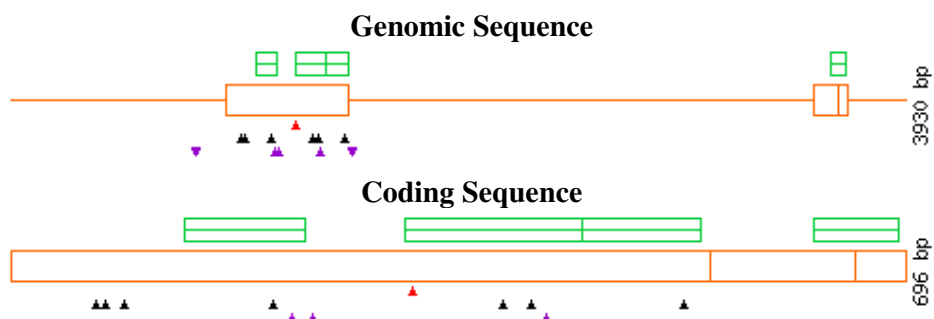


Iratb_temp

IPB007053, IPB012502, IPB001036, IPB011591, IPB001686, IPB007696, IPB003888, IPB002077, IPB001487, IPB000064, and IPB006069



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	A812G	Non-coding					4851	Homo
2	G C	T1006G	H22Q					2863	Homo
3	G C	T1014A	F25Y					902	Homo
4	G C	T1028C	S30P					7377	Homo
5	G C	T1144G	D68E			6.1	0.31	6706	Homo
6	G C	C1159T	H73=		MnlI			1270	Homo
7	G C	C1175T	L79=					2730	Homo
8	G C	C1252A	Y104*					6753	Homo
9	G C	T1323A	M128K		BccI	2.0	0.73	2447	Homo
10	G C	G1345T	Q135H	FokI , Hin4I	AlwNI , CviJI , Fnu4HI , TauI	7.0	0.02	8412	Homo
11	G C	T1357C	A139=	SecI	BbvCI , Bpu10I , BseMII , DdeI , NspBII			6630	Homo
12	G C	T1464A	V175E		HphI , MslI , OliI	7.9	0.96	345	Homo
13	G	T1497C	Intron	AccI , HgaI , HindII , Hpy99I , MjaIV , Sall	BsaBI , CviRI , SfaNI			6972	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: [Browse...](#)

Sequence Alignment: [Browse...](#)

[Redo analysis with homology model](#)

-OR-

[Reverse PSI-Blast/SIFT for Models](#)

Genomic Sequence

tggaggagaaaacactatggagaggtcagggaaatgtacgatttttaaaggaggcgtggcacccaacacca	0 72
ccctaaccccaaccgtcattggatgatgagcaagtcataactaaattgtaagaattagatcgtacgaattca	0 144
tacaaattagccactaaatcaaaaagttacgaattggcgtgagattgcgcttggtggacatgtactgaggac	0 216
caggagcgcaactacacatcttactgaggggtatgcggtttaaagttttgtgttaaagattttgaattaaac	0 288
atgtgtgccagcgtatgcaattaatggtataatTTTTTatttaataaaatacattattatacttgtataaaa	0 360
tgcaaaataagcaattttaaccaaacatatttattttattttattatctaatactttaaaataaggataatt	0 432
tcaaaaatagttttggcacaatggcgccacccaaaatatttgatagaattgtacacacattagttcatttat	0 504
aaagtttttttaaagttattcatttttagttcagcttagtctctttattcataaggggtcgccacagcaga	0 576
atgcagaatgttttacttagtggatgcccttcagctgcaaccagtagtgggaaacatccatacacacaca	0 648
ttcactacggccaatttattttatactattaactgtagggaaaccggagcaccagggggaaaccccgcgaa	0 720
cactgccagaacatgcaaacctacacaaaactgccagcttcccagcgggactcgaaccagcgaccttct	0 792

gaaccCGTTTTTAAAAGTATTCCTTTATTCTTTGATGTTCTCATTTTCACAGCTCTTCAGTGGTAGCCAAT	0
g[1]	864
AGTCTCTCCCCTAGGGTCGTGACGTCACGACAGACCGCTGCTCCTTAGAATAAAACCAAGCGCGGAGGTTAGA	0
	936
G Q H C K M L D S L S L L L E K T	17
acca ggg cag cac tgc aaa atg tta gat tct ctc tcc ttg ctg ttg gag aaa acc	991
L L L A H F N F F S T T S S K Q E R	35
tta ctt cta gcg cat ttc aac ttt ttc agc acc act tcc tct aag caa gag aga	1045
gH22Q[2] aF25Y[3] cS30P[4]	
	IPB007053A (1.2e-24) IC 2.20
C T K R R E E S T Y <u>F Q R G D L L E</u>	53
tgc acg aag cga cgc gag gag agc act tac ttc cag cgc ggg gat ctg ttg gag	1099
<u>V P R T L F T H F G I Y L G D N K V</u>	71
gtt ccg cgc act ttg ttc act cat ttt ggc att tac ctc ggc gat aac aaa gtc	1153
gD68E[5]	
<u>A H L M P</u> D I L P V L T S N K S H L	89
gca cac ctc atg cct gat ata ctg ccg gtg ctg acg agc aac aaa agt cac ctc	1207
tH73=[6] tL79=[7]	
	IPB007053B (8.8e-21) IC 1.63
Q N V V T N K R L L L G V <u>L Y K Y A</u>	107
cag aat gta gtg acg aac aag aga ctg ctt ctc ggt gtg ctc tac aag tac gcc	1261
aY104*[8]	
<u>S V R V D T V E D F A Y G S N I L L</u>	125
tca gta cgg gtg gac aca gtg gag gat ttc gcc tac ggg tcc aat att ttg ctg	1315
<u>N T M D T T L R K Q P L A A E E V A</u>	143
aac acg atg gac act acc ttg aga aaa cag ccg ctg gct gct gag gag gtc gcc	1369
aM128K[9] tQ135H[10] cA139=[11]	
	IPB007053C (1.1e-26) IC 2.19
R R A E K <u>L V G H F P Y S L M W N N</u>	161
aga aga gcc gaa aaa ctt gtc ggt cat ttt ccc tac agt ctt atg tgg aat aac	1423
<u>C E H F V T Y C R Y G T A V S L Q T</u>	179
tgc gaa cat ttt gtc act tac tgc cgc tac ggc aca gcg gtg agc ctg cag acg	1477
aV175E[12]	
D Q	181
gac cag gtaacactgtcgatgacacatctgcagctcttctgccgagtgaagacttcactgtgattacaag	1547
c[13]	
ttaatcattacatggttgtcgatttcgcgcttttcttctgctgaaacttgcgagatgtatagaagataaatta	181
	1619
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	1691
aagtgtaacgtagcattttatacaagctttcattagctctgcacaaatgtgatttgaacttttaatagtt	181
	1763
	181

tgттаатgcatgtagactatattccagttggтаааатacgtttaacagтаааacagtcaaattaggctctta	1835
taaactttagaaaccctttttatacaaaatataaaattttaaatggcaagaattacactaagacagatata	181 1907
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 3419

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 3491

atctcacatgccatctttttccctcaacag ttc tgc gaa agt tta aag tca ata atc cgg 191
 3551

F C E S L K S I I R

D Q R S I L L T T V I G M L S M F F IPB001036D (1.9e-05) IC 1.97
 209
 gac cag agg agc att ctc ctg acc act gtc atc ggg atg ctt tcc atg ttt ttt 3605

V G I A P S T A L P T F I I P F I 226
 gtt gga ata gcg ccg tcg acc gca ctt ccc g acc ttc atc att ccc ttc atc 3657

L W M A G * 232
 ttg tgg atg gct gga taa tgcatagtctgaacacacatactgtatgaactatttaacgtatcaaac 3723

tttgtatTTTTGGCTTTATCATAGAGAGTCACTGCAAGATTTTTTTGCAAGTTGATGATTGTATTTTTCTC 232
 3795

gggcattgataacttaatcttttcattctttatagctacctttatatattaacattttttgtacattttt 232
 3867

tacgatcgTTTTTCAAACATACTGTACAATATAACAAAATAATAAATGTCATTTAAATGGT 232
 3930

Coding Sequence

G Q H C K M L D S L S L L L E K T L 18
 ggg cag cac tgc aaa atg tta gat tct ctc tcc ttg ctg ttg gag aaa acc tta 54

L L A H F N F F S T T S S K Q E R C 36
 ctt cta gcg cat ttc aac ttt ttc agc acc act tcc tct aag caa gag aga tgc 108
 gH22Q[2] aF25Y[3] cS30P[4]

IPB007053A (1.2e-24) IC 2.20

T K R R E E S T Y F Q R G D L L E V 54
 acg aag cga cgc gag gag agc act tac ttc cag cgc ggg gat ctg ttg gag gtt 162

P R T L F T H F G I Y L G D N K V A 72
 ccg cgc act ttg ttc act cat ttt ggc att tac ctc ggc gat aac aaa gtc gca 216
 gD68E[5]

H L M P D I L P V L T S N K S H L Q 90

cac ctc atg cct gat ata ctg ccg gtg ctg acg agc aac aaa agt cac ctc cag 270
 tH73=[6] tL79=[7]

IPB007053B (8.8e-21) IC 1.63
 N V V T N K R L L L G V L Y K Y A S 108
 aat gta gtg acg aac aag aga ctg ctt ctc ggt gtg ctc tac aag tac gcc tca 324
 aY104*[8]

V R V D T V E D F A Y G S N I L L N 126
 gta cgg gtg gac aca gtg gag gat ttc gcc tac ggg tcc aat att ttg ctg aac 378

T M D T T L R K Q P L A A E E V A R 144
 acg atg gac act acc ttg aga aaa cag ccg ctg gct gct gag gag gtc gcc aga 432
 aM128K[9] tQ135H[10] cA139=[11]

IPB007053C (1.1e-26) IC 2.19
R A E K L V G H F P Y S L M W N N C 162
 aga gcc gaa aaa ctt gtc ggt cat ttt ccc tac agt ctt atg tgg aat aac tgc 486

E H F V T Y C R Y G T A V S L Q T D 180
 gaa cat ttt gtc act tac tgc cgc tac ggc aca gcg gtg agc ctg cag acg gac 540
 aV175E[12]

Q | F C E S L K S I I R D Q R S I L 197
 cag | ttc tgc gaa agt tta aag tca ata atc cgg gac cag agg agc att ctc 591

IPB001036D (1.9e-05) IC 1.97
 L T T V I G M L S M F F V G I A P S 215
 ctg acc act gtc atc ggg atg ctt tcc atg ttt ttt gtt gga ata gcg ccg tcg 645

T A L P | T F I I P F I L W M A G * 232
 acc gca ctt ccc | acc ttc atc att ccc ttc atc ttg tgg atg gct gga taa 696