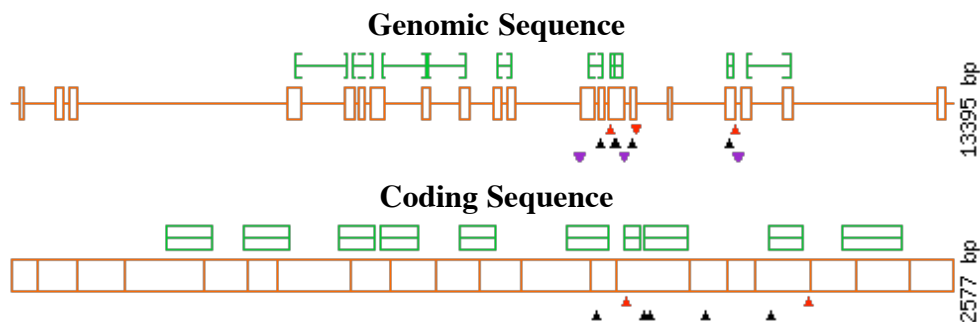


ZiWI

IPB003165, IPB003100, IPB005034, IPB002389, IPB007860, and IPB007695



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	C8054T	Intron	Hpy188I	Hpy178III			5914	Homo
2	G	T8083A	Intron		TspDTI			5462	Homo
3	G C	T8371A	D533E	MaeII	DpnI , MboI	-0.8	0.27	260	Homo
4	G C	C8525T	R561*	MfeI , TspEI	TaqI			5023	Homo
5	G C	C8577T	T578I			-5.1	0.59	5208	Homo
6	G C	T8592C	V583A	AciI		4.2	1.00	5690	Homo
7	G	C8721T	Intron		MslI			815	Homo
8	G C	T8827G	D633E	BsmAI , Eco31I				4754	Homo
9	G	G8890A	Splice Junction	Hpy178III				4236	Homo
10	G C	T10195A	I694N		SfaNI	22.3	0.00	211	Homo
11	G C	T10298A	Y728*	MseI				4796	Homo
12	G	T10312G	Intron	BceFI	FaiI , TspDTI			1289	Homo
13	G	T10327C	Intron	TaqII				5924	Homo
14	G	T10357C	Intron	Tsp4CI , TspRI	TspDTI			3293	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.

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F N I P O H R 243
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T I L Q Y E S S I M L C S D V S H K 270
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IPB007860C (7.5e-07) IC 1.66
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G P M G I R M O R A V M 528
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D R O E S L L R A L O O N V A R E T 550
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ad533E[3]

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IPB002389H (9.6e-05) IC 4.13

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IPB003165B (3.9e-20) IC 1.09

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<u>M O S I</u> K T M G Q D Y E	729
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c[13] c[14]	

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IPB003165D (2.9e-38) IC 1.47

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gataagaaacatgctaagtaaacattcttgtttatctgaaaaacaatgctgatgtcagataaatctgctttaa	12173
	820
aaatgtgtttttctgtgccgaaagctgtctttgttttggggtttttaaccgcccaatgccagtttagcca	12245
	820
attatattccagcaacctgggttgccgtggtgtaaaactgcatatttcattcagtcaggaaggctctcaaag	12317
	820
catgcattcgtaaccaaaatgacacctcctgtcgagagtagcagactcaaagagacgcagattcagttcca	12389
	820
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	820
ccctgaatattaacaacatgctttgtgactagttatgcaatgatatgcaatttggctgtttgcatcagaaga	12533
	820
aacatgacaaatttaaataatggccgttcagaagtacagaatatgcaactcaccacgaaatggtaaggtttat	12605
	820
aatctaatacatattaaccctctttaacattattaaatgtagatgctgtaccactgatatgtgttctaaagt	12677

tcaatttcagacggtttattttcaagatctgaggtgctgctgctttcagtatatagcaataaatgtcaggta	820	12749
aaatggcattcaaactcacattgttaacatttaacagtgaataaagcactgtagctgagctgatcattgtca	820	12821
gtttccggttgttcacttggtgccaatagacggcggttttaaatatatgttcgaggagtttgttagaacaaaa	820	12893
actccttttaatatgaaaaaatattccttctattatgtgctggtgcttttatttagaacacttttaatttt	820	12965
ctcgcgcttgctcctcaatctggcaacctgcgctttgcatttgtttgatccaggagtgaataacctagttca	820	13037
accactgggtgtgaaacttgcatgttattgagctgtggaggtcagacagaaccagtcaatattatgagtat	820	13109
tgtggcatccctaattaacacagtgctgtgatatggattctttatgactatctctgtttccttag gg	G 821	13180
I V R V P A P C Q Y A H K L A F L	838	
g att gtg cga gtg cca gct cca tgc cag tat gcc cac aaa ttg gcc ttc ctg	13232	
V G Q S I H K E P N M N L D D F L Y	856	
gtt ggc cag agc att cac aag gag cct aac atg aat ctg gat gac ttc ctg tat	13286	
Y L *	859	
tac ctg taa ctggtaaagagtcaagatgcagggctcctgaaggaacagtgtagccgtagtttctttttc	13355	
gagttgaatgaaaagagtatgctattcggagaactttca	859	13395

Coding Sequence

M T G R A R A R S R G R G R G Q E P	18
atg aca gga cga gca aga gca aga tcg agg ggc aga ggt cgt ggt cag gag cct	54
A A P G A Q P P V S Q E A A K P V	35
gct gct cct ggc gca caa cca cct gta tct caa gag gct gca aag cct gtt	105
V S T P S E G Q L V G R G R Q K P A	53
gtg tcc act ccg tct gaa gga caa ctg gtg ggc aga ggg aga cag aaa cct gca	159
P G A M S E E A M L Q I S A G F Q	70
cct gga gcc atg tct gaa gaa g cg atg ctc cag att tct gct ggc ttt cag	210

Q V K I G E R G G R R R D F H D S G 88
cag gtg aag atc ggg gag aga ggt gga cgc aga cgg gat ttc cac gat tct ggt 264

V H T R Q L M E H V K E S K T G | V 105
gtc cat act cgt caa ctt atg gaa cac gtg aaa gaa tcc aaa aca g | gt gtt 315

S G T A I E L R A N F M R L L S R P 123
tct ggg act gcc att gag ctg agg gcc aat ttt atg cgt ctg ctt tca cgt cct 369

M W A L Y Q Y H V D Y K P P M E S R 141
atg tgg gct ttg tat cag tat cat gtg gac tac aag cca cca atg gag tcc aga 423

IPB005034J (2.5e-05) IC 2.78

R L R S A L L F O H E E T L G K A H 159
cga ctg cgt tcg gct ttg ctt ttc cag cac gag gag act ctg ggg aaa gca cac 477

T F D G A I L F L P N K L R N A | E 176
acc ttt gat gga gcc att ctc ttt ctc ccc aac aaa ctg cgc aac gct | gag 528

T V L C S E T R N G E K V E I T V T 194
aca gtc ctg tgc agt gag acc aga aat gga gag aag gtt gag atc act gtg aca 582

L T N E L P P S S P V C L Q F Y N I 212
ctg acc aat gag ctg ccg ccg tcc tct cct gta tgc ctg cag ttt tac aac atc 636

IPB003165A (1.9e-20) IC 0.91

L F R R | I L R I L N M O O I G R H 229
ctc ttc agg ag | a atc cta aga ata cta aac atg cag cag atc gga cgt cat 687

Y Y N P D D P F N I P O H R | L T I 246
tac tac aat cct gat gac cca ttc aac atc cca cag cac ag | g ctg aca att 738

W P G F M T T I L Q Y E S S I M L C 264
tgg cct ggc ttc atg acc acc atc cta cag tac gag tcc agc atc atg ctg tgc 792

S D V S H K V L R S E T V L D F M Y 282
tct gat gtg agc cac aag gtt ctg cgc agt gag acg gtt ctt gac ttt atg tac 846

IPB003100A (7.6e-18) IC 0.81

S L R Q Q C G D Q R F P E A C T K E 300
agt ctg aga cag cag tgt gga gac cag cgc ttc cct gaa gcc tgc acg aag gag 900

L V G L I I L T K | Y N N K T Y R I 317
ctt gtg ggc ctg atc att ctg acc aa | g tac aac aac aag aca tac agg att 951

D D I A W D H T P N N T F K K G D T 335
gat gac att gcc tgg gat cat act ccc aac aac aca ttc aag aaa gga gat aca 1005

IPB003100B (2.6e-13) IC 0.97

E I S F K N Y F K S | O Y G L D I T 352
gaa att tca ttc aag aac tac ttc aaa tcg | caa tat ggt ctt gac ata aca 1056

D G N O V L L V S H V K R L G P S G 370

gat ggc aac cag gtt ctt ctc gtt agc cat gtg aag aga ctt ggc ccc tca gga 1110

R P P P G P A M L V P E F C Y L T G | 388
cgc cct cca ccg gga cca gct atg ctt gtc ccc gag ttc tgc tac ctc act g | g 1163

L T D K M R A D F N I M K D L A S 405
t cta acc gat aaa atg cgt gct gat ttt aac atc atg aag gat ctt gct tca 1215

IPB005034L (3.7e-05) IC 2.97

H T R L S P E O R E G R I N R L I S 423
cat aca cgg cta agt cct gaa cag aga gag ggc aga att aac cgc tta atc tcc 1269

N I N R | N G D V O N E L T T W G L 440
aac atc aac ag | a aat gga gac gtg cag aat gaa ctg act act tgg ggt ctg 1320

S F E N K L L S L N G R V L P S E R 458
agc ttt gag aac aag ctt ctt agt ctt aat ggg aga gtt ttg ccc tct gag agg 1374

I I Q G G R A | F E Y N P W T A D W 475
atc ata cag gga ggc aga gca | ttt gag tat aac cca tgg aca gca gac tgg 1425

S K E M R G L P L I S C M S L D N W 493
tct aaa gag atg aga ggt ctc cct ctg att agc tgc atg tct ctg gac aac tgg 1479

IPB007860C (7.5e-07) IC 1.66

L M F Y T R R N A D V A Q S L L Q T 511
ctc atg ttc tac acg cgc aga aat gca gat gtt gcc caa tct ctg ctt cag act 1533

L N K V S G P M G I R M O R A V M | _ 528
ctc aac aaa gtg tct gga ccc atg ggg atc cgc atg cag agg gct gtc at | g 1584

I E Y E D R O E S L L R A L O O N V 546
att gag tat gaa gat cgt cag gaa tct ctc ctt aga gct ttg caa caa aac gta 1638
ad533E[3]

IPB002389H (9.6e-05) IC 4.13

A R E T Q M | V V V I L P T N R K D 563
gca cgt gaa act cag atg | gtg gtg gtg atc ttg cct acc aat cga aaa gac 1689
tr561*[4]

IPB003165B (3.9e-20) IC 1.09

K Y D C V K K Y L C V D C P T P S O 581
aag tac gac tgt gta aag aag tac ctg tgt gtg gac tgc cct act cct agt cag 1743
tT578I[5]

C V V S R T I S K P O A L M T V A T 599
tgt gtg gtg tct cgc acc atc agc aaa cct caa gca ctt atg act gtg gcc acc 1797
cV583A[6]

K I A L O M N C K M G G E L W S V E 617
aag att gct ttg cag atg aac tgc aaa atg gga gga gag ctg tgg agt gta gaa 1851

I P | L R Q L M I V G I D C Y H D T 634
att cca | ctc cgg cag ctc atg att gta ggt ata gac tgc tac cat gat acc 1902

A A G K R S I G A M V A S L N Q G M 652
 gct gct gga aaa agg tcc atc ggc gca atg gtg gcc agt cta aat cag ggc atg 1956

S R | W F S K C V L Q N R G Q E I I 669
 tca ag | g tgg ttc tcc aag tgt gtc ttg caa aac cgt gga cag gag atc atc 2007

D A L K G S L Q G | A L K A Y L K Y 686
 gat gca ctg aag ggg tca ttg cag g | gt gct ctg aag gcc tat ctg aaa tac 2058

IPB003165C (8.0e-21) IC 1.70
 N N S L P S R I I V Y R D G V G D G 704
 aac aat tct ctg ccc tcg cgc atc att gtt tac cga gat gga gtt gga gat ggc 2112
 aI694N[10]

M L O S V V D Y E V P O I M O S I K 722
 atg ctg cag agc gtt gtg gac tat gaa gtt cct cag atc atg cag tct atc aag 2166

T M G Q D Y E | P K L S V V V V K K 739
 acc atg ggg caa gat tat ga | g ccc aag ctc tca gta gtg gtg gtg aaa aag 2217
 aY728*[11]

R I S S R F F A R I D G K I A N P P 757
 cgc atc agc tcc cga ttc ttt gct cgg att gat ggc aaa att gcc aat ccc cct 2271

IPB003165D (2.9e-38) IC 1.47
 P G T V I D T E V T R P E W | Y D F 774
 cct ggg aca gtc att gac act gaa gtc act cgt cca gag tg | g tat gat ttc 2322

F I V S Q A V R F G C V A P T H Y N 792
 ttc att gta agc cag gct gtg cgc ttt ggg tgt gtc gca cct act cac tac aat 2376

V V F D N S G L K P D H M O R L T Y 810
 gtg gtg ttt gac aac agc ggc ctt aaa cca gat cac atg cag aga ctc acc tac 2430

K L C H M Y Y N W Q | G I V R V P A 827
 aaa ctt tgc cac atg tac tac aac tgg cag | ggg att gtg cga gtg cca gct 2481

P C Q Y A H K L A F L V G Q S I H K 845
 cca tgc cag tat gcc cac aaa ttg gcc ttc ctg gtt ggc cag agc att cac aag 2535

E P N M N L D D F L Y Y L * 859
 gag cct aac atg aat ctg gat gac ttc ctg tat tac ctg taa 2577