

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/HAUSatp Tue Feb 1 12:17:09 2022

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[illegible]

	*::: :: . * . :: * :	. *::* ::. . * . **	
Rattus_norvegicus	RDRD VNLVIEDLKQKASEYESEA	KRLD FLMESVNFSPANLSNT	90
Mus_musculus	RDRDISLVIEDLKQKASEYESEA	KRLD FLMESVNFSPANLSKS	90
Homo_sapiens	RDRDVYLVIEDLKQKASEYESEA	KYLD LLMESVNFSPANLSST	90
Pan_troglodytes	RDRDVYLVIEDLKQKASEYESEA	KYLD LLMESVNFSPANLSST	90
Macaca_mulatta	RDRDVYLVVEDLKQKASEYESEA	KYLD LLMESVNFSPANLSST	90
Callithrix_jacchus	RDRDVYLVIEDLKQKASEYESEGRVSRCPGWSAVVPSS	KYLD LLMESVNFSPANLSST	106
Canis_lupus_familiaris	RDRDVYLVIEDLKQKASEYESEA	KHLQ NLLMESVNFSPANLSST	90
Equus_caballus	RDRDVYLVIEDLKQKASEYESEA	KHLQ D LLMESVNFSPANLSST	90
Bos_taurus	RDRDVYLVIEDLKQKASEYESEA	KHLQ D LLMESVNFSPANLSST	90
Xenopus_tropicalis	RDKDLTLVIEDLKLKSAEVKAEE	KYLD L L L T E G L G P S Y T N L S R M	87
Rhinatrema_bivittatum	RDKDITLVIEDLKLKTAETAAEE	SFLQ D L L L E M G P S Y T L S R M	87
Latimeria_chalumnae	RDRDVSLLIKDLKQKTAEYGESE	SYLD Q FLMESVGLSFTSLSSST	87
Chelonia_mydas	RDRDVSLVIDDMKQKTAEYSEV	NYLD L L L M E S V N L S F N S L S S A	87
Pavo_muticus	RERDVSFLIEDMKQRAAEYDADA	EYLD Q S L L T E S L N L S P S S L S K E	103
Pavo_cristatus	RERDVSFLIEDMKQRAAEYDADA	EYLD Q S L L T E S L N L S P S S L S K E	103
Gallus_gallus	RERDVSFLIEDMKKRAAEYDAGA	EYLD Q S L L T E S L G L S P S S L S E E	104
Anas_platyrhynchos	RERDLAFLVEDTEQKAAEYEAQA	KYLD L L L K G L G L S L S S L S S E	92
70.....80.....90.....100.....110.....120		

[illegible]

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/HAS1_001.fasta Tue Feb 1 12:17:09 2022

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* : * : * : * : * : * : * : * : * : * : * : * : * :
LVLEKCLREDLKKADVHLSAERAKAEGRLQNMDFLKAKAAEFRRFGIRAAEEQLSSRGMDA 210
LVLEKCLREDLKKAEQLQLSAEKAKVDSRLQNMDFLKAKAAEFRRFGIKAAEEQLSARGMDA 210
LVLEKCLQEDVKKAEHLHLSTERAKVDNRRQNMDFLKAKSEEFRRFGIKAAEEQLSARGMDA 210
LVLEKCLQEDVKKAEHLHLSTERAKVDNRRQNMDFLKAKSEEFRRFGIKAAEEQLSARGMDA 210
LVLEKCLQEDVKKAEHLHSIERAKVDNRRQNMDFLKAKSEEFRRFGIKAAEEQLSARGMDA 210
LVLEKCLQEDLKKAEHLHLSTERAKVDHRRQNMDFLKAKSEEFRRFIKAAEEQLSARGMDA 226
LVLEKCLREDLKKAEHLHLSTERAKVDNRLQNMDFLKAKSEEFRRFGIRTAEEQLSARGMDA 210
LVLEKCLREDLKKAEHLHLSTERAKVDNRLQNMNFLKAKSEEFRRFGIRAAEEQLSARGLDA 210
LVLEKCLQEDLKKAEHLHLSTERARVDNRLQNMDFLKAKSEEFRRGIRTAEEQLSARGMDA 210
LVLEKSLQDLKKAAEEQCNEFEKAKVEVRAQNMKKLKDSEYKYKIHAAKDLSSAGMEE 207
LVLEKTLQEDLRKAAEEQCTVEKAKVDSRMQNMFLKAKSEEFRRVRIKAAEEQLSANGMDS 207
LVLEKSLEEDLVKTEDKLAVETARTEVRIQNVEMIKAKLDSLRFKSKAAEKKLSDNGMNS 207
LVLEKHLKEDLKKTEEHLATEKAKADSRQNMKFLKDKSEDFKFRIKAAEEQLSASGMDP 207
LMLEKQLEEDLEKAKTHLEIEGAKSESRCNLQFLKDKSEDLRIRIKIAKEQLAATGLDQ 223
LMLEKQLEEDLEKAKTHLEIEGAKSESRCNLQFLKDKSEDLRIRIKIAKEQLAATGLDQ 223
LVLEKQLEKDLKTKTHLEIEVAKSENRLQFLKDKSEDLKIRIKTAEQQLAASGLDQ 224
LAMEKRLLEDLRKTRDYLEVERVKAESRSNLKFLRDKSEDFKIRIKAAEEKLAANGLDY 212
.....190.....200.....210.....220.....230.....240

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SLSHRSIVALS250DKLS251ELKQOTIPLKKKLESYLDLMPNP252SLAQVKIEEAKRELD253ATEAELT254 270
SLSHRSIAALS255EKLS256ELKEQTIPLKKKLESYLDLMPSP257SLAQVKIEEAKRELD258ATEAELT259 270
SLSHQSIVALS260EKLARLKQOTIPLKKKLESYLDLMPNP261SLAQVKIEEAKRELD262STIEAELT263 270
SLSHQSIVALS264EKLARLKQOTIPLKKKLESYLDLMPNP265SLAQVKIEEAKRELD266STIEAELT267 270
SLSHQSIVALS268EKLARLKQOTIPLKKKLESYLDLMPNP269SLARVKIEEAKRELD270STIEAELT271 270
SLSHQSIVALS272EKLAKLKQOTIPLKKKLESYLDLMPNP273SLAQVKIEEAKRELD274STIEAELT275 286
SLSHQSIVALS276EKLAELKQOTIPLKKKLESYLDLMPNP277SLAQVKIEEAKRELD278TIEAELT279 270
SLSHQSIVALS280EKLAELKQOTIPLKKKLESYLDLMPNP281SLAQVKIEEAKRELD282ITIEAELT283 270
SLSHQSIVALS284EKLAELKQOTIPLKKKLESYLDLMPNP285SLAQVKIEEAKRELD286TIEAELT287 270
SLTHRSIVLS288ETQ289TELNAQSM290AAKEKLSYLDLAPNP291SLVKVIEEAKRELK292ATEAELT293 267
SLSHQSIVALS294EKRTIKLKEQAVPLKKKLESYLDLSPNP295SLAQVKIEEAKRELD296NSTIDEAELT297 267
SLSHQSIVHLS298EKLAKLKEETVPLKKKLESYLDLTPNP299SLAQVKIEEAKRELA300ALEAELD301 267
SLTHQSIVLS302EKLTELKQOTVPLKKKLESYLDLTPNP303SLARVKIEEAKRELN304ALEAEFS305 267
SLMHPELVCLS306EKLAGMQEEMEHLKKELECYLDLPPNLP307SLARVKVEEAKRELN308ALEEEFS309 283
SLMHPELVCLS310EKLAGMQEEMEHLKKELECYLDLPPNLP311SLARVKVEEAKRELN312ALEEEFS313 283
SLMHESIVLSMSEKLAEMQ314EEHVHKKKLEY315YLDLPPNLP316SLARVKVEEAKRELN317ALEEEFS318 284
SLMHQSIVLSMSEKLEEMQ319KEVVPVKRELD320SYLDLTPNP321SLVQVKVEEARRELD322EAELS323 272
.....250.....260.....270.....280.....290.....300

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KKVDMMEL----- 278
KKVDMMGL----- 278
RRVDMMEL----- 278
RRVDMMEL----- 278
RRVDMMEL----- 278
RRVDMMEL----- 294
KKVDMMEL----- 278
KKVDMMEL----- 278
KRVNMMEL----- 278
TKVNMMEFVVPESKRRLK 286
QKVDMMELALPEQKKYRFP 286
EKVDVMEFSLPEQYKRRII 286
SKVDMMALSVPEPSKRFRF 286
KQIEMLTLDLLETKRL--- 299
KQIEMLTLDLLETKRL--- 299
KQIEMLTLDVQETKKL--- 300
KEILMLLTLEMPSRKNKFT 291

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