

|    |           |     |                |  |     |
|----|-----------|-----|----------------|--|-----|
| gi | 145611760 | ref | XP_369103.2    | MEPSEKRLGDAPEAVVAQTPSNRNRSGSSESSKQKDD-----LTKADSKVLKPTADAVADPDDIYKHLPPHVAEILKROV-DTPSVKVGIAILYRVARSNLIIILSLICAVASGAALPLMIVIFGNLQGSFQDRFLGVT---     | 137 |
| gi | 164423939 | ref | XP_959059.2    | MAAGLSLSEKGEPSALPVSHEGGSTKG--DTIHKPDPLE-----LEKADTQVVSPPKSLDDDP--YKHLPEREAKILKEQV-FTPDVKVGIAILYRVARNDLLIIAIVSAICAAAGAAALPLMIVIFGNLQGTFFQNYFAGVT--- | 132 |
| gi | 19075765  | ref | NP_588265.1    | MSLHKKSTSTVKDNEHSLDLSIKSTPSNEKNFSTEKSE-----NEASESHVVDVVKDP-----FEQVTPPEQETILYKQINDTPAKLSGYPRLLSVADKWDIMLQLAGTTIGAGLGMPLMSLVSGQLAQAFDTLDSAGK---     | 130 |
| gi | 45382457  | ref | NP_990225.1    | -----MHSEDEKQKHTVD-----GNTYFIANSNQDQDP-----EDEKKGKKKKG--KPKQMVSPPLALFRYSSTDKLLMIFGSLLAIAHGTSLPIAMIIFGDMTDSFVTSGMTNITGN                             | 101 |
| gi | 118085766 | ref | XP_418636.2    | -----MLRQEGREDPQGIKMGSEEE-IKHYIN-----GRDDNIAVSYQNYQS-----EGKCSDEKKKP--EKMNNVSPFLAVFRYSRQDKLLMVLGTMAMVHLGASLPLMMIVFGDMTDTFIASENTYYPAN               | 114 |
| gi | 42741659  | ref | NP_000918.2    | -----MDLEGDRN-----GGAKKKNFFKLNKNS-----KDKKKEKKT-----VSVFMFRYSNWLKLYMVGTLAAI IHGAGLPLMMLVFGEMTDIFANAGN-LEDLM  | 89  |
| gi | 114614338 | ref | XP_001163342.1 | -----MDLEGDRN-----GGAKKKNFFKLNKNS-----KDKKKEKKT-----VSVFMFRYSNWLKLYMVGTLAAI IHGAGLPLMMLVFGEMTDIFANAGN-LEDLM  | 89  |
| gi | 50978984  | ref | NP_001003215.1 | -----MDPEGGRR-----GSAEK-NFWMKGKKS-----KKEKKEKKT-----VSTFAMFRYSNWLRLMLVGTMAAIIHGAAALPLMMLVFGNMTDSFANAGISRNKTF                                       | 89  |
| gi | 6755048   | ref | NP_035206.1    | -----MELEEDLK-----GRADK-NFSKMGKKS-----KKEKKEKKT-----VSVLMFRYAGWLDRLYMLVGTAAI IHGVALPLMMLIFGDMTDSFASVGN---VS  | 85  |
| gi | 25453402  | ref | NP_596892.1    | -----MELEEDLN-----GRADK-NFSKMGKKS-----KKEKKEKKT-----VSVLMFRYAGWLDRLFYMLLGTAAI IHGIALPLMMLVFGDMTDSFANVG---  | 82  |
| gi | 194685301 | ref | XP_590317.4    | -----MEWGTTRRQNRGGGQSPGRAAALPLGSRAEAGCLALSNVP-----AATLGGHEPAGSCGRALRPSARRAVFRYSNWLDRLYMVLGTAAI IHGAGLPLMMLVFGDMTDSFAAVGSSGNITF                     | 116 |
| gi | 17541710  | ref | NP_502413.1    | -----MLRNGSLRQSLRLDSFSLAPEDVLYKTAIKT-----VDEYEGDNIDSNCEI-----KITRDAKEVVP--NKVSIPLQLYRYTTLEKLLFTGLTVAVITGAGLPLMSILQGVSVQAFINEQIVINNGN               | 116 |
| gi | 17558664  | ref | NP_507487.1    | -----MGLFKKKKDDSSSEG-----SSEKKEEAPP-----PKISIFQLRYTSTVDRMLAVGIIVVSCATGVGLPMSIIMGNVSNQFVLTGLTIFLDPN   | 85  |
| gi | 85726357  | ref | NP_523740.3    | -----MLVKNCDVVKDDVNRQYKNIIVLQAKLEDSDRD-----RKSFEFNKSKKSKKH-----ESDASDEEDGSEQYHEDVKQVSYFQLFRVATKDRALYVIGLISAVATGLTIPANSLIFGNLNDMIDLGG-LLESQ         | 126 |
| gi | 15232977  | ref | NP_189479.1    | -----MGKEDEKESGRDKMKKSF-----SIRSIIFMHADGVDWMLMALGLIGAVDGFIPFIVVVFENTLNNLGTSSS---   | 68  |
| gi | 15232978  | ref | NP_189480.1    | -----MMKSFQ-----SIRSIIFMHADGVDWMLMALGLIGAVDGFIPFIFFFICSKLLNNVGGSSF---  | 56  |
| gi | 240255457 | ref | NP_189477.4    | -----MKTWG-----SMRISIFMHADGVDWMLMGLGLIGAVDGFIPILFFIITAMLLNDFGSSF---  | 55  |
| gi | 22331385  | ref | NP_683599.1    | -----MKSFG-----SVRSIFMHANSVDLMLMGLGLIGAVDGFIPPIIFFITGLLNDIGDSSF---   | 55  |
| gi | 15229473  | ref | NP_189475.1    | -----MGKKEEKESGRNKMNCFQ-----SVRSIFMHADGVDWMLMGLGLIGAVDGFITPVLVLLISKLMNIIIGSSF---   | 68  |
| gi | 115444737 | ref | NP_001046148.1 | -----MGGGGGAGKAKARPVFS-----SFMVFMHADAADVLMVLGGLGAMGGISIPVMLLITSRIFNDLGSAD---   | 68  |
| gi | 115444735 | ref | NP_001046147.1 | -----MGGDDRSAG--KAKPVLG-----SFMVFMHADAADVLMVLGGLGAVDGLSMFVLLLITGSVYNNFGGGAD---   | 66  |



|    |           |     |                |  |     |
|----|-----------|-----|----------------|--|-----|
| gi | 145611760 | ref | XP_369103.2    | -----SYDEFMTMLNLVLYEVLAIAGEFISVIATVGLIYGERISAKIRAHVLESCMRQNGFFDKL--GAGEVTIRIADTNLVOEGISEKVGLTAAAVAFVSFAVIFGVFMYWKLILILSIFFFALIFVMGG                          | 266 |
| gi | 164423939 | ref | XP_959059.2    | -----TYDDFTDELARLVLYEVLAIAGEFVIMYITVGFVYSGEHSIGKIREHVLESCMRQNGFFDKL--GAGEVTIRIADTNLVOEGISEKVGLTALALAFIAAFVIGFVSFWKLLILLSIVVALITLVMGG                         | 261 |
| gi | 19075765  | ref | NP_588265.1    | -----GASSFQHTVDHFLCYFYIYLAIGVFGCSYIYTVFIIAGERIARRIRQDYLHALLSNIGYFDRL--GAGEITIRIADTNLVOEGISEKVGLVFFALATFVSGVFIARFHKKFLLISMFPAICGGIGL                          | 259 |
| gi | 45382457  | ref | NP_990225.1    | -----VFNKLEEMERYAYYYSAIAAAVLVAAYIOTSFVFLAAGROVKKIREKFFHAIMROEIGWFDVN--DAGELNRLRDDVSKINEGIGDKIGFLISETPLTGFIVGFTRGWKLTLVLILAVSPVLGSAAL                         | 239 |
| gi | 118085766 | ref | XP_418636.2    | -----FSLLSNLSVNFMEFFYILIGLEEMERYAYYYSGIGAGVLFVAAYIOVSFWFLAAGROIKRIRQEFFHAVMROEIGWFDVN--DVCELNTRIVDDISKINEGIGEKIAMFFQAVATFFTGFIVGFTKGWKLTLVLILAVSPVLGSSAL     | 262 |
| gi | 42741659  | ref | NP_000918.2    | -----DNITNRSIDIN--DTCGFMMN-LEEDMTRAYAYYYSGIGAGVLFVAAYIOVSFWCLAAAGROIHKIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTLVLILAVSPVLGSAAV | 231 |
| gi | 114614338 | ref | XP_001163342.1 | -----DNITNRSIDIN--DTCGFMMN-LEEDMTRAYAYYYSGIGAGVLFVAAYIOVSFWCLAAAGROIHKIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTLVLILAVSPVLGSAAV | 231 |
| gi | 50978984  | ref | NP_001003215.1 | -----PVIINESIITN--NIQHFINHLEEMERYAYYYSGIGAGVLFVAAYIOVSFWCLAAAGROILKIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKVMFFQSIATFFTGFIVGFTPGWKLTLVLILAVSPVLGSAAI     | 232 |
| gi | 6755048   | ref | NP_035206.1    | -----KNSTNMSIAD--KRAMFAK-LEBEMERYAYYYTGIGAGVLFVAAYIOVSFWCLAAAGROIHKIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKIGMFFQAMATFFGGFIIIGFTRGWKLTLVLILAVSPVLGSAI    | 227 |
| gi | 25453402  | ref | NP_596892.1    | -----NNRSMSEFYN--AADIYAK-LEDEMERYAYYYTGIGAGVLFVAAYIOVSLWCLAAAGROIHKIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKIGMFFQAMATFFGGFIIIGFTRGWKLTLVLILAVSPVLGSAI    | 223 |
| gi | 194685301 | ref | XP_590317.4    | -----PNINISGSELG--IVRTEYGGKLEKEMERYAYYYSGIGAGVLFVAAYIOVSFWCLAAAGROVHRIRKQFFHAIMROEIGWFDVH--DVGELNRLRDDVSKINEGIGDKIGMFFQAMATFFGGFIIIGFTEGWKLTLVLILAVSPVLGSAAI | 261 |
| gi | 17541710  | ref | NP_502413.1    | -----STFLPTGQNY-----TKTDFERDVMNVVMSAAMTVGMMAAGQITVFCILYVAEQMNNRLRREPVKSIILROEISWFDIN--HSGTLANRKLFLERVKEGTGDKIGMAFQYLSQPIITGFIVAFTHSQQLLMLAVTPIQALCGFA        | 255 |
| gi | 17558664  | ref | NP_507487.1    | -----KST--ASEKAA-----ARAEFSHEVIQNCCLKIVLGCQIFAAGFLQASCFMVICELSNRFRQFFHSVMRQETAWYDKN--TSGTLNKLFLNLERVREGTQDKVGLAFQMAAQFICGFVAVFTYDWLLTLIMMSLSPFMMICGLF        | 222 |
| gi | 85726357  | ref | NP_523740.3    | -----KSYRADDAIS-----TLLLDKVRQFLQNTYIGIIMLVCSYLSIFCFNYAAHSLITIRSKFFRSILHODMKWYDFN--QSGEVAARMNEDLSKMEGLAEKVVVFVHLYVAVFVGLVLAFAVKGLSLVCLTSLPLTIFAMGL            | 263 |
| gi | 15232977  | ref | NP_189479.1    | -----NNTTFMPTIKNVVALLVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                       | 199 |
| gi | 15232978  | ref | NP_189480.1    | -----NDETFMPTIKNVALVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                         | 187 |
| gi | 240255457 | ref | NP_189477.4    | -----NDETFMPTIKNVALVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                         | 186 |
| gi | 22331385  | ref | NP_683599.1    | -----NDETFMPTIKNVALVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                         | 178 |
| gi | 15229473  | ref | NP_189475.1    | -----NDETFMPTIKNVALVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                         | 199 |
| gi | 115444737 | ref | NP_001046148.1 | -----NDETFMPTIKNVALVACGSWVICFLGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                         | 199 |
| gi | 115444735 | ref | NP_001046147.1 | -----NVQEFSSKVNMMARNLLFLAA-----EGYCWTRIGEROAARMREKYLRAVLRODVGYPDLHVITSDSVIIISVSDSLVIQDFLSEKLPNLFMNASAFVASIVSIFILMWRLTIVGFPFIIILLVPLGLM                       | 199 |



|    |           |     |                |    |            |   |     |    |      |    |    |    |    |     |    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |     |     |   |   |     |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |     |   |   |   |     |     |
|----|-----------|-----|----------------|----|------------|---|-----|----|------|----|----|----|----|-----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|-----|-----|---|---|-----|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|---|---|---|-----|---|---|---|-----|-----|
| gi | 145611760 | ref | XP_369103.2    | GS | SAFTIVKFSK | T | IDS | VA | EGGS | VA | EV | IS | SV | RNA | VA | F | G | T | D | R | L | A | R | R | Y | D | S | H | L | V | K | A | E | G | F | G | V | K | A | S | I | G | M | V | A | G | M | S | V | L | V | L | N | V | G | L | A | F | W | G | S | R | L | V | D | --- | G | V | I | P | L | S | K | V | L | V | M | S | V | M | I | G | A | F   | N | I | G   | N   | V | A | F   | V   | Q | A | F | T | T | L | G | A | A | K | I | Y | T | I | D | R | S | V | 409 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |     |   |   |   |     |     |
| gi | 164423939 | ref | XP_959059.2    | GS | QF         | I | K   | F  | S    | K  | N  | I  | A  | A   | V  | A | E | G | S | V | A | E | V | I | S | V | R | N | A | I | A | F | G | T | D | R | L | A | R | R | Y | D | A | H | L | T | R | A | E | H | F | G | F | R | L | K | G | S | I | G | M | V | A | G | M | T   | V | L | V | L | N | V | G | L | A | F | W | G | S | R | F | L | S | --- | G | D | E   | L   | R | K | L   | I   | L | V | M | S | V | M | I | G | A | F | N | L | G | N | I | A | P | N | L   | Q | A | F | V | T | L | G | A | A | K | I | Y | N | I | D | R | S | V | 404 |   |   |   |   |   |     |   |   |   |     |     |
| gi | 19075765  | ref | NP_588265.1    | G  | V          | P | F   | I  | T    | K  | N  | K  | G  | Q   | I  | A | V | A | E | S | T | F | V | E | E | F | S | N | I | R | N | A | F | A | F | G | T | O | D | I | L | A | K | L | N | K | Y | L | I | T | A | Q | R | F | G | I | N | K | A | T | A | M | G | L | M | V   | G | M | F | F | V | A | V | G | V | G | L | A | F | W | E | G | R | L   | L | H | A   | --- | G | D | L   | D   | V | S | K | L | I | G | C | F | F | A | V | L | I | A | S | Y | S | L | A   | N | I | S | P | K | M | O | S | V | S | C | A | S | A | A | K | I | F | D   | I | D | R | S | V | 402 |   |   |   |     |     |
| gi | 45382457  | ref | NP_990225.1    | W  | A          | K | I   | L  | T    | A  | F  | T  | D  | K   | E  | Q | A | A | Y | A | K | A | G | A | V | A | E | V | L | S | A | V | R | V | I | A | F | G | G | O | E | K | I | K | R | V | H | K | N | L | E | D | A | K | R | I | G | I | R | K | A | I | T | S | N | I   | S | M | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W   | G | T | L   | I   | L | A | --- | N   | E | Y | S | I | G | N | V | L | T | V | F | F | S | V | L | I | G | A | F   | S | I | G | T | A | P | S | I | E | A | F | A | N | A | R | G | A | A | Y   | A | I | F | N | I | D   | N | E | P | 382 |     |
| gi | 118085766 | ref | XP_418636.2    | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | Q | K | N | L | E | D | A | K | R | M | G | I | K | A | I | S | A | N | I | S   | M | G | V | S | F | F | L | I | Y | G | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | E | D | Y | T | I | G | K | V | T | V | F | F | S | I | L | V | G | A | F   | S | V | G | Q | A | F | S | M | E | A | F | A | N | A | R | G | A | A | Y   | A | I | F | N | I | D   | N | E | P | 405 |     |
| gi | 42741659  | ref | NP_000918.2    | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | K | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | G | E | Y | S | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | V | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | I | F | K | I   | D | N | K | P   | 374 |
| gi | 114614338 | ref | XP_001163342.1 | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | K | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | G | E | Y | S | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | V | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | I | F | K | I   | D | N | K | P   | 374 |
| gi | 50978984  | ref | NP_001003215.1 | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | N | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | S | E | T | T | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | V | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | I | F | K | I   | D | N | K | P   | 375 |
| gi | 6755048   | ref | NP_035206.1    | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | N | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | K | E | Y | T | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | V | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | V | F | K | I   | D | N | K | P   | 370 |
| gi | 25453402  | ref | NP_596892.1    | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | N | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | K | E | Y | T | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | V | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | V | F | K | I   | D | N | K | P   | 366 |
| gi | 194685301 | ref | XP_590317.4    | W  | A          | K | I   | L  | S    | S  | F  | T  | D  | K   | E  | L | L | A | Y | A | K | A | G | A | V | A | E | V | L | A | A | I | R | V | I | A | F | G | G | O | K | E | L | E | R | Y | N | K | N | L | E | E | A | K | R | I | G | I | K | A | I | T | A | N | I | S   | I | G | A | A | F | L | L | I | Y | A | S | Y | A | L | A | F | W | G   | T | L | I   | L   | V | L | S   | --- | K | E | Y | S | I | G | Q | V | L | T | V | F | F | S | V | L | I | G | A   | F | S | I | G | Q | A | S | P | I | E | A | F | A | N | A | R | G | A | A   | Y | E | V | F | K | I   | D | N | K | P   | 404 |
| gi | 17541710  | ref | NP_502413.1    | L  | A          | K | S   | M  | S    | T  | F  | A  | I  | R   | E  | L | R | Y | A | K | A | G | K | V | V | E | E | I | S | I | S | I | R | V | V | S | L | N | G | L | R | L | E | R | V | S | T | A | V | E | E | A | K | A | G | V | L | K | G | L | F | L | G | I | S | E   | G | A | M | Q | A | N | F | S | F | A | L | A | F | I | V | G | V | W   | H | D | --- | G   | S | L | N   | F   | G | D | M | L | T | F | F | S | V | M | M | G | S | M | A | L | G | L | A   | G | F | Q | L | A | V | L | G | T | A | Q | C | A | S | G | I | V | E | L   | D | R | K | P | V | 398 |   |   |   |     |     |
| gi | 17558664  | ref | NP_507487.1    | L  | A          | K | L   | A  | T    | A  | A  | T  | K  | E   | A  | K | Q | Y | A | V | A | G | G | I | A | E | V | L | I | S | I | R | V | I | A | F | N | G | C | E | Y | E | C | K | R | Y | E | D | A | L | E | H | G | K | K | I | G | I | K | S | F | L | I | G | A | L   | S | F | F | V | I | Y | A | S | Y | C | L | A | F | W | G | T | I | N   | F | V | S   | --- | G | R | L   | E   | S | G | T | V | L | T | V | F | F | S | V | M | M | G | S | M | A | L | G   | Q | A | Q | O | F | A | T | I | G | T | A | L | G | A | A | S | L | E | V   | I | D | R | K | P | 365 |   |   |   |     |     |
| gi | 85726357  | ref | NP_523740.3    | V  | A          | V | A   | S  | R    | L  | A  | K  | K  | E   | V  | I | M | Y | A | C | A | A | V | A | E | G | A | L | S | G | I | R | V | K | A | F | E | G | E | A | K | V | A | A | K | E | R | V | A | A | K | I | N | K | R | N | M | F | S | G | I | G | F | L | L | W   | F | F | I | Y | A | S | Y | A | L | A | F | W | G | V | G | L | V | I   | K | G | Y   | H   | E | P | A   | V   | E | N | N | D | A | G | T | M | I | T | V | F | F | S | V | M | M | G | S   | M | N | I | G | M | A | A | Y | E | A | F | A | G | I | A | K | A | C | A   | K | V | F | H | I | E   | Q | I | P | E   | 413 |
| gi | 15232977  | ref | NP_189479.1    | Y  | G          | R | A   | L  | V    | S  | I  | S  | R  | K   | I  | H | E | Q | V | N | E | A | G | S | I | A | E | Q | A |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |     |     |   |   |     |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |   |   |   |   |   |     |   |   |   |     |     |

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gi |145611760|ref |XP_369103.2| LPEGYDINVGGRGFLMSGGQKORIAIARAIVSDPKILLLDEATSALDTRFEGVVQAALVVAEGRTTIIIAHRLSTIKDAHNIVVMSEGRIVEQGNHNDLLE-KRGAYYNLVTAQETAKVT--ELSPHEEEAINEKEE-VLIRKATSNK 704
gi |164423939|ref |XP_959059.2| LPEGYDINVGGRGFLMSGGQKORIAIARAIVSDPKILLLDEATSALDTRFEGVVQAALVVAEGRTTIIIAHRLSTIKDAHNIVVMSEGRIVEQGNHNDLLE-KRGAYYNLVTAQETAKVT--EMTAEHEEAALDQQEEAALIRKATRNS 701
gi |19075765|ref |NP_588265.1| LPEQFSTNVGGRGFLMSGGQKORIAIARAIVSDPKILLLDEATSALDTRFEGVVQAALVVAEGRTTIIIAHRLSTIRNADNIVVMNAGKIVBQGNHNDLLE-LNGAYARLVTAQETAKVT--EMVHEHELEDAPRETPTTSPGDDDEDN 707
gi |45382457|ref |NP_990225.1| LPKKFEIVVGERGAQMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 667
gi |118085766|ref |XP_418636.2| LPKKFEIVVGERGAQMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNDLLE-LNGAYARLVTAQETAKVT--EMVHEHELEDAPRETPTTSPGDDDEDN 685
gi |42741659|ref |NP_000918.2| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 658
gi |114614338|ref |XP_001163342.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 658
gi |50978984|ref |NP_001003215.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 659
gi |6755048|ref |NP_035206.1| LPHQFDLVGERGAHVGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 654
gi |25453402|ref |NP_596892.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 650
gi |194685301|ref |XP_590317.4| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 688
gi |17541710|ref |NP_502413.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 683
gi |17558664|ref |NP_507487.1| FPEGNLTLVGDGRGQMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 648
gi |85726357|ref |NP_523740.3| LPKGYDILVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 694
gi |15232977|ref |NP_189479.1| FPLGYKTVQVGERGVMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 627
gi |15232978|ref |NP_189480.1| FPNVYQTVQVGERGVMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 612
gi |240255457|ref |NP_189477.4| FPHGYQTVQVGERGVMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 613
gi |22331385|ref |NP_683599.1| FPLGYKTVQVGERGVMSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 606
gi |15229473|ref |NP_189475.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 623
gi |115444737|ref |NP_001046148.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 626
gi |115444735|ref |NP_001046147.1| LPHKFDLVGERGAQLSGGQKORIAIARALVHNPKILLLDEATSALDTESEAVVQAALDKAREGRTTIVVVAHRLSTVRNADLIAVFEVSGVIEEQGNHNSQLIE-KKGIYVYKLVNMQTETED---PSEKSENAVSVKRSQSQSNLDE 616
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi |145611760|ref |XP_369103.2| E---SGSFIPD--PNDKLAHKMER-----LKS---ASSVALQ-----GRSKDAPK-----KYLWTKIKLIAAFN--APEWKLWVIGLLFSLICGGGNPQAVFFAKLITSMVSP-VNEQTIPIGIRDVSVFQCLMVLMLA 818
gi |164423939|ref |XP_959059.2| QKEGGAAGYVED--PEDNIAEKLDNR-----SKSQSVSSVALA-----ARKKEEPK-----EYGLWTLIKLIAAFN--KKEWHMLLVGIFFAICGAGNPPQAVFFAKLITSMVSP-VNEQTIPIGIRDVSVFQCLMVLMLA 822
gi |19075765|ref |NP_588265.1| DNASLEAPMMHNTDTTLNKNKLNEDNVVFDKTLQHVASEIVNLPADVGELNEEKKKSKKSKKNHINSLTALWFIHSFVRTMIEIICLLIGILASMICGAAYPQAAVAFARFLN---IFDLSSTDFLKHVNVFAVYWLILA 846
gi |45382457|ref |NP_990225.1| L-----KKELRRGSTRRSMKFP-----GEPND--DEKQ-----SSPDEEL-----PPVSLKMLKLNKNWVYFVAGFCAIVNGALQPAFVIFSEIIG---IFSET-DQKVLREKLNLYSLLFLALG 771
gi |118085766|ref |XP_418636.2| V-----LFGQRQSTRKSLKRV-----RIQNDDELVKA-----DQLDKNM-----PPSFFKIMKLNKTEWPFVVGFLCAIINGALQPAFVIFSEIIG---MFVEK-GKAAIRETNSYALLFLFGF 790
gi |42741659|ref |NP_000918.2| R-----SLIRKRSTRRSVRGS-----QAQDRKLSLK-----EALDESI-----PPVSWRIMKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---VFRIDDPETKRONSNLFLFLALG 763
gi |114614338|ref |XP_001163342.1| R-----SLIRKRSTRRSVRGS-----QAQDRKLSLK-----EALDESI-----PPVSWRIMKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---VFRIDDPETKRONSNLFLFLALG 763
gi |50978984|ref |NP_001003215.1| G-----SLIKRSTRRSIHAP-----QQDRKLSLK-----EDLNENV-----PSVSWRILKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---IFTRDEDPETKRONSNLFLFLALG 764
gi |6755048|ref |NP_035206.1| G-----SLIRRRSTRRSICGP-----HDQDRKLSLK-----EALDEDV-----PPASFWRILKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---VFTNGGPPETQRONSNLFLFLALG 759
gi |25453402|ref |NP_596892.1| G-----SLIRRRSTRRSIRGP-----HDQDRKLSLK-----EALDDDV-----PPASFWRILKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---VFTKNDTPEIQRONSNLFLFLALG 755
gi |194685301|ref |XP_590317.4| R-----SLIRKRSTRRSIRGS-----QSRDRKLSSE-----ETLDES V-----PPVSWRILKLNLEWPFVVGFLCAIINGALQPAFVIFSEIIG---IFTRNDVDETKRONSNLFLFLALG 793
gi |17541710|ref |NP_502413.1| SRGASEMDDIMNRVRSSTIGSTING-----FVIDEKEERIKDALSRLKQLEENNA-----QKLNLEFELYHARPHALSIFIGMSTAIIGGFYTPVYVFFTSFNM---VFAQN-PADFLS-QGHFWALMFLVLA 804
gi |17558664|ref |NP_507487.1| E-----VNFKTSQESQVDEKPGA-----PPAPEAAEKE-----IKRLKKELEEGA-----VKANLFXILRWARPEWYIFFAIAALIQAVMPAFSLFFSQIIN---VFSNF-DRDKKDKGHFWALMFLVLA 757
gi |85726357|ref |NP_523740.3| E-----EIKVLSDEDEDEMVT-----DEKNKKKKK-----KVDKPN-----VKP-MLEVMMKMPKPEWQIAGVCISVIMGCAMPFAVLFSGSILQ---ILSVKNDQVYRENSQVSLYFLIAG 798
gi |15232977|ref |NP_189479.1| Q-----HNSIGTS-----SSIVTNVSDL-----IPNDNQF-----LVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VFFLTSHDQIKKTRIVYLLFVGLA 723
gi |15232978|ref |NP_189480.1| P-----KEFIHST-----SNIVRDFPNL-----SPKDGKS-----LVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLASHDQIKKTRIVYLLFVGLA 708
gi |240255457|ref |NP_189477.4| P-----RDLAHSMS-----SSIVTNVSDL-----IPNDNQF-----LVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLASHDQIKKTRIVYLLFVGLA 709
gi |22331385|ref |NP_683599.1| S-----RLSIQSRSLFAT-----SSIDTNLGS-----IPDKKP-----LVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLTSHDEKTRIVYLLFVGLA 704
gi |15229473|ref |NP_189475.1| S-----RVSTLSRS-SAN-----SVTGPSTIKN-----LSEDNKP-----QLPSPFKRLLAMNLPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLTSHDEKTRIVYLLFVGLA 723
gi |115444737|ref |NP_001046148.1| R-----RFSAAARS-----SA-----RSLGDARDD-----NTEKPKL-----PVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLTSHDEKTRIVYLLFVGLA 725
gi |115444735|ref |NP_001046147.1| R-----RFSAAARS-----SV-----RSLGDARDD-----NTEKPKL-----PVPFTRLMVMNRPKPEWKHALYGCLSAALVGLQVPSAYSAGSVIS---VYFLTSHDEKTRIVYLLFVGLA 715
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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|    |           |     |                |  |   |     |
|----|-----------|-----|----------------|--|---|-----|
| gi | 145611760 | ref | XP_369103.2    |  | IVQFIATFVIGILFAKCSERLIHRVDRAFRMLRMDIGEFVDFKEENIAGALTSFLETHVAGISGVTLGLTLMVITLVSFTLILALGKWLALVCSIVPVLACGFLRFWMLAHYQRRAKRAYDNASAYASEAITAIRIVASLIRE       | 968 |
| gi | 164423939 | ref | XP_959059.2    |  | LVQCLAFVCGWLFKAGCSERLIHRVDRMAFRSFLRQDVEFFDRDENISAGALTSFLETHVAGISGVTLGLTLMVITLVAIACTVALALGWKLVLCIAIPILLGCGFYRFWMLAHYQRRAKSAVAGSASYASEAITAMRIVASLIRE    | 972 |
| gi | 19075765  | ref | NP_588265.1    |  | IVQFFAYAINFAMTYAMEAVLQRIRYHLFRLLRQDVEFFDRDENISVGAITISLSTKIQSLEGLSGPTLGFPIILNTNISVITLISLATGWKLVLSLSPVITIIAGYVRVRLDQVQKLSAAVRESAAAFACESIAIRIVASLIRE     | 996 |
| gi | 45382457  | ref | NP_990225.1    |  | IISFFTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 921 |
| gi | 118085766 | ref | XP_418636.2    |  | LISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 940 |
| gi | 42741659  | ref | NP_000918.2    |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 913 |
| gi | 114614338 | ref | XP_001163342.1 |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 913 |
| gi | 50978984  | ref | NP_001003215.1 |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 914 |
| gi | 6755048   | ref | NP_035206.1    |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 909 |
| gi | 25453402  | ref | NP_596892.1    |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 905 |
| gi | 194685301 | ref | XP_590317.4    |  | IISFVTFVVGAFPGKAGEILMKLRFMAFKAMLRQDMAWFDDPKNSTGALITRLANDASQVKGATGVRLLALIAQNTANLGTGIIISLVYGWQLLLLLLAVPPIIAVAGMIEMKMLAGHAKDKKIELEBAAGKIATEAENIRIVASLIRE | 943 |
| gi | 17541710  | ref | NP_502413.1    |  | AAQGCISFLMTFFMGIAASESLRDLRNLKLFNRVLSOHIGFDFSPQNASGKISIRLATDVPNLRITAFDRFSTVITLVSVMVAGIAGLAFYGGWQALLIIAIPVAVPQQLRGRRTGKNVKSASEFADSGKIAIEAENIRIVASLIRE   | 954 |
| gi | 17558664  | ref | NP_507487.1    |  | AVQGTSMFLFCCLFVGAARLIMRIRSKYVRNVLQDATYFDMPKHSPGRITRLATDAPNIKSAIDYRIGSIFNALSASVGGGLGIAFYGGWQMAFLVMAIFPFMVAVGQALMMKYHGGSATSDAKEMNAGKTAMEAENIRIVASLIRE   | 907 |
| gi | 85726357  | ref | NP_523740.3    |  | IVVGIATFLIIVFGIAGERLTERLRLMFEAMLRQEVAVFDDKANGTGLCARLGGDAAAQVQAGQORIGIVQISITLALGIALSMYYEWSLGLVALAFTPFILIAFMORTLMAKENMGSATIMNCTKLAVEVSNIRIVASLIRE       | 948 |
| gi | 15232977  | ref | NP_189479.1    |  | IFSFVNLNISHYGFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS | 873 |
| gi | 15232978  | ref | NP_189480.1    |  | LFVFLNLSHYGFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS   | 858 |
| gi | 240255457 | ref | NP_189477.4    |  | LFVFLNLSHYGFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS   | 859 |
| gi | 22331385  | ref | NP_683599.1    |  | QTRVILNLSHYGFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS  | 854 |
| gi | 15229473  | ref | NP_189475.1    |  | VLSFLINISQHYNFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS | 875 |
| gi | 115444737 | ref | NP_001046148.1 |  | VLSFLINISQHYNFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS | 873 |
| gi | 115444735 | ref | NP_001046147.1 |  | VLSFLINISQHYNFAYMGEVLTKRIRERMLKILTFEWNWFDKIDENSSGAICRRLAKDANVRSVLDGRMSLLVQITISAVSITCAIGLVIASWRFLIVMMSVQPVIVVCFYTORVLLKSMRINAIRKQDESSKLAAEAVSNIRITAFSS | 865 |



|    |           |     |                |  |  |      |
|----|-----------|-----|----------------|--|--|------|
| gi | 145611760 | ref | XP_369103.2    |  | NDVLRKRYQNSLDEQGRASLQSVLKSSILMAASQSLIFLVIALAFWYGGSLLRG--EYGMFQFFLVFSAIIFGAQSGTMAFAPDMGKAHAAELKTLFDRKPTDITWSDGERIGEVN-GTIEFRDVHFRVPTRPEQVPLRGDLTV       | 1115 |
| gi | 164423939 | ref | XP_959059.2    |  | QDVLRKRYQNSLDEQGRASLQSVLKSSILMAASQSLIFLVIALAFWYGGSLLRG--EYDMFTFFLVFSAIIFGAQSGTMAFAPDMGKAHAAELKTLFDRKPTDITWSDGERIGEVN-GTIEFRDVHFRVPTRPEQVPLRGDLTV       | 1119 |
| gi | 19075765  | ref | NP_588265.1    |  | ENVFAEYCDLSLIKPGRESALIASLKSGLFFSAAGVITLINALTFWYGSTLMRKG--EYNIQVFTCFIAIVFGIQQAGFFGYSADVTKAKAAAGEIKYLSBSKPKIDITWSTEGKVESLQSAAEFRQVEFSVPTRRHKVLRGLNLTV    | 1144 |
| gi | 45382457  | ref | NP_990225.1    |  | KRFELMYGHEHLLVPRNSVVKKAHIFGCFPSLQAMMFFTYAGCFRFGAYLVVNG--HIEYKTVFLVFSAVVFGAMALGQSSFPADYAKAKISAAHLFVLFNRPVPLDYSREDEG-KPEKFGGNIRIKDKVFNPNRPEVKILQGLNLAV   | 1068 |
| gi | 118085766 | ref | XP_418636.2    |  | RKFEYMYGONLQVSYRNSIKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVKNG--HMRFKDVLVFSAVVFGAMALGQSSFPADYAKAKISAAHLFVLFNRPVPLDYSREDEG-KPKMFGGNITFKDVAFKVPTRPEVKVLOGLNIEV    | 1087 |
| gi | 42741659  | ref | NP_000918.2    |  | QKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVAKH--LMSFEDVLLVFSAVVFGAMAVGQVSSFPADYAKAKISAAHIMIIEKTPLDISYSTEGL-MPNTLEGNVTFGEVFNVPTRPDIPVLQGLSLEV    | 1060 |
| gi | 114614338 | ref | XP_001163342.1 |  | QKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVAKH--LMSFEDVLLVFSAVVFGAMAVGQVSSFPADYAKAKISAAHIMIIEKTPLDISYSTEGL-MPNTLEGNVTFGEVFNVPTRPDIPVLQGLSLEV    | 1060 |
| gi | 50978984  | ref | NP_001003215.1 |  | QKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVANE--FMNFQDVLVFSAVVFGAMAVGQVSSFPADYAKAKISAAHIMIIEKTPLDISYSTEGL-MPNTLEGNVTFGEVFNVPTRPDIPVLQGLSLEV     | 1061 |
| gi | 6755048   | ref | NP_035206.1    |  | QKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVQ--LMTFENVLLVFSAVVFGAMAVGQVSSFPADYAKATVSASHIIRIIEKTEPEIDSYSTEGL-KPNMLEGNVQFSGVFNVPTRPDIPLQGLSLEV     | 1056 |
| gi | 25453402  | ref | NP_596892.1    |  | QKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVARE--LMTFENVLLVFSAVVFGAMAVGQVSSFPADYAKAKISAAHIMIIEKTEPEIDSYSTEGL-KPNMLEGNVQFSGVFNVPTRPDIPLQGLSLEV    | 1052 |
| gi | 194685301 | ref | XP_590317.4    |  | RKFEHMYAOSLQVPRNSLRKKAHIFGTFAPFOAIMYFTYAGCFRFGAYLVAG--IMEFQDVLVFSAVVFGAMAVGQVSSFPADYAKAKISAAHIMIIEKTEPEIDSYSTEGL-KPSTVEGNVQFSGVFNVPTRPDIPLQGLSLEV      | 1090 |
| gi | 17541710  | ref | NP_502413.1    |  | DTFVENFCRKLIDIPHEKAIKEAFIQGLSQCASVLYLILNCAIRMLGALITDPTMQPMRVLRVMYAIISTSLGFSATSVFPEYAKATFAGCIIFGMIRKIKSKIDSLSLAGE-KKK-LYGVKIFKNVFAFERPEIETIKGLSFSV      | 1102 |
| gi | 17558664  | ref | NP_507487.1    |  | TKLVNIFCSHLDAFHGGNISKAIIRGLTYGFANSIQFFVYAAAFRGLFLIFDKNVLMEPENVLRVLFALISFSGIIGFAASVFPYIKATFAAGLIFNMLEEPRIDGMTSSG--YFQ-LSGEVKNLNVFRVFERPAVILQGLNVHV      | 1055 |
| gi | 85726357  | ref | NP_523740.3    |  | EMFHQNYIGMLIPAVEISKRNTHFRGLVYGLARSIMFAYAACMYGTWCVIHR--GILFGDVFVKSQALMGTSANALAFAPNMQKGVSAAKTIFTLRRQPSIVDRPQVSR-DPWHSEGYVRFDRKVKFSVPTRSEIQVLKGLLAV       | 1095 |
| gi | 15232977  | ref | NP_189479.1    |  | ERIKLKLKVVQEGPRRESVHRSLAGIVLGTSRSLITCTSALNFWYGGRLIADG--KIVSKAFFEILFLIFVITGRVITADAGTMTDLARGLDVAGSVFAVLDRCITTEPKNPDGY-VAEKIRGQITFLNVDFAVPTRPDVIIFENFSIEI | 1020 |
| gi | 15232978  | ref | NP_189480.1    |  | ERIKLKLKVVQEGPRRESVHRSLAGIVLGTSRSLITCTSALNFWYGGRLIADG--KIVSKAFFEILFLIFVITGRVITADAGTMTDLARGLDVAGSVFAVLDRCITTEPKNPDGY-VAEKIRGQITFLNVDFAVPTRPDVIIFENFSIEI | 1005 |
| gi | 240255457 | ref | NP_189477.4    |  | ERIKLKLKVVQEGPRRESVHRSLAGIVLGTSRSLITCTSALNFWYGGRLIADG--KIVSKAFFEILFLIFVITGRVITADAGTMTDLARGLDVAGSVFAVLDRCITTEPKNPDGY-VAEKIRGQITFLNVDFAVPTRPDVIIFENFSIEI | 1006 |
| gi | 22331385  | ref | NP_683599.1    |  | ERIKLKLKVVQEGPRRESVHRSLAGIVLGTSRSLITCTSALNFWYGGRLIADG--KIVSKAFFEILFLIFVITGRVITADAGTMTDLARGLDVAGSVFAVLDRCITTEPKNPDGY-VAEKIRGQITFLNVDFAVPTRPDVIIFENFSIEI | 1001 |
| gi | 15229473  | ref | NP_189475.1    |  | ERIKLKLKVVQEGPRRESVHRSLAGIVLGTSRSLITCTSALNFWYGGRLIADG--KIVSKAFFEILFLIFVITGRVITADAGTMTDLARGLDVAGSVFAVLDRCITTEPKNPDGY-VAEKIRGQITFLNVDFAVPTRPDVIIFENFSIEI | 1020 |
| gi | 115444737 | ref | NP_001046148.1 |  | ERILRLFEQDGRPKRESIQSWFAGLGLGTSMSLMTCTWALDFWYGGRLIAEH--HISAKELFQFMILVSTGRVIADAGSMTDLARGDVAVASVFAVLDRETEIDPDNPQGY-KPEKIKGEVDIRRVDFAVPSRPDVIIFKGFILSI     | 1022 |
| gi | 115444735 | ref | NP_001046147.1 |  | ERILRLFEQDGRPKRESIQSWFAGLGLGTSMSLMTCTWALDFWYGGRLIAEH--HISAKELFQFMILVSTGRVIADAGSMTDLARGDVAVASVFAVLDRETEIDPDNPQGY-KPEKIKGEVDIRRVDFAVPSRPDVIIFKGFILSI     | 1012 |



