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MMs     1 RPTTLCETMGKAEIWLMRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFVQTSGE
RN      1 RPTTLCETMGKAEIWLMRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFVQTSGE
CF      1 RPTTLCEIMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFVQSSGE
PT      1 RPTTLCETMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFIQSSGK
HS      1 RPTTLCETMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGLHCKPAKPLPKEMEEFIQSSGK
MMa     1 RPTTLCETVGKAEIWLIRTYWDFEYPQPYQPNFEFVGGLHCKPAKPLPKEMENFVQSSGE
DR      1 KPTTMCETMGKADIWLIRTYWDFEYPRPFPPNFKFVGGLHCKPAKPLSKEMEEFVQSSGD

MMs    61 HGIVVFSLGSMVKNLTDEKANLIASALAQIPQKVLWRYKGKIPDTLGSNTRLFDWIPQND
RN     61 HGVVVFSLGSMVKNLTEEKANLIASALAQIPQKVLWRYKGKIPATLGSNTRLFDWIPQND
CF     61 DGVVVFSLGSMVKNLTDEKANLIASALAQIPQKVLWRYKGNKPATLGTNTRLYDWIPQND
PT     61 DGVVVFSLGSMVKNLTEEKANLIASALAQIPQKVLWRYKGKKPATLGNNTQLFDWIPQND
HS     61 NGVVVFSLGSMVKNLTEEKANLIASALAQIPQKVLWRYKGKKPATLGNNTQLFDWIPQND
MMa    61 DGIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGTNTRLYDWIPQND
DR     61 HGVVVFSLGSMIKNLTSERANTIAAALGQIPQKVVWRYSGKTPETLAPNTKIYDWIPQND

MMs   121 LLGHPKTRAFITHGGTNGIYEAIYHGIPMVGVPMFADQPDNIAHMKAKGAAVEVNMNTMT
RN    121 LLGHPKTRAFITHGGTNGIYEAIYHGIPMVGVPMFADQPDNIAHMKAKGAAVEVNMNTMT
CF    121 LLGHPKTKAFITHGGTNGIYEAIYHGVPMVGVPMFADQPDNIAHMKAKGAAVEVNINTMT
PT    121 LLGHPKTKAFITHGGTNGIYEAIYHGVPMVGIPMFADQPDNIAHMKAKGAAVEVNLNTMT
HS    121 LLGHPKTKAFITHGGTNGIYEAIYHGVPMVGVPMFADQPDNIAHMKAKGAAVEVNLNTMT
MMa   121 LLGHPQTKAFITHGGMNGVYEAIYHGVPMVGVPIFGDQPDNIAHMKAKGAAVEINFKTMT
DR    121 LLGHPKTKAFITHGGTNGLYEAIYHGVPMVGLPLFADQPDNLLHMKTKGAAVVLDINTLE

MMs   181 SSDLLNALRTVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAH
RN    181 SADLLSAVRAVINEPFYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAH
CF    181 SADLLHALRTVINEPSYKENATRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRPASH
PT    181 SVDLLSALRTVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAH
HS    181 SVDLLSALRTVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAH
MMa   181 SEDLLRAVRTVITDSSYKENAMRLSRIHHDQSVKPLDRAVFWIEFVMRHKGAKHLRSAAH
DR    181 SKDLVDALKTVLNNPSYKESIMRLSRIHHDQPMKPLDQAVYWIEFVMRNKGAKHLRVQAH

MMs   241 DLSWFQYHSLDVIGFLLACVASAILLVAKCCLFIFQK.VGKTGKKKKRD~~~~~
RN    241 DLSWFQYHSLDVIGFLLACMASAILLVIKCCLFVFQK.IGKTGKKNKRD~~~~~
CF    241 DLTWFQYHSLDVIGFLLACVATAIFLVTKCCLFSCRK.FNKAGKKKKRE~~~~~
PT    241 NLTWFQYHSLDVIGFLLVCVTTAIFLVIQCCLFSCQK.FVKIGKKKKRE~~~~~
HS    241 DLTWFQYHSLDVIGFLLVCVTTAIFLVIQCCLFSCQK.FGKIGKKKKRE~~~~~
MMa   241 DLNWFQHHSIDVIAFLLACVATAIFLFTRCFLFSCQN.FNKTRKIEKRE~~~~~
DR    241 ELSWYQYHCLDVAAFLLSITALITFLWVKTCCFLFRRCVRKTHPERKTQKSKKE
Transmembrane segment  ────────────────
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