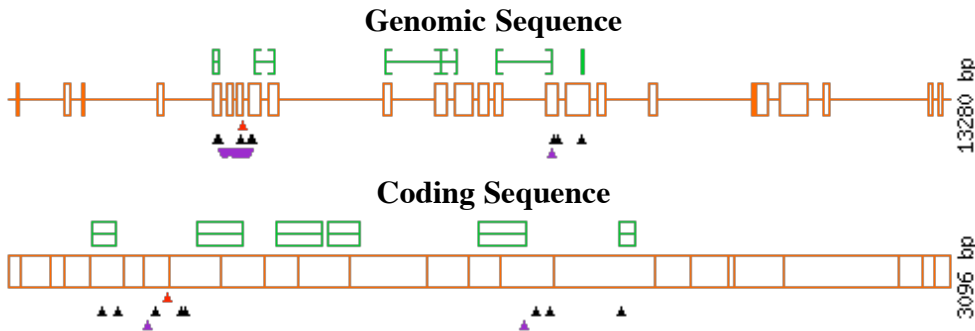


TDRD1

IPB008191, IPB002893, IPB003894, IPB010304, IPB008395, and IPB001782



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	T2923G	C102W	BsrI	Tsp4CI	34.5	0.00	1603	Homo
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4	G	T3008A	Intron					7712	Homo
5	G	T3061G	Intron		SspI			7214	Homo
6	G	T3079G	Intron		TspDTI			3278	Homo
7	G	T3079G	Intron		TspDTI			654	Homo
8	G	G3162T	Intron		MaeIII			5051	Homo
9	G	T3209C	Intron	FokI				4942	Homo
10	G C	T3236C	D153=	AccI , HgaI , HindII , MjaIV	CviRI , SfaNI			6835	Homo
11	G C	C3261T	R162C		FnuDII , Hpy178III , Hpy99I , NruI			7405	Homo
12	G C	G3297T	E174*		BseMII , Hpy188I			8685	Homo
13	G	T3321A	Intron	FalI , XmnI				7212	Homo
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16	G	T3326A	Intron	BsaBI , TspDTI	MboII			648	Homo
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26	G C	T7649C	Y565=	BsaXI				915	Homo
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29	G C	T8075G	I672S			23.4	0.00	5360	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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aat tgg tac aga gct gtt gtg ttg gag gta acc aca aag cat gca cat gtc att	10594
	833
Y S D Y G N M E T V P L S S I L P I	833
tac tct gat tat ggg aac atg gag act gtt cct ctc tcc agt atc ctt ccc atc	10648
	851
T K E L L Q H P F Q I V R C A L T G	851
acc aaa gaa ctt ctc cag cat cca ttc cag ata gtt aga tgt gcc ctg aca g gt	10702
	851
aaaattaccaactgatttcaactaaatctacaaattttaataagtaaaatccgctcatgtaggactatgga	10774
	851
ttgtttgtgaaggctcattttatgctaagatgtaatttcatttaaataagtaatttctcaaaatgaggatacaag	10846

	K E H F P V	857
tacatggatggaacatggttgttttaatacatttttgcacag	gt aaa gag cac ttc cct gta	10909
V W P T E V L E L F G I Q L S G G V		875
gtg tgg cct act gaa gtg ctg gaa ctc ttt ggc att cag ttg agt ggg ggt gtc		10963
L A S F Q G F D G T S N L L T L T Q		893
ctg gca tcc ttt cag ggc ttt gat gga acc tcc aac ctg tta acc ctt acc cag		11017
Q S G Q S D R D I N S I I L G A L Q		911
cag tca ggt caa tct gac aga gac att aat tcc att atc ctt gga gct ctg cag		11071
K G Q I K P S S K L P A N V N E E K		929
aaa gga cag atc aag cct agc tca aag ctg cct gcc aat gtc aat gaa gag aaa		11125
K D V E Q K Q T Q P I S S N K A V E		947
aag gat gtt gaa cag aag cag acg cag cct atc agc tca aat aag gcc gta gag		11179
Q T L S T N V E K P A L D D Q T L P		965
caa act cta tct aca aat gtt gag aaa cct gcc ctg gat gat caa acc ctg cct		11233
L S V S L K H E E P E		976
tta agt gtc agc ttg aag cac gag gaa cca g gtgaggaattaaacattgagcagaatttat		11294
		976
gttggcaggactgtgttgtaatgtatgggtttacaggacctgtgttaggaatttgctcaggaccttttagcaat		11366
		976
gaaattctggtgcacaggtgctgttccacctggtgttctcagctgtaactctaaggtgttattttaaaggag		11438
	N M S	979
ccttgtcatcatatccagagcagcagttgtcaaacatttattatgtctaatttcag	aa aac atg tcc	11505
K T K T A E E C T S T P D T V S S I		997
aag acg aag act gca gag gaa tgt act tca aca ccc gac act gtg agc agt att		11559
E S S H A		1002
gag agc agc cat g gtgggtattactgtttcaaattgtatcactcataactttttggtagggtgaaaa		11626
		1002
ggagcacatcctggaccgatataagtctttaagttagggctgggcaatataaaaaataatgtcaataacaa		11698
		1002
ttataagctctggatatttttactctatattgatctaagagccaatagcccctttcacgcagtgataccggt		11770
		1002
aaatatctggaatccggaacgactttaccggtatattcaaaaaagcgctgttcacacaggcgaggacg		11842

Q S C C C Q E L K Q K 1014
 caa tct tgc tgt tgt cag gag ctg aag caa aag gtttgaataataaattaaaaattgcatt 13051

1014
 ttttttttttaatcctcaaattcttttagtactgttttttttttaatcatcaattctttacccaccttt 13123

M D R I E E L V L L L V K Q V G S 1031
 cag atg gag cgt atc gag gag ttg gtt ctc ctg ctt gtg aag caa gtt gga tcc 13177

R 1032
 aga tagtaaccaagatcttcaatacccaaagatttaagggatagtcacccataaatgaaaatgatcatt 13248

1032
 tactcactctttgcttttttaagctattatga 13280

Coding Sequence

M R V H H I S P R G R V E V | K Q G 17
 atg cgc gtt cat cat att tca ccg cgt ggt cgt gtc gaa g | tg aaa caa ggg 51

N N E S S L R S A N D E T Q S P T E 35
 aat aat gaa tcc agc ctt cgc tca gcc aat gat gag acc caa tct ccc act gag 105

E T C H W T Q F T F S | G P K I D T 52
 gag acc tgc cac tgg acc cag ttc act ttc tcc | ggt ccc aag att gac acc 156

M R K D I S Q N | C G D V L S S P Q 69
 atg aga aag gat atc agt cag aat | tgt gga gat gtc ttg tct tct cca cag 207

T A V S M M G Q V V K L C N Y C S H 87
 aca gcg gtg tct atg atg ggc caa gta gta aag ttg tgc aat tac tgc agc cac 261

IPB002893 (3.2e-22) IC 0.87
 Q G | N L R C T R C K K T C Y C S V 104
 cag g | gc aac tta agg tgc act cgg tgt aaa aaa act tgc tac tgt tct gta 312
gC102W[1]

A C O T O D W I A H R H V C K P S I 122
 gct tgt cag act cag gat tgg atc gca cat cga cat gtt tgc aaa ccc agc att 366
 tP120S[2]
 tP120S[3]

P E V T S | E K P K E S K A V P Y A 139
 cca gaa gtc aca ag | t gaa aaa cct aag gag tca aaa gct gtg cca tat gca 417

N G L G G T Q A K | E I S V D A Q P 156
 aat gga ctt ggt ggc act caa gct aag | gag atc tct gtt gat gca cag cct 468
 cD153=[10]

K R I Y R R D L H K K V V S K G S E 174
 aag aga ata tat cgt cgc gac ttg cac aaa aaa gtg gtt tcc aaa ggt tct gag 522

I K | G T V I D L R N P G M F S I H 191
 ata aag | ggc aca gta att gac ctg aga aac cct ggg atg ttc tcc atc cac 573
 aI190N[22]
 aI190N[23]

IPB010304B (1.5e-07) IC 2.87

C Q C E E M I E S L K K I T Q Q L O 209
 tgt cag tgc gag gag atg ata gaa tcc ctg aag aag att acc caa cag ctt cag 627
 aC194S[24]
 aC194S[25]

K T Y C S S F A O E Y K P E V G E L 227
 aag acc tat tgc tct tca ttc gca caa gag tat aag cct gaa gtt ggt gag ctc 681

C A V K F S | N W Y R A E I O A V D 244
 tgt gct gtc aaa ttt tct | aac tgg tat cga gct gag att cag gca gtt gat 732

V A R K T A G V F Y I D F G N E E N 262
 gtg gcc cgc aag act gct ggt gtg ttt tac att gac ttt ggg aat gaa gag aat 786

V A L D H I R P L S E N I D A V P P 280
 gtt gca ctt gac cac ata cga ccc ctt tct gaa aac att gat gct gtg cca cca 840

IPB010304B (7.7e-09) IC 2.87

F | G I I Q Q L Q M N L R V H C S N 297
 ttt | ggt ata atc cag cag ttg caa atg aac ttg aga gtt cat tgt tca aac 891

T A A S D D F R P A P G T V C C S L 315
 act gct gcc agt gat gac ttc aga cct gca cca gga act gtc tgc tgc tct ctc 945

F S E | D N O W Y R A K V L A Y S S 332
 ttc tcc g | ag gac aac cag tgg tac aga gct aaa gtt ctg gca tat tcc tct 996

IPB008395B (1.3e-05) IC 2.92

E D R V C V G Y I D F G N S E E V E 350
 gag gat cgt gtg tgt gtt gga tac ata gac ttt gga aac tct gag gag gtt gag 1050

L N R L R P I S K E L L A L A T O A 368
 cta aat cgc tta agg ccg atc agc aag gag ctg ttg gct ttg gca aca caa gca 1104

I P C S L A G | I K S L T D T W S D 385
 atc ccc tgt tct cta gca g | gt ata aag tct cta aca gac acc tgg tct gat 1155

E A V L M L K H L V C N R F I R V E 403
 gag gca gtt ctg atg tta aaa cat ctg gtg tgc aac cgc ttc att cgg gtt gag 1209

I L G K K D G R A L V S M I D E S S 421
 att ctg ggt aaa aag gac ggt agg gct ctg gtg tcc atg atc gat gag tcc agt 1263

D P Q A S V T E L L V N M G F A A I 439
 gat cct cag gcc agt gtc aca gag ctg ttg gtt aac atg ggt ttt gct gct ata 1317

E S V E T K K N E P D P A T S T E I 457
 gaa agt gtg gaa acc aag aag aat gaa cca gat cca gct acc tcc act gaa att 1371

P P | L S Q P V V E K L E W T G A E 474
 ccc c | cc cta agt caa cct gtt gtt gag aaa ttg gag tgg act ggt gct gaa 1422

L P F D G Q K V E L V I S T L K S L 492
 ctt ccc ttt gat ggc cag aag gtg gag ctg gtg att agt aca ctg aag agc ctt 1476

D E F Y C Y N Y S K T D | E H T L T 509
 gat gaa ttc tac tgt tac aac tac agt aaa aca g | ac gaa cac acc ctg aca 1527

IPB010304B (1.0e-07) IC 2.87

E M S F E L M K H C E S E R A P F T 527
 gag atg tcc ttt gag ctt atg aaa cac tgt gaa tca gag aga gct ccc ttt acc 1581

P I V G E P C C A L F T G | D A R W 544
 cct att gta gga gaa cca tgt tgt gct ctc ttc aca g | ga gac gcc cgc tgg 1632

Y R A M V L E V C G E G K A R V C F 562
 tac aga gcc atg gtg tta gag gtg tgt gga gag ggt aaa gct aga gtt tgt ttt 1686

V D Y G N S C E V D A A H L K A I T 580
 gtg gat tat ggg aac tcc tgt gag gtg gat gca gca cac ctc aag gcc atc aca 1740
 cY565=[26] gI579S[27]

Q S L L K L P F Q A I R C W L A G | E 598
 cag agc ctg cta aaa ctg ccc ttc cag gca ata cgc tgc tgg ctt gca ggt | ga 1793
 gC593G[28]

G Q W K K E A M L R F Q A L C A G 615
 g ggc cag tgg aaa aaa gaa gct atg ctt agg ttt cag gct ctt tgt gcc ggc 1845

Q P L S G K V L S I T E K G Y G M E 633
 cag cct ttg agt ggc aaa gtg ctt tcc atc act gag aag ggt tat ggg atg gag 1899

L E S A G Q T V A S V L I S E H L A 651
 ctg gaa agt gct gga caa act gtt gct tct gtg ctc atc tct gag cac ctg gct 1953

K P Y G Q V R Q P P Q I Q P A K P A 669
 aaa cct tac gga cag gtc aga cag cct ccg caa ata cag cca gct aaa ccc gcc 2007

IPB001782A (6.9e-05) IC 2.45

S Q I E D L P S L K P I D Q N P S V 687
 agt cag att gaa gat ctg ccc tct ctt aaa ccc att gat cag aat cca tct gtt 2061
 gI672S[29]

E E P L K V S S K G A A T T P E D L 705
 gaa gag cct ttg aaa gtt agc agc aag gga gct gcc act acc cca gaa gat tta 2115

P V S S G C F P L N W K T L E L S	722
cca gtg tca a gt ggc tgt ttt cct tta aac tgg aag aca ttg gag ctg tct	2166
C S G T F Q P R V A A V I S P S L F	740
tgc agt ggc act ttc caa cca aga gtg gca gca gta atc agc cct agt ctc ttt	2220
Y I M N P G Q V N V E G L K A V M	757
tac att atg aat cct gga caa g tg aat gta gag ggt ctg aag gct gtt atg	2271
T D V A K Y C S K Q P V P N Q C H P	775
act gat gtt gca aag tac tgc agc aaa cag cca gtt ccc aat cag tgc cat cct	2325
L P G A S C C A Q F S G Q I P N T	792
tta cca gga gcc tcc tgt tgt gcg cag ttt tca ggt ca a ata cca aat aca	2376
T I K D K N W Y R A V V L E V T T	809
act atc aaa gac aaa aat tgg tac aga gct gtt gtg ttg gag gta acc aca	2427
K H A H V I Y S D Y G N M E T V P L	827
aag cat gca cat gtc att tac tct gat tat ggg aac atg gag act gtt cct ctc	2481
S S I L P I T K E L L Q H P F Q I V	845
tcc agt atc ctt ccc atc acc aaa gaa ctt ctc cag cat cca ttc cag ata gtt	2535
R C A L T G K E H F P V V W P T E	862
aga tgt gcc ctg aca g gt aaa gag cac ttc cct gta gtg tgg cct act gaa	2586
V L E L F G I Q L S G G V L A S F Q	880
gtg ctg gaa ctc ttt ggc att cag ttg agt ggg ggt gtc ctg gca tcc ttt cag	2640
G F D G T S N L L T L T Q Q S G Q S	898
ggc ttt gat gga acc tcc aac ctg tta acc ctt acc cag cag tca ggt caa tct	2694
D R D I N S I I L G A L Q K G Q I K	916
gac aga gac att aat tcc att atc ctt gga gct ctg cag aaa gga cag atc aag	2748
P S S K L P A N V N E E K K D V E Q	934
cct agc tca aag ctg cct gcc aat gtc aat gaa gag aaa aag gat gtt gaa cag	2802
K Q T Q P I S S N K A V E Q T L S T	952
aag cag acg cag cct atc agc tca aat aag gcc gta gag caa act cta tct aca	2856
N V E K P A L D D Q T L P L S V S L	970
aat gtt gag aaa cct gcc ctg gat gat caa acc ctg cct tta agt gtc agc ttg	2910
K H E E P E N M S K T K T A E E C	987
aag cac gag gaa cca g aa aac atg tcc aag acg aag act gca gag gaa tgt	2961
T S T P D T V S S I E S S H A A Q	1004

act tca aca ccc gac act gtg agc agt att gag agc agc cat g | ct gca caa 3012

S C C C Q E L K Q K | M D R I E E L 1021
tct tgc tgt tgt cag gag ctg aag caa aag | atg gac cgt atc gag gag ttg 3063

V L L L V K Q V G S R 1032
gtt ctc ctg ctt gtg aag caa gtt gga tcc aga 3096