

|    |           |     |                |                                                                                                                                                |     |
|----|-----------|-----|----------------|------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| gi | 27370160  | ref | NP_766374.1    | -----MHTPGTPAPG-----HDPDPPPLLLTLL                                                                                                              | 150 |
| gi | 34852635  | ref | XP_218776.2    | -----MHTPETPAPG-----RLAPRPPPLPTLL                                                                                                              | 150 |
| gi | 31083156  | ref | NP_055247.2    | -----MRAPG-----RPALRPLPLPPLL                                                                                                                   | 150 |
| gi | 114609471 | ref | XP_518765.2    | -----MRAPG-----RPALRPLPLPPLL                                                                                                                   | 150 |
| gi | 73946036  | ref | XP_541119.2    | -----MWARPPAPGTHRGVAPAPGQALRLLLL                                                                                                               | 150 |
| gi | 194669941 | ref | XP_585919.4    | MVGRSODIKDKDSTQPKKWLKLEGGGKSRILGAASPNGLEEKSDTFLALAPSPGSGGTRVGLRRSSASPGTQPIGARRAARALAQEEGRPFSQRPRPEGESHADGCLQRCDDPAPAPMCAPGFSARAARGAPAPGLPAL--- | 150 |
| gi | 50742701  | ref | XP_419723.1    | -----MGTCQ-----PRRGAVALSLLL                                                                                                                    | 150 |
| gi | 118918377 | ref | NP_001073144.1 | -----MDVVLSCCLC                                                                                                                                | 150 |



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| gi | 27370160  | ref | NP_766374.1    | LLLAAS--GRAVPCVFCGLPKPTNIFLSINMKNVLHWNPPESLHGVEVYTYVQYFIYGOK-----KWLNAASKCGSINRTYCDLSVETSDEYEQFYAKVKAIWEARCSWAE-TERFYPFLETQVSPPEVALTTGKKSISIALTAPAE | 300 |
| gi | 34852635  | ref | XP_218776.2    | LLLAAS--GRAVPCVFCGLPKPTNIFLSINMKNVLHWNPPESLHGVEVYTYVQYFIYGOR-----KWLNAASKCTSISRTYCDLSVETSDEYEQFYAKVKAIWEARCSWAE-TERFYPFLETQVSPPEVALTTGKKSISIALTAPAE | 300 |
| gi | 31083156  | ref | NP_055247.2    | LLLLAAPWGRAVPCVSGGLPKPANIIFLSINMKNVLQWTPPEGLQGVKVVYTYVQYFIYGOK-----KWLNSKCRNINRTYCDLSAETSDEYEQFYAKVKAIWGTCKSKWAE-SGRFYPFLETQIGPPEVALTTGKKSISVVLTAPE | 300 |
| gi | 114609471 | ref | XP_518765.2    | LLLLAAPWGRAVPCVSGGLPKPANIIFLSINMKNVLQWTPPEGLQGVKVVYTYVQYFIYGOK-----KWLNSKCRNINRTYCDLSAETSDEYEQFYAKVKAIWGTCKSKWAE-SGRFYPFLETQIGPPEVALTTGKKSISVVLTAPE | 300 |
| gi | 73946036  | ref | XP_541119.2    | LLLLAAPSGRAVLCISGGLPKPANIIFLSINMKNVLQWTPPEGLQGAEVYTYVQYFIYGOK-----KWLNSKCRNINRTYCDLSAETSDEYEQFYAKVKAIWGTCKSKWAE-SGRFYPFLETQIGPPEVALTTGKKSISVVLTAPE  | 300 |
| gi | 194669941 | ref | XP_585919.4    | LLLLAAPWGRAVPCVSGGLPKPNTVAFISINMKNVLQWTPPEGLQGMVEVYTYVQYFIYGOK-----KWLNSKCRNISRITYCDLSAETSDEYEQFYAKVKAWGTCKSKWAE-SGRFYPFLETQIGPPEVALTTGKKSISVVLTAPE | 300 |
| gi | 50742701  | ref | XP_419723.1    | PLLLPPPAAHTGELYCSLNPFRNVHVESINMKNVLHVLAPPEG-TGDGVLYNPKYVYVYGDG-----KWKIRPECRNINRTYCDLSAETSDEYEQFYAKVKALVNGKSNWIE-STRFNPLDTHKIGPMVNVNSTEKKSISITLIVPE | 300 |
| gi | 118918377 | ref | NP_001073144.1 | FLLRALSASSAD---GPEPRDVEHFYSERLNRVVRNTAGHG-SPSDTYTYVEYAIYDADEKLEPEQVWRPVDQIRISVQIECDVSOETFLDLDEYFARVRAISKHGQVWSEIGRFRPLSDVILGAPLVDVTVRQNHIDITLKGPF   | 300 |



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| gi | 27370160  | ref | NP_766374.1    | KWKRNPQDHTVSMQCIYPNLKNVSVYNTKSRRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRLPMPQKQKISLVEVQTSAWKAKVIFWYVFLTSVIVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL   | 450 |
| gi | 34852635  | ref | XP_218776.2    | KWKRNPQDHTVSMQCIYPNLKNVSVYNTKSRRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRLPMPQKQKISLVEVQTSAWKAKVIFWYVFLTSVIVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL   | 450 |
| gi | 31083156  | ref | NP_055247.2    | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |
| gi | 114609471 | ref | XP_518765.2    | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |
| gi | 73946036  | ref | XP_541119.2    | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |
| gi | 194669941 | ref | XP_585919.4    | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |
| gi | 50742701  | ref | XP_419723.1    | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |
| gi | 118918377 | ref | NP_001073144.1 | KWKRNPEDLPVSMQCIYPNLKNVSVLNTKSNRTWSQCVTNSLVLVSWLEPNILYCVHVESLVPGPPRRAPQSEKQCARLTKDQSSSEFKAKIIFWVFLVPSITVFLFSAIGYLVYRVIHVGEKHPANLVLVIRNEIGTRVFEPTETITL | 450 |



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| gi | 27370160  | ref | NP_766374.1    | NFITFSMLDDTKISPKDMNLLDKSSDDISVNDPEHNEAEPHWEEVEGQHLGCSHLLMDAVCG--AEQRDGDLSLQHGWLNSLTPTEGIDNEPOYKVLG-DFYGEGEILGCEPEEAARTEKISEPLVNSANLD-----POLED       | 600 |
| gi | 34852635  | ref | XP_218776.2    | --ITLSDLDSSKISQTDMLNLLDRSSDEVSVNNEPFGSGWEPNWEDAEQGHGSSHLVDIVCG--VEQSDRDLSLQHGWLNSLTPTEGIDNEPOYKVLG-DFYKKEGRDQFCGSEEAARTEKLAEPQALANLD-----POLED       | 600 |
| gi | 31083156  | ref | NP_055247.2    | NFITLNISSDDSKIHQDMSLLGKSSDVSFLNDPQPSGNLRPPQEEVEVKHLGVAHLMEIFCD--SEENEGSLTQOESLERTIPPDKTVIEYEYDVRTTIDICAGPEEQELSLQEEVSTQGTLLSAAALAVLGPOTLQYSYTPQLQD   | 600 |
| gi | 114609471 | ref | XP_518765.2    | NFITLNISSDDSKIHQDMSLLGKSSDVSFLNDPQPSGNLRPPQEEVEVKHLGVAHLMEIFCD--SEENEGSLTQOESLERTIPPDKTVIEYEYDVRTTIDICAGPEEQELSLQEEVSTQGTLLSAAALAVLGPOTLQYSYTPQLQD   | 600 |
| gi | 73946036  | ref | XP_541119.2    | NFITLNISSDDSKIHQDMSLLGKSSDVSFLNDPQPSGNLRPPQEEVEVKHLGVAHLMEIFCN--SEETKGLPLTQOESLERTIPPDKTVIEYEYDVRTTIDICAGPEEQELSLQEEVSTQGTLLSAAALAVLGPOTLQYSYTPQLQD  | 600 |
| gi | 194669941 | ref | XP_585919.4    | NFITLNISSDDSKIHQDMSLLGKSSDVSFLNDPQPSGNLRPPQEEVEVKHLGVAHLMEIFCD--FEKSKGSLTQOESLERTIPPDKTVIEYEYDVRTTIDICAGPEEQELSLQEEVSTQGTLLSAAALAVLGPOTLQYSYTPQLQD   | 600 |
| gi | 50742701  | ref | XP_419723.1    | NLITVNV-DESKPQESIHPEMKSERYTYVSYSGAEGRDVSLKVEPBAKYLDDISHEEISQEEEDLLAEGDHTPKNDQPMKNTMRQKNGGSVEALGVRADDFSPQSLLEELSLKREKSTPPGGLGEPOTALGNLVNKKRKAQCPQLQEV | 600 |
| gi | 118918377 | ref | NP_001073144.1 | FNIKLDDSSVLRPPLPFPVEDSSEEPVNAVQPAQYAAQQPLPAPASISGDLQD-----GDSLSDSEPLADHSEAG--DYAFVIRAKVDHSEVEVSYRITQGHADP                                            | 600 |



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| gi | 27370160  | ref | NP_766374.1    | -----LHHLGQEHVTSEDG-----PEEETSILVVDWDPQTRGLCIPSLPIFGRDPENYGHYERDQLEGGLLSRLYENQAPDKPEKENENCLTRFMEEWGLVQMES-                                 | 741 |
| gi | 34852635  | ref | XP_218776.2    | -----LQHLGQEHVTSEDG-----PEEESTILVVDWDPQTRGLCIPSLPIFGRDLNENYCYERDHLSEDGLLSRLYENQAPDKPEKENENCLTRFMEEWGLVQMES-                                | 741 |
| gi | 31083156  | ref | NP_055247.2    | -----LDPLAQEHVTSSEEG-----PEEESTILVVDWDPQTRGLCIPSLPIFGRDSEGCPESEGDGLGEEGLLSRLYEEAPDRPGENETYLQFMEEWGLVQMEN-                                  | 741 |
| gi | 114609471 | ref | XP_518765.2    | -----LDPLAQEHVTSSEEG-----PEEESTILVVDWDPQTRGLCIPSLPIFGRDSEGCPESEGDGLGEEGLLSRLYEEAPDRPGENETYLQFMEEWGLVQMEN-                                  | 741 |
| gi | 73946036  | ref | XP_541119.2    | -----LDQRQWHPDTRKE-----PDEKSTILVVDWDPQTRGLCIPSLPIFGRDSEGCPESEGEFTTEEGLLSRLYEEQALDEPSEHSVILMKFMEEWGLVQMEN-                                  | 741 |
| gi | 194669941 | ref | XP_585919.4    | -----LDHLRQGHVDTSEEG-----PEEESTILVVDWDPQTRGLCIPSLPIFGRDSEGCPESEGLGEEGLLSRLYQDAPDKAPEENBAYLMFMEEWGLVQMED-                                   | 741 |
| gi | 50742701  | ref | XP_419723.1    | RATDPSSGQELLEELKLMADIVDELGKGRINLVLDLHDEKSGHYSYRRLGKIAHGTTEKESQIVLVDWDPQTRGLYPIPLFVENV-EVCKGVFRCDGPNKBEGLLSRLYKQVSESSQDQEMYLRLQEQWGLHVEMED- | 741 |
| gi | 118918377 | ref | NP_001073144.1 | -----LDH-----HIEEAQIFVDWSPSEGLKIPLMGLLGLDESGVQTEAVSLLNLLITQTSVDGCEQDD-----FSMERNWGLVHSSPE                                                  | 741 |

