

gi	24584474	ref	NP_723925.1	MGLNAKSVCSSTSEPNQSIIVTITAPSNCEVSSSIVVVVSSSSISSSSSDPTAILPHDPPIPTSTFSSASQRSEELPGTSAASRTDEMCSCDSONLAASTAAATSNGNKRKRRLSSDSEEDPELGFEPPEAKRQORLPALYGEQGNLSSV	150
gi	158296948	ref	XP_317276.4	-----	
gi	110227586	ref	NP_031659.2	-----	
gi	109458606	ref	XP_574426.2	-----	
gi	17318559	ref	NP_001229.1	-----	
gi	114676470	ref	XP_512559.2	-----	
gi	73948568	ref	XP_541724.2	-----	
gi	119910263	ref	XP_612960.3	-----	
gi	71897105	ref	NP_001026529.1	-----	
gi	18858511	ref	NP_571070.1	-----	
gi	71981558	ref	NP_001021028.1	-----MAGRKRSSRFAERVPPTQKPERKSAILSPHDELRELLLETAIDMKENIPQRNTR	53

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

gi	24584474	ref	NP_723925.1	ASSVYSPVVSVDGQSTPELLSIRSSPAEDLSFAPHSPLPDSPPSPDRGSKQTPVVVRYAAEQVVISVVTIKTEDDDLLDSCEDYSYDDEDDVEEEDDDVEIYSSGISPASSGCSQQQAVNGERTFGLPKHGEQIHHFVLDLM	300
gi	158296948	ref	XP_317276.4	-----	
gi	110227586	ref	NP_031659.2	-----MPREK---DSTD-----HSNMKEEGGSDLSVR--SRKRKANVAVF-----LQDPDEEIAKIDKIVKSEDSQP-WDNNACVDPCCSIFIPFNKEEDN---ELEYPRK	88
gi	109458606	ref	XP_574426.2	-----MPREKREKRSKD-----HSNMKEEGGSDLSVR--SRKRKANVAVF-----LQDPDEEIAKIDKIVKSEDSQP-WDNNACVDPCCSIFIPFNKEEDN---ELEYPKT	91
gi	17318559	ref	NP_001229.1	-----MPREKREKREDAKE-----RDTMKEDGGAEFSAR--SRKRKANVAVF-----LQDPDEEMAKIDRTARDCCGSSQP-WDNNACVADPCSLIPFPDKEDD---DRVVPNS	90
gi	114676470	ref	XP_512559.2	-----MPREKREKREDAKE-----RDTMKEDGGAEFSAR--SRKRKANVAVF-----LQDPDEEMAKIDRTARDCCGSSQP-WDNNACVADPCSLIPFPDKEDD---DRVVPNS	72
gi	73948568	ref	XP_541724.2	-----MPIGQASRLCKAQSLLVLRGKHFAREARSADAPFPPPPPLLAQPSGSRCPALPEKARASQASSIAHTFPQGLGVNVPSP---QHSFLQDPDEEIVAKIDRTARGCCGSSQP-WDNNACENPCSLIPFPDKEDD---EPAYPSS	136
gi	119910263	ref	XP_612960.3	-----MPREKREKREDAKE-----RDTMKEDGGAEFSAR--SRKRKANVAVF-----LQDPDEEIAKIDRTARDCCGSSQP-WDNNACVADPCSLIPFPDKEDD---DRVVPNS	89
gi	71897105	ref	NP_001026529.1	-----MRRRESDAEE---KAPAKGEGGAEFTVR--ARKRKADVAIF-----LQDPDEEIAKIDRTARDCCGSSQP-WDNNACVADPCSLIPFPDKEDD---ELEYVPH	87
gi	18858511	ref	NP_571070.1	-----MPSKKVLQTEH---INTTDEAPKTSVR--PRKRKADVAIF-----LQDPDEEIVTEMTR--KKQCAACACNPPDTGTSFCRRIPFPDEVEEVEVAFSGVGTQY	92
gi	71981558	ref	NP_001021028.1	-----NSVVGSKSDCSETRKRKRSKKEGPAARRHSGEKHRNGSREDSLEYISDREVEVSSSQSERTGQPLPAMPBEEVVFQKSSSSDN-----LAESSESHEMVRLERQDIEEIEDFDEEEDVVNDKEEVEEIESEDEDDYFVQNEG	196

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

gi	24584474	ref	NP_723925.1	INMRTFMSPAVENGLRQCPLPALAWA---NAADVWRMLMCHRDEQDRLRSISMLEQHPGLQPRMRAILLDWLIEVCEVYKLRHRETFYLAVDYLDRLYLV-AHKVQKTHLQIGIICLFVAAKVEEYPPKIGEFAYVTDGACTERDILN	446
gi	158296948	ref	XP_317276.4	-----	
gi	110227586	ref	NP_031659.2	-----AFQPRKIRP---PRASPLPVLNWG---NREEVWRIMLNKEK---TYLRDEHFLQRHPLLOARMRAVLLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QHNITKTLLOLIGISALFIAASKLEEYPPKLFQFAYVTDGACSGDEILTM	227
gi	109458606	ref	XP_574426.2	-----AFQPRKIRP---PRASPLPVLNWG---NREEVWRIMLNKEK---TYLRDEHFLQRHPLLOARMRAVLLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QHNITKTLLOLIGISALFIAASKLEEYPPKLFQFAYVTDGACSGDEILTM	230
gi	17318559	ref	NP_001229.1	-----TCKPRIIAP---SRGSPLPVLNSWA---NREEVWKIMLNKEK---TYLRDQHFLQHPPLLOPKMRAILLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLFQFAYVTDGACSGDEILTM	229
gi	114676470	ref	XP_512559.2	-----TCKPRIIAP---SRGSPLPVLNSWA---NREEVWKIMLNKEK---TYLRDQHFLQHPPLLOPKMRAILLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLFQFAYVTDGACSGDEILTM	211
gi	73948568	ref	XP_541724.2	-----VCGPQSFMP---SRASPLPLLNWA---NRDEVWKIMLNKEK---TYLRDKHFMQRHPLLOPKMRAILLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLFQFAYVTDGACSGDEILTM	275
gi	119910263	ref	XP_612960.3	-----AVKPRQSTPS---SRASPLPVLNWA---NREEVWKIMLNKEK---TYLRDKHFMQRHPLLOPKMRAILLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLFQFAYVTDGACSGDEILTM	230
gi	71897105	ref	NP_001026529.1	-----HFIHLNVA---TRSSPLPILQWA---NRDQVWKIMLNKEE---TYVRDKLYMQRHPLLOPKMRAILLDWLMEVCEVYKLYRRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLFQFAYVTDGACTEDELISM	226
gi	18858511	ref	NP_571070.1	-----ASESIFITP---TRSSPLPILQWA---SKDEVWNNLLGKDK---LYLRDTRVMERHPNLOPKMRAILLDWLMEVCEVYKLRHRETFYLAODFFDRYMA--QENVVKTLLQLIGISLFIAAKLEEYPPKLVQFAYVTDGACTEEDILSM	231
gi	71981558	ref	NP_001021028.1	-----FAVTKRLMNDHMHVAPHFLSIAKCDGIGSPTKVWSLWVKRDE--IPRATERFLGNHPDMDDEKRRILLDWMEVCESEKLRHRETFYLAVDYVDRVLESSEVCESTDNFLVGTAAFLIAAKVEEYPPKCIDFAHLDFAFTCDNIRIM	344

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

gi	24584474	ref	NP_723925.1	EKILLQALDWDISPITITGWLGVYMLNVLNRRTPAFSFGIGRQKSAEADDAFIYQFSGFEFVOTSQLDLCLTDVGMANYSVLAALAAISH-LFREMALRCGLDQVITPCARWMEFFFRVISKAP--YLQLNQNEQVSNKFGI	593
gi	158296948	ref	XP_317276.4	-----	
gi	110227586	ref	NP_031659.2	-----ELMMMKALKWRLSPLTIIVSWLNVVQVAYVN---DTGEVLMPOVPOQVFOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIEKCVKWMVPPFAMVIREMGSS---KL	344
gi	109458606	ref	XP_574426.2	-----ELMMMKALKWRLSPLTIIVSWLNVVQVAYVN---DTGEVLMPOVPOQVFOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIEKCVKWMVPPFAMVIREMGSS---KL	347
gi	17318559	ref	NP_001229.1	-----ELMIMKALKWRLSPLTIIVSWLNVVQVAYLN---DLHEVLLPOVPOQIFIOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIENCVWVPPFAMVIRETGSS---KL	346
gi	114676470	ref	XP_512559.2	-----ELMIMKALKWRLSPLTIIVSWLNVVQVAYLN---DLHEVLLPOVPOQIFIOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIENCVWVPPFAMVIRETGSS---KL	328
gi	73948568	ref	XP_541724.2	-----ELIIMKALKWHLSPLTIVSWLNVVQVAYLN---DLHEVLLPOVPOQIFIOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIEKCVKWMVPPFAMVIRETGSS---KL	392
gi	119910263	ref	XP_612960.3	-----ELIIMKALKWHLSPLTIVSWLNVVQVAYLN---DVVEVLLPOVPOQIFIOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIEKCVKWMVPPFAMVIRETGSS---KL	347
gi	71897105	ref	NP_001026529.1	-----ELIIMKALNWNLNPITVSWLNVVQVAYLN---ELVEVLLPOVPOQIFIOIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELMQKVSQYQWCDIEKCVKWMVPPFAMVIRETGSS---KL	343
gi	18858511	ref	NP_571070.1	-----ELIIMKELNWSLSPITVAVLNIYQVAYLK---ETAEVLTAAQVPAIAEILLDCLVDVGCLEFPYGVLAASALYH-FSSLELVTKVSGLKWCDIEKCVWVPPFAMVIREAGSS---AL	348
gi	71981558	ref	NP_001021028.1	-----EVLIVKVIQWLSGPTISIQWLSYVQLLGLGKK---NKSDEHYEQNMVPELRRSEVLEMCKILLDFLLFEIDSTFTSVRTIAAAVLFVNYEPTCAVKAATGFMAQLEKVIYVEFVCRAPAKORQLD	472

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

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gi | 24584474 |ref| NP_723925.1 | GLICPNIVTDDSHIIQTHTTTMDMYDEVLMADAAHAMRARIQASPAALRALRAPESLLTPPASSHKFDDEYLGDGDETGARSGISSTTTCNTAASNKGGKSSSNNSVTSCSSRSNP 709
gi | 158296948 |ref| XP_317276.4 | KHICPNLVSDSSHIIQTHTT-----AQAKKAILSEQNRIS-PPPSVVLTPPPSSKKQSSSEQEIE----- 110
gi | 110227586 |ref| NP_031659.2 | KHFRG-VPMEDSHNIQTHINSLDLLDR-----AQAKKAILSEQNRIS-PPPSVVLTPPPSSKKQSSSEQEIE----- 408
gi | 109458606 |ref| XP_574426.2 | KHFRG-VPMEDSHNIQTHINSLDLLDR-----AQAKKAILSEQNRIS-PPPSVVLTPPPSSKKQSSSEQEIE----- 411
gi | 17318559 |ref| NP_001229.1 | KHFRG-VADEDAHNIQTHRDRLDLLDR-----ARAKKAMLEQNRRAS-PLPSGLLTPPSSGKKQSSGPEMA----- 410
gi | 114676470 |ref| XP_512559.2 | KHFRG-VADEDAHNIQTHRDRLDLLDR-----ARAKKAMLEQNRRAS-PLPSGLLTPPSSGKKQSSGPEMA----- 393
gi | 73948568 |ref| XP_541724.2 | KHFRG-VPAEDAHNIQTHINSLDLLDR-----AQAKKAILSEQNRIS-PPPTGVLTTPPSSKKQSSGQDTA----- 456
gi | 119910263 |ref| XP_612960.3 | KHFRG-VPAEDAHNIQTHINSLDLLDR-----AQAKKAILSEQNRIS-PLPTGVLTTPPSSKKQSSGQSSA----- 411
gi | 71897105 |ref| NP_001026529.1 | KHFRG-IAPEDLHNIQTHINSLDLLDR-----AQAKKAILSEQNRIS-PPPTGVLTTPPSSKKQSSGAGLKPI----- 407
gi | 18858511 |ref| NP_571070.1 | KTFKG-IAADDMHNIQTHVPLEWLGR-----VHSYQLVDIESSQRS-PVPTGVLTTPPSSKKQSSGPESTIS----- 410
gi | 71981558 |ref| NP_001021028.1 | IPKHESIKSDSSHNIQVNVK-----RSSMEPIVKSEERERIQHLKARRLHPQRLF----- 521
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....

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