

spork

Genomic Sequence



Coding Sequence



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

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		Description	Zygosity
				Gained in Variant	Lost from Reference		
1	G C	T1653A	C65S			5200	Homo
2	G C	G1665A	V69I		AccI , AvaI , MjaIV , PspXI , SmlI , XhoI	595	Homo
3	G C	T1852G	V131G	BccI , BsiYI , MaeIII , Tsp45I	MjaIV	5442	Homo
4	G C	C1985T	D175=		AflIII , BspLU11I , NlaIII , NspI	6105	Homo
5	G C	T2052C	S198P		MnII	4383	Homo
6	G C	C2095T	T212I			6768	Homo
7	G C	T2096C	T212=	AsuI , AvaII		3716	Homo
8	G C	G2173A	S238N	BspMI	Cac8I , CviJI	7821	Homo
9	G C	C2250T	R264C	CviRI , SfaNI	HgaI , Hpy99I	2858	Homo
10	G C	C2260T	T267M		Esp3I , MaeII , RsaI	5081	Homo
11	G C	T2289C	S277P	MnII		3439	Homo
12	G C	T2300A	P280=		MnII	2433	Homo
13	G C	C2433T	H325Y		NlaIII	3025	Homo
14	G C	C2433T	H325Y		NlaIII	3766	Homo
15	G C	T2477A	D339E			8318	Homo
16	G C	C2492T	S344=			6836	Homo
17	G C	C2600T	S380=		NlaIV	4224	Homo

18	G C	T2603G	H381Q			119	Homo
19	G C	T2613G	S385A	HaeII , HhaI	AluI , CviJI , Eco57MI , GsuI , Hpy178III	1170	Homo
20	G C	T2663C	N401=	TspGWI	BsrDI	3844	Homo
21	G C	G2725T	R422L		ApoI , TaqI	557	Homo
22	G C	A2741T	A427=		CviRI , SfaNI	6909	Homo
23	G C	G2763A	A435T		CviJI	8029	Homo
24	G C	T2765C	A435=	AsuI , HaeIII		8597	Homo
25	G C	G2790T	G444W	BstXI	AlwNI , BsiYI , PfiMI	8029	Homo
26	G C	T2806C	V449A	CviRI , NspBII , PstI		7367	Homo
27	G C	T2829C	S457P			5961	Homo
28	G C	C2869T	T470I	TspEI	BseMII , DdeI	1962	Homo
29	G C	C2878T	T473I			5035	Homo
30	G C	C2878T	T473I			7169	Homo
31	G C	G2885A	S475=	Bce83I	AvaI , MnII , PspXI , TaqI , XhoI	2646	Homo
32	G C	T2891A	D477E		FokI	5349	Homo
33	G C	T2891A	D477E		FokI	6820	Homo
34	G C	T2916C	S486P	AsuI , CviJI , HaeIII		3121	Homo
35	G C	T2918C	S486=	AsuI , AvaII , BsrI , BstXI , NlaIV	MaeI	4229	Homo
36	G C	T2938A	V493D	AccI , MjaIV		3711	Homo
37	G C	C2976T	Q506*		BsaXI , TstI	308	Homo
38	G C	C2979T	P507S		MnII	6526	Homo
39	G C	T2997C	Y513H	AlfI	RsaI	6786	Homo
40	G C	C3019T	T520M	NlaIII	TspGWI	3554	Homo
41	G C	T3049C	V530A	Cac8I , HgiCI , NlaIV		3659	Homo
42	G C	T3065G	N535K	FokI , SecI , StyI		4482	Homo
43	G C	C3084T	R542C	CviRI	FspAI , HhaI , MstI , SfaNI	3047	Homo
44	G C	C3084T	R542C	CviRI	FspAI , HhaI , MstI , SfaNI	8692	Homo
45	G C	T3097C	L546P	CauII , Eco31I , HpaII , ScrFI , SecI	AlwNI , BfiI , BsrI	7913	Homo
46	G C	G3100A	G547E	BseRI , Eco57MI , GsuI , MnII	BfiI	6464	Homo

47	G C	C3118T	S553F	MboII	BseRI, MnlI	4518	Homo
48	G	T3191C	Intron			7862	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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T G S D E D K Q      37
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Coding Sequence

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Q | A Y S Q D A Y L K G H D A Y S G 53
cag | gcc tat tct caa gat gcc tac ctt aag ggt cat gat gca tac agt gga 159

N A R H I P E P P P I C Y P R V D C 71
aat gct cgc cat atc cca gag cca ccc cct ata tgt tat cct cga gta gac tgc 213
aC65S[1] aV69I[2]

K P P G M A Q A T E T S A P G V V S 89
aag ccc ccg ggg atg gcc cag gcc act gag aca tca gcc ccg ggg gtt gta tct 267

S D L G Y R V E I P V P P S P P P P 107
tcc gat cta gga tac cgt gtg gag ata ccg gta cct ccc tca cct cca cca ccc 321

I P K T Q T A V C V C N E S V R T V 125
att cca aaa aca cag acc gca gtg tgt gtg tgc aat gaa agt gta cgg aca gtg 375

V V P P D V H M G L M V Q G H R G D 143
gtg gta cct cct gat gtt cac atg ggc ctt atg gtc caa ggt cac aga gga gac 429
gV131G[3]

Y G L V G P D P M L I R A R P G T V 161
tat ggt cta gtt ggt cca gat cca atg ctt atc cga gcc agg cct gga act gtg 483

S G G R P P Y L H P R K A D M F P S 179
 tct ggt ggt cgt ccg cca tat cta cac ccg cgc aaa gct gac atg ttc ccg tca 537
 tD175=[4]

G Y H G D P Y A I P P T H Y V P A S 197
 ggt tac cat ggt gat cct tat gcc att cca ccc aca cac tat gtg cct gct tcc 591

S I T S P A T H Q N I D W R T Y Q T 215
 tca atc acc tcc cct gct act cac cag aac att gac tgg cgg act tac cag aca 645
 cS198P[5] tT212I[6]
 cT212=[7]

Y R E Y I D N K G I H A Y S R T V Q 233
 tac cgg gaa tat att gac aac aaa ggt att cat gct tac agt cga act gtt caa 699

E R L D S L R A A S Q S T H G G P H 251
 gaa cgt tta gac agc ctg cga gct gca tct caa agt aca cat ggt ggc cct cac 753
 aS238N[8]

C G P Q P G W G N K L R R R S T S H 269
 tgt gga ccc caa cct ggc tgg ggc aat aag tta cga cgc aga agt acg tct cat 807
 tR264C[9] tT267M[10]

D R A Y Q G P S M L P P R S A S Q D 287
 gat cgg gcc tac cag ggc cct tct atg ctt cct cca cgc agt gct tcg cag gat 861
 cS277P[11] aP280=[12]

R M S G A E R A A H A R D W P P R S 305
 agg atg agt ggg gca gag aga gca gct cac gcc agg gac tgg cct cct cgt agt 915

V S S D G L I R K P R A H S S D Y V 323
 gtg tcc tct gat ggt ctc ata cgg aag ccc cgt gct cat tca tca gac tat gtg 969

E H G E L V S A A P W A A P V D R Q 341
 gaa cat ggt gaa cta gtt tct gct gca cca tgg gca gca cct gtg gat agg cag 1023
 tH325Y[13] aD339E[15]
 tH325Y[14]

L Y S R V D Q R S R P S R Q S L P P 359
 ctt tat agc aga gta gac cag agg agt cgt ccc agt aga cag tct ctc cca cca 1077
 tS344=[16]

R A V L Y R P P T G Y G M S V R G N 377
 agg gcg gtg ctt tac cgc cca cca aca ggg tat ggt atg agc gtc agg ggt aat 1131

A G S H K H S S R T D I P P T A G F 395
gct ggc tcc cat aag cat agc tcc aga acg gat atc cca cct act gct ggt ttt 1185
tS380=[17] gS385A[19]
gH381Q[18]

P E R P R N G I N Q A K E P P S K D 413
cca gag cga cct cgc aat gga ata aac cag gcc aaa gaa cct cct tcc aaa gac 1239
cN401=[20]

Q S G T V V G N R I L N S A S N Q S 431
caa agt gga act gta gtt gga aat cga att tta aat tct gca tca aac caa tca 1293
tR422L[21] tA427=[22]

R T R A E T M Q S P E S G K D I S V 449
aga act agg gct gaa acc atg caa agc cca gaa tct ggg aaa gat att tct gta 1347
aA435T[23] tG444W[25] cV449A[26]
cA435=[24]

G Y R S A S Y S A P P L Q R P K G G 467
gga tat agg tcg gca tct tac tct gct cca cct ctt caa agg ccc aag ggt ggt 1401
cS457P[27]

A S T Q R T S S R D V K G L P V N G 485
gca tca act cag agg aca agc tcg agg gat gtc aag ggc tta cca gta aat ggg 1455
tT470I[28] tT473I[29] aD477E[32]
tT473I[30] aD477E[33]
aS475=[31]

S S P V E G V V L R E K P P T G K G 503
tct agt cct gtg gag ggt gta gtc ctc aga gag aaa ccg cca aca ggg aag ggg 1509
cS486P[34] aV493D[36]
cS486=[35]

T P Q P L R H P S Y I L A V N D T D 521
acc cca caa cct ctc cgc cat ccc tcg tac atc ctt gca gta aat gac acg gat 1563
tQ506*[37] cY513H[39] tT520M[40]
tP507S[38]

G S E P A G G G V C W L P N D A R R 539
ggg tct gag cca gca ggg ggc ggt gtc tgc tgg tta ccc aat gat gct cgc cgg 1617
cV530A[41] gN535K[42]

E M R M Q R L G E R L D S S F C S S 557
gag atg cgc atg cag aga ctg ggg gag cgg ctt gac tcc tcc ttc tgt tcc agt 1671
tR542C[43] cL546P[45] tS553F[47]
tR542C[44] aG547E[46]

N	L	D	E	S	L	D	S	I	P	F	I	D		E	P	A	S	574	
aat	ctg	gac	gaa	tca	ctt	gac	tcc	att	ccc	ttc	atc	g		at	gaa	cca	gcc	agc	1722
P	S	V	D	H	D	G	S	H	I	P	A	S	V	V	I	S	G	592	
cct	agt	gta	gat	cat	gat	ggc	agt	cat	att	cct	gca	tca	gtt	gtg	att	tct	gga	1776	
A	Q	A	A	L	S	D	S	P	S	P	S	T	P	S	P	L	M	610	
gct	caa	gct	gca	ctt	tct	gat	agc	cca	agc	cct	tcc	acg	cct	agt	ccc	ctc	atg	1830	
R	R	Q	L	S	H	D	*											618	
cgc	cga	caa	ctg	tcc	cat	gac	taa											1854	