

```
#####
# Program: needle
# Rundate: Sun 24 May 2020 17:21:07
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20200524-172200-0614-74180216-p1m.asequence
#   -bsequence emboss_needle-I20200524-172200-0614-74180216-p1m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: M3W594_FELCA
# 2: P09958_FURIN_HUMAN
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 794
# Identity:      766/794 (96.5%)
# Similarity:   772/794 (97.2%)
# Gaps:         1/794 ( 0.1%)
# Score: 4083.0
#
#=====
```

M3W594_FELCA	1	MELRPWLLWVVAAGALVLLAADACGQKVYTNWAVHIPGGPAVADSLAR	50
		. .	
P09958_FURIN_	1	MELRPWLLWVVAATGTLVLLAADAQGQKVFTNTWAVRIPGGPAVANSVAR	50
M3W594_FELCA	51	KHGFLNLGQIFGDYYHFWHRAVTKRSLSPHRPRHSRLQREPQVQWLEQQV	100
		. .	
P09958_FURIN_	51	KHGFLNLGQIFGDYYHFWHRGVTKRSLSPHRPRHSRLQREPQVQWLEQQV	100
M3W594_FELCA	101	AKRRTKRDVYQEPTDPKFPQQWYLSGVTQRDLNVKEAWAQGYTGHGIVVS	150
		. .	
P09958_FURIN_	101	AKRRTKRDVYQEPTDPKFPQQWYLSGVTQRDLNVKAAWAQGYTGHGIVVS	150

M3W594_FELCA	151	ILDDGIEKNHPDLAGNYDPGASFDVNDQDPDPQPRYTQMNDNRHGTRCAG 	200
P09958_FURIN_	151	ILDDGIEKNHPDLAGNYDPGASFDVNDQDPDPQPRYTQMNDNRHGTRCAG 	200
M3W594_FELCA	201	EVAAVANNGVCGVGVAYNARIGGVRMLDGEVTDAVEARSLGLNPNIHIY 	250
P09958_FURIN_	201	EVAAVANNGVCGVGVAYNARIGGVRMLDGEVTDAVEARSLGLNPNIHIY 	250
M3W594_FELCA	251	SASWGPEDDGKTVDGPARLAEAEAFRQVSVQGRGGLGSIFVWASGNGGREH 	300
P09958_FURIN_	251	SASWGPEDDGKTVDGPARLAEAEAFRQVSVQGRGGLGSIFVWASGNGGREH 	300
M3W594_FELCA	301	DSCNCDGYTNSIYTLSSISSATQLGNVPWYSEACSSTLATTYSSGSQNEKQ 	350
P09958_FURIN_	301	DSCNCDGYTNSIYTLSSISSATQFGNVPWYSEACSSTLATTYSSGNQNEKQ 	350
M3W594_FELCA	351	IVTTDLRQKCTESHTGTSASAPLAAGIALTLEANKNLTWRDMQHLVVQT 	400
P09958_FURIN_	351	IVTTDLRQKCTESHTGTSASAPLAAGIALTLEANKNLTWRDMQHLVVQT 	400
M3W594_FELCA	401	SKPAHLNANDWATNGVGRKVSYSYGYGLLDAGAMVTLAQNWTTVAPQRKC 	450
P09958_FURIN_	401	SKPAHLNANDWATNGVGRKVSYSYGYGLLDAGAMVALAQNWTTVAPQRKC 	450
M3W594_FELCA	451	IIDILTEPKDIGKRLEVRKMVTAACLGEPHITRLEHAQARLTLSYNRRGD 	500
P09958_FURIN_	451	IIDILTEPKDIGKRLEVRKVTACLGEPNHITRLEHAQARLTLSYNRRGD 	500
M3W594_FELCA	501	LAIHLVSPMGTRSTLLAARPHDYSADGFNDWAFMTTHSWDEDPSGEWVLE 	550
P09958_FURIN_	501	LAIHLVSPMGTRSTLLAARPHDYSADGFNDWAFMTTHSWDEDPSGEWVLE 	550
M3W594_FELCA	551	IENTSEANNYGTLTKFTLVLYGTAPEGLHAPPESSGCKLTSSQACVVCE 	600
P09958_FURIN_	551	IENTSEANNYGTLTKFTLVLYGTAPEGLPVPESSGCKLTSSQACVVCE 	600
M3W594_FELCA	601	EGFSLHQKSCVQHCPPGFTPQVLDTHYSTENDVEIIRASVCAPCHASCAT 	650
P09958_FURIN_	601	EGFSLHQKSCVQHCPPGFAPQVLDTHYSTENDVETIRASVCAPCHASCAT 	650
M3W594_FELCA	651	CQGLAPTDCLSCPSHASLDPVEQTCRSQSQSSRES-PEQQPPRPPPEVEA . .	699
P09958_FURIN_	651	CQGPALTDCLSCPSHASLDPVEQTCRSQSQSSRESPPQQQPPRLPPEVEA . .	700
M3W594_FELCA	700	EPRARAELLPSHLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFSFRGVKVV	749
P09958_FURIN_	701	GQRLRAGLLPSHLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFSFRGVKVV	750

M3W594_FELCA 750 TMDRGLISYKGLPPEAWQEEG PSDSEED EGRGERTAFIKDQSAL 793
||||| . |||||
P09958_FURIN_ 751 TMDRGLISYKGLPPEAWQEEC PSDSEED EGRGERTAFIKDQSAL 794

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#####

Program: water
Rundate: Fri 22 May 2020 15:19:38
Commandline: water
-auto
-stdout
-asequence emboss_water-I20200522-151937-0280-4325025-p2m.asequence
-bsequence emboss_water-I20200522-151937-0280-4325025-p2m.bsequence
-datafile EBLOSUM62
-gapopen 10.0
-gapextend 0.5
-aformat3 pair
-sprotein1
-sprotein2
Align_format: pair
Report_file: stdout
#####

#=====

Aligned_sequences: 2
1: ACE2_FELCA
2: ACE2_HUMAN
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 805
Identity: 686/805 (85.2%)
Similarity: 743/805 (92.3%)
Gaps: 0/805 (0.0%)
Score: 3717.0

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ACE2_FELCA	1	MSGSFWLLLSFAALTAQSTTEELAKTFLEKFNHEAEELSYQSSLASWNY	50
	 : . . : : .	
ACE2_HUMAN	1	MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNY	50
ACE2_FELCA	51	NTNITDENVQKMNEAGAKWSAFYEEQSKLAKTYPLAEIHNTTVKRQLQAL	100
		: :. 	
ACE2_HUMAN	51	NTNITEENVQNMNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKQLQAL	100
ACE2_FELCA	101	QQSGSSVLSADKSQRLNTILNAMSTIYSTGKACNPNNPQECLLLEPGLDD	150
		: . : . .. :	
ACE2_HUMAN	101	QQNGSSVLSSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNE	150

ACE2_FELCA	151	IMENSKDYNERLWAWEGWRAEVGKQLRPLYEEYVALKNEMARANNYEDYG . . : :	200
ACE2_HUMAN	151	IMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYG	200
ACE2_FELCA	201	DYWRGDYEEEWTDGYNYSRSQLIKDVEHTFTQIKPLYQHLHAYVRAKLMD : : . : : :	250
ACE2_HUMAN	201	DYWRGDYEVNGVDGYDYSRQLIEDVEHTFEEIKPLYEHLHAYVRAKLMD	250
ACE2_FELCA	251	TYPSRISPTGCLPAHLLGDMWGRFWTNLYPLTVPFQKPNIDVTDAMVNQ . . . : : :	300
ACE2_HUMAN	251	AYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFQKPNIDVTDAMVDQ	300
ACE2_FELCA	301	SWDARRIFKEAEKFFVSVGLPNMTQGFWENSMLTEPGDSRKVVCHPTAWD : : : : : . :	350
ACE2_HUMAN	301	AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWD	350
ACE2_FELCA	351	LGKGDFRIMCTKVTMDDFLTAHHEMGGHIQYDMAYAVQPFLLRNGANEGF . : :	400
ACE2_HUMAN	351	LGKGDFRILMCTKVTMDDFLTAHHEMGGHIQYDMAYAAQPFLLRNGANEGF	400
ACE2_FELCA	401	HEAVGEIMSLSAATPNHLKTIGLLSPGFSEDETEINFLKQALTIVGTL : : . : :	450
ACE2_HUMAN	401	HEAVGEIMSLSAATPKHLKSIIGLLSPDFQEDNETEINFLKQALTIVGTL	450
ACE2_FELCA	451	PFTYMLEKWRWVFKGEIPKEQWMQKWWEMKREIVGVVEPVPHDETYCDP : : :	500
ACE2_HUMAN	451	PFTYMLEKWRWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDP	500
ACE2_FELCA	501	ASLFHVANDYSFIRYYTRTIYQFQFQEALCRIAKHEGPHKCDISNSSEA : : : . :	550
ACE2_HUMAN	501	ASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPHKCDISNSTEA	550
ACE2_FELCA	551	GKKLLQMLTLGKSKPWTLALAHVVGEEKMNVTPLLKYFEPLFTWLKEQNR : . . . : : : :	600
ACE2_HUMAN	551	GQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK	600
ACE2_FELCA	601	NSFVGWNTDWRPYADQSIKVRISLKSALGDEAYEWNENMYLFRSSVAYA : . : :	650
ACE2_HUMAN	601	NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNENMYLFRSSVAYA	650
ACE2_FELCA	651	MREYFSKVKVQTIQFVEDNVVSNLKPRIFFVTASKNVSDVIPRSEV : : . : : : : :	700
ACE2_HUMAN	651	MRQYFLKVKVQMIQFGEEDVRVANLKPRIFFVTAPKNVSDIIPRTEV	700
ACE2_FELCA	701	EEAIRMSRSRINDAFRLDDNSLEFLGIQPTLSPPYQPPVTIWLIVFGVVM : : : . . :	750
ACE2_HUMAN	701	EKAIRMSRSRINDAFRLDNDNSLEFLGIQPTLGPPNQPPVTIWLIVFGVVM	750

ACE2_FELCA	751	GVVVGVLLIVSGIRNRRKNNQARSEENPYASVDLSKGENNPQFHADD	800
		: : .:.: : .:.: . : : : .	
ACE2_HUMAN	751	GVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPQFQNTDD	800
ACE2_FELCA	801	VQTSF	805
ACE2_HUMAN	801	VQTSF	805

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#####
# Program: needle
# Rundate: Sat 23 May 2020 11:28:56
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20200523-112955-0071-59784166-
p1m.asequence
#   -bsequence emboss_needle-I20200523-112955-0071-59784166-
p1m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: SPIKE_SARS2
# 2: AJO26983.1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1618
# Identity:      408/1618 (25.2%)
# Similarity:    648/1618 (40.0%)
# Gaps:          497/1618 (30.7%)
# Score: 1110.5
#
#
#=====
```

```
SPIKE_SARS2      1 MFVFLVLLPLVSS-QCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLH
49
      |.:.||||.:|.:. . . . . |..|...:|.|      || |.:.:.
AJO26983.1      1 MILLLVLFVSVVGAHDAPHGVTLPQFNTSYNN-----DK-FELNFYN
40

SPIKE_SARS2      50 --STQDL-----FLPFF---SNVTWFHAIHVS--GTNGTKRF---
79
      .|. |:           :||:.   :|..|:..:..   |:||....
AJO26983.1      41 FLQTDWIDIPPNTETILGGYLPYCGTGANCGWYNFVYQQNVGSGNGKYSYINT
90

SPIKE_SARS2      80 DNPVLPFNDGVYFASTEKSN-----IIRGWIFGTTLDSTQ-S
116
      .|.:|.|...|...|...|...|.:.           :|           .:..|:| |
AJO26983.1      91 QNLNIPNVHGVYFDVREHNSDGVWDARDRVGLLI-----AIHGKSQYS
```

133

SPIKE_SARS2	117	LLIV-----NNATNVVIKVCEF-----QF-----C-----
136		
		: . .:. :. : :.:
AJO26983.1	134	LLMVLQDDVEENQPHVAVKICHWKPGNISSIHQFSVNLGDGGQCVFNQRF
183		
SPIKE_SARS2	137	-----NDPFLGVYHKN-----NKSWMESSEFRVYSSANNCTF
168		
		. .:.:. . . .:.:. . . .:.:.:
AJO26983.1	184	SLDTILTND-FYGFQWTNMYVNIYLGTTITKVWVENDWSVVESSISYHW
232		
SPIKE_SARS2	169	EYVSQPFLMDLEGKQGNFKNLREFVFKNIDG-----YFKIY
204		
		:.:.:. . .:.: . .:.:
AJO26983.1	233	SRLNYGYMQFVNR-----TTYVYNNVTGGANYTHLQLEECHSEYCYAGY
276		
SPIKE_SARS2	205	SKHTPINLVRDLPQGFSAL-----EPLVDLPIGINITRFQT
240		
		: .:.:.:.:.:. . .:
AJO26983.1	277	AKNVFVPIDGKIPDGFSFSNWFLLSDKSTSVQGRVLSKQPVFVQCLR---
323		
SPIKE_SARS2	241	LLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTF-----LLKYNENG
283		
		:... :.::
AJO26983.1	324	-----AVPSWSNNSA---VVHFSNDDFCPNVTAEVLRFNLF
357		
SPIKE_SARS2	284	TITDAVDCALDPLSETKCTLKSFTVE----KGI--YQTSNFR-VQPTESI
326		
		:.:.:
AJO26983.1	358	SDTDVY-----VASNSDDRLYFTFEDNTTAGVACYSSANITDYKPN---
398		
SPIKE_SARS2	327	VRFPNITNLCPFGEVFNA-----TRFASV-----YAWNRKR
357		
		. .:.:
AJO26983.1	399	---TNASSQTPFGKTTHSYFCFANFSSSHVTQFLGILPPIVREFAFGK---
443		
SPIKE_SARS2	358	ISNCVADYSVL---YNSASFSTFKCYGVSPTKLND-----LCFTNVYADS
399		
		. .:.:
AJO26983.1	444	-----DGSIFVNGYKYFSFPPIKSVNFSISSVENFGFWTIAYTN-YTDV
486		
SPIKE_SARS2	400	FV-IRGDEVRQI----APGQTGKIADYNYKLPDFTGCVIAWNSNLDISK
444		
		. .:
AJO26983.1	487	MVDVNGTGITRLFYCDSPINRIKQQLKYELPDGF-----YSASMLVKK
530		
SPIKE_SARS2	445	-----VGGNYNYL-----YRFRKSNLKPFERDIST

470
AJ026983.1 531 DLPKTFVVTMPQFYNNWNVTLHVVLNDTEKKADIILAKASELASL-ADVHF
579
SPIKE_SARS2 471 EIYQAGSTPCN-----GVEGFNCY---FPLQSYG--F
497
AJ026983.1 580 EIAQANGSVVNATSLCVQTRQLALFYKYTSLQGLYTYSNLVELQNYDCPF
629
SPIKE_SARS2 498 QPTNGVGYQPYP-----VVVLSFELLH-----
519
AJ026983.1 630 SPHQFNYYLQFETLCFDTSPAVAGCKWSLVHDVWRWRTQFATITISYKDGA
679
SPIKE_SARS2 520 ---APATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKF---LPF
562
AJ026983.1 680 KITTMPKAKLGFQDISNIVKDECTDYNIYGLQGTGIIRNTTTRIVAGLYY
729
SPIKE_SARS2 563 QQFGRDIADTTDAVRDPQTLLEILDITPCSFSGG-----VSVITPGTN
603
AJ026983.1 730 TSISGDLL---AFKNSTTGEIFTVVPCGLTAQAAVINDEIVGVITAVNQ
775
SPIKE_SARS2 604 TSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA
653
AJ026983.1 776 TD-----LFEFVNHTQARRARS-----STGSQTVQTYT-----
803
SPIKE_SARS2 654 EHVNSYECDIPIGAGICASYQTQTNPPRRARSVASQSI IAYTM-----
697
AJ026983.1 804 --MPQFY-----YITKWNNND---SSTNCTSVITYSSFAICNT
835
SPIKE_SARS2 698 -----SLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSM
731
AJ026983.1 836 GEIKYVNVTHVEIVDDSIGVIKPI--STGNISIPKNFTVAVQAEYIQIQV
883
SPIKE_SARS2 732 TKTSVDCTMYICGDSSTECNLLLQYGSFCTQLNRALT-GIAVE-----
773
AJ026983.1 884 KPVVVDCAKYVCNGNSHCLTLLAQYTSACQTIENALNFGARLESMLNDM
933
SPIKE_SARS2 774 ---QDKNTQEVFAQVKQIYKTP-PIKDFGGFNFS---QILPDPSKPS--K
814
AJ026983.1 934 ITVSDRSLE--LATVEKFNTTVLGAEKLGGFYFDGLRELLP----PTIGK

SPIKE_SARS2 815 RSFIEDLLFNKVTLADAGFI-KQYGDCLGDIAARDLICAQKFNGLTVLPP
863

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AJO26983.1 978 RSAIEDLLFNKVVT SGLGTVDDDYKKCSAGTDVADLVCAQYYNGIMVLP
1027

SPIKE_SARS2 864 LLTDEMIAQYTSALLA----GTITSGWTFGAGAALQIPFAMQMAYRFNGI
909

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AJO26983.1 1028 VVDQNKMSMYTASLIGGMALGSITS-----AVAVPFAMQVQARLNYV
1069

SPIKE_SARS2 910 GVTQNVLYENQKLIANQFNSAIGKI-----QDSLSTASAL
945

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AJO26983.1 1070 ALQTDVLQENQKILANAFNNAIGNITLALGKVSNAITTTSDGFNTMASAL
1119

SPIKE_SARS2 946 GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLDILSRLDKVEAEVQIDR
995

. |:|.||||.....|:|. . .|. .|. .|. .|. .|. .:|. :||:| | | :. |:| |

AJO26983.1 1120 TKIQSVVNHQGDALSQLTSQLQKNFQAISSSIAEIYNRLEKVEADAQVDR
1169

SPIKE_SARS2 996 LITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGK
1045

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AJO26983.1 1170 LITGRLAALNAYVSQTLTQYSEVKASRQLAMEKVNCECVKSQSNRYGF
1219

SPIKE_SARS2 1046 GYHLMSFPQSAPHGVVFLHVTVPAQEKNFTTAPAIC-HDGKAHFPRE--
1092

|. | | |. |. .| | |. |:|. .|. . .:|.|| | :|. .| :. . . .

AJO26983.1 1220 GTHLFSLVNSAPDGLLFFHTVLLPTEWEVVTAWSGICVNDTYAYVLKDFE
1269

SPIKE_SARS2 1093 -GVFVSNGTHWVFVTQRNFYEP-----QIIITDNTFVSGNC----DV
1128

.:|. .| | | | :|. | | | |. :| | | |. :| | | | |. :. :. : :

AJO26983.1 1270 YSIFSYNGT-YMVT PRNMFPQRK PQMSDFVQITSCEVTFLNTTYTTFQEI
1318

SPIKE_SARS2 1129 VIGI--VNNTVYDPLQPELDSFKEELDKYFKNHSTPDVDLGDISGINASV
1176

| | | . :|. | :. | | | | | :|:| | | | :|:|:|:| | :. . . |. . . :

AJO26983.1 1319 VIDYIDINKTIAD-----MLEQYNLNYYTSELNL-QLEIFNQTK
1356

SPIKE_SARS2 1177 VNIQKEIDRLNEVA-----KNL NESLIDLQELGKYEQYIKW
1212

:|:|. .| | | | :|. . . | | | | :|:|:|:| | :. |. . . |. | :| |

AJO26983.1 1357 LNLTAEIDQLEQRADNLTNIAHELQQYIDNLNKTLVDLEWLN RVET YVKW
1406

SPIKE_SARS2 1213 PWYIWLGFIAGLIAIVMVTIML-CCM-TSCC SCLKGCCSCGSCC-----K

1255

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AJO26983.1 1407 PWYVWL--LIGLVVVFICIPLLLFCCLSTGCCGCF-GC--LGSCCHSLCSR
1451

SPIKE_SARS2 1256 FDEDDSEPVLKGVKLHYT 1273

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AJO26983.1 1452 RQFESYEPIEK-VHIH-- 1466

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