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| gi | 10863887 | ref | NP_066924.1 | MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 114591092 | ref | XP_516949.2 | MANAGLQLLGFILAFLGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGVIAIFVAIVGMKCMKCLEDDDEVQKMRMAVIGGAIIFLLAGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 7710002 | ref | NP_057883.1 | MANAGLQLLGFILAFSLGWIGSIVSTALPQWKIYSYAGDNIVTAQAIYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGLIAIFVSIIGMKCMRCLLEDDDEVQKMRMAVIGGIIIFLISGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 61889099 | ref | NP_113887.2 | MANAGLQLLGFILAFSLGWIGSIVSTALPQWKIYSYAGDNIVTAQAIYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGLIAIFVSIIGMKCMRCLLEDDDEVQKMRMAVIGGIIIFVLSGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 74003604 | ref | XP_850248.1 | MANAGLQLLGFILAFSLGWIGSIVSTALPQWKIYSYAGDNIVTAQAIYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGLIAIFVSIIGMKCMKCMEDDEVQKMRMAVIGGVIFLIAGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 49258204 | ref | NP_001001854.1 | MANAGLQLLGFILAFSLGWIGSIVSTALPQWKVYSYASDNIVTAQAIYEGLWMSCVSOSTGQIQCKVFDSELLNLSSTLQATRALMVGILLGLIAIFVSIIGMKCMKCMEDDEAQKMRMAVFGGVIFLISGLAILVATAWYGNRIVQEFYD | 150 |
| gi | 61889131 | ref | NP_001013629.1 | MASGGQLLGFVLAFLGWMGIIITSTAMPQWKMASYAGDNIVTAQALYEGLWMSCAMOSTGQIQCKVFDSELLKLEGSLOATRALMVAAILLGLVGFVAIVIGMKCMKCMEDDQVKKMRMAVFGGVIFLIAGLAILVATAWYGNRVARAFYD | 150 |
| gi | 18858435 | ref | NP_571845.1 | MAHAGLQMLGYCLGFLGLLGLIASTAMAEWKMSYSYAGDNITTAQAQYEGLWQSCVSOSTGQLQCKKYDSELLKLPGEIQGARGLMMLTGIFLCGLSLVSVFGMKCTTCLSEAPQVKSVALAGGVLFITGGLFALIAISWYGEKIRQKFFD | 150 |



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| gi | 10863887 | ref | NP_066924.1 | PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV | 211 |
| gi | 114591092 | ref | XP_516949.2 | PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV | 211 |
| gi | 7710002 | ref | NP_057883.1 | PLTIPINARVEFGQALFTGWAAAALCLLGGVLLSCSCPRKTTSYPTPRPYPKPTPSSGKDYV | 211 |
| gi | 61889099 | ref | NP_113887.2 | PMTFPVNARYEFGQALFTGWAAAALCLLGGALLSCSCPRKTTSYPTPRPYPKPTPSTGKDYV | 211 |
| gi | 74003604 | ref | XP_850248.1 | PMTFPVNARYEFGQALFTGWAAAALCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV | 211 |
| gi | 49258204 | ref | NP_001001854.1 | PMTFPVNARYEFGQALFIGWAAAALCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV | 211 |
| gi | 61889131 | ref | NP_001013629.1 | PFTFPVNTREFGSALEFIGWAAAALCLLGGALLCCSCPRSETSYPPSRGYPKNAPSTGKDYV | 211 |
| gi | 18858435 | ref | NP_571845.1 | PFTFPVNARYEFGKALYVGVGSSALSIIGSLLCCIIGSEASEKPE--YPPARAAGRPGTDRV | 210 |

