

Block annotations

Block info

genomic range	chr3:190,287,162-190,290,917 <i>e!</i>
block size	3,756 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.081$ [-0.149 – -0.013]	gene(s) hit or close-by	IL1RAP <i>e!</i>
phastCons	$\mu = 0.000$ [0 – 0]	eQTL gene(s)	-
GERP++	$\mu = 1.190$ [0 – 2.38]	potentially regulated gene(s)	-
CADD score	$\mu = 6.082$ [3.796 – 8.369]	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
IL1RAP <i>e!</i>	downstream gene variant	4856	ENST00000461629 <i>e!</i>	?	?	1
IL1RAP <i>e!</i>	downstream gene variant	4955	ENST00000482913 <i>e!</i>	?	?	1
IL1RAP <i>e!</i>	downstream gene variant	4705	ENST00000473566 <i>e!</i>	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
IL1RAP <i>e!</i>	ENST00000317757 <i>e!</i>	NM_001167931.1	ENSP00000314807 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000439062 <i>e!</i>	NM_001167928.1	ENSP00000401132 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000342550 <i>e!</i>	?	ENSP00000345829 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000453359 <i>e!</i>	?	ENSP00000412008 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000072516 <i>e!</i>	NM_001167929.1	ENSP00000072516 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000422940 <i>e!</i>	NM_001167930.1	ENSP00000387371 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000434491 <i>e!</i>	?	ENSP00000391899 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000422485 <i>e!</i>	NM_134470.3	ENSP00000409352 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000447382 <i>e!</i>	NM_002182.3	ENSP00000390541 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000422625 <i>e!</i>	?	ENSP00000389149 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000413869 <i>e!</i>	?	ENSP00000416296 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000412504 <i>e!</i>	?	ENSP00000412053 <i>e!</i>	2
IL1RAP <i>e!</i>	ENST00000443369 <i>e!</i>	?	ENSP00000408893 <i>e!</i>	2

