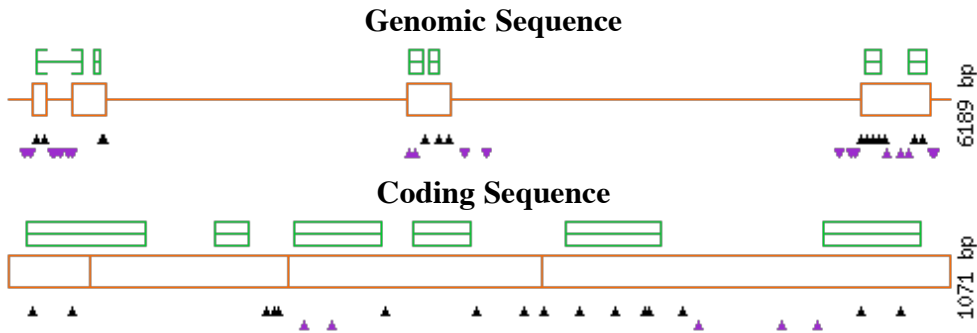


wnt16A

IPB005816, IPB003859, IPB013223, IPB004193, IPB007677, and IPB007360



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	G101A	Non-coding	AccI	AsuI , AvaII , BtsI , TspRI			8575	Homo
2	G	T144C	Non-coding	AsuI , AvaII , DraII , NlaIV , PpuMI				8072	Homo
3	G C	T188A	H9Q		CviRI , NlaIII , NspI	0.3	0.01	6080	Homo
4	G C	T234A	C25S	AluI , CviJI , HgiJII , SacI		1.3	0.34	5249	Homo
5	G	A282G	Intron		MseI			5774	Homo
6	G	A294T	Intron	ApoI				7795	Homo
7	G	C338T	Intron		AsuI , BsiYI , EcoRII , HaeIII , ScrFI			8033	Homo
8	G	G394A	Intron					7022	Homo
9	G	A411T	Intron		SfaNI			6823	Homo
10	G C	A618C	N98T	McrI , Tsp4CI	AflIII , MaeII , XmnI			5765	Homo
11	G C	G627A	G101D	TaqI	CviJI			7422	Homo
12	G C	G632A	E103K		BseSI , HgiAI , HgiJII , SacI , SduI			5867	Homo
13	G C	G2638A	A112=	BsmI	PpiI			3154	Homo
14	G C	T2671C	V123=	AsuI , AvaII	TspDTI			8067	Homo
15	G C	C2732A	L144M	MslI , NlaIII , NspI	BglI , CviJI			8107	Homo
16	G C	G2834T	A178S	Hin4I , SfaNI , TaqI	BbvI , BsgI , Fnu4HI , TseI			4491	Homo

17	G C	A2889G	N196S	BtsI	Tsp4CI			661	Homo
18	G	T2994A	Intron					1208	Homo
19	G	T3136G	Intron					1683	Homo
20	G	A5461G	Intron	MnlI				6885	Homo
21	G	A5533G	Intron	CviRI				905	Homo
22	G	A5565T	Intron	BsrI	BglII , DpnI , Hpy178III , MboI , XhoII			927	Homo
23	G C	G5601A	V204M	BccI , BtgZI	AciI			3201	Homo
24	G C	G5640A	V217I			11.4	0.04	7409	Homo
25	G C	G5682A	A231T		BbvI , CviJI , Fnu4HI , TseI	13.2	0.01	5142	Homo
26	G C	A5716T	D242V		BinI , DpnI , MboI	9.7	0.07	6245	Homo
27	G C	G5719T	R243L	XhoII		7.0	0.13	5739	Homo
28	G C	C5757T	R256C		MaeII			2964	Homo
29	G C	C5757T	R256C		MaeII			5813	Homo
30	G C	T5777C	D262=					6337	Homo
31	G C	G5870A	V293=		Tsp45I			7585	Homo
32	G C	G5912A	G307=	AvaII	ApaI , BseSI , CauII , CviJI , HaeIII , HgiIII , ScrFI , SduI			2365	Homo
33	G C	T5960A	H323Q		AflIII , BspLU11I , NlaIII , NspI	1.7	0.65	6785	Homo
34	G C	T6006A	C339S	BsgI , CviRI		24.1	0.00	333	Homo
35	G	G6076A	Non-coding	TaqI				6847	Homo
36	G	G6089A	Non-coding	HinfI , MboII , TfiI	BinI , DpnI , MboI , XhoII			6830	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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72

attacaggtgctacatattagatgcagtgaccggcatgaatcgtctttgtcaaaacggtcagttcgggact 0
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326
g[5] t[6]

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398
t[7] a[8]

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N V F G Y E L T S G 107
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aE103K[12]

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822

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2118

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2190

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2334

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2550

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IPB005816C (2.5e-20) IC 2.28
S L L G S G S P T E G W H W G G C S 160
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aL144M[15]

D D I A F G T S F S R R F I D S A A 178
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tA178S[16]

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gN196S[17]

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c a g t t g a a g t c c a a a c t a t t a g c c c a c c t g a g a a t t t t c t t t t c c t t t t t a a a t a t t t c c c a a g a g c a a g g a 202
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IPB005816D (9.7e-31) IC 2.48

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 aV217I[24]

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 aA231T[25] tD242V[26]
 tR243L[27]

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 tR256C[28]
 tR256C[29]

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 aG307=[32]

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 aH323Q[33]

K F V W C C Y V R C R R C E T M N D 351
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 aC339S[34]

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 a[35] a[36]

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6182

cataaag 357
6189

Coding Sequence

IPB007360A (4.4e-07) IC 2.11

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aH9Q[3]

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aC25S[4]

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K Q K E L C A R K P H L L P S V K E 71
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IPB005816A (5.1e-15) IC 2.32

G A R L G I T E C O T O F R H E R W 89
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N C S T R R D P N V F G Y E L T S G | 107
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cN98T[10] aG101D[11]
aE103K[12]

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IPB005816C (2.5e-20) IC 2.28

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aL144M[15]

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tA178S[16]

K N T S T R G E E A L L I M K Q H N 196
aaa aac acc tcg acc cgt ggt gag gag gcc ctg ctc att atg aag cag cat aac 588
gN196S[17]

IPB005816D (9.7e-31) IC 2.48

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aV204M[23]

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tR243L[27]

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357
1071