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gi|5453722|ref|NP_006321.1|-----
gi|114620143|ref|XP_519760.2|-----
gi|77736321|ref|NP_001029860.1|-----
gi|6678760|ref|NP_032892.1|-----
gi|6981362|ref|NP_037138.1|-----
gi|73999380|ref|XP_851288.1|-----
gi|62955209|ref|NP_001017616.1|-----
gi|17508057|ref|NP_492213.1|-----
gi|145341423|ref|NP_193961.2|-----
gi|115461208|ref|NP_001054204.1|-----
MARTFILWLHGLGDSGPANEPITQPKSSELSNAEWLFPSPAPFNPVTCNNGAVMREWFDVPELPPKVGSPIDESSVLEAVKNVHAIIDOBIAEGTNPENVFICGLSOGGALTLASVLLYPKTLGGGAVLSCWVPPFTSSIIISQFPPEAKKV 150
                                                                                                                                -----M
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|5453722|ref|NP_006321.1|-----
gi|114620143|ref|XP_519760.2|-----
gi|77736321|ref|NP_001029860.1|-----
gi|6678760|ref|NP_032892.1|-----
gi|6981362|ref|NP_037138.1|-----
gi|73999380|ref|XP_851288.1|-----
gi|62955209|ref|NP_001017616.1|-----
gi|17508057|ref|NP_492213.1|-----
gi|145341423|ref|NP_193961.2|-----
gi|115461208|ref|NP_001054204.1|-----
MCHLCLFLINPILWVSHGTDGDRMLVFEAGQAALPFLKQAVTCEFKAYPGLGHSISNKKELKYIESWIKRRLKLDILONKTFEERSIRENGEGMRTSRLLKPIVLLITALLSIVFFFAFFLTKSDVSSSTALRNRRDSMARTFILWLHGLGDS 300
SRLRFLFS-----LAAATAAASLLAAA-----LRRRAP-----PSGLAARLVPAAPMA-----AAAAANR-----SPVLWLHGLGDS 63
                                                                                                                                -----MLH-----
1.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|5453722|ref|NP_006321.1|-----
gi|114620143|ref|XP_519760.2|-----
gi|77736321|ref|NP_001029860.1|-----
gi|6678760|ref|NP_032892.1|-----
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gi|62955209|ref|NP_001017616.1|-----
gi|17508057|ref|NP_492213.1|-----
gi|145341423|ref|NP_193961.2|-----
gi|115461208|ref|NP_001054204.1|-----
GHWAEAFAG---IRSSHIIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIGGANRDISILQCHGDCDPLVP 178
GHWAEAFAG---IRSSHIIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIGGANRDISILQCHGDCDPLVP 178
GHWAEAFAG---IRSAHIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSLQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIGGANRDISILQCHGDCDPLVP 178
GHWAEAFAG---IKSPHIIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSQEDSGIKQAAETVKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIINSANRDISVLQCHGDCDPLVP 178
GHWAEAFAG---IKSSHIIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSQEDSGIKQAAETVKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIINSANRDISVLQCHGDCDPLVP 178
--GWAFAFVG---IRSSHIIKYICPHAPVMPVILNMMNVAMPWFVDIIGLSP--DSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSOGGALSPLYTALTTOOKLAGVTALSCWLPLRASFPQGGPIINSANRDISVLQCHGDCDPLVP 146
GHWADAMAG---IRTPHVYIYICPHAPVMPVILNMMNVAMPWFVDIISLNP--NAQEDSGIKRAAENIKALIDQEVKNGIPSHRIVLGGFSQ-----VISKNKDISVLQCHGDCDPLVP 143
GHWADAFKTE--AKHDNIKFCIPHSSESRPVILNMMNVAMPWFVDIIGLSP--NAQEDSGIKRAAENIKALIDQEVKNGIPSHRIVLGGFSQ-----SFTANNAIPFLGHTDDPLVP 175
GPANEPKILFRSQEFRNTKWLFPSPAPPNPVSCNYGAVMPWFVDIPELPLTAGSPKDESLKAVKNVHAIDKEIAGGINPENVFICGFSOGGALTLASVLLYPKTLGGGAVFSGWLPFSSVTPTRISPEARK--TPILWVSHGIDDKTVL 449
GPANEPKIRNFSAPEFRLTKWAFSPAPNPVSCNYGAVMPWFVDIHELPMSSGSPQDSSGVLKAVENVHAMIDKEVADGIPPENIFVCGFSOGGALTLASVLLYPKTLGGGAVFSGWLPFSSVTPTRISPEARK--TPILWVSHGIDDKTVL 212
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|5453722|ref|NP_006321.1|-----
gi|114620143|ref|XP_519760.2|-----
gi|77736321|ref|NP_001029860.1|-----
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gi|73999380|ref|XP_851288.1|-----
gi|62955209|ref|NP_001017616.1|-----
gi|17508057|ref|NP_492213.1|-----
gi|145341423|ref|NP_193961.2|-----
gi|115461208|ref|NP_001054204.1|-----
LMFGSLTVEKLTILVNPANVTFKTYEGMMHSSCOQEMM-----DVKQFIDKLLP-----PID--- 230
LMFGSLTVEKLTILVNPANVTFKTYEGMMHSSCOQEMM-----DVKQFIDKLLP-----PID--- 230
LMFGSLTAEKLTILVNPANVTFRTYAGMMHSSCOQEMM-----DIKQFIDKLLP-----PVD--- 230
LMFGSLTVERLKLINPANVTFKTYEGMMHSSCOQEMM-----DVKHFIDKLLP-----PID--- 230
LMFGSLTVERLKLINPANVTFKTYEGMMHSSCOQEMM-----DVKYFIDKLLP-----PID--- 230
LTFASLTAEKLTILVNPANVTFKTYEGMMHSSCOQELINEFTLNHRLQDLDSLSNLIQRIFFVPIITCNF 216
LIFGQLTVEKLTMLKPSNVTFKTYSGMTHSACPQEMM-----DIKQFIEKQLP-----PINE--- 196
LQFGQMSQEQYIKKFN--PKVELHTYRGMCHSSCGEEMR-----DVKTFLSAHIAH----- 223
FEAQQAALPFLQAG--VTCEFKAYPGLGHSISNBEELQ-----YLESWLKLRMQSSSSSS----- 502
FEAQQAAGPPFLQAG--FSCEFKAYPGLGHSISKEELY-----SLESWIKNHLKASQEKEN----- 266
.....460.....470.....480.....490.....500.....510.....520

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