

CLUSTAL O(1.2.4) multiple sequence alignment

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sp|P36334|SPIKE_CVHOC      ----MFLILLISLPT-AFAVIGDLKCTSDNINDK-----DTGPPPISTDTVDVTNGLGT  49
sp|Q0ZME7|SPIKE_CVHN5     -----MFLIIFILPT-TLAVIGDFNCTNSFINDY-----NKTIPRISEDVVDVSLGLGT  48
sp|K9N5Q8|SPIKE_MERS1     MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTWP----RPIDVSKADGI   56
sp|P59594|SPIKE_SARS      ----MFIFLLFLTLT-SG-----SDLDRCTTFD-----DVQAPN---YTQHTSSMRGV   40
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  ----MFVFLVLLPLV-SS-----QCV----NLT-----TRTQLP---PAYTNSSTRGV   36
sp|P0DTC2|SPIKE_SARS2     ----MFVFLVLLPLV-SS-----QCV----NLT-----TRTQLP---PAYTNSFTRGV   36
OM858820.1               ----MFVFLVLLPLV-SS-----QCV----NLR-----TRTQLP---PAYTNSFTRGV   36
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sp|P36334|SPIKE_CVHOC      YYVLDRVYLNNTTLFLNGYYPTSGSTYRNMALKGSVLLS----RLW----FKPPFLSDFIN  101
sp|Q0ZME7|SPIKE_CVHN5     YYVLNRVYLNNTLLFTGYFPKSGANFRDLALKGSIYLS----TLW----YKPPFLSDFNN  100
sp|K9N5Q8|SPIKE_MERS1     IYPQGRYTSNITITYQGLF-PYQGDHGDYVYSAGHATGTPQKLFVANYSQD-VKQFAN  114
sp|P59594|SPIKE_SARS      YYPDEIFRSDTLYLTQDLFLPFYSNVT---GFHTIN-----HT----FGNP-VIPFKD   85
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  YYPDKVFRSSVLHLTQDLFLPFFSNVT---WFHAIHVSGTNGIKR---FDNP-VLPFND   88
sp|P0DTC2|SPIKE_SARS2     YYPDKVFRSSVLHSTQDLFLPFFSNVT---WFHAIHVSGTNGTKR---FDNP-VLPFND   88
OM858820.1               YYPDKVFRSSVLHSTQDLFLPFFSNVT---WFHAIHVSGTNGTKR---FDNP-VLPFND   88
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sp|P36334|SPIKE_CVHOC      GIFAKVKNTKVIKDRV-----MYSEFPAITIGSTFVNtsy-----SVVVQPR  143
sp|Q0ZME7|SPIKE_CVHN5     GIFSKVKNTKLYVNNT-----LYSEFSTIVIGSVFVNtsy-----TIVVQPH  142
sp|K9N5Q8|SPIKE_MERS1     GFVVRIGAAANSTGTVIIISPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTLVLLPD  174
sp|P59594|SPIKE_SARS      GIYFAATE-----KSNVVRGWVFGSTMNKSQ-----SVIINN  119
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  GVVFASTE-----KSNIIRGWIFGTTLDSTQ-----SLLIVNN  122
sp|P0DTC2|SPIKE_SARS2     GVVFASTE-----KSNIIRGWIFGTTLDSTQ-----SLLIVNN  122
OM858820.1               GVVFASTE-----KSNIIRGWIFGTTLDSTQ-----SLLIVNN  122
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sp|P36334|SPIKE_CVHOC      TINSTQDGDNKLQGLLEVSVVCQYNMCEYPQTICHPNLGNHRK-----  185
sp|Q0ZME7|SPIKE_CVHN5     -----NGILEITACQYTMCEYPHTVCKS-KGSIRN-----  171
sp|K9N5Q8|SPIKE_MERS1     -----G-----CGTLLRAF--YCILEPRSGNHCPAGNSYTSFATYHTPATDCSDGNYN  220
sp|P59594|SPIKE_SARS      -----S-----TNVIRACNFEELCDNPFFAVSKPMGT-----  146
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  -----A-----TNVVIKVECFQFCNDPFLGVYYHKNN-----  149
sp|P0DTC2|SPIKE_SARS2     -----A-----TNVVIKVECFQFCNDPFLGVYYHKNN-----  149
OM858820.1               -----A-----TNVVIKVECFQFCNDPFLDVYYHKNN-----  149
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sp|P36334|SPIKE_CVHOC      ELWHLDTGV-VSCLYKRNFTYDVNA-----DYL-----YFHFYQEGGTFYAYFTDT-  230
sp|Q0ZME7|SPIKE_CVHN5     ESWHIDSSE-PLCLFKKNFTYNVSA-----DWL-----YFHFYQERG VFYAYYADV-  216
sp|K9N5Q8|SPIKE_MERS1     RNASLNSFKEYFNLRNCTFMYTYNITEDEILEWFGITQTAQG-VHLFSSRYVDLYGGN--  277
sp|P59594|SPIKE_SARS      ----QTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGLFVYVKGYP  202
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  KSWMESEFRVYSSANNCTFEYVSQPF LMDLEGGQGNFKNLRNFVFKNIDGYFKIYSKHTP  209
sp|P0DTC2|SPIKE_SARS2     KSWMESEFRVYSSANNCTFEYVSQPF LMDLEGGQGNFKNLRNFVFKNIDGYFKIYSKHTP  209
OM858820.1               KSWMES--GVYSSANNCTFEYVSQPF LMDLEGGQGNFKNLRNFVFKNIDGYFKIYSKHTP  207
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sp|P36334|SPIKE_CVHOC      -GV-----V-TKFLFNVLGMALSHYYVPLTCN-----S-----KLITLEYWVTP  268
sp|Q0ZME7|SPIKE_CVHN5     -GM-----P-TTFLFSLYLGITLSHYYVPLTCN-----AISSNTDNETLEYWVTP  260
sp|K9N5Q8|SPIKE_MERS1     -----MFQFATLPVYDTIKYYSIIPHSIR---SIQSDRKAW----AAFYVYK  317
sp|P59594|SPIKE_SARS      IDVVRDLP SGFNTLKPIFKLPLGINITNFRAILTAFS-----PAQDIWGTSAAYFVG  256
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  INLVRDLP PGFSALEPLVDLPIGINITRFQTL LALHRSYLT PGDSSSGWTAGAAAYVGY  269
sp|P0DTC2|SPIKE_SARS2     INLVRDLP QGFSALEPLVDLPIGINITRFQTL LALHRSYLT PGDSSSGWTAGAAAYVGY  269
OM858820.1               INLVRDLP QGFSALEPLVDLPIGINITRFQTL LALHRSYLT PGDSSSGWTAGAAAYVGY  267
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sp|P36334|SPIKE_CVHOC      LTSRQYLLAFNQDGIIFNAEDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRR  328
sp|Q0ZME7|SPIKE_CVHN5     LSRQYLLNFDEHGVITNAVDCSSSFLSEIQCKTQSFAPNTGVYDLSGFTVKPVATVYRR  320
sp|K9N5Q8|SPIKE_MERS1     LQPLTFL LDFSDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQ  377
sp|P59594|SPIKE_SARS      LKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVP SGDVVRF  316
tr|A0A6B9WHD3|A0A6B9WHD3_SARS  LQPRTFLLKYNENGITITDAVDCALDPLSETKCTLKSF TVEKGIYQTSNFRVQPTDSIVRF  329
sp|P0DTC2|SPIKE_SARS2     LQPRTFLLKYNENGITITDAVDCALDPLSETKCTLKSF TVEKGIYQTSNFRVQPTESIVRF  329
OM858820.1               LQPRTFLLKYNENGITITDAVDCALDPLSETKCTLKSF TVEKGIYQTSNFRVQPTESIVRF  327

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sp P36334 SPIKE_CVHOC	KNPLPNCNIEAWLNDKSVPSPLNWERKTFSNCFNMSSLSMFIQADSFTCNNIDAAKIYG	388
sp Q0ZME7 SPIKE_CVHN5	IPNLPDCDIDNWLNNVSVPSPLNWERRIFSNCNFNLTLLRLVHVSFSCNNLDSKIFG	380
sp K9N5Q8 SPIKE_MERS1	AEG-VECDFSPLLSG-TPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIAS	435
sp P59594 SPIKE_SARS	PNITNLCPFGEVFNATKFPVSVAWERKKISNCVADYSVLNYSFSTFKCYGVSATKLN	376
tr A0A6B9WHD3 A0A6B9WHD3_SARS	PNITNLCPFGEVFNATTFASVYAWNRKRISNCVADYSVLNYSFSTFKCYGVSPTKLN	389
sp P0DTC2 SPIKE_SARS2	PNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNYSASFSTFKCYGVSPTKLN	389
OM858820.1	PNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNYSASFSTFKCYGVSPTKLN	387

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sp P36334 SPIKE_CVHOC	MCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAVSVSR-F	447
sp Q0ZME7 SPIKE_CVHN5	SCFNSITVDKFAIPNRRRDDQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNTINN-F	439
sp K9N5Q8 SPIKE_MERS1	NCYSSLILDYFSYPLSMKSDLVSSAGPISQFNYKQSFNSPTCLILATVPHNLTTITKPL	495
sp P59594 SPIKE_SARS	LCFSNVYADSFVVGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNY	436
tr A0A6B9WHD3 A0A6B9WHD3_SARS	LCFTNVYADSFVITGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSKHIDAKEGGNF	449
sp P0DTC2 SPIKE_SARS2	LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNY	449
OM858820.1	LCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNY	447

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sp P36334 SPIKE_CVHOC	NPSTWNKRFGFIEDSVFKPRPAGVLTNHDEVVYAQHCFAKPNFCPCCK--LNGSCVGS	505
sp Q0ZME7 SPIKE_CVHN5	NPSSWNRRYGFSGF-----NLSSYDVVYSDHCFVNSDFCPCA--DPSV-VNSCAK	487
sp K9N5Q8 SPIKE_MERS1	KYSYINKCSRFLSD-----DRTEVPQLVNAN--QYSPCVSIVPST-VW----	535
sp P59594 SPIKE_SARS	NYKYRYLRHGKLRP-----FERDISNVPFSP--DGKPCTP-PALNCYW----	476
tr A0A6B9WHD3 A0A6B9WHD3_SARS	NYLYRLFRKANLKP-----FERDISTEIIYQA--GSKPCNGQTGLNCYY----	490
sp P0DTC2 SPIKE_SARS2	NYLYRLFRKSNLKP-----FERDISTEIIYQA--GSTPCNGVEGFNCYF----	490
OM858820.1	NYRYRLFRKSNLKP-----FERDISTEIIYQA--GSKPCNGVEGFNCYF----	488

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sp P36334 SPIKE_CVHOC	KNNGIGTCPAGTNYLTCD-----NLCTPDPITFTGTQYKCPQTKSLVGIGEHC	553
sp Q0ZME7 SPIKE_CVHN5	SKPPSAICPAGTKYRHCDLDTLYVKNWCRCSCLPDPISTYSPNTCPQKKVVVGIGEHCP	547
sp K9N5Q8 SPIKE_MERS1	-----EDGDYYRK-----QLSPLEGGGWLW-----	555
sp P59594 SPIKE_SARS	-----PLNDYGFYF-----	485
tr A0A6B9WHD3 A0A6B9WHD3_SARS	-----PLYRYGFYP-----	499
sp P0DTC2 SPIKE_SARS2	-----PLQSYGFQP-----	499
OM858820.1	-----PLQSYGFQP-----	497

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sp P36334 SPIKE_CVHOC	GLAVKSDYCGG---NSCTCRPQAFLGWSADSCSQGDKCNIFANFILHDVNSGLTCST--	607
sp Q0ZME7 SPIKE_CVHN5	GLGINEEEKCGTQLNHSSCFSPDAFLGWSFDSCISNNRCNIFSNFIFNGINS GTTCSN--	605
sp K9N5Q8 SPIKE_MERS1	-----ASGSTVAMTEQLQMGGFI-----TVQYGTDTNSVCPKLE	589
sp P59594 SPIKE_SARS	-----TTGIGYQPYRVVLSFEL-----L----NAPATVCGP--	513
tr A0A6B9WHD3 A0A6B9WHD3_SARS	-----TDGVGHQPYRVVLSFEL-----L----NAPATVCGP--	527
sp P0DTC2 SPIKE_SARS2	-----TNGVGYPYRVVLSFEL-----L----HAPATVCGP--	527
OM858820.1	-----TNGVGYPYRVVLSFEL-----L----HAPATVCGP--	525

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sp P36334 SPIKE_CVHOC	DLQKANTDIILGVCVNYDLYGILGQGFVEVNATYYNSWQNLLYDSNGNLY-GFRDYIIN	666
sp Q0ZME7 SPIKE_CVHN5	DLLYSNTEISTGVCVNYDLYGITGQGFKEVSAAYYNNWQNLLYDSNGNII-GFKDFLTN	664
sp K9N5Q8 SPIKE_MERS1	FANDTKIASQLGNCVEYSLYGVSGRGVFQNC TAVG-VRQQRFVYDAYQNLVGYYS--DG	646
sp P59594 SPIKE_SARS	---KLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRF-QPFQQFGRDVSDFDFT-DSVRDPKTS	568
tr A0A6B9WHD3 A0A6B9WHD3_SARS	---KKSTNLVKNKCVNFNFNGLTGTGVLTESNKKF-LPFQQFGRDIADTT-DAVRDPQTL	582
sp P0DTC2 SPIKE_SARS2	---KKSTNLVKNKCVNFNFNGLTGTGVLTESNKKF-LPFQQFGRDIADTT-DAVRDPQTL	582
OM858820.1	---KKSTNLVKNKCVNFNFNGLTGTGVLTESNKKF-LPFQQFGRDIADTT-DAVRDPQTL	580

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sp P36334 SPIKE_CVHOC	RTFMIRSCYSGRVSAAFH--ANSSEPALLFRNIKCNYVFNNLSLTRLQLQ-----PI	714
sp Q0ZME7 SPIKE_CVHN5	KTYTILPCYSGRVSAAFY--QNSSSPALLYRNLCYSVLNNIS--FIS-----QP	710
sp K9N5Q8 SPIKE_MERS1	NYYLCLACVSVPSVIYD--KETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTY	704
sp P59594 SPIKE_SARS	EILDIPCSFSGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLT--PAWRIYSTGN	626
tr A0A6B9WHD3 A0A6B9WHD3_SARS	EILDITPCSFSGGVSVITPGTNASNQVAVLYQDVNCTEVPVAIHADQLT--PTWRVYSTGS	640
sp P0DTC2 SPIKE_SARS2	EILDITPCSFSGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT--PTWRVYSTGS	640
OM858820.1	EILDITPCSFSGGVSVITPGTNTSNQVAVLYQGVNCTEVPVAIHADQLT--PTWRVYSTGS	638

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sp P36334 SPIKE_CVHOC	NYFDSYLGCVVNAYNSTAISVQCDLTVGSGYCVDYSK--NRRSGAIIITGTYFTN-FEP	771
sp Q0ZME7 SPIKE_CVHN5	FYFDSYLGCVLNAVNLTSYSVSSCDLRMGSGFCIDYALPSSRRKRRGISSPYRFVT-FEP	769
sp K9N5Q8 SPIKE_MERS1	GPLQTPVGCVLGLVNSS-LFVEDCKLPLGQSLCALPDPSTLTPRSVRSVPGEMRLASIA	763
sp P59594 SPIKE_SARS	NVFQQTQAGCLIGAEHVD--TSYECDIPIGAGICASYHTVS-L---LRSTSQKSI---VA	676
tr A0A6B9WHD3 A0A6B9WHD3_SARS	NVFQTRAGCLIGAEHVN--NSYECDIPIGAGICASYQTQT-NS----RSVASQSI---IA	690
sp P0DTC2 SPIKE_SARS2	NVFQTRAGCLIGAEHVN--NSYECDIPIGAGICASYQTQT-NSPRRARSVASQSI---IA	694
OM858820.1	NVFQTRAGCLIGAEHVN--NSYECDIPIGAGICASYQTQT-NSRRRARSVASQSI---IA	692
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sp P36334 SPIKE_CVHOC	FTVNSVNDLSLEPVGGLYEIQIPSEFTIGNMVEFIQTSSPKVTIDCAAFVCGDYAACKSQL	831
sp Q0ZME7 SPIKE_CVHN5	FNVSFVNDSVETVGGFLFEIQIPTNFTIAGHEEFIQTSSPKVTIDCSAFVCSNYAACHDLL	829
sp K9N5Q8 SPIKE_MERS1	FNHPIQ-V-DQLNSSYFKLSIPTNFSFGVTQEYIQTTIQKVTVDCKQYVCNGFQKCEQLL	821
sp P59594 SPIKE_SARS	YTMSLG-ADSSIAYSNNIIAIPTNFISISITTEVMPVSMAKTSVDNMYICGDSTECANLL	735
tr A0A6B9WHD3 A0A6B9WHD3_SARS	YTMSLG-AENSVAYSNNIIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLL	749
sp P0DTC2 SPIKE_SARS2	YTMSLG-AENSVAYSNNIIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLL	753
OM858820.1	YTMSLG-AENSVAYSNNIIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLL	751
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sp P36334 SPIKE_CVHOC	VEYGSFCDNINAILTEVNELLDTTQLQVANS LMNGVTLSTKLKDGVNFNVDINFPVLG	891
sp Q0ZME7 SPIKE_CVHN5	SEYGTFCDNINSILNEVNLDLDTQLQVANALMQGVTLSSNLNTNLHSDVDNIDFKSLLG	889
sp K9N5Q8 SPIKE_MERS1	REYQGFCSKINQALHGANLRQDSDVRNLFASVKSSQSSPI-----IPFGGGFNLTLEP	876
sp P59594 SPIKE_SARS	LQYGSFCTQLNRALSGIAAEQDRNTREVFQVQKMYKTPT-----LKYFGGF-NFSQILP	789
tr A0A6B9WHD3 A0A6B9WHD3_SARS	LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVQKIYKTPP-----IKDFGGF-NFSQILP	803
sp P0DTC2 SPIKE_SARS2	LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVQKIYKTPP-----IKDFGGF-NFSQILP	807
OM858820.1	LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVQKIYKTPP-----IKDFGGF-NFSQILP	805
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sp P36334 SPIKE_CVHOC	CLGSECSKASSRSAIEDLLFDKVKLSDVGFVEAYNNCT--GGAERDLCVQSYKGIKVL	949
sp Q0ZME7 SPIKE_CVHN5	CLGSQCGS-SSRSLLEDLLFNKVKLSDVGFVEAYNNCT--GGSEIRDLLCVQSFNGIKVL	946
sp K9N5Q8 SPIKE_MERS1	-VSISTGSRARSIAIEDLLFDKVTIADPGYMQGYDDCMQQGPASARDLCAQYVAGYKVL	935
sp P59594 SPIKE_SARS	-DP---LKPTKRSFIEDLLFNKVTADAGFMKQYGECL--GDINARDLCAQKFNGLTVL	843
tr A0A6B9WHD3 A0A6B9WHD3_SARS	-DP---SKPSKRSFIEDLLFNKVTADAGFIKQYGDCL--GDIAARDLCAQKFNGLTVL	857
sp P0DTC2 SPIKE_SARS2	-DP---SKPSKRSFIEDLLFNKVTADAGFIKQYGDCL--GDIAARDLCAQKFNGLTVL	861
OM858820.1	-DP---SKPSKRSFIEDLLFNKVTADAGFIKQYGDCL--GDIAARDLCAQKFNGLTVL	859
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sp P36334 SPIKE_CVHOC	PPLLSENQISGYTLAATSASLFPWTA-----AGVPFYLNVQYRINGLGVTMDVLSQNQK	1005
sp Q0ZME7 SPIKE_CVHN5	PPILSETQISGYTTAATVAAMFPWSA-----AGVPFSLNVQYRINGLGVTMDVLNKNQK	1002
sp K9N5Q8 SPIKE_MERS1	PPLMDVNMEAAYTSSLGSIAGVGWTAGLSSFAAIPFAQSI FYRLNGVGITQQVLSNQK	995
sp P59594 SPIKE_SARS	PPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK	903
tr A0A6B9WHD3 A0A6B9WHD3_SARS	PPLLTDemiaQYTSALLAGTITSWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK	917
sp P0DTC2 SPIKE_SARS2	PPLLTDemiaQYTSALLAGTITSWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK	921
OM858820.1	PPLLTDemiaQYTSALLAGTITSWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK	919
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sp P36334 SPIKE_CVHOC	LIANAFNNALYAIQEGFDATNSALVKIQAVVNANAEALNLLQQLSNRFGAISASLQEIL	1065
sp Q0ZME7 SPIKE_CVHN5	LIANAFNKALLSIQNGFTATNSALAKIQSVVNANAQALNLLQQLFNKFGAISSSLQEIL	1062
sp K9N5Q8 SPIKE_MERS1	LIANKFNQALGAMQTGFTTNEAFHKVQDAVNNNNAQALSKLASELSNTFGAISASIGDII	1055
sp P59594 SPIKE_SARS	QIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDIL	963
tr A0A6B9WHD3 A0A6B9WHD3_SARS	LIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDIL	977
sp P0DTC2 SPIKE_SARS2	LIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDIL	981
OM858820.1	LIANQFNSAIGKIQDSLSTASALGKLQNVVNQNAQALNTLVKQLSSNFGAISSVLNDIL	979
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sp P36334 SPIKE_CVHOC	SRLDALEAEQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNCEVKSSSRIN	1125
sp Q0ZME7 SPIKE_CVHN5	SRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNCEVKSSPRIN	1122
sp K9N5Q8 SPIKE_MERS1	QRLDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLAKDKVNCEVKAQSKRSG	1115
sp P59594 SPIKE_SARS	SRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1023
tr A0A6B9WHD3 A0A6B9WHD3_SARS	SRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1037
sp P0DTC2 SPIKE_SARS2	SRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1041
OM858820.1	SRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1039
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sp P36334 SPIKE_CVHOC	FCGNGNHIISLVQNAPYGLYFIHFSYVPTKYVTARVSPGLCIAGDR--GIAPKSGYFVNV	1183
sp Q0ZME7 SPIKE_CVHN5	FCGNGNHILSLVQNAPYGLLFIHFSYKPTSFKTVLVSPGLCLSGDR--GIAPKOGYFIKO	1180

sp K9N5Q8 SPIKE_MERS1	FCGQGTHIVSFVVNAPNGLYFMHVGYYPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKT	1175
sp P59594 SPIKE_SARS	FCGKGHYHLSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKA---YFPREGVFFVN	1080
tr A0A6B9WHD3 A0A6B9WHD3_SARS	FCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKA---HFPREGVFFVS	1094
sp P0DTC2 SPIKE_SARS2	FCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKA---HFPREGVFFVS	1098
OM858820.1	FCGKGHYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKA---HFPREGVFFVS	1096
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sp P36334 SPIKE_CVHOC	-----NNTWMTGSGYYYPEPITENNVMSTCAVNYTKAPYVML--NTSIPNLPDFKEE	1236
sp Q0ZME7 SPIKE_CVHN5	-----NDSWMFTGSSYYYPEPISDKNVVFMNSCSVNFTKAPFIYL--NNSIPNLSDFEAE	1233
sp K9N5Q8 SPIKE_MERS1	NNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQN-ISTNLPPPLLGNSTGIDFQDE	1234
sp P59594 SPIKE_SARS	-----GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQ--PELDSFKEE	1133
tr A0A6B9WHD3 A0A6B9WHD3_SARS	-----GTHWFTQRNFYEPQIITTDNTFVSGSDVVIGIVNNTVYDPLQ--PELDSFKEE	1147
sp P0DTC2 SPIKE_SARS2	-----GTHWFTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ--PELDSFKEE	1151
OM858820.1	-----GTHWFTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ--PELDSFKEE	1149
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sp P36334 SPIKE_CVHOC	LDQWFKNQTSVAPDLSLD-YINVTFDLQLQVEMNRLQEAIKVLNQSYINLKDIGTYEYVK	1295
sp Q0ZME7 SPIKE_CVHN5	LSLWFKNHTSIAPNLTFNSHINATFLDLYEMNVIQESIKSLNSSFINLKEIGTYEMYVK	1293
sp K9N5Q8 SPIKE_MERS1	LDEFFKNVSTSIPIFGLTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNK	1294
sp P59594 SPIKE_SARS	LDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK	1193
tr A0A6B9WHD3 A0A6B9WHD3_SARS	LDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK	1207
sp P0DTC2 SPIKE_SARS2	LDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK	1211
OM858820.1	LDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK	1209
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sp P36334 SPIKE_CVHOC	WPWYVWLLICLAGVAMLVLLFFICCCTGCGTSCFK--KCGGCCDDYTGQELVIK-TSHD	1352
sp Q0ZME7 SPIKE_CVHN5	WPWYIWLILVILFIIFLMILFFICCCTGCGSACFS--KCHNCCDEYGGHNDFVIK-ASHD	1350
sp K9N5Q8 SPIKE_MERS1	WPWYIWLGFIAGLVALALCVFFILCCTGCGTNCMGKLCNRCCDRYEEYDLEPHKVHVH-	1353
sp P59594 SPIKE_SARS	WPWYVWLGFIAGLIAIVMVTILCCMTSCCCLKGACSCGSCCKF-DEDDSEPVLKGVKL	1252
tr A0A6B9WHD3 A0A6B9WHD3_SARS	WPWYIWLGFIAGLIAIMVTIMLCCMTSCCCLKGCCSCGSCCKF-DEDDSEPVLKGVKL	1266
sp P0DTC2 SPIKE_SARS2	WPWYIWLGFIAGLIAIVMVTIMLCCMTSCCCLKGCCSCGSCCKF-DEDDSEPVLKGVKL	1270
OM858820.1	WPWYIWLGFIAGLIAIVMVTIMLCCMTSCCCLKGCCSCGSCCKF-DEDDSEPVLKGVKL	1268
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sp P36334 SPIKE_CVHOC	D--	1353
sp Q0ZME7 SPIKE_CVHN5	D--	1351
sp K9N5Q8 SPIKE_MERS1	---	1353
sp P59594 SPIKE_SARS	HYT	1255
tr A0A6B9WHD3 A0A6B9WHD3_SARS	HYT	1269
sp P0DTC2 SPIKE_SARS2	HYT	1273
OM858820.1	HYT	1271