

Ensembl Gene: ATG14 ENSG00000126775

Chromosome 14: 55,366,366,391-55,411,830 reverse strand

ATG14-201 - ENST0000247178 with 10 exons encoding for ATG14L

ATG14-202 - ENST0000558189 with 7 exons encoding for ATG14S

[Translated sequence](#) / [Flanking sequence](#) / [intron sequence](#) / [UTR](#)

ATG transcription start site for *ATG14L* in exon 1 and *ATG14S* in alternative exon 4' are indicated.

Exon / Intron	Length	Sequence
5' upstream sequence	cagaatgcaccggttgaaaacaaaatcccacgtgactggctctcctctc
Exon 1 with ATG14L start site	229	AGGCCATC ATG GCGTCTCCAGTGGGAAGGGAGCCCGGGCGCTGGAGGCTCCTGGCTGCG GGCCCCGGCCGCTCGCCCGGGACCTGGTGGACTCCGTGGACGATGCGGAGGGGCTGTACG TGGCTGTGGAGCGCTGCCCGCTGTGCAACACTACCCGCCGGCGGCTGACCTGCCCAAAT GCGTTCAGAGCGCGATTTTCGTCTACTTCGACGCCGCGACCGGGAGAG
Intron 1-2	14,167	gtacggcgccgcccacggccctatt.....aagacattgaatTTTTTTgttacag
Exon 2	63	GTTTATCGACAAGAAGGAAAGGTTAAGCCGACTTAAGAGCAAGCAAGAAGAATTCAGAA AGA
Intron 2-3	1,389	gtgagtgttttgttttgtcttttaa.....tattttctgtctcttttctcacag
Exon 3	43	AGTGTTAAAAGCTATGGAAGGAAAATGGATAACAGATCAGTTG
Intron 3-4	4,947	gtaagttgtaatacatgttcttttt.....gatatttattacatgcttttttcag
5' upstream sequence	aggcatgcgccaccacgccagctaattTTTTgtattTTTTtagtagagat
Exon 4' with ATG14S start site		GGGGTTTCACCATGTTGGCCAGGATGGTCTTGATCTCCTAACCTCTTGATCTGCCCTCCT TGGCCTCCCAAAGTGCTGCGATTACAGGCGTGAGCCACCGCACTGGCCTAATTTCTCTTT TCTCTGCATTGAACTAGAAAAACATCGTTCTCTTTTTTCGTAATGTTCCATAGTTACAAAA GCTATAACATAAGGTCTTTTTCTTCATTATGTTTTCTGCATATCTGAAAATAAGCAGTG ATCCCAGGTAGATAATCATATTAACCATAAGAGACCAACGTTTGTGATATTTATTACATG CTTTTTTCAGAGATGGAAAATA ATG TCCTGCAAGATGAGGATTGAACAGTTAAAACAAAC AATATGTAAGGAAATGAAGAAATGGAGAAA
Exon 4	82	AGATGGAAAATAATGTCTGCAAGATGAGGATTGAACAGTTAAAACAAACAATATGTAAA GGAAATGAAGAAATGGAGAAA
Intron 4-5	4,814	gtaagtaattcgtgtccttccctcc.....gttgggtgtgatttatttatttttag
Exon 5	238	ATTCTGAAGCCTTCTCAAACCAAGGAAAAGAATCAGAAGCTTTACAGTCGAGCACAAAC GGCACCAAGGAAAAAGGAGAAGATTCAGAGGCATAATCGCAAACCTGGTGACCTGGTAG AAAAAAGACCATTGACTTAAGAAGTCATTATGAGCGTCTGGCAAATCTTCGACGATCCC ATATATTAGAGCTCACCTCTGTCAATTTTCCAATCGAGGAAGTAAAGACGGGTGTGAG
Intron 5-6	3,667	gtacattaagcaagtcttttgactc.....tccgtgtgtgtcttctactttag
Exon 6	230	AGACCCCGCAGATGTGTCTTCAGAGAGTGACAGTGCCATGACCTCCAGCACTGTGAGCAA GCTTGCTGAAGCCCGGAGGACAACCTTACCTCTCAGGACGATGGGTCTGTGACGATCACAA CGGAGACACCAGCATTAGCATTACAGGGCCTGGATTAGCCTCCCTAACAAATGGGGACTA CTCTGCCTACTACAGCTGGGTGGAGGAGAAGAAAACAACCCAGGGGCCTG
Intron 6-7	1,271	gtgagaagcagcatatcctttgaaa.....catgggtgggtgttttcttactgcag
Exon 7	118	ACATGGAGCAGAGTAACCCTGCCTACCCATCAGTGTGCGCTGTGCTATGCAACTCAGC TGGTCAACATCTGTCTCATATACTTGATGTAATCTTCCCAAAAAGCTCTGCAACAG
Intron 7-8	2,498	gcaagtaattgaaggtggtaatgtc.....tataaattgtatgtttgttttacag
Exon 8	91	TGAATTTTGTGGCGAAAATCTAAGCAAGCAGAAATTTACTCGAGCAGTGAAGAACTGAA TGCAAATATTCTTTACCTTTGTTTTTCTCAG
Intron 8-9	79	gtatgaaaaataggttgtgaactaa.....taaccaattctttaatTTTTTTtag
Exon 9	86	CATGTAATTTAGATCAATTACAACCACTGCATACCCCTCAGGAATCTAATGTACCTGGTC AGTCCAAGCTCTGAACACCTAGGCAG

Exon / Intron	Length	Sequence
Intron 9-10	7,893	gtaagaagatatttgttgcttttct.....agagaccctcattgtctgcacacag
Exon 10	3,535	<p>GTCAGGGCCCTTTGAAGTACGAGCAGACCTTGAGGAGTCCATGGAATTTGTGGATCCCGG AGTTGCTGGAGAATCAGATGAGAGCGGAGATGAGCGCGTCAGCGATGAAGAAACCGACCT GGGCACAGACTGGGAGAACTTGCTAGTCCCGGTTTTGTGATATCCCTTCCCAGTCTGT GGAAGTCTCCAGAGTCAGAGCACCCAGGCGTCCCCACCCATCGCGAGCAGCAGTGCAGG TGGGATGATCTCCTCTGCAGCAGCCTCGGTGACCTCCTGGTTAAAGCTTACACTGGACA CCGTTAACGAGCATGGACAAAAACATAACCAATCTGCATCAAGAAAAGTTCTTCTCCCACT ACACTCTAGTAAACATTTTCTGTTTAAAGTTAAGATAGTGTCTGGAACAAAGAGGTTAAAG TGTGTTTTTGTCTTTTTAAGCAGGGAGACAAAATTTCTATTTGCCAAGTGGCCT GTGATGGTGACCAACATGCTTATGATAATTAAGAGAACAGGGGTGCAAGGTCTTTCTACC CAGACCAGTCTGGTGAAGGAGGACCTGTGCGTGTGGCCAGTTCTGCCAAGGAAGCAGT TGATTTGGGTCCCTCTGGGCCCGGGCCACCGGGCCACAGATATGGGTGAGTGTCTGG TCCTTGGCGTCTGAGACTGTTCTGACACTTTAAGTTTTAGAGGTTGGTTGAATCACAA GAGGTGATCTTGATTATTAGGACATGAAAGATAAAAGCTCTTTAATAAGAGTTTTTCTG CCATTGTTTTTGTATGAGAACCAGCAGGCAATTTAAAATTTCTAATTTGGTCCCTTTGAT TTTTGTTGGGAGGGGTGAGTTACACGTATTTTATTCATGCTGCTCTGTCGTAGTTTGTCA GACATTCCTGTTTTCTTTCCCCCACACACCAAGAAAATGAAAGTCTTTTTCTTTAGGA CCCACATCCATAAATGGAAGAAATCCTGGCTGCAATAATGTCTAGAGAGTTTTTAACTAT TTTCTTGTATCTGAGGGGAATTAAGCTTATCTTACCTAGTTGAATTCCTGCCATCCAC ACTATGAGCATTTTGAATTTGAAGTTATATTTTCTGGGTGAAAATAAGTCATGAAGGTCA TTCCCTTATGTAAGCTCAATGCCTGCCTGGGCACAGGGGAAAAGCCACTTAGTTAAGTGG CCTCTGGTCATTCTTGTGGTGTCCACTTTCTTTCTATGGGATTGAGTAGGTGGCAGGTGT TTTCAGGGGAAACCATCTACTTGTTCCTCCCGAACTCTTTGTTGCTCTGAGGACACAGCT TTGCTCAGAAATGCAGCGCAGATCCTTACGGCTGATGCTACTCTGCTCTGTTCTGGGGAA AGCACAAATAAAGAAAGAATTTCCAGCCAGGCGAGTGCTCACGCCTACCCAGTAAATCCCAG CACTTTAGGAGCCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTTGAAGCAGCCTGGC TAACATGGTGAAACCTGTTTCTACTAAAAATACAAAAAATACCAGGTTGGTGGCGCA CGCCTGTAATCCAGCTACTCGGGAGGCTGCGGCAGGAGAATCGCTTGAACCGGGAGGCA GAGGTTGCAGTGAGCCGAGATTGTGCCATGCACTCCAGCCTGGGCAACAAGAGCGAAAC TCCGTCACAAAAAAGAAATTTCCCTCAGCAGGAGATCATTTTTCAGCTCACGTGTCT TGTCATTCCTTTAGTGACAATCTTACAAGAAACTATAATGAGAGAGGCATTATGTACAA ATATGTAAGTAGTTTATTTTTAATAACTGCAAAAAATCCTATGTAACAACCTACCAAAAG AAATCCATGAAAGAGTCCTAACAGGCATTTATACCATATCTTATGTGATGGCATGATA GCACCTCTGATAAATCATTACAGAGTTTGGCATGCCAGCTCTTTTTCTCATCATAATA ATTGTAGTTGATACTTTGCCTCCAAGTCCGAGGTGCTATATAGCTTTTGGTAAATGGTATA TTTTGGTGTTTGTATAGTTTTTGGGTAGAGTTGCAGAACGGAGTTTTATTTCTATCCGGTAG TCACAAATTCCTTGGCTCTATGAATTTTCCATGAAAGGAGGAAGTAGGCTTTTCTCGTTG TGGGTGGTCTTTTTTTTTTTTGGAGACGGAGTCTCACTCAGCTGCCAGGCTGGAGTGTA GTGGCACCATCTCCGCTCACTGCAACCACCATCTCCTGGGTTCAAGCAATTCCTCCATCT CAACCTCCCAGTAGCTGGGATTATAGGCACCTGCCATCATGCCAGCTAATTTTTGTAT TTTAGTAAAGACGGGGTTTTTACCATGTTGGCCAGGCTGGTCTTGAAGTCTGACTTCA GGTGATCCGCTTGCCTTGGCCTCCTAAAGTGTAGGATTACAGGCCTGAGCCACCGCGCC CGGCCCCTTATGGGTTCTTCTACACTGCTGGGATCTCTGTTTTAAGTGTCTCAGCTTCATG ATTGATTGCTGGGCTTCCATTTTCCCAGTCTGAGGTTTCGTAGAGAGTGAAGATGG TAGACTTGAACAGATAAATAAACTTAACGATCTTGTAAAGAGTTGTCTAGCTACTTAAAC CCTCAGAAGTAAAGACTTAGTCTCACGAGTTGTAAGAGTGGGATTTGGAGCTTGGTGGTG GAGACTGACTTCACTGAGAGATGCACAACAGTCATGGTTTTCTTAAAGCCTCTTATGAAA CCATGAATGAGAGATGAAGCTAAAGAATAGAATCCAGAGATCACAACTCATCTAGAGTA CTTCCACAAAATTTACAAGATGTGGGAACTTTATGGATAGGATATATTTTTGTTTGTGT TGTTAATATCAACTAGAGGCACTTTACATAGGGTTAAGTGTGCAACCTTTTTGTGGTTT TGAACCCAACATACTGGCTTACACTGCTGAAATATTTTGGGTTTCATTATTTTGCCTG GATCCACCCTGTAATACTCTTAAAGTATACATTTCAACCATGTTTTTTTCTACTCTTTTT GCTGCTCATTAATACTTTTCTAGTGTAGGTGCCAGAACCATATGTAACAGCTTTTTAAAAA ATTGAAGCTGGTATTTTTGTTTTAAACAAAAAGCCATAGAAGTGGTCACTTTTTCCATTTT AAAATGATTTACTGAAACAAAGTAATACTAATAAAAAACCCACAGGCACCAAAACAGGCTGC TTAAAATGGTCTGTAAAGACATTTTTTGGTTATGGAATATAAGAAAAGTTTTGCACATC TGTAAGGGGGAAAAACAGTATATCACCATTGGGTAGAGTGGACGGGACTCATGTAAGGAC TCAATTTGGGGAAGAGCATTCAGTGGCATGCTGTTAGAGGACTAGTGTCCGAGAATCTCC TCACAGTATCATGTTGCAGGAATTCCTTCTGCAACTTCAAACAGTTTTGAGTC ATACAAATGTTTTCTAAACTTTTTATTGATTTACTGCAATAAATCTTTTAAACAGTA</p>
3' downstream sequence		ctttgctcatgtgatgtctttttcctaactgttccatttgcactgctgcat.....