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```
# Program: needle
# Rundate: Wed 11 Jan 2023 08:39:38
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20230111-083937-0108-9752-p2m.asequence
#   -bsequence emboss_needle-I20230111-083937-0108-9752-p2m.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
```

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```
#
# Aligned_sequences: 2
# 1: MERS-CoV
# 2: SARS-CoV
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 803
# Identity:      190/803 (23.7%)
# Similarity:    292/803 (36.4%)
# Gaps:          222/803 (27.6%)
# Score: 383.5
#
#
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```

MERS-CoV	1	YVDVGPDSVKSACIEVDIQTFDDKTWPRPID-VSKADGIIYPQGRITYSN	49
		.: ...  ... ... . ... : ... :	
SARS-CoV	1	-----SDLDRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSD	37
MERS-CoV	50	ITITYQGLF-PYQGDHGDYVYSAGHATGTTTPQKLFVANYSQD--VKQFA	96
		..... ... :    :   ..... :   .. .	
SARS-CoV	38	TLYLTQDLFLPF-----YS--NVTG-----FHTINHTFDNPVIPFK	71
MERS-CoV	97	NGF-----VVR---IGAAAN--STGTVIISPSTSATIRKI-----	126
		: .     ...   ... : ... ..	
SARS-CoV	72	DGIYFAATEKSNVVRGWVFGSTMNKSQSVIIINNSTNVVIRACNFELCD	121
MERS-CoV	127	YPAFMLGSSVGNFSDGKMGRFFNHTLVLLPDGCGTLLRAFYCILEPRSGN	176
		. . :.... ...:   :..   ... . .	
SARS-CoV	122	NPFFFAVSKPMGTQT-----HTMIF--D-----NAFNCTFE-----	149
MERS-CoV	177	HCPAGNSYTSFATYHTPATDCSD--GNYNRNASLNSFKEYFNLRNCTFMY	224
		...  .: ...    :.. .: :..... :	
SARS-CoV	150	-----YISDAF-----SLDVSEKSGNFKH-----LREFVFKNKDGLY	182
MERS-CoV	225	TY-----NITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATL-	267
		.  :...  ... :..... ... ...:	
SARS-CoV	183	VYKGYPIDVVRD-----LPSGFNTLKPIFKLPLGINITNFRAIL	222
MERS-CoV	268	----PVYDTIKYYSIIPHSIRSIQSDRKAW----AAFYVYKLQPLTFLLD	309
		..     ... ... : ...	
SARS-CoV	223	TAFSPAQDT-----WGTSAAAYFVGYLKPTTFMLK	252
MERS-CoV	310	FSDVGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVE	359
		:... . ... : ... : ... : ... : ... : ... : ...	

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