

Calculations for Putative GR-beta Arising from Exon 9

A

Donor site predictions for mGR beta in Exon 9

Start	End	Score	Exon	Intron
1187	1201	0.62		agaccaagtaacttc
1890	1904	0.82	AAAACAGGTTTGCTC	32bp product
2189	2203	0.58		gcaatatgtaaatac
2262	2276	0.70		tttccaagtaagatg

Acceptor site predictions for mGR beta in Exon 9

Start	End	Score	Intron	Exon
213	253	0.72	acttatcaacttgtcttgtgatggtttgtcgcttctttttg	
328	368	0.41	gccatcacttttcagtgacaggaaagcagacagtgatgtgc	
470	510	0.60	aactttctgctcaactttcagttggctggataacactttct	
525	565	0.71	gtgtatcccccatgtatagtttaggatagcattttgattt	
610	650	0.52	gggaagtgtgaccttttatagctattactgtctggttttaa	
694	734	0.58	taaataatgttattctagttattgtatagctgtttaaag	
705	745	0.47	tgtattctagttattgtatagctgtttaaagatgggcagctg	
1041	1081	0.56	cccaatgcaccatctcttcagtggtgctgtagcaacaaagt	
1081	1121	0.78	tttgaactcagctctttcaggaccttcgggagtagttgt	
1128	1168	0.82	ttttaaagtattattccagataaccagctgtgataaagc	
1321	1361	0.69	tactgatttttgttatttgaactgaatgtcaggcatcca	
1615	1655	0.87	CTAATATATTTTTATATTTAGTTCTAGTTTCAGATATATAT	295bp product
1786	1826	0.96	CATGTTATATATTTTTTGTAGGGGTCAAAGAAATGTTGATG	124bp product
1929	1969	0.45	ctggccctgtgtgcagtgacaggtcctgagggtttgaccgca	
2307	2347	0.66	tttgaatgttatttttcagttattttgcagaaattattta	
2317	2357	0.56	gttattttcagttattttgcagaaattatttaaaaaaaaa	

B

Primer 4: 3' CTAGGGAGAGGGAGCTGGGA 5'

Primer 5: 3' CTCTAAGCTAGGGAGAGGGA 5'

C

Predicted PCR product sizes of GR beta from Intron 8 or Exon 9

Exon 7+8 = 289bp

GRbeta Intron 8:

Primer1 GR beta1-R: 73+289 = **362bp product**

Primer2 GR beta2-R: 187+289 = **476bp product**

Primer3 GR beta3-R: 189+289 = **478bp product**

GRbeta Exon 9 (Primer4):

GT Donor (highest score): 289+32 = **321bp product**

AG Acceptor 1 (highest score): 289+124 = **413bp product**

AG Acceptor 2 (2nd highest score): 289+295 = **584bp product**

D

Green = mGRalpha mRNA Exon 9 sequence

Blue = Highest scores for splice-site predictions

mGR Exon 9

GTGGTTGAAAATCTCCTTAGCTACTGCTTCCAAACATTTTTGGATAAGTCCATG
 AGTATTGAATTCAGAGATGTTAGCTGAAATCATCACTAATCAGATAACAAAA
 TACTCAAATGGAATATCAAAAAGCTTCTGTTTCATCAGAAATGACTGCCTTAC
 TAAGAAAGGCTGCCTTAAAGAAAGTTGAATTTATAGCTTTTACTGTACAAAAT
 ATCAACTTGTCTTGTAGATGTTTTGTCGTTCTTTTTGTTTGTCTTGTGTTTT
 CTATACGCACTACATGTGGTCTCTAGAGGGCCAAGACTTGGCAACAGAAGCAGA
 TGAGCCATCACTTTTCAGTGACAGGAAAGCAGACAGTGATGTGCATTGGCTGGT
 GTATCACAGAACTAGAACAGTTAGTGGAGACATGTCCACTATCAGAGAAGGAC
 CGCACCTGAACCACCAGTGCCCAAAGTCCATGTGATCAACTTTCTGCTCAACTT
 TCAGTTGGCTGGATAACACTTTCTAGACTTTTCTGTTGGTGTATTTTTCCCATG
 TATAGTTAGGATAGCATTTTTGATTTATGCATGGAAACCTGAAAAAAGTTTACAC
 GTGTATATCAGAAAAGGGAAGTTGTGCCTTTTATAGCTATTACTGTCTGGTTTT
 AACAAATTCCTTTATATTCAGTGAACATGCTTGTCTCGTTTTCTTAAATAATT
 TTTGTATTCAGTTATTGTATAGCTGTTTAAAGTGGGCAGCTGCCTCACAGCTC
 TCCTAGACGCTAACATTAATTTCCGTGTGAAAATGGGTCCGTGCTCCTACCCTG
 ATGGCACTCAGCTATCAGAAGACCACAGAAATGACTCAGATCTCCAGTATTCT
 TGTCAAAGCTCTTACTCTGTATATATCTGCTTCCATGGGGAATTATATAGGTT
 GTGCAGATTAACCGTCTTAAGTGGTATAGAGCACCTAGTCCAGTGACCTGCTGG
 GTAAACTGTGGATGATGGTTACAAAAGACTAATTGTAACAGTGCACCACCAAC
 AGGCCCGTTTTGCACCAATGCACCATCTCTTCAGTGGTGCATAGCAACAAAG
 TTTGTAACCTCAGCTCTTTCAGGACCTTCGGGAGTAGTTTGTGTAACATTTTAA
 ATGTATTATTCAGATAACCAGCTGTGATAAAGCCGAGAGATTGTTTTAATCAG
 ACCAAGTAACTCTCTCATTAACGTTACCCTCAACTAAGTCTCTAATATGGCA
 AGAATGGCTAGACACCACTTTTACATCCCACCTGTCCACCAATTTGGTCTAGCTT
 TCCTGGTGGTACAGAAAATCAGCTACTGATTTTTTGTATTATTAGAACTGAATG
 TCAGGCATCCATGTTTGTCCAACATACATCCCTACATGTGCCATAGAATCTAA
 CACAAGTCTTGTGAACTTCTTACACTGAGAGTTATCATTTTTAAACAAAACAGA
 AGCTGTAGTAGCCCTTTCTGTGTGCACCTTACCAACTTTCTGTGACTCAAAGCT
 TAACACACTTACTAAGCCACAAGAAATCTGATTTCTACTTAAAGGTGGCCAAATT
 ATTTGTGTAATAGAAAATGAAAATCTAATATTAATAAATATGAAACTTCTAATA
 TATTTTTATATTTAGTTCTAGTTTCAGATATATATCATATTGGTATTCACATA
 CTGGGAAGGGAAGGGCTACTGCAGCTGTACATGCAATTTATTAACATGATTGTA
 AAATAGCTGTATAGTGTAAAATAAGAATGATTTTTAGATGAGATTGTTTTATCA
 TGACATGTTATATATTTTTTGTAGGGGTCAAAGAAATGTTGATGGATATCCTAT
 AAGATTTATAGTATATAAGAGCATCCATACAGGCCTCAGTGGTCTGGAAATTA
 AAACAGGTTTGTCTTAAGCTAGGGAGAGGGGACTGGCCCTGTGTGCAG
 TGCAGGTCCTGAGGGTTTTGACCCGATCAGATCACAGGGGAACATAATCCCTCCC
 ATCTAACCATCCTCATCCGACCATGGCCCTGTGAGTGCAGGCTGGCTTTATTAA
 ATCCAGGACAGAAAGGTGGCGCTTATGTACTTAGAGGCACCGTCCAGTAACAGG
 GTTGTTCACATGCAGCCTCCGCACGGGTTAACAGAAACAGAGGCTTTAGAAG
 TTTGGCAATAATGTGCATAGAGGTTCCAGCAATATGTAATACTAAAGAATCGC
 ATAGGAAGCCAATAATACACTAATCCTCTCCATCCTACAAGAGTCCATTTCCAA
 GTAAGATGAGGACATGTTTATGTTTTCTTTGAATGCTTTTTGAATGTTGTTATT
 TTCAGTATTTTGCAGAAATTAATTAATAAAAAAAGTATAATCATTGCTTTTT
 GAATTTCTCTTAAAGGGAATGTTGAGTTTGTAAATGTTTAAATTTGGTCTCAAA
 GACTTTTAAATAATTGTAACCCAGCTGGATGTGAAATTTATGGTGCCTAAGAA
 ATACCACCTGAAGATTATCAATGACAGTGTAAAGTTTCAAATGAGCTTCTCAA
 AAATAGATTATTGTACATTTATGGAATGTTATATGGTTAAACCCAAAAAGCACA
 TCACACATAAATCTGCTTTTTCAGTTCCAACCAGCTTGGCTTTCAAATAAGAGCT
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