

gi|58331148|ref|NP_005931.2| MAAWLRSAARALLPPM-----LLLLLQPPLLAR-ALPPDAHHLHAERRGPOPWHAALPSSPAPAP-AIQEAPRPASSLR-PPRCGVDP-----SDGLSARNRQKRFVLSGGRWEKTDLTYRILRFPWLVQEG 125
gi|114685393|ref|XP_515022.2| MCAAVQRRRCCEP-----GSPADAHHLHAERRGPOPWHAALPSSPAPAP-AIQEAPRPASSLR-PPRCGVDP-----PDGLSARNRQKRFVLSGGRWEKTDLTYRILRFPWLVQEG 106
gi|73995874|ref|XP_543534.2| MARAPRLRGAALRALLLPL-----LLLLLPPPPLLAWAPRPDAHRRHPVRRGPOPWHEAGPSSLVLPAP-AIQDTPQPASSPR-PPRCGVDP-----PDGLSARNRQKRFVLSGGRWDTLTYRILRFPWLVQEG 126
gi|6678894|ref|NP_032632.1| MARAACLLRAISRVLPLP-----LLLLLLLLLPSPLMAR-ARPPESRHRHPVKKGPRLLHAALPNTLSVP-ASHWVPSPAGSSR-PLRCGVDP-----PDVLNARNRQKRFVLSGGRWEKTDLTYRILRFPWLVQEG 129
gi|6981212|ref|NP_037112.1| MGRSRGRPGAHILS-----DAPRRHPVSRGPOPWPDAPPDSDAPAL-AIQEALPLAGRPR-PPRCGVDP-----PDGLSARNRQKRFVLSGGRWEKTDLTYRILRFPWLVQEG 96
gi|119909610|ref|XP_584877.3| MQESDRPGRSSPPGMARPLPAAALAAALLHCAPAAPARRHKPKHRRKHTKWEKSPHLSLVGTGVPKAGFPMGADEQAARWN-PPRCGVDP-----LFDGNGRNRQKRFVLSGGRWDTLTYRILRFPWLVQEG 103
gi|118098674|ref|XP_001232777.1| MRVSGLLACAFALHMLTAR-CLPLHGQGLAKHRESPLGYSIPLHLSRHRKRRVSPWLDQDTFKPAPWKPEPHNTPLRNSRATGPKRCGVDP-----LFDGNGRNRQKRFVLSGGRWDTLTYRILRFPWLVQEG 137
gi|189522615|ref|XP_692205.3| MRSAQLLSALFYCIACIHS-----LVPPDGNRHRTPAADWPKLTHHHLKKRGRLLHVQDILNEDFNKRAOPHTQFWRPRRCGVDP-----PSSEKGGSSLHFAHKGGLLGRHRRKRFDFPGRWDTLTYRILRFPWLVQEG 134
gi|125825560|ref|XP_694153.2| 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|58331148|ref|NP_005931.2| VROITMAEALKVWSDVTPLETFEVEHGRADIMIDFARYWHGDDLFPDGGGILAHAFPPKTHREGDVHFYDDETWIIGDDGGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDCRGVOHLYGQWPPTV---TSRTPAL 271
gi|114685393|ref|XP_515022.2| VROITMAEALKVWSDVTPLETFEVEHGRADIMIDFARYWHGDDLFPDGGGILAHAFPPKTHREGDVHFYDDETWIIGDDGGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDRRGVQHLYGQWPPTV---TSRTPAL 252
gi|73995874|ref|XP_543534.2| VROITVAEALQVSEVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDRRGIQHLYGQWPPTV---TSRTPAV 272
gi|6678894|ref|NP_032632.1| VROITVAEALQVSEVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDRRGIQHLYGQWPPTV---TSRTPAL 275
gi|6981212|ref|NP_037112.1| VROITVAEALQVSEVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDRRGIQHLYGQWPPTV---TSRTPAL 241
gi|119909610|ref|XP_584877.3| VROITVAEALQVSDVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSPDDRRGIQHLYGQWPPTV---TSRTPAL 249
gi|118098674|ref|XP_001232777.1| VRRITVEEALKVWSDVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSEDDKIGIQLYLGKPKLDPDE---TPTQPAE 285
gi|189522615|ref|XP_692205.3| VRRITVEEALKVWSDVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSEDDKIGIQLYLGKPKLDPDE---TPTQPAE 273
gi|125825560|ref|XP_694153.2| VRYVIREALRAWSDVTPLETFEVEHGRADIMIDFARYWHGDNLPFDGGGILAHAFPPKTHREGDVHFYDDETWIIGNGQGTDLQVAAEHFGHVLGLQHTTAAKALMSAFYTFRYPLSLSEDDKIGIQLYLGKPKLDPDE---TPTQPAE 289
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|58331148|ref|NP_005931.2| GPOAGIDTNEIAPLEP-DAPPDACEASFDAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLTELGLVRFVVAHAL-VWGPEKNKIYFFRGRDYWRFPHSRRVD 419
gi|114685393|ref|XP_515022.2| GPOAGIDTNEIAPLEP-DAPPDACEASFDAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLTELGLVRFVVAHAL-VWGPEKNKIYFFRGRDYWRFPHSRRVD 400
gi|73995874|ref|XP_543534.2| GPOAGVDTNEIAPLEP-EAPPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 420
gi|6678894|ref|NP_032632.1| SSOAGTDNEIAPLEP-EAPPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 423
gi|6981212|ref|NP_037112.1| SSOAGTDNEIAPLEP-EAPPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 389
gi|119909610|ref|XP_584877.3| GPGIGADTNEIAPLEP-DAPPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 397
gi|118098674|ref|XP_001232777.1| LPDPDLETNEIAPLEP-SCRPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 433
gi|189522615|ref|XP_692205.3| ~PQIPAEITNIPSP---APPDACHDFDAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 418
gi|125825560|ref|XP_694153.2| TERNEIDATFPPVHPNPSPPDACEITFDVAVSTIRGELFFFKAGFVWRLRGGQLPGYPALASRHWGLPSPVDAAFEDAAGHIWFFGGAQYVWYDGEKPVLPAPLSELGLLGSPIQAAL-AWGPEKNKIYFFRGRDYWRFPHSRRVD 439
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|58331148|ref|NP_005931.2| SPVPRRA-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCAEPA-NTFL----- 488
gi|114685393|ref|XP_515022.2| SPVPRRA-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCAEPA-NTFL----- 469
gi|73995874|ref|XP_543534.2| SPVPRRA-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCTEPA-NTFR----- 489
gi|6678894|ref|NP_032632.1| NPVPRRS-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCAEPA-NTFR----- 492
gi|6981212|ref|NP_037112.1| NPVPRRS-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCAEPA-NTFR----- 458
gi|119909610|ref|XP_584877.3| SPVPRRV-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCTEPA-NTFR----- 466
gi|118098674|ref|XP_001232777.1| NVVPRRM-ADWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCTEPA-NTFR----- 502
gi|189522615|ref|XP_692205.3| SAPRRIQDWWGVPEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCTEPA-NTFR----- 501
gi|125825560|ref|XP_694153.2| SMHPRSM-TDWRGVSEIDAADFQDADGYAYFLRGRLYWKFDPVVKVKALEGFPRLVGPDFFGCTEPA-NTFR----- 506
.....460.....470.....480.....490.....500.....510.....520.....530.....

