

gi	39973979	ref	XP_368380.1	-----MDLLEQLQKLLTLWLDSEASHAFQR-----VPGSAVLIRYVKSSVQNDPVR-----SAIELVLVVFFIRLMA	150
gi	85089501	ref	XP_957979.1	-----MELQLEQLHLTEWLNELATAFQR-----VPGSAVLIRYVRSSVQNDPVR-----SAIELVLVVFFIRLMA	150
gi	19112640	ref	NP_595848.1	-----MSYSYVPPFDVDAAYNQIVTFQKALDVLPGSPVTKRYIKSSVQNDPLR-----TFIFIFLLLVFAAYVVL	150
gi	24653276	ref	NP_610842.1	-----MVAIQ-LFNEIGSIFRNPTR-----ALVLTLLLIIVTWLHL	150
gi	158289895	ref	XP_311520.4	-----MVNTPYIINEYDILQKSSPF-----ELTLBALLALGVWIVFY	150
gi	29244577	ref	NP_033295.2	-----MATVAEQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	109504676	ref	XP_341496.3	-----MATVAEQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	5454084	ref	NP_006406.1	-----MATATEQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	73946708	ref	XP_541308.2	-----MATAAEQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	77736443	ref	NP_001029921.1	-----MATVAEQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	118104215	ref	XP_423815.2	-----MVAQAFYEVRRVCRGGMLGGCEPRPGVATGSEOTAAGPRPSRDCGLSRRLPAALAVAVGIVSWHRQRKAGFRLSGSCEESGRELERCASAGPPAPCALVYQFLHSILNWLKLLNSVYQAPY-----HLILEGILILWIIRLVS	150
gi	66472918	ref	NP_001018307.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	71982617	ref	NP_001021978.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	115449375	ref	NP_001048451.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	115481358	ref	NP_001064272.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	115451951	ref	NP_001049576.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	79326362	ref	NP_001031796.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	6323954	ref	NP_014025.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	50302995	ref	XP_451435.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150
gi	45185375	ref	NP_983092.1	-----MAGCQQQWLVEMVQALYEAPY-----HLILEGILILWIIRLVS	150



gi	39973979	ref	XP_368380.1	-----PYSYHKNFIKLREDEIDELVEDWTEPELVFARLAQEEAAEAKLPLVIGPTGPKTKLASGRT-----VTNLSTNYNFNANAQIKKAIQILRTYVGVGCGPFPQFYGQDVHMKTEADIAAYIGTEGCIIVYAHAFSAVTSVTPSF	300
gi	85089501	ref	XP_957979.1	-----PAYSRSKQNFIKLDDDEIDELVDEWTEPELVFNMLVLEEMSEKLPILVIGATGPKSKLANGRT-----VTNLASYNFYLNANAQIKKAIQILRTYVGVGCGPFPQFYGQDVHMRAEADIKTEGCIIVYAHAFSAVTSVTPSF	300
gi	19112640	ref	NP_595848.1	-----KRPTSPDNNYVEFKKINELVDWDPKPELVLAELDDEKLEKLEIPVLESVH-LHFKLLIDGRP-----ITNFASFNFLDLAEKHTTECAVALRECEGLGACGPPGFYQDKHLRLEKDIASFGLBRAIVYQAQSCFTSSVIPA	300
gi	24653276	ref	NP_610842.1	-----RRGGG---RRRLKKEKERLIADYEPELVLA---DDEPNPLLHTRVQSRVQKRIQVDGHD-----CLNLGSHNVLFLAEDEILBEACKSLRKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	158289895	ref	XP_311520.4	-----KR-----TTKMPMSSEELARWTEPELVLA---EVDQDPALPKTKRIVEGPGVKMNVNNGKE-----CINMATHNVLGLAEBEDIKQAARKSLRKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	29244577	ref	NP_033295.2	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKNHPALNNYIVSGPPTNIVVNGKE-----CVNFASFNFLGLLANPRVKATAFSLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	109504676	ref	XP_341496.3	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSRNHPALNNYIVSGPPTNIVVNGKE-----CVNFASFNFLGLLANPRVKAAAFSLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	5454084	ref	NP_006406.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVPKHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	73946708	ref	XP_541308.2	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PISKHPALNNYIVSGPPTNIVVNGKE-----CVNFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	77736443	ref	NP_001029921.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	118104215	ref	XP_423815.2	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CVNFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	66472918	ref	NP_001018307.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	71982617	ref	NP_001021978.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	115449375	ref	NP_001048451.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	115481358	ref	NP_001064272.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	115451951	ref	NP_001049576.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	79326362	ref	NP_001031796.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	6323954	ref	NP_014025.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	50302995	ref	XP_451435.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300
gi	45185375	ref	NP_983092.1	-----KTYKLO---ERSDLVAKEKEBELIEEWOPEPLV---PVSKDHPALNNYIVSGPPTNIVVNGKE-----CINFASFNFLGLLANPRVKAALASLKKYGVGCGPRGFYGFDFVHLDLEDRLAKFMGLEBRAIVYQAQSCFTSSVIPA	300



gi	39973979	ref	XP_368380.1	-----CKRGDVIIVADRMANYSIRKLELERSIRWGHGDMEELEAAMAKVAKEQAK--NKK-LTRRFVVEIALSELLGLDIADLPKLELKEKFKRLLIIDEWFSFVGLGRGRLTEAQNVDF--FTQVDMIVGSMAGPLCAGGGFCAGSRVDVEH	450
gi	85089501	ref	XP_957979.1	-----CKRGDIIIVADRMANYSIRKLELERSIRWGHGDMEELEAAMAKVAKEQAK--TKK-LTRRFVVEIALSELLGLDIADLPKLELKEKFKRLLIIDEWFSFVGLGRGRLTEAQNVDF--FTQVDMIVGSMAGPLCAGGGFCAGSRVDVEH	450
gi	19112640	ref	NP_595848.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	24653276	ref	NP_610842.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	158289895	ref	XP_311520.4	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	29244577	ref	NP_033295.2	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	109504676	ref	XP_341496.3	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	5454084	ref	NP_006406.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	73946708	ref	XP_541308.2	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	77736443	ref	NP_001029921.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	118104215	ref	XP_423815.2	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	66472918	ref	NP_001018307.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	71982617	ref	NP_001021978.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	115449375	ref	NP_001048451.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	115481358	ref	NP_001064272.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	115451951	ref	NP_001049576.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	79326362	ref	NP_001031796.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	6323954	ref	NP_014025.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	50302995	ref	XP_451435.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450
gi	45185375	ref	NP_983092.1	-----SKRGDILVVDVDAACFAIQKGLQASRSDIKLFKHNMDADLERLLKQEIETDQKNPRKARVRRFIVVEGLYMNVTGICPLPELVKLYKRYKARIFLEESLSPFVGLGEGHGRVTEHFGIS-IDDDILISANMENALASVGGFCAGSRVDVEH	450



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gi | 39973979 | ref | XP_368380.1 | ORIMSTAVYFSAALPAMTAVLASEIENLNLOSPE-ILSQCRENIKALRAQLDPRSD--WVFCYTSIDNPILLGLKPEV-----IASRRLTAEQDNRLLEQCVDELAN-GVWITRLKIQPVLNITGPKK 600
gi | 85089501 | ref | XP_957979.1 | ORLTAASYTFSAALPAMLAIIASESLHVIQENPEALGVCRENIRLMRAQLDPKSD--WVICTSAPENPILLVLRKQV-----VEARRLTAEQDERLLQEVADCLAN-NILVTRKGGPITTHMGLKD 600
gi | 19112640 | ref | NP_595848.1 | ORLSGMAIYFSAALPAPSLAVAAEYEAISILSRDGGMLNDLRKSKALFPAKLS-RNK---FFETSSEDIESPITHLRFK-----DKDITSDKQVFLLEEVLELCTAE-GFLTARAKRVESLERVK 600
gi | 24653276 | ref | NP_610842.1 | ORLSGLGYIFSAALPPMLTQAASALDRFEREPQ-IFEQLQAKSKTLHQKFLRFK---LTLRGDEVSPVKHLYLAQP-----AENFDKELKLLTELADKCIAR-GVAVVQAAYLQNRERQP 600
gi | 158289895 | ref | XP_311520.4 | ORLSGLGYCFASLPPLLAQAASALDRFESNPR-IFVELRERCRMVSNKLSQLKH---FQSRGDPLSPVKHLYLKHK-----HESWAHEKMLLDEISTEICTDN-GLAVIAAEVLETMEKHC 600
gi | 29244577 | ref | NP_033295.2 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPD-IFAVLKKKQNIHKSLOQVSG---LKVVGESLSPALHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 109504676 | ref | XP_341496.3 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPG-IFAVLKKKQNIHKSLOQVSG---LKVVGESLCPALHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 5454084 | ref | NP_006406.1 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPG-IFAVLKEKCKQIHKALQGISG---LKVVGESLSPAFHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 73946708 | ref | XP_541308.2 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPG-IFSVLKEKCKRIHKALQGISG---LKVVGESLSPAFHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 77736443 | ref | NP_001029921.1 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPG-IFAVLKEKCKRIHKALQGISG---LKVVGESLSPALHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 118104215 | ref | XP_423815.2 | ORLSGGQYCFASLPPLLAAAAEALNIMEENPD-IFAVLKEKCKRIHKALQGISG---LKVVGESLSPALHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 66472918 | ref | NP_001018307.1 | ORLSGGQYCFASLPPMLAAAEALNIMEEDPG-IFRVLREKCRNVKHALQGTAG---LKVVGESFAPALHLQLEES---LGSREKDVKLLQAVDQCMDK-GIALTQARYLDKEEKCL 600
gi | 71982617 | ref | NP_001021978.1 | ORLSGLGYCFASLPPLLATAASEAISIIDEEPS-RVQKVTETMAINGQKQLQDALSGS-KFSLQGCPESPMKHIYVNG-----EDEEKQLDTFVETVFTKNHLLLRARYLDKDELFK 600
gi | 115449375 | ref | NP_001048451.1 | ORLSSGVVFSASLPPVLAASAASAVDHLLEENPS-VLANLRSNITLLHKLSDVQG---LEIASNILSPIVFLKLLTP---LGSVADLELELLEIIEKVLKE-DSVFIAATKRSSLDKCR 600
gi | 115481358 | ref | NP_001064272.1 | ORLSSGVVFSASLPPVLAASAASAVNHLLEENPS-VLANLRSNITALLHKLSDIPG---LEIASNILSPIVFLKLLTP---LGSVADLELEIIEKVLME-DSVFIAATKRSSLDKCR 600
gi | 115451951 | ref | NP_001049576.1 | ORLSSGVVFSASLPPVLAASAASAVSYLEGNPS-VLADLRSNISFLLHKLSDIPG---LEIASNILSPIVFLKLLTP---LGSVADLELEIIEKVLME-DSVFIAATKRSSLDKCR 600
gi | 79326362 | ref | NP_001031796.1 | ORLSSGVVFSASLPPVLAASAATIDVIDQNDP-MLVKLQNVALLWKLSDIKG---MSLITNRESPIVFLKLLTP---LGSVADLELEIIEKVLME-DSVFIAATKRSSLDKCR 600
gi | 6323954 | ref | NP_014025.1 | ORIGSNACFSAALPAMTAVTSVSKVLKLMDSNND-AVQTLQKLSKSLHDSFASDDSLRSVIVTSPVAVLHLQLTAPAYRSRKFYGTCEQLFETMSALQKKSQNKFIETPYEEBEKFLQSIVDHALINYNVLTIRNTIVLKQETLP 600
gi | 50302995 | ref | XP_451435.1 | ORIGSNACFSAALPAMTAVTSVSKVLKLMDSNND-AVQTLQKLSKSLHDSFASDDSLRSVIVTSPVAVLHLQLTAPAYRSRKFYGTCEQLFETMSALQKKSQNKFIETPYEEBEKFLQSIVDHALINYNVLTIRNTIVLKQETLP 600
gi | 45185375 | ref | NP_983092.1 | ORIGSNACYASALPAMTAVTSVSKVLKLMDSNND-AVQTLQKLSKSLHDSFASDDSLRSVIVTSPVAVLHLQLTAPAYRSRKFYGTCEQLFETMSALQKKSQNKFIETPYEEBEKFLQSIVDHALINYNVLTIRNTIVLKQETLP 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi | 39973979 | ref | XP_368380.1 | NI-TIQPALKVCVTSGLSRKDIERAGTIRHAITKVMKSNAKLSPAVAPA 650
gi | 85089501 | ref | XP_957979.1 | NVYIATPALKVCVTSGLSKKETEKAGIAIRHAITKVMTKKGNKLGVPVA 650
gi | 19112640 | ref | NP_595848.1 | ---VQPSLRICISLGHSAEIEKLLALLKKEKTEIVFDKHKVINQV--- 650
gi | 24653276 | ref | NP_610842.1 | ---VRPSIRIHAVNRLLESSEIDNAFEVIESVSSSVL----- 650
gi | 158289895 | ref | XP_311520.4 | ---PRPSIRLTVNRLLEKTEIDDAFRILEHVSEKVFASAG----- 650
gi | 29244577 | ref | NP_033295.2 | ---PPPSIRVVVTVVEQTEEELQRAASTIREAAQAVLL----- 650
gi | 109504676 | ref | XP_341496.3 | ---PPPSIRVVVTVVEQTEEELQRAASTIREAAQAVLL----- 650
gi | 5454084 | ref | NP_006406.1 | ---PPPSIRVVVTVVEQTEEELQRAASTIKEVAQAVLL----- 650
gi | 73946708 | ref | XP_541308.2 | ---PPPSIRVVVTVVEQTEEELQRAASTIKEVAQAVLL----- 650
gi | 77736443 | ref | NP_001029921.1 | ---PPPSIRVVVTVVEQTEEELQRAASTISEVAQTVLL----- 650
gi | 118104215 | ref | XP_423815.2 | ---PSPSIRVVVTVVEQTEQELDKAASLIKEAAKSVLN----- 650
gi | 66472918 | ref | NP_001018307.1 | ---PPPSIRVVVTVVEQTEEIEKKAQCIIEAALHVLK----- 650
gi | 71982617 | ref | NP_001021978.1 | ---IRPSIRVMFQHDLEEEIQRAVDAIRVVVAHKF----- 650
gi | 115449375 | ref | NP_001048451.1 | ---LPVGIRLRFVSAAGHTESDILKVESLKRVAASVVL----- 650
gi | 115481358 | ref | NP_001064272.1 | ---LPVGIRLRFVSAAGHTESDIFKVSASLKRVAASVV----- 650
gi | 115451951 | ref | NP_001049576.1 | ---LPVGIRLRFMSAGHTSDSIDKVSSSLKRVASASVLSDYI----- 650
gi | 79326362 | ref | NP_001031796.1 | ---LPVGIRKLYVSAAGHTESDLLKASESLKRVAASVLLK----- 650
gi | 6323954 | ref | NP_014025.1 | ---IVPSLKICCNAAAMPSELKNAGESVKQILACCQESNK----- 650
gi | 50302995 | ref | XP_451435.1 | ---VTNISICCNSSMESEQLLDANVIRIAIKKCSSEA----- 650
gi | 45185375 | ref | NP_983092.1 | ---IVPSLKAYCHAAMSCSELERAEVIAKAAIACCAQPSL----- 650
.....610.....620.....630.....640.....650

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