<html><head></head><body><pre style="word-wrap: break-word; white-space: pre-wrap;">
```
#######################################
# Program: matcher
# Rundate: Wed 24 Jan 2018 13:29:12
# Commandline: matcher
#    -auto
#    -stdout
#    -asequence emboss_matcher-I20180124-132911-0542-39055053-p1m.asequence
#    -bsequence emboss_matcher-I20180124-132911-0542-39055053-p1m.bsequence
#    -datafile EDNAFULL
#    -gapopen 10
#    -gapextend 4
#    -alternatives 1
#    -aformat3 pair
#    -snucleotide1
#    -snucleotide2
# Align_format: pair
# Report_file: stdout
#######################################

#=======================================
#
# Aligned_sequences: 2
# 1: human
# 2: fugu
# Matrix: EDNAFULL
# Gap_penalty: 10
# Extend_penalty: 4
#
# Length: 603
# Identity:     327/603 (54.2%)
# Similarity:   327/603 (54.2%)
# Gaps:         102/603 (16.9%)
# Score: 189
#
#
#=======================================

human             798 TGCCGGCGAGGAGATC-ATGCGGGATGAGATGGGGGTGTGGAGACGCC--    844
                      |.|.||||.|||.||. |.|..|.|||..|..|.|||.|| ||....|
fugu               34 TTCAGGCGGGGACATAGAAGTCGCATGCAAACGTGGTTTG-AGCTTTCAT     82

human             845 TGCACAATTTCAGCCCAAGC---TTCTAGAGAGTGGTGATGACTTGCATA    891
                      |.|.|. ||..||.|..|.|   ||.|..|..|.|| |||   |.|.|.|
fugu               83 TTCTCC-TTATAGACTGACCCCTTTTTTCAATGCGG-GAT---TGGAAGA    127

human             892 -TGAGGGCAGCAATGCAAGTCG-GTGTGCTCCCCATTCTGTGG-GAC-AT    937
                       |.|||.||..|||  ||.||| |||.|.||.||  ||.|||. ||. |.
fugu              128 GTAAGGACAATAAT--AACTCGTGTGAGGTCTCC--TCAGTGAAGAGGAG    173

human             938 GACCTGGTTGCTTCACAGCTCCGAGATGA---CACAGAC--TTGCT-TAA    981
                      |.|.||  ||.| ||.|||...|||||||   |...|.|  ||||| ||.
fugu              174 GGCATG--TGAT-CATAGCCAAGAGATGAATGCGTTGGCCTTTGCTGTAT    220

human             982 -AGGAAGTGACTATTG-TGACTTGG-G-----CATCACTTGACTGATGGT   1023
                       ||||||||..|...| |||..||| |     |||||.|.|..|||||..
fugu              221 TAGGAAGTGGTTGCAGATGAGATGGTGGTTGTCATCAGTGGTTTGATGAC    270

human            1024 A--ATCAGT--TGTCTAAAGAAGTGCACAG-ATTACATGTCCGTG-TGCT   1067
                      |  ||||..  ||.|   |....|..|||. |||.||||.|..|| || |
fugu              271 ATCATCAAACCTGCC---ATTTTTCAACATCATTTCATGGCTTTGGTG-T    316

human            1068 CATTGGGTCTAT-CTGGCCGCGTTGAACACCACCAGGCTTTGTATTCAGA   1116
                      |.|.|...||.| |.||||.|.|....|..|.||.|.|||||. |||.||
fugu              317 CCTGGACACTGTTCAGGCCACTTCCTTCTTCCCCTGACTTTGC-TTCTGA    365

human            1117 AACAGGAGGGAGGTCCTGCACTTTC-CCAGGAGGGGTGGCCCTTTCAGAT   1165
                      ||..|.|.. ||...|...|.|.|. |||..     ||   |..|.|.|.
fugu              366 AAGTGTAAA-AGCAACAAAAATATGTCCATC-----TG---CAATGAAAA    406

human            1166 GCAATCGA-GATTGTTAGGCTCTGGGAGAGTAGTTGCCTGGTTGTGGCAG   1214
                      ||||..|| ||.. ||.|..||||  ||| |.|  |||..|.    |||.
fugu              407 GCAAGTGATGAGC-TTTGTTTCTG--AGA-TCG--GCCAAGA----GCAC    446
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human            1215 TTGGTAAATTTCTATTCAAACAGTTGCCATGCACCAGTTGTTCACAACAA   1264
                      | |||   ||||    |.|| |||| |.|||        |..| ||||||
fugu              447 T-GGT---TTTC----CTAA-AGTT-CTATG--------GGAC-CAACAA    477

human            1265 GGGTA-CGTAATCTGTCTGGCATTACTTCTA-CTT-T-TGTACAAAGGAT   1310
                      |  || ||.|||||..||. | ||..||.|| ||| | |||.|.||.|||
fugu              478 G--TAGCGGAATCTTGCTT-C-TTCTTTATAACTTATATGTCCTAAAGAT    523

human            1311 ---CAAAAAAAAAAAAGATACTG-TT-AAGATATGATTTTTCTCAGACTT   1355
                         ||.|........|||.|||| || ||...||..||||.||||.|.||
fugu              524 ACTCATATCCTTGTCAGAAACTGCTTGAATCAATTGTTTTCCTCACATTT    573

human            1356 TGG   1358
                      |.|
fugu              574 TAG    576


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