

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

NM_000518.5

ACATTTGCTTCTGACACAACACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCATC
ex1 -----
ATGGTGCATC

NM_000518.5

TGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGCAAGGTGAACGTGGATGAAG
ex1
TGACTCCTGTGGAGAAGTCTGCCGTTACTGCCCTGTGGGCAAGGTGAACGTGGATGAAG

NM_000518.5

TTGGTGGTGAGGCCCTGGCAGGCTGCTGGTGGTACCCCTGGACCCAGAGGTTCTTG
ex1
TTGGTGGTGAGGCCCTGGCAGGCTGCTGGTGGTACCCCTGGACCCAGAGGTTCTTG

NM_000518.5

AGTCCTTGGGATCTGTCCACTCCTGATGCTGTTATGGCAACCTAAGGTGAAGGCTC
ex1
AGTCCTTGGGATCTGTCCACTCCTGATGCAATTATGGCAACCTAAGGTGAAGGCTC

NM_000518.5

ATGGCAAGAAAGTGCCTGGCTTAGTGATGGCCTGGCTCACCTGGACAAACCTCAAGG
ex1
ATGGCAAGAAAGTGCCTGGCTTAGTGATGGCCTGGCTCACCTGGACAAACCTCAAGG

NM_000518.5

GCACCTTGCCACACTGAGTGAGCTGACTGTGACAAGCTGCACGTGGATCCTGAGAACT
ex1
GCACCTTGCCACACTGAGTGAGCTGACTGTGACAAGCTGCACGTGGATCCTGAGAACT

NM_000518.5

TCAGGGCTCCTGGCAACGTGCTGGTCTGTGCTGGCCATCACTTGGCAAAGAATTCA
ex1
TCAGGGCTCCTGGCAACGTGCTGGTCTGTGCTGGCCATCACTTGGCAAAGAATTCA

NM_000518.5

CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCC

ex1

CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCC

NM_000518.5

ACAAGTATCACTAACGCTCGTTCTTGCTGTCCAATTCTATTAAAGGTTCTTGTCC

ex1

ACAAGTATCACTAACGCTCGTTCTTGCTGTCCAATT-----

NM_000518.5

CTAAGTCCAACACTAAACTGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCC

ex1

NM_000518.5

ex1

TAATAAAAACATTTATTTTCATTGCAA
