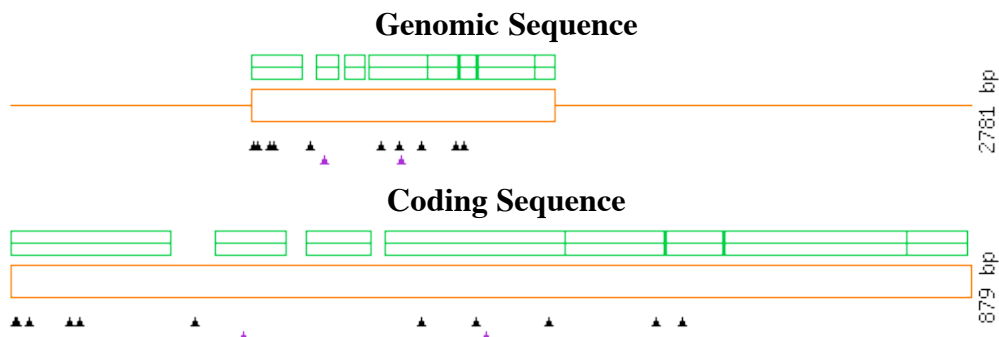


atoh1a

IPB003023, IPB012502, IPB001092, IPB003888, IPB007696, IPB003141, IPB009448, IPB011591, IPB003024, IPB006127, and User BLOCKs



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	A702T	D2V	MmeI	BccI , FokI	9.0	0.00	3083	Homo
2	G C	T703A	D2E		BccI , FokI	7.3	0.00	892	Homo
3	G C	C714T	T6M	NlaIII	BseSI , HgiAI , SduI , TspGWI	5.7	0.00	7912	Homo
4	G C	T752C	S19P	BsiYI , FokI , Hpy188I , SfaNI	BsmI , TaqI	7.5	0.15	2676	Homo
5	G C	G760T	L21F			1.0	0.18	3053	Homo
6	G C	G760T	L21F			1.0	0.18	3604	Homo
7	G C	G760T	L21F			1.0	0.18	3933	Homo
8	G C	G760T	L21F			1.0	0.18	4038	Homo
9	G C	G866A	A57T		MwoI		0.26	3047	Homo
10	G C	G910A	V71=	BciVI				8623	Homo
11	G C	C1073T	R126W	EcoNI , EcoRII , PfiMI	AvaI , CauII , HpaII , SmaI	24.2	0.00	6263	Homo
12	G C	A1124C	S143R	Bcefi	BtsI , MstI , TspRI	4.7	0.19	1374	Homo

13	G C	C1132T	I145=		BseYI , FokI			6839	Homo
14	G C	A1190G	I165V	AccI , EcoRII , MjaIV , ScrFI , SceI	BglII , BsaBI , DpnI , MboI , XhoII	8.3	0.13	6270	Homo
15	G C	C1288A	D197E		AseI , AvaII , RsrII , TaqII	0.4	1.00	6222	Homo
16	G C	G1311A	G205D	AatII , BetI , MaeII , PshAI	CauII , HgaI , ScrFI	16.2	0.04	3080	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

```

taatagcattgTTTTTaaagctatcctctaaaagattgTTTgggtaactaaaagttcttgtgtgctatt      0
                                                                    72

TTTTGcaaaccaactctcttcaaactTTaattTTaagtgtgaagacggctgaatacagttgcctgtgtttac    0
                                                                    144

gagcatttaatgaagaaaagtaccttcaaagcacgatgttcttagataaaagatTTTTgataacctctttat    0
                                                                    216

tccatttagaccgccgaggtaagTTTTgTTTTcctgtcgcgtTTaatagactatctaatttccaaaacatg    0
                                                                    288

gcgtgaggaggccccgccacataactTTattcagtcctccaactTTTTgagtacgtcctatgggacgaccatt    0
                                                                    360
    
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cac gga ttg aac cac gcg ttc gac gag ctg cgc agt gtc atc cca gcc ttt gac 1144
 cS143R[12]
 tI145=[13]

N D K K L S K Y E T L O M A O I Y I 167
 aac gac aag aaa ctc tcc aag tac gaa acc ctg cag atg gcc cag atc tac atc 1198
 gI165V[14]

User BLOCK 5 (4.0e-21) IC 2.03

N A L S D L L Q G P G A K A D P P N 185
 aac gcc ctg tcc gac tta cta cag ggc ccc ggt gct aaa gcc gac ccg cca aac 1252

User BLOCK 6 (1.1e-14) IC 2.49

C D L L H A N V L E T D R S P R G S 203
 tgc gac ctg ctg cat gcc aac gtg tta gaa acg gac cga tct ccc aga gga tca 1306
 aD197E[15]

User BLOCK 7 (5.7e-55) IC 3.50

P G V C R R G T G V G Y P Y Q Y E D 221
 ccg ggc gtc tgt cgg aga ggc acg ggc gtg ggt tac ccg tac cag tac gag gac 1360
 aG205D[16]

G T F N S F M E O D L O S P S G T S 239
 gga aca ttc aac tct ttc atg gag caa gac ctc cag tcg ccc tct gga acg agc 1414

K S G S E A S K D S P R S N R S D G 257
 aag tct ggt tcg gag gcc agt aaa gac tcg cct cgg tcg aac cgg agt gat gga 1468

User BLOCK 8 (2.4e-23) IC 4.32

E F S P H S H F S D S D E T H L E L 275
 gag ttc tcg cct cac tcg cac ttc agt gac tca gac gaa acg cac ttg gag ctg 1522

O S E D E L S E L K L A K R R A F * 293
 cag agt gaa gac gag ctg tcg gaa ctg aaa ctg gcc aag cgc cgc gct ttt taa g 1577

293
 aaaacacaccgccgactgtccctcaatcgtgtcaatcgcataatctgggctttgtaatgggttgctttattt 1649

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293
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 taaaactgtcttccgcaaactgttttgagactattcattcacacatgattgtcatggacctatttcacagat 1865

293
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Coding Sequence

User BLOCK 1 (8.1e-60) IC 3.43

<u>M D G M S T D T R E V V E L D V O H</u>	18
atg gat gga atg agc acg gat aca aga gag gtg gtt gaa ctc gac gtc cag cat	54
tD2V[1] tT6M[3]	
aD2E[2]	

<u>S S L G R G E O S E Y P P A L A L M</u>	36
tcg agc ttg ggg cgg ggg gag cag agc gag tac cca cca gcc ttg gca ctc atg	108

cS19P[4]

tL21F[5]
tL21F[6]
tL21F[7]
tL21F[8]

A S S D P R A W L A P V O A G T C A 54
gcc agc agt gac cca cgc gcc tgg ctg gct ccc gtg cag gct ggc acc tgc gcg 162

User BLOCK 2 (2.1e-13) IC 1.92

A H A E Y L L H S P G S S A E G V S 72
gca cac gcc gaa tac ctg ctg cac tcg ccc ggc tcg agc gcg gaa ggc gtg tcc 216
aa57T[9] aV71=[10]

S A S N F R K S S K S P V K V R E L 90
tct gcc tcc aac ttc agg aag agc agc aag agt cct gtc aaa gta cgc gag ctc 270

User BLOCK 3 (5.7e-18) IC 1.85

C R L K G A V G A D E G R O R A P S 108
tgc cgg ctt aaa gga gct gtg ggg gca gat gag ggc aga cag cgg gcc cca tcc 324

User BLOCK 4 (5.4e-64) IC 3.89

S K S T N V V O K O R R M A A N A R 126
agc aaa tcc acc aac gtc gtg cag aaa cag agg cga atg gct gcc aat gcc cgg 378
tR126W[11]

E R R R M H G L N H A F D E L R S V 144
gag agg cga aga atg cac gga ttg aac cac gcg ttc gac gag ctg cgc agt gtc 432
cS143R[12]

I P A F D N D K K L S K Y E T L O M 162
atc cca gcc ttt gac aac gac aag aaa ctc tcc aag tac gaa acc ctg cag atg 486
tI145=[13]

User BLOCK 5 (4.0e-21) IC 2.03

A O I Y I N A L S D L L O G P G A K 180
gcc cag atc tac atc aac gcc ctg tcc gac tta cta cag ggc ccc ggt gct aaa 540
gI165V[14]

A D P P N C D L L H A N V L E T D R 198
gcc gac ccg cca aac tgc gac ctg ctg cat gcc aac gtg tta gaa acg gac cga 594
aD197E[15]

User BLOCK 6 (1.1e-14) IC 2.49

S P R G S P G V C R R G T G V G Y P 216
tct ccc aga gga tca ccg ggc gtc tgt cgg aga ggc acg ggc gtg ggt tac ccg 648
aG205D[16]

User BLOCK 7 (5.7e-55) IC 3.50

Y Q Y E D G T F N S F M E O D L O S 234
tac cag tac gag gac gga aca ttc aac tct ttc atg gag caa gac ctc cag tcg 702

P S G T S K S G S E A S K D S P R S 252
ccc tct gga acg agc aag tct ggt tcg gag gcc agt aaa gac tcg cct cgg tcg 756

<u>N R S D G E F S P H S H F S D S D E</u>	270
aac cgg agt gat gga gag ttc tcg cct cac tcg cac ttc agt gac tca gac gaa	810
User BLOCK 8 (2.4e-23) IC 4.32	
<u>T H L E L Q S E D E L S E L K L A K</u>	288
acg cac ttg gag ctg cag agt gaa gac gag ctg tcg gaa ctg aaa ctg gcc aag	864
<u>R R A F</u> *	293
cgc cgc gct ttt taa	879