

Variant Annotation Model Schema

id <i>String</i>	Unique variant ID, this consists of chromosome, position, reference and alternate alleles in this format: <i>chrom:pos:ref:alt</i>																								
chromosome <i>String</i>	The chromosome where the genomic variant is located																								
start <i>int</i>	The 1-based position where the genomic variant starts. For variants coming from VCF files, this position is likely to be normalised																								
end <i>int</i>	The 1-based position where the genomic variant ends. For variants coming from VCF files, this position is likely to be normalised																								
reference <i>String</i>	Reference allele. For variants coming from VCF files, this position is likely to be normalised																								
alternate <i>String</i>	Alternate allele. For variants coming from VCF files, this position is likely to be normalised																								
ancestralAllele <i>String</i>																									
xrefs <i>List<Xref></i>																									
hgvs <i>List<String></i>																									
displayConsequenceType <i>String</i>																									
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transcriptAnnotationFlags <i>List<String></i>	
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cdsPosition <i>int</i>	
codon <i>String</i>	

proteinVariantAnnotation

ProteinVariantAnnotation

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reference <i>String</i>											
alternate <i>String</i>											
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source <i>String</i>											
description <i>String</i>											
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features <i>List<ProteinFeature></i>	<table><tr><td>id <i>String</i></td><td></td></tr><tr><td>start <i>int</i></td><td></td></tr><tr><td>end <i>int</i></td><td></td></tr><tr><td>type <i>String</i></td><td></td></tr><tr><td>description <i>String</i></td><td></td></tr></table>	id <i>String</i>		start <i>int</i>		end <i>int</i>		type <i>String</i>		description <i>String</i>	
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start <i>int</i>											
end <i>int</i>											
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description <i>String</i>											

	sequenceOntologyTerms accession <i>String</i> name <i>String</i> <i>List<SequenceOntologyTerm></i>
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cytoband

List<Cytoband>

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String	
stain	
String	
name	
String	
start	
int	
end	
int	

repeat

List<Repeat>

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score	
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sequence	
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source	
String	

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