

Clinical Variant Evidence Data Model Schema

interpretationMethodName <i>String</i>	Interpretation method name.										
phenotypes <i>List<Phenotype></i>	List of phenotypes for that evicende.<table><tr><td>ageOfOnset <i>String</i></td><td>Age at which the proband acquired a condition or symptoms of a that disorder.</td></tr><tr><td>status <i>Status</i></td><td> Status.<table><tr><td>OBSERVED</td><td></td></tr><tr><td>NOT_OBSERVED</td><td></td></tr><tr><td>UNKNOWN</td><td></td></tr></table> </td></tr></table>	ageOfOnset <i>String</i>	Age at which the proband acquired a condition or symptoms of a that disorder.	status <i>Status</i>	Status.<table><tr><td>OBSERVED</td><td></td></tr><tr><td>NOT_OBSERVED</td><td></td></tr><tr><td>UNKNOWN</td><td></td></tr></table>	OBSERVED		NOT_OBSERVED		UNKNOWN	
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consequenceTypes <i>List<SequenceOntologyTerm></i>	List of Sequence Ontology terms that describe the consequence types.<table><tr><td>accession <i>String</i></td><td>Accession identifier. e.g.: SO:0001583</td></tr><tr><td>name <i>String</i></td><td>Term name, e.g.: missense_variant</td></tr></table>	accession <i>String</i>	Accession identifier. e.g.: SO:0001583	name <i>String</i>	Term name, e.g.: missense_variant						
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	other List<String> Custom values for classifying variants.												
score Double	Score.												
fullyExplainPhenotypes Boolean	Fully explain phenotypes.												
compoundHeterozygousVariantIds List<String>	List of compound heterozygous variant IDs.												
roleInCancer RoleInCancer	Role in Cancer. <table><tr><td>ONCOGENE</td><td></td></tr><tr><td>TUMOR_SUPPRESSOR_GENE</td><td></td></tr><tr><td>BOTH</td><td></td></tr></table>	ONCOGENE		TUMOR_SUPPRESSOR_GENE		BOTH							
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