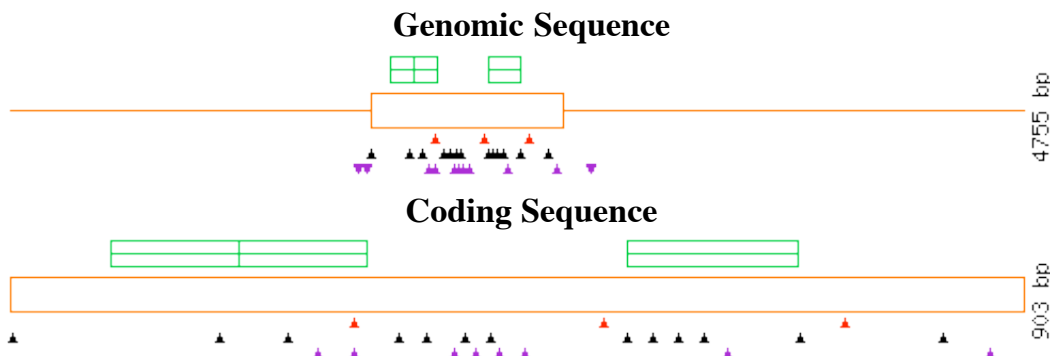


Sox3

IPB000135, IPB012502, IPB003888, IPB013558, IPB011591, IPB001686, IPB003056, IPB009448, IPB007275, IPB007696, and IPB007252



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	Zygotity
				Gained in Variant	Lost from Reference				
1	G	G1636A	Non-coding		BsmAI			7951	Homo
2	G	G1636A	Non-coding		BsmAI			7952	Homo
3	G	T1673G	Non-coding	BseSI , BseYI , SduI				3552	Homo
4	G C	G1692A	M1I					8040	Homo
5	G C	G1692A	M1I					8394	Homo
6	G C	T1876C	S63P	CauII , HpaII , ScrFI	Hpy188I	8.7	0.02	5346	Homo
7	G C	C1936T	P83S	BinI , DpnI , Hin4I , MboI , XhoII	BsmAI , Eco31I	11.0	0.13	3503	Homo
8	G C	C1963A	R92=	MseI	MaeIII			1298	Homo
9	G C	C1963A	R92=	MseI	MaeIII			537	Homo
10	G C	C1995A	Y102*	MseI				4754	Homo

11	G C	C1995T	Y102=	PsiI				7133	Homo
12	G C	A2035G	K116E	BbvII , BsiYI , EcoNI				811	Homo
13	G C	G2060A	G124E		FlnI , Hinfl , PleI			6868	Homo
14	G C	T2085C	A132=	Bcefl				7662	Homo
15	G C	C2094A	N135K		FnuDII			5941	Homo
16	G C	G2103T	S138=					7248	Homo
17	G C	T2117C	M143T	TspGWI	BccI , FokI , PfiMI			717	Homo
18	G C	C2124T	Y145=		MslI			8366	Homo
19	G C	C2148T	N153=		PsrI			5076	Homo
20	G C	C2218T	Q177*	BglIII , MaeI	BinI , NspBII			8148	Homo
21	G C	C2238A	D183E		NlaIII			3743	Homo
22	G C	T2261A	M191K			-0.9	0.87	8229	Homo
23	G C	T2285G	M199R	SfeI	NlaIII , TspDTI	9.5	0.25	6026	Homo
24	G C	T2285G	M199R	SfeI	NlaIII , TspDTI	9.5	0.25	6047	Homo
25	G C	A2308T	S207C	AluI , CviJI , CviRI , PvuII		9.5	0.04	6845	Homo
26	G C	G2328T	T213=					2954	Homo
27	G C	C2393T	S235F		BplI			282	Homo
28	G C	T2433A	C248*					7522	Homo
29	G C	C2521T	H278Y		MaeIII			4769	Homo
30	G C	G2562T	V291=	AccI , HindII , HpaI , MseI				6194	Homo
31	G C	G2562T	V291=	AccI , HindII , HpaI , MseI				8289	Homo
32	G	T2726C	Non-coding					6757	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

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                                a[2]

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gM199R[23]

tS207C[25]

gM199R[24]

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 tS235F[27]

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 aC248*[28]

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 tH278Y[29]

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Coding Sequence

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aM1I[5]																		

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G	S	V	T	G	G	K	N	N	S	A	N	<u>D</u>	<u>Q</u>	<u>D</u>	<u>R</u>	<u>V</u>	<u>K</u>	36
ggc	tcg	gtg	acg	ggc	ggc	aaa	aac	aac	agt	gcc	aac	gac	cag	gac	cgg	gtg	aag	108
<u>R</u>	<u>P</u>	<u>M</u>	<u>N</u>	<u>A</u>	<u>F</u>	<u>M</u>	<u>V</u>	<u>W</u>	<u>S</u>	<u>R</u>	<u>G</u>	<u>Q</u>	<u>R</u>	<u>R</u>	<u>K</u>	<u>M</u>	<u>A</u>	54
cgg	cct	atg	aat	gct	ttc	atg	gtg	tgg	tct	cgc	ggg	cag	cgg	agg	aag	atg	gct	162

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<u>O</u>	<u>E</u>	<u>N</u>	<u>P</u>	<u>K</u>	<u>M</u>	<u>H</u>	<u>N</u>	<u>S</u>	<u>E</u>	<u>I</u>	<u>S</u>	<u>K</u>	<u>R</u>	<u>L</u>	<u>G</u>	<u>A</u>	<u>D</u>	72
cag	gag	aat	cct	aaa	atg	cac	aac	tcg	gag	atc	agc	aag	cgc	ctc	ggt	gct	gac	216
																		cS63P[6]
<u>W</u>	<u>K</u>	<u>L</u>	<u>L</u>	<u>T</u>	<u>D</u>	<u>A</u>	<u>E</u>	<u>K</u>	<u>R</u>	<u>P</u>	<u>F</u>	<u>I</u>	<u>D</u>	<u>E</u>	<u>A</u>	<u>K</u>	<u>R</u>	90
tgg	aaa	ctt	ttg	act	gac	gcc	gag	aag	aga	ccc	ttc	att	gac	gag	gcc	aag	cgg	270
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<u>L</u>	<u>R</u>	<u>A</u>	<u>M</u>	<u>H</u>	<u>M</u>	<u>K</u>	<u>E</u>	<u>H</u>	<u>P</u>	<u>D</u>	<u>Y</u>	<u>K</u>	<u>Y</u>	<u>R</u>	<u>P</u>	R	R	108
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																		tQ177*[20]
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cgg	tac	gac	atg	gcg	gga	ctt	cag	tac	cca	atg	atg	tcc	acg	gct	cag	acc	tac	594
																		aD183E[21]
																		aM191K[22]
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																		gM199R[24]
<u>S</u>	<u>S</u>	<u>A</u>	<u>M</u>	<u>G</u>	<u>L</u>	<u>G</u>	<u>S</u>	<u>M</u>	<u>A</u>	<u>S</u>	<u>V</u>	<u>C</u>	<u>K</u>	<u>T</u>	<u>E</u>	<u>P</u>	<u>S</u>	234
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S	P	P	P	A	I	T	S	H	S	Q	R	A	C	L	G	D	L	252
tcc	cct	cct	ccg	gcc	ata	acc	tct	cac	tct	cag	cgt	gct	tgt	ttg	gga	gac	ctg	756
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																		aC248*[28]

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