Selected Sequences: 55 /Selected Residues: 128
Deleted Sequences: 0 /Deleted Residues: 22

Gaps Scores: =0=   <.001   <.050   <.100   <.150   <.200   <.250   <.350   <.500   <.750   <1.00   =1=
Similarity Scores: =0=   <1e-6   <1e-5   <1e-4   <.001   <.010   <.100   <.250   <.500   <.750   <1.00   =1=

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                    10        20        30        40        50        60        70        80        90       100       110       120
        ========+=========+=========+=========+=========+=========+=========+=========+=========+=========+=========+=========+=========+

ACoV-WA1087                AGKQTELATNSSLLTLCA-----FSVDPAKTYVEAVRSGHKPVSNCIKMLANGSGNGQAITNGVEANTNQDSYG---GASVCIYCRAHVCHP----SMDGVCRLKGKYVQVPIG-TTDPI
BtCoV/020_16/M.dau/FIN/2016 AGKQTEHASNSSILTLCS-----FAVDPAKTYIDAVKSGQKPVGNCIKMLSNGSGNGMAITNGVEATGNQDSYG---GASVCLYCRAHVEHP---AMDGICRLKGKYVQMPIG-TTDPI
PEDV                       AGKQTEQAINSSLLTLCA-----FAVDPAKTYIDAVKSGHKPVGNCVKMLANGSGNGQAVTNGVEASTNQDSYG---GASVCLYCRAHVEHP----SMDGFCRLKGKYVQVPLG-TVDPI
Sc-BatCoV_512              AGKQTEQATNSSLLTLCA-----FAVDPPKTYLDAVKSGHRPVGNCVKMLANGSGNGQAITNGVEASTNQDSYG---GASVCLYCRAHVEHP----DMDGFCKLRGKYVQVPLG-TLDPI
ACoV-WA3607                AGKQTELASNSPLLTMCA-----FAVDPAKTYVDAVKKGVKPVGNCIKMLSNGSGTGQAITVGVEANTNQESYG---GASVCLYCRAHVEHP----TMDGACRFRGKYVQVPIG-TPDPI
BtRf-AlphaCoV              AGKQTELATNSPLLTMCA-----FSVDPAKTYLDAVKRGVKPVGNCIKMLSNGAGTGQAITVGVESNTNQDSYG---GASVCLYCRAHVEHP----SMDGRCRLKGKYVQVPLG-TIDPI
HipPBCoV-CHB25             AGKQTEMAVNSPLLTMCA-----FSVDPAKTYVDAVKRGAKPVGNCIRMLSNGSGNGQAITNGVEANTNQDSYG---GSSVCLYCRAHVEHP----SMDGHCRLKGKYVQVPSG-TIDPI
BtCoV_HKU10               AGKQTELAVNSPLLTMCA-----FAVDPAKTYLDAVKRGAKPVGNCIKMLANGSGTGQAVTTGVEANTNQDSYG---GASVCLYCRAHVEHP----SMDGYCKLKGRYVQVPMG-TIDPI
BtMr-AlphaCoV             AGKQTEQAANSSLLTMCA-----FAVDPAKCYLDAVKGGVKPVGNCIKMLSNGSGNGQAITHGVESNTSQDTYG---GASVCLYCRAHVDHP----SMDGFCRLKGKYVQVPLG-TLDPI
Mi-BatCoV_1A              AGKQTELVVNSSLLTLCS-----FAVDPAKCYLDAVKSGVKPVNNCVKMLSNGSGNGQAVTNGVEANTNQDSYG---GASVCLYCRAHVDHP----SIDGFCQFKGRYVQIPVG-TVDPI
Mi-BatCoV_HKU8           AGTQTELVANSSLLTMCS-----FAVDPRKCYLDAVKNGVKPVGNCIKMLSNGSGNGQAITNGVEANTNQDSYG---GASVCLYCRAHIDHP----SMDGFCQFKGRYVQVPIG-TVDPI
ACoV-WA2028               AGRQTELVANSSLLTLCA-----FAVDPEKTYIDAVKSGTKPVGNCVKMLSNGAGNGQAITNTVSEANTNQDSYG---GASVCLYCRAHVAHP----TMDGQCRFRGKYVQVPTG-TTDPI
BtNv-AlphaCoV            AGKQTELATNSSLLTLCA-----FAVDPPKMYIDSVKAGIKPVGNCIKMLSNGSGNGQAITTSVEANTNQDSYG---GASVCLYCRAHVEHP----GMDGCQFKGKYVQVPLG-TADPI
TyBCoV-HKU33             AGKQTELASNCALLTLCS-----FAVDPAKMYIDSVKSGMKPVGNCVKMLANGSGNGQAITVGVEANTNQDSYG---GASVCLYCRAHVCHP----SMDGQCKYKGKYVQVPLG-TLDPI
PK-BatCoV                AGKQTEIAANSGLLTLCA-----FSPDPAKMYLDAVKSGIKPVGNCIKMLSNGAGNGQAITVGVEANTNQDSFG---GASVCLYCRAHVEHP----AMDGRCQFKGKYVQIPVG-TVDPI
Rh-BatCoV_HKU2          AGKQTELACNSSLLTLCA-----FAVDPAKAYVSAVKQGAKPVGNCVKMLANGSGSGQAVTNGVEANMQDSYG---GASVCIYCRAHVDHP----AMDGACRFKGKYVQIPIG-VNDPI
BtCoV_CDPHE15           AGKQTEQVMNSSLLTMCA-----FSTDPAKTYLDAVKSGVKPIGNCVKMLANGAGNGQAITNGVEANSQDSYG---GASVCLWCRAYVEHP----AMDGFCKYRGKYVQVPIG-TVDPI
BtCoV-AMA-L-F          AGRQTEVATNSSLLTVCA-----FAVDPAAAYVDAVKSGIKPIGNCVKMLSNGAGNGQAITNGVEANTAQDSYG---GASVCLYCRCHIDHP----GMDGRCKFKGKYVQVPMS-VTDPI
BtKYNL63               AGKQTELAANSGLLTVCA-----FAVDPAAAYLDAVKQGAKPVGNCVKMLTNGAGNGQAVTATVDANSNQDSYG---GASVCLYCRAHVPHN----TMDGYCKYKGKYVQIPMG-CMDPI
HCoV_NL63              AGKQTELAVNSGLLTACA-----FSVDPATTYLEAVKHGAKPVSNCIKMLSNGAGNGQAITTSVDANTNQDSYG---GASICLYCRAHVPHP----SMDGYCKFKGKCVQVPIG-CLDPI
HCoV_229E             AGKQTEFVSNSHLLTHCS-----FAVDPAAAYLDAVKQGAKPVGNCVKMLTNGSGSGQAITCTIDSNTTQDTYG---GASVCIYCRAHVAHP----TMDGFCQYKGKWVQVPIG-TNDPI
MCoV                  AGKQTEHPSNSSLLTLCA-----FAPEPAKAYVELVKKGMQPVNNCVKMLSNGSGNGMAITNGVEATPNQDSYG---GASVCIYCRSHTAHP----SIDGMCRFKGKFVQVPAG-TADPI
TGEV                  AGKPTEHPSNSSLLTLCA-----FSPDPAKAYVDAVKRGMQPVGNCVKMLSNGAGNGQAITNGVEANTQQDSYG---GASVCIYCRAHVEHP----AIDGLCRYKGKYVQIPTG-TQDPI
Sm-CoV_X74            AGRPTEFPENSNLSICA-----FAVDPAKAYLDAIKSGVKPLSNCIKMLSNGSNGQAVSYTVDAKTNQDSYG---GASVCIYCRAYVEHP----TVDGLCQFKGRFVQVPLG-TKDPV
LRNV                  AGKPTEYATDCQLLTLCA-----FAVDPKDAYLTAVRQGHKLSNCIRMINNGSGNGLAITHRVEANTNQDSYG---GASCCLYCRASVEHP----GMDGNCILRGKYVQVPTG-TTDPI
Sa-CoV_T14            AGKSTEVPENVNILSMCA-----FSVDPEKTYLDYVKSGQNPLKSCVKMLDRTGNGMAITPRPEATYNQDSYG---GASVCIYCRSYTAHP----GYDGVCKLKGKFVQVPKG-TVDPV
Bat_Hp-BetaCoV        AGKPTEVAANSKCLTFCA-----FAVDPEKAYFDFVNSGGQPLNNCVRVLCTHTGTGRAITADPEATADQESYG---GSSCCLYCRCHISHP----SHNGLCKYKGKYVQIPNVCTNDPV
SARSr-CoV             AGNATEVPANSTVLSFCA-----FAVEPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFG---GASCCLYCRCHIDHP----NPKGFCDFKGRYVQIPTTCVNDPV
SARS-CoV              AGNATEVPANSTVLSFCA-----FAVDPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFG---GASCCLYCRCHIDHP----NPKGFCDLKGRYVQIPTTCANDPV
SARS-CoV-2            AGNATEVPANSTVLSFCA-----FAVDAAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQESFG---GASCCLYCRCHIDHP----NPKGFCDLKGKYVQIPTTCANDPV
Ei-BatCoV_C704       AGSATEVTSNSSILLCA-----FSVDPEATYKEYVDNGGAPIGNCVKMLTPHTGTGLAVTAKPDANMEQESFG---GASVCLYCRCHIEHP----GPNGVCKFKGRYVQLPLAGVQDPI
Ro-BatCoV_GCCDC1    AGSATEVASNSAILSLCA-----FSVDPEATYKDYLDNGGTPIGNCVKMLTTHTGTGLALTAKPDASIDQESFG---GASCCIYCRCHIEHP----GASGVCKFKGRFVQIPLCGVPDPI
Ro-BatCoV_HKU9      AGSATEVASNSSILSLCS-----FSVDPEATYKDYLDNGGSPIGNCVKMLTPHTGTGLAITAKPDANIDQESFG---GASCCLYCRCHIEHP----GASGVCKYKGKFVQIPLVGVNDPI
EriCoV             AGSNTEYASNSSVLSLVN-----FAVDPAKAYTDYVNAGGAPLTNCVKMLTPKTGTGIAISVKPESNLDQETYG---GASVCLYCRAHIEHP----DVSGVCKFKGKFVQIPAQCTRDPV
MERS-CoV           AGSNTEFASNSSVLSLVN-----FTVDPQKAYLDFVNAGGAPLTNCVKMLTPKTGTGIAISVKPESTADQETYG---GASVCLYCRAHIEHP----DVSGVCKYKGKFVQIPAQCVRDPV
Pi-BatCoV_HKU5    AGSNTEFAINSSVLSAVT-----FSVDPGKAYLDFVNAGGAPLTNCVKMLTPKTGTGIAVSVKPEANADQDTYG---GASVCLYCRAHVEHP----DVTGVCKFKGKFVQVPLH-IRDPV
Ty-BatCoV-HKU4    AGANTEFASNSTVLTLVA-----FAVDPAKAYLDYVGSGGTPLSNYVKMLAPKTGTGQAITAKPEATADQETYG---GASVCKYKGKFVQIPAH-VRDPV
ChRCoV_HKU24      AGHATEYAANSAILSLCA-----FSVDPKKTYLDYIQQGGIPIANCVKMLCDHAGTGMAITVKPDATTNQDSYG---GASVCIYCRARIEHP----DVDGLCKLRGKYVQVPIG-IKDPV
MHV               AGTATEYASNSSVILSLCA-----FSVDPKKTYLDYIKQGGVPVTNCVKMLCDHAGTGMAITIKPEATTNQDSYG---GASVCIYCRSRVEHP----DVDGLCKLKGRYVQVPLG-IKDPV
MrufCoV_2JL14     AGTPTEYASNSSVLSLCA-----FSVDPKKTYLDYQQGGVPLTNCVKMLCDHAGTGMAITVKPEATTNQDSYG---GASVCIYCRARVEHP----DVDGLCKLRGKYVQVPIG-IKDPV
HCoV_OC43         AGTATEYASNSSILSLCA-----FSVDPKKTYLDFIQQGGTPIANCVKMLCDHAGTGMAITVKPDATTSQDSYG---GASVCIYCRAHVEHP----DVDGLCKLRGKYVQVPLG-IKDPV
HCoV_HKU1         AGVATEYAANSSILSLCA-----FSVDPKKTYLDYIQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYG---GASVCIYCRARVEHP----DVDGICKLRGKYVQVPLG-IKDPV
BcanCoV_CB17      KGHDTEEVEAVGILSLCS-----FAVDPASCYKEYIAGGGKPLANCVKMLTVHNGSGFAITTKPSPTPDQDSYG---GASVCLYCRAHVAHP----NMDGKCPYKGSFVQIPSV-EQDPV
DuCoV_2714        KGHETEELESVGILSLCA-----FAVNPEETYLKYSAGNQPLGNCVKMLTVHNGNGFAITTKPSPTPDQDSYG---GASVCLYCRAHIAHPGASGTLDGRCPFKGSFVQIPTS-EKDPV
ACoV_9203         KGHETEEVDAVGILSLCA-----FAVDPADTYCKYVAAGNQPLGNCVKMLTVHNGSGFAITSKPSPTPDQDSYG---GVSVCLYCRAHIAHPGGAGNLDARCQFKGSFVQIPTT-EKDPV
IBV               KGHETEEVDAVGILSLCS-----FAVDPADTYCKYVAAGNQPLGNCVKMLTVHNGSGFAITSKPSPTPDQDSYG---GASVCLYCRAHIAHPGSVGNLDGRCQFKGSFVQIPTT-EKDPV
BWCoV             HGVSTESVENCGILSLCS-----FALDAKECYLEYIKEGGAPLSNCVKMLTLHTGSGAAVTVKPAPTPEQDSFG---GASVCLYCRAHISHP----GVYGVCQFKGKFVQIPVE-EKDPV
CMCoV_HKU21       TGTHVEYQENASLLTYLA-----FAVNPKEAYLKHVADGGKPIQGVIQMIAP-IGSGFAVTTKPQPNEMQYSYG---GASVCLYCRAHITHP----GVDGRCVYKGRFVHIDKD--KEPV
BulCV_HKU11       NGTQIEYQENASLLTYLA-----FAVNPKEAYLKHLADGGKPIQGCIQMIAS-LGPGFAVTTKPQPNEHQFSYG---GASICLYCRAHIPHP----GVDGRCVYKGRFVHIDKD--KEPV
WECoV_HKU16       NGTQIEYQENASLLTYLA-----FSVDPKAAYLKHIADGGKPIQGCIQMIAT-LGPGFAVTTKPQPNEQQFSYG---GASICLYCRAHIPHP----GVDGRCTYKGRFVQIDKD--KEPV
PoCoV_HKU15       SGTQIEYQQNASLLTYLA-----FSVDPKTAYLKHLADGGSPIQGCVQMVAA-MGPGFAVTTKPQPNEHQYSYG---GASICLYCRAHIPHP----GVDGRCPYKGRFVHIDKD--KEPV
MunCV_HKU13       NGTHIEYQENASLLTYLA-----FSVDPKAAYLKHLADGGKPIQGCVQMVAA-MGPGFAVTIKPQPSEHQNSYG---GASICLYCRAHVEHP----SMDGRCNYKGRFVHIDKD--KEPV
NHCoV_HKU19       SGTSVEYQENNSLLTYLA-----FAVNPREAYLAHISNGGKPIQGAVRVIAP-QGEGFAVTTKPQPNAMQHAYG---GASICLYCRAHVTHP----SMDGRCNYKGKFVQVIDKD--LEPT
WiCoV_HKU20       NGTAIEYQQNASLLTYLA-----FAADPKDAYLKHVQAGGKPLMGAVKMVAP-IGEGFAVTTKPQPNANQHSYG---GASICVYCRAHVPHN----TVNGQCLYKGIFVQIDKD--LDPF
PsNV              STNLCILCGVPSVVS-CADCVRKFPLCCSCLYHHVADTNHSTIQSFNEMKCNAPGCEVS-------DCRLLSYGLSSGNDGSMRCEVH---------------------------SSSSV
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Selected Cols:

Gaps Scores:

Similarity Scores: