Homo-oligomer Protein Binding Sites:

ws homotrimer-Conf1-5X58

Host-Virus Interaction Protein Binding Sites:

```
wS heterodimer-IGHV3-30-3-2GHW
   wS trimer-ACE2-Conf1-6ACG
   wS_trimer-ACE2-Conf2-6ACJ
   wS trimer-ACE2-Conf3-6ACK
   wS trimer-IGHV3-30-3-Conf1-6NB6
   wS trimer-IGHV3-30-3-Conf2-6NB7
                                MFV-----FLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQD 53
YP 009724390
SP|P59594|SPIKE CVHSA
                                MFI--FLL-FLTLTSGSDLDRCTTFDDVOAPNYTOHTSSMRGVYYPDEIFRSDTLYLTOD 57
                                MFI--FLL-FLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQD 57
TR | Q6UZF4 | Q6UZF4_CVHSA
TR Q6UZF0 Q6UZF0_CVHSA
                                MFI--FLL-FLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQD 57
TR Q6JH46 Q6JH46_CVHSA
TR Q692E4 Q692E4_CVHSA
                                MFI--FLL-FLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQD 57
                                MFI--FLL-FLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQD 57
SP Q3LZX1 SPIKE BCHK3
                                MKILIF---AFLANLAKAQEGCGIISRKPQPKMAQVSSSRRGVYYNDDIFRSDVLHLTQD 57
SP Q315J5 SPIKE_BCRP3
                                MKILIL---AFLASLAKAQEGCGIISRKPQPKMAQVSSSRRGVYYNDDIFRSNVLHLTQD 57
SP | Q0Q475 | SPIKE_BC279
                                MKVLIF---ALLFSLAKAOEGCGIISRKPOPKMEKVSSSRRGVYYNDDIFRSDVLHLTOD 57
TR R9QTA0 R9QTAO CVHSA
                                --MILL---LLFLSSAKAQEGCGVISNKPQRTFDQYSSTFRGVYYNDDIFRSDVLHLTQD 55
TR R9QTH3 R9QTH3_CVHSA
                                MKIFLF---SLLFSAALAOEGCGLLSFKPOPKLAOFSSSKRGVYYNDDIFRSDVLHLTOD 57
TR A0A0K1Z074 A0A0K1Z074 CVHSA MKILIF---AFLVTLVKAQEGCGVINLRTQPKLSQVSSSRRGVYYNDDIFRSDVLHLTQD 57
TR A0A0U1WH16 A0A0U1WH16 CVHSA MKILIF---AFLVTLVKAQEGCGVINLKTQPTLTQVSSSRRGVYYNDDIFRSDVLHLTQD 57
TR | A0A166ZL64 | A0A166ZL64 | 9NIDO MFIVFLISYTTFLIPYTATTTC--FSGPTIENKLNISSGSRGVYYPDDIFRSNVSVLVTG 58
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA MFIVFLISYTTFLIPYTATTTC--FKGPTTENKLNISSGSRGVYYPDDIFRSNVSVLVTG 58
                                                                     .* **** *..***..
YP 009724390
                                LFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSK 113
                                LFLPFYSNVTGFHTINH-----TFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNK 110
LFLPFYSNVTGFHTINH-----TFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNK 110
SP P59594 SPIKE_CVHSA
TR | Q6UZF4 | Q6UZF4_CVHSA
                                LFLPFYSNVTGFHTINH-----TFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNK 110
TR | Q6UZF0 | Q6UZF0 CVHSA
                                LFLPFYSNVTGFHTINH-----TFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNK 110
TR Q6JH46 Q6JH46 CVHSA
TR | Q692E4 | Q692E4 CVHSA
                                LFLPFYSNVTGFHTINH-----TFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNK 110
SP | O3LZX1 | SPIKE BCHK3
                                YFLPFDSNLTOYFSLNVDS-DRYTYFDNPILDFGDGVYFAATEKSNVIRGWIFGSSFDNT 116
SP Q315J5 SPIKE_BCRP3
                                YFLPFDSNLTQYFSLNVDS-DRFTYFDNPILDFGDGVYFAATEKSNVIRGWIFGSTFDNT 116
SP Q0Q475 | SPIKE BC279
                                YFLPFDSNLTQYFSLNIDS-NKYTYFDNPILDFGDGVYFAATEKSNVIRGWIFGSSFDNT 116
TR R9QTAO R9QTAO CVHSA
                                YFLPFNTNVTRYLSLNAAQ-NTIVYFDNHVIPFYDGIYFAATERSNVIRGWIFGSTFDNR 114
TR | R9QTH3 | R9QTH3_CVHSA
                                YFLPFHSNLTQYFSLNVDS-DRQVYFDNPTLNFGDGVYFAATEKSNVIRGWIFGSTMDNS 116
TR A0A0K1Z074 A0A0K1Z074 CVHSA YFLPFHSNLTQYFSLSIQS-DKIVYFDNPILKFGDGIYFAATEKSNVIRGWVFGSTFDNT 116
TR A0A0U1WH16 A0A0U1WH16 CVHSA YFLPFHSNLTQYFSLNIES-D--IYFDNPILKFGDGVYFAATEKSNVIRGWVFGSTFDNT 114
TR|A0A166ZL64|A0A166ZL64_9NIDO RFLRFNTTLTWYNSWNQ-----AYSSPVLPFGHGVYFSTIDKSNVVRGWIFGTTLDNT 111
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA RFLRFNTTLTWYNSWNQ-----AYSSPVLPFGHGVYFSTIDKSNVVRGWIFGTTLDNT 111
                                 ** * :.:* : :
                                                         :.. : * .*:**:: ::**::**::::.
                                TOSLLIVNNATNVVIKVCEFOFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSO 173
YP 009724390
SP|P59594|SPIKE CVHSA
                                SQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMG----TQTHTMIFDNAFNCTFEYISD 166
TR Q6UZF4 Q6UZF4_CVHSA
                                SQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMG----TQTHTMIFDNAFNCTFEYISD 166
TR Q6UZF0 Q6UZF0 CVHSA
                                SOSVIIINNSTNVVIRACNFELCDNPFFAVSKPMG----TOTHTMIFDNAFNCTFEYISD 166
                                SQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMG----TQTHTMIFDNAFNCTFEYISD 166
TR | Q6JH46 | Q6JH46_CVHSA
TR | Q692E4 | Q692E4 CVHSA
                                SQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMG----TQTHTMIFDNAFNCTFEYISD 166
                                TOSAVIVNNSTHIIIRVCNFNLCKEPMYTVSR--G----TOONAWVYOSAFNCTYDRVEK 170
SP | O3LZX1 | SPIKE BCHK3
                                TQSAVIVNNSTHIIIRVCNFNLCKEPMYTVSR--G----AQQSSWVYQSAFNCTYDRVEK 170
SP Q3I5J5 | SPIKE_BCRP3
                                TQSAIIVNNSTHIIIRVCNFNLCKEPMYTVSK--G----TQQSSWVYQSAFNCTYDRVEK 170
SP|Q0Q475|SPIKE BC279
TR R9QTA0 R9QTA0_CVHSA
                                SQSAIIVNNSTHILVKVCNFVLCTEPMFTVSR--N----QHYKSWVYQHARNCTYDVAYP 168
TR R9QTH3 R9QTH3 CVHSA
                                TQSAIIVNNSTHIIIRVCNFNLCKEPMFTVSR--G----VHFSSWVYQSAFNCTYDRVEK 170
TR A0A0K1Z074 A0A0K1Z074 CVHSA TQSAIIVNNSTHIIIRVCYFNLCKDPMYTVSA--G----TQISSWVYQNAFNCTYDRVEK 170
TR A0A0U1WH16 A0A0U1WH16 CVHSA TQSAIIVNNSTHIIIRVCYFNLCKDPMYTVSA--G----TQVSSWVYQSAFNCTYDRVEK 168
```

TR|A0A166ZL64|A0A166ZL64_9NIDO TQSALLVNNGSAITIEVCYFQFCDNPAFIISG--G---AQTNTAIYINLRNCTYVDTLR 165 TR|A0A0U1UYX4|A0A0U1UYX4 CVHSA TQSALLVNNGSAITIEVCYFQFCDNPAFIIRD--G---AQINTAIYINLRNCTYVDTLR 165

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YP 009724390
                              PFLMDLEGK-QGNFKNLREFVFKNIDGYFKIYSKHTPINLVR----DLPQGFSALEPLVD 228
SP P59594 SPIKE CVHSA
                              AFSLDVSEK-SGNFKHLREFVFKNKDGFLYVYKGYOPIDVVR----DLPSGFNTLKPIFK 221
TR Q6UZF4 Q6UZF4 CVHSA
                              AFSLDVSEK-SGNFKHLREFVFKNKDGFLYVYKGYQPIDVVR----DLPSGFNTLKPIFK 221
TR | O6UZFO | O6UZFO CVHSA
                              AFSLDVSEK-SGNFKHLREFVFKNKDGFLYVYKGYOPIDVVR----DLPSGFNTLKPIFK 221
TR Q6JH46 Q6JH46_CVHSA
                              AFSLDVSEK-SGNFKHLREFVFKNKDGFLYVYKGYQPIDVVR----DLPSGFNTLKPIFK 221
                              AFSLDVSEK-SGNFKHLREFVFKNKDGFLYVYKGYQPIDVVR----DLPSGFNTLKPIFK 221
TR | Q692E4 | Q692E4 CVHSA
                              SFOLDTTPK-TGNFKDLREYVFKNRDGFLSVYOTYTAVNLPR----GLPTGFSVLKPILK 225
SP | O3LZX1 | SPIKE BCHK3
SP Q315J5 SPIKE_BCRP3
                              SFQLDTAPK-TGNFKDLREYVFKNRDGFLSVYQTYTAVNLPR----GLPIGFSVLRPILK 225
                              SFQLDTAPK-TGNFKDLREYVFKNRDGFLSVYQTYTAVNLPR----GFPAGFSVLRPILK 225
SP|Q0Q475|SPIKE BC279
TR R9QTA0 R9QTA0_CVHSA
                              SFQLDVSLKNNVNFQHLREFIFKNVDGFLKIYSSYEPINVVS----GIPSGFSVLKPVMS 224
TR | R9QTH3 | R9QTH3_CVHSA
                              SFQLDTAPK-TGNFKDLREYVFKNRDGFLSVYHSYTPVDIIR----GIPVGFSVLKPILK 225
TR | A0A0K1Z074 | A0A0K1Z074 CVHSA SFQLDTAPK-SGNFIALREFVFKNRDGFFTVYQDYTPVNLLR----GLPAGLSVLKPILK 225
TR A0A0U1WH16 A0A0U1WH16 CVHSA SFQLDTSPK-TGNFTDLREFVFKNRDGFFTVYQTYTPVNLLR----GLPSGLSVLKPILK 223
TR A0A166ZL64 A0A166ZL64 9NIDO DLPLSFED-VDGGFKHLREFVFKNSDGFLHIYGAYQPYDLAIGATAALPAQFLPLKPLWK 224
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA DLPLSFAE-VDGGFKHLREFVFKNSDGFLHIYGAYQPYDLAIGATAALPAQFLPLKPLWK 224
                                          .* ***::** **::: :
                               : :.
YP 009724390
                              LPIGINITRFOTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLOPRTFLLKYNENGTITDA 288
                              LPLGINITNFRAILTAFS-----PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDA 275
SP|P59594|SPIKE CVHSA
TR Q6UZF4 Q6UZF4 CVHSA
                              LPLGINITNFRAILTAFS----PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDA 275
TR Q6UZF0 Q6UZF0 CVHSA
                              LPLGINITNFRAILTAFS-----PAODIWGTSAAAYFVGYLKPTTFMLKYDENGTITDA 275
                              LPLGINITNFRAILTAFS-----PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDA 275
TR|Q6JH46|Q6JH46_CVHSA
TR | Q692E4 | Q692E4 CVHSA
                              LPLGINITNFRAILTAFS----PAQDTWGTSAAAYFVGYLKPTTFMLKYDENGTITDA 275
SP Q3LZX1 SPIKE BCHK3
                              LPFGINITSYRVVMAMFS-----QTTSNFLPESAAYYVGNLKYSTFMLRFNENGTITDA 279
                              LPFGINITSYRVVMAMFS-----QTTSNFLPESAAYYVGNLKYTTFMLSFNENGTITNA 279
SP Q3I5J5 | SPIKE_BCRP3
SP Q0Q475 | SPIKE BC279
                              LPFGINITSYRVVMTMFS-----QFNSNFLPESAAYYVGNLKYTTFMLSFNENGTITDA 279
TR R9QTA0 R9QTA0_CVHSA
                              LPLGINITGMRVVMTMFS-----NTQANFLTENAAYYVGYLKPRTFMLQFNTNGTIVNA 278
TR R9QTH3 R9QTH3 CVHSA
                              LPIGINITSFKVVMTMYS-----QTTSNFLSESAAYYVGNLKYVTFMFQFNENGTIADA 279
TR A0A0K1Z074 A0A0K1Z074 CVHSA LPFGINITSFRVVMAMFS-----KTTSNYVPESAAYYVGNLKQSTFMLSFNQNGTITDA 279
TR A0A0U1WHI6 A0A0U1WHI6_CVHSA LPFGINITSFRVVMAMFS-----KTTSNYVPESAAYYVGNLKQSTFMLSFNQNGTIVDA 277
TR A0A166ZL64 A0A166ZL64 9NIDO LPLGLNITNYKVVTTLKP----TNQ---AFQAAYIVGNLKHTTMMLSFNENGTMSNA 274
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA LPLGLNITNYKVVTTLKP----TNQ---AFQAAYIVGNLKHTTMMLSFNENGTMSNA 274
                                                                *** ** *: :: :: ***: :*
                               **:*:**
                                                       YP 009724390
                              VDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFA 348
SP P59594 SPIKE_CVHSA
                              VDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFP 335
TR Q6UZF4 Q6UZF4 CVHSA
                              VDCSONPLAELKCSVKSFEIDKGIYOTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFP 335
TR Q6UZF0 Q6UZF0 CVHSA
                              VDCSONPLAELKCSVKSFEIDKGIYOTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFP 335
TR Q6JH46 Q6JH46_CVHSA
                              VDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFP 335
TR | Q692E4 | Q692E4 CVHSA
                              VDCSONPLAELKCSVKSFEIDKGIYOTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFP 335
SP Q3LZX1 SPIKE_BCHK3
                              VDCSQNPLAELKCTIKNFNVDKGIYQTSNFRVSPTQEVIRFPNITNRCPFDKVFNATRFP 339
SP Q315J5 SPIKE BCRP3
                              IDCAQNPLAELKCTIKNFNVSKGIYQTSNFRVSPTQEVIRFPNITNRCPFDKVFNATRFP 339
SP Q0Q475 SPIKE BC279
                              VDCSQNPLAELKCTIKNFNVSKGIYQTSNFRVTPTQEVVRFPNITNRCPFDKVFNASRFP 339
TR R9QTA0 R9QTA0_CVHSA
                              VDCSQDPLSELKCTLKNFNITKGIYQTSNFRVSPTQEVVRFPNITNRCPFDKVFNATRFP 338
TR R9QTH3 R9QTH3 CVHSA
                              VDCSQNPLAELKCTLKNFNVSKGIYQTSNFRVSPSTEVIRFPNITNRCPFDRVFNASRFP 339
TR A0A0K1Z074 A0A0K1Z074 CVHSA VDCSQNPLAELKCTTKSFNVSKGIYQTSNFRVAPVTEVVRFPNITNLCPFDKVFNATRFP 339
TR A0A0U1WH16 A0A0U1WH16_CVHSA VDCSQDPLAELKCTTKSFNVSKGIYQTSNFRVSPVTEVVRFPNITNLCPFDKVFNATRFP 337
TR A0A166ZL64 A0A166ZL64 9NIDO IDCSQDPLAELKCTLKQFDVGKGIYQTSNFRVQPTVDVARFPNITNVCPFDKVFNATRFP 334
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA IDCSQDPLAELKCTLKQFDVGKGIYQTSNFRVQPTVDVARFPNITNVCPFDKVFNATRFP 334
                               . ****** *** ****
YP 009724390
                               SVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVR 408
SP|P59594|SPIKE CVHSA
                              SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVR 395
                               SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVR 395
TR | Q6UZF4 | Q6UZF4_CVHSA
TR | Q6UZF0 | Q6UZF0_CVHSA
                              SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVR 395
TR Q6JH46 Q6JH46 CVHSA
                              SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVR 395
TR | Q692E4 | Q692E4 CVHSA
                              SVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVR 395
SP Q3LZX1 SPIKE_BCHK3
                              NVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRSSEVR 399
SP Q3I5J5 SPIKE BCRP3
                              NVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRSSEVR 399
SP|Q0Q475|SPIKE_BC279
                              NVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRSSEVR 399
TR R9QTA0 R9QTA0_CVHSA
                              SVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRSSEVR 398
TR R90TH3 R90TH3 CVHSA
                              SVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRFSEVR 399
TR A0A0K12074 A0A0K12074 CVHSA SVYAWERTKISDCVADYTVFYNSTSFSTFNCYGVSPSKLIDLCFTSVYADTFLIRFSEVR 399
TR A0A0U1WH16 A0A0U1WH16_CVHSA SVYAWERTKISDCVADYTVFYNSTSFSTFNCYGVSPSKLIDLCFTSVYADTFLIRFSEVR 397
TR A0A166ZL64 A0A166ZL64 9NIDO SVYAWERTKISDCVADYTVFYNSTSFSTFNCYGVSPSKLIDLCFTSVYADTFLIRFSEVR 394
TR A0A0U1UYX4 A0A0U1UYX4_CVHSA SVYAWERTKISDCVADYTVFYNSTSFSTFNCYGVSPSKLIDLCFTSVYADTFLIRFSEVR 394
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YP 009724390
                              OTAPGOTGKTADYNYKI,PDDFTGCVTAWNSNNI,DSKVGGNYNYI,YRI,FRKSNI,KPFERDT 468
SP|P59594|SPIKE CVHSA
                              QIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDI 455
TR | O6UZF4 | O6UZF4 CVHSA
                              OIAPGOTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDI 455
TR Q6UZF0 Q6UZF0_CVHSA
                              QIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDI 455
TR Q6JH46 Q6JH46 CVHSA
                              QIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRSLRHGKLRPFERDI 455
TR | Q692E4 | Q692E4 CVHSA
                              QIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDI 455
SP Q3LZX1 SPIKE_BCHK3
                              QVAPGETGVIADYNYKLPDDFTGCVIAWNTAKHDTG----NYYYRSHRKTKLKPFERDL 454
SP Q3I5J5 SPIKE BCRP3
                              QVAPGETGVIADYNYKLPDDFTGCVIAWNTAKQDQG----QYYYRSHRKTKLKPFERDL 454
SP Q0Q475 SPIKE BC279
                              QVAPGETGVIADYNYKLPDDFTGCVIAWNTAQQDQG----QYYYRSYRKEKLKPFERDL 454
                              QVAPGETGVIADYNYKLPDDFTGCVIAWNTANQDQG----QYYYRSSRKEKLKPFERDL 453
TR | R9QTA0 | R9QTA0_CVHSA
TR R9QTH3 R9QTH3 CVHSA
                              QIAPGETGVIADYNYKLPDEFTGCVIAWNTANQDRG----QYYYRSSRKTKLKPFERDL 454
TR A0A0K1Z074 A0A0K1Z074 CVHSA OVAPGOTGVIADYNYKLPDDFTGCVIAWNTAKYDVG----SYFYRSHRSSKLKPFERDL 454
TR A0A0U1WHI6 A0A0U1WHI6_CVHSA QVAPGQTGVIADYNYKLPDDFTGCVIAWNTAKQDVG----SYFYRSHRSSKLKPFERDL 452
TR A0A166ZL64 A0A166ZL64 9NIDO QVAPGQTGVIADYNYKLPDDFIGCVIAWNTAKQDVG----SYFYRSHRSSKLKPFERDL 449
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA QVAPGQTGVIADYNYKLPDDFIGCVIAWNTAKQDVG----SYFYRSHRSSKLKPFERDL 449
                                                                      .* **
                              *:***:** ********* ***:* *
                              STEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPK 528
YP 009724390
SP|P59594|SPIKE CVHSA
                              SNVPFSPDGKPCTPP-ALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK 514
TR Q6UZF4 Q6UZF4_CVHSA
                              SNVPFSPDGKPCTPP-ALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK 514
TR | Q6UZF0 | Q6UZF0_CVHSA
                              SNVPFSPDGKPCTPP-ALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK 514
TR Q6JH46 Q6JH46 CVHSA
                              SNVPFSPDGKPCTPP-ALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK 514
TR | Q692E4 | Q692E4 CVHSA
                              SNVPFSPDGKPCTPP-ALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPK 514
SP Q3LZX1 SPIKE BCHK3
                              SSDD----GNGVYTLSTYDFNPNVPVAYQATRVVVLSFELLNAPATVCGPK 501
SP Q3I5J5 SPIKE BCRP3
                              SSD----ENGVRTLSTYDFYPSVPVAYQATRVVVLSFELLNAPATVCGPK 500
                              SSD-----ENGVYTLSTYDFYPSIPVEYQATRVVVLSFELLNAPATVCGPK 500
SP|Q0Q475|SPIKE BC279
                              SSD----ENGVYTLSTYDFYPSVPLDYQATRVVVLSFELLNAPATVCGPK 499
TR R9QTA0 R9QTA0_CVHSA
TR R90TH3 R90TH3 CVHSA
                              SSD-----ENGVRTLSTYDFYPSVPLEYQATRVVVLSFELLNAPATVCGPK 500
TR A0A0K12074 A0A0K12074 CVHSA SSE-----ENGARTLSTYDFNQNVPLEYQATRVVVLSFELLNAPATVCGPK 500
TR A0A0U1WH16 A0A0U1WH16 CVHSA SSE-----ENGVRTLSTYDFNQYVPLEYQATRVVVLSFELLNAPATVCGPK 498
TR A0A166ZL64 A0A166ZL64 9NIDO SSE-----ENGVLTLSTYDFNQNVPLEYQATRVVVLSFELLNAPATVCGPK 495
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA SSE-----ENGVLTLSTYDFNQNVPLEYQATRVVVLSFELLNAPATVCGPK 495
                                                    * * * *
                                                               : **
                                                                    *******
YP 009724390
                              KSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDIT 588
SP|P59594|SPIKE_CVHSA
                              LSTDLIKNOCVNFNFNGLTGTGVLTPSSKRFOPFOOFGRDVSDFTDSVRDPKTSEILDIS 574
TR Q6UZF4 Q6UZF4_CVHSA
                              LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS 574
TR Q6UZF0 Q6UZF0 CVHSA
                              LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS 574
TR Q6JH46 Q6JH46 CVHSA
                              LSTDLIKNOCVNFNFNGLTGTGVLTPSSKRFOPFOOFGRDVSDFTDSVRDPKTSEILDIS 574
TR | Q692E4 | Q692E4 CVHSA
                              LSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS 574
SP Q3LZX1 SPIKE BCHK3
                              LSTELVKNQCVNFNFNGLKGTGVLTSSSKRFQSFQQFGRDTSDFTDSVRDPQTLEILDIS 561
SP Q315J5 SPIKE_BCRP3
                              LSTQLVKNQCVNFNFNGLKGTGVLTESSKRFQSFQQFGRDTSDFTDSVRDPQTLEILDIS 560
SP|Q0Q475|SPIKE BC279
                              LSTQLVKNQCVNFNFNGLRGTGVLTTSSKRFQSFQQFGRDTSDFTDSVRDPQTLEILDIS 560
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TR A0A0U1UYX4 A0A0U1UYX4_CVHSA LSTPLVKNQCVNFNFNGLKGTGVLTDSSKTFQSFQQFGRDASDFTDSVRDPQTLQILDIS 555
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TR Q6JH46 Q6JH46 CVHSA
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TR | Q692E4 | Q692E4 CVHSA
SP Q3LZX1 SPIKE_BCHK3
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SP Q3I5J5 SPIKE BCRP3
                               PSQERNFTTAPAICHEGKAYFPREGVFVSNGTSWFITQRNFYSPQIITTDNTFVAGSCDV 1096
                               PSOERNFTTAPAICHEGKAYFPREGVFVSNGTSWFITORNFYSPOIITTDNTFVAGNCDV 1096
SP|000475|SPIKE BC279
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TR | R9QTH3 | R9QTH3 CVHSA
                               PSQERNFTTAPAICHQGKAYFPREGVFVSNGTSWFITQRNFFSPQIITTDNTFVSGNCDV 1096
TR A0A0K12074 A0A0K12074 CVHSA PSQEKNFTTAPAICHEGKAYFPREGVFVFNGTSWFITQRNFYSPQTITTDNTFVAGNCDV 1096
TR A0A0U1WHI6 A0A0U1WHI6_CVHSA PSQERNFTTAPAICHEGKAYFPREGVFVSNGSSWFITQRNFYSPQIITTDNTFVAGSCDV 1094
TR | A0A166ZL64 | A0A166ZL64 9NIDO PAQEKNFTTAPAICHEGKAYFPREGVFVSNGSSWFITQRNFYSPQIITTDNTFVAGSCDV 1091
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA PAQEKNFTTAPAICHEGKAYFPREGVFVSNGSSWFITQRNFYSPQIITTDNTFVAGSCDV 1091
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                               VIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNE 1170
TR Q6UZF0 Q6UZF0 CVHSA
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TR | Q6JH46 | Q6JH46_CVHSA
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SP Q315J5 SPIKE BCRP3
                               VIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNE 1156
SP Q0Q475 | SPIKE BC279
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TR R9QTH3 R9QTH3_CVHSA
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TR A0A0U1WH16 A0A0U1WH16 CVHSA VIGIINNTVYDPLQPELDSFKQELDKYFKNHTSPDVDFGDISGINASVVDIQKEIDRLNE 1154
TR A0A166ZL64 A0A166ZL64 9NIDO VIGIINNTVYDPLQPELDSFKQELDKYFKNHTSPDVDLGDISGINASVVDIQKEIDRLNE 1151
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SP Q315J5 SPIKE_BCRP3
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SP 000475 | SPIKE BC279
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TR|A0A166ZL64|A0A166ZL64|9NIDO VAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLVGLFMAIILLCYFTSCCSCCKGMC 1211
TR A0A0U1UYX4 A0A0U1UYX4 CVHSA VAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLVGLFMAIILLCYFTSCCSCCKGMC 1211
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SP|P59594|SPIKE CVHSA
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TR Q6UZF4 Q6UZF4_CVHSA
                               SCGSCCKFDEDDSEPVLKGVKLHYT 1255
TR | Q6UZF0 | Q6UZF0 CVHSA
                               SCGSCCKFDEDDSEPVLKGVKLHYT 1255
                               SCGSCCKFDEDDSEPVLKGVKLHYT 1255
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SP|Q0Q475|SPIKE_BC279
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