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| gi | 24645837 | ref | NP_652625.2 | MR---WLLNSWLLLLALFQGSW----GYSVLMISHTASRSHYAVCFALAKGLAAAGHEVTLVSPFPQPKIKNIIDVETPNITITVMGVYKARILENAKPKVLLR-----VPRISLMLGLDITESLLKEPKVQELLKQNR | 129 |
| gi | 21357701 | ref | NP_652626.1 | MKPTAGQTFGLALLLFCLLSCVSS----AYNLVVLHTAARSHYVGSALAKGLAAAGHOVITISPFELKPKIKNIKDVPAKISILTSMOGRITANLLQSSKEPIIKQ-----IINFHEMGLEIEHELLKEPSVIELMKSNO | 132 |
| gi | 24645835 | ref | NP_652620.1 | MR-----TFTLILGLLCLLGYSS----GYNLMLVNSAGRSHNVGHALAKGLVAKGHTITVVSVPFPKPKIPGYTDVSVNVIIVMGGDITGALWASTIQKTYTON-----LIDHYQMGRIRGLFEDSNFQDFLKSNO | 127 |
| gi | 158295576 | ref | XP_001688832.1 | MLGGKNNVASVALLCLVFAIGHNSVVVESAKILGIFPTSSKSHWILGSAIMKELADGHEV--YVCPFLKNAKPTVTRDVKIDYKGLFEAAMDKVFDMINDINSIVOK-----MTKLGNFANAIINTLSSPEVQALLQSDTE | 136 |
| gi | 158295574 | ref | XP_316292.4 | MISSKNNVAVAFLCLVFIIGNNRVMSAKILGIFPTASRSHWILGSAIMKELADGHEV--YVCPFLKNAKPTVTRDVKIDYKGLFEAAMDKVFDMINDINSIVOK-----MTKLGNFANAIINTLSSPEVQALLQSDTE | 137 |
| gi | 118778599 | ref | XP_308743.3 | ML--KWAVAVALLAALYAAKTP--VEGAKILAVFPTSSRSHYVIGSALMKELARRGHEVSVINPFPQKPKLNRVDIDVSGSEELVKDLVPMNFEMADQSVVES-----ITMUYKFGQMLANYILMHENVAKLKSNKE | 132 |
| gi | 8850236 | ref | NP_000454.1 | MAVESQGRPLVVLG--LILLCVLGPVSHAGKILLIPVDG--SHWLSMLGAIQQLQGRHEIVVLAPDASLYIRDGFYTLKTYVVPFQREDVKESFVLGHNVFENDFLQRVIKTKKIKKDSAMLLSGCSHLLHNKELMASLAE | 145 |
| gi | 157785611 | ref | NP_001099106.1 | MTAGSQGDRPVILL--LILLCVLGPVSHAGKILLIPVDG--SHWLSMLGAIQQLQGRHEIVVLAPDASLYIRDGFYTLKTYVVPFQREDVKESFVLGHNVFENDFLQRVIKTKKIKKDSAMLLSGCSHLLHNKELMASLAE | 145 |
| gi | 47059135 | ref | NP_964007.1 | MTVVCWSRLLLLLPLLLCVFGPSASHAGRLVFPMDG--SHWLSMLGVIQQLQKQHEVVVIAPESAIHIKESGFYTLRKPFPVFPQKENVTAALVELGRVAFNQDSFLLRVVKIYMKVKRDSMLLAGCSHLLHNAEFMASLEES | 147 |
| gi | 28849913 | ref | NP_036815.1 | MSVVCRSCLLLLLPCLLVCVLPGPSASHAGKLLVLPIDG--SHWLSMLGVIQQLQKQHEVVVIAPESAIHIKESGFYTLRKPFPVFPQKENVTAALVELGRVAFNQDSFLLRVVKIYMKVKRDSMLLAGCSHLLHNAEFMASLEES | 147 |
| gi | 118093321 | ref | XP_421883.2 | MALVLPSPHPQVSVSLLLLSVLSLAAG--GKLLVVSVVDG--SPWFSVLEMLVQLQKQHEVVVIAPESAIHIKESGFYTLRKPFPVFPQKENVTAALVELGRVAFNQDSFLLRVVKIYMKVKRDSMLLAGCSHLLHNAEFMASLEES | 145 |
| gi | 47087385 | ref | NP_998587.1 | ---MKRILFVPAQLGLFAFLCLFSSSESVQAGKVLVMPVDG--SHWLSMKILVLEEMSRGHEMVLVPEEISILIKESGNFTTKTSFRVYSDDELNAVVDHRIKATLAKAPRITIDVIGALGNLIQFTMVKACEGLLLYDEPLMKSLRDM | 144 |
| gi | 82658296 | ref | NP_001032505.1 | ---MRILFVPAQLGLLCLFSSFEVQAGKVLVMPVDG--SHWLSMKILVLEEMSRGHEMVLVPEEISILIKESGNFTTKTSFRVYSDDELNAVVDHRIKATLAKAPRITIDVIGALGNLIQFTMVKACEGLLLYDEPLMKSLRDM | 143 |



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| gi | 24645837 | ref | NP_652625.2 | DGVI CETFMNDAAHGF AEFH KAPLII LLSLGLA GWTSDLVGTPSPPPSYVPHSLRFGDRMNVWERAQNLGFIQIEFYAENLNLPRHEALYRKYFPNNKQDFYRMRKD--TSLVLLNNHVISINPRPYSFNMIIEVGGMHVNRKAPKPLPN | 278 |
| gi | 21357701 | ref | NP_652626.1 | DAVIEVFLNEAHEGF AEFH KAPLII LLSLGLA GWTSDLVGTPSPPPSYVPHSLRFGDRMNVWERAQNLGFIQIEFYAENLNLPRHEALYRKYFPNNKQDFYRMRKD--TSLVLLNNHVISINPRPYSFNMIIEVGGMHVNRKAPKPLPN | 280 |
| gi | 24645835 | ref | NP_652620.1 | DAIICETFMNDAAHGF AEFH KAPLII LLSLGLA GWTSDLVGTPSPPPSYVPHSLRFGDRMNVWERAQNLGFIQIEFYAENLNLPRHEALYRKYFPNNKQDFYRMRKD--TSLVLLNNHVISINPRPYSFNMIIEVGGMHVNRKAPKPLPN | 275 |
| gi | 158295576 | ref | XP_001688832.1 | DLVILEIFLDDALLGFADRFNCPVVMGSMFTFGASSVWNSLIGSPQPLSYVPHSPSFTDKMNFWRQVNLVLSAFDELLTAMCNPIQRHYNHYPNATRSLDEMRRHGVSLVLSINSHFSLSPFRPPLNLEVGGFHVNRKV-NPLPED | 285 |
| gi | 158295574 | ref | XP_316292.4 | DLVILEIFLDDALLGFADRFNCPVVMGSMFTFGASSVWNSLIGSPQPLSYVPHSPSFTDKMNFWRQVNLVLSAFDELLTAMCNPIQRHYNHYPNATRSLDEMRRHGVSLVLSINSHFSLSPFRPPLNLEVGGFHVNRKV-NPLPED | 286 |
| gi | 118778599 | ref | XP_308743.3 | DLIIMESFLNDAHGF AEFH KAPCVALSFTGASRWTNDMVGTPSPLSYVPHSPSFTDKMNFWRQVNLVLSAFDELLTAMCNPIQRHYNHYPNATRSLDEMRRHGVSLVLSINSHFSLSPFRPPLNLEVGGFHVNRKV-NPLPED | 281 |
| gi | 8850236 | ref | NP_000454.1 | DVMLTDFPLPCGPI--VAQYLSLPTVFFLNLPCSLDFOGTSPPSPSYVPRYLSFNSDHMTFLQVKKMFTLSESLCDMVSYP--YGLLASEIILQKEMTVQDLSLPA--SVWLLRSDVFKVYPRFIMPVNFVFG--GINCLQKPLSQE | 289 |
| gi | 157785611 | ref | NP_001099106.1 | DVMLTDFPLPCGPI--VAQYLSLPTVFFLNLPCSLDFOGTSPPSPSYVPRYLSFNSDHMTFLQVKKMFTLSESLCDMVSYP--YGLLASEIILQKEMTVQDLSLPA--SVWLLRSDVFKVYPRFIMPVNFVFG--GINCLQKPLSQE | 289 |
| gi | 47059135 | ref | NP_964007.1 | DALLTDFPLPCGSI--VAQYLVPTVFFLNLPCSLDSEATCPVPLSYVPKLSFNSDRMLNLRVKNVLLAVSENFMCRVVSYP--YGLLASEIILQKEMTVQDLSLPA--SVWLLRSDVFKVYPRFIMPVNFVFG--GINCLQKPLSQE | 291 |
| gi | 28849913 | ref | NP_036815.1 | DALLTDFPLPCGSI--VAQYLVPTVFFLNLPCSLDSEATCPVPLSYVPKLSFNSDRMLNLRVKNVLLAVSENFMCRVVSYP--YGLLASEIILQKEMTVQDLSLPA--SVWLLRSDVFKVYPRFIMPVNFVFG--GINCLQKPLSQE | 291 |
| gi | 118093321 | ref | XP_421883.2 | DALFTDFVPCGAI--LAHLSIPSVYFMRGMPCLDFEATCPNPPSYIPRAFDTHTDHMNFQRVKNVIEDLSNLFCLDFIFPK--YEKLASEFLQKEDVTDLLRKA--SVWLLRYDFVLDYPRFLMNIIVVG--GINCAHQK-LPQE | 288 |
| gi | 47087385 | ref | NP_998587.1 | DALLTDFPLPCGSI--IADYFPIPAVYVFLRGIICRDLDEAAA--CSPSPFPIPRFTTGTIDKMTFPRMINTFMTVEKLLCHQLFAS--FDELAIRYLKKTTSYAEILLGHG--AVWLLRYDFVFEVFPKQPMFNVIG--GINCAKRAPLTKE | 288 |
| gi | 82658296 | ref | NP_001032505.1 | DAMLTDFPLPCGII--IADYFPIPAVYVFLRGIICRDLDEAAA--CSPSPFPIPRFTTGTIDKMTFPRMINTFMTVEKLLCHQLFAS--FDELAIRYLKKTTSYAEILLGHG--AVWLLRYDFVFEVFPKQPMFNVIG--GINCAKRAPLTKE | 287 |



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| gi | 24645837 | ref | NP_652625.2 | IRKFTIEEA--EHGVLYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 427 |
| gi | 21357701 | ref | NP_652626.1 | ILEFTIEGA--EHGVLYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 429 |
| gi | 24645835 | ref | NP_652620.1 | IERTFINE--EHGAIYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 424 |
| gi | 158295576 | ref | XP_001688832.1 | IKSFTEQ--EHGVLYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 431 |
| gi | 158295574 | ref | XP_316292.4 | IKSFTEQ--EHGVLYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 431 |
| gi | 118778599 | ref | XP_308743.3 | IQRVLDGA--EHGVLYFSLGSLNLSKDLPEENKRKAIVEILRGLKYRVIWVYEEETFVDKPDNVLISNWLPODDILAHEKVIAFITHGGLLS--TMSIYHGKPVVVGIPFGDQFMNMAAEQMGYGVKVAQLTASLFRSAIERIISDPSFT | 430 |
| gi | 8850236 | ref | NP_000454.1 | FEAYVNA--GERGIVVFLSLS--MVSIEPPEKAMEIADALGKIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 437 |
| gi | 157785611 | ref | NP_001099106.1 | FEAYVNA--GERGIVVFLSLS--MVSIEPPEKAMEIADALGKIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 437 |
| gi | 47059135 | ref | NP_964007.1 | FEAYVNA--GERGIVVFLSLS--MVSIEPPEKAMEIADALGKIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 439 |
| gi | 28849913 | ref | NP_036815.1 | FEAYVNA--GERGIVVFLSLS--MVSIEPPEKAMEIADALGKIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 439 |
| gi | 118093321 | ref | XP_421883.2 | FEAYVNA--GERGIVVFLSLS--MVSIEPPEKAMEIADALGKIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 436 |
| gi | 47087385 | ref | NP_998587.1 | LEEFVNGSGEHRFVVFILGS--MVSQLEPAKAREFFFAFRQIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 436 |
| gi | 82658296 | ref | NP_001032505.1 | LEEFVNGSGEHRFVVFILGS--MVSQLEPAKAREFFFAFRQIPQTVLWRVYGTGTRPSNLAKNITLKVLPONDLLGHPKTRAFITHSGSHGIVEGICNGVPMVMPLFGDQMDNAKRMEIRGAGVTLNLEMSDEDLKALKAVINEKTYK | 435 |



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| gi | 24645837 | ref | NP_652625.2 | ERVKVIS--SQYRDQKETPLERAVYVVEVHRHKGAKYLRSACQDLNFIQYHNDVLAFFSVIGLVIFVFLVLRFLVTIVNGFLYK----PSSKLLKI | 521 |
| gi | 21357701 | ref | NP_652626.1 | QRVDRMS--DRYRDQOQTPLERAVYVVEVHRHKGAKYLRSACQDLNFIQYHNDVLAFFSVIGLVIFVFLVLRFLVTIVNGFLYK----PSSKLLKI | 528 |
| gi | 24645835 | ref | NP_652620.1 | KVVOGIS--FRYRDQOQTPLERAVYVVEVHRHKGAKYLRSACQDLNFIQYHNDVLAFFSVIGLVIFVFLVLRFLVTIVNGFLYK----PSSKLLKI | 519 |
| gi | 158295576 | ref | XP_001688832.1 | -----RYVLLLN--LVNFS | 443 |
| gi | 158295574 | ref | XP_316292.4 | ANVKTISRMRDQPLAPMDIAKFWVEYVLRHDCAKHLISSAQDLNFIQYHNDVLAFFSVIGLVIFVFLVLRFLVTIVNGFLYK----PSSKLLKI | 529 |
| gi | 118778599 | ref | XP_308743.3 | TVAQSI--ARYRDQOPEPLBLAAPFWVEYVLRHDCAKHLISSAQDLNFIQYHNDVLAFFSVIGLVIFVFLVLRFLVTIVNGFLYK----PSSKLLKI | 522 |
| gi | 8850236 | ref | NP_000454.1 | ENIMRSL--SLHKDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 533 |
| gi | 157785611 | ref | NP_001099106.1 | ENIMRSL--SLHKDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 533 |
| gi | 47059135 | ref | NP_964007.1 | ENIMRSL--SLHKDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 535 |
| gi | 28849913 | ref | NP_036815.1 | ENIMRSL--SLHKDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 535 |
| gi | 118093321 | ref | XP_421883.2 | ENIQRL--DLHLDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 532 |
| gi | 47087385 | ref | NP_998587.1 | EKMMLK--AIHRDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 526 |
| gi | 82658296 | ref | NP_001032505.1 | EKMMLK--AIHRDRPIEPLDLAVFWVEYVMRHKGAPHLRPAADHLTWQYHSLDVIQGLLAVLTVAFITFKCCAYGRKCLGKGRVVKSHKSKTH | 525 |

