

<html><head></head><body><pre style="word-wrap: break-word; white-space: pre-wrap;">#####

```
# Program: needle
# Rundate: Wed 24 Jan 2018 13:29:59
# Commandline: needle
# -auto
# -stdout
# -asequence emboss_needle-I20180124-132957-0052-68239585-plm.asequence
# -bsequence emboss_needle-I20180124-132957-0052-68239585-plm.bsequence
# -datafile EDNAFULL
# -gapopen 10.0
# -gapextend 0.5
# -endopen 10.0
# -endextend 0.5
# -aformat3 pair
# -snucleotide1
# -snucleotide2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: human
# 2: fugu
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 6675
# Identity: 419/6675 ( 6.3%)
# Similarity: 419/6675 ( 6.3%)
# Gaps: 6152/6675 (92.2%)
# Score: 656.5
#
#
#=====
```

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human	101	ccctctctccccactacttgctctcacagtactcgctgagggtgaacaag	150
fugu	1	-----	0
human	151	aaaagacctgataaagattaaccagaagaaaacaaggagggaacaaccg	200
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fugu       577 ----- 576
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