

#####

Program: needle
Rundate: Wed 12 Apr 2017 21:16:55
Commandline: needle
-auto
-stdout
-asequence emboss_needle-I20170412-211654-0624-90352445-pg.asequence
-bsequence emboss_needle-I20170412-211654-0624-90352445-pg.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: 103
Identity: 10/103 (9.7%)
Similarity: 21/103 (20.4%)
Gaps: 56/103 (54.4%)
Score: 11.5

#

#

#=====

EMBOSS_001 1 MAVDEWVNNSGRRRKIAKEML-----PKGVTVRC-----WICKQP 35
EMBOSS_001 1 -----MHEVLSRGRGGDPTDPENILCLCRWCHHWVTVNP 34
EMBOSS_001 36 -GANQLDHIKPRSKYPELIWDRSNIVPAHDTCNNLKSDGDGPGGLGFHSE 84
EMBOSS_001 35 KAATELGLLRGRRTASEHVAKFRISQIGTZ----- 63
EMBOSS_001 85 VWZ 87
EMBOSS_001 64 --- 63

#-----

#-----