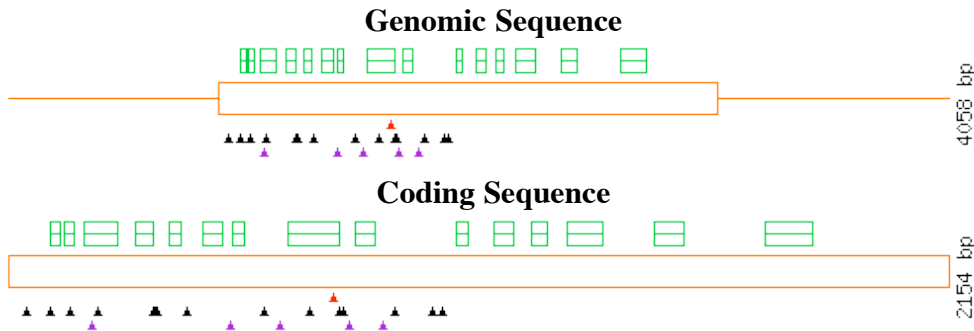


Your Gene

IPB008112, IPB000372, IPB003598, IPB002182, IPB000157, IPB013716, IPB003599, IPB009138, 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 C	T950G	C15G					2288	Homo
2	G C	T1004A	C33S			22.6	0.00	2032	Homo
3	G C	T1004A	C33S			22.6	0.00	2567	Homo
4	G C	C1046A	P47T			19.6	0.00	7173	Homo
5	G C	T1099C	L64=	TstI				5212	Homo
6	G C	G1112T	G69C		BstEII , CauII , HpaII , ScrFI	7.8	0.05	7818	Homo
7	G C	T1239G	I111S	BcefI , CviJI	FokI , TspGWI	21.1	0.00	2212	Homo
8	G C	T1239A	I111N	Tsp4CI	FokI , TspGWI	21.4	0.00	8020	Homo
9	G C	G1242T	R112L		MaeIII , Tsp4SI , TspGWI			6413	Homo
10	G C	T1248A	I114N	BcefI				3346	Homo
11	G C	T1248A	I114N	BcefI				3512	Homo
12	G C	G1316T	D137Y					3715	Homo
13	G C	T1417A	L170=	BsaXI	HpyI88I			2291	Homo

14	G C	T1494G	I196S	CviJI	BinI , DpnI , MboI , XhoII			1229	Homo
15	G C	T1494G	I196S	CviJI	BinI , DpnI , MboI , XhoII			5145	Homo
16	G C	T1528C	I207=	FokI , SfaNI	BsmI , Hpy178III			7965	Homo
17	G C	C1597A	D230E		FokI	15.6	0.00	3796	Homo
18	G C	T1651A	Y248*	DdeI				5548	Homo
19	G C	G1664T	V253F		MaeI , SpeI	0.7	0.02	1754	Homo
20	G C	C1674T	P256L	Eco57MI , GsuI , Hpy178III	NlaIV			2241	Homo
21	G C	G1687T	L260=	Eco57I , Eco57MI , Hpy188I , Ksp632I , MboII , SapI	CviRI , NspBII , PstI , SfeI			8416	Homo
22	G C	G1687T	L260=	Eco57I , Eco57MI , Hpy188I , Ksp632I , MboII , SapI	CviRI , NspBII , PstI , SfeI			8410	Homo
23	G C	C1765T	N286=		NlaIII , NspI			4920	Homo
24	G C	T1791G	I295S	MaeIII	MseI			624	Homo
25	G C	T1791G	I295S	MaeIII	MseI			906	Homo
26	G C	C1878T	P324L	Bce83I , SmlI	TstI			3199	Homo
27	G C	G1899A	R331H		Bcefi			7848	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

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aataattattaaataaattatgaaattaccattgcagtcagtacataccttcaccccactagcctcaattg	0 216
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gC15G[1]

IPB000372A (2.7e-08) IC 0.47

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 aC33S[3]

IPB013716D (9.5e-05) IC 4.32

IPB000372B (3.6e-13) IC 0.68

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 aI111N[8] aI114N[11]
 tR112L[9]

IPB000372C (6.1e-08) IC 1.06

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IPB008112B (1.2e-09) IC 3.95

E M P D F S L Q D L T N L Q E L Y I 151
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L L R L H L N S N R L K A I D S R W 187
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IPB013716I (3.2e-06) IC 3.33

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aD230E[17]

L E S L S F Y D N K L V R V P Q T A 259
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 aY248*[18] tV253F[19] tP256L[20]

IPB013716G (4.1e-06) IC 3.60

L Q K L P N L K F L D L N K N P I H 277
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E L T K L E A T N N P K F S Y V S R 331
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L N S L Y Q A T A D S L P N L R E I 367
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IPB000157B (5.9e-08) IC 1.41

S I H S N P L R C D C V I Q W M S S 385
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N K T T I R F M E P L S M F C T M P 403
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I E V R G Q R V R D V F S R E P S G 421
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IPB009138A (1.8e-05) IC 2.41

Q C L P M I S H D T F P N H L N L D 439
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I G M T V D L D C R A M A E P E P E 457
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I Y W V T P S G N K V M M D T V S D 475
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K Y Q L N S A G T L R I S Y I Q V D 493
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IPB003598B (1.8e-12) IC 0.46

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V T A I R V N G T L L D S T Q L M K 529
 gtg acc gcc att cga gtt aac ggg act ctt ctg gat agc acg cag ctt atg aag 2494

I Y V K H T E S H S I L V S W K V N 547
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S N V M T S N L K W S S A T M K I D 565
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IPB013716L (3.4e-05) IC 3.56

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L T H L O P A T E Y E V C L S V S N 601
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I H Q Q T O K S C V N V T T K H A T 619
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F A V E I S E Q G T N T A L A A V M 637
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G T I L A I I S L G S I T L Y I A K 655
 ggc acc att ctg gcc atc atc agc ctg ggc tct atc acg ttg tac att gcg aag 2872

R W K R K N Y H H S L K K Y M Q K T 673
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S S I P L N E L Y P P L I N L W E A 691
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D S E K D K D G S S D N K Q T Q V D 709
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T T R S Y Y M W * 718
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718

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Coding Sequence

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L  L  A  V  L  G  L  S  S  V  H  S  T  E    IPB000372A (2.7e-08) IC 0.47
C  P  Q  L    36
    
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ctt ctg gct gta ctt ggt ctc tct tcg gtt cac agt aca gaa tgt ccg cag ctt 108
aC33S[2]
aC33S[3]

IPB013716D (9.5e-05) IC 4.32

C V C E I R P W F T P O S T Y R E A 54
 tgt gtg tgc gag atc cgg cct tgg ttc aca ccc cag tcc acc tac aga gaa gca 162
aP47T[4]

IPB000372B (3.6e-13) IC 0.68

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IPB013716G (1.9e-07) IC 3.60

E L E Q L L N L T E L D L S O N N F 108
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IPB000372C (6.1e-08) IC 1.06

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 agc aac atc cgt gac atc ggc ctg acc aac atg tca caa ctc acg act ctt cac 378
gI111S[7] aI114N[10]
aI111N[8] aI114N[11]
tR112L[9]

L E E N O I V E M P D F S L Q D L T 144
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tD137Y[12]

IPB008112B (1.2e-09) IC 3.95

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IPB000372C (1.6e-08) IC 1.06

A F A G L R N L L R L H L N S N R L 180
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K A I D S R W F E S T P N L E I L M 198
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gI196S[14]
gI196S[15]

IPB013716I (3.2e-06) IC 3.33

I G E N P V V G I L D L N F K P L T 216
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cI207=[16]

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aD230E[17]

A F V G L D N L E S L S F Y D N K L 252

gca ttt gtt gga ctg gac aac ctg gag agt ctc tcc ttc tat gac aat aaa cta 756
aY248*[18]

IPB013716G (4.1e-06) IC 3.60

V R V P Q T A L Q K L P N L K F L D 270
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 tL260=[22]

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 gI295S[25]

F A L D N L P E L T K L E A T N N P 324
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 tP324L[26]

IPB000372C (1.5e-05) IC 1.06

K F S Y V S R L A F R D L P A L E S 342
 aag ttt tcc tac gtg agc cgt tta gcg ttc cgt gat ttg ccg gca cta gag agc 1026
 aR331H[27]

L M L N N N A L N S L Y Q A T A D S 360
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IPB000157B (5.9e-08) IC 1.41

L P N L R E I S I H S N P L R C D C 378
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V I O W M S S N K T T I R F M E P L 396
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IPB000157C (3.3e-05) IC 0.91

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IPB009138A (1.8e-05) IC 2.41

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P N H L N L D I G M T V D L D C R A 450
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M A E P E P E I Y W V T P S G N K V 468
 atg gct gaa ccc gaa ccg gaa ata tac tgg gtg aca cca tct ggt aac aaa gtc 1404

M M D T V S D K Y Q L N S A G T L R 486
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IPB003598B (1.8e-12) IC 0.46

I S Y I Q V D D S G H Y T C V A Q N 504
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T E G A D T R V T A I R V N G T L L 522
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D S T Q L M K I Y V K H T E S H S I 540
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L V S W K V N S N V M T S N L K W S 558
 cta gtg tcc tgg aaa gtg aac tcc aac gtc atg acg tcc aat ctg aag tgg tca 1674

S A T M K I D N P H I T Y T A K V P 576
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IPB013716L (3.4e-05) IC 3.56

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V T T K H A T F A V E I S E Q G T N 630
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T A L A A V M G T I L A I I S L G S 648
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I T L Y I A K R W K R K N Y H H S L 666
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K K Y M Q K T S S I P L N E L Y P P 684
 aag aag tac atg cag aaa acc tca tcc atc cct cta aat gaa ctc tat cct ccc 2052

L I N L W E A D S E K D K D G S S D 702
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N K Q T Q V D T T R S Y Y M W * 718
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