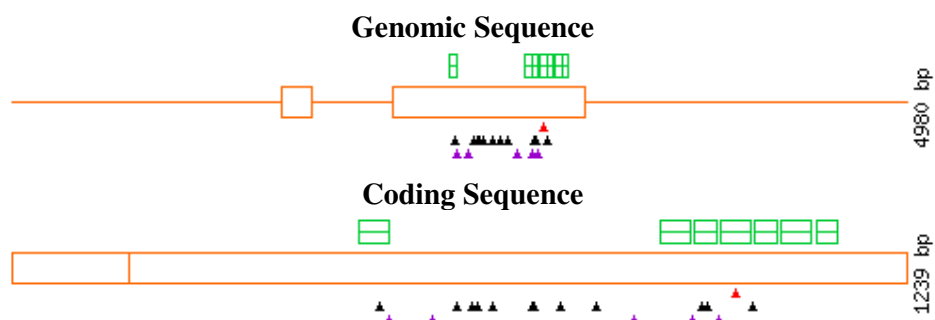


# Your Gene

IPB007086, IPB006794, and IPB001293



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>	G2460A	V170I	<a href="#">BglII</a> , <a href="#">DpnI</a> , <a href="#">MboI</a> , <a href="#">XhoII</a>	<a href="#">MnlI</a>	4.8	0.09	7748	Homo
2	<a href="#">G C</a>	G2474T	P174=					4940	Homo
3	<a href="#">G C</a>	T2534C	S194=					8513	Homo
4	<a href="#">G C</a>	A2568G	I206V					6841	Homo
5	<a href="#">G C</a>	T2589G	F213V	<a href="#">SgrAI</a>	<a href="#">CviJI</a>			3305	Homo
6	<a href="#">G C</a>	C2598T	P216S		<a href="#">MmeI</a> , <a href="#">MnlI</a>			2178	Homo
7	<a href="#">G C</a>	C2598T	P216S		<a href="#">MmeI</a> , <a href="#">MnlI</a>			6892	Homo
8	<a href="#">G C</a>	T2617A	M222K		<a href="#">CviRI</a> , <a href="#">NlaIII</a> , <a href="#">NspI</a>			4288	Homo
9	<a href="#">G C</a>	T2617A	M222K		<a href="#">CviRI</a> , <a href="#">NlaIII</a> , <a href="#">NspI</a>			4377	Homo
10	<a href="#">G C</a>	C2673A,C2674T	P241M	<a href="#">MseI</a> , <a href="#">VspI</a>	<a href="#">AciI</a>			7830	Homo
11	<a href="#">G C</a>	C2674T	P241L		<a href="#">AciI</a>			7830	Homo
12	<a href="#">G C</a>	C2711A	F253L	<a href="#">MseI</a>				6517	Homo
13	<a href="#">G C</a>	C2761T	T270I					8662	Homo
14	<a href="#">G C</a>	C2813T	N287=					4950	Homo
15	<a href="#">G C</a>	C2894T	D314=	<a href="#">FokI</a> , <a href="#">TspDTI</a>				7272	Homo
16	<a href="#">G C</a>	C2907T	H319Y			37.0	0.00	6938	Homo
17	<a href="#">G C</a>	A2916T	I322F		<a href="#">FokI</a> , <a href="#">SfaNI</a>	17.5	0.10	974	Homo
18	<a href="#">G C</a>	C2930T	H326=					7802	Homo

19	<a href="#">G C</a>	C2954A	C334*	<a href="#">TspDTI</a> , <a href="#">TspRI</a>	<a href="#">AvaIII</a> , <a href="#">CviRI</a> , <a href="#">NlaIII</a>			8726	Homo
20	<a href="#">G C</a>	A2977G	D342G	<a href="#">AciI</a> , <a href="#">CfrI</a> , <a href="#">CviJI</a> , <a href="#">HaeIII</a> , <a href="#">NspBII</a> , <a href="#">TauI</a>				7365	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:](#)

[Sequence Alignment:](#)

**-OR-**

## Genomic Sequence

```

caaatggccttatatgaaaatgtaaaaaattattacatgaggtagaataagctattaggtgacagtttgtcca 0
                                                                                   72

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                                                                                   144

caataattacataataattgcaataactgtggttattttcactttcttgcattatatttcactctgagatgtg 0
                                                                                   216

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D  L  A  Y  S  S  S  F  A  Q  P  A  G  P  R  N  Q  T	87
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T  L  S  C  T  M  A  Q  N  Q  A  D  M  E  H  I  Y  S	159
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gF213V[5]	
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tP241L[11]	
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T K I H L R Q K E R K S S S S S T G 393  
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V S S S E R G V A T S I C S S S S N 411  
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413

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## Coding Sequence

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P L A D S I Y S V D E L G T T L P A	36
cct ctt gcc gat agc atc tat tcg gtg gac gag ctt ggc aca aca ctg cca gcc	108

S V T I Y N D L G G H Y E Q I N A G 54  
 tct gtg act ata tat aac gat tta gga gga cat tac gag cag ata aac gca gga 162

D | G L I N G D M S T E K R A L D L 71  
 g | at ggc ctg att aac ggg gat atg agc acg gag aag cgc gcc ctc gac tta 213

A Y S S S F A Q P A G P R N Q T F T 89  
 gcc tac tcc agc agc ttc gcg caa cca gct ggc cct cgc aac caa act ttt acc 267

Y M G K F S I D S Q Y P G N W N P E 107  
 tac atg gga aag ttt tcc atc gac tcc cag tac ccg gga aac tgg aac cca gag 321

G V I N I V S A G I L G M T Q P S S 125  
 ggc gtg atc aac atc gtg agc gcg ggg atc ctg ggc atg acc cag cca tcc tca 375

A S S S P A S S V S P S H F S S T L 143  
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S C T M A Q N Q A D M E H I Y S P P IPB007086A (7.4e-05) IC 1.00  
 agc tgc acc atg gcg cag aac caa gca gac atg gag cac atc tac tct ccc ccg 161  
 483

P P Y S G C G E V Y Q D P S A F L S 179  
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 tP216S[7] aM222K[9]

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 tP241L[11]

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 aF253L[12]

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 tT270I[13] tN287=[14]

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 915

C D R R F S R S D E L T R H I R I H IPB007086B (1.1e-11) IC 1.47  
 tgc gac agg cgc ttc tcg cgc tcg gac gaa ctt acc aga cac atc cgc atc cac 323  
 969

