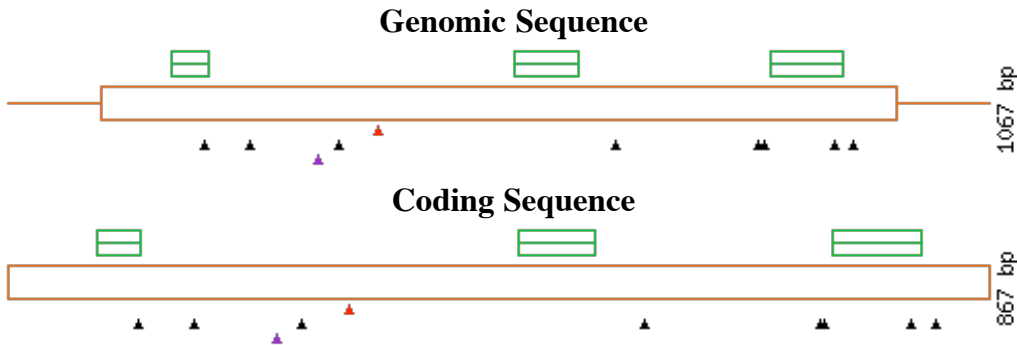


# Left-Over

IPB002884, IPB003971, and IPB007689



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	<a href="#">G C</a>	A215G	T39A	<a href="#">AciI</a> , <a href="#">MwoI</a>		5.8	0.58	7920	Homo
2	<a href="#">G C</a>	A264T	K55I					5332	Homo
3	<a href="#">G C</a>	C337T	Y79=					5321	Homo
4	<a href="#">G C</a>	T360C	L87P	<a href="#">BamHI</a> , <a href="#">NlaIV</a>				6270	Homo
5	<a href="#">G C</a>	T402A	L101*					46	Homo
6	<a href="#">G C</a>	A662T	I188L					5135	Homo
7	<a href="#">G C</a>	T817A	N239K	<a href="#">ApoI</a>				456	Homo
8	<a href="#">G C</a>	T822C	L241P		<a href="#">EcoNI</a> , <a href="#">MnII</a> , <a href="#">TaqI</a>			4855	Homo
9	<a href="#">G C</a>	T899A	S267T	<a href="#">MjaIV</a>	<a href="#">Eco57MI</a> , <a href="#">GsuI</a>	-2.7	0.00	1923	Homo
10	<a href="#">G C</a>	G920A	D274N		<a href="#">BsiYI</a> , <a href="#">MnII</a> , <a href="#">Tth111I</a>			3979	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:](#)  no file selected

[Sequence Alignment:](#)  no file selected

**-OR-**

## Genomic Sequence

```
ccacagcctattttaacaaacatctgccttatccccgagcctttggaagccctttgcgcacaaatcgcgagt 0
                                                                                               72

                                M  A  L  A  D  P  E  C  G  I  S  11
gactggcatcttcagcagaggagacgcg atg gct ttg gca gac ccc gag tgt gga ata tca 133

                                IPB003971A (9.4e-07) IC 2.03
N  G  A  D  S  A  S  P  F  S  V  I  I  E  L  N  V  G 29
aac ggc gct gat tcc gcg tct ccg ttt tcc gtc att atc gaa ctt aac gtg gga 187

G  O  V  Y  V  T  R  H  T  T  L  I  A  V  P  D  S  L  47
gga cag gtg tat gta acg cgg cac acc act tta ata gcc gta ccg gac tct ctg 241
                                gT39A[1]

L  W  N  M  F  S  K  K  T  P  A  E  L  A  R  D  S  K  65
ctg tgg aac atg ttc agt aag aaa aca ccg gct gag ctg gcg cgg gac agc aaa 295
                                tK55I[2]

G  R  F  F  L  D  R  D  G  F  L  F  R  Y  I  L  D  Y  83
ggt cgt ttt ttt ctg gac cgg gac ggc ttt ctt ttc cgc tac att tta gac tac 349
                                tY79=[3]

L  R  D  L  N  L  V  L  P  D  Y  F  P  E  K  S  R  L  101
cta cgg gat cta aac ctg gtt ctg ccg gac tat ttt cca gag aaa agt aga tta 403
                                cL87P[4]
                                                                aL101*[5]

Q  R  E  A  E  F  F  Q  L  R  D  L  S  K  L  L  S  P  119
cag aga gag gct gag ttc ttt cag ctg cgg gac ctt agc aag ctc ttg agt ccc 457

K  M  S  K  D  N  S  I  T  D  E  I  C  Q  S  D  S  E  137
aaa atg agt aaa gac aac tcc atc act gac gag atc tgc cag agt gac tcg gag 511

                                IPB007689L (4.2e-08) IC 3.48
E  P  S  A  S  A  T  P  V  V  G  P  E  T  S  R  T  L 155
gag ccg agc gcg agc gcg act ccg gtg gtc gga ccc gag act tct cgc act ctg 565

S  V  A  S  S  A  H  S  P  S  L  E  S  R  K  S  G  Y 173
```

tcc gtc gcc agc agc gca cat tct ccc tcc ctg gag tcc aga aag tct ggg tac 619

I T V G Y R G S Y T M G R D I Q T D 191  
atc acg gtt ggt tac cga ggc tcg tac aca atg gga aga gac ata cag aca gac 673  
tI188L[6]

A K F R R V A R I T V C G K T S L A 209  
gcc aaa ttc agg cgg gtc gcg cgg atc acg gtt tgc ggg aag act tct ttg gca 727

K E V F G D T L N E S R D P D R P P 227  
aag gag gtg ttt gga gac aca ttg aac gaa agc aga gac ccg gac cgg ccc cca 781

IPB007689G (1.3e-06) IC 4.32  
E R Y T S R Y Y L K Y N F L E Q A F 245  
gag agg tac acc tcg cgc tat tat ctg aaa tat aat ttc ctc gaa cag gcg ttt 835  
aN239K[7]  
cL241P[8]

D K L S E F G F O M V A C S S T G T 263  
gac aaa ctg tca gag ttt ggc ttc cag atg gtc gcg tgc agc tcc acg ggc acg 889

C A Y S S S D P N E D K V W T S Y T 281  
tgc gcg tac tcc agc agc gac cca aac gag gac aaa gtc tgg aca agc tac aca 943  
aS267T[9] aD274N[10]

E Y V F C R E \* 289  
gag tat gtt ttc tgt cga gaa tga gccaaaagcgctttatttaagagagagagcggtgtgtacat 1007

aggcgtcctactacgagagtgaaatcttatccggttaggagatgtgtattggagttttcc 289  
1067

## Coding Sequence

M A L A D P E C G I S N G A D S A S 18  
atg gct ttg gca gac ccc gag tgt gga ata tca aac ggc gct gat tcc gcg tct 54

IPB003971A (9.4e-07) IC 2.03  
P F S V I I E L N V G G O V Y V T R 36  
ccg ttt tcc gtc att atc gaa ctt aac gtg gga gga cag gtg tat gta acg cgg 108

H T T L I A V P D S L L W N M F S K 54  
cac acc act tta ata gcc gta ccg gac tct ctg ctg tgg aac atg ttc agt aag 162  
gT39A[1]

K T P A E L A R D S K G R F F L D R 72  
aaa aca ccg gct gag ctg gcg cgg gac agc aaa ggt cgt ttt ttt ctg gac cgg 216  
tK55I[2]

D G F L F R Y I L D Y L R D L N L V 90  
gac ggc ttt ctt ttc cgc tac att tta gac tac cta cgg gat cta aac ctg gtt 270

tY79=[3]

cL87P[4]

L P D Y F P E K S R L Q R E A E F F 108  
 ctg ccg gac tat ttt cca gag aaa agt aga tta cag aga gag gct gag ttc ttt 324  
 aL101\*[5]

Q L R D L S K L L S P K M S K D N S 126  
 cag ctg cgg gac ctt agc aag ctc ttg agt ccc aaa atg agt aaa gac aac tcc 378

I T D E I C Q S D S E E P S A S A T 144  
 atc act gac gag atc tgc cag agt gac tcg gag gag ccg agc gcg agc gcg act 432

IPB007689L (4.2e-08) IC 3.48

P V V G P E T S R T L S V A S S A H 162  
 ccg gtg gtc gga ccc gag act tct cgc act ctg tcc gtc gcc agc agc gca cat 486

S P S L E S R K S G Y I T V G Y R G 180  
 tct ccc tcc ctg gag tcc aga aag tct ggg tac atc acg gtt ggt tac cga ggc 540

S Y T M G R D I Q T D A K F R R V A 198  
 tcg tac aca atg gga aga gac ata cag aca gac gcc aaa ttc agg cgg gtc gcg 594  
 tI188L[6]

R I T V C G K T S L A K E V F G D T 216  
 cgg atc acg gtt tgc ggg aag act tct ttg gca aag gag gtg ttt gga gac aca 648

L N E S R D P D R P P E R Y T S R Y 234  
 ttg aac gaa agc aga gac ccg gac cgg ccc cca gag agg tac acc tcg cgc tat 702

IPB007689G (1.3e-06) IC 4.32

Y L K Y N F L E Q A F D K L S E F G 252  
 tat ctg aaa tat aat ttc ctc gaa cag gcg ttt gac aaa ctg tca gag ttt ggc 756  
 aN239K[7]  
 cL241P[8]

F O M V A C S S T G T C A Y S S S D 270  
 ttc cag atg gtc gcg tgc agc tcc acg ggc acg tgc gcg tac tcc agc agc gac 810  
 aS267T[9]

P N E D K V W T S Y T E Y V F C R E 288  
 cca aac gag gac aaa gtc tgg aca agc tac aca gag tat gtt ttc tgt cga gaa 864  
 aD274N[10]

\* 289  
 tga 867