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gi | 20129349 | ref | NP_609176.1 | MSGTSQKHRNFVAEPMGNKSVTELAGIGETLGGRLKDGAFDMAYTVLGOYLVLKKDEELFKDWMKEVCHASSKQASDCYNCLNDWCHEEFL 90
gi | 31211799 | ref | XP_314872.1 | MSSTSQKHRNFVAEPMGEKPVTDLAGVGDVLGKRLEAAGFDRAYTVLGOYLILKKDAELFKEWMDTCGANASKQAADCYQCLSDWCDEFL 90
gi | 84042521 | ref | NP_001033320.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGDVLGKRLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 16758438 | ref | NP_446083.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGDALGKRLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 221316573 | ref | NP_001137457.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 114638636 | ref | XP_001170547.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 73983656 | ref | XP_854776.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 194670921 | ref | XP_001787260.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 33695131 | ref | NP_892033.1 | -MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGOFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWDAFL 89
gi | 45387555 | ref | NP_991125.1 | MSSTSQKHKDFVAEPMGEKSVMALAGIGEVLGKRLEEKGFDKAYVVLGOFLVLRKDEELFREWLKDTCGANTKQQGDCYSCLREWDSFL 90
gi | 17551886 | ref | NP_499085.1 | -MSTSVKHFREFVGEPMGDKEVTCIAGIGPTYGTKLTDAGFDKAYVVLFGQYLLKKDEDLFIEWLKETAGVTANHAKTAFNCLNEWADQFM 89
1.....10.....20.....30.....40.....50.....60.....70.....80.....90

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