

gi | 118026946 | ref | NP_032705.2 | MSGLGESLDPLAESRKRK-LPCDAPGGLVYSGEKWRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 149
gi | 109469257 | ref | XP_215947.4 | MSGLGESLDPLAESRKRK-LPCDAPGGLVYSGEKWRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 149
gi | 291490683 | ref | NP_001167558.1 | MSGLGEN-LDPLAEDSRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 148
gi | 73992554 | ref | XP_543039.2 | MSGLGENSLDPLAEDSRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 149
gi | 119905976 | ref | XP_602010.3 | MSGLGENALDPLAEDSRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 149
gi | 118100627 | ref | XP_417385.2 | MSGLGESLDSLINESRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 150
gi | 292618880 | ref | XP_002663806.1 | MSGLGENSLPLCSLDRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 145
gi | 292618878 | ref | XP_692938.4 | MSGLGENSLPLCSLDRKRK-LPCDTPGGGLCSGEKRRRQESKYIEELAEELISANLSDIDNFVVKPDKCAILKETVRRQIRQIKQKTIISDDDDVQKADVSTGGQVIDKDSLGLPLLLQALDGLFLVFNVDGNIVFVSENVTOYLOVK 145



gi | 118026946 | ref | NP_032705.2 | QEDLVNTSVYSILHEQDRKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMLEBEGEDLQCCMIVARRVIT-DRPFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 293
gi | 109469257 | ref | XP_215947.4 | QEDLVNTSVYSILHEQDRKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMLEBEGEDLQCCMIVARRVIT-DRPFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 295
gi | 291490683 | ref | NP_001167558.1 | QEDLVNTSVYILHEEDRDKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMMEBEGEDLQCCMIVARRIT-GERAFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 296
gi | 73992554 | ref | XP_543039.2 | QEDLVNTSVYSILHEEDRDKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMMEBEGEDLQCCMIVARRIT-GERAFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 297
gi | 119905976 | ref | XP_602010.3 | QEDLVNTSVYILHEEDRDKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMMEBEGEDLQCCMIVARRIT-GERAFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 297
gi | 118100627 | ref | XP_417385.2 | QEDLVNTSVYILHEEDRDKDFLKHLPKST-VNGVSWTNENQRQKSHTFNCRMLMKI-HDILEDVNASPETRQRYETMQCFALSQPRAMMEBEGEDLQCCMIVARRIT-GERAFSSPESFIRHDLGSKVVNIDTNSLR-SSMRPGFEDI 298
gi | 292618880 | ref | XP_002663806.1 | QBELINTSIYILHEEDREBLKHLPKSTNGP-SVSWGDS-SRQKSHTFNCRMLVKGFGGGPGEAGGPP--RYETMQCFALQPRAMMEBEGEDLQCCMIVARRVIT-GERAFSSPESFIRHDLGSKLLEIQQLLHTMRPGWEDI 288
gi | 292618878 | ref | XP_692938.4 | QBELINTSIYILHEEDREBLKHLPKSTNGP-SVSWGDS-SRQKSHTFNCRMLVKGFGGGPGEAGGPP--RYETMQCFALQPRAMMEBEGEDLQCCMIVARRVIT-GERAFSSPESFIRHDLGSKLLEIQQLLHTMRPGWEDI 288



gi | 118026946 | ref | NP_032705.2 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GVMSPNQNVOMMGSRITYG-----VDPDNTTG 418
gi | 109469257 | ref | XP_215947.4 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 420
gi | 291490683 | ref | NP_001167558.1 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 426
gi | 73992554 | ref | XP_543039.2 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 427
gi | 119905976 | ref | XP_602010.3 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 427
gi | 118100627 | ref | XP_417385.2 | IRRCIQRFSSLNDGQSWQKRHYQEAYVHGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDRHGFISTHFLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 427
gi | 292618880 | ref | XP_002663806.1 | VRRCMQMFHRSEGPWSYKRHYQEAYVHGHAETPPYRFSLADGTIVTAQTRSELCRNPVTSDPHTFLSTHLLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 438
gi | 292618878 | ref | XP_692938.4 | VRRCMQMFHRSEGPWSYKRHYQEAYVHGHAETPPYRFSLADGTIVTAQTRSELCRNPVTSDPHTFLSTHLLQREONGYRPNPAGQGIR---PPAAGC---GMLSPSQSVOMLGSRTYG-----VADPNTTG 438



gi | 118026946 | ref | NP_032705.2 | QMGGARYGASSSVASLTPGQSLQSPSSYQSN-----SYGLSMSSPPHSGPGLGNQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 542
gi | 109469257 | ref | XP_215947.4 | QMGGARYGASSSVASLTPGQSLQSPSSYQSN-----SYGLSMSSPPHSGPGLGNQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 544
gi | 291490683 | ref | NP_001167558.1 | QMSGARYGSSSNIASLTPGPGMQSPSSYQSN-----NYGLNMSPPHSGPGLGNQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 550
gi | 73992554 | ref | XP_543039.2 | QMSGARYGASNPASLTPGPGMQSPSSYQSN-----NYGLNMSPPHSGPGLGSSQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 551
gi | 119905976 | ref | XP_602010.3 | QMSGARYGASGSIASLTPGPGMQSPSSYQSN-----NYGLNMSPPHSGPGLGSSQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 551
gi | 118100627 | ref | XP_417385.2 | QLNSSRYGGPQNMGPVNSGPGMQSN-SAYQSN-----SYGLNMSPPHSGPGLTSSQONLMIISPRNRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 550
gi | 292618880 | ref | XP_002663806.1 | QMNNMNMCMNMQSMNMQNMNMNMNMNMNMQMHPGMNQHQQGGPHFGGGYGMVMTSPSQSGPMMNPGQONLMSPPRIRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 587
gi | 292618878 | ref | XP_692938.4 | QMNNMNMCMNMQSMNMQNMNMNMNMNMQMHPGMNQHQQGGPHFGGGYGMVMTSPSQSGPMMNPGQONLMSPPRIRGSPKMAHQFSPAAGVHSPMG-----SSGNTGSHSFSSSSLALQAISEGVGTSLLSTLSSPGPKLDN 587



gi | 118026946 | ref | NP_032705.2 | SPNMNISQPS-----KVSQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 662
gi | 109469257 | ref | XP_215947.4 | SPNMNISQPS-----KASQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 664
gi | 291490683 | ref | NP_001167558.1 | SPNMNISQPS-----KVSQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 670
gi | 73992554 | ref | XP_543039.2 | SPNMNISQPS-----KVSQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 671
gi | 119905976 | ref | XP_602010.3 | SPNMNISQPS-----KVSQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 671
gi | 118100627 | ref | XP_417385.2 | SPNVSIAGQSN-----KANNQDQSKPLGLYCDQNPVSSMCSQNSRDHLSKESKESGEGVETPRGPLESKGHKLLQLLTCSSDDRGHSSLTN-----SPLDNCCKDSSISVTSFS-----GVSSS-----TSGVSSST 670
gi | 292618880 | ref | XP_002663806.1 | SPNINISTQSSQGGIIGNKPIISDSKSPSSAHSSTGLDQSQASSTEN-TDKPDSQSNKDGSAAGGVNRRVP-DGKGHKLLQLLTCSPTEIGTGTATSGVPVGRASIPMGDPKETGSGMMSPSSTGVSSSSGSSSGNNVQOQSSGGVSSST 735
gi | 292618878 | ref | XP_692938.4 | SPNINISTQSSQGGIIGNKPIISDSKSPSSAHSSTGLDQSQASSTEN-TDKPDSQSNKDGSAAGGVNRRVP-DGKGHKLLQLLTCSPTEIGTGTATSGVPVGRASIPMGDPKETGSGMMSPSSTGVSSSSGSSSGNNVQOQSSGGVSSST 735



gi	118026946	ref	NP_032705.2	PQPTPMYQPSDMKGWPSGNLARNGSPFOQQ-FAPQGNPAAYNMVHMNSGG-----HLGQAMTFPMPMSGMPMGPDQKYC	1403
gi	109469257	ref	XP_215947.4	PQTAPMYQSSSEMKGWPSGNLARNGSPFOQQ-FAPQANPAAYNMVHMNSGGS-----HLGQMTMTPMPMSGMPMGPDQKYC	1399
gi	291490683	ref	NP_001167558.1	PQAASIQSSSEMKGWPSGNLARNSSPFOQQ-FAHQGNPAVYSMVHMNSGSG-----HMQQMNMPMPMSGMPMGPDQKYC	1423
gi	73992554	ref	XP_543039.2	PQTAPMYQSSSEIKGWPSGNLARNSSPFOQQ-FAHQGNPAAYSMVHMNSGSG-----PMGQMNMSMPMAGMPMGPDQKYC	1416
gi	119905976	ref	XP_602010.3	PQTAPMYQSSSEMKGWPSGTLARNSTPFOQQ-FAHQGNPAAYSMVHMNSGSG-----PMGQMNMSMPMAGMPMGPDQKYC	1411
gi	118100627	ref	XP_417385.2	PQTAPMYQSPSEMKGWPSGSMARSSPFOQQ-FSHQGNPATYMMHMNSGSG-----HIGQMNITVPMSGMPMGPDQKYC	1399
gi	292618880	ref	XP_002663806.1	PQSNPMYQSAEMKGWQQPMPMNNSYPQQQYPOQIGAPGQYGGMMNNGSMQGGVNGGAGQMPPMQGMGNTMGMRMPMGPDQKYC	1497
gi	292618878	ref	XP_692938.4	-----	1375

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