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gi|11968156|ref|NP_071303.1|MPADLSGTWNLSSDNFEGYMLALGIDFATRKIALLKPKVIEQNGDSFTIQCSSLRNVLVFKVGEFEEDNKGLDNRKCTSLVTWENDKLCVORGEKKNRGWSHWIEGDLHLEMFCEGOVCKQTFORA- 134
gi|62650039|ref|XP_575960.1|MPADLSGTWNLSSDNFEGYMLALGIDFATRKIALLKPKVIEQNGDSFSINCSSLRNVLVFKVGEFEEDNKGLDNRKCTSLVTWENDKLCVORGEKKNRGWSHWIEGDLHLEMFCEGOVCKQTFORA- 134
gi|16418455|ref|NP_443192.1|MPADLSGTWNLSSDNFEGYMLALGIDFATRKIALLKPKVIEQNGDSFTIHTNSSLRNYFVKVGEFEEDNRGLDNRKCKSLVIWVNDRLTCIQKGEKKNRGWTHWIEGDKLHLEMFCEGOVCKQTFORA- 134
gi|114553870|ref|XP_001161299.1|MPADLSGTWNLSSDNFEGYMLALGIDFATRKIALLKPKVIEQNGDSFTIHTNSSLRNYFVKVGEFEEDNRGLDNRKCKSLVIWVNDRLTCIQKGEKKNRGWTHWIEGDKLHLEMFCEGOVCKQTFORA- 134
gi|57086929|ref|XP_536740.1|MPLPPYGVAKSSASQDCL-----IGIDFATRKIALLKPKVIEQNGDSFTIHTYSSLRNVLVTFKVGEFEEDNKGLDNRKCKSLVTWVNDRLTCIQKGEKKNRGWTHWIEGDKLHLEMFCEGOVCKQTFORA- 129
gi|194674079|ref|XP_871364.3|-----IDFATRKIALLKPKVIEQNGDSFTIHTNSTFRNYVVKVGEFEEDNKGLDNRKCKSLVTWVNDRLTCIQKGEKKNRGWTHWIEGDKLHLEMFCEGOVCKQTFORA- 109
gi|118101075|ref|XP_417606.2|MPVDFSGTWNLVSNDFEGYMLALGIDFATRKIALLKPKVIEQNGDSFSIHTTSTFRDYMLQFKIGEEFEEDNKGLDNRKCKSLVTWVNDRLTCIQAGEKKNRGWTHWIEGDDLHL-VFDLLQNC----- 127
gi|192455692|ref|NP_001122222.1|MPVNYSGTWDIVDHNDFEGYMLALGIDFATRKIALLKPKVIEQNGDSFTIKLITFRNYSSFKIGEEFEETKGLDNRKCTVNVWVNDRLTCIQKGEKKNRGWTHWIEGDTLYLELTCEDOI CKQTYKRSA 135
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....

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