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gi | 17737561 | ref | NP_524023.1 | ---MFHFSGFN-----MMFPEG---RNFHANYKCFVSMLPG---NERDVEKGGKIIMPPSALDQLRLNVEYPMFLKLTINVKKRSRHAGVLEFVADEGKCYLPHWMMENLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 132
gi | 118794962 | ref | XP_321840.2 | ---MFQFNGFN-----MMFPDHS---RPNTTYKCYVSMLPG---NERQDVENGKGIIMPPSALDQLRLNVEYPMFLKLTINVSINRSRHAGVLEFVADEGKCYLPHWMMENLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 133
gi | 31981443 | ref | NP_035802.2 | ---MFSFNMFED-----HPIPRVFQNRFFSTQYRCFSVSMLAG---NDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTINKNSDRMTHCGVLEFVADEGICYLPHWMMONLLLEEGGLVQVESVNLQVAITSKFQPHHDFLDI 135
gi | 16758158 | ref | NP_445870.1 | ---MFSFNMFED-----HPIPRVFQNRFFSTQYRCFSVSMLAG---NDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTINKNSDRMTHCGVLEFVADEGICYLPHWMMONLLLEEGGLVQVESVNLQVAITSKFQPHHDFLDI 135
gi | 29501813 | ref | NP_005650.2 | ---MFSFNMFED-----HPIPRVFQNRFFSTQYRCFSVSMLAG---NDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTINKNSDRMTHCGVLEFVADEGICYLPHWMMONLLLEEGGLVQVESVNLQVAITSKFQPHHDFLDI 135
gi | 45383542 | ref | NP_989632.1 | ---MFSFNMFED-----HPIPRVFQNRFFSTQYRCFSVSMLAG---NDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTINKNSDRMTHCGVLEFVADEGICYLPHWMMONLLLEEGGLVQVESVNLQVAITSKFQPHHDFLDI 135
gi | 50539970 | ref | NP_001002451.1 | ---MFSFNMFED-----HPVGRVFQNRFFSTQYRCFSVSMLAG---NDRSDVEKGGKIIMPPSALDQLSRLNITYPMLFKLTINKNSDRMTHCGVLEFVADEGICYLPHWMMONLLLEEGGLVQVESVNLQVAITSKFQPHHDFLDI 135
gi | 18420341 | ref | NP_568048.1 | ---MFYDGYA-----YHG---TTFEQYRQYCPASFDK---PQIESGDKIIMPPSALDRLASLHIDYPMFLFELRNASDPSFHCGVLEFIAEBEGMIMYPYMMONLLLEGDIVRVRNVLTKPGTYVVKLOPHHDFLDI 125
gi | 18399646 | ref | NP_565504.1 | ---MFFDGVH-----YHG---TTFEQYRQYCPASFDK---PQIESGDKIIMPPSALDRLASLHIDYPMFLFELRNASDPSFHCGVLEFIAEBEGMIMYPYMMONLLLEGDIVRVRNVLTKPGTYVVKLOPHHDFLDI 125
gi | 115444631 | ref | NP_001046095.1 | ---MYFEGY-----YRG---STFEQYRQYCPASFDK---PQLETGDKIIMPPSALDRLASLHIDYPMFLFELRNASDPSFHCGVLEFIAEBEGMIMYPYMMONLLLEGDIVRVRNVLTKPGTYVVKLOPHHDFLDI 125
gi | 17539898 | ref | NP_502348.1 | ---MQAWIQQLH-----GMQMGRRVGNVDTQTFVYVYGGVFLPNATGSKI---EINYGGKILLPSSALDRLNLMQYIMPMFLFKLTAMAVQRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 139
gi | 6321485 | ref | NP_011562.1 | MFSG---FSSFGG---GNGFVN---MPQTFEEFFRCYPTAMMNDR---TRKDDANVGGKIFLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 137
gi | 50304703 | ref | XP_452307.1 | MFSG---FSGYG---NAYAN---IPQRLEEFRFCYPTAMMNDR---TRKDDANVGGKIFLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 135
gi | 45199181 | ref | NP_986210.1 | MFSG---FSGYG---GGFV---MPQKFEDEFRCYPTAMMNDR---TRKEDANYGGKIFLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 135
gi | 19113572 | ref | NP_596780.1 | MFSG---FSSDDG---FSSMQLRSFAFNANNVQRFDRYRCYPMVAMIPGE---ERP---NVNYGGKIVLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 147
gi | 39942190 | ref | XP_360632.1 | MYAS---AMR---GGRR---IVQRFDYRRCYPMVAMIPGE---ERP---ELNHGSKILLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 132
gi | 32413324 | ref | XP_327142.1 | MYGD---IYSRA---TGRSR---CAQRFDYRRCYPMVAMIPGE---ERP---ELNYGSKILLPPSALNKLKSLMNLNRYPMFLFKLTANEGRVTHCGVLEFIAEBEGMIMYPYMMONLLLEGDILNIEVSLPVAIFSKFQPHHDFLDI 134
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 17737561 | ref | NP_524023.1 | TNPKAVLENALRNFACLTTRGDVIAIKYNTTYVELSVLETKPGN---AVSIIEDCMNVFEAPVGYKDISETQAS---GSGQQGAAGTV---GGEIAGANAILLEVVEFKGSGVRLDGKKKES-QLETFFVK 256
gi | 118794962 | ref | XP_321840.2 | TNPKAVLENALRNFACLTTRGDVIAIKYNTTYVELSVLETKPGN---AVTIIEDCMNVFEAPVGYTEPEREKE---EEMTIDTPEL---MPEPTG---FVAFKGEGRTRLDGKKKNDGNTDAPAAQ 249
gi | 31981443 | ref | NP_035802.2 | TNPKAVLENALRDFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EESIEGADHS---GYAGEVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 16758158 | ref | NP_445870.1 | TNPKAVLENALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EESIEGADHS---GYAGEVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 29501813 | ref | NP_005650.2 | TNPKAVLENALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 45383542 | ref | NP_989632.1 | TNPKAVLENALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 50539970 | ref | NP_001002451.1 | TNPKAVLENALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 18420341 | ref | NP_568048.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 18399646 | ref | NP_565504.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 115444631 | ref | NP_001046095.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 17539898 | ref | NP_502348.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 6321485 | ref | NP_011562.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 50304703 | ref | XP_452307.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 45199181 | ref | NP_986210.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 19113572 | ref | NP_596780.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 39942190 | ref | XP_360632.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
gi | 32413324 | ref | XP_327142.1 | ANPKAILETALRNFACLTTRGDVIAINYNKIIYELRVMETKPKD---AVSIIEDCMNVDFDAPLGKKEPERVQH---EETDVEADHS---GYVSDVG---FRAFSGSGNRLDGKKKGV-E-PSPIPK 251
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 17737561 | ref | NP_524023.1 | ---KVLARGVDPDYDFQGLIRFDRNRIPISDRG---EDDAVAGNADASDAESFHGTGFSMKKT-RK--- 316
gi | 118794962 | ref | XP_321840.2 | R---QTVYRGIPIYDHPYGLLRFRDRSVR---KTDQLESKLEDSKFEQFQEGGFNLKKN-RK--- 303
gi | 31981443 | ref | NP_035802.2 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 16758158 | ref | NP_445870.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 29501813 | ref | NP_005650.2 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 45383542 | ref | NP_989632.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 50539970 | ref | NP_001002451.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 18420341 | ref | NP_568048.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 18399646 | ref | NP_565504.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 115444631 | ref | NP_001046095.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 17539898 | ref | NP_502348.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 6321485 | ref | NP_011562.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 50304703 | ref | XP_452307.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 45199181 | ref | NP_986210.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 19113572 | ref | NP_596780.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 39942190 | ref | XP_360632.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
gi | 32413324 | ref | XP_327142.1 | ---GDIKRGIPNYEFKLGKIFIRNSRP---LVKKVEDEAGGRFVAFSGEGQSLRKKGRKP--- 307
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....

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