

# SNiPAcad

## Block annotations

### Block info

genomic range	chr4:76,943,947-76,943,947 <i>e!</i>
block size	1 bp
variant count	1 variants

### Basic features

Conservation/deleteriousness		Linked genes	
phyloP	4.616	gene(s) hit or close-by	ART3 <i>e!</i> , CXCL10 <i>e!</i>
phastCons	0.999	eQTL gene(s)	-
GERP++	4.93	potentially regulated gene(s)	-
CADD score	14.66	disease gene(s)	-

## Direct effect on transcript

### Amino acid sequence alteration

gene	effect type	affected transcript	RefSeq id	protein	exchanged AA's	exchanged codons	SIFT prediction	PolyPhen prediction	variant(s)
CXCL10 <i>e!</i>	missense variant	ENST00000306602 <i>e!</i>	NM_001565.3	ENSP00000305651	C/R	Tgc/Cgc	?	?	1

## Putative effect on transcript

### Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ART3 <i>e!</i>	ENST00000510669 <i>e!</i>	?	?	1
ART3 <i>e!</i>	ENST00000513353 <i>e!</i>	?	ENSP00000421345 <i>e!</i>	1
ART3 <i>e!</i>	ENST00000504914 <i>e!</i>	?	ENSP00000421431 <i>e!</i>	1
ART3 <i>e!</i>	ENST00000341029 <i>e!</i>	NM_001130017.2	ENSP00000343843 <i>e!</i>	1
ART3 <i>e!</i>	ENST00000513122 <i>e!</i>	?	ENSP00000422287 <i>e!</i>	1

