

CLUSTAL O(1.2.4) multiple sequence alignment

NM_001324803.1	-----ATGGAAGGTCACCA	15
GQ903730.1	ATGGTTGCAATGAGGAAGCCTGCAGGCTATGGTGAGAAGAAAAGCACAAAGAAAAGAGTT	60
	* * *	
NM_001324803.1	TGTTGTGAAAAGGCTCATACAAACAAAGGAGCATGGACTAAAGAAGAAGATGAAAGGCTT	75
GQ903730.1	GGGTGTGAAAAGAAATTCATAACAAGGGGGCTTGGTCCAAGCAAGAAGACCAGAAGCTC	120
	* * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	ATTGCTTACATTAAAGCTCATGGCGAAGGTTGTTGGAGGTCTCTTCCTAAAGCTGCTGGC	135
GQ903730.1	ATTGATTATATCCAAAAGCATGGTGAAGGTTGCTGGAGTTCACCTCCTCAGTCTGCAGGC	180
	**** *	
NM_001324803.1	CTTCTCAGATGTGGTAAAAGCTGCCGTCTTCGTTGGATTAATTACTTACGACCTGATCTT	195
GQ903730.1	TTGCTTCGTTGCGGGAAAAGTTGCCGGCTGAGATGGGTGAACCTAACGCTGATGTT	240
	* * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	AAACGTGGTAACTTCACTGATGAAGAAGATGAACTCATTATCAAACCTCCATAGCCTCCTC	255
GQ903730.1	AAGCGTGGGAACTTTGGGGAAGACGAAGAGGACCTCATCATTAAAGCTCCATGCGCTTCTT	300
	** *	
NM_001324803.1	GGTAACAAGTGGTCACTTATAGCGGGAAGATTACCAGGAAGAACAGATAATGAGATAAAG	315
GQ903730.1	GGAACAGGTGGTCATTGATAGCGGGAAGATTGCCCAGGAAGGACAGACAATGAAGTAAAG	360
	** *	
NM_001324803.1	AATTATTGGAACACACATATAAGAAGGAAGCTTTTGAGTAGGGGTATTGATCCAACAACA	375
GQ903730.1	AACTATTGGAATTCTCATCTAAAGAAAAAGCTAATGCGGATGGGCATTGATCCTAATAAC	420
	** *	
NM_001324803.1	CATAGGCCAATGAGTGAGCCTACCCCTTGGTACGCAAAAAGTGACAACCATTCTTTTGT	435
GQ903730.1	CATCGCCTGGGAGAAAGGGCTTCGGGTACTAGCAAATCATTTGAATCCAGGGACCAGACA	480
	*** * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	GCTGATGATCA-AGATCAGA--AGATTAAGATCAAATCCGA-ATTAATTGAGACGATGA	490
GQ903730.1	AGCAATCCTCTAATCTCAGCTGCCGATAATAATGCAGTCTTGATTCTACATGTGGCTCA	540
	* * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	GCAAAGAAGAAGATCATGAAATTCAAGAACGGTGTCTGACTTGAATCTTGAGCTTAGAA	550
GQ903730.1	GCGAGCAAGACAACA-----AGCAGTTTGCCTGACCTAAACCTTAATCTCAATG	589
	** * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	TTAGTCCTCCTCATGA--CCAACAAAACCAACTTGATCATAATCAAAGAGCAAACCTTT	607
GQ903730.1	TGGGGGCTCCATCAGTAGATGAACAAATGCAGCTAACTGGGG-----CAATAGT	639
	* * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	TGTGTTTTACATGTAGTTTGGGTATACAAATAGTAAAGATTGCAGTTGCAGTACTAAAA	667
GQ903730.1	CATAAGGAACCTTGAACCTGC-----TCCCTTTACAACCTCT--AC	676
	* * * * * * * * * * * * * * * * * * * *	
NM_001324803.1	GTAGTAATGGAAATGGCTGTAGTAATATTATAAGTATGAATATGAATATTTCTGGTTATG	727
GQ903730.1	TTCTTTTGGATGA-----	690
	* * * * *	
NM_001324803.1	ATTTTTTAGGGTTGAAGAATAATGGTCTTGTTTTGGACTATAGAACATTGGAACTAAGT	787
GQ903730.1	-----	690
NM_001324803.1	GA	789
GQ903730.1	--	690