

gi | 39972847 | ref | XP_367814.1 | ----MAPSSKRKAINDDFITLISDNEADEFVVEE--VIQEAPPKKSKLTPKKQKRSKSKASNDDAE-----EEDGHIEGVWGQNDDDGAMGDF--EFVVGAGVEDLDDNPEFEGWGDFGAKK 117

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 39972847 | ref | XP_367814.1 | AMGCGN---GVLDDEIIRRRER--KEGGTK--GAAPEAKAEEGE---ALGLDDDDDE--VLARDAFGMGAGSDDEDSAEASEGQDG--SEAEGEGED--SDESVAPVPHPD 218

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 39972847 | ref | XP_367814.1 | DDQSESEEDDEEEAAKMKFFAADPEKSDITNKG-NAISMSLSRPILRGLTISVGFQAKPIIISKILIPALSMKGKDVVGGAVTGSKTAAPFVPIERLRYRPPKV---PISRVLVLPVRELAIQCHAVATKIASFTD-IK 356

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 39972847 | ref | XP_367814.1 | FCLAVGGLSLKVQESSELRLRPDVIIATPGRFIDHMNRNSASFAVD-----TVEILVLDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 451
gi | 32403416 | ref | XP_322321.1 | FCLAVGGLSLKVQEAELRLRPDVIIATPGRFIDHMNRNSASFAVD-----TVEILVLDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 489
gi | 19114126 | ref | NP_593214.1 | VCLCTIGGLSLKLEQELRKRKRPDIVIATPGRFIDHMNRNSQGFVTE-----NIETIMVMDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 455
gi | 50311527 | ref | XP_455788.1 | FGLAVGGNLNRQOEQALKRTPDIVIATPGRFIDHMNRNSASFSVD-----SVEILVLDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 430
gi | 45184660 | ref | NP_982378.1 | FGLAVGGNLNRQOEQALKRTPDIVIATPGRFIDHMNRNSASFSVD-----SVEILVLDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 416
gi | 6323021 | ref | NP_013093.1 | FGLAVGGNLNRQOEQMLKSRPDIIVATPGRFIDHMNRNSASFNVD-----SVEILVLDLDEAD-----RMLDEGFADLNEILITLTPKSRQIMLFSAMTSSVDNLR 428
gi | 21356161 | ref | NP_651970.1 | VGLAIGGLDVKAQEAHLRKNPDIIVATPGRLLIDHILKNTSPSTLD-----SIEVLILDEAD-----RMLDEYFABQMKKIIINSCCKTQIMLFSAMTSEVQKDLAA 354
gi | 158287566 | ref | XP_309566.4 | VGLAIGGLDVKAQEAHLRKNPDIIVATPGRLLIDHILKNTSPSTLD-----SIEVLILDEAD-----RMLDEYFABQMKKIIINSCCKTQIMLFSAMTSEVQKDLAA 371
gi | 124249330 | ref | NP_694705.2 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 380
gi | 109469261 | ref | XP_342583.3 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 407
gi | 224593278 | ref | NP_060365.7 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 414
gi | 114682553 | ref | XP_514711.2 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 445
gi | 122692565 | ref | NP_001073740.1 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 383
gi | 73992237 | ref | XP_534451.2 | FCLAVGGLDVKSQEAALRAAPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 381
gi | 57529371 | ref | NP_001006293.1 | FCLAVGGLDVKTQEAALRSQPDILIIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTDEVKDLA 376
gi | 50838814 | ref | NP_001002869.1 | FCLAVGGLDLKSQEAALRAGFDVLIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTSEVQKDLA 397
gi | 17510559 | ref | NP_490891.1 | CCLCAGGLDLKQEAALRSQPDVLIATPGRLLIDHLHNCPSFHL-----SIEVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTSEVQKDLA 368
gi | 30683736 | ref | NP_193396.3 | VGLVGGLSVREQEVVLRSPDIIIVATPGRMIDHLHNSMVDLD-----DLAVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTSEVQKDLA 363
gi | 115488568 | ref | NP_001066771.1 | CCLIVGGLSLKVQEAALRSQPDIIIVATPGRLLIDHLHNSLVLG-----DLAVLILDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTSEVQKDLA 420
gi | 124807064 | ref | XP_001350899.1 | VSLFCGGIDIKQOEYEFKKRNDLFCVCTPGRLLIDHLHNSLVDLFIN-----YLIVVLDLDEAD-----RMLDEYFEEQMKKIIIRMSCSHRQIMLFSAMTSEVQKDLA 293



gi | 39972847 | ref | XP_367814.1 | VGLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 552
gi | 32403416 | ref | XP_322321.1 | AGLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 590
gi | 19114126 | ref | NP_593214.1 | LSLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 556
gi | 50311527 | ref | XP_455788.1 | LSLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 533
gi | 45184660 | ref | NP_982378.1 | LSLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 519
gi | 6323021 | ref | NP_013093.1 | LSLNKPVRIMVDSQKKI-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 531
gi | 21356161 | ref | NP_651970.1 | VSLDKPKVIFVNNNQV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 455
gi | 158287566 | ref | XP_309566.4 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 472
gi | 124249330 | ref | NP_694705.2 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 481
gi | 109469261 | ref | XP_342583.3 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 508
gi | 224593278 | ref | NP_060365.7 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 515
gi | 114682553 | ref | XP_514711.2 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 546
gi | 122692565 | ref | NP_001073740.1 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 484
gi | 73992237 | ref | XP_534451.2 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 482
gi | 57529371 | ref | NP_001006293.1 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 477
gi | 50838814 | ref | NP_001002869.1 | VSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 498
gi | 17510559 | ref | NP_490891.1 | MSLKQPKVIFINENTD-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 469
gi | 30683736 | ref | NP_193396.3 | LSLNKPVRLEADSPSKR-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 464
gi | 115488568 | ref | NP_001066771.1 | LSLNKPVRLEADSPSKR-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 521
gi | 124807064 | ref | XP_001350899.1 | FSLNKPVRIFVNSNDV-----VVTLTQEFVRLRPGREBEKRMGYLVYLCKNLY-----TERRVIFFRQKKIAHARIIFGLLGLSCAELHGHSGMSIQRIQSVDFRQKVS 438



gi | 39972847 | ref | XP_367814.1 | FLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 692
gi | 32403416 | ref | XP_322321.1 | FLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 730
gi | 19114126 | ref | NP_593214.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 696
gi | 50311527 | ref | XP_455788.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 677
gi | 45184660 | ref | NP_982378.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 663
gi | 6323021 | ref | NP_013093.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 677
gi | 21356161 | ref | NP_651970.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 588
gi | 158287566 | ref | XP_309566.4 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 613
gi | 124249330 | ref | NP_694705.2 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 619
gi | 109469261 | ref | NP_342583.3 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 646
gi | 224593278 | ref | NP_060365.7 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 653
gi | 114682553 | ref | XP_514711.2 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 684
gi | 122692565 | ref | NP_001073740.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 622
gi | 73992237 | ref | XP_534451.2 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 622
gi | 57529371 | ref | NP_001006293.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 616
gi | 50838814 | ref | NP_001002869.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 634
gi | 17510559 | ref | NP_490891.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 608
gi | 30683736 | ref | NP_193396.3 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 601
gi | 115488568 | ref | NP_001066771.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 658
gi | 124807064 | ref | XP_001350899.1 | VLLAIDLASRGLDIKGVDIVINYEAPQSLIYVHRVGR TARAGRSQTAIILAAEF--DRKVKAQVKAQKAGQ--AKISSRIIDAADSDVQAKIDELEDEVEAVMREBEKQVLAQADMRRKQNMNR---YEDD IKARPKRTWF 579



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gi|39972847|ref|XP_367814.1|EPEKDKKAAREAGRAA--LNQVREALKKKHGGKNSLNDKDKKLDAMAEAKEARVVKKGAAERAGKGAVLNFK--KDKSSKGGPVVGG775
gi|32403416|ref|XP_322321.1|ETQEDKKKAKAAGRAE--LNQVREALKKKHGGKNSLNDKDKKLDAMAEAKEARVVKKGAAERAGKGAVLNFK--KDKSSKGGPVVGG815
gi|19114126|ref|NP_593214.1|QSEKDKQASKAS-----EAKDKKSLAKRKKQ-----MEKEEVPRAYKTKNDR-----LSN-----742
gi|50311527|ref|XP_455788.1|QSEAEKKNKMLQ-----VLAKNKPIINSKRRKQ--EALAE--PRLYKTKQDR-----VEYOE-----729
gi|45184660|ref|NP_982378.1|QSESEKKNSSILQ-----ALSNKKVINSKRRKEEAQEVG--SRQYKTKQDR-----VINDOE-----716
gi|6323021|ref|NP_013093.1|QSESDKKNKVLG-----ALSRNKKVINSKRRKEEAQEVG--SRQYKTKQDR-----VINDOE-----731
gi|21356161|ref|NP_651970.1|QTKQREAEKDLRLALTGDEDKASGGKGGKLAGKRRKRPYGGDGGPPVKDLEAKRNNKKKPERK-KTPEQLAKERAMKEIEKVSIVRAKMAKLRKRPG--KLGAAIVFHRSGA--DGGKPK-----KRRGG712
gi|158287566|ref|XP_309566.4|QTKHERREEKNRLAGEEQQE-----KKKAAKRKRKRRDD--DEDFDVPVRYHEEKRRKQKAAAGGGGATAKQLARERALEVVRVSMVQAKLAKIRNRRPGRVNAAEVEHNGPADGRAGGKSNKRRSKN735
gi|124249330|ref|NP_694705.2|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--AKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRTK--RARAMPEDEPTG--PAKQK-----KQQQ709
gi|109469261|ref|XP_342583.3|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--VKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRTK--RARAMPEEPEAAGPAKKQ-----KQHK737
gi|224593278|ref|NP_060365.7|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--AKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRAK--RARAMPEEPEVVRGPAKKQ-----KQKQ744
gi|114682553|ref|XP_514711.2|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--AKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRAK--RARAMPEEPEVVRGPAKKQ-----KQKQ775
gi|122692565|ref|NP_001073740.1|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--AKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRAK--RARAMPEEPEVVRGPAKKQ-----KQVK713
gi|73992237|ref|XP_534451.2|QTKBERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--AKKKGEMTAEERSQFEILKAOMFAERLAKRNNRRAK--RARAMPEEPEAARGPAKKQ-----KQVN713
gi|57529371|ref|NP_001006293.1|QTKREERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--TORKAQMTPEERSQFEILKSONYFAERLAKRNNRVK--RARALPEEPEAAAPKQPK-----RKKK707
gi|50838814|ref|NP_001002869.1|QTKNEERKKEKIAKALC--EFDLALRGKKKKRKKFMKD--GKRRK-ELTAEERAQLEVLKSONYFAERLAKRNNRVK--RARALPEEPEAAAPKQPK-----RKKK726
gi|17510559|ref|NP_490891.1|MKESIEIEKQR-----KREKRQMKVDA-----RKKAEAAKTPEDITEHEAAFHVRAAKRANRHSK--KRIRAVVVSAGTKGAGKAAQNKKKASSNK694
gi|30683736|ref|NP_193396.3|MTEKELKLVQAQAEKDSAGN--PAGGELVSADEADLKKMKEKRRERKKNLPRKKRRKLEBAAREMLEDNEGEEEEEDEEGDEKRRGRSRGKDKKKQETDKKGLTLKDLGYMRAKAVKAK-QRAIDSGK724
gi|115488568|ref|NP_001066771.1|AKTEKELKLVQAQAEKDSAGN--PAGGELVSADEADLKKMKEKRRERKKNLPRKKRRKLEBAAREMLEDNEGEEEEEDEEGDEKRRGRSRGKDKKKQETDKKGLTLKDLGYMRAKAVKAK-QRAIDSGK770
gi|124807064|ref|XP_001350899.1|LREKELKLVQAQAEKDSAGN--PAGGELVSADEADLKKMKEKRRERKKNLPRKKRRKLEBAAREMLEDNEGEEEEEDEEGDEKRRGRSRGKDKKKQETDKKGLTLKDLGYMRAKAVKAK-QRAIDSGK671
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi|39972847|ref|XP_367814.1|RVAKKCAPRGKPRRR-----GNVAGKGG-KGKGRKRLP--SPYPRPNFNLPEPSPKPFWSQPSKASEATQQSTKIALFPFLRRLFGPRAHTRS--LVRVLLPSVTRDREYREHLNFRHRNLPKHKVRLQTRIRYRFILEERRRKKQAGGRLVDIIRRQSRRLVYGGGAGVRR790
gi|32403416|ref|XP_322321.1|RVAKKCAPRGKPRRR-----GNVAGKGG-KGKGRKRLP--SPYPRPNFNLPEPSPKPFWSQPSKASEATQQSTKIALFPFLRRLFGPRAHTRS--LVRVLLPSVTRDREYREHLNFRHRNLPKHKVRLQTRIRYRFILEERRRKKQAGGRLVDIIRRQSRRLVYGGGAGVRR964
gi|19114126|ref|NP_593214.1|---KKSTKSKSKRKK-----RQYKSKCAAYGKKGK--KGKK-----LAERK-QKGGNKKK--KVRK-----754
gi|50311527|ref|XP_455788.1|---KKSTKSKSKRKK-----RQYKSKCAAYGKKGK--KGKK-----LAERK-QKGGNKKK--KVRK-----748
gi|45184660|ref|NP_982378.1|---KKSTKSKSKRKK-----RQYKSKCAAYGKKGK--KGKK-----LAERK-QKGGNKKK--KVRK-----734
gi|6323021|ref|NP_013093.1|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK752
gi|21356161|ref|NP_651970.1|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK809
gi|158287566|ref|XP_309566.4|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK760
gi|124249330|ref|NP_694705.2|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK788
gi|109469261|ref|XP_342583.3|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK796
gi|224593278|ref|NP_060365.7|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK827
gi|114682553|ref|XP_514711.2|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK765
gi|122692565|ref|NP_001073740.1|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK765
gi|73992237|ref|XP_534451.2|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK758
gi|57529371|ref|NP_001006293.1|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK776
gi|50838814|ref|NP_001002869.1|RTFFKQKSTNSNKKKGFPSRR-----QSAFTNDLTDVSRGGALRLRSEANRHKMTKTAAKK---KASVVKLTNKGAKNKFNGKNFGGPRHAKDKKK--KSFVFEELTNTSKKALKOYRAGPS--FEERK--QSGLPORRG-NFKSKSRVYKRRK757
gi|17510559|ref|NP_490891.1|TSLRDIPLVNAAGSRGVQAKQKQK--PGAKKGF--SALASVSKKSVKAAARHGPEDSKFKARVVAHRMKT--KQYMERPKPDKKQSRKPRNPRGEEEMKDLFKSDMGEKK--QGRGGAAAAAKPRTKSNKSFKARVYKRR--GKNDKAKQHS--GKGPTRC--EEMELFQNDMSEWK--QGRS--LKKNNVMRKKSKNSFKSKRNVNRRK763
gi|30683736|ref|NP_193396.3|TSLRDIPLVNAAGSRGVQAKQKQK--PGAKKGF--SALASVSKKSVKAAARHGPEDSKFKARVVAHRMKT--KQYMERPKPDKKQSRKPRNPRGEEEMKDLFKSDMGEKK--QGRGGAAAAAKPRTKSNKSFKARVYKRR--GKNDKAKQHS--GKGPTRC--EEMELFQNDMSEWK--QGRS--LKKNNVMRKKSKNSFKSKRNVNRRK789
gi|115488568|ref|NP_001066771.1|TSLRDIPLVNAAGSRGVQAKQKQK--PGAKKGF--SALASVSKKSVKAAARHGPEDSKFKARVVAHRMKT--KQYMERPKPDKKQSRKPRNPRGEEEMKDLFKSDMGEKK--QGRGGAAAAAKPRTKSNKSFKARVYKRR--GKNDKAKQHS--GKGPTRC--EEMELFQNDMSEWK--QGRS--LKKNNVMRKKSKNSFKSKRNVNRRK832
gi|124807064|ref|XP_001350899.1|TSLRDIPLVNAAGSRGVQAKQKQK--PGAKKGF--SALASVSKKSVKAAARHGPEDSKFKARVVAHRMKT--KQYMERPKPDKKQSRKPRNPRGEEEMKDLFKSDMGEKK--QGRGGAAAAAKPRTKSNKSFKARVYKRR--GKNDKAKQHS--GKGPTRC--EEMELFQNDMSEWK--QGRS--LKKNNVMRKKSKNSFKSKRNVNRRK717
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200

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gi|39972847|ref|XP_367814.1|SIGIGRAAGGGLGPGVLRRELPWKQORLLRDRETSNTNTNGPDDSOAQPQRKIDANDKMTSPYTHGYTGQYCANEPYEGSRRRKLAMAGSVYRAGVAAASREIREOYSOTRLTRDMGDGSPGVHPIGAFPEVPIIHKGQEQLT790
gi|32403416|ref|XP_322321.1|SIGIGRAAGGGLGPGVLRRELPWKQORLLRDRETSNTNTNGPDDSOAQPQRKIDANDKMTSPYTHGYTGQYCANEPYEGSRRRKLAMAGSVYRAGVAAASREIREOYSOTRLTRDMGDGSPGVHPIGAFPEVPIIHKGQEQLT1114
gi|19114126|ref|NP_593214.1|-----754
gi|50311527|ref|XP_455788.1|-----748
gi|45184660|ref|NP_982378.1|-----734
gi|6323021|ref|NP_013093.1|-----752
gi|21356161|ref|NP_651970.1|-----782
gi|158287566|ref|XP_309566.4|-----809
gi|124249330|ref|NP_694705.2|-----760
gi|109469261|ref|XP_342583.3|-----788
gi|224593278|ref|NP_060365.7|-----796
gi|114682553|ref|XP_514711.2|-----827
gi|122692565|ref|NP_001073740.1|-----765
gi|73992237|ref|XP_534451.2|-----765
gi|57529371|ref|NP_001006293.1|-----758
gi|50838814|ref|NP_001002869.1|-----776
gi|17510559|ref|NP_490891.1|-----763
gi|30683736|ref|NP_193396.3|-----789
gi|115488568|ref|NP_001066771.1|-----832
gi|124807064|ref|XP_001350899.1|-----717
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	LFPSYAKRHVKGIIHLPRRPDLGGNAYGTPNGGGNGIGPGVDERDYWTAEWNRHEDEKAVVDVDIRGWIYMPKGPMSRKNRVMVGVARREGLPDTAALQAGAGPQQGGDLRRITVDLEGLGEERIATAKEARETERRGGGEKEAATRG	1264
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500		

gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	EYSERPRADDMDGFGAMRORRSPSPPNSTAPVRINSGLGAFPPSEMTEAEIAAANASLNARLAPFMANPLVGLPIILFFVNDORSKSKNIEINAEGHFIAARVPLDFVPTHFRVLANENISTTQPVIEPRGVSLISDVDDTIKRSNINQ	1414
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650		

gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	GAREIFRNTFVRELADQITIDGVKELYTSLHNMGVKLVHVSNSPWQLYPVLATFFHKAGLPPGSIDLKQYSQMLQGIFEPVAERKKGTLERILRDFPERKFLLVGDSGEADLVYTDLALAYPGRILAVFIRDVITPEQVDMGYFTSNTQA	1564
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800		

gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	DRNNGLERSDSGRRRAQTMRATAATNTRDVAPPPPKLPPRSSPOPKGPIMGDLIDLSDPPQPAYDPRTSLSNAMHASRSTGDIPQRKGGPPPRPAKPTALRSSPARINTGGAPPLPKPRESPRPNTSHONSSASASAPGSGSGR	1714
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950		

gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	PAPPPPPRRRTSTVNLSSQSQRQSQPPPLPPRRVQITNSSSYDSDTDEWGLPLPLENRTLGSGNGGRNTFLPVRPATSYDTMNGVNGASVYATNNSASGGGANSFVNKKLEIWLRLAEAEHELLEKQGVKLYTWREGRDVAEAGLV	1864
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100		

gi	39972847	ref	XP_367814.1	-----	790
gi	32403416	ref	XP_322321.1	REAMRGFNQGVGRRS	1880
gi	19114126	ref	NP_593214.1	-----	754
gi	50311527	ref	XP_455788.1	-----	748
gi	45184660	ref	NP_982378.1	-----	734
gi	6323021	ref	NP_013093.1	-----	752
gi	21356161	ref	NP_651970.1	-----	782
gi	158287566	ref	XP_309566.4	-----	809
gi	124249330	ref	NP_694705.2	-----	760
gi	109469261	ref	XP_342583.3	-----	788
gi	224593278	ref	NP_060365.7	-----	796
gi	114682553	ref	XP_514711.2	-----	827
gi	122692565	ref	NP_001073740.1	-----	765
gi	73992237	ref	XP_534451.2	-----	765
gi	57529371	ref	NP_001006293.1	-----	758
gi	50838814	ref	NP_001002869.1	-----	776
gi	17510559	ref	NP_490891.1	-----	763
gi	30683736	ref	NP_193396.3	-----	789
gi	115488568	ref	NP_001066771.1	-----	832
gi	124807064	ref	XP_001350899.1	-----	717
		2110.....		