

Variant Annotation Schema

Here you can find a detailed information about annotation 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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cdsPosition <i>int</i>	
codon <i>String</i>	

proteinVariantAnnotation

ProteinVariantAnnotation

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<i>String</i>																																	

cytoband

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stain	
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name	
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int	
end	
int	

repeat

List<Repeat>

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percentageMatch	
float	
score	
float	
sequence	
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source	
String	

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