

gi | 121247453 | ref | NP_032199.3 | MDSKESLAPPGRDEV-PSSLLGQGRGSMVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFSKGSAASNAOQ---0000000000000000PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 6980988 | ref | NP_036708.1 | MDSKESLAPPGRDEV-PSSLLGQGRGSMVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFSKGSAASNAOQ---0000000000000000PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 66528677 | ref | NP_001019265.1 | MDSKESLAPPGRDEV-PSSVLAQERGNVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFPKGSSVNAOQ---PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 114602488 | ref | XP_001154683.1 | MDSKESLAPPGRDEV-PSSVLAQERGNVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFPKGSSVNAOQ---PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 73949531 | ref | XP_535225.2 | MDSKESLAPPGRDEV-PSSVLAQERGNVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFPKGSSVNAOQ---PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 76662652 | ref | XP_612999.2 | MDPKESLAPPGRDEV-PSSVLAQERGNVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFPKGSSVNAOQ---PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 83721947 | ref | NP_001032915.1 | MDSKESLAPPGRDEV-PSSVLAQERGNVDFYKTLRGGATVKVSSASSPSVAASQADSKQRILLDFPKGSSVNAOQ---PDLKSKAVLSMGLYMGETETKVMGNDLGYPOOQGLGLSSGETDFRLLLEESIAN 150
gi | 99028943 | ref | NP_001018547.2 | MDQGLLENGKRRER--LNLLDYNKRATGILP-----RRIQSTMSVAPISMVPCAGFMVPSGDIENLSN-----SPTLEETHSVSSVSLFGDSELEKLLGKQRALQQTLVPTLGLDLSGLASL 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 121247453 | ref | NP_032199.3 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 6980988 | ref | NP_036708.1 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 66528677 | ref | NP_001019265.1 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 114602488 | ref | XP_001154683.1 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 73949531 | ref | XP_535225.2 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 76662652 | ref | XP_612999.2 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 83721947 | ref | NP_001032915.1 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
gi | 99028943 | ref | NP_001018547.2 | LNRSTSRPENPKSSTPAAGCATPTEKEFPQTHSDPSSEQ--QNRKSPGTNGGSKVLYTDDOSTFDI---LQDLFESAGSPGKETNESPWRSDDLIDEN--LLSPLAGEDDFPFLLEGDNVEDCKPLILPDKPKIKDGTGDIILSSPSSVAL 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 121247453 | ref | NP_032199.3 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 6980988 | ref | NP_036708.1 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 66528677 | ref | NP_001019265.1 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 114602488 | ref | XP_001154683.1 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 73949531 | ref | XP_535225.2 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 76662652 | ref | XP_612999.2 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 83721947 | ref | NP_001032915.1 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
gi | 99028943 | ref | NP_001018547.2 | PDKTEKDDFIELCTPGVIRKQELKGPVYCOAASFSGTNIIGNKMSAIVHGVSTSGGOMHYDMN---TASLQQQDQKPFVFNVIPPVPGSENNWRCOGSGEDNLSLGLAMNFAGRVFNNGYSS--FGMRPVDVSSPPSSS--AAGPPPKL 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 121247453 | ref | NP_032199.3 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 6980988 | ref | NP_036708.1 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 66528677 | ref | NP_001019265.1 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 114602488 | ref | XP_001154683.1 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 73949531 | ref | XP_535225.2 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 76662652 | ref | XP_612999.2 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 83721947 | ref | NP_001032915.1 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
gi | 99028943 | ref | NP_001018547.2 | CLVCSDEASGCHYGVLCGSKVFFKRAVEG--QHNLYCAGRNDICIIDKIRKNCPCACRYRCKLQAGMNLKARKTKKIKG---IQQATAGVSDTSENA--NKTIVPAALPOLPPTLVSLLEVEIEPEVLVYAGVDSVSPDSTWRIMTILNML 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 121247453 | ref | NP_032199.3 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 6980988 | ref | NP_036708.1 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 66528677 | ref | NP_001019265.1 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 114602488 | ref | XP_001154683.1 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 73949531 | ref | XP_535225.2 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 76662652 | ref | XP_612999.2 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 83721947 | ref | NP_001032915.1 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
gi | 99028943 | ref | NP_001018547.2 | GGRQVIAAVKAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWSRYQSSGNLLCFAPDILLIENQRMPLCMYDQCKHMLFVSSSELRLQVSYEYLCMKTLILLSSVPEKGLKSOELFDEIRMTYIKELGKAIVKREGNSSQWRFY 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi |121247453|ref|NP_032199.3| QLTKLLDSMHDVVENLLSYCFQTFLDKSMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |6980988|ref|NP_036708.1| QLTKLLDSMHEVVENLLTYCFQTFLDKTMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |66528677|ref|NP_001019265.1| QLTKLLDSMHEVVENLLNYCFQTFLDKTMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |114602488|ref|XP_001154683.1| QLTKLLDSMHEVVENLLNYCFQTFLDKTMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |73949531|ref|XP_535225.2| QLTKLLDSMHDVVENLLNFCFQTFLDKTMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |76662652|ref|XP_612999.2| QLTKLLDSMHDVVENLLNYCFQTFLDKTMSEFFPEMLAEIITNQIPKYSNGNIKKLLFHQK 811
gi |83721947|ref|NP_001032915.1| QLTKLLDSMHDVVENLLSFCFQTFLDKSMSEFFPEMLAEIISNQIPKYSNGNIKKLLFHQK 811
gi |99028943|ref|NP_001018547.2| QLTKLLDSMHDLVGGLLNF CFYTFVNKSLSEFFPEMLAEIISNQLPKFKDGSVKPLLFHQK 811
.....760.....770.....780.....790.....800.....810.

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