

```
#####
# Program: needle
# Rundate: Sun 6 Jun 2021 17:42:25
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210606-174729-0659-85770980-plm.asequence
#   -bsequence emboss_needle-I20210606-174729-0659-85770980-plm.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: linR
# 2: MAE_62070
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 396
# Identity:      60/396 (15.2%)
# Similarity:    110/396 (27.8%)
# Gaps:          183/396 (46.2%)
# Score: 71.0
#
#=====

linR          1 MNIDDLDFRHLVLLDALLKRHSVSAAARELDLPQPTASHGLARLRKALGD      50
               :.....|:::|.....|:..||..|:..|||..|.....|:|::|.
MAE_62070     1 --MIQATLHQLIVFEATARHGSFTRAAEELSITQPTVSTQMKQLTKAVGL      48

linR          51 PL-----LVRARDGMEPTPRA-----EAIAGVVQQLLEL      79
               ||          |..|..|:..|:|          .||..|:..|..|.
MAE_62070     49 PLFEQIGKRLYLTEAGRGLLVTCQAVLKIDINFEMAIAAIKGIKQGKRLR      98

linR          80 RRLAEGGQTFS PDRLKREFIIAGSDIAHLVVLTAHSAARFEAPH----      125
               |..|..|:..|.
MAE_62070     99 -----AAVSTAQYLI PQILGP      114

linR          126 --TSYR---ALTLSGDEMVSALETGHV-DIAVGAYPSLVAGIKTQRLYQ      168
               ..|:      :|..|:.....|.....| |:::..|.....:.....:
MAE_62070     115 FCQQYQGVDVSLLEL TNHQELEARII NNVDLYILSEPPEDLNLEIRPFLE      164

linR          169 EEYLCFGKEGHPF-----IKSGETDDFMA-----ADH-      195
               .....:..|.      ||.....|:..      .||
MAE_62070     165 NPLVVIARKDHP LAGQKKIP IKRLQGEPFIMREMGS GIRRAVQQIFLDHG      214

linR          196 IVSTKGMAHAHRAVERA-----LLDKIHPD-----      221
               |..|:.....|:..|          :|:..||:
MAE_62070     215 ITVSIRLEIGNNEAIKQAVAGGLGISVLSQHVLNLDHPNGEFTILDVEDF      264

linR          222 -----RIRIVASSFLVALAACFESDLIILAPARVIGRLAEV      257
               ::::|:..|..|.....|:      ..::|.
MAE_62070     265 PIQRHWYVVYPKDKKLSVIAKTFLDYLLNIQPQSLL--KVKISG-----      306

linR          258 YGLRAVRPPI LMEAFEVRQYWHARNQDDPPHRWLRLQLLHKVLSARM      303
MAE_62070     307 -----      306

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