```
CLUSTAL O(1.2.4) multiple sequence alignment


sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS 60
sp|Q2KI99|STING_BOVIN      -------MP-------------------HSSLHPSIPQP-RGLRAQK---AALVLLS-AC 29
sp|E1C7U0|STING_CHICK      -------MP-------------QDPSTRSSPARLLIPEP-RAGRARH---AACVLLA-VC 35
sp|Q86WV6|STING_HUMAN      -------MP-------------------HSSLHPSIPCP-RGHGAQK---AALVLLS-AC 29
sp|Q3TBT3|STING_MOUSE      -------MP-------------------YSNLHPAIPRP-RGHRSKY---VALIFLV-AS 29
sp|A7SLZ2|STING_NEMVE      -------MR----------------RAEENNGFGTIPKR-RNQHTPF---YASIGMI-VV 32
sp|B8XX90|STING_PIG        -------MP-------------------YSSLHPSIPQP-RGLRAQV---AALVLLG-AC 29
sp|F1M391|STING_RAT        -------MP-------------------YSNLHPSIPRP-RSYRFKL---AAFVLLV-GS 29
                                  :                     .     :    :            : :

sp|P0DTC2|SPIKE_SARS2      NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV 120
sp|Q2KI99|STING_BOVIN      LVALW------GLG--------------------EPPDYTLKW----LVLHLA------- 52
sp|E1C7U0|STING_CHICK      FVVLF------LSG--------------------EPLAPIIRS----VCTQLA------- 58
sp|Q86WV6|STING_HUMAN      LVTLW------GLG--------------------EPPEHTLRY----LVLHLA------- 52
sp|Q3TBT3|STING_MOUSE      LMILW------VAK--------------------DPPNHTLKY----LALHLA------- 52
sp|A7SLZ2|STING_NEMVE      IIVAFTSYHITSYG--------------------DDRNRAMRQYSFTFSLAYL------- 65
sp|B8XX90|STING_PIG        LVALW------GLG--------------------ELPEYTLRW----LVLHLA------- 52
sp|F1M391|STING_RAT        LMSLW------MTG--------------------EPPSHTLHY----LALHVA------- 52
                            :  :                                   ::

sp|P0DTC2|SPIKE_SARS2      NNATNVVI-KVCEF----QFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFE-YVSQP 174
sp|Q2KI99|STING_BOVIN      SQQMGLLIKGICSLAEELCHVHSRYHGSYWRAVR--------ACLCSSMRCGALLLLSCY 104
sp|E1C7U0|STING_CHICK      ALQLGVLLKGCCCLAEEIFHLHSRHHGSLWQVLC--------SCFPPR-WYLALLLVGGS 109
sp|Q86WV6|STING_HUMAN      SLQLGLLLNGVCSLAEELRHIHSRYRGSYWRTVR--------ACLGCPLRRGALLLLSIY 104
sp|Q3TBT3|STING_MOUSE      SHELGLLLKNLCCLAEELCHVQSRYQGSYWKAVR--------ACLGCPIHCMAMILLSSY 104
sp|A7SLZ2|STING_NEMVE      AFLVGELLRRCCLFAEEYRHIETRYNGSLKKAIQ--------TTFSFGHN-NVLFVASLL 116
sp|B8XX90|STING_PIG        SQQIGLLVKGLCSLAEELCHVHSRYQSSYWRAAR--------ACLGCPIRCGALLLLSCY 104
sp|F1M391|STING_RAT        SQQLGLLLKKLCCLAEELCHVQSRYQGSYWKAVR--------ACVGSPICFMALILLSFY 104
                               . ::   * :     . .  . .   :                          .

sp|P0DTC2|SPIKE_SARS2      FLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQ------GFSALEPLVD 228
sp|Q2KI99|STING_BOVIN      FYCSL-------PN------------------------MADLPFTWML--ALLGLSQALN 131
sp|E1C7U0|STING_CHICK      AYLDP-------PE------------------------DNGHSPRLAL--TLSCLCQLLV 136
sp|Q86WV6|STING_HUMAN      FYYSL-------PN------------------------AVGPPFTWML--ALLGLSQALN 131
sp|Q3TBT3|STING_MOUSE      FYF-L-------QN------------------------TADIYLSWMF--GLLVLYKSLS 130
sp|A7SLZ2|STING_NEMVE      FFVVFVASND--PNGSSSV---IQGNS-TAEPHTEMRQTSGWQGLWGQFIISALLTPLVV 170
sp|B8XX90|STING_PIG        FYFSI-------RD------------------------KAGLPLPWML--ALLGLSQALN 131
sp|F1M391|STING_RAT        FYCSL-------EN------------------------TSDLRLAWHL--GILVLSKSLS 131
                                        :                          .             *   :

sp|P0DTC2|SPIKE_SARS2      LPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLK-----YNE-- 281
sp|Q2KI99|STING_BOVIN      ILLGL-----QGLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLILPGLPARIQIYNQFH 186
sp|E1C7U0|STING_CHICK      LALGL-----QKLSAVEVSELTESSKKNVAHGLAWSYYIGYLKVVLPRLKECMEELSRTN 191
sp|Q86WV6|STING_HUMAN      ILLGL-----KGLAPAEISAVCEKGNFNVAHGLAWSYYIGYLRLILPELQARIRTYNQHY 186
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sp|Q3TBT3|STING_MOUSE      MLLGL-----QSLTPAEVSAVCEEKKLNVAHGLAWSYYIGYLRLILPGLQARIRMFNQLH 185
sp|A7SLZ2|STING_NEMVE      HLLGL-----RELSKVEESQLNEKENKNVADGLAWSYYFGYLKFVLPELEKQIEKTSKFR 225
sp|B8XX90|STING_PIG        ILLGL-----QHLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLILPGLRARIQAYNQRH 186
sp|F1M391|STING_RAT        MTLDL-----QSLAPAEVSAVCEEKNFNVAHGLAWSYYIGYLKLILPGLQARIRMFNQLH 186
                             :.:     : *   . * :    . .   . * :**.***:     *       ..

sp|P0DTC2|SPIKE_SARS2      NGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITN--LCPFG 339
sp|Q2KI99|STING_BOVIN      NNTLQGAGSHRLHILFPLDCGVPDDL------NVAD-------PNIRFLHELPQQSADRA 233
sp|E1C7U0|STING_CHICK      PMLRAHRDTWKLHILVPLGCDIWDDL------EKAD-------SNIQYLADLPETILTRA 238
sp|Q86WV6|STING_HUMAN      NNLLRGAVSQRLYILLPLDCGVPDNL------SMAD-------PNIRFLDKLPQQTGDHA 233
sp|Q3TBT3|STING_MOUSE      NNMLSGAGSRRLYILFPLDCGVPDNL------SVVD-------PNIRFRDMLPQQNIDRA 232
sp|A7SLZ2|STING_NEMVE      SK---EKFVKKMFILIPSNCFWDDKI------PGSDYDPQ---NRITFEGNTEPLEKTRG 273
sp|B8XX90|STING_PIG        KNVLGGIGNHRLHILFPLDCGVPDDL------SVAD-------PNIRFLHELPQQSADRA 233
sp|F1M391|STING_RAT        NNMLSGAGSRRLYILFPLDCGVPDDL------SVAD-------PNIRFRDMLPQQNTDRA 233
                                      :  *    *   .           :         : :           .

sp|P0DTC2|SPIKE_SARS2      EVFNATRFASVYAW--NRKRISNCVADYSVLYNS-ASFSTFKCYGVSPTKLNDLCFTNVY 396
sp|Q2KI99|STING_BOVIN      GIKGRVYTNSIYELLENGQRAGVCVLEYATPLQTLFAMSQDGRAGFSREDRLE--Q---- 287
sp|E1C7U0|STING_CHICK      GIKRRVYKHSLYVIRDKDNKLRPCVLEFASPLQTLCAMSQDDCAAFSREQRLE--Q---- 292
sp|Q86WV6|STING_HUMAN      GIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLE--Q---- 287
sp|Q3TBT3|STING_MOUSE      GIKNRVYSNSVYEILENGQPAGVCILEYATPLQTLFAMSQDAKAGFSREDRLE--Q---- 286
sp|A7SLZ2|STING_NEMVE      GVFLRHYKHSVYEIKDGENEPWFCIMEYATPLLTLYDMSVAQPGELSREERDA--Q---- 327
sp|B8XX90|STING_PIG        GIKGRVYTNSIYELLENGQPAGVCVLGYATPLQTLFAMSQDGRAGFSREDRLE--Q---- 287
sp|F1M391|STING_RAT        GVKNRAYSNSVYELLENGQPAGACILEYATPLQTLFAMSQDGKAGFSREDRLE--Q---- 287
                            :       *:*      :    *:  ::    :   :*      .*  .

sp|P0DTC2|SPIKE_SARS2      ADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTG----CVIAWNSNNLD---SKVGGNY 449
sp|Q2KI99|STING_BOVIN      AKLFCRTLEDILANAPESQNNCRLIVYQEPAEGSSFSLSQEILQHLRQEER-EVTMGSTE 346
sp|E1C7U0|STING_CHICK      ARLFYRSLRDILGSSKECAGLYRLIAYEEPAEPESHFLSGLILWHLQQQQREEYMVQEEL 352
sp|Q86WV6|STING_HUMAN      AKLFCRTLEDILADAPESQNNCRLIAYQEPADDSSFSLSQEVLRHLRQEEKEEVTVGSLK 347
sp|Q3TBT3|STING_MOUSE      AKLFCRTLEEILEDVPESRNNCRLIVYQEPTDGNSFSLSQEVLRHIRQEEKEEVTMNAPM 346
sp|A7SLZ2|STING_NEMVE      VVVFLRKLQDILEGDRACQGKYELVTFSPDRDLA-----DVMLRKLKDSE---LEIGG-- 377
sp|B8XX90|STING_PIG        AKLFCRTLEDILADAPEAQNNCRLIVYQEPTEGGSFSLSQEILRHLRQEER-EVTMGSAE 346
sp|F1M391|STING_RAT        AKLFCRTLEEILADVPESRNHCRLIVYQESEEGNSFSLSQEVLRHIRQEEKEEVTMSGPP 347
                           .  *     ::        .      :.   :         :  : .: :     :

sp|P0DTC2|SPIKE_SARS2      NYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYR 509
sp|Q2KI99|STING_BOVIN      TSV---------MPG-------SSVLSQEPELLISGLEKPLPLRSDVF------------ 378
sp|E1C7U0|STING_CHICK      P---------------------LGTSSVELSLQVSSSDLPQPLRSDCP------------ 379
sp|Q86WV6|STING_HUMAN      TSA---------VPS-------TSTMSQEPELLISGMEKPLPLRTDFS------------ 379
sp|Q3TBT3|STING_MOUSE      TSV---------APP-------PSVLSQEPRLLISGMDQPLPLRTDLI------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        TSV---------VPT-------SSTLSQEPELLISGMEQPLPLRSDIF------------ 378
sp|F1M391|STING_RAT        TSV---------APR-------PSLLSQEPRLLISGMEQPLPLRTDLI------------ 379


sp|P0DTC2|SPIKE_SARS2      VVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDI 569
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sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      ADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQL 629
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      TPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVAS 689
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      QSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC 749
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDP 809
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
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sp|P0DTC2|SPIKE_SARS2      SKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEM 869
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379

sp|P0DTC2|SPIKE_SARS2      IAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNS 929
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379

sp|P0DTC2|SPIKE_SARS2      AIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEA 989
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379

sp|P0DTC2|SPIKE_SARS2      EVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL 1049
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379

sp|P0DTC2|SPIKE_SARS2      MSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNF 1109
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
```

```
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      YEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDI 1169
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVM 1229
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|P0DTC2|SPIKE_SARS2      VTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT 1273
sp|Q2KI99|STING_BOVIN      -------------------------------------------- 378
sp|E1C7U0|STING_CHICK      -------------------------------------------- 379
sp|Q86WV6|STING_HUMAN      -------------------------------------------- 379
sp|Q3TBT3|STING_MOUSE      -------------------------------------------- 378
sp|A7SLZ2|STING_NEMVE      -------------------------------------------- 377
sp|B8XX90|STING_PIG        -------------------------------------------- 378
sp|F1M391|STING_RAT        -------------------------------------------- 379
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1      ----MLLIIFILPTT--LAVIGDFNCTNFAIN----D--LNTTVPRISEY---------- 38
sp|Q14EB0|SPIKE_CVHN2      ----MFLIIFILPTT--LAVIGDFNCTNSFIN----D--YNKTIPRISED---------- 38
sp|Q0ZME7|SPIKE_CVHN5      ----MFLIIFILPTT--LAVIGDFNCTNSFIN----D--YNKTIPRISED---------- 38
sp|Q6Q1S2|SPIKE_CVHNL      --MKLFLILLVLPLASCFFT-----CNSN-AN----LSMLQLGVPDNSSTIVTGLLPTHW 48
sp|P36334|SPIKE_CVHOC      ---MFLILLISLPTA--FAVIGDLKCTSDNIN----D--KDTGPPPISTD---------- 39
sp|K9N5Q8|SPIKE_MERS1      MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTWP---RP---------- 47
sp|P59594|SPIKE_SARS       ----MFIFLLFLTLT-S----------GSDLD--RCTTFDDVQAP---NY---------- 30
sp|P0DTC2|SPIKE_SARS2      ----MFVFLVLLPLV-S----------SQCVN--LTT--RTQLPP---AY---------- 28


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1      -----VVDVSYGLGTYYILDRVYLNTTILFTGYFPKSGANFRDLS------LKGTTYLST 87
sp|Q14EB0|SPIKE_CVHN2      -----VVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLA------LKGSKYLST 87
sp|Q0ZME7|SPIKE_CVHN5      -----VVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLA------LKGSIYLST 87
sp|Q6Q1S2|SPIKE_CVHNL      FCANQSTSVYSANGFFYIDVGNHRSAFALHTGYYDANQ---YYIYVTNEIGLNASVTLKI 105
sp|P36334|SPIKE_CVHOC      -----TVDVTNGLGTYYVLDRVYLNTTLFLNGYYPTSGSTYRNMA------LKGSVLLSR 88
sp|K9N5Q8|SPIKE_MERS1      ------IDVSKADGIIYPQGRTYSNITITYQGLF-PYQGDHGDMYVYSAGHATGTTPQKL 100
sp|P59594|SPIKE_SARS       -----TQHTSSMRGVYYPDEIFRSDTLYLTQDLFLPFYSNVT---GFHTIN-------HT 75
sp|P0DTC2|SPIKE_SARS2      -------TNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVT---WFHAIHVSGTNGTKR 78


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
```

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sp|Q5MQD0|SPIKE_CVHN1      --LWYQKPFLSDFNNGIFSRVK---N------TKLYVNKTL---------YSEFSTIVIG 127
sp|Q14EB0|SPIKE_CVHN2      --LWYKPPFLSDFNNGIFSKVK---N------TKLYVNNTL---------YSEFSTIVIG 127
sp|Q0ZME7|SPIKE_CVHN5      --LWYKPPFLSDFNNGIFSKVK---N------TKLYVNNTL---------YSEFSTIVIG 127
sp|Q6Q1S2|SPIKE_CVHNL      --CKFSRNTTFDFLSNASSSFDCIVNLLFTEQLGAPLGITISGETVRLHLYNVTRTFYVP 163
sp|P36334|SPIKE_CVHOC      --LWFKPPFLSDFINGIFAKVK---N------TKVIKDRVM---------YSEFPAITIG 128
sp|K9N5Q8|SPIKE_MERS1      FVANYSQD-VKQFANGFVVRIG---A------AANSTGTVIISPSTSATIRKIYPAFMLG 150
sp|P59594|SPIKE_SARS       ----FGNP-VIPFKDGIYFAAT---E-----------------------KSNVVRGWVFG 104
sp|P0DTC2|SPIKE_SARS2      ----FDNP-VLPFNDGVYFAST---E-----------------------KSNIIRGWIFG 107


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      -------------MFVLLVAYA---LLHIAGCQTTNGLNTSYSVCNGCVGYSENVFAVES 44
sp|Q5MQD0|SPIKE_CVHN1      SVFINNSY---------TIV----VQPH-------------------------------- 142
sp|Q14EB0|SPIKE_CVHN2      SVFVNTSY---------TIV----VQPH-------------------------------- 142
sp|Q0ZME7|SPIKE_CVHN5      SVFVNTSY---------TIV----VQPH-------------------------------- 142
sp|Q6Q1S2|SPIKE_CVHNL      AAYKLTKL-SVKCYFNYSCVFSVVNATVTVNVTTHNGRVVNYTVCDDCNGYTDNIFSVQQ 222
sp|P36334|SPIKE_CVHOC      STFVNTSY---------SVV----VQPRTINST-QDG----------------------- 151
sp|K9N5Q8|SPIKE_MERS1      SSVGNFSDGKMGRFFNHTLV----LLPD--------G----------------------- 175
sp|P59594|SPIKE_SARS       STMNNKSQ---------SVI----IINN--------S----------------------- 120
sp|P0DTC2|SPIKE_SARS2      TTLDSKTQ---------SLL----IVNN--------A----------------------- 123


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      GGYIPSDFAFNNWFLLTNTSSVVDGVVRSFQPLLLNCLWSVSGLRFTTGFVY-----FNG 99
sp|Q5MQD0|SPIKE_CVHN1      -----------------------NGVLEITACQYTMCEYPHTICKS-KGSSRN------- 171
sp|Q14EB0|SPIKE_CVHN2      -----------------------NGILEITACQYTMCEYPHTVCKS-KGSIRN------- 171
sp|Q0ZME7|SPIKE_CVHN5      -----------------------NGILEITACQYTMCEYPHTVCKS-KGSIRN------- 171
sp|Q6Q1S2|SPIKE_CVHNL      DGRIPNGFPFNNWFLLTNGSTLVDGVSRLYQPLRLTCLWPVPGLKSSTGFVY-----FNA 277
sp|P36334|SPIKE_CVHOC      -------------------DNKLQGLLEVSVCQYNMCEYPQTICHPNLGNHRK------- 185
sp|K9N5Q8|SPIKE_MERS1      ------------------------CGTLLRAF--YCILEPRSGNHCPAGNSYTSFATYHT 209
sp|P59594|SPIKE_SARS       ------------------------TNVVIRACNFELCDNPFFAVSKPMGT---------- 146
sp|P0DTC2|SPIKE_SARS2      ------------------------TNVVIKVCEFQFCNDPFLGVYYHKNN---------- 149


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
```

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sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      TGR-GDCKGFSSDVLSD-----VIRYNLNFEE-------NLRRG--------TILFKTSY 138
sp|Q5MQD0|SPIKE_CVHN1      -----------ESWHFDKSE-PLCLFKKNFTYN--VST----DWL-------YFHFYQER 206
sp|Q14EB0|SPIKE_CVHN2      -----------ESWHIDSSE-PLCLFKKNFTYN--VSA----DWL-------YFHFYQER 206
sp|Q0ZME7|SPIKE_CVHN5      -----------ESWHIDSSE-PLCLFKKNFTYN--VSA----DWL-------YFHFYQER 206
sp|Q6Q1S2|SPIKE_CVHNL      TGSDVNCNGYQHNSVVD-----VMRYNLNFSANS---LDNLKSG--------VIVFKTLQ 321
sp|P36334|SPIKE_CVHOC      -----------ELWHLDTGV-VSCLYKRNFTYD--VNA----DYL-------YFHFYQEG 220
sp|K9N5Q8|SPIKE_MERS1      PATDCSDGNYNRNASLNSFKEYFNLRNCTFMYTYNITEDEILEWFGITQTAQG-VHLFSS 268
sp|P59594|SPIKE_SARS       ---------------QTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKD 191
sp|P0DTC2|SPIKE_SARS2      -----------KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNID 198


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      GVVVFYCTNNTLV------------SGDAHIPFGTVLGNFYCFVNTTIGNETTSAFVGAL 186
sp|Q5MQD0|SPIKE_CVHN1      GTFYAYYADS----------GMP-TTFLFSLYLGTLLSHYYVL----------------- 238
sp|Q14EB0|SPIKE_CVHN2      GVFYAYYADV----------GMP-TTFLFSLYLGTILSHYYVM----------------- 238
sp|Q0ZME7|SPIKE_CVHN5      GVFYAYYADV----------GMP-TTFLFSLYLGTILSHYYVM----------------- 238
sp|Q6Q1S2|SPIKE_CVHNL      YDVLFYCSNSSSG------------VLDTTIPFGPSSQPYYCFINSTINTTHVSTFVGIL 369
sp|P36334|SPIKE_CVHOC      GTFYAYFTDT----------GVV-TKFLFNVYLGMALSHYYVM----------------- 252
sp|K9N5Q8|SPIKE_MERS1      RYVDLYGGN---------------MFQFATLPVYDTIKYYSII----------------- 296
sp|P59594|SPIKE_SARS       GFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAI----------------- 234
sp|P0DTC2|SPIKE_SARS2      GYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTL----------------- 241


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      PKTVREFVISRTGHFYINGYRYFTLGNVEAVNFNVTTAETTDFCTVALASYADVLVNVSQ 246
sp|Q5MQD0|SPIKE_CVHN1      PLTCN---------------------A----ISSNTDNETLQYWVTPLSKRQYLLKFDNR 273
sp|Q14EB0|SPIKE_CVHN2      PLTCK---------------------A----ISSNTDNETLEYWVTPLSRRQYLLNFDEH 273
sp|Q0ZME7|SPIKE_CVHN5      PLTCN---------------------A----ISSNTDNETLEYWVTPLSRRQYLLNFDEH 273
sp|Q6Q1S2|SPIKE_CVHNL      PPTVREIVVARTGQFYINGFKYFDLGFIEAVNFNVTTASATDFWTVAFATFVDVLVNVSA 429
```

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sp|P36334|SPIKE_CVHOC      PLTCN---------------------S----------KLTLEYWVTPLTSRQYLLAFNQD 281
sp|K9N5Q8|SPIKE_MERS1      PHSIR------------------SIQS----DRKAW----AAFYVYKLQPLTFLLDFSVD 330
sp|P59594|SPIKE_SARS       LTAFS---------------------P----AQDIWGTSAAAYFVGYLKPTTFMLKYDEN 269
sp|P0DTC2|SPIKE_SARS2      LALHRSYL---------------TPGD----SSSGWTAGAAAYYVGYLQPRTFLLKYNEN 282


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      TSIANIIYCN-SVINRLRCDQLSFDVPDGFYSTSPIQSVELPVSIVSLPVYH-------- 297
sp|Q5MQD0|SPIKE_CVHN1      GVITNAVDCSSSFFSEIQCKTKSLLPNTGVYDLSGFTVKPVATVHRRIPDLPDCDIDKWL 333
sp|Q14EB0|SPIKE_CVHN2      GVITNAVDCSSSFLSEIQCKTQSFAPNTGVYDLSGFTVKPVATVYRRIPNLPDCDIDNWL 333
sp|Q0ZME7|SPIKE_CVHN5      GVITNAVDCSSSFLSEIQCKTQSFAPNTGVYDLSGFTVKPVATVYRRIPNLPDCDIDNWL 333
sp|Q6Q1S2|SPIKE_CVHNL      TNIQNLLYCD-SPFEKLQCEHLQFGLQDGFYSANFLDDNVLPETYVALPIYY-------- 480
sp|P36334|SPIKE_CVHOC      GIIFNAEDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRRKPNLPNCNIEAWL 341
sp|K9N5Q8|SPIKE_MERS1      GYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEG-VECDFSPLL 389
sp|P59594|SPIKE_SARS       GTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVF 329
sp|P0DTC2|SPIKE_SARS2      GTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVF 342


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
sp|P15423|SPIKE_CVH22      ------------KHTFIVLY-----------------VDFKPQSGGGKCFNCYPAGVNIT 328
sp|Q5MQD0|SPIKE_CVHN1      NNFNVPSPLNWERKIFSNCNFNLSTLLRLVHTDSFSCNNFDESKIYGSCFKSI------V 387
sp|Q14EB0|SPIKE_CVHN2      NNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSI------T 387
sp|Q0ZME7|SPIKE_CVHN5      NNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSI------T 387
sp|Q6Q1S2|SPIKE_CVHNL      ------------QHTDINFT--------------------ATASFGGSCYVCKPHQVNIS 508
sp|P36334|SPIKE_CVHOC      NDKSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSI------T 395
sp|K9N5Q8|SPIKE_MERS1      SG-TPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSL------I 442
sp|P59594|SPIKE_SARS       NATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNV------Y 383
sp|P0DTC2|SPIKE_SARS2      NATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNV------Y 396


sp|Q2KI99|STING_BOVIN      -----------------------------------------MP----------------- 2
sp|E1C7U0|STING_CHICK      -----------------------------------------MPQD---------P---ST 7
sp|Q86WV6|STING_HUMAN      -----------------------------------------MP----------------- 2
sp|Q3TBT3|STING_MOUSE      -----------------------------------------MP----------------- 2
sp|A7SLZ2|STING_NEMVE      -----------------------------------------MR---------------RA 4
```

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sp|B8XX90|STING_PIG         -----------------------------------------MP----------------- 2
sp|F1M391|STING_RAT         -----------------------------------------MP----------------- 2
sp|P15423|SPIKE_CVH22       LANFNE---TKGPLCVDTSHFTTKYVAVYA-----NVGRWSASIN--TG---------NC 369
sp|Q5MQD0|SPIKE_CVHN1       LDKFAIPNSRRSDLQLGSSGFLQSSNYKIDTTSSSCQLYYSLPAINVTINN-YNPSSWNR 446
sp|Q14EB0|SPIKE_CVHN2       VDKFAIPNRRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINN-FNPSSWNR 446
sp|Q0ZME7|SPIKE_CVHN5       VDKFAIPNRRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINN-FNPSSWNR 446
sp|Q6Q1S2|SPIKE_CVHNL       LNG-------NTSVCVRTSHFSIRYIYNRVKSGSPGDSSWHIYLK--SG---------TC 550
sp|P36334|SPIKE_CVHOC       IDKFAIPNGRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSR-FNPSTWNK 454
sp|K9N5Q8|SPIKE_MERS1       LDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNLTTITKPLKYSYINK 502
sp|P59594|SPIKE_SARS        ADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYL 443
sp|P0DTC2|SPIKE_SARS2       ADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLF 456


sp|Q2KI99|STING_BOVIN       -HSSLHP--SIPQPRGLRA---------------QKAALVLLSACLVALW---------- 34
sp|E1C7U0|STING_CHICK       RSSPARL--LIPEPRAGRA---------------RHAACVLLAVCFVVLF---------- 40
sp|Q86WV6|STING_HUMAN       -HSSLHP--SIPCPRGHGA---------------QKAALVLLSACLVTLW---------- 34
sp|Q3TBT3|STING_MOUSE       -YSNLHP--AIPRPRGHRS---------------KYVALIFLVASLMILW---------- 34
sp|A7SLZ2|STING_NEMVE       EENNGFG--TIPKRRNQHT---------------PFYASIGMIVVIIVAFTSYHI-T--- 43
sp|B8XX90|STING_PIG         -YSSLHP--SIPQPRGLRA---------------QVAALVLLGACLVALW---------- 34
sp|F1M391|STING_RAT         -YSNLHP--SIPRPRSYRF---------------KLAAFVLLVGSLMSLW---------- 34
sp|P15423|SPIKE_CVH22       PFSFGKVNNFV------------KFGSVCFSLKDIPGGCAMPI---VANWA--------- 405
sp|Q5MQD0|SPIKE_CVHN1       RYGFNNFN---------LSSHSVVYSRYCFSVNNTFCPCAKPSFASSCKSHK----PPSA 493
sp|Q14EB0|SPIKE_CVHN2       RYGFGSFN---------VSSYDVVYSDHCFSVNSDFCPCADPSVVNSCVKSK----PLSA 493
sp|Q0ZME7|SPIKE_CVHN5       RYGFGSFN---------LSSYDVVYSDHCFSVNSDFCPCADPSVVNSCAKSK----PPSA 493
sp|Q6Q1S2|SPIKE_CVHNL       PFSFSKLNNFQ------------KFKTICFSTVEVPGSCNFPL---EATWH--------- 586
sp|P36334|SPIKE_CVHOC       RFGFIEDSVFKPRPAGVLTNHDVVYAQHCFKAPKNFCPCKLNG---SCVGSGPGKNNGIG 511
sp|K9N5Q8|SPIKE_MERS1       CSRFLSD-----DRT--------EVPQLVNA--NQYSPCVSIV-PST-VW---------- 535
sp|P59594|SPIKE_SARS        RHGKLRP-----FER--------DISNVPFS--PDGKPCTP-P-ALNCYW---------- 476
sp|P0DTC2|SPIKE_SARS2       RKSNLKP-----FER--------DISTEIYQ--AGSTPCNGVE-GFNCYF---------- 490


sp|Q2KI99|STING_BOVIN       --GLGE---------------------PPDYTLKW----LVLH-LASQQMGLLIKGICSL 66
sp|E1C7U0|STING_CHICK       --LSGE---------------------PLAPIIRS----VCTQ-LAALQLGVLLKGCCCL 72
sp|Q86WV6|STING_HUMAN       --GLGE---------------------PPEHTLRY----LVLH-LASLQLGLLLNGVCSL 66
sp|Q3TBT3|STING_MOUSE       --VAKD---------------------PPNHTLKY----LALH-LASHELGLLLKNLCCL 66
sp|A7SLZ2|STING_NEMVE       --SYGD---------------------DRNRAMRQYSFTFSLA-YLAFLVGELLRRCCLF 79
sp|B8XX90|STING_PIG         --GLGE---------------------LPEYTLRW----LVLH-LASQQIGLLVKGLCSL 66
sp|F1M391|STING_RAT         --MTGE---------------------PPSHTLHY----LALH-VASQQLGLLLKKLCCL 66
sp|P15423|SPIKE_CVH22       -----------------------------------YSKYYT------------------- 411
sp|Q5MQD0|SPIKE_CVHN1       SCPIGTNYRSCESTTVLDHTDWCRCSCLPDP-ITAYDPRSCSQKKSLVGVGEHCAGF-GV 551
sp|Q14EB0|SPIKE_CVHN2       ICPAGTKYRHCDLDTTLYVNNWCRCSCLPDP-ISTYSPNTCPQKKVVVGIGEHCPGL-GI 551
sp|Q0ZME7|SPIKE_CVHN5       ICPAGTKYRHCDLDTTLYVKNWCRCSCLPDP-ISTYSPNTCPQKKVVVGIGEHCPGL-GI 551
sp|Q6Q1S2|SPIKE_CVHNL       -----------------------------------YTSYTI------------------- 592
sp|P36334|SPIKE_CVHOC       TCPAGTNYLTCD------------NLCTPDP-ITFTGTYKCPQTKSLVGIGEHCSGL-AV 557
sp|K9N5Q8|SPIKE_MERS1       --EDGDYYRK---------------Q--LSP-LEGGGWLVA-------------SGS-TV 561
sp|P59594|SPIKE_SARS        ------------------------------P-LNDYGFYTT-------------TGI-GY 491
sp|P0DTC2|SPIKE_SARS2       ------------------------------P-LQSYGFQPT-------------NGV-GY 505
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sp|Q2KI99|STING_BOVIN      AEELCHVHSR-YHGSYWRAVRACLCSSMRCGALLLLSCYF-----------YCSL----- 109
sp|E1C7U0|STING_CHICK      AEEIFHLHSR-HHGSLWQVLCSCFPPR-WYLALLLVGGSA-----------YLDP----- 114
sp|Q86WV6|STING_HUMAN      AEELRHIHSR-YRGSYWRTVRACLGCPLRRGALLLLSIYF-----------YYSL----- 109
sp|Q3TBT3|STING_MOUSE      AEELCHVQSR-YQGSYWKAVRACLGCPIHCMAMILLSSYF-----------YF-L----- 108
sp|A7SLZ2|STING_NEMVE      AEEYRHIETR-YNGSLKKAIQTTFSFGHN-NVLFVASLLF-----------FVVFV-ASN 125
sp|B8XX90|STING_PIG        AEELCHVHSR-YQSSYWRAARACLGCPIRCGALLLLSCYF-----------YFSI----- 109
sp|F1M391|STING_RAT        AEELCHVQSR-YQGSYWKAVRACVGSPICFMALILLSFYF-----------YCSL----- 109
sp|P15423|SPIKE_CVH22      -------------------------IG----S-LYVSWSDGDGITGVP------------ 429
sp|Q5MQD0|SPIKE_CVHN1      DEEKCGVLDGSYNVS-----CLC--ST----D-AFLGWSYDTCVSNNRCNIFSNFILNGI 599
sp|Q14EB0|SPIKE_CVHN2      NEEKCGTQLN--HSS-----CSC--SP----D-AFLGWSFDSCISNNRCNIFSNFIFNGI 597
sp|Q0ZME7|SPIKE_CVHN5      NEEKCGTQLN--HSS-----CFC--SP----D-AFLGWSFDSCISNNRCNIFSNFIFNGI 597
sp|Q6Q1S2|SPIKE_CVHNL      -------------------------VG----A-LYVTWSEGNSITGVP------------ 610
sp|P36334|SPIKE_CVHOC      KSDYCG------GNS-----CTC--RP----Q-AFLGWSADSCLQGDKCNIFANFILHDV 599
sp|K9N5Q8|SPIKE_MERS1      AM-----------------------TE----Q-LQMGF--------------GITVQYGT 579
sp|P59594|SPIKE_SARS       QP-----------------------YR----V-VVLSF--------------ELL----N 505
sp|P0DTC2|SPIKE_SARS2      QP-----------------------YR----V-VVLSF--------------ELL----H 519


sp|Q2KI99|STING_BOVIN      -PN--------------------------------------MADLPFTWML--ALL---- 124
sp|E1C7U0|STING_CHICK      -PE--------------------------------------DNGHSPRLAL--TLS---- 129
sp|Q86WV6|STING_HUMAN      -PN--------------------------------------AVGPPFTWML--ALL---- 124
sp|Q3TBT3|STING_MOUSE      -QN--------------------------------------TADIYLSWMF--GLL---- 123
sp|A7SLZ2|STING_NEMVE      DPNG-----------SSSVIQGNSTAEPHT------EMR-QTSGWQGLWGQFIISA---- 163
sp|B8XX90|STING_PIG        -RD--------------------------------------KAGLPLPWML--ALL---- 124
sp|F1M391|STING_RAT        -EN--------------------------------------TSDLRLAWHL--GIL---- 124
sp|P15423|SPIKE_CVH22      --QPVE-----GVSSFMNVTLDKCTKYNIYDVSGVGVIRVSNDTFLNGIT--YTSTSGNL 480
sp|Q5MQD0|SPIKE_CVHN1      NSGTTCSND--LLQPNTEVFTDVCVDYDLYGITGQGIFKEVSAVYYNSWQNLLYDSNGNI 657
sp|Q14EB0|SPIKE_CVHN2      NSGTTCSND--LLYSNTEVSTGVCVNYDLYGITGQGIFKEVSAAYYNNWQNLLYDSNGNI 655
sp|Q0ZME7|SPIKE_CVHN5      NSGTTCSND--LLYSNTEISTGVCVNYDLYGITGQGIFKEVSAAYYNNWQNLLYDSNGNI 655
sp|Q6Q1S2|SPIKE_CVHNL      --YPVS-----GIREFSNLVLNNCTKYNIYDYVGTGIIRSSNQSLAGGIT--YVSNSGNL 661
sp|P36334|SPIKE_CVHOC      NSGLTCSTD--LQKANTDIILGVCVNYDLYGILGQGIFVEVNATYYNSWQNLLYDSNGNL 657
sp|K9N5Q8|SPIKE_MERS1      DTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVGV-RQQRFVYDAYQNL 638
sp|P59594|SPIKE_SARS       APATVCGP-----KLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQ-PFQQFGRDVSDFT 559
sp|P0DTC2|SPIKE_SARS2      APATVCGP-----KKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFL-PFQQFGRDIADTT 573


sp|Q2KI99|STING_BOVIN      -G--LSQALNILLGLQGLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLILPGLPARIQI 181
sp|E1C7U0|STING_CHICK      -C--LCQLLVLALGLQKLSAVEVSELTESSKKNVAHGLAWSYYIGYLKVVLPRLKECMEE 186
sp|Q86WV6|STING_HUMAN      -G--LSQALNILLGLKGLAPAEISAVCEKGNFNVAHGLAWSYYIGYLRLILPELQARIRT 181
sp|Q3TBT3|STING_MOUSE      -V--LYKSLSMLLGLQSLTPAEVSAVCEEKKLNVAHGLAWSYYIGYLRLILPGLQARIRM 180
sp|A7SLZ2|STING_NEMVE      -L--LTPLVVHLLGLRELSKVEESQLNEKENKNVADGLAWSYYFGYLKFVLPELEKQIEK 220
sp|B8XX90|STING_PIG        -G--LSQALNILLGLQHLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLILPGLRARIQA 181
sp|F1M391|STING_RAT        -V--LSKSLSMTLDLQSLAPAEVSAVCEEKNFNVAHGLAWSYYIGYLKLILPGLQARIRM 181
sp|P15423|SPIKE_CVH22      LG-FKDVTKGTIYSITPCNPPDQLVVYQQ------------------------AVVGAML 515
sp|Q5MQD0|SPIKE_CVHN1      IG-FKDFVTNKTYNIFPCYAGRVSAAFH--QNASSLALLYR------------NLKCSYV 702
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sp|Q14EB0|SPIKE_CVHN2      IG-FKDFLTNKTYTILPCYSGRVSAAFY--QNSSSPALLYR------------NLKCSYV 700
sp|Q0ZME7|SPIKE_CVHN5      IG-FKDFLTNKTYTILPCYSGRVSAAFY--QNSSSPALLYR------------NLKCSYV 700
sp|Q6Q1S2|SPIKE_CVHNL      LG-FKNVSTGNIFIVTPCNQPDQVAVYQQ------------------------SIIGAMT 696
sp|P36334|SPIKE_CVHOC      YG-FRDYIINRTFMIRSCYSGRVSAAFH--ANSSEPALLFR------------NIKCNYV 702
sp|K9N5Q8|SPIKE_MERS1      VGYYSD--DGNYYCLRACVSVPVSVIYD--KETKTHATLFG------------SVACEHI 682
sp|P59594|SPIKE_SARS       -DSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQ------------DVNCTDV 606
sp|P0DTC2|SPIKE_SARS2      -DAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQ------------DVNCTEV 620
                                         :                                             

sp|Q2KI99|STING_BOVIN      YNQFHNNTLQGAGS------HRLHILFPLDCGVPDD----LNVAD------PNIRFLHEL 225
sp|E1C7U0|STING_CHICK      LSRTNPMLRAHRDT------WKLHILVPLGCDIWDD----LEKAD------SNIQYLADL 230
sp|Q86WV6|STING_HUMAN      YNQHYNNLLRGAVS------QRLYILLPLDCGVPDN----LSMAD------PNIRFLDKL 225
sp|Q3TBT3|STING_MOUSE      FNQLHNNMLSGAGS------RRLYILFPLDCGVPDN----LSVVD------PNIRFRDML 224
sp|A7SLZ2|STING_NEMVE      TSKFRSK---EKFV------KKMFILIPSNCFWDDK----IPGSDYDPQ--NRITFEGNT 265
sp|B8XX90|STING_PIG        YNQRHKNVLGGIGN------HRLHILFPLDCGVPDD----LSVAD------PNIRFLHEL 225
sp|F1M391|STING_RAT        FNQLHNNMLSGAGS------RRLYILFPLDCGVPDD----LSVAD------PNIRFRDML 225
sp|P15423|SPIKE_CVH22      SENFTSYGFS-----NVVELPKFFYASNGT-----YNCTD----AVLTYSSFGVCADGSI 561
sp|Q5MQD0|SPIKE_CVHN1      LNNISL--TT----------QP-YFDSYLGCVFNADNLTDYSVSSCALRMGSGFCVDYNS 749
sp|Q14EB0|SPIKE_CVHN2      LNNISF--IS----------QPFYFDSYLGCVLNAVNLTSYSVSSCDLRMGSGFCIDYAL 748
sp|Q0ZME7|SPIKE_CVHN5      LNNISF--IS----------QPFYFDSYLGCVLNAVNLTSYSVSSCDLRMGSGFCIDYAL 748
sp|Q6Q1S2|SPIKE_CVHNL      AVNESRYGLQ-----NLLQLPNFYYVSNGG-----NNCTT----AVMTYSNFGICADGSL 742
sp|P36334|SPIKE_CVHOC      FNNSLTRQLQ----------PINYFDSYLGCVVNAYNSTAISVQTCDLTVGSGYCVDYSK 752
sp|K9N5Q8|SPIKE_MERS1      SSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGLVNSS-LFVEDCKLPLGQSLCALPDT 741
sp|P59594|SPIKE_SARS       STAIHADQLT--PAWRIYSTGNNVFQTQAGCLIGAEHVD--TSYECDIPIGAGICASYHT 662
sp|P0DTC2|SPIKE_SARS2      PVAIHADQLT--PTWRVYSTGSNVFQTRAGCLIGAEHVN--NSYECDIPIGAGICASYQT 676


sp|Q2KI99|STING_BOVIN      PQQS---ADRAGIK-------GRVYTNSI------------YELLENGQRAGVCVLEYA- 262
sp|E1C7U0|STING_CHICK      PETI---LTRAGIK-------RRVYKHSL------------YVIRDKDNKLRPCVLEFA- 267
sp|Q86WV6|STING_HUMAN      PQQT---GDHAGIK-------DRVYSNSI------------YELLENGQRAGTCVLEYA- 262
sp|Q3TBT3|STING_MOUSE      PQQN---IDRAGIK-------NRVYSNSV------------YEILENGQPAGVCILEYA- 261
sp|A7SLZ2|STING_NEMVE      EPLE---KTRGGVF-------LRHYKHSV------------YEIKDGENEPWFCIMEYA- 302
sp|B8XX90|STING_PIG        PQQS---ADRAGIK-------GRVYTNSI------------YELLENGQPAGVCVLGYA- 262
sp|F1M391|STING_RAT        PQQN---TDRAGVK-------NRAYSNSV------------YELLENGQPAGACILEYA- 262
sp|P15423|SPIKE_CVH22      IA-------------------VQPRNVSY---DSV-SAIVTANLSIPSNWTTSVQVEYLQ 598
sp|Q5MQD0|SPIKE_CVHN1      PSSSSSRRKRRSISASYRFVTFEPFNVSF-VNDSIESVGGLYEIKIPTNFTIVGQEEFIQ 808
sp|Q14EB0|SPIKE_CVHN2      PS---SRRKRRGISSPYRFVTFEPFNVSF-VNDSVETVGGLFEIQIPTNFTIAGHEEFIQ 804
sp|Q0ZME7|SPIKE_CVHN5      PS---SRRKRRGISSPYRFVTFEPFNVSF-VNDSVETVGGLFEIQIPTNFTIAGHEEFIQ 804
sp|Q6Q1S2|SPIKE_CVHNL      IP-------------------VRPRNSSD---NGI-SAIITANLSIPSNWTTSVQVEYLQ 779
sp|P36334|SPIKE_CVHOC      -----NRRSRGAITTGYRFTNFEPFTVNS-VNDSLEPVGGLYEIQIPSEFTIGNMVEFIQ 806
sp|K9N5Q8|SPIKE_MERS1      PSTLTPRSVRSVPG-EMRLASI-AFNHPIQV-DQL--NSSYFKLSIPTNFSFGVTQEYIQ 796
sp|P59594|SPIKE_SARS       VS-L----LRSTSQ-KSI---V-AYTMSLGADSSI--AYSNNTIAIPTNFSISITTEVMP 710
sp|P0DTC2|SPIKE_SARS2      QT-NSPRRARSVAS-QSI---I-AYTMSLGAENSV--AYSNNSIAIPTNFTISVTTEILP 728
                                                    .                 :    :            

sp|Q2KI99|STING_BOVIN      -TPLQTLFAMSQDGRAGFSR-EDRLEQAKLFCRTLEDILANAPESQNNCRLIVYQEPAEG 320
sp|E1C7U0|STING_CHICK      -SPLQTLCAMSQDDCAAFSR-EQRLEQARLFYRSLRDILGSSKECAGLYRLIAYEEPAEP 325
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sp|Q86WV6|STING_HUMAN       -TPLQTLFAMSQYSQAGFSR-EDRLEQAKLFCRTLEDILADAPESQNNCRLIAYQEPADD 320
sp|Q3TBT3|STING_MOUSE       -TPLQTLFAMSQDAKAGFSR-EDRLEQAKLFCRTLEEILEDVPESRNNCRLIVYQEPTDG 319
sp|A7SLZ2|STING_NEMVE       -TPLLTLYDMSVAQPGELSR-EERDAQVVVFLRKLQDILEGDRACQGKYELVTFSPDRDL 360
sp|B8XX90|STING_PIG         -TPLQTLFAMSQDGRAGFSR-EDRLEQAKLFCRTLEDILADAPEAQNNCRLIVYQEPTEG 320
sp|F1M391|STING_RAT         -TPLQTLFAMSQDGKAGFSR-EDRLEQAKLFCRTLEEILADVPESRNHCRLIVYQESEEG 320
sp|P15423|SPIKE_CVH22       ITSTPIVVDCSTYVCNGNVRCVELLKQYTSACKTIEDALRNSARLESADVSEMLTFDKKA 658
sp|Q5MQD0|SPIKE_CVHN1       TNSPKVTIDCSLFVCSNYAACHDLLSEYGTFCDNINSILDEVNGLLDTTQLHVADTLMQG 868
sp|Q14EB0|SPIKE_CVHN2       TSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQG 864
sp|Q0ZME7|SPIKE_CVHN5       TSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQG 864
sp|Q6Q1S2|SPIKE_CVHNL       ITSTPIVVDCATYVCNGNPRCKNLLKQYTSACKTIEDALRLSAHLETNDVSSMLTFDSNA 839
sp|P36334|SPIKE_CVHOC       TSSPKVTIDCAAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNG 866
sp|K9N5Q8|SPIKE_MERS1       TTIQKVTVDCKQYVCNGFQKCEQLLREYGQFCSKINQALHGANLRQDDSVRNLFASVKSS 856
sp|P59594|SPIKE_SARS        VSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQM 770
sp|P0DTC2|SPIKE_SARS2       VSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQI 788
                             .                    .   :       :.  *                   .

sp|Q2KI99|STING_BOVIN       SSFSLSQEILQHLRQEER-EVTMGSTETSVMPGSSV-------LSQEPELLISGLEKPLP 372
sp|E1C7U0|STING_CHICK       ESHFLSGLILWHLQQQREEYMVQEELP-----LGT-------SSVELSLQVSSSDLPQP 373
sp|Q86WV6|STING_HUMAN       SSFSLSQEVLRHLRQEEKEEVTVGSLKTSAVPSTST-------MSQEPELLISGMEKPLP 373
sp|Q3TBT3|STING_MOUSE       NSFSLSQEVLRHIRQEEKEEVTMNAPMTSVAPPPSV-------LSQEPRLLISGMDQPLP 372
sp|A7SLZ2|STING_NEMVE       A-----DVMLRKLKDSE---LEIGG----------------------------------- 377
sp|B8XX90|STING_PIG         GSFSLSQEILRHLRQEER-EVTMGSAETSVVPTSST-------LSQEPELLISGMEQPLP 372
sp|F1M391|STING_RAT         NSFSLSQEVLRHIRQEEKEEVTMSGPPTSVAPRPSL-------LSQEPRLLISGMEQPLP 373
sp|P15423|SPIKE_CVH22       --FTLAN-----VSSFG-D-Y----NLSSVIPSLPTSGSRVAGRSAIEDILFSKLVTSGL 705
sp|Q5MQD0|SPIKE_CVHN1       --VTLSSNLNTNLHFDV-DNI----NFKSLVGCLGPHCGS-SSRSFFEDLLFDKVKLSDV 920
sp|Q14EB0|SPIKE_CVHN2       --VTLSSNLNTNLHSDV-DNI----DFKSLLGCLGSQCGS-SSRSLLEDLLFNKVKLSDV 916
sp|Q0ZME7|SPIKE_CVHN5       --VTLSSNLNTNLHSDV-DNI----DFKSLLGCLGSQCGS-SSRSLLEDLLFNKVKLSDV 916
sp|Q6Q1S2|SPIKE_CVHNL       --FSLAN-----VTSFG-D-Y----NLSSVLPQRNIRSSRIAGRSALEDLLFSKVVTSGL 886
sp|P36334|SPIKE_CVHOC       --VTLSTKLKDGVNFNV-DDI----NFSPVLGCLGSECSKASSRSAIEDLLFDKVKLSDV 919
sp|K9N5Q8|SPIKE_MERS1       --QSSPI-----IPGFG-GDF----NLTLLEP-VSISTGSRSARSAIEDLLFDKVTIADP 903
sp|P59594|SPIKE_SARS        --YKTPT-----LKYFG-GF-----NFSQILP-DP---LKPTKRSFIEDLLFNKVTLADA 813
sp|P0DTC2|SPIKE_SARS2       --YKTPP-----IKDFG-GF-----NFSQILP-DP---SKPSKRSFIEDLLFNKVTLADA 831
                                        :

sp|Q2KI99|STING_BOVIN       L-----RSDVF------------------------------------------------- 378
sp|E1C7U0|STING_CHICK       L-----RSDCP------------------------------------------------- 379
sp|Q86WV6|STING_HUMAN       L-----RTDFS------------------------------------------------- 379
sp|Q3TBT3|STING_MOUSE       L-----RTDLI------------------------------------------------- 378
sp|A7SLZ2|STING_NEMVE       ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG         L-----RSDIF------------------------------------------------- 378
sp|F1M391|STING_RAT         L-----RTDLI------------------------------------------------- 379
sp|P15423|SPIKE_CVH22       GTVDADYKKCT--KGLSIADLACAQYYNGIMVLPGVADAERMAMYTGSLIGGIALGGLTS 763
sp|Q5MQD0|SPIKE_CVHN1       GFVE-AYNNCT--GGSEIRDLLCVQSFNGIKVLPPILSESQISGYTTAATVAAMFPPWSA 977
sp|Q14EB0|SPIKE_CVHN2       GFVE-AYNNCT--GGSEIRDLLCVQSFNGIKVLPPILSETQISGYTTAATVAAMFPPWSA 973
sp|Q0ZME7|SPIKE_CVHN5       GFVE-AYNNCT--GGSEIRDLLCVQSFNGIKVLPPILSETQISGYTTAATVAAMFPPWSA 973
sp|Q6Q1S2|SPIKE_CVHNL       GTVDVDYKSCT--KGLSIADLACAQYYNGIMVLPGVADAERMAMYTGSLIGGMVLGGLTS 944
sp|P36334|SPIKE_CVHOC       GFVE-AYNNCT--GGAEIRDLICVQSYKGIKVLPPLLSENQISGYTLAATSASLFPPWTA 976
```

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sp|K9N5Q8|SPIKE_MERS1      GYMQ-GYDDCMQQGPASARDLICAQYVAGYKVLPPLMDVNMEAAYTSSLLGSIAGVGWTA 962
sp|P59594|SPIKE_SARS       GFMK-QYGECL--GDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTF 870
sp|P0DTC2|SPIKE_SARS2      GFIK-QYGDCL--GDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTF 888


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22      A----VSIPFSLAIQARLNYVALQTDVLQENQKILAASFNKAMTNIVDAFTGVNDAITQT 819
sp|Q5MQD0|SPIKE_CVHN1      A----AGIPFSLNVQYRINGLGVTMDVLNKNQKLIATAFNNALLSIQNGFSATN------ 1027
sp|Q14EB0|SPIKE_CVHN2      A----AGVPFSLNVQYRINGLGVTMDVLNKNQKLIANAFNKALLSIQNGFTATN------ 1023
sp|Q0ZME7|SPIKE_CVHN5      A----AGVPFSLNVQYRINGLGVTMDVLNKNQKLIANAFNKALLSIQNGFTATN------ 1023
sp|Q6Q1S2|SPIKE_CVHNL      A----AAIPFSLALQARLNYVALQTDVLQENQKILAASFNKAINNIVASFSSVNDAITQT 1000
sp|P36334|SPIKE_CVHOC      A----AGVPFYLNVQYRINGLGVTMDVLSQNQKLIANAFNNALYAIQEGFDATN------ 1026
sp|K9N5Q8|SPIKE_MERS1      GLSSFAAIPFAQSIFYRLNGVGITQQVLSENQKLIANKFNQALGAMQTGFTTTN------ 1016
sp|P59594|SPIKE_SARS       GAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTS------ 924
sp|P0DTC2|SPIKE_SARS2      GAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTA------ 942


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22      SQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNFQAISSSIQAIYDRLDTIQADQQVD 879
sp|Q5MQD0|SPIKE_CVHN1      --------SALAKIQSVVNSNAQALNSLLQQLFNKFGAISSSLQEILSRLDALEAQVQID 1079
sp|Q14EB0|SPIKE_CVHN2      --------SALAKIQSVVNANAQALNSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQID 1075
sp|Q0ZME7|SPIKE_CVHN5      --------SALAKIQSVVNANAQALNSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQID 1075
sp|Q6Q1S2|SPIKE_CVHNL      AEAIHTVTIALNKIQDVVNQQGSALNHLTSQLRHNFQAISNSIQAIYDRLDSIQADQQVD 1060
sp|P36334|SPIKE_CVHOC      --------SALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQEILSRLDALEAEAQID 1078
sp|K9N5Q8|SPIKE_MERS1      --------EAFHKVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQID 1068
sp|P59594|SPIKE_SARS       --------TALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQID 976
sp|P0DTC2|SPIKE_SARS2      --------SALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQID 994


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
```

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sp|F1M391|STING_RAT      ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22    RLITGRLAALNVFVSHTLTKYTEVRASRQLAQQKVNECVKSQSKRYGFCGNGTHIFSIVN 939
sp|Q5MQD0|SPIKE_CVHN1    RLINGRLTALNAYVSQQLSDISLVKFGAALAMEKVNECVKSQSPRINFCGNGNHILSLVQ 1139
sp|Q14EB0|SPIKE_CVHN2    RLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHILSLVQ 1135
sp|Q0ZME7|SPIKE_CVHN5    RLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHILSLVQ 1135
sp|Q6Q1S2|SPIKE_CVHNL    RLITGRLAALNAFVSQVLNKYTEVRGSRRLAQQKINECVKSQSNRYGFCGNGTHIFSIVN 1120
sp|P36334|SPIKE_CVHOC    RLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNGNHIISLVQ 1138
sp|K9N5Q8|SPIKE_MERS1    RLINGRLTTLNAFVAQQLVRSESAALSAQLAKDKVNECVKAQSKRSGFCGQGTHIVSFVV 1128
sp|P59594|SPIKE_SARS     RLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQ 1036
sp|P0DTC2|SPIKE_SARS2    RLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQ 1054


sp|Q2KI99|STING_BOVIN    ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK    ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN    ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE    ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE    ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG      ------------------------------------------------------------ 378
sp|F1M391|STING_RAT      ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22    AAPEGLVFLHTVLLPTQYKDVEAWSGLCVDGTN--GYVLRQPNLALY---KEGNYYRITS 994
sp|Q5MQD0|SPIKE_CVHN1    NAPYGLLFMHFSYKPISFKTVLVSPGLCISGDV--GIAPKQGYFIKH-----NDHWMFTG 1192
sp|Q14EB0|SPIKE_CVHN2    NAPYGLLFIHFSYKPTSFKTVLVSPGLCLSGDR--GIAPKQGYFIKQ-----NDSWMFTG 1188
sp|Q0ZME7|SPIKE_CVHN5    NAPYGLLFIHFSYKPTSFKTVLVSPGLCLSGDR--GIAPKQGYFIKQ-----NDSWMFTG 1188
sp|Q6Q1S2|SPIKE_CVHNL    SAPDGLLFLHTVLLPTDYKNVKAWSGICVDGIY--GYVLRQPNLVLY---SDNGVFRVTS 1175
sp|P36334|SPIKE_CVHOC    NAPYGLYFIHFSYVPTKYVTARVSPGLCIAGDR--GIAPKSGYFVNV-----NNTWMYTG 1191
sp|K9N5Q8|SPIKE_MERS1    NAPNGLYFMHVGYYPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIVDEWSYTG 1188
sp|P59594|SPIKE_SARS     AAPHGVVFLHVTYVPSQERNFTTAPAICHEGKA---YFPREGVFVFN-----GTSWFITQ 1088
sp|P0DTC2|SPIKE_SARS2    SAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA---HFPREGVFVSN-----GTHWFVTQ 1106


sp|Q2KI99|STING_BOVIN    ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK    ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN    ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE    ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE    ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG      ------------------------------------------------------------ 378
sp|F1M391|STING_RAT      ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22    RIMFEPRIPTMADFVQIENCNVTFVNISRSE--LQTIVPEYIDVNKTLQELSYKLPNYTV 1052
sp|Q5MQD0|SPIKE_CVHN1    SSYYYPEPISDKNVVFMNTCSVNFTKAPLVY--LNHSVPKLSDFESELSH-------WFK 1243
sp|Q14EB0|SPIKE_CVHN2    SSYYYPEPISDKNVVFMNSCSVNFTKAPFIY--LNNSIPNLSDFEAEFSL-------WFK 1239
sp|Q0ZME7|SPIKE_CVHN5    SSYYYPEPISDKNVVFMNSCSVNFTKAPFIY--LNNSIPNLSDFEAELSL-------WFK 1239
sp|Q6Q1S2|SPIKE_CVHNL    RVMFQPRLPVLSDFVQIYNCNVTFVNISRVE--LHTVIPDYVDVNKTLQEFAQNLPKYVK 1233
sp|P36334|SPIKE_CVHOC    SGYYYPEPITENNVVVMSTCAVNYTKAPYVM--LNTSIPNLPDFKEELDQ-------WFK 1242
sp|K9N5Q8|SPIKE_MERS1    SSFYAPEPITSLNTKYVAPQVTYQN-ISTNLPPPLLGNSTGIDFQDELDE-------FFK 1240
sp|P59594|SPIKE_SARS     RNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQ--PELDSFKEELDK-------YFK 1139
sp|P0DTC2|SPIKE_SARS2    RNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ--PELDSFKEELDK-------YFK 1157
```

```
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22      PDLVVEQYNQTILNLTSEISTLENKSAELNYTVQKLQTLIDNINSTLVDLKWLNRVETYI 1112
sp|Q5MQD0|SPIKE_CVHN1      NQT------SIAPNLTLNLHTINATFLDLYYEMNLIQESIKSLNNSYINLKDIGTYEMYV 1297
sp|Q14EB0|SPIKE_CVHN2      NHT------SIAPNLTFNSH-INATFLDLYYEMNVIQESIKSLNSSFINLKEIGTYEMYV 1292
sp|Q0ZME7|SPIKE_CVHN5      NHT------SIAPNLTFNSH-INATFLDLYYEMNVIQESIKSLNSSFINLKEIGTYEMYV 1292
sp|Q6Q1S2|SPIKE_CVHNL      PNFDLTPFNLTYLNLSSELKQLEAKTASLFQTTVELQGLIDQINSTYVDLKLLNRFENYI 1293
sp|P36334|SPIKE_CVHOC      NQT------SVAPDLSLD--YINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIGTYEYYV 1294
sp|K9N5Q8|SPIKE_MERS1      NVS------TSIPNFGS-LTQINTTLLDLTYEMLSLQQVVKALNESYIDLKELGNYTYYN 1293
sp|P59594|SPIKE_SARS       NHT------SPDVDLGD-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI 1192
sp|P0DTC2|SPIKE_SARS2      NHT------SPDVDLGD-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI 1210


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|P15423|SPIKE_CVH22      KWPWWVWLCISVVLIFVVSMLLLCCCSTGCCGFFSCFASSIRGCCE--STKLPYYDVEKI 1170
sp|Q5MQD0|SPIKE_CVHN1      KWPWYVWLLISFSFIIFLVLLFFICCCTGCGSACF-------S--KCHNCCDEYGGHHDF 1348
sp|Q14EB0|SPIKE_CVHN2      KWPWYIWLLIVILFIIFLMILFFICCCTGCGSACF-------S--KCHNCCDEYGGHNDF 1343
sp|Q0ZME7|SPIKE_CVHN5      KWPWYIWLLIVILFIIFLMILFFICCCTGCGSACF-------S--KCHNCCDEYGGHNDF 1343
sp|Q6Q1S2|SPIKE_CVHNL      KWPWWVWLIISVVFVVLLSLLVFCCLSTGCCGCCNCLTSSMRGCCDCGSTKLPYYEFEKV 1353
sp|P36334|SPIKE_CVHOC      KWPWYVWLLICLAGVAMLVLLFFICCCTGCGTSCF-------K--KCGGCCDDYTGYQEL 1345
sp|K9N5Q8|SPIKE_MERS1      KWPWYIWLGFIAGLVALALCVFFILCCTGCGTNCM-------GKLKCNRCCDRYEEYDLE 1346
sp|P59594|SPIKE_SARS       KWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCLK-------GACSCGSCCKF-DEDDSE 1244
sp|P0DTC2|SPIKE_SARS2      KWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLK-------GCCSCGSCCKF-DEDDSE 1262


sp|Q2KI99|STING_BOVIN      -----------  378
sp|E1C7U0|STING_CHICK      -----------  379
sp|Q86WV6|STING_HUMAN      -----------  379
sp|Q3TBT3|STING_MOUSE      -----------  378
sp|A7SLZ2|STING_NEMVE      -----------  377
sp|B8XX90|STING_PIG        -----------  378
sp|F1M391|STING_RAT        -----------  379
sp|P15423|SPIKE_CVH22      HIQ--------  1173
sp|Q5MQD0|SPIKE_CVHN1      VIK-TSHDD--  1356
sp|Q14EB0|SPIKE_CVHN2      VIK-ASHDD--  1351
```

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sp|Q0ZME7|SPIKE_CVHN5      VIK-ASHDD--  1351
sp|Q6Q1S2|SPIKE_CVHNL      HVQ--------  1356
sp|P36334|SPIKE_CVHOC      VIK-TSHDD--  1353
sp|K9N5Q8|SPIKE_MERS1      PHKVHVH----  1353
sp|P59594|SPIKE_SARS       PVLKGVKLHYT  1255
sp|P0DTC2|SPIKE_SARS2      PVLKGVKLHYT  1273
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CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q2KI99|STING_BOVIN      MP-------------------HS-SLHPSIPQP------RGLRAQ--KA------ALVLL 26
sp|E1C7U0|STING_CHICK      MPQ--------DPSTR-----SS-PARLLIPEP------RAGRAR--HA------ACVLL 32
sp|Q86WV6|STING_HUMAN      MP-------------------HS-SLHPSIPCP------RGHGAQ--KA------ALVLL 26
sp|Q3TBT3|STING_MOUSE      MP-------------------YS-NLHPAIPRP------RGHRSK--YV------ALIFL 26
sp|A7SLZ2|STING_NEMVE      MR-----------RAE-----EN-NGFGTIPKR------RNQHTP--FY------ASIGM 29
sp|B8XX90|STING_PIG        MP-------------------YS-SLHPSIPQP------RGLRAQ--VA------ALVLL 26
sp|F1M391|STING_RAT        MP-------------------YS-NLHPSIPRP------RSYRFK--LA------AFVLL 26
sp|O14924|RGS12_HUMAN      MFR--------AGEAS-----KRPLPGPSPPRVRSVEVARGRAGY--GF------TLSGQ 39
sp|Q8CGE9|RGS12_MOUSE      MYR--------AGEPG-----KR-QPGPAPPRVRSVEVARGRAGY--GF------TLSGQ 38
sp|O08774|RGS12_RAT        MYR--------AGEPG-----KR-QSGPAPPRVRSVEVARGRAGY--GF------TLSGQ 38
sp|P59594|SPIKE_SARS       MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQ--HTSSMRGVYYPDEIFRSDTLYLTQDL 58
sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTT--RTQLPPAY----TNSFTRGVYYPDKVFRSSVLHSTQDL 54
                           *                                      *

sp|Q2KI99|STING_BOVIN      SACLVALW-------GLGEPPDYTL-KW---------LVLHLASQQ-------------- 55
sp|E1C7U0|STING_CHICK      AVCFVVLF-------LSGEPLAPII-RS---------VCTQLAALQ-------------- 61
sp|Q86WV6|STING_HUMAN      SACLVTLW-------GLGEPPEHTL-RY---------LVLHLASLQ-------------- 55
sp|Q3TBT3|STING_MOUSE      VASLMILW-------VAKDPPNHTL-KY---------LALHLASHE-------------- 55
sp|A7SLZ2|STING_NEMVE      IVVIIVAFTSYHIT-SYGDDRNRAM-RQYSF-----TFSLAYLAFL-------------- 68
sp|B8XX90|STING_PIG        GACLVALW-------GLGELPEYTL-RW---------LVLHLASQQ-------------- 55
sp|F1M391|STING_RAT        VGSLMSLW-------MTGEPPSHTL-HY---------LALHVASQQ-------------- 55
sp|O14924|RGS12_HUMAN      APCVLSCV-------MRGSPADFVGLRAGDQILAVNEINVKKASHE-------------- 78
sp|Q8CGE9|RGS12_MOUSE      APCVLSCV-------MRGSPADFVGLRAGDQILAINEINVKKASHE-------------- 77
sp|O08774|RGS12_RAT        APCVLSCV-------MRGSPADFVGLRAGDQILAINEINVKKASHE-------------- 77
sp|P59594|SPIKE_SARS       FLPFYSNVTGFHTIN----------HTFGNPVIPFKD-GIYFAATEKSNVVRGWVFGSTM 107
sp|P0DTC2|SPIKE_SARS2      FLPFFSNVTWFHAIHVSGTNGT---KRFDNPVLPFND-GVYFASTEKSNIIRGWIFGTTL 110
                              .                                       :

sp|Q2KI99|STING_BOVIN      ----MGLLIKGICS------LAEELCHVHS----------RYHGSYWRAVRA-CLCSSMR 94
sp|E1C7U0|STING_CHICK      ----LGVLLKGCCC------LAEEIFHLHS----------RHHGSLWQVLCS-CFPPR-W 99
sp|Q86WV6|STING_HUMAN      ----LGLLLNGVCS------LAEELRHIHS----------RYRGSYWRTVRA-CLGCPLR 94
sp|Q3TBT3|STING_MOUSE      ----LGLLLKNLCC------LAEELCHVQS----------RYQGSYWKAVRA-CLGCPIH 94
sp|A7SLZ2|STING_NEMVE      ----VGELLRRCCL------FAEEYRHIET----------RYNGSLKKAIQT-TFSFGHN 107
sp|B8XX90|STING_PIG        ----IGLLVKGLCS------LAEELCHVHS----------RYQSSYWRAARA-CLGCPIR 94
sp|F1M391|STING_RAT        ----LGLLLKKLCC------LAEELCHVQS----------RYQGSYWKAVRA-CVGSPIC 94
sp|O14924|RGS12_HUMAN      ----DVVKLIGKCSGVLHMVIAEGVGRFESCSSDEEGG--LYEGKGWLKPKLDSKALGIN 132
sp|Q8CGE9|RGS12_MOUSE      ----DVVKLIGKCSGVLHMVIAEGTSHVESCSSDEEGG--LYEGKGWLRPKLDSKALGIN 131
sp|O08774|RGS12_RAT        ----DVVKLIGKCSGVLRMVISEGSSHVEPSSSDEEGG--LCEGKGWLRPKLDSKALGIN 131
sp|P59594|SPIKE_SARS       NNKSQSVIIINNSTNV-----VIRACNFELCDNPFFAVSKPMGT----QTHTMIF----- 153
sp|P0DTC2|SPIKE_SARS2      DSKTQSLLIVNNATNV-----VIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVY----- 160
                                   :   .             ...

sp|Q2KI99|STING_BOVIN      CG----ALLLLSCYFYCSL-----PN--------------------MADLPFTWML--AL 123
sp|E1C7U0|STING_CHICK      YL----ALLLVGGSAYLDP-----PE--------------------DNGHSPRLAL--TL 128
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sp|Q86WV6|STING_HUMAN      RG----ALLLLSIYFYYSL-----PN--------------------AVGPPFTWML--AL 123
sp|Q3TBT3|STING_MOUSE      CM----AMILLSSYFYF-L-----QN--------------------TADIYLSWMF--GL 122
sp|A7SLZ2|STING_NEMVE      -N----VLFVASLLFFVVFVASNDPNGSSSVIQGNSTAEPHTEMRQTSGWQGLWGQFIIS 162
sp|B8XX90|STING_PIG        CG----ALLLLSCYFYFSI-----RD--------------------KAGLPLPWML--AL 123
sp|F1M391|STING_RAT        FM----ALILLSFYFYCSL-----EN--------------------TSDLRLAWHL--GI 123
sp|O14924|RGS12_HUMAN      RAERVVEEMQSGGIFNMIFEN---PS----LCA--SNSEP-----------LKLKQ--RS 170
sp|Q8CGE9|RGS12_MOUSE      RAERVVEEVQSGGIFNMIFES---SS----LCA--SGPEP-----------LKLKQ--RS 169
sp|O08774|RGS12_RAT        RAERVVEEVQSGGIFNMIFES---PS----LCA--SGSEP-----------LKLKQ--RS 169
sp|P59594|SPIKE_SARS       -----------DNAFNCTFEYISDAFSL--------------DVSEKSGNFKHLREFVFK 188
sp|P0DTC2|SPIKE_SARS2      -----------SSANNCTFEYVSQPFLM--------------DLEGKQGNFKNLREFVFK 195
                                      .                                                 

sp|Q2KI99|STING_BOVIN      LGLSQALNILLGLQG-----------------------LAPAEVSAICEK-RNFNV---- 155
sp|E1C7U0|STING_CHICK      SCLCQLLVLALGLQK-----------------------LSAVEVSELTES-SKKNV---- 160
sp|Q86WV6|STING_HUMAN      LGLSQALNILLGLKG-----------------------LAPAEISAVCEK-GNFNV---- 155
sp|Q3TBT3|STING_MOUSE      LVLYKSLSMLLGLQS-----------------------LTPAEVSAVCEE-KKLNV---- 154
sp|A7SLZ2|STING_NEMVE      ALLTPLVVHLLGLRE-----------------------LSKVEESQLNEK-ENKNV---- 194
sp|B8XX90|STING_PIG        LGLSQALNILLGLQH-----------------------LAPAEVSAICEK-RNFNV---- 155
sp|F1M391|STING_RAT        LVLSKSLSMTLDLQS-----------------------LAPAEVSAVCEE-KNFNV---- 155
sp|O14924|RGS12_HUMAN      LSESAATRFDVGHESIN----------NPNPNM-----LSKEEISKVIHDDSVFSIGLES 215
sp|Q8CGE9|RGS12_MOUSE      LSESAALRLDAGQAGLC----------APHPSM-----LSKEDISKVINDDSVFTVGLDS 214
sp|O08774|RGS12_RAT        LSESAALRLDVGQDSLC----------TPHPSM-----LSKEEISKVINDDSVFTVGLDN 214
sp|P59594|SPIKE_SARS       NKD-GFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFS------PA 241
sp|P0DTC2|SPIKE_SARS2      NID-GYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDS 254
                                                                 :       :              

sp|Q2KI99|STING_BOVIN      -------AHGLAWSYYIGYLRLI-LPGLPARIQI--YNQFHNNTLQGAGSHRLHILFPLD 205
sp|E1C7U0|STING_CHICK      -------AHGLAWSYYIGYLKVV-LPRLKECMEE--LSRTNPMLRAHRDTWKLHILVPLG 210
sp|Q86WV6|STING_HUMAN      -------AHGLAWSYYIGYLRLI-LPELQARIRT--YNQHYNNLLRGAVSQRLYILLPLD 205
sp|Q3TBT3|STING_MOUSE      -------AHGLAWSYYIGYLRLI-LPGLQARIRM--FNQLHNNMLSGAGSRRLYILFPLD 204
sp|A7SLZ2|STING_NEMVE      -------ADGLAWSYYFGYLKFV-LPELEKQIEK--TSKFRSK---EKFVKKMFILIPSN 241
sp|B8XX90|STING_PIG        -------AHGLAWSYYIGYLRLI-LPGLRARIQA--YNQRHKNVLGGIGNHRLHILFPLD 205
sp|F1M391|STING_RAT        -------AHGLAWSYYIGYLKLI-LPGLQARIRM--FNQLHNNMLSGAGSRRLYILFPLD 205
sp|O14924|RGS12_HUMAN      HDDFALDASILNVAMIVGYLGSIELPSTSSNLESDSLQAIRGCMRRLRAEQKIHSLVTM- 274
sp|Q8CGE9|RGS12_MOUSE      HDDFGLDASILNVAMVVGYLGSIELPSTSSNLEHDSLQAIRGCMRRLRAEQKIHSLVTM- 273
sp|O08774|RGS12_RAT        HDDFGLDASILNVAMVVGYLGSIELPSTSSNLEHDSLQAIRGCMRRLRAEQKIHSLVTM- 273
sp|P59594|SPIKE_SARS       QDIW----GTSAAAYFVGYLKPTTFMLKYD--ENGTITDAVDCSQNP--------LAELK 287
sp|P0DTC2|SPIKE_SARS2      SSGW----TAGAAAYYVGYLQPRTFLLKYN--ENGTITDAVDCALDP--------LSETK 300
                                        :  .***    :       .                      *    

sp|Q2KI99|STING_BOVIN      CGVPDDLNVAD----PNIRFLHELPQQSADRAGIKGRVYTNSIYELLENGQRAGVCVLEY 261
sp|E1C7U0|STING_CHICK      CDIWDDLEKAD----SNIQYLADLPETILTRAGIKRRVYKHSLYVIRDKDNKLRPCVLEF 266
sp|Q86WV6|STING_HUMAN      CGVPDNLSMAD----PNIRFLDKLPQQTGDHAGIKDRVYSNSIYELLENGQRAGTCVLEY 261
sp|Q3TBT3|STING_MOUSE      CGVPDNLSVVD----PNIRFRDMLPQQNIDRAGIKNRVYSNSVYEILENGQPAGVCILEY 260
sp|A7SLZ2|STING_NEMVE      CFWDDKIPGSDYDPQNRITFEGNTEPLEKTRGGVFLRHYKHSVYEIKDGENEPWFCIMEY 301
sp|B8XX90|STING_PIG        CGVPDDLSVAD----PNIRFLHELPQQSADRAGIKGRVYTNSIYELLENGQPAGVCVLGY 261
sp|F1M391|STING_RAT        CGVPDDLSVAD----PNIRFRDMLPQQNTDRAGVKNRAYSNSVYELLENGQPAGACILEY 261
```

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sp|O14924|RGS12_HUMAN      ------------------KIMHDCVQLSTDKAGVVAEYPAEKL---------AFSAVCPD 307
sp|Q8CGE9|RGS12_MOUSE      ------------------KVMHDCVQLVTDRAGVVAEYPAEKL---------AFSAVCPD 306
sp|O08774|RGS12_RAT        ------------------KVMHDCVQLVTDRAGVVAEYPAEKL---------AFSAVCPD 306
sp|P59594|SPIKE_SARS       CSVKSFEIDKGIYQTSNFRV---------VPSGDVVRFP-------------NITNLCPF 325
sp|P0DTC2|SPIKE_SARS2      CTLKSFTVEKGIYQTSNFRV---------QPTESIVRFP-------------NITNLCPF 338
                                                               .                   :

sp|Q2KI99|STING_BOVIN      ATPLQ-----TLFAMSQDG-RAGFSRED-------------------------------- 283
sp|E1C7U0|STING_CHICK      ASPLQ-----TLCAMSQDD-CAAFSREQ-------------------------------- 288
sp|Q86WV6|STING_HUMAN      ATPLQ-----TLFAMSQYS-QAGFSRED-------------------------------- 283
sp|Q3TBT3|STING_MOUSE      ATPLQ-----TLFAMSQDA-KAGFSRED-------------------------------- 282
sp|A7SLZ2|STING_NEMVE      ATPLL-----TLYDMSVAQ-PGELSREE-------------------------------- 323
sp|B8XX90|STING_PIG        ATPLQ-----TLFAMSQDG-RAGFSRED-------------------------------- 283
sp|F1M391|STING_RAT        ATPLQ-----TLFAMSQDG-KAGFSRED-------------------------------- 283
sp|O14924|RGS12_HUMAN      DRRFF-----GLVTMQTND-DGSLAQEEEGALRTSCHVFMVDPDLFNHKIHQGIARRFGF 361
sp|Q8CGE9|RGS12_MOUSE      DRRFF-----GLVTMQTND-DGGLAQEDEGALRTSCHVFMVDPDLFHHKIHQGIARRFGF 360
sp|O08774|RGS12_RAT        DRRFF-----GLVTMQTND-DGCLAQEDEGALRTSCHVFMVDPDLFHHKIHQGIARRFGF 360
sp|P59594|SPIKE_SARS       GEVFNATKFPSVYAWERKKISNCVADY--SVL-------------Y-------------- 356
sp|P0DTC2|SPIKE_SARS2      GEVFNATRFASVYAWNRKRISNCVADY--SVL-------------Y-------------- 369
                              :       :   .       .:

sp|Q2KI99|STING_BOVIN      --------------------RLEQAKLFCRTLEDILANAPESQNNCRLIV------YQEP 317
sp|E1C7U0|STING_CHICK      --------------------RLEQARLFYRSLRDILGSSKECAGLYRLIA------YEEP 322
sp|Q86WV6|STING_HUMAN      --------------------RLEQAKLFCRTLEDILADAPESQNNCRLIA------YQEP 317
sp|Q3TBT3|STING_MOUSE      --------------------RLEQAKLFCRTLEEILEDVPESRNNCRLIV------YQEP 316
sp|A7SLZ2|STING_NEMVE      --------------------RDAQVVVFLRKLQDILEGDRACQGKYELVT------FSPD 357
sp|B8XX90|STING_PIG        --------------------RLEQAKLFCRTLEDILADAPEAQNNCRLIV------YQEP 317
sp|F1M391|STING_RAT        --------------------RLEQAKLFCRTLEEILADVPESRNHCRLIV------YQES 317
sp|O14924|RGS12_HUMAN      ECTADPDTNGCLEFPASSLPVLQFISVLYRDMGELIEGMRARAFLDGDAD------AH-- 413
sp|Q8CGE9|RGS12_MOUSE      ACTADPDTSGCLEFPASSLPVLQFISVLYRDMGELIEGVRARAFLDGDAD------AH-- 412
sp|O08774|RGS12_RAT        ACTADPDTSGCLEFPASSLPVLQFISVLYRDMGELIEGVRARAFLDGDAD------AH-- 412
sp|P59594|SPIKE_SARS       -NSTFFSTFKCYGVSATKLNDLCFSNVYADSF--VVKGDDVRQIAPGQTGVIADYNYKLP 413
sp|P0DTC2|SPIKE_SARS2      -NSASFSTFKCYGVSPTKLNDLCFTNVYADSF--VIRGDEVRQIAPGQTGKIADYNYKLP 426
                                                     :    :  :: .

sp|Q2KI99|STING_BOVIN      AEGS------SFSLS-QEILQHLRQEER-E------------------------------ 339
sp|E1C7U0|STING_CHICK      AEPE------SHFLS-GLILWHLQQQQREE------------------------------ 345
sp|Q86WV6|STING_HUMAN      ADDS------SFSLS-QEVLRHLRQEEKEE------------------------------ 340
sp|Q3TBT3|STING_MOUSE      TDGN------SFSLS-QEVLRHIRQEEKEE------------------------------ 339
sp|A7SLZ2|STING_NEMVE      RDLA------------DVMLRKLKDSE--------------------------------- 372
sp|B8XX90|STING_PIG        TEGG------SFSLS-QEILRHLRQEER-E------------------------------ 339
sp|F1M391|STING_RAT        EEGN------SFSLS-QEVLRHIRQEEKEE------------------------------ 340
sp|O14924|RGS12_HUMAN      QNNS------TSSNS-DSGIGNFHQEEKSNRVLVVDLGGSSSRHGPGG-SAWDGVGGRGA 465
sp|Q8CGE9|RGS12_MOUSE      QNNS------TSSNS-DSGIGNFNQEEKSNRVLVVDLGGGSSRHGQGSSPGWESGGGRGS 465
sp|O08774|RGS12_RAT        QNNS------TSSNS-DSGIGNFNQEEKSNRVLVVDLGGGSSRHGQGSSPGWESVSGRGS 465
sp|P59594|SPIKE_SARS       DDFMGCVLAWNTRNIDATSTGNYNYKYRYL-------------------------RHGKL 448
sp|P0DTC2|SPIKE_SARS2      DDFTGCVIAWNSNNLDSKVGGNYNYLYRLF-------------------------RKSNL 461
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                            :                   : .

sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      QPWGAPWTGPFCPDPEGSPPFEAAHQTDRFWDLNKHLG-PA--------------SPVEV 510
sp|Q8CGE9|RGS12_MOUSE      QPWSAPWNGAFCHDSEAGSPLETSPNTDRFWDLTKHSG-PV--------------SHMEV 510
sp|O08774|RGS12_RAT        QPWSAPWNGTFCHDSEAGSPLETSPNTDRFWDLTKHSG-PV--------------FHMEV 510
sp|P59594|SPIKE_SARS       RPFERDIS--NVPFSPDGKPCTP-PALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLN 505
sp|P0DTC2|SPIKE_SARS2      KPFERDIS--TEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLH 519


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      PPASLRS-----------SVPPSKRGTVGAG--CGFNQRWLPVHVLREW----------- 546
sp|Q8CGE9|RGS12_MOUSE      PPATLRS-----------SIPPSKRGAAGSS--CGFNQRWLPVHVLQEW----------- 546
sp|O08774|RGS12_RAT        PPATLRS-----------SIPPSKRGATGSS--CGFNQRWLPVHVLQEW----------- 546
sp|P59594|SPIKE_SARS       APATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDP 565
sp|P0DTC2|SPIKE_SARS2      APATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDP 579


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      ---------QCGHT--S----DQDSYTDSTDGWSSINCGTLPPPMSKIPADRYRVEGSFA 591
sp|Q8CGE9|RGS12_MOUSE      ---------QCGHA--S----DQESYTDSTDGWSSVNCGTLPPPMSKIPADRYRVEGSFA 591
sp|O08774|RGS12_RAT        ---------QCGHA--S----DQESYTDSTDGWSSVNCGTLPPPMSKIPADRYRVEGSFA 591
sp|P59594|SPIKE_SARS       KTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHAD---Q-------- 614
sp|P0DTC2|SPIKE_SARS2      QTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHAD---Q-------- 628


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
```

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sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      QPPLNAPKREWSRKAFGMQSIFGPHRNVRKTKE-----DKKGSKFGRGTGLTQPSQRTSA 646
sp|Q8CGE9|RGS12_MOUSE      QAPLSTQKRDWSRKAFGMQNLFGPHRNVRKTKE-----DKKSSKLGRGVALAQTSQRTSA 646
sp|O08774|RGS12_RAT        QAPLSTQKRDWSRKAFGMQNLFGPHRNVRKTKE-----DKKSSKLGRGVALAQTSQRTSA 646
sp|P59594|SPIKE_SARS       ------LTPAWRIYSTGN-NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSL-- 665
sp|P0DTC2|SPIKE_SARS2      ------LTPTWRVYSTGS-NVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSP 681


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      RRSF--GRSKRFSITRSLDDLESATVSDGELTGADLKDCVSNNSLSSNASLPSVQSCRRL 704
sp|Q8CGE9|RGS12_MOUSE      RRSF--GRSRRFSITRSLDDLESATVSDGELTGADLKDCISNNSLSSNASLPSVQSCRRL 704
sp|O08774|RGS12_RAT        RRSF--GRSRRFSLTRSLDDLESATVSDGELTGADLKDCISNNSLSSNASLPSVQSCRRL 704
sp|P59594|SPIKE_SARS       --LRSTSQKSIVAYTMSL--------------GADSSIAYSNNTIAIPTNFS-------- 701
sp|P0DTC2|SPIKE_SARS2      RRARSVASQSIIAYTMSL--------------GAENSVAYSNNSIAIPTNFT-------- 719


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      RERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACEYFNHVPAHDKKELSY 764
sp|Q8CGE9|RGS12_MOUSE      RERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACECFSHVPAHDKKELSY 764
sp|O08774|RGS12_RAT        RERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACECFSHVPAHDKKELSY 764
sp|P59594|SPIKE_SARS       ---------ISI------------TTEVMPVSMA-------------------------- 714
sp|P0DTC2|SPIKE_SARS2      ---------ISV------------TTEILPVSMT-------------------------- 732


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      RAREIFSKFLCSKATTPVNIDSQAQLADDVLRAPHPDMFKEQQLQIFNLMKFDSYTRFLK 824
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sp|Q8CGE9|RGS12_MOUSE      RAREIFSKFLCSKATTPVNIDSQAQLADDILNAPHPDMFKEQQLQIFNLMKFDSYTRFLK 824
sp|O08774|RGS12_RAT        RAREIFSKFLCSKATTPVNIDSQAQLADDILNAPHPDMFKEQQLQIFNLMKFDSYTRFLK 824
sp|P59594|SPIKE_SARS       KTSVDCNMYICGDSTECAN----------------------------------------- 733
sp|P0DTC2|SPIKE_SARS2      KTSVDCTMYICGDSTECSN----------------------------------------- 751


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      SPLYQECILAEVEGRALPDSQQVPSSPASKHSLGSDHSSVSTPKKLSGKSKSGRSLNEEL 884
sp|Q8CGE9|RGS12_MOUSE      SQLYQECVLAEVEGRTLPDSQQVPSSPASKHSISSDHSNVSTPKKLSGKSKSGRSLNEDV 884
sp|O08774|RGS12_RAT        SQLYQECVLAEVEGRTLPDSQQVPSSPASKHSISSDHSNVSTPKKLSGKSKSGRSLNEDV 884
sp|P59594|SPIKE_SARS       ------------------------------------------------------------ 733
sp|P0DTC2|SPIKE_SARS2      ------------------------------------------------------------ 751


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 339
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 345
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 340
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 339
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 372
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 339
sp|F1M391|STING_RAT        ------------------------------------------------------------ 340
sp|O14924|RGS12_HUMAN      GDEDSEKKRKGAFFSWSRTRSTGRSQKKREHGDHADDALHANGGLCRRESQGSVSSAGSL 944
sp|Q8CGE9|RGS12_MOUSE      GEEDSEKKRRGAFFSWSRSRSTGRSQKKKDHGDHAHDAPHANGGLCRRESQGSVSSAGSL 944
sp|O08774|RGS12_RAT        GEEDSEKKRKGAFFSWSRSRSTGRSQKKKDHGDHAHDALHANGGLCRRESQGSVSSAGSL 944
sp|P59594|SPIKE_SARS       -------------------------------------LLLQYGSFCTQLN---------- 746
sp|P0DTC2|SPIKE_SARS2      -------------------------------------LLLQYGSFCTQLN---------- 764


sp|Q2KI99|STING_BOVIN      --------------------------------------VTMGSTETSVMPGSSVLSQEPE 361
sp|E1C7U0|STING_CHICK      --------------------------------------YMVQEELP-----LGTSSVELS 362
sp|Q86WV6|STING_HUMAN      --------------------------------------VTVGSLKTSAVPSTSTMSQEPE 362
sp|Q3TBT3|STING_MOUSE      --------------------------------------VTMNAPMTSVAPPPSVLSQEPR 361
sp|A7SLZ2|STING_NEMVE      --------------------------------------LEIGG----------------- 377
sp|B8XX90|STING_PIG        --------------------------------------VTMGSAETSVVPTSSTLSQEPE 361
sp|F1M391|STING_RAT        --------------------------------------VTMSGPPTSVAPRPSLLSQEPR 362
sp|O14924|RGS12_HUMAN      DLSEACRTLAPEKDKATKHCCIHLPDGT-SCVVAVKAGFSIKDILSGLCERHGINGAAAD 1003
sp|Q8CGE9|RGS12_MOUSE      DLSEACRTSALEKDKAAKHCCVHLPDGT-SCVVAVKSGFSIKEILSGLCERHGINGAAVD 1003
sp|O08774|RGS12_RAT        DLSEACRTSALERDKAAKHCCVHLPDGT-SCVVAVKSGFSIKEILSGLCERHGINGAAVD 1003
sp|P59594|SPIKE_SARS       ---RALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLK---------- 793
sp|P0DTC2|SPIKE_SARS2      ---RALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSK---------- 811
                                                                   .
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```
sp|Q2KI99|STING_BOVIN      LLISGLEKPLPLRSDVF------------------------------------------- 378
sp|E1C7U0|STING_CHICK      LQVSSSDLPQPLRSDCP------------------------------------------- 379
sp|Q86WV6|STING_HUMAN      LLISGMEKPLPLRTDFS------------------------------------------- 379
sp|Q3TBT3|STING_MOUSE      LLISGMDQPLPLRTDLI------------------------------------------- 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        LLISGMEQPLPLRSDIF------------------------------------------- 378
sp|F1M391|STING_RAT        LLISGMEQPLPLRTDLI------------------------------------------- 379
sp|O14924|RGS12_HUMAN      LFLVGGDKPLVLHQDSSILESRDLRLEKRTLF----------------RLDLVPINRSVG 1047
sp|Q8CGE9|RGS12_MOUSE      LFLVGGDKPLVLHQDSSILATRDLRLEKRTLF----------------RLDLVPINRSVG 1047
sp|O08774|RGS12_RAT        LFLVGGDKPLVLHQDSSILATRDLRLGKRTLF----------------RLDLVPINRSVG 1047
sp|P59594|SPIKE_SARS       --------PT---KRSF---IEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNG 839
sp|P0DTC2|SPIKE_SARS2      --------PS---KRSF---IEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNG 857


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      LKAKPTKPVTEVLRPVVARYGLDLSGLLVRLSGEKEPLDLGA----PIS-----SLDG-- 1096
sp|Q8CGE9|RGS12_MOUSE      LKAKPTKPVTEVLRPVVAKYGLDLGSLLVRLSGEKEPLDLGA----PIS-----SLDG-- 1096
sp|O08774|RGS12_RAT        LKAKPTKPVTEVLRPVVAKYGLDLGSLLVRLSGEKEPLDLGA----PIS-----SLDG-- 1096
sp|P59594|SPIKE_SARS       LTVLPPLLTDD----MIAAYTAALVS---GTATAGWTFGAGAALQIPFAMQMAYRFNGIG 892
sp|P0DTC2|SPIKE_SARS2      LTVLPPLLTDE----MIAQYTSALLA---GTITSGWTFGAGAALQIPFAMQMAYRFNGIG 910


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      --QRVVLEEKDPSRGKASADKQKGVPVKQNTAVNSSSRNHSATGEERTLGKSNSIKIKGE 1154
sp|Q8CGE9|RGS12_MOUSE      --QRVILEERDPSRGKVSTDKQKGAPVKQNSAVNSSPRNHLAMGEERTLGKSNSIKIRGE 1154
sp|O08774|RGS12_RAT        --QRVILEERDPSRGKVSTEKQKGAPVKQSSAVNSSPRNHSAMGEERTLGKSNSIKIRGE 1154
sp|P59594|SPIKE_SARS       VTQNVLYEN------------QKQIANQFNKAISQI--QESLTTTSTALGKLQDVVNQNA 938
sp|P0DTC2|SPIKE_SARS2      VTQNVLYEN------------QKLIANQFNSAIGKI--QDSLSSTASALGKLQDVVNQNA 956


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
```

```
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      NGKNARDPRLSKREESIAKIGKKKYQKINLDEAEEFFE-LIS-KAQSNRADDQRGLLRKE 1212
sp|Q8CGE9|RGS12_MOUSE      NGKSARDPRLSKREESIAKIGKKKYQKINLDEAEEFFE-LIS-KAQSNRADDQRGLLRKE 1212
sp|O08774|RGS12_RAT        NGKSARDPRLSKREESIAKIGKKKYQKINLDEAEEFFE-LIS-KAQSNRADDQRGLLRKE 1212
sp|P59594|SPIKE_SARS       QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA 998
sp|P0DTC2|SPIKE_SARS2      QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA 1016


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      DLVLPEFLRLPPGSTELTLPTPAAVAKGFSKRSA-TGNGRESASQPGEQWEP-------- 1263
sp|Q8CGE9|RGS12_MOUSE      DLVLPEFLRLPAGSSELALSSPPP-VKGYSKRAV-TGHGQEGAAQTEESYSDSPATSPAS 1270
sp|O08774|RGS12_RAT        DLVLPEFLRLPPGSSELALSSPPP-VKGFSKRAV-TSHGQEGAVQTEESYSDSPATSPAS 1270
sp|P59594|SPIKE_SARS       EIR---------ASANLAATKMSECVLGQSKRVDFCGKGY--------HLMSFPQAAPHG 1041
sp|P0DTC2|SPIKE_SARS2      EIR---------ASANLAATKMSECVLGQSKRVDFCGKGY--------HLMSFPQSAPHG 1059


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      ----------VQESSDSPSTSPGSASSPPGPPGTTPPGQKSPSGPFCTPQSPVSLAQEGT 1313
sp|Q8CGE9|RGS12_MOUSE      AQSPCSAYSPGSAHS------PGSAHSTPGPPGTTQPGEKPT-KPS-----CVSMVQEGT 1318
sp|O08774|RGS12_RAT        AQSPCSAYSPGSAHSPGSAHSPGSAHSTPGPPGTAQPGEKPT-KPS-----CISTVQEGT 1324
sp|P59594|SPIKE_SARS       VVFLHVTYVPSQERNFT--TAPA----------ICHEGK------AYFPREGV-FVF--N 1080
sp|P0DTC2|SPIKE_SARS2      VVFLHVTYVPAQEKNFT--TAPA----------ICHDGK------AHFPREGV-FVS--N 1098


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      AQIWKRQSQEVEAGGIQTVEDEHVAELTLMGEGD--ISSPNSTLLPPPSTPQEVPGPSRP 1371
sp|Q8CGE9|RGS12_MOUSE      TQAWRRLSPEMEAGGIQTVEDEQVADLTLMGEGD--ISSPNSTLLPPPPTPQDTPGPPRP 1376
```

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sp|O08774|RGS12_RAT        TQAWRRLSPELEAGGIQTVEEEQVADLTLMGEGD--ISSPNSTLLPPPPLPQDTPGPTRP 1382
sp|P59594|SPIKE_SARS       GTSWFITQRNFFSPQIITTDNTFVS-----GNCDVVIGIINNTVYD----------PLQP 1125
sp|P0DTC2|SPIKE_SARS2      GTHWFVTQRNFYEPQIITTDNTFVS-----GNCDVVIGIVNNTVYD----------PLQP 1143


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      GSGTHGSR-DLPVNRIIDVDLVTGSAPGRDGGIAGAQAGPGRSQASG---GPPTSDLPGL 1427
sp|Q8CGE9|RGS12_MOUSE      GTSRF------------------------------------------------------- 1381
sp|O08774|RGS12_RAT        GTSRF------------------------------------------------------- 1387
sp|P59594|SPIKE_SARS       ELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL 1185
sp|P0DTC2|SPIKE_SARS2      ELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL 1203


sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|O14924|RGS12_HUMAN      GPVPGEPAKPKTSAHHATFV---------------------------------------- 1447
sp|Q8CGE9|RGS12_MOUSE      ------------------------------------------------------------ 1381
sp|O08774|RGS12_RAT        ------------------------------------------------------------ 1387
sp|P59594|SPIKE_SARS       GKYEQYIKWPWY--VWLGFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDS 1243
sp|P0DTC2|SPIKE_SARS2      GKYEQYIKWPWY--IWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDS 1261


sp|Q2KI99|STING_BOVIN      ------------ 378
sp|E1C7U0|STING_CHICK      ------------ 379
sp|Q86WV6|STING_HUMAN      ------------ 379
sp|Q3TBT3|STING_MOUSE      ------------ 378
sp|A7SLZ2|STING_NEMVE      ------------ 377
sp|B8XX90|STING_PIG        ------------ 378
sp|F1M391|STING_RAT        ------------ 379
sp|O14924|RGS12_HUMAN      ------------ 1447
sp|Q8CGE9|RGS12_MOUSE      ------------ 1381
sp|O08774|RGS12_RAT        ------------ 1387
sp|P59594|SPIKE_SARS       EPVLKGVKLHYT 1255
sp|P0DTC2|SPIKE_SARS2      EPVLKGVKLHYT 1273
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|O14924|RGS12_HUMAN      ------------------------------------------------------------ 0
sp|Q8CGE9|RGS12_MOUSE      ------------------------------------------------------------ 0
sp|O08774|RGS12_RAT        ------------------------------------------------------------ 0
sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS 60


sp|O14924|RGS12_HUMAN      -------MFRAGEASKRPLPGPSPPRVRSVEVAR-----GRAGY--GFTLSGQAPCVLSC 46
sp|Q8CGE9|RGS12_MOUSE      -------MYRAGEPGKR-QPGPAPPRVRSVEVAR-----GRAGY--GFTLSGQAPCVLSC 45
sp|O08774|RGS12_RAT        -------MYRAGEPGKR-QSGPAPPRVRSVEVAR-----GRAGY--GFTLSGQAPCVLSC 45
sp|P0DTC2|SPIKE_SARS2      NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQS---- 116
                                  :. :*  ..:   .*  *   .* .*         *:  * **..:: .

sp|O14924|RGS12_HUMAN      VMRGSPADFVGLRAGDQILAVNEINVKKASHEDVVKLIGKCSGVLHMVIAEGVGRFESCS 106
sp|Q8CGE9|RGS12_MOUSE      VMRGSPADFVGLRAGDQILAINEINVKKASHEDVVKLIGKCSGVLHMVIAEGTSHVESCS 105
sp|O08774|RGS12_RAT        VMRGSPADFVGLRAGDQILAINEINVKKASHEDVVKLIGKCSGVLRMVISEGSSHVEPSS 105
sp|P0DTC2|SPIKE_SARS2      -----------------LLIVN-----------------NATNV---VI--KVCEFQFCN 137
                                            :* :*                 :.:.*   **     ..: ..

sp|O14924|RGS12_HUMAN      SDEEGGLY--EGKGWLKPKLDSKALGINRAERVV------E---------------EMQS 143
sp|Q8CGE9|RGS12_MOUSE      SDEEGGLY--EGKGWLRPKLDSKALGINRAERVV------E---------------EVQS 142
sp|O08774|RGS12_RAT        SDEEGGLC--EGKGWLRPKLDSKALGINRAERVV------E---------------EVQS 142
sp|P0DTC2|SPIKE_SARS2      DPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNI 197
                           .   *     :.*.*:. ::   : . * : . *      :                 :

sp|O14924|RGS12_HUMAN      GGIFNMIFENPSLCASNSEPLKLKQRSLSES----AATRFDVGHESINNPNPNMLSKEEI 199
sp|Q8CGE9|RGS12_MOUSE      GGIFNMIFESSSLCASGPEPLKLKQRSLSES----AALRLDAGQAGLCAPHPSMLSKEDI 198
sp|O08774|RGS12_RAT        GGIFNMIFESPSLCASGSEPLKLKQRSLSES----AALRLDVGQDSLCTPHPSMLSKEEI 198
sp|P0DTC2|SPIKE_SARS2      DGYFKIYSK--------HTPINLVRDLPQGFSALEPLVDLPIGINI-----------TRF 238
                           .* *::  :          *::* :   .          :  *                :

sp|O14924|RGS12_HUMAN      SKVIHDDSVFSIGLESHDDFALDASILNVAMIVGYLGSIELPSTSSNLESDSLQAIRGCM 259
sp|Q8CGE9|RGS12_MOUSE      SKVINDDSVFTVGLDSHDDFGLDASILNVAMVVGYLGSIELPSTSSNLEHDSLQAIRGCM 258
sp|O08774|RGS12_RAT        SKVINDDSVFTVGLDNHDDFGLDASILNVAMVVGYLGSIELPSTSSNLEHDSLQAIRGCM 258
sp|P0DTC2|SPIKE_SARS2      QTLLALHRSYLTPGDSSSGWTA----GAAAYYVGYLQPRTFLLKY--NENGTITDAVDCA 292
                           ..::  .  :    :. ..:        .*  ****    :  .    * .::    .*

sp|O14924|RGS12_HUMAN      RRLRAEQK--IHSLVTMKIMHDCVQLSTDKAGVVAEYPAEKLAFSAVCPDDRRFFGLVTM 317
sp|Q8CGE9|RGS12_MOUSE      RRLRAEQK--IHSLVTMKVMHDCVQLVTDRAGVVAEYPAEKLAFSAVCPDDRRFFGLVTM 316
sp|O08774|RGS12_RAT        RRLRAEQK--IHSLVTMKVMHDCVQLVTDRAGVVAEYPAEKLAFSAVCPDDRRFFGLVTM 316
sp|P0DTC2|SPIKE_SARS2      LDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFP----NITNLCPFGEVFNATRF- 347
                               :* *  ::*:.. * :::  :: .: :  :..:*     :: :** .. * .

sp|O14924|RGS12_HUMAN      QTNDDGSLAQEEEGALRTSCHVFMVDPDLFNHKIHQGIARRFGFECTADPDTNGCLEFPA 377
sp|Q8CGE9|RGS12_MOUSE      QTNDDGGLAQEDEGALRTSCHVFMVDPDLFHHKIHQGIARRFGFACTADPDTSGCLEFPA 376
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sp|O08774|RGS12_RAT        QTNDDGCLAQEDEGALRTSCHVFMVDPDLFHHKIHQGIARRFGFACTADPDTSGCLEFPA 376
sp|P0DTC2|SPIKE_SARS2      ----AS---------------VYAWN----RKRISNCVADYSVLYNSASFSTFKCYGVSP 384
                                .               *:  :    .::* : :*    :  :*. .*  *  .

sp|O14924|RGS12_HUMAN      SSLPVLQFISVLYRDMGELIEGMRARAFLDGDADAHQN--------------NSTSSNSD 423
sp|Q8CGE9|RGS12_MOUSE      SSLPVLQFISVLYRDMGELIEGVRARAFLDGDADAHQN--------------NSTSSNSD 422
sp|O08774|RGS12_RAT        SSLPVLQFISVLYRDMGELIEGVRARAFLDGDADAHQN--------------NSTSSNSD 422
sp|P0DTC2|SPIKE_SARS2      TKLNDLCFTNVYADS--FVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLD 442
                           :.*  * * .*   .   :*.* ..* :  *::.   :                .*.* *

sp|O14924|RGS12_HUMAN      SGIG-NFHQEE----KSN-----RVLV--VDLGGSSSRHGPG--------G-SAWDGVGG 462
sp|Q8CGE9|RGS12_MOUSE      SGIG-NFNQEE----KSN-----RVLV--VDLGGGSSRHGQG--------SSPGWESGGG 462
sp|O08774|RGS12_RAT        SGIG-NFNQEE----KSN-----RVLV--VDLGGGSSRHGQG--------SSPGWESVSG 462
sp|P0DTC2|SPIKE_SARS2      SKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNG 502
                           * :* *::       ***     * :   :  .*.:  :*             .::  .*

sp|O14924|RGS12_HUMAN      RGAQPWGAPWTGPFCPDPEGSPPFEAAHQTDRFWDLNKHLGPASPVEVPPASLRSSVPPS 522
sp|Q8CGE9|RGS12_MOUSE      RGSQPWSAPWNGAFCHDSEAGSPLETSPNTDRFWDLTKHSGPVSHMEVPPATLRSSIPPS 522
sp|O08774|RGS12_RAT        RGSQPWSAPWNGTFCHDSEAGSPLETSPNTDRFWDLTKHSGPVFHMEVPPATLRSSIPPS 522
sp|P0DTC2|SPIKE_SARS2      VGYQPYRVVVLS-----------FELLHAP------ATVCGPKKSTNLV---KNKCVNFN 542
                            * **: .   .           :*            .  **    ::     ...:  .

sp|O14924|RGS12_HUMAN      KRGTVG--AGCGFNQRWLPVHVLRE--------------------WQCGHT--S----DQ 554
sp|Q8CGE9|RGS12_MOUSE      KRGAAG--SSCGFNQRWLPVHVLQE--------------------WQCGHA--S----DQ 554
sp|O08774|RGS12_RAT        KRGATG--SSCGFNQRWLPVHVLQE--------------------WQCGHA--S----DQ 554
sp|P0DTC2|SPIKE_SARS2      FNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGT 602
                            .* .*       *:::**.: : .                      *..   *    .

sp|O14924|RGS12_HUMAN      DSYTDSTDGWSSINCGTLPPPMSKIPADRYRVEGSFAQPPLNAPKREWSRKAFGMQSIFG 614
sp|Q8CGE9|RGS12_MOUSE      ESYTDSTDGWSSVNCGTLPPPMSKIPADRYRVEGSFAQAPLSTQKRDWSRKAFGMQNLFG 614
sp|O08774|RGS12_RAT        ESYTDSTDGWSSVNCGTLPPPMSKIPADRYRVEGSFAQAPLSTQKRDWSRKAFGMQNLFG 614
sp|P0DTC2|SPIKE_SARS2      NTSNQVAVLYQDVNCTEVPVAIHAD-----------------QLTPTWRVYSTGSN-VFQ 644
                           :: .: :  :..:**  :*  :                      .  *   : * : :*

sp|O14924|RGS12_HUMAN      PHRNVRKT-----KEDKKGSKFGRGTGLTQPSQRTSARRSFG--RSKRFSITRSLDDLES 667
sp|Q8CGE9|RGS12_MOUSE      PHRNVRKT-----KEDKKSSKLGRGVALAQTSQRTSARRSFG--RSRRFSITRSLDDLES 667
sp|O08774|RGS12_RAT        PHRNVRKT-----KEDKKSSKLGRGVALAQTSQRTSARRSFG--RSRRFSLTRSLDDLES 667
sp|P0DTC2|SPIKE_SARS2      TRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENS 704
                            : .         :. : .  :* *   :  :* .* **: .   .  :: * **.  :*

sp|O14924|RGS12_HUMAN      ATVSDGELT--------------G----ADLKDCVS---NNS-LSSNASLPSVQSCRRLR 705
sp|Q8CGE9|RGS12_MOUSE      ATVSDGELT--------------G----ADLKDCIS---NNS-LSSNASLPSVQSCRRLR 705
sp|O08774|RGS12_RAT        ATVSDGELT--------------G----ADLKDCIS---NNS-LSSNASLPSVQSCRRLR 705
sp|P0DTC2|SPIKE_SARS2      VAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLN 764
                           .: *:..::                       **     .:*  .**  *   . * :*.

sp|O14924|RGS12_HUMAN      ERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACEYFNHVPAHDKKELSYR 765
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sp|Q8CGE9|RGS12_MOUSE      ERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACECFSHVPAHDKKELSYR 765
sp|O08774|RGS12_RAT        ERRVASWAVSFERLLQDPVGVRYFSDFLRKEFSEENILFWQACECFSHVPAHDKKELSYR 765
sp|P0DTC2|SPIKE_SARS2      R-ALTGIAVEQDKN--------------------TQEVFAQVKQIYKTPPIKDFGGFNF- 802
                           .  ::. **. ::                      : :* *. : :.  * :*   :.:

sp|O14924|RGS12_HUMAN      AREIFSKFLCSKATTPVNIDSQAQLADDVLRAPHPDMFKEQQLQIFNLMKFDSYTRFLKS 825
sp|Q8CGE9|RGS12_MOUSE      AREIFSKFLCSKATTPVNIDSQAQLADDILNAPHPDMFKEQQLQIFNLMKFDSYTRFLKS 825
sp|O08774|RGS12_RAT        AREIFSKFLCSKATTPVNIDSQAQLADDILNAPHPDMFKEQQLQIFNLMKFDSYTRFLKS 825
sp|P0DTC2|SPIKE_SARS2      -----SQILPD----PS--------------KPSKRSFIED--LLFNKVTLAD-AGFI-- 834
                                *::* .    *                *    * *:   :** :.: . : *:

sp|O14924|RGS12_HUMAN      PLYQECILAEVEGRALPDSQQVPSSPASKHSLGSDHSSVSTPKKLSGKSKSGRSLNEELG 885
sp|Q8CGE9|RGS12_MOUSE      QLYQECVLAEVEGRTLPDSQQVPSSPASKHSISSDHSNVSTPKKLSGKSKSGRSLNEDVG 885
sp|O08774|RGS12_RAT        QLYQECVLAEVEGRTLPDSQQVPSSPASKHSISSDHSNVSTPKKLSGKSKSGRSLNEDVG 885
sp|P0DTC2|SPIKE_SARS2      KQYGDCLG-DIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGA--- 890
                             * :*:  :: .* *  :*:. .  .    : .:     *   *:*. .** ::.

sp|O14924|RGS12_HUMAN      DEDSEKKRKGAFFSWSRTRSTGRSQKKREHGDHADDALHANGGLCRRESQGSVSSAGSLD 945
sp|Q8CGE9|RGS12_MOUSE      EEDSEKKRRGAFFSWSRSRSTGRSQKKKDHGDHAHDAPHANGGLCRRESQGSVSSAGSLD 945
sp|O08774|RGS12_RAT        EEDSEKKRKGAFFSWSRSRSTGRSQKKKDHGDHAHDALHANGGLCRRESQGSVSSAGSLD 945
sp|P0DTC2|SPIKE_SARS2      ------------------------------------------------------------ 890


sp|O14924|RGS12_HUMAN      LSEACRTLAPEKDKATKHCCIHLPDGTSCVVAVKAGFSIKDILSGLCERHGINGAAADLF 1005
sp|Q8CGE9|RGS12_MOUSE      LSEACRTSALEKDKAAKHCCVHLPDGTSCVVAVKSGFSIKEILSGLCERHGINGAAVDLF 1005
sp|O08774|RGS12_RAT        LSEACRTSALERDKAAKHCCVHLPDGTSCVVAVKSGFSIKEILSGLCERHGINGAAVDLF 1005
sp|P0DTC2|SPIKE_SARS2      ------------------------------------------------------------ 890


sp|O14924|RGS12_HUMAN      LVGGDKPLVLHQDSSILESRDLRLEKRTLFRLDLVPINRSVGLKAKPTKPVTEVLRPVVA 1065
sp|Q8CGE9|RGS12_MOUSE      LVGGDKPLVLHQDSSILATRDLRLEKRTLFRLDLVPINRSVGLKAKPTKPVTEVLRPVVA 1065
sp|O08774|RGS12_RAT        LVGGDKPLVLHQDSSILATRDLRLGKRTLFRLDLVPINRSVGLKAKPTKPVTEVLRPVVA 1065
sp|P0DTC2|SPIKE_SARS2      ----GAALQI------------PFAMQMAYRFNGI------------------------- 909
                               .  * :             :  :  :*:: :

sp|O14924|RGS12_HUMAN      RYGLDLSGLLVRLSGEKEPLDLGAPIS-SLDGQRVVLEEKDPSRGKASADKQKGVPVKQN 1124
sp|Q8CGE9|RGS12_MOUSE      KYGLDLGSLLVRLSGEKEPLDLGAPIS-SLDGQRVILEERDPSRGKVSTDKQKGAPVKQN 1124
sp|O08774|RGS12_RAT        KYGLDLGSLLVRLSGEKEPLDLGAPIS-SLDGQRVILEERDPSRGKVSTEKQKGAPVKQS 1124
sp|P0DTC2|SPIKE_SARS2      ----------------------GVTQNVLYENQKLIANQFNSAIGKIQDS---------- 937
                                                 *.  .   :.*::: :: : : ** . .

sp|O14924|RGS12_HUMAN      TAVNSSSRNHSATGEERTLGKSNSIKIKGENGKNARDPRLSKREESIAKIGKKKYQKINL 1184
sp|Q8CGE9|RGS12_MOUSE      SAVNSSPRNHLAMGEERTLGKSNSIKIRGENGKSARDPRLSKREESIAKIGKKKYQKINL 1184
sp|O08774|RGS12_RAT        SAVNSSPRNHSAMGEERTLGKSNSIKIRGENGKSARDPRLSKREESIAKIGKKKYQKINL 1184
sp|P0DTC2|SPIKE_SARS2      -----LSSTA------SALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDK 986
                                   .        :*** :.:  :. :. .:   :**..  :*:.: :.  .:::
```

```
sp|O14924|RGS12_HUMAN      DEAEEFFE-LIS-KAQSNRADDQRGLLRKEDLVLPEFLRLPPGSTELTLPTPAAVAKGFS 1242
sp|Q8CGE9|RGS12_MOUSE      DEAEEFFE-LIS-KAQSNRADDQRGLLRKEDLVLPEFLRLPAGSSELALSSPPP-VKGYS 1241
sp|O08774|RGS12_RAT        DEAEEFFE-LIS-KAQSNRADDQRGLLRKEDLVLPEFLRLPPGSSELALSSPPP-VKGFS 1241
sp|P0DTC2|SPIKE_SARS2      VEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA---------SANLAATKMSECVLGQS 1037
                            ***  :: **: : ** ::   : *:*  ::           *::*:  .    . * *

sp|O14924|RGS12_HUMAN      KRSA-TGNGRESASQPGEQWEP------------------VQESSDSPSTSPGSASSPPG 1283
sp|Q8CGE9|RGS12_MOUSE      KRAV-TGHGQEGAAQTEESYSDSPATSPASAQSPCSAYSPGSAHS------PGSAHSTPG 1294
sp|O08774|RGS12_RAT        KRAV-TSHGQEGAVQTEESYSDSPATSPASAQSPCSAYSPGSAHSPGSAHSPGSAHSTPG 1300
sp|P0DTC2|SPIKE_SARS2      KRVDFCGKGY--------HLMSFPQSAPHGVVFLHVTYVPAQEKNFT--TAP-------- 1079
                           **    .:*                                .  .      *

sp|O14924|RGS12_HUMAN      PPGTTPPGQKSPSGPFCTPQSPVSLAQEGTAQIWKRQSQEVEAGGIQTVEDEHVAELTLM 1343
sp|Q8CGE9|RGS12_MOUSE      PPGTTQPGEKPT-KPS-----CVSMVQEGTTQAWRRLSPEMEAGGIQTVEDEQVADLTLM 1348
sp|O08774|RGS12_RAT        PPGTAQPGEKPT-KPS-----CISTVQEGTTQAWRRLSPELEAGGIQTVEEEQVADLTLM 1354
sp|P0DTC2|SPIKE_SARS2      --AICHDGKA------HFPREG---VFVSNGTHWFVTQRNFYEPQIITTDNTFV-----S 1123
                             .    *:                .  ..   *   . :.    * *.::  *

sp|O14924|RGS12_HUMAN      GEGDI--SSPNSTLLPPPSTPQEVPGPSRPGSGTHGSR-DLPVNRIIDVDLVTGSAPGRD 1400
sp|Q8CGE9|RGS12_MOUSE      GEGDI--SSPNSTLLPPPPTPQDTPGPPRPGTSRF------------------------- 1381
sp|O08774|RGS12_RAT        GEGDI--SSPNSTLLPPPPLPQDTPGPTRPGTSRF------------------------- 1387
sp|P0DTC2|SPIKE_SARS2      GNCDVVIGIVNNTVYD----------PLQPELDSFKEELDKYFKNHTSPDVDLGDISGIN 1173
                           *: *:  .  *.*:            * :*  . .

sp|O14924|RGS12_HUMAN      GGIAGAQAGPGRSQASG---GPPTSDLPGLGPVPGEPAKPKTSAHHATFV---------- 1447
sp|Q8CGE9|RGS12_MOUSE      ------------------------------------------------------------ 1381
sp|O08774|RGS12_RAT        ------------------------------------------------------------ 1387
sp|P0DTC2|SPIKE_SARS2      ASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWY--IWLGFIAGLIAIVMVT 1231


sp|O14924|RGS12_HUMAN      ------------------------------------------   1447
sp|Q8CGE9|RGS12_MOUSE      ------------------------------------------   1381
sp|O08774|RGS12_RAT        ------------------------------------------   1387
sp|P0DTC2|SPIKE_SARS2      IMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT   1273
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|K9N5Q8|SPIKE_MERS1      MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTWPRP-IDVSKADGIIYP 59
sp|P59594|SPIKE_SARS       ----MFIFLLFLTLT-S----------GSDLD--RCTTFDDVQAPNYTQHTSSMRGVYYP 43
sp|P0DTC2|SPIKE_SARS2      ----MFVFLVLLPLV-S----------SQCVN--LTT--RTQLPPAY--TNSFTRGVYYP 39
                               :*:::.:*  . *          .  ::            *      *   *: **

sp|K9N5Q8|SPIKE_MERS1      QGRTYSNITITYQGLF-PYQGDHGDMYVYSAGHATGTTPQKLFVANYSQDVKQFANGFVV 118
sp|P59594|SPIKE_SARS       DEIFRSDTLYLTQDLFLPFYSNVT---GFHTIN-------HT----FGNPVIPFKDGIYF 89
sp|P0DTC2|SPIKE_SARS2      DKVFRSSVLHSTQDLFLPFFSNVT---WFHAIHVSGTNGTKR----FDNPVLPFNDGVYF 92
                           :    *.     *.** *: .:      : : :       :     :.: *  * :*. .

sp|K9N5Q8|SPIKE_MERS1      RIGAAANSTGTVIISPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTLVLLPDGCGT 178
sp|P59594|SPIKE_SARS       AATE-----------------KSNVVRGWVFGSTMNNKSQ---------SVIIINNSTNV 123
sp|P0DTC2|SPIKE_SARS2      ASTE-----------------KSNIIRGWIFGTTLDSKTQ---------SLLIVNNATNV 126
                                                  ::  .:::*:::.. ::         ::::: :. ..

sp|K9N5Q8|SPIKE_MERS1      LLRAF--YCILEPRSGNHCPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNLRN 236
sp|P59594|SPIKE_SARS       VIRACNFELCDNPFFAVSKPMGT-------------------------QTHTMIFDNAFN 158
sp|P0DTC2|SPIKE_SARS2      VIKVCEFQFCNDPFLGVYYHKNN---------------------KSWMESEFRVYSSANN 165
                           :::.       :*  .     ..                          .    : .  *

sp|K9N5Q8|SPIKE_MERS1      CTFMYTYNITEDEILEWFGITQTAQG-VHLFSSRYVDLYGGN---------------MFQ 280
sp|P59594|SPIKE_SARS       CTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKP 218
sp|P0DTC2|SPIKE_SARS2      CTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEP 225
                           *** *  :    ::    *  :  :  *.   . :. :*                  :

sp|K9N5Q8|SPIKE_MERS1      FATLPVYDTIKYYSIIPHSIR---SIQSDRKAW----AAFYVYKLQPLTFLLDFSVDGYI 333
sp|P59594|SPIKE_SARS       IFKLPLGINITNFRAILTAFS------PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTI 272
sp|P0DTC2|SPIKE_SARS2      LVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTI 285
                           :  **:  .*. :  :              . *    **::*  *:* **:*.:. :* *

sp|K9N5Q8|SPIKE_MERS1      RRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEG-VECDFSPLLSG- 391
sp|P59594|SPIKE_SARS       TDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNAT 332
sp|P0DTC2|SPIKE_SARS2      TDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNAT 345
                             *:**. : *:: :*: :** ::.*:*..*.*.. *: .:*.  :    * *. ::..

sp|K9N5Q8|SPIKE_MERS1      TPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPLS 451
sp|P59594|SPIKE_SARS       KFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGD 392
sp|P0DTC2|SPIKE_SARS2      RFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGD 405
                              .** ::*  ::**  : : * .   .. *.*  :* : : . *::.:  * *    .

sp|K9N5Q8|SPIKE_MERS1      MKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNLTTITKPLKYSYINKCSRFLSDDR 511
sp|P59594|SPIKE_SARS       DVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFE 452
sp|P0DTC2|SPIKE_SARS2      EVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFE 465
                              ::: ..:* *:::***   .   *::  .  :  :.     :* *       *   .
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sp|K9N5Q8|SPIKE_MERS1      TEVPQLVNANQYSPCVSIVPST-VWEDGDYYRKQLSPLEGGGWLVASGSTVAMTEQLQMG 570
sp|P59594|SPIKE_SARS       RDISNVPFSPDGKPCTP-PALNCYW-----------PLNDYGFYTTTGIGYQPYRVVVLS 500
sp|P0DTC2|SPIKE_SARS2      RDISTEIYQAGSTPCNGVEGFNCYF-----------PLQSYGFQPTNGVGYQPYRVVVLS 514
                            ::         .**      .  :           **:. *:  :.*      . : :.

sp|K9N5Q8|SPIKE_MERS1      FGITVQYGTDTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVGVRQQRF 630
sp|P59594|SPIKE_SARS       FELL----NAPATVCGP-----KLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQF 551
sp|P0DTC2|SPIKE_SARS2      FELL----HAPATVCGP-----KKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQF 565
                           * :         :**       . .     .:**::.: *::* **:  ..      *:*

sp|K9N5Q8|SPIKE_MERS1      VYDAYQNLVGYYSD--DGNYYCLRACVSVPVSVIYD--KETKTHATLFGSVACEHISSTM 686
sp|P59594|SPIKE_SARS       GRDVSDFT-DSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAI 610
sp|P0DTC2|SPIKE_SARS2      GRDIADTT-DAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAI 624
                             *  :   .   *    :   :  *    ****    : :.  *.*: .* * .:  ::

sp|K9N5Q8|SPIKE_MERS1      SQYSRSTRSMLKRRDSTYGPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTPSTLT 746
sp|P59594|SPIKE_SARS       HADQLT--PAWRIYSTGNNVFQTQAGCLIGAEHVD-TSYECDIPIGAGICASYHTVS-L- 665
sp|P0DTC2|SPIKE_SARS2      HADQLT--PTWRVYSTGSNVFQTRAGCLIGAEHVN-NSYECDIPIGAGICASYQTQT-NS 680
                              . :     :  .:  . :** .**::*  : .    :*.:*:* .:**  .* :

sp|K9N5Q8|SPIKE_MERS1      PRSVRSVPGEMRLASIAFNHPIQV-DQLNSSYFKLSIPTNFSFGVTQEYIQTTIQKVTVD 805
sp|P59594|SPIKE_SARS       ---LRSTSQKSI---VAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVD 719
sp|P0DTC2|SPIKE_SARS2      PRRARSVASQSI---IAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVD 737
                               **.  :     :*:.  : ..:  *  .::*****::.:* * : .:: *.:**

sp|K9N5Q8|SPIKE_MERS1      CKQYVCNGFQKCEQLLREYGQFCSKINQALHGANLRQDDSVRNLFASVKSSQSSPIIPGF 865
sp|P59594|SPIKE_SARS       CNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYF 779
sp|P0DTC2|SPIKE_SARS2      CTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDF 797
                           *. *:*..  :* :** :**.**:::*:** *   .** ..:::**.**.  .:* :  *

sp|K9N5Q8|SPIKE_MERS1      GGDFNLTLLEPVSISTGSRSARSAIEDLLFDKVTIADPGYMQGYDDCMQQGPASARDLIC 925
sp|P59594|SPIKE_SARS       GGF-NFSQILPDP---LKPTKRSFIEDLLFNKVTLADAGFMKQYGECL--GDINARDLIC 833
sp|P0DTC2|SPIKE_SARS2      GGF-NFSQILPDP---SKPSKRSFIEDLLFNKVTLADAGFIKQYGDCL--GDIAARDLIC 851
                           **  *:: : *      . : ** ******:***:** *::: *.:*:  *   ******

sp|K9N5Q8|SPIKE_MERS1      AQYVAGYKVLPPLMDVNMEAAYTSSLLGSIAGVGWTAGLSSFAAIPFAQSIFYRLNGVGI 985
sp|P59594|SPIKE_SARS       AQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGV 893
sp|P0DTC2|SPIKE_SARS2      AQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGV 911
                           ** . * .*****:  :* * **::*:..    *** * .:   **** .: **:**:*:

sp|K9N5Q8|SPIKE_MERS1      TQQVLSENQKLIANKFNQALGAMQTGFTTTNEAFHKVQDAVNNNAQALSKLASELSNTFG 1045
sp|P59594|SPIKE_SARS       TQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFG 953
sp|P0DTC2|SPIKE_SARS2      TQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFG 971
                           **:** **** ***:**.*:. :* .:::*  *: *:**.**:*****..*..:**..**

sp|K9N5Q8|SPIKE_MERS1      AISASIGDIIQRLDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLAKDKVNE 1105
```

```
sp|P59594|SPIKE_SARS       AISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE 1013
sp|P0DTC2|SPIKE_SARS2      AISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE 1031
                           ***: :.**:.*** :* :.******.*** :*:::*:***:*: .   **:**  *:.*

sp|K9N5Q8|SPIKE_MERS1      CVKAQSKRSGFCGQGTHIVSFVVNAPNGLYFMHVGYYPSNHIEVVSAYGLCDAANPTNCI 1165
sp|P59594|SPIKE_SARS       CVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKA---Y 1070
sp|P0DTC2|SPIKE_SARS2      CVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA---H 1088
                           ** .**** .***:* *::**   **:*: *:** * *::. :..:* .:*. .:

sp|K9N5Q8|SPIKE_MERS1      APVNGYFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQN-ISTNLPPPLLG 1224
sp|P59594|SPIKE_SARS       FPREGVFVFN-----GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQ- 1124
sp|P0DTC2|SPIKE_SARS2      FPREGVFVSN-----GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ- 1142
                            * :* *: .        *  *  .*: *: **: **   .   .  . :...:  **

sp|K9N5Q8|SPIKE_MERS1      NSTGIDFQDELDEFFKNVSTSIPNFGSLTQINTTLLDLTYEMLSLQQVVKALNESYIDLK 1284
sp|P59594|SPIKE_SARS       -PELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQ 1183
sp|P0DTC2|SPIKE_SARS2      -PELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQ 1201
                                .*::***::*** ::   ::*.:: **::::::  *:  *::*.* **** ***:

sp|K9N5Q8|SPIKE_MERS1      ELGNYTYYNKWPWYIWLGFIAGLVALALCVFFILCCTGCGTNCMGKLKCNRCCDRYEEYD 1344
sp|P59594|SPIKE_SARS       ELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKF-DEDD 1242
sp|P0DTC2|SPIKE_SARS2      ELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKF-DEDD 1260
                           ***:*  * *****:********:*:.: .::: * *.* :   *  .*. **.  :* *

sp|K9N5Q8|SPIKE_MERS1      LEPHKVHVH----        1353
sp|P59594|SPIKE_SARS       SEPVLKGVKLHYT        1255
sp|P0DTC2|SPIKE_SARS2      SEPVLKGVKLHYT        1273
                            **    *:
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CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q0Q4F2|SPIKE_BC133      ----MTRLMCLLMSLSIFVRGFDSQFVDMSPASNASECLESQVDAAAFS---------KL 47
sp|Q0Q475|SPIKE_BC279      ----MKVLI----FALLFSL-----------AKAQEGCGIISR---------------KP 26
sp|Q0Q466|SPIKE_BC512      --MKYTLLFCV-VFATVSF-G----------FADNERCN--------KTVNLTR--LF-S 35
sp|Q3LZX1|SPIKE_BCHK3      ----MKILI----FAFLANL-----------AKAQEGCGIISR---------------KP 26
sp|A3EX94|SPIKE_BCHK4      ----MTLLMCLLMSLLIFVRGCDSQFVDMSPASNTSECLESQVDAAAFS---------KL 47
sp|A3EXD0|SPIKE_BCHK5      MIRSVLVLMCSLTFIGNLTRG---QSVDMG-HNGTGSCLDSQVQPDYFE-S------VHT 49
sp|A3EXG6|SPIKE_BCHK9      ----MLLIL----VLGVSLA-----------AASRPECFNPRFT---LT-P------LNH 31
sp|Q3I5J5|SPIKE_BCRP3      ----MKILI----LAFLASL-----------AKAQEGCGIISR---------------KP 26
sp|Q91A26|SPIKE_CVBEN      ---MFLILL----ISLPTAFA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|P25190|SPIKE_CVBF       ---MFLILL----ISLPMALA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|P25191|SPIKE_CVBL9      ---MFLILL----ISLPMAFA----------VIGDLKCTTV-SINDVDT-G------APS 35
sp|Q9QAR5|SPIKE_CVBLS      ---MFLILL----ISLPTAFA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|Q8V436|SPIKE_CVBLU      ---MFLILL----ISLPTAFA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|P25192|SPIKE_CVBLY      ---MFLILL----ISLPMALA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|P15777|SPIKE_CVBM       ---MFLILL----ISLPMAFA----------VIGDLKCTTV-SINDVDT-G------APS 35
sp|Q9QAQ8|SPIKE_CVBOK      ---MFLILL----ISLPTAFA----------VIGDLKCTTV-SINDVDT-G------VPS 35
sp|P25193|SPIKE_CVBQ       ---MFLILL----ISLPMAFA----------VIGDLKCTTV-SINDVDT-G------APS 35
sp|P25194|SPIKE_CVBV       ---MFLILL----ISLPMAFA----------VIGDLKCTTV-SINDVDT-G------APS 35
sp|P36300|SPIKE_CVCAI      ---MIVLTLCLF-LFLYSSVS----------CTSNNDCVQVNVTQLPGNENIIKDFLFQ- 45
sp|Q65984|SPIKE_CVCAK      ---MIVLILCLL-LFSYNSVI----------CTSNNDCVQGNVTQLPGNENIIKDFLFH- 45
sp|Q7T6T3|SPIKE_CVCBG      ---MIVLTLCLF-LVLYNSVI----------CTSNNECVQVNVTQLPGNENIIRDFLFQ- 45
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1      ----MLLII----FILPTTLA----------VIGDFNCTNF-AINDLNT-T------VPR 34
sp|Q14EB0|SPIKE_CVHN2      ----MFLII----FILPTTLA----------VIGDFNCTNS-FINDYNK-T------IPR 34
sp|Q0ZME7|SPIKE_CVHN5      ----MFLII----FILPTTLA----------VIGDFNCTNS-FINDYNK-T------IPR 34
sp|Q6Q1S2|SPIKE_CVHNL      --MKLFLILLVLPLASCF-----------------FTCN--------SNANLSM-----L 28
sp|P36334|SPIKE_CVHOC      ---MFLILL----ISLPTAFA----------VIGDLKCTSD-NINDKDT-G------PPP 35
sp|P22432|SPIKE_CVM4       ---MLFVFI----LLLPSCLG----------YIGDFRCIQTVNYNGNNA-S------APS 36
sp|P11224|SPIKE_CVMA5      ---MLFVFI----LFLPSCLG----------YIGDFRCIQLVNSNGANV-S------APS 36
sp|Q02385|SPIKE_CVMJC      ---MLFVFI----LFLPSCLG----------YIGDFRCIQTVNYNGNNA-S------APS 36
sp|P11225|SPIKE_CVMJH      ---MLFVFI----LLLPSCLG----------YIGDFRCIQTVNYNGNNA-S------APS 36
sp|P18450|SPIKE_CVPFS      ---MKK----LFVVLVVMPLI----------YGDNFPCSKLTNRTIGNHWNLIETFLLNY 43
sp|P33470|SPIKE_CVPMI      ---MKK----LFVVLVVMPLI----------YGDNFPCSKLTNRTIGNHWNLIETFLLNY 43
sp|P07946|SPIKE_CVPPU      ---MKK----LFVVLVVMPLI----------YGDNFPCSKLTNRTIGNQWNLIETFLLNY 43
sp|P27655|SPIKE_CVPR8      ------------------------------------------------------------ 0
sp|P24413|SPIKE_CVPRM      ------------------------------------------------------------ 0
sp|Q01977|SPIKE_CVPRT      ---MKK----LFVVLVVMPLI----------YGDNFPCSKLTNRTIGNQWNLIETFLLNY 43
sp|Q9IKD1|SPIKE_CVRSD      ---MLFVFL----TLLPSCLG----------YIGDFRCINLVNTRISNA-R------APS 36
sp|P10033|SPIKE_FIPV       ---MIVLVTCLLLLCSYHTVL----------STTNNECIQVNVTQLAGNENLIRDFLFS- 46
sp|K9N5Q8|SPIKE_MERS1      MIHSVFLLM--------FLLTPTESYVDVGPDSVKSACIEVDIQQTFFD----------K 42
sp|P59594|SPIKE_SARS       ----MFIFL----LFLTLTS-----------GSDLDRCTTFDD---------------VQ 26
sp|P0DTC2|SPIKE_SARS2      ----MFVFL----VLLP---------------LVSSQCVNLTT---------------RT 22
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
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sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      VWPYPIDPAKVDGIIYPLGRTYSNITLEY-----------TGLFPLQGDLGMQYLYS-VS 95
sp|Q0Q475|SPIKE_BC279      QPKMEKVSSSRRGVYYNDDIFRSDVLHLT-----------QDYFLPFDS--NLTQYF-SL 72
sp|Q0Q466|SPIKE_BC512      KFDIQPPSQVVLAGLLPNQTAQWKCTTETNKR-DEGV-GVKGVFLS------Y-----VS 82
sp|Q3LZX1|SPIKE_BCHK3      QPKMAQVSSSRRGVYYNDDIFRSDVLHLT-----------QDYFLPFDS--NLTQYF-SL 72
sp|A3EX94|SPIKE_BCHK4      MWPYPIDPSKVDGIIYPLGRTYSNITLAY-----------TGLFPLQGDLGSQYLYS-VS 95
sp|A3EXD0|SPIKE_BCHK5      TWPMPIDTSKAEGVIYPNGKSYSNITLTY-----------TGLYPKANDLGKQYLFS-DG 97
sp|A3EXG6|SPIKE_BCHK9      TLNYTSIKAKVSNVLLPDPYIAYSGQTLR-----------QNLFMADMS--NTILYPVTP 78
sp|Q3I5J5|SPIKE_BCRP3      QPKMAQVSSSRRGVYYNDDIFRSNVLHLT-----------QDYFLPFDS--NLTQYF-SL 72
sp|Q91A26|SPIKE_CVBEN      ISTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P25190|SPIKE_CVBF       ISTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P25191|SPIKE_CVBL9      ISTDIVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|Q9QAR5|SPIKE_CVBLS      ISTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|Q8V436|SPIKE_CVBLU      ISTDTVDVTKGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P25192|SPIKE_CVBLY      VSTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P15777|SPIKE_CVBM       ISTDIVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|Q9QAQ8|SPIKE_CVBOK      ISTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P25193|SPIKE_CVBQ       ISTDIVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P25194|SPIKE_CVBV       ISTDTVDVTNGLGTYYVLDRVYLNTTLLL-----------NGYYPTSGSTYRN------M 78
sp|P36300|SPIKE_CVCAI      --NFKEEGSLVVGGYYPT-EVWYNCSTTQQTTAYKYFSNIHAFYFDMEAMENS-----TG 97
sp|Q65984|SPIKE_CVCAK      --TFKEEPSVVVGGYYPT-EVWYNCSRSATTTAYKDFSNIHAFYFDMEAMENS-----TG 97
sp|Q7T6T3|SPIKE_CVCBG      --NFKEEGTVVVGGYYPT-EVWYNCSRTARTQAFKTFSNIHAFYFDMEAMENS-----TG 97
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1      ISEYVVDVSYGLGTYYILDRVYLNTTILF-----------TGYFPKSGANFRD------L 77
sp|Q14EB0|SPIKE_CVHN2      ISEDVVDVSLGLGTYYVLNRVYLNTTLLF-----------TGYFPKSGANFRD------L 77
sp|Q0ZME7|SPIKE_CVHN5      ISEDVVDVSLGLGTYYVLNRVYLNTTLLF-----------TGYFPKSGANFRD------L 77
sp|Q6Q1S2|SPIKE_CVHNL      QLGVPDNSSTIVTGLLPT---HWFCANQSTSV-YSA----NGFFYI------D-----VG 69
sp|P36334|SPIKE_CVHOC      ISTDTVDVTNGLGTYYVLDRVYLNTTLFL-----------NGYYPTSGSTYRN------M 78
sp|P22432|SPIKE_CVM4       ISTEAVDVSKGLGTYYVLDRVYLNATLLL-----------TGYYPVDGSNYRN------L 79
sp|P11224|SPIKE_CVMA5      ISTETVEVSQGLGTYYVLDRVYLNATLLL-----------TGYYPVDGSKFRN------L 79
sp|Q02385|SPIKE_CVMJC      ISTEAVDVSKGLGTYYVLDRVYLNATLLL-----------TGYYPVDGSNYRN------L 79
sp|P11225|SPIKE_CVMJH      ISTEAVDVSKGRGTYYVLDRVYLNATLLL-----------TGYYPVDGSNYRN------L 79
sp|P18450|SPIKE_CVPFS      SSRLSPNSDVVLGDYFPTVQPWFNCIHNNSNDLYVTLENLKALYWDYATENST-----W- 97
sp|P33470|SPIKE_CVPMI      SSRLSPNSDVVLGDYFPTVQPWFNCIRNNSNDLYVTLENLKALYWDYATENIT-----L- 97
sp|P07946|SPIKE_CVPPU      SSRLPPNSDVVLGDYFPTVQPWFNCIRNNSNDLYVTLENLKALYWDYATENIT-----W- 97
sp|P27655|SPIKE_CVPR8      ------------------------------------------------------------ 0
sp|P24413|SPIKE_CVPRM      ------------------------------------------------------------ 0
sp|Q01977|SPIKE_CVPRT      SSRLPPNSDVVLGDYFPTVQPWFNCIRNNSNDLYVTLENLKALYWDYATENIT-----W- 97
sp|Q9IKD1|SPIKE_CVRSD      VSTEVVDVSKGLGTYYVLDRVYLNATLLL-----------TGYYPVDGSMYRN------M 79
sp|P10033|SPIKE_FIPV       --NFKEEGSVVVGGYYPT-EVWYNCSRTARTTAFQYFNNIHAFYFVMEAMENS-----TG 98
sp|K9N5Q8|SPIKE_MERS1      TWPRPIDVSKADGIIYPQGRTYSNITITY-----------QGLFPYQGDHGDMYVYS-AG 90
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sp|P59594|SPIKE_SARS        APNYTQHTSSMRGVYYPDEIFRSDTLYLT-----------QDLFLPFYS--NVTGFH-TI 72
sp|P0DTC2|SPIKE_SARS2       QLPPAYTNSFTRGVYYPDKVFRSSVLHST-----------QDLFLPFFS--NVTWFH-AI 68
sp|Q2KI99|STING_BOVIN       ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK       ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN       ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE       ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE       ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG         ------------------------------------------------------------ 0
sp|F1M391|STING_RAT         ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133       HAVGNDGDPTKAYISNYS-LLVNDFDNGFVVRI-GAAANSTGTI----------VISP-- 141
sp|Q0Q475|SPIKE_BC279       NIDS-NKY------TYFD-NPILDFGDGVYFAA-TE------------------------ 99
sp|Q0Q466|SPIKE_BC512       SG---RGFTIGVSQYNFDPSTYQLYLHR--------------DTNGNSNAFAYLRICKWP 125
sp|Q3LZX1|SPIKE_BCHK3       NVDS-DRY------TYFD-NPILDFGDGVYFAA-TE------------------------ 99
sp|A3EX94|SPIKE_BCHK4       HAVGHDGDPTKAYISNYS-LLVNDFDNGFVVRI-GAAANSTGTI----------VISP-- 141
sp|A3EXD0|SPIKE_BCHK5       HSA--PGRLNNLFVSNYS-SQVESFDDGFVVRI-GAAANKTGTT----------VISQ-- 141
sp|A3EXG6|SPIKE_BCHK9       PANGANGG------FIYN-TSIIPVSAGLFVNT-WM------------------YRQP-- 110
sp|Q3I5J5|SPIKE_BCRP3       NVDS-DRF------TYFD-NPILDFGDGVYFAA-TE------------------------ 99
sp|Q91A26|SPIKE_CVBEN       ALKGTLLL----STLWFKPPFLSDFTNGIFAKV-KNTKV--------------------- 112
sp|P25190|SPIKE_CVBF        ALKGTLLL----STLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|P25191|SPIKE_CVBL9       ALKGTLLL----SRLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|Q9QAR5|SPIKE_CVBLS       ALKGTLLL----STLWFKPPFLSDFTNGIFAKV-KNTKV--------------------- 112
sp|Q8V436|SPIKE_CVBLU       ALKGTLLL----STLWFKPPFLSDFTNGIFAKV-KNTKV--------------------- 112
sp|P25192|SPIKE_CVBLY       ALKGTLLL----STLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|P15777|SPIKE_CVBM        ALKGTLLL----SRLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|Q9QAQ8|SPIKE_CVBOK       ALKGTLLL----STLWFKPPFLSDFTNGIFAKV-KNTKV--------------------- 112
sp|P25193|SPIKE_CVBQ        ALKGTLLL----SRLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|P25194|SPIKE_CVBV        ALKGTLLL----SRLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|P36300|SPIKE_CVCAI       NA---RGKPLLVHV-HGNPVSIIVYISAYRDDVQFRPLLKHGLLCITKNDT--VDYNSFT 151
sp|Q65984|SPIKE_CVCAK       NA---RGKPLLVHV-HGDPVSIIIYISAYRDDVQPRPLLKHGLLCITKNKI--IDYNTFT 151
sp|Q7T6T3|SPIKE_CVCBG       DA---RGKPLLVHV-HGNPVSIIVYISAYRHDVQGRPKLKHGLLCITKNST--TDYDRFT 151
sp|P15423|SPIKE_CVH22       ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1       SLKGTTYL----STLWYQKPFLSDFNNGIFSRV-KNTKL--------------------- 111
sp|Q14EB0|SPIKE_CVHN2       ALKGSKYL----STLWYKPPFLSDFNNGIFSKV-KNTKL--------------------- 111
sp|Q0ZME7|SPIKE_CVHN5       ALKGSIYL----STLWYKPPFLSDFNNGIFSKV-KNTKL--------------------- 111
sp|Q6Q1S2|SPIKE_CVHNL       NH---RS-AFALHTGYYDANQYYIYVTN--------------EI--GLNASVTLKICKFS 109
sp|P36334|SPIKE_CVHOC       ALKGSVLL----SRLWFKPPFLSDFINGIFAKV-KNTKV--------------------- 112
sp|P22432|SPIKE_CVM4        ALTGTNTL----SLTWFKPPFLSEFNDGIFAKV-QNLKT--------------------- 113
sp|P11224|SPIKE_CVMA5       ALRGTNSV----SLSWFQPPYLNQFNDGIFAKV-QNLKT--------------------- 113
sp|Q02385|SPIKE_CVMJC       ALTGTNTL----SLTWFKPPFLSEFNDGIFAKV-QNLKT--------------------- 113
sp|P11225|SPIKE_CVMJH       ALTGTNTL----SLTWFKPPFLSEFNDGIFAKV-QNLKT--------------------- 113
sp|P18450|SPIKE_CVPFS       NH----KQRLNVVV-NGYPYSITVTTTRN------FNSAEGAIICICKGSPPTTTTESSL 146
sp|P33470|SPIKE_CVPMI       NH----KQRLNVVV-NGYPYSITVTTTRN------FNSAEGAIICICKGSPPTTTTESSL 146
sp|P07946|SPIKE_CVPPU       NH----RQRLNVVV-NGYPYSITVTTTRN------FNSAEGAIICICKGSPPTTTTESSL 146
sp|P27655|SPIKE_CVPR8       ------------------------------------------------------------ 0
sp|P24413|SPIKE_CVPRM       ------------------------------------------------------------ 0
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sp|Q01977|SPIKE_CVPRT      NH----RQRLNVVV-NGYPYSITVTTTRN------FNSAEGAIICICKGSPPTTTTESSL 146
sp|Q9IKD1|SPIKE_CVRSD      ALMGTNTL----SLNWFEPPFLSEFNDGIYAKV-KNLKA--------------------- 113
sp|P10033|SPIKE_FIPV       NA---RGKPLLFHV-HGEPVSVI--ISAYRDDVQQRPLLKHGLVCITKNRH--INYEQFT 150
sp|K9N5Q8|SPIKE_MERS1      HATGT--TPQKLFVANYS-QDVKQFANGFVVRI-GAAANSTGTV----------IISP-- 134
sp|P59594|SPIKE_SARS       N-------------HTFG-NPVIPFKDGIYFAA-TE------------------------ 93
sp|P0DTC2|SPIKE_SARS2      HVSGTNGT------KRFD-NPVLPFNDGVYFAS-TE------------------------ 96
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      ---------------------SVNTKIKKAYPAFILGSSLTNTSA------GKP------ 168
sp|Q0Q475|SPIKE_BC279      --------------------------KSNVIRGWIFGSSFDNTTQS-------------- 119
sp|Q0Q466|SPIKE_BC512      SKKWLQSTSNMDTSGRFCLVNKKIPAAFTDHANMVVGITWDQDRVT--FYTDKVYHFYVP 183
sp|Q3LZX1|SPIKE_BCHK3      --------------------------KSNVIRGWIFGSSFDNTTQS-------------- 119
sp|A3EX94|SPIKE_BCHK4      ---------------------SVNTKIKKAYPAFILGSSLTNTSA------GQP------ 168
sp|A3EXD0|SPIKE_BCHK5      ---------------------STFKPIKKIYPAFLLGHSVGNYTPSN----RTG------ 170
sp|A3EXG6|SPIKE_BCHK9      ---------------------ASSRAYCQEPFGVAFGDTFENDRIA-------------- 135
sp|Q3I5J5|SPIKE_BCRP3      --------------------------KSNVIRGWIFGSTFDNTTQS-------------- 119
sp|Q91A26|SPIKE_CVBEN      ---------------------IKDGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P25190|SPIKE_CVBF       ---------------------IKHGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P25191|SPIKE_CVBL9      ---------------------IKKGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|Q9QAR5|SPIKE_CVBLS      ---------------------IKDGVKYSEFPAITIGSTFVNTSYS-------------- 137
sp|Q8V436|SPIKE_CVBLU      ---------------------IKDGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P25192|SPIKE_CVBLY      ---------------------IKNGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P15777|SPIKE_CVBM       ---------------------IKKGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|Q9QAQ8|SPIKE_CVBOK      ---------------------IKDGVKYSEFPAITIGSTFVNTSYS-------------- 137
sp|P25193|SPIKE_CVBQ       ---------------------IKKGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P25194|SPIKE_CVBV       ---------------------IKKGVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P36300|SPIKE_CVCAI      INQWRDICLGDDR-------KIPFSVVPTDNGTKLFGLEWNDDYVTAYI-SDESHRLNIN 203
sp|Q65984|SPIKE_CVCAK      SAQWSAICLGDDR-------KIPFSVIPTDNGTKIFGLEWNDDYVTAYI-SDRSHHLNIN 203
sp|Q7T6T3|SPIKE_CVCBG      ANQWRDICLGEDR-------KIPFSVVPTDNGTKLFGLEWNDDYVTAYI-SDDSHYLNIN 203
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 0
sp|Q5MQD0|SPIKE_CVHN1      ---------------------YVNKTLYSEFSTIVIGSVFINNSYT-------------- 136
sp|Q14EB0|SPIKE_CVHN2      ---------------------YVNNTLYSEFSTIVIGSVFVNTSYT-------------- 136
sp|Q0ZME7|SPIKE_CVHN5      ---------------------YVNNTLYSEFSTIVIGSVFVNTSYT-------------- 136
sp|Q6Q1S2|SPIKE_CVHNL      RNTTFDFLSNAS-SSFDCIVNL----LFTEQLGAPLGITISGETVRLHLYN-VTRTFYVP 163
sp|P36334|SPIKE_CVHOC      ---------------------IKDRVMYSEFPAITIGSTFVNTSYS-------------- 137
sp|P22432|SPIKE_CVM4       ---------------------NTPTGATSYFPTIVIGSLFGNTSYT-------------- 138
sp|P11224|SPIKE_CVMA5      ---------------------STPSGATAYFPTIVIGSLFGYTSYT-------------- 138
sp|Q02385|SPIKE_CVMJC      ---------------------NTPTGATSYFPTIVIGSLFGNTSYT-------------- 138
sp|P11225|SPIKE_CVMJH      ---------------------NTPTGATSYFPTIVIGSLFGNTSYT-------------- 138
sp|P18450|SPIKE_CVPFS      TCNWGSECRLNHK------FPICPSNSEANCGNMLYGLQWFADAVVAYL-HGASYRISFE 199
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sp|P33470|SPIKE_CVPMI      TCNWGSECRLNHK------FPICPSNSEANCGNMLYGLQWFADAVVAYL-HGASYRISFE 199
sp|P07946|SPIKE_CVPPU      TCNWGSECRLNHK------FPICPSNSEANCGNMLYGLQWFADEVVAYL-HGASYRISFE 199
sp|P27655|SPIKE_CVPR8      ------------------------------------------------------------ 0
sp|P24413|SPIKE_CVPRM      ------------------------------------------------------------ 0
sp|Q01977|SPIKE_CVPRT      TCNWGSECRLNHK------FPICPSNSEANCGNMLYGLQWFADEVVAYL-HGASYRISFE 199
sp|Q9IKD1|SPIKE_CVRSD      ---------------------SLPIGSASYFPTIIIGSNFVNTSYT-------------- 138
sp|P10033|SPIKE_FIPV       SNQWNSTCTGADR-------KIPFSVIPTDNGTKIYGLEWNDDFVTAYI-SGRSYHLNIN 202
sp|K9N5Q8|SPIKE_MERS1      ---------------------STSATIRKIYPAFMLGSSVGNFSDG-----KMG------ 162
sp|P59594|SPIKE_SARS       --------------------------KSNVVRGWVFGSTMNNKSQS-------------- 113
sp|P0DTC2|SPIKE_SARS2      --------------------------KSNIIRGWIFGTTLDSKTQS-------------- 116
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      -LYANY-SLTIIPDGCGTVL--------------HAFYCILKPRTGNRCPSGSDYNAYFI 212
sp|Q0Q475|SPIKE_BC279      -------AIIV--------------------------------NNSTHI--------IIR 132
sp|Q0Q466|SPIKE_BC512      NN---------RWSRVVSWCSAADSCAMQY--INSTIYYNLNVTTPGP-----GGITYSV 227
sp|Q3LZX1|SPIKE_BCHK3      -------AVIV--------------------------------NNSTHI--------IIR 132
sp|A3EX94|SPIKE_BCHK4      -LYANY-SLTIIPDGCGTVL--------------HAFYCILKPRTVNRCPSGTGYVSYFI 212
sp|A3EXD0|SPIKE_BCHK5      -RYLNH-TLVILPDGCGTIL--------------HAFYCVLHPRTQQNCAGETNFKSLSL 214
sp|A3EXG6|SPIKE_BCHK9      -------ILIMAPDNLGSWS-------------------AVAPRNQTNI--------YLL 161
sp|Q3I5J5|SPIKE_BCRP3      -------AVIV--------------------------------NNSTHI--------IIR 132
sp|Q91A26|SPIKE_CVBEN      --------VVVQPHTTI-----------------------L--GNKLQGFLEISVCQYTM 164
sp|P25190|SPIKE_CVBF       --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|P25191|SPIKE_CVBL9      --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|Q9QAR5|SPIKE_CVBLS      --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|Q8V436|SPIKE_CVBLU      --------VVVQPHTTI-----------------------L--GNKLQGFLEISVCQYTM 164
sp|P25192|SPIKE_CVBLY      --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|P15777|SPIKE_CVBM       --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|Q9QAQ8|SPIKE_CVBOK      --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|P25193|SPIKE_CVBQ       --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|P25194|SPIKE_CVBV       --------VVVQPHTTN-----------------------L--DNKLQGLLEISVCQYTM 164
sp|P36300|SPIKE_CVCAI      NNWFNNVTLLYSRTSTATW---QHSAAYVYQGVSNFTYYKLNK---TA-----GLKSYEL 252
sp|Q65984|SPIKE_CVCAK      NNWFNNVTILYSRSSSATW---QKSAAYVYQGVSNFTYYKLNN---TN-----GLKSYEL 252
sp|Q7T6T3|SPIKE_CVCBG      NNWFNNVTLLYSRSSTATW---QHSAAYVYQGVSNFTYYKLNN---TN-----GLKSYEL 252
sp|P15423|SPIKE_CVH22      --------------------MFVLLVAYA-----LL--HIAGCQTTNG-----LNTSYSV 28
sp|Q5MQD0|SPIKE_CVHN1      --------IVVQPH---------------------------------NGVLEITACQYTM 155
sp|Q14EB0|SPIKE_CVHN2      --------IVVQPH---------------------------------NGILEITACQYTM 155
sp|Q0ZME7|SPIKE_CVHN5      --------IVVQPH---------------------------------NGILEITACQYTM 155
sp|Q6Q1S2|SPIKE_CVHNL      AAY--------KLTKLSVKCYFNYSCVFSV--VNAT--VTVNVTTHNG-----RVVNYTV 206
sp|P36334|SPIKE_CVHOC      --------VVVQPRTINSTQ-------------------DG--DNKLQGLLEVSVCQYNM 168
sp|P22432|SPIKE_CVM4       --------VVLEPY---------------------------------NNIIMASVCTYTI 157
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sp|P11224|SPIKE_CVMA5      --------VVIEPY---------------------------------NGVIMASVCQYTI 157
sp|Q02385|SPIKE_CVMJC      --------VVLEPY---------------------------------NNIIMASVCTYTI 157
sp|P11225|SPIKE_CVMJH      --------VVLEPY---------------------------------NNIIMASVCTYTI 157
sp|P18450|SPIKE_CVPFS      NQWSGTVTLGDMRATTLETAG-TLVDLWWFNPVYDVSYYRVNN---KN-----GTTVVSN 250
sp|P33470|SPIKE_CVPMI      NQWSGTVTLGDMRATTLETAG-TLVDLWWFNPVYDVSYYRVNN---KN-----GTTVVSN 250
sp|P07946|SPIKE_CVPPU      NQWSGTVTFGDMRATTLEVAG-TLVDLWWFNPVYDVSYYRVNN---KN-----GTTVVSN 250
sp|P27655|SPIKE_CVPR8      -----------------------MKKLFVV---LVVMPLIYGD---KF-----PTSVVSN 26
sp|P24413|SPIKE_CVPRM      -----------------------MKKLFVV---LVVMPLIYGD---KF-----PTSVVSN 26
sp|Q01977|SPIKE_CVPRT      NQWSGTVTFGDMRATTLEVSG-TLVDLWWFNPVYDVSYYRVNN---KN-----GTTVVSN 250
sp|Q9IKD1|SPIKE_CVRSD      --------VVLEPY---------------------------------NGIIMASICQYTI 157
sp|P10033|SPIKE_FIPV       TNWFNNVTLLYSRSSTATW---EYSAAYAYQGVSNFTYYKLNN---TN-----GLKTYEL 251
sp|K9N5Q8|SPIKE_MERS1      -RFFNH-TLVLLPDGCGTLL--------------RAFYCILEPRSGNHCPAGNSYTSFAT 206
sp|P59594|SPIKE_SARS       -------VIII--------------------------------NNSTNV--------VIR 126
sp|P0DTC2|SPIKE_SARS2      -------LLIV--------------------------------NNATNV--------VIK 129
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      YETIHSDCQST------------------INRNASLNS--------FKSFFD-LVNCTFF 245
sp|Q0Q475|SPIKE_BC279      VC-NFNLCKEPM-----------------YTVSK--G-----TQQSSWVYQS-AFNCTYD 166
sp|Q0Q466|SPIKE_BC512      C---TKHCTGLADNVFSTDQGGHIPPIFPYNNWFLLTNTSTLVQGVTRVFQPFLVNCLVA 284
sp|Q3LZX1|SPIKE_BCHK3      VC-NFNLCKEPM-----------------YTVSR--G-----TQQNAWVYQS-AFNCTYD 166
sp|A3EX94|SPIKE_BCHK4      YETVHNDCQST------------------INRNASLNS--------FKSFFD-LVNCTFF 245
sp|A3EXD0|SPIKE_BCHK5      WDTPASDCVSGS-----------------YNQEATLGA--------FKVYFD-LINCTFR 248
sp|A3EXG6|SPIKE_BCHK9      VCSNATLCINPG-----------------FNRWGPAGS-F--IAPDA-LVDH-SNSC--- 196
sp|Q3I5J5|SPIKE_BCRP3      VC-NFNLCKEPM-----------------YTVSR--G-----AQQSSWVYQS-AFNCTYD 166
sp|Q91A26|SPIKE_CVBEN      CEYPNTICNPN------------------LGN-QRVE---------LWHWDTGVVSCLYK 196
sp|P25190|SPIKE_CVBF       CEYPNTICHPN------------------LGN-RRVE---------LWHWDTGVVSCLYK 196
sp|P25191|SPIKE_CVBL9      CEYPHTICHPN------------------LGN-KRVE---------LWHWDTGVVSCLYK 196
sp|Q9QAR5|SPIKE_CVBLS      CEYPNTICNPN------------------LGN-QRVE---------LWHWDTGVVSCLYK 196
sp|Q8V436|SPIKE_CVBLU      CEYPNTICNPN------------------LGN-RRVE---------LWHWDTGVVSCLYK 196
sp|P25192|SPIKE_CVBLY      CEYPHTICHPN------------------LGN-RRIE---------LWHWDTGVVSCLYK 196
sp|P15777|SPIKE_CVBM       CEYPHTICHPN------------------LGN-KRVE---------LWHWDTGVVSCLYK 196
sp|Q9QAQ8|SPIKE_CVBOK      CEYPNTICNPN------------------LGN-QRVE---------LWHWDTGVVSCLYK 196
sp|P25193|SPIKE_CVBQ       CEYPHTICHPK------------------LGN-KRVE---------LWHWDTGVVSCLYK 196
sp|P25194|SPIKE_CVBV       CEYPHTICHPN------------------LGN-QRVE---------LWHWDTGVVSCLYK 196
sp|P36300|SPIKE_CVCAI      CE-DYEYCTGYATNVFAPTSGGYIPDGFSFNNWFMLTNSSTFVSGRFVTNQPLLVNCLWP 311
sp|Q65984|SPIKE_CVCAK      CE-DYEYCTGYATNVFAPTVGGYIPHGFSFNNWFMRTNSSTFVSGRFVTNQPLLVNCLWP 311
sp|Q7T6T3|SPIKE_CVCBG      CE-DYEYCTGYATNVFAPTPGGYIPEGFSFNNWFMLTNSSTFVSGRFVTNQPLLVNCLWP 311
sp|P15423|SPIKE_CVH22      C----NGCVGYSENVFAVESGGYIPSDFAFNNWFLLTNTSSVVDGVVRSFQPLLLNCLWS 84
sp|Q5MQD0|SPIKE_CVHN1      CEYPHTICKSK--------------------GSSRNE---------SWHFDKSEPLCLFK 186
sp|Q14EB0|SPIKE_CVHN2      CEYPHTVCKSK--------------------GSIRNE---------SWHIDSSEPLCLFK 186
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sp|Q0ZME7|SPIKE_CVHN5      CEYPHTVCKSK--------------------GSIRNE---------SWHIDSSEPLCLFK 186
sp|Q6Q1S2|SPIKE_CVHNL      C----DDCNGYTDNIFSVQQDGRIPNGFPFNNWFLLTNGSTLVDGVSRLYQPLRLTCLWP 262
sp|P36334|SPIKE_CVHOC      CEYPQTICHPN------------------LGN-HRKE---------LWHLDTGVVSCLYK 200
sp|P22432|SPIKE_CVM4       CQLPYTPCKPN------------------TNGNRVIG---------FWHTDVKPPICLLK 190
sp|P11224|SPIKE_CVMA5      CQLPYTDCKPN------------------TNGNKLIG---------FWHTDVKPPICVLK 190
sp|Q02385|SPIKE_CVMJC      CQLPYTPCKPN------------------TNGNRVIG---------FWHTDVKPPICLLK 190
sp|P11225|SPIKE_CVMJH      CQLPYTPCKPN------------------TNGNRVIG---------FWHTDVKPPICLLK 190
sp|P18450|SPIKE_CVPFS      C---TDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTKQPLLVNCLWP 307
sp|P33470|SPIKE_CVPMI      C---TDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTKQPLLVNCLWP 307
sp|P07946|SPIKE_CVPPU      C---TDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTKQPLLVNCLWP 307
sp|P27655|SPIKE_CVPR8      C---TDQCASYVANVFTTQPGGFIPSDFSFNNWFILTNSSTLVSGKLVTKQPLLVNCLWP 83
sp|P24413|SPIKE_CVPRM      C---TDQCASYVANVFTILPGGFIPSDFSFNNWFLLTNSSTLVNGKLVTKQPLLVNCLWP 83
sp|Q01977|SPIKE_CVPRT      C---TDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTKQPLLVNCLWP 307
sp|Q9IKD1|SPIKE_CVRSD      CQLPHTDCKPN------------------TGGNTLIG---------FWHTDLRPPVCILK 190
sp|P10033|SPIKE_FIPV       CE-DYEHCTGYATNVFAPTSGGYIPDGFSFNNWFLLTNSSTFVSGRFVTNQPLLINCLWP 310
sp|K9N5Q8|SPIKE_MERS1      YHTPATDCSDGN-----------------YNRNASLNS--------FKEYFN-LRNCTFM 240
sp|P59594|SPIKE_SARS       AC-NFELCDNPF-----------------FAVSKPMG-----TQTHTMIFDN-AFNCTFE 162
sp|P0DTC2|SPIKE_SARS2      VC-EFQFCNDPF-----------------LGVYYHKNN-KSWMESEFRVYSS-ANNCTFE 169
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      NSWDI-----TADETK--------------E----------------------------- 257
sp|Q0Q475|SPIKE_BC279      RVEKS-----FQLDTA--------------PKTGNFKDLREYV-------------FKNR 194
sp|Q0Q466|SPIKE_BC512      LPKLQGLTTTLSFDSPLNVPGFSCNGANGSSSAEAFRFNVNDTKLF---VGAGAVTLNTV 341
sp|Q3LZX1|SPIKE_BCHK3      RVEKS-----FQLDTT--------------PKTGNFKDLREYV-------------FKNR 194
sp|A3EX94|SPIKE_BCHK4      NSWDI-----TADETK--------------E----------------------------- 257
sp|A3EXD0|SPIKE_BCHK5      YNYTI-----TEDENA--------------E----------------------------- 260
sp|A3EXG6|SPIKE_BCHK9      FVNNT-----FSVNIS--------------TS----RISLAFL-------------FKDG 220
sp|Q3I5J5|SPIKE_BCRP3      RVEKS-----FQLDTA--------------PKTGNFKDLREYV-------------FKNR 194
sp|Q91A26|SPIKE_CVBEN      ---------------------------------------RNFT-------------YDVN 204
sp|P25190|SPIKE_CVBF       ---------------------------------------RNFT-------------YDVN 204
sp|P25191|SPIKE_CVBL9      ---------------------------------------RNFT-------------YDVN 204
sp|Q9QAR5|SPIKE_CVBLS      ---------------------------------------RNFT-------------YDVN 204
sp|Q8V436|SPIKE_CVBLU      ---------------------------------------RNFT-------------YDVN 204
sp|P25192|SPIKE_CVBLY      ---------------------------------------RNFT-------------YDVN 204
sp|P15777|SPIKE_CVBM       ---------------------------------------RNFT-------------YDVN 204
sp|Q9QAQ8|SPIKE_CVBOK      ---------------------------------------RNFT-------------YDVN 204
sp|P25193|SPIKE_CVBQ       ---------------------------------------RNFT-------------YDVN 204
sp|P25194|SPIKE_CVBV       ---------------------------------------RNFT-------------YDVN 204
sp|P36300|SPIKE_CVCAI      VPSFGVAAQEFCFEGAQ---FSQCNGVSLNNTVDVIRFNLNFTTDVQSGMGATVFSLNTT 368
sp|Q65984|SPIKE_CVCAK      VPSFGVAAQQFCFEGAQ---FSQCNGVSLNNTVDVIRFNLNFTALVQSGMGATVFSLNTT 368
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sp|Q7T6T3|SPIKE_CVCBG      VPSFGVAAQEFCFEGAQ---FSQCNGVSLNNTVDVIRFNLNFTTDVQSGMGATVFSLNTT 368
sp|P15423|SPIKE_CVH22      VSGLRFTTGFVYFNGTG--R-GDCKGFSSDVLSDVIRYNLNFEE----NLRRGTILFKTS 137
sp|Q5MQD0|SPIKE_CVHN1      ---------------------------------------KNFT-------------YNVS 194
sp|Q14EB0|SPIKE_CVHN2      ---------------------------------------KNFT-------------YNVS 194
sp|Q0ZME7|SPIKE_CVHN5      ---------------------------------------KNFT-------------YNVS 194
sp|Q6Q1S2|SPIKE_CVHNL      VPGLKSSTGFVYFNATG--SDVNCNGYQHNSVVDVMRYNLNFSANSLDNLKSGVIVFKTL 320
sp|P36334|SPIKE_CVHOC      ---------------------------------------RNFT-------------YDVN 208
sp|P22432|SPIKE_CVM4       ---------------------------------------RNFT-------------FNVN 198
sp|P11224|SPIKE_CVMA5      ---------------------------------------RNFT-------------LNVN 198
sp|Q02385|SPIKE_CVMJC      ---------------------------------------RNFT-------------FNVN 198
sp|P11225|SPIKE_CVMJH      ---------------------------------------RNFT-------------FNVN 198
sp|P18450|SPIKE_CVPFS      VPSFEEAASTFCFEGAG---FDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 364
sp|P33470|SPIKE_CVPMI      VPSFEEAASTLCFEGAG---FDQCNGPVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 364
sp|P07946|SPIKE_CVPPU      VPSFEEAASTFCFEGAG---FDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 364
sp|P27655|SPIKE_CVPR8      VPSFEEAASTFCFEGAD---FDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 140
sp|P24413|SPIKE_CVPRM      VPSFEEVASTFCFEGAD---FDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 140
sp|Q01977|SPIKE_CVPRT      VPSFEEAASTFCFEGAG---FDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGATVFSLNTT 364
sp|Q9IKD1|SPIKE_CVRSD      ---------------------------------------RNFT-------------FNVN 198
sp|P10033|SPIKE_FIPV       VPSFGVAAQEFCFEGAQ---FSQCNGVSLNNTVDVIRFNLNFTADVQSGMGATVFSLNTT 367
sp|K9N5Q8|SPIKE_MERS1      YTYNI-----TEDEIL--------------E----------------------------- 252
sp|P59594|SPIKE_SARS       YISDA-----FSLDVS--------------EKSGNFKHLREFV-------------FKNK 190
sp|P0DTC2|SPIKE_SARS2      YVSQP-----FLMDLE--------------GKQGNFKNLREFV-------------FKNI 197
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      --W---FGITQDTQGVHLHSSRKGDLYGG----N--MFRFATLPVYEGIKYYTVIPRSFR 306
sp|Q0Q475|SPIKE_BC279      DGFLSVYQTYTAVNLPRGFPA-----GFS----V--LRPILKLPFGINITSYRVVMTMFS 243
sp|Q0Q466|SPIKE_BC512      DGVNVSIVCSNNATQ----PT-R--SNNLQEDLPYYCFTNTSSGTNHTVKFLSVFPPIIR 394
sp|Q3LZX1|SPIKE_BCHK3      DGFLSVYQTYTAVNLPRGLPT-----GFS----V--LKPILKLPFGINITSYRVVMAMFS 243
sp|A3EX94|SPIKE_BCHK4      --W---FGITQDTQGVHLYSSRKGDLYGG----N--MFRFATLPVYEGIKYYTVIPRSFR 306
sp|A3EXD0|SPIKE_BCHK5      --W---FGITQDTQGVHLYSSRKENVFRN----N--MFHFATLPVYQKILYYTVIPRSIR 309
sp|A3EXG6|SPIKE_BCHK9      DLLIYHSGWLPTSNFEHGFSR-----GSH----P--MTYFMSLPVGGNLPRAQFFQSIVR 269
sp|Q3I5J5|SPIKE_BCRP3      DGFLSVYQTYTAVNLPRGLPI-----GFS----V--LRPILKLPFGINITSYRVVMAMFS 243
sp|Q91A26|SPIKE_CVBEN      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
sp|P25190|SPIKE_CVBF       ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
sp|P25191|SPIKE_CVBL9      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVLPLTCN 253
sp|Q9QAR5|SPIKE_CVBLS      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
sp|Q8V436|SPIKE_CVBLU      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
sp|P25192|SPIKE_CVBLY      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
sp|P15777|SPIKE_CVBM       ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVLPLTCS 253
sp|Q9QAQ8|SPIKE_CVBOK      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVMPLTCN 253
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sp|P25193|SPIKE_CVBQ       ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVLPLTCS 253
sp|P25194|SPIKE_CVBV       ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGTVLSHYYVLPLTCY 253
sp|P36300|SPIKE_CVCAI      GGVILEISCYNDTVSESSFYS-YGEIPFGVTDGPRYCYVLY---NGTALKYLGTLPPSVK 424
sp|Q65984|SPIKE_CVCAK      GGVILEISCYNDTVSESSFYS-YGEISFGVTDGPRYCFALY---NGTALKYLGTLPPSVK 424
sp|Q7T6T3|SPIKE_CVCBG      GGVILDISCYNDTVSESSFYS-YGEIPFGVIDGPRYCYVLY---NGTALKYLGTLPPSVK 424
sp|P15423|SPIKE_CVH22      YG-VVVFYCTNNTLV----SG-DAHIPFGTVLGNFYCFVNTTIGNETTSAFVGALPKTVR 191
sp|Q5MQD0|SPIKE_CVHN1      TDWLYFHFYQERGTFYAY----YAD-SGM----P--TTFLFSLYLGTLLSHYYVLPLTCN 243
sp|Q14EB0|SPIKE_CVHN2      ADWLYFHFYQERGVFYAY----YAD-VGM----P--TTFLFSLYLGTILSHYYVMPLTCK 243
sp|Q0ZME7|SPIKE_CVHN5      ADWLYFHFYQERGVFYAY----YAD-VGM----P--TTFLFSLYLGTILSHYYVMPLTCN 243
sp|Q6Q1S2|SPIKE_CVHNL      QY-DVLFYCSNSSSG----VL-DTTIPFGPSSQPYYCFINSTINTTHVSTFVGILPPTVR 374
sp|P36334|SPIKE_CVHOC      ADYLYFHFYQEGGTFYAY----FTD-TGV----V--TKFLFNVYLGMALSHYYVMPLTCN 257
sp|P22432|SPIKE_CVM4       APWLYFHFYQQGGTFYAY----YAD-KPS----A--TTFLFSVYIGDILTQYFVLPFICT 247
sp|P11224|SPIKE_CVMA5      ADAFYFHFYQHGGTFYAY----YAD-KPS----A--TTFLFSVYIGDILTQYYVLPFICN 247
sp|Q02385|SPIKE_CVMJC      APWLYFHFYQQGGTFYAY----YAD-KPS----A--TTFLFSVYIGDILTQYFVLPFICT 247
sp|P11225|SPIKE_CVMJH      APWLYFHFYQQGGTFYAY----YAD-KPS----A--TTFLFSVYIGDILTQYFVLPFICT 247
sp|P18450|SPIKE_CVPFS      GGVTLEISCYNDTVSDSSFSS-YGEIPFGVTDGPRYCYVLY---NGTALKYLGTLPPSVK 420
sp|P33470|SPIKE_CVPMI      GGVTLEISCYNDTVSDSSFSS-YGEMPFGVTDGPRYCYVLY---NGTALKYLGTLPPSVK 420
sp|P07946|SPIKE_CVPPU      GGVTLEISCYT--VSDSSFFS-YGEIPFGVTDGPRYCYVHY---NGTALKYLGTLPPSVK 418
sp|P27655|SPIKE_CVPR8      GGVTLEISCYNDTVSDSSFSS-YGEIPFGVTNGPRYCYVLY---NGTALKYLGTLPPSVK 196
sp|P24413|SPIKE_CVPRM      GGVTLEISCYNDTVSDSSFSS-YGEIPFGVTNGPRYCYVLY---NGTALKYLGTLPPSVK 196
sp|Q01977|SPIKE_CVPRT      GGVTLEISCYT--VSDSSFFS-YGEIPFGVTDGPRYCYVHY---NGTALKYLGTLPPSVK 418
sp|Q9IKD1|SPIKE_CVRSD      AEWLYFHFYQQGGTFYAY----YAD-VSS----A--TTFLFSSYIGAVLTQYFVLPYMCS 247
sp|P10033|SPIKE_FIPV       GGVILEISCYSDTVSESSSYS-YGEIPFGITDGPRYCYVLY---NGTALKYLGTLPPSVK 423
sp|K9N5Q8|SPIKE_MERS1      --W---FGITQTAQGVHLFSSRYVDLYGG----N--MFQFATLPVYDTIKYYSIIPHSIR 301
sp|P59594|SPIKE_SARS       DGFLYVYKGYQPIDVVRDLPS-----GFN----T--LKPIFKLPLGINITNFRAILTAFS 239
sp|P0DTC2|SPIKE_SARS2      DGYFKIYSKHTPINLVRDLPQ-----GFS----A--LEPLVDLPIGINITRFQTLLALHR 246
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      SKANKR------------------------EA----WAAFYVYKLHQLTYLLDFSVDGYI 338
sp|Q0Q475|SPIKE_BC279      -------QFN--------------------SNFLPESAAYYVGNLKYTTFMLSFNENGTI 276
sp|Q0Q466|SPIKE_BC512      EFVITKYGNVYVNGYIYLRTRPLTAVHLNASSHSQDVAGFWTIAATNFTDVLVEVNNTGI 454
sp|Q3LZX1|SPIKE_BCHK3      -------QTT--------------------SNFLPESAAYYVGNLKYSTFMLRFNENGTI 276
sp|A3EX94|SPIKE_BCHK4      SKANKR------------------------EA----WAAFYVYKLHQLTYLLDFSVDGYI 338
sp|A3EXD0|SPIKE_BCHK5      SPFNDR------------------------KA----WAAFYIYKLHPLTYLLNFDVEGYI 341
sp|A3EXG6|SPIKE_BCHK9      SNAIDKGD----------------------GMCTNFDVNLHVAHLINRDLLVSYFNNGSV 307
sp|Q3I5J5|SPIKE_BCRP3      -------QTT--------------------SNFLPESAAYYVGNLKYTTFMLSFNENGTI 276
sp|Q91A26|SPIKE_CVBEN      S---------------------------------ALTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P25190|SPIKE_CVBF       S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P25191|SPIKE_CVBL9      S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|Q9QAR5|SPIKE_CVBLS      S---------------------------------ALTLEYWVTPLTSKQYLLAFNQDGVI 280
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sp|Q8V436|SPIKE_CVBLU      S---------------------------------ALTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P25192|SPIKE_CVBLY      S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P15777|SPIKE_CVBM       S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|Q9QAQ8|SPIKE_CVBOK      S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P25193|SPIKE_CVBQ       S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P25194|SPIKE_CVBV       S---------------------------------AMTLEYWVTPLTSKQYLLAFNQDGVI 280
sp|P36300|SPIKE_CVCAI      EIAISKWGHFYINGYNFFSTFPIDCIAFNLTT--GASGAFWTIAYTSYTEALVQVENTAI 482
sp|Q65984|SPIKE_CVCAK      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSGAFWTIAYTSYTDALVQVENTAI 482
sp|Q7T6T3|SPIKE_CVCBG      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GASGAFWTIAYTSYTEALVQVENTAI 482
sp|P15423|SPIKE_CVH22      EFVISRTGHFYINGYRYFTLGNVEAVNFNVTT--AETTDFCTVALASYADVLVNVSQTSI 249
sp|Q5MQD0|SPIKE_CVHN1      AISS---------------------------NTDNETLQYWVTPLSKRQYLLKFDNRGVI 276
sp|Q14EB0|SPIKE_CVHN2      AISS---------------------------NTDNETLEYWVTPLSRRQYLLNFDEHGVI 276
sp|Q0ZME7|SPIKE_CVHN5      AISS---------------------------NTDNETLEYWVTPLSRRQYLLNFDEHGVI 276
sp|Q6Q1S2|SPIKE_CVHNL      EIVVARTGQFYINGFKYFDLGFIEAVNFNVTT--ASATDFWTVAFATFVDVLVNVSATNI 432
sp|P36334|SPIKE_CVHOC      S---------------------------------KLTLEYWVTPLTSRQYLLAFNQDGII 284
sp|P22432|SPIKE_CVM4       PTAG---------------------------S--TLLPLYWVTPLLKRQYLFNFNEKGVI 278
sp|P11224|SPIKE_CVMA5      PTAG---------------------------S--TFAPRYWVTPLVKRQYLFNFNQKGVI 278
sp|Q02385|SPIKE_CVMJC      PTAG---------------------------S--TLLPLYWVTPLLKRQYLFNFNEKGVI 278
sp|P11225|SPIKE_CVMJH      PTAG---------------------------S--TLAPLYWVTPLLKRQYLFNFNEKGVI 278
sp|P18450|SPIKE_CVPFS      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 478
sp|P33470|SPIKE_CVPMI      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 478
sp|P07946|SPIKE_CVPPU      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 476
sp|P27655|SPIKE_CVPR8      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 254
sp|P24413|SPIKE_CVPRM      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 254
sp|Q01977|SPIKE_CVPRT      EIAISKWGHFYINGYNFFSTFPIDCISFNLTT--GDSDVFWTIAYTSYTEALVQVENTAI 476
sp|Q9IKD1|SPIKE_CVRSD      PTTS---------------------------G--VSSPQYWVTPLVKRQYLFNFNQKGII 278
sp|P10033|SPIKE_FIPV       EIAISKWGHFYINGYNFFSTFPIGCISFNLTT--GVSGAFWTIAYTSYTEALVQVENTAI 481
sp|K9N5Q8|SPIKE_MERS1      SIQSDR------------------------KA----WAAFYVYKLQPLTFLLDFSVDGYI 333
sp|P59594|SPIKE_SARS       -------PAQ--------------------DIWGTSAAAYFVGYLKPTTFMLKYDENGTI 272
sp|P0DTC2|SPIKE_SARS2      SYLT-PGDSS--------------------SGWTAGAAAYYVGYLQPRTFLLKYNENGTI 285
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      RRAIDCGHDDLSQLHCSYTSFEVDTGVYSVSSYEASATGTFIEQPNVT-ECD-FSP-MLT 395
sp|Q0Q475|SPIKE_BC279      TDAVDCSQNPLAELKCTIKNFNVSKGIYQTSNFRVTPTQEVVRFPNITNRCP-FDKVFNA 335
sp|Q0Q466|SPIKE_BC512      QRLLYCD-TPENSVKCSQLSFELEDGFYSMTADNVYAVTKPHTFVT-L------------ 500
sp|Q3LZX1|SPIKE_BCHK3      TDAVDCSQNPLAELKCTIKNFNVDKGIYQTSNFRVSPTQEVIRFPNITNRCP-FDKVFNA 335
sp|A3EX94|SPIKE_BCHK4      RRAIDCGHDDLSQLHCSYTSFEVDTGVYSVSSYEASATGTFIEQPNAT-ECD-FSP-MLT 395
sp|A3EXD0|SPIKE_BCHK5      TKAVDCGYDDLAQLQCSYESFEVETGVYSVSSFEASPRGEFIEQATTQ-ECD-FTP-MLT 398
sp|A3EXG6|SPIKE_BCHK9      ANAADCADSAAEELYCVTGSFDPPTGVYPLSRYRAQVAGFV-RVTQRGSYCTPPYSV--L 364
sp|Q3I5J5|SPIKE_BCRP3      TNAIDCAQNPLAELKCTIKNFNVSKGIYQTSNFRVSPTQEVIRFPNITNRCP-FDKVFNA 335
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sp|Q91A26|SPIKE_CVBEN      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P25190|SPIKE_CVBF       FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P25191|SPIKE_CVBL9      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|Q9QAR5|SPIKE_CVBLS      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|Q8V436|SPIKE_CVBLU      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P25192|SPIKE_CVBLY      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P15777|SPIKE_CVBM       FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|Q9QAQ8|SPIKE_CVBOK      FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P25193|SPIKE_CVBQ       FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P25194|SPIKE_CVBV       FNAVDCKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLND 339
sp|P36300|SPIKE_CVCAI      KKVTYCN-SHINNIKCSQLTANLQNGFYPVASSEVGLV--NKSVVL-L------------ 526
sp|Q65984|SPIKE_CVCAK      KKVTYCN-SHINNIKCSQLTANLQNGFYPVASSEVGLV--NKSVVL-L------------ 526
sp|Q7T6T3|SPIKE_CVCBG      KKVTYCN-SHVNSIKCSQLTANLQNGFYPVASSEVGLV--NKSVVL-L------------ 526
sp|P15423|SPIKE_CVH22      ANIIYCN-SVINRLRCDQLSFDVPDGFYSTSP--IQSVELPVSIVS-L------------ 293
sp|Q5MQD0|SPIKE_CVHN1      TNAVDCSSSFFSEIQCKTKSLLPNTGVYDLSGFTVKPVATVHRRIPDLPDCD-IDKWLNN 335
sp|Q14EB0|SPIKE_CVHN2      TNAVDCSSSFLSEIQCKTQSFAPNTGVYDLSGFTVKPVATVYRRIPNLPDCD-IDNWLNN 335
sp|Q0ZME7|SPIKE_CVHN5      TNAVDCSSSFLSEIQCKTQSFAPNTGVYDLSGFTVKPVATVYRRIPNLPDCD-IDNWLNN 335
sp|Q6Q1S2|SPIKE_CVHNL      QNLLYCD-SPFEKLQCEHLQFGLQDGFYSANF--LDDNVLPETYVA-L------------ 476
sp|P36334|SPIKE_CVHOC      FNAEDCMSDFMSEIKCKTQSIAPPTGVYELNGYTVQPIADVYRRKPNLPNCN-IEAWLND 343
sp|P22432|SPIKE_CVM4       TSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPNLPDCK-IEEWLTA 337
sp|P11224|SPIKE_CVMA5      TSAVDCASSYTSEIKCKTQSMLPSTGVYELSGYTVQPVGVVYRRVANLPACN-IEEWLTA 337
sp|Q02385|SPIKE_CVMJC      TSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPNLPDCK-IEEWLTA 337
sp|P11225|SPIKE_CVMJH      TSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVYRRVPNLPDCK-IEEWLTA 337
sp|P18450|SPIKE_CVPFS      TKVTYCN-SYVNNIKCSQLTANLNNGFYPVSSSEVGFV--NKSVVL-L------------ 522
sp|P33470|SPIKE_CVPMI      TKVTYCN-SYVNNIKCSQLTANLNNGFYPVSSSEVGLV--NKSVVL-L------------ 522
sp|P07946|SPIKE_CVPPU      TKVTYCN-SHVNNIKCSQITANLNNGFYPVSSSEVGLV--NKSVVL-L------------ 520
sp|P27655|SPIKE_CVPR8      TNVTYCN-SYVNNIKCSQLTANLNNGFYPVSSSEVGSV--NKSVVL-L------------ 298
sp|P24413|SPIKE_CVPRM      TNVTYCN-SYVNNIKCSQLTANLNNGFYPVSSSEVGSV--NKSVVL-L------------ 298
sp|Q01977|SPIKE_CVPRT      TKVTYCN-SHVNNIKCSQITANLNNGFYPVSSSEVGLV--NKSVVL-L------------ 520
sp|Q9IKD1|SPIKE_CVRSD      TSAVDCASSYTSEIKCKTQSMNPNTGVYDLSGYTVQPVGLVYRRVRNLPDCK-IEEWLAA 337
sp|P10033|SPIKE_FIPV       KNVTYCN-SHINNIKCSQLTANLNNGFYPVASSEVGFV--NKSVVL-L------------ 525
sp|K9N5Q8|SPIKE_MERS1      RRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQAEGV-ECD-FSP-LLS 390
sp|P59594|SPIKE_SARS       TDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCP-FGEVFNA 331
sp|P0DTC2|SPIKE_SARS2      TDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCP-FGEVFNA 344
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0


sp|Q0Q4F2|SPIKE_BC133      GVAPQVYNFKRLVFSNCNYNLTKLLSLFAVDEFSCNGISPDAIARGCYSTLTVDYFAYPL 455
sp|Q0Q475|SPIKE_BC279      SRFPNVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRS 395
sp|Q0Q466|SPIKE_BC512      ---PT---FNDHGFVNVTV------------------------GGNFDSSY-PPKFTAN- 528
sp|Q3LZX1|SPIKE_BCHK3      TRFPNVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRS 395
```

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sp|A3EX94|SPIKE_BCHK4      GVAPQVYNFKRLVFSNCNYNLTKLLSLFAVDEFSCNGISPDSIARGCYSTLTVDYFAYPL 455
sp|A3EXD0|SPIKE_BCHK5      GTPPPIYNFKRLVFTNCNYNLTKLLSLFQVSEFSCHQVSPSSLATGCYSSLTVDYFAYST 458
sp|A3EXG6|SPIKE_BCHK9      QDPPQPVVWRRYMLYDCVFDFTVVVDSLPTHQLQCYGVSPRRLASMCYGSVTLDVMRINE 424
sp|Q3I5J5|SPIKE_BCRP3      TRFPNVYAWERTKISDCVADYTVLYNSTSFSTFKCYGVSPSKLIDLCFTSVYADTFLIRS 395
sp|Q91A26|SPIKE_CVBEN      KSVPSPLNWERKTFSNCNFNMSSLMSFIQAYSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P25190|SPIKE_CVBF       KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P25191|SPIKE_CVBL9      KSVPSPLNWERKTFSNCNFNMSCLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|Q9QAR5|SPIKE_CVBLS      KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|Q8V436|SPIKE_CVBLU      KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P25192|SPIKE_CVBLY      KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P15777|SPIKE_CVBM       KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|Q9QAQ8|SPIKE_CVBOK      KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P25193|SPIKE_CVBQ       KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 399
sp|P25194|SPIKE_CVBV       KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIEAAKIYGMCFSSITIDKFAIPN 399
sp|P36300|SPIKE_CVCAI      ---PS---FYSHTSVNITID-----------------LGMKRSV-TV-TIA-SPLSNITL 560
sp|Q65984|SPIKE_CVCAK      ---PS---FYSHTSVNITID-----------------LGMKRSGYGQ-PIA-STLSNITL 561
sp|Q7T6T3|SPIKE_CVCBG      ---PS---FYSHTSVNITID-----------------LGMRRSGYGQ-PVA-SSLSNISL 561
sp|P15423|SPIKE_CVH22      ---PV---YHKHTFIVLYVD-----------------FKPQSGGGKCFNCY-PAGVNITL 329
sp|Q5MQD0|SPIKE_CVHN1      FNVPSPLNWERKIFSNCNFNLSTLLRLVHTDSFSCNNFDESKIYGSCFKSIVLDKFAIPN 395
sp|Q14EB0|SPIKE_CVHN2      VSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPN 395
sp|Q0ZME7|SPIKE_CVHN5      VSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPN 395
sp|Q6Q1S2|SPIKE_CVHNL      ---PI---YYQHTDINFT--------------------ATASFGGSCYVCK-PHQVNISL 509
sp|P36334|SPIKE_CVHOC      KSVPSPLNWERKTFSNCNFNMSSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPN 403
sp|P22432|SPIKE_CVM4       KSVPSPLNWERRTFQNCNFNLSSLLRYVQAESLSCNNIDASKVYGMCFGSVSVDKFAIPR 397
sp|P11224|SPIKE_CVMA5      RSVPSPLNWERKTFQNCNFNLSSLLRYVQAESLFCNNIDASKVYGRCFGSISVDKFAVPR 397
sp|Q02385|SPIKE_CVMJC      KSVPSPLNWERRTFQNCNFNLSSLLRYVQAESLSCNNIDASKVYGMCFGSVSVDKFAIPR 397
sp|P11225|SPIKE_CVMJH      KSVPSPLNWERRTFQNCNFNLSSLLRYVQAESLSCNNIDASKVYGMCFGSVSVDKFAIPR 397
sp|P18450|SPIKE_CVPFS      ---PT---FYTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 557
sp|P33470|SPIKE_CVPMI      ---PS---FYTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 557
sp|P07946|SPIKE_CVPPU      ---PS---FYTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 555
sp|P27655|SPIKE_CVPR8      ---PS---FLTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 333
sp|P24413|SPIKE_CVPRM      ---PS---FLTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 333
sp|Q01977|SPIKE_CVPRT      ---PS---FYTHTIVNITIG-----------------LGMKRSGYGQ-PIA-STLSNITL 555
sp|Q9IKD1|SPIKE_CVRSD      NTVPSPLNWERKTFQNCNFNLSSLLRFVQAESLSCSNIDASKVYGMCFGSISIDKFAIPN 397
sp|P10033|SPIKE_FIPV       ---PS---FFTYTAVNITID-----------------LGMKLSGYGQ-PIA-STLSNITL 560
sp|K9N5Q8|SPIKE_MERS1      GTPPQVYNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSSLILDYFSYPL 450
sp|P59594|SPIKE_SARS       TKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKG 391
sp|P0DTC2|SPIKE_SARS2      TRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRG 404
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 0
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 0
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 0
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 0
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 0
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 0
sp|F1M391|STING_RAT        ------------------------------------------------------------ 0
```

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sp|Q0Q4F2|SPIKE_BC133      SMKSYIRPGSAGNIPLYNYKQSFANPTCRVMASVPDNV-TITK--PGAYGYISKCS---R 509
sp|Q0Q475|SPIKE_BC279      SEVRQVAPGETGVIADYNYKLPDDFTGCVIAWNTAQQDQ-------G--QYYYRSYRKEK 446
sp|Q0Q466|SPIKE_BC512      GTLVNN-----------------GTVVCVTSNQF--TLRHDFMV-----------GYSAD 558
sp|Q3LZX1|SPIKE_BCHK3      SEVRQVAPGETGVIADYNYKLPDDFTGCVIAWNTAKHDT-------G--NYYYRSHRKTK 446
sp|A3EX94|SPIKE_BCHK4      SMKSYIRPGSAGNIPLYNYKQSFANPTCRVMASVLANV-TITK--PHAYGYISKCS---R 509
sp|A3EXD0|SPIKE_BCHK5      DMSSYLQPGSAGAIVQFNYKQDFSNPTCRVLATVPQNLTTITK--PSNYAYLTECY---K 513
sp|A3EXG6|SPIKE_BCHK9      THLNNLFNRVPDTFSLYNYALPDNFYGCLHAFYLNSTAPYAV-------------ANRFP 471
sp|Q3I5J5|SPIKE_BCRP3      SEVRQVAPGETGVIADYNYKLPDDFTGCVIAWNTAKQDQ-------G--QYYYRSHRKTK 446
sp|Q91A26|SPIKE_CVBEN      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|P25190|SPIKE_CVBF       GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSLSRFNPSIWNRRFGFTEQSV 459
sp|P25191|SPIKE_CVBL9      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|Q9QAR5|SPIKE_CVBLS      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|Q8V436|SPIKE_CVBLU      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|P25192|SPIKE_CVBLY      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|P15777|SPIKE_CVBM       GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQFV 459
sp|Q9QAQ8|SPIKE_CVBOK      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSIWNRRFGFTEQSV 459
sp|P25193|SPIKE_CVBQ       GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQFV 459
sp|P25194|SPIKE_CVBV       GRKVDLQLGNLGYLQSFNYRIDTTAASCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQSV 459
sp|P36300|SPIKE_CVCAI      PMQDNN-----------------IDVYCIRSNQF--SVYVHSTCKSSLWDNNFNSACTDV 601
sp|Q65984|SPIKE_CVCAK      PMQDNN-----------------TDVYCIRSNRF--SVYFHSTCKSSLWDDVFNSDCTDV 602
sp|Q7T6T3|SPIKE_CVCBG      PMQDNN-----------------TDVYCIRSNQF--SFYVHSNCKSASWDNIFNSACTDV 602
sp|P15423|SPIKE_CVH22      ANFNET-----------------KGPLCVDTSHF--TTKYVAVYA-------------NV 357
sp|Q5MQD0|SPIKE_CVHN1      SRRSDLQLGSSGFLQSSNYKIDTTSSSCQLYYSLPAINVTINNYNPSSWNRRYGFNNFNL 455
sp|Q14EB0|SPIKE_CVHN2      RRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINNFNPSSWNRRYGFGSFNV 455
sp|Q0ZME7|SPIKE_CVHN5      RRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINNFNPSSWNRRYGFGSFNL 455
sp|Q6Q1S2|SPIKE_CVHNL      NG---------------------NTSVCVRTSHF--SIRYIYNRV--------KSGSPGD 538
sp|P36334|SPIKE_CVHOC      GRKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAANVSVSRFNPSTWNKRFGFIEDSV 463
sp|P22432|SPIKE_CVM4       SRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVTINNYNPSSWNRRYGFNDAGV 457
sp|P11224|SPIKE_CVMA5      SRQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVTINNHNPSSWNRRYGFNDAGV 457
sp|Q02385|SPIKE_CVMJC      SRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVTINNYNPSSWNRRYGFNDAGV 457
sp|P11225|SPIKE_CVMJH      SRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVTINNYNPSSWNRRYGFK---- 453
sp|P18450|SPIKE_CVPFS      PMQDNN-----------------IDVYCIRSDQF--SVYVHSTCKSALWDNVFKRNCTDV 598
sp|P33470|SPIKE_CVPMI      PMQDNN-----------------TDVYCIRSDQF--SVYVHSTCKSSLWDNVFKRNCTDV 598
sp|P07946|SPIKE_CVPPU      PMQDHN-----------------TDVYCIRSDQF--SVYVHSTCKSALWDNIFKRNCTDV 596
sp|P27655|SPIKE_CVPR8      PMQDNN-----------------TDVYCVRSDQF--SVYVHSTCKSALWDNVFKRNCTDV 374
sp|P24413|SPIKE_CVPRM      PMQDNN-----------------NDVYCVRSDQF--SVYVHSTCKSVLWDNVFKRNCTDV 374
sp|Q01977|SPIKE_CVPRT      PMQDHN-----------------TDVYCIRSDQF--SVYVHSTCKSALWDNIFKRNCTDV 596
sp|Q9IKD1|SPIKE_CVRSD      SRRVDLQLGKSGLLQSFNYKIDTRATSCQLYYSLAQDNVTVINHNPSSWNRRYGFNDVAT 457
sp|P10033|SPIKE_FIPV       PMQDNN-----------------TDVYCIRSNQF--SVYVHSTCKSSLWDNIFNQDCTDV 601
sp|K9N5Q8|SPIKE_MERS1      SMKSDLSVSSAGPISQFNYKQSFSNPTCLILATVPHNLTTITK--PLKYSYINKCS---R 505
sp|P59594|SPIKE_SARS       DDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATST----GNYNYKYRYLRHGK 447
sp|P0DTC2|SPIKE_SARS2      DEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG----GNYNYLYRLFRKSN 460
sp|Q2KI99|STING_BOVIN      ---------------------------------MP----------------------HSS 5
sp|E1C7U0|STING_CHICK      ---------------------------------MPQDPS----------------TRSSP 11
sp|Q86WV6|STING_HUMAN      ---------------------------------MP----------------------HSS 5
sp|Q3TBT3|STING_MOUSE      ---------------------------------MP----------------------YSN 5
sp|A7SLZ2|STING_NEMVE      ---------------------------------MR---R----------------AEENN 8
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sp|B8XX90|STING_PIG        ---------------------------------MP----------------------YSS 5
sp|F1M391|STING_RAT        ---------------------------------MP----------------------YSN 5


sp|Q0Q4F2|SPIKE_BC133      LTG----------V-------NQDIETPLYINPGEYSICRDFAPLG-------------- 538
sp|Q0Q475|SPIKE_BC279      LKP----------F-------ERDLSSD----------------E--------------- 458
sp|Q0Q466|SPIKE_BC512      MRKGIFEYSSTCPFNRETINNYLTFGRICFSTSPADGACELKYYV--------------- 603
sp|Q3LZX1|SPIKE_BCHK3      LKP----------F-------ERDLSSDD---------------G--------------- 459
sp|A3EX94|SPIKE_BCHK4      LTG----------A-------NQDVETPLYINPGEYSICRDFSPGG-------------- 538
sp|A3EXD0|SPIKE_BCHK5      TSA----------Y-------GK---NYLYNAPGAYTPCLSLASRG-------------- 539
sp|A3EXG6|SPIKE_BCHK9      IKP----------G-------GRQSNSAFI------------------------------ 484
sp|Q3I5J5|SPIKE_BCRP3      LKP----------F-------ERDLSSD----------------E--------------- 458
sp|Q91A26|SPIKE_CVBEN      FKP--------QPAGVF-TDHDVVYAQHCFKASTNFCPCKLDGSLCVGNGPGIDAGYKTS 510
sp|P25190|SPIKE_CVBF       FKP--------QPVGVF-TDHDVVYAQHCFKAPTNFCPCKLDGSLCVGNGPGIDAGYKNS 510
sp|P25191|SPIKE_CVBL9      FKP--------QPVGVF-THHDVVYAQHCFKAPTNFCPCKLDGSLCVGNGPGIDAGYKNS 510
sp|Q9QAR5|SPIKE_CVBLS      FKP--------QPAGVF-TDHDVVYAQHCFKAPTNFCPCKLDGSLCVGSGSGIDAGYKNT 510
sp|Q8V436|SPIKE_CVBLU      FKP--------QPAGVF-TDHDVVYAQHCFKAPTNFCPCKLDGSLCVGNGPGIDAGYKTS 510
sp|P25192|SPIKE_CVBLY      FKP--------QPVGVF-TDHDVVYAQHCFKAPTNFCPCKLDGSLCVGSGSGIDAGYKNS 510
sp|P15777|SPIKE_CVBM       FKP--------QPVGVF-THHDVVYAQHCFKAPSNFCPCKLDGSLCVGNGPGIDAGYKNS 510
sp|Q9QAQ8|SPIKE_CVBOK      FKP--------QPAGVF-TDHDVVYAQHCFKAPTNFCPCKLDGSLCVGSGSGIDAGYKNT 510
sp|P25193|SPIKE_CVBQ       FKP--------QPVGVF-THHDVVYAQHCFKAPKNFCPCKLDGSLCVGNGPGIDAGYKNS 510
sp|P25194|SPIKE_CVBV       FKP--------QPVGVF-THHDVVYAQHCFKAPTNFCPCKLDGSLCVGNGPGIDAGYKNS 510
sp|P36300|SPIKE_CVCAI      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLNPVGANCKLDVAA--------------- 646
sp|Q65984|SPIKE_CVCAK      LYATAVIKTGTCPFSFDKLNNYLTFNKFCLSLNPVGANCKFDVAA--------------- 647
sp|Q7T6T3|SPIKE_CVCBG      LEATAVIKTGTCPFSFDKLNNYLTFNKFCLSLNPTGANCKFDVVA--------------- 647
sp|P15423|SPIKE_CVH22      GRWSASINTGNCPFSFGKVNNFVKFGSVCFSLKDIPGGCAMPIVA--------------- 402
sp|Q5MQD0|SPIKE_CVHN1      ------------------SSHSVVYSRYCFSVNNTFCPCAKPSFASSCKSH-------KP 490
sp|Q14EB0|SPIKE_CVHN2      ------------------SSYDVVYSDHCFSVNSDFCPCADPSVVNSCVKS-------KP 490
sp|Q0ZME7|SPIKE_CVHN5      ------------------SSYDVVYSDHCFSVNSDFCPCADPSVVNSCAKS-------KP 490
sp|Q6Q1S2|SPIKE_CVHNL      SSWHIYLKSGTCPFSFSKLNNFQKFKTICFSTVEVPGSCNFPLEA--------------- 583
sp|P36334|SPIKE_CVHOC      FKP--------RPAGVL-TNHDVVYAQHCFKAPKNFCPCKLNGS-CVGSGPG-----KNN 508
sp|P22432|SPIKE_CVM4       FGK---------------SKHDVAYAQQCFTVRPSYCPCAQPDIVSACTSQT------KP 496
sp|P11224|SPIKE_CVMA5      FGK---------------NQHDVVYAQQCFTVRSSYCPCAQPDIVSPCTTQT------KP 496
sp|Q02385|SPIKE_CVMJC      FGK---------------SKHDVAYAQQCFIVRPSYCPCAQPDIVSACTSQT------KP 496
sp|P11225|SPIKE_CVMJH      ------------------------------------------------------------ 453
sp|P18450|SPIKE_CVPFS      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 643
sp|P33470|SPIKE_CVPMI      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 643
sp|P07946|SPIKE_CVPPU      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 641
sp|P27655|SPIKE_CVPR8      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 419
sp|P24413|SPIKE_CVPRM      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 419
sp|Q01977|SPIKE_CVPRT      LDATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 641
sp|Q9IKD1|SPIKE_CVRSD      FHS---------------GEHDVAYAEACFTVGASYCPCAKPSTVYSCVT-G------KP 495
sp|P10033|SPIKE_FIPV       LEATAVIKTGTCPFSFDKLNNYLTFNKFCLSLSPVGANCKFDVAA--------------- 646
sp|K9N5Q8|SPIKE_MERS1      FLS----------D-------DR-TEVPQLVNANQYSPCVSIVPST-------------- 533
sp|P59594|SPIKE_SARS       LRP----------F-------ERDISNVPFSPD--GKPCTPP-AL--------------- 472
sp|P0DTC2|SPIKE_SARS2      LKP----------F-------ERDISTEIYQAG--STPCNGVEGF--------------- 486
sp|Q2KI99|STING_BOVIN      LHP--------------------------------------------------------- 8
```

```
sp|E1C7U0|STING_CHICK      ARL--------------------------------------------------------- 14
sp|Q86WV6|STING_HUMAN      LHP--------------------------------------------------------- 8
sp|Q3TBT3|STING_MOUSE      LHP--------------------------------------------------------- 8
sp|A7SLZ2|STING_NEMVE      GFG--------------------------------------------------------- 11
sp|B8XX90|STING_PIG        LHP--------------------------------------------------------- 8
sp|F1M391|STING_RAT        LHP--------------------------------------------------------- 8


sp|Q0Q4F2|SPIKE_BC133      ---FSEDGQVFKRTLT-------------------------QFEGG-------------G 557
sp|Q0Q475|SPIKE_BC279      ------------NGVY-------------------------TLSTY-------------D 468
sp|Q0Q466|SPIKE_BC512      ------------------------------------------------------------ 603
sp|Q3LZX1|SPIKE_BCHK3      ------------NGVY-------------------------TLSTY-------------D 469
sp|A3EX94|SPIKE_BCHK4      ---FSEDGQVFKRTLT-------------------------QFEGG-------------G 557
sp|A3EXD0|SPIKE_BCHK5      ---FSTKYQS---------------------------------HSD-------------G 550
sp|A3EXG6|SPIKE_BCHK9      ------------DT---------------------------------------------- 486
sp|Q3I5J5|SPIKE_BCRP3      ------------NGVR-------------------------TLSTY-------------D 468
sp|Q91A26|SPIKE_CVBEN      GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKAT---GPYKCPQTK 553
sp|P25190|SPIKE_CVBF       GIGTCPAGTNYLTC--------------HNAAQCNCLCTPDPITSKST---GPYKCPQTK 553
sp|P25191|SPIKE_CVBL9      GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKST---GPYKCPQTK 553
sp|Q9QAR5|SPIKE_CVBLS      GIGTCPAGTNYLTC--------------HNAAQCGCLCTPDPITSKAT---GPYKCPQTK 553
sp|Q8V436|SPIKE_CVBLU      GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKAT---GPYKCPQTK 553
sp|P25192|SPIKE_CVBLY      GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKST---GPYKCPQTK 553
sp|P15777|SPIKE_CVBM       GIGTCPAGTNYLTC--------------HNAAQCNCLCTPDPITSKST---GPYKCPQTK 553
sp|Q9QAQ8|SPIKE_CVBOK      GIGTCPAGTNYLTC--------------HNAAQCGCLCTPDPITSKAT---GPYKCPQTK 553
sp|P25193|SPIKE_CVBQ       GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKST---GPYKCPQTK 553
sp|P25194|SPIKE_CVBV       GIGTCPAGTNYLTC--------------HNAAQCDCLCTPDPITSKST---GPYKCPQTK 553
sp|P36300|SPIKE_CVCAI      ------------------------------------------------------------ 646
sp|Q65984|SPIKE_CVCAK      ------------------------------------------------------------ 647
sp|Q7T6T3|SPIKE_CVCBG      ------------------------------------------------------------ 647
sp|P15423|SPIKE_CVH22      ------------------------------------------------------------ 402
sp|Q5MQD0|SPIKE_CVHN1      PSASCPIGTNYRSCESTTV--------LDHTDWCRCSCLPDPITAY-----DPRSCSQKK 537
sp|Q14EB0|SPIKE_CVHN2      LSAICPAGTKYRHCDLDTT--------LYVNNWCRCSCLPDPISTY-----SPNTCPQKK 537
sp|Q0ZME7|SPIKE_CVHN5      PSAICPAGTKYRHCDLDTT--------LYVKNWCRCSCLPDPISTY-----SPNTCPQKK 537
sp|Q6Q1S2|SPIKE_CVHNL      ------------------------------------------------------------ 583
sp|P36334|SPIKE_CVHOC      GIGTCPAGTNYLTC--------------DN------LCTPDPIT--FT---GTYKCPQTK 543
sp|P22432|SPIKE_CVM4       MSAYCPTGTIHRECSLWNGPHLRSARVGSGTYTCECTCKPNPFDT------YDLRCGQIK 550
sp|P11224|SPIKE_CVMA5      KSA--------------------------------------------------------- 499
sp|Q02385|SPIKE_CVMJC      MSAYCPTGTIHRECSLWNGPHLRSARVGSGTYTCECTCKPNPFDT------YDLRCGQIK 550
sp|P11225|SPIKE_CVMJH      ------------------------------------------------------------ 453
sp|P18450|SPIKE_CVPFS      ------------------------------------------------------------ 643
sp|P33470|SPIKE_CVPMI      ------------------------------------------------------------ 643
sp|P07946|SPIKE_CVPPU      ------------------------------------------------------------ 641
sp|P27655|SPIKE_CVPR8      ------------------------------------------------------------ 419
sp|P24413|SPIKE_CVPRM      ------------------------------------------------------------ 419
sp|Q01977|SPIKE_CVPRT      ------------------------------------------------------------ 641
sp|Q9IKD1|SPIKE_CVRSD      KSANCPTGTSNRECNVQAS---------GFKSKCDCTCNPSPLTT------YDPRCLQAR 540
sp|P10033|SPIKE_FIPV       ------------------------------------------------------------ 646
```

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sp|K9N5Q8|SPIKE_MERS1      ---VWEDGDYYRKQLS-------------------------PLEGG-------------G 552
sp|P59594|SPIKE_SARS       ------------NCYW-------------------------PLNDY-------------G 482
sp|P0DTC2|SPIKE_SARS2      ------------NCYF-------------------------PLQSY-------------G 496
sp|Q2KI99|STING_BOVIN      -----------------SIPQPRGLRAQKAALVLLSACLVALW------GLGEPPDYTLK 45
sp|E1C7U0|STING_CHICK      -----------------LIPEPRAGRARHAACVLLAVCFVVLF------LSGEPLAPIIR 51
sp|Q86WV6|STING_HUMAN      -----------------SIPCPRGHGAQKAALVLLSACLVTLW------GLGEPPEHTLR 45
sp|Q3TBT3|STING_MOUSE      -----------------AIPRPRGHRSKYVALIFLVASLMILW------VAKDPPNHTLK 45
sp|A7SLZ2|STING_NEMVE      -----------------TIPKRRNQHTPFYASIGMIVVIIVAFTSYHITSYGDDRNRAMR 54
sp|B8XX90|STING_PIG        -----------------SIPQPRGLRAQVAALVLLGACLVALW------GLGELPEYTLR 45
sp|F1M391|STING_RAT        -----------------SIPRPRSYRFKLAAFVLLVGSLMSLW------MTGEPPSHTLH 45


sp|Q0Q4F2|SPIKE_BC133      L---LIGVGTRVPMTANLE---------------------------------M----GFV 577
sp|Q0Q475|SPIKE_BC279      F---YPSIPVEYQA----T---------------------------------R----VVV 484
sp|Q0Q466|SPIKE_BC512      ----WNTIGAVSHLAGTLY----------------------------------------- 618
sp|Q3LZX1|SPIKE_BCHK3      F---NPNVPVAYQA----T---------------------------------R----VVV 485
sp|A3EX94|SPIKE_BCHK4      L---LIGVGTRVPMTDNLQ---------------------------------M----SFI 577
sp|A3EXD0|SPIKE_BCHK5      E---LTTTGYIYPVTGNLQ---------------------------------M----AFI 570
sp|A3EXG6|SPIKE_BCHK9      -----VINAAHYSPFSYVY---------------------------------G----LAV 504
sp|Q3I5J5|SPIKE_BCRP3      F---YPSVPVAYQA----T---------------------------------R----VVV 484
sp|Q91A26|SPIKE_CVBEN      Y---LVGIGEHCSGLAIKSDHCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P25190|SPIKE_CVBF       Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P25191|SPIKE_CVBL9      Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|Q9QAR5|SPIKE_CVBLS      Y---LVGIGEHCSGLAIKSDYCGGN------PCSCQPQAFLGWSVDSCLQGDR----CNI 600
sp|Q8V436|SPIKE_CVBLU      Y---LVGIGEHCSGLAIKSDHCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P25192|SPIKE_CVBLY      Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P15777|SPIKE_CVBM       Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|Q9QAQ8|SPIKE_CVBOK      Y---LVGIGEHCSGLAIKSDYCGGN------PCSCRPQAFLGWSVDSCLQGDR----CNI 600
sp|P25193|SPIKE_CVBQ       Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P25194|SPIKE_CVBV       Y---LVGIGEHCSGLAIKSDYCGGN------PCTCQPQAFLGWSVDSCLQGDR----CNI 600
sp|P36300|SPIKE_CVCAI      R---TR---TNEQVFGSLY----------------------------------------- 659
sp|Q65984|SPIKE_CVCAK      R---TR---TNEQVVRSLY----------------------------------------- 660
sp|Q7T6T3|SPIKE_CVCBG      R---TR---TNEQGVGSLY----------------------------------------- 660
sp|P15423|SPIKE_CVH22      N---WAY--SKYYTIGSLY----------------------------------------- 416
sp|Q5MQD0|SPIKE_CVHN1      S---LVGVGEHCAGFGVDEEKCGVLDGSYNVSCLCSTDAFLGWSYDTCVSNNR----CNI 590
sp|Q14EB0|SPIKE_CVHN2      V---VVGIGEHCPGLGINEEKCGTQLN--HSSCSCSPDAFLGWSFDSCISNNR----CNI 588
sp|Q0ZME7|SPIKE_CVHN5      V---VVGIGEHCPGLGINEEKCGTQLN--HSSCFCSPDAFLGWSFDSCISNNR----CNI 588
sp|Q6Q1S2|SPIKE_CVHNL      T---WHY--TSYTIVGALY----------------------------------------- 597
sp|P36334|SPIKE_CVHOC      S---LVGIGEHCSGLAVKSDYCGGN------SCTCRPQAFLGWSADSCLQGDK----CNI 590
sp|P22432|SPIKE_CVM4       T---IVNVGDHCEGLGVLEDKCGNSDP--HKGCSCANDSFIGWSHDTCLVNDR----CQI 601
sp|P11224|SPIKE_CVMA5      ----FVNVGDHCEGLGVLEDNCGNADP--HKGCICANNSFIGWSHDTCLVNDR----CQI 549
sp|Q02385|SPIKE_CVMJC      T---IVNVGDHCEGLGVLEDKCGNSDP--HKGCSCAHDSFIGWSHDTCLVNDH----SQI 601
sp|P11225|SPIKE_CVMJH      -------------------------------------------------VNDR----CQI 460
sp|P18450|SPIKE_CVPFS      R---TR---ANDQVVRSLY----------------------------------------- 656
sp|P33470|SPIKE_CVPMI      R---TR---TNDQVVRSLY----------------------------------------- 656
sp|P07946|SPIKE_CVPPU      R---TR---TNEQVVRSLY----------------------------------------- 654
sp|P27655|SPIKE_CVPR8      R---TR---TNDQFVRSLY----------------------------------------- 432
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sp|P24413|SPIKE_CVPRM      R---TR---TNDQVVRSLY----------------------------------------- 432
sp|Q01977|SPIKE_CVPRT      R---TR---TNEQVVRSLY----------------------------------------- 654
sp|Q9IKD1|SPIKE_CVRSD      S---MLGVGDHCEGLGILEDKCGGSN-----ICNCSADAFVGWAMDSCLSNAR----CHI 588
sp|P10033|SPIKE_FIPV       R---TR---TNEQVVRSLY----------------------------------------- 659
sp|K9N5Q8|SPIKE_MERS1      W---LVASGSTVAMTEQLQ---------------------------------M----GFG 572
sp|P59594|SPIKE_SARS       F---YTTTGIGYQP----Y---------------------------------R----VVV 498
sp|P0DTC2|SPIKE_SARS2      F---QPTNGVGYQP----Y---------------------------------R----VVV 512
sp|Q2KI99|STING_BOVIN      W----LVLHLASQQMGLLIKGICSLAEELCHVHSRY-HGSYWRAVRACLCSSMRCGALLL 100
sp|E1C7U0|STING_CHICK      S----VCTQLAALQLGVLLKGCCCLAEEIFHLHSRH-HGSLWQVLCSCFPPR-WYLALLL 105
sp|Q86WV6|STING_HUMAN      Y----LVLHLASLQLGLLLNGVCSLAEELRHIHSRY-RGSYWRTVRACLGCPLRRGALLL 100
sp|Q3TBT3|STING_MOUSE      Y----LALHLASHELGLLLKNLCCLAEELCHVQSRY-QGSYWKAVRACLGCPIHCMAMIL 100
sp|A7SLZ2|STING_NEMVE      QYSFTFSLAYLAFLVGELLRRCCLFAEEYRHIETRY-NGSLKKAIQTTFSFGHN-NVLFV 112
sp|B8XX90|STING_PIG        W----LVLHLASQQIGLLVKGLCSLAEELCHVHSRY-QSSYWRAARACLGCPIRCGALLL 100
sp|F1M391|STING_RAT        Y----LALHVASQQLGLLLKKLCCLAEELCHVQSRY-QGSYWKAVRACVGSPICFMALIL 100


sp|Q0Q4F2|SPIKE_BC133      IS--VQYGT---GTDSVCPMLDLGDSLTITNRLGKCVDYSLYGVTGRGVFQNCTAVG-VK 631
sp|Q0Q475|SPIKE_BC279      LS--FELLN---APATVCGPKL-----STQLVKNQCVNFNFNGLRGTGVLTTSSKRF-QS 533
sp|Q0Q466|SPIKE_BC512      ----VQHTK--GDIITGTPKPLQGLNDISELHLDTCTTYTIYGFRGDGVIRLTNQTF--- 669
sp|Q3LZX1|SPIKE_BCHK3      LS--FELLN---APATVCGPKL-----STELVKNQCVNFNFNGLKGTGVLTSSSKRF-QS 534
sp|A3EX94|SPIKE_BCHK4      IS--VQYGT---GTDSVCPMLDLGDSLTITNRLGKCVDYSLYGVTGRGVFQNCTAVG-VK 631
sp|A3EXD0|SPIKE_BCHK5      IS--VQYGT---DTNSVCPMQALRNDTSIEDKLDVCVEYSLHGITGRGVFHNCTSVG-LR 624
sp|A3EXG6|SPIKE_BCHK9      IT--LKPAA---GSKLVCPVAN-----DTVVITDRCVQYNLYGYTGTGVLSKNTSLV-IP 553
sp|Q3I5J5|SPIKE_BCRP3      LS--FELLN---APATVCGPKL-----STQLVKNQCVNFNFNGLKGTGVLTESSKRF-QS 533
sp|Q91A26|SPIKE_CVBEN      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P25190|SPIKE_CVBF       FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEANATYYNS 655
sp|P25191|SPIKE_CVBL9      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNAPYYNS 655
sp|Q9QAR5|SPIKE_CVBLS      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|Q8V436|SPIKE_CVBLU      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P25192|SPIKE_CVBLY      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P15777|SPIKE_CVBM       FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|Q9QAQ8|SPIKE_CVBOK      FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P25193|SPIKE_CVBQ       FANFIFHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P25194|SPIKE_CVBV       FANFILHDV---NSGTTCSTDL--QKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNS 655
sp|P36300|SPIKE_CVCAI      ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRKTNSTL--- 710
sp|Q65984|SPIKE_CVCAK      ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGITGVGIIRQTNSTL--- 711
sp|Q7T6T3|SPIKE_CVCBG      ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRNGVGIIRKTNSTL--- 711
sp|P15423|SPIKE_CVH22      ----VSWSD--GDGITGVPQPVEGVSSFMNVTLDKCTKYNIYDVSGVGVIRVSNDTF--- 467
sp|Q5MQD0|SPIKE_CVHN1      FSNFILNGI---NSGTTCSNDL--LQPNTEVFTDVCVDYDLYGITGQGIFKEVSAVYYNS 645
sp|Q14EB0|SPIKE_CVHN2      FSNFIFNGI---NSGTTCSNDL--LYSNTEVSTGVCVNYDLYGITGQGIFKEVSAAYYNN 643
sp|Q0ZME7|SPIKE_CVHN5      FSNFIFNGI---NSGTTCSNDL--LYSNTEISTGVCVNYDLYGITGQGIFKEVSAAYYNN 643
sp|Q6Q1S2|SPIKE_CVHNL      ----VTWSE--GNSITGVPYPVSGIREFSNLVLNNCTKYNIYDYVGTGIIRSSNQSL--- 648
sp|P36334|SPIKE_CVHOC      FANFILHDV---NSGLTCSTDL--QKANTDIILGVCVNYDLYGILGQGIFVEVNATYYNS 645
sp|P22432|SPIKE_CVM4       FANILLNGI---NSGTTCSTDL--QLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNS 656
sp|P11224|SPIKE_CVMA5      FANILLNGI---NSGTTCSTDL--QLPNTEVVTGICVKYDLYGITGQGVFKEVKADYYNS 604
sp|Q02385|SPIKE_CVMJC      FANILLNGI---NSGTTCSTDL--QLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNS 656
sp|P11225|SPIKE_CVMJH      FANILLNGI---NSGTTCSTDL--QLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNS 515
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sp|P18450|SPIKE_CVPFS       ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRSGVGIIRQTNRTL--- 707
sp|P33470|SPIKE_CVPMI       ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRQTNRTL--- 707
sp|P07946|SPIKE_CVPPU       ----VIYEE--GDNIVGVPSDNSGVHDLSVLHLDSCTDYNIYGRTGVGIIRQTNRTL--- 705
sp|P27655|SPIKE_CVPR8       ----VIYEE--GDSIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRQTNRTL--- 483
sp|P24413|SPIKE_CVPRM       ----VIYEE--GDSIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRQTNRTI--- 483
sp|Q01977|SPIKE_CVPRT       ----VIYEE--GDNIVGVPSDNSGVHDLSVLHLDSCTDYNIYGRTGVGIIRKTNRTL--- 705
sp|Q9IKD1|SPIKE_CVRSD       FSNLMLNGI---NSGTTCSTDF--QLPNTEVVTGVCVKYDLYGSTGQGVFKEVKADYYNS 643
sp|P10033|SPIKE_FIPV        ----VIYEE--GDNIVGVPSDNSGLHDLSVLHLDSCTDYNIYGRTGVGIIRRTNSTL--- 710
sp|K9N5Q8|SPIKE_MERS1       IT--VQYGT---DTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVG-VR 626
sp|P59594|SPIKE_SARS        LS--FELLN---APATVCGPKL-----STDLIKNQCVNFNFNGLTGTGVLTPSSKRF-QP 547
sp|P0DTC2|SPIKE_SARS2       LS--FELLH---APATVCGPKK-----STNLVKNKCVNFNFNGLTGTGVLTESNKKF-LP 561
sp|Q2KI99|STING_BOVIN       LSCYFYCSL-----PN-------------------------------------MADLPFT 118
sp|E1C7U0|STING_CHICK       VGGSAYLDP-----PE-------------------------------------DNGHSPR 123
sp|Q86WV6|STING_HUMAN       LSIYFYYSL-----PN-------------------------------------AVGPPFT 118
sp|Q3TBT3|STING_MOUSE       LSSYFYF-L-----QN-------------------------------------TADIYLS 117
sp|A7SLZ2|STING_NEMVE       ASLLFFVVFVASNDPNGSSSVIQGN-STAEPHTEMRQ----------------TSGWQGL 155
sp|B8XX90|STING_PIG         LSCYFYFSI-----RD-------------------------------------KAGLPLP 118
sp|F1M391|STING_RAT         LSFYFYCSL-----EN-------------------------------------TSDLRLA 118


sp|Q0Q4F2|SPIKE_BC133       QQRFVYDSFD---N--LVGY-YSDDGNYYCVRPCVSVPVSVIYDK--STNLHATLFGSVA 683
sp|Q0Q475|SPIKE_BC279       FQQFGRDTSD---FTDSVR--DPQTLEILDISPCSFGGVSVITPGTNASSEVAVLYQDVN 588
sp|Q0Q466|SPIKE_BC512       -LSGVYYTSE---SGQLLAFKNVTTGQIYSVTPCQLVQQVAFVEDRIVGVISSANNTG-- 723
sp|Q3LZX1|SPIKE_BCHK3       FQQFGRDTSD---FTDSVR--DPQTLEILDISPCSFGGVSVITPGTNASSEVAVLYQDVN 589
sp|A3EX94|SPIKE_BCHK4       QQRFVYDSFD---N--LVGY-YSDDGNYYCVRPCVSVPVSVIYDK--STNLHATLFGSVA 683
sp|A3EXD0|SPIKE_BCHK5       NQRFVYDTFD---N--LVGY-HSDNGNYYCVRPCVSVPVSVIYDK--ASNSHATLFGSVA 676
sp|A3EXG6|SPIKE_BCHK9       DGKVFTASS----TGTIIG--VSINSTTYSIMPCVTVPVS---VGYHPNFERALLFNGLS 604
sp|Q3I5J5|SPIKE_BCRP3       FQQFGRDTSD---FTDSVR--DPQTLEILDISPCSFGGVSVITPGTNASSEVAVLYQDVN 588
sp|Q91A26|SPIKE_CVBEN       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P25190|SPIKE_CVBF        WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P25191|SPIKE_CVBL9       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|Q9QAR5|SPIKE_CVBLS       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNFK 708
sp|Q8V436|SPIKE_CVBLU       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P25192|SPIKE_CVBLY       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P15777|SPIKE_CVBM        WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|Q9QAQ8|SPIKE_CVBOK       WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P25193|SPIKE_CVBQ        WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P25194|SPIKE_CVBV        WQNLLYDSNG---N--LYGFRDYLTNRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 708
sp|P36300|SPIKE_CVCAI       -LSGLYYTSL---SGDLLGFKNVSDGVVYSVTPCDVSAQAAVIDGAIVGAMTSINSEL-- 764
sp|Q65984|SPIKE_CVCAK       -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAHAAVIDGAIVGAMTSINSEL-- 765
sp|Q7T6T3|SPIKE_CVCBG       -LSGLYYTSL---SGDLLGFKNVSDGVVYSVTPCEVSAQAAVIDGAIVGAMTSINSEL-- 765
sp|P15423|SPIKE_CVH22       -LNGITYTST---SGNLLGFKDVTKGTIYSITPCNPPDQLVVYQQAVVGAMLSENFTS-- 521
sp|Q5MQD0|SPIKE_CVHN1       WQNLLYDSNG---N--IIGFKDFVTNKTYNIFPCYAGRVSAAFHQ--NASSLALLYRNLK 698
sp|Q14EB0|SPIKE_CVHN2       WQNLLYDSNG---N--IIGFKDFLTNKTYTILPCYSGRVSAAFYQ--NSSSPALLYRNLK 696
sp|Q0ZME7|SPIKE_CVHN5       WQNLLYDSNG---N--IIGFKDFLTNKTYTILPCYSGRVSAAFYQ--NSSSPALLYRNLK 696
sp|Q6Q1S2|SPIKE_CVHNL       -AGGITYVSN---SGNLLGFKNVSTGNIFIVTPCNQPDQVAVYQQSIIGAMTAVNESR-- 702
sp|P36334|SPIKE_CVHOC       WQNLLYDSNG---N--LYGFRDYIINRTFMIRSCYSGRVSAAFHA--NSSEPALLFRNIK 698
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sp|P22432|SPIKE_CVM4           WQALLYDVNG---N--LNGFRDLTTNKTYTIRSCYSGRVSAAYHK--EAPEPALLYRNIN 709
sp|P11224|SPIKE_CVMA5          WQTLLYDVNG---N--LNGFRDLTTNKTYTIRSCYSGRVSAAFHK--DAPEPALLYRNIN 657
sp|Q02385|SPIKE_CVMJC          WQALLYDVNG---N--LNGFRDLTTNKTYTIRSCYSGRVSAAYHK--EAPEPALLYRNIN 709
sp|P11225|SPIKE_CVMJH          WQALLYDVNG---N--LNGFRDLTTNKTYTIRSCYSGRVSAAYHK--EAPEPALLYRNIN 568
sp|P18450|SPIKE_CVPFS          -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAVIDGTIVGAITSINSEL-- 761
sp|P33470|SPIKE_CVPMI          -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAVIDGTIVGAITSINSEL-- 761
sp|P07946|SPIKE_CVPPU          -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAVIDGTIVGAITSINSEL-- 759
sp|P27655|SPIKE_CVPR8          -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAIIDGAIVGAITSINSEL-- 537
sp|P24413|SPIKE_CVPRM          -LSGLYYTSL---SGDLLGFTNVSDGVIYSVTPCDVSAQAAIIDGTIVGAITSINSEL-- 537
sp|Q01977|SPIKE_CVPRT          -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAVIDGTIVGAITSINSEL-- 759
sp|Q9IKD1|SPIKE_CVRSD          WQNLLYDVNG---N--LNGFRDIVTNKTYLLRSCYSGRVSAAYHQ--DAPEPALLYRNLK 696
sp|P10033|SPIKE_FIPV           -LSGLYYTSL---SGDLLGFKNVSDGVIYSVTPCDVSAQAAVIDGAIVGAMTSINSEL-- 764
sp|K9N5Q8|SPIKE_MERS1          QQRFVYDAYQ---N--LVGY-YSDDGNYYCLRACVSVPVSVIYDK--ETKTHATLFGSVA 678
sp|P59594|SPIKE_SARS           FQQFGRDVSD---FTDSVR--DPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVN 602
sp|P0DTC2|SPIKE_SARS2          FQQFGRDIAD---TTDAVR--DPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVN 616
sp|Q2KI99|STING_BOVIN          WML--ALLGLSQALNILLGL-----------QGLAPAEVSAICEKRNFNVAHGL-----A 160
sp|E1C7U0|STING_CHICK          LAL--TLSCLCQLLVLALGL-----------QKLSAVEVSELTESSKKNVAHGL-----A 165
sp|Q86WV6|STING_HUMAN          WML--ALLGLSQALNILLGL-----------KGLAPAEISAVCEKGNFNVAHGL-----A 160
sp|Q3TBT3|STING_MOUSE          WMF--GLLVLYKSLSMLLGL-----------QSLTPAEVSAVCEEKKLNVAHGL-----A 159
sp|A7SLZ2|STING_NEMVE          WGQFIISALLTPLVVHLLGL-----------RELSKVEESQLNEKENKNVADGL-----A 199
sp|B8XX90|STING_PIG            WML--ALLGLSQALNILLGL-----------QHLAPAEVSAICEKRNFNVAHGL-----A 160
sp|F1M391|STING_RAT            WHL--GILVLSKSLSMTLDL-----------QSLAPAEVSAVCEEKNFNVAHGL-----A 160
                                                                                   .

sp|Q0Q4F2|SPIKE_BC133          CEHVTTMMSQFSRLTQSNLRRRD-SNTPLQTAVGCVIGLSNN-SLVVSDCKLPLGQSLCA 741
sp|Q0Q475|SPIKE_BC279          CTDVPTSIHADQL--TPAWRVYSTGVNVFQTQAGCLIGAEHVNA--SYECDIPIGAGICA 644
sp|Q0Q466|SPIKE_BC512          --F-FNST-----RTFPGFYYHSNDTTN--------------CTSPR---LVYSNIGVCT 758
sp|Q3LZX1|SPIKE_BCHK3          CTDVPTAIRADQL--TPAWRVYSTGVNVFQTQAGCLIGAEHVNA--SYECDIPIGAGICA 645
sp|A3EX94|SPIKE_BCHK4          CEHVTTMMSQFSRLTQSNLRRRD-SNIPLQTAVGCVIGLSNN-SLVVSDCKLPLGQSLCA 741
sp|A3EXD0|SPIKE_BCHK5          CSHVTTMMSQFSRMTKTNLLART-TPGPLQTTVGCAMGFINS-SMVVDECQLPLGQSLCA 734
sp|A3EXG6|SPIKE_BCHK9          CSQRSRAVT-EPV--SVLWSASATAQDAFDTPSGCVVNVELRNTTIVNTCAMPIGNSLCF 661
sp|Q3I5J5|SPIKE_BCRP3          CTDVPAAIHADQL--TPAWRVYSTGTNVFQTQAGCLIGAEHVNA--SYECDIPIGAGICA 644
sp|Q91A26|SPIKE_CVBEN          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|P25190|SPIKE_CVBF           CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTASAVQTCDLTVGSGYCV 758
sp|P25191|SPIKE_CVBL9          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|Q9QAR5|SPIKE_CVBLS          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|Q8V436|SPIKE_CVBLU          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|P25192|SPIKE_CVBLY          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSAVQTCDLTVGSGYCV 758
sp|P15777|SPIKE_CVBM           CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|Q9QAQ8|SPIKE_CVBOK          CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|P25193|SPIKE_CVBQ           CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|P25194|SPIKE_CVBV           CNYVFNNTL----------SRQLQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCV 758
sp|P36300|SPIKE_CVCAI          --LGLTHW-----TTTPNFYYYSIYNYTNVMNRGTAI-DNDIDCEPI---ITYSNIGVCK 813
sp|Q65984|SPIKE_CVCAK          --LGLTHW-----TTTPNFYYYSIYNYTNERTRGTAIDSNDVDCEPI---ITYSNIGVCK 815
sp|Q7T6T3|SPIKE_CVCBG          --LGLTHW-----TTTPNFYYYSIYNYTNERVRGTVTDSNDVDCEPI---ITYSNIGVCK 815
sp|P15423|SPIKE_CVH22          --YGFSNV-----VELPKFFYASNGTYN--------------CTDAV---LTYSSFGVCA 557
sp|Q5MQD0|SPIKE_CVHN1          CSYVLNNI-----------SLTTQ-P-YFDSYLGCVFNADNLTDYSVSSCALRMGSGFCV 745
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sp|Q14EB0|SPIKE_CVHN2      CSYVLNNI-----------SFISQ-PFYFDSYLGCVLNAVNLTSYSVSSCDLRMGSGFCI 744
sp|Q0ZME7|SPIKE_CVHN5      CSYVLNNI-----------SFISQ-PFYFDSYLGCVLNAVNLTSYSVSSCDLRMGSGFCI 744
sp|Q6Q1S2|SPIKE_CVHNL      --YGLQNL-----LQLPNFYYVSNGGNN--------------CTTAV---MTYSNFGICA 738
sp|P36334|SPIKE_CVHOC      CNYVFNNSL----------TRQLQPINYFDSYLGCVVNAYNSTAISVQTCDLTVGSGYCV 748
sp|P22432|SPIKE_CVM4       CSYVFTNNI----------SREENPLNYFDSYLGCVVNADNRTDEALPNCDLRMGAGLCV 759
sp|P11224|SPIKE_CVMA5      CSYVFSNNI----------SREENPLNYFDSYLGCVVNADNRTDEALPNCDLRMGAGLCV 707
sp|Q02385|SPIKE_CVMJC      CSYVFTNNI----------SREENPLNYFDSYLGCVVNADNRPDEALPNCDLRMGAGLCV 759
sp|P11225|SPIKE_CVMJH      CSYVFTNNI----------SREENPLNYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCV 618
sp|P18450|SPIKE_CVPFS      --LGLTHW-----TTTPNFYYYSIYNYTNDMTRGTAIDSNDVDCEPV---ITYSNIGVCK 811
sp|P33470|SPIKE_CVPMI      --LGLTHW-----TTTPNFYYYSIYNYTNDRTRGTAIDSNDVDCEPV---ITYSNIGVCK 811
sp|P07946|SPIKE_CVPPU      --LGLTHW-----TTTPNFYYYSIYNYTNDRTRGTAIDSNDVDCEPV---ITYSNIGVCK 809
sp|P27655|SPIKE_CVPR8      --LALTHW-----TITPNFYYYSIYNYTNDKTRGTPIGSNDVDCEPV---ITYSNIGVCK 587
sp|P24413|SPIKE_CVPRM      --LGLTHW-----TTTPNFYYYSIYNYTNDKTRGTPIGSNDVDCEPV---ITYSNIGVCK 587
sp|Q01977|SPIKE_CVPRT      --LGLTHW-----TTTPNFYYYSIYNYTNDRTRGTAIDSNDVDCEPV---ITYSNIGVCK 809
sp|Q9IKD1|SPIKE_CVRSD      CDYVFNNNI----------SREETPLNYFDSYLGCVINADNSTEQSVDACDLRMGSGLCV 746
sp|P10033|SPIKE_FIPV       --LGLTHW-----TTTPNFYYYSIYNYTSERTRGTAIDSNDVDCEPV---ITYSNIGVCK 814
sp|K9N5Q8|SPIKE_MERS1      CEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGLVNS-SLFVEDCKLPLGQSLCA 737
sp|P59594|SPIKE_SARS       CTDVSTAIHADQL--TPAWRIYSTGNNVFQTQAGCLIGAEHVDT--SYECDIPIGAGICA 658
sp|P0DTC2|SPIKE_SARS2      CTEVPVAIHADQL--TPTWRVYSTGSNVFQTRAGCLIGAEHVNN--SYECDIPIGAGICA 672
sp|Q2KI99|STING_BOVIN      WSYY----IGYLRLILPGLPARIQIYNQFHNNTLQGAGSHRLHILFPLDCGVPDDLNVAD 216
sp|E1C7U0|STING_CHICK      WSYY----IGYLKVVLPRLKECMEELSRTNPMLRAHRDTWKLHILVPLGCDIWDDLEKAD 221
sp|Q86WV6|STING_HUMAN      WSYY----IGYLRLILPELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLSMAD 216
sp|Q3TBT3|STING_MOUSE      WSYY----IGYLRLILPGLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDNLSVVD 215
sp|A7SLZ2|STING_NEMVE      WSYY----FGYLKFVLPELEKQIEKTSKFRSK---EKFVKKMFILIPSNCFWDDKIPGSD 252
sp|B8XX90|STING_PIG        WSYY----IGYLRLILPGLRARIQAYNQRHKNVLGGIGNHRLHILFPLDCGVPDDLSVAD 216
sp|F1M391|STING_RAT        WSYY----IGYLKLILPGLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDDLSVAD 216


sp|Q0Q4F2|SPIKE_BC133      ---------VPPVSMFR-SY-----SASQFQLAV-LNYTSPIVV--TPINSSGFTAAIPT 783
sp|Q0Q475|SPIKE_BC279      ---------SYHTAS-----VLR----STGQKSI-VAYTMSLGAEN-SIAYANNSIAIPT 684
sp|Q0Q466|SPIKE_BC512      ---------SGAIGLLS--------------------PKAA-QPQVQPMF--QGNISIPT 786
sp|Q3LZX1|SPIKE_BCHK3      ---------SYHTAS-----VLR----STGQKSI-VAYTMSLGAEN-SIAYANNSIAIPT 685
sp|A3EX94|SPIKE_BCHK4      ---------VPPVSTFR-SY-----SASQFQLAV-LNYTSPIVV--TPINSSGFTAAIPT 783
sp|A3EXD0|SPIKE_BCHK5      ---------IPPTTSSR-VRRATSGASDVFQIAT-LNFTSPLTL--APINSTGFVVAVPT 781
sp|A3EXG6|SPIKE_BCHK9      ---------INGSIATA---NAD----SLPRLQL-VNYDPLYDNSTATPMTPVYWVKVPT 704
sp|Q3I5J5|SPIKE_BCRP3      ---------SYHTAS-----TLR----SVGQKSI-VAYTMSLGAEN-SIAYANNSIAIPT 684
sp|Q91A26|SPIKE_CVBEN      ---------DYST-----KRRSRRSITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P25190|SPIKE_CVBF       ---------DYST-----KRRSVRAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P25191|SPIKE_CVBL9      ---------DYST-----KRRSRRAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|Q9QAR5|SPIKE_CVBLS      ---------DYST-----KRRSRRSITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|Q8V436|SPIKE_CVBLU      ---------DYST-----KRRSRRSITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P25192|SPIKE_CVBLY      ---------DYST-----KRRSRRAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P15777|SPIKE_CVBM       ---------DYST-----KRRSRRAITTGYRFTTFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|Q9QAQ8|SPIKE_CVBOK      ---------DYST-----KRRSRRSITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P25193|SPIKE_CVBQ       ---------DYST-----KRRSRRAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P25194|SPIKE_CVBV       ---------DYST-----KRRSRRAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 804
sp|P36300|SPIKE_CVCAI      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 841
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sp|Q65984|SPIKE_CVCAK      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 843
sp|Q7T6T3|SPIKE_CVCBG      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 843
sp|P15423|SPIKE_CVH22      ---------DGSIIAVQ--------------------PRNVSYDSVSAIV--TANLSIPS 586
sp|Q5MQD0|SPIKE_CVHN1      ---------DYNSPSSSSSRRKRRSISASYRFVTFEPFNVSFVNDSIESVGGLYEIKIPT 796
sp|Q14EB0|SPIKE_CVHN2      ---------DYALPS---SRRKRRGISSPYRFVTFEPFNVSFVNDSVETVGGLFEIQIPT 792
sp|Q0ZME7|SPIKE_CVHN5      ---------DYALPS---SRRKRRGISSPYRFVTFEPFNVSFVNDSVETVGGLFEIQIPT 792
sp|Q6Q1S2|SPIKE_CVHNL      ---------DGSLIPVR--------------------PRNSSDNGISAII--TANLSIPS 767
sp|P36334|SPIKE_CVHOC      ---------DYSK-----NRRSRGAITTGYRFTNFEPFTVNSVNDSLEPVGGLYEIQIPS 794
sp|P22432|SPIKE_CVM4       ---------DYSK-----SRRARRSVSTGYRLTTFEPYMPMLVNDSVQSVGGLYEMQIPT 805
sp|P11224|SPIKE_CVMA5      ---------DYSK-----SRRAHRSVSTGYRLTTFEPYTPMLVNDSVQSVDGLYEMQIPT 753
sp|Q02385|SPIKE_CVMJC      ---------DYSK-----SRRARRSVSTGYRLTTFEPYMPMLVNDSVQSVGGLYEMQIPT 805
sp|P11225|SPIKE_CVMJH      ---------DYSK-----SRRARRSVSTGYRLTTFEPYMPMLVNDSVQSVGGLYEMQIPT 664
sp|P18450|SPIKE_CVPFS      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 839
sp|P33470|SPIKE_CVPMI      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 839
sp|P07946|SPIKE_CVPPU      ---------NGAFVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 837
sp|P27655|SPIKE_CVPR8      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 615
sp|P24413|SPIKE_CVPRM      ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 615
sp|Q01977|SPIKE_CVPRT      ---------NGAFVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 837
sp|Q9IKD1|SPIKE_CVRSD      ---------NYSI-----AHRARRSVSTGYKLTTFEPFTVSIVNDSVESVGGLYEMQIPT 792
sp|P10033|SPIKE_FIPV       ---------NGALVFIN--------------------VTHS-DGDVQPIS--TGNVTIPT 842
sp|K9N5Q8|SPIKE_MERS1      ---------LPDTPSTL-TPRSVRSVPGEMRLAS-IAFNHPIQV--DQLNSSYFKLSIPT 784
sp|P59594|SPIKE_SARS       ---------SYHTVS-----LLR----STSQKSI-VAYTMSLGADS-SIAYSNNTIAIPT 698
sp|P0DTC2|SPIKE_SARS2      ---------SYQTQTNS-PRRAR----SVASQSI-IAYTMSLGAEN-SVAYSNNSIAIPT 716
sp|Q2KI99|STING_BOVIN      ----PNIRFLHELPQQS---ADRA----GIKGR---VYTNS-----------IYELLENG 251
sp|E1C7U0|STING_CHICK      ----SNIQYLADLPETI---LTRA----GIKRR---VYKHS-----------LYVIRDKD 256
sp|Q86WV6|STING_HUMAN      ----PNIRFLDKLPQQT---GDHA----GIKDR---VYSNS-----------IYELLENG 251
sp|Q3TBT3|STING_MOUSE      ----PNIRFRDMLPQQN---IDRA----GIKNR---VYSNS-----------VYEILENG 250
sp|A7SLZ2|STING_NEMVE      YDPQNRITFEGNTEPLE---KTRG----GVFLR---HYKHS-----------VYEIKDGE 291
sp|B8XX90|STING_PIG        ----PNIRFLHELPQQS---ADRA----GIKGR---VYTNS-----------IYELLENG 251
sp|F1M391|STING_RAT        ----PNIRFRDMLPQQN---TDRA----GVKNR---AYSNS-----------VYELLENG 251


sp|Q0Q4F2|SPIKE_BC133      NFSFSLTQEYIETSIQKVTVDCKQYVCNGFTRCEKLLVEYGQFCSKINQALHGANLRQDE 843
sp|Q0Q475|SPIKE_BC279      NFSISVTTEVMPVSIAKTSVDCTMYICGDSLECSNLLLQYGSFCTQLNRALTGIAIEQDK 744
sp|Q0Q466|SPIKE_BC512      NFTMSVRTEYIQLFNKPVSVDCAMYVCNGNDRCKQLLSQYTSACKNIESALQLSARLESM 846
sp|Q3LZX1|SPIKE_BCHK3      NFSISVTTEVMPVSMAKTAVDCTMYICGDSLECSNLLLQYGSFCTQLNRALTGIAIEQDK 745
sp|A3EX94|SPIKE_BCHK4      NFSFSVTQEYIETSIQKVTVDCKQYVCNGFTRCEKLLVEYGQFCSKINQALHGANLRQDE 843
sp|A3EXD0|SPIKE_BCHK5      NFTFGVTQEFIETTIQKITVDCKQYVCNGFKKCEDLLKEYGQFCSKINQALHGANLRQDE 841
sp|A3EXG6|SPIKE_BCHK9      NFTLSATEEYIQTTAPKITIDCARYLCGDSSRCLNVLLHYGTFCNDINKALSRVSTILDS 764
sp|Q3I5J5|SPIKE_BCRP3      NFSISVTTEVMPVSMAKTSVDCTMYICGDSLECSNLLLQYGSFCTQLNRALSGIAIEQDK 744
sp|Q91A26|SPIKE_CVBEN      EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P25190|SPIKE_CVBF       EFTIGNMEEFIQTSSPKVTIDCSAFVCGDCAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P25191|SPIKE_CVBL9      EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|Q9QAR5|SPIKE_CVBLS      EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|Q8V436|SPIKE_CVBLU      EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P25192|SPIKE_CVBLY      EFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P15777|SPIKE_CVBM       EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
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sp|Q9QAQ8|SPIKE_CVBOK           EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P25193|SPIKE_CVBQ            EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P25194|SPIKE_CVBV            EFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 864
sp|P36300|SPIKE_CVCAI           NFTISVQVEYIQVYTTPVSIDCARYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 901
sp|Q65984|SPIKE_CVCAK           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 903
sp|Q7T6T3|SPIKE_CVCBG           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNSRCNKLLTQYVSACHTIEQALAMGARLENM 903
sp|P15423|SPIKE_CVH22           NWTTSVQVEYLQITSTPIVVDCSTYVCNGNVRCVELLKQYTSACKTIEDALRNSARLESA 646
sp|Q5MQD0|SPIKE_CVHN1           NFTIVGQEEFIQTNSPKVTIDCSLFVCSNYAACHDLLSEYGTFCDNINSILDEVNGLLDT 856
sp|Q14EB0|SPIKE_CVHN2           NFTIAGHEEFIQTSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDI 852
sp|Q0ZME7|SPIKE_CVHN5           NFTIAGHEEFIQTSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDI 852
sp|Q6Q1S2|SPIKE_CVHNL           NWTTSVQVEYLQITSTPIVVDCATYVCNGNPRCKNLLKQYTSACKTIEDALRLSAHLETN 827
sp|P36334|SPIKE_CVHOC           EFTIGNMVEFIQTSSPKVTIDCAAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELLDT 854
sp|P22432|SPIKE_CVM4            NFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLVEYGSFCDNVNAILNEVNNLLDN 865
sp|P11224|SPIKE_CVMA5           NFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNEVNNLLDN 813
sp|Q02385|SPIKE_CVMJC           NFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLVEYGSFCDNVNAILNEVNNLLDN 865
sp|P11225|SPIKE_CVMJH           NFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACRQQLVEYGSFCDNVNAILNEVNNLLDN 724
sp|P18450|SPIKE_CVPFS           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAVGARLENM 899
sp|P33470|SPIKE_CVPMI           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 899
sp|P07946|SPIKE_CVPPU           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 897
sp|P27655|SPIKE_CVPR8           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 675
sp|P24413|SPIKE_CVPRM           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 675
sp|Q01977|SPIKE_CVPRT           NFTISVQVEYIQVYTTPVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 897
sp|Q9IKD1|SPIKE_CVRSD           NFTIASHQEFIQTRSPKVTIDCAAFVCGDYTACRQQLVDYGSFCDNINAILGEVNNLIDT 852
sp|P10033|SPIKE_FIPV            NFTISVQVEYMQVYTTPVSIDCARYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLENM 902
sp|K9N5Q8|SPIKE_MERS1           NFSFGVTQEYIQTTIQKVTVDCKQYVCNGFQKCEQLLREYGQFCSKINQALHGANLRQDD 844
sp|P59594|SPIKE_SARS            NFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDR 758
sp|P0DTC2|SPIKE_SARS2           NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK 776
sp|Q2KI99|STING_BOVIN           QRAGVCVLEYA--TPLQTLFAMSQDGRAGFSR-EDRLEQAKLFCRTLEDILANAPESQNN 308
sp|E1C7U0|STING_CHICK           NKLRPCVLEFA--SPLQTLCAMSQDDCAAFSR-EQRLEQARLFYRSLRDILGSSKECAGL 313
sp|Q86WV6|STING_HUMAN           QRAGTCVLEYA--TPLQTLFAMSQYSQAGFSR-EDRLEQAKLFCRTLEDILADAPESQNN 308
sp|Q3TBT3|STING_MOUSE           QPAGVCILEYA--TPLQTLFAMSQDAKAGFSR-EDRLEQAKLFCRTLEEILEDVPESRNN 307
sp|A7SLZ2|STING_NEMVE           NEPWFCIMEYA--TPLLTLYDMSVAQPGELSR-EERDAQVVVFLRKLQDILEGDRACQGK 348
sp|B8XX90|STING_PIG             QPAGVCVLGYA--TPLQTLFAMSQDGRAGFSR-EDRLEQAKLFCRTLEDILADAPEAQNN 308
sp|F1M391|STING_RAT             QPAGACILEYA--TPLQTLFAMSQDGKAGFSR-EDRLEQAKLFCRTLEEILADVPESRNH 308
                                :                                 .   .       :.  *

sp|Q0Q4F2|SPIKE_BC133           SVYSLYS----NI------------KTTST-Q----------TLEYGLNGDFNLTLLQ-V 875
sp|Q0Q475|SPIKE_BC279           NTQEVFA----QV------------K--QMYK----------TPAIKDFGGFNFSQI--- 773
sp|Q0Q466|SPIKE_BC512           EVNSMLTVSDEAL------------KLATISQFPGG--------------GYNFTNILPA 880
sp|Q3LZX1|SPIKE_BCHK3           NTQEVFA----QV------------K--QMYK----------TPAIKDFGGFNFSQI--- 774
sp|A3EX94|SPIKE_BCHK4           SVYSLYS----NI------------KTTST-Q----------TLEYGLNGDFNLTLLQ-V 875
sp|A3EXD0|SPIKE_BCHK5           SIANLFS----SI------------KTQNT-Q----------PLQAGLNGDFNLTMLQ-I 873
sp|A3EXG6|SPIKE_BCHK9           ALLSLVK----EL------------SINTRDE----------VTTFSFDGDYNFTGLMGC 798
sp|Q3I5J5|SPIKE_BCRP3           NTQEVFA----QV------------K--QMYK----------TPAIKDFGGFNFSQI--- 773
sp|Q91A26|SPIKE_CVBEN           TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P25190|SPIKE_CVBF            TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P25191|SPIKE_CVBL9           TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
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sp|Q9QAR5|SPIKE_CVBLS      TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|Q8V436|SPIKE_CVBLU      TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P25192|SPIKE_CVBLY      TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P15777|SPIKE_CVBM       TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|Q9QAQ8|SPIKE_CVBOK      TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P25193|SPIKE_CVBQ       TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P25194|SPIKE_CVBV       TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 902
sp|P36300|SPIKE_CVCAI      EIDSMLFVSENAL------------KLASVEAFNSTENLDPIYKEWPNIGGSWLGGLKDI 949
sp|Q65984|SPIKE_CVCAK      EIDSMLFVSENAL------------KLASVEAFNSTETLDPIYKEWPNIGGSWLGGLKDI 951
sp|Q7T6T3|SPIKE_CVCBG      EIDSMLFVSENAL------------KLASVEAFNSTDNLDPIYREWPNIGGSWLGGLKDI 951
sp|P15423|SPIKE_CVH22      DVSEMLTFDKKAF------------TLANVSSF--G--------------DYNLSSVIPS 678
sp|Q5MQD0|SPIKE_CVHN1      TQLHVADTLMQGV------------TLSSNLN----------TNLHFDVDNINFKSLVGC 894
sp|Q14EB0|SPIKE_CVHN2      TQLQVANALMQGV------------TLSSNLN----------TNLHSDVDNIDFKSLLGC 890
sp|Q0ZME7|SPIKE_CVHN5      TQLQVANALMQGV------------TLSSNLN----------TNLHSDVDNIDFKSLLGC 890
sp|Q6Q1S2|SPIKE_CVHNL      DVSSMLTFDSNAF------------SLANVTSF--G--------------DYNLSSVLPQ 859
sp|P36334|SPIKE_CVHOC      TQLQVANSLMNGV------------TLSTKLK----------DGVNFNVDDINFSPVLGC 892
sp|P22432|SPIKE_CVM4       MQLQVASALMQGV------------TISSRLP----------DGISGPIDDINFSPLLGC 903
sp|P11224|SPIKE_CVMA5      MQLQVASALMQGV------------TISSRLP----------DGISGPIDDINFSPLLGC 851
sp|Q02385|SPIKE_CVMJC      MQLQVASALMQGV------------TISSRLP----------DGISGPIDDINFSPLLGC 903
sp|P11225|SPIKE_CVMJH      MQLQVASALMQGV------------TISSRLP----------DGISGPIDDINFSPLLGC 762
sp|P18450|SPIKE_CVPFS      EVDSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGSWLEGLKYI 947
sp|P33470|SPIKE_CVPMI      EVGSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGSWLEGLKYI 947
sp|P07946|SPIKE_CVPPU      EVDSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGSWLEGLKYI 945
sp|P27655|SPIKE_CVPR8      EVDSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGFWLEGLKYI 723
sp|P24413|SPIKE_CVPRM      EVDSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGFWLEGLKYI 723
sp|Q01977|SPIKE_CVPRT      EVDSMLFVSENAL------------KLASVEAFNSSETLDPIYKEWPNIGGSWLEGLKYI 945
sp|Q9IKD1|SPIKE_CVRSD      MQLQVASALIQGV------------TLSSRLA----------DGISGQIDDINFSPLLGC 890
sp|P10033|SPIKE_FIPV       EVDSMLFVSENAL------------KLASVEAFNSTENLDPIYKEWPSIGGSWLGGLKDI 950
sp|K9N5Q8|SPIKE_MERS1      SVRNLFA----SV------------KSSQS-S----------PIIPGFGGDFNLTLLE-P 876
sp|P59594|SPIKE_SARS       NTREVFA----QV------------K--QMYK----------TPTLKYFGGFNFSQI--- 787
sp|P0DTC2|SPIKE_SARS2      NTQEVFA----QV------------K--QIYK----------TPPIKDFGGFNFSQI--- 805
sp|Q2KI99|STING_BOVIN      CRLIVYQEPAEGSSFSLSQEILQHLRQEER-EVTMGSTETS---VMP---GSSVLSQEPE 361
sp|E1C7U0|STING_CHICK      YRLIAYEEPAEPESHFLSGLILWHLQQQREEYMVQEELP------------LGTSSVELS 362
sp|Q86WV6|STING_HUMAN      CRLIAYQEPADDSSFSLSQEVLRHLRQEEKEEVTVGSLKTS---AVP---STSTMSQEPE 362
sp|Q3TBT3|STING_MOUSE      CRLIVYQEPTDGNSFSLSQEVLRHIRQEEKEEVTMNAPMTS---VAP---PPSVLSQEPR 361
sp|A7SLZ2|STING_NEMVE      YELVTFSPDRDLA-----DVMLRKLKDSE---LEIGG----------------------- 377
sp|B8XX90|STING_PIG        CRLIVYQEPTEGGSFSLSQEILRHLRQEER-EVTMGSAETS---VVP---TSSTLSQEPE 361
sp|F1M391|STING_RAT        CRLIVYQESEEGNSFSLSQEVLRHIRQEEKEEVTMSGPPTS---VAP---RPSLLSQEPR 362


sp|Q0Q4F2|SPIKE_BC133      PQIGGS---------SYRSAIEDLLFDKVTIADPGYM-QGYDDCMKQG-PQSARDLICAQ 924
sp|Q0Q475|SPIKE_BC279      -LPDPSK-------PTKRSFIEDLLFNKVTLADAGFM-KQYGECLGDI---SARDLICAQ 821
sp|Q0Q466|SPIKE_BC512      NP-------------GARSVIEDILFDKVVTSGLGTVDEDYKRCSNGL---SIADLACAQ 924
sp|Q3LZX1|SPIKE_BCHK3      -LPDPSK-------PTKRSFIEDLLFNKVTLADAGFM-KQYGDCLGDV---SARDLICAQ 822
sp|A3EX94|SPIKE_BCHK4      PQIGGSS-------SSYRSAIEDLLFDKVTIADPGYM-QGYDDCMKQG-PQSARDLICAQ 926
sp|A3EXD0|SPIKE_BCHK5      PQVTTGE-------RKYRSTIEDLLFNKVTIADPGYM-QGYDECMQQG-PQSARDLICAQ 924
sp|A3EXG6|SPIKE_BCHK9      LGPNCGA-------TTYRSAFSDLLYDKVRITDPGFM-QSYQKCIDSQWGGSIRDLLCTQ 850
```

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sp|Q3I5J5|SPIKE_BCRP3      -LPDPSK-------PTKRSFIEDLLFNKVTLADAGFM-KQYGECLGDI---SARDLICAQ 821
sp|Q91A26|SPIKE_CVBEN      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P25190|SPIKE_CVBF       LGSECNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P25191|SPIKE_CVBL9      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|Q9QAR5|SPIKE_CVBLS      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|Q8V436|SPIKE_CVBLU      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P25192|SPIKE_CVBLY      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P15777|SPIKE_CVBM       LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|Q9QAQ8|SPIKE_CVBOK      LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P25193|SPIKE_CVBQ       LGSACNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P25194|SPIKE_CVBV       LGSDCNK-------VSSRSAIEDLLFSKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 951
sp|P36300|SPIKE_CVCAI      LPSHNSK-------RKYRSAIEDLLFDKVVTSGLGTVDEDYKRSAGGY---DIADLVCAR 999
sp|Q65984|SPIKE_CVCAK      LPSHNSK-------RKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 1001
sp|Q7T6T3|SPIKE_CVCBG      LPSHNSK-------RKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 1001
sp|P15423|SPIKE_CVH22      LPTSGSR-------VAGRSAIEDILFSKLVTSGLGTVDADYKKCTKGL---SIADLACAQ 728
sp|Q5MQD0|SPIKE_CVHN1      LGPHCGS--------SSRSFFEDLLFDKVKLSDVGFV-EAYNNCTGGS---EIRDLLCVQ 942
sp|Q14EB0|SPIKE_CVHN2      LGSQCGS--------SSRSLLEDLLFNKVKLSDVGFV-EAYNNCTGGS---EIRDLLCVQ 938
sp|Q0ZME7|SPIKE_CVHN5      LGSQCGS--------SSRSLLEDLLFNKVKLSDVGFV-EAYNNCTGGS---EIRDLLCVQ 938
sp|Q6Q1S2|SPIKE_CVHNL      RNIRSSR-------IAGRSALEDLLFSKVVTSGLGTVDVDYKSCTKGL---SIADLACAQ 909
sp|P36334|SPIKE_CVHOC      LGSECSK-------ASSRSAIEDLLFDKVKLSDVGFV-EAYNNCTGGA---EIRDLICVQ 941
sp|P22432|SPIKE_CVM4       IGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFV-EAYNNCTGGQ---EVRDLLCVQ 959
sp|P11224|SPIKE_CVMA5      IGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFV-EAYNNCTGGQ---EVRDLLCVQ 907
sp|Q02385|SPIKE_CVMJC      IGSTCAEDGNGPSAMRGRSAIEDLLFDKVKLSDVGFV-EAYNNCTGGQ---EVRDLLCVQ 959
sp|P11225|SPIKE_CVMJH      IGSTCAEDGNGPSAIRGRSAIEDLLFDKVKLSDVGFV-EAYNNCTGGQ---EVRDLLCVQ 818
sp|P18450|SPIKE_CVPFS      LPSDNSK-------RKYRSAIEDLLFSKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 997
sp|P33470|SPIKE_CVPMI      LPSDNSK-------RKYRSAIEDLLFAKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 997
sp|P07946|SPIKE_CVPPU      LPSHNSK-------RKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 995
sp|P27655|SPIKE_CVPR8      LPSDNSK-------RKYRSAIEDLLFSKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 773
sp|P24413|SPIKE_CVPRM      LPSDNSK-------RKYRSAIEDLLFSKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 773
sp|Q01977|SPIKE_CVPRT      LPSHNSK-------RKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 995
sp|Q9IKD1|SPIKE_CVRSD      LGSDCSE---GTKAAQGRSAIEDVLFDKVKLSDVGFV-ESYNNCTGGQ---EVRDLLCVQ 943
sp|P10033|SPIKE_FIPV       LPSHNSK-------RKYGSAIEDLLFDKVVTSGLGTVDEDYKRCTGGY---DIADLVCAQ 1000
sp|K9N5Q8|SPIKE_MERS1      VSISTGS-------RSARSAIEDLLFDKVTIADPGYM-QGYDDCMQQG-PASARDLICAQ 927
sp|P59594|SPIKE_SARS       -LPDPLK-------PTKRSFIEDLLFNKVTLADAGFM-KQYGECLGDI---NARDLICAQ 835
sp|P0DTC2|SPIKE_SARS2      -LPDPSK-------PSKRSFIEDLLFNKVTLADAGFI-KQYGDCLGDI---AARDLICAQ 853
sp|Q2KI99|STING_BOVIN      LLISGLE-----KPLPLRSDV---F----------------------------------- 378
sp|E1C7U0|STING_CHICK      LQVSSSD-----LPQPLRSDC---P----------------------------------- 379
sp|Q86WV6|STING_HUMAN      LLISGME-----KPLPLRTDF---S----------------------------------- 379
sp|Q3TBT3|STING_MOUSE      LLISGMD-----QPLPLRTDL---I----------------------------------- 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        LLISGME-----QPLPLRSDI---F----------------------------------- 378
sp|F1M391|STING_RAT        LLISGME-----QPLPLRTDL---I----------------------------------- 379


sp|Q0Q4F2|SPIKE_BC133      YVSGYKVLPPLYDPNMEAAYTSSLLGSIAGAGWTAGLSSFAAIPFAQSMFYRLNGVGITQ 984
sp|Q0Q475|SPIKE_BC279      KFNGLTVLPPLLTDEMIAAYTAALVSGTATAGWTFGAGSALQIPFAMQMAYRFNGIGVTQ 881
sp|Q0Q466|SPIKE_BC512      HYNGIMVLPGVADWEKVHMYSASLVGGMTLGGIT---S-AAALPFSYAVQARLNYVALQT 980
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sp|Q3LZX1|SPIKE_BCHK3      KFNGLTVLPPLLTDEMVAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQ 882
sp|A3EX94|SPIKE_BCHK4      YVSGYKVLPPLYDPNMEAAYTSSLLGSIAGAGWTAGLSSFAAIPFAQSMFYRLNGVGITQ 986
sp|A3EXD0|SPIKE_BCHK5      YVAGYKVLPPLYDPYMEAAYTSSLLGSIAGASWTAGLSSFAAIPFAQSIFYRLNGVGITQ 984
sp|A3EXG6|SPIKE_BCHK9      TYNGIAVLPPIVSPAMQALYTSLLVGAVASSGYTFGITSAGVIPFATQLQFRLNGIGVTT 910
sp|Q3I5J5|SPIKE_BCRP3      KFNGLTVLPPLLTDEMIAAYTAALVSGTATAGWTFGAGSALQIPFAMQMAYRFNGIGVTQ 881
sp|Q91A26|SPIKE_CVBEN      SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P25190|SPIKE_CVBF       SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P25191|SPIKE_CVBL9      SYNGIKVLPPLLSVNQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|Q9QAR5|SPIKE_CVBLS      SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|Q8V436|SPIKE_CVBLU      SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P25192|SPIKE_CVBLY      SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P15777|SPIKE_CVBM       SYNGIKVLPPLLSVNQISGYTLAATSASLFPPLS----AAVGVPFYLNVQYRINGIGVTM 1007
sp|Q9QAQ8|SPIKE_CVBOK      SYNGIKVLPPLLSENQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P25193|SPIKE_CVBQ       SYNGIKVLPPLLSVNQISGYTLAATSASLFPPLS----AAVGVPFYLNVQYRINGIGVTM 1007
sp|P25194|SPIKE_CVBV       SYNGIKVLPPLLSVNQISGYTLAATSASLFPPWS----AAAGVPFYLNVQYRINGIGVTM 1007
sp|P36300|SPIKE_CVCAI      YYNGIMVLPGVANDDKMTMYTASLTGGITLGALS---GGAVAIPFAVAVQARLNYVALQT 1056
sp|Q65984|SPIKE_CVCAK      YYNGIMVLPGVANDDKMAMYTASLAGGITLGSLG---GGAVSIPFAIAVQARLNYVALQT 1058
sp|Q7T6T3|SPIKE_CVCBG      YYNGIMVLPGVANDDKMAMYTASLAGGITLGALG---GGAVSIPFAVAVQARLNYVALQT 1058
sp|P15423|SPIKE_CVH22      YYNGIMVLPGVADAERMAMYTGSLIGGIALGGLT---S-AVSIPFSLAIQARLNYVALQT 784
sp|Q5MQD0|SPIKE_CVHN1      SFNGIKVLPPILSESQISGYTTAATVAAMFPPWS----AAAGIPFSLNVQYRINGLGVTM 998
sp|Q14EB0|SPIKE_CVHN2      SFNGIKVLPPILSETQISGYTTAATVAAMFPPWS----AAAGVPFSLNVQYRINGLGVTM 994
sp|Q0ZME7|SPIKE_CVHN5      SFNGIKVLPPILSETQISGYTTAATVAAMFPPWS----AAAGVPFSLNVQYRINGLGVTM 994
sp|Q6Q1S2|SPIKE_CVHNL      YYNGIMVLPGVADAERMAMYTGSLIGGMVLGGLT---S-AAIPFSLALQARLNYVALQT 965
sp|P36334|SPIKE_CVHOC      SYKGIKVLPPLLSENQISGYTLAATSASLFPPWT----AAAGVPFYLNVQYRINGLGVTM 997
sp|P22432|SPIKE_CVM4       SFNGIKVLPPVLSESQISGYTAGATAAAMFPPWT----AAAGVPFSLNVQYRINGLGVTM 1015
sp|P11224|SPIKE_CVMA5      SFNGIKVLPPVLSESQISGYTTGATAAAMFPPWS----AAAGVPFSLSVQYRINGLGVTM 963
sp|Q02385|SPIKE_CVMJC      SFNGIKVLPPVLSESQISGYTAGATAAAMFPPWT----AAAGVPFSLNVQYRINGLGVTM 1015
sp|P11225|SPIKE_CVMJH      SFNGIKVLPPVLSESQISGYTAGATAAAMFPPWT----AAAGVPFSLNVQYRINGLGVTM 874
sp|P18450|SPIKE_CVPFS      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 1054
sp|P33470|SPIKE_CVPMI      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 1054
sp|P07946|SPIKE_CVPPU      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 1052
sp|P27655|SPIKE_CVPR8      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 830
sp|P24413|SPIKE_CVPRM      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 830
sp|Q01977|SPIKE_CVPRT      YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 1052
sp|Q9IKD1|SPIKE_CVRSD      SFNGIKVLPPVLSESQISGYTAGATASAMFPPWS----AAAGVPFALSVQYRINGLGVTM 999
sp|P10033|SPIKE_FIPV       YYNGIMVLPGVANADKMTMYTASLAGGITLGALG---GGAVAIPFAVAVQARLNYVALQT 1057
sp|K9N5Q8|SPIKE_MERS1      YVAGYKVLPPLMDVNMEAAYTSSLLGSIAGVGWTAGLSSFAAIPFAQSIFYRLNGVGITQ 987
sp|P59594|SPIKE_SARS       KFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQ 895
sp|P0DTC2|SPIKE_SARS2      KFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQ 913
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
```

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sp|Q0Q4F2|SPIKE_BC133      QVLSENQKLIANKFNQALGAMQTGFTT--------------SNLAFSKVQDAVNANAQAL 1030
sp|Q0Q475|SPIKE_BC279      NVLYENQKQIANQFNKAISQIQESLTT--------------TSTALGKLQDVVNDNAQAL 927
sp|Q0Q466|SPIKE_BC512      DVLQRNQQMLANSFNSAISNITLAFESVNNAIYQTSAGLNTVAEALSKVQDVVNGQGNAL 1040
sp|Q3LZX1|SPIKE_BCHK3      NVLYENQKLIANQFNSAIGKIQESLSS--------------TASALGKLQDVVNQNAQAL 928
sp|A3EX94|SPIKE_BCHK4      QVLSENQKLIANKFNQALGAMQTGFTT--------------SNLAFSKVQDAVNANAQAL 1032
sp|A3EXD0|SPIKE_BCHK5      QVLSENQKIIANKFNQALGAMQTGFTT--------------TNLAFNKVQDAVNANAMAL 1030
sp|A3EXG6|SPIKE_BCHK9      QVLVENQKLIASSFNNALVNIQKGFTE--------------TSIALSKMQDVINQHAAQL 956
sp|Q3I5J5|SPIKE_BCRP3      NVLYENQKQIANQFNKAISQIQESLTT--------------TSTALGKLQDVVNQNAQAL 927
sp|Q91A26|SPIKE_CVBEN      DVLSQNQKLIANAFNNALGAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P25190|SPIKE_CVBF       DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P25191|SPIKE_CVBL9      DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|Q9QAR5|SPIKE_CVBLS      DVLSQNQKLIANAFNNALGAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|Q8V436|SPIKE_CVBLU      DVLSQNQKLIANAFNNALGAIQEGFDA--------------TNSALVKIQAVVNANAETL 1053
sp|P25192|SPIKE_CVBLY      DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P15777|SPIKE_CVBM       DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|Q9QAQ8|SPIKE_CVBOK      DVLSQNQKLIANAFNNALGAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P25193|SPIKE_CVBQ       DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P25194|SPIKE_CVBV       DVLSQNQKLIANAFNNALDAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1053
sp|P36300|SPIKE_CVCAI      DVLNKNQQILANAFNQAIGNITQAFGKVNDAIHQTSKGLATVAKALAKVQDVVNTQGQAL 1116
sp|Q65984|SPIKE_CVCAK      DVLNKNQQILANAFNQAIGNITQAFGKVNDAIHQTSQGLATVAKVLAKVQDVVNTQGQAL 1118
sp|Q7T6T3|SPIKE_CVCBG      DVLNKNQQILANAFNQAIGNITQAFGNVNDAIHQTSKGLATVAKALAKVQDVVNTQGQAL 1118
sp|P15423|SPIKE_CVH22      DVLQENQKILAASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSL 844
sp|Q5MQD0|SPIKE_CVHN1      DVLNKNQKLIATAFNNALLSIQNGFSA--------------TNSALAKIQSVVNSNAQAL 1044
sp|Q14EB0|SPIKE_CVHN2      DVLNKNQKLIANAFNKALLSIQNGFTA--------------TNSALAKIQSVVNANAQAL 1040
sp|Q0ZME7|SPIKE_CVHN5      DVLNKNQKLIANAFNKALLSIQNGFTA--------------TNSALAKIQSVVNANAQAL 1040
sp|Q6Q1S2|SPIKE_CVHNL      DVLQENQKILAASFNKAINNIVASFSSVNDAITQTAEAIHTVTIALNKIQDVVNQQGSAL 1025
sp|P36334|SPIKE_CVHOC      DVLSQNQKLIANAFNNALYAIQEGFDA--------------TNSALVKIQAVVNANAEAL 1043
sp|P22432|SPIKE_CVM4       NVLSENQKMIASAFNNALGAIQEGFDA--------------TNSALGKIQSVVNANAEAL 1061
sp|P11224|SPIKE_CVMA5      NVLSENQKMIASAFNNALGAIQDGFDA--------------TNSALGKIQSVVNANAEAL 1009
sp|Q02385|SPIKE_CVMJC      NVLSENQKMIASAFNNALGAIQEGFDA--------------TNSALGKIQSVVNANAEAL 1061
sp|P11225|SPIKE_CVMJH      NVLSENQKMIASAFNNALGAIQEGFDA--------------TNSALGKIQSVVNANAEAL 920
sp|P18450|SPIKE_CVPFS      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHQTSRGLATVAKALAKVQDVVNTQGQAL 1114
sp|P33470|SPIKE_CVPMI      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHQTSRGLATVAKALAKVQDVVNTQGQAL 1114
sp|P07946|SPIKE_CVPPU      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHQTSRGLATVAKALAKVQDVVNIQGQAL 1112
sp|P27655|SPIKE_CVPR8      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHQTSRGLTTVAKALAKVQDVVNTQGQAL 890
sp|P24413|SPIKE_CVPRM      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHQTSRGLTTVAKALAKVQDVVNTQGQAL 890
sp|Q01977|SPIKE_CVPRT      DVLNKNQQILASAFNQAIGNITQSFGKVNDAIHXTSRGLATVAKALAKVQDVVXIQGQAL 1112
sp|Q9IKD1|SPIKE_CVRSD      NVLSENQKMIASSFNNAIGAIQEGFDA--------------TNSALAKIQSVVNANAEAL 1045
sp|P10033|SPIKE_FIPV       DVLNKNQQILANAFNQAIGNITQAFGKVNDAIHQTSQGLATVAKALAKVQDVVNTQGQAL 1117
sp|K9N5Q8|SPIKE_MERS1      QVLSENQKLIANKFNQALGAMQTGFTT--------------TNEAFHKVQDAVNNNAQAL 1033
sp|P59594|SPIKE_SARS       NVLYENQKQIANQFNKAISQIQESLTT--------------TSTALGKLQDVVNQNAQAL 941
sp|P0DTC2|SPIKE_SARS2      NVLYENQKLIANQFNSAIGKIQDSLSS--------------TASALGKLQDVVNQNAQAL 959
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
```

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sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      SKLASELSNTFGAISSSISDILARLDTVEQDAQIDRLINGRLTSLNAFVSQQLVRSETAA 1090
sp|Q0Q475|SPIKE_BC279      NTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR 987
sp|Q0Q466|SPIKE_BC512      SQLTVQLQNNFQAISNSIGDIYSRLDQITADAQVDRLITGRLAALNAFVAQSLTKYAEVQ 1100
sp|Q3LZX1|SPIKE_BCHK3      NTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR 988
sp|A3EX94|SPIKE_BCHK4      SKLASELSNTFGAISSSISDILARLDTVEQDAQIDRLINGRLISLNAFVSQQLVRSETAA 1092
sp|A3EXD0|SPIKE_BCHK5      SKLAAELSNTFGAISSSISDILARLDTVEQEAQIDRLINGRLTSLNAFVAQQLVRTEAAA 1090
sp|A3EXG6|SPIKE_BCHK9      HTLVVQLGNSFGAISSSINEIFSRLEGLAANAEVDRLINGRMMVLNTYVTQLLIQASEAK 1016
sp|Q3I5J5|SPIKE_BCRP3      NTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR 987
sp|Q91A26|SPIKE_CVBEN      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|P25190|SPIKE_CVBF       NNLLQQLSNRFGAISSSLQEILSRLDALEAQRQIDRLINGRFTALNAYVSQQLSDSTLVK 1113
sp|P25191|SPIKE_CVBL9      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|Q9QAR5|SPIKE_CVBLS      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|Q8V436|SPIKE_CVBLU      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|P25192|SPIKE_CVBLY      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|P15777|SPIKE_CVBM       NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNVYVSQQLSDSTLVK 1113
sp|Q9QAQ8|SPIKE_CVBOK      NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|P25193|SPIKE_CVBQ       NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNVYVSQQLSDSTLVK 1113
sp|P25194|SPIKE_CVBV       NNLLQQLSNRFGAISSSLQEILSRLDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVK 1113
sp|P36300|SPIKE_CVCAI      SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1176
sp|Q65984|SPIKE_CVCAK      SHLTLQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1178
sp|Q7T6T3|SPIKE_CVCBG      SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1178
sp|P15423|SPIKE_CVH22      NHLTSQLRQNFQAISSSIQAIYDRLDTIQADQQVDRLITGRLAALNVFVSHTLTKYTEVR 904
sp|Q5MQD0|SPIKE_CVHN1      NSLLQQLFNKFGAISSSLQEILSRLDALEAQVQIDRLINGRLTALNAYVSQQLSDISLVK 1104
sp|Q14EB0|SPIKE_CVHN2      NSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIK 1100
sp|Q0ZME7|SPIKE_CVHN5      NSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIK 1100
sp|Q6Q1S2|SPIKE_CVHNL      NHLTSQLRHNFQAISNSIQAIYDRLDSIQADQQVDRLITGRLAALNAFVSQVLNKYTEVR 1085
sp|P36334|SPIKE_CVHOC      NNLLQQLSNRFGAISASLQEILSRLDALEAEAQIDRLINGRLTALNAYVSQQLSDSTLVK 1103
sp|P22432|SPIKE_CVM4       NNLLNQLSNRFGAISASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIK 1121
sp|P11224|SPIKE_CVMA5      NNLLNQLSNRFGAISASLQEILTRLEAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIK 1069
sp|Q02385|SPIKE_CVMJC      NNLLNQLSNRFGAISASLQEILTRLDRVEAKAQIDRLINGRLTALNAYISKQLSDSTLIK 1121
sp|P11225|SPIKE_CVMJH      NNLLNQLSNRFGAISASLQEILTRLDAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIK 980
sp|P18450|SPIKE_CVPFS      SHLTVQLQNNFQAISSSISDIYNRLDELSADAHVDRLITGRLTALNAFVSQTLTRQAEVR 1174
sp|P33470|SPIKE_CVPMI      SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1174
sp|P07946|SPIKE_CVPPU      SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1172
sp|P27655|SPIKE_CVPR8      RHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 950
sp|P24413|SPIKE_CVPRM      RHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 950
sp|Q01977|SPIKE_CVPRT      SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1172
sp|Q9IKD1|SPIKE_CVRSD      NNLLNQLSNRFGAISASLQEILSRLDALEAQAQIDRLINGRLTALNAYVSKQLSDMTLIK 1105
sp|P10033|SPIKE_FIPV       SHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVR 1177
sp|K9N5Q8|SPIKE_MERS1      SKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAA 1093
sp|P59594|SPIKE_SARS       NTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR 1001
sp|P0DTC2|SPIKE_SARS2      NTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR 1019
```

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sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      RSAQLASDKVNECVKSQSKRNGFCGS-GTHIVSFVVNAPNGFYFFHVGYVPTNYTNVTAA 1149
sp|Q0Q475|SPIKE_BC279      ASANLAATKMSECVLGQSKRVDFCGK-GYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTA 1046
sp|Q0Q466|SPIKE_BC512      ASRTLAKQKVNECVKSQSPRYGFCGDEGEHIFSLTQAAPQGLMFLHTVLVPNGFINVTAV 1160
sp|Q3LZX1|SPIKE_BCHK3      ASANLAATKMSECVLGQSKRVDFCGK-GYHLMSFPQSAPHGVVFLHVTYVPSQEKNFTTA 1047
sp|A3EX94|SPIKE_BCHK4      RSAQLASDKVNECVKSQSKRNGFCGS-GTHIVSFVVNAPNGFYFFHVGYVPTNYTNVTAA 1151
sp|A3EXD0|SPIKE_BCHK5      RSAQLAQDKVNECVKSQSKRNGFCGT-GTHIVSFAINAPNGLYFFHVGYQPTSHVNATAA 1149
sp|A3EXG6|SPIKE_BCHK9      AQNALAAQKISECVKAQSLRNDFCGN-GTHVLSIPQLAPNGVLFIHYAYTPTEYAFVQTS 1075
sp|Q3I5J5|SPIKE_BCRP3      ASANLAATKMSECVLGQSKRVDFCGK-GYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTA 1046
sp|Q91A26|SPIKE_CVBEN      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P25190|SPIKE_CVBF       FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P25191|SPIKE_CVBL9      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|Q9QAR5|SPIKE_CVBLS      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|Q8V436|SPIKE_CVBLU      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P25192|SPIKE_CVBLY      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P15777|SPIKE_CVBM       FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|Q9QAQ8|SPIKE_CVBOK      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P25193|SPIKE_CVBQ       FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P25194|SPIKE_CVBV       FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVS 1172
sp|P36300|SPIKE_CVCAI      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1235
sp|Q65984|SPIKE_CVCAK      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1237
sp|Q7T6T3|SPIKE_CVCBG      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1237
sp|P15423|SPIKE_CVH22      ASRQLAQQKVNECVKSQSKRYGFCGN-GTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAW 963
sp|Q5MQD0|SPIKE_CVHN1      FGAALAMEKVNECVKSQSPRINFCGN-GNHILSLVQNAPYGLLFMHFSYKPISFKTVLVS 1163
sp|Q14EB0|SPIKE_CVHN2      AGASRAIEKVNECVKSQSPRINFCGN-GNHILSLVQNAPYGLLFIHFSYKPTSFKTVLVS 1159
sp|Q0ZME7|SPIKE_CVHN5      AGASRAIEKVNECVKSQSPRINFCGN-GNHILSLVQNAPYGLLFIHFSYKPTSFKTVLVS 1159
sp|Q6Q1S2|SPIKE_CVHNL      GSRRLAQQKINECVKSQSNRYGFCGN-GTHIFSIVNSAPDGLLFLHTVLLPTDYKNVKAW 1144
sp|P36334|SPIKE_CVHOC      FSAAQAMEKVNECVKSQSSRINFCGN-GNHIISLVQNAPYGLYFIHFSYVPTKYVTARVS 1162
sp|P22432|SPIKE_CVM4       FSAAQAIEKVNECVKSQTTRINFCGN-GNHILSLVQNAPYGLCFIHFSYVPTSFKTANVS 1180
sp|P11224|SPIKE_CVMA5      VSAAQAIEKVNECVKSQTTRINFCGN-GNHILSLVQNAPYGLYFIHFSYVPISFTTANVS 1128
sp|Q02385|SPIKE_CVMJC      FSAAQAIEKVNECVKSQTTRINFCGN-GNHILSLVQNAPYGLCFIHFSYVPTSFKTANVS 1180
sp|P11225|SPIKE_CVMJH      FSAAQAIEKVNECVKSQTTRINFCGN-GNHILSLVQNAPYGLCFIHFSYVPTSFKTANVS 1039
sp|P18450|SPIKE_CVPFS      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHAVLLPTAYETVTAW 1233
sp|P33470|SPIKE_CVPMI      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1233
sp|P07946|SPIKE_CVPPU      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1231
sp|P27655|SPIKE_CVPR8      ASRQLAKDKVNECVKSQSHRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1009
sp|P24413|SPIKE_CVPRM      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1009
sp|Q01977|SPIKE_CVPRT      ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1231
sp|Q9IKD1|SPIKE_CVRSD      VSAAQAIEKVNECVKSQSPRINFCGN-GNHILSLVQNAPYGLYFIHFSYVPTSFTTVNVS 1164
```

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sp|P10033|SPIKE_FIPV       ASRQLAKDKVNECVRSQSQRFGFCGN-GTHLFSLANAAPNGMIFFHTVLLPTAYETVTAW 1236
sp|K9N5Q8|SPIKE_MERS1      LSAQLAKDKVNECVKAQSKRSGFCGQ-GTHIVSFVVNAPNGLYFMHVGYYPSNHIEVVSA 1152
sp|P59594|SPIKE_SARS       ASANLAATKMSECVLGQSKRVDFCGK-GYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTA 1060
sp|P0DTC2|SPIKE_SARS2      ASANLAATKMSECVLGQSKRVDFCGK-GYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1078
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      YGLCN-HNNPPLCIAPIDGYFITNQTTTY--SVDTEWYYTGSSFFKPEPITQANSRYV-S 1205
sp|Q0Q475|SPIKE_BC279      PAICH-EGK---AYFPREGVFVS--NG-------TSWFITQRNFYSPQIITTDNTFVAGN 1093
sp|Q0Q466|SPIKE_BC512      TGLCV---DETIAMTLRQSGFVL------FVQ-NGNYLVSPRKMFEPRRPEVADFVQVKT 1210
sp|Q3LZX1|SPIKE_BCHK3      PAICH-EGK---AYFPREGVFVS--NG-------TSWFITQRNFYSPQLITTDNTFVSGN 1094
sp|A3EX94|SPIKE_BCHK4      YGLCN-NNNPPLCIAPIDGYFITNQTTTY--SVDTEWYYTGSSFYKPEPITQANSRYV-S 1207
sp|A3EXD0|SPIKE_BCHK5      YGLCN-TENPQKCIAPIDGYFVLNQTTSTVADSDQQWYYTGSSFFHPEPITEANSKYV-S 1207
sp|A3EXG6|SPIKE_BCHK9      AGLCH-NGT---GYAPRQGMFVLPNNT-------NMWHFTTMQFYNPVNISASNTQVLTS 1124
sp|Q3I5J5|SPIKE_BCRP3      PAICH-EGK---AYFPREGVFVS--NG-------TSWFITQRNFYSPQIITTDNTFVAGS 1093
sp|Q91A26|SPIKE_CVBEN      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P25190|SPIKE_CVBF       PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P25191|SPIKE_CVBL9      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|Q9QAR5|SPIKE_CVBLS      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|Q8V436|SPIKE_CVBLU      PGLCI-AGG--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P25192|SPIKE_CVBLY      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P15777|SPIKE_CVBM       PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|Q9QAQ8|SPIKE_CVBOK      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P25193|SPIKE_CVBQ       PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P25194|SPIKE_CVBV       PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMFTGSGYYYPEPITGNNVVVMST 1220
sp|P36300|SPIKE_CVCAI      SGICASDGSRTFGLVVEDVQLTL------FRNLDEKFYLTPRTMYQPRVATSSDFVQIEG 1289
sp|Q65984|SPIKE_CVCAK      SGICASDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPIVATSSDFVQIEG 1291
sp|Q7T6T3|SPIKE_CVCBG      SGICASDGNRTFGLVVKDVQLTL------FRNLDYKFYLTPRTMYQPRVATSSDFVQIEG 1291
sp|P15423|SPIKE_CVH22      SGLCV---DGTNGYVLRQPNLAL------YKE-GNYYRITSRIMFEPRIPTMADFVQIEN 1013
sp|Q5MQD0|SPIKE_CVHN1      PGLCI-SGD--VGIAPKQGYFIKHN---------DHWMFTGSSYYYPEPISDKNVVFMNT 1211
sp|Q14EB0|SPIKE_CVHN2      PGLCL-SGD--RGIAPKQGYFIKQN---------DSWMFTGSSYYYPEPISDKNVVFMNS 1207
sp|Q0ZME7|SPIKE_CVHN5      PGLCL-SGD--RGIAPKQGYFIKQN---------DSWMFTGSSYYYPEPISDKNVVFMNS 1207
sp|Q6Q1S2|SPIKE_CVHNL      SGICV---DGIYGYVLRQPNLVL------YSD-NGVFRVTSRVMFQPRLPVLSDFVQIYN 1194
sp|P36334|SPIKE_CVHOC      PGLCI-AGD--RGIAPKSGYFVNVN---------NTWMYTGSGYYYPEPITENNVVVMST 1210
sp|P22432|SPIKE_CVM4       PGLCI-SGD--RGLAPKAGYFVQDN---------GEWKFTGSNYYYPEPITDKNSVVMIS 1228
sp|P11224|SPIKE_CVMA5      PGLCI-SGD--RGLAPKAGYFVQDD---------GEWKFTGSSYYYPEPITDKNSVIMSS 1176
sp|Q02385|SPIKE_CVMJC      PGLCI-SGD--RGLAPKAGYFVQDN---------GEWKFTGSNYYYPEPITDKNSVVMIS 1228
sp|P11225|SPIKE_CVMJH      PGLCI-SGD--RGLAPKAGYFVQDN---------GEWKFTGSNYYYPEPITDKNSVAMIS 1087
sp|P18450|SPIKE_CVPFS      AGICALDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1287
sp|P33470|SPIKE_CVPMI      AGICALDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1287
sp|P07946|SPIKE_CVPPU      PGICASDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1285
```

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sp|P27655|SPIKE_CVPR8      SGICALDGDRTFGLVVKDVQLTL------FRNLDDNFYLTPRTMYQPRVATSSDFVQIEG 1063
sp|P24413|SPIKE_CVPRM      SGICALDVDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1063
sp|Q01977|SPIKE_CVPRT      PGICASDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1285
sp|Q9IKD1|SPIKE_CVRSD      PGLCI-SGD--RGLAPKAGYFVQDH---------GEWKFTGSNYYYPESITDKNSVVMSS 1212
sp|P10033|SPIKE_FIPV       SGICASDGDRTFGLVVKDVQLTL------FRNLDDKFYLTPRTMYQPRVATSSDFVQIEG 1290
sp|K9N5Q8|SPIKE_MERS1      YGLCD-AANPTNCIAPVNGYFIKTNNTR----IVDEWSYTGSSFYAPEPITSLNTKYV-A 1206
sp|P59594|SPIKE_SARS       PAICH-EGK---AYFPREGVFVF--NG-------TSWFITQRNFFSPQIITTDNTFVSGN 1107
sp|P0DTC2|SPIKE_SARS2      PAICH-DGK---AHFPREGVFVS--NG-------THWFVTQRNFYEPQIITTDNTFVSGN 1125
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      SDVKFEKLENNLPPPLLENSTDVDFKDELEEFFKNVTS--HGPNFA-EISKINTTLLDLS 1262
sp|Q0Q475|SPIKE_BC279      CDVVIGIINNTVYDPLQP--ELDSFKEELDKYFKNHTS--PDVDLG-DISGINASVVNIQ 1148
sp|Q0Q466|SPIKE_BC512      CTISYVNITNNQLPDIIP--DYVDVNKTIDEILAN-LPNNTVPDLP--LDVFNQTFLNLT 1265
sp|Q3LZX1|SPIKE_BCHK3      CDVVIGIINNTVYDPLQP--ELDSFKEELDKYFKNHTS--PDVDLG-DISGINASVVNIQ 1149
sp|A3EX94|SPIKE_BCHK4      SDVKFDKLENNLPPPLLENSTDVDFKDELEEFFKNVTS--HGPNFA-EISKINTTLLDLS 1264
sp|A3EXD0|SPIKE_BCHK5      MDVKFENLTNRLPPPLLSNSTDLDFKEELEEFFKNVSS--QGPNFQ-EISKINTTLLNLN 1264
sp|A3EXG6|SPIKE_BCHK9      CSVNYTSVNYTVLEPSVP--GDYDFQKEFDKFYKNLST--IFNNTF-NPNDFNFSTVDVT 1179
sp|Q3I5J5|SPIKE_BCRP3      CDVVIGIINNTVYDPLQP--ELDSFKEELDKYFKNHTS--PDVDLG-DISGINASVVNIQ 1148
sp|Q91A26|SPIKE_CVBEN      CAVNYTKAPDVMLNISTP--NLPYFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P25190|SPIKE_CVBF       CAVNYTKAPDVMLNISTP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P25191|SPIKE_CVBL9      CAANYTKAPDVMLNISTP--NLHDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|Q9QAR5|SPIKE_CVBLS      CAVNYTKAPDVMLNISTP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|Q8V436|SPIKE_CVBLU      CAVNYTKAPDVMLNISTP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P25192|SPIKE_CVBLY      CAVNYTKAPDVMLNISTP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P15777|SPIKE_CVBM       CAVNYTKAPDVMLNISTP--NLHDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|Q9QAQ8|SPIKE_CVBOK      CAVNYTKAPDVMLNISTP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P25193|SPIKE_CVBQ       CAVNYTKAPDVMLNISTP--NLHDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P25194|SPIKE_CVBV       CAVNYTKAPDVMLNISTP--NLHDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1274
sp|P36300|SPIKE_CVCAI      CDVLFVNGTVIELPSIIP--DYIDINQTVQDILENFRPNWTVPELP--LDIFHATYLNLT 1345
sp|Q65984|SPIKE_CVCAK      CDVLFVNATVIDLPSIIP--DYIDINQTVQDILENFRPNWTVPELP--LDIFNATYLNLT 1347
sp|Q7T6T3|SPIKE_CVCBG      CDVLFVNATVIELPSIIP--DYIDINQTVQDILENFRPNWTVPELP--LDIFNATYLNLT 1347
sp|P15423|SPIKE_CVH22      CNVTFVNISRSELQTIVP--EYIDVNKTLQELSYK-LPNYTVPDLV--VEQYNQTILNLT 1068
sp|Q5MQD0|SPIKE_CVHN1      CSVNFTKAPLVYLNHSVP--KLSDFESELSHWFKNQTS--IAPNLTLNLHTINATFLDLY 1267
sp|Q14EB0|SPIKE_CVHN2      CSVNFTKAPFIYLNNSIP--NLSDFEAEFSLWFKNHTS--IAPNLTFNSH-INATFLDLY 1262
sp|Q0ZME7|SPIKE_CVHN5      CSVNFTKAPFIYLNNSIP--NLSDFEAELSLWFKNHTS--IAPNLTFNSH-INATFLDLY 1262
sp|Q6Q1S2|SPIKE_CVHNL      CNVTFVNISRVELHTVIP--DYVDVNKTLQEFAQN-LPKYVKPNFD--LTPFNLTYLNLS 1249
sp|P36334|SPIKE_CVHOC      CAVNYTKAPYVMLNTSIP--NLPDFKEELDQWFKNQTS--VAPDLSLDY--INVTFLDLQ 1264
sp|P22432|SPIKE_CVM4       CAVNYTKAPEVFLNNSIP--NLPDFKEELDKWFKNQTS--IAPDLSLDFEKLNVTFLDLT 1284
sp|P11224|SPIKE_CVMA5      CAVNYTKAPEVFLNTSIP--NPPDFKEELDKWFKNQTS--IAPDLSLDFEKLNVTLLDLT 1232
sp|Q02385|SPIKE_CVMJC      CAVNYTKAPEVFLNNSIP--NLPDFKEELDKWFKNQTS--IAPDLSLDFEKLNVTFLDLT 1284
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sp|P11225|SPIKE_CVMJH      CAVNYTKAPEVFLNNSIP--NLPDFKEELDKWFKNQTS--IAPDLSLDFEKLNVTFLDLT 1143
sp|P18450|SPIKE_CVPFS      CDVLFVNATLSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--FDIFNATYLNLT 1343
sp|P33470|SPIKE_CVPMI      CDVLFVNATVSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--FDIFNATYLNLT 1343
sp|P07946|SPIKE_CVPPU      CDVLFVNATVSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--FDIFNATYLNLT 1341
sp|P27655|SPIKE_CVPR8      CDVLFVNTTVSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--MDVFNATYLNLT 1119
sp|P24413|SPIKE_CVPRM      CDVLFVNTTVSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--LDVFNATYLNLT 1119
sp|Q01977|SPIKE_CVPRT      CDVLFVNATVSDLPSIIP--DYIDINQTVQDILENFRPNWTVPELT--FDIFNATYLNLT 1341
sp|Q9IKD1|SPIKE_CVRSD      CAVNYTKAPEVFLNTSIT--NLPDFKEELDKWFKNQTS--IVPDLSFDIGKLNVTFLDLS 1268
sp|P10033|SPIKE_FIPV       CDVLFVNATVIDLPSIIP--DYIDINQTVQDILENYRPNWTVPEFT--LDIFNATYLNLT 1346
sp|K9N5Q8|SPIKE_MERS1      PQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVST--SIPNFG-SLTQINTTLLDLT 1263
sp|P59594|SPIKE_SARS       CDVVIGIINNTVYDPLQP--ELDSFKEELDKYFKNHTS--PDVDLG-DISGINASVVNIQ 1162
sp|P0DTC2|SPIKE_SARS2      CDVVIGIVNNTVYDPLQP--ELDSFKEELDKYFKNHTS--PDVDLG-DISGINASVVNIQ 1180
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      DEMAI--------------LQEVVKQLNDSYIDLKELGNYTYYNKWPWYIWLGFIAGLVA 1308
sp|Q0Q475|SPIKE_BC279      KEIDR--------------LNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIA 1194
sp|Q0Q466|SPIKE_BC512      GEIADLEARSESLKNTSEELRQLIQNINNTLVDLQWLNRVETFIKWPWYVWLAIVIALIL 1325
sp|Q3LZX1|SPIKE_BCHK3      KEIDR--------------LNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIA 1195
sp|A3EX94|SPIKE_BCHK4      DEMAM--------------LQEVVKQLNDSYIDLKELGNYTYYNKWPWYVWLGFIAGLVA 1310
sp|A3EXD0|SPIKE_BCHK5      TELMV--------------LSEVVKQLNESYIDLKELGNYTFYQKWPWYIWLGFIAGLVA 1310
sp|A3EXG6|SPIKE_BCHK9      AQIKS--------------LHDVVNQLNQSFIDLKKLNVYEKTIKWPWYVWLAMIAGIVG 1225
sp|Q3I5J5|SPIKE_BCRP3      KEIDR--------------LNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIA 1194
sp|Q91A26|SPIKE_CVBEN      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P25190|SPIKE_CVBF       DEMNR--------------LQEAIKLLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P25191|SPIKE_CVBL9      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|Q9QAR5|SPIKE_CVBLS      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|Q8V436|SPIKE_CVBLU      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P25192|SPIKE_CVBLY      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA 1320
sp|P15777|SPIKE_CVBM       DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|Q9QAQ8|SPIKE_CVBOK      DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P25193|SPIKE_CVBQ       DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P25194|SPIKE_CVBV       DEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGFAGVA 1320
sp|P36300|SPIKE_CVCAI      GEINDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1405
sp|Q65984|SPIKE_CVCAK      GEINDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1407
sp|Q7T6T3|SPIKE_CVCBG      GEINDLEFRSEKLHNTTLELATLIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1407
sp|P15423|SPIKE_CVH22      SEISTLENKSAELNYTVQKLQTLIDNINSTLVDLKWLNRVETYIKWPWWVWLCISVVLIF 1128
sp|Q5MQD0|SPIKE_CVHN1      YEMNL--------------IQESIKSLNNSYINLKDIGTYEMYVKWPWYVWLLISFSFII 1313
sp|Q14EB0|SPIKE_CVHN2      YEMNV--------------IQESIKSLNSSFINLKEIGTYEMYVKWPWYIWLLIVILFII 1308
sp|Q0ZME7|SPIKE_CVHN5      YEMNV--------------IQESIKSLNSSFINLKEIGTYEMYVKWPWYIWLLIVILFII 1308
sp|Q6Q1S2|SPIKE_CVHNL      SELKQLEAKTASLFQTTVELQGLIDQINSTYVDLKLLNRFENYIKWPWWVWLIISVVFVV 1309
```

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sp|P36334|SPIKE_CVHOC      VEMNR--------------LQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLICLAGVA 1310
sp|P22432|SPIKE_CVM4       YEMNR--------------IQDAIKKLNESYINLKEVGTYEMYVKWPWYVWLLIGLAGVA 1330
sp|P11224|SPIKE_CVMA5      YEMNR--------------IQDAIKKLNESYINLKEVGTYEMYVKWPWYVWLLIGLAGVA 1278
sp|Q02385|SPIKE_CVMJC      YEMNR--------------IQDAIKKLNESYINLKEVGTYEMYVKWPWYVWLLIGLAGVA 1330
sp|P11225|SPIKE_CVMJH      YEMNR--------------IQDAIKKLNESYINLKEVGTYEMYVKWPWYVWLLIGLAGVA 1189
sp|P18450|SPIKE_CVPFS      GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1403
sp|P33470|SPIKE_CVPMI      GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1403
sp|P07946|SPIKE_CVPPU      GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1401
sp|P27655|SPIKE_CVPR8      GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1179
sp|P24413|SPIKE_CVPRM      GEIDDLEFRSEKLHNTTVELAILIDNINNTVVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1179
sp|Q01977|SPIKE_CVPRT      GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVIF 1401
sp|Q9IKD1|SPIKE_CVRSD      YEMNR--------------IQDAIKNLNESYINLKEIGTYEMYVKWPWYVWLLIGLAGVA 1314
sp|P10033|SPIKE_FIPV       GEIDDLEFRSEKLHNTTVELAILIDNINNTLVNLEWLNRIETYVKWPWYVWLLIGLVVVF 1406
sp|K9N5Q8|SPIKE_MERS1      YEMLS--------------LQQVVKALNESYIDLKELGNYTYYNKWPWYIWLGFIAGLVA 1309
sp|P59594|SPIKE_SARS       KEIDR--------------LNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIA 1208
sp|P0DTC2|SPIKE_SARS2      KEIDR--------------LNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIA 1226
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379


sp|Q0Q4F2|SPIKE_BC133      LLLCVFFLLCCTGCGTSCLGKM-KCKNCCDSYEE--YDVEK----IHVH-----       1350
sp|Q0Q475|SPIKE_BC279      IVMVTILLCCMTSCCSCLKGAC-SCGSCCKFDED--DSEPVLKG-VKLHYT---       1241
sp|Q0Q466|SPIKE_BC512      VVSLLVFCCISTGCCGCCGCCGSCFSGCCRG-TKLQHYEPI----EKVHVQ---       1371
sp|Q3LZX1|SPIKE_BCHK3      IVMVTILLCCMTSCCSCLKGAC-SCGSCCKFDED--DSEPVLKG-VKLHYT---       1242
sp|A3EX94|SPIKE_BCHK4      LLLCVFFLLCCTGCGTSCLGKM-KCKNCCDSYEE--YDVEK----IHVH-----       1352
sp|A3EXD0|SPIKE_BCHK5      LALCVFFILCCTGCGTSCLGKL-KCNRCCDSYDE--YEVEK----IHVH-----       1352
sp|A3EXG6|SPIKE_BCHK9      LVLAVIMLMCMTNCCSCFKGMC-DCRRCCGSYDS--YD-DVYPA-VRVNKKRTV       1274
sp|Q3I5J5|SPIKE_BCRP3      IVMVTILLCCMTSCCSCLKGAC-SCGSCCKFDED--DSEPVLKG-VKLHYT---       1241
sp|Q91A26|SPIKE_CVBEN      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHED---       1363
sp|P25190|SPIKE_CVBF       MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|P25191|SPIKE_CVBL9      MLVLLFFICCCTGCGTSCFK---ICGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|Q9QAR5|SPIKE_CVBLS      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|Q8V436|SPIKE_CVBLU      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHED---       1363
sp|P25192|SPIKE_CVBLY      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|P15777|SPIKE_CVBM       MLVLLFFICCCTGCGTSCFK---ICGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|Q9QAQ8|SPIKE_CVBOK      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|P25193|SPIKE_CVBQ       MLVLLFFICCCTGCGTSCFK---ICGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|P25194|SPIKE_CVBV       MLVLLFFICCCTGCGTSCFK---ICGGCCDDYTG--HQELVIKT---SHDD---       1363
sp|P36300|SPIKE_CVCAI      CIPILLFCCCSTGCCGCIGCLGSCCHSICSR-GQFESYEPI----EKVHVH---       1451
sp|Q65984|SPIKE_CVCAK      CIPILLFCCCSTGCCGCIGCLGSCCHSICSR-RQFESYEPI----EKVHVH---       1453
sp|Q7T6T3|SPIKE_CVCBG      CIPLLLFCCCSTGCCGCFGCIGSCCHSMCSR-RQFESYEPI----EKVHVH---       1453
sp|P15423|SPIKE_CVH22      VVSMLLLCCCSTGCCGFFSCFASSIRGCCE--STKLPYYDV----EKIHIQ---       1173
```

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sp|Q5MQD0|SPIKE_CVHN1      FLVLLFFICCCTGCGSACFS---KCHNCCDEYGG--HHDFVIKT---SHDD---       1356
sp|Q14EB0|SPIKE_CVHN2      FLMILFFICCCTGCGSACFS---KCHNCCDEYGG--HNDFVIKA---SHDD---       1351
sp|Q0ZME7|SPIKE_CVHN5      FLMILFFICCCTGCGSACFS---KCHNCCDEYGG--HNDFVIKA---SHDD---       1351
sp|Q6Q1S2|SPIKE_CVHNL      LLSLLVFCCLSTGCCGCCNCLTSSMRGCCDCGSTKLPYYEF----EKVHVQ---       1356
sp|P36334|SPIKE_CVHOC      MLVLLFFICCCTGCGTSCFK---KCGGCCDDYTG--YQELVIKT---SHDD---       1353
sp|P22432|SPIKE_CVM4       VCVLLFFICCCTGCGSCCFR---KCGSCCDEYGG--HQDSIVIHNISAHED---       1376
sp|P11224|SPIKE_CVMA5      VCVLLFFICCCTGCGSCCFK---KCGNCCDEYGG--HQDSIVIHNISSHED---       1324
sp|Q02385|SPIKE_CVMJC      VCVLLFFICCCTGCGSCCFR---KCGSCCDEYGG--HQDSIVIYNISAHED---       1376
sp|P11225|SPIKE_CVMJH      VCVLLFFICCCTGCGSCCFR---KCGSCCDEYGG--HQDSIVIHNISAHED---       1235
sp|P18450|SPIKE_CVPFS      CIPLLLFCCCSTGCCGCIGCLGSCCHSICSR-RQFENYEPI----EKVHIH---       1449
sp|P33470|SPIKE_CVPMI      CIPLLLFCCCSTGCCGCIGCLGSCCHSICSR-RQFENYEPI----EKVHVH---       1449
sp|P07946|SPIKE_CVPPU      CIPLLLFCCCSTGCCGCIGCLGSCCHSICSR-RQFENYEPI----EKVHVH---       1447
sp|P27655|SPIKE_CVPR8      CIPLLLFCCCSTGCCGCIGCLGSCCHSIFSR-RQFENYEPI----EKVHVH---       1225
sp|P24413|SPIKE_CVPRM      CIPLLLFCCCSTGCCGCIGCLGSCCHSIFSR-RQFENYEPI----EKVHVH---       1225
sp|Q01977|SPIKE_CVPRT      CIPLLLFCCCSTGCCGCIGCLGSCCHSICSR-RQFENYEPI----EKVHVH---       1447
sp|Q9IKD1|SPIKE_CVRSD      VCVLLFFICCCTGCGSCCFK---KCGNCCDEYGG--RQAGIVIHNISSHED---       1360
sp|P10033|SPIKE_FIPV       CIPLLLFCCFSTGCCGCIGCLGSCCHSICSR-RQFENYEPI----EKVHVH---       1452
sp|K9N5Q8|SPIKE_MERS1      LALCVFFILCCTGCGTNCMGKL-KCNRCCDRYEE--YDLEP----HKVHVH---       1353
sp|P59594|SPIKE_SARS       IVMVTILLCCMTSCCSCLKGAC-SCGSCCKFDED--DSEPVLKG-VKLHYT---       1255
sp|P0DTC2|SPIKE_SARS2      IVMVTIMLCCMTSCCSCLKGCC-SCGSCCKFDED--DSEPVLKG-VKLHYT---       1273
sp|Q2KI99|STING_BOVIN      -------------------------------------------------------      378
sp|E1C7U0|STING_CHICK      -------------------------------------------------------      379
sp|Q86WV6|STING_HUMAN      -------------------------------------------------------      379
sp|Q3TBT3|STING_MOUSE      -------------------------------------------------------      378
sp|A7SLZ2|STING_NEMVE      -------------------------------------------------------      377
sp|B8XX90|STING_PIG        -------------------------------------------------------      378
sp|F1M391|STING_RAT        -------------------------------------------------------      379
```

```
CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q93971|TRPG_CAEEL          MMSDDMLDENDENFACQDVDEIIIYVPEFAGYREVNIDTAVSVCPTPIQQARRESSCRNL	60
sp|Q7Z4N2|TRPM1_HUMAN         ------------------------------------------------------------	0
sp|Q2TV84|TRPM1_MOUSE         ------------------------------------------------------------	0
sp|Q2WEA5|TRPM1_RAT           ------------------------------------------------------------	0
sp|A0A0R4IMY7|TRPM2_DANRE     ------------------------------------------------------------	0
sp|O94759|TRPM2_HUMAN         ------------------------------------------------------------	0
sp|Q91YD4|TRPM2_MOUSE         ------------------------------------------------------------	0
sp|E9PTA2|TRPM2_RAT           ------------------------------------------------------------	0
sp|Q9HCF6|TRPM3_HUMAN         ------------------------------------------------------------	0
sp|Q8TD43|TRPM4_HUMAN         ------------------------------------------------------------	0
sp|Q7TN37|TRPM4_MOUSE         ------------------------------------------------------------	0
sp|Q9ESQ5|TRPM4_RAT           ------------------------------------------------------------	0
sp|P0DTC2|SPIKE_SARS2         ------------------------------------------------------------	0


sp|Q93971|TRPG_CAEEL          EMRRRFEKLRREKKEEKKLLADDEKDFDEDDDVFEDGEGLQMRTFQPNASIRDENGSMPS	120
sp|Q7Z4N2|TRPM1_HUMAN         ------------------------------------------------------------	0
sp|Q2TV84|TRPM1_MOUSE         ------------------------------------------------------------	0
sp|Q2WEA5|TRPM1_RAT           ------------------------------------------------------------	0
sp|A0A0R4IMY7|TRPM2_DANRE     ------------------------------------------------------------	0
sp|O94759|TRPM2_HUMAN         ------------------------------------------------------------	0
sp|Q91YD4|TRPM2_MOUSE         ------------------------------------------------------------	0
sp|E9PTA2|TRPM2_RAT           ------------------------------------------------------------	0
sp|Q9HCF6|TRPM3_HUMAN         ------------------------------------------------------------	0
sp|Q8TD43|TRPM4_HUMAN         ------------------------------------------------------------	0
sp|Q7TN37|TRPM4_MOUSE         ------------------------------------------------------------	0
sp|Q9ESQ5|TRPM4_RAT           ------------------------------------------------------------	0
sp|P0DTC2|SPIKE_SARS2         -----------------------------------------MFVFLVL---------LPL	10


sp|Q93971|TRPG_CAEEL          LLPRTAPIKKTRKHRRRRSGSFTGGVYP-RKGHRNRSLLGHAIPPPNVHSADWRDMLAIT	179
sp|Q7Z4N2|TRPM1_HUMAN         ------------------------------------------------------------	0
sp|Q2TV84|TRPM1_MOUSE         ------------------------------------------------------------	0
sp|Q2WEA5|TRPM1_RAT           ------------------------------------------------------------	0
sp|A0A0R4IMY7|TRPM2_DANRE     ------------------------------------------------------------	0
sp|O94759|TRPM2_HUMAN         ------------------------------------------------------------	0
sp|Q91YD4|TRPM2_MOUSE         ------------------------------------------------------------	0
sp|E9PTA2|TRPM2_RAT           ------------------------------------------------------------	0
sp|Q9HCF6|TRPM3_HUMAN         ------------------------------------------------MPEPWGTVYFL-	11
sp|Q8TD43|TRPM4_HUMAN         ------------------------------------------------------------	0
sp|Q7TN37|TRPM4_MOUSE         ------------------------------------------------------------	0
sp|Q9ESQ5|TRPM4_RAT           ------------------------------------------------------------	0
sp|P0DTC2|SPIKE_SARS2         VSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSS------------------------	46
```

```
sp|Q93971|TRPG_CAEEL         DNKDDKLMKTLGVTRYLQSKGGDQVPPTSTTTGGAGGDGNAVPTTSQAQAQTFNSG-RQT    238
sp|Q7Z4N2|TRPM1_HUMAN        ------------------------------------------------------------    0
sp|Q2TV84|TRPM1_MOUSE        ------------------------------------------------------------    0
sp|Q2WEA5|TRPM1_RAT          ------------------------------------------------------------    0
sp|A0A0R4IMY7|TRPM2_DANRE    ------------------------------------------------------------    0
sp|O94759|TRPM2_HUMAN        ------------------------MEPSALRK------------AGSE----------QE    14
sp|Q91YD4|TRPM2_MOUSE        ------------------------MESLDRRR------------TGSE----------QE    14
sp|E9PTA2|TRPM2_RAT          ------------------------MEPLDQRR------------TDSD----------QE    14
sp|Q9HCF6|TRPM3_HUMAN        ---------------------------------------------GIAQVFSFLFSWWNL    26
sp|Q8TD43|TRPM4_HUMAN        ------------------------------------------------------------    0
sp|Q7TN37|TRPM4_MOUSE        ------------------------------------------------------------    0
sp|Q9ESQ5|TRPM4_RAT          ------------------------------------------------------------    0
sp|P0DTC2|SPIKE_SARS2        ------------------------------------------------------------    46


sp|Q93971|TRPG_CAEEL         TGMSSGDRLNEDVSATANSAQLVLPTPL-------FNQMRFTESNMSLNRHNWVRETFTR    291
sp|Q7Z4N2|TRPM1_HUMAN        ------------------------------------------------------------    0
sp|Q2TV84|TRPM1_MOUSE        MG---------------SMRKM------SSSFKR--GSIKSSTSGSQKGQKAWIEKTFCK    37
sp|Q2WEA5|TRPM1_RAT          MG---------------SMRKM------SSSFKR--GSIKSSTSGSQKGQKAWIEKTFCK    37
sp|A0A0R4IMY7|TRPM2_DANRE    ---------MDEAALEPTLVQTLA----VSTAKGG-RYLSLSPSFQRCSLASWIKENIKK    46
sp|O94759|TRPM2_HUMAN        EGFEGLPRRVTDLGMVSNLRRSNS-----SLFKSWRLQCPFGNNDKQESLSSWIPENIKK    69
sp|Q91YD4|TRPM2_MOUSE        EGFGVQSRRATDLGMVPNLRRSNS-----SLCKSRRFLCSFSS-EKQENLSSWIPENIKK    68
sp|E9PTA2|TRPM2_RAT          EGFGVQSRRATDLGMVPNLRRSNS-----SLCKSRRLLCSFSS-EKQENLSSWIPENIKK    68
sp|Q9HCF6|TRPM3_HUMAN        EG---------------VMNQADAPRPLNWTIRKLCHAAFLPSVRLLKAQKSWIERAFYK    71
sp|Q8TD43|TRPM4_HUMAN        -------------------------------------------MVVPEKEQSWIPKIFKK    17
sp|Q7TN37|TRPM4_MOUSE        -------------------------------------------MVGPEKEQSWIPKIFRK    17
sp|Q9ESQ5|TRPM4_RAT          -------------------------------------------MVGQEKEQSWIPKIFRK    17
sp|P0DTC2|SPIKE_SARS2        ------------------------------------------------------------    46


sp|Q93971|TRPG_CAEEL         RECSRFIASSR----DLHKCGCGRTRDAHRNIPELTSEFLRQKRSVAALEQQRSISNVND    347
sp|Q7Z4N2|TRPM1_HUMAN        ---------MK----DSNRCCCGQFTNQHIPPLPSA-------------------TPSK-    27
sp|Q2TV84|TRPM1_MOUSE        RECIFVIPSTK----DPNRCCCGQLTNQHIPPLPSG-------------------APST-    73
sp|Q2WEA5|TRPM1_RAT          RECIFVIPSTK----DPNRCCCGQLTNQHIPPLPSV-------------------TPSS-    73
sp|A0A0R4IMY7|TRPM2_DANRE    KECCFYVEDG-----REGICKCGYPKVQHCDEAIKP------------------------    77
sp|O94759|TRPM2_HUMAN        KECVYFVESSKLSDAGKVVCQCGYTHEQHLEEATKP------------------------    105
sp|Q91YD4|TRPM2_MOUSE        KECVYFVESSKLSDAGKVVCACGYTHEQHLEVAIKP------------------------    104
sp|E9PTA2|TRPM2_RAT          KECVYFVESSKLSDAGKVVCECGYTHEQHIEVAIKP------------------------    104
sp|Q9HCF6|TRPM3_HUMAN        RECVHIIPSTK----DPHRCCCGRLIGQHVGLTPSI-------------------SVLQN    108
sp|Q8TD43|TRPM4_HUMAN        KTCTTFIVDS-T-DPGGTLCQCGRPRTAHPAVAMED------------------------    51
sp|Q7TN37|TRPM4_MOUSE        KVCTTFIVDL-SDDAGGTLCQCGQPRDAHPSVAVED------------------------    52
sp|Q9ESQ5|TRPM4_RAT          KVCTTFIVDL-HDDAGGTLCQCGQPRDAHPSVAVED------------------------    52
sp|P0DTC2|SPIKE_SARS2        ------------------------------------------------------------    46


sp|Q93971|TRPG_CAEEL         DINTQNMYTKRGANEKWSLRKHTVSLATNAFGQVEFQGGPHPYKAQYVRVNFDTEPAYIM    407
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```
sp|Q7Z4N2|TRPM1_HUMAN          --NEEESKQVETQPEKWSVAKHTQSYPTDSYGVLEFQGGGYSNKAMYIRVSYDTKPDSLL     85
sp|Q2TV84|TRPM1_MOUSE          --TGEDTKQADTQSGKWSVSKHTQSYPTDSYGILEFQGGGYSNKAMYIRVSYDTKPDSLL     131
sp|Q2WEA5|TRPM1_RAT            --TAEDTKQGDAQSGKWSVSKHTQSYPTDSYGILEFQGGGYSNKAMYIRVSYDTKPDSLL     131
sp|A0A0R4IMY7|TRPM2_DANRE      -------E--DYMGEQWDKHRHVRETPTDAFGDISFGGLGQK-TGKYVRVSSDTSCENLY     127
sp|O94759|TRPM2_HUMAN          -------H--TFQGTQWDPKKHVQEMPTDAFGDIVFTGLSQK-VKKYVRVSQDTPSSVIY     155
sp|Q91YD4|TRPM2_MOUSE          -------H--TFQGKEWDPKKHVQEMPTDAFGDIVFTDLSQK-VGKYVRVSQDTPSSVIY     154
sp|E9PTA2|TRPM2_RAT            -------H--TFQGKEWDPKKHVHEMPTDAFGDIVFTGLSQK-VGKYVRLSQDTSSIVIY     154
sp|Q9HCF6|TRPM3_HUMAN          EKNESRLSRNDIQSEKWSISKHTQLSPTDAFGTIEFQGGGHSNKAMYVRVSFDTKPDLLL     168
sp|Q8TD43|TRPM4_HUMAN          -------AFGAAVVTVWDSDAHTTEKPTDAYGELDFTGAGRK-HSNFLRLSDRTDPAAVY     103
sp|Q7TN37|TRPM4_MOUSE          -------AFGAAVVTEWNSDEHTTEKPTDAYGDLDFTYSGRK-HSNFLRLSDRTDPATVY     104
sp|Q9ESQ5|TRPM4_RAT            -------AFGAAVVTEWNSDEHTTEKPTDAYGDLDFTYSGRK-SSNFLRLSDRTDPATVY     104
sp|P0DTC2|SPIKE_SARS2          -------------------------------------------------VLHST-QDLFL     56
                                                                                :   *    .

sp|Q93971|TRPG_CAEEL           SLF-EHVWQISPPRLIITVHGGTSNFDLQPKLARVFRKGLLKA----ASTTGAWIITSGC     462
sp|Q7Z4N2|TRPM1_HUMAN          HLM-VKDWQLELPKLLISVHGGLQNFEMQPKLKQVFGKGLIKA----AMTTGAWIFTGGV     140
sp|Q2TV84|TRPM1_MOUSE          HLM-VKDWQLELPKLLISVHGGLQSFEMQPKLKQVFGKGLIKA----AMTTGAWIFTGGV     186
sp|Q2WEA5|TRPM1_RAT            HLM-VKDWQLELPKLLISVHGGLQSFEMQPKLKQVFGKGLIKA----AMTTGAWIFTGGV     186
sp|A0A0R4IMY7|TRPM2_DANRE      QLM-TEQWKLRSPNLLISVTGGAKNFYIKTHLKDKFRRGLIKV----AQTTGAWILTGGT     182
sp|O94759|TRPM2_HUMAN          HLM-TQHWGLDVPNLLISVTGGAKNFNMKPRLKSIFRRGLVKV----AQTTGAWIITGGS     210
sp|Q91YD4|TRPM2_MOUSE          QLM-TQHWGLDVPNLLISVTGGAKNFNMKLRLKSIFRRGLVKV----AQTTGAWIITGGS     209
sp|E9PTA2|TRPM2_RAT            QLM-TQHWGLDVPSLLISVTGGAKNFNMKLRLKSIFRRGLVKV----AQTTGAWIITGGS     209
sp|Q9HCF6|TRPM3_HUMAN          HLM-TKEWQLELPKLLISVHGGLQNFELQPKLKQVFGKGLIKA----AMTTGAWIFTGGV     223
sp|Q8TD43|TRPM4_HUMAN          SLV-TRTWGFRAPNLVVSVLGGSGGPVLQTWLQDLLRRGLVRA----AQSTGAWIVTGGL     158
sp|Q7TN37|TRPM4_MOUSE          SLV-TRSWGFRAPNLVVSVLGGSGGPVLQTWLQDLLRRGLVRA----AQSTGAWIVTGGL     159
sp|Q9ESQ5|TRPM4_RAT            SLV-TRSWGFRAPNLVVSVLGGSEGPVLQTWLQDLLRRGLVRA----AQSTGAWIVTGGL     159
sp|P0DTC2|SPIKE_SARS2          PFFSNVTWFH---AIHVSGTNGTKRFDNPV---LPFNDGVYFASTEKSNIIRGWIFGTTL     110
                                :.    *      : ::  .*             :  *:  .    :    .**.

sp|Q93971|TRPG_CAEEL           DTGVVKHVAAALEGAQSAQ---RNKIVCIGIAPWGLLKKREDFIGQDKTVPYYPSS----     515
sp|Q7Z4N2|TRPM1_HUMAN          STGVISHVGDALKDHSSKS---RGRVCAIGIAPWGIVENKEDLVGKDVTRVYQTMS--N-     194
sp|Q2TV84|TRPM1_MOUSE          STGVVSHVGDALKDHSSKS---RGRLCAIGIAPWGMVENKEDLIGKDVTRVYQTMS--N-     240
sp|Q2WEA5|TRPM1_RAT            STGVVSHVGDALKDHSSKS---RGRLCAIGIAPWGMVENKEDLVGKDVTRVYQTMS--N-     240
sp|A0A0R4IMY7|TRPM2_DANRE      HAGVMKHVGMAVRDYTLSSGSMEGQIVVIGVAPWGVIHNRSTLIHPEGRFPAYYSLDEQG     242
sp|O94759|TRPM2_HUMAN          HTGVMKQVGEAVRDFSLSSSYKEGELITIGVATWGTVHRREGLIHPTGSFPAEYILDEDG     270
sp|Q91YD4|TRPM2_MOUSE          HTGVMKQVGEAVRDFSLSSSCKEGEVITIGVATWGTIHNREGLIHPMGGFPAEYMLDEEG     269
sp|E9PTA2|TRPM2_RAT            HTGVMKQVGEAVRDFSLSSSCKEGDVITIGIATWGTIHNREALIHPMGGFPAEYMLDEEG     269
sp|Q9HCF6|TRPM3_HUMAN          NTGVIRHVGDALKDHASKS---RGKICTIGIAPWGIVENQEDLIGRDVVRPYQTMS--N-     277
sp|Q8TD43|TRPM4_HUMAN          HTGIGRHVGVAVRDHQMAST-GGTKVVAMGVAPWGVVRNRDTLINPKGSFPARYRWRGDP     217
sp|Q7TN37|TRPM4_MOUSE          HTGIGRHVGVAVRDHQTAST-GSSKVVAMGVAPWGVVRNRDMLINPKGSFPARYRWRGDP     218
sp|Q9ESQ5|TRPM4_RAT            HTGIGRHVGVAVRDHQTAST-GGSKVVAMGVAPWGVVRNRDMLINPKGSFPARYRWRGDP     218
sp|P0DTC2|SPIKE_SARS2          DSKTQSLLIVN-----------NATNVVIKVCEFQFC--NDPFLGVYYHK-NNKSWMESE     156
                                :     :                    : :. :     .. ::

sp|Q93971|TRPG_CAEEL           ----SKGRFTGLNNRHSYFLLVDNGTVGRYGAEVILR-KRLEMYISQKQK----------     560
sp|Q7Z4N2|TRPM1_HUMAN          ----PLSKLSVLNNSHTHFILADNGTLGKYGAEVKLR-RLLEKHISLQKINTR-------     242
sp|Q2TV84|TRPM1_MOUSE          ----PLSKLSVLNNSHTHFILADNGTLGKYGAEVKLR-RQLEKHISLQKINTR-------     288
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sp|Q2WEA5|TRPM1_RAT            ----PLSKLSVLNNSHTHFILADNGTLGKYGAEVKLR-RQLEKHISLQKINTR-------     288
sp|A0A0R4IMY7|TRPM2_DANRE      -----QGRLSCLDINHTHFLLVDDGTQGHYGVEIELR-ARLEKLISKLSLGNR-------     289
sp|O94759|TRPM2_HUMAN          -----QGNLTCLDSNHSHFILVDDGTHGQYGVEIPLR-TRLEKFISEQTKERG-------     317
sp|Q91YD4|TRPM2_MOUSE          -----QGNLTCLDSNHSHFILVDDGTHGQYGVEIPLR-TKLEKFISEQTKERG-------     316
sp|E9PTA2|TRPM2_RAT            -----QGNLTCLDSNHSHFILVDDGTHGQYGVEIPLR-TKLEKFISEQTKERG-------     316
sp|Q9HCF6|TRPM3_HUMAN          ----PMSKLTVLNSMHSHFILADNGTTGKYGAEVKLR-RQLEKHISLQKINTRCLPFFSL     332
sp|Q8TD43|TRPM4_HUMAN          ----EDGVQFPLDYNYSAFFLVDDGTHGCLGGENRFR-LRLESYISQQKTGVG-------     265
sp|Q7TN37|TRPM4_MOUSE          ----EDGVEFPLDYNYSAFFLVDDGTYGRLGGENRFR-LRFESYVAQQKTGVG-------     266
sp|Q9ESQ5|TRPM4_RAT            ----EDGVEFPLDYNYSAFFLVDDGTYGRMGGENRFR-LRFESYVAQQKTGVG-------     266
sp|P0DTC2|SPIKE_SARS2          FRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTP---I-NL     212
                                     .    ::     *::  :*. *       :    ::  .

sp|Q93971|TRPG_CAEEL           ---------------IFGGTRSVPVVCVVLEGGSCTIRSV----LDYVTNVPRVPVVVCD     601
sp|Q7Z4N2|TRPM1_HUMAN          ------------------LGQGVPLVGLVVEGGPNVVSIV----LEYLQEEPPIPVVICD     280
sp|Q2TV84|TRPM1_MOUSE          ------------------LGQGVPVVGLVVEGGPNVVSIV----LEYLKEDPPVPVVVCD     326
sp|Q2WEA5|TRPM1_RAT            ------------------LGQGVPVVGLVVEGGPNVVSIV----LEYLREDPPVPVVVCD     326
sp|A0A0R4IMY7|TRPM2_DANRE      -----------------ESGVTIPVVCVVLDGGPGTLNTI----YNSMLN--HTPCVVLE     326
sp|O94759|TRPM2_HUMAN          -----------------GVAIKIPIVCVVLEGGPGTLHTI----DNATTN--GTPCVVVE     354
sp|Q91YD4|TRPM2_MOUSE          -----------------GVAIKIPIVCVVLEGGPGTLHTI----YNAINN--GTPCVIVE     353
sp|E9PTA2|TRPM2_RAT            -----------------GVAIKIPIVCVVLEGGPGTLHTI----YNAITN--GTPCVIVE     353
sp|Q9HCF6|TRPM3_HUMAN          DSRLFYSFWGSCQLDSVGIGQGVPVVALIVEGGPNVISIV----LEYLRDTPPVPVVVCD     388
sp|Q8TD43|TRPM4_HUMAN          -----------------GTGIDIPVLLLLIDGDEKMLTRI----ENATQA--QLPCLLVA     302
sp|Q7TN37|TRPM4_MOUSE          -----------------GTGIDIPVLLLLIDGDEKMLKRI----EDATQA--QLPCLLVA     303
sp|Q9ESQ5|TRPM4_RAT            -----------------GTGIDIPVLLLLIEGDEKMLKRI----EDATQA--QLPCLLVA     303
sp|P0DTC2|SPIKE_SARS2          VRDL-----------PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTP-----G--DS     254
                                                      *:: : :  .   .  :     .

sp|Q93971|TRPG_CAEEL           GSGRAADLLAFAHQNVTE---------DGLLPDDIRRQVLLLVETTF-GCSEAAAHRLLH     651
sp|Q7Z4N2|TRPM1_HUMAN          GSGRASDILSFAHKYCEE---------GGIINESLREQLLVTIQKTF-NYNKAQSHQLFA     330
sp|Q2TV84|TRPM1_MOUSE          GSGRASDILSFAHKYCDE---------GGVINESLRDQLLVTIQKTF-NYSKSQSYQLFA     376
sp|Q2WEA5|TRPM1_RAT            GSGRASDILSFAHKYCDE---------GGVINESLRDQLLVTIQKTF-NYSKSQSHQLFA     376
sp|A0A0R4IMY7|TRPM2_DANRE      GSGRLADVIAHVASVPVS------KVTM----ALINRLLKRFFMQEYKNFTELQIIEWTK     376
sp|O94759|TRPM2_HUMAN          GSGRVADVIAQVANLPVS------DITI----SLIQQKLSVFFQEMFETFTESRIVEWTK     404
sp|Q91YD4|TRPM2_MOUSE          GSGRVADVIAQVATLPVS------EITI----SLIQQKLSIFFQEMFETFTENQIVEWTK     403
sp|E9PTA2|TRPM2_RAT            GSGRVADVIAQVAALPVS------EITI----SLIQQKLSVFFQEMFETFTENQIVEWTK     403
sp|Q9HCF6|TRPM3_HUMAN          GSGRASDILAFGHKYSEE---------GGLINESLRDQLLVTIQKTF-TYTRTQAQHLFI     438
sp|Q8TD43|TRPM4_HUMAN          GSGGAADCLAETLEDTLA------PGSGGARQGEARDRIRRFFPK-------GDLEVLQA     349
sp|Q7TN37|TRPM4_MOUSE          GSGGAADCLVETLEDTLA------PGSGGLRRGEARDRIRRYFPK-------GDPEVLQA     350
sp|Q9ESQ5|TRPM4_RAT            GSGGAADCLVETLEDTLA------PGSGGLRRGEARDRIRRYFPK-------GDPEVLQA     350
sp|P0DTC2|SPIKE_SARS2          SSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCAL---------------------     293
                               .**  :.                               :

sp|Q93971|TRPG_CAEEL           ELTVCAQHKNLLTIFRLGEQ--GEHDVDHAILTALLK--GQNLSAA-------DQLALAL     700
sp|Q7Z4N2|TRPM1_HUMAN          IIMECMKKKELVTVFRMGSE--GQQDIEMAILTALLK--GTNVSAP-------DQLSLAL     379
sp|Q2TV84|TRPM1_MOUSE          IIMECMKKKELVTVFRMGSE--GQQDVEMAILTALLK--GTNASAP-------DQLSLAL     425
sp|Q2WEA5|TRPM1_RAT            IIMECMKKKELVTVFRMGSE--GQQDVEMAILTALLK--GTNVSAP-------DQLSLAL     425
sp|A0A0R4IMY7|TRPM2_DANRE      KIQDILRMPHLLTVFRIDED--KNYDVDVAILQALLK--ASRSDEHAGRHCWERQLELAV     432
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sp|O94759|TRPM2_HUMAN          KIQDIVRRRQLLTVFREGKD--GQQDVDVAILQALLK--ASRSQDHFGHENWDHQLKLAV     460
sp|Q91YD4|TRPM2_MOUSE          KIQDIVRRRQLLTIFREGKD--GQQDVDVAILQALLK--ASRSQDHFGHENWDHQLKLAV     459
sp|E9PTA2|TRPM2_RAT            KIQDIVRRRQLLTVFREGKD--GQQDVDVAILQALLK--ASRSQDHFGHENWDHQLKLAV     459
sp|Q9HCF6|TRPM3_HUMAN          ILMECMKKKELITVFRMGSE--GHQDIDLAILTALLK--GANASAP-------DQLSLAL     487
sp|Q8TD43|TRPM4_HUMAN          QVERIMTRKELLTVYS-SED--GSEEFETIVLKALVK--ACGSSEA---SAYLDELRLAV     401
sp|Q7TN37|TRPM4_MOUSE          QVERIMTRKELLTVYS-SED--GSEEFETIVLRALVK--ACGSSEA---SAYLDELRLAV     402
sp|Q9ESQ5|TRPM4_RAT            QVERIMTRKELLTVYS-SED--GSEEFETIVLRALVK--ACGSSEA---SAYLDELRLAV     402
sp|P0DTC2|SPIKE_SARS2          --DPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVY     351
                                          :. :   .      :.      ::::                 .:  .

sp|Q93971|TRPG_CAEEL           AWNRVDIARSDV----FAMGHEWPQ-----------------------------------     721
sp|Q7Z4N2|TRPM1_HUMAN          AWNRVDIARSQI----FVFGPHWPPLGSL--APPTDSKATEKEKKPPMATTKGGRGKG-K     432
sp|Q2TV84|TRPM1_MOUSE          AWNRVDIARSQI----FVFGPHWPPLGSL--APPVDTKATEKEKKPPTATTK-GRGKG-K     477
sp|Q2WEA5|TRPM1_RAT            AWNRVDIARSQI----FVFGPHWPPLGSL--APPVDTKVAEKEKKPPTATTK-GRGKG-K     477
sp|A0A0R4IMY7|TRPM2_DANRE      AWNRVDIAESEI----FTEESQWTS-----------------------------------     453
sp|O94759|TRPM2_HUMAN          AWNRVDIARSEI----FMDEWQWKP-----------------------------------     481
sp|Q91YD4|TRPM2_MOUSE          AWNRVDIARSEI----FTDEWQWKP-----------------------------------     480
sp|E9PTA2|TRPM2_RAT            AWNRVDIARSEI----FTDEWQWKP-----------------------------------     480
sp|Q9HCF6|TRPM3_HUMAN          AWNRVDIARSQI----FIYGQQWPV-----------------------------------     508
sp|Q8TD43|TRPM4_HUMAN          AWNRVDIAQSEL----FRGDIQWRS-----------------------------------     422
sp|Q7TN37|TRPM4_MOUSE          AWNRVDIAQSEL----FRGDIQWRS-----------------------------------     423
sp|Q9ESQ5|TRPM4_RAT            AWNRVDIAQSEL----FRGDIQWRS-----------------------------------     423
sp|P0DTC2|SPIKE_SARS2          AWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIA     411
                               ****  *:..      :     :

sp|Q93971|TRPG_CAEEL           --------------------------AALHNAMMEALIHDRVDFVRLLLEQGINMQKFLT     755
sp|Q7Z4N2|TRPM1_HUMAN          GKKKGKVKEEVEEETDPRKIELLNWVNALEQAMLDALVLDRVDFVKLLIENGVNMQHFLT     492
sp|Q2TV84|TRPM1_MOUSE          GKKKGKVKEEVEEETDPRKLELLNWVNALEQAMLDALVLDRVDFVKLLIENGVNMQHFLT     537
sp|Q2WEA5|TRPM1_RAT            GKKKGKVKEEVEEETDPRKIELLNWVNALEQAMLDALVLDRVDFVKLLIENGVNMQHFLT     537
sp|A0A0R4IMY7|TRPM2_DANRE      --------------------------SDLHPAMFSALVGDKPEFVRLLLENGVCVREFLE     487
sp|O94759|TRPM2_HUMAN          --------------------------SDLHPTMTAALISNKPEFVKLFLENGVQLKEFVT     515
sp|Q91YD4|TRPM2_MOUSE          --------------------------ADLHPMMTAALISNKPEFVRLFLENGVRLKEFVT     514
sp|E9PTA2|TRPM2_RAT            --------------------------SDLHPMMTAALISNKPEFVRLFLENGVRLKEFVT     514
sp|Q9HCF6|TRPM3_HUMAN          --------------------------GSLEQAMLDALVLDRVDFVKLLIENGVSMHRFLT     542
sp|Q8TD43|TRPM4_HUMAN          --------------------------FHLEASLMDALLNDRPEFVRLLISHGLSLGHFLT     456
sp|Q7TN37|TRPM4_MOUSE          --------------------------FHLEASLMDALLNDRPEFVRLLISHGLSLGHFLT     457
sp|Q9ESQ5|TRPM4_RAT            --------------------------FHLEASLMDALLNDRPEFVRLLISHGLSLGHFLT     457
sp|P0DTC2|SPIKE_SARS2          PGQTGKIADYNYKLPDDFTGCVIAWNS----NNLDSKVGGNYNYLYRLFRK-SNLKPFE-     465
                                                                  : : .. :::  :: :   :  *

sp|Q93971|TRPG_CAEEL           ISRLDELYNTDKGPPNTLFYIVRDVVR-----------VRQGYRFKLPDIGLVIEKLMGN     804
sp|Q7Z4N2|TRPM1_HUMAN          IPRLEELYNTRLGPPNTLHLLVRDVKKS--N-------LPPDYHISLIDIGLVLEYLMGG     543
sp|Q2TV84|TRPM1_MOUSE          IPRLEELYNTRLGPPNTLHLLVRDVKKS--N-------LPPDYHISLIDIGLVLEYLMGG     588
sp|Q2WEA5|TRPM1_RAT            IPRLEELYNTRLGPPNTLHLLVRDVKKS--N-------LPPDYHISLIDIGLVLEYLMGG     588
sp|A0A0R4IMY7|TRPM2_DANRE      REETLCELYSH--LPSCFFLRKLAKRVQGGKMRRGQEPLPGSRKVCLSHVSEEVRHLLGS     545
sp|O94759|TRPM2_HUMAN          WDTLLYLYENL--DPSCLFHSKLQKVLVEDPERPAC--APAAPRLQMHHVAQVLRELLGD     571
sp|Q91YD4|TRPM2_MOUSE          WDTLLCLYENL--EPSCLFHSKLQKVLAEE-QRLAY--ASATPRLHMHHVAQVLRELLGD     569
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sp|E9PTA2|TRPM2_RAT          WDTLLCLYENL--EPSCLFHSKLQKVLAEEHERLAY--ASETPRLQMHHVAQVLRELLGD     570
sp|Q9HCF6|TRPM3_HUMAN        ISRLEELYNTRHGPSNTLYHLVRDVKKG--N-------LPPDYRISLIDIGLVIEYLMGG     593
sp|Q8TD43|TRPM4_HUMAN        PMRLAQLYSAA--PSNSLIRNLLDQASHS-AGTKAPALKGGAAELRPPDVGHVLRMLLGK     513
sp|Q7TN37|TRPM4_MOUSE        PVRLAQLYSAV--SPNSLIRNLLDQASHA-SSSKSPPVN-GTVELRPPNVGQVLRTLLGE     513
sp|Q9ESQ5|TRPM4_RAT          PVRLAQLYSAV--SPNSLIRNLLDQASHA-SSSKSPPAN-GAAELRPPNVGQVLRTLLGE     513
sp|P0DTC2|SPIKE_SARS2        RDISTEIYQAGSTPCNGV-----------------------------------------E     484
                                            . .

sp|Q93971|TRPG_CAEEL         SYQCSYTTSEFRDKY-KQR-MKRVKHAQKKA--MGVFSSRPSR--TGSGI-----ASRQS     853
sp|Q7Z4N2|TRPM1_HUMAN        AYRCNYTRKNFRTLY-NNL-FGPKRPKALKL--LGMEDDEPPA--KGKKK-----KKK--     590
sp|Q2TV84|TRPM1_MOUSE        AYRCNYTRKSFRTLY-NNL-FGPKRPKALKL--LGMEDDEPPA--KGKKK-----KKK--     635
sp|Q2WEA5|TRPM1_RAT          AYRCNYTRKSFRTLY-NNL-FGPKRPKALKL--LGMEDDEPPA--KGKKK-----KKK--     635
sp|A0A0R4IMY7|TRPM2_DANRE    FTQPLYIASRYKPTK-DDVRLKVPSKGALDLPC---------------------------     577
sp|O94759|TRPM2_HUMAN        FTQPLYPRPRHNDRL----RLLLPVPH-VKLNVQGVSLRS--------------------     606
sp|Q91YD4|TRPM2_MOUSE        STQLLYPRPRYTDRP----RLSMTVPH-IKLNVQGVSLRS--------------------     604
sp|E9PTA2|TRPM2_RAT          STQLLYPRPRYTDRP----RLSLPMPH-IKLNVQGVSLRS--------------------     605
sp|Q9HCF6|TRPM3_HUMAN        AYRCNYTRKRFRTLY-HNL-FGPKRPKALKL--LGMEDDIPLR--RGRKT------TK--     639
sp|Q8TD43|TRPM4_HUMAN        MCAPRYPSGGAWDPH-PGQGFGESMYL---------LSDK--------------------     543
sp|Q7TN37|TRPM4_MOUSE        TCAPRYPARNTRDSY-LGQDHRENDSL---------LMDW--------------------     543
sp|Q9ESQ5|TRPM4_RAT          TCAPRYPARNTRHSL-LGQDHRENDSL---------LMDW--------------------     543
sp|P0DTC2|SPIKE_SARS2        GFNCYFPLQSYGFQPTNGVGYQPYRVVVLSF-----ELLHAPATVCGPKKSTNLVKNKCV     539
                                  :

sp|Q93971|TRPG_CAEEL         TEGMGGVGGGSSVA---------GVFGNSFGNQD-PPLDPHVN------RSALSGSRA--     895
sp|Q7Z4N2|TRPM1_HUMAN        ------------------------------------------------------------     590
sp|Q2TV84|TRPM1_MOUSE        ------------------------------------------------------------     635
sp|Q2WEA5|TRPM1_RAT          ------------------------------------------------------------     635
sp|A0A0R4IMY7|TRPM2_DANRE    ------------------------------------------------------------     577
sp|O94759|TRPM2_HUMAN        ------------------------------------------------------------     606
sp|Q91YD4|TRPM2_MOUSE        ------------------------------------------------------------     604
sp|E9PTA2|TRPM2_RAT          ------------------------------------------------------------     605
sp|Q9HCF6|TRPM3_HUMAN        ------------------------------------------------------------     639
sp|Q8TD43|TRPM4_HUMAN        ------------------------------------------------------------     543
sp|Q7TN37|TRPM4_MOUSE        ------------------------------------------------------------     543
sp|Q9ESQ5|TRPM4_RAT          ------------------------------------------------------------     543
sp|P0DTC2|SPIKE_SARS2        NFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVIT     599


sp|Q93971|TRPG_CAEEL         ---------------------------LSNHILWRSAFRGNFPAN-----PMRPPNLGDS     923
sp|Q7Z4N2|TRPM1_HUMAN        ------------------------------------------------------------     590
sp|Q2TV84|TRPM1_MOUSE        ------------------------------------------------------------     635
sp|Q2WEA5|TRPM1_RAT          ------------------------------------------------------------     635
sp|A0A0R4IMY7|TRPM2_DANRE    ------------------------------------------------------------     577
sp|O94759|TRPM2_HUMAN        ------------------------------------L-----------------------     607
sp|Q91YD4|TRPM2_MOUSE        ------------------------------------L-----------------------     605
sp|E9PTA2|TRPM2_RAT          ------------------------------------L-----------------------     606
sp|Q9HCF6|TRPM3_HUMAN        ------------------------------------------------------------     639
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sp|Q8TD43|TRPM4_HUMAN          ------------------------------------A-----------------------      544
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------A-----------------------      544
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------A-----------------------      544
sp|P0DTC2|SPIKE_SARS2          PGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNS      659


sp|Q93971|TRPG_CAEEL           RDCG---------SEFDEE------------------LSLTS-----ASDGSQTE--PDF      949
sp|Q7Z4N2|TRPM1_HUMAN          --------------KKEEE------------------IDI--------DVDDPAV--SRF      608
sp|Q2TV84|TRPM1_MOUSE          --------------KKEEE------------------IDI--------DVDDPAV--SRF      653
sp|Q2WEA5|TRPM1_RAT            --------------KKEEE------------------IDI--------DVDDPAV--SRF      653
sp|A0A0R4IMY7|TRPM2_DANRE      ------------------------------------------------SGEEWSA--DTV      587
sp|O94759|TRPM2_HUMAN          --------------Y---------------------------------KRSSGHV--TFT      618
sp|Q91YD4|TRPM2_MOUSE          --------------Y---------------------------------KRSTGHV--TFT      616
sp|E9PTA2|TRPM2_RAT            --------------Y---------------------------------KRSTGHV--TFT      617
sp|Q9HCF6|TRPM3_HUMAN          --------------KREEE------------------VDI--------DLDDPEI--NHF      657
sp|Q8TD43|TRPM4_HUMAN          --------------T---------------------------------SPLSLDA--GLG      555
sp|Q7TN37|TRPM4_MOUSE          --------------N---------------------------------KQPSTDA--SFE      555
sp|Q9ESQ5|TRPM4_RAT            --------------N---------------------------------MQ--QDA--SFE      553
sp|P0DTC2|SPIKE_SARS2          YECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFT      719


sp|Q93971|TRPG_CAEEL           RYPYSELMIWAVLTKRQDMAMCMWQHGEEAMAKALVACR----LYKSLATEAAEDYLE-V      1004
sp|Q7Z4N2|TRPM1_HUMAN          QYPFHELMVWAVLMKRQKMAVFLWQRGEESMAKALVACK----LYKAMAHESSESDLV-D      663
sp|Q2TV84|TRPM1_MOUSE          QYPFHELMVWAVLMKRQKMAVFLWQRGEECMAKALVACK----LYKAMAHESSESELV-D      708
sp|Q2WEA5|TRPM1_RAT            QYPFHELMVWAVLMKRQKMAVFLWQRGEECMAKALVACK----LYKAMAHESSESELV-D      708
sp|A0A0R4IMY7|TRPM2_DANRE      WDPGRDLFLWAVVQNNRELAEIGWEQCRDCIAAALAASK----ILRKLAQESGEDDS---      640
sp|O94759|TRPM2_HUMAN          MDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSK----ILKELSKEEE--DT---      669
sp|Q91YD4|TRPM2_MOUSE          IDPVRDLLIWAVIQNHRELAGIIWAQSQDCTAAALACSK----ILKELSKEEE--DT---      667
sp|E9PTA2|TRPM2_RAT            IDPVRDLLIWAIIQNHRELAGIIWAQSQDCTAAALACSK----ILKELSKEEE--DT---      668
sp|Q9HCF6|TRPM3_HUMAN          PFPFHELMVWAVLMKRQKMALFFWQHGEEAMAKALVACK----LCKAMAHEASENDMV-D      712
sp|Q8TD43|TRPM4_HUMAN          QAPWSDLLLWALLLNRAQMAMYFWEMGSNAVSSALGACL----LLRVMARLEP--DA---      606
sp|Q7TN37|TRPM4_MOUSE          QAPWSDLLIWALLLNRAQMAIYFWEKGSNSVASALGACL----LLRVMARLES--EA---      606
sp|Q9ESQ5|TRPM4_RAT            QAPWSDLLIWALLLNRAQMAIYFWEKGSNSVASALGACL----LLRVMARLEW--EA---      604
sp|P0DTC2|SPIKE_SARS2          ISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQ      779
                                    :::  ::  .  . :        :.    *        : : ::

sp|Q93971|TRPG_CAEEL           EICEELKKY-----AEEFRILSLELL-DHCYHVDD-AQTLQLLTYELSNWSNETCLALAV      1057
sp|Q7Z4N2|TRPM1_HUMAN          DISQDLDNN-----SKDFGQLALELL-DQSYKHDE-QIAMKLLTYELKNWSNSTCLKLAV      716
sp|Q2TV84|TRPM1_MOUSE          DISQDLDNN-----SKDFGQLAVELL-DQSYKHDE-QVAMKLLTYELKNWSNSTCLKLAV      761
sp|Q2WEA5|TRPM1_RAT            DISQDLDNN-----SKDFGQLAVELL-DQSYKHDE-QVAMKLLTYELKNWSNSTCLKLAV      761
sp|A0A0R4IMY7|TRPM2_DANRE      EEATEMLEL-----ANHYEKQAIGVF-SECHSWDA-QRAQKLLIRISPSWGRSTCLWLAL      693
sp|O94759|TRPM2_HUMAN          DSSEEMLAL-----AEEYEHRAIGVF-TECYRKDE-ERAQKLLTRVSEAWGKTTCLQLAL      722
sp|Q91YD4|TRPM2_MOUSE          DSSEEMLAL-----ADEFEHRAIGVF-TECYRKDE-ERAQKLLVRVSEAWGKTTCLQLAL      720
sp|E9PTA2|TRPM2_RAT            DSSEEMLAL-----ADEFEHRAIGVF-TECYRKDE-ERAQKLLVRVSEAWGKTTCLQLAL      721
sp|Q9HCF6|TRPM3_HUMAN          DISQELNHN-----SRDFGQLAVELL-DQSYKQDE-QLAMKLLTYELKNWSNATCLQLAV      765
sp|Q8TD43|TRPM4_HUMAN          EEAARRKDL-----AFKFEGMGVDLF-GECYRSSE-VRAARLLLRRCPLWGDATCLQLAM      659
sp|Q7TN37|TRPM4_MOUSE          EEAARRKDL-----AATFESMSVDLF-GECYHNSE-ERAARLLLRRCPLWGEATCLQLAM      659
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sp|Q9ESQ5|TRPM4_RAT            EEAARRKDL-----AAKFESMSVDLF-GECYHNSE-YRAARLLLRRCPLWGEATCLQLAM     657
sp|P0DTC2|SPIKE_SARS2          EVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLL-------------FNKV     826
                               :                :    .  :  .    .       **                :

sp|Q93971|TRPG_CAEEL           IVNNKHFLAHPCCQILLADLWHGGLRMRTHSNIKVVLG-LICPPFIQ--MLEFKTREELL     1114
sp|Q7Z4N2|TRPM1_HUMAN          AAKHRDFIAHTCSQMLLTDMWMGRLRMRKNPGLKVIMG-ILLPPTIL--FLEFRTYDDFS     773
sp|Q2TV84|TRPM1_MOUSE          AAKHRDFIAHTCSQMLLTDMWMGRLRMRKNPGLKVIMG-ILIPPTIL--FLEFRTYDDFS     818
sp|Q2WEA5|TRPM1_RAT            AAKHRDFIAHTCSQMLLTDMWMGRLRMRKNPGLKVIMG-ILIPPTIL--FLEFRSYDDFS     818
sp|A0A0R4IMY7|TRPM2_DANRE      EAHDKSFIAHSGVQALLTQIWCGELSV-DNPHWKVLLC-MIFFPLIYTGFLTFRRDEDIQ     751
sp|O94759|TRPM2_HUMAN          EAKDMKFVSHGGIQAFLTKVWWGQLSV-DNGLWRVTLC-MLAFPLLLTGLISFREKRLQD     780
sp|Q91YD4|TRPM2_MOUSE          EAKDMKFVSHGGIQAFLTKVWWGQLCV-DNGLWRIILC-MLAFPLLFTGFISFREKRLQA     778
sp|E9PTA2|TRPM2_RAT            EAKDMKFVSHGGIQAFLTKVWWGQLCV-DNGLWRIILC-MLAFPLLFTGFISFREKRLQA     779
sp|Q9HCF6|TRPM3_HUMAN          AAKHRDFIAHTCSQMLLTDMWMGRLRMRKNSGLKVILG-ILLPPSIL--SLEFKNKDDMP     822
sp|Q8TD43|TRPM4_HUMAN          QADARAFFAQDGVQSLLTQKWWGDMAS-TTPIWALVLA-FFCPPLIYTRLITFRKSEEEP     717
sp|Q7TN37|TRPM4_MOUSE          QADARAFFAQDGVQSLLTQKWWGEMDS-TTPIWALLLA-FFCPPLIYTNLIVFRKSEEEP     717
sp|Q9ESQ5|TRPM4_RAT            QADARAFFAQDGVQSLLTQKWWGEMDS-TNPIWALLLT-FFCPPLIYTNLILFRKSEEEP     715
sp|P0DTC2|SPIKE_SARS2          TLADAGFIKQYGD-------CLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTS----     875
                                     *. :            * :               .  * :    :

sp|Q93971|TRPG_CAEEL           NQPQTAAEHQNDMNYSSSSSSSSSSSSSSSSSDSSSFEDDDDENNAHNHDQKRTRKTSQG     1174
sp|Q7Z4N2|TRPM1_HUMAN          YQTSKENED---------------------------------------------------     782
sp|Q2TV84|TRPM1_MOUSE          YQTSKENED---------------------------------------------------     827
sp|Q2WEA5|TRPM1_RAT            YQTSKENED---------------------------------------------------     827
sp|A0A0R4IMY7|TRPM2_DANRE      RQAERTEQQKLAMESVFAGQSD--------------------GK------IKR-------     778
sp|O94759|TRPM2_HUMAN          V-----------------------------------------------------------     781
sp|Q91YD4|TRPM2_MOUSE          L-----------------------------------------------------------     779
sp|E9PTA2|TRPM2_RAT            L-----------------------------------------------------------     780
sp|Q9HCF6|TRPM3_HUMAN          YMSQAQEIHLQEKEA---------------------------EE----PE-KP-------     843
sp|Q8TD43|TRPM4_HUMAN          TREE----LEFDMDSVINGEGP--------------------VG-TADPAEKT-------     745
sp|Q7TN37|TRPM4_MOUSE          TQKD----LDFDMDSSINGAGP--------------------PG-TVEPSAKV-------     745
sp|Q9ESQ5|TRPM4_RAT            TQKD----LDFDMDSSMNGAGP--------------------LG-PAEPSAKV-------     743
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     875


sp|Q93971|TRPG_CAEEL           SAQSLNITSLFHSRRRKAKKNEKCDRETDASACEAGNRQIQNGGLTAEYGTFGESNGVSP     1234
sp|Q7Z4N2|TRPM1_HUMAN          ---------------GKEKEEE----NT---------------D---------ANADA--     797
sp|Q2TV84|TRPM1_MOUSE          ---------------GKEKEEE----NV---------------D---------ANADA--     842
sp|Q2WEA5|TRPM1_RAT            ---------------GKEKEEE----NV---------------D---------ANADA--     842
sp|A0A0R4IMY7|TRPM2_DANRE      -----------------------------------------------HL-----------     780
sp|O94759|TRPM2_HUMAN          ------------------------------------------------------------     781
sp|Q91YD4|TRPM2_MOUSE          ------------------------------------------------------------     779
sp|E9PTA2|TRPM2_RAT            ------------------------------------------------------------     780
sp|Q9HCF6|TRPM3_HUMAN          ---------------TKEKEEE----DM---------------ELTAMLG---RNNGE--     864
sp|Q8TD43|TRPM4_HUMAN          -----------------------------------------------PLG---V------     749
sp|Q7TN37|TRPM4_MOUSE          -----------------------------------------------ALE---RRQ----     751
sp|Q9ESQ5|TRPM4_RAT            -----------------------------------------------ALE---RRR----     749
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     875
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sp|Q93971|TRPG_CAEEL           PPPYMRANSRSRYNNRSDMSKTSSVIFGSDPNLSKLQKSNITSTDRPNPMEQFQGTRKIK     1294
sp|Q7Z4N2|TRPM1_HUMAN          ------------------------------------------GSRKGDEENEHKKQRSIP     815
sp|Q2TV84|TRPM1_MOUSE          ------------------------------------------GSRKGDEENEHKKQRSIP     860
sp|Q2WEA5|TRPM1_RAT            ------------------------------------------GSRKGDEENEHKKQRSIP     860
sp|A0A0R4IMY7|TRPM2_DANRE      -----------------------------------------------RGFSQKSELKPLN     793
sp|O94759|TRPM2_HUMAN          ----------------------------------------------------------GT     783
sp|Q91YD4|TRPM2_MOUSE          ----------------------------------------------------------CR     781
sp|E9PTA2|TRPM2_RAT            ----------------------------------------------------------CR     782
sp|Q9HCF6|TRPM3_HUMAN          ------------------------------------------SSRKKDEEEVQSKHRLIP     882
sp|Q8TD43|TRPM4_HUMAN          ------------------------------------------PRQSGRPGCCGGRCGGRR     767
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------------RRRPGRALCCGK------     763
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------------RRRPGHTLCCGG------     761
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     875


sp|Q93971|TRPG_CAEEL           MRRRFYEFYSAPISTFWSWTISFILFITFFTYTLLVKTPPR-PT----VIEYILIAYVAA     1349
sp|Q7Z4N2|TRPM1_HUMAN          IGTKICEFYNAPIVKFWFYTISYLGYLLLFNYVILVRMDGW-PS----LQEWIVISYIVS     870
sp|Q2TV84|TRPM1_MOUSE          IGTKICEFYNAPIVKFWFYTISYLGYLLLFNYVILVRMDGW-PS----PQEWIVISYIVS     915
sp|Q2WEA5|TRPM1_RAT            IGTKICEFYNAPIVKFWFYTISYLGYLLLFNYVILVRMDGW-PS----PQEWIVISYIVS     915
sp|A0A0R4IMY7|TRPM2_DANRE      CSSRLMSFLKSPQVKFYWNIASYFGFLWLFAVVLMIDFQTS-PS----WRELLLYVWLTS     848
sp|O94759|TRPM2_HUMAN          PAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPV-PS----WCECAIYLWLFS     838
sp|Q91YD4|TRPM2_MOUSE          P-ARVRAFFNAPVVIFHMNILSYFAFLCLFAYVLMVDFQPS-PS----WCEYLIYLWLFS     835
sp|E9PTA2|TRPM2_RAT            L-ARVRAFFNAPVVIFYLNILSYFAFLCLFAYVLMVDFQPS-PS----WCEYLIYLWLFS     836
sp|Q9HCF6|TRPM3_HUMAN          LGRKIYEFYNAPIVKFWFYTLAYIGYLMLFNYIVLVKMERW-PS----TQEWIVISYIFT     937
sp|Q8TD43|TRPM4_HUMAN          CLRRWFHFWGAPVTIFMGNVVSYLLFLLLFSRVLLVDFQPAPPG----SLELLLYFWAFT     823
sp|Q7TN37|TRPM4_MOUSE          FSKRWSDFWGAPVTAFLGNVVSYLLFLLLFAHVLLVDFQPTKPS----VSELLLYFWAFT     819
sp|Q9ESQ5|TRPM4_RAT            CSKRWSYFWGAPVTAFLGNVVSYLLFLLLFAHVLLVDFQPTKPG----VFELLLYFWAFT     817
sp|P0DTC2|SPIKE_SARS2          ------ALLAGTITSGWTFGAGAAL-QIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN     928
                                      :  .          .       *   :                ::  :

sp|Q93971|TRPG_CAEEL           FGLEQVRKIIMS--------------DAKPFYEKIRTYVCSFWNCVTILAIIFYIVGFFM     1395
sp|Q7Z4N2|TRPM1_HUMAN          LALEKIREILMS--------------EPGKLSQKIKVWLQEYWNITDLVAISTFMIGAIL     916
sp|Q2TV84|TRPM1_MOUSE          LALEKIREILMS--------------EPGKLSQKIKVWLQEYWNITDLVAISMFMVGAIL     961
sp|Q2WEA5|TRPM1_RAT            LALEKIREILMS--------------EPGKLSQKIKVWLQEYWNITDLVAISMFMVGAIL     961
sp|A0A0R4IMY7|TRPM2_DANRE      LVCEEIRQLYHD-------------FDGSGFRRKAKMYIKDLWNILDVLSIVLFIAGLIC     895
sp|O94759|TRPM2_HUMAN          LVCEEMRQLFYD-------------PDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTC     885
sp|Q91YD4|TRPM2_MOUSE          LVCEETRQLFYD-------------PDGCGLMKMASLYFSDFWNKLDVGAILLFIVGLTC     882
sp|E9PTA2|TRPM2_RAT            LVCEETRQLFYD-------------PDGCGLMKMASLYFSDFWNKLDVGAILLFIAGLTC     883
sp|Q9HCF6|TRPM3_HUMAN          LGIEKMREILMS--------------EPGKLLQKVKVWLQEYWNVTDLIAILLFSVGMIL     983
sp|Q8TD43|TRPM4_HUMAN          LLCEELRQGLSGGGGSLASGG--PGPGHASLSQRLRLYLADSWNQCDLVALTCFLLGVGC     881
sp|Q7TN37|TRPM4_MOUSE          LLCEELRQGLGGGWGSLASGG--RGPDRAPLRHRLHLYLSDTWNQCDLLALTCFLLGVGC     877
sp|Q9ESQ5|TRPM4_RAT            LLCEELRQGLGGGWGTLANGG--PGPGKAPLRHRLHLYLLDTWNQCDLLALTCFLLGVGC     875
sp|P0DTC2|SPIKE_SARS2          SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSN------FGAISSVLNDILS     982
                                   : :.   .                  :         .      . ::     .
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sp|Q93971|TRPG_CAEEL           RCFG---SVAYGRVIL---------------------------------A----CDSVLW     1415
sp|Q7Z4N2|TRPM1_HUMAN          RLQNQ-PYMGYGRVIY---------------------------------C----VDIIFW     938
sp|Q2TV84|TRPM1_MOUSE          RLQSQ-PYMGYGRVIY---------------------------------C----VDIILW     983
sp|Q2WEA5|TRPM1_RAT            RLQNQ-PYMGYGRVIY---------------------------------C----VDIILW     983
sp|A0A0R4IMY7|TRPM2_DANRE      RLQASDTVFYIGKVIL---------------------------------C----IDFIIF     918
sp|O94759|TRPM2_HUMAN          RLIP--ATLYPGRVIL---------------------------------S----LDFILF     906
sp|Q91YD4|TRPM2_MOUSE          RLIP--ATLYPGRIIL---------------------------------S----LDFIMF     903
sp|E9PTA2|TRPM2_RAT            RLIP--ATLYPGRIIL---------------------------------S----LDFIMF     904
sp|Q9HCF6|TRPM3_HUMAN          RLQDQ-PFRSDGRVIY---------------------------------C----VNIIYW     1005
sp|Q8TD43|TRPM4_HUMAN          RLTP--GLYHLGRTVL---------------------------------C----IDFMVF     902
sp|Q7TN37|TRPM4_MOUSE          RLTP--GLFDLGRTVL---------------------------------C----LDFMIF     898
sp|Q9ESQ5|TRPM4_RAT            RLTP--GLFDLGRTVL---------------------------------C----LDFMIF     896
sp|P0DTC2|SPIKE_SARS2          RLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDF     1042
                               *          .: :                                  .     . : :

sp|Q93971|TRPG_CAEEL           TMKLLDYMSVHPKLGPYVTMAGKMIQNMSYIIVML-----VVTLL---SFGLARQSITYP     1467
sp|Q7Z4N2|TRPM1_HUMAN          YIRVLDIFGVNKYLGPYVMMIGKMMIDMLYFVVIM-----LVVLM---SFGVARQAILHP     990
sp|Q2TV84|TRPM1_MOUSE          YIRVLDIFGVNKYLGPYVMMIGKMMIDMLYFVVIM-----LVVLM---SFGVARQAILHP     1035
sp|Q2WEA5|TRPM1_RAT            YIRVLDIFGVNKYLGPYVMMIGKMMIDMLYFVVIM-----LVVLM---SFGVARQAILHP     1035
sp|A0A0R4IMY7|TRPM2_DANRE      CLRLMAIFSISRTLGPKIIIVRRMMLDLFFFMFLL-----SIWVV---AYGVAKQGILIE     970
sp|O94759|TRPM2_HUMAN          CLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLL-----AVWVV---SFGVAKQAILIH     958
sp|Q91YD4|TRPM2_MOUSE          CLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLL-----AVWVV---SFGVAKQAILIH     955
sp|E9PTA2|TRPM2_RAT            CLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLL-----AVWVV---SFGVAKQAILIH     956
sp|Q9HCF6|TRPM3_HUMAN          YIRLLDIFGVNKYLGPYVMMIGKMMIDMMYFVIIM-----LVVLM---SFGVARQAILFP     1057
sp|Q8TD43|TRPM4_HUMAN          TVRLLHIFTVNKQLGPKIVIVSKMMKDVFFFLFFL-----GVWLV---AYGVATEGLLRP     954
sp|Q7TN37|TRPM4_MOUSE          TLRLLHIFTVNKQLGPKIVIVSKMMKDVFFFLFFL-----CVWLV---AYGVATEGILRP     950
sp|Q9ESQ5|TRPM4_RAT            TLRLLHIFTVNKQLGPKIVIVSKMMKDVFFFLFFL-----CVWLV---AYGVATEGILRP     948
sp|P0DTC2|SPIKE_SARS2          CGKGYHLMSFPQSA-P----HGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGV-FV     1096
                                 :    : .     *       :: .: :.            :       .  :.:

sp|Q93971|TRPG_CAEEL           DETWHWILVRNIFLKPYFMLYGEVYADEI-DT--------------CGDEAWDQHLEN--     1510
sp|Q7Z4N2|TRPM1_HUMAN          EEKPSWKLARNIFYMPYWMIYGEVFADQI-------DLYAMEINPPCGENLYDEE-----     1038
sp|Q2TV84|TRPM1_MOUSE          EEKPSWKLARNIFYMPYWMIYGEVFADQI-------DLYAMEINPPCGENLYDEE-----     1083
sp|Q2WEA5|TRPM1_RAT            EEKPSWKLARNIFYMPYWMIYGEVFADQI-DRKTRIHIYAMEINPPCGENLYDEE-----     1089
sp|A0A0R4IMY7|TRPM2_DANRE      NEERLNWIIRGAVYEPYITIFGNFPTNI--DNTLFD-------ISSCSVNASDPLKPK--     1019
sp|O94759|TRPM2_HUMAN          NERRVDWLFRGAVYHSYLTIFGQIPGYI--DGVNFN-------PEHCSPNGTDPYKPK--     1007
sp|Q91YD4|TRPM2_MOUSE          NESRVDWIFRGVVYHSYLTIFGQIPTYI--DGVNFS-------MDQCSPNGTDPYKPK--     1004
sp|E9PTA2|TRPM2_RAT            NESRVDWIFRGVIYHSYLTIFGQIPTYI--DGVNFS-------MDQCSPNGTDPYKPK--     1005
sp|Q9HCF6|TRPM3_HUMAN          NEEPSWKLAKNIFYMPYWMIYGEVFADQI--------------DPPCGQNETRED-----     1098
sp|Q8TD43|TRPM4_HUMAN          RDSDFPSILRRVFYRPYLQIFGQIPQEDM-DVALME-------HSNCSSEPGFWAHPP--     1004
sp|Q7TN37|TRPM4_MOUSE          QDRSLPSILRRVFYRPYLQIFGQIPQEEM-DVALMI-------PGNCSMERGSWAHPE--     1000
sp|Q9ESQ5|TRPM4_RAT            QDRSLPSILRRVFYRPYLQIFGQIPQEEM-DVALMN-------PSNCSAERGSWAHPE--     998
sp|P0DTC2|SPIKE_SARS2          SNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGI----------VNNTVYDPLQPELD     1146
                                :     : :  .        .:                        .

sp|Q93971|TRPG_CAEEL           -------------GGP-VILGNGTTGLSCVP--GYWIPPLLMTFFLLIANILLMSMLIAI     1554
sp|Q7Z4N2|TRPM1_HUMAN          --------------------GK--RLPPCIP--GAWLTPALMACYLLVANILLVNLLIAV     1074
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sp|Q2TV84|TRPM1_MOUSE          --------------------GK--RLPPCIP--GAWLTPALMACYLLVANILLVNLLIAV     1119
sp|Q2WEA5|TRPM1_RAT            --------------------GK--RLPPCIP--GAWLTPALMACYLLVANILLVNLLIAV     1125
sp|A0A0R4IMY7|TRPM2_DANRE      ---------------CP------MLNA-DNTPVFPEWLTIMMLCVYLLFANILLLNLLIAI     1058
sp|O94759|TRPM2_HUMAN          ---------------CP------ESDATQQRPAFPEWLTVLLLCLYLLFTNILLLNLLIAM     1047
sp|Q91YD4|TRPM2_MOUSE          ---------------CP------ESDWTGQAPAFPEWLTVTLLCLYLLFANILLLNLLIAM     1044
sp|E9PTA2|TRPM2_RAT            ---------------CP------ESDWTGQAPAFPEWLTVTLLCLYLLFANILLLNLLIAM     1045
sp|Q9HCF6|TRPM3_HUMAN          --------------------GKIIQLPPCKT--GAWIVPAIMACYLLVANILLVNLLIAV     1136
sp|Q8TD43|TRPM4_HUMAN          ---------------GA------Q--AGTCVSQYANWLVVLLLVIFLLVANILLVNLLIAM     1042
sp|Q7TN37|TRPM4_MOUSE          ---------------GP------V--AGSCVSQYANWLVVLLLIVFLLVANILLLNLLIAM     1038
sp|Q9ESQ5|TRPM4_RAT            ---------------GP------V--AGSCVSQYANWLVVLLLIVFLLVANILLLNLLIAM     1036
sp|P0DTC2|SPIKE_SARS2          SFKEELDKYFKNHTSPDVDLGDISGINAS--------------VVNIQKEIDRLNEVAKN     1192
                                                                              :  :*  :. :

sp|Q93971|TRPG_CAEEL           FNHIFDATDEM--SQQIWLFQRYKQVMEYESTPFLPPPLTPLYHG----------VLILQ     1602
sp|Q7Z4N2|TRPM1_HUMAN          FNNTFFEVKSI--SNQVWKFQRYQLIMTFHDRPVLPPPMIILSHI----------YIIIM     1122
sp|Q2TV84|TRPM1_MOUSE          FNNTFFEVKSI--SNQVWKFQRYQLIMTFHDRPVLPPPMIILSHI----------YIIIM     1167
sp|Q2WEA5|TRPM1_RAT            FNNTFFEVKSI--SNQVWKFQRYQLIMTFHDRPVLPPPMIILSHI----------YIIVM     1173
sp|A0A0R4IMY7|TRPM2_DANRE      FNYTFQEVQDN--TDTIWKFQRYELIKEYHSRPALPPPFILLSHL----------ILFIR     1106
sp|O94759|TRPM2_HUMAN          FNYTFQQVQEH--TDQIWKFQRHDLIEEYHGRPAAPPPFILLSHL----------QLFIK     1095
sp|Q91YD4|TRPM2_MOUSE          FNYTFQEVQEH--TDQIWKFQRHDLIEEYHGRPPAPPPLILLSHL----------QLLIK     1092
sp|E9PTA2|TRPM2_RAT            FNYTFQEVQEH--TDQIWKFQRHDLIEEYHGRPPAPPPLILLSHL----------QLLIK     1093
sp|Q9HCF6|TRPM3_HUMAN          FNNTFFEVKSI--SNQVWKFQRYQLIMTFHERPVLPPPLIIFSHM----------TMIFQ     1184
sp|Q8TD43|TRPM4_HUMAN          FSYTFGKVQGN--SDLYWKAQRYRLIREFHSRPALAPPFIVISHL----------RLLLR     1090
sp|Q7TN37|TRPM4_MOUSE          FSYTFSKVHGN--SDLYWKAQRYSLIREFHSRPALAPPLIIISHV----------RLLIK     1086
sp|Q9ESQ5|TRPM4_RAT            FSYTFNKVHGN--SDLYWKAQRYSLIREFHSRPALAPPLIIISHL----------RLLFK     1084
sp|P0DTC2|SPIKE_SARS2          LNESLIDLQELGKYEQYIKWPWYIWL------GFI-AGLIAIVMVTIMLCCMTSCCSCLK     1245
                               :.  :   .     :       :  :            :  :                .

sp|Q93971|TRPG_CAEEL           FVRTRLSCSKSQ-ERNPMFDFSLKLFLDNDQIEKLHDFEEDCMEDLARQKLNEKNTSNEQ     1661
sp|Q7Z4N2|TRPM1_HUMAN          RLSGR--CRKKREGDQEERDRGLKLFLSDEELKRLHEFEEQCVQEHFREKEDEQQSSSDE     1180
sp|Q2TV84|TRPM1_MOUSE          RLSGR--CRKKREGDQEERDRGLKLFLSDEELKKLHEFEEQCVQEHFREKEDEQQSSSDE     1225
sp|Q2WEA5|TRPM1_RAT            RLSGR--CRKKREGDQEERDRGLKLFLSDEELKKLHEFEEQCVQEHFREKEDEQQSSSDE     1231
sp|A0A0R4IMY7|TRPM2_DANRE      GVFLRDLP---------QRHKNFRQELEQTEEEELLSWEAYMKDNYLASTRQDESQSVEH     1157
sp|O94759|TRPM2_HUMAN          RVVLKTPA---------KRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQKQRPEQ     1146
sp|Q91YD4|TRPM2_MOUSE          RIVLKIPA---------KRHKQLKNKLEKNEETALLSWELYLKENYLQNQQYQQKQRPEQ     1143
sp|E9PTA2|TRPM2_RAT            RIVLKIPA---------KRHKQLKNKLEKNEEAALLSWELYLKENYLQNQQYQHKQRPEQ     1144
sp|Q9HCF6|TRPM3_HUMAN          HLCCR--WR-KHESDPDERDYGLKLFITDDELKKVHDFEEQCIEEYFREKDDRFNSSNDE     1241
sp|Q8TD43|TRPM4_HUMAN          QLCR---RPRSPQ-PSSPALEHFRVYLSKEAERKLLTWESVHKENFLLARARDKRESDSE     1146
sp|Q7TN37|TRPM4_MOUSE          WLRRCRRCRRANL-PASPVFEHFRVCLSKEAERKLLTWESVHKENFLLAQARDKRDSDSE     1145
sp|Q9ESQ5|TRPM4_RAT            WLRRC---HRTNL-PASPVFEHFRVCLSKEAERTLLTWESVHKENFLLAQARDKRDSDSE     1140
sp|P0DTC2|SPIKE_SARS2          GCCSCGSCCKFDEDDSEPVLKGVKLHYT--------------------------------     1273
                                                     .:

sp|Q93971|TRPG_CAEEL           RILRADIRTDQILNRLIDLQAKESMGRDVINDVESRLASVEKAQNEILECVRALLNQNNA     1721
sp|Q7Z4N2|TRPM1_HUMAN          RIRVTSERVENMSMRLEEINERETFMKTSLQTVDLRLAQLEELSNRMVNALENLAGIDRS     1240
sp|Q2TV84|TRPM1_MOUSE          RIRVTSERVENMSMRLEEINERENFMKTSLQTVDLRLSQLEELSGRMVSALENLAGIDRS     1285
sp|Q2WEA5|TRPM1_RAT            RIRVTSERVENMSMRLEEINERENFMKASLQTVDLRLSQLEELSGRMVGALENLAGIDRS     1291
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sp|A0A0R4IMY7|TRPM2_DANRE      RIHDTAEKVGAMSELLEREQEM------VSATMAKRLARLEEQVSESAKALRWIIDALKS     1211
sp|O94759|TRPM2_HUMAN          KIEDISNKVDAMVDLLDLDPLK------RSGSMEQRLASLEEQVAQTAQALHWIVRTLRA     1200
sp|Q91YD4|TRPM2_MOUSE          KIQDISEKVDTMVDLLDMDQVK------RSGSTEQRLASLEEQVTQVTRALHWIVTTLKD     1197
sp|E9PTA2|TRPM2_RAT            KIQDISEKVDTMVDLLDMDRVK------RSGSTEQRLASLEEQVTQMGRSLHWIVTTLKD     1198
sp|Q9HCF6|TRPM3_HUMAN          RIRVTSERVENMSMRLEEVNEREHSMKASLQTVDIRLAQLEDLIGRMATALERLTGLERA     1301
sp|Q8TD43|TRPM4_HUMAN          RLKRTSQKVDLALKQL-----G------HIREYEQRLKVLEREVQQCSRVLGWVAEALSR     1195
sp|Q7TN37|TRPM4_MOUSE          RLKRTSQKVDTALKQL-----G------QIREYDRRLRGLEREVQHCSRVLTWMAEALSH     1194
sp|Q9ESQ5|TRPM4_RAT            RLKRTSQKVDTALKQL-----G------QIREYDRRLRGLEREVQHCSRVLTWMAEALSH     1189
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           -------PTA------IGRCFSPSPDPLVETANGTPGPLLLKL-----PGTDPILEEKDH     1763
sp|Q7Z4N2|TRPM1_HUMAN          -------DLIQARSRASSECE-ATYLLRQSSINSADGYSLYRYH---FNGEELLFED---     1286
sp|Q2TV84|TRPM1_MOUSE          -------DLIQARSRASSECE-ATYLLRQSSINSADGYSLYRYH---FNGEELLFEE---     1331
sp|Q2WEA5|TRPM1_RAT            -------DLIQARSRASSECE-ATYLLRQSSINSADGYSMYRYH---FNGEELLFEE---     1337
sp|A0A0R4IMY7|TRPM2_DANRE      QGCKSKVQPPLMRSKS-SDRDDGDSSGQET--DDEEAPHMFARQLQYPDSTVRRF-----     1263
sp|O94759|TRPM2_HUMAN          SGFSSEADVPTLASQKAAEEPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRF-----     1255
sp|Q91YD4|TRPM2_MOUSE          SGFGSGAGALTLAPQRAFDEPDAELSIRRKVEEPGDGYHVSARHLLYPNARIMRF-----     1252
sp|E9PTA2|TRPM2_RAT            SGFGSGAGALTLA-QRAFDEPDAELSIRKKGEEGGDGYHVSARHLLYPDARIMRF-----     1252
sp|Q9HCF6|TRPM3_HUMAN          -------ESNKIRSRTSSDCTDAAYIVRQSSFNSQEGNTFKLQESIDPAGEET-------     1347
sp|Q8TD43|TRPM4_HUMAN          SALLPPGGPPPPDLPGSKD-----------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE          SALLPPGAPPPPSPTGSKD-----------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT            SALLPPGGPPPPSPTGSKD-----------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           DSGENSNSLPPGRIRRNRT-----ATICGGYVSEERNMMLL-------------------     1799
sp|Q7Z4N2|TRPM1_HUMAN          ----TSLSTSPGTGVRKKT-----CSF---RIKEEKDVKT--HLVPECQNSLHL------     1326
sp|Q2TV84|TRPM1_MOUSE          ----PALSTSPGTAFRKKT-----YSF---RVKDEDA-KS--HLD--QPSNLHH------     1368
sp|Q2WEA5|TRPM1_RAT            ----PALSTSPGTVFRKKT-----CSF---RVKEEDV-KP--HLD--QPSSLHH------     1374
sp|A0A0R4IMY7|TRPM2_DANRE      -------PVPEEKVSWEVNFSPYQPPVYNQQDSSESDTS---------------------     1295
sp|O94759|TRPM2_HUMAN          -------PVPNEKVPWETEFLIYDPPFYTAERKDAAAMDPMGD-----------------     1291
sp|Q91YD4|TRPM2_MOUSE          -------PVPNEKVPWAAEFLIYDPPFYTAEK-DVALTDPVGD-----------------     1287
sp|E9PTA2|TRPM2_RAT            -------PVPNEKVPWEAEFLIYDPPFYTAEKKDATLTDPVGD-----------------     1288
sp|Q9HCF6|TRPM3_HUMAN          -----MSPTSPTLMPRMRS-----HSFYSVNMKDKGGIEKLESIFKERSLSLHRATSSHS     1397
sp|Q8TD43|TRPM4_HUMAN          ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           -SPKPSDVSGIPQQRLM-------------------SVTSMDPLPLPLA-----------     1828
sp|Q7Z4N2|TRPM1_HUMAN          -SLGTST-SATPDGSHLAVDDLKNAEESKLGPDIGISKED-------DERQTD-------     1370
sp|Q2TV84|TRPM1_MOUSE          -TPGPSP-PATPGRSRLALEGPLST-ELRPGSDPGISAGE-------FDPRAD-------     1411
sp|Q2WEA5|TRPM1_RAT            -TPGPSP-PATPGRSRLALDGPLST-ELRPGLDPGISAGE-------LDPRAD-------     1417
sp|A0A0R4IMY7|TRPM2_DANRE      ------------------------------------------ALDKHRNPGG-RTGIRGK     1312
sp|O94759|TRPM2_HUMAN          -TLE--PLST---IQYNVVDGLRDRRSF-----HGPYTV---QAGLPLNPMG-RTGLRGR     1336
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sp|Q91YD4|TRPM2_MOUSE            -TAE--PLSK---ISYNVVDGPTDRRSF-----HGVYVV---EYGFPLNPMG-RTGLRGR     1332
sp|E9PTA2|TRPM2_RAT              -TAE--PLSK---INYNVVDGLMDRCSF-----HGTYVV---QYGFPLNPMG-RTGLRGR     1333
sp|Q9HCF6|TRPM3_HUMAN            VAKEPKA-PAAPANTLAIVPD-----SRRPSSCIDIYVSAMDELHCDIDPLDNSVNILGL     1451
sp|Q8TD43|TRPM4_HUMAN            ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE            ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT              ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2            ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL             ------------------------------------KLSTMSIRRRHEEYTSITDS----     1848
sp|Q7Z4N2|TRPM1_HUMAN            ----SK-KEETISPSLNKTDVIHGQDKS-----------DVQNTQLTV---------ETT     1405
sp|Q2TV84|TRPM1_MOUSE            ----FK--STEAAPSLNAA--------------------GVTGTQL--------------     1431
sp|Q2WEA5|TRPM1_RAT              ----FK--SAEVAPSLNTA--------------------NVASTQL--------------     1437
sp|A0A0R4IMY7|TRPM2_DANRE        GALNTLGPNHILHPIFTRWRDAE------H--------------KVLEFLAVWEDAEKRW     1352
sp|O94759|TRPM2_HUMAN            GSLSCFGPNHTLYPMVTRWRRNE------DG-----AICRKSIKKMLEVLVVKLPLSEHW     1385
sp|Q91YD4|TRPM2_MOUSE            GSLSWFGPNHTLQPVVTRWKRNQ------GG-----AICRKSVRKMLEVLVMKLPRSEHW     1381
sp|E9PTA2|TRPM2_RAT              GSLSWFGPNHTLQPVVTRWKRNQ------GG-----GICRKSVRKMLEVLVVKLPQSEHW     1382
sp|Q9HCF6|TRPM3_HUMAN            GEPSFSTPVPSTAPSSSAYATLAPTDRPPSRSIDFEDITSMDTRSFSSDYTHLPECQNPW     1511
sp|Q8TD43|TRPM4_HUMAN            ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE            ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT              ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2            ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL             ---IAIRHP-------ERRIRNNRSNSSEHD-ESAVDSEGGGNVTSSPRKRSTRDLRMTP     1897
sp|Q7Z4N2|TRPM1_HUMAN            NIEGTISYP-------LEETKITRYFPDET--INACTKMKSRSFVYSRGRKLVG--GV-N     1453
sp|Q2TV84|TRPM1_MOUSE            TVESTDSHP-------LRESKLVRYYPGD---PNTYKTMKSRSFVYTEGRKLVR--GL-S     1478
sp|Q2WEA5|TRPM1_RAT              TVESTVSHP-------LRESKLARYYPGD---LNTYKTMKSRSFVYSEGRKLVR--GL-S     1484
sp|A0A0R4IMY7|TRPM2_DANRE        ALLGGPAQPDEPLAQVLERILGKKLNEKTKTLLKA------GEEVYK---GYVDDSRNTD     1403
sp|O94759|TRPM2_HUMAN            ALPGGSREPGEMLPRKLKRILRQEHWPSFENLLKC------GMEVYK---GYMDDPRNTD     1436
sp|Q91YD4|TRPM2_MOUSE            ALPGGSREPGEMLPRKLKRVLRQEFWVAFETLLMQ------GTEVYK---GYVDDPRNTD     1432
sp|E9PTA2|TRPM2_RAT              ALPGGSREPGKMLPRKLKQVLQQEYWVTFETLLRQ------GTEVYK---GYVDDPRNTD     1433
sp|Q9HCF6|TRPM3_HUMAN            DSEPPMYHT-------IERSKSSRYLATTPFLLEEAPIVKSHSFMFSPSRSYYANFGV-P     1563
sp|Q8TD43|TRPM4_HUMAN            ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE            ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT              ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2            ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL             SSQVEESTSR---------------------------DQIFEI----------------D     1914
sp|Q7Z4N2|TRPM1_HUMAN            -QDVEYSSIT---------------------------DQQL-TTEWQCQVQKITRSHSTD     1484
sp|Q2TV84|TRPM1_MOUSE            NWSAEYSSIM---------------------------DQAWNATEWRCQVQRITRSRSTD     1511
sp|Q2WEA5|TRPM1_RAT              NWGAEYSSIM---------------------------DQTWNSAEWRCQVQRITRSRSTD     1517
sp|A0A0R4IMY7|TRPM2_DANRE        NAWVETSIITLHCDKNTPLMA-DLNHMVE------SSLSSHQPLQWREVSSDACRCSYQ-     1455
sp|O94759|TRPM2_HUMAN            NAWIETVAVSVHFQDQNDVELNRLNSNLHACDSG-------ASIRWQVVDRRIPLYANH-     1488
sp|Q91YD4|TRPM2_MOUSE            NAWIETVAVSIHFQDQNDMELKRLEENLHTHDPKELTRDLKLSTEWQVVDRRIPLYANH-     1491
sp|E9PTA2|TRPM2_RAT              NAWIETVAVSIHFQDQNDVELKRLEENLQTHDPKESARGLEMSTEWQVVDRRIPLYVNH-     1492
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sp|Q9HCF6|TRPM3_HUMAN          VKTAEYTSIT---------------------------DCI----DTRCVNA---------     1583
sp|Q8TD43|TRPM4_HUMAN          ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           HPEHEEDEAQADCELTDVITEEEDEEEDDEEDDSHERHHIHPRRKSSRQNR-QPSHTLET     1973
sp|Q7Z4N2|TRPM1_HUMAN          IPYIVS-EAAVQAEHKEQFADMQDEHHV---------AEAIPR---------IPRLSLTI     1525
sp|Q2TV84|TRPM1_MOUSE          IPYIVS-EAASQDEL-------EDEHRG---------SLLDPQ---------ISRSALTV     1545
sp|Q2WEA5|TRPM1_RAT            IPYIVS-EAASQDEF-------EDEHRE---------SLLAPQ---------ISRSALTV     1551
sp|A0A0R4IMY7|TRPM2_DANRE      -REALR---QIAHHHNTYF-----------------------------------------     1470
sp|O94759|TRPM2_HUMAN          -KTLLQ---KAAAEFGAHY-----------------------------------------     1503
sp|Q91YD4|TRPM2_MOUSE          -KTILQ---KVASLFGAHF-----------------------------------------     1506
sp|E9PTA2|TRPM2_RAT            -KKILQ---KVASLFGAHF-----------------------------------------     1507
sp|Q9HCF6|TRPM3_HUMAN          -PQAIADRAAFPGGLGDKVEDLTCCHPE------REAELSHPSSDSEENEAKGRRATIAI     1636
sp|Q8TD43|TRPM4_HUMAN          ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           DLSEGEEVDPLDVLKM-KELPIIHQILN-EEEQAGAPHSTPVIASPSSSRADLTSQK---     2028
sp|Q7Z4N2|TRPM1_HUMAN          TDRNGM---------ENLLSVKPDQTLGFPSLRSKSLHGHPRNVKSIQGKLDRSGHASSV     1576
sp|Q2TV84|TRPM1_MOUSE          SDRPEK---------ENLLSVKPHQTLGFPCLRSRSLHGRPRSAEPAPSKLDRAGHASST     1596
sp|Q2WEA5|TRPM1_RAT            SDRPEK---------ENLLSVKPHQTLGFPCLRSRSLHGHPRSAKPSPSKLDRAGHASST     1602
sp|A0A0R4IMY7|TRPM2_DANRE      ------------------------------------------------------------     1470
sp|O94759|TRPM2_HUMAN          ------------------------------------------------------------     1503
sp|Q91YD4|TRPM2_MOUSE          ------------------------------------------------------------     1506
sp|E9PTA2|TRPM2_RAT            ------------------------------------------------------------     1507
sp|Q9HCF6|TRPM3_HUMAN          SSQEGDNSE--RTLSNNITVPKIERANSYSAEEPSAPYAHTRKSFSISDKLDRQRNTASL     1694
sp|Q8TD43|TRPM4_HUMAN          ------------------------------------------------------------     1214
sp|Q7TN37|TRPM4_MOUSE          ------------------------------------------------------------     1213
sp|Q9ESQ5|TRPM4_RAT            ------------------------------------------------------------     1208
sp|P0DTC2|SPIKE_SARS2          ------------------------------------------------------------     1273


sp|Q93971|TRPG_CAEEL           ----------------------------CSDV------   2032
sp|Q7Z4N2|TRPM1_HUMAN          SSLVIVSGM-TAEEKKVKKE-KASTETEC---------   1603
sp|Q2TV84|TRPM1_MOUSE          SNLAVMSVV-P-EGQNTQQE-KRSAETEC---------   1622
sp|Q2WEA5|TRPM1_RAT            SNLAVMSDA-P-EGQNTQQE-KGNPETEC---------   1628
sp|A0A0R4IMY7|TRPM2_DANRE      --------------------------------------   1470
sp|O94759|TRPM2_HUMAN          --------------------------------------   1503
sp|Q91YD4|TRPM2_MOUSE          --------------------------------------   1506
sp|E9PTA2|TRPM2_RAT            --------------------------------------   1507
sp|Q9HCF6|TRPM3_HUMAN          RNPFQRSKSSKPEGRGDSLSMRRLSRTSAFQSFESKHN   1732
sp|Q8TD43|TRPM4_HUMAN          --------------------------------------   1214
```

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sp|Q7TN37|TRPM4_MOUSE          --------------------------------------   1213
sp|Q9ESQ5|TRPM4_RAT            --------------------------------------   1208
sp|P0DTC2|SPIKE_SARS2          --------------------------------------   1273
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CLUSTAL O(1.2.4) multiple sequence alignment


sp|P75606|Y087_MYCPN       ------------------------------------------------------------ 0
sp|Q2KI99|STING_BOVIN      MP------HSSLHPSIPQPRGLRAQKAALVLLSACLVALWGLGEPPDY------T----L 44
sp|E1C7U0|STING_CHICK      MPQDPSTRSSPARLLIPEPRAGRARHAACVLLAVCFVVLFLSGEPLAP------I----I 50
sp|Q86WV6|STING_HUMAN      MP------HSSLHPSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEH------T----L 44
sp|Q3TBT3|STING_MOUSE      MP------YSNLHPAIPRPRGHRSKYVALIFLVASLMILWVAKDPPNH------T----L 44
sp|A7SLZ2|STING_NEMVE      MR---RAEENNGFGTIPKRRNQHTPFYASIGMIVVIIVAFTSYHITSYGDDRNRAMRQYS 57
sp|B8XX90|STING_PIG        MP------YSSLHPSIPQPRGLRAQVAALVLLGACLVALWGLGELPEY------T----L 44
sp|F1M391|STING_RAT        MP------YSNLHPSIPRPRSYRFKLAAFVLLVGSLMSLWMTGEPPSH------T----L 44
sp|A8E5V9|STING_XENTR      --------------------------MACVLAIGSILFVWILGKGKYSGAQ---L----I 27


sp|P75606|Y087_MYCPN       --MTLIYVPTTLNL--IDSFNYSESIYKWGDYFFRHLESRD--FYF----SNFGFISLFL 50
sp|Q2KI99|STING_BOVIN      KWLVLHLASQQMGLLIKGICSLAEE--------LCHVHSRYHGSYWRAVRACLCSSM--- 93
sp|E1C7U0|STING_CHICK      RSVCTQLAALQLGVLLKGCCCLAEE--------IFHLHSRHHGSLWQVLCSCFPPR---- 98
sp|Q86WV6|STING_HUMAN      RYLVLHLASLQLGLLLNGVCSLAEE--------LRHIHSRYRGSYWRTVRACLGCPL--- 93
sp|Q3TBT3|STING_MOUSE      KYLALHLASHELGLLLKNLCCLAEE--------LCHVQSRYQGSYWKAVRACLGCPI--- 93
sp|A7SLZ2|STING_NEMVE      FTFSLAYLAFLVGELLRRCCLFAEE--------YRHIETRYNGSLKKAIQTTFSFGH--- 106
sp|B8XX90|STING_PIG        RWLVLHLASQQIGLLVKGLCSLAEE--------LCHVHSRYQSSYWRAARACLGCPI--- 93
sp|F1M391|STING_RAT        HYLALHVASQQLGLLLKKLCCLAEE--------LCHVQSRYQGSYWKAVRACVGSPI--- 93
sp|A8E5V9|STING_XENTR      YRMATNFAISQGCCLVTCACELTEE--------IKHLHTRYNGHYWRALKASFNLS---- 75
                             .                   :*.          *:.:*          : .

sp|P75606|Y087_MYCPN       LLFVIPTITLTTLGCFLFSY---------------------------------------- 70
sp|Q2KI99|STING_BOVIN      -----RCGALLLLSCYFY--CSLPN-----------------------MADLPFTWM--L 121
sp|E1C7U0|STING_CHICK      -----WYLALLLVGGSAY--LDPPE-----------------------DNGHSPRLA--L 126
sp|Q86WV6|STING_HUMAN      -----RRGALLLLSIYFY--YSLPN-----------------------AVGPPFTWM--L 121
sp|Q3TBT3|STING_MOUSE      -----HCMAMILLSSYFY--F-LQN-----------------------TADIYLSWM--F 120
sp|A7SLZ2|STING_NEMVE      -----NNV-LFVASLLFFVVFVASNDPNGSSSVIQGNSTAEPHTEMRQTSGWQGLWGQFI 160
sp|B8XX90|STING_PIG        -----RCGALLLLSCYFY--FSIRD-----------------------KAGLPLPWM--L 121
sp|F1M391|STING_RAT        -----CFMALILLSFYFY--CSLEN-----------------------TSDLRLAWH--L 121
sp|A8E5V9|STING_XENTR      -----CAAFVTAILCYVF--YEPKL-----------------------MASLPLTID--I 103
                                    :       :

sp|P75606|Y087_MYCPN       ------------LRFTDINKIKIQIYSLLTVFIFIDVFGLVVSVLFGYLLPLAFDSLPFS 118
sp|Q2KI99|STING_BOVIN      ALLGLSQALNILLGLQGLAPAEV--SAICEKRNFNVAHGLAWSYYIGYLRLIL-PGLPAR 178
sp|E1C7U0|STING_CHICK      TLSCLCQLLVLALGLQKLSAVEV--SELTESSKKNVAHGLAWSYYIGYLKVVL-PRLKEC 183
sp|Q86WV6|STING_HUMAN      ALLGLSQALNILLGLKGLAPAEI--SAVCEKGNFNVAHGLAWSYYIGYLRLIL-PELQAR 178
sp|Q3TBT3|STING_MOUSE      GLLVLYKSLSMLLGLQSLTPAEV--SAVCEEKKLNVAHGLAWSYYIGYLRLIL-PGLQAR 177
sp|A7SLZ2|STING_NEMVE      ISALLTPLVVHLLGLRELSKVEE--SQLNEKENKNVADGLAWSYYFGYLKFVL-PELEKQ 217
sp|B8XX90|STING_PIG        ALLGLSQALNILLGLQHLAPAEV--SAICEKRNFNVAHGLAWSYYIGYLRLIL-PGLRAR 178
sp|F1M391|STING_RAT        GILVLSKSLSMTLDLQSLAPAEV--SAVCEEKNFNVAHGLAWSYYIGYLKLIL-PGLQAR 178
sp|A8E5V9|STING_XENTR      TLTLLSWLFCWILGIQGPTPATI--SEITEIKQLNVAHGLAWSYYVGYLQFVL-PALKES 160
                                       * :            :        . **. *  .***  :    *
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sp|P75606|Y087_MYCPN       V--------NLTREVFLSLAMIVIFANSVIFT-L-----RQKRNID-------------- 150
sp|Q2KI99|STING_BOVIN      IQIYNQFHNNTLQGAGSHRLHILFPLDCGVPDDLN----VADPNIRFLHELPQQSADRAG 234
sp|E1C7U0|STING_CHICK      MEELSRTNPMLRAHRDTWKLHILVPLGCDIWDDLE----KADSNIQYLADLPETILTRAG 239
sp|Q86WV6|STING_HUMAN      IRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLS----MADPNIRFLDKLPQQTGDHAG 234
sp|Q3TBT3|STING_MOUSE      IRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDNLS----VVDPNIRFRDMLPQQNIDRAG 233
sp|A7SLZ2|STING_NEMVE      IEKTSKFRS---KEKFVKKMFILIPSNCFWDDKIPGSDYDPQNRITFEGNTEPLEKTRGG 274
sp|B8XX90|STING_PIG        IQAYNQRHKNVLGGIGNHRLHILFPLDCGVPDDLS----VADPNIRFLHELPQQSADRAG 234
sp|F1M391|STING_RAT        IRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDDLS----VADPNIRFRDMLPQQNTDRAG 234
sp|A8E5V9|STING_XENTR      IQKFNEENHNLLKFPETCRLHILIPLSCRLYGDLK----DVDENITFLKEIPPLYIDRAG 216
                           :                    *:.  ..     :       . .*

sp|P75606|Y087_MYCPN       ------------------------------------------------------------ 150
sp|Q2KI99|STING_BOVIN      IKGRVYTNSIYELLENGQRAGVCVLEYATPLQTLFAMSQDGRAGFSREDRLEQAKLFCRT 294
sp|E1C7U0|STING_CHICK      IKRRVYKHSLYVIRDKDNKLRPCVLEFASPLQTLCAMSQDDCAAFSREQRLEQARLFYRS 299
sp|Q86WV6|STING_HUMAN      IKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAKLFCRT 294
sp|Q3TBT3|STING_MOUSE      IKNRVYSNSVYEILENGQPAGVCILEYATPLQTLFAMSQDAKAGFSREDRLEQAKLFCRT 293
sp|A7SLZ2|STING_NEMVE      VFLRHYKHSVYEIKDGENEPWFCIMEYATPLLTLYDMSVAQPGELSREERDAQVVVFLRK 334
sp|B8XX90|STING_PIG        IKGRVYTNSIYELLENGQPAGVCVLGYATPLQTLFAMSQDGRAGFSREDRLEQAKLFCRT 294
sp|F1M391|STING_RAT        VKNRAYSNSVYELLENGQPAGACILEYATPLQTLFAMSQDGKAGFSREDRLEQAKLFCRT 294
sp|A8E5V9|STING_XENTR      IKGRVFKNNVYRILDEDGRPYNCIVEYATPLASLLKMTDIPSAAFSADDRLQQTKLFYRT 276


sp|P75606|Y087_MYCPN       ------------------------------------------------------------ 150
sp|Q2KI99|STING_BOVIN      LEDILANAPESQNNCRLIVYQEPA---EGSSFSLSQEILQHLRQEER-EVTMGSTETSVM 350
sp|E1C7U0|STING_CHICK      LRDILGSSKECAGLYRLIAYEEPA---EPESHFLSGLILWHLQQQQREEYMVQEELP--- 353
sp|Q86WV6|STING_HUMAN      LEDILADAPESQNNCRLIAYQEPA---DDSSFSLSQEVLRHLRQEEKEEVTVGSLKTSAV 351
sp|Q3TBT3|STING_MOUSE      LEEILEDVPESRNNCRLIVYQEPT---DGNSFSLSQEVLRHIRQEEKEEVTMNAPMTSVA 350
sp|A7SLZ2|STING_NEMVE      LQDILEGDRACQGKYELVTFSPDRD--------LADVMLRKLKDSE---LEIGG------ 377
sp|B8XX90|STING_PIG        LEDILADAPEAQNNCRLIVYQEPT---EGGSFSLSQEILRHLRQEER-EVTMGSAETSVV 350
sp|F1M391|STING_RAT        LEEILADVPESRNHCRLIVYQESE---EGNSFSLSQEVLRHIRQEEKEEVTMSGPPTSVA 351
sp|A8E5V9|STING_XENTR      LKDILENAHELQNTYRLIVYEDFPETKDHSRHLLSQEILKHIRQQHSEEYSML------- 329


sp|P75606|Y087_MYCPN       ---------------------------- 150
sp|Q2KI99|STING_BOVIN      PGSSVLSQEPELLISGLEKPLPLRSDVF 378
sp|E1C7U0|STING_CHICK      --LGTSSVELSLQVSSSDLPQPLRSDCP 379
sp|Q86WV6|STING_HUMAN      PSTSTMSQEPELLISGMEKPLPLRTDFS 379
sp|Q3TBT3|STING_MOUSE      PPPSVLSQEPRLLISGMDQPLPLRTDLI 378
sp|A7SLZ2|STING_NEMVE      ---------------------------- 377
sp|B8XX90|STING_PIG        PTSSTLSQEPELLISGMEQPLPLRSDIF 378
sp|F1M391|STING_RAT        PRPSLLSQEPRLLISGMEQPLPLRTDLI 379
sp|A8E5V9|STING_XENTR      ---------------------------- 329
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CLUSTAL O(1.2.4) multiple sequence alignment


sp|P9WGC0|Y1339_MYCTO      -----------MRRCIPHRCIGHGTVVSVRITVLGCSGSVVGPDSPA-SGYL---LRAPH 45
sp|P9WGC1|Y1339_MYCTU      -----------MRRCIPHRCIGHGTVVSVRITVLGCSGSVVGPDSPA-SGYL---LRAPH 45
sp|Q2KI99|STING_BOVIN      MP------HSSLHPSIPQPRGLRAQKA-ALVLLSACLVALWGLGEPPDY------T---- 43
sp|E1C7U0|STING_CHICK      MPQDPSTRSSPARLLIPEPRAGRARHA-ACVLLAVCFVVLFLSGEPLAP------I---- 49
sp|Q86WV6|STING_HUMAN      MP------HSSLHPSIPCPRGHGAQKA-ALVLLSACLVTLWGLGEPPEH------T---- 43
sp|Q3TBT3|STING_MOUSE      MP------YSNLHPAIPRPRGHRSKYV-ALIFLVASLMILWVAKDPPNH------T---- 43
sp|A7SLZ2|STING_NEMVE      MR---RAEENNGFGTIPKRRNQHTPFY-ASIGMIVVIIVAFTSYHITSYGDDRNRAMRQY 56
sp|B8XX90|STING_PIG        MP------YSSLHPSIPQPRGLRAQVA-ALVLLGACLVALWGLGELPEY------T---- 43
sp|F1M391|STING_RAT        MP------YSNLHPSIPRPRSYRFKLA-AFVLLVGSLMSLWMTGEPPSH------T---- 43
sp|A8E5V9|STING_XENTR      --------------------------M-ACVLAIGSILFVWILGKGKYSGAQ---L---- 26
                                                       . :

sp|P9WGC0|Y1339_MYCTO      TPPLVIDFGGGVLGALQRHADPASVHVLLSHLHAD----------HC---------LDLP 86
sp|P9WGC1|Y1339_MYCTU      TPPLVIDFGGGVLGALQRHADPASVHVLLSHLHAD----------HC---------LDLP 86
sp|Q2KI99|STING_BOVIN      LKWLVLHLASQQMGLLIKGICS--LAEELCHVHSRYHGSYWRAVRACLCSSMRCGALLLL 101
sp|E1C7U0|STING_CHICK      IRSVCTQLAALQLGVLLKGCCC--LAEEIFHLHSRHHGSLWQVLCSCFPPR-WYLALLLV 106
sp|Q86WV6|STING_HUMAN      LRYLVLHLASLQLGLLLNGVCS--LAEELRHIHSRYRGSYWRTVRACLGCPLRRGALLLL 101
sp|Q3TBT3|STING_MOUSE      LKYLALHLASHELGLLLKNLCC--LAEELCHVQSRYQGSYWKAVRACLGCPIHCMAMILL 101
sp|A7SLZ2|STING_NEMVE      SFTFSLAYLAFLVGELLRRCCL--FAEEYRHIETRYNGSLKKAIQTTFSFGHNNV-LFVA 113
sp|B8XX90|STING_PIG        LRWLVLHLASQQIGLLVKGLCS--LAEELCHVHSRYQSSYWRAARACLGCPIRCGALLLL 101
sp|F1M391|STING_RAT        LHYLALHVASQQLGLLLKKLCC--LAEELCHVQSRYQGSYWKAVRACVGSPICFMALILL 101
sp|A8E5V9|STING_XENTR      IYRMATNFAISQGCCLVTCACE--LTEEIKHLHTRYNGHYWRALKASFNLS-CAAFVTAI 83
                              .           *        .     *:.:                      :

sp|P9WGC0|Y1339_MYCTO      GLFVWRRYHPSR-PSGKALL----------------YGPSDTWSRLGAASSPYGGEIDDC 129
sp|P9WGC1|Y1339_MYCTU      GLFVWRRYHPSR-PSGKALL----------------YGPSDTWSRLGAASSPYGGEIDDC 129
sp|Q2KI99|STING_BOVIN      SCYFY--CSLPN-----------------------MADLPFTWM--LAL----------- 123
sp|E1C7U0|STING_CHICK      GGSAY--LDPPE-----------------------DNGHSPRLA--LTL----------- 128
sp|Q86WV6|STING_HUMAN      SIYFY--YSLPN-----------------------AVGPPFTWM--LAL----------- 123
sp|Q3TBT3|STING_MOUSE      SSYFY--F-LQN-----------------------TADIYLSWM--FGL----------- 122
sp|A7SLZ2|STING_NEMVE      SLLFFVVFVASNDPNGSSSVIQGNSTAEPHTEMRQTSGWQGLWGQFIIS----------- 162
sp|B8XX90|STING_PIG        SCYFY--FSIRD-----------------------KAGLPLPWM--LAL----------- 123
sp|F1M391|STING_RAT        SFYFY--CSLEN-----------------------TSDLRLAWH--LGI----------- 123
sp|A8E5V9|STING_XENTR      LCYVF--YEPKL-----------------------MASLPLTID--ITL----------- 105
                               :                                .

sp|P9WGC0|Y1339_MYCTO      SDIFDVHHWADSEPVTLGALTIVPRLVAHPTESFGLRITDPSGASLAYSGDTGICDQL-V 188
sp|P9WGC1|Y1339_MYCTU      SDIFDVHHWADSEPVTLGALTIVPRLVAHPTESFGLRITDPSGASLAYSGDTGICDQL-V 188
sp|Q2KI99|STING_BOVIN      ------LGLSQALNILLGLQGLAPAEVSAICEKRNFNV----AHGLAWSYYIGYLRLILP 173
sp|E1C7U0|STING_CHICK      ------SCLCQLLVLALGLQKLSAVEVSELTESSKKNV----AHGLAWSYYIGYLKVVLP 178
sp|Q86WV6|STING_HUMAN      ------LGLSQALNILLGLKGLAPAEISAVCEKGNFNV----AHGLAWSYYIGYLRLILP 173
sp|Q3TBT3|STING_MOUSE      ------LVLYKSLSMLLGLQSLTPAEVSAVCEEKKLNV----AHGLAWSYYIGYLRLILP 172
sp|A7SLZ2|STING_NEMVE      ------ALLTPLVVHLLGLRELSKVEESQLNEKENKNV----ADGLAWSYYFGYLKFVLP 212
sp|B8XX90|STING_PIG        ------LGLSQALNILLGLQHLAPAEVSAICEKRNFNV----AHGLAWSYYIGYLRLILP 173
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sp|F1M391|STING_RAT        ------LVLSKSLSMTLDLQSLAPAEVSAVCEEKNFNV----AHGLAWSYYIGYLKLILP 173
sp|A8E5V9|STING_XENTR      ------TLLSWLFCWILGIQGPTPATISEITEIKQLNV----AHGLAWSYYVGYLQFVLP 155
                                           *.         :   *    .:    . .**:*   *    :

sp|P9WGC0|Y1339_MYCTO      ELARGVDVFL--------------------CEASWTH-SP----KHPPDLHLSGTEAGMV 223
sp|P9WGC1|Y1339_MYCTU      ELARGVDVFL--------------------CEASWTH-SP----KHPPDLHLSGTEAGMV 223
sp|Q2KI99|STING_BOVIN      GLPARIQIYNQFHNNTLQGAGSHRLHILFPLDCGVPDDLN----VADPNIRFLHELPQQS 229
sp|E1C7U0|STING_CHICK      RLKECMEELSRTNPMLRAHRDTWKLHILVPLGCDIWDDLE----KADSNIQYLADLPETI 234
sp|Q86WV6|STING_HUMAN      ELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNLS----MADPNIRFLDKLPQQT 229
sp|Q3TBT3|STING_MOUSE      GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDNLS----VVDPNIRFRDMLPQQN 228
sp|A7SLZ2|STING_NEMVE      ELEKQIEKTSKFRS---KEKFVKKMFILIPSNCFWDDKIPGSDYDPQNRITFEGNTEPLE 269
sp|B8XX90|STING_PIG        GLRARIQAYNQRHKNVLGGIGNHRLHILFPLDCGVPDDLS----VADPNIRFLHELPQQS 229
sp|F1M391|STING_RAT        GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDDLS----VADPNIRFRDMLPQQN 229
sp|A8E5V9|STING_XENTR      ALKESIQKFNEENHNLLKFPETCRLHILIPLSCRLYGDLK----DVDENITFLKEIPPLY 211
                            *   :                          .                :

sp|P9WGC0|Y1339_MYCTO      AAQAGVR---------ELLLTHIPPWTSR-----------------------EDVISEAK 251
sp|P9WGC1|Y1339_MYCTU      AAQAGVR---------ELLLTHIPPWTSR-----------------------EDVISEAK 251
sp|Q2KI99|STING_BOVIN      ADRAGIKGRVYTNSIYELLENGQRAGVCVLEYATPLQTLFAMSQDGRAGFSREDRLEQAK 289
sp|E1C7U0|STING_CHICK      LTRAGIKRRVYKHSLYVIRDKDNKLRPCVLEFASPLQTLCAMSQDDCAAFSREQRLEQAR 294
sp|Q86WV6|STING_HUMAN      GDHAGIKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAK 289
sp|Q3TBT3|STING_MOUSE      IDRAGIKNRVYSNSVYEILENGQPAGVCILEYATPLQTLFAMSQDAKAGFSREDRLEQAK 288
sp|A7SLZ2|STING_NEMVE      KTRGGVFLRHYKHSVYEIKDGENEPWFCIMEYATPLLTLYDMSVAQPGELSREERDAQVV 329
sp|B8XX90|STING_PIG        ADRAGIKGRVYTNSIYELLENGQPAGVCVLGYATPLQTLFAMSQDGRAGFSREDRLEQAK 289
sp|F1M391|STING_RAT        TDRAGVKNRAYSNSVYELLENGQPAGACILEYATPLQTLFAMSQDGKAGFSREDRLEQAK 289
sp|A8E5V9|STING_XENTR      IDRAGIKGRVFKNNVYRILDEDGRPYNCIVEYATPLASLLKMTDIPSAAFSADDRLQQTK 271
                             :.*:           :         .                        ::   :.

sp|P9WGC0|Y1339_MYCTO      -------------AEFDGPVHAVVCDETFEVRRAG------------------------- 273
sp|P9WGC1|Y1339_MYCTU      -------------AEFDGPVHAVVCDETFEVRRAG------------------------- 273
sp|Q2KI99|STING_BOVIN      LFCRTLEDILANAPESQNNCRLIVYQEPA---EGSSFSLSQEILQHLRQEER-EVTMGST 345
sp|E1C7U0|STING_CHICK      LFYRSLRDILGSSKECAGLYRLIAYEEPA---EPESHFLSGLILWHLQQQQREEYMVQEE 351
sp|Q86WV6|STING_HUMAN      LFCRTLEDILADAPESQNNCRLIAYQEPA---DDSSFSLSQEVLRHLRQEEKEEVTVGSL 346
sp|Q3TBT3|STING_MOUSE      LFCRTLEEILEDVPESRNNCRLIVYQEPT---DGNSFSLSQEVLRHIRQEEKEEVTMNAP 345
sp|A7SLZ2|STING_NEMVE      VFLRKLQDILEGDRACQGKYELVTFSPDRD--------LADVMLRKLKDSE---LEIGG- 377
sp|B8XX90|STING_PIG        LFCRTLEDILADAPEAQNNCRLIVYQEPT---EGGSFSLSQEILRHLRQEER-EVTMGSA 345
sp|F1M391|STING_RAT        LFCRTLEEILADVPESRNHCRLIVYQESE---EGNSFSLSQEVLRHIRQEEKEEVTMSGP 346
sp|A8E5V9|STING_XENTR      LFYRTLKDILENAHELQNTYRLIVYEDFPETKDHSRHLLSQEILKHIRQQHSEEYSML-- 329
                                            .  . :. .

sp|P9WGC0|Y1339_MYCTO      ---------------------------------    273
sp|P9WGC1|Y1339_MYCTU      ---------------------------------    273
sp|Q2KI99|STING_BOVIN      ETSVMPGSSVLSQEPELLISGLEKPLPLRSDVF    378
sp|E1C7U0|STING_CHICK      LP-----LGTSSVELSLQVSSSDLPQPLRSDCP    379
sp|Q86WV6|STING_HUMAN      KTSAVPSTSTMSQEPELLISGMEKPLPLRTDFS    379
sp|Q3TBT3|STING_MOUSE      MTSVAPPPSVLSQEPRLLISGMDQPLPLRTDLI    378
sp|A7SLZ2|STING_NEMVE      ---------------------------------    377
```

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sp|B8XX90|STING_PIG        ETSVVPTSSTLSQEPELLISGMEQPLPLRSDIF    378
sp|F1M391|STING_RAT        PTSVAPRPSLLSQEPRLLISGMEQPLPLRTDLI    379
sp|A8E5V9|STING_XENTR      ---------------------------------    329
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|B5Y008|BETA_KLEP3       MQFDYIIIGAGSAGNVLATRLTEDPNTTVLLLEAGGPDYRFDFRTQMPAALAYPLQGKRY 60
sp|A6T613|BETA_KLEP7       MQFDYIIIGAGSAGNVLATRLTEDPNTTVLLLEAGGPDYRFDFRTQMPAALAYPLQGKRY 60
sp|A7FKL6|BETA_YERP3       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|Q1C932|BETA_YERPA       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|B2K8U4|BETA_YERPB       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|Q8ZGW0|BETA_YERPE       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|Q1CFR7|BETA_YERPN       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|A4TNP2|BETA_YERPP       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|Q66D54|BETA_YERPS       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|B1JSR0|BETA_YERPY       MEYDYIIIGAGSAGNVLAARLTEDADVTVLLLEAGGPDYRLDFRTQMPAALAFPLQGKRY 60
sp|Q2KI99|STING_BOVIN      ----------------------------------------------MP-----------H 3
sp|E1C7U0|STING_CHICK      ----------------------------------------------MPQD-----PSTRS 9
sp|Q86WV6|STING_HUMAN      ----------------------------------------------MP-----------H 3
sp|Q3TBT3|STING_MOUSE      ----------------------------------------------MP-----------Y 3
sp|A7SLZ2|STING_NEMVE      ----------------------------------------------MR--------RAEE 6
sp|B8XX90|STING_PIG        ----------------------------------------------MP-----------Y 3
sp|F1M391|STING_RAT        ----------------------------------------------MP-----------Y 3
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 0


sp|B5Y008|BETA_KLEP3       NWAYETEPEPYMNHRRM------------------------------------ECGRGKG 84
sp|A6T613|BETA_KLEP7       NWAYETEPEPYMNNRRM------------------------------------ECGRGKG 84
sp|A7FKL6|BETA_YERP3       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|Q1C932|BETA_YERPA       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|B2K8U4|BETA_YERPB       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|Q8ZGW0|BETA_YERPE       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|Q1CFR7|BETA_YERPN       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|A4TNP2|BETA_YERPP       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|Q66D54|BETA_YERPS       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|B1JSR0|BETA_YERPY       NWAYETDPEPHMNNRRM------------------------------------ECGRGKG 84
sp|Q2KI99|STING_BOVIN      SSLHPSIPQPRGLRAQKAALVLLSACLVALWGLGEPPDY------T----LKWLVLHLAS 53
sp|E1C7U0|STING_CHICK      SPARLLIPEPRAGRARHAACVLLAVCFVVLFLSGEPLAP------I----IRSVCTQLAA 59
sp|Q86WV6|STING_HUMAN      SSLHPSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEH------T----LRYLVLHLAS 53
sp|Q3TBT3|STING_MOUSE      SNLHPAIPRPRGHRSKYVALIFLVASLMILWVAKDPPNH------T----LKYLALHLAS 53
sp|A7SLZ2|STING_NEMVE      NNGFGTIPKRRNQHTPFYASIGMIVVIIVAFTSYHITSYGDDRNRAMRQYSFTFSLAYLA 66
sp|B8XX90|STING_PIG        SSLHPSIPQPRGLRAQVAALVLLGACLVALWGLGELPEY------T----LRWLVLHLAS 53
sp|F1M391|STING_RAT        SNLHPSIPRPRSYRFKLAAFVLLVGSLMSLWMTGEPPSH------T----LHYLALHVAS 53
sp|A8E5V9|STING_XENTR      -----------------MACVLAIGSILFVWILGKGKYSGAQ---L----IYRMATNFAI 36


sp|B5Y008|BETA_KLEP3       LGGSSLINGMCYIRGNAMDLDN------WAKEP---GLEHW----SYLDCLPYYRKAETR 131
sp|A6T613|BETA_KLEP7       LGGSSLINGMCYIRGNAMDLDN------WAKEP---GLEHW----SYLDCLPYYRKAETR 131
sp|A7FKL6|BETA_YERP3       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|Q1C932|BETA_YERPA       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
```

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sp|B2K8U4|BETA_YERPB       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|Q8ZGW0|BETA_YERPE       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|Q1CFR7|BETA_YERPN       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|A4TNP2|BETA_YERPP       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|Q66D54|BETA_YERPS       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|B1JSR0|BETA_YERPY       LGGSSLINGMCYIRGNAMDFDH------WASLS---GLEDW----SYLDCLPYFRKAETR 131
sp|Q2KI99|STING_BOVIN      QQMGLLIKGICSLAEELCHVHSRYHGSYWRAVRACLCSSMRCGALLLLSCYFY--C---- 107
sp|E1C7U0|STING_CHICK      LQLGVLLKGCCCLAEEIFHLHSRHHGSLWQVLCSCFPPR-WYLALLLVGGSAY--L---- 112
sp|Q86WV6|STING_HUMAN      LQLGLLLNGVCSLAEELRHIHSRYRGSYWRTVRACLGCPLRRGALLLLSIYFY--Y---- 107
sp|Q3TBT3|STING_MOUSE      HELGLLLKNLCCLAEELCHVQSRYQGSYWKAVRACLGCPIHCMAMILLSSYFY--F---- 107
sp|A7SLZ2|STING_NEMVE      FLVGELLRRCCLFAEEYRHIETRYNGSLKKAIQTTFSFGHNNV-LFVASLLFFVVF---- 121
sp|B8XX90|STING_PIG        QQIGLLVKGLCSLAEELCHVHSRYQSSYWRAARACLGCPIRCGALLLLSCYFY--F---- 107
sp|F1M391|STING_RAT        QQLGLLLKKLCCLAEELCHVQSRYQGSYWKAVRACVGSPICFMALILLSFYFY--C---- 107
sp|A8E5V9|STING_XENTR      SQGCCLVTCACELTEEIKHLHTRYNGHYWRALKASFNLS-CAAFVTAILCYVF--Y---- 89
                                *:   * :  :  ...                               :

sp|B5Y008|BETA_KLEP3       DIGPNDYHGGDGPVSVTTPKPGNNPLFEAMVTAGVQAGYP----------RTDDLNGYQQ 181
sp|A6T613|BETA_KLEP7       DIGPNDYHGGDGPVSVTTPKPGNNPLFEAMVEAGVQAGYP----------RTDDLNGYQQ 181
sp|A7FKL6|BETA_YERP3       DIGPNDFHGGEGPVNVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|Q1C932|BETA_YERPA       DIGPNDFHGGEGPVSVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|B2K8U4|BETA_YERPB       DVGPNDFHGGEGPVSVTTPKIDNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|Q8ZGW0|BETA_YERPE       DIGPNDFHGGEGPVSVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|Q1CFR7|BETA_YERPN       DIGPNDFHGGEGPVSVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|A4TNP2|BETA_YERPP       DIGPNDFHGGEGPVSVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|Q66D54|BETA_YERPS       DVGPNDFHGGEGPVSVTTPKIDNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|B1JSR0|BETA_YERPY       DIGPNDFHGGEGPVNVTTPKIGNNPLFHAMVAAGVQAGYP----------RTDDLNGYQQ 181
sp|Q2KI99|STING_BOVIN      -SLPN--------------------------MADLPFTWM--LALLGLSQALNILLGLQ- 137
sp|E1C7U0|STING_CHICK      -DPPE--------------------------DNGHSPRLA--LTLSCLCQLLVLALGLQ- 142
sp|Q86WV6|STING_HUMAN      -SLPN--------------------------AVGPPFTWM--LALLGLSQALNILLGLK- 137
sp|Q3TBT3|STING_MOUSE      --LQN--------------------------TADIYLSWM--FGLLVLYKSLSMLLGLQ- 136
sp|A7SLZ2|STING_NEMVE      -VASNDPNGSS---SVIQGNSTAEPHTEMRQTSGWQGLWGQFIISALLTPLVVHLLGLR- 176
sp|B8XX90|STING_PIG        -SIRD--------------------------KAGLPLPWM--LALLGLSQALNILLGLQ- 137
sp|F1M391|STING_RAT        -SLEN--------------------------TSDLRLAWH--LGILVLSKSLSMTLDLQ- 137
sp|A8E5V9|STING_XENTR      -EPKL--------------------------MASLPLTID--ITLTLLSWLFCWILGIQ- 119
                                                            .                      . :

sp|B5Y008|BETA_KLEP3       EGFGPMD--------RTVTPQGRRASTARGYLDQARGRPNLTIRTHALTDHIIFAGKRAV 233
sp|A6T613|BETA_KLEP7       EGFGPMD--------RTVTPQGRRASTARGYLDQARGRPNLTIRTHALTDHIIFAGKRAV 233
sp|A7FKL6|BETA_YERP3       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|Q1C932|BETA_YERPA       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|B2K8U4|BETA_YERPB       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|Q8ZGW0|BETA_YERPE       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|Q1CFR7|BETA_YERPN       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|A4TNP2|BETA_YERPP       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|Q66D54|BETA_YERPS       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|B1JSR0|BETA_YERPY       EGFGPMD--------RTVTPKGRRASTARGYLDQARPRNNLTIITHALTDRILFEGKRAT 233
sp|Q2KI99|STING_BOVIN      -GLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLI------------------------- 171
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sp|E1C7U0|STING_CHICK      -KLSAVEVSELTESSKKNVAHGLAWSYYIGYLKVV------------------------- 176
sp|Q86WV6|STING_HUMAN      -GLAPAEISAVCEKGNFNVAHGLAWSYYIGYLRLI------------------------- 171
sp|Q3TBT3|STING_MOUSE      -SLTPAEVSAVCEEKKLNVAHGLAWSYYIGYLRLI------------------------- 170
sp|A7SLZ2|STING_NEMVE      -ELSKVEESQLNEKENKNVADGLAWSYYFGYLKFV------------------------- 210
sp|B8XX90|STING_PIG        -HLAPAEVSAICEKRNFNVAHGLAWSYYIGYLRLI------------------------- 171
sp|F1M391|STING_RAT        -SLAPAEVSAVCEEKNFNVAHGLAWSYYIGYLKLI------------------------- 171
sp|A8E5V9|STING_XENTR      -GPTPATISEITEIKQLNVAHGLAWSYYVGYLQFV------------------------- 153
                                          .  . .*   *   ***

sp|B5Y008|BETA_KLEP3       GVEWLEGESTIPSKATANKEVLLCAGAIASPQILQRSGVGNPELLRQFDIPVVHDLPGVG 293
sp|A6T613|BETA_KLEP7       GVEWLEGESTIPSKATANKEVLLCAGAIASPQILQRSGVGNPELLRQFDIPVVHDLPGVG 293
sp|A7FKL6|BETA_YERP3       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|Q1C932|BETA_YERPA       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|B2K8U4|BETA_YERPB       GVSYLKGDAGTGQTAHARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|Q8ZGW0|BETA_YERPE       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|Q1CFR7|BETA_YERPN       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|A4TNP2|BETA_YERPP       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|Q66D54|BETA_YERPS       GVSYLKGDAGTGQTAHARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|B1JSR0|BETA_YERPY       GVRYLKGDAGTGQTAYARREVLLCGGAIASPQILQRSGIGPAELLQRLDIPLVQALPGVG 293
sp|Q2KI99|STING_BOVIN      -------------------------------------------------------LPGLP 176
sp|E1C7U0|STING_CHICK      -------------------------------------------------------LPRLK 181
sp|Q86WV6|STING_HUMAN      -------------------------------------------------------LPELQ 176
sp|Q3TBT3|STING_MOUSE      -------------------------------------------------------LPGLQ 175
sp|A7SLZ2|STING_NEMVE      -------------------------------------------------------LPELE 215
sp|B8XX90|STING_PIG        -------------------------------------------------------LPGLR 176
sp|F1M391|STING_RAT        -------------------------------------------------------LPGLQ 176
sp|A8E5V9|STING_XENTR      -------------------------------------------------------LPALK 158
                                                                                  ** :

sp|B5Y008|BETA_KLEP3       ENLQDHLEMYLQYEC--------KEPVSLYPAL-QWWNQPKIGAEWLFGGTGIGASNQFE 344
sp|A6T613|BETA_KLEP7       ENLQDHLEMYLQYEC--------KEPVSLYPAL-QWWNQPKIGAEWLFGGTGIGASNQFE 344
sp|A7FKL6|BETA_YERP3       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|Q1C932|BETA_YERPA       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|B2K8U4|BETA_YERPB       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|Q8ZGW0|BETA_YERPE       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|Q1CFR7|BETA_YERPN       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|A4TNP2|BETA_YERPP       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|Q66D54|BETA_YERPS       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|B1JSR0|BETA_YERPY       ENLQDHLEMYLQYSC--------KQPVSLYPAL-LWFNQPKIGIEWLFNGTGVGASNQFE 344
sp|Q2KI99|STING_BOVIN      A----RIQIYNQFHNNTLQGAGSHRLHILFPLDCGVPDDL-N------------------ 213
sp|E1C7U0|STING_CHICK      E----CMEELSRTNPMLRAHRDTWKLHILVPLGCDIWDDL-E------------------ 218
sp|Q86WV6|STING_HUMAN      A----RIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPDNL-S------------------ 213
sp|Q3TBT3|STING_MOUSE      A----RIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDNL-S------------------ 212
sp|A7SLZ2|STING_NEMVE      K----QIEKTSKFRS---KEKFVKKMFILIPSNCFWDDKI-PGS---------------- 251
sp|B8XX90|STING_PIG        A----RIQAYNQRHKNVLGGIGNHRLHILFPLDCGVPDDL-S------------------ 213
sp|F1M391|STING_RAT        A----RIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPDDL-S------------------ 213
sp|A8E5V9|STING_XENTR      E----SIQKFNEENHNLLKFPETCRLHILIPLSCRLYGDL-K------------------ 195
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                                 :.   .            .   * *      ..

sp|B5Y008|BETA_KLEP3       AGGFIRSRAEFAWPNIQYHFLPVAINYNGSNAVKEHGFQCHVGSMRSPSRGHVRLKSRDP 404
sp|A6T613|BETA_KLEP7       AGGFIRSRAEFAWPNIQYHFLPVAINYNGSNAVKEHGFQCHVGSMRSPSRGHVRLKSRDP 404
sp|A7FKL6|BETA_YERP3       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|Q1C932|BETA_YERPA       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|B2K8U4|BETA_YERPB       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|Q8ZGW0|BETA_YERPE       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|Q1CFR7|BETA_YERPN       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|A4TNP2|BETA_YERPP       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|Q66D54|BETA_YERPS       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|B1JSR0|BETA_YERPY       AGGFIRSRDAFTWPNIQYHFLPVAINYNGSNAVKEHGFQAHVGSMRSPSRGRIQVKSKDP 404
sp|Q2KI99|STING_BOVIN      ----------VADPNIRFLHELPQQ-SADRAGIKGRVYTNSI----------YELLENGQ 252
sp|E1C7U0|STING_CHICK      ----------KADSNIQYLADLPET-ILTRAGIKRRVYKHSL----------YVIRDKDN 257
sp|Q86WV6|STING_HUMAN      ----------MADPNIRFLDKLPQQ-TGDHAGIKDRVYSNSI----------YELLENGQ 252
sp|Q3TBT3|STING_MOUSE      ----------VVDPNIRFRDMLPQQ-NIDRAGIKNRVYSNSV----------YEILENGQ 251
sp|A7SLZ2|STING_NEMVE      --------DYDPQNRITFEGNTEPL-EKTRGGVFLRHYKHSV----------YEIKDGEN 292
sp|B8XX90|STING_PIG        ----------VADPNIRFLHELPQQ-SADRAGIKGRVYTNSI----------YELLENGQ 252
sp|F1M391|STING_RAT        ----------VADPNIRFRDMLPQQ-NTDRAGVKNRAYSNSV----------YELLENGQ 252
sp|A8E5V9|STING_XENTR      ----------DVDENITFLKEIPPL-YIDRAGIKGRVFKNNV----------YRILDEDG 234
                                         .* :             .:  : :   :            : .

sp|B5Y008|BETA_KLEP3       HAHPAI--------LFNYMSHE--------QDWQEFRDAIRITREIMNQPALDKYRGREI 448
sp|A6T613|BETA_KLEP7       HAHPAI--------LFNYMSHE--------QDWQEFRDAIRITREIMNQPALDKYRGREI 448
sp|A7FKL6|BETA_YERP3       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|Q1C932|BETA_YERPA       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|B2K8U4|BETA_YERPB       RQHPSI--------LFNYMSNE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|Q8ZGW0|BETA_YERPE       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|Q1CFR7|BETA_YERPN       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|A4TNP2|BETA_YERPP       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|Q66D54|BETA_YERPS       RQHPSI--------LFNYMSNE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|B1JSR0|BETA_YERPY       RQHPSI--------LFNYMSSE--------QDWHEFRDAIRITREIIAQPALDPYRGREI 448
sp|Q2KI99|STING_BOVIN      RAGVCVLEYATPLQTLFAMSQDGRAGFSREDRLEQAKLFCRTLEDILAN----------- 301
sp|E1C7U0|STING_CHICK      KLRPCVLEFASPLQTLCAMSQDDCAAFSREQRLEQARLFYRSLRDILGS----------- 306
sp|Q86WV6|STING_HUMAN      RAGTCVLEYATPLQTLFAMSQYSQAGFSREDRLEQAKLFCRTLEDILAD----------- 301
sp|Q3TBT3|STING_MOUSE      PAGVCILEYATPLQTLFAMSQDAKAGFSREDRLEQAKLFCRTLEEILED----------- 300
sp|A7SLZ2|STING_NEMVE      EPWFCIMEYATPLLTLYDMSVAQPGELSREERDAQVVVFLRKLQDILEG----------- 341
sp|B8XX90|STING_PIG        PAGVCVLGYATPLQTLFAMSQDGRAGFSREDRLEQAKLFCRTLEDILAD----------- 301
sp|F1M391|STING_RAT        PAGACILEYATPLQTLFAMSQDGKAGFSREDRLEQAKLFCRTLEEILAD----------- 301
sp|A8E5V9|STING_XENTR      RPYNCIVEYATPLASLLKMTDIPSAAFSADDRLQQTKLFYRTLKDILEN----------- 283
                               .:         :  *:          :   :     *  .:*:

sp|B5Y008|BETA_KLEP3       SPGTECQSDAELDEFVRNHA--E-TAF--------H----PCGTCKMGYDEMAVVDGEGR 493
sp|A6T613|BETA_KLEP7       SPGIECQSDAELDEFVRNHA--E-TAF--------H----PCGTCKMGYDEMAVVDGEGR 493
sp|A7FKL6|BETA_YERP3       SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|Q1C932|BETA_YERPA       SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|B2K8U4|BETA_YERPB       SPGANVQSDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
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sp|Q8ZGW0|BETA_YERPE      SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|Q1CFR7|BETA_YERPN      SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|A4TNP2|BETA_YERPP      SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|Q66D54|BETA_YERPS      SPGANVQSDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|B1JSR0|BETA_YERPY      SPGANVQNDDELDAFIREHA--E-TAY--------H----PSCSCKMGDDKMAVVDGQGR 493
sp|Q2KI99|STING_BOVIN     --APESQNNCRLIVYQEPA---EGSSFSLSQEILQHLRQEER-EVTMGSTETSVMPGSSV 355
sp|E1C7U0|STING_CHICK     --SKECAGLYRLIAYEEPA---EPESHFLSGLILWHLQQQQREEYMVQEELP-----LGT 356
sp|Q86WV6|STING_HUMAN     --APESQNNCRLIAYQEPA---DDSSFSLSQEVLRHLRQEEKEEVTVGSLKTSAVPSTST 356
sp|Q3TBT3|STING_MOUSE     --VPESRNNCRLIVYQEPT---DGNSFSLSQEVLRHIRQEEKEEVTMNAPMTSVAPPPSV 355
sp|A7SLZ2|STING_NEMVE     --DRACQGKYELVTFSPDRD--------LADVMLRKLKDSE---LEIGG----------- 377
sp|B8XX90|STING_PIG       --APEAQNNCRLIVYQEPT---EGGSFSLSQEILRHLRQEER-EVTMGSAETSVVPTSST 355
sp|F1M391|STING_RAT       --VPESRNHCRLIVYQESE---EGNSFSLSQEVLRHIRQEEKEEVTMSGPPTSVAPRPSL 356
sp|A8E5V9|STING_XENTR     --AHELQNTYRLIVYEDFPETKDHSRHLLSQEILKHIRQQHSEEYSML------------ 329
                                 .  .*  :                    :          :

sp|B5Y008|BETA_KLEP3      VHGLEGVRVVDASIMPQIITGNLNATTIMIGEKMADAIRGRQPLPRSTAAYYVAGGAPVR 553
sp|A6T613|BETA_KLEP7      VHGLEGLRVVDASIMPQIITGNLNATTIMIGEKMADAIRGRQPLPRSTATYYVAGDAPVR 553
sp|A7FKL6|BETA_YERP3      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|Q1C932|BETA_YERPA      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|B2K8U4|BETA_YERPB      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|Q8ZGW0|BETA_YERPE      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|Q1CFR7|BETA_YERPN      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|A4TNP2|BETA_YERPP      VHGVQGLRVVDASIMSQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|Q66D54|BETA_YERPS      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|B1JSR0|BETA_YERPY      VHGVQGLRVVDASIMPQIITGNLNATTIMIAEKIADRIRGCQPLAKSNAAYFIAGDTPAR 553
sp|Q2KI99|STING_BOVIN     L-----------SQEPELLI---------S--------GLEKPLPL-------------- 373
sp|E1C7U0|STING_CHICK     S-----------SVELSLQV---------S--------SSDLPQPL-------------- 374
sp|Q86WV6|STING_HUMAN     M-----------SQEPELLI---------S--------GMEKPLPL-------------- 374
sp|Q3TBT3|STING_MOUSE     L-----------SQEPRLLI---------S--------GMDQPLPL-------------- 373
sp|A7SLZ2|STING_NEMVE     ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG       L-----------SQEPELLI---------S--------GMEQPLPL-------------- 373
sp|F1M391|STING_RAT       L-----------SQEPRLLI---------S--------GMEQPLPL-------------- 374
sp|A8E5V9|STING_XENTR     ------------------------------------------------------------ 329


sp|B5Y008|BETA_KLEP3      R-------------       554
sp|A6T613|BETA_KLEP7      R-------------       554
sp|A7FKL6|BETA_YERP3      TSPVRHSLPVTSYP       567
sp|Q1C932|BETA_YERPA      TSPVRHSLPVTSYP       567
sp|B2K8U4|BETA_YERPB      TSPVRHSLPVTSYP       567
sp|Q8ZGW0|BETA_YERPE      TSPVRHSLPVTSYP       567
sp|Q1CFR7|BETA_YERPN      TSPVRHSLPVTSYP       567
sp|A4TNP2|BETA_YERPP      TSPVRHSLPVTSYP       567
sp|Q66D54|BETA_YERPS      TSPVRHSLPVTSYP       567
sp|B1JSR0|BETA_YERPY      TSPVRHSLPVTSYP       567
sp|Q2KI99|STING_BOVIN     ----RSDVF-----       378
sp|E1C7U0|STING_CHICK     ----RSDCP-----       379
```

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sp|Q86WV6|STING_HUMAN      ----RTDFS-----       379
sp|Q3TBT3|STING_MOUSE      ----RTDLI-----       378
sp|A7SLZ2|STING_NEMVE      --------------       377
sp|B8XX90|STING_PIG        ----RSDIF-----       378
sp|F1M391|STING_RAT        ----RTDLI-----       379
sp|A8E5V9|STING_XENTR      --------------       329
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 0
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 0
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|Q2KI99|STING_BOVIN      -----------------------------------------------------------M 1
sp|E1C7U0|STING_CHICK      -----------------------------------------------------------M 1
sp|Q86WV6|STING_HUMAN      -----------------------------------------------------------M 1
sp|Q3TBT3|STING_MOUSE      -----------------------------------------------------------M 1
sp|A7SLZ2|STING_NEMVE      -----------------------------------------------------------M 1
sp|B8XX90|STING_PIG        -----------------------------------------------------------M 1
sp|F1M391|STING_RAT        -----------------------------------------------------------M 1
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 60
sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTT--RTQLPPAY--TNSFTRGVYYPDKVFRSSVLHSTQDLFL 56


sp|Q9BXJ3|C1QT4_HUMAN      --------------------------------------MLPLLLGLLGPAACWALGPTPG 22
sp|Q8R066|C1QT4_MOUSE      --------------------------------------MLLLLLGFLGPAACWALGPA-G 21
sp|P0A5I7|BLAC_MYCBO       ----------------------------MRNRGFGRRELLVAMAMLVSVTGCARHASGAR 32
sp|A5U493|BLAC_MYCTA       ----------------------------MRNRGFGRRELLVAMAMLVSVTGCARHASGAR 32
sp|P9WKD2|BLAC_MYCTO       ----------------------------MRNRGFGRRELLVAMAMLVSVTGCARHASGAR 32
sp|P9WKD3|BLAC_MYCTU       ----------------------------MRNRGFGRRELLVAMAMLVSVTGCARHASGAR 32
sp|Q2KI99|STING_BOVIN      P-------------------HSSLHPSIPQPRGLRA-QKAALVLLSACLVALWGLGEPPD 41
sp|E1C7U0|STING_CHICK      P-------------QDPSTRSSPARLLIPEPRAGRA-RHAACVLLAVCFVVLFLSGEPLA 47
sp|Q86WV6|STING_HUMAN      P-------------------HSSLHPSIPCPRGHGA-QKAALVLLSACLVTLWGLGEPPE 41
sp|Q3TBT3|STING_MOUSE      P-------------------YSNLHPAIPRPRGHRS-KYVALIFLVASLMILWVAKDPPN 41
sp|A7SLZ2|STING_NEMVE      R----------------RAEENNGFGTIPKRRNQHT-PFYASIGMIVVIIVAFTSYHITS 44
sp|B8XX90|STING_PIG        P-------------------YSSLHPSIPQPRGLRA-QVAALVLLGACLVALWGLGELPE 41
sp|F1M391|STING_RAT        P-------------------YSNLHPSIPRPRSYRF-KLAAFVLLVGSLMSLWMTGEPPS 41
sp|A8E5V9|STING_XENTR      ---------------------------------------MACVLAIGSILFVWILGKGKY 21
sp|P59594|SPIKE_SARS       PFYSNVTGFHTIN-------HTFGNPVIPFKDGIYF---A--ATEKSNVVRGWVFGSTMN 108
sp|P0DTC2|SPIKE_SARS2      PFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYF---A--STEKSNIIRGWIFGTTLD 111


sp|Q9BXJ3|C1QT4_HUMAN      PGSSELRSAFS----------AA-RTTPLEGTSEMAV---TFDKVYVNIGGDFDVATGQF 68
sp|Q8R066|C1QT4_MOUSE      PGSSELRSAFS----------AA-RTTPLEGTSEMAV---TFDKVYVNIGGDFDAATGRF 67
sp|P0A5I7|BLAC_MYCBO       PASTTLPA-----------------------GADLAD---R----FAELERRYDARLGVY 62
sp|A5U493|BLAC_MYCTA       PASTTLPA-----------------------GADLAD---R----FAELERRYDARLGVY 62
sp|P9WKD2|BLAC_MYCTO       PASTTLPA-----------------------GADLAD---R----FAELERRYDARLGVY 62
sp|P9WKD3|BLAC_MYCTU       PASTTLPA-----------------------GADLAD---R----FAELERRYDARLGVY 62
sp|Q2KI99|STING_BOVIN      Y------T----LKWLVLHLASQQMGLLIKGICSLAE---ELCHVHSRYHGSYWRAV-RA 87
sp|E1C7U0|STING_CHICK      P------I----IRSVCTQLAALQLGVLLKGCCCLAE---EIFHLHSRHHGSLWQVL-CS 93
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sp|Q86WV6|STING_HUMAN      H------T----LRYLVLHLASLQLGLLLNGVCSLAE---ELRHIHSRYRGSYWRTV-RA 87
sp|Q3TBT3|STING_MOUSE      H------T----LKYLALHLASHELGLLLKNLCCLAE---ELCHVQSRYQGSYWKAV-RA 87
sp|A7SLZ2|STING_NEMVE      YGDDRNRAMRQYSFTFSLAYLAFLVGELLRRCCLFAE---EYRHIETRYNGSLKKAI-QT 100
sp|B8XX90|STING_PIG        Y------T----LRWLVLHLASQQIGLLVKGLCSLAE---ELCHVHSRYQSSYWRAA-RA 87
sp|F1M391|STING_RAT        H------T----LHYLALHVASQQLGLLLKKLCCLAE---ELCHVQSRYQGSYWKAV-RA 87
sp|A8E5V9|STING_XENTR      SGAQ---L----IYRMATNFAISQGCCLVTCACELTE---EIKHLHTRYNGHYWRAL-KA 70
sp|P59594|SPIKE_SARS       NKSQSVII------------INN-STNVVIRACNFELCDNPFFAVSKPMGT----QTHTM 151
sp|P0DTC2|SPIKE_SARS2      SKTQSLLI------------VNN-ATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFR 158
                                                           . :

sp|Q9BXJ3|C1QT4_HUMAN      ----------RCRVPGAYFF--SFT-------AGKAPHKSLSVMLVRNRDEVQALAFD-- 107
sp|Q8R066|C1QT4_MOUSE      ----------RCRVPGAYFF--SFT-------AGKAPHKSLSVMLVRNRDEVQALAFD-- 106
sp|P0A5I7|BLAC_MYCBO       VPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLDKLITYTSDDIRSISPV-- 120
sp|A5U493|BLAC_MYCTA       VPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLDKLITYTSDDIRSISPV-- 120
sp|P9WKD2|BLAC_MYCTO       VPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLDKLITYTSDDIRSISPV-- 120
sp|P9WKD3|BLAC_MYCTU       VPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLDKLITYTSDDIRSISPV-- 120
sp|Q2KI99|STING_BOVIN      CLCSSMRCGALLLLSCYFY------------------------CSLPN------------ 111
sp|E1C7U0|STING_CHICK      CFPPR-WYLALLLVGGSAY------------------------LDPPE------------ 116
sp|Q86WV6|STING_HUMAN      CLGCPLRRGALLLLSIYFY------------------------YSLPN------------ 111
sp|Q3TBT3|STING_MOUSE      CLGCPIHCMAMILLSSYFY------------------------F-LQN------------ 110
sp|A7SLZ2|STING_NEMVE      TFSFGHNNV-LFVASLLFFVV----------------------FVASNDPNGSSSVIQGN 137
sp|B8XX90|STING_PIG        CLGCPIRCGALLLLSCYFY------------------------FSIRD------------ 111
sp|F1M391|STING_RAT        CVGSPICFMALILLSFYFY------------------------CSLEN------------ 111
sp|A8E5V9|STING_XENTR      SFNLS-CAAFVTAILCYVF------------------------YEPKL------------ 93
sp|P59594|SPIKE_SARS       IFDNAFNCTFEY-ISDAFSLD---------VSEKSGNFKHLREFVFKN-KDGFLYVYKG- 199
sp|P0DTC2|SPIKE_SARS2      VYSSANNCTFEY-VSQPFLMD---------LEGKQGNFKNLREFVFKN-IDGYFKIYSK- 206


sp|Q9BXJ3|C1QT4_HUMAN      -----------EQRRPG------ARRAASQSAMLQLDYGDTVWLRLHGAP-------QYA 143
sp|Q8R066|C1QT4_MOUSE      -----------EQRRPG------ARRAASQSAMLQLDYGDTVWLRLHGAP-------QYA 142
sp|P0A5I7|BLAC_MYCBO       -----------AQQHVQ------TGMTIGQLCDAAIRYSDGTAANLL----------LAD 153
sp|A5U493|BLAC_MYCTA       -----------AQQHVQ------TGMTIGQLCDAAIRYSDGTAANLL----------LAD 153
sp|P9WKD2|BLAC_MYCTO       -----------AQQHVQ------TGMTIGQLCDAAIRYSDGTAANLL----------LAD 153
sp|P9WKD3|BLAC_MYCTU       -----------AQQHVQ------TGMTIGQLCDAAIRYSDGTAANLL----------LAD 153
sp|Q2KI99|STING_BOVIN      -----------MADLPFTWM--LALLGLSQALNILLGL-----QGLAPAEVSAICEKRNF 153
sp|E1C7U0|STING_CHICK      -----------DNGHSPRLA--LTLSCLCQLLVLALGL-----QKLSAVEVSELTESSKK 158
sp|Q86WV6|STING_HUMAN      -----------AVGPPFTWM--LALLGLSQALNILLGL-----KGLAPAEISAVCEKGNF 153
sp|Q3TBT3|STING_MOUSE      -----------TADIYLSWM--FGLLVLYKSLSMLLGL-----QSLTPAEVSAVCEEKKL 152
sp|A7SLZ2|STING_NEMVE      STAEPHTEMRQTSGWQGLWGQFIISALLTPLVVHLLGL-----RELSKVEESQLNEKENK 192
sp|B8XX90|STING_PIG        -----------KAGLPLPWM--LALLGLSQALNILLGL-----QHLAPAEVSAICEKRNF 153
sp|F1M391|STING_RAT        -----------TSDLRLAWH--LGILVLSKSLSMTLDL-----QSLAPAEVSAVCEEKNF 153
sp|A8E5V9|STING_XENTR      -----------MASLPLTID--ITLTLLSWLFCWILGI-----QGPTPATISEITEIKQL 135
sp|P59594|SPIKE_SARS       -----YQPIDVVRDLPS------GFNTLKPIFKLPLGINITNFRAILTAFS------PAQ 242
sp|P0DTC2|SPIKE_SARS2      -----HTPINLVRDLPQ------GFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSS 255
                                                              :

sp|Q9BXJ3|C1QT4_HUMAN      LGAPG---ATFSGYLVYADAD-----ADAP--ARGPPAPPEPRS---AFSAARTRS---- 186
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sp|Q8R066|C1QT4_MOUSE      LGAPG---ATFSGYLVYADAD-----ADAP--ARGPA-APEPRS---AFSAARTRS---- 184
sp|P0A5I7|BLAC_MYCBO       LGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQL---- 209
sp|A5U493|BLAC_MYCTA       LGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQL---- 209
sp|P9WKD2|BLAC_MYCTO       LGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQL---- 209
sp|P9WKD3|BLAC_MYCTU       LGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQL---- 209
sp|Q2KI99|STING_BOVIN      NVAHGLAWSYYIGYLRLILP---GLPARIQIYNQFHNNTLQGAGSHRLHILFPLDCGVPD 210
sp|E1C7U0|STING_CHICK      NVAHGLAWSYYIGYLKVVLP---RLKECMEELSRTNPMLRAHRDTWKLHILVPLGCDIWD 215
sp|Q86WV6|STING_HUMAN      NVAHGLAWSYYIGYLRLILP---ELQARIRTYNQHYNNLLRGAVSQRLYILLPLDCGVPD 210
sp|Q3TBT3|STING_MOUSE      NVAHGLAWSYYIGYLRLILP---GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPD 209
sp|A7SLZ2|STING_NEMVE      NVADGLAWSYYFGYLKFVLP---ELEKQIEKTSKFRS---KEKFVKKMFILIPSNCFWDD 246
sp|B8XX90|STING_PIG        NVAHGLAWSYYIGYLRLILP---GLRARIQAYNQRHKNVLGGIGNHRLHILFPLDCGVPD 210
sp|F1M391|STING_RAT        NVAHGLAWSYYIGYLKLILP---GLQARIRMFNQLHNNMLSGAGSRRLYILFPLDCGVPD 210
sp|A8E5V9|STING_XENTR      NVAHGLAWSYYVGYLQFVLP---ALKESIQKFNEENHNLLKFPETCRLHILIPLSCRLYG 192
sp|P59594|SPIKE_SARS       DIWGTSAAAYFVGYLKPTTF---MLK-----YDE--NGTITDAVDCSQNPLAELKCSVKS 292
sp|P0DTC2|SPIKE_SARS2      SGWTAGAAAYYVGYLQPRTF---LLK-----YNE--NGTITDAVDCALDPLSETKCTLKS 305
                                   : : ***                  .

sp|Q9BXJ3|C1QT4_HUMAN      ---------------LVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFR-CRLPGAYF 230
sp|Q8R066|C1QT4_MOUSE      ---------------LVGSDAAPGPRHRPLAFDTELVNIGGDFDAAAGVFR-CRLPGAYF 228
sp|P0A5I7|BLAC_MYCBO       ---------------VLGNALPPDKRA--LLTDWMARNTTG-----AKRIR-AGFPA--- 243
sp|A5U493|BLAC_MYCTA       ---------------VLGNALPPDKRA--LLTDWMARNTTG-----AKRIR-AGFPA--- 243
sp|P9WKD2|BLAC_MYCTO       ---------------VLGNALPPDKRA--LLTDWMARNTTG-----AKRIR-AGFPA--- 243
sp|P9WKD3|BLAC_MYCTU       ---------------VLGNALPPDKRA--LLTDWMARNTTG-----AKRIR-AGFPA--- 243
sp|Q2KI99|STING_BOVIN      DL--------------N----VADPNIRFLHE---LPQQSA---DRAGIKGRVYTNSIYE 246
sp|E1C7U0|STING_CHICK      DL--------------E----KADSNIQYLAD---LPETIL---TRAGIKRRVYKHSLYV 251
sp|Q86WV6|STING_HUMAN      NL--------------S----MADPNIRFLDK---LPQQTG---DHAGIKDRVYSNSIYE 246
sp|Q3TBT3|STING_MOUSE      NL--------------S----VVDPNIRFRDM---LPQQNI---DRAGIKNRVYSNSVYE 245
sp|A7SLZ2|STING_NEMVE      KI--------------PGSDYDPQNRITFEGN---TEPLEK---TRGGVFLRHYKHSVYE 286
sp|B8XX90|STING_PIG        DL--------------S----VADPNIRFLHE---LPQQSA---DRAGIKGRVYTNSIYE 246
sp|F1M391|STING_RAT        DL--------------S----VADPNIRFRDM---LPQQNT---DRAGVKNRAYSNSVYE 246
sp|A8E5V9|STING_XENTR      DL--------------K----DVDENITFLKE---IPPLYI---DRAGIKGRVFKNNVYR 228
sp|P59594|SPIKE_SARS       FEIDKGIYQTSNFRVVPSGDVVRFPNITNLCP-------------FGEVFNATKFPSVYA 339
sp|P0DTC2|SPIKE_SARS2      FTVEKGIYQTSNFRVQPTESIVRFPNITNLCP-------------FGEVFNATRFASVYA 352
                                                    .                    .

sp|Q9BXJ3|C1QT4_HUMAN      FSFTLGKLPRKTLSVKLMKNRDEVQA---MIY--DDGASRRREM--Q--SQSVMLALRRG 281
sp|Q8R066|C1QT4_MOUSE      FSFTLGKLPRKTLSVKLMKNRDEVQA---MIY--DDGASRRREM--Q--SQSVMLPLRRG 279
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 243
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 243
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 243
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 243
sp|Q2KI99|STING_BOVIN      LL-----ENGQRAGVCVLEYATPLQTLFAMSQDGRAGFSREDRL--E----QAKLFCRTL 295
sp|E1C7U0|STING_CHICK      IR-----DKDNKLRPCVLEFASPLQTLCAMSQDDCAAFSREQRL--E----QARLFYRSL 300
sp|Q86WV6|STING_HUMAN      LL-----ENGQRAGTCVLEYATPLQTLFAMSQYSQAGFSREDRL--E----QAKLFCRTL 295
sp|Q3TBT3|STING_MOUSE      IL-----ENGQPAGVCILEYATPLQTLFAMSQDAKAGFSREDRL--E----QAKLFCRTL 294
sp|A7SLZ2|STING_NEMVE      IK-----DGENEPWFCIMEYATPLLTLYDMSVAQPGELSREERD--A----QVVVFLRKL 335
sp|B8XX90|STING_PIG        LL-----ENGQPAGVCVLGYATPLQTLFAMSQDGRAGFSREDRL--E----QAKLFCRTL 295
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sp|F1M391|STING_RAT         LL-----ENGQPAGACILEYATPLQTLFAMSQDGKAGFSREDRL--E----QAKLFCRTL 295
sp|A8E5V9|STING_XENTR       IL-----DEDGRPYNCIVEYATPLASLLKMTDIPSAAFSADDRL--Q----QTKLFYRTL 277
sp|P59594|SPIKE_SARS        W-------ERKKISNCVADYSVLYNSTF-FSTFKCYGVSATKLNDLCFSNVYADSFVVKG 391
sp|P0DTC2|SPIKE_SARS2       W-------NRKRISNCVADYSVLYNSAS-FSTFKCYGVSPTKLNDLCFTNVYADSFVIRG 404


sp|Q9BXJ3|C1QT4_HUMAN       DAVWLLSHDH-----------------------------DGYGAYSNHGKYITF------ 306
sp|Q8R066|C1QT4_MOUSE       DAVWLLSHDH-----------------------------DGYGAYSNHGKYITF------ 304
sp|P0A5I7|BLAC_MYCBO        --DWKV-IDK-----------------------------TGTGDYGRANDIAVVW----- 266
sp|A5U493|BLAC_MYCTA        --DWKV-IDK-----------------------------TGTGDYGRANDIAVVW----- 266
sp|P9WKD2|BLAC_MYCTO        --DWKV-IDK-----------------------------TGTGDYGRANDIAVVW----- 266
sp|P9WKD3|BLAC_MYCTU        --DWKV-IDK-----------------------------TGTGDYGRANDIAVVW----- 266
sp|Q2KI99|STING_BOVIN       EDILANAPESQNNCRLIVYQEPA-----------------EGSSFSLSQEILQHLR--QE 336
sp|E1C7U0|STING_CHICK       RDILGSSKECAGLYRLIAYEEPA-----------------EPESHFLSGLILWHLQ--QQ 341
sp|Q86WV6|STING_HUMAN       EDILADAPESQNNCRLIAYQEPA-----------------DDSSFSLSQEVLRHLR--QE 336
sp|Q3TBT3|STING_MOUSE       EEILEDVPESRNNCRLIVYQEPT-----------------DGNSFSLSQEVLRHIR--QE 335
sp|A7SLZ2|STING_NEMVE       QDILEGDRACQGKYELVTFSPDR--------------D--------LADVMLRKLK--DS 371
sp|B8XX90|STING_PIG         EDILADAPEAQNNCRLIVYQEPT-----------------EGGSFSLSQEILRHLR--QE 336
sp|F1M391|STING_RAT         EEILADVPESRNHCRLIVYQESE-----------------EGNSFSLSQEVLRHIR--QE 336
sp|A8E5V9|STING_XENTR       KDILENAHELQNTYRLIVYEDFP--------------ETKDHSRHLLSQEILKHIR--QQ 321
sp|P59594|SPIKE_SARS        DDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPF 451
sp|P0DTC2|SPIKE_SARS2       DEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPF 464


sp|Q9BXJ3|C1QT4_HUMAN       -----------SGFLV-------------------------------------------- 311
sp|Q8R066|C1QT4_MOUSE       -----------SGFLV-------------------------------------------- 309
sp|P0A5I7|BLAC_MYCBO        ---------SPTGVPY----------------------V--------------------- 274
sp|A5U493|BLAC_MYCTA        ---------SPTGVPY----------------------V--------------------- 274
sp|P9WKD2|BLAC_MYCTO        ---------SPTGVPY----------------------V--------------------- 274
sp|P9WKD3|BLAC_MYCTU        ---------SPTGVPY----------------------V--------------------- 274
sp|Q2KI99|STING_BOVIN       E----R-EVTMGSTETSVMPGSSVLSQEPELLISGLEKPLPLRSDVF------------- 378
sp|E1C7U0|STING_CHICK       Q----REEYMVQEELP-----LGTSSVELSLQVSSSDLPQPLRSDCP------------- 379
sp|Q86WV6|STING_HUMAN       E----KEEVTVGSLKTSAVPSTSTMSQEPELLISGMEKPLPLRTDFS------------- 379
sp|Q3TBT3|STING_MOUSE       E----KEEVTMNAPMTSVAPPPSVLSQEPRLLISGMDQPLPLRTDLI------------- 378
sp|A7SLZ2|STING_NEMVE       E-------LEIGG----------------------------------------------- 377
sp|B8XX90|STING_PIG         E----R-EVTMGSAETSVVPTSSTLSQEPELLISGMEQPLPLRSDIF------------- 378
sp|F1M391|STING_RAT         E----KEEVTMSGPPTSVAPRPSLLSQEPRLLISGMEQPLPLRTDLI------------- 379
sp|A8E5V9|STING_XENTR       H----SEEYSML------------------------------------------------ 329
sp|P59594|SPIKE_SARS        ERDISNVPFSPDGKPCT--------------P-PALNCYWPLNDYGFYTTTGIGYQPYRV 496
sp|P0DTC2|SPIKE_SARS2       ERDISTEIYQAGSTPCN--------------GVEGFNCYFPLQSYGFQPTNGVGYQPYRV 510


sp|Q9BXJ3|C1QT4_HUMAN       ------------------------------------------------------------ 311
sp|Q8R066|C1QT4_MOUSE       ------------------------------------------------------------ 309
sp|P0A5I7|BLAC_MYCBO        ------------------------------------------------------------ 274
sp|A5U493|BLAC_MYCTA        ------------------------------------------------------------ 274
sp|P9WKD2|BLAC_MYCTO        ------------------------------------------------------------ 274
```

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sp|P9WKD3|BLAC_MYCTU      ------------------------------------------------------------ 274
sp|Q2KI99|STING_BOVIN     ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK     ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN     ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE     ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE     ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG       ------------------------------------------------------------ 378
sp|F1M391|STING_RAT       ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR     ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS      VVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVS 556
sp|P0DTC2|SPIKE_SARS2     VVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIA 570


sp|Q9BXJ3|C1QT4_HUMAN     -------------YPDLAPAA-------PPGLGA---SELL------------------- 329
sp|Q8R066|C1QT4_MOUSE     -------------YPDLAAAG-------PPALKP---PEL-------------------- 326
sp|P0A5I7|BLAC_MYCBO      -------------VAVMSDRA-------GGGYDAEPREALLAEAATC------------- 301
sp|A5U493|BLAC_MYCTA      -------------VAVMSDRA-------GGGYDAEPREALLAEAATC------------- 301
sp|P9WKD2|BLAC_MYCTO      -------------VAVMSDRA-------GGGYDAEPREALLAEAATC------------- 301
sp|P9WKD3|BLAC_MYCTU      -------------VAVMSDRA-------GGGYDAEPREALLAEAATC------------- 301
sp|Q2KI99|STING_BOVIN     ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK     ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN     ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE     ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE     ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG       ------------------------------------------------------------ 378
sp|F1M391|STING_RAT       ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR     ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS      DFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLT 616
sp|P0DTC2|SPIKE_SARS2     DTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT 630


sp|Q9BXJ3|C1QT4_HUMAN     ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE     ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO      -------------------VAGVLA----------------------------------- 307
sp|A5U493|BLAC_MYCTA      -------------------VAGVLA----------------------------------- 307
sp|P9WKD2|BLAC_MYCTO      -------------------VAGVLA----------------------------------- 307
sp|P9WKD3|BLAC_MYCTU      -------------------VAGVLA----------------------------------- 307
sp|Q2KI99|STING_BOVIN     ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK     ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN     ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE     ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE     ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG       ------------------------------------------------------------ 378
sp|F1M391|STING_RAT       ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR     ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS      PAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSL----LRSTSQK 672
sp|P0DTC2|SPIKE_SARS2     PTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQ 690
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sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       SIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA 732
sp|P0DTC2|SPIKE_SARS2      SIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECS 750


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPL 792
sp|P0DTC2|SPIKE_SARS2      NLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPS 810


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
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sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMI 852
sp|P0DTC2|SPIKE_SARS2      KPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMI 870


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA 912
sp|P0DTC2|SPIKE_SARS2      AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSA 930


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE 972
sp|P0DTC2|SPIKE_SARS2      IGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE 990


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
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sp|P0A5I7|BLAC_MYCBO        ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA        ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO        ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU        ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN       ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK       ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN       ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE       ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE       ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG         ------------------------------------------------------------ 378
sp|F1M391|STING_RAT         ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR       ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS        VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM 1032
sp|P0DTC2|SPIKE_SARS2       VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM 1050


sp|Q9BXJ3|C1QT4_HUMAN       ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE       ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO        ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA        ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO        ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU        ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN       ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK       ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN       ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE       ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE       ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG         ------------------------------------------------------------ 378
sp|F1M391|STING_RAT         ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR       ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS        SFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFNGTSWFITQRNFF 1092
sp|P0DTC2|SPIKE_SARS2       SFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFY 1110


sp|Q9BXJ3|C1QT4_HUMAN       ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE       ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO        ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA        ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO        ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU        ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN       ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK       ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN       ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE       ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE       ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG         ------------------------------------------------------------ 378
sp|F1M391|STING_RAT         ------------------------------------------------------------ 379
```

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sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       SPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS 1152
sp|P0DTC2|SPIKE_SARS2      EPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDIS 1170


sp|Q9BXJ3|C1QT4_HUMAN      ------------------------------------------------------------ 329
sp|Q8R066|C1QT4_MOUSE      ------------------------------------------------------------ 326
sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|Q2KI99|STING_BOVIN      ------------------------------------------------------------ 378
sp|E1C7U0|STING_CHICK      ------------------------------------------------------------ 379
sp|Q86WV6|STING_HUMAN      ------------------------------------------------------------ 379
sp|Q3TBT3|STING_MOUSE      ------------------------------------------------------------ 378
sp|A7SLZ2|STING_NEMVE      ------------------------------------------------------------ 377
sp|B8XX90|STING_PIG        ------------------------------------------------------------ 378
sp|F1M391|STING_RAT        ------------------------------------------------------------ 379
sp|A8E5V9|STING_XENTR      ------------------------------------------------------------ 329
sp|P59594|SPIKE_SARS       GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMV 1212
sp|P0DTC2|SPIKE_SARS2      GINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMV 1230


sp|Q9BXJ3|C1QT4_HUMAN      -------------------------------------------  329
sp|Q8R066|C1QT4_MOUSE      -------------------------------------------  326
sp|P0A5I7|BLAC_MYCBO       -------------------------------------------  307
sp|A5U493|BLAC_MYCTA       -------------------------------------------  307
sp|P9WKD2|BLAC_MYCTO       -------------------------------------------  307
sp|P9WKD3|BLAC_MYCTU       -------------------------------------------  307
sp|Q2KI99|STING_BOVIN      -------------------------------------------  378
sp|E1C7U0|STING_CHICK      -------------------------------------------  379
sp|Q86WV6|STING_HUMAN      -------------------------------------------  379
sp|Q3TBT3|STING_MOUSE      -------------------------------------------  378
sp|A7SLZ2|STING_NEMVE      -------------------------------------------  377
sp|B8XX90|STING_PIG        -------------------------------------------  378
sp|F1M391|STING_RAT        -------------------------------------------  379
sp|A8E5V9|STING_XENTR      -------------------------------------------  329
sp|P59594|SPIKE_SARS       TILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT  1255
sp|P0DTC2|SPIKE_SARS2      TIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT  1273
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|P0A5I7|BLAC_MYCBO       MRNRGFGRRELLVAMAMLVSVTGCARHASGARPASTTLPA------------GADLADR- 47
sp|A5U493|BLAC_MYCTA       MRNRGFGRRELLVAMAMLVSVTGCARHASGARPASTTLPA------------GADLADR- 47
sp|P9WKD2|BLAC_MYCTO       MRNRGFGRRELLVAMAMLVSVTGCARHASGARPASTTLPA------------GADLADR- 47
sp|P9WKD3|BLAC_MYCTU       MRNRGFGRRELLVAMAMLVSVTGCARHASGARPASTTLPA------------GADLADR- 47
sp|Q9BXJ3|C1QT4_HUMAN      ----------MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTF 50
sp|Q8R066|C1QT4_MOUSE      ----------MLLLLLGFLGPAACWALGPA-GPGSSELRSAFSAARTTPLEGTSEMAVTF 49
                                     :*  :  ::. :.*   .    *.*: * :             :::*

sp|P0A5I7|BLAC_MYCBO       ---FAELERRYDARLGVYVPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLD 104
sp|A5U493|BLAC_MYCTA       ---FAELERRYDARLGVYVPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLD 104
sp|P9WKD2|BLAC_MYCTO       ---FAELERRYDARLGVYVPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLD 104
sp|P9WKD3|BLAC_MYCTU       ---FAELERRYDARLGVYVPATGTTAAIEYRADERFAFCSTFKAPLVAAVLHQNPLTHLD 104
sp|Q9BXJ3|C1QT4_HUMAN      DKVYVNIGGDFDVATGQF----------RCRVPGAYFF--SFT-------AGKAPHKSLS 91
sp|Q8R066|C1QT4_MOUSE      DKVYVNIGGDFDAATGRF----------RCRVPGAYFF--SFT-------AGKAPHKSLS 90
                              :.::   :*.  * :          . *.   : *  :*.         : * . *.

sp|P0A5I7|BLAC_MYCBO       KLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIRYSDGTAANLL---LADLGGPGGGT 161
sp|A5U493|BLAC_MYCTA       KLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIRYSDGTAANLL---LADLGGPGGGT 161
sp|P9WKD2|BLAC_MYCTO       KLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIRYSDGTAANLL---LADLGGPGGGT 161
sp|P9WKD3|BLAC_MYCTU       KLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIRYSDGTAANLL---LADLGGPGGGT 161
sp|Q9BXJ3|C1QT4_HUMAN      VMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPQYALGAPG--- 148
sp|Q8R066|C1QT4_MOUSE      VMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPQYALGAPG--- 147
                            ::. . *::::::   *::  :  : .* .   : *.* .  .*       **.**

sp|P0A5I7|BLAC_MYCBO       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA 221
sp|A5U493|BLAC_MYCTA       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA 221
sp|P9WKD2|BLAC_MYCTO       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA 221
sp|P9WKD3|BLAC_MYCTU       AAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPHAIALVLQQLVLGNALPPDKRA 221
sp|Q9BXJ3|C1QT4_HUMAN      ATFSGYLVYADAD-----ADAP--ARGPPAPPEPRS---AFSAARTRSLVGSDAGPGPRH 198
sp|Q8R066|C1QT4_MOUSE      ATFSGYLVYADAD-----ADAP--ARGPA-APEPRS---AFSAARTRSLVGSDAAPGPRH 196
                           *:*:***   .       *: *   *.*    .  :   *:: .  : ::*.   *. *

sp|P0A5I7|BLAC_MYCBO       --LLTDWMARNTTG-----AKRIRAGFPA------------------------------- 243
sp|A5U493|BLAC_MYCTA       --LLTDWMARNTTG-----AKRIRAGFPA------------------------------- 243
sp|P9WKD2|BLAC_MYCTO       --LLTDWMARNTTG-----AKRIRAGFPA------------------------------- 243
sp|P9WKD3|BLAC_MYCTU       --LLTDWMARNTTG-----AKRIRAGFPA------------------------------- 243
sp|Q9BXJ3|C1QT4_HUMAN      QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMI 258
sp|Q8R066|C1QT4_MOUSE      RPLAFDTELVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMI 256
                             *  *    *  *     *  :*. :*.

sp|P0A5I7|BLAC_MYCBO       -------------------------DWKV-IDKTGTGDYGRANDIAVVWSPTGVPYVVAV 277
sp|A5U493|BLAC_MYCTA       -------------------------DWKV-IDKTGTGDYGRANDIAVVWSPTGVPYVVAV 277
sp|P9WKD2|BLAC_MYCTO       -------------------------DWKV-IDKTGTGDYGRANDIAVVWSPTGVPYVVAV 277
sp|P9WKD3|BLAC_MYCTU       -------------------------DWKV-IDKTGTGDYGRANDIAVVWSPTGVPYVVAV 277
```

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sp|Q9BXJ3|C1QT4_HUMAN      YDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITF---SGFLV-YPD 314
sp|Q8R066|C1QT4_MOUSE      YDDGASRRREMQSQSVMLPLRRGDAVWLLSHDHDGYGAYSNHGKYITF---SGFLV-YPD 312
                                                     * :  *: * * *.. ..  ..   :*.

sp|P0A5I7|BLAC_MYCBO       MSDRAGGGYDAEPREALLAEAATCVAGVLA       307
sp|A5U493|BLAC_MYCTA       MSDRAGGGYDAEPREALLAEAATCVAGVLA       307
sp|P9WKD2|BLAC_MYCTO       MSDRAGGGYDAEPREALLAEAATCVAGVLA       307
sp|P9WKD3|BLAC_MYCTU       MSDRAGGGYDAEPREALLAEAATCVAGVLA       307
sp|Q9BXJ3|C1QT4_HUMAN      LAPAAPPGLGA---SELL------------       329
sp|Q8R066|C1QT4_MOUSE      LAAAGPPALKP---PEL-------------       326
                           ::  .  .        *
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 0
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 60
sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTT--RTQLPPAY--TNSFTRGVYYPDKVFRSSVLHSTQDLFL 56


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 0
sp|Q2FPJ8|RL30E_METHJ      ---------------------------MDFNTSL------RRAIKTGK------------ 15
sp|P59594|SPIKE_SARS       PFYSNVTGFHTIN-------HTFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQS 113
sp|P0DTC2|SPIKE_SARS2      PFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQS 116


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 0
sp|Q2FPJ8|RL30E_METHJ      VILGQNETKDSIE------------------------KGSAKLVVVA------------- 38
sp|P59594|SPIKE_SARS       VIIINNSTNVVIRACNFELCDNPFFAVSKPMGT----QTHTMIFDNAFNCTFEYISDAFS 169
sp|P0DTC2|SPIKE_SARS2      LLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL 176


sp|Q6LYT4|Y903_METMP       ----------MGLKYLAFKNRGQ---------------------------ISLELGVLV- 22
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 38
sp|P59594|SPIKE_SARS       LDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINIT 229
sp|P0DTC2|SPIKE_SARS2      MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINIT 236


sp|Q6LYT4|Y903_METMP       ---------------------LAVAMVAVFAGYLYIQSTLE------------------- 42
sp|Q2FPJ8|RL30E_METHJ      -----------------------ANCPAEFSGYLSGKDGVKTY----------------- 58
sp|P59594|SPIKE_SARS       NFRAILTAFS------PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDAVDCSQNPL 283
sp|P0DTC2|SPIKE_SARS2      RFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPL 296
                                                  .   * : ***     :

sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 42
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS       AELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERK 343
sp|P0DTC2|SPIKE_SARS2      SETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRK 356


sp|Q6LYT4|Y903_METMP       ----------------------------------------------SAVKINQTA----- 51
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS       KISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG 403
sp|P0DTC2|SPIKE_SARS2      RISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTG 416


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 58
```

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sp|P59594|SPIKE_SARS        VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPD 463
sp|P0DTC2|SPIKE_SARS2       KIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG 476


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        GKPCTP-PALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKN 522
sp|P0DTC2|SPIKE_SARS2       STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKN 536


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        QCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVS 582
sp|P0DTC2|SPIKE_SARS2       KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS 596


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV 642
sp|P0DTC2|SPIKE_SARS2       VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV 656


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        DTSYECDIPIGAGICASYHTVSL----LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT 698
sp|P0DTC2|SPIKE_SARS2       NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT 716


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        NFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDR 758
sp|P0DTC2|SPIKE_SARS2       NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK 776


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        NTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQ 818
sp|P0DTC2|SPIKE_SARS2       NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ 836


sp|Q6LYT4|Y903_METMP        ------------------------------------------------------------ 51
sp|Q2FPJ8|RL30E_METHJ       ------------------------------------------------------------ 58
sp|P59594|SPIKE_SARS        YGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQI 878
sp|P0DTC2|SPIKE_SARS2       YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQI 896


sp|Q6LYT4|Y903_METMP        ------------------------NGTVGMYNSAVNRITESVGNLSNN------------ 75
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sp|Q2FPJ8|RL30E_METHJ      --------TYEGSGVQLG------------------------------------------ 68
sp|P59594|SPIKE_SARS       PFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNA 938
sp|P0DTC2|SPIKE_SARS2      PFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNA 956


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 75
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 68
sp|P59594|SPIKE_SARS       QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA 998
sp|P0DTC2|SPIKE_SARS2      QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA 1016


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 75
sp|Q2FPJ8|RL30E_METHJ      ------------------------RACGKPFIVSALAIEE-------------------- 84
sp|P59594|SPIKE_SARS       EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFT 1058
sp|P0DTC2|SPIKE_SARS2      EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFT 1076


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 75
sp|Q2FPJ8|RL30E_METHJ      ----------------------------------------------SGDSDILT------ 92
sp|P59594|SPIKE_SARS       TAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT 1118
sp|P0DTC2|SPIKE_SARS2      TAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNT 1136


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 75
sp|Q2FPJ8|RL30E_METHJ      ------------------------------------------------------------ 92
sp|P59594|SPIKE_SARS       VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES 1178
sp|P0DTC2|SPIKE_SARS2      VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES 1196


sp|Q6LYT4|Y903_METMP       ------------------------------------------------------------ 75
sp|Q2FPJ8|RL30E_METHJ      ---LSR------------------------------------------------------ 95
sp|P59594|SPIKE_SARS       LIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKF 1238
sp|P0DTC2|SPIKE_SARS2      LIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKF 1256


sp|Q6LYT4|Y903_METMP       -----------------    75
sp|Q2FPJ8|RL30E_METHJ      -----------------    95
sp|P59594|SPIKE_SARS       DEDDSEPVLKGVKLHYT    1255
sp|P0DTC2|SPIKE_SARS2      DEDDSEPVLKGVKLHYT    1273
```

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CLUSTAL O(1.2.4) multiple sequence alignment


sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 60
sp|P0DTC2|SPIKE_SARS2      MFVFLVLLPLVSSQCVNLTT--RTQLPPAY--TNSFTRGVYYPDKVFRSSVLHSTQDLFL 56

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       PFYSNVTGFHTIN-------HTFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQS 113
sp|P0DTC2|SPIKE_SARS2      PFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQS 116

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       VIIINNSTNVVIRACNFELCDNPFFAVSKPMGT----QTHTMIFDNAFNCTFEYISDAFS 169
sp|P0DTC2|SPIKE_SARS2      LLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL 176

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       LDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINIT 229
sp|P0DTC2|SPIKE_SARS2      MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINIT 236

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS       NFRAILTAFS------PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDAVDCSQNPL 283
sp|P0DTC2|SPIKE_SARS2      RFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPL 296

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 0
```

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sp|P59594|SPIKE_SARS      AELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERK 343
sp|P0DTC2|SPIKE_SARS2     SETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRK 356


sp|P0A5I7|BLAC_MYCBO      ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA      ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO      ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU      ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS      KISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG 403
sp|P0DTC2|SPIKE_SARS2     RISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTG 416


sp|P0A5I7|BLAC_MYCBO      ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA      ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO      ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU      ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS      VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPD 463
sp|P0DTC2|SPIKE_SARS2     KIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG 476


sp|P0A5I7|BLAC_MYCBO      ------------------------------------------------------------ 0
sp|A5U493|BLAC_MYCTA      ------------------------------------------------------------ 0
sp|P9WKD2|BLAC_MYCTO      ------------------------------------------------------------ 0
sp|P9WKD3|BLAC_MYCTU      ------------------------------------------------------------ 0
sp|P59594|SPIKE_SARS      GKPCTP-PALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKN 522
sp|P0DTC2|SPIKE_SARS2     STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKN 536


sp|P0A5I7|BLAC_MYCBO      --------------------------------------------------MRNRGFGRRE 10
sp|A5U493|BLAC_MYCTA      --------------------------------------------------MRNRGFGRRE 10
sp|P9WKD2|BLAC_MYCTO      --------------------------------------------------MRNRGFGRRE 10
sp|P9WKD3|BLAC_MYCTU      --------------------------------------------------MRNRGFGRRE 10
sp|P59594|SPIKE_SARS      QCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVS 582
sp|P0DTC2|SPIKE_SARS2     KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS 596
                                                                            :   .**  .

sp|P0A5I7|BLAC_MYCBO      LLV-------AMAML--------------------------------VSVTGCARHASGA 31
sp|A5U493|BLAC_MYCTA      LLV-------AMAML--------------------------------VSVTGCARHASGA 31
sp|P9WKD2|BLAC_MYCTO      LLV-------AMAML--------------------------------VSVTGCARHASGA 31
sp|P9WKD3|BLAC_MYCTU      LLV-------AMAML--------------------------------VSVTGCARHASGA 31
sp|P59594|SPIKE_SARS      VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV 642
sp|P0DTC2|SPIKE_SARS2     VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV 656
                          ::.        :*:*                                  : :**   *. .

sp|P0A5I7|BLAC_MYCBO      -RPASTTLPAGADLADRFAELERR-------YDARLGVYVPATGTTAAIEYRADE----- 78
sp|A5U493|BLAC_MYCTA      -RPASTTLPAGADLADRFAELERR-------YDARLGVYVPATGTTAAIEYRADE----- 78
sp|P9WKD2|BLAC_MYCTO      -RPASTTLPAGADLADRFAELERR-------YDARLGVYVPATGTTAAIEYRADE----- 78
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sp|P9WKD3|BLAC_MYCTU       -RPASTTLPAGADLADRFAELERR-------YDARLGVYVPATGTTAAIEYRADE----- 78
sp|P59594|SPIKE_SARS       DTSYECDIPIGAGICASYHTVSL----LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT 698
sp|P0DTC2|SPIKE_SARS2      NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT 716
                               .  :* **.:.  :              .  : .*. : *:  :: *  :

sp|P0A5I7|BLAC_MYCBO       ---------------------------------------RFAFCSTFKAPLVA------- 92
sp|A5U493|BLAC_MYCTA       ---------------------------------------RFAFCSTFKAPLVA------- 92
sp|P9WKD2|BLAC_MYCTO       ---------------------------------------RFAFCSTFKAPLVA------- 92
sp|P9WKD3|BLAC_MYCTU       ---------------------------------------RFAFCSTFKAPLVA------- 92
sp|P59594|SPIKE_SARS       NFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDR 758
sp|P0DTC2|SPIKE_SARS2      NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK 776
                                                                    :**: ::  * .

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 92
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 92
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 92
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 92
sp|P59594|SPIKE_SARS       NTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQ 818
sp|P0DTC2|SPIKE_SARS2      NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ 836


sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 92
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 92
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 92
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 92
sp|P59594|SPIKE_SARS       YGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQI 878
sp|P0DTC2|SPIKE_SARS2      YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQI 896


sp|P0A5I7|BLAC_MYCBO       ------------AVLHQNPLTHLDKLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIR 140
sp|A5U493|BLAC_MYCTA       ------------AVLHQNPLTHLDKLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIR 140
sp|P9WKD2|BLAC_MYCTO       ------------AVLHQNPLTHLDKLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIR 140
sp|P9WKD3|BLAC_MYCTU       ------------AVLHQNPLTHLDKLITYTSDDIRSISPVAQQHVQTGMTIGQLCDAAIR 140
sp|P59594|SPIKE_SARS       PFAMQMAYRFNGIGVTQNVLYENQKQIANQFN--KAISQIQESLTTTSTALGKLQDVVNQ 936
sp|P0DTC2|SPIKE_SARS2      PFAMQMAYRFNGIGVTQNVLYENQKLIANQFN--SAIGKIQDSLSSTASALGKLQDVVNQ 954
                                         : ** * . :* *:   :   :*. : :.   *. ::*:* *.. :

sp|P0A5I7|BLAC_MYCBO       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH 200
sp|A5U493|BLAC_MYCTA       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH 200
sp|P9WKD2|BLAC_MYCTO       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH 200
sp|P9WKD3|BLAC_MYCTU       YSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNRDPPGDERDTTTPH 200
sp|P59594|SPIKE_SARS       --NAQALNTLVKQLSS------NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS--- 985
sp|P0DTC2|SPIKE_SARS2      --NAQALNTLVKQLSS------NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQS--- 1003
                             :. * * *: :*..       * .    *.* :****  * *:: *     *  :

sp|P0A5I7|BLAC_MYCBO       AIALVLQQLVLGNALPPDKRALLTDWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRAN 260
sp|A5U493|BLAC_MYCTA       AIALVLQQLVLGNALPPDKRALLTDWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRAN 260
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sp|P9WKD2|BLAC_MYCTO       AIALVLQQLVLGNALPPDKRALLTDWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRAN 260
sp|P9WKD3|BLAC_MYCTU       AIALVLQQLVLGNALPPDKRALLTDWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRAN 260
sp|P59594|SPIKE_SARS       LQTYVTQQLIRAAEIRASA-NLAATKMSECVLG----------QSKRVDFCGKGYHLM-- 1032
sp|P0DTC2|SPIKE_SARS2      LQTYVTQQLIRAAEIRASA-NLAATKMSECVLG----------QSKRVDFCGKGYHLM-- 1050
                             : * ***: .  :  .   * :  *:. . *          : * :*  *.* :

sp|P0A5I7|BLAC_MYCBO       DIAVVWSPTGVPYVVAVMSDRAGGGYDAEPREALLAEAATCVAGVLA------------- 307
sp|A5U493|BLAC_MYCTA       DIAVVWSPTGVPYVVAVMSDRAGGGYDAEPREALLAEAATCVAGVLA------------- 307
sp|P9WKD2|BLAC_MYCTO       DIAVVWSPTGVPYVVAVMSDRAGGGYDAEPREALLAEAATCVAGVLA------------- 307
sp|P9WKD3|BLAC_MYCTU       DIAVVWSPTGVPYVVAVMSDRAGGGYDAEPREALLAEAATCVAGVLA------------- 307
sp|P59594|SPIKE_SARS       -SFPQAAPHGVVFLHVTYVPSQER--------NFTTAPAICHEGKAYFPREGVFVFNGTS 1083
sp|P0DTC2|SPIKE_SARS2      -SFPQSAPHGVVFLHVTYVPAQEK--------NFTTAPAICHDGKAHFPREGVFVSNGTH 1101
                                 :* ** :: ..                : :  * *  *

sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|P59594|SPIKE_SARS       WFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS 1143
sp|P0DTC2|SPIKE_SARS2      WFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTS 1161


sp|P0A5I7|BLAC_MYCBO       ------------------------------------------------------------ 307
sp|A5U493|BLAC_MYCTA       ------------------------------------------------------------ 307
sp|P9WKD2|BLAC_MYCTO       ------------------------------------------------------------ 307
sp|P9WKD3|BLAC_MYCTU       ------------------------------------------------------------ 307
sp|P59594|SPIKE_SARS       PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFI 1203
sp|P0DTC2|SPIKE_SARS2      PDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFI 1221


sp|P0A5I7|BLAC_MYCBO       ---------------------------------------------------- 307
sp|A5U493|BLAC_MYCTA       ---------------------------------------------------- 307
sp|P9WKD2|BLAC_MYCTO       ---------------------------------------------------- 307
sp|P9WKD3|BLAC_MYCTU       ---------------------------------------------------- 307
sp|P59594|SPIKE_SARS       AGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT 1255
sp|P0DTC2|SPIKE_SARS2      AGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT 1273
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