

Splice site predictions for 2 sequences with donor score cutoff 0.40, acceptor score cutoff 0.40 (exon/intron boundary shown in larger font):

Donor site predictions for NM_001134831.2 :

Start	End	Score	Exon	Intron
596	610	0.99	tgatgat	gt aagtgc
861	875	0.62	cagaaaa	gt gagaag
1101	1115	0.42	gaaacaa	gt acattg
1448	1462	0.89	cccaatg	gt aaaaat
1942	1956	0.88	caacact	gt acgtaa
1952	1966	0.79	cgtaact	gt aagagg
2025	2039	0.97	gaaaaag	gt aaacca
3317	3331	0.50	cacagag	gt gatacg
3500	3514	0.90	ccatcag	gt agatac
4486	4500	0.89	acctaag	gt caggag
4821	4835	0.60	catatag	gt aacttc
5341	5355	0.69	aaaattg	gt aaacat
5497	5511	0.59	gtgtcag	gt acagct
5866	5880	0.98	tgacaaa	gt aagact

Acceptor site predictions for NM_001134831.2 :

Start	End	Score	Intron	Exon
3	43	0.86	agagccgcggccttgctttc	ag gacacgggtcgctggcgggt
140	180	0.68	gttctgcgtacccctctcc	ag tgtcaacctggggctgaatc
318	358	0.57	gtcaatgctttgcattctc	ag tcctctgcataaagctgaga
1003	1043	0.97	agttgacttactttccctc	ag atactttattccatgatgac
1162	1202	0.90	cagttagatcagttttcttc	ag attctcatcaagatgatgaa
2001	2041	0.77	cgctctatgatggctcttc	ag gaggaaaaaggtaaaccagt
2605	2645	0.67	cactttgttttgatactga	ag gtcatcatatgtattcagga
3114	3154	0.41	gattttccatgttgcccagc	ag gaggctgaaatgttcaaacg
3225	3265	0.95	ccccatcaaggctcttttc	ag attgatgaatttgtccacac
4005	4045	0.80	ccaaatggaattttctcttc	ag agttcagaattttcagatac
4793	4833	0.58	taaaattttgtgtttctta	ag atcaaatacatataggttaact
5002	5042	0.80	tttattttttctaaagttcc	ag aataatagtgtcattattat
5590	5630	0.94	aaaatatctgtttctctgc	ag tttcagctaataattttgag

Donor site predictions for NM_001134831.2(AHI1):c.2106G>A :

Start	End	Score	Exon	Intron
596	610	0.99	tgatgat	gt aagtgc
861	875	0.62	cagaaaa	gt gagaag

1101	1115	0.42	gaaacaa gt acattg
1448	1462	0.89	cccaatg gt aaaaat
1942	1956	0.88	caacact gt acgtaa
1952	1966	0.79	cgtaact gt aagagg
2025	2039	0.97	gaaaaag gt aaacca
3317	3331	0.50	cacagag gt gatacg
3500	3514	0.90	ccatcag gt agatac
4486	4500	0.89	acctaag gt caggag
4821	4835	0.60	catatag gt aacttc
5341	5355	0.69	aaaattg gt aaacat
5497	5511	0.59	gtgtcag gt acagct
5866	5880	0.98	tgacaaa gt aagact

Acceptor site predictions for NM_001134831.2(AHI1):c.2106G>A :

Start	End	Score	Intron	Exon
3	43	0.86	agagccgcggttgctttc	ag gacacgggtcgctggcgggt
140	180	0.68	gttctgcgtacccctctcc	ag tgtcaacctggggctgaatc
318	358	0.57	gtcaatgctttgcattctc	ag tcctctgcataaagctgaga
1003	1043	0.97	agttgacttactttccctc	ag atactttattccatgatgac
1162	1202	0.90	cagttagatcagtttcttc	ag attctcatcaagatgatgaa
2001	2041	0.77	cgctctatgatggctcttc	ag gaggaaaaaggtaaaccagt
2605	2645	0.67	cactttgttttgatactga	ag gtcatcatatgtattcagga
3114	3154	0.41	gatttccatggtgcccagc	ag gaggctgaaatgttcaaacg
3225	3265	0.95	ccccatcaaggctcttttc	ag attgatgaatttgtccacac
4005	4045	0.80	ccaaatggaatttctcttc	ag agttcagaattttcagatac
4793	4833	0.58	taaaattttgtgtttctta	ag atcaaatacatataggtaact
5002	5042	0.80	tttattttttctaaagttcc	ag aataatagtgtcattattat
5590	5630	0.94	aaaatatctgtttctctgc	ag tttcagctaataattttgag
