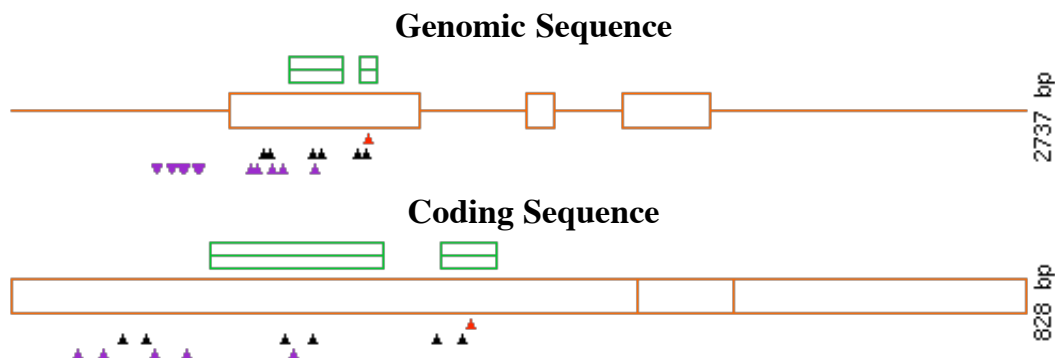


myod

IPB002546, IPB001092, IPB007869, IPB002418, and IPB000502



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	Zygoticity
				Gained in Variant	Lost from Reference				
1	G	C390T	Non-coding					5868	Homo
2	G	C431T	Non-coding		AsuI , AvaII , DraII , PpuMI			1230	Homo
3	G	T461A	Non-coding	AclI	MaeII , RsaI , SplI			3999	Homo
4	G	T465G	Non-coding	Tsp4CI	MaeII			8037	Homo
5	G	A503T	Non-coding		TspEI			7294	Homo
6	G	A504G	Non-coding	MaeI	TspEI			2180	Homo
7	G	T508C	Non-coding					8355	Homo
8	G	G509A	Non-coding		BsiYI			8687	Homo
9	G C	C643T	D18=		Hpy99I			3601	Homo
10	G C	C664T	N25=					7606	Homo
11	G C	G680A	E31K	AhaIII , MseI	BbvII , MboII			8283	Homo
12	G C	T699G	L37R		CviJI			6897	Homo

13	G C	C706T	H39=	NlaIII , TspDTI	BsaAI , MaeII , MjaIV , PmaCI			2861	Homo
14	G C	T733C	H48=	BseSI , HgiAI , SduI	HphI , SfaNI			2551	Homo
15	G C	C813T	A75V		AluI , Cac8I , CviJI , HindIII	5.1	0.27	7945	Homo
16	G C	G820A	K77=	MwoI				4268	Homo
17	G C	T835A	N82K	AluI , CviJI		8.8	0.24	2096	Homo
18	G C	A936C	N116T					7202	Homo
19	G C	A957T	E123V	HphI		2.3	0.30	6394	Homo
20	G C	A965T	R126*	BsaXI , TstI	BseMII , DdeI , Hpy188I			8438	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

caaatatattagacttatcaaattcagcactagtaaattatacaattagaaaatgtattaattagaaattag 0
72

aaaccaattggttgttttttccattaacaagcaaagtaaagcaaagctcatgcttgaatttatttgtaa 0
144

gttgaaatttgatggaaaataaacaagtaggcctaaatgtaatttggtatacaagcaataaaaacttctat 0
216

0

aaggcgaatccgacctttaacgacaaaagaaagacttttgatccactgctggaaactaggaaagaatgcttt	276 2022
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ctttctttcatagactaattctttttttctttctttctttctttctttctttctttctttctttcttttttt	276 2166
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acaactatttatactggaatatctatgtgatttgttgtgatttattggatgtataaacattttagcctactgt	276 2670
acacgtgatatatcaatttgttgaaatcaaatcggtttagcgttacacaataaacaggcctgtacaa	276 2737

Coding Sequence

M E L S D I P F P I P S A D D F Y D	18
atg gag ttg tcg gat atc ccc ttc ccc atc cca tca gct gat gac ttc tac gac	54
	tD18=[9]

D P C F N T N D M H F F E D L D P R	36
gac cct tgc ttc aac acc aac gac atg cac ttc ttt gaa gac ttg gac ccc agg	108
	tN25=[10] aE31K[11]

L V H V S L L K P D E H H H I E D E	54
ctt gtt cac gtg agc ctg ctc aaa ccc gac gag cat cac cac atc gag gac gag	162

gL37R[12]

cH48=[14]

tH39=[13]

IPB002546 (3.0e-52) IC 3.06

<u>H V R A P S G H H O A G R C L L W A</u>	72
cac gtg agg gcg ccc agt ggg cat cat cag gcc ggc agg tgc cta ctg tgg gca	216

<u>C K A C K R K T T N A D R R K A A T</u>	90
tgc aaa gct tgc aag aga aaa act acc aat gct gac cgt cgc aaa gcc gcc acc	270

tA75V[15]

aN82K[17]

aK77=[16]

<u>M R E R R R L S K V N</u> D A F E T L K	108
atg agg gag agg agg cga ctg agc aag gtc aac gac gct ttc gag acc ctc aag	324

IPB001092B (7.2e-12) IC 0.74

R C T S T N P N Q <u>R L P K V E I L R</u>	126
aga tgc acg tcc acc aac ccg aac cag agg ctg ccc aaa gtg gag att ctg aga	378

cN116T[18]

tE123V[19] tR126*[20]

<u>N A I S Y I</u> E S L Q A L L R S Q E D	144
aac gcc att agt tat atc gag tct ctg cag gct ctt ctc aga agt caa gag gat	432

N Y Y P V L E H Y S G D S D A S S P	162
aac tac tat ccc gtt ctg gaa cat tac agt gga gac tct gat gct tcc agt ccg	486

R S N C S D G M M D F M G P T C Q	179
aga tcc aac tgc tct gat ggc atg atg gat ttt atg ggc cca acg tgt cag	537

T R R R N S Y D S S Y F N D T P N A	197
acg aga aga cgg aac agc tat gac agc tct tac ttc aat gac aca cca aat g c	590

D A R N N K N S V V S S L D C L S	214
t gac gca cgg aat aat aaa aac tca gtg gtg tcg agt ttg gat tgt ctg tcc	642

S I V E R I S T E T P A C P V L S V	232
agc atc gtg gag cga att tcc aca gag act cct gca tgt ccc gtg ctg tca gta	696

P E G H E E S P C S P H E G S V L S	250
ccg gag ggg cac gaa gag agc ccg tgt tct ccg cat gag gga tct gtc ctg agt	750

D T G T T A P S P T S C P Q Q Q A Q	268
gac acc gga acc acc gca ccg tcc ccg acc agc tgc cct caa cag cag gct cag	804

E T I Y Q V L *	276
gaa acc att tat caa gtg ctt taa	828