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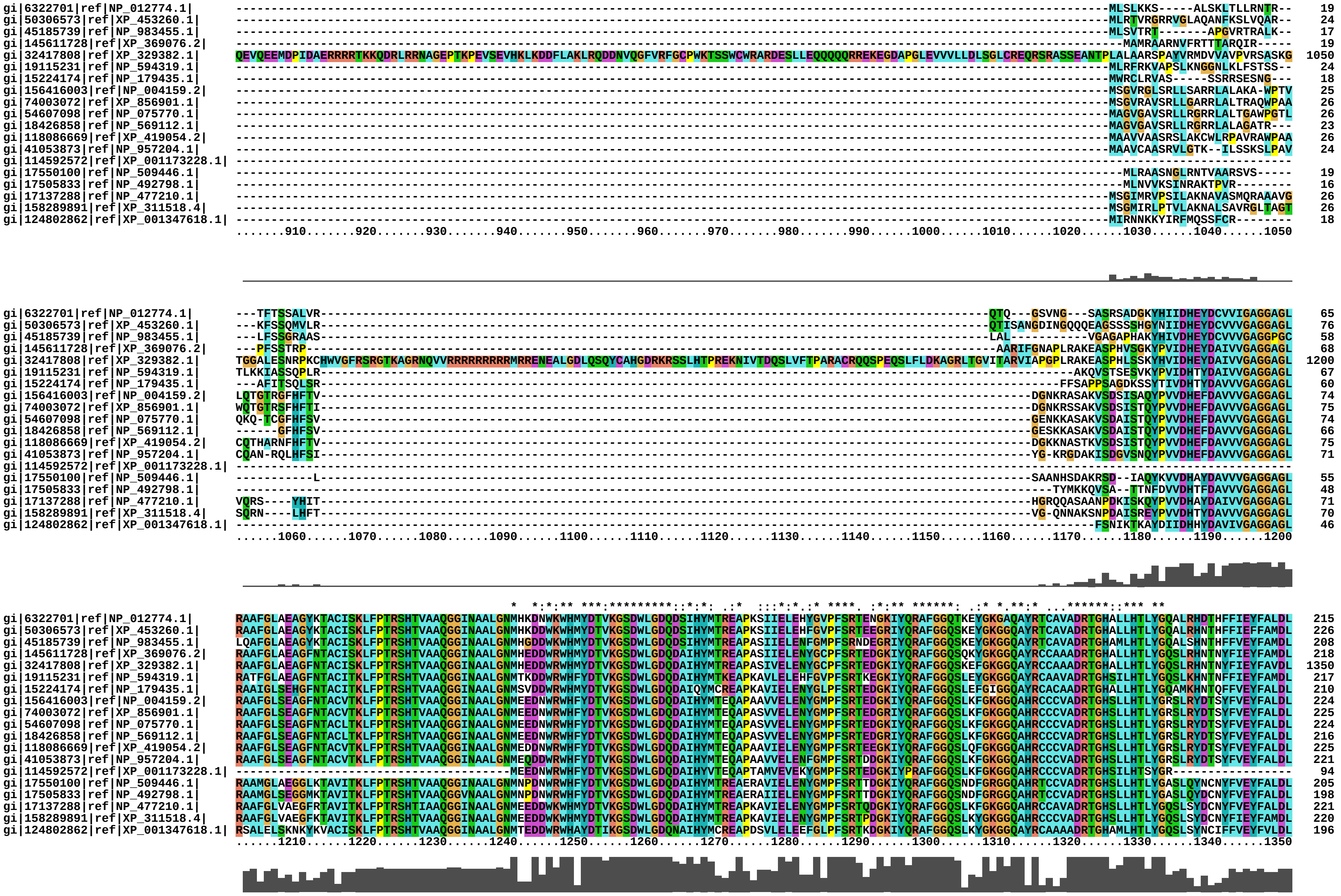

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gi|17137288|ref|NP_477210.1|      ----------------------------------------------------------------------------------------------------------------------------MSGIMRVPSILAKNAVASMQRAAAVG   26
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gi|45185739|ref|NP_983455.1|      ---LFSSGRAAS-----------------------------------------------------------------------------------------------LAL-----------VGAGAPHAKYHIVDHEYDCVVVGAGGPGC   58
gi|145611728|ref|XP_369076.2|     ---PFSSTRP--------------------------------------------------------------------------------------------------AARIFGNAPLRAKEASPHVSGKYPVIDHEYDAIVVGAGGAGL   68
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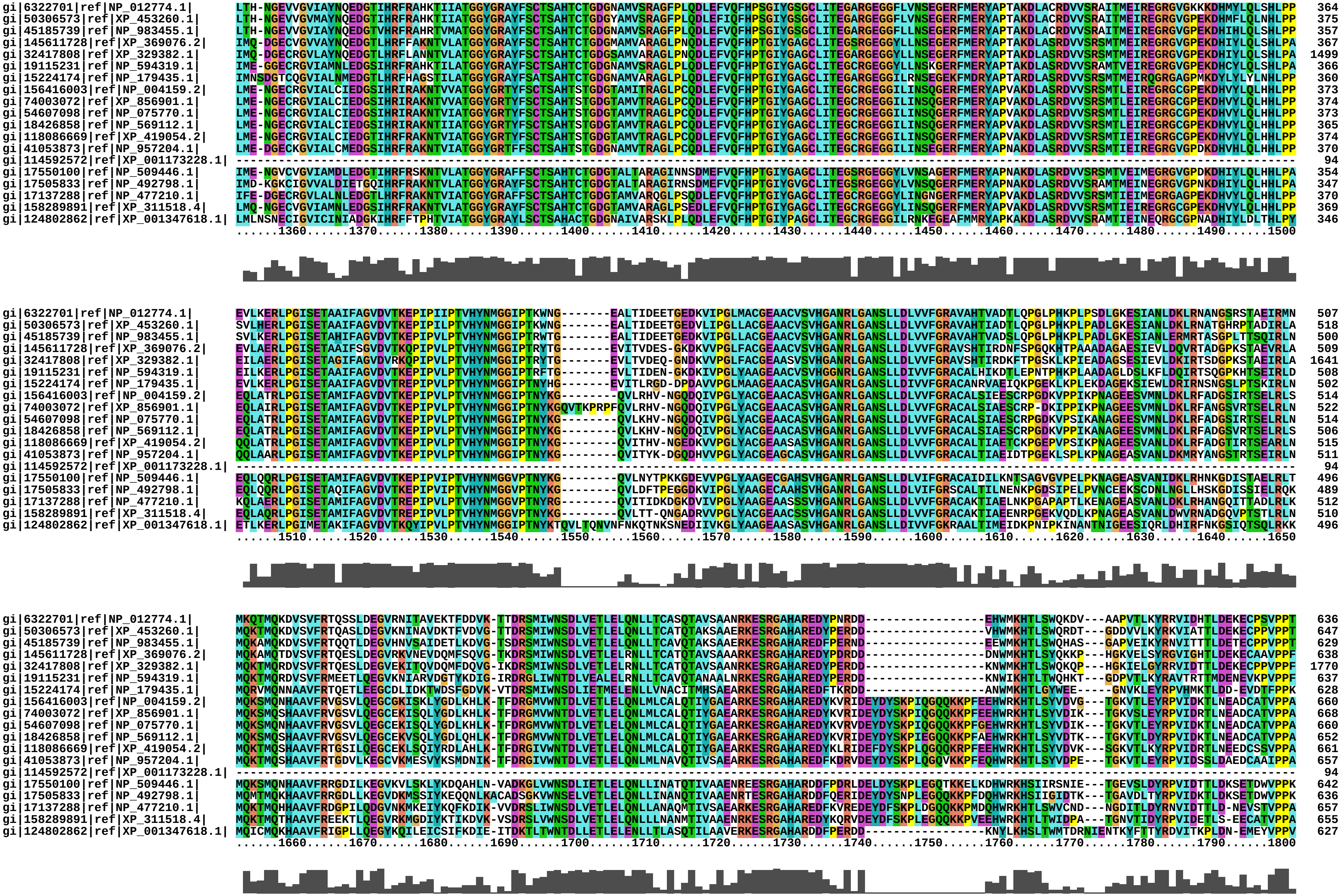

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gi|15224174|ref|NP_179435.1|         IMNSDGTCQGVIALNMEDGTLHRFHAGSTILATGGYGRAYFSATSAHTCTGDGNAMVARAGLPLQDLEFVQFHPTGIYGAGCLITEGARGEGGILRNSEGEKFMDRYAPTARDLASRDVVSRSMTMEIRQGRGAGPMKDYLYLYLNHLPP   360
gi|156416003|ref|NP_004159.2|        LME-NGECRGVIALCIEDGSIHRIRAKNTVVATGGYGRTYFSCTSAHTSTGDGTAMITRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPEKDHVYLQLHHLPP   373
gi|74003072|ref|XP_856901.1|         LME-NGECRGVIALCIEDGSIHRIRAKNTVVATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPEKDHVYLQLHHLPP   374
gi|54607098|ref|NP_075770.1|         LME-NGECRGVIALCIEDGSIHRIRAKNTVIATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPEKDHVYLQLHHLPP   373
gi|18426858|ref|NP_569112.1|         LME-NGECRGVIALCIEDGSIHRIRAKNTIIATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPEKDHVYLQLHHLPP   365
gi|118086669|ref|XP_419054.2|        LME-NGECRGVIALCIEDGTIHRFRAKNTVIATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTIEIREGRGCGPEKDHVYLQLHHLPP   374
gi|41053873|ref|NP_957204.1|         LME-DGECKGVIALCMEDGSIHRFRAKNTVIATGGYGRTFFSCTSAHTSTGDGNAMVTRAGLPCQDLEFVQFHPTGIYGAGCLITEGCRGEGGILINSEGERFMERYAPNAKDLASRDVVSRSMTIEIREGRGVGPDKDHVHLQLHHLPP   370
gi|114592572|ref|XP_001173228.1|     ------------------------------------------------------------------------------------------------------------------------------------------------------    94
gi|17550100|ref|NP_509446.1|         IME-NGVCVGVIAMDLEDGTIHRFRSKNTVLATGGYGRAFFSCTSAHTCTGDGTALTARAGINNSDMEFVQFHPTGIYGAGCLITEGSRGEGGYLVNSAGERFMERYAPNAKDLASRDVVSRSMTVEIMEGRGVGPDKDHIYLQLHHLPA   354
gi|17505833|ref|NP_492798.1|         IMD-KGKCIGVVALDIETGQIHRFRAKNTVLATGGYGRAYFSCTSAHTCTGDGTALTARAGIRNSDMEFVQFHPTGIYGVGCLITEGSRGEGGYLVNSQGERFMERYAPNAKDLASRDVVSRAMTMEINEGRGVGPNKDHIYLQLHHLPA   347
gi|17137288|ref|NP_477210.1|         IFE-DGECRGVLALNLEDGTLHRFRAKNTVIATGGYGRAFFSCTSAHTCTGDGTAMVARQGLPSQDLEFVQFHPTGIYGAGCLITEGCRGEGGYLINGNGERFMERYAPVAKDLASRDVVSRSMTIEIMEGRGAGPEKDHVYLQLHHLPP   370
gi|158289891|ref|XP_311518.4|        LMQ-NGECVGVIAMNLEDGSIHRFRAKNTVLATGGYGRAYFSCTSAHTCTGDGTAMVARAGLPSEDLEFVQFHPTGIYGAGCLITEGCRGEGGYLINSQGERFMERYAPVAKDLASRDVVSRSMTIEIREGRGCGPEKDHVYLQLHHLPP   369
gi|124802862|ref|XP_001347618.1|     LMLNSNECIGVICINIADGKIHRFFTPHTVIATGGYGRAYLSCTSAHACTGDGNAIVARSKLPLQDLEFVQFHPTGIYPAGCLITEGCRGEGGILRNKEGEAFMMRYAPKAKDLASRDVVSRAMTIEINEQRGCGPNADHIYLDLTHLPY   346
                                     ......1360......1370......1380......1390......1400......1410......1420......1430......1440......1450......1460......1470......1480......1490......1500

gi|6322701|ref|NP_012774.1|          EVLKERLPGISETAAIFAGVDVTKEPIPIIPTVHYNMGGIPTKWNG-------EALTIDEETGEDKVIPGLMACGEAACVSVHGANRLGANSLLDLVVFGRAVAHTVADTLQPGLPHKPLPSDLGKESIANLDKLRNANGSRSTAEIRMN   507
gi|50306573|ref|XP_453260.1|         SVLHERLPGISETAAIFAGVDVTKEPIPILPTVHYNMGGIPTKWNG-------EALTIDEETGEDVLIPGLLACGEAACVSVHGANRLGANSLLDLVVFGRAVAHTIADTLQPGLPHKPLPADLGKESIANLDKLRNATGHRPTADIRLA   518
gi|45185739|ref|NP_983455.1|         SVLKERLPGISETAHIFAGVDVTKEPIPVLPTVHYNMGGIPTRWTG-------EALTIDEETGEDKVIPGLLACGEAACVSVHGANRLGANSLLDLVVFGRAVAHTVADSLQPGLPHKPLPADLGKESIANLERMRTASGPLTTSQIRLN   500
gi|145611728|ref|XP_369076.2|        EVLAERLPGISETAAIFSGVDVTKQPIPVLPTVHYNMGGIPTRYTG-------EVITVDES-GKDKVVPGLFACGEAACVSVHGANRLGANSLLDLVVFGRAVSHTIRDNFSPGQKHTPAAADAGAESIEVLDQVRTADGPKSTAEVRLA   509
gi|32417808|ref|XP_329382.1|         EILAERLPGISETAGIFAGVDVRKQPIPVLPTVHYNMGGIPTRYTG-------EVLTVDEQ-GNDKVVPGLFACGEAASVSVHGANRLGANSLLDLVVFGRAVSHTIRDKFTPGSKLKPIEADAGSESIEVLDKIRTSDGPKSTAEIRLA  1641
gi|19115231|ref|NP_594319.1|         EILKERLPGISETAAIFAGVDVTKEPIPVLPTVHYNMGGIPTRFTG-------EVLTIDEN-GKDKIVPGLYAAGEAACVSVHGGNRLGANSLLDIVVFGRACALHIKDTLEPNTPHKPLAADAGLDSLKFLDQIRTSQGPKHTSEIRLD   508
gi|15224174|ref|NP_179435.1|         EVLKERLPGISETAAIFAGVDVTREPIPVLPTVHYNMGGIPTNYHG-------EVITLRGD-DPDAVVPGLMAAGEAACASVHGANRLGANSLLDIVVFGRACANRVAEIQKPGEKLKPLEKDAGEKSIEWLDRIRNSNGSLPTSKIRLN   502
gi|156416003|ref|NP_004159.2|        EQLATRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKG--------QVLRHV-NGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIEESCRPGDKVPPIKPNAGEESVMNLDKLRFADGSIRTSELRLS   514
gi|74003072|ref|XP_856901.1|         EQLAIRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKGQVTKPRPFQVLRHV-NGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIAESCRP-DKIPPIKPNAGEESVMNLDKLRFANGSVRTSELRLN   522
gi|54607098|ref|NP_075770.1|         EQLATRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKG--------QVLKHV-NGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIAESCRPGDKVPSIKANAGEESVMNLDKLRFADGSIRTSELRLN   514
gi|18426858|ref|NP_569112.1|         EQLATRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKG--------QVLKHV-NGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIAESCRPGDKVPPIKANAGEESVMNLDKLRFADGSVRTSELRLS   506
gi|118086669|ref|XP_419054.2|        QQLATRLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKG--------QVITHV-NGEDKVVPGLYACGEAASASVHGANRLGANSLLDLVVFGRACALTIAETCKPGEPVPSIKPNAGEESVANLDKLRFADGTIRTSEARLN   515
gi|41053873|ref|NP_957204.1|         QQLAARLPGISETAMIFAGVDVTKEPIPVLPTVHYNMGGIPTNYKG--------QVITYK-DGQDHVVPGLYACGEAGCASVHGANRLGANSLLDLVVFGRACALTIAEIDTPGEKLSPLKPNAGEASVANLDKMRYANGSTRTSEIRLN   511
gi|114592572|ref|XP_001173228.1|     ------------------------------------------------------------------------------------------------------------------------------------------------------    94
gi|17550100|ref|NP_509446.1|         EQLQQRLPGISETAMIFAGVDVTKEPIPVIPTVHYNMGGVPTNYKG--------QVLNYTPKKGDEVVPGLYAAGECGAHSVHGANRLGANSLLDLVIFGRACAIDILKNTSAGVGVPELPKNAGEASVANIDKLRHNKGDISTAELRLT   496
gi|17505833|ref|NP_492798.1|         EQLQQRLPGISETAQIFAGVDVTKEPIPVIPTVHYNMGGVPTNYKG--------QVLDFTPEGGDKVIPGLYAAGECAAHSVHGANRLGANSLLDLVIFGRSCALTILNENKPGDSIPELPVNCEEKSCDNLNGLLHSKGDISSIELRQK   489
gi|17137288|ref|NP_477210.1|         KQLAERLPGISETAMIFAGVDVTREPIPVLPTVHYNMGGVPTNYRG--------QVITIDKDGKDVIVPGLYAAGEAASSSVHGANRLGANSLLDLVVFGRACAKTIAELNKPGAPAPTLKENAGEASVANLDKLRHANGQITTADLRLK   512
gi|158289891|ref|XP_311518.4|        EQLAQRLPGISETAMIFAGVDVTREPIPVLPTVHYNMGGVPTNYKG--------QVLTT-QNGADRVVPGLYACGEAACSSVHGANRLGANSLLDLVVFGRACAKTIAEENRPGEKVQDLKPNAGEASVANLDWVRNADGQVPTSTLRLN   510
gi|124802862|ref|XP_001347618.1|     ETLKERLPGIMETAKIFAGVDVTKQYIPVLPTVHYNMGGIPTNYKTQVLTQNVNFNKQTNKSNEDIIVKGLYAAGEAASASVHGANRLGANSLLDIVVFGKRAALTIMEIDKPNIPKINANTNIGEESIQRLDHIRFNKGSIQTSQLRKK   496
                                     ......1510......1520......1530......1540......1550......1560......1570......1580......1590......1600......1610......1620......1630......1640......1650

gi|6322701|ref|NP_012774.1|          MKQTMQKDVSVFRTQSSLDEGVRNITAVEKTFDDVK-TTDRSMIWNSDLVETLELQNLLTCASQTAVSAANRKESRGAHAREDYPNRDD-----------------EHWMKHTLSWQKDV---AAPVTLKYRRVIDHTLDEKECPSVPPT   636
gi|50306573|ref|XP_453260.1|         MQKTMQKDVSVFRTQASLDEGVKNINAVDKTFVDVG-TTDRSMIWNSDLVETLELQNLLTCATQTAKSAAERKESRGAHAREDYPERDD-----------------VHWMKHTLSWQRDT---GDDVVLKYRKVIATTLDEKECPPVPPT   647
gi|45185739|ref|NP_983455.1|         MQKAMQKDVSVFRTQQTLDEGVHNVSAIDETLKDVG-TSDRSMIWNSDLVETLELQNLLTCAVQTAKSAAERKESRGAHAREDFPERND-----------------EEWMKHTLSWQHAS---GAPVEIKYRNVITTTLDETECPPVPPT   629
gi|145611728|ref|XP_369076.2|        MQKAMQTDVSVFRTQESLDEGVRKVNEVDQMFSQVG-TKDRSMIWNSDLVETLELRNLLTCATQTAVSAAARKESRGAHAREDYPDRDD-----------------DNWMKHTLSYQKKP---HGKVELSYRGVIGHTLDEKECAAVPPF   638
gi|32417808|ref|XP_329382.1|         MQKTMQRDVSVFRTQESLDEGVEKITQVDQMFDQVG-IKDRSMIWNSDLVETLELRNLLTCATQTAVSAANRKESRGAHAREDYPERDD-----------------KNWMKHTLSWQKQP---HGKIELGYRRVIDTTLDEKECPPVPPF  1770
gi|19115231|ref|NP_594319.1|         MQKTMQRDVSVFRMEETLQEGVKNIARVDGTYKDIG-IRDRGLIWNTDLVEALELRNLLTCAVQTANAALNRKESRGAHAREDYPERDD-----------------KNWIKHTLTWQHKT---GDPVTLKYRAVTRTTMDENEVKPVPPF   637
gi|15224174|ref|NP_179435.1|         MQRVMQNNAAVFRTQETLEEGCDLIDKTWDSFGDVK-VTDRSMIWNSDLIETMELENLLVNACITMHSAEARKESRGAHAREDFTKRDD-----------------ANWMKHTLGYWEE----GNVKLEYRPVHMKTLDD-EVDTFPPK   628
gi|156416003|ref|NP_004159.2|        MQKSMQNHAAVFRVGSVLQEGCGKISKLYGDLKHLK-TFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVRIDEYDYSKPIQGQQKKPFEEHWRKHTLSYVDVG---TGKVTLEYRPVIDKTLNEADCATVPPA   660
gi|74003072|ref|XP_856901.1|         MQKSMQSHAAVFRVGSVLQEGCEKISQLYGDLKHLK-TFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVRIDEYDYSKPIQGQQKKPFEEHWRKHTLSYVDIK---TGKVSLEYRPVIDRTLNEADCATVPPA   668
gi|54607098|ref|NP_075770.1|         MQKSMQNHAAVFRVGSVLQEGCEKISQLYGDLKHLK-TFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVRVDEYDYSKPIQGQQKKPFGEHWRKHTLSYVDIK---TGKVTLEYRPVIDKTLNEADCATVPPA   660
gi|18426858|ref|NP_569112.1|         MQKSMQSHAAVFRVGSVLQEGCEKVSQLYGDLQHLK-TFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVRIDEYDYSKPIEGQQKKPFAEHWRKHTLSYVDTK---TGKVTLDYRPVIDKTLNEADCATVPPA   652
gi|118086669|ref|XP_419054.2|        MQKTMQSHAAVFRTGSILQEGCEKLSQIYRDLAHLK-TFDRGIVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKLRIDEFDYSKPLQGQQKRPFEEHWRKHTLSYVDVK---SGKVTLKYRPVIDRTLNEEDCSSVPPA   661
gi|41053873|ref|NP_957204.1|         MQKTMQSHAAVFRTGDVLKEGCVKMESVYKSMDNIK-TFDRGIVWNTDLVETLELQNLMLNAVQTIVSAEARKESRGAHAREDFKDRVDEYDYSKPLQGQVKKPFEQHWRKHTLSYVDPE---TGKVTLEYRPVIDSSLDAEDCAAIPPA   657
gi|114592572|ref|XP_001173228.1|     ------------------------------------------------------------------------------------------------------------------------------------------------------    94
gi|17550100|ref|NP_509446.1|         MQKSMQNHAAVFRRGDILKEGVKVLSKLYKDQAHLN-VADKGLVWNSDLIETLELQNLLINATQTIVAAENREESRGAHARDDFPDRLDELDYSKPLEGQTKKELKDHWRKHSIIRSNIE---TGEVSLDYRPVIDTTLDKSETDWVPPK   642
gi|17505833|ref|NP_492798.1|         MQMTMQKHAAVFRRGDLLKEGVDKMSSIYKEQQNLKACADSGKVWNSELVETLELQNLLINANQTIVAAENRTESRGAHARDDFQERIDEYDYSNPLEGQQKKPFDQHWRKHSIIGIDTK---TGAVDLTYRPVIDKTLDKSETDWVPPK   636
gi|17137288|ref|NP_477210.1|         MQKTMQHHAAVFRDGPILQDGVNKMKEIYKQFKDIK-VVDRSLIWNSDLVETLELQNLLANAQMTIVSAEARKESRGAHAREDFKVREDEYDFSKPLDGQQKKPMDQHWRKHTLSWVCND---NGDITLDYRNVIDTTLD-NEVSTVPPA   657
gi|158289891|ref|XP_311518.4|        MQKTMQTHAAVFREEKTLQEGVRKMGDIYKTIKDVK-VSDRSLVWNSDLVETLELQNLLLNANMTIVAAENRKESRGAHAREDYKQRVDEYDFSKPLEGQQKKPVEEHWRKHTLTWIDPA---TGNVTIDYRPVIDETLS-EECATVPPA   655
gi|124802862|ref|XP_001347618.1|     MQICMQKHAAVFRIGPLLQEGYKQILEICSIFKDIE-ITDKTLTWNTDLLETLELENLLTLASQTILAAVERKESRGAHARDDFPERDD-----------------KNYLKHSLTWMTDRNIENTKYFTTYRDVITKPLDN-EMEYVPPV   627
                                     ......1660......1670......1680......1690......1700......1710......1720......1730......1740......1750......1760......1770......1780......1790......1800
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gi|50306573|ref|XP_453260.1|      VRAY   651
gi|45185739|ref|NP_983455.1|      VRAY   633
gi|145611728|ref|XP_369076.2|     KRVY   642
gi|32417808|ref|XP_329382.1|      KRVY  1774
gi|19115231|ref|NP_594319.1|      KRVY   641
gi|15224174|ref|NP_179435.1|      PRVY   632
gi|156416003|ref|NP_004159.2|     IRSY   664
gi|74003072|ref|XP_856901.1|      IRSY   672
gi|54607098|ref|NP_075770.1|      IRSY   664
gi|18426858|ref|NP_569112.1|      IRSY   656
gi|118086669|ref|XP_419054.2|     IRSY   665
gi|41053873|ref|NP_957204.1|      IRSY   661
gi|114592572|ref|XP_001173228.1|  ----    94
gi|17550100|ref|NP_509446.1|      VRSY   646
gi|17505833|ref|NP_492798.1|      VRSY   640
gi|17137288|ref|NP_477210.1|      IRSY   661
gi|158289891|ref|XP_311518.4|     IRSY   659
gi|124802862|ref|XP_001347618.1|  KRVY   631
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