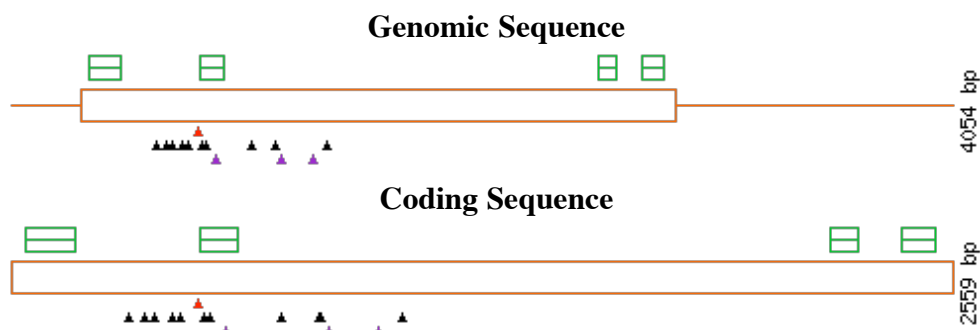


tsh1

IPB006176, IPB006180, IPB006794, IPB012568, and IPB012580



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	C620A	S107R	Hpy178III , XbaI	MwoI			6610	Homo
2	G C	T662A	D121E		BinI , DpnI , MboI , TstI , XhoII			7966	Homo
3	G C	C688A	T130K		BceFI , MaeIII , Tsp45I			4743	Homo
4	G C	C735A	Q146K					8457	Homo
5	G C	T760A	I154N		ApoI , TspEI			2759	Homo
6	G C	C804T	Q169*		BbvI , Fnu4HI , NspBII , TseI			1285	Homo
7	G C	T820A	M174K		MslI , NlaIII	-1.1	0.06	4285	Homo
8	G C	T836A	H179Q	TspEI		15.8	0.04	6872	Homo
9	G C	A881G	L194=					7926	Homo
10	G C	A1031T	K244N					7050	Homo
11	G C	G1137A	D280N	HinfI , TfiI	BinI , DpnI , MboI , MnlI , XhoII			5051	Homo
12	G C	A1138G	D280G		BinI , DpnI , MboI , XhoII			7967	Homo
13	G C	C1163A	G288=	MjaI	CviJI , HaeIII			6610	Homo
14	G C	A1298C	I333=		BspMI			1037b	Homo
15	G C	C1360T	T354I	DpnI , MboI	MnlI			1037	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

agacaaacgtgacacagagcagcaattctacaaaagccaccacattaaccaatgccaaacaatggaaccatca 0
72

atggtgctaacagtggggggtgttgcatatgactggcaccaagcagcacttgctaaaaccttacagcatacgc 0
144

cctaccacttaatgctgaaccaagtctcttcagcacagtgagctgtaccggcaaaacaataagctgtatg 0
216

ggcctgtgtttacaggtgccagcaaattcagatgcaaggactgtagtgagcctacgacacgcttgtaggtc 0
288

IPB006794F (1.9e-05) IC 3.81

M N E T G H Y R D D N K D K E 15
tcacggtagac atg aat gaa aca ggt cat tac cgt gat gat aac aag gac aag gag 344

E D R G K K W S K P R K R S L M E M 33
gag gac agg ggc aaa aaa tgg tct aag cca agg aag cga tcc tta atg gag atg 398

E G K E D A O K V L K C M Y C G H S 51
gag ggt aaa gaa gat gca cag aaa gtt ttg aaa tgc atg tat tgt ggc cac tgc 452

F E S L O D L S V H M I K T K H Y Q 69
ttt gaa tcc cta caa gac ttg agt gtc cac atg atc aaa act aaa cac tac cag 506

K V P L K E P M P A L A S K L V P S 87
aaa gtg cct cta aaa gaa cca atg cca gct ctt gcc tca aag ctg gtg ccc tcc 560

T K K R V F Q D L M S P C S P D S I 105
acc aaa aag cga gtg ttc cag gac ctg atg tct cca tgc tca cct gac tca atc 614

S S T P G I P L A E T A P T K D P K 123
tct agc acc cct ggc att cca tta gct gag act gca ccc acc aaa gat cca aaa 668
aS107R[1] aD121E[2]

I S N P Y V T A N N R Y G Y Q N G A 141
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aT130K[3]

S Y T W Q F E A R K A Q I L K C M E 159
agt tat acc tgg cag ttt gag gcc aga aaa gct caa att ctc aag tgt atg gaa 776
aQ146K[4] aI154N[5]

IPB006794B (6.8e-05) IC 2.91
C G S S H D T L Q Q L T A H M M V T 177
tgt ggg agt tcc cat gac acc ttg cag cag ttg aca gcc cac atg atg gtg acc 830
tQ169*[6] aM174K[7]

G H F L K V T N S A S K K G K Q L V 195
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aH179Q[8] gL194=[9]

F D P V V E E K I O S I P L P P T T 213
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T R L P A P A I K S Q P D S P I H P 231
aca cgc tta cca gct cct gct atc aag tcc caa cca gac tct cca ata cac ccc 992

S I M D D R K E L E E E K F E E P E 249
tcc att atg gat gat cgg aag gag ttg gaa gaa gag aaa ttt gag gaa cct gag 1046
tK244N[10]

E K K I K Q E K E D P S E R V E K S 267
gaa aag aaa atc aag caa gag aag gaa gac cct tct gag agg gtt gaa aag tct 1100

E K L S H Y K Y L R E E D L E E S P 285
gag aaa ctc agc cat tac aaa tat ctt cga gaa gag gat ctt gaa gag tct cct 1154
aD280N[11]
gD280G[12]

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A Y Q L Q G S V K S S I P A I Q S V 339
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agc	act	ctg	ata	cat	tct	cct	agc	agc	cca	tca	cca	cca	cca	aac	cat	aaa	agc	1424
N	V	L	A	M	E	E	L	V	E	K	V	T	G	K	I	P	S	393
aat	gtc	cta	gcc	atg	gag	gag	ttg	gtg	gag	aaa	gtg	aca	ggg	aaa	att	cca	tca	1478
K	K	D	R	D	E	K	L	T	E	R	N	S	K	H	L	T	A	411
aag	aaa	gac	agg	gat	gaa	aaa	tta	act	gaa	cgt	aat	tcc	aaa	cat	ctt	act	gct	1532
E	L	P	S	P	V	L	K	E	R	K	D	L	P	K	P	D	D	429
gaa	tta	ccc	tct	ccg	gtt	ctc	aaa	gag	aga	aaa	gac	ctg	cca	aaa	cca	gat	gat	1586
L	T	K	P	T	K	N	G	T	V	D	K	D	L	E	H	T	P	447
ctt	act	aag	cca	aca	aag	aat	ggc	act	gta	gat	aaa	gac	cta	gag	cac	act	cca	1640
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T	D	A	L	K	T	Q	V	S	N	G	C	G	N	L	G	I	I	483
acg	gat	gcc	ctc	aaa	acg	caa	gtc	agc	aat	ggt	tgc	ggt	aat	tta	gga	atc	atc	1748
T	D	H	S	P	E	Q	P	L	V	N	P	L	S	A	L	Q	S	501
act	gac	cac	tca	cca	gag	cag	cct	tta	gtt	aac	ccc	ctc	agt	gca	ttg	cag	tct	1802
I	M	N	T	H	L	G	K	A	S	K	T	V	S	P	L	L	D	519
atc	atg	aac	act	cat	ttg	ggt	aag	gct	tcc	aaa	aca	gtc	agt	cca	ctc	ctg	gac	1856
P	L	A	M	L	Y	K	I	S	N	N	M	M	E	K	P	M	Y	537
ccc	tta	gca	atg	ttg	tac	aag	att	agc	aac	aac	atg	atg	gaa	aaa	ccc	atg	tac	1910
N	P	A	Q	V	K	Q	V	E	P	I	N	R	Y	Y	E	N	D	555
aat	cca	gct	cag	gtc	aaa	caa	gtg	gag	ccc	atc	aac	aga	tat	tat	gaa	aat	gac	1964
D	D	Q	P	M	D	L	T	K	S	K	S	G	I	G	P	T	N	573
gac	gat	cag	ccc	atg	gac	ttg	aca	aag	tcc	aaa	agt	ggc	att	ggc	ccc	aca	aat	2018
N	C	T	S	T	I	I	S	N	S	S	I	T	N	S	T	R	P	591
aac	tgt	aca	tcc	acc	att	ata	agc	aac	agc	agc	atc	aca	aac	agc	acc	cga	ccc	2072
I	L	S	T	L	A	E	Q	V	S	S	P	L	R	E	N	A	L	609
atc	tta	tcc	acg	ttg	gct	gaa	caa	gtc	tca	tct	cct	ctt	cgg	gag	aat	gcc	cta	2126
M	D	I	S	D	M	V	K	N	L	T	G	R	L	T	P	K	S	627
atg	gac	atc	tct	gac	atg	gta	aag	aac	ctg	act	ggt	cgc	ttg	aca	cca	aag	tcg	2180
S	T	P	S	S	I	S	E	K	S	D	A	D	G	C	A	F	E	645
tca	aca	cct	tcc	tct	ata	tca	gaa	aag	tca	gat	gca	gat	gga	tgt	gct	ttt	gag	2234

D G L E D L S P I Q K R K G R Q S N 663
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W N P Q H L L I L Q A Q F A S S L R 681
tgg aac cct cag cat ctg ctg att ctt caa gct cag ttt gca tcc agc ctt cga 2342

E T P D G K Y I I T D L G P Q E R V 699
gaa acc cct gac gga aag tac ata att aca gac tta ggt cct cag gag cgt gta 2396

H I C K F T G L S M T T I S H W L A 717
cat att tgt aag ttt aca ggt ctc tct atg acc acc atc tcc cac tgg ttg gcg 2450

N V K Y Q L R R T G G T K F L K N I 735
aac gtc aag tac caa ctc aga cgg aca ggt gga acc aag ttc ctg aag aac ata 2504

IPB0067940 (1.2e-06) IC 4.32

D S G H P L F L C S D C A S O F R T 753
gac tcg ggc cat cca ctg ttc ctg tgt agt gat tgt gcc tcc cag ttt aga act 2558

P S T Y I N H L E S H L G F S L K D 771
ccc tcc aca tac att aac cac tta gag tcc cat ttg ggc ttt agt ttg aag gac 2612

L S K L S I D L I R D Q Q A V T K M 789
ctc tca aag tta tca ata gac ctc ata aga gac cag caa gca gtc aca aaa atg 2666

IPB006794M (1.4e-06) IC 4.32

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I F O C K L C N R T F V S K H A V K 825
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ctg cac ctc agc aaa aca cac ggg aag tca ccg gag gac cac ctg atc ttt gtt 2828

T E L E K L E K A * 853
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tatgacttgactgaaggagttgcatcgtgctgatgcatggcatacgagttggaaccaagcaatgcaaaaca	853	3970
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aaaaaaggaaaa	853	4054

Coding Sequence

	IPB006794F (1.9e-05) IC 3.81
M N E T G H Y R D D N K <u>D K E E D R</u>	18
atg aat gaa aca ggt cat tac cgt gat gat aac aag gac aag gag gag gac agg	54
<u>G K K W S K P R K R S L M E M E G K</u>	36
ggc aaa aaa tgg tct aag cca agg aag cga tcc tta atg gag atg gag ggt aaa	108
<u>E D A O K V L K C M Y C G H S F E S</u>	54

gaa gat gca cag aaa gtt ttg aaa tgc atg tat tgt ggc cac tcg ttt gaa tcc 162

L Q D L S V H M I K T K H Y Q K V P 72
cta caa gac ttg agt gtc cac atg atc aaa act aaa cac tac cag aaa gtg cct 216

L K E P M P A L A S K L V P S T K K 90
cta aaa gaa cca atg cca gct ctt gcc tca aag ctg gtg ccc tcc acc aaa aag 270

R V F Q D L M S P C S P D S I S S T 108
cga gtg ttc cag gac ctg atg tct cca tgc tca cct gac tca atc tct agc acc 324
aS107R[1]

P G I P L A E T A P T K D P K I S N 126
cct ggc att cca tta gct gag act gca ccc acc aaa gat cca aaa att tca aat 378
aD121E[2]

P Y V T A N N R Y G Y Q N G A S Y T 144
cca tac gtc acg gct aat aac cgt tat ggc tac caa aat ggt gca agt tat acc 432
aT130K[3]

W Q F E A R K A Q I L K C M E C G S 162
tgg cag ttt gag gcc aga aaa gct caa att ctc aag tgt atg gaa tgt ggg agt 486
aQ146K[4] aI154N[5]

IPB006794B (6.8e-05) IC 2.91
S H D T L Q Q L T A H M M V T G H F 180
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tQ169*[6] aM174K[7] aH179Q[8]

L K V T N S A S K K G K O L V F D P 198
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gL194=[9]

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P A P A I K S Q P D S P I H P S I M 234
cca gct cct gct atc aag tcc caa cca gac tct cca ata cac ccc tcc att atg 702

D D R K E L E E E K F E E P E E K K 252
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tK244N[10]

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S H Y K Y L R E E D L E E S P K G G 288
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aD280N[11] aG288=[13]
gD280G[12]

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Q T G T P T W G G Y P S I H A A Y Q	324
cag acc ggt aca ccc acc tgg ggt gga tat ccc agc att cat gct gcc tac cag	972
L Q G S V K S S I P A I Q S V Q I Q	342
ctc caa ggg tct gtg aaa tca tct ata cct gct atc cag agt gtc cag att caa	1026
cI333=[14]	
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tT354I[15]	
I H S P S S P S P P P N H K S N V L	378
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A M E E L V E K V T G K I P S K K D	396
gcc atg gag gag ttg gtg gag aaa gtg aca ggg aaa att cca tca aag aaa gac	1188
R D E K L T E R N S K H L T A E L P	414
agg gat gaa aaa tta act gaa cgt aat tcc aaa cat ctt act gct gaa tta ccc	1242
S P V L K E R K D L P K P D D L T K	432
tct ccg gtt ctc aaa gag aga aaa gac ctg cca aaa cca gat gat ctt act aag	1296
P T K N G T V D K D L E H T P V R E	450
cca aca aag aat ggc act gta gat aaa gac cta gag cac act cca gtt cga gaa	1350
G E Y K E S H A D N P I K N G T D A	468
gga gaa tac aag gaa agc cat gca gat aat ccc ata aaa aat gga acg gat gcc	1404
L K T Q V S N G C G N L G I I T D H	486
ctc aaa acg caa gtc agc aat ggt tgc ggt aat tta gga atc atc act gac cac	1458
S P E Q P L V N P L S A L Q S I M N	504
tca cca gag cag cct tta gtt aac ccc ctc agt gca ttg cag tct atc atg aac	1512
T H L G K A S K T V S P L L D P L A	522
act cat ttg ggt aag gct tcc aaa aca gtc agt cca ctc ctg gac ccc tta gca	1566
M L Y K I S N N M M E K P M Y N P A	540
atg ttg tac aag att agc aac aac atg atg gaa aaa ccc atg tac aat cca gct	1620
Q V K Q V E P I N R Y Y E N D D D Q	558
cag gtc aaa caa gtg gag ccc atc aac aga tat tat gaa aat gac gac gat cag	1674
P M D L T K S K S G I G P T N N C T	576
ccc atg gac ttg aca aag tcc aaa agt ggc att ggc ccc aca aat aac tgt aca	1728

S T I I S N S S I T N S T R P I L S 594
 tcc acc att ata agc aac agc agc atc aca aac agc acc cga ccc atc tta tcc 1782

T L A E Q V S S P L R E N A L M D I 612
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S D M V K N L T G R L T P K S S T P 630
 tct gac atg gta aag aac ctg act ggt cgc ttg aca cca aag tcg tca aca cct 1890

S S I S E K S D A D G C A F E D G L 648
 tcc tct ata tca gaa aag tca gat gca gat gga tgt gct ttt gag gat ggt ctg 1944

E D L S P I Q K R K G R Q S N W N P 666
 gag gat ctt tca cct att caa aag agg aaa ggc agg cag tca aac tgg aac cct 1998

Q H L L I L Q A Q F A S S L R E T P 684
 cag cat ctg ctg att ctt caa gct cag ttt gca tcc agc ctt cga gaa acc cct 2052

D G K Y I I T D L G P Q E R V H I C 702
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K F T G L S M T T I S H W L A N V K 720
 aag ttt aca ggt ctc tct atg acc acc atc tcc cac tgg ttg gcg aac gtc aag 2160

Y Q L R R T G G T K F L K N I D S G 738
 tac caa ctc aga cgg aca ggt gga acc aag ttc ctg aag aac ata gac tcg ggc 2214

IPB0067940 (1.2e-06) IC 4.32
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Y I N H L E S H L G F S L K D L S K 774
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L S I D L I R D Q Q A V T K M I T D 792
 tta tca ata gac ctc ata aga gac cag caa gca gtc aca aaa atg atc aca gac 2376

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C K L C N R T F V S K H A V K L H L 828
 tgc aaa ctg tgc aat agg act ttt gtc agc aag cac gca gtg aaa ctg cac ctc 2484

S K T H G K S P E D H L I F V T E L 846
 agc aaa aca cac ggg aag tca ccg gag gac cac ctg atc ttt gtt act gag ctg 2538

E K L E K A * 853
 gaa aag tta gaa aaa gcc taa 2559

