

gi		10863887		ref		NP_066924.1		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		114591092		ref		XP_516949.2		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		7710002		ref		NP_057883.1		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		61889099		ref		NP_113887.2		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		74003604		ref		XP_850248.1		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		49258204		ref		NP_001001854.1		MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD	150
gi		61889131		ref		NP_001013629.1		MASSGLQLLGFVLAFLGWMGIIITSTAMPQWKMASYAGDNIVTAQALYEGLWMSCAMQSTGQIQCKVFDSELLKLEGSLOATRALMVAAILLGLVGFVAIVGMKCMKCMEDDQKMRMAVFGGVIFIIAGLEALVATSWYGNRVARAFYD	150
gi		18858435		ref		NP_571845.1		MAHAGLQMLGVCYCLGFLGLGLIASTAMAEWKMSSYAGDNITTAQAQYEGLWQSCVQSQTGQLQCKKYDSELLKLPGEIQGARGLMMLTGIFLCGLSLVSVFGMKCTTCLSEAPQVKSVALAGGVLPFITGGLFALIAISWYGEKIRQKFFD	150



gi		10863887		ref		NP_066924.1		PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCS CPRKTTSYPTPRPYPKPAPSSGKDYV	211
gi		114591092		ref		XP_516949.2		PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCS CPRKTTSYPTPRPYPKPAPSSGKDYV	211
gi		7710002		ref		NP_057883.1		PLTIPINARVEFGQALFTGWAAAALCLLGGVLLSCS CPRKTTSYPTPRPYPKPTPSSGKDYV	211
gi		61889099		ref		NP_113887.2		PMTFPVNARYEFGQALFTGWAAAALCLLGGALLSCS CPRKTTSYPTPRPYPKPTPSTGKDYV	211
gi		74003604		ref		XP_850248.1		PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCS CPRKTTSYPTPRPYPKPAPSSGKDYV	211
gi		49258204		ref		NP_001001854.1		PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCS CPRKTTSYPTPRPYPKPAPSSGKDYV	211
gi		61889131		ref		NP_001013629.1		PFTFPVNTREFGSALEFIGWAAAALALLGGAFLCCS CPRSETSYPPSRGYPKNAPSTGKDYV	211
gi		18858435		ref		NP_571845.1		PFTFPVNARYEFGKALYVGVGSSALSIIGSLLCCI GSEASEKPE--YPPARAAGRPGTRV	211

