

gi | 62955651 | ref | NP_001017839.1 | MSVGADLQH-----LDYLTENELM-----GMD 22
gi | 292611289 | ref | XP_002661045.1 | MSVGADLQH-----LDYLTENELM-----GMD 22
gi | 4507271 | ref | NP_000446.1 | MEV-VDPOC-----LGMFTEGELMS-----VGMD 23
gi | 114674399 | ref | XP_524028.2 | MEV-VDPOC-----LGMFTEGELMS-----VGMD 23
gi | 73987574 | ref | XP_542206.2 | MDV-ADPOC-----LGMFTEGELMS-----VGMD 23
gi | 194668554 | ref | XP_593229.4 | MEV-ADPOC-----LGMFTEGELMS-----VGMD 23
gi | 7106425 | ref | NP_035622.1 | MDV-ADPEP-----LGLFTEGELMS-----VGMD 23
gi | 109480249 | ref | XP_234900.3 | MDV-ADPEP-----LGLFTEGELMS-----VGMD 23
gi | 113951717 | ref | NP_001039298.1 | -----LGMFTEGELMS-----VGMD 23
gi | 21358043 | ref | NP_650302.1 | -----LGMFTEGELMS-----VGMD 23
gi | 17566086 | ref | NP_507533.1 | -----LGMFTEGELMS-----VGMD 23



gi | 62955651 | ref | NP_001017839.1 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 155
gi | 292611289 | ref | XP_002661045.1 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 155
gi | 4507271 | ref | NP_000446.1 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 114674399 | ref | XP_524028.2 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 73987574 | ref | XP_542206.2 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 194668554 | ref | XP_593229.4 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 7106425 | ref | NP_035622.1 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 109480249 | ref | XP_234900.3 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 113951717 | ref | NP_001039298.1 | RRRAKRLIGKYLMDLLGEGSYGKVKEMLDPELTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 156
gi | 21358043 | ref | NP_650302.1 | KKSISKVMGKYLMDVLEGSYGVKVEAMNSENLCLRAVKILTKRKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 279
gi | 17566086 | ref | NP_507533.1 | AMRPFNQRVNMAMFNQDNSEFQHLIEFPIVVKRQKPIIEGVMWGGQIGTGSYGVKVECIDMYLTCRAVILKIKKKLRRIPNGEAVKKEIQLLRLRHKHNVQLVDVLYNEEKQKMYMMEYCVCGMQLDSDVPEKRFVPCQAHGY 290



gi | 62955651 | ref | NP_001017839.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---ECG--- 278
gi | 292611289 | ref | XP_002661045.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---ECG--- 278
gi | 4507271 | ref | NP_000446.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGSVAIFG---DCG--- 279
gi | 114674399 | ref | XP_524028.2 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGSVAIFG---DCG--- 279
gi | 73987574 | ref | XP_542206.2 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 194668554 | ref | XP_593229.4 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 7106425 | ref | NP_035622.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 109480249 | ref | XP_234900.3 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 113951717 | ref | NP_001039298.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 21358043 | ref | NP_650302.1 | FCOLLIDGLEVYLSQGVVHKDIKPGNLLLTGALKISDLGVAEALHFFAADDTCRTSQGSPAFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---NIYKLFENIG---KGDYSIPE---DCG--- 279
gi | 17566086 | ref | NP_507533.1 | FIELCQGLNLYLSKRVSHKDIKPGNLLSIDFVVKICDFGVAEQINLFGRCITKVNGLPKFOPPEIANG-LDTFSGFKVDIWSAGVILYNIITGLYPFEGD---VLLKLYECIG---TEPLQMTN---VQLT--- 416



gi | 62955651 | ref | NP_001017839.1 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 292611289 | ref | XP_002661045.1 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 4507271 | ref | NP_000446.1 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 114674399 | ref | XP_524028.2 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 73987574 | ref | XP_542206.2 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 194668554 | ref | XP_593229.4 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 7106425 | ref | NP_035622.1 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 109480249 | ref | XP_234900.3 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 113951717 | ref | NP_001039298.1 | -PILLSLLRGMLEYEPKRFPSIRQIRQHSWFRKKHPPAEAEVPPVPPSPDKDRWRSMVTVPVLEDLHGAGED---EDLFDIEDDIYTDQDFVPGQVLEEEAS---HNGORRG---LPKAVC 391
gi | 21358043 | ref | NP_650302.1 | -ADNFANLILGMLQADPKRLLSLOEIRHDFWFRSAPVKGPPPIPPPLK---CDKYNSTVPIVLEAYHYGTQ---EDVYFVHVDVQELARQAAAAEIRAKQS---AAALAACHTVEPPST 519
gi | 17566086 | ref | NP_507533.1 | -KDLQDLITLLEKDFNERPCLLETMIHPWFLSTPEPQGLGRIMERMRGDRP---LTLSSMTALYDGTPEDELLIEDNLGIHQOILFINLTSVAVLEGRSFGKFKLEAKPGDGPDGVGSESDSAAPLGPDRRPPSSSMTCPAPPFG 563



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gi|62955651|ref|NP_001017839.1| VNGTESAALKP--KCERRSWSSWSNPWSR--KGLSAASKIRRLSTCKQQ----- 440
gi|292611289|ref|XP_002661045.1| VNGTESAALKP--KCERRSWSSWSNPWSR--KGLSAASKIRRLSTCKQQ----- 438
gi|4507271|ref|NP_000446.1| MNGTEAAQLSTKSRAEGR---APNPWAR--KACSASSKIRRLSACKQQ----- 433
gi|114674399|ref|XP_524028.2| MNGTEAAQLSTKSRAEGR---APNPWAR--KACSASSKIRRLSACKQQ----- 433
gi|73987574|ref|XP_542206.2| MNGTESAQLSTKSKVERRASAAWSNPWAR--KACSASSKIRRLSACKQQ----- 439
gi|194668554|ref|XP_593229.4| VNGDWTTQLNWTRSRWAERRASAAWSNPWAR--KACSASSKIRRLSACKQQ----- 465
gi|7106425|ref|NP_035622.1| VNGTEFW-QLSSKVKWPEGR-PGTANWPAR--KVCSW-SNKIRRLSACKQQ----- 436
gi|109480249|ref|XP_234900.3| VNGTEFW-QLSSKVKWPEGR-PGAANWPAR--KVCSW-SNKIRRLSACKQQ----- 436
gi|113951717|ref|NP_001039298.1| MNGTEPGQLSTKSKAERRASAAWSNPWSR--KACSASSKIRRLSTCKQQ----- 440
gi|21358043|ref|NP_650302.1| SAAAAASNLGNGSREWAPVKKKGSALWKRRAKLTSWCISVWRKLSHWCRWTS----- 567
gi|17566086|ref|NP_507533.1| AAGNAQNSTAENGAETDGVASASWDPWPPWTAWAPWGAPWPRWRKWRNWFFWSWCIFWRSWRTWEA----- 617
.....610.....620.....630.....640.....650.....

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