MARBURG_L GHPPLYNDVALDKVKKHAQSTKILKPKVMFETFCVFKFIVAKNHYHSQ.GSWSYVTSDRN

VSV_L GHPPLIDYVTGLEKLLHSQVTMKKIDIVSYAKALASDLARIVLFQQFNH.KKWFVNGDPLL

RABIES_L GHPYIDYRKGLSKLYDQVHMKKVIDKSYQECCLASDLARRILRWGFQDKY.SKWFYLDLDRFLA

α16 α17 α18 α19

HMPV_L 430 440 450 460 470 480

HMPV_L LSKRWTMFYKAKNYPSQLELSEQDFLEAAIQFEQEFSVPKKTNLEMLVNDKAITSPKRL

RSV_L LPLRWLTYYKLNITPSLLELTERDLIVLDSLRFYREFRIPKPVLDLEMITNDKAITSPKRL

hPIV3_L AHEFIINAYGNSAISYEN.AVDYYSFIGIKFNKFIQPOLDEDLTYMKDKALSPKSN

MUMPS_L APKSLIEMRHNSSELKYEY.VLKNWKSISMLRIHKCFDASPEDLSTFMDKAITSPKQD

MEASLES_L AADTIRNAQASGEGTHEQ.CVDNWKSFAGVFKFCFMPPLSLDSDLTMYLKD KALAAALQRE

NIPAH_L ASKHIIIRLKNSESITIDD.CVKNWESFCGIQDFCMECLKLSDLSMYMKDKALSPKIDE

EBOLA_L LTPGLNSYIKRNQFPPLPM.IKELLWEFYHLDHPPFSTKIIISDLSIFIKDRATAVERTC

MARBURG_L LTPYLRQHIVSNSSPSQAE.IYQHLWEWYFVEHEPLFSTKIIISDLSIFIKDRATAVNQEC

VSV_L HDHPFKSHVKNETWPTAAQ.VQDFGDKWHEPLIKCFEIPDLLDPSIYSDKSHMNRSE

RABIES_L QDHP LTPYVKETQTWPPEPRHI.ADLVGDTHWKLPITQI FEIFESM DPELTDKSHLSTR

Motif G

α20 α21 α22 α23

HMPV_L 490 500 510 520 530 540 TT

HMPV_L IWSVYPKNYLPETIKNRYLEETFNASDSLKTRRVLEYYLKDNKFDQKE LKSYVVRQGEYLN

RSV_L IWTSPRNYMPSHIQNYIEHEKLFSESDKSRRLVEY YLRDNKFNEDCLYNCVVNQSYLN

hPIV3_L WD TVY PANSNLLYRT NASN SRRLVEYV IADSKF FDPHQLD YVESGDWLD

MUMPS_L WMGVFRRSLIKQRYR DANRPLPQPF NRLLLNFL EDDRFD DPKELEYVTSGEYLR

MEASLES_L WD SVYPKEFLRYDP PKGTG SRRLVDVFLNDSSFPDPYDVIMYVSSGAYLH

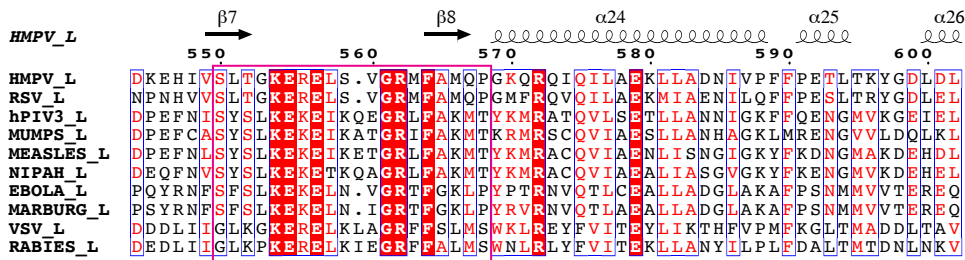
NIPAH_L WD SVYPREVLSYTP PKSTE PRRLVDV FVNDENFDPYVML EYVLSGAYLH

EBOLA_L WDAVFEPNVLGYNP PHKFS KRVPEQFL EQENF SIENVLSYQKLEYLH

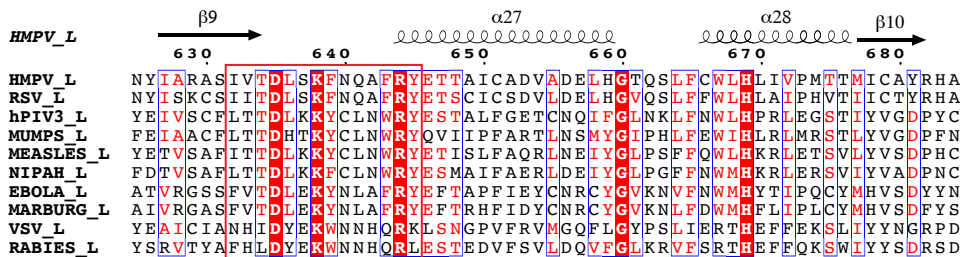
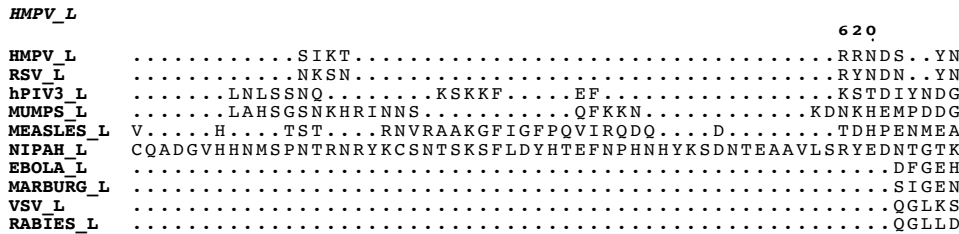
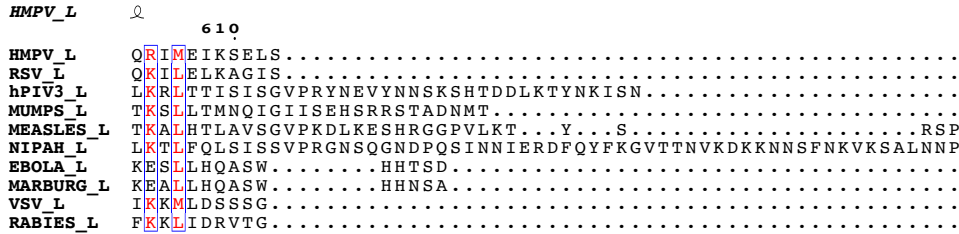
MARBURG_L WDSVDFR SVLGYNP PVRFO SKRVPEQFL GQADFSLNQILEFAEKLEYLA

VSV_L VLKHHVMN P NTPIP SKKVLQTM LDTKATNWKEFLKEID.EKGLD

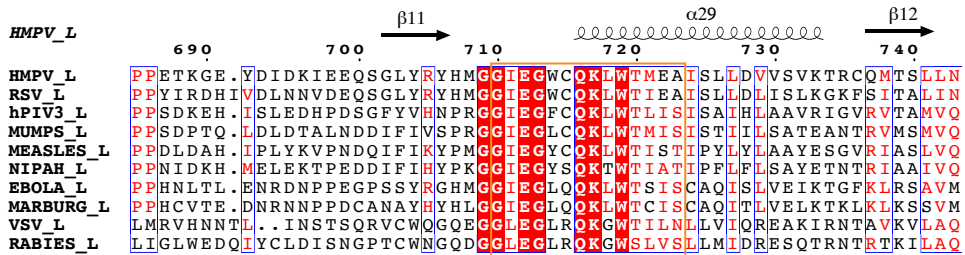
RABIES_L LASHVLE R GGPVPSEKVIITALE SKPPINPREFLKSID.LGGLP



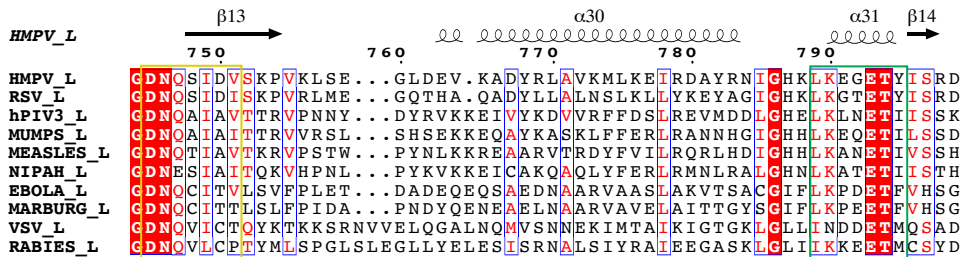
Motif F



Motif A



Motif B



Motif C

Motif D

$\beta 15$ $\beta 16$ $\alpha 32$ $\alpha 33$
 HMPV_L 800 810 820 830 840 850
 HMPV_L IQSEGVVHPFKKVLRVGPWINTLDDIKTSAESIGSLCQEL...EFRGES
 RSV_L MQFMSKTIQHNGVYYPASIKKVLRVGPWINTLDDFKVLSLEIGSLTQEL...EYRGES
 hPIV3_L MFIYSKRVIYDGRILTQALKALSRVVFVSETVIETRASSNLATSAFAK...IENGY
 MUMPS_L FFYYSKRVIYDGRILTQALKALSRVVFVSETVIETRASSNLATSAFAK...TENGE
 MEASLES_L FFVYSKGIHYDGLLVVQSLLKSIARCVFVSETVIETRASSNLATSAFAK...IERGYD
 NIPAH_L LFIYSKGIHYDGLLVVQSLLKSIARCVFVSETVIETRASSNLATSAFAK...IENGLS
 EBOLA_L FIYFQKKQYLVNGLVLPQSLKATRMAPLSDAIFDDLOGTLASIGTAFERS...ISETRH
 MARBURG_L FIYFQKKQYLVNGLVLPQSLKATRMAPLSDAIFDDLOGTLASIGTAFERS...ISETRH
 VSV_L YLNYGKIPIFRGVIRGLETKRWSRVTCVTND...QIPTCANIMSSVSTNALTVAHFAEN
 RABIES_L FLIYKTPLFRRGNILVPEESKRWARVSCISND...QIVNLANIMSTVSTNALTVAQHSQS

Motif E

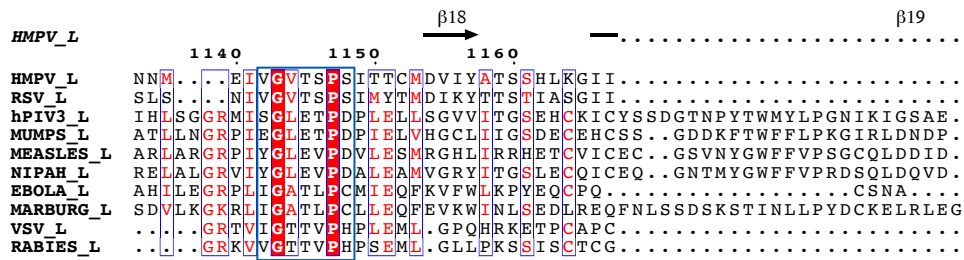
$\alpha 34$ $\alpha 35$ $\alpha 36$
 HMPV_L 860 870 880 890 900 910
 HMPV_L IIVSLILRNFWLYNLYMHESKQHPFLAGKQLFKQLNKTLTSVQRFPEIKRENEVDLWMMNI
 RSV_L LLCSLIFRNWVLYNQIALQ LKNHALCANNKLYLDLKV LKHLKTFNLDNIDTALPLIYMMNI
 hPIV3_L PVLGYACSIKFNQI...QLYIALG...MNIPTITQNIIRD.QYFRNPWMOYASLI
 MUMPS_L KDLCYFLNAPMTIR...QCYDLV...FPQTKLSQDITN.AYLNHPILISRLCLL
 MEASLES_L RYLAYS LNVLKVIQ...QILISLG...FTINSTMRDVI.PLLTNNDLIRMALL
 NIPAH_L RNVGYCINILKVIQ...QLLISTE...FSINETLTDVTS.PISNNLDWLIITAAI
 EBOLA_L IFPCRITAAFHTFFSVRILQYHHLG...FNKGFDLGQLTLG.KPLDF.GTISLALAV
 MARBURG_L IFPSRWIASFHSMLAINLLNQNHG...FPLGFNIDISCFK.KPIITF.SKLIITIT
 VSV_L PINAMIQYNYFGTFARLLLMMHDPALRQSLYEVQDK...IPGLHSSTFKYAMLYL
 RABIES_L LIKPMRDFLLMSVQAVFHYLFLSPILKGRVYKLSA...E.GESFLLAMSRITLYL

$\alpha 37$ $\alpha 38$ $\alpha 39$
 HMPV_L 920 930 940 950 960
 HMPV_L PMQFGGDPPVVFYRSFYRRTPDFLTEAISHVDILLKISAN...IKNETKVSFFK
 RSV_L PMLFGGDPPNLLYRSFYRRTPDFLTEAIVHSVFLSYTNDLKDQLDSDDRLNKFLT
 hPIV3_L PASVGGFNFMAMSRCFVRNIGDPSVAALADIKRFIKANQLD...RSVVL
 MUMPS_L PSQLGCLNFLSCSRFLFRNIGDPLVSAIADVKRLIKAGCLD...IWVVL
 MEASLES_L PAPIGGFNLYLNMSRFLFRNIGDPLVSAIADVKRMLIASLMP...EETL
 NIPAH_L PAPIGGFNLYLNMSRFLFRNIGDPLVSAIADVKRMLIASLMP...EETL
 EBOLA_L PQVLLGGLSFLNPEKCFYRNIGDPLVSGFLQKTYLRMIEMD...DLF
 MARBURG_L PQVLLGGLSFLNPEKCFYRNIGDPLVSGFLQKTYLRMIEMD...DLF
 VSV_L DPSIGGVSGMSLSRFLIRAFDPDVTESLSFWRFIHVHARSE...HLKE
 RABIES_L DPSIGGVSGMSLSRFLIRAFDPDVTESLSFWRFIHVHARSE...HLKE

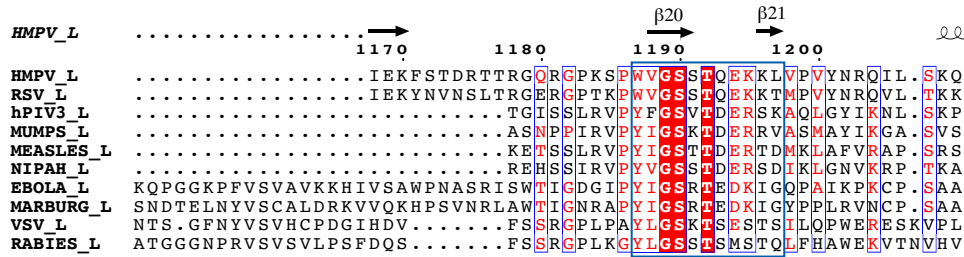
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 RSV_L CIIITFDKN...PNAEFVTLMRDPAQVGSERQAKVTSINRNTAVTSTLSPNQLFSDS
 hPIV3_L YRIMNQEP...GESSFLDWAADPYSYCNLPQSQNTTMIKNITARNVLDSPNPLLSGL
 MUMPS_L YNILLGRRP...GKQKSTLAAADPYSYCNLPQSQNTTMIKNITARNVLDSPNPLLSGL
 MEASLES_L HQVMTQQP...GDSFSLDWAADPYSYCNLPQSQNTTMIKNITARNVLDSPNPLLSGL
 NIPAH_L QKVMNQEP...GDSFSLDWAADPYSYCNLPQSQNTTMIKNITARNVLDSPNPLLSGL
 EBOLA_L LPLIAKNP...GNCTAIDFVLPNLSGFLNVPQSITRLLKNTARFVLIHSPNPLLSGL
 MARBURG_L YLIISSKP...GLADASDFVLPNLSGFLNVPQSITRLLKNTARFVLIHSPNPLLSGL
 VSV_L MSAVFGNPEIAKFRITHIDKLVEDPSTLNIAMGMSPANLKTVEVK.KCLIESRQTRNQV
 RABIES_L LCHEAGNPDLDGERTLESFTRLLEDPSTLNIAMGMSPANLKTVEVK.KCLIESRQTRNQV

$\alpha 42$ $\alpha 43$ $\alpha 44$
 HMPV_L 1030 1040 1050 1060 1070 TT
 HMPV_L AI...HYS.RNEEVGIIAENITPVYPHGLRVLYESLPFKAEKVVNMI SGTKSITNLLQ
 RSV_L AQ...HYT.TTEIDLNDIMQNIETPYPHGLRVLYESLPFKAEKIVNLI SGTKSITNILE
 hPIV3_L FT...NTMIEEDELAEFLMDRVIILPRVAHDILDNSLTGIRNAIAGMLDTKSLIRVGI
 MUMPS_L FS...ENAAEEDELAQYLLDREVVMPRVAHDILDNSLTGIRNAIAGMLDTKSLIRVGI
 MEASLES_L FH...DSSKEEDELAAFLMDRHIIVPRAAHEILDH SVTGAREE IAGMLDTKSLIRASM
 NIPAH_L FH...DKSFEDELAAFLMDRVIILPRAAHEILDH SVTGAREE IAGMLDTKSLIRASM
 EBOLA_L FH...ASADFEDMVCWLLSSTPVMSSRFADIFSRTPSGKRLQILGYLEGTRTLASKI
 MARBURG_L FH...IGSDLEDQRCVCEWLLSSTPVMSSRFADIFSRTPSGKRLQILGYLEGTRTLASKI
 VSV_L IKDATIYLYHEEDRLRSFLWSINLFPRLFSEFKSGTFLGVADGLISLIFQNSRTIRNSFK
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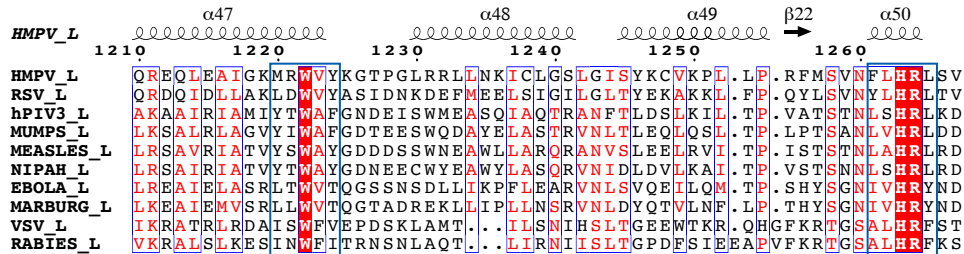
$\beta 17$ $\alpha 45$ $\alpha 46$
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 RSV_L KTSADLTDIDRAVSMMLLENLGLLSRITLSV.VVDSIEIPFKSNGRLICCCQISRTLRBTSSW
 hPIV3_L NRGGLTYSLLRKISNYDLAQYETLSRT...LRLIVSDKIR.YEDMCSVDLAIAIRQKMW
 MUMPS_L EVRPLSARKLNTVIEYNLLYLSYNLEIEKPNIVQPFNAI.NVDTCSIDIAIRSRKLSW
 MEASLES_L RKGGLTSRVITRLSNYDYEQFRAGMVL...LTGRKRNVLI.DKESCSVQLARARSHMW
 NIPAH_L RKGGLTSRVITRLSNYDYEQFRAGMVL...LTGRKRNVLI.DKESCSVQLARARSHMW
 EBOLA_L INNNTETPVLDRLRKITLQRWSLWFSYLDH...CDNILAEAL.TQITCTVDVAQIEEYSSW
 MARBURG_L ISLTTTEGTM LMKLRELTRNRWKSWSYIDA..LDDDLSESL.EKFTCTVDVANFBRAYSSW
 VSV_L KKYHRELDLIVRSEV...SSLTLH...GKHLHRRGSCKMWTCSATHADTDRYKSW
 RABIES_L KSLSRTELESFYNSEI...HGINRM...TQTPQR..VGRVWP.CSSEADLREISW



Motif A'

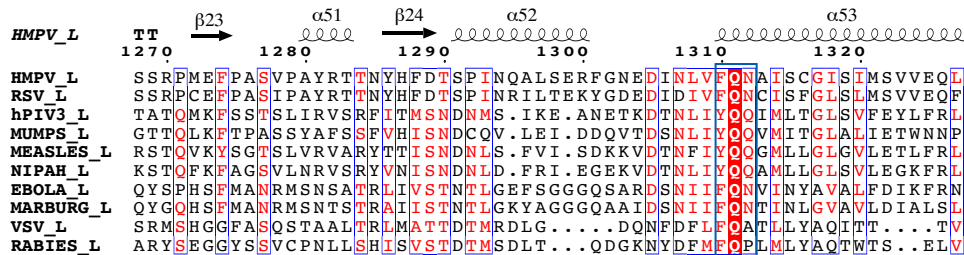


Motif B'

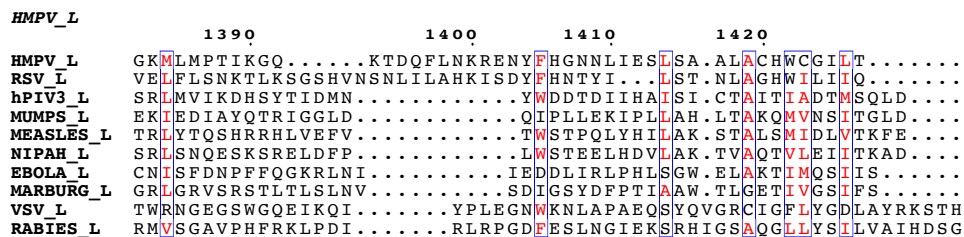
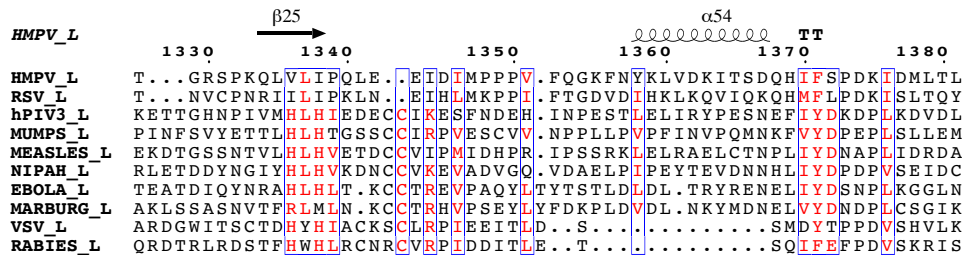


Motif C'

Motif D'



Motif E'



Supplementary figure 2 - Structure-based alignment of L from HMPV, RSV, human parainfluenza virus 3 (hPIV3), Mumps virus, Measles virus, Nipah virus, Ebola virus, Marburg virus, VSV and Rabies Virus. Accession codes for the sequences included in the alignment are: HMPV_L: Q6WB93.1; RSV_L: NP_044598.1; hPIV3: ACJ70091.1; MUMPS_L: ACH78356.1; MEASLES_L: AAF85706.1; NIPAH_L: NP_112028.1; EBOLA_L: Q05318.2; MARBURG_L: ABA87130.1; VSV_L: Q98776.1 and Rabies_virus L: BAA24082.1. Secondary structures of HMPV-L (this work) are displayed above the alignment. The domains of L are indicated by a colored bar below the alignment (NTD, grey; RdRp, aquamarine and capping domain, green). Evolutionary conserved motifs of the RdRp and capping domains are boxed. Polymerase motifs A-G were defined according to previous work⁴⁰⁻⁴³. In particular, we made use of the structure-based sequence alignment of HMPV-L (this work) with the poliovirus polymerase (PDB code: 1RA6). The five capping motifs are labeled A'-E'. The r.m.s.d. between the structure of HMPV-L and RSV_L¹⁶ is 1.21 Å over 1282 residues.