

>ENSCGRG00001005116/1-684

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QAKKRWWWGPNWGWGAILLVNCPAETEDL-DD-QSSDQEAPKDIQNLSQMTLTVGPTSVFKNYMLILHTSK  
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SHDKSIPEMPLYKDTVMFRVAPYIFTSTQMPLEVYLCREMQLQGFVDTVTRLSEKISVQVASVYEDPSRQG  
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>ENSM AUG00000018048/1-642

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>ENSP EMG00000017319/1-692

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>ENSM SIG00000013004/1-682

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>ENSM USG00000040935/1-682

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>MGP\_SPRETEij\_G0027703/1-682

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>MGP\_CAROLIEIJ\_G0026723/1-682  
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>ENSRNOG00000037079/1-683  
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>ENSNAG00000014612/1-682  
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>ENSJJAG00000019685/1-672  
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EEASKTRVYCS-RG----LSLVLGPNKHFYALPP----LEDHGTETFYVEATEFFSASFGLISFVSLVER  
SRDVSIPDIPIYKDTVMFRVAPYIFTPSTQMPIEVYLCSELQQLQGFADTVSRLSERSDVHVSVYEDPSRLG  
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>ENSSTOG00000019498/1-674  
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QAKKKWVWGPNGWGAILLNCSPANMSQI-TD-KS--KVFSDEIRKLSQMSLTVQGPSCILKNYKLILHTSK  
EEAETRVYRPQKD-SCAYQLVLGLGWHCHALGP----LETLRKETFYVEATEFFSASFGLVSVSVLVEE  
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GFRLLIASPSSCYKLFQEQKEEGYGEATLFEDIRADQLLANGRKARTINQLLADESRRQNDYVERCIDLNR  
AILKRELGLGEKDIIDVPLFCLELRTNIPSEQQTPKLLARAYFPNMLCMIVMDMNLGIPKPYGPQIKGICC  
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>ENSUPAG00010017599/1-685  
VVSMECRAVAFQSTVHLTLDTPAHAICVGLGTEISLDIRCAPKNCQSFTVRASPRVLVDVAGT--VISGKED  
AVICRSLDTSVHLVLRMVSVXSASVDEDKVLVSYHPNEEVPMATALLYLTGIEFLWGS---PGPSPPENS  
WSQKKWVWGPNGWGAILLNCSPANMSQI-TD-KS--KVFSDEIRKLSQMSLTVQGPSCILKNYKLILHTSK  
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>ENSMG00000020848/1-685

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>ENSSVLG00005001183/1-688

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QAKKKWWWGPNWGWAILLVNCSPTDVSQ-LD-KT-NKEFLDEMKNLSQMTLTVQGPSCILKNYKLVHTSE  
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>ENSHGLG00000019075/1-680

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QMKKWLWGWPTGWGAILLVNCSPEAVNQD-----TKTVLSEDIKDLQMTLTVQGPSTALKNYKLVHTSE  
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SPVPSIPETPVYKDTVFRVAPCIFTPTQMPLEVYLYRDVKIQGFVDMVAALSEKTDSDQVSVYEDPNRLG  
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>ENSODEG00000016131/1-673

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QTKETWVWGPAGWGWAILLVNCSPADVNP-----TQMVQRQPQKLLTQMTLSIQGPTCILKNYKLVHTSE  
EEAKKARVFWPHG-----ELLGPDNRNSYIFNP----LVNLGKETIYVEAIEFSPANFAGLISFSVSLIED  
PPISCLPEIPVYKDTVFRVAPCIFTPTQMPLEVYLYRDVKVQGFVDAVVALSEKTDSDQMASVYEDSNRSG  
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DFRLLASPCACYLLREKQEEGYGDATLFEGVSPDLLHANGREAKTINQFLSDKSLKNQNDYAEKCIHLNR  
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>ENSCLAG00000003328/1-672

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QTKETWVWGPAGWGWAILLVNCSPADVNSQD-----TKTVISEDIKDLQMTLSIQGPTCILKNYKLVHTSV  
EEADKARVYFWPHG-----EIVLGPGHNSYTFSP----LVNLGKETIYVEAIEFSPANFAGLISFSISLIED  
PP--SIPAPVYKDTVFRVAPCIFTPTQMPLEVYLYRDVKVQGFVDTVVALSEKTDSDQMASVYEDPSRQG  
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>ENSCPOG00000024187/1-667

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QIKEKWWVWGPSGWGAVLLVNCSPADLRQE-----SKMVVSEHIKDLSQMTLNVNGPNCALKNYHLVLTHTSA  
EEAEKTRVYWPQG-----EVLGPDRESSYFTP----LENL-EETFYVEALEFSPASFSGLISFSISLIED  
PP-----GPVYKDTVFRVAPCIFTSTQMPLEMYLYRDVVKIQGFVDAVTALESEKSDSQVASVYEDFNRMG  
RWLQDEMAFCYTETPNKMMSFVLDTPRTTTPDEFPMKYALSPGVGYLIQNITDHTVASLDTIGNLMVSPPVK  
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GFRLLLASPCACYNLFRKQEEGFGGVLFGGVNPDTLHANGREAKTINQLLADQTMRNQNNYVEKCIHLNR  
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>ENSODRG0000005081/1-658

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LAKKKWWVWGPNGWGAILLVNCSVDLSQV-TD----KAIFSKEIKTLAEVTLTVQGPSSTLKNYGLVLTHTSE  
EEAKKIRIYWPQ-DAQSTFKLVGSPSQHFHTLSP----LES-MEQTLYAEAIDFPSSSFGLISFSLSLVEQ  
PQDSAIETPIYKDTVFRVAPCIFTSTQMPLEVLCREVQFTGSSEVLLRLS-----G  
SWLTDEMAFCYSQAPHGTISMVIDSPRTAKLEDFPMKYSLSPGISYMTHTSTEDHQVASLDSVGNMMVSPPVK  
AQQGDYPLGRILIGSSFYF---SRTMGKSLQAFLYAQVQAPLELFSDWLMTGHVDEFMCFVVEN-SRDTK  
DFRLLLASPSACYELFKKQREGYGNATLFEVVRTDQLISNGRKAKTIDQLLADEKLRKENDYVEKCIHLNR  
ILLKRELGLVEKDIIDIPQLFYLEKLTNIPSDQQTTLKFAKPYFPDLLQMIVMGNNLGIKPFPGPQIKGICC  
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>ENSOCUG00000025853/1-693

GVSLEGRAMSFQNTLCLSPDSPAHAICVLGTEINLDSRAAPDNCEFFTVSGSQRVLVNVCDV--VITEKEA  
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QEKEKWWVWGPKGRGPILLVNTGPANVDQL-IDKETNKVFLSDEIKNLSRMILNLQGPSCVLKRYRLVLTHTSR  
EEAEKARVYWPQKDGSSAFELVLPGRHSYTFTS----IENPLKETFYLEATEFSPASFSGLISYSASLVEE  
SEDPSIPETVYKDTVFRVAPCIFTSTQMPLEVLCRELQLQGFVNMVTELEKSNSQLASVYEDPNRLG  
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GFRLLLASPSCYNLFEKQKEGYGDAVLFEGVRGDQLLSNGREARTINQLLADESLRKQNDYVEKCLRLNR  
TILKSELGLAEEDIVEVPLFCLEQLSNVSEEQSRKPLARPYFPDLLQMIVMDKNLGVKPFPGPQIKGSCC  
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>ENSPTRG00000052623/1-693

MVSVEGRAMSFQSIHLSLSDSPVHAVCVLGEICLDLSGCAPQKQCFTIHGSGRVLIDVANT--VISEKED  
ATIWWPLSDPTYATVKMTSPSPMDADKVSVTYYGPNEDAPVGTAVLYLTGIEVSLEVDIYRNGQVEMSSDK  
QAKKKWIWGPSGWGAILLVNCPADVGGQLEDKTKKVFSEITNLSQMTLNVQGPCILTKYRLVLTHTSK  
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GFRLLLASPSCYKLFREKQKEGYGDALLFDELRADQLLSNGREACTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIEIPQLFCEKLTNIPSDQPKRSFARPYFPDLLRMIVMGKDLGIPKPFPGPQIKGTCC  
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>ENSPAG00000040946/1-694

MVSVEGRAMSFQSIHLSLSDSPVHAVCVLGEICLDLSGCAPQKQCFTIHGSGRVLIDVANT--VISEKED  
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QAKKKWIWGPSGWGAILLVNCPADVGGQLEDKTKKVFSEITNLSQMTLNVQGPCILTKYRLVLTHTSK  
EESKARVYWPQKDNSSFELVLPDQHAYTLA----LGNHLKETFYVEAIAFSPAEFSGLISYSVSLVEE  
SQDPSIPETVLYKDTVFRVAPCVFIPCTQVPLEVYLCRELQLQGFVDTVTKLSEKSNSQLASVYEDPNRLG  
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VEGKEYPLGRVLIGSSFYPSAEGRAMSKTLRDFLYAQVQAPVELYSDWLMTGHVDEFMCFIPTDDKNEGKK  
GFRLLLASPSCYKLFREKQKEGYGDALLFDELRADQLLSNGREACTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIEIPQLFCEKLTNIPSDQPKRSFARPYFPDLLRMIVMGKDLGIPKPFPGPQIKGTCC  
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>ENSG00000276747/1-694

MVSVEGRAMSFQSIHLSLSDSPVHAVCVLGEICLDLSGCAPQKQCFTIHGSGRVLIDVANT--VISEKED  
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QAKKKWIWGPSGWGAILLVNCPADVGGQLEDKTKKVFSEITNLSQMTLNVQGPCILTKYRLVLTHTSK  
EESKARVYWPQKDNSSFELVLPDQHAYTLA----LGNHLKETFYVEAIAFSPAEFSGLISYSVSLVEE  
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GFRLLLASPSCYKLFREKQKEGYGDALLFDELRADQLLSNGREACTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIEIPQLFCEKLTNIPSDQPKRSFARPYFPDLLRMIVMGKDLGIPKPFPGPQIKGTCC

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>ENSGGOG00000015257/1-694

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QAKKKWIWGPGSWGAILLVNCPADVGGQLEDKTKKVFSEITNLSQMTLNVQGPSCILKRYRLVHTSK  
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GFLLLASPSACYKLFREKQKEGYGDALLFDELRADQLLSNGREAKTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIIEIPQLFCLEKLTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGQIKGTCC  
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>ENSPPYG00000001806/1-694

VVSVEGRAMSFQSIHVLSLSDSPAHAVCVLGTICLDLSDGAPQKQCQCFTHGSGRVLINMANT--VISEEKED  
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QAKKKWIWGPGSWGAILLVNCPADVGGQLEDKTKKVFSEITNLSQMTLSVQGPCTCILKRYRLVHTSK  
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GFQLLASPSACYKLFREKQKEGYGDALLFDELRADQLLSNGREAKTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIIEIPQLFCLEKLTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGQIKGTCC  
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>ENSNLEG00000007782/1-642

VVSVEGRAMSFQSIHVLSLSDSPAHAVCVLGTIEI-----YSAHGVG-----LCSR---

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EESKKARVYWPQKDNSSSTFELVLPDQHVYTLAL----LGSHLKETFYVEAIAFSPAEFSGLISYSVSLVEE  
SQDPSIPETLLYKDTVFRVAPCVFIPCTQVPLEVYLCRELQLQGFVDTVTELSEKSNSQVASVYEDPNRLG  
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VQGREYPLGRVLIGSSFYPSAEGRAMSKTLRDFLYAQVQAPVELYSDWLMTGHVDEFMCFIPTDDKNEGKK  
GFQLLASPSACYKLFREKQKEGYGDALLFDELRADQLLSNGKGTPE-----AQN---RKCIHLNR  
DILKTELGLVEQDIIIEIPQLFCLEKLTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGQIKGTCC  
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>ENSMLEG000000029519/1-694

MVSVEARMSFQSIHVLSLSDSPAHAVCVLGTICLDLSDGAPQKQCQCFTHGSGRVLIDVANT--VISEED  
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QAKKKWIWGPGSWGAILLVNCPADVGGQPEDKTKKVFSEIKNLSQMTLSVQGPSCILKRYRLVHTSK  
EESKKARVYWPQKDNSSSTFELVLPDQHVYTLAL----LGNHLKETFYVEAIAFSPAEFSGLISYSASLVEE  
SQDPSIPETLLYKDTVFRVAPCVFVPCQVPLEVYLCRELQLQGFVDTVTELSEKSNSQVASVYEDPNRLG  
RWLQDEMAFCYTQAPHKTTSLILDTPQAADLDEFPMKYLSLPGIGYMIQDIEDHKVASMDSIGNLMVSPPVK  
VQEKEYPLGRVLIGSSFYPSAEGRAMSKTLRDFLYAQVQAPVELYSDWLMTGHVDEFMCFIPTDDKNEGKK  
GFQLLASPSACYKLFREKQKEGYGDALLFDELRADQLLSNGREARTIDQLLADESLKKQNEYVEKCIHLNR  
DILKTELGLVEQDIIIEIPQLFCLEKMTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGQIKGTCC  
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>ENSPANG000000031439/1-694

MVSVEGRAMSFQSIHVLSLSDSPAHAVCVLGTICLDLSDGAPQKQCQCFTHGSGRVLIDVANT--VISEED  
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QAKKKWIWGPGSWGAILLVNCPADVGGQPEDKTKKVFSEIKNLSQMTLSVQGPSCILKRYRLVHTSK  
EESKKARVYWPQKDNFSTFELVLPDQHVYTLAL----LGNHLKETFYVEAIAFSPAAGFSGLISYSASLVEE  
SQDPSIPETLLYKDTVFRVAPCVFVPCQVPLEVYLCRELQLQGFVDTVTELSEKSNSQVASVYEDPNRLG  
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DILKTELGLVEQDIIIEIPQLFCLEKMTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGQIKGTCC  
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>ENSCATG000000040335/1-694

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QAKKKWIWGPGSWGAILLVNCPADVGGQPEDKTKKVFSEIKNLSQMTLSVQGPSCILKRYRLVHTSK  
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>ENSMUG00000022437/1-694

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QAKKKWIWGSPSGWGAILLVNCNPADVGGQPEDKTKKVFSEEIKNLSQMTLSVQGPSCILKYYRVLVHTSK  
EESKKARVYWPQKDNSSTFELVLPQGHAYTLAL----LGNHLKETFYVEAIAFPSAEFSGLISYSASLVEE  
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DILKTELGLVEQDIIIEIPQLFCLEKMTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIKPFPGQIKGTCC  
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>ENSMFAG00000002560/1-694

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QAKKKWIWGSPSGWGAILLVNCNPADVGGQPEDKTKKVFSEEIKNLSQMTLSVQGPSCILKYYRVLVHTSK  
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>ENSMNEG000000039952/1-694

MVSVEGRAMSFQSIVRSLDSPAHAHVCVLGTEICLDLSGCAPQKQCFTIHGSGRVLIDVANT--VISEEED  
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>ENSCSAG00000000865/1-694

MVSVEGRAMSFQSIVRSLSPAHAHVCVLGTEICLDLSGCAPQKQCFTIHGSGRVLIDVANT--VISEEED  
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DILKTELGLVEQDIIIEIPQLFCLEKMTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIKPFPGQIKGTCC  
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>ENSRROG000000039820/1-694

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SQDPSIPETLLYKDTVFRVAPCVFPCTQVPLEVYLCRELQLQGFVDTVTELSKNSQVASVYEDPNRLG  
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>ENSRBIG000000035034/1-694

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EESKKARVYWPQKDNSSTFELVLGPGQHAYTLAL----LGNHLKETFYVEAIAFPSAEFSG LISYSASLVEE  
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VQEKEYPLGRVLIGSSFYFSTEGRAMSKTLRDFLYAQVQAPVELYSDWLMGSHVDEFMCFIPTDDKNEGRK  
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DILKTELGLVEQDIIIEIPQLFCLEKLTNIPSDQQPKRPFARPYFPDLLRMIVMGKNLGIPKPFPGPQIKGTCC  
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>ENSCCAG00000036970/1-693

KVSVEGQAMSFQNIIRLSLDSPAHAVCVMGTEICLDLSCAPEKQCQCFIRGSGRVMIDVANT--VISEKES  
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QAKKKWTWGPSGWGAILLVNCPADAGQQLD-KTNRVIFSEEIKNLSQMTLKVQGPSCLLKKYRLVLTSE  
EESKKARVYWRKDNSSTFELVLGSPQHAYTLAL----LGDHLKETFYLEAMVFPSAEFSG LITYSVSLVEE  
SQDPLIPETPLYKDTVFRVAPCIPCTQVPLEVYLCRELQLQGFDVTTELSEKSNSQVASVYEDPSRLG  
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>ENSCJAG00000007733/1-693

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QAKKKWTWGPSGWGAILLVNCPADAGQQLD-ETKRVIFSEEIKNLSQMTLNVQGPSCLLKKFRLVLTSE  
EESKKARVYWRKDNSSTFELVLGSPQHAYTLAL----LGDHLKETFYLEAMEFPSAEFSG LITYSVSLVEE  
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>ENSCCAG000000026784/1-571

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-----SEPTYQWTS-VSPSCEKH-----TL-----TEMSSHL

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>ENSEASG0000005015759/1-687

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RAKKNWWWGPGSWGAILLVNCSPADMGQL-TDRNTTKAFFPEEMKNLSQMTLSVQGPNCILKXHLVHTSE  
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GFRLLLASPSSCYRLFQEKQKEGYGDMHLFEGVRADQLLSNGREANTIHQLLADENMRRQNDYVQKICINLNR  
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>ENSCDRG0000005005429/1-695

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DFRLLLASPSSCYKLFKEKQKEGYGDMPLFEEVRKQDLISNGREASTINQLLADENMRKQNDYVENCINLNR  
DILKRELGLVEKDIIDIPQLFCLEQLTNVPSSEQTQKLFARPYFPDLLQIIVMGTNLGIKPFGRINGTCC  
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>ENSRFEG00010015258/1-693

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QAKKNWWWGPKGWGAILLVNCSPTDMGQL-IDKKTTRVIFSEEIKLSQMTLNVQGPSCILKNHQLVLYTSE  
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-FRLLLASPACYKLFQEKQKEGYGDMPLFEEVREDQLLSNGREANTINQLLADENMRKQDAYVEKCVNLNR  
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>ENSDLEG00000017509/1-676

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SILKRELGLVEEQDIIDIPQLFCLEHIANIPSSSEQTEKLYARPYFPDLLQMVVMGQNLGIKPFQKINGACC  
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>ENSDLEG00000017924/1-676

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SQDLSIPETVYKDTVFRVAPCVFVSSTQMPLLEVYLCRELQVQGFVNTVMELSESNIQVASVYEDPNRLG  
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SILKRELGLVEEQDIIDIPQLFCLEHIANIPSSSEQTEKLYARPYFPDLLQMVVMGQNLGIKPFQKINGACC  
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>ENSDLEG00000009237/1-676

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SQDLSIPETVYKDTVFRVAPCVFVSSTQMPLLEVYLCRELQVQGFVNTVMELSESNIQVASVYEDPNRLG  
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>ENSMNMG00015008836/1-680

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SILKRELGLVEEQDIIDIPQLFCLEHIANIPSSSEQTEKLYARPYFPDLLQMVVMGQNLGIKPFQKINGACC  
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>ENSPSNG0000000724/1-676

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SQDLSIPETVVYKDTVFRVAPCVFVSSTQMPLEVYLCRELQVQGFVNTVMELSESNIQVASVYEDPNRLG  
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SILKRELGLEEQDIIDIPQLFCLHEIANIPSSQTEKLYARPYFPDLLQMVMGQNLGIPKPFPGPQINGACC  
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>ENSPCTG00005022042/1-643

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SQDLSIPETVVYKDTVFRVAPCVFVPSTQ-----ILPGPGRFC  
NWLQDEMAFCYTQAPHKTIISLVLDTPRLPKLDDFPMKYSLSPGVGYMTQRTQDHAVASIDSIGNLMVSPPVK  
AQQKEYPLGRILIGSSFYPSKDCRNLSKTLRDFLYAQVQAPVELFSDWLMIGHAYEFMCFIPAQYKVEDEK  
GFRLLASPSSCYKLFKEKQKEGYGDARLFEGIRKQDQLLSNGREANTINQLLADENMRKQNSYVEKCIDLNR  
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>ENSBMSG00010001172/1-676

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SPDPSIPETVVYKDTVFRVAPCVFVPSTQMPLEVYLCRELQVQGFVNTVMELSESNIQVASVYEDPNRLG  
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>ENSOARG00020012854/1-688

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SQDPLVPETVLYKDTVFRVAPCIFAFTTQMPLEVYLCRELQVQGFVSAVTELSERSNSQVASVYEDPNRLG  
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>ENSCHIG00000014830/1-688

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>ENSBIXG00005026457/1-695

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>ENSBTAG00000038945/1-688

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SQDPLVPEAVLCKDVTFLFRVAPCIVFPSTQMPLEVLVLCRELQVQGFVSTVTELSERSNSQVASVYEDPNRLG  
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>ENSBMUG0000003419/1-695

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>ENSBGRG0000003075/1-635

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>ENSBGRG00000020369/1-672

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SQDPLVPEAVLCKDVTFLFRVAPCIVFPSTQMPLEVLVLCRELQVQGFVSTVTELSERSNSQVASVYEDPNRLG  
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>ENSMMSG00000007431/1-687

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DFRLLASPSSCYKLFKERQKEGYGDVMLFEGLRKQDQLSNGRKAITINQLLADEKMRKQNDYAEKCIHLNR  
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>ENSBHYG00000003136/1-695

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>ENSSSCG00000003484/1-687

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>ENSMUG00000014390/1-656

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>ENSLAFG00000010718/1-682

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