

gi	94400840	ref	NP_941044.2	-----MNSRVTPGTTAIGELCFEIVHS	23
gi	109501882	ref	XP_224403.4	MAILAPLGTIRSSSLAHRSSDPDLSPRGKVAIRWIKRPGDVIDECCGRREAKITGVPAASWHLPGPECMSSRFDAVTEPGLVLEURLCKPHTALLANPYDSDPFEQSIYDITQHYCNKLIRPLAGHVMSRIITPSGTTAIGELSFHVVHS	150
gi	156151402	ref	NP_079389.2	-----	
gi	114651507	ref	XP_001156463.1	-----	
gi	156120729	ref	NP_001095511.1	-----	
gi	73989288	ref	XP_542570.2	-----	
gi	118084876	ref	XP_417049.2	-----MSVSSSCLVVPVWLGAFRRGSGKLSAPSLKVDFTESAFPSNLSVIRISGLAPIPQISVLSDEYRPAVIGHAG-----LSLASYPSAEAIKIDILVSVLSASGLKPSL	101
gi	125825979	ref	XP_690079.2	-----	

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

gi	94400840	ref	NP_941044.2	IIPGKMVSSQIGWGDSPVDLCEGSNRAFDQTD-----QPACOLDVRLLRKASWINPLCVOOPLDELCPORPTVQSFENHVVDLTPSPRLRLILSVRDSLAEMLSENTADVICNSAHCSSGGKEGDFFLATEEVEVHLQ-----QE	160
gi	109501882	ref	XP_224403.4	IIPGKMVSQSTGQDYPMDCSERISHAFQADAGLFSVLDTDQACOLDVRLVRHKASWINPLCVOOPLRESGLORPTVQSFENHVVDLTPSPDLILFQDRLAEMLSENTADVICNSAHCSSGGKEGDFFLATEEVEVHLQ-----QE	296
gi	156151402	ref	NP_079389.2	-----MVSQSTVRODPSVPEWEGISDHSGLIDGSPRLNLDHPPCOLDIRLMRHKAWINPQDVOQQPDLSQVPAAGNSGTHFVTDAAASPSGPPSCLGDSLAETILSEDTDSVGSASPHGSSEKSSSFLSSSTVHMVVRPGYSHRV	146
gi	114651507	ref	XP_001156463.1	-----MVSQFTVRODPSVPEWEGISDHSGLIDGSPRLNLDHPPCOLDIRLMRHKAWINPQDVOQQPDLSQVPAAGNSGTHFVTDAAASPSGPPSCLGDSLAETILSEDTDSVGSASPHGSSEKSSSFLSSSTVHMVVRPGYSHRV	146
gi	156120729	ref	NP_001095511.1	-----MVSQSSGRODPSVPEWEGISDHSGLIDGSPRLNLDHPPCOLDIRLMRHKAWINPQDVOQQPDLSQVPAAGNSGTHFVTDAAASPSGPPSCLGDSLAETILSEDTDSVGSASPHGSSEKSSSFLSSSTVHMVVRPGYSHRV	146
gi	73989288	ref	XP_542570.2	-----MTAVLVCVSNHFLVAVPR-----RFAAARPRPAGRVASRR-PESASPP-----AAADTCSPSE--PGRWCPERRAGRPHPERPSCPSGQCVAATGGPHS	86
gi	118084876	ref	XP_417049.2	LSSEHILAMCAEHPDSDLERWEEESDGENDDTDSDSAHQSTACTQTDVFRTRERACWDIRNCSSRPALDTFFHPCSDSDPATSSLNQFTLSDSPLKRCDCFTQVLLTGGTVTSAVVHPEKEQNLFKQDQLLRLPPDSTVSKPADL	251
gi	125825979	ref	XP_690079.2	-----MFAILLSCFLCAQAGSR-----SITGDLHFPAKLVDWEPSPNPITDDDDDEEBEENDEIRESEVKECNFVSECDSDFLNDEYHLPSSSVPICRKRPNIDTKQCKGSLVTPPLWISITSP-----	118

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

gi	94400840	ref	NP_941044.2	LLKNPKTIVATSPSPKESARSESPIHTASTDDG-DARSSRSRAWNPFFPLETFMLPADVEKENLHFYAADIIIVIVNMKCNLENQOQPERWDTEDAARLRGTG---AEMTFYTHIKQEPGSSAASHHCCEGCAALQVSPVAEILSYCFV	306
gi	109501882	ref	XP_224403.4	LLKNPKAVATSPFSK-ASVHSESPIHTASTDDG-DACSS-RSHSWNPFFLETFILPADMEKENLHFYAADIIIVIVENLKCNCILLSQOQPGSGTBEAARSCGTG---AEMTFYTHIKQEPGSSAASHHCCEGCAALQVSPVAEILSYCFV	440
gi	156151402	ref	NP_079389.2	LFITSPGILATSPPEETDIAFFEPESHLTSADEG-AVQVSRRTIISNFSFSEVFLVVDVEKENAHFYVADMIISAMEKMKCNILSQOQTESWSK-EVSGLLGSDQDSEMFDINIKQESGSSSTSSYSGYEGCAVLQVSPVTEIRIYHV	294
gi	114651507	ref	XP_001156463.1	LFITSPRILATSPPETDIAFFEPESHLTSADEG-AVQVSRRTIISNFSFSEVFLVVDVEKENAHFYVADMIISAMEKMKCNILSQOQTESWSK-EVSGLLGSDQDSEMFDINIKQESGSSSTSSYSGYEGCAVLQVSPVTEIRIYHV	295
gi	156120729	ref	NP_001095511.1	LITSSKIVSGPPCPEDGRAFFPKPSQLTADAD-AVQVGGRTVSNFSFSEVFLVVDVEKENAHFYVADMIISAMEKMKCNILSQOQTESWTSTBEAARSLGNRADLEGTFYTHVQKESGSSSTSSDGYEGC-VLQVSPVTEIRIYFSEV	294
gi	73989288	ref	XP_542570.2	---GPILVATSEFSSEVC---PPHADSAQRQ-AVQGR---HLNRFSPAEFLVVDVEKENAHFYVADMIISAMEKMKCNILSQOQTESWTSTBEAARSLGNRADLEGTFYTHVQKESGSSSTSSDGYEGC-VLQVSPVTEIRIYFSEV	223
gi	118084876	ref	XP_417049.2	FKYPAASAPKAVSNADSSSPAFSQLEPPNQGTGASLNLNIAVPLNRLQDTPVLPEDVEKENAHFYVADMIISAMEKMKCNILSQOQTESWTSTBEAARSLGNRADLEGTFYTHVQKESGSSSTSSDGYEGC-VLQVSPVTEIRIYFSEV	400
gi	125825979	ref	XP_690079.2	---GLKSNASSPHRLBELRRSENERNFDECDLSQSSRQMLLLDKQHGTRISHVSDTQFHSLPFFGRRLHEELTKRACSDIPIINRKSDDQAKHWFPIGDSNEDINSLDQENAHFVVVDMLLEVLVAVKWAVCLQQSNINPNNRD	265

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

gi	94400840	ref	NP_941044.2	AGEACKHD-LNKLVMLELQKYNIDIKGCRCSYNSSKSAATCESNLSAPAGCLARELFRGFCKCWMLL-EVNCQLPGSPITASGVGDDEEYAEEDFSSVDAAREVLMKSRVPGTEDDVLPRCQIILTVPHPKIRDIAVVAONFFCAGCGTPI	454
gi	109501882	ref	XP_224403.4	ATEACTLD-LNKLVMLELQKYNIDIKGCRCSYNSSKSAATCESNLSAPAGCLARELFRGFYKYNMLESSEVTRPPGSLIPASGVGEEQAEELDSSVDIAREVLMKSRVPGTEDDVLPRCQIILTVPHPKIRDIAVVAONFFCAGCGTPI	589
gi	156151402	ref	NP_079389.2	-KEICKCD-VDEFVILELGFNDITETCSKSCSSSSKSVIYEPDFNSAELLAELAKELYRVFKCWMLL-VVNSQLAGSLAAGSIVVNEEHRVDFESSMNVQVEIKFKSRIRGTEWAPPRFOIIFNHPPLKRDLVVAONFFCAGCGTPI	441
gi	114651507	ref	XP_001156463.1	-KEICKCD-VDEFVILELGFNDITETCSKSCSSSSKSVIYEPDFNSAELLAELAKELYRVFKCWMLL-VVNSQLAGSLAAGSIVVNEEHRVDFESSMNVQVEIKFKSRIRGTEWAPPRFOIIFNHPPLKRDLVVAONFFCAGCGTPI	442
gi	156120729	ref	NP_001095511.1	TEEDCKCD-FDDFVIVELGDFNSNTEPCGSSDTSKSVIHEPNFNSAELLAELAKELYRVFKCWMLL-EVHYDLTGLSDDAAGSIVNEERVQKDFESSVDVQVEIKLRSIRGTEWAPPRFOIIFNHPPLKRDLVVAONFFCAGCGTPI	442
gi	73989288	ref	XP_542570.2	LKEACKCD-FDDFVIVELGDFNSNTEPCGSSDTSKSVIHEPNFNSAELLAELAKELYRVFKCWMLL-EVHYDLTGLSDDAAGSIVNEERVQKDFESSVDVQVEIKLRSIRGTEWAPPRFOIIFNHPPLKRDLVVAONFFCAGCGTPI	371
gi	118084876	ref	XP_417049.2	TGLPCHSDSEDEVVILEHELENLVSINERNSLAPAGCLARELFRGFCKCWMLL-EVNCQLPGSPITASGVGDDEEYAEEDFSSVDAAREVLMKSRVPGTEDDVLPRCQIILTVPHPKIRDIAVVAONFFCAGCGTPI	547
gi	125825979	ref	XP_690079.2	RCETHDLSKIDSIASSDGFEEISERYSLASFSQ--CLQSRTQCAENLAHRLVSEFRKQWFS---ELLKNPVLNLS-ALQEVLPFIMGERISLSEIIMMKRMRGTFWAPPRFOIIFVQVPTRRSVDIASOHPLCAGCGTPI	407

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

gi	94400840	ref	NP_941044.2	GPKFVKRLRYCEYLGKVFCDCHSSAESCIPARILTMWDFRKYQVDFSKWLLDSVWHQPVFKLLGGHSLYAKAKELDRVKDIEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	604
gi	109501882	ref	XP_224403.4	GPKFVKRLRYCEYLGKVFCDCHSSAESCIPARILTMWDFRKYQVDFSKWLLDSVWHQPVFKLLGGHSLYAKAKELDRVKDIEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	739
gi	156151402	ref	NP_079389.2	EPKFVKRLRYCEYLGKVFCDCHSSAESCIPARILMMWDFKKYVVSFNFSKRLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFANSALKFEQVPGHLDDELHLSLEDLVRIKKGLLAPLLKDLKASLHV	591
gi	114651507	ref	XP_001156463.1	EPKFVKRLRYCEYLGKVFCDCHSSAESCIPARILMMWDFKKYVVSFNFSKRLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFANSALKFEQVPGHLDDELHLSLEDLVRIKKGLLAPLLKDLKASLHV	592
gi	156120729	ref	NP_001095511.1	EPKFVKRLRYCEYLGKVFCDCHSSAESCIPARILMMWDFRKYVVSFNFSKRLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	592
gi	73989288	ref	XP_542570.2	EPKFVRLRYCDYLGKVFCDCHSYAESCIPARILTMWDFRKYVVSFNFSKRLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	521
gi	118084876	ref	XP_417049.2	ESKYIRRLRYCDYLGKVFCDCHSYAQAIPARILMMWDFRKYVVSFNFSKRLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	697
gi	125825979	ref	XP_690079.2	EARYMKLRYCDYLGKVFCDCHGGLETVIPGRVLLNNWDFARYVPCNFSRQLDLSIWHQPIFNLLSIQSLYAKAKELDRVKEIQEQLPHIKKLLKTCRFADSVLKEFEQVPSHLTDECHIFSMDDFLRTKKGGLLAPLLKDLKASLHV	557

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

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gi|94400840|ref|NP_941044.2|DSCELCQKGFICEFCQSTTVIIPFFQTTTCRRCAACRACFHKCFQSSRCPCARIARROHLESLPAA 675
gi|109501882|ref|XP_224403.4|DSCELCQKGFICEFCQSTTVIIPFFQTTTCRRCAACRACFHKCFQSSRCPCARIARROHLESLPAA 808
gi|156151402|ref|NP_079389.2|AGCELCQKGFICEFCQNTTVIIPFFQTAACRRCSACRACFHKCFQSSRCPCARIARRRLLSVASAA 662
gi|114651507|ref|XP_001156463.1|AGCELCQKGFICEFCQNTTVIIPFFQTAACRRCSACRACFHKCFQSSRCPCARIARRRLLSVASAA 663
gi|156120729|ref|NP_001095511.1|ASCELCQKGFICEFCRSTAVIIPFFQTAACRRCSACRACFHKCFQSSRCPCARIARRRLLSVASAA 663
gi|73989288|ref|XP_542570.2|ASCELCQKGFICEFCQSTAVIIPFFQTEICRRCAACRACFHKCFQSSRCPCARIARRRLLSVASAA 592
gi|118084876|ref|XP_417049.2|DGCELCQAKGFICEFCQSDLLFAFQISKCKRCFECKACFHKCFKAGGCPKCLRIARRTLSETPSQVPL 768
gi|125825979|ref|XP_690079.2|DFCELCQAKGFICEFCQSGKEVLFQFQRTICTRCQDCRACFHISCFRDESCPKCARLQKRRKLEQDMV--- 625
.....760.....770.....780.....790.....800.....810.....820.

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