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

# Program: needle

# Rundate: Fri 21 Sep 2018 04:36:50

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20180921-043649-0975-11804965-p1m.asequence

# -bsequence emboss\_needle-I20180921-043649-0975-11804965-p1m.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: intermed\_3

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

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 565

# Identity: 433/565 (76.6%)

# Similarity: 486/565 (86.0%)

# Gaps: 0/565 ( 0.0%)

# Score: 2177.0

#

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intermed\_3 1 MARAAGPERRLLAIYTGGTIGMRSEGGVLVPGRGLAAVLRTLPMFHDEEY 50

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Cavia\_porcell 1 MARASGSERHLLLIYTGGTLGMQSKGGVLVPGPGLVTLLRTLPMFHDKEF 50

intermed\_3 51 AQAHSLPEDTLVLPPASPDQRIIYTVLECQPLFDSSDMTITEWVQIAQTI 100

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Cavia\_porcell 51 AQAQGLPDHALALPPASHGPRVLYTVLECQPLLDSSDMTIDDWIRIAKII 100

intermed\_3 101 ERHYEQYHGFVVIHGTDTMAFAASVLSFMLENLQKPVILTGAQVPIHALW 150

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Cavia\_porcell 101 ERHYEQYQGFVVIHGTDTMASGASMLSFMLENLHKPVILTGAQVPIRVLW 150

intermed\_3 151 NDGRENLLGALLMAGQYIIPEVCLFFQNQLFRGNRATKVDARRFAAFCSP 200

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Cavia\_porcell 151 NDARENLLGALLVAGQYIIPEVCLFMNSQLFRGNRVTKVDSQKFEAFCSP 200

intermed\_3 201 NLPPLATVGADVTINRELVRKASGKDRLVVHSSMERDVGLLRLYPGIPAS 250

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Cavia\_porcell 201 NLSPLATVGADVTIAWDLVRKVKWKDPLVVHSNMEHDVALLRLYPGIPAS 250

intermed\_3 251 LVRAFLQPPLKGVVMETFGSGNGPTKPDLLQELRAAAERGLIIVNCTHCL 300

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Cavia\_porcell 251 LVRAFLQPPLKGVVLETFGSGNGPSKPDLLQELRAAAQRGLIMVNCSQCL 300

intermed\_3 301 QGAVTSDYASAMAGAGIVSGFDMTSEAALAKLSYVLGQPGLSLDDRKKLL 350

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Cavia\_porcell 301 RGSVTPGYATSLAGANIVSGLDMTSEAALAKLSYVLGLPELSLERRQELL 350

intermed\_3 351 AKDLRGEMTLPTADERRSSLQGSTLGRGVAWLLSLSGSQEADAMRDALMP 400

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Cavia\_porcell 351 AKDLRGEMTLPTADLHQSSPPGSTLGQGVARLFSLFGCQEEDSVQDAVMP 400

intermed\_3 401 SLALAAAHAGDLEALQALVELGSDLSLKDSNGQTPLHVAARRGHAGVVAM 450

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Cavia\_porcell 401 SLALALAHAGELEALQALMELGSDLRLKDSNGQTLLHVAARNGRDGVVTM 450

intermed\_3 451 LLQRGVDVNARDQDGLSPLLLAVRGRHQGVIGLLRAAGACLSPQELEDAG 500

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Cavia\_porcell 451 LLHRGMDVNARDRDGLSPLLLAVQGRHRECIRLLRKAGACLSPQDLKDAG 500

intermed\_3 501 TELCRLASRADSEGLQAWWQAGADLGQPGYDGHSALHVAEAAGNPEVVAL 550

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Cavia\_porcell 501 TELCRLASRADMEGLQAWGQAGADLQQPGYDGRSALCVAEAAGNQEVLAL 550

intermed\_3 551 LQSLEGGVGEVLPGV 565

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Cavia\_porcell 551 LRNLALVGPEVPPAI 565

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