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CLUSTAL O(1.2.4) multiple sequence alignment


Mammalia_concensus      ---------------------MGGNSGQAGRH---IYQSLAEDGPFDSVEPPKRPTGRLI      36
Amniota+_concensus      MTLTKEDSFHEALPPPSEVASADLDPSTRDKEFSEEKAAQMSGARFGAVEPKRRSTGRLI      60
Laevis_NCBI             MTLSKEVEY---QTPQKQVSSTGLYPSTKDVEFSAS-LEQMNGEIFQSVEPPRRSTGRLI      56
Tropicalis_NCBI         MTLSKEVEY---PAPQKQLSSTGLYPSTKDMEFSAS-LEQMNGEVFQAVEPPRRSTGRLI      56
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Mammalia_concensus      MHSMAMFGREFCYAVEAAYVTPVLLSVGLPKSLYSIVWFLSPILGFLLQPVVGSASDHCR      96
Amniota+_concensus      MHSMAMFGREFCYAVEAAFVTPVLLSVGLPKSLYSLVWLISPILGFILQPVVGSASDHCR      120
Laevis_NCBI             MHSMAMFGREFCYAVEAAYVTPVLLSVGLPKSLYSLVWLISPILGFILQPVVGSASDHCR      116
Tropicalis_NCBI         MHSMAMFGREFCYAVEAAFVTPVLLSVGLPRSLYSLVWLISPILGFILQPVVGSASDYCR      116
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Mammalia_concensus      SRWGRRRPYILTLGVMMLVGMALYLNGDTVVAALIA-NPRRKLVWAISVTMIGVVLFDFA      155
Amniota+_concensus      SSWGRRRPYILGLGIIMLLGMALYLNGDEMISAFIGERDQKKRTWAIVITMLGVVLFDFA      180
Laevis_NCBI             SRWGRRRPYILCLGIIMVLGMTLYLNGDTAVTAVLGTSA-EKTTWAIVITMLGVVAFDFA      175
Tropicalis_NCBI         SRWGRRRPYILCLGIIMVLGMTLYLNGDTAVTAVLGTSP-EKTTWAIVITMLGVVAFDFA      175
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Mammalia_concensus      ADFIDGPIKAYLFDVCSHQDKEKGLHYHALFTGFGGALGYLLGAIDWAHLELGRLLGTEF      215
Amniota+_concensus      ADFIDGPIKAYLFDVCSHQDKEKGLHYHALFTGLGGALGYLTGAMDWGHTVLGRILGSEF      240
Laevis_NCBI             ADFIDGPIKAYLFDVCSHHDKERGLHYHALFTGLGGALGYLTGAMDWGSTFLGRIMGSEF      235
Tropicalis_NCBI         ADFIDGPIKAYLFDVCSHHDKERGLHYHALFTGLGGALGYLTGAMDWGSTFLGRIMGSEF      235
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Mammalia_concensus      QVMFFFSALVLTLCFIVHLCSISEAPLTDVAKGIIPPQQTPQDPPLSSDGMYEYGSIEKV      275
Amniota+_concensus      QVIFFFSALVFLICLTVHLCSIPEVPLRYEKEETKCPS---ASLLLEVDEPYKYGSIEKE      297
Laevis_NCBI             QVMFFFASAVFLILLVVHLCSIPEIPIADEKQESQ--------MLLKHDHLGAYGSIDKT      287
Tropicalis_NCBI         QVMFFFASSVFLIFLAVHLCSIPEIPLEDEKQETQ--------MLLKHDHLGAYGSIDKA      287
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Mammalia_concensus      KNGYVNPELAMQ------------GAKNKNHAEQTRRAMTLKSLLRALVSMPPHYRYLCI      323
Amniota+_concensus      IKNCCKQEGYLKCTDTNISAAAKPEKCTDDSCTEVQRRMTLKSLLKALLSMPSHYRYLCV      357
Laevis_NCBI             QN------GILKT-KTTRSLSQVEENDSSDREEQVQKRMTVKSLINALLTMPAHYRYLCI      340
Tropicalis_NCBI         QN------GILKNRKTSRSLSQVEENNPNDREEQVQKRMTVKSLISALFTMPAHYRYLCL      341
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Mammalia_concensus      SHLIGWTAFLSNMLFFTDFMGQIVYRGDPYSAHNSTEFLIYERGVEVGCWGLCINSVF--      381
Amniota+_concensus      SHLFGWTAFLSNMLFFTDFMGQIVYHGNPYAEHNSTAYLTYERGVEVGCWGLCINAISHQ      417
Laevis_NCBI             SHLIGWTAFLSNMLFFTDFMGQIVYHGNPYAEHNSTAHLIYERGVEVGCWGMCINAIS--      398
Tropicalis_NCBI         SHLIGWTAFLSNMLFFTDFMGQIVYHGNPYAEHNSTAYLTYERGVEVGCWGMCINAIS--      399
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Mammalia_concensus      -----SSLYSYFQKVLVSYIGLKGLYFTGYLLFGLGTGFIGLFPNVYSTLVLCSLFGVMS      436
Amniota+_concensus      SILVSSSLYSYLQKALLPYIGLKGLYFIGYLLFGLGTGLIGLFPNVYSTLVLCSLFGVMS      477
Laevis_NCBI             -----SALYSYLQKALLPFIGLKGLYFLGYLLFGLGTGFIGLFPNVYSTLVLCSLFGVMS      453
Tropicalis_NCBI         -----SALYSYIQKALLPYIGLKGLYFLGYLLFGLGTGFIGLFPNVYSTLVLCSLFGVMS      454
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Mammalia_concensus      STLYTVPFNLIAEYHREEEKERQQQAPGGDPDNSGRGKGMDCAALTCMVQLAQILVGGGL      496
Amniota+_concensus      STLYTVPFNLIAEYHREEEDLKLQEKEQGPEHGRGKGKGIDCAALTCMVQLAQIIVGVGL      537
Laevis_NCBI             STLYTVPFNLISEYHREEEQ-KMQPNGKTPTPSDNRGKGIDCAALTCMVQLAQIIVGGGL      512
Tropicalis_NCBI         STLYTVPFNLISEYHREEEQ-ETQPNGKTPTPSDNRGKGIDCAALTCMVQLAQIIVGGGL      513
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Mammalia_concensus      GFLVNTAGSVVVVVITASAVALIGCCFVALFVRYVD       532
Amniota+_concensus      GFLVSVAGSVVVTVISASAVALIGCCFVAFCVRYVD       573
Laevis_NCBI             GFLVSLAGSVVVVVISASAASLIGCCFVALFVRYVE       548
Tropicalis_NCBI         GFLVSLAGSVVVVVISASAASLIGCCFVALFVRYVD       549
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