

gi | 73964173 | ref | XP_547841.2 | MGGWRANLGGKERSLVLVNPKRVPGRPRALAEAPCGLADRHSPGVGKVVAKAKPRRVGETPQCTISASDKCRAAHSQAQAGSQAIVCKNLDPLEPSVFWVDCKDTSYVDCTDGGQLNFFRPTTPQAPQRPGDNVEPVFSGAARRGRVF 150
gi | 33859494 | ref | NP_033215.1 |
gi | 109478354 | ref | XP_343080.3 |
gi | 5174681 | ref | NP_005973.1 |
gi | 114653353 | ref | XP_509988.2 |
gi | 119902749 | ref | XP_588692.2 | MHVHHPSLFNLVGG AAVVLALR AVSLERQGN IMLQP DGYWS 41
gi | 113206154 | ref | NP_001038150.1 |
gi | 46309555 | ref | NP_996978.1 |
110.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi | 73964173 | ref | XP_547841.2 | SSCPGEPLFVQVWAGGGGLPAASPRALDPLTKEAGGSPRGPPLPGENSLLPYIHAYISGDKSSLFGNKPRRPADSPWPSRTSREPLPATSALAFCIKQLSAPGRVLRGGTEPEPGVGCRLVAIRVTLGSRREAAAGASCSPFI 300
gi | 33859494 | ref | NP_033215.1 |
gi | 109478354 | ref | XP_343080.3 |
gi | 5174681 | ref | NP_005973.1 |
gi | 114653353 | ref | XP_509988.2 |
gi | 119902749 | ref | XP_588692.2 | RYCFMLIYTPSSAFPSPSR GAARPRS F ARRACWPAPDRRRPOPTISAPRILR-ALRQLQ GEQKPSR ATSSIHPPAGGRSQ RGPKSCG 128
gi | 113206154 | ref | NP_001038150.1 |
gi | 46309555 | ref | NP_996978.1 |
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi | 73964173 | ref | XP_547841.2 | NLRRISVFRVICIDSKGFKLLEQLKAFCAAAGRTETKFPGNEQHOPGGRPEPERPRLRSEPAARCPARP PPPSSAAOPIITGTFAYGNPREGVRSSCAPLAAAAPCLVGAAPCRVRPGGAPROAPAMSLPSFGFTQEQVACVCEV 450
gi | 33859494 | ref | NP_033215.1 | MSMLPSFGFTQEQVACVCEV 20
gi | 109478354 | ref | XP_343080.3 | MSMLPSFGFTQEQVACVCEV 20
gi | 5174681 | ref | NP_005973.1 | MSMLPSFGFTQEQVACVCEV 20
gi | 114653353 | ref | XP_509988.2 | MSMLPSFGFTQEQVACVCEV 20
gi | 119902749 | ref | XP_588692.2 | VSRPFLEQ RALYSSAY SAASLQVLRVAFAPREGVRS CRAPLAAAAPCFGFAPCRVRPGSAPROAPAMSLPSFGFTQEQVACVCEV 220
gi | 113206154 | ref | NP_001038150.1 | MSMLPSFGFTQEQVACVCEV 20
gi | 46309555 | ref | NP_996978.1 | MSMLPSFGFTQEQVACVCEV 20
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi | 73964173 | ref | XP_547841.2 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 600
gi | 33859494 | ref | NP_033215.1 | LQQGNLERQGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
gi | 109478354 | ref | XP_343080.3 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
gi | 5174681 | ref | NP_005973.1 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
gi | 114653353 | ref | XP_509988.2 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
gi | 119902749 | ref | XP_588692.2 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 370
gi | 113206154 | ref | NP_001038150.1 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
gi | 46309555 | ref | NP_996978.1 | LQQGNLERLGRFLWSLPA CDHLHKNESVLKAKAVVAFHRGNFRELYKILESHQFSPHNHPKLOQLWLKAHYVBAEKLGRPLGAVGKYRVRKKFPLPRTIWDGEETS YCFKEKSRGVLRWYAHNPVPSPREKRELAEAATGLTTQVSN 170
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

gi | 73964173 | ref | XP_547841.2 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 714
gi | 33859494 | ref | NP_033215.1 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 284
gi | 109478354 | ref | XP_343080.3 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 284
gi | 5174681 | ref | NP_005973.1 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 284
gi | 114653353 | ref | XP_509988.2 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 284
gi | 119902749 | ref | XP_588692.2 | WFKNRRQRDRAAEAKERENTENNNSSNKQNLSPLEGGKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 484
gi | 113206154 | ref | NP_001038150.1 | WFKNRRQRDRAAEAKERENTENNNAATKPNQNLSPLDGSKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 282
gi | 46309555 | ref | NP_996978.1 | WFKNRRQRDRAAEAKERENTENNNTGANKQNLSPLDGSKPLMSSSEEEFSPPOS PDQNSVLLLGNMGHARSSNYSLPGLTASQPSHGLQAHQHQLODSSLGPLTSSLVDLGS 284
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....