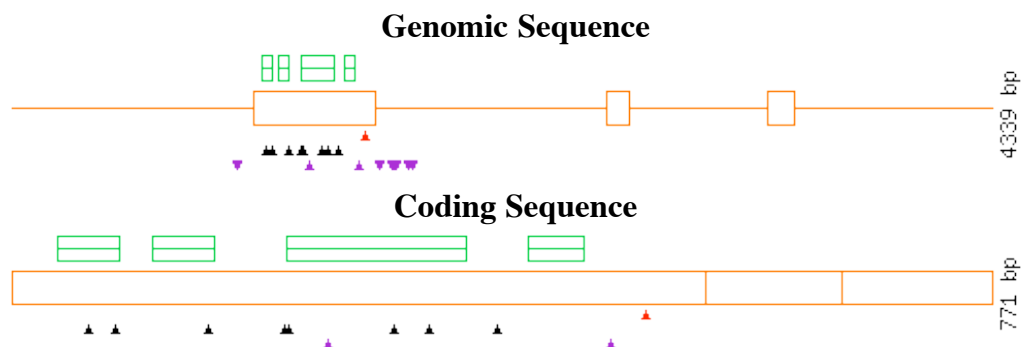


myogenin

IPB002546, IPB001092, IPB001686, IPB007696, IPB002418, IPB003650, IPB005147, and IPB012502



For help interpreting these results, view the [PARSENP Introduction](#) page.

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		PSSM Difference	SIFT Score	Description	Zygoty
				Gained in Variant	Lost from Reference				
1	G	C996T	Non-coding					2643	Homo
2	G C	G1127A	D21N			-1.2	0.18	4451	Homo
3	G C	A1148G	I28V	PleI	TfiI	-0.1	0.01	6002	Homo
4	G C	A1220T	M52L	Tsp4CI	FokI , SfaNI , TspGWI	8.1	0.05	1376	Homo
5	G C	C1281T	S72F	TspDTI				2837	Homo
6	G C	T1284A	M73K		NlaIII	1.6	0.90	7875	Homo
7	G C	C1315T	P83=	Ball , EcoRII	CauII , HpaII			7873	Homo
8	G C	A1367G	M101V	AlwNI , Tsp4CI		1.8	1.00	617	Homo
9	G C	A1394G	R110G	SecI , StyI	Bce83I , SmlI	18.4	0.00	8052	Homo
10	G C	A1448T	S128C	ApaI , CviRI , MjaIV	BseRI			4231	Homo
11	G C	A1448T	S128C	ApaI , CviRI	BseRI			4337	Homo

				MjaIV					
12	G C	A1448T	S128C	ApaLI , CviRI , MjaIV	BseRI			6157	Homo
13	G C	A1448T	S128C	ApaLI , CviRI , MjaIV	BseRI			6504	Homo
14	G C	C1537A	V157=					3303	Homo
15	G C	C1565T	Q167*					5327	Homo
16	G	T1626A	Intron					4891	Homo
17	G	G1682A	Intron	BsrDI	BclI , BtgZI , FnuDII			7983	Homo
18	G	A1688T	Intron	MseI				7852	Homo
19	G	T1701C	Intron	MnII	MseI			1805	Homo
20	G	G1753C	Intron	BglII , DpnI , MboI , XhoII	RsaI , TatI			6248	Homo
21	G	A1774C	Intron	MaeI				6841	Homo

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[View Variants on 3D Structure](#)

No [protein homology model](#) was submitted. You may add one using any or all of the fields below.

Blocks Families:

Blocks File: no file selected

Sequence Alignment: no file selected

-OR-

Genomic Sequence

aatattactatTTTTattgtagTTTTatgTTaatataagaagTaaataagaatggcaaattatggTgtga 0
72

cagaaaaaaaaatgagaagaaaatTTTTaattTTTTacatactaattTgtggattagTtctactTgttat 0
144

tatatttgataatgtaaaaatgtaatgtcagataaaagtattattgtggttggttatttctgtattcttc	0 216
cattgtatattcaattcaaatacattattattagtagtagtagtggtggttagtagtagtagttatagcagca	0 288
gtagttgtagtcggagttatagtagtatatactgtataataaattaaaatacactattgttattaggtcact	0 360
aaatagatttggtagatttgttaaactgtcactctacattttcaaattttacaaactaattaattttagaat	0 432
cagattacaaacttttctattacatacattgccatttactagttccagtagtaccatttaattgcaatttac	0 504
aattataaacttttattgttttgtcttttaaacagccagaataaacattacactttgtcttgagcttcttct	0 576
ctgaccaaattacagaaataatgaaacataaacacgatgccacatttcacatcttcagcaaatcctgtctga	0 648
tgaggatttatcttagtcagttaattaaggagccgtgctacatctttcatactccaacagcctgtagtttg	0 720
atttccacggccccagatcatattcctggactttcaccgctggcctgccgccgttcctcaagcaaaccctg	0 792
tcccaaatccccagaagattgaagaatgaaaagagatgtaaagtttagatgtgtggcaacagctaaacgacg	0 864
gctcaggtttctccaagcctggctatatttaacctactgatctaaccaggcagagagtttaaatgccac	0 936
cagtgcagttggtgtggagcagttgtcgtccacagatcttcttcagaaacaccacaaaacgctcacaaggac	0 1008
	t[1]
	M E L 3
ctgtacagcttttcagaggagacacagcacagccggtggactctaaaccagcaagac atg gag ctt	1075
	IPB002418E (8.1e-05) IC 3.13
F E T N P Y F F N <u>D Q R F Y E G A D</u>	21
ttc gag acc aac ccc tac ttt ttc aac gac cag cgt ttt tac gaa ggc gcc gat	1129
	aD21N[2]

IPB005147A (7.2e-05) IC 1.84
N F F O S R I N G G F E Q A G Y Q D 39
 aat ttc ttc cag tcc aga atc aat ggt ggc ttc gag caa gcc gga tat cag gac 1183
 gI28V[3]

R S S M M G L C G D G R M L T T T V 57
 agg agc tcc atg atg ggc ttg tgt ggg gat gga cgg atg ctg acc acc aca gtt 1237
 tM52L[4]

IPB002546 (5.3e-42) IC 3.06
 G L E D K P S P S S S L G L S M S P 75
 ggg ttg gaa gac aaa cca tct cca tcg tcc agc ctc ggt ttg tcc atg tct cct 1291
 tS72F[5]
 aM73K[6]

H O E O O H C P G O C L P W A C K V 93
 cat cag gag caa cag cac tgc ccc ggc cag tgt ctc ccc tgg gcc tgc aag gtg 1345
 tP83=[7]

C K R K S V T M D R R K A A T L R E 111
 tgc aag cgc aag tca gtg act atg gat cga aga aag gcc gct acc ttg aga gag 1399
 gM101V[8] gR110G[9]

K R R L K K V N E A F E A L K R S T 129
 aag agg agg ttg aag aag gtg aac gag gcc ttt gag gct ctg aag agg agc aca 1453
 tS128C[10]
 tS128C[11]
 tS128C[12]
 tS128C[13]

IPB001092B (9.7e-12) IC 0.74
 L M N P N Q R L P K V E I L R S A I 147
 ttg atg aac ccc aac cag agg ctg ccg aag gtg gag atc ctg cgc agt gct ata 1507

O Y I E R L Q A L V S S L N Q Q E H 165
 cag tac atc gag agg ctg cag gca ctg gtc agt tca ctc aac cag cag gag cat 1561
 aV157=[14]

E Q G N L H Y R A T A A A P H T G 182
 gaa cag ggg aat ctg cat tat aga gcc aca gcc gct gct cca cat act ggg gtga 1616
 tQ167*[15]

182
 gtgcagatttgagaaacaagacaggtgtgtggtgggattttttgagtttatacactttcaagcgcgatggta 1688
 a[16] a[17] t[18]

182
 aagctgtcaccttaatcaacagatacactttatacctaaagggtcaaaattagtagcttgagatgtacttat 1760
 c[19] c[20]

caatgcttttgaccaattttatttttaatttaaaactagttccgaatgccagtccttgtaaataatgttcctattt 3841
 257
 tctacagagtgcTTTTgttatgttattttgtattttttccctgtgtgtttgctattattttatttgactt 3913
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 ttataataaagattgttgtgtatttgtatattttcatttcaaactgtattcctttacctttcaaatgttttc 3985
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 ttgaagtcagaattattagccccctttgaatttttttaattgtttttaatatttctcaaattgatg 4339

Coding Sequence

IPB002418E (8.1e-05) IC 3.13
 M E L F E T N P Y F F N D O R F Y E 18
 atg gag ctt ttc gag acc aac ccc tac ttt ttc aac gac cag cgt ttt tac gaa 54

G A D N F F O S R I N G G F E Q A G 36
 ggc gcc gat aat ttc ttc cag tcc aga atc aat ggt ggc ttc gag caa gcc gga 108
 aD21N[2] gI28V[3]

IPB005147A (7.2e-05) IC 1.84
 Y Q D R S S M M G L C G D G R M L T 54
 tat cag gac agg agc tcc atg atg ggc ttg tgt ggg gat gga cgg atg ctg acc 162
 tM52L[4]

T T V G L E D K P S P S S S L G L S 72
 acc aca gtt ggg ttg gaa gac aaa cca tct cca tcg tcc agc ctc ggt ttg tcc 216
 tS72F[5]

IPB002546 (5.3e-42) IC 3.06
M S P H O E O O H C P G O C L P W A 90
 atg tct cct cat cag gag caa cag cac tgc ccc ggc cag tgt ctc ccc tgg gcc 270
 aM73K[6] tP83=[7]

C K V C K R K S V T M D R R K A A T 108
 tgc aag gtg tgc aag cgc aag tca gtg act atg gat cga aga aag gcc gct acc 324
 gM101V[8]

L R E K R R L K K V N E A F E A L K 126
 ttg aga gag aag agg agg ttg aag aag gtg aac gag gcc ttt gag gct ctg aag 378
 gR110G[9]

R S T L M N P N Q R L P K V E I L R IPB001092B (9.7e-12) IC 0.74 144
 agg agc aca ttg atg aac ccc aac cag agg ctg ccg aag gtg gag atc ctg cgc 432
 tS128C[10]
 tS128C[11]
 tS128C[12]
 tS128C[13]

S A I Q Y I E R L Q A L V S S L N Q 162
 agt gct ata cag tac atc gag agg ctg cag gca ctg gtc agt tca ctc aac cag 486
 aV157=[14]

Q E H E Q G N L H Y R A T A A A P H 180
 cag gag cat gaa cag ggg aat ctg cat tat aga gcc aca gcc gct gct cca cat 540
 tQ167*[15]

T G | V S S S S D Q G S G S T C C S 197
 act ggg | gtg tgc tcc tct agt gat cag ggc tct ggc agc acc tgc tgc agc 591

S P E W S S A S D H C V P A Y S S A 215
 agt cca gaa tgg agc agc gcg tct gat cac tgt gtc ccc gcc tat agc tcc gcc 645

H E D | L L N D D S S E Q S N L R S 232
 cac gag g | at ctg ctg aac gac gac tcg tca gag caa tcc aac ctg agg tct 696

L T S I V D S I T G T E A T P V A Y 250
 ctg acg tct ata gtg gac agc ata acg gga aca gag gcg act cca gtg gcc tat 750

S V D I S K * 257
 tca gtg gac ata agc aaa taa 771