# Program: needle
# Rundate: Tue 24 May 2022 21:14:12
# Commandline: needle
#    -auto
#    -stdout
#    -asequence emboss_needle-E20220524-213020-0874-21503531-p1m.asequence
#    -bsequence emboss_needle-E20220524-213020-0874-21503531-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: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 209
# Identity:      19/209 ( 9.1%)
# Similarity:    31/209 (14.8%)
# Gaps:         136/209 (65.1%)
# Score: 12.5
#
#=======================================

EMBOSS_001         1 CPFGEVFNATRFASVYAWNRKISRISNCVADYSVLYNSASFSTFKCYGVSP    50
EMBOSS_001         1 --------------------------------------------------    0
EMBOSS_001        51 KLNDLCFTNVYADSFVIRGDEVRIAIRPQTGKIADYNYKLPDDFTGCVIA    100
EMBOSS_001         1 ---------------------------------------------PQITL      5
EMBOSS_001       101 WNSNNLDSKVGGNYLYRLFRKSNLKPFERDISTE--IYQAGSTP----    144
EMBOSS_001 6 WQRPLVTIKIGG--------------QLKEALLDTADTVLEEMSLPGRWK 43
EMBOSS_001 145 ---CNGVEGFNCYFPLQSY--------GFQPTNGVGYQRYRVVLSFELL 183
EMBOSS_001 44 PKMIGGIGG---IKVRQYDQILIEICGHKAIGTVALVGPTVNIICRNLL 90
EMBOSS_001 184 ------- 183
EMBOSS_001 91 TQIGCTLNF 99

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