

File: /media/morpheus/disk1/fst/pep_msa/METABOLITE
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	** : ** : * . ** : ** : ***** ***** *	
Pavo_muticus	KQEEYEVNAKRYWDDFYKIHENGFFKDRHWLFTTEFPELVPTIRNPSQNEDSLCELSCKEVS	119
Pavo_cristatus	KQEEYEVNAKRYWDDFYKIHENGFFKDRHWLFTTEFPELVPTIRNPSQNEDSLCELSCKEVS	119
Gallus_gallus	KQEEYEVNAKRYWDDFYKIHENGFFKDRHWLFTTEFPELAPNRPSONEDSLCEFSCKEVS	119
Anas_platyrhynchos	KQEEYEVNAKRYWDDFYKIHENGFFKDRHWLFTTEFPELAPNRSQHNENSVREHIKES	120
Chelonia_mydas	KQDEYELNANEYWNDFYKIHENGFFKDRHWLFTTEFPELAPNQLSQPEASAYKDGSTRKP	180
Mus_musculus	KQVDYEVNAHKYWDDFYRIHENGFFKDRHWLFTTEFPELAPSHS--HLTGVPLEKQRSDVC	123
Rattus_norvegicus	KQADYEVNAHKYWDDFYKVHENGFFKDRHWLFTTEFPELAPSHD--HLVNLHLEKQKNEVS	123
Canis_lupus_familiaris	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQNQNHLDLLPENKRSKVP	125
Equus_caballus	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPAQNQDPLKDLPLENKRSVP	125
Bos_taurus	KQADYEINANKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQ--HLKNLLSENKRSEVY	123
Homo_sapiens	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQNQNHLDKDFLENK-SEVP	124
Pan_troglodytes	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQNQNHLDKDSFLENK-SEVS	124
Macaca_mulatta	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQNQNHLDKDFLENKRSVP	125
Callithrix_jacchus	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFTTEFPELAPSQNQNHLDKDFLENKRSSEIS	125
Heterocephalus_glaber	KQVDYEVNAHKYWNDFYKIHENGFFKDRHWLFMEFPELAPSQNENHLKDLLMENKRNEIS	125
Rhinatrema_bivittatum	KQAEYETKASKYWNDFYMIHENGFFKDRHWLFTTEFPELAPNWHQRQSENVVPPAASLDN	120
130.....140.....150.....160.....170.....180	

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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Pavo_muticus	KNEGLGSCENGHCM	-LETRAEN--	QLNLIKSRP----	TFCTKELAPRK---	LKQSD	EDYP	169
Pavo_cristatus	KNEGLGSCENGHCT	-LETRAEN--	QLNLIKSRP----	TFCTKELAPRK---	LKQSD	EDYP	169
Gallus_gallus	KNEGLGSCENGHCT	-LENRAEN--	QLNLLKSSP----	RFCTEELAPOK---	LKQSY	EDYP	169
Anas_platyrhynchos	NNEGLGSCENGHCS	-LETRAEN--	QLNFMKSTP----	TFCTEELAPOKHGEV	NSY	GDYP	173
Chelonia_mydas	RNTGLGSCEKGLSS	-LETRTEEHQDLMDSS	NIINRLD	TGDGEGILKGLDKLSD	GDFP		239
Mus_musculus	-----	EDGPGLTA--	EQHKCS	CASPGCETQVP----	PLEEPV	TQKLGHLEISGEEFP	169
Rattus_norvegicus	KP-RSSE	EDGPGLAA--	EQHKRPCTSHGCE	TRVP-----	PVEEPV	TQKLTHLEICADDFP	174
Canis_lupus_familiaris	QC-RSNE	DGPGLQI--	EEQHKCSSNSLGHKM	OMP-----	PVEENV	TQKLSHLEICVDEFP	177
Equus_caballus	EY-RSSE	DRPGLII--	EEQHKFSSNSLGHET	TQTL-----	PVEESV	TQKLSHLEICADDFP	177
Bos_taurus	EYRSGED	GPLDITI--	EEQHRCS	SVSLGDKTOPP----	LTEESV	TQKLHHLEICANFP	176
Homo_sapiens	EC-RNNED	GPGLIM--	EEQHKCSSKSLEHKT	QTL-----	PVEENV	TQKISDLAICADFP	176
Pan_troglodytes	EC-RNNED	GPGLIM--	EEQHKCSSKSLEYKT	TQTL-----	PMEENV	TQKISDLAICADFP	175
Macaca_mulatta	EC-RNNED	GPLSLIM--	EEQHKCSSKSLEHKT	ETP-----	PVEENV	TQKISDLAICADFP	177
Callithrix_jacchus	EC-RNNED	GPLVIM--	EEQHKCSSKSLEHKT	QVP-----	PVEENV	TQKISDLAICADFP	177
Heterocephalus_glaber	EC-QSSK	GGPKLTTSE	EQPKCSSTGLGPKT	QLA-----	PEEE--	TQNFSLQICA-KFP	175
Rhinatrema_bivittatum	SNGDARDS	KGHPCA-AD	QELDT	EQSSHKLHLG----	GSDLHCE	VPRLGDMKIHNCFP	175
190.....	200.....	210.....	220.....	230.....	240	

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Pavo_muticus	GSSASYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSTTAVDLVQSNVEYDSSRCFAF	229
Pavo_cristatus	GSSASYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSTTAVDLVQSNVEYDSSRCFAF	229
Gallus_gallus	GSSASYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSTTAVDLVQSNVEYDSSRCFAF	229
Anas_platyrhynchos	GSSASYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSTTAVDLVRNNAEYDSSRCFAF	233
Chelonia_mydas	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSNTAVDLVQTNSEYDSSRCFAF	299
Mus_musculus	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSATAIELLKTNSQYDPSRCYAF	229
Rattus_norvegicus	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSATAIELVKTNSQYDPSRCFAF	234
Canis_lupus_familiaris	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	237
Equus_caballus	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	237
Bos_taurus	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	236
Homo_sapiens	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	236
Pan_troglodytes	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	235
Macaca_mulatta	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	237
Callithrix_jacchus	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	237
Heterocephalus_glaber	GSSATYRILEVGCAGNTVFPILQTNNDPGLFVYCCDFSSTAVELVQTNSEYDPSRCFAF	235
Rhinatrema_bivittatum	GSLASFRVLEVGCAGNTVFPVLQTNNDPALFVYCCDFSSTAVELLKGHAAYDPSRCFAF	235
250.....260.....270.....280.....290.....300	

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Pavo_muticus	VHDLCDNDQSPFPVPDESIDVILIFVL\$AILPEKMORVINKLSRLLKPGGMILLRDYGRY	289
Pavo_cristatus	VHDLCDNDQSPFPVPDESIDVILIFVL\$AILPEKMORVINKLSRLLKPGGMILLRDYGRY	289
Gallus_gallus	VHDLCDNDQSPFPMPE\$SLDIVILIFVL\$AILPEKMQCVINKLSRLLKPGGMILLRDYGRY	289
Anas_platyrhynchos	VHDLCDNDQSPFMPDESLDVIIILIFVL\$AILPEKMCVVNRLSRLLKPGGMILLRDYGRY	293
Chelonia_mydas	VHDLCKDQSPYPMPPE\$SLDIIILIFVL\$AILPEKMQCIVNRLSQLLKPGGMILLRDYGRY	359
Mus_musculus	VHDLCDDEDQSYPPVEDSLDVIVLIFVL\$AIVPDKMOKAISKL\$RLLKPGGVMLLRDYGRY	289
Rattus_norvegicus	VHDLCDDEDQSYPPMKD\$SLDVIVLIFVL\$AIVPDKMOKAISKL\$RLLKPGGVMLLRDYGRY	294
Canis_lupus_familiaris	VHDLCDDEDKSYPPVRD\$SLDIIILIFVL\$AVVPDKMOKAINRLSRLLKPGGLMLLRDYGRY	297
Equus_caballus	VHDLCDDEDKSYPPVD\$SLDIIILIFVL\$AVVPDKMOKAINRLSRLLKPGGMLLRDYGRY	297
Bos_taurus	VHDLCDDEDKSYPPNPEN\$SLDVIIILIFVL\$AIVPDKMONAINRLSRLLKPGGIMLLRDYGRY	296
Homo_sapiens	VHDLCDDEEKSYPPVKGS\$LDIIILIFVL\$AIVPDKMOKAINRLSRLLKPGGMMLLRDYGRY	296
Pan_troglodytes	VHDLCDDEEKSYPPVKGS\$LDIIILIFVL\$AIVPDKMOEAINRLSRLLKPGGMMMLLRDYGRY	295
Macaca_mulatta	VHDLCDDEEKSYPPVKGS\$LDIIILIFVL\$AIVPDKMOKAINRLSRLLKPGGMMMLLRDYGRY	297
Callithrix_jacchus	VHDLCDDEEKSYPPVEGS\$LDIIILIFVL\$AIVPDKMOKAINRLSKLLKPGGMMMLLRDYGRY	297
Heterocephalus_glaber	VHDLCDGDQSYPPPEN\$SDVIVLIFVL\$AIVPDKMOKVNVNRLSRLLKSGGVMLVRDYGRY	295
Rhinatrema_bivittatum	VHDVSEECNYPVEQ\$SLDIIILIFVL\$SLLPDKMQSAINRM\$SHLLKPGGLILLRDYGRY	295
310.....320.....330.....340.....350.....360	

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

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DLAQLRFKKGQCLSANFYVRGDGTRVYFFTQDELDDLFTFRAGLQKVQNLVDRRLQVNRGK
DLAQLRFKKGQCLSANFYVRGDGTRVYFFTQDELDDLFTFRAGLQKVQNLVDRRLQVNRGK
DLAQLRFKKGQCLSANFYVRGDGTRVYFFTQDELDDLFTFRAGLQKIQNLVDRRLQVNRGK
DLAQLRFKKGQCLSDNFYVRGDGTRVYFFTQDELDDLFTFRAGLEKIQNLVDRRLQVNRGK
DLAQLRFKKGRCLSDNFYVRGDGTRVYFFTQDELDALFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQGEELDTLFTTAAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQDELDTLFTTAAGLEKVQNVVDRRLQVNRGK
DMAQLRFKKGQCLSENFYVRGDGTRVYFFTQDELDTLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSENFYVRGDGTRVYFFTQDELDTLFTTAAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSENFYVRGDGTRVYFFTQDELDTLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQEELDTLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQEELDTLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQEELDMLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQEELDVLFMTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGQCLSGNFYVRGDGTRVYFFTQGEELDTLFTTAGLEKVQNLVDRRLQVNRGK
DMAQLRFKKGRCLSDNFYVRGDGTRVYFFTQDELDRLFTAAGLQKVQNLVDRRLQVNRGK
.....370.....380.....390.....400.....410.....420

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QMTMYRVWVIOCKYQKPAAPQL-----	370
QMTMYRVWVIOCKYQKPAAPQL-----	370
QMTMYRVWVIOCKYQKPAAPQL-----	370
QMTMYRVWVIOCKYQKPAAPQL-----	374
QVTMHRVWVIOCKYRKPFPAHGKENGVRH--	447
QLTMYRVWVIOCKYSKPLALRSSQHVPPIPHATESSSSHSGLL	389
QLTMYRVWVIOCKYSKPLVPSASQHVPITPHTT---	385
QLTMYRVWVIOCKYRKPLLSTGT-----	379
QLTMYRVWVIOCKYRKPLPCRAAESACS-----	384
QLTMYRVWVIOCKYRKPLGSSSTG-----	378
QLTMYRVWVIOCKYCKPLLSSTS-----	378
QLTMYRVWVIOCKYCKPLLSSTS-----	377
QLTMYRVWVIOCKYCKPLLSSTS-----	379
QLTMYRVWVIOCKYRKPLLSTGS-----	379
QLTMYRVWVIOCKYRKPLQPST-----	377
QLTMYRVWVIOCKYRRPFLSGQEMNGHVH-----	383

.....430.....440.....450.....460