

gi |124249086|ref|NP\_796264.2| --- MCGSALAFLLAAL 13  
gi |62651421|ref|XP\_343127.2| --- MCGSALAFLLAAL 13  
gi |4504779|ref|NP\_002205.1| --- MCGSALAFFTAAF 13  
gi |114612260|ref|XP\_518987.2| --- MCGSALAFFTAAF 13  
gi |57096028|ref|XP\_532487.1| --- MCGSALAFFAAAF 13  
gi |119922193|ref|XP\_616412.3| --- MCRSALVFFLAAL 13  
gi |118085920|ref|XP\_418706.2| MGRKLRALGEVERSDQGERIDLAVRHGRYRNNVLEVYGGDRYARKLGDPPSPQLGRNPPDQHKGRSLRALPLIFGAPLPHGFAAFLNCRAGRPPGPAAAAAAAGAGTERRAAPPSRGPEERARERERRRRMMVPELLACLTAGI 150  
gi |189532775|ref|XP\_001919626.1| --- MTCSCM 5



gi |124249086|ref|NP\_796264.2| LSLHNCQRGPALVLGAAWVFLVVLGLGQSEHNRCGSANVVS CARCLQLGPECGWCVOEDFVSGGSGSERCDIVSNLISKGCVPVDSIEYLSVHVVSSENEINIQVTPGEVSVQLHPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 163  
gi |62651421|ref|XP\_343127.2| LCLHNCQRGPALVLGAAWVFLVVLGLGQSEHNRCDSANVVS CARCLQLGPECGWCVOEDFVSGGSRSEKCDIVSNLISKGCVPVDSIEYLSVHVVSSENEINIQVTPGDVSIQLHPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 163  
gi |4504779|ref|NP\_002205.1| VCLONDRRGPASFLWAAWVFLVVLGLGQGEDNRCASSNAASCARCLALGPECGWCVOEDFISGGSRSEKCDIVSNLISKGCVPVDSIEYPSVHVIPTEINEINTQVTPGEVSIQLRPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 163  
gi |114612260|ref|XP\_518987.2| VCLONDRRGPASFLWAAWVFLVVLGLGQGEDNRCASSNAASCARCLALGPECGWCVOEDFISGGSRSEKCDIVSNLISKGCVPVDSIEYPSVHVIPTEINEINTQVTPGEVSIQLRPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 163  
gi |57096028|ref|XP\_532487.1| VRLONCRPGPAPFLRAAWLVLVVLGLGQSEHNRCASSNAASCARCLALGPECGWCVOEDFISGGSKNERCDIVSNLISKGCVPVDSIEYPSVHVIPTEINEINTQVTPGEVSIQLRPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 162  
gi |119922193|ref|XP\_616412.3| VRLONCRPGPAPFLRAAWLVLVVLGLGQSEHNRCASSNAASCARCLALGPECGWCVOEDFISGGSKNERCDIVSNLISKGCVPVDSIEYPSVHVIPTEINEINTQVTPGEVSIQLRPGAEANFMLKVRPLKXY PVDLYLVDVVSASMHNII 162  
gi |118085920|ref|XP\_418706.2| VSVKCRQRPAGALLGAVRLLAAVPLGCRPENRCATSNNAVCTKCLALGPECGWCVOEDFMADSSCKGRCDIVSNLISKGCVPVDSIEYPSVHVIPTEINEINTQVTPGRVSVQLSPGSEASFLKVRPLEKYPVDLYLVDVVSASMHNII 300  
gi |189532775|ref|XP\_001919626.1| RPYCDLIARMLLLLLIIVLILLVLR--SNADNRCLLALISLCECLRRGPECAWCSEERFLDGAHVSRQRCVSDLVRRGCEEFINPKVVEVNAITISS--SQVAPREIITHLRPGSEASFLVIEVQQLERY PVDLYLVDVVSASMODNL 152



gi |124249086|ref|NP\_796264.2| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 313  
gi |62651421|ref|XP\_343127.2| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 313  
gi |4504779|ref|NP\_002205.1| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 313  
gi |114612260|ref|XP\_518987.2| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 313  
gi |57096028|ref|XP\_532487.1| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 312  
gi |119922193|ref|XP\_616412.3| EKLNSVGNLDSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 312  
gi |118085920|ref|XP\_418706.2| EKLNSVGFALSKKNMAYSRDFRLGFGSYVDKIVSPYIISHPERIHNCSDYNLDCMPPHGYIHVLSLLENITFEKAVHRQKISGNIDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQTSHLALDSKLAGIVVDPDGNCHLKNNV 450  
gi |189532775|ref|XP\_001919626.1| DRLLKIVGLALSHQMKQSSDFRVGFGFVDPKVPYIIVDHPKSKLLNPCSEYEVHCRPAHGFIHVLVPTQNMSEFTRVIQEORISGNMDTPEGGFDAMLQAACVESHIGWRKEAKRLLLVMTDQPSHLALDSKLAGIVVDPDGRCHLEDNV 302



gi |124249086|ref|NP\_796264.2| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VHGVHFNITAIICPDGARKPGISGGCNVTSNDEVLFNVTVMKCDVITGGKN--YAIIKPIGFNE 457  
gi |62651421|ref|XP\_343127.2| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VHGVHFNITAIICPDGARKPGTSGCCNVTSNDEVLFNVTVMKCDIIGGKN--YAIIKPIGFNE 457  
gi |4504779|ref|NP\_002205.1| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VQGIYFNITAIICPDGSRKPGMEGCRNVTNDEVLFNVTVMKCDVITGGKN--YAIIKPIGFNE 457  
gi |114612260|ref|XP\_518987.2| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VQGVYFNITAIICPDGSRKPGMEGCRNVTNDEVLFNVTVMKCDVITGGKN--YAIIKPIGFNE 457  
gi |57096028|ref|XP\_532487.1| VVRSTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VQGVYFNITAIICPDGTRKPGTGGCCNVTSNDEVLFNVTVMKCDVITGGKS--YAIIKPIGFNE 456  
gi |119922193|ref|XP\_616412.3| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---VQGIYFNITAIICPDGTRKPGTGGCCNVTSNDEVLFNVTVMKCDVITGGKS--YAIIKPIGFNE 456  
gi |118085920|ref|XP\_418706.2| VVKSTTMEHPSLGLSEKLLIDNNINVIFAVQKGFHWYKDLLPLLPGLAIAGEIESKAANLNLVVEAYKLLISEVKKVQLEN---HICDLFNITAIICPDGSKTGMGCKNIGYNQEVLFNVTVMKCDITGGRK--YAIIKPIGFNE 594  
gi |189532775|ref|XP\_001919626.1| YSQTSTMEHPTVAQLAEKLENSIYSIFAVDHLQYQWYEDLVLDLIPGSYVGRFLPKASLKDLDLVVAYKLLSDVEVQMLEDPQQAERFWVNVSAICPGGSSAAGNSKSGVQPKQTVFFQITVGMLSCPAGSADQVLMMLVRPVGFNE 452



gi |124249086|ref|NP\_796264.2| LTKVHIHRSCSCQEDNRHGLKGCABAAAP-DPKPCQCDSDRCHDFDEDFPSEI CKPKQEDQPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYLHGDVLCAGHGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 606  
gi |62651421|ref|XP\_343127.2| LTKVHIHRSCSCQEDNRHGLKGCABAAAP-DPKPCQCDSDRCHDFDEDFPSEI CKPKQEDQPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYLHGDVLCAGHGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 606  
gi |4504779|ref|NP\_002205.1| LAKIHIHRSCSCQEDNRGPKGKCVDETFLDSKCFQDENKCHDFDEDFPSEI CKSHKQDPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 607  
gi |114612260|ref|XP\_518987.2| LAKIHIHRSCSCQEDNRGPKGKCVDETFLDSKCFQDENKCHDFDEDFPSEI CKSHKQDPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 607  
gi |57096028|ref|XP\_532487.1| LTKIHIHRSCSCQDDGRGSKRCVDEIFLDAKFCQENKCHDFDEDFPSEI CKSHKQDPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 606  
gi |119922193|ref|XP\_616412.3| LTKIHIHRSCSCQDDSRGPKRCVBEFLDTKFCQDENKCHDFDEDFPSEI CKSHKQDPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 606  
gi |118085920|ref|XP\_418706.2| LTIINVKSCACQNGDNAKPKRWADEIFPDGKQPHCSDSGCSVSRITLPSSECRHQDQPCISGRGCI EGKCFYKKNLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFADWEGDRCCPSASAOHCVNSKGOVCSGRGTC 744  
gi |189532775|ref|XP\_001919626.1| VYVVRIRLCSGGCTD---PKPEPSSCTIN---ASDSCREHNTPVCSGRGVCI CGKCLCHKTKLGRVYGYCEKDDFSCPYHGNLCAHGGECEAGRCOCFSGWEGDRCCPSASAOHCVNSKGOVCSGRGTC 579



