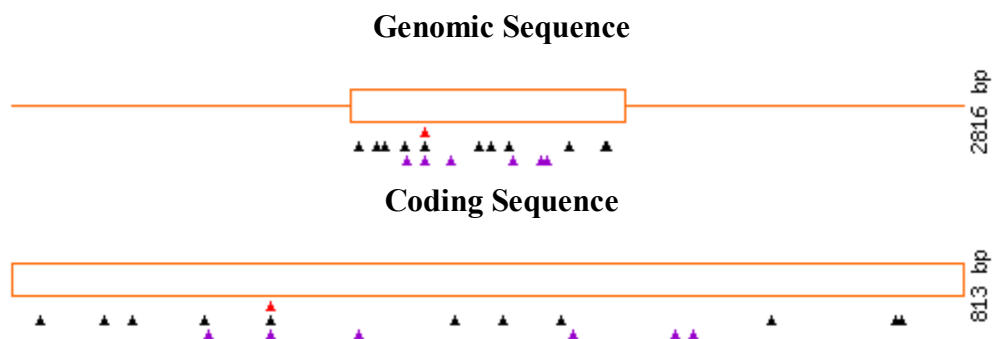


kctd12.2



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

#	View On Sequence	Nucleotide Change	Effect	Restriction Enzyme Differences from REBASE		Description	Zygoty
				Gained in Variant	Lost from Reference		
1	G C	T1025C	S9P		MboII	8082fh	Homo
2	G C	G1079A	V27I		MaeII , MaeIII	6318fh	Homo
3	G C	T1103G	S35A	BcefI , Cac8I	TspGWI	5247fh	Homo
4	G C	C1164T	T55I	TaqI		5824fh	Homo
5	G C	C1168T	D56=			5325fh	Homo
6	G C	T1221A	L74*			2240fh	Homo
7	G C	G1222A	L74=			2469fh	Homo
8	G C	G1222T	L74F			3712fh	Homo
9	G C	A1297G	E99=	MnII	SspI	6172fh	Homo
10	G C	A1379C	S127R	Cac8I , FnuDII , HhaI		2574fh	Homo
11	G C	C1419T	T140I	DpnI , MboI	BspMI	2587fh	Homo
12	G C	T1470C	I157T		TspDTI	5809fh	Homo
13	G C	G1480T	G160=	MaeIII	RsaI	6422fh	Homo
14	G C	G1567A	T189=		BsmAI , Esp3I , MaeII	5853fh	Homo
15	G C	A1582G	E194=	MnII		7980fh	Homo
16	G C	A1650G	Y217C	MaeIII , MslI		2193fh	Homo
17	G C	C1756A	N252K		MaeIII	5923fh	Homo
18	G C	C1760A	P254T		BsiYI	5863fh	Homo

[Download Tab-Separated table](#)

No [protein homology model](#) was submitted. You may add one using any or all of the fields below.

Blocks Families: **Blocks File:** **Sequence Alignment:** **-OR-**

Genomic Sequence

aggaaaaaaaaataaacaggtcaactatatatatatatatatataacgtttacttaattattaattataa	0 72
ccattaaccattattgttacagtaaaacctaataaaatataaaacaaaataaagcttgatgaataaccagat	0 144
taaaagtgagtagtcttttcaaaggaatgcaataaatataggctataaatcaaaagctgagtatatttaca	0 216
atacagcaccatgggatattgtaatggaaaggagcgccctctactaggtaggctgtaagcgtataaaaact	0 288
cttaatcttctgtccactagatgtcactacatgcactgctgctgctgcagcagcctgttcacactctcttgg	0 360
atgttttgcataaaaactaataataaaccaaagttctatggtttggttaataatTTTTTTTgaaagttaaaaa	0 432
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aaggcaaataaaacactcaagttgtgattttttcacaaatgaagcaataattaagtagattttgtctacaac	0 720
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tagtaaattcataatcacaacattctatgatgccccattcggtaagcatttagatttttcgcaggggtgga	0 864
gtaaagagttaatacagccgtcagattccccctcctacgtaactctgttttagcctacataaacaagcagaa	0 936
atatttctttccactcttcttcagttctgtgattgcactggaggtctcgcgcagctgtgcaaag atg gat	M D 2 1006
K T R A D A S S P R F S E I I E L N aag act cgc gcg gac gct tct tca ccg cga ttc tcc gaa atc att gag ctc aat	20 1060
	cS9P[1]
V G G Q V Y V T R H S T L L S V P N gtc gga ggg caa gtt tac gtt acg cgc cac tca act ttg ctc tcc vtg ccc aat	38 1114
	aV27I[2] gS35A[3]
S L L W T M F S Q K K P A E L T T D tct tta ctt tgg acc atg ttc agt cag aag aaa ccc gcg gaa ctt act acc gac	56 1168
	tT55I[4] tD56=[5]
S K G R F F L D R D G F L F R Y I L agc aaa gga cgc ttc ttt ttg gac agg gac ggc ttt ttg ttc cgt tat att ttg	74 1222
	aL74*[6] aL74=[7] tL74F[8]
D Y L R D Q T L V L P D Y F K E K A gat tac ttg cgg gac cag act ctg gtt ttg cct gat tac ttc aaa gag aaa gcg	92 1276
S L L K E A E Y F Q L Q D L A K R L agc ctc ctc aaa gag gca gaa tat ttc caa ctt caa gac ctg gca aag cgc ctg	110 1330
	gE99=[9]
K P A V S K E N S I S E E V C Q S D aaa cct gcg gtc agt aag gag aac tcc atc agc gag gag gtt tgc cag agc gac	128 1384
	cS127R[10]
P E E A A L A G T S M T C T G P R S ccg gag gag gct gcg ctc gcc gga acc agc atg acc tgc acc ggc ccc cgc tca	146 1438
	tT140I[11]
P S L D A R K T G F I T I G Y R G S ccg tct ttg gac gcg agg aaa acc ggc ttc ata acc atc ggg tac agg ggc tcc	164 1492
	cI157T[12] tG160=[13]
Y T I G R D L Q Q D A K F R R V A R tac act ata gga cga gac ctt caa cag gac gcc aaa ttc cga cgg gtg gcg aga	182 1546
I T V C G K T S L A K E V F G E T L atc act gtg tgc ggc aaa acg tct ctc gcc aaa gaa gtt ttc ggg gag acg ctg	200 1600

aT189=[14]

gE194=[15]

N E S R D P D R P P E R Y T S R Y Y 218
 aac gag agc aga gac ccc gac aga ccc cca gag aga tac aca tct cgg tat tac 1654
 gY217C[16]

L K Y N F L E Q A F D R L A E V G F 236
 ctg aag tat aat ttc ctg gag caa gcc ttt gac agg ctg gca gag gtg ggc ttc 1708

H M V A C S S T G T C A Y A S N D P 254
 cac atg gtt gcg tgc agc tct acg ggc acc tgt gcg tac gcg agt aac gac ccc 1762
 aN252K[17]
 aP254T[18]

N E D K I W T S Y T E Y V F C R E 271
 aac gag gac aaa atc tgg acg agt tac acc gag tat gtt ttt tgt agg gag tgaa 1817

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 1889

gcgcaacgaacgtgtagttgtgtgccacaatgtcaatatgtcaagacgaattagggaccatcaatcgctgcg 271
 1961

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 2033

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 2321

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 2393

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 2609

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2681

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2753

tggaataactaggagacagaacaggaactaggcctgtgtctgccagcagtcctgtgactaaaca 271
2816

Coding Sequence

M D K T R A D A S S P R F S E I I E 18
atg gat aag act cgc gcg gac gct tct tca ccg cga ttc tcc gaa atc att gag 54
cS9P[1]

L N V G G Q V Y V T R H S T L L S V 36
ctc aat gtc gga ggg caa gtt tac gtt acg cgc cac tca act ttg ctc tcc gtg 108
aV27I[2] gS35A[3]

P N S L L W T M F S Q K K P A E L T 54
ccc aat tct tta ctt tgg acc atg ttc agt cag aag aaa ccc gcg gaa ctt act 162

T D S K G R F F L D R D G F L F R Y 72
acc gac agc aaa gga cgc ttc ttt ttg gac agg gac ggc ttt ttg ttc cgt tat 216
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tL74F[8]

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aaa gcg agc ctc ctc aaa gag gca gaa tat ttc caa ctt caa gac ctg gca aag 324
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cgc ctg aaa cct gcg gtc agt aag gag aac tcc atc agc gag gag gtt tgc cag 378

S D P E E A A L A G T S M T C T G P 144
agc gac ccg gag gag gct gcg ctc gcc gga acc agc atg acc tgc acc ggc ccc 432
cS127R[10] tT140I[11]

R S P S L D A R K T G F I T I G Y R 162
cgc tca ccg tct ttg gac gcg agg aaa acc ggc ttc ata acc atc ggg tac agg 486
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ggc tcc tac act ata gga cga gac ctt caa cag gac gcc aaa ttc cga cgg gtg 540

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gcg	aga	atc	act	gtg	tgc	ggc	aaa	acg	tct	ctc	gcc	aaa	gaa	gtt	ttc	ggg	gag	594
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T	L	N	E	S	R	D	P	D	R	P	P	E	R	Y	T	S	R	216
acg	ctg	aac	gag	agc	aga	gac	ccc	gac	aga	ccc	cca	gag	aga	tac	aca	tct	cgg	648
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ggc	ttc	cac	atg	gtt	gcg	tgc	agc	tct	acg	ggc	acc	tgt	gcg	tac	gcg	agt	aac	756
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D	P	N	E	D	K	I	W	T	S	Y	T	E	Y	V	F	C	R	270
gac	ccc	aac	gag	gac	aaa	atc	tgg	acg	agt	tac	acc	gag	tat	gtt	ttt	tgt	agg	810
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E																		271
gag																		813