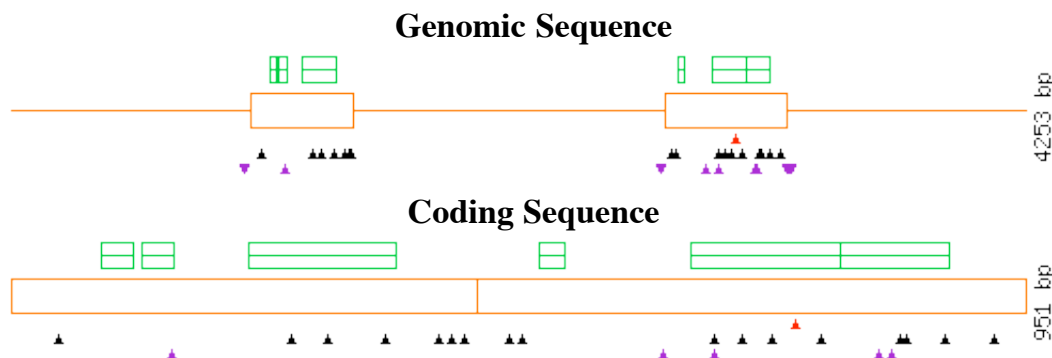


gbx1

IPB001827, IPB013847, IPB000747, IPB006711, IPB006820, IPB000047, IPB003106, IPB000327, IPB012502, IPB003025, IPB003022, IPB006712, IPB003888, and IPB003654



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	Zygoticity
				Gained in Variant	Lost from Reference				
1	G	T975A	Non-coding	AhaIII , MseI				187	Homo
2	G C	C1044A	S15Y		HinfI , TfiI			3893	Homo
3	G C	G1150A	S50=	TspDTI				6175	Homo
4	G C	C1263T	T88I			12.3	0.01	3315	Homo
5	G C	A1296G	D99G	EcoRII , ScrFI	Hpy178III	4.2	0.36	5431	Homo
6	G C	C1350T	T117M	BccI , FokI	FniI	-5.2	0.07	3822	Homo
7	G C	T1401C	L134P		BseRI			8433	Homo
8	G C	A1412G	T138A	AciI , FnuDII	TspGWI			8242	Homo
9	G C	A1425G	Q142R	TaqI				6339	Homo
10	G	T2724C	Intron	Ksp632I , MboII				3140	Homo
11	G C	A2769C	E156A	FnuDII , HgaI				4369	Homo

12	G C	T2781A	L160Q					3905	Homo
13	G C	G2914A	A204=		AflIII , FnuDII , MaeIII , MluI			5564	Homo
14	G C	C2961T	A220V	Tsp4CI	AluI , CviJI	16.6	0.02	4709	Homo
15	G C	T2962C	A220=		AluI			4073	Homo
16	G C	C2987A	L229I		AvaI , SmlI , XhoI	15.6	0.02	7976	Homo
17	G C	T2988G	L229R	FnuDII	AvaI , Hpy178III , SmlI , TaqI , XhoI	20.4	0.00	1234	Homo
18	G C	A3015T	Y238F			21.2	0.00	8544	Homo
19	G C	C3038T	Q246*		Cac8I , MwoI			6532	Homo
20	G C	A3062T	S254C		BseMII , DdeI	10.4	0.01	7518	Homo
21	G C	G3115C	R271=	SfaNI	BlnI , DpnI , MboI , TspGWI			25	Homo
22	G C	A3127G	G275=	CauI , ScrFI				7399	Homo
23	G C	C3136A	N278K		HindII , MjaIV	3.8	0.57	6800	Homo
24	G C	G3141A	R280K		DpnI , MboI	10.3	0.11	3762	Homo
25	G C	T3177C	V292A	AcyI , HaeII , HhaI , NarI	BseSI , SduI	-1.6	0.28	1540	Homo
26	G C	T3223A	H307Q		Hin4I			6701	Homo
27	G	T3255A	Non-coding					5333	Homo
28	G	T3255A	Non-coding					5345	Homo
29	G	G3256T	Non-coding	MseI , TspEI				258	Homo
30	G	A3266G	Non-coding	BseMII , DdeI , TspDTI				5397	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

tgacgcttagggagggttcagaagctaagaggggggtcagaacctcccaaaattcacaccctgctggtgac	0 72
tcaaaattcatgatggttttagctaacaaaagtaagactaaaatgtatgctatgtaaagactacaataat	0 144
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a[1] 1006

R P S G T G T A F S I D S L I G T P 20
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IPB003025A (7.0e-05) IC 2.82
Q P R P G H L L Y T G Y P M F M P Y 38
cag cca cga ccg ggc cac ctg ctc tac acg ggc tac ccg atg ttt atg ccg tac 1114

IPB003022B (6.8e-05) IC 3.39
R P L M I P O A L S H S S L P S G I 56
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P P L A P L A S F A G R L T N T F C 74
cca cct ttg gca ccg ctg gca tct ttc gca ggg cgt ctg acc aac act ttt tgc 1222

IPB000327A (8.0e-06) IC 1.61
A G L G O G M P S M V A L T T T L P 92
gcg ggg tta gga cag gga atg ccc tcc atg gtg gcg ctc acc acc acc ctg cct 1276
tT88I[4]

S F S D P P D S F Y P P O E M P G P 110
agt ttc tcg gac cct cca gat agt ttc tac ccc ccg cag gag atg ccg gga ccc 1330
gD99G[5]

R L G A D G T G M N R Q E S P H D E 128
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tT117M[6]

L K G S E L L N F T E T F Q A V A G 146
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cL134P[7] gT138A[8] gQ142R[9]

146

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IPB006712D (1.1e-05) IC 2.83
 A E A A C S D R E D S S A D S E N E 180
 gcg gag gcc gcg tgc agt gac cgg gag gac agc tcg gcc gac agc gag aac gaa 2842

S F S D G N T C A S A S Q K G K L K 198
 agc ttc tcc gac ggg aac acc tgc gcc tct gcg tcc cag aaa ggc aaa ctg aaa 2896

IPB000747C (4.8e-25) IC 3.09
 G G S Q D A L P P G G S A G K S R R 216
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 aA204=[13]

R R T A F T S E O L L E L E K E F H 234
 aga cgg aca gct ttc acg agc gag cag ctg ctg gaa ctc gag aag gag ttt cac 3004
 tA220V[14] aL229I[16]
 cA220=[15] gL229R[17]

C K K Y L S L T E R S O I A H A L K 252
 tgt aag aag tat ctg tcc ctc acc gag cgc tcg cag atc gcg cat gcg ctc aaa 3058
 tY238F[18] tQ246*[19]

IPB000747D (5.2e-12) IC 2.99
L S E V O V K I W F O N R R A K W K 270
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 tS254C[20]

R I K A G N V N N R S G E P V R N P 288
 cgg atc aaa gcc gga aat gtc aac aac aga tca ggc gag ccc gtc cgg aac ccc 3166
 cR271=[21] gG275=[22] aR280K[24]
 aN278K[23]

K I V V P I P V H V N R F A V R S Q 306
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cV292A[25]

H Q Q I E P G S R P *	317
cat caa cag atc gaa ccg ggc agc agg cca tga atgaactcctcaatataaatgactcctc	3281
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	t[29]
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 4217

acatatgtgggtatggaaaatgcaacattgcttgtt 317
 4253

Coding Sequence

M Q R P S G T G T A F S I D S L I G 18
 atg cag aga ccg agc ggt acg ggc acg gcg ttt tcc att gat tct ttg att ggc 54
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IPB003025A (7.0e-05) IC 2.82
 T P Q P R P G H L L Y T G Y P M F M 36
 act cca cag cca cga ccg ggc cac ctg ctc tac acg ggc tac ccg atg ttt atg 108

IPB003022B (6.8e-05) IC 3.39
P Y R P L M I P Q A L S H S S L P S 54
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IPB000327A (8.0e-06) IC 1.61
 F C A G L G O G M P S M V A L T T T 90
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 tT88I[4]

L P S F S D P P D S F Y P P Q E M P 108
 ctg cct agt ttc tcg gac cct cca gat agt ttc tac ccc ccg cag gag atg ccg 324
 gD99G[5]

G P R L G A D G T G M N R Q E S P H 126
 gga ccc ccg tta ggc gca gac ggg acg ggg atg aac cgg caa gag agc ccg cat 378
 tT117M[6]

D E L K G S E L L N F T E T F Q A V 144
 gac gaa ctc aaa ggc tct gaa ctc ctc aat ttc acg gaa act ttt caa gca gtc 432
 cL134P[7] gT138A[8] gQ142R[9]

A G | E T K L Y S S D D E K L D L K 161
 gca g | gc gaa acc aaa ctc tac agt tca gat gac gag aaa ctg gac ctg aaa 483
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IPB006712D (1.1e-05) IC 2.83
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E S F S D G N T C A S A S Q K G K L 197
 gaa agc ttc tcc gac ggg aac acc tgc gcc tct gcg tcc cag aaa ggc aaa ctg 591

IPB000747C (4.8e-25) IC 3.09
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 aA204=[13]

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 cA220=[15] gL229R[17]

H C K K Y L S L T E R S O I A H A L 251
 cac tgt aag aag tat ctg tcc ctc acc gag cgc tcg cag atc gcg cat gcg ctc 753
 tY238F[18] tQ246*[19]

IPB000747D (5.2e-12) IC 2.99
K L S E V O V K I W F O N R R A K W 269
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 tS254C[20]

K R I K A G N V N N R S G E P V R N 287
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 cR271=[21] gG275=[22] aR280K[24]
 aN278K[23]

P K I V V P I P V H V N R F A V R S 305
 ccc aaa atc gtg gtg ccc att cca gtg cac gtc aac agg ttc gcg gtg cgg agt 915
 cV292A[25]

Q H Q Q I E P G S R P * 317
 caa cat caa cag atc gaa ccg ggc agc agg cca tga 951
 aH307Q[26]