

gi|221329623|ref|NP_001096860.2|MQWTAASCDQHDQDPPAVNRNIEQRTFANNCEVDPMDATGSKTHPLPKQREADRVPVSGSGGGSSSLTLLGAVTTSMSEVTVSTTTTTITIESSSNTTILEKNSPFAGGSCSSGSLSPAYLQHHLQHGSPHLHLQVHHHTAPP 150
gi|158301435|ref|XP_321129.4|
gi|29243976|ref|NP_808274.1|
gi|109477888|ref|XP_233830.4|
gi|217416392|ref|NP_742066.2|
gi|114577175|ref|XP_525888.2|
gi|73970111|ref|XP_538474.2|
gi|118087949|ref|XP_419455.2|
gi|292620003|ref|XP_001921439.2|
gi|133900950|ref|NP_001041092.2|

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

gi|221329623|ref|NP_001096860.2|PLAAVRS AQMGSSVANGAGPAAACLAVCCSPGSSHHHLGHVGHLAGHPLPHQLPHQLPPLSLYPLMAAALGVAGSSGPPSLVNSPALGRKRKRYTSSNSNCSQFNNNYAGLDVDSLDDMLRKLTELEQVIEAEERAEEAEKVRAME 300
gi|158301435|ref|XP_321129.4|.....PLLSPHVVRAME 12
gi|29243976|ref|NP_808274.1|.....MEEPSPEPEGLIDWKERCVALEAQLMKFRVQASK 33
gi|109477888|ref|XP_233830.4|.....MEESXPERPIDWKERCVALEAQLMKFRVQASK 33
gi|217416392|ref|NP_742066.2|.....MAELSEPEGPVDWKERCVALESQLMKFRVQASK 33
gi|114577175|ref|XP_525888.2|.....MAELSEPEGPVDWKERCVALESQLMKFRVQASK 33
gi|73970111|ref|XP_538474.2|.....MLNGPLLPHLVDVDCICDRDIECAEVRGKSKLNDLRINMAELSETEGPVDWKERCVALESQLMKFRVQASK 71
gi|118087949|ref|XP_419455.2|.....MADLSEPEGTVNWKERCLTLESQLMKFRVQASK 33
gi|292620003|ref|XP_001921439.2|.....MAECDSESTG-GAWKEKYMALRALLFKFRGQMSM 32
gi|133900950|ref|NP_001041092.2|

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



gi|221329623|ref|NP_001096860.2|QRLEWPKPPQQAACHPHSHHPPIPSHPQEQAKNHCSPSHQASGGATAGAAGSGLPPTQETEKIITSLEIQVEEORQLRLHDAEQIEAKAAKIKEWVNNKLRLEEQNQLLREQNVKCNQOLELLRNHIANQSQRRHSIVG---PVR 447
gi|158301435|ref|XP_321129.4|QRLCDWPKSPNLTGPSPPSSNP-----AAAAAAGAGQAIAAAVAGGPPGTEPPKGTDPVKISQLESAIEEQQLRLQDARQVGAKAAKIKEWVNNKLRLEEQNQLLREQNICKCNQOLELLRNHIATQSTRHSVAPTPQVPR 152
gi|29243976|ref|NP_808274.1|IRELLADKMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 183
gi|109477888|ref|XP_233830.4|IRELLADKMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 183
gi|217416392|ref|NP_742066.2|IRELLAEMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 183
gi|114577175|ref|XP_525888.2|IRELLAEMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 183
gi|73970111|ref|XP_538474.2|IRELLAEMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 221
gi|118087949|ref|XP_419455.2|IRELLAEMOQLEROVIDAERQAEKAFQEVQVMEKLAANIQTSESETRLYKCCODLESVMQEKDDLIQNLALRLEEQQVRIQEAIIIEKAAKIKEWVTVKLNLELEVENQNLRFINQTEELRAIQSKLQELKIKVSCVSPKTS 182
gi|292620003|ref|XP_001921439.2|VRELTTEKMOQLERQVLEAEQRAYEANQGVQVMEERLKASDIQSSDQVRLFRRCNQLQSVLQEKDELIAITLQKLEEQKQNRIOQARTVIEKAAKIKEWVMMKLNAFETENTSLRDRHQLEAETQVLRRLQAMQCSQSDGTLQI-IVG 181
gi|133900950|ref|NP_001041092.2|.....MSDSSASPLRSPDEELLKASRIQLRWVKKMKLEEDQNERLRAQNLRCITDQMLRFTIEKSRKIKAEEMERSIT 77

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



gi|221329623|ref|NP_001096860.2|NSLSLDVQDFTGSGSNPEHRRRSSES LDPQEIIGRPLTSS-----YPHHQHRRNLSMEPELERNLVAAVDGD---LILAPLSSISNKAPEGVPTESEGVVTRPDSDDTDAHYDAEITYIPSCFKLPAMKNNPALMASGGN 578
gi|158301435|ref|XP_321129.4|TSLSLDVQDVKRRSG---RRRSSES LDPPEHRS LHAGSSGSGSHHPHHHHHHHHHHRRNLSMEPELARDLAAAVDGD---LNLPLSQQQPHQSHPPPPGMCASP-GSDVDVAVHYDAEITYIPSRKAPAWLKG---LPGGGS 287
gi|29243976|ref|NP_808274.1|EGORN--LTFGCFLSRAKSPPCVVRCEEVSKMASNEPEITTEGRVCEMEIAEKPADNQVENSRSORLKHETSCSSEON---DKTRASFAMDGGTSONSGVPPVSDWSSDDEDDGSKGRSKRCTSTLSSHTSEEGQCGRLGSEAYLTASD 328
gi|109477888|ref|XP_233830.4|EGORLSSSLTFGCFLSRAKSPPCAVRSEAEKMASSEPEFAEARCVEEMEIAEKPADNQVENSRSORLKHETSCSSEON---RKTGASFVADGGTPEHSGLPVSDWSSDDEDDGSKGRSKRCTSTLSSHTSEEGQCGRLGSEAYLTASD 330
gi|217416392|ref|NP_742066.2|EGORLSSSLTFGCFLSRAKSPPCVVRSEEMSKISSKEPEFTTEGKDMEMEIEPEKSVDNQVLENNRQRTLHQTPCGSEON---RKTGASFVADGGTSONSGAPVSDWSSDDEDDGSKGRSKRCTSTLSSHTSEEGVQCRMGSEMYLTASD 330
gi|114577175|ref|XP_525888.2|EGORLSSSLTFGCFLSRAKSPPCVVRSEEMSKISSKEPEFTTEGKDMEMEIEPEKSVDNQVLENNRQRTLHQTPCGSEON---RKTGASFVADGGTSONSGAPVSDWSSDDEDDGSKGRSKRCTSTLSSHTSEEGVQCRMGSEMYLTASD 330
gi|73970111|ref|XP_538474.2|EGORLSSSLTFGCFLSRAKSPPCVVRSEEMSKISSKEPEFTTEGKDIEMEMEIEPEKSGENIQEENRQRTLHQTPCVPEON---QNRGTSFATDGGTSONSGAPGSDWSSDDEDDGSKGRSKRYTSTLSSHTSEEGVQCRMGSEMYLTASD 368
gi|118087949|ref|XP_419455.2|EGORLSSSLTFGCFNSRARSPPQSPKFEIISKSSSKELDYAESKNLLEKILLETTSAGSAHESNKGOKSLQDSSSGSEONKRVTRSSSKDVSDDMSKNSCTGSDWSSDDEDDGDNKGLKRCASLTSSHTSEENARYSRVGSSEMYLTASD 332
gi|292620003|ref|XP_001921439.2|EPKRLSSSLTFGCFQIRGKSPQVQVIGPEPQRSISITLQEDSGDK-----QESPETOR---ISRCSEKERS-----ENEGEQUESTGHKLSGASVLSSTASEGERSLFEGFCFS---HTT---SEAVHTTSD 292
gi|133900950|ref|NP_001041092.2|G-----TLFVLRLENRTSDSGLTSDADRQMS----- 106

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi	221329623	ref	NP_001096860.2	SFTTTTTSSELGVPRPPPLPLHRFP-----SWEAKIYQVANDGLAGACTGTSTAESLASEPDIQDQMGCTNLSNGRRHGCHGSGCTGIGTGDCGHTLGSFPGTLPPLPSRQQVTASGGFCDIIVPVYAVTVKG	704
gi	158301435	ref	XP_321129.4	SFTTSDSVADLGTPRPPPLPLHRFP-----SWEAKIYQVANDGLAGAGSNAGAGAGEEGEQDQESGSGMTASVG-----GGGGN-----SRSTVSGGVCDLIVPVYAVTVKG	386
gi	29243976	ref	NP_808274.1	DSSSIFEEETFDGNRPEQKLLKCSWQOKAPWKAQGN-LAKGRSSG--VKEDSSDELNKKFHSORLDYSSSSSEANTPSPILTPALTPRYN-----SLPGKGGAPLVPPPFQPPPKLRVNVFSSISVALTKRRLSOPOLCSDRMFGNRRN	472
gi	109477888	ref	XP_233830.4	DSSSIFEEETFDANRPEHKKLYSWQOKAPWKAQSN-LAKGSSQSE--VKQRDSSDELNKKFQSORLDYSSSSSEANTPSPILTPALTPKHPN-----SLPGKG--TLPVPPPFQPPPKLRIPNVFSSISVALTKRRLSOPOLCSDRMFGNRRN	473
gi	217416392	ref	NP_742066.2	DSSSIFEEETFGIKRPEHKKLYSWQOEAQWKAQNSPLGKGNSELS--KKEQDSSDELNKKFQSORLDYSSSSSEANTPSPILTPALMPKHPN-----SLSGKG--TQLVPSHLLPPPKLRIIPNVFSSISVALAKRRLSOPOLCSDRMFGNRRN	474
gi	114577175	ref	XP_525888.2	DSSSIFEEETFGIKRPEHKKLYSWQOEAQWKAQNSPLGKGNSELS--KKEQDSSDELNKKFQSORLDYSSSSSEANTPSPILTPALMPKHPD-----SLSGKG--TQLVPSHLLPPPKLRIIPNVFSSISVALAKRRLSOPOLCSDRMFGNRRN	474
gi	73970111	ref	XP_538474.2	DSSSIFEEETFGIKRRLPEHKKLYSWQOEAQWKAQNSPLGKGNSELS--KKEHSSDELNKKFQSORLDYSSSSSEANTPSPILTPALMPKHPN-----SLGPRG--TQLASSYLPPPKLRIIPNVFSSISVALAKRRLSOPOLCSDRMFGNRRN	512
gi	118087949	ref	XP_419455.2	DSSSLFEEESLGVORTPEHKKLYSWQOEAQWKAQNSPLGKGNSELS--KKEHSSDELNKKFQSORLDYSSSSSEANTPSPILTPALAMKHAIRA--SADS--TLPSSDFSNLPPPKLRIIPNVFSSISVALAKRRLSOPOLCSDRMFGNRRN	482
gi	29262003	ref	XP_001921439.2	DSSSLFDDDD--MORLECSRLISDTKSTLK-----KGMKVED--TEDGSSDELNKKFQSYLSSSSSDNTRPSPILTPVLPKRP-----PSGD--SQDTPASPKQPRLRNFAFEVSLALLKXHSOPFVYKAAHGRTRN	421
gi	133900950	ref	NP_001041092.2610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750	155



gi	221329623	ref	NP_001096860.2	RASQIRSMF-FTGDSDDSSDGED-HAVMLT-----HSHNSSTDTTETSTSGSASSPSKSLKTSSLSLPAKRSSESPPKNAKARVHIOSRTSTPSSRNQHQLPQSOHHTLQNHGHQLGAYVTPSS--GGLLPRYHANALQ	844
gi	158301435	ref	XP_321129.4	RASQIRSMF-FTGDSDDSSDGEDHGAMLT-CATSTHNSHNSSTDTTETSTSGSASSPSKSLKTSSLSLPAKRSSESPPKN-KGRGKORHEFFVVFLLSYDIFLR-IMYTKHNIHYNTSFIQTHTHYINID--VLLFFFAFFIFSFT	530
gi	29243976	ref	NP_808274.1	AISMIRPLRPOETDLDVVDGDAEAVNRMDTGCDDGLFSYDQPPPCADDQENSSEAPKAPCNKPPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	622
gi	109477888	ref	XP_233830.4	AISMIRPLRPOETDLDVVDGDAEAVNRMDTGCDDGLFSYDQPP--SAEDPENSEATKAKASCSPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	621
gi	217416392	ref	NP_742066.2	AISMIRPLRPOETDLDVVDGDSFVLENMDTSCDDGLFSYDQPP--NSDDQENCSAKKVAKSPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	623
gi	114577175	ref	XP_525888.2	AISMIRPLRPOETDLDVVDGDSFVLENMDTSCDDGLFSYDQPP--NSDDQENCSAKKVAKSPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	623
gi	73970111	ref	XP_538474.2	AISMIRPLRPOETDLDVVDGDSFVLENMDTSCDDGLFSYDQPP--NSDDQENCSAKKVAKSPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	623
gi	118087949	ref	XP_419455.2	AISMIRWRPQETDIDQVQDGEDLAILEKMEICDQGVFVYDCTEAQ-DAEAQEPDQMTKVASNKPPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	661
gi	118087949	ref	XP_419455.2	AISMIRWRPQETDIDQVQDGEDLAILEKMEICDQGVFVYDCTEAQ-DAEAQEPDQMTKVASNKPPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	631
gi	29262003	ref	XP_001921439.2	AISMIRSLRLEPQETDMNED-----QKMETGEK-----HSDVLP--EETPTNLSAIPGSKPPPLPRLRFPWESRIYAVAKSGIRVSEAFNMEHANKNSADILSYAASLYTSLIYKMTTPVYTLKGGKATQISSSPFLDSSG	555
gi	133900950	ref	NP_001041092.2760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	305



gi	221329623	ref	NP_001096860.2	PGSLPPLQHMGRGTVI--DLSFESGLS-----DDYALPPDAVS--ESTCMASMPSSLMRQSYVD--PSKIKIESLEKMGHLAKLGG--KLTWKRWFVFLKNGSINVWVQHQHVDVQRKPGQQLDLEVCIRINRAE	967
gi	158301435	ref	XP_321129.4	LLCFPLLLCLFP--ISELSFESGLS-----DDYALPPDAVS--ESTCMASMPSSLMRQSYVD--PSKIKIESLEKMGHLAKLGG--KLTWKRWFVFLKNGSINVWVQHQHVDVQRKPGQQLDLEVCIRINRAE	652
gi	29243976	ref	NP_808274.1	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSDSSAASEDYAIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	760
gi	109477888	ref	XP_233830.4	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSD--SEGDAYIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	757
gi	217416392	ref	NP_742066.2	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSLSSVASEDYAIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	761
gi	114577175	ref	XP_525888.2	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSLSSVASEDYAIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	761
gi	73970111	ref	XP_538474.2	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSLSSVASEDYAIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	799
gi	118087949	ref	XP_419455.2	SEEDSSRSSSR--LSESDARSRSGPS-----SPRAMKRGVSLSSVASEDYAIPPDAYS--IDAECSPQEQLLKTCCLASCDNGKNEPLEKSGYLLKMGV--RVKTKRRWFVFLKGGELLYYKSPDVIKPKQGHIELASCSILRGD	769
gi	29262003	ref	XP_001921439.2	SEEESSSEEFQSN--GDEKAQTS--GSESHKSHRS--SHSFKRAVSLSSMTSESDYAIPPDAYS--IDAECFEPESKQPKTCSSSGN-----ILN-----SDVIKPKQGHIELASCSILRGD	662
gi	133900950	ref	NP_001041092.2	HSYEDGAAAYARDLCLG-----DDYALPPDAVS-----RCSGGTPTRTSLIPSRMETMEKSGYVTLQLDPSRIKSLKRRVYVFKNGQLISYRKHNRDEEPAKSIISIDIRSVTKLE	412



gi	221329623	ref	NP_001096860.2	--GASTFEIDTGGKVVYLTADSHAMDDWIRVLQNVQRNATKLLLSRDD-QKPTVQGWVTKVKNHGPKKCWCVLLGKMFYFKAPAE--TN-----PLGQINMRDARVEVEHVSDSEEREDAQAQD	1087
gi	158301435	ref	XP_321129.4	--GASTFEIDTGGKVVYLTADSHAMDDWIRVLQNVQRNATKLLLSRDD-QKPTVQGWVTKVKNHGPKKCWCVLLGKMFYFKAPAE--TN-----PLGQINMRDARVEVEHVSDSEEREDAQAQD	772
gi	29243976	ref	NP_808274.1	--NKQTVQLAKTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLCLQPE--GKPAVKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLWEAKVEEVDRCSDSEDEYETRGCYLL	880
gi	109477888	ref	XP_233830.4	--NKQTVQLAKTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLCLQPE--GKPAVKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLWEAKVEEVDRCSDSEDEYETRGCYLL	877
gi	217416392	ref	NP_742066.2	--NKQTVQLTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLSLQPE--GKPTMKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLWEAKVEEVDRCSDSEDEYETRGCYLL	881
gi	114577175	ref	XP_525888.2	--NKQTVQLTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLSLQPE--GKPTMKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLWEAKVEEVDRCSDSEDEYETRGCYLL	881
gi	73970111	ref	XP_538474.2	--NKQTVQLTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLFLQPE--GKPTVKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLWEANVEEVDRCSDSEDEYETRGCYLL	919
gi	118087949	ref	XP_419455.2	--GKQTIQLTEKHTYYLTADSPNILEEWIKVQLVLRVQAANPLFLQPE--IKPTMKGLLTKVKGYSKRVCMLVGVKLYYFRNED-----KFPLGQIKLFEAKVEEVDRCSDSEDEYETRGCYLL	889
gi	29262003	ref	XP_001921439.2	--EKQMLQVVGKSVCLKADSPNILEEWRVRLQSVQRKAASPVFTQLD-MRPVLIKGLLTVKKGYSKRVCMLVGVKLYYFRNEDVVFCLLQKXVILYDICTFMXLLSNFPTQFPLGQIKMWEARVEEHSCLDAE-----L	800
gi	133900950	ref	NP_001041092.2	QGAAYAFQLIISTDKMNFMTSERT--HDWVITLSSAAIKATLREMASRVTPIDASISGWLTVKCGLSKVFALVNLKMFKNSDLVPMNG-----FLCLOGAQIKSEKNGTEEYSSDQELTKHEPNQR	542



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gi | 221329623 | ref | NP_001096860.2 | ARLVVAIVPAHQG-PTYLILSGKPERDNWLYHLTVVSGGG-PSAGTQYBQLVQKLMETDGDPCNVLWRHPILLLTKDITIAPLSSMHTETMOPBAIKLFKFIOLFMFSVAVNQPGIDYHVVLAQNALQHALDMPLELTEMICILIKOTSRH 1235
gi | 158301435 | ref | XP_321129.4 | ARLVVAIVPQGGPTYLILPGKQERDNWLYHLTVVSGGG-PNAGTQYBQLVQKLMETDGDPCNVLWRHPILLLTKDNIISPLTSLHSETLQAEAIKLFKFCOLFLSVAVNQPGIDYHVVLAQNALQCLDMPLELQSELICALIKOTSRH 921
gi | 29243976 | ref | NP_808274.1 | STHYTIIVHPKDGPTYLLIGSKHEKEAWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1030
gi | 109477888 | ref | XP_233830.4 | STHYTIIVHPKDGPTYLLIGSKHEKEAWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1027
gi | 217416392 | ref | NP_742066.2 | STHYTIIVHPKDGPTYLLIGSKHEKDTWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1031
gi | 114577175 | ref | XP_525888.2 | STHYTIIVHPKDGPTYLLIGSKHEKDTWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1031
gi | 73970111 | ref | XP_538474.2 | STHYTIIVHPKDGPTYLLIGSKHEKDTWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1069
gi | 118087949 | ref | XP_419455.2 | STHYTIIVHPKDGPTYLLIGSKHEKDTWLYHLTVAAAGSNNINVGSEFEQLVCKLLNIEGEPSSQIWRHPMLCHSKGEGILSPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTRRR 1039
gi | 292620003 | ref | XP_001921439.2 | SAQHTISVQSGRQGSTYLLIDSPHEKMAWVYHLSVAAGTAVGQVGTVEFQLVCKLLNMDGNQSSQLWRHPMLCFKSEKGLFLPPLTSLPSEALQTEAIKLFKFCOLFINAAVDSPAIDYHISLAQSAQLOVCLTHPELONEICCOLIKOTWKK 950
gi | 133900950 | ref | NP_001041092.2 | KNNDLVCQIANEDPVLILLIRSEDEKWKLYLKSASGTA-ALCGTFFETLVRORMAENVANDSPLWED-LLFASGSEI PKDTMTTVDHSDRKKTLLETARACOLFVSVLMDRAQATQYHIDLQNLISLAVQOQYLRNEVVSQILKMHSSG 690
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi | 221329623 | ref | NP_001096860.2 | LGOKLSVGVVKNKLGKQTROLLCCATOSLFTCDTQQAGHAQAGSSPTSIAQAPSAPIIDCKSNPPVYSFVQWOLLALAVSLFVPRSSRLWYKHLHLSRNADTKTEFG--KYAAYCERALERTLNKGGRETKPSRMEVLSILLKNPY 1383
gi | 158301435 | ref | XP_321129.4 | TGOKLGVGVVKNKLAAPAROLLCCATOSLFTCDTQQGSAQAAGSSPTSIAQAP-IVPPIDCKSNPPSYTFIQWOLLALAVSLFVPKNSRLWYKHLHLSRNADSKTDCG--KYAAYCERALERTMONGGRETKPSRMEVLSILLKNPY 1068
gi | 29243976 | ref | NP_808274.1 | QLONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLQHLQRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1114
gi | 109477888 | ref | XP_233830.4 | QONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLQVHLQRSADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1111
gi | 217416392 | ref | NP_742066.2 | QPONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLSLHLKRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1115
gi | 114577175 | ref | XP_525888.2 | QPONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLSLHLKRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1115
gi | 73970111 | ref | XP_538474.2 | QPONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLSLHLKRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1153
gi | 118087949 | ref | XP_419455.2 | HPONQPG-----PLOGWOLLALCVGLFPLPHF--FLWLLSLHLKRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1123
gi | 292620003 | ref | XP_001921439.2 | TNGPPG-----PLOGWOLLALCVGLFPLPHF--FLWLLQVHLKRNADSRTEFG--KYAIYQRCVVERTQONGDREARPSRMEILSTLLRNPY 1034
gi | 133900950 | ref | NP_001041092.2 | MPFGTQG-----WKLLALTRPFLPKQVSLLLWLLKRLHLSRNADTKTEFG--KYAAYCERALERTLNKGGRETKPSRMEVLSILLKNPY 773
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500

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gi | 221329623 | ref | NP_001096860.2 | HHSLLPHAIIPVHMNNTSYQVVSFDGSTTIEEFQATLAHELGRDATN-GFCLFSDDFIEKDLHEHYLEPLAKLCDVVISKWTALREKGSKGFENSRVIOISYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1532
gi | 158301435 | ref | XP_321129.4 | HHSLLPHAIIPVHMNNTSYQVVSFDGSTTIEEFHGLTLAGIGCRDATN-GFTLFSDDPIEKDLHEHYLDPAKLCDVVISKWTALREKGSKGFENSRVIOISYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1217
gi | 29243976 | ref | NP_808274.1 | HHSRPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1264
gi | 109477888 | ref | XP_233830.4 | HHSRPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1261
gi | 217416392 | ref | NP_742066.2 | HHSLPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1265
gi | 114577175 | ref | XP_525888.2 | HHSLPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1265
gi | 73970111 | ref | XP_538474.2 | HHSLPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1303
gi | 118087949 | ref | XP_419455.2 | HHSLPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1273
gi | 292620003 | ref | XP_001921439.2 | HHSLPFIPVHFMNGLYQVVFDASTTVEEFLNTLNQDTGMRKPAQSGGFALFDDPSGRDLEHCLQGNIKICDIIISKWEQASKEQPGKCEGSRVRLTYKNRNLWYKHTIKCTDKERLLLYCYQVINSIQVGRFPLSRDLALSLALMS 1132
gi | 133900950 | ref | NP_001041092.2 | RTKFPFHSISVKLPISEYQIVVEFDGSTEIGCCSLCLKLMRPAALLSGVALVMDPMTHS-LLLLKQKQLCDALS-TWETRSRDAIRGRVSDCAALSLRMRHYWGHALLETPIERQFLVWRASBEIVGRFPLSNQCESLAALYAG 922
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650

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gi | 221329623 | ref | NP_001096860.2 | IDMGDYSL-----EKSRDVGVLKGLDKFYPRYRDALGAEQLKDVQELLVSKWMLLKGRSTLDCVRIYLTCCRKWPYFGACLFQAKPRQSPESNTASGATPVAWLVAEDALNVLELSMAPVARYPYSSVMTFGGCCDDDFMLV 1672
gi | 158301435 | ref | XP_321129.4 | IDMGDFAS-----DKSKLN--SLQALDKFYPRYRDALNQEGLKELQELLAKWALLRGRSVLDCVRIYLTCCRKWPYFGACLFQAKPRHS-----DQAMAWLVAEDALNVLELSMAPVARYPYSSVMTFGGCCDDDFMLV 1347
gi | 29243976 | ref | NP_808274.1 | VDIDGFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SSLGNVCVLAHVENGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1409
gi | 109477888 | ref | XP_233830.4 | VDIDGFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SSLGNVCVLAHVENGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1406
gi | 217416392 | ref | NP_742066.2 | VEIGDFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SSLGSTFWLVAHVEDGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1410
gi | 114577175 | ref | XP_525888.2 | VEIGDFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SSLGSTFWLVAHVEDGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1410
gi | 73970111 | ref | XP_538474.2 | VEIGDFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SALGSTFWLVAHVEDGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1448
gi | 118087949 | ref | XP_419455.2 | VEIGDFERPFPSTPAGVTVNCKANQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SALGSTFWLVAHVEDGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1418
gi | 292620003 | ref | XP_001921439.2 | VEFQDFEHPLESPSGSNTPTKSNQILKQVIERFYPKRYREGCSSEELRQLYQLRSTRWMLRGRHSAADCRIYLTVARKWPFFGAKLFLAKPIAP-----SALKNVRVWVAHVEDGLSILEYTSRMLVTSYMYKGLMTFGGYQDFMVV 1277
gi | 133900950 | ref | NP_001041092.2 | MVFG-----DANQSLSDQEFYISQRFYPSKMLDVAIKSLR--LQINSNWSELIGMSENECRVILQVLGWKPLFGSDLHEASMRD-----NEKIFLALNDHVSLLDRRHDFVIRLIPSSLSLTFQGLQDFMLV 1049
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800

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gi | 221329623 | ref | NP_001096860.2 | VSHDD---GGGGE---KLLFAMSKPKILEIILLIADYMNALGHTVPGTPQMNSLIRNGSHRSLRITSRPNLGGGSAVATGFSTNATTAAHNTLNSHATHTLNSNHSHLSSSHHAGGGSQPGLTSSGHQHQQHHPDILKSTPDE 1816
gi | 158301435 | ref | XP_321129.4 | VSAEDTLQSAANEQ---KLLFAMSKPKILEIILLIADYMNALGHTLPGTPQMNTLIRNGSHRSIR----- 1409
gi | 29243976 | ref | NP_808274.1 | VS---TQSKDRPTE---KLLFAMAKHKILEILLIASYINSFHQQKTFPHHLCAPALLSPRTPQAPQARVMGSOPLLESNRPTKGPILL----- 1491
gi | 109477888 | ref | XP_233830.4 | IS---TQAKDRPTE---KLLFAMAKPKILEILLIASYINNFYQOKAAPHHLSAPALLSAKVQEPQAKAMGSOPLLESNNRPTKGPILL----- 1488
gi | 217416392 | ref | NP_742066.2 | INNTHSKDKPTE---KLLFAMAKPKILEILLIASYINNFHQQKAAPHHLSAPALLSAQIRGPOARMGSOPLLESRRPTKGPILL----- 1493
gi | 114577175 | ref | XP_525888.2 | INNTHSKDKPTE---KLLFAMAKPKILEILLIASYINNFHQQKAAPHHLSAPALLSAQIRGPOARMGSOPLLESRRPTKGPILL----- 1493
gi | 73970111 | ref | XP_538474.2 | INNTHSKDKPTE---KLLFAMAKPKILEILLIASYINNFHQQKAAPHHLSAPALLSAQIRGPEARAVGSOPLLESRRPTKGPILL----- 1531
gi | 118087949 | ref | XP_419455.2 | VMDAQTKDKATE---KLLFAMTKPKILEILLIASYINNFHQQKGAHHLSAPALLTPQ---GQKLEMGSOPLLINNRPTKCPILL----- 1500
gi | 292620003 | ref | XP_001921439.2 | VAESGSGTSGK---KHLFAMTSSKVRDLVLLIASYIKSITQAHMAAAHHLAPALLLALAEEMKNNPRSKSPPVACRCKAPILL----- 1360
gi | 133900950 | ref | NP_001041092.2 | IIRPLTPGSHPEAPKERLTFSMQKNEIEQLLHLAEYIRCQLVWVKVK----- 1099
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950

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gi | 221329623 | ref | NP_001096860.2 | QRIK 1820
gi | 158301435 | ref | XP_321129.4 | ---- 1409
gi | 29243976 | ref | NP_808274.1 | ---- 1491
gi | 109477888 | ref | XP_233830.4 | ---- 1488
gi | 217416392 | ref | NP_742066.2 | ---- 1493
gi | 114577175 | ref | XP_525888.2 | ---- 1493
gi | 73970111 | ref | XP_538474.2 | ---- 1531
gi | 118087949 | ref | XP_419455.2 | ---- 1500
gi | 292620003 | ref | XP_001921439.2 | ---- 1360
gi | 133900950 | ref | NP_001041092.2 | ---- 1099
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