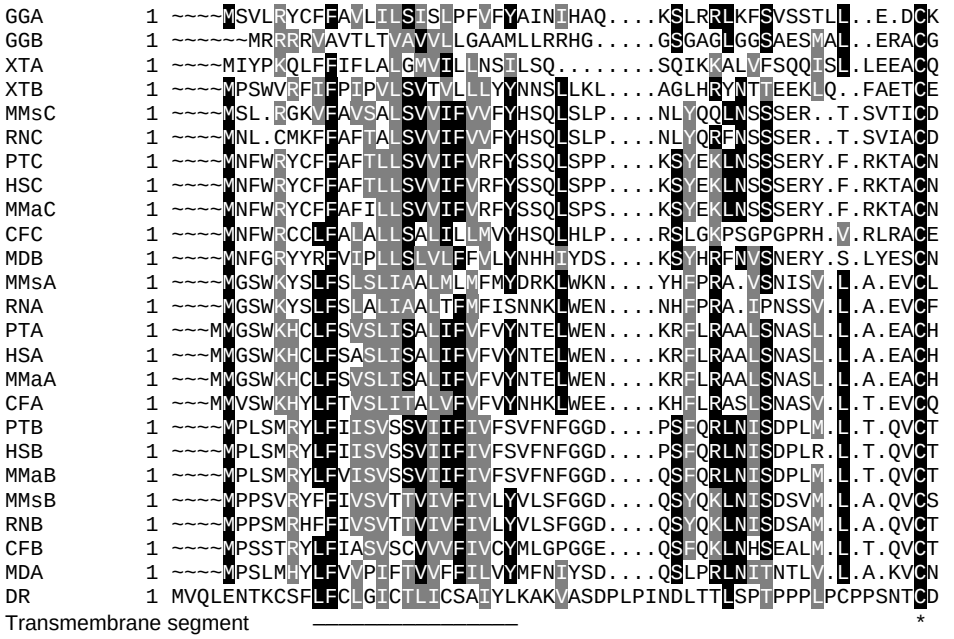
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XTA 1 ~~~~MIYPKQLFFIFLALGMVILLNSTLSQ.....SQIKKALVFSQQISL.LEEACQ
XTB 1 ~~~~MPSWVRFIFPIPVLSVTVLLLYYNNSLLKL....AGLHRYNTTEEKLQ..FAETCE
MMsC 1 ~~~~MSL.RGKVFAVSALSVVIFVVFYHSQLSLP....NLYQQLNSSSER..T.SVTICD
RNC 1 ~~~~MNL.CMKFFAFTALSVVIFVVFYHSQLSLP....NLYQRFNSSSER..T.SVIACD
PTC 1 ~~~~MNFWRYCFFAFTLLSVVIFVRFYSSQLSPP....KSYEKLNSSSERY.F.RKTACN
HSC 1 ~~~~MNFWRYCFFAFTLLSVVIFVRFYSSQLSPP....KSYEKLNSSSERY.F.RKTACN
MMaC 1 ~~~~MNFWRYCFFAFILLSVVIFVRFYSSQLSPS....KSYEKLNSSSERY.F.RKTACN
CFC 1 ~~~~MNFWRCCLFALALLSALILLMVYHSQLHLP....RSLGKPSGPGPRH.V.RLRACE
MDB 1 ~~~~MNFGRYYRFVIPLLSLVLFFVLYNHHIYDS....KSYHRFNVSNERY.S.LYESCN
MMsA 1 ~~~~MGSWKYSLFSLSLIAALMLMFMYDRKLWKN....YHFPRA.VSNISV.L.A.EVCL
RNA 1 ~~~~MGSWKYSLFSLALIAALTFMFISNNKLWEN....NHFPRA.IPNSSV.L.A.EVCF
PTA 1 ~~~MMGSWKHCLFSVSLISALIFVFVYNTELWEN....KRFLRAALSNASL.L.A.EACH
HSA 1 ~~~MMGSWKHCLFSASLISALIFVFVYNTELWEN....KRFLRAALSNASL.L.A.EACH
MMaA 1 ~~~MMGSWKHCLFSVSLISALIFVFVYNTELWEN....KRFLRAALSNASL.L.A.EACH
CFA 1 ~~~MMVSWKHYLFTVSLITALVFVFVYNHKLWEE....KHFLRASLSNASV.L.T.EVCQ
PTB 1 ~~~~MPLSMRYLFIISVSSVIIFIVFSVFNFGGD....PSFQRLNISDPLM.L.T.QVCT
HSB 1 ~~~~MPLSMRYLFIISVSSVIIFIVFSVFNFGGD....PSFQRLNISDPLR.L.T.QVCT
MMaB 1 ~~~~MPLSMRYLFVISVSSVIIFIVFSVFNFGGD....QSFQRLNISDPLM.L.T.QVCT
MMsB 1 ~~~~MPPSVRYFFIVSVTTVIVFIVLYVLSFGGD....QSYQKLNISDSVM.L.A.QVCS
RNB 1 ~~~~MPPSMRHFFIVSVTTVIVFIVLYVLSFGGD....QSYQKLNISDSAM.L.A.QVCT
CFB 1 ~~~~MPSSTRYLFIASVSCVVVFIVCYMLGPGGE....QSFQKLNHSEALM.L.T.QVCT
MDA 1 ~~~~MPSLMHYLFVVPIFTVVFFILVYMFNIYSD....QSLPRLNITNTLV.L.A.KVCN
DR 1 MVQLENTKCSFLFCLGICTLICSAIYLKAKVASDPLPINDLTTLSPTPPPLPCPPSNTCD
Transmembrane segment
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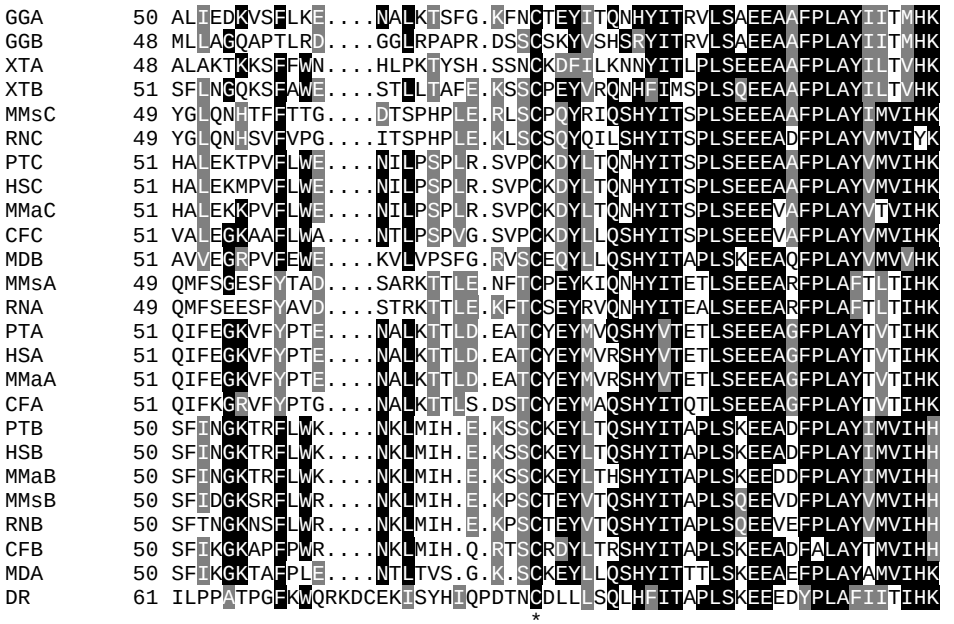
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XTA 48 ALAKTKKSFFWN....HLPKTYSH.SSNCKDFILKNNYITLPLSEEEAAFPLAYILTVHK
XTB 51 SFLNGQKSFAWE....STLLTAFE.KSSCPEYVRQNHFIMSPLSQEEAAFPLAYILIVHK
MMsC 49 YGLQNHTFFTTG....DTSPHPLE.RLSCPQYRIQSHYITSPLSEEEAAFPLAYIMVIHK
RNC 49 YGLQNHSVFVPG....ITSPHPLE.KLSCSQYQILSHYITSPLSEEEADFPLAYVMVIYK
PTC 51 HALEKTPVFLWE....NILPSPLR.SVPCKDYLTQNHYITSPLSEEEAAFPLAYVMVIHK
HSC 51 HALEKMPVFLWE....NILPSPLR.SVPCKDYLTQNHYITSPLSEEEAAFPLAYVMVIHK
MMaC 51 HALEKKPVFLWE....NILPSPLR.SVPCKDYLTQNHYITSPLSEEEVAFPLAYVTVIHK
CFC 51 VALEGKAAFLWA....NTLPSPVG.SVPCKDYLLQSHYITSPLSEEEVAFPLAYVMVIHK
MDB 51 AVVEGRPVFEWE....KVLVPSFG.RVSCEQYLLQSHYITAPLSKEEAQFPLAYVMVVHK
MMsA 49 QMFSGESFYTAD....SARKTTLE.NFTCPEYKIQNHYITETLSEEEARFPLAFTLTIHK
RNA 49 QMFSEESFYAVD....STRKTTLE.KFTCSEYRVQNHYITEALSEEEARFPLAFTLTIHK
PTA 51 QIFEGKVFYPTE....NALKTTLD.EATCYEYMVQSHYVTETLSEEEAGFPLAYTVTIHK
HSA 51 QIFEGKVFYPTE....NALKTTLD.EATCYEYMVRSHYVTETLSEEEAGFPLAYTVTIHK
MMaA 51 QIFEGKVFYPTE....NALKTTLD.EATCYEYMVRSHYVTETLSEEEAGFPLAYTVTIHK
CFA 51 QIFKGRVFYPTG....NALKTTLS.DSTCYEYMAQSHYITQTLSEEEAGFPLAYTVTIHK
PTB 50 SFINGKTRFLWK....NKLMIH.E.KSSCKEYLTQSHYITAPLSKEEADFPLAYIMVIHH
HSB 50 SFINGKTRFLWK....NKLMIH.E.KSSCKEYLTQSHYITAPLSKEEADFPLAYIMVIHH
MMaB 50 SFINGKTRFLWK....NKLMIH.E.KSSCKEYLTHSHYITAPLSKEEDDFPLAYIMVIHH
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RNB 50 SFTNGKNSFLWR....NKLMIH.E.KPSCTEYVTQSHYITAPLSQEEVEFPLAYVMVIHH
CFB 50 SFIKGKAPFPWR....NKLMIH.Q.RTSCRDYLTRSHYITAPLSKEEADFALAYTMVIHH
MDA 50 SFIKGKTAFPLE....NTLTVS.G.K.SCKEYLLQSHYITTTLSKEEAEFPLAYAMVIHK
DR 61 ILPPATPGFKWQRKDCEKISYHIQPDTNCDLLLSQLHFITAPLSKEEEDYPLAFIITIHK
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GGB 103 EFETFERLFRAVYMPQNVYCIHVDGKAPAALKQAVRRLVDCFPNAFLASRTERVVYGGVS
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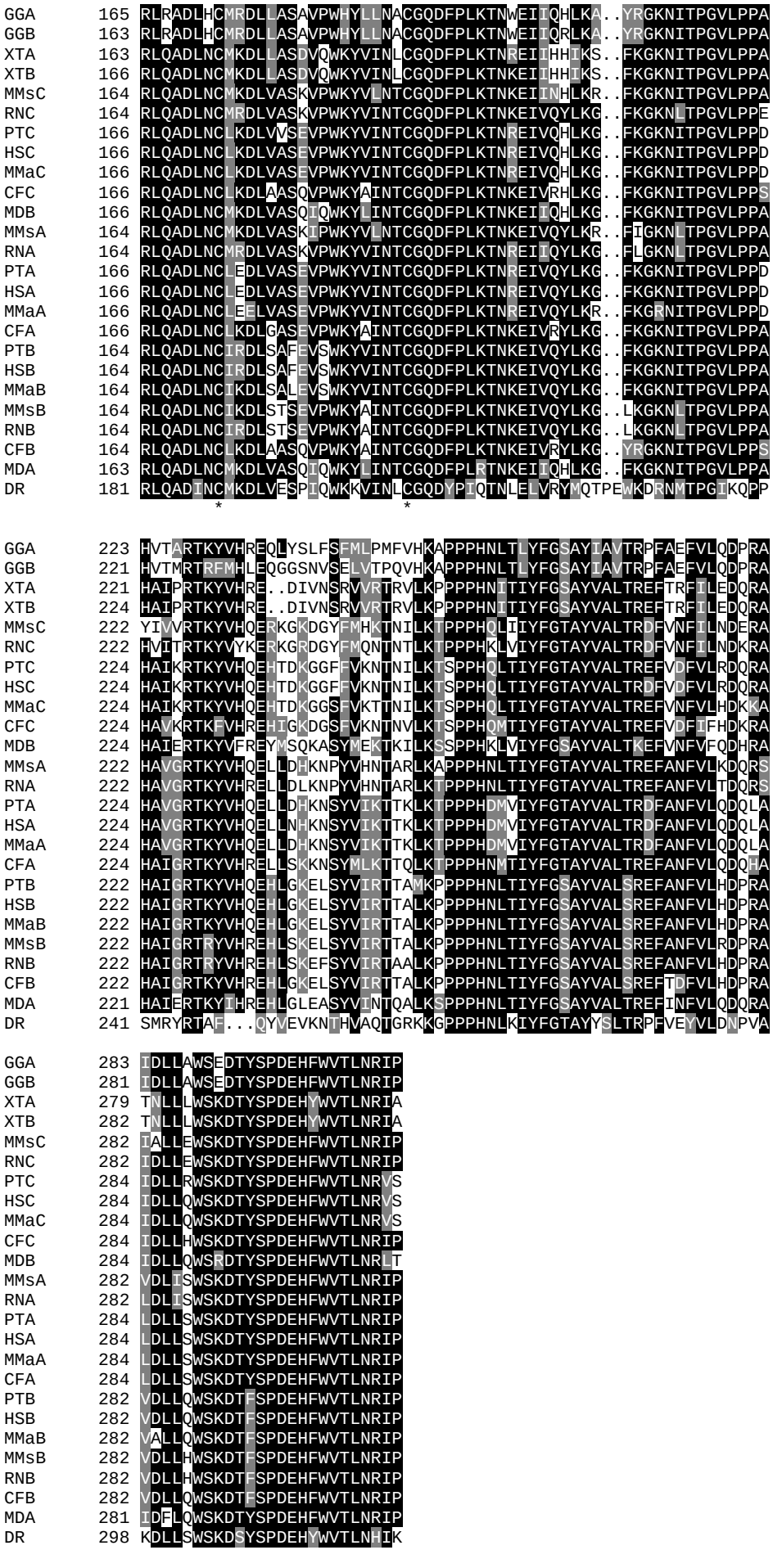
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