########################################

# Program: needle

# Rundate: Fri 21 Sep 2018 04:15:34

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20180921-041532-0595-19915816-p2m.asequence

# -bsequence emboss\_needle-I20180921-041532-0595-19915816-p2m.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

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#

# Aligned\_sequences: 2

# 1: Homo\_sapiens\_@human@\_1\_

# 2: Cavia\_porcellus\_@domestic\_guinea\_pig@\_1\_

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 573

# Identity: 399/573 (69.6%)

# Similarity: 464/573 (81.0%)

# Gaps: 8/573 ( 1.4%)

# Score: 1988.5

#

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Homo\_sapiens\_ 1 MARAVGPERRLLAVYTGGTIGMRSELGVLVPGTGLAAILRTLPMFHDEEH 50

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Cavia\_porcell 1 MARASGSERHLLLIYTGGTLGMQSKGGVLVPGPGLVTLLRTLPMFHDKEF 50

Homo\_sapiens\_ 51 ARARGLSEDTLVLPPASRNQRILYTVLECQPLFDSSDMTIAEWVCLAQTI 100

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Cavia\_porcell 51 AQAQGLPDHALALPPASHGPRVLYTVLECQPLLDSSDMTIDDWIRIAKII 100

Homo\_sapiens\_ 101 KRHYEQYHGFVVIHGTDTMAFAASMLSFMLENLQKTVILTGAQVPIHALW 150

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Cavia\_porcell 101 ERHYEQYQGFVVIHGTDTMASGASMLSFMLENLHKPVILTGAQVPIRVLW 150

Homo\_sapiens\_ 151 SDGRENLLGALLMAGQYVIPEVCLFFQNQLFRGNRATKVDARRFAAFCSP 200

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Cavia\_porcell 151 NDARENLLGALLVAGQYIIPEVCLFMNSQLFRGNRVTKVDSQKFEAFCSP 200

Homo\_sapiens\_ 201 NLLPLATVGADITINRELVRKVDGKAGLVVHSSMEQDVGLLRLYPGIPAA 250

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Cavia\_porcell 201 NLSPLATVGADVTIAWDLVRKVKWKDPLVVHSNMEHDVALLRLYPGIPAS 250

Homo\_sapiens\_ 251 LVRAFLQPPLKGVVMETFGSGNGPTKPDLLQELRVATERGLVIVNCTHCL 300

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Cavia\_porcell 251 LVRAFLQPPLKGVVLETFGSGNGPSKPDLLQELRAAAQRGLIMVNCSQCL 300

Homo\_sapiens\_ 301 QGAVTTDYAAGMAMAGAGVISGFDMTSEAALAKLSYVLGQPGLSLDVRKE 350

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Cavia\_porcell 301 RGSVTPGYAT--SLAGANIVSGLDMTSEAALAKLSYVLGLPELSLERRQE 348

Homo\_sapiens\_ 351 LLTKDLRGEMTPPSVEERRPSLQGNTLGGGVSWLLSLSGSQEADALRNAL 400

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Cavia\_porcell 349 LLAKDLRGEMTLPTADLHQSSPPGSTLGQGVARLFSLFGCQEEDSVQDAV 398

Homo\_sapiens\_ 401 VPSLACAAAHAGDVEALQALVELGSDLGLVDFNGQTPLHAAARGGHTEAV 450

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Cavia\_porcell 399 MPSLALALAHAGELEALQALMELGSDLRLKDSNGQTLLHVAARNGRDGVV 448

Homo\_sapiens\_ 451 TMLLQRGVDVNTRDTDGFSPLLLAVRGRHPGVIGLLREAGASLSTQELEE 500

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Cavia\_porcell 449 TMLLHRGMDVNARDRDGLSPLLLAVQGRHRECIRLLRKAGACLSPQDLKD 498

Homo\_sapiens\_ 501 AGTELCRLAYRADLEGLQVWWQAGADLGQPGYDGHSALHVAEAAGNLAVV 550

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Cavia\_porcell 499 AGTELCRLASRADMEGLQAWGQAGADLQQPGYDGRSALCVAEAAGNQEVL 548

Homo\_sapiens\_ 551 AFLQSLEGAVGAQAPCPEVLPGV 573

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Cavia\_porcell 549 ALLRNL-ALVG-----PEVPPAI 565

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