

gi|23956238|ref|NP\_291093.1| 150  
gi|109468836|ref|XP\_230607.4| 150  
gi|18252045|ref|NP\_079496.1| 150  
gi|194672523|ref|XP\_601929.3| 150  
gi|73991928|ref|XP\_542918.2| 150  
gi|118090896|ref|XP\_420886.2| 150

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1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|23956238|ref|NP\_291093.1| 300  
gi|109468836|ref|XP\_230607.4| 300  
gi|18252045|ref|NP\_079496.1| 300  
gi|194672523|ref|XP\_601929.3| 300  
gi|73991928|ref|XP\_542918.2| 300  
gi|118090896|ref|XP\_420886.2| 300

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160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|23956238|ref|NP\_291093.1| 450  
gi|109468836|ref|XP\_230607.4| 450  
gi|18252045|ref|NP\_079496.1| 450  
gi|194672523|ref|XP\_601929.3| 450  
gi|73991928|ref|XP\_542918.2| 450  
gi|118090896|ref|XP\_420886.2| 450

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310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|23956238|ref|NP\_291093.1| 600  
gi|109468836|ref|XP\_230607.4| 600  
gi|18252045|ref|NP\_079496.1| 600  
gi|194672523|ref|XP\_601929.3| 600  
gi|73991928|ref|XP\_542918.2| 600  
gi|118090896|ref|XP\_420886.2| 600

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460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|23956238|ref|NP\_291093.1| 750  
gi|109468836|ref|XP\_230607.4| 750  
gi|18252045|ref|NP\_079496.1| 750  
gi|194672523|ref|XP\_601929.3| 750  
gi|73991928|ref|XP\_542918.2| 750  
gi|118090896|ref|XP\_420886.2| 750

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610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|23956238|ref|NP\_291093.1| 900  
gi|109468836|ref|XP\_230607.4| 900  
gi|18252045|ref|NP\_079496.1| 900  
gi|194672523|ref|XP\_601929.3| 900  
gi|73991928|ref|XP\_542918.2| 900  
gi|118090896|ref|XP\_420886.2| 900

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760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



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gi | 23956238 | ref | NP_291093.1 | RDAPFLAMLLSFLLPPLPGAGLAWCYQLP-TFCHRRGLCCRRDPLWN-----RDIPLGTVHPVEFGSIITGEPSPPPPWTSCQQRSHP--PSLDLLSDPANSELT----- 1015
gi | 109468836 | ref | XP_230607.4 | PDAPFLAMLLSFLLPPLPGAGLAWCYQLP-TLCOQPGRCRRDALCN-----RDQPLGTVHPVEFGSIITGEPSPFP-----NPESELT----- 1015
gi | 18252045 | ref | NP_079496.1 | HDIFLLAMLLSVLLPPLPGAGLAWCYRLPGAHLQRCVSWGRRDPACSGPKDGPHRDHPLGGVHPMELGPTATGQPWPLDPENSHPESSHPEKPLPAVSPDQADQVQMPRSCLW 1015
gi | 194672523 | ref | XP_601929.3 | PDAPFLAMLLSFLLPPLPGAGLAWCYRRPGLCLQCFCWGSRRALMCSGSKDGPCRGHPLGSIHPVELRLIAPQESQPLDLEN-----SARTQQPP----- 1015
gi | 73991928 | ref | XP_542918.2 | HKIFLLGVILSFLLPPLPGAGLAWCCCRQPRSGLQCCLWGLRRDPCSRPKDGNRRDPSSSIHPMELGPAATGEPQPLGE----- 1015
gi | 118090896 | ref | XP_420886.2 | HEAILVILLIFLLFPLALVGSIVFWYRRENGLLNKWKEDRNDLLDG-----MLESDDGSPVPRISLAICS----- 1015
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....

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