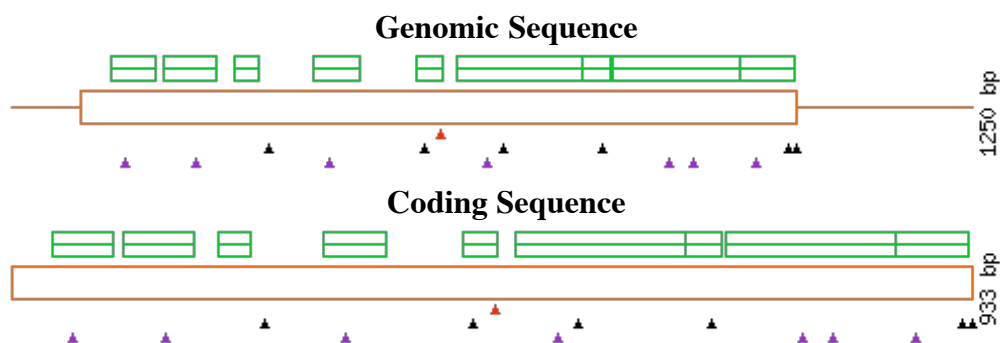


# ztl8788

## User BLOCKs

Variant C413C is not a proper nucleotide change.



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	<a href="#">G C</a>	G149T	P20=		<a href="#">BceI</a> , <a href="#">MaeIII</a>			zfish none	Homo
2	<a href="#">G C</a>	C239T	N50=					zfish none	Hetero
3	<a href="#">G C</a>	C336G	P83A	<a href="#">NlaIII</a>	<a href="#">BccI</a> , <a href="#">FokI</a> , <a href="#">Hpy188I</a>		1.00	zfish none	Hetero
4	<a href="#">G C</a>	C336G	P83A	<a href="#">NlaIII</a>	<a href="#">BccI</a> , <a href="#">FokI</a> , <a href="#">Hpy188I</a>		1.00	zfish none	Hetero
5	<a href="#">G C</a>	C413T	I108=		<a href="#">BccI</a> , <a href="#">NspBII</a>			zfish none	Homo
6	<a href="#">G C</a>	T538A	I150K			4.7	0.88	zfish none	Hetero
7	<a href="#">G C</a>	A558T	<b>K157*</b>		<a href="#">MseI</a>			zfish none	Homo
8	<a href="#">G C</a>	G620A	G177=		<a href="#">FauI</a>			zfish none	Homo
9	<a href="#">G C</a>	T639A	C184S		<a href="#">ApaBI</a> , <a href="#">BsmI</a> , <a href="#">CviRI</a>	27.2	0.00	zfish none	Hetero
10	<a href="#">G C</a>	A769G	E227G	<a href="#">BccI</a> , <a href="#">FinI</a> , <a href="#">XcmI</a>	<a href="#">MnII</a>	14.1	0.01	zfish none	Hetero
11	<a href="#">G C</a>	A857T	S256=					zfish none	Hetero
12	<a href="#">G C</a>	A887G	L266=	<a href="#">Cac8I</a>	<a href="#">BspMI</a>			zfish none	Hetero
13	<a href="#">G C</a>	G968A	Q293=		<a href="#">BfiI</a> , <a href="#">BsrI</a>			zfish none	Hetero
14	<a href="#">G C</a>	G968A	Q293=		<a href="#">BfiI</a> , <a href="#">BsrI</a>			zfish none	Hetero
15	<a href="#">G C</a>	A1012T	Q308L	<a href="#">MaeI</a>		7.2	0.00	zfish none	Hetero
16	<a href="#">G C</a>	A1022C	*311C		<a href="#">BccI</a> , <a href="#">BspHI</a> , <a href="#">Hpy178III</a>			zfish none	Hetero



D H A A P T P V V D P Y T T G N S H 139  
gat cac gca gct cct act cct gtt gtg gat ccg tat acg acc ggg aat tcc cac 506

User BLOCK 5 (1.4e-08) IC 2.26

G R T L A A E Q P K I L S S K N I K 157  
ggc agg act cta gct gcg gag cag ccc aag ata ctg agc tcc aag aac att aag 560  
aI150K[6] tK157\*[7]

User BLOCK 6 (3.1e-57) IC 3.69

T L A A L P E E K K K H V L L C E K 175  
aca ctg gca gcc ttg cct gaa gag aag aaa aag cat gtg ctg ctg tgc gag aaa 614

C G K C R C T E C T L P R T L P S C 193  
tgc ggg aaa tgc cga tgc acc gaa tgc acg ctg ccc cga acc ttg cct tct tgt 668  
aG177=[8] aC184S[9]

W V C N O E C L C S A O N L V D S V 211  
tgg gtt tgc aac caa gag tgt ctg tgc tcc gca caa aac cta gtg gac tcg gtg 722

User BLOCK 7 (4.1e-14) IC 3.41

T C M C L V K G V F Y H C T D E D E 229  
act tgc atg tgt cta gtc aag ggg gtt ttc tac cac tgc act gat gag gac gag 776  
gE227G[10]

User BLOCK 8 (1.2e-57) IC 3.78

E G S C A D K P C S C S H S N C C A 247  
gaa ggc tcc tgc gcg gac aaa cca tgc tcc tgt tcg cac tcg aac tgt tgc gca 830

R W S F M A A V S L V L P C L V C Y 265  
cgc tgg tcc ttc atg gca gcc gtc tca ttg gtt ttg ccc tgc ctg gtg tgc tat 884  
tS256=[11]

L P A T G C A K L S O K C Y D G V S 283  
tta cct gcc act ggc tgt gcc aag ctt tcg cag aaa tgc tac gac ggc gtc agc 938  
gL266=[12]

User BLOCK 9 (1.3e-22) IC 3.32

R P G C R C K S T O S C K V A E I K 301  
cgc cca gga tgc cga tgc aaa agc acc cag tcc tgc aag gtg gca gaa atc aag 992  
aQ293=[13]  
aQ293=[14]

A C O P E K O A S \* 311  
gcc tgt cag cca gaa aaa caa gcc tca tga tggtttgcaggaccttccctcccaaatcatgg 1054  
tQ308L[15] c\*311C[16]

tacttaaggtgttgaaatcagtagcaatgtttgactgaagggcacaaatgatcatttcacgtactgcaaaga 311  
1126

agttcttctcctcagatggttctacgtattagcctctactaaaggaccttgcaaacacagaatgctgcatt 311  
1198

tccaaaagatctctgtttgttttctctttgagaaaccaccattcagaagcg 311  
1250



D K P C S C S H S N C C A R W S F M 252  
gac aaa cca tgc tcc tgt tcg cac tcg aac tgt tgc gca cgc tgg tcc ttc atg 756

A A V S L V L P C L V C Y L P A T G 270  
gca gcc gtc tca ttg gtt ttg ccc tgc ctg gtg tgc tat tta cct gcc act ggc 810  
tS256=[11] gL266=[12]

C A K L S Q K C Y D G V S R P G C R 288  
tgt gcc aag ctt tcg cag aaa tgc tac gac ggc gtc agc cgc cca gga tgc cga 864  
User BLOCK 9 (1.3e-22) IC 3.32

C K S T O S C K V A E I K A C O P E 306  
tgc aaa agc acc cag tcc tgc aag gtg gca gaa atc aag gcc tgt cag cca gaa 918  
aQ293=[13]  
aQ293=[14]

K O A S \* 311  
aaa caa gcc tca tga 933  
tQ308L[15] c\*311C[16]