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gi|6679144|ref|NP_032768.1|-----MSILFVVFIFLAYLRGIQGN 19
gi|47271540|ref|NP_112335.2|-----MSILFVVFIFLAYLRGIQGN 19
gi|114642998|ref|XP_522331.2|-----MSILFVVFIFLAYLRGIQGN 19
gi|73997470|ref|XP_543858.2|-----MSILFVVFIFLAYLRGIQGN 19
gi|156630995|ref|NP_001096124.1|-----MVTPTITLQVNVKMSILFVVFIFLAYLRGIQGN 32
gi|118151064|ref|NP_001071456.1|-----MSILFVVMFLAYLRGVQGN 19
gi|118083230|ref|XP_425658.2|-----MVTPTITLQVNVKMSILFVVFIFLAYLRGIQST 32
gi|189517902|ref|XP_697445.3|MNKEWRKKKKKKKCPMINKETHSVNRKFTPSFNLSLRVSCDIYGLFDWLKLLKAKCKSSRRKKKHILCHQEVHSSFLQCEITLSTHRAFLYLETVDKRIYKLYLHLVGSAEYFLDAMVTFITLQVNLVMSILLVVMFLAYLYGISAS 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6679144|ref|NP_032768.1|SMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPREPEQGEATRSEFOPMIATDTPELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGNPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 169
gi|47271540|ref|NP_112335.2|NMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPREPEQGEATRSEFOPMIATDTPELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGNPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 169
gi|114642998|ref|XP_522331.2|NMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPREPERGEPKSAFOPVMIAMDTELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGNPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 168
gi|73997470|ref|XP_543858.2|NMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPRKPERGEPKSAFOPVMIAMDTELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGNPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 168
gi|156630995|ref|NP_001096124.1|NMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPREPERGEPKSAFOPVMIAMDTELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGSPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 181
gi|118151064|ref|NP_001071456.1|SMDQRSLPEDSLNSLIILKLIQADILKNKLSKQMV DVKENYQSTLPKAEAPPR---EPKSAFOPVMIAMDTELLRQORRYNSPRVLLSDSTPLEPPPLYLMEDVVGSPVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 164
gi|118083230|ref|XP_425658.2|NMDQRSLPEDSMNSLIILKLIQADILKNKLSKQMV DVKENYQNIYQKVEDHCEMDGDNVKSDFOPVISMIDLLRQORRYNSPRVLLSDNTPLEPPPLYLTEDVVGSSVVAANRTSPRRKRYAEHKSHRGEYSVCDSESLWVTDKSSAIDI 181
gi|189517902|ref|XP_697445.3|TMDKQRPTDPIALILKLIQADISKQKQG---DVIPTSLNVTSTVADYKKE---KDNNTPMVDSSEELLRQYKRYNSPRVLLSDRPPMPPAFYLMDFKFTSG-QDSNKLR--QKRFAEHSYRGEFVCDSESNWVTDKSSAIDS 286
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|6679144|ref|NP_032768.1|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 258
gi|47271540|ref|NP_112335.2|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 258
gi|114642998|ref|XP_522331.2|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 257
gi|73997470|ref|XP_543858.2|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 257
gi|156630995|ref|NP_001096124.1|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 270
gi|118151064|ref|NP_001071456.1|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 253
gi|118083230|ref|XP_425658.2|RGHQVTVLGEIKTGNSPVKQYFYETRCKEARPVKNG-CRGIDDKHWNSQCKTSQTYVVRALTSENNKLVGWRWIRIDTSCVCALSRKIGRT 270
gi|189517902|ref|XP_697445.3|RGNHVTVLNSFTVKQK-XTQYFYETRCKTPHSHRKSRCIGIDEKHWNSQCKTTQTYVVRALT-QHKSLSVSNWIRIDTACVCALSKKHRT 374
.....310.....320.....330.....340.....350.....360.....370.....380.....390

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