Variant Annotation Model Schema

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

geneName *String*	HGNC gene name
ensemblGeneId *String*	
ensemblTranscriptId *String*	
strand *String*	
biotype *String*	
exonOverlap *List<ExonOverlap>*	

number *String*	
percentage *float*	

transcriptAnnotationFlags *List<String>*	
cdnaPosition *int*	
cdsPosition *int*	
codon *String*	

proteinVariantAnnotation *ProteinVariantAnnotation*	
	uniprotAccession *String*
	uniprotName *String*
	position int
	reference *String*
	alternate *String*
	uniprotVariantId *String*
	functionalDescription *String*
	substitutionScores *List<Score>*
	keywords *List<String>*
	features *List<ProteinFeature>*

score *double*
source *String*
description *String*

id *String*
start *int*
end *int*
type *String*
description *String*

	sequenceOntologyTerms *List<SequenceOntologyTerm>* **accession** *String* **name** *String*
populationFrequencies *List<PopulationFrequency>*	**study** *String* **population** *String* **refAllele** *String* **altAllele** *String* **refAlleleFreq** *float* **altAlleleFreq** *float* **refHomGenotypeFreq** *float* **hetGenotypeFreq** *float* **altHomGenotypeFreq** *float*
minorAllele *String*	
minorAlelleFreq *float*	
conservation *List<Score>*	**score** *double* **source** *String* **description** *String*

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String</td><td></td></tr>
<tr><td>name
String</td><td></td></tr>
<tr><td>hpo
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<tr><td>score
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cytoband *List<Cytoband>*	**chromosome** *String* **stain** *String* **name** *String* **start** *int* **end** *int*
repeat *List<Repeat>*	**id** *String* **chromosome** *String* **start** *int* **end** *int* **period** *int* **consensusSize** *int* **copyNumber** *float* **percentageMatch** *float* **score** *float* **sequence** *String* **source** *String*

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<tr><td>additionalAttributes

Map<String, AdditionalAttribute></td><td></td></tr>
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