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CLUSTAL 2.0.3 multiple sequence alignment


Homo_sapie      MVLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHG
Bos_taurus      MVLSAADKGNVKAAWGKVGGHAAEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHG
Mus_muscul      MVLSGEDKSNIKAAWGKIGGHGAEYGAEALERMFASFPTTKTYFPHFDVSHGSAQVKGHG
Rattus_nor      MVLSADDKTNIKNCWGKIGGHGGEYGEEALQRMFAAFPTTKTYFSHIDVSPGSAQVKAHG
Gallus_gal      MVLSAADKNNVKGIFTKIAGHAEEYGAETLERMFTTYPPTKTYFPHFDLSHGSAQIKGHG
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Homo_sapie      KKVADALTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTP
Bos_taurus      AKVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSDFTP
Mus_muscul      KKVADALANAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTP
Rattus_nor      KKVADALAKAADHVEDLPGALSTLSDLHAHKLRVDPVNFKFLSHCLLVTLACHHPGDFTP
Gallus_gal      KKVVAALIEAANHIDDIAGTLSKLSDLHAHKLRVDPVNFKLLGQCFLVVVAIHHPAALTP
                 **. ** :*. *::*:..:** *****************:*.:.:**.:* * *. :**

Homo_sapie      AVHASLDKFLASVSTVLTSKYR
Bos_taurus      AVHASLDKFLANVSTVLTSKYR
Mus_muscul      AVHASLDKFLASVSTVLTSKYR
Rattus_nor      AMHASLDKFLASVSTVLTSKYR
Gallus_gal      EVHASLDKFLCAVGTVLTAKYR
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