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#=====
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 209
# Identity:      5/209 ( 2.4%)
# Similarity:    8/209 ( 3.8%)
# Gaps:          192/209 (91.9%)
# Score: 11.5
#
#
#=====

EMBOSS_001      1  -----CPFGEVFNATRFASVYAWNKRIS
24
                                     ..|...:|::  |.|...
EMBOSS_001      1  GLEHMADEEKLPPGWEKRMSRSSGRVYYFNHITNASQ-----WERPSG-
43

EMBOSS_001      25  NCVADYSVLYNASAFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRO
74

EMBOSS_001      44  -----
43

EMBOSS_001      75  IAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKS
124

EMBOSS_001      44  -----
43

EMBOSS_001      125 NLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYR
174

EMBOSS_001      44  -----
43

EMBOSS_001      175 VVVLSEFELL      183
EMBOSS_001      44  -----      43

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