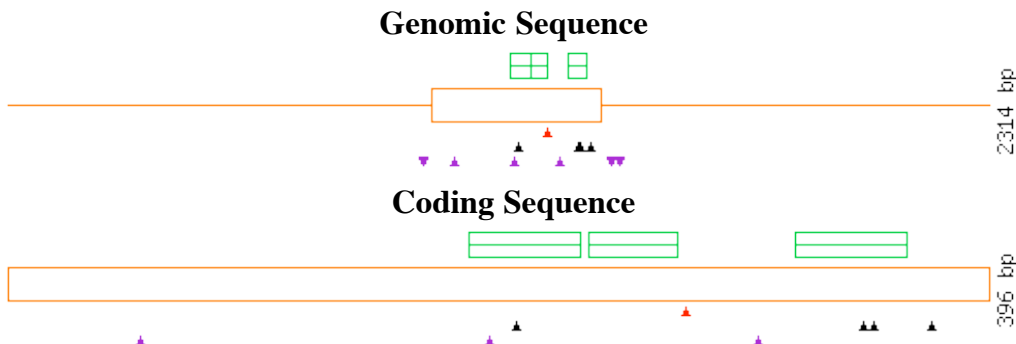


mesogenin

IPB003888, IPB002077, IPB001092, IPB003024, IPB001686, IPB003975, 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	C980T	Non-coding		BsgI			8513	Homo
2	G C	C1054T	D18=		BsrI , Eco57MI , FlnI , GsuI			8003	Homo
3	G C	G1195T	V65=	MseI	MboII			5171	Homo
4	G C	T1206A	M69K			11.2	0.02	8319	Homo
5	G C	C1274T	Q92*		SfaNI			508	Homo
6	G C	C1303T	Y101=		NspBII , RsaI			6948	Homo
7	G C	T1346C	Y116H			-7.3	0.15	7850	Homo
8	G C	C1350T	T117I		BccI	4.3	0.13	5395	Homo
9	G C	T1373A	S125T	AccI , Cfr10I , HindII , HpaI , MjaIV , MseI				6039	Homo
10	G	T1424A	Non-coding					734	Homo
11	G	A1442C	Non-coding	Tsp4CI	AclI , MaeII			7792	Homo

[Download Tab-Separated table](#)

[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: [Choose File](#) no file selected

Sequence Alignment: [Choose File](#) no file selected

[Redo analysis with homology model](#)

-OR-

[Reverse PSI-Blast/SIFT for Models](#)

Genomic Sequence

tcgagatcacaacattatgattaggctttaaaaaagagttttgaaccttttattttggaatattttgtgtaa	0 72
agtgttttctaattcgttgtagactacagaggctaataaacagtatatccgtatatatatatatatat	0 144
atatatatatatatatatatatatatatatatatatataattattagccccaatTTTTTcccc	0 216
ccaatttctgtttaacggagagcagatTTTTTcaacacattTTTaaatataatagttttaactcatct	0 288
ctaatgactaatttattttatcttctgtcatgatgactgttaataatatttgatagatattagatatactaga	0 360
tattcttcaagacacttgattcagcttaaagtgacatttaaaggcttactaggttaattagggttaactag	0 432
gcaggttagggtaatcaagtcattgtataatgatggtttctgttagaatatcgaaaaatatataactta	0 504
aaggggtttaataatattgtcctaaaaaattaaaaactgcttttattccagccaaaataaaacaataagac	0 576
	0

tttctacagaagaaaaatattatcagacatactgtgaacatttccttgctctgttaaacaatcatttgggaa 648

0

atatttgaaaaagaaaaagagtttcaagcactttatTTTTgaatgTTTgtaagtgttccctgCGctttaaact 720

0

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0

cgccaacatcaccttattcgcgcacgggtgtcaagcgcgcgtccgccctgCGccttTgaactccgcgctc 936

0

gtaaagTTTTgCGgtataaaagcgcagccccgcgcacctgcacatttctctaaccgTccggac atg gcg 1006
 M A
 t[1]

Q I D V D V F T A K V L S H W D W S 20
 caa atc gac gtg gat gtg ttc aca gcc aag gtt ttg tcc cat tgg gac tgg agc 1060
 tD18=[2]

R E D R S F G D S A S S P E S E S F 38
 cgt gag gac agg tca ttt gga gac agc gcg tcc tcg ccg gag tcc gag tcc ttc 1114

D S A C S S P D A R S S P T A G C E 56
 gat tct gcc tgc tcg tcg ccc gac gcg cgc tcc agc ccc aca gca ggg tgc gag 1168

IPB003975C (3.9e-05) IC 2.81
 H A E Q Q K P K V K M S M R R R M K 74
 cat gcg gag cag cag aag ccg aaa gtg aag atg agt atg agg agg agg atg aag 1222
 tV65=[3] aM69K[4]

IPB001092A (4.4e-06) IC 0.70
A S E R E K L R M R S L A E A L H Q 92
 gcc agc gag cgg gag aag ctc cgc atg agg agt ctg gcg gag gcg ctg cat cag 1276
 tQ92*[5]

IPB001092B (5.8e-08) IC 0.74
 L R D Y L P P G Y S R R G Q P L T K 110
 cta cgg gat tac ctt ccg ccg ggg tac agc agg aga gga cag ccg ctc acc aag 1330
 tY101=[6]

I O T L K Y T I O Y I K E L S G I L 128
 atc cag acg ctc aaa tac acc atc cag tac atc aaa gag tta tcc ggc atc ctc 1384
 cY116H[7] aS125T[9]
 tT117I[8]

E Q Q * 132

```

gag cag cag tga gacccgcgggaaaccttcccacaacgcttttaggaacgtttagacaacgttgtttcg 1452
                                a[ 10 ]                                c[ 11 ]

agaacgtcattttcgaatgttcctttttgaaaaaatgtttcaggaagcttttcgaagatgtcaaaacaaaga 132
1524

ttgaaacattcgaacatgggcattcgcattttcgacttatgcgcaaaaaacctacagacaacgaactttatt 132
1596

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1740

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1812

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1884

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1956

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2028

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2100

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2172

aaacatcctggaaatgttacttttccaaatgttttctgaacgtttaaaaaacatttaaacataaacgttcaa 132
2244

ttaaagaaaattccaaaaaaaaaaaaaaaaacgtacaatgttatttatgaattttctcttttttaaattactt 132
2314

```

Coding Sequence

```

M  A  Q  I  D  V  D  V  F  T  A  K  V  L  S  H  W  D  18
atg gcg caa atc gac gtg gat gtg ttc aca gcc aag gtt ttg tcc cat tgg gac 54
                                tD18=[ 2 ]

```

W S R E D R S F G D S A S S P E S E 36
 tgg agc cgt gag gac agg tca ttt gga gac agc gcg tcc tcg ccg gag tcc gag 108

S F D S A C S S P D A R S S P T A G 54
 tcc ttc gat tct gcc tgc tcg tcg ccc gac gcg cgc tcc agc ccc aca gca ggg 162

IPB003975C (3.9e-05) IC 2.81
 C E H A E Q Q K P K V K M S M R R R 72
 tgc gag cat gcg gag cag cag aag ccg aaa gtg aag atg agt atg agg agg agg 216
 tV65=[3] aM69K[4]

IPB001092A (4.4e-06) IC 0.70
M K A S E R E K L R M R S L A E A L 90
 atg aag gcc agc gag cgg gag aag ctc cgc atg agg agt ctg gcg gag gcg ctg 270

IPB001092B (5.8e-08) IC 0.74
 H Q L R D Y L P P G Y S R R G Q P L 108
 cat cag cta cgg gat tac ctt ccg ccg ggg tac agc agg aga gga cag ccg ctc 324
 tQ92*[5] tY101=[6]

T K I O T L K Y T I O Y I K E L S G 126
 acc aag atc cag acg ctc aaa tac acc atc cag tac atc aaa gag tta tcc ggc 378
 cY116H[7] aS125T[9]
 tT117I[8]

I L E Q Q * 132
 atc ctc gag cag cag tga 396