

CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/PUMaps: Tue Feb 1 14:22:36 2022

Page 1 of 4

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Pavo_muticus          -----*.:MKAWNKKKKF9
Pavo_cristatus        -----MKAWNKKKKF9
Gallus_gallus         -----MKAWNKKKKF9
Anas_platyrhynchos    -----MEGRARRKP9
Chelonia_mydas        -----MEAKGKKRF9
Latimeria_chalumnae   -----MEAQSKKKQ9
Mus_musculus          -----MMEVKGKKKF10
Rattus_norvegicus     -----MEVKGKKKI9
Homo_sapiens          -----MEVKGKKQF9
Pan_troglodytes       -----MEVKGKKQF9
Macaca_mulatta        -----MMDIAKVATMEVKGKKQF18
Callithrix_jacchus    MEKMGQVFPTTEKFKITNVKIIREIEDHHLNKRSHCCROSPLTNKVSRVAAMEVKGKKQF60
Canis_lupus_familiaris -----MMEVKGKKKF10
Bos_taurus            -----MEVKGKKKL9
Equus_caballus        -----MEVKGKKKF9
Heterocephalus_glaber -----MEVKGKKKF9
Rhinatrema_bivittatum -----METKSKKQF9
Xenopus_tropicalis    -----MDSRGTKQF9
1.....10.....20.....30.....40.....50.....60

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Pavo_muticus          P--GKSGKVSRGKQLHGKKKFKKDDDSVPSKTFH-SKGDEEEKPKSISKPPVRGNLRP--64
Pavo_cristatus        P--GKSGKVSRGKQLHGKKKFKKDDDSVPSKTFH-SKGDEEEKPKSISKPPVRGNLRP--64
Gallus_gallus         P--GKNGKVSRGKQLRGKKKFKKDDDSVPLKTFH-SKGDEEEKPKSISKPPVKGNLRP--64
Anas_platyrhynchos    A--ARSGKAPAGKAPQGRRKFKRDHDSGPPKKFP-NKGDEEGPKPSISKPFVKGNLRP--64
Chelonia_mydas        M--GKNGKAP-----QRKHKFKKDNDSGPPKKFY-TKRGEEGPKPFSKKSEKGNKKL--59
Latimeria_chalumnae   SS-GKGGKPS-----FRKGGRDGNESAPSRKIK-GKGSTEGKAKFKPKFEKGGKKFDDK62
Mus_musculus          T--GKSPQTS-----QGKNKFHKNSSESSSKTFP-RKAVKEGGPKVTSKNFEKGATKP--60
Rattus_norvegicus     T--GKSPQTS-----QGKNKFHKNSSESSAKAFP-RKAAKEGGPKVTSKNFEKGATKP--59
Homo_sapiens          T--GKSTKTA-----QEKNRFHKNSDSGSSKTFP-TRKVAKEGGPKVTSRNFESKITKL--60
Pan_troglodytes       T--GKSTKTA-----QEKNRFHKNSDSGSSKTFP-TRKVAKEGGPKVTSRNFESKITKL--60
Macaca_mulatta        T--GKSTKTS-----QEKNRFHKNSDSGSSKITLP-RKVAKEGGPKITSRNFESKITKP--68
Callithrix_jacchus    T--GKSTKTS-----QEKPRFHKNSDSGSSKKFP-RKVAKEGGSKITSNNFEKNITKP--110
Canis_lupus_familiaris I--GKGAKTS-----QEKRFHKNSDSGSSKTFP-RKVVEGGPKITSKNFEKCAIKP--60
Bos_taurus            T--GKGTKMS-----QEKSKFHKNNDSGSSKTFP-KKVVEGGPKITSKNFEKTATKP--59
Equus_caballus        T--GKGTKTS-----QEKRFHKNSDSGSSKTFP-RKVLKEGGPKITSKNFEKSATKP--59
Heterocephalus_glaber T--GRSTKVS-----QEKNNFQKNRDSFSKTFP-KKVK-EGGPKVPSPKKFEKSAMKP--58
Rhinatrema_bivittatum K--GKGRKAS-----HGKGKSRKAAGSCLPKNFQ-ARAGEKGPKPFSQKFEKGKKSEKT61
Xenopus_tropicalis    KKKEKSFQKKT---TDSPKFKKIKGSAQHNS-TGQSPKGNK--SNKFEKGAKKDRP62
.....70.....80.....90.....100.....110.....120

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Pavo_muticus          --GRASVKQVKNK-----QOSEKLAKRRKYQDG-TQGESDSKKPKWDDFKKKKK110
Pavo_cristatus        --GRASVKQVKNK-----QOSEKLAKRRKYQDG-TQGESDSKKPKWDDFKKKKK110
Gallus_gallus         --GRASVKQFKNK-----QOSEKLAKRRYQDS-TQGESDSKKPKWDDFKKKKK110
Anas_platyrhynchos    --GKATIKQFKNK-----QOSGLAKRRKLQDG-EEGGSDSKKPKWDDFKKKKK110
Chelonia_mydas        --GKTSVKQFKSK-----QPEKFSRKRKLPEDE-NEGGSVPKPKWDDLKRKKK105
Latimeria_chalumnae   TGGKAGVKQFKGK-----QPAEKFPKKRKLQOGDEEDDGAAKPKWDEFKKKKK111
Mus_musculus          --GKKGVKQFKNKPOGGGKPKDKFQKANKFSKKRRKFQPDGESDESGAKPKWDDFKKKKK118
Rattus_norvegicus     --GKKRVKQFKNKPOGGGKPKDKFQKANKFNKKRRKFQPDGKSDESAAKPKWDDFKKKKK117
Homo_sapiens          --GKKGVKQFKNKQOGDKSPKNKFQANKFNKKRRKFQPDGRSDESAAKPKWDDFKKKKK118
Pan_troglodytes       --GKKGVKQFKNKQOGDKSPKNKFQANKFNKKRRKFQPDGKSDESAAKPKWDDFKKKKK118
Macaca_mulatta        --GKKGVKQFKNKQOGDKSPKNKFQANKFNKKRRKFQPDGKSDESAAKPKWDDFKKKKK126
Callithrix_jacchus    --GKKGVKQFKNKQOGDKSPKNKFQANKFNKKRRKFQPDGKSDESAAKPKWDDFKKKKK168
Canis_lupus_familiaris --GKKGVKQFKNKQOGDKIPKNKFQANKFNKKRRKFQADGKSDESAAKPKWDDFKKKKK118
Bos_taurus            --GKKGVKQFKNKQOGDRIPKNKFQANKFNKKRRKFQPDGKSDESAAKPKWDEFKKKKK117
Equus_caballus        --GKKGVKQFKNKQOGDKILKNKFQANKFQKKRRKFQPDGKSDESAAKPKWDDFKKKKK117
Heterocephalus_glaber --GKRGVKQFKNKQOGDKGLKNKFQANKFNKKRRKFHPSKSDSASAKPKWDDFKKKKK116
Rhinatrema_bivittatum G-GKAVAKQFAAKP-----ROKDSPOKKRRKQEGDLEGGPDSKKPKWEDFKKKKK110
Xenopus_tropicalis    G-GKAGVKQFAAKN-----AKOGGGFTKKRKHQEDQEGGSEAKPKWDDFKKKKK112
.....130.....140.....150.....160.....170.....180

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/PUMDaps: Tue Feb 1 14:22:36 2022

Page 2 of 4

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/PUMDaps Tue Feb 14:22:36 2022

Page 3 of 4

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      .:  *  .  *:*****:*.*:*****:*****:*****  *  *  :*:***:***:.*
Pavo_muticus      QPEKREAILDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTHALPKQRMSEIEAIREAVIY  349
Pavo_cristatus    QPEKREAILDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTHALPKQRMSEIEAIREAVIY  349
Gallus_gallus      QPEKREAILDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTHALPKQRMSEIEAIREAVIY  349
Anas_platyrhynchos QPEKREAILDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYALPKQRMSEIEAIREAVIY  349
Chelonia_mydas     HPEKQEAIMDEMKQILTPVAQKEAVIKHSLVHKVFLDFFTHALPKQRMSEIEAIREAVIY  344
Latimeria_chalumnae QPEKRKAIMEEMKQMLTPMAQKEAVVKHSLVHKVFLDFFTHAPDKLKTEMIEAVREAVLY  351
Mus_musculus       QPAKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKPRSELIEAIREAVVY  357
Rattus_norvegicus  QPGKLELILDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSELIEAIREAVVY  356
Homo_sapiens        QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  357
Pan_troglodytes     QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  357
Macaca_mulatta      QSEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  365
Callithrix_jacchus  RPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  407
Canis_lupus_familiaris QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVIY  357
Bos_taurus          QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  356
Equus_caballus      QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPPKLRSEMEIEAIREAVVY  356
Heterocephalus_glaber QPEKLELIMDEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYATPKLRSELIEAIREAVVY  355
Rhinatrema_bivittatum HPEKQETIMEEMKQILTPMAQKEAVIKHSLVHKVFLDFFTYAPVKLKTEMIEAIREALTY  349
Xenopus_tropicalis  QPEKKSILDEMKQILVPLGQKEAVIKHSLVHKVFLDFFSNASPKIRSEMEIEAIREAVVY  351
.....370.....380.....390.....400.....410.....420

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      :  *****:*.*:  :*****  :  .  :*  :  :  :*:***:.*  ***:*****
Pavo_muticus      LAHTHDGSRVAMHCLWHGTPKDRKVIVKT-MKTYIEKIATGEFSLVLLAAFDICIDDTKL  408
Pavo_cristatus    LAHTHDGSRVAMHCLWHGTPKDRKVIVKT-MKTYIEKIATGEFSLVLLAAFDICIDDTKL  408
Gallus_gallus      LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYIEKIATGEFSLVLLAAFDICIDDTKL  408
Anas_platyrhynchos LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYIEKIATGEFSLVLLAAFDICIDDTKL  408
Chelonia_mydas     LAHTHDGARVAMHALWHGTPKDRKIIMKT-MKTYVEKIATGEFSLVLLAAFDICIDDTKL  403
Latimeria_chalumnae MAHTHDGARVAMHCLWHGTPKVSQTDFGNGLKLVLSFVLQGEFSLAVLAAFDICIDDTKL  411
Mus_musculus       LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  416
Rattus_norvegicus  LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKIANGQYSHLVLLAAFDICIDDTKL  415
Homo_sapiens        LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  416
Pan_troglodytes     LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  416
Macaca_mulatta      LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  424
Callithrix_jacchus  LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  466
Canis_lupus_familiaris LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYIEKVANGQYSHLVLLAAFDICIDDTKL  416
Bos_taurus          LAHTHDGARVAMYCLWHGTPKDRKVIVKT-MKTYIEKVANGQYSHLVLLAAFDICIDDTKL  415
Equus_caballus      LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  415
Heterocephalus_glaber LAHTHDGARVAMHCLWHGTPKDRKVIVKT-MKTYVEKVANGQYSHLVLLAAFDICIDDTKL  414
Rhinatrema_bivittatum MAHTHDGARVAMHGVWHGTPKDRKVIVKT-MKTFIEKIATGEFSLVLLAAFDICIDDTKL  408
Xenopus_tropicalis  IITHDGDARVGMHSVWHGTPKDRKVIKT-MKTYIEKIATGEFSLVLLAAFDICVDDTKL  410
.....430.....440.....450.....460.....470.....480

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Pavo_muticus      VKQLIITELNASLPSLISNKHGKKVLLYLLSPRDPAHFVPEIVTLLQQGDGNAYSKKNTIE  468
Pavo_cristatus    VKQLIITELNASLPSLISNKHGKKVLLYLLSPRDPAHFVPEIVTLLQQGDGNAYSKKNTIE  468
Gallus_gallus      VKQLIITELNASLPSLISNKHGKKVLLYLLSPRDPAHFVPEIITLLQQGDGNAYSKKSTIE  468
Anas_platyrhynchos VKQLIISEINASLPSIINNKHGKKVLLYLLSPRDPAHFVPEIITLLQQGDGNAYSKKNTIE  468
Chelonia_mydas     MKQLIISEISGSLPNIVNKKYGRKVLLYLLSPRDPAHFLPEIVKILQQGDGNAYSKKDSD  463
Latimeria_chalumnae VKQIIISEITNTLPNLINNKYGRKVLLYLLSPRDPAHFLPEITKVLLQQGDGNVHSHKKDAE  471
Mus_musculus       VKQIIISEIISLSPSIVNDKYGRKVLLYLLSPRDPAHTVPELIELLQKGDGNAHSHKKDTA  476
Rattus_norvegicus  VKQIIISEVISSLPSIVNDKYGRKVLLYLLSPRAPAHLVPEIITQLQKGDGNAHSHKKDTA  475
Homo_sapiens        VKQIIISEIISLSPSIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTE  476
Pan_troglodytes     VKQIIISEIISLSPSIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTE  476
Macaca_mulatta      VKQIIISEIISLSPSIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTE  484
Callithrix_jacchus  VKQIIIVSEIISLSPSIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTE  526
Canis_lupus_familiaris VKQIIISEIINSLPNIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTA  476
Bos_taurus          VKQIIISEIINSLPNIVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTE  475
Equus_caballus      VKQIIISEIISLSPNIINDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNAHSHKKDTA  475
Heterocephalus_glaber VKQIIISEIISLSPNVNDKYGRKVLLYLLSPRDPAHTVREIIEVLQKGDGNSHSHKKDTA  474
Rhinatrema_bivittatum VKQLIISEIISLSPSIASNKYGRKVLLYLLSPRDPAHFVPEIIVLQGDENAHSHKKDTE  468
Xenopus_tropicalis  LKQLILSELISLSPSIINDKYGRKVLLYLLNWRNPAPHFVPEIIVLQKGDGNAHSHKKDPT  470
.....490.....500.....510.....520.....530.....540

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CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: /media/morpheus/disk1/fst/pep_msa/PUMaPs Tue Feb 1 14:22:36 2022

Page 4 of 4

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*: ****:***.** **: : ::::: : *:.* * *: **.: :.*:**
LRRRELLEAISPPLLLEYLQEHTEQEVVMDKAAAFVLVADILRTATGDIQPTLNAIANLAAEE
LRRRELLEAISPPLLLEYLQEHTEQEVVMDKAAAFVLVADILRTATGDIQPTLNAIANLAAEE
LRRHELLEAISPPLLLEYLQEHIQEIVMDKAAAFVLVADILRTATGDIQPTLNAIANLAAEE
LRRRELLEAISPPLLLEYLQEHCEQEVVMDKATFVLVADILRTAVGEIQPTLDAIANLAAEE
VRRCELLEAISPALGLYLQEHAEQEMVMDKATCVLVADVGLSALGDVQPAMNAIASLAAEE
VRRRELLEAISPPLLKYLQEHAREVVMKDVTCTVMVADILGSLGELQPALDVIADIAAEE
IRRRELLESISPALLSYLQHTQEVVLDKSACVLVSDMLGSATGDVQPAMDAIASLAAEE
IRRRELLESISPALLSYLQHTREVVLVDKSVCLVSDILGSATGDAQPAMDAIAGLAAEE
VRRRELLESISPALLSYLQEHAEQEVVLDKSACVLVSDILGSATGDVQPTMNAIASLAATG
VRRRELLESISPALLSYLQEHAEQEVVLDKSACVLVSDILGSATGDVQPTMNAIASLAATG
VRRRELLESISPALLSYLQEHAREVVLVDKSACVLVSDILGSATGDAQPAMNAIASLAATE
VRRRELLESISPALLSYLQEHTEQEVVLDKSACVLVSDILGSATGDVQPAMNAIASLAATE
IRRRELLESISPALLSYLQGHAEQEVVLDKSACVLVSDILGAAIGDVQPAMDAIASLAATE
IRRRELLESISPALLSYLQGHAEQEVVLDKSACVLVADILGTATGDVQPAMDAVASLAAEE
IRRRELLESISPALLSYLQGHAEQEVVLDKSACVLVSDILGAAIGDVQPAMDAIASLAAEE
IRRHELLESISPALLNYLQRNAQEMVLVDKSACVLVSDILGSATGDTQAMDAIASLAAEE
IRRRELLEAISPALPKYLQENAEQEMVMDKAMCVLVANILESAHGNLQPMAMDSIAGLAAEE
VRQHELLESISPPLLKYLEEHIQDVVLQNALCGMVTISILLCALGDQPQVMNAIASMAAEE
.....550.....560.....570.....580.....590.....600

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[illegible]

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** : **** : * ** : * : * : * : * : * : * :
WAEVNRGAIVLCCLLRSTDQKVTNAVRKGLKKIVPKLKLNN--VKGV EALLEKLT-- 638
WAEVNRGAIVLCCLLQSTDQKVTNAVRKGLKKIVPKLKLNN--VKGV EALLEKLT-- 638
WAEVNRGAIVLCCLLRSTDQKVTNAVKKGLKKIVPKLKLNN--VKGIEALLEKLT-- 638
WAKVNRGAIVLCCLLRSTDQEVANAVKKGLKKLVPQLKLNN--VKGIEALLEKLTs- 639
WAEVNRGAMVLCCLLRSTDQEVANKVKGGLSLIPKLCKNN--VKGIEALLEMLTs- 634
WATVNRGAMVLCRLLSQVDEEVRNKSKEGLKLIPPLKKNION--VKGV EALLEKLT- 642
WASINRGAILLSSLLQSCDQEVVNKVKGGLKPLIPTLEKNKSSSRGIQTILLEKLT- 648
WASINRGAI V LSSLLQSCDQDVVNKVKAGLKLIPPTLEKTKSTSKGIQTILLEKLT- 647
WASVNRGAILLSSLLQSCDLEVANKVKAALKSLIPTLEKTKSTSKGIEITILLEKLT- 648
WASVNRGAILLSSLLQSCDLEVANKVKAALKSLIPTLEKTKSTSKGIEITILLEKLT- 648
WASVNRGAILLSSLLQSCDLEVANKVKAALKSLIPTLEKNKSTSKGIEITILLEKLT- 656
WASINRGAILLSSLLQSCDPEVANKVKAALKSLIPALEKTKSTSKGV EALLEKLT- 698
WASVNRGAILLSSLLQSSDHEVAHKIKAGLKLIPPTLEKNKNTSKGIEMLLEKLAA- 648
WASVNRGAILLSSLLQSSDQEVANKVKAGLKLIPALEKSKNTSKGIEMLLEKLT- 651
WASVNRGAILLSSLLQSSDQEVADKVKAGLKLIPALEKHKSTSKGIEITILLEKLT- 651
WASVNRGAILLSSLLQSTDQEVANKVKVGLKSLIPTLEKNKNTSKGIEITILLEKLAA- 646
WAEVNRGAIVLCCLLQSDADKEVAMNVRSGRLSLVPKLKSNK--IKGIGALLDRLSSs- 640
WAQVNRGAIVLCCLLQSSDEETIAAQVKNLGLVSKPKNSTN--TKATEALTEQLHSP- 642
.....670.....680.....690.....700.....710.....

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