

gi	6679695	ref	NP_031982.1	MTMLHTKASGMALLHQIQGNELEPLNRPOLKMPMERALGEVYVDSKPTVFNYPGEAAVEFNAAAAAASAPVYQSGIAYGPGSE---AAAFSANSLGAFPPQLNSVSPSPMLMLLHPPQ-LSPFLHPHG-----QQVPHYLENE	139
gi	6978815	ref	NP_036821.1	MTMLHTKASGMALLHQIQGNELEPLNRPOLKMPMERALGEVYVDSKPAVFNYPGEAAVEFNAAAAAASAPVYQSGIAYGPGSE---AAAFGANSLGAFPPQLNSVSPSPMLMLLHPPH-VSPFLHPHG-----HQVPHYLENE	140
gi	62821794	ref	NP_000116.2	MTMLHTKASGMALLHQIQGNELEPLNRPOLKIPLERPLGEVYVDSKPAVFNYPGEAAVEFNAAAA---ANAQVYQSGIAYGPGSE---AAAFGANSLGAFPPQLNSVSPSPMLMLLHPPQ-LSPFLHPHG-----QQVPHYLENE	135
gi	47824866	ref	NP_001001443.1	MTMLHTKASGMALLHQIQGNELEPLNRPOLKIPLERPLGEVYVDSKPAVFNYPGEAAVEFNAAAA---ASAPVYQSGIAYGPGSE---AAAFGANSLGAFPPQLNSVSPSPMLMLLHPPQ-LSPFLHPHG-----QQVPHYLENE	136
gi	73945701	ref	XP_533454.2	--MMLHTKASGMALLHQIQGPELDSLNRPLKIPLERPLGEVYVDSKPAVFNYPGEAAVEFNAAAA---APAPLYQSGIAYGPGSEAAVAAAFGANLGGFPPLNSMSPFPVLLHPPQ-LSPFLHPHG-----QQVPHYLENE	136
gi	45383986	ref	NP_990514.1	MTMLHTKASGMALLHQIQGTELETLRPLKIPLERLSDMYVESNKTGVFNYPGEATYDFG---ITAPVYQSGIAYGPGSE---EFGSSSLAGFHSLSLNVVSPVVFLOTAP-LSPFIHHS-----QQVPHYLENE	129
gi	23308675	ref	NP_694491.1	--MYPKEEHSAGGISVNVN---YLDG---AYEYFN-PTQTFG---TSPAEPA---VGYYPAPP---DFHEEHLQTLGGGSSPLMFAPSSPQ-LSPFLSHHGHHITPHGVSYLDDSS	101



gi	6679695	ref	NP_031982.1	PS-AVAVRDTGPPAFYRNSDNRROGRERLSSNEKGNMIMESAKEYTRICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	288
gi	6978815	ref	NP_036821.1	PS-AVAVRDTGPPAFYRNSDNRROGRERLSSSEKGNMIMESAKEYTRICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	289
gi	62821794	ref	NP_000116.2	PS-GYVREAGPPAFYRNSDNRROGRERLSTNDKGSMAIMESAKEYTRICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	284
gi	47824866	ref	NP_001001443.1	SS-GYAVREAGPPAFYRNSDNRROGRERLSTSDKGSMAIMESAKEYTRICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	285
gi	73945701	ref	XP_533454.2	PS-GYAVRQAGPPAFYRNSDNRROGRERLSTSDKGNMIMESAKEYTRICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	285
gi	45383986	ref	NP_990514.1	QG-SFGMREAAPAFYRNSDNRHRSIRERLSTNEKGSLSMESTIKETRYICAVCNDYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	278
gi	23308675	ref	NP_694491.1	SSIVYRSVSVSSQAAVGLCELCSATDRRELYTGSRAAGGFDSEKTEKRFCAVCSYASGYHYGVVSCBCKAFAFKRSIQGHNDYMCPTAQCCTIDKNRKSCQACRLRKCCEVGMKGGIRKDRRGGRLMKHKRQRDDLEGRNEVSG	250



gi	6679695	ref	NP_031982.1	DMRAANLWPSPLVIKHTKKN--SPALSLTADQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	436
gi	6978815	ref	NP_036821.1	DMRAANLWPSPLVIKHTKKN--SPALSLTADQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	437
gi	62821794	ref	NP_000116.2	DMRAANLWPSPLMIKRSKKN--SLALSLTADQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	432
gi	47824866	ref	NP_001001443.1	DMRAANLWPSPLMIKRSKKN--SPVLSLTADQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	433
gi	73945701	ref	XP_533454.2	DVRTSSLWPSPLVIKHTKKN--SPALSLTADQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	433
gi	45383986	ref	NP_990514.1	ELRAPTLWTSPLVVKHKNKN--SPALSLTAEQMVSAALLDAEPPMIYSEYDPSRPFSEASMMGLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	426
gi	23308675	ref	NP_694491.1	CSRAGVRTTGPQDKKRSKGGVSVTLGMSDQVLLLLGAEPPAVCSRQKHSRPTETITMSLLTLNADRELVHMINWAKRVPVGFQDLNLHDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGEMVEIFDMLLATS	400



gi	6679695	ref	NP_031982.1	SRFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPASRMGVPEE-EPSQQLATTSSTSAHSLQI	585
gi	6978815	ref	NP_036821.1	SRFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPASRMGVPEE-EPSQQLATTSSTSAHSLQI	586
gi	62821794	ref	NP_000116.2	SRFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPASRMGVPEE-EPSQQLATTSSTSAHSLQI	581
gi	47824866	ref	NP_001001443.1	SRFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHFRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPANFGSAPPE-DVNSQQLATTSSTSAHSLQI	582
gi	73945701	ref	XP_533454.2	SRFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPASRMGVPEE-EPSQQLATTSSTSAHSLQI	582
gi	45383986	ref	NP_990514.1	ARFRMMNLQGEFVCLKSIIILLNSGVYTFLLSILKSLSEKDHHRVLDKIINDTLIHLMAKAGLTQQOHRRLAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAHRLHAPASRMGVPEE-EPSQQLATTSSTSAHSLQI	574
gi	23308675	ref	NP_694491.1	ARFRSLKLEEFVCLKSIIILLNSGAFSFCSSPVEPLMDFNFVQCMLENTIDALIYCSKSGASLQLSRRQAQLLLILSHIRHMSNKGMEHLYNMCKKNVPLVDLLEMLDAQRQSSGKQVQVWSSEKNSPPSTPTSSSSNNSPR	550



gi	6679695	ref	NP_031982.1	YYIIPP-EAEGFPNTI---	599
gi	6978815	ref	NP_036821.1	YYIIPP-EAEGFPNTI---	600
gi	62821794	ref	NP_000116.2	YYITG-EAEGFPATV---	595
gi	47824866	ref	NP_001001443.1	YYITG-EAENFPSTV---	596
gi	73945701	ref	XP_533454.2	YYITE-EAGNFPSTV---	596
gi	45383986	ref	NP_990514.1	FVINSKEESMONTI---	589
gi	23308675	ref	NP_694491.1	GGAAAI-SNGACHSHSPDP	569

