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gi | 45552723 | ref | NP_995886.1 | -----MQAAAAMEEINNATITIEQPIALINGEQEVANEQQPSSPTSVATPTTSG-----GTGNATPAFVYDLPALPANTSAQSQSGAGS---TL-ARVTSQK-----THI 97
gi | 158294225 | ref | XP_001237663.2 | -----MEDSINAMGMDQ-----OOHGAAAYENNGPAPATP-----CYDDLFPALPESEPPRFNSTLS---ATNMRVGSVV-----TOV 71
gi | 4885409 | ref | NP_005327.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 114584294 | ref | XP_001161053.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 19527028 | ref | NP_598569.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 25282449 | ref | NP_742036.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 73994293 | ref | XP_534628.2 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 119930773 | ref | XP_001256511.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 79
gi | 45384156 | ref | NP_990427.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 78
gi | 41393109 | ref | NP_958882.1 | -----MSSVAVLTOESFAEHRGLVPOQIKVAT-----LNSSEEDPPP-----TYKDAFPPLPEKAACLESAGEPAGAWNKIRPIKASVI-----TOV 82
gi | 17531677 | ref | NP_496136.1 | -----MDNGHIEETINNVIEDPANGGAVMS-----FSYASDFPTLPDAAPASAPLAKQTHVWRP---TLSKSEV-----NTI 64
gi | 6322381 | ref | NP_012455.1 | -----MSEEQTAIDSPSTVEGSEVETVTITIDSPSTASTIAATAEEHP-----OLEKKPTPLPSLKDPLSLGSAAFAN---VKVSWGNPMKPAVSNFSPSPSPAPSLITGLG-----AKRM 104
gi | 45184647 | ref | NP_982365.1 | -----MESQAAVEEPQHSVVIETPTTAESSETPVADTATGAEPEGAGC-----AAVVPKRMPTRADFPPLSS-VIFET---KQVWGNPMKPESSQASPPSPG---FVSGG-----AKPM 102
gi | 50306403 | ref | XP_453175.1 | -----MSEITPDVAEDYSQIVVDTPSSADSSKLAGQTIHQTEKSNNG-----EEAATAPAVKVLFPRLGGNAASASGNASVWGSILKSGSSVNVSLSLHGKNGRASG---GSAKPL 107
gi | 39977187 | ref | XP_369981.1 | -----MSSAALADRVDLDQSTSLADQLRQKHTVTIEDAEDPDLVPTLTKQKSEYCG-----QSKSLDKSHELFPDLGGPKKANS---GVAPITWNAKPTIDGNVHGNCANGGSESKS---GPP----- 110
gi | 32405206 | ref | XP_323216.1 | -----MADSTEQAAAQLLQCHLETASNAGSSHRVLEVEVEDDHLKHPVSSSETPAAP-----KPKPTLTDQSRBELFPELGGPKPKAS---VVAFTWCAKSNNTNGS---SNGAAPANGTQCSAPPSPGVSTPIGSGRGGPGPH 129
gi | 19075606 | ref | NP_588106.1 | MDSYDFOKLINDENLQCTESQVPSGSKSASTNGLLSAASSAAGSSFLPTPSAILQQKHENAQGGKKNNSKFSKPAIDVHSEDAPFTLLSKLGPSPKTRIVSVWRKASNTSVAGSDSVSRDKIFFASR-----ASTTK 137
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 45552723 | ref | NP_995886.1 | VHVPCERKSTSEK-----FGESEKRI-----CQIITKEGQAQIEIVSGKNIS-----LTFLLIKGQSELLDARRKILMGFSQAAROVTVPREHFRVILKGGQRLREIERTV---AATRINIP 206
gi | 158294225 | ref | XP_001237663.2 | FIVASGERK-YDSK-----FGESESLR-----CQAIMKEGNAHIEISSGKDS-----LTFLLVTKGVQEVMEARRKILVHFQTAASKTINIPREHHRWILKGGKERLRELERTH---AATKINVP 179
gi | 4885409 | ref | NP_005327.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 114584294 | ref | XP_001161053.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 19527028 | ref | NP_598569.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 25282449 | ref | NP_742036.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 73994293 | ref | XP_534628.2 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 119930773 | ref | XP_001256511.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLEIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKDIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 188
gi | 45384156 | ref | NP_990427.1 | FHVPLEERKYMNQ-----FGEEOAKI-----CLDIMORGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKEIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 187
gi | 41393109 | ref | NP_958882.1 | FHVPLEERKYMNQ-----FGEEOAKV-----CLDIMHKGGAHLELSLAKDQG-----LSIMVSGKLDVAMKARKEIVARLQTAASATVAIPKEHHRFVIGKNGEKIQDLELKT---AATKIQIP 191
gi | 17531677 | ref | NP_496136.1 | FRLASDERSNKVKFSF-----GSTSESKK-----AQAIATAKTRITELSESKDGE-----LTVVVGGERAKAEERARIRLRLQTAASREIDIPKDHGRLIGKEGALLRNLBAET---NCRITQIPN 173
gi | 6322381 | ref | NP_012455.1 | RSKNICEAFTLQLSLSITKPELSRI-----VQSVKKNHDVSVESTLSKNAR-----TFLVSGVAANVHEAKRELVKLTKPINAIVIEVPSCKCAIIGSGGRTIREISDAY---EVKINVSKEVNVENS 222
gi | 45184647 | ref | NP_982365.1 | RSKTMOEAFSLDLQVTTISKAFESKF-----VQSVKQSHSVSISTLSKLSR-----TFLITGSPITNVNAKRELVKLTKPYNVVIQVPSKIVSIIIGPGGRMIREITNAAGGIKIDIAKTAEDAY 221
gi | 50306403 | ref | XP_453175.1 | RSRNICEVFSLLDLDAQVQITKTFSSFI-----VQSVKQKYDVSVESTLSKTSR-----TFLISGSSDKIGLAKRELVKLTKPYNVNFVPSKIRSAIIGSGGKTRASDAA---GVKIVVPKEVDEVD 225
gi | 39977187 | ref | XP_369981.1 | LSIPIGRNVAVHLLPEQVMPRLKRP-----LPDILKDLNRKRANVSMVTPNGLRLEFATGPSDVANQALRDVQIGAKQIVTVSVPSVPHIIGKQGAALKALERT---GARIQLPKDNNAQF 232
gi | 32405206 | ref | XP_323216.1 | LSIPIGRNVETMLLDPHILPRTLKRPP-----LPDILKDLNRKRANVSMHALNGQLRFDAVGPQEHAAQALKDLVNIIGKQNIIVQIPSSARAHILKGGSTIKAIQEKI---GARIQLKRADESQF 232
gi | 19075606 | ref | NP_588106.1 | STLSSVKETDFVETLILSPDNAPRMSFVGGKPNVAEIVRTVMHQSTRINVSIAASKTKN---TFLIQGKSAVKAARRQIKLIGRREKIMPVCFVVFVVGAIITGNGNLKSMDR---STRITIPKRNITANE---SDDAKKPEKENS 283
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 45552723 | ref | NP_995886.1 | -----QSDEEFTTIAGTKEGIAQAEQEIROLSEAEYKKSDDRITVPK-VYHPFIVGF-----YSENLNKLOBETGARINVPVQVQKDEIVISGEKDAVAAAKAVEAIVKMEKKCTSVSEVAKPKH 325
gi | 158294225 | ref | XP_001237663.2 | ISDEDAITITGKTEGIEKAHEIRIIMSDECSRKAERFNVPK-IYHPFVLGA-----YGENLQKMMBETGAKINVPVQVQKDEIITIGEGEVLAAKARIEAIVKMEKKCTSVAVEVVRADH 298
gi | 4885409 | ref | NP_005327.1 | PDDPBNQIKITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 114584294 | ref | XP_001161053.1 | PDDPBNQIKITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 19527028 | ref | NP_598569.1 | PDDPBNQIKITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 25282449 | ref | NP_742036.1 | PDDPBNQIKITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 73994293 | ref | XP_534628.2 | PDDAANQIRITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 119930773 | ref | XP_001256511.1 | PDDAANQIRITGKTEGIEKARHEVLLISAEDOKRAVERLEVEK-AFHPFIAGP-----YNRLVGEIMOETGTRINIPPPSVNRTIEIVTGEKEQLAQAVARIKIVYEEKKKTITLAVEVKSQH 307
gi | 45384156 | ref | NP_990427.1 | PDDPBNQIKITGKTEGIEKARHEVLLISAEDOKRAVERLDVEK-VYHPFIAGP-----YNRLVSELMODGTRINIPPPSVNRTIEIVTGEKEQLAQAVARVKKIVYEEKKKTITLAVEVKSQH 306
gi | 41393109 | ref | NP_958882.1 | PDDPBNQIKITGKTEGIEKAKHEILLISAEDOKRAVERMNDK-VFHPFITGA-----HGKLVGDLMOETGARINVPVPSVNTKIEIVTGEKEQVALAMVKKIKLYEKKKNATLAVEVKSQH 310
gi | 17531677 | ref | NP_496136.1 | RDGPKSKITITIPREGIORAAAHILAVSEREAKLATERIVCPK-NLVAFVRGB-----KNETVDRLLQNNGVKINIPPPHVNTNEIVSVTGEKDGVLVRAAEIRQIIES-KKNVSSIQVAVARTQ 291
gi | 6322381 | ref | NP_012455.1 | DEDMDDTISNVSLFGDFESVNLAKAKILAIVKEETKNAITIKLVVEDEKYLPIYD-----VSEFASDEGDEEVKQVQYK---SGDIVLGPREKAKAKISIQDYLLKKLASNLDEEKVKIPSKFQ 339
gi | 45184647 | ref | NP_982365.1 | DADLDDQLINISLHGDAVSNFAKDKILSIVKEETKNAISVAVENKQLPFIS-----LADVEIS---EDVVKAFPNG-SEKIVLMGPRDEAKEAKVNVQNYLNTLASKVSEKKSIPRKFQ 336
gi | 50306403 | ref | XP_453175.1 | DSDLEDYVVTISLHGDAVSNVLAQKILVDEKVEETKNAIVLVEDSKLVPFID-----LESVEIP---ADVKAQFLTNDPDAEIALNGPRDNLKAKVINYLNELGLKLVVKEKVPKFKF 341
gi | 39977187 | ref | XP_369981.1 | IDDDDEAMVDVIEGNAVSARAAQDAILNIAKERSANVTTLKLNIPAEFVPLS-----RALQLGDDVVVRIPPPPTIGRPHFSPAPVENLIQVAGDRAAVQSARAEIRIAEQLHQLLEQASIQGRH 369
gi | 32405206 | ref | XP_323216.1 | -----ADEDDDTMINVHIEGNAFSAAAAQOEDIRIAGERAAVQTKLRNIPAEFVPIAGPKNNLVHKLBEDMGVIRVPPVQGRSLQPPSIPAPGRPIFAPAPQDYNIQLAGERTAVQNARAATERRAELRRLALEQLSIQGRH 396
gi | 19075606 | ref | NP_588106.1 | AASTLDDLEPYEMTTITLGDPEGVLAQKIDIEATINERTSNITVRSISISTELLSLRGE-----DGKNIKLEBGRDLKVIQFPAALDPSAVNPIVLSGKSAVRECALYLGQAEELRRTITPMLPIPRRH 416
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 45552723 | ref | NP\_995886.1 | .....-SDLSKDVIRGPKDVEKAKVOLLLELANER-.....-LAFSFTAERAKOQHKKFLIKNGASIRKIRDAIGARIIFPSNEDTDE-.....-VITIIIGKESVKKAREOLEAIKCEDEVTEGEVS-VDPKH 826  
gi | 158294225 | ref | XP\_001237663.2 | .....-SDLSKDVIRGPKDVEKAKVOLLLELANER-.....-ELSSYSVOIRAKPOHKKFLIKNGASIKKIRKDGARVIFPNVNDQNE-.....-AIIIIIGKKEHVEAKTELEAIKKNIDNIVDEIS-VQPKF 798  
gi | 4885409 | ref | NP\_005327.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 811  
gi | 114584294 | ref | XP\_001161053.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 825  
gi | 19527028 | ref | NP\_598569.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 811  
gi | 25282449 | ref | NP\_742036.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 811  
gi | 73994293 | ref | XP\_534628.2 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 824  
gi | 119930773 | ref | XP\_001256511.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 723  
gi | 45384156 | ref | NP\_990427.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 811  
gi | 41393109 | ref | NP\_958882.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 814  
gi | 17531677 | ref | NP\_496136.1 | .....-EGSGSDTVVIRGPKSSDVEKAKVOLLLELANER-.....-DTKSFYVDIRAKPEYHKFLIKGGGKIRKVRDSTGARIIFPAEDDKDQ-.....-LIIIIIGKEDAVREAQKLEALIQNLNVDNVEDSML-VDPKH 794  
gi | 6322381 | ref | NP\_012455.1 | .....-DNEIVTIRGSRGPNKAHEELKALLDFEM-.....-ENGVEMDIPAEHVPRIVKNGNDINIRAEYGVEMDPLQKSTDPKAEQETGEVELEITGSRNINIKDAKRRESVIAEASDFVTEVLK-IDHY 872  
gi | 45184647 | ref | NP\_982365.1 | .....-EGEVVITIKGSRGPNKAHEELKALLDFEI-.....-ENGHKSVINVPVAVHVRIVKNGNDINIRAEYGVEMDPLQKSTDPKAEQETGEVELEITGSRNINIKDAKRRESVIAEASDFVTEVLK-IDHY 862  
gi | 50306403 | ref | XP\_453175.1 | .....-DSELVTIRGSRGPNKAHEELKALLDFEI-.....-ENGHKELLVVVDVTRVIRGSGSETINDIAEYGVEMDPLQKSTDPKAEQETGEVELEITGSRNINIKDAKRRESVIAEASDFVTEVLK-IDHY 870  
gi | 39977187 | ref | XP\_369981.1 | .....-AGSEAGAKPRRQAPDEVIIRGPKKGADEARDELLSLVQYLK-.....-DNEFTATTIVQKQLPHFISGGGNDMDALRQOIGAKIDIPNGRDTDS-.....-TVEILIKGTSQVAAAKKILKEKSVFDDIVREVE-VDRKF 925  
gi | 32405206 | ref | XP\_323216.1 | .....-AGSDAG-KPRRQQAADDEVIIRGPKKGADEARDELLSLVQYLK-.....-DNYTATVIVQKQLPHFISGGGNDMDALRQOIGAKIDIPNGRDTDS-.....-LVEIQKGTKEVAVAAAKKILKEKSVFDDIVREVE-VDRKF 950  
gi | 19075606 | ref | NP\_588106.1 | .....-NELMKPSPDVEVIRGGKKSVAIAAKOELLEVEYEK-.....-SIAVITSTIDIPSKAVSRVVRGNSSTVENIRIQDFVQKIDIGVSTETT-.....-FVVRGAKADVENAIKEISAIAEVKNLVEKVIK-IDREY 966



gi | 45552723 | ref | NP\_995886.1 | .....HKHFVAKRGLILHRISIEECGG-.....-VMISFPRVGIN-SDKVIKGAKDCIEAARQRIEIEIVADLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-DATEPVEGLTNGGSGENGGNEGQGE-..... 952  
gi | 158294225 | ref | XP\_001237663.2 | .....HKHFVAKRGLILHRISIEECGG-.....-MSISFPRMRRDRNRVRLKGPDKCIEAARQRIEIEIVADLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-DATEPVEGLTNGGSGENGGNEGQGE-..... 940  
gi | 4885409 | ref | NP\_005327.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 934  
gi | 114584294 | ref | XP\_001161053.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 948  
gi | 19527028 | ref | NP\_598569.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 934  
gi | 25282449 | ref | NP\_742036.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 948  
gi | 73994293 | ref | XP\_534628.2 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 934  
gi | 119930773 | ref | XP\_001256511.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 947  
gi | 45384156 | ref | NP\_990427.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 746  
gi | 41393109 | ref | NP\_958882.1 | .....HRHFVIRRGQVLRRIAEIEYGG-.....-VMYSFPR-SGTOSDKVILKGAKDCVAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 935  
gi | 17531677 | ref | NP\_496136.1 | .....YKNFLARGAALVKIEIQONGG-.....-VVISFPK-NGDSSEVIRGSKQCVEAAKRRIOEIIEDLEAQTIEVVIPQRHRRIMGARGFKVQVTFEFDVQIKFPDR-.....-EENAVHSTEPVQVQNGEAGEG-..... 902  
gi | 6322381 | ref | NP\_012455.1 | .....HKSIVSGGHHILREIISKAGGEEIRN-.....-KSVDIIPN-ASDENKDIIVGPKFVKVVEENKLVKDAENSVIKTIDIPAERKAGALIGPGGIVRRROLESSEFNINLFPVKNDDF-..... 981  
gi | 45184647 | ref | NP\_982365.1 | .....HKLIVGPGGSLKDFIISKAGGDDIRN-.....-KRVNDIPN-ASDENKDIIVGPKFVKVVEENKLVKDAENSVIKTIDIPAERKAGALIGPGGIVRRROLESSEFNINLFPVKNDDF-..... 970  
gi | 50306403 | ref | XP\_453175.1 | .....VSDIIGRSGSLKDFIISKAGGDDIRN-.....-KRVNDIPN-ASDENKDIIVGPKFVKVVEENKLVKDAENSVIKTIDIPAERKAGALIGPGGIVRRROLESSEFNINLFPVKNDDF-..... 979  
gi | 39977187 | ref | XP\_369981.1 | .....HRSLLIGGGSILRDIVVAGGSDRRRELARVRFPP-.....-QDSGNTIKIEGRTEVVEKILAKIIEVLSQRSVSDVLDVPEKRRILIGRGGDVKRONENKFKYSIDIPKIGDG-..... 1037  
gi | 32405206 | ref | XP\_323216.1 | .....HRSLLIGGGSILRDIVVAGGSDRRRELARVRFPP-.....-QDSGNTIKIEGRTEVVEKILAKIIEVLSQRSVSDVLDVPEKRRILIGRGGDVKRONENKFKYSIDIPKIGDG-..... 1062  
gi | 19075606 | ref | NP\_588106.1 | .....HRYLIGPNSKLGNTIKIECGGS-.....-TDKTEIARLISFNGNSEERNSVVLGRDKKIVEALTELLIEVELKNGVEEKTEVPRCIS-.....-IIGRMGS-TRRDIERK-.....-STMLNIPNVLDPE-..... 1081



gi | 45552723 | ref | NP\_995886.1 | .....-GEQVEKEAQEVEVR-CDVIRITGRIEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1087  
gi | 158294225 | ref | XP\_001237663.2 | .....-TIDGGEVVNGGAAGE-ITTPAEPVORASDLVRISGNKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1086  
gi | 4885409 | ref | NP\_005327.1 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1066  
gi | 114584294 | ref | XP\_001161053.1 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1080  
gi | 19527028 | ref | NP\_598569.1 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1066  
gi | 25282449 | ref | NP\_742036.1 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1066  
gi | 73994293 | ref | XP\_534628.2 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1079  
gi | 119930773 | ref | XP\_001256511.1 | .....-REAKDPCGSPRR-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 746  
gi | 45384156 | ref | NP\_990427.1 | .....-KDGKADPSSPRK-CDIIIIISGRKEKCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1068  
gi | 41393109 | ref | NP\_958882.1 | .....-KEP-VDRTPAKK-CDVIVLSGRKERCCEAAKQALLDLPIE-.....-EELSVPFLDHRITIGPRGANVRFMSKDHVHVELPPSELKE-.....-DVIKVCGTPARVAEAREALVKMIEDVEADRDRLEKSFVQVDFTEFHSK 1065  
gi | 17531677 | ref | NP\_496136.1 | .....-SQDVTVGRDTKVBEAKALLAMVPTIS-.....-KVIQIPVDMHRSITIGRGETVTRKLMQDYVNMISIPKDNSE-.....-DIITVIGQTEVVDQALEALRGKIGEYEAQEDRKLKQWMSINVPDTHQK 1020  
gi | 6322381 | ref | NP\_012455.1 | .....-SGKITITGAPENVKAEKLLNEIIRENFDRVDPASIVYVS-ERGAFIQKLRMDLNVNRFVFG-.....-NNSK-.....-KANKLARAPITIEPLEKVCSS-EGENAETKFTIEEVGAPITSSSEGITM 1098  
gi | 45184647 | ref | NP\_982365.1 | .....-EGKVIIRGRPEAVEKCEKEIFSIIRDSVDQEMVPAVYHAFVS-ERGLINLKRMTYFVNVKHG-.....-NNSK-.....-KANKLARAPITIEPLEKVCSS-EGENAETKFTIEEVGAPITSSSEGITM 1083  
gi | 50306403 | ref | XP\_453175.1 | .....-DEKVTVGSNPANISCKKIKLEKILRDSFDLEIAPVAKYHVS-NSGLIFQTLRNEIDVSHG-.....-NLTR-.....-KACLSRANKVVP-ENVAGGE-.....-NNSNVLITIEVSAPEASANDNPW 1090  
gi | 39977187 | ref | XP\_369981.1 | .....-LTDKVISGSPSDVNAAKEHILS-LIKEQOQETVEPRNLHHAIS-GGGQFRKLRDLNLTVDHAGHVP-.....-KPSQQRNSNG-GGALLITDEPDS-.....-NAHSHVVEANTSSGSDGDLIPW 1152  
gi | 32405206 | ref | XP\_323216.1 | .....-QTIKIVGQASADVAKAHIQS-LTKDQPGETLQVPRALHSHVS-NNGQIFRRLKSDHVTVDHAGHVP-.....-KPAAPASIRANGGSLPLITDDE-.....-STADAHSWVVDQTS-.....-EGDIPW 1177  
gi | 19075606 | ref | NP\_588106.1 | .....-ETVITITVGSPEKCAKEMIQEKVASYE-.....-QMITVPTDVEYSIM-.....-KGLIMKLRSDLVKVFDP-.....-PEIKPVO-.....-FTEVLEDHEDGVFPWKLVTVDY-.....-GSSSSWAVR-..... 1184



