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gi|15218927|ref|NP_176191.1|-----150
gi|115481986|ref|NP_001064586.1|-----150
gi|117168245|ref|NP_057613.4|-----150
gi|114649166|ref|XP_522636.2|-----150
           MQLMGLSLACMRKEVWFKGDREGSWFS-----SWAGRSKDPFRKPSRAQFPLEGLGQMGAGGAA-----150
gi|7656912|ref|NP_056618.1|-----150
gi|118085026|ref|XP_417130.2|-----150
gi|292627610|ref|XP_002666695.1|-----150
gi|145602111|ref|XP_001403448.1|-----150
           --MAGQPPPRPGAPRNSNDDLLLLENDQPVYGGGQRSNVNDDDLRFHNN--DDQAAGRPSVSYDDFVGGGGGRDYTPSPSSSRDTDPDRPETATSRQGPY--MOPFARQYSQTSSELGNRYQYADDDFYF--EDGQSYQHGGGAPR-----150
           --MAAGRPPPPGAP-S--AQHDDLLLDFGNEQFPYGGGQRSTLNDDDLRLRLHSDDAQGAAQPRPSVSYDDFVGGG-----DTIQPTTAPRPTQAPGATGGGGPISPYPDRRLDRHFGTSDLGNRYQYADSDDYFDESTTSYYQHGGAIYF-----150
           MARDVDNKO--NAKRISRDEDE--DEFAGES-----MVGRTLDNPFLEGEDEFDIFGSESQ--YISSSGQNS-----150
           MKPKYFERETQSQRGATHRSTCFPMSGSTKHGDSALFDFVDLDDSYTPD--LRDSPPRRNSPFAVIDSGMD--TSQRTLLPQETIDLSDN--IEND-IENPKN-----150
           --MSGRDKHNEETLFDIDFLDDRYTPEPARPVNDSGSRSGP--IIDSGLDD--LVQMORTGFPEVIDLDDPFRPHDSDIENDLIENPFD-----150
           --MNDRETFPKRKGEDTLDLFDLDDTSHS--GSRKVTNSHANG-----YIFPSSHVLPEETIDLADDDNLENDVHENLDFMNSNHD-----150
           --MSLVYRKLNLFLKGNEDDKVKININGEN-----KRTCNNSVITSKYVTFNEIFLNMYEQFHKLSNV-----150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|15218927|ref|NP_176191.1|-----300
gi|115481986|ref|NP_001064586.1|-----300
gi|117168245|ref|NP_057613.4|-----300
gi|114649166|ref|XP_522636.2|-----300
           LDKALKMSLPRLRSR-----IRSSVGPVRSSTLGYKKAEDEMSRATSVGDQLEAPARTIYLN--QPHLNKFRDNQISTAKYSVLTFLPRFLYEQIR-----300
           LGAPAVPARSPFPARQAASLSPARSLQGSAGAGGSGPGAGLAPAPGAARCVGVGGAGGGAGLCCGGRGGGVSRSQGPVRSSTLGYKKAEDEMSRATSVGDQLEAPARTIYLN--QPHLNKFRDNQISTAKYSVLTFLPRFLYEQIR-----300
           -----MSRATSVGDQLEAPARTIYLN--QSHLNKFRDNQISTAKYSVLTFLPRFLYEQIR-----300
           -----MESMGKNRPVCSPTGYKKAEDEMSGATSSADLDEAPARTIYLN--QPPQSKFRDNQISTAKYSVLTFLPRFLYEQIR-----300
ADDPPQNSRDNAKRNK--VLSMGGGLMGRANMLGMSGGSYSEMDLPLTEPGQQRGGAPGGAATGDAHQPPSQKKSQKFFDMGNFKFGRGKPDSTLG--PRIIHLNPPANAANKVVDNHNVTAKYNFATFLPKFLYEQFS-----300
           PDS--AAARDSARARNS--VLSMGGGLIGRAKMLGMPGEGYSEMDLPLTDPRATAR--VDHSHEPPPPKPAKFD--FKFPGGGKPEDPATLG--PRIIHLNPPANSLNKVVDNHNVTAKYNFATFLPKFLYEQFS-----300
           TNP--FLADRISIEN--PLGSES--KANQLNKQGTNVNHIIEPLRFDNPTQ-----PFSLPPPKNFTFSRIKKIKNLFKKEKQVQVPEDLG--PRQIILN--DYSANHPLHNAVSTCKYSAFTFLPKFLYEQFS-----300
           DR--WSASFADNPNRN--VLPQPSGFNRFMSVKSAVGMGGHKGQFQSFEMNDY--DQNTN-RYESSTRKFDIKVLFNRYILRK-GRTSCKSDPEPTILLNDSASNRFGRDHNHISTTKYNAATFLPKFLYEQFS-----300
           DE--RCQORVLASANRL--SVPPQPSGQRLVGGLRDSVGGRTNSQVSFEMQDY--RPHSGDRYQSRNKFNKALFDHYVLRKPAADTGCAGEPRVIVINERRANGAMGYDGNHISTTKYNAATFLPKFLYEQFS-----300
           DQTSWNANRFDSDAYQPOSRAVKKPPLGFARFGNGLKNAFTFK--RKKGPESFEMNHYN--AVTNNELDDNYLDSRNKFNKILFNRYILRKVNGDAEKGEPVHIHINDSLANSFFGYSDNHISTTKYNAATFLPKFLYEQFS-----300
           YFFFTIGILQVTPQFTANGIPTVFFPLLVLTANAIKDAFEDWNRHKTDRKIENNRMCYG--TVSBEKKIVQEKSNNKNIFFKILKRYFFGNRKCICNENYDEDDMCDDTDTINDVINNYEDNLENTEGTVKKRWDIKAGDIT-----300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|15218927|ref|NP_176191.1|RIANIFFLGISCLSMTP-ISPVSPITINVAPLSMVLLVSLIKEAFEDWKRFDNMSINNTEVIELQDQ--WVSIWPKRLQVDIVKIKKDGFPFADILFMSSTNSDGICVETANLDGETNLKIRKALERWDVIVPEKAYEFKGETICE-----450
gi|115481986|ref|NP_001064586.1|-----450
gi|117168245|ref|NP_057613.4|RAANAFFLFIALLQCPDVSPTGRYTLVPLIILTIAGIKEIVEDFKRHKADNAVKKKIVLNRGM--WHTIMWKEVAVGDIVKVVNGOYLPAADVLLSSSEPOAMCVETANLDGETNLKIRKGLSHADMOTREVLMLKSGTICE-----450
gi|114649166|ref|XP_522636.2|RAANAFFLFIALLQCPDVSPTGRYTLVPLIILTIAGIKEIVEDFKRHKADNAVKKKIVLNRGM--WHTIMWKEVAVGDIVKVVNGOYLPAADVLLSSSEPOAMCVETANLDGETNLKIRKGLSHADMOTREVLMLKSGTICE-----450
gi|7656912|ref|NP_056618.1|RAANAFFLFIALLQCPDVSPTGRYTLVPLIILTIAGIKEIVEDFKRHKADNAVKKKIVLNRGM--WHTIMWKEVAVGDIVKVVNGOYLPAADVLLSSSEPOAMCVETANLDGETNLKIRKGLSHADMOTREVLMLKSGTICE-----450
gi|118085026|ref|XP_417130.2|KAANAFFLFIALLQCPDVSPTGRYTLVPLLFIITVAVIKETIEDYKRHKADNAVKKKIVLNRGM--WQDIVKKEVAVGDIVKVVNGOYHLPADMILIISSSEPOAMCVETANLDGETNLKIRKGLSLASLQREELMKVSGTICE-----450
gi|292627610|ref|XP_002666695.1|-----450
gi|145602111|ref|XP_001403448.1|KFIANIFFLFTAALQCPRLSPTNRYTTIGPLIVLVMVSAKEMVEDYRRKMAKALNMSKARVLRGSS--FEETKWINIAGDIVRVESEEPFPADLVLLASSEPEGLCYIETANLDGETNLKIRKQALPETSHLVSSSELSRLGGRIRSE-----450
gi|85087076|ref|XP_957823.1|KFIANIFFLFTAGLQCPPLSPTNRYTTIGPLAVLLVSAKEMVEDYRRKQADKALNMSKARILRGST--FEETKWINVSVGDIIRVESEEFPPADLVLLASSEPEGLCYIETANLDGETNLKIRKQALPETSSWVSSSELSRLGGRIRSE-----450
gi|19113278|ref|NP_596486.1|KYANLFFLFTAVVQCIPGIPVVRVYTTIGPMLIVLVSAGIKEMEDIKRKKQDQELNESPCYVLOGTG--FVERQWKDVVVGDIVKIVSETFFPADLVLLSSSEPEGLCYIETANLDGETNLKIRKQALPETAGLLKPVGLQSLSGEVKSE-----450
gi|50302485|ref|XP_451177.1|KYANLFFLFTSIIQCVNVPVPTNRYTTIGTLIVLVLSAIVESVEDLKRNSADKELNHSRCDVLDERSGPFVRKKWIDIAVGDIIRVRSEEAIPADLVLLSSSEPEGLCYIETANLDGETNLKIRKQALPETANLDEKALCKLHGRVQSE-----450
gi|45188223|ref|NP_984446.1|KYANLFFLFTSIIQCVNVPVPTNRYTTIGTLIVLVLSAIVESVEDLKRNSADKELNHSRCDVLDERSGPFVIRKKWIDIAVGDIIRVRSEEAIPADLVLLSSSEPEGLCYIETANLDGETNLKIRKQALPETSKILDVRELSAMRGKILSE-----450
gi|6319293|ref|NP_009376.1|KYANLFFLFTSIIQCVPHVSPVPTNRYTTIGTLIVLVLSAMKECIEDIKRANSDELNNTAEIFSEAHDYVEKRWDIRVGDIIIRVSEEPADLVLLSSSEPEGLCYIETANLDGETNLKIRKQALPETAKFIDVKTLMNMGKVVSE-----450
gi|124805991|ref|XP_001350596.1|LCRRFEFFCADILLCTSHKNGIAFVESLLDGETNLVKEANVFLFNILGNDRNAIDNVKNLQGLFSLDKPKNKDLSMYG--TIYFKDKKIDVENIQTQELLKKTTEEIYRKKRSLVDLSKSSAIGSNLGNNSNNSDSEKSLIKNY-----450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 15218927 | ref | NP_176191.1 | **QPNN**SLYFTGNLVVQK---QTLPSPDOLLRRGCSLRNTEYIVGAVVFTGHETKVMNANMAPSKRSTLEKIKLKLIIIFCVLVTCMLIGATGCSIVTDREDKYLGLNSDWEYRN---GLMIGFTFFLLVTLFSSIIPIISLVYSI 600
 gi | 115481986 | ref | NP_001064586.1 | ----- 600
 gi | 117168245 | ref | NP_057613.4 | **GNRHL**YDFTGNLNLDD---KSLVALGPDQILLRGTQLRNTQWVFGIVVYTGHDTKLMQNSTKAPLKRNSVEKVTNVOILLVLFGLILLVVALVSSAGALYWNRSHG-EKNWYIKKMDTT---SDNFGYNLLTFIILYNNLIPISLLVTL 600
 gi | 114649166 | ref | XP_522636.2 | **GNRHL**YDFTGNLNLDD---KSLVALGPDQILLRGTQLRNTQWVFGIVVYTGHDTKLMQNSTKAPLKRNSVEKVTNVOILLVLFGLILLVVALVSSAGALYWNRSHG-EKNWYIKKMDTT---SDNFGYNLLTFIILYNNLIPISLLVTL 600
 gi | 7656912 | ref | NP_056618.1 | **GNRHL**YDFTGNLNLDD---KSSVALGPDQILLRGTQLRNTQWVFGIVVYTGHDSTKLMQNSTKAPLKRNSVEKVTNVOILLVLFGLILLVVALVSSVGGALVFNWNGSHG-GKSWYIKKMDTT---SDNFGYNLLTFIILYNNLIPISLLVTL 600
 gi | 118085026 | ref | XP_417130.2 | **GNRHL**YDFTGNLRLDD---QSPVFPVGPDQILLRGAQLRNTQWVLGIVVYTGFDTKLMQNSTKAPLKRNSVEKVTNMQILLVLFGLILLVVALVSSVGGALLWNRTHG-EVWVWLGSNKML---SVNFGYNLLTFIILYNNLIPISLLVTL 600
 gi | 292627610 | ref | XP_002666695.1 | -----MQILLVLFGLILLVVALVSSVGGALLWNRTHG-EVWVWLGSNKML---SVNFGYNLLTFIILYNNLIPISLLVTL 600
 gi | 145602111 | ref | XP_001403448.1 | **QPNS**SLYTYEATLTMQAGGGEKELPLNPEQLLLRGATLRNTPWLYGVVFTGHETKLMRNAAAPIKRRTKVERQLNLAVLGLVAIILLVLSVCTVGDVLTFRSVPFG-SISVIMLDNATDALEIFKVFRLDMVTWVWLFSAVLPISLFTVTL 600
 gi | 85087076 | ref | XP_957823.1 | **QPNS**SLYTYEATLTMQAGGGEKELPLNPEQLLLRGATLRNTPWVHGIVVFTGHETKLMRNAAAPIKRRTKVERQLNLAVLGLVAIILLVLSVCTVGDVLTFRSVPFG-SISVIMLDNATDALEIFKVFRLDMVTWVWLFSAVLPISLFTVTL 600
 gi | 19113278 | ref | NP_596486.1 | **QPNN**SLYTFDAILKLLP---SDRELPLSPDOLLRGAQLRNTQWVYGVVFTGHESKLMQNTETPIKRRTSVEKQVNSQILFLLCIVFLFCFASLIGALHRSVYGS-ALSVYKYTSNR---AGMFFKGLLTFWILYSNLVPIISLFTVTL 600
 gi | 50302485 | ref | XP_451177.1 | **HPNS**SLYTYEATMLNG---STFPLSPDOMLLRGATLRNTAWIFGLIVFTGHETKLMRNAAATPIKRRTAVERVINMOILALFGVLIIVLALISSGQNVIMTKRDSA-HLGVLYIEGTN---KAGLFFKDLITFWILFSNLVPIISLFTVTL 600
 gi | 45188223 | ref | NP_984446.1 | **QPNT**SLYTYEATMLNHN---NRIPLSPDQILLRGATLRNTVWIFGLIVFTGHETKLMRNAAATPIKRRTAVERVINMOILALFGVLIIVLALISSGQNVIMTKRDSA-HLGVLYIEGTN---KAGLFFKDLITFWILFSNLVPIISLFTVTL 600
 gi | 6319293 | ref | NP_009376.1 | **QPNS**SLYTYEATMLND---RQIPLSPDOMLLRGATLRNTAWIFGLIVFTGHETKLMRNAAATPIKRRTAVERVINMOILALFGVLIIVLALISSGQNVIMTKRDSA-HLGVLYIEGTN---KAGLFFKDLITFWILFSNLVPIISLFTVTL 600
 gi | 124805991 | ref | XP_001350596.1 | **NKDDDD**DDDDENNILKNDNYIRIPFDEKQFVLRGCKLKNIDWIMGIVIVGRETQIQMNSKSKIKKTKLEILTKMIIIVVIQMIICLISAYNNAITVSSSRKNRFRVLPFNLEKAK-KPVIIGIISFFSVMVVICNFVPIISLFTVTL 600
460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 15218927 | ref | NP_176191.1 | **EMIKFI**CSQFINRDLNMYHAEINIP-----ASARTSNLNEELGQV 750
 gi | 115481986 | ref | NP_001064586.1 | ----- 750
 gi | 117168245 | ref | NP_057613.4 | **EVVKY**TQA-LFINWDTDMYIIGNDTF-----AMARTSNLNEELGQV 750
 gi | 114649166 | ref | XP_522636.2 | **EVVKY**TQA-LFINWDTDMYIIGNDTF-----AMARTSNLNEELGQV 750
 gi | 7656912 | ref | NP_056618.1 | **EVVKY**TQA-LFINWDMMYIENDTF-----AMARTSNLNEELGQV 750
 gi | 118085026 | ref | XP_417130.2 | **EVVKY**TQA-LFINWDMMYIPEDTF-----AMARTSNLNEELGQV 750
 gi | 292627610 | ref | XP_002666695.1 | **EVVKY**TQA-LFINWDMMYIPEDTF-----AMARTSNLNEELGQV 750
 gi | 145602111 | ref | XP_001403448.1 | **EVVKY**WHG-ILINDDLDMYHDKEDTF-----ANCRTSSLVEELGMV 750
 gi | 85087076 | ref | XP_957823.1 | **EMVKY**WHG-ILINDDLDMYDVNDTF-----ANCRTSSLVEELGMV 750
 gi | 19113278 | ref | NP_596486.1 | **ELVRY**IQA-QLISSDDLMYNEEDTF-----AACRTSSLVEELGQV 750
 gi | 50302485 | ref | XP_451177.1 | **EMIKY**IQA-YMIGSDLLDLYHEESDTP-----TVVRTSSLVEELGQI 750
 gi | 45188223 | ref | NP_984446.1 | **EMIKY**IQA-YMIASDLDLDFHEESNMF-----TVVRTSSLVEELGQI 750
 gi | 6319293 | ref | NP_009376.1 | **ELIKY**IQA-FMIGSDLLDLYYKEDTF-----TVVRTSSLVEELGQI 750
 gi | 124805991 | ref | XP_001350596.1 | **SFVKV**VQAYFISCDKNMIHKVQADVPFSGEQKEIPNIPKDDISSDADVIKRMRTKRIADSSLLHIDENOTEEDNMDMKSDCIAFKNNSSHONINGNKNQYSSSSLGIIISNAPKREISSRVISFKDSKEKNYVFNNAVPTSSSLVEELGQI 750
610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 15218927 | ref | NP_176191.1 | **EYIF**SDKTGTLTRNLMFEFKCSIGGVSYCGVTEIEKGIAQRHGLKVQERQRSIGAIREFKGFNDDPRLRMGAWNEP-NPDLCKELFRCLAICHTVLPPEGDESPEKIVYQAAAPDEAALVTAAKNFGFFFYRRTPTMVVRESHVVKMG 900
 gi | 115481986 | ref | NP_001064586.1 | ----- 900
 gi | 117168245 | ref | NP_057613.4 | **KMLF**SDKTGTLTRNIMNFKKCSIAGVYGHFPELARE-----PSDDFCRMPPPCSDSCDFDDPRLLNIEDRHP-TAPCIQEFLLAVCHTVVPE--KDGDNIIYQASSPDEAALVKGAKKLGVFVFTARTPF-----SVIIEA 900
 gi | 114649166 | ref | XP_522636.2 | **KMLF**SDKTGTLTRNIMNFKKCSIAGVYGHFPELARE-----PSDDFCRMPPPCSDSCDFDDPRLLNIEDRHP-TAPCIQEFLLAVCHTVVPE--KDGDNIIYQASSPDEAALVKGAKKLGVFVFTARTPF-----SVIIEA 900
 gi | 7656912 | ref | NP_056618.1 | **KMLF**SDKTGTLTRNIMNFKKCSIAGVYGHFPELARE-----QSDDFCRMTSCTNDSCDFNDPRLLNIEDQHP-TAPCIQEFLLAVCHTVVPE--KDGDEIIYQASSPDEAALVKGAKKLGVFVFTGRTFY-----SVIIEA 900
 gi | 118085026 | ref | XP_417130.2 | **KMLF**SDKTGTLTRNIMNFKKCSIAGVYGHFPELARE-----RSSEDFSQLPPTSSECFDDPRLLNIEDNHP-TAVHIQEFLLAVCHTVVPE--RQGNKIIYQASSPDEALVKGAKKLGVFVFTGRTPH-----SVIIDA 900
 gi | 292627610 | ref | XP_002666695.1 | **KMLF**SDKTGTLTRNIMNFKKCSIAGVYGHFPELARE-----RMEDFSHLPSISHSNTEFDDPALIQIEKNHP-TSPQICEFLIMAVCHTVVPE--REDNQIIYQASSPDEALVKGAKKLGVFVFTARTPH-----SVIIEA 900
 gi | 145602111 | ref | XP_001403448.1 | **EYVFS**DKTGTLTRNMEFEKQSSIAGIMYGEDIPEDRR-ANVQDGV-----EIGIHDFQ--LAQNLKTHKT--APAIEHFLALLAICHTVPERDEKSDRIKYQAAAPDEGALVEGAALGVKVFVARKPR-----AVIIEV 900
 gi | 85087076 | ref | XP_957823.1 | **EYVFS**DKTGTLTRNMEFEKQSSIAGIMYADKVPEDRI-PSGEDG-----EDGIDDFQ--LQNLKESHQS--AQVIDQFLLLAICHTVPIPEQAEQGS-IKYQAAAPDEGALVQGAADLGVKVFVARKPR-----AVIIEA 900
 gi | 19113278 | ref | NP_596486.1 | **GVYFS**DKTGTLTRNMEFEKQSSIAGVAYADVIPEDRR-FISEDL-----SDMYIYDFDT--LKENLKHSEN--ASLIHFLLVLSICHTVPIPEYDESTNSIKYQASSPDEGALVGAASIGYKFLARKPH-----LVTVSI 900
 gi | 50302485 | ref | XP_451177.1 | **EYIFS**DKTGTLTRNMEFEKSVSIAGRCYIETIPEDRR-AIVEDG-----IEIGFHSFES--LKDKMTPDEDEAGVIEFLLLAICHTVPIPETQSDGT-IKYQAAAPDEGALVQGAADLGVKVFDIRRPNV-----SIS-TP 900
 gi | 45188223 | ref | NP_984446.1 | **EYIFS**DKTGTLTRNMEFEKSCSIAGRCYIQSIPEDKR-AAFDEG-----IEVGYRTYDD--MHELLHTPGSGDGAIDEFLLLAICHTVPIPEQENGSI-KYQAAAPDEGALVQGAADLGVKVFDIRRPNV-----TILRED 900
 gi | 6319293 | ref | NP_009376.1 | **EYIFS**DKTGTLTRNMEFEKSCSIAGRCYIDKIPEDKT-AIVEDG-----IEVGYRKFDD--LKKKLNDSDEPSLIINDFLLAICHTVPIPEQSDGS-IKYQAAAPDEGALVQGAADLGVKVFDIRRPNV-----LVLLRE 900
 gi | 124805991 | ref | XP_001350596.1 | **EYIFS**DKTGTLTRNMEFEKCAINGISYKGLTEIKRNLKKNLEIPEVEPTMKFKKKTPTVNIINDLINHLKDPNHFVNVLINFFLHLAINHAVICE-KDKEGVTTSSSPDEALVNAAKHFDITELVREG-----KYGISI 900
760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi|15218927|ref|NP_176191.1| KI DVAVEILLNVLEFNSRKRQSVVCRFPDGG-----RLVLYCKG----- 1050
gi|115481986|ref|NP_001064586.1| -----NSTRKRQSVVCRFPNG-----RLVLYCKG----- 1050
gi|117168245|ref|NP_057613.4| MGQEQTFGILNVLEFSDRKRMSVIVRTPSG-----RLRLYCKG----- 1050
gi|114649166|ref|XP_522636.2| MGQEQTFGILNVLEFSDRKRMSVIVRTPSG-----RLRLYCKG----- 1050
gi|7656912|ref|NP_056618.1| MGQEQTFGILNVLEFSDRKRMSVIVRTPSG-----QLRLYCKG----- 1050
gi|118085026|ref|XP_417130.2| LGKEKTFEILLNVLEFSDRKRMSVIVRTPAG-----QLRLYCKG----- 1050
gi|292627610|ref|XP_002666695.1| RGKEQTYELLNVLEFSDRKRMSVIVRTPAG-----QLRLYCKG----- 1050
gi|145602111|ref|XP_001403448.1| EGQEFYELLAVCFEFSNSTRKRMSIIVRCPDGG-----KIRVYCKG----- 1050
gi|85087076|ref|XP_957823.1| NGQOLEVELLAVCFEFSNSTRKRMSIIVRCPDGG-----KVRVYCKG----- 1050
gi|19113278|ref|NP_596486.1| FGKDESYELLHICFNFSTRKRMSIIVRCPDGG-----KIRLYVKG----- 1050
gi|50302485|ref|XP_451177.1| FSEOLEYQLLNICEFNSRKRMSAIFRMPDGG-----SIRLFCKG----- 1050
gi|45188223|ref|NP_984446.1| ITEEVVYELLNICEFNSRKRMSAIFRFPDGG-----SIRLLCKG----- 1050
gi|6319293|ref|NP_009376.1| GEEKEYQLLNICEFNSRKRMSAIFRFPDGG-----SIRLFCKG----- 1050
gi|124805991|ref|XP_001350596.1| FGKIYEIDLAALIEFTSKRMSVIVRCPVPI NPDYVHPDAKSSNMDDKKNMDDHLVVGKNEEKEDDLLNVVPPKKAHSLKLNNNNNNNNNNNIRIDNLYDDKNNFNILYNHNEGRUPEVILCKNSKSKIMLFCCKG----- 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi|15218927|ref|NP_176191.1| ---ADNVIFERLANGMDDVRKVYREHLEHFSSGLRLNLCAYKDLNPEYDSWNEKFIQAKSLRD-REKKLDEVAELIEKDLILLIGSAIEDKIQEGVPTCETLSRAGIKIWLVTGDKMETAINIAYACNLINEMKQFVLSSETDA 1200
gi|115481986|ref|NP_001064586.1| ---ADNVVYERLDAGNNDIKKISREHLQFSGAGRLNLCAYRDLREYYSWNEKFIQAKSLRD-RDKKLEVAELIEKDLVLVGCIAIEDKIQEGVPACQTLAAGIKIWLVTGDKMETAINIAYACNLINEMKQFVLSSETDV 1200
gi|117168245|ref|NP_057613.4| ---ADNVIFERLSKD-SKYMEETLCHLEYFATEGLRLNLCVAYADLSENEYEBEWLVKYQEAETILKDR-RAORLEECYETIEKNLLLLGATAIEDRLQAGVPETIATLLKAEIKIWLVTGDKMETAINIGYSCRLVSONMALILLKEDS-- 1200
gi|114649166|ref|XP_522636.2| ---ADNVIFERLSKD-SKYMEETLCHLEYFATEGLRLNLCVAYADLSENEYEBEWLVKYQEAETILKDR-RAORLEECYETIEKNLLLLGATAIEDRLQAGVPETIATLLKAEIKIWLVTGDKMETAINIGYSCRLVSONMALILLKEDS-- 1200
gi|7656912|ref|NP_056618.1| ---ADNVIFERLSKD-SKYMEETLCHLEYFATEGLRLNLCVAYADLSENEYEBEWLVKYQEAETILKDR-RAORLEECYETIEKNLLLLGATAIEDRLQAGVPETIATLLKAEIKIWLVTGDKMETAINIGYSCRLVSONMALILLKEDS-- 1200
gi|118085026|ref|XP_417130.2| ---ADNVIFERLSKD-SQYMEQTLCHLEYFATEGLRLNLCVAYADLSENYRRLNLYVNEASILLKDR-RTQKLEECYETIEKNLLLLGATAIEDRLQAGVPETIATLMKAEIKIWLVTGDKMETAINIGYSCRLVSONMALILLKEDS-- 1200
gi|292627610|ref|XP_002666695.1| IDVLDQNVIFERLNVT-SQYKELTVAHLQFQFATEGLRLNLCVAYADLSENYRRLNLYVNEASILLKDR-RAQKLEECYETIEKNLLLLGATAIEDRLQAGVPETIATLMRADIKIWLVTGDKMETAINIGYSCRLVSONMALILLKEDS-- 1200
gi|145602111|ref|XP_001403448.1| ---ADTVILERLNES-NPHVEVTLCHLEBYASEGLRLNLCIAMREVDPHEFTWMAVYKCAQNTVSGNRAEELDKAAELIEHDFYLLGATAIEDRLQAGVPETIHTLQAGIKVWVLTGDRQETAINIGMSCKLLSEDMMLLIVNEET-- 1200
gi|85087076|ref|XP_957823.1| ---ADTVILERLNDQ-NPHVDAATLRHLEBYASEGLRLNLCIAMREVDPHEFTWMAVYKCAQNTVSGNRAEELDKAAELIEHDFYLLGATAIEDRLQAGVPETIHTLQAGIKVWVLTGDRQETAINIGMSCKLLSEDMMLLIVNEET-- 1200
gi|19113278|ref|NP_596486.1| ---ADTVIMERLASD-NPVLGTHIHHLLEDYATVGLRLNLCIAMREVDPHEFTWMAVYKCAQNTVSGNRAEELDKAAELIEHDFYLLGATAIEDRLQAGVPETIHTLQAGIKIWLVTGDRQETAINIGMSCKLLSEDMMLLIVNEET-- 1200
gi|50302485|ref|XP_451177.1| ---ADTVILERLDESENPVVSRLRHLLEDYAAEGLRLNLCIASRTIPESEYEWKSLYDAAATMHN-RSEELDKVAEMIEKGLVLLGATAIEDKLDQGVPEIHTLQAGIKVWVLTGDRQETAINIGMSCKLLSEDMMLLIVNEET-- 1200
gi|45188223|ref|NP_984446.1| ---ADTVILERLDAATSNPVVAATLRHLEDYAAEGLRLNLCIASRTIPESEYEWKSLYDAAATMHN-RSEELDKVAEMIEKGLVLLGATAIEDKLDQGVPEIHTLQAGIKVWVLTGDRQETAINIGMSCKLLSEDMMLLIVNEET-- 1200
gi|6319293|ref|NP_009376.1| ---AGSIIILKKLAKR-TDVEETIIEHMETYADEGLRLNLCIAQRELSSEFAWYHLYKAEALSISKD-REKLEESVAEYIENDLILQGITIETEDKIQEGVSSITIEDLRMAGITHIWLVTGDKMETAINIGIAANLIDNYSEQFYITEBYTE 1200
gi|124805991|ref|XP_001350596.1|1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi|15218927|ref|NP_176191.1| IR-----EAERGDQVEIARVIKEEVKREIKKSLLEEAQHSLEHTVAGPK-LSLVIDGKCLMVALDPSLRVMLLSLSINCTSVCVRVSPLOKAVVTSIVRKG-AQKITLSIGDGDVSMIQAAH 1350
gi|115481986|ref|NP_001064586.1| IR-----EAERGDQVEIARVIKESVRSQSLKSYHEEARGSLISTVPGQR-LALIIDGKCLMVALDPTLRVDLLGLSLIHSVVCVRVSPLOKAVVSLVKKG-AHKITLSIGDGDVSMIQAAH 1350
gi|117168245|ref|NP_057613.4| ---LDATRAAITQHCTDLGN---LLGKENDVALIIDGHTLKVYLSFEVRRSFLDLALSCKAVICCRVSPLOKSEIVDVVKKR-VKAITLAIAGDGDVSMIQAAH 1350
gi|114649166|ref|XP_522636.2| ---LDATRAAITQHCTDLGN---LLGKENDVALIIDGHTLKVYLSFEVRRSFLDLALSCKAVICCRVSPLOKSEIVDVVKKR-VKAITLAIAGDGDVSMIQAAH 1350
gi|7656912|ref|NP_056618.1| ---LDATRAAITQHCTDLGN---LLGKENDVALIIDGHTLKVYLSFEVRRSFLDLALSCKAVICCRVSPLOKSEIVDVVKKR-VKAITLAIAGDGDVSMIQAAH 1350
gi|118085026|ref|XP_417130.2| ---LDATRAAITQHCTDLGN---LLGKENDVALIIDGHTLKVYLSFEVRRSFLDLALSCKAVICCRVSPLOKSEIVDVVKKR-VKAITLAIAGDGDVSMIQAAH 1350
gi|292627610|ref|XP_002666695.1| ---LDATRAAITQHCTDLGN---LLGKENDVALIIDGHTLKVYLSFEVRRSFLDLALSCKAVICCRVSPLOKSEIVDVVKKR-VKAITLAIAGDGDVSMIQAAH 1350
gi|145602111|ref|XP_001403448.1| AAATRDNIQKKLEAIRTQGDGTTEMETLALVIDGKSLTYALEPELDRMFLDLAIMCKAVICCRVSPLOKALVVKLVKKYDKESITLAIAGDGDVSMIQAAH 1350
gi|85087076|ref|XP_957823.1| AEATRDNIQKKLEAIRTQGDGTTEMETLALVIDGKSLTYALEPELDRMFLDLAIMCKAVICCRVSPLOKALVVKLVKKYDKESITLAIAGDGDVSMIQAAH 1350
gi|19113278|ref|NP_596486.1| KEATAESVMAKLSSIIYRNEATIGNVESMALVIDGVSILTYALDFSLERRFFELASLCAVVICCRVSPLOKALIVKMKRRN-TGEVLLAIAGDGDVSMIQAAH 1350
gi|50302485|ref|XP_451177.1| KEDTRNLQSKLNAIESHQISQQDMNLSLALVIDGKSLTYALEPELDRMFLDLAIMCKAVICCRVSPLOKALVVKLVKKR-TSSLLAIAGDGDVSMIQAAH 1350
gi|45188223|ref|NP_984446.1| KESTRNLLIDKLRANDHQISQQDMNLSLALVIDGKSLTYALEPELDRMFLDLAIMCKAVICCRVSPLOKALVVKLVKKR-TSSLLAIAGDGDVSMIQAAH 1350
gi|6319293|ref|NP_009376.1| RDTTERNLLEKINALNEHQISTHDMKSLALVIDGKSLTYALEPELDRMFLDLAIMCKAVICCRVSPLOKALVVKLVKKR-TSSLLAIAGDGDVSMIQAAH 1350
gi|124805991|ref|XP_001350596.1| SEEAALKKIDDDILMVEKSLNIPHYMFDDENNVEDEKRRKTFFRNNEIKNFCAKKNKSGLLNPDYKNLINTLNLVVLVDGSDVIDLLELSEKMERKFFYLADKSSVICGRVSPYQKAVLSANRL-LNKITLAIAGDGDVSMIQAAH 1350
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



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gi | 15218927 | ref | NP_176191.1 | VGIISGMEGMOAVMASDFALIAQFRFLTDLLLVHGRWSYLRLCKVITFYFFYKNTLFTLQFWFRTGFSGRFYDDWFOQLFNVVFALPVLVILGLFEKDVASLKKRYPFLYREGIRNSFFKWRVVAWVAISAVVQLSLVCLYFVITSS 1500
gi | 115481986 | ref | NP_001064586.1 | VGIISGMEGMOAVMASDFALIAQFRFLTDLLLVHGRWSYLRLCKVITFYFFYKNTLFTLQFWFRTGFSGRFYDDWFOQLFNVVFALPVLVILGLFEKDVASLKKRYPFLYREGIRNSFFKWRVVAWVAISAVVQLSLVCLYFVITSS 1500
gi | 117168245 | ref | NP_057613.4 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 114649166 | ref | XP_522636.2 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 7656912 | ref | NP_056618.1 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 118085026 | ref | XP_417130.2 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 292627610 | ref | XP_002666695.1 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 145602111 | ref | XP_001403448.1 | VGVGISGNEGMOAANNNDYAIAQFSYLEKLLLVHGAWSYNRVTKCILCYFYKVVLYIIEELWFAFVNGFSGOILFERWCIGLYNVIFATLPPFTLGFIFERSCQESMLRFPOLYKRTONAEFGNTKVFVGHICINALVHSLILFWFPMKAL 1500
gi | 85087076 | ref | XP_957823.1 | IGVGISGMEGLQAARSADVSIAQFRFLRLKLLLVHGAWSYHRVSKTILFSFYKNTLFTLQFWFRTGFSGEVYIESWTLFSFNVEFTVLPPLALGILDQFVSARLLDRYPOLYNLGNORNTFFKRVFGEWIINAVYHSLILVGGCLFV 1500
gi | 19113278 | ref | NP_596486.1 | VGVGISGMEGLQAARSADVSIAQFRFLRLKLLLVHGSWCYQRLSKLILYSFYKNTALYMQFVYAFNAFSGOVIFESWSISLNVNLTLPVPIVIGIFDQFVSAGQLFQYPLYQLGORSFENLKRFRWSIITNGFYHSLILFLCSIAFV 1500
gi | 50302485 | ref | XP_451177.1 | VGVGISGMEGMOAARSADFAIGQFRFLRLKLLLVHGSWSYQRISLAILYSFYKNTALYMQFVYAFNAFSGOVIFESWSISLNVNLTLPVPIVIGIFDQFVSAGQLFQYPLYQLGORSFENLKRFRWSIITNGFYHSLILFLCSIAFV 1500
gi | 45188223 | ref | NP_984446.1 | VGVGISGMEGMOAARSADFAIGQFRFLRLKLLLVHGSWSYQRISLAILYSFYKNTALYMQFVYAFNAFSGOVIFESWSISLNVNLTLPVPIVIGIFDQFVSAGQLFQYPLYQLGORSFENLKRFRWSIITNGFYHSLILFLCSIAFV 1500
gi | 6319293 | ref | NP_009376.1 | VGVGISGMEGMOAARSADIALGQFRFLKLLLVHGSWSYQRISVAILYSFYKNTALYMQFVYAFNAFSGOVIFESWSISLNVNLTLPVPIVIGIFDQFVSAGQLFQYPLYQLGORSFENLKRFRWSIITNGFYHSLILFLCSIAFV 1500
gi | 124805991 | ref | XP_001350596.1 | IGVGISGMEGLQAARSADVSIAQFRFLKLLLVHGRLSYRRISKLIVVMFYKNTLVLIFFLFIQGISLISYSGOKIYFELLHLFVNLFTALPVVIVHAVLDQDISLNTAMEKENLYKLGIIHYYFNIRTFISVWVMSLFGS VVFLIPLIYFL 1500
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500

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gi | 15218927 | ref | NP_176191.1 | FG--AVNLSGKVFGLWDVSTMVTFCLVIAVNRILLMNSLRWHYLVGGSLANLVFAFYVCGIMTDRHNSNVFVYIVLMSLFYFVFTLLLVPIVSLGDFIFCGVVERFFPYDYQIVQELRHESDASKADQLEVENELTPOEAR 1650
gi | 115481986 | ref | NP_001064586.1 | RY--GHGSSGKILGLWDVSTMAFTCVVVNLRLLMSCNSTRWHYLSVAGSITAWFMFIFYLSAIMTSDFRQENVFVYIVLMSLFFYVFTLLLVPIVSLGDFIFCGVVERFFPYDYQIVQELRHESDASKADQLEVENELTPOEAR 1650
gi | 117168245 | ref | NP_057613.4 | EH-DTVLRSGHADYLFVGNIVTYVVVVVCLKAGLETAWTKFSLHAVGSMLELWLVFFGIYSITWPTTIPADDMRGQATMVLSAHFWLGLFLVPTACLIEDVAVRAAKHTCKKTLLEEQBELTKSRVLGKAVLRDSNGKR--LNER 1650
gi | 114649166 | ref | XP_522636.2 | EH-DTVLRSGHADYLFVGNIVTYVVVVVCLKAGLETAWTKFSLHAVGSMLELWLVFFGIYSITWPTTIPADDMRGQATMVLSAHFWLGLFLVPTACLIEDVAVRAAKHTCKKTLLEEQBELTKSRVLGKAVLRDSNGKR--LNER 1650
gi | 7656912 | ref | NP_056618.1 | EH-DTVLRSGHADYLFVGNIVTYVVVVVCLKAGLETAWTKFSLHAVGSMLELWLVFFGIYSITWPTTIPADDMRGQATMVLSAHFWLGLFLVPTACLIEDVAVRAAKHTCKKTLLEEQBELTKSRVGMKAVLRDSNGKR--MNER 1650
gi | 118085026 | ref | XP_417130.2 | EH-DAVFNGOGIDYLFVGNIVTYVVVVVCLKAGLETAWTKFSLHAVGSMLELWLVFFGIYSITWPTTIPADDMRGQATMVLSAHFWLGLFLVPTACLIEDVAVRAAKHTCKKTLLEEQBELTKSRVGMKAVLRDSNGKR--MNER 1650
gi | 292627610 | ref | XP_002666695.1 | EH-DTPFDNNSVDYLFVGNIVTYVVVVVCLKAGLETAWTKFSLHAVGSMLELWLVFFGIYSITWPTTIPADDMRGQATMVLSAHFWLGLFLVPTACLIEDVAVRAAKHTCKKTLLEEQBELTKSRVGMKAVLRDSNGKR--MNER 1650
gi | 145602111 | ref | XP_001403448.1 | RR-SSPNKRVIVNVVIFVYASVFPFRFNISIEYDGLVPLRFPSEAVFVQVQLVPLVLCCLLRDVAWVYAKRMVPEAVHHIQEIQKYNIDYRPRMDQFQKAI--RKVR 1650
gi | 85087076 | ref | XP_957823.1 | LN-DGPOGDGFPGGKVVWGTAMYGAVLLVGLKAAALVNNWTKYHVAIAPGSMFAWILFVAVYGEVAPKLNISVEYFGVPLRFTSPFIWQMPPLAIIICLLRDFAWKFSKRLWRPEAVHHIQEIQKYNIDYRPRMDQFQKAI--RKVR 1650
gi | 19113278 | ref | NP_596486.1 | YF-DGNKDGSLASHWVWGTLLVAAIILAVLGAALINHWTKYTVIAITLGSFLLNIVFMPYIAVAAPAIIGFSKEYYGIIPHLVGNLKFVWASLLVLPPTIALLRDVFVWVYSSRMVPEAVHHIQEIQKYNIDYRPRMDQFQKAI--RKVR 1650
gi | 50302485 | ref | XP_451177.1 | RYGNCLNMGCEADHWVWGVGVIYTSIIIVLGAALISQWTKFTLVAIPGSLVIVLWLLFFPYSVAVFRVNVSKYVYGIIGHYVGSATPWLMLCIVLVPFALLRDFVWVYKRYRYSPESHVVOEMKYNISDYRPRMDQFQKAI--RKVR 1650
gi | 45188223 | ref | NP_984446.1 | RYGAAGAMHGEADHWVWGVVAIQPSSIIIVLGAALINHWTKFTLVAIPGSLVIVLWLLFFPIYAYLLPGLNVSKYVYGVVSHVYGSFTFWAMCVLVPFALLRDLWVYKRYRYSPESHVVOEMKYNISDYRPRMDQFQKAI--RKVR 1650
gi | 6319293 | ref | NP_009376.1 | RYGFALNMHGEADHWVWGVVYVTHSVIIVLGAALVNNWTKFTLVAIPGSLVIVLWLLFFPIYASIFPHANISREYVGVVKTYSVGSVWTLVIVLPIFALVRDFLWVYKRYRYSPESHVVOEMKYNISDYRPRMDQFQKAI--RKVR 1650
gi | 124805991 | ref | XP_001350596.1 | SYNYNPTSDGIPYDIWVGCATYFLTVLIVNFKILFEYYINLIPISGIALSIFSVLLVITAFSEMCVGS--IHLIGTVLVVQSLRFVWLVVILGLFALLRDFVYKRYRYSPESHVVOEMKYNISDYRPRMDQFQKAI--KDD 1650
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650

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gi | 15218927 | ref | NP_176191.1 | SVAISQLPREL-----SKHTGFADSPGYESFFASQLGIYAPQKAWDVARRASMRSRPKVPKK----- 1762
gi | 115481986 | ref | NP_001064586.1 | SVAISMLPRES-----SKHTGFADSPGYESFFASQOQGVVPHKVDVARRASMKQRKTEGGS----- 1762
gi | 117168245 | ref | NP_057613.4 | DRLLKRLGRKTPPLFRGSLQOQGVPHGYAFSQ--EEHGAVSQEEVIRAYDTTKKSRKK----- 1762
gi | 114649166 | ref | XP_522636.2 | DRLLKRLGRKTPPLFRGSLQOQGVPHGYAFSQ--EEHGAVSQEEVIRAYDTTKKSRKK----- 1762
gi | 7656912 | ref | NP_056618.1 | DRLLKRLSRKTPPLFRGSLQOQGVPHGYAFSQ--EEHGAVSQEEVIRAYDTTKKSRKK----- 1762
gi | 118085026 | ref | XP_417130.2 | DRLLKRLGRKTPPLFRGSLQOQGVPHGYAFSQ--EEHGAVSQEEVIRAYDTTKKSRKK----- 1762
gi | 292627610 | ref | XP_002666695.1 | AALLTRVFRKTPPSVGRSNVQQTVSHGYAFSQ--EEHGAVSQEEVIRAYDTTKRQPSL----- 1762
gi | 145602111 | ref | XP_001403448.1 | --QVORMRKQR-----GYAFSQ-ADE--SOTRVLQAYDTTQNRGRYGEASSRGR----- 1762
gi | 85087076 | ref | XP_957823.1 | --QVORMRKQR-----GYAFSQ-ADE--SOTRVLQAYDTTQNRGRYGEASSRPNQ----- 1762
gi | 19113278 | ref | NP_596486.1 | --QVORMRKQR-----GYAFSQ-GEE--DQSRILLDAYDTTTRGAVGEMR----- 1762
gi | 50302485 | ref | XP_451177.1 | --QVORMKQR-----GFASFQ-SEEG--GQDRILRIMYDTTLKRGVHGEADASLNPFDTP-----AQVEPSSNVGLRGSFESTNPKVDV----- 1762
gi | 45188223 | ref | NP_984446.1 | --QVORMKQR-----GFASFQ-SEEA--GQDRIVRMYDTTKRGTGELQDPSMNPFKDL----- 1762
gi | 6319293 | ref | NP_009376.1 | --QVORMKQR-----GFASFQ-AEEG--GQEKIVRMYDTTKRGTGELQDASANPFNDNGLGNDPESAEPTIENPFADGNQENRFSSSRDDISFDI----- 1762
gi | 124805991 | ref | XP_001350596.1 | DIRIEKRS-----LGVAFSE-----ADPACIQILIRKQDNMI----- 1762
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760..

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