

Uploaded Variation	Location	Allele	Gene	Feature type	Consequence	Position in cDNA	Position in CDS	Position in protein	Amino acid change	Codon change
rs11576243	chr1:92101761	C	-	-	intergenic_variant	-	-	-	-	-
rs4658257	chr1:92129685	G	-	-	intergenic_variant	-	-	-	-	-
rs284177	chr1:92224698	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284177	chr1:92224698	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284177	chr1:92224698	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284177	chr1:92224698	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284180	chr1:92227848	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284180	chr1:92227848	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284180	chr1:92227848	C	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284191	chr1:92236048	G	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284191	chr1:92236048	G	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284191	chr1:92236048	G	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284191	chr1:92236048	G	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284198	chr1:92238167	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284198	chr1:92238167	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284198	chr1:92238167	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs284198	chr1:92238167	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs4658265	chr1:92240685	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs4658265	chr1:92240685	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs4658265	chr1:92240685	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs4658265	chr1:92240685	T	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs6604053	chr1:92244566	A	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs6604053	chr1:92244566	A	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs6604053	chr1:92244566	A	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs6604053	chr1:92244566	A	TGFBR3	Transcript	intron_variant	-	-	-	-	-
rs6604053	chr1:92244566	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs17131593	chr1:92503338	C	EPHX4	Transcript	intron_variant	-	-	-	-	-
rs6662618	chr1:92935411	G	GFI1	Transcript	downstream_gene_variant	-	-	-	-	-
rs6662618	chr1:92935411	G	GFI1	Transcript	downstream_gene_variant	-	-	-	-	-
rs6662618	chr1:92935411	G	GFI1	Transcript	downstream_gene_variant	-	-	-	-	-
rs11804321	chr1:93009313	C	EVI5	Transcript	intron_variant	-	-	-	-	-
rs11804321	chr1:93009313	C	EVI5	Transcript	intron_variant	-	-	-	-	-
rs11804321	chr1:93009313	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6698352	chr1:170339511	A	-	-	intergenic_variant	-	-	-	-	-
rs10797527	chr1:234250281	G	SLC35F3	Transcript	intron_variant	-	-	-	-	-
rs10797527	chr1:234250281	G	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs7095226	chr10:2809279	G	-	-	intergenic_variant	-	-	-	-	-
rs7914915	chr10:6173416	C	-	-	intergenic_variant	-	-	-	-	-
rs16936011	chr10:35679866	A	CCNY	Transcript	intron_variant	-	-	-	-	-
rs16936011	chr10:35679866	A	CCNY	Transcript	intron_variant	-	-	-	-	-

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rs16936011	chr10:35679866	A	CCNY	Transcript	intron_variant	-	-	-	-	-
rs16936011	chr10:35679866	A	CCNY	Transcript	intron_variant	-	-	-	-	-
rs16936011	chr10:35679866	A	CCNY	Transcript	intron_variant	-	-	-	-	-
rs16936011	chr10:35679866	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs10768177	chr11:36125835	G	LDLRAD3	Transcript	intron_variant	-	-	-	-	-
rs10768177	chr11:36125835	G	LDLRAD3	Transcript	intron_variant	-	-	-	-	-
rs10768177	chr11:36125835	G	LDLRAD3	Transcript	intron_variant	-	-	-	-	-
rs10768177	chr11:36125835	G	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs12865017	chr13:46908398	C	-	-	intergenic_variant	-	-	-	-	-
rs12865017	chr13:46908398	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs1095070	chr13:64450447	A	-	-	intergenic_variant	-	-	-	-	-
rs2414428	chr15:56007695	C	PRTG	Transcript	intron_variant	-	-	-	-	-
rs2414428	chr15:56007695	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	PPCDC	Transcript	intron_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	PPCDC	Transcript	intron_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	PPCDC	Transcript	intron_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	PPCDC	Transcript	intron_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	PPCDC	Transcript	intron_variant	-	-	-	-	-
rs4886649	chr15:75328595	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs12447897	chr16:87738888	T	KLHDC4	Transcript	downstream_gene_variant	-	-	-	-	-
rs12447897	chr16:87738888	T	KLHDC4	Transcript	downstream_gene_variant	-	-	-	-	-
rs12447897	chr16:87738888	T	KLHDC4	Transcript	downstream_gene_variant	-	-	-	-	-
rs12447897	chr16:87738888	T	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs2970065	chr17:16416867	T	-	-	intergenic_variant	-	-	-	-	-
rs10512460	chr17:32459020	G	ASIC2	Transcript	intron_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	CDK5RAP3	Transcript	upstream_gene_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	CDK5RAP3	Transcript	upstream_gene_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	CDK5RAP3	Transcript	upstream_gene_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	CDK5RAP3	Transcript	upstream_gene_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	CDK5RAP3	Transcript	upstream_gene_variant	-	-	-	-	-
rs2597167	chr17:46047656	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs8066209	chr17:59798591	T	BRIP1	Transcript	intron_variant	-	-	-	-	-
rs7214718	chr17:65239455	C	HE LZ	Transcript	intron_variant	-	-	-	-	-
rs7214718	chr17:65239455	C	LOC101928021	Transcript	upstream_gene_variant	-	-	-	-	-
rs7214718	chr17:65239455	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6501667	chr17:71859152	G	-	-	intergenic_variant	-	-	-	-	-
rs1987925	chr17:71866651	T	-	-	intergenic_variant	-	-	-	-	-
rs532804	chr18:66067465	G	-	-	intergenic_variant	-	-	-	-	-
rs8109892	chr19:14842242	T	ZNF333	Transcript	3_prime_UTR_variant	1308	-	-	-	-
rs8109892	chr19:14842242	T	ADGRE2	Transcript	downstream_gene_variant	-	-	-	-	-
rs8109892	chr19:14842242	T	ADGRE2	Transcript	downstream_gene_variant	-	-	-	-	-

[illegible]

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rs6550402	chr3:20219885	T	SGO1	Transcript	intron_variant	-	-	-	-	-
rs6550402	chr3:20219885	T	SGO1	Transcript	intron_variant	-	-	-	-	-
rs6550402	chr3:20219885	T	SGO1-AS1	Transcript	intron_variant	-	-	-	-	-
rs7631044	chr3:30730722	C	TGFBR2	Transcript	intron_variant	-	-	-	-	-
rs7631044	chr3:30730722	C	TGFBR2	Transcript	intron_variant	-	-	-	-	-
rs7631044	chr3:30730722	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs326255	chr3:96201175	A	-	-	intergenic_variant	-	-	-	-	-
rs587321	chr3:114590028	T	ZBTB20	Transcript	intron_variant	-	-	-	-	-
rs587321	chr3:114590028	T	ZBTB20	Transcript	intron_variant	-	-	-	-	-
rs587321	chr3:114590028	T	ZBTB20	Transcript	intron_variant	-	-	-	-	-
rs587321	chr3:114590028	T	ZBTB20-AS3	Transcript	upstream_gene_variant	-	-	-	-	-
rs17236537	chr3:160275031	A	KPNA4	Transcript	intron_variant	-	-	-	-	-
rs743695	chr4:2307574	C	ZFYVE28	Transcript	intron_variant	-	-	-	-	-
rs743695	chr4:2307574	C	ZFYVE28	Transcript	intron_variant	-	-	-	-	-
rs743695	chr4:2307574	C	ZFYVE28	Transcript	intron_variant	-	-	-	-	-
rs2660943	chr4:58935943	G	-	-	intergenic_variant	-	-	-	-	-
rs9312960	chr5:204082	A	CCDC127	Transcript	downstream_gene_variant	-	-	-	-	-
rs9312960	chr5:204082	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs1054174	chr5:204952	T	CCDC127	Transcript	3_prime_UTR_variant	1343	-	-	-	-
rs9763161	chr5:207618	A	CCDC127	Transcript	intron_variant	-	-	-	-	-
rs9763161	chr5:207618	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs11133943	chr5:246152	C	SDHA	Transcript	intron_variant	-	-	-	-	-
rs11133943	chr5:246152	C	SDHA	Transcript	intron_variant	-	-	-	-	-
rs11133943	chr5:246152	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs16900804	chr5:305595	C	PDCD6	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	PDCD6	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	PDCD6	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	PDCD6	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	PDCD6	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	AHRR	Transcript	intron_variant	-	-	-	-	-
rs16900804	chr5:305595	C	AHRR	Transcript	intron_variant	-	-	-	-	-
rs11745733	chr5:360739	A	AHRR	Transcript	intron_variant	-	-	-	-	-
rs11745733	chr5:360739	A	AHRR	Transcript	intron_variant	-	-	-	-	-
rs11745733	chr5:360739	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6899226	chr5:393377	T	AHRR	Transcript	intron_variant	-	-	-	-	-
rs6899226	chr5:393377	T	AHRR	Transcript	intron_variant	-	-	-	-	-
rs6899226	chr5:393377	T	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs10067993	chr5:7281915	G	-	-	intergenic_variant	-	-	-	-	-
rs3891746	chr5:11702017	A	CTNND2	Transcript	intron_variant	-	-	-	-	-
rs3891746	chr5:11702017	A	CTNND2	Transcript	intron_variant	-	-	-	-	-
rs3891746	chr5:11702017	A	CTNND2	Transcript	intron_variant	-	-	-	-	-

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rs6880511	chr5:124597571	G	LOC101927421	Transcript	intron_variant	-	-	-	-	-
rs4976609	chr5:167863844	A	WWC1	Transcript	intron_variant	-	-	-	-	-
rs4976609	chr5:167863844	A	WWC1	Transcript	intron_variant	-	-	-	-	-
rs4976609	chr5:167863844	A	WWC1	Transcript	intron_variant	-	-	-	-	-
rs4976609	chr5:167863844	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs594930	chr6:114170427	C	-	-	intergenic_variant	-	-	-	-	-
rs3808340	chr7:962371	G	ADAP1	Transcript	upstream_gene_variant	-	-	-	-	-
rs3808340	chr7:962371	G	ADAP1	Transcript	intron_variant	-	-	-	-	-
rs3808340	chr7:962371	G	ADAP1	Transcript	intron_variant	-	-	-	-	-
rs3808340	chr7:962371	G	ADAP1	Transcript	intron_variant	-	-	-	-	-
rs3808340	chr7:962371	G	ADAP1	Transcript	intron_variant	-	-	-	-	-
rs3808340	chr7:962371	G	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6977682	chr7:8269678	C	ICA1	Transcript	intron_variant	-	-	-	-	-
rs6977682	chr7:8269678	C	ICA1	Transcript	intron_variant	-	-	-	-	-
rs6977682	chr7:8269678	C	ICA1	Transcript	intron_variant	-	-	-	-	-
rs6977682	chr7:8269678	C	ICA1	Transcript	intron_variant	-	-	-	-	-
rs6977682	chr7:8269678	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs2877301	chr7:44995327	T	-	-	intergenic_variant	-	-	-	-	-
rs2877301	chr7:44995327	T	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6946581	chr7:44998714	A	MYO1G	Transcript	downstream_gene_variant	-	-	-	-	-
rs6946581	chr7:44998714	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs6976664	chr7:45014304	T	MYO1G	Transcript	intron_variant	-	-	-	-	-
rs6976664	chr7:45014304	T	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	TBRG4	Transcript	intron_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	TBRG4	Transcript	intron_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	TBRG4	Transcript	intron_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	TBRG4	Transcript	intron_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	SNORA5A	Transcript	downstream_gene_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	SNORA5C	Transcript	downstream_gene_variant	-	-	-	-	-
rs7792895	chr7:45141785	T	SNORA5B	Transcript	downstream_gene_variant	-	-	-	-	-
rs1524395	chr7:54198501	A	-	-	intergenic_variant	-	-	-	-	-
rs10229129	chr7:103950365	C	-	-	intergenic_variant	-	-	-	-	-
rs6979610	chr7:138463724	G	ATP6V0A4	Transcript	upstream_gene_variant	-	-	-	-	-
rs6979610	chr7:138463724	G	ATP6V0A4	Transcript	intron_variant	-	-	-	-	-
rs6979610	chr7:138463724	G	ATP6V0A4	Transcript	intron_variant	-	-	-	-	-
rs11761588	chr7:151094048	C	WDR86	Transcript	intron_variant	-	-	-	-	-
rs11761588	chr7:151094048	C	WDR86	Transcript	intron_variant	-	-	-	-	-
rs11761588	chr7:151094048	C	WDR86	Transcript	intron_variant	-	-	-	-	-
rs11761588	chr7:151094048	C	WDR86	Transcript	intron_variant	-	-	-	-	-
rs11761588	chr7:151094048	C	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs13257816	chr8:5181443	A	-	-	intergenic_variant	-	-	-	-	-

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rs1436149	chr8:23732888	T	-	-	intergenic_variant	-	-	-	-	-
rs28921387	chr8:107682407	A	OXR1	Transcript	intron_variant	-	-	-	-	-
rs28921387	chr8:107682407	A	OXR1	Transcript	intron_variant	-	-	-	-	-
rs28921387	chr8:107682407	A	OXR1	Transcript	intron_variant	-	-	-	-	-
rs28921387	chr8:107682407	A	OXR1	Transcript	intron_variant	-	-	-	-	-
rs28921387	chr8:107682407	A	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-
rs10975176	chr9:5551385	A	PDCD1LG2	Transcript	intron_variant	-	-	-	-	-
rs3010671	chr9:81078138	A	-	-	intergenic_variant	-	-	-	-	-
rs11137862	chr9:81442685	C	-	-	intergenic_variant	-	-	-	-	-
rs12378461	chr9:81474084	A	-	-	intergenic_variant	-	-	-	-	-
rs11137922	chr9:81493973	T	-	-	intergenic_variant	-	-	-	-	-
rs10819528	chr9:132260350	G	LINC00963	Transcript	intron_variant	-	-	-	-	-
rs10819528	chr9:132260350	G	-	RegulatoryFeature	regulatory_region_variant	-	-	-	-	-