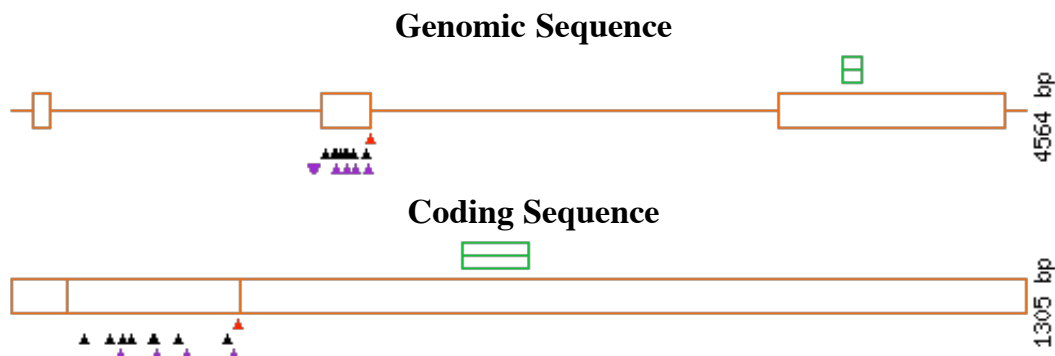


pard6gb

IPB003888, IPB004172, IPB012502, IPB002077, and IPB001940



For help interpreting these results, view the [PARSENP Introduction](#) page.

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		PSSM Difference	Description	Zygoty
				Gained in Variant	Lost from Reference			
1	G	T1351G	Intron	NspI			2789	Homo
2	G	T1361C	Intron	AflI , BbvI , CviRI , Fnu4HI , NspBII , TseI			4804	Homo
3	G C	T1416A	F32I	ApoI , TspEI			8415	Homo
4	G C	G1449A	E43K		MnlI , TaqI		6894	Homo
5	G C	A1463G	K47=	AluI , CviJI			4254	Homo
6	G C	C1464T	L48F	ApoI , TspDTI , TspEI			7552	Homo
7	G C	T1477A	I52N		BccI , FokI		8030	Homo
8	G C	T1504A	M61K	MboII			233	Homo
9	G C	A1506G	I62V	BccI , MmeI	DpnI , MboI		6814	Homo
10	G C	C1508T	I62=		DpnI , Hpy188I , MboI		8067	Homo
11	G C	T1537C	L72P		BplI , BseRI , MnlI		5233	Homo
12	G C	C1547T	N75=				8427	Homo
13	G C	A1599G	I93V	FauI	BinI , BsaBI , DpnI , MboI , XhoII		6478	Homo
14	G C	C1607T	I05=	Hpy188I , NspBII	BsaBI ,		7151	Homo

14	G C	C10071	199=	Hpy100I, NspDI	Hpy178III		7151	Homo
15	G C	C1614T	Q98*		BsmAI		2447	Homo

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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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IPB004172B (8.4e-17) IC 3.28																		
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<u>E</u>	<u>V</u>	<u>N</u>	<u>G</u>	<u>I</u>	E	V	T	G	K	T	L	D	Q	V	T	D	M	235
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Coding Sequence

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IPB004172B (8.4e-17) IC 3.28

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