

gi	40317626	ref	NP_003237.2	MGCEPQGFPPARAEILWISSFYLCPLGASPIALDHSRGEAAADVPSRRDEWNSRQLES CWLGTVAWRPFDNDRSTRQRHSWCVHPQKCNPHLGFRSRKMKRTFREKGRVNNRQRKAAVLPGLDENHHLAKRPAEGAPRQRERRIC	150
gi	114656320	ref	XP_510294.2	-----	
gi	41386685	ref	NP_776621.1	-----	
gi	73999965	ref	XP_544610.2	-----MLPQVLPQGVILRSTSGHRNCFSSRKARFG	30
gi	47059073	ref	NP_035710.2	-----	
gi	118091761	ref	XP_421205.2	-----	
gi	189533247	ref	XP_690395.3	-----	

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

gi	40317626	ref	NP_003237.2	-----	13
gi	114656320	ref	XP_510294.2	GPPGSRGRKAPESSEGERRRARRNLPAPPTRSPSPSPGPGVGAQDRSSGDACPHPTGTVESQRGPEGQRAAPPCCPLRPSWPASSGLLPLSRSNLYSGRTGSPRAPPALAALATAPGRRAPVHTGSLGINSSTMGLAWGLGVLFILM	300
gi	41386685	ref	NP_776621.1	-----	13
gi	73999965	ref	XP_544610.2	CLVLLGGRS-----LRGRGQAAAGAGPPIRVQDRPQAHRPAAPP-----AIASSGLPPRASPDAPPRAAPERIGSRLGTSGSTMGLAWALGVLFLL	120
gi	47059073	ref	NP_035710.2	-----	13
gi	118091761	ref	XP_421205.2	-----	12
gi	189533247	ref	XP_690395.3	-----	10

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

gi	40317626	ref	NP_003237.2	HVCC--TNRIPES--GGDNSVDFDIFELT---GAARKGSGRRLVKGPDSPSPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	157
gi	114656320	ref	XP_510294.2	HVCC--TNRIPES--GGDNSVDFDIFELT---GAARKGSGRRLVKGPDSPSPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	444
gi	41386685	ref	NP_776621.1	HACC--SNRIPES--GGDNSVDFDIFELT---GAARKGSGRRLVKGPDSPSPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	157
gi	73999965	ref	XP_544610.2	RVCA--SSRLPES--GGDNSVDFDIFELT---GAARKGSGRRLVKGPDSPSPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	264
gi	47059073	ref	NP_035710.2	HMCG--SNRIPES--GGDNGVDFDIFELI---GGARRGPGRRLVKGQDLSPPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	157
gi	118091761	ref	XP_421205.2	ALGCPPEAKRTAESRQDDSVDFDIFELVVRKAGRRAPGVHLVKGPDSPSPAFRIEDANLIPVPPDDKFDLVDVAVRAEKGFLLASLRQMKTRGTLALERKDHSGQVFSVVSNGKAGTLDLSTVQGRQHVVSVEALLATGOWKSIIT	162
gi	189533247	ref	XP_690395.3	MLWNCESARVAES--RDDNSVDFDIFELV---QVPRKNHGVTLVKGDDEYEPAYKILNPLDILPPVPSAFRDLIDSLHAEKGFLLVNVKQPKFRTRGSLTVERKDGSGVFEIVSNGKANTLDIVFSTENKQQLVSVVEADLAVGHWKNIT	156

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

gi	40317626	ref	NP_003237.2	LFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSVLLTLDNNVVGSSPAIRTNYIGHKTKDLQAIICGIS CDELSMVLRLGLRTIVTITLQDSIRKVTTEENK	306
gi	114656320	ref	XP_510294.2	LFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSVLLTLDNNVVGSSPAIRTNYIGHKTKDLQAIICGIS CDELSMVLRLGLRTIVTITLQDSIRKVTTEENK	593
gi	41386685	ref	NP_776621.1	LFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSVLLTLDNNVVGSSPAIRTNYIGHKTKDLQAIICGIS CDELSMVLRLGLRTIVTITLQDSIRKVTTEENK	306
gi	73999965	ref	XP_544610.2	LFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSVLLTLDNNVVGSSPAIRTNYIGHKTKDLQAIICGIS CDELSMVLRLGLRTIVTITLQDSIRKVTTEENK	413
gi	47059073	ref	NP_035710.2	LFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSVLLTLDNNVVGSSPAIRTNYIGHKTKDLQAIICGIS CDELSMVLRLGLRTIVTITLQDSIRKVTTEENK	310
gi	118091761	ref	XP_421205.2	LFVQEDRAQLYVGCCKMENAEILDVPIQSVFTRDLAS IARLRIAKGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSS--STSAITLTDK-PMNGSSPAIRTNYIGHKTKDLQAVCGFS CDELINMFLRLGLRTIVTITLQDSIRKVTTEENK	307
gi	189533247	ref	XP_690395.3	LFVQEDRVQVYVGCCEVNVAEILDASIHITLQETIPGVAKMRIKGAVKDRFQGVLQNVRFVFGTTPEDILRNKGCSS--AMTDITLDN-PINGSSPAIRTNYIGHKTKDLQAVCGFS CDELIAAMFKELKGLGVVQELS NELRKLTDKRN	305

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

gi	40317626	ref	NP_003237.2	ELANELRRPP--LCYHNGVQYRNNEEWTVDSCTECHCONSVTIICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSTSCGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGDG	454
gi	114656320	ref	XP_510294.2	ELANELRRPP--LCYHNGVQYRNNEEWTVDSCTECHCONSVTIICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSTSCGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGDG	741
gi	41386685	ref	NP_776621.1	ELANELRRPP--LCYHNGVQYRTGDEWTVDSCTECHCONSVTIICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSTSCGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGDG	454
gi	73999965	ref	XP_544610.2	ELAIELRRPP--LCYHNGVQYRNNEEWTVDSCTECHCONSVTIICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSAACGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGDG	561
gi	47059073	ref	NP_035710.2	ELVSELKRRP--LCFHNGVQYKNNNEEWTVDSCTECHCONSVTIICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSAACGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGDG	455
gi	118091761	ref	XP_421205.2	LIAKVQITPQVIHNGILHKKEEWTVDSCTECHCONSATICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CSVTSCGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGTG	459
gi	189533247	ref	XP_690395.3	MLNMQGIRAGVCLHNGVHKNKEEWTVDSCTECHCONSATICKKVSQCPIMPNSNATVPDGECCPRC-WPDSADDDGWSWSEWTS CGRGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHSPWSSCSVT CGAG	455

.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

gi|40317626|ref|NP\_003237.2| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 604  
gi|114656320|ref|XP\_510294.2| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 891  
gi|41386685|ref|NP\_776621.1| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 604  
gi|73999965|ref|XP\_544610.2| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 711  
gi|47059073|ref|NP\_035710.2| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 605  
gi|118091761|ref|XP\_421205.2| MITRIRLNCNSPVPOLNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 609  
gi|189533247|ref|XP\_690395.3| VITRIRLNCNSPSPOMNGKPCGEARETKACKKDACPIINGGWGWPSPWDICSVTCGGGVQKRRLCNPPTPFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGWSKCGACPPGYSNGIQCCTDVDECKEVPDACEFNHNG 605



gi|40317626|ref|NP\_003237.2| EHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 754  
gi|114656320|ref|XP\_510294.2| EHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 1041  
gi|41386685|ref|NP\_776621.1| EHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 754  
gi|73999965|ref|XP\_544610.2| EHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 861  
gi|47059073|ref|NP\_035710.2| EHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 755  
gi|118091761|ref|XP\_421205.2| VHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 759  
gi|189533247|ref|XP\_690395.3| VHRCENTDPGYNCLPCPPRFTGSPFFGQVEHAIAHAKOVCKPRNPCTDGTGTHDCNKNAKCNLYLGHYSDDPMYRCECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGOEDYDKDGIADACDDDDNDKIPDDRDC 755



gi|40317626|ref|NP\_003237.2| PFHYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 904  
gi|114656320|ref|XP\_510294.2| PFHYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 1191  
gi|41386685|ref|NP\_776621.1| PFHYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 904  
gi|73999965|ref|XP\_544610.2| PFHYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 1011  
gi|47059073|ref|NP\_035710.2| PFHYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 905  
gi|118091761|ref|XP\_421205.2| PFIYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 909  
gi|189533247|ref|XP\_690395.3| PFIYNPAQYDVRDDVGRDCNCPYVNHNPQADIDNNEGEGDACAADIDGDLNERDNCQYVYVNDQRDITDMDGVGDQCDNCPLEHNPDLSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPAQAADHDKDGKDA CDHDDNDGIP 905



gi|40317626|ref|NP\_003237.2| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1054  
gi|114656320|ref|XP\_510294.2| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1341  
gi|41386685|ref|NP\_776621.1| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1054  
gi|73999965|ref|XP\_544610.2| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1161  
gi|47059073|ref|NP\_035710.2| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1055  
gi|118091761|ref|XP\_421205.2| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1059  
gi|189533247|ref|XP\_690395.3| DDKDNCRVLVNPDLQKSDGDRGDAKDDDFDHSVVDIDDIICPENVDISETDFRRFOMIPLDPKGTSONDPNWWVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGVFVGYQSSSRFYVVMWKOVTQSYWDTNPTK 1055



gi|40317626|ref|NP\_003237.2| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1170  
gi|114656320|ref|XP\_510294.2| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1457  
gi|41386685|ref|NP\_776621.1| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1170  
gi|73999965|ref|XP\_544610.2| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1277  
gi|47059073|ref|NP\_035710.2| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1171  
gi|118091761|ref|XP\_421205.2| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1175  
gi|189533247|ref|XP\_690395.3| ACGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADS GPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECDP 1171

