

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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genomicFeature <i>GenomicFeature</i>	Genomic feature. <table border="1"> <tr> <td data-bbox="488 184 618 268"> id <i>String</i> </td><td data-bbox="618 184 992 268"> Genomic feature ID. </td></tr> <tr> <td data-bbox="488 268 618 474"> type <i>String</i> </td><td data-bbox="618 268 992 474"> Type. <table border="1"> <tr> <td data-bbox="634 325 743 369">GENE</td><td data-bbox="743 325 781 369"></td></tr> <tr> <td data-bbox="634 369 743 413">VARIANT</td><td data-bbox="743 369 781 413"></td></tr> <tr> <td data-bbox="634 413 743 457">REGION</td><td data-bbox="743 413 781 457"></td></tr> </table> </td></tr> <tr> <td data-bbox="488 474 618 558"> transcriptId <i>String</i> </td><td data-bbox="618 474 992 558"> Transcript ID. </td></tr> <tr> <td data-bbox="488 558 618 653"> geneName <i>String</i> </td><td data-bbox="618 558 992 653"> Gene name. </td></tr> <tr> <td data-bbox="488 653 618 1081"> xrefs <i>List<Xref></i> </td><td data-bbox="618 653 992 1081"> List of synonymous. <table border="1"> <tr> <td data-bbox="634 709 802 800"> id <i>String</i> </td><td data-bbox="802 709 980 800"> ID. </td></tr> <tr> <td data-bbox="634 800 802 890"> dbName <i>String</i> </td><td data-bbox="802 800 980 890"> DB name. </td></tr> <tr> <td data-bbox="634 890 802 980"> dbDisplayName <i>String</i> </td><td data-bbox="802 890 980 980"> DB display name. </td></tr> <tr> <td data-bbox="634 980 802 1071"> description <i>String</i> </td><td data-bbox="802 980 980 1071"> Description. </td></tr> </table> </td></tr> </table>	id <i>String</i>	Genomic feature ID.	type <i>String</i>	Type. <table border="1"> <tr> <td data-bbox="634 325 743 369">GENE</td><td data-bbox="743 325 781 369"></td></tr> <tr> <td data-bbox="634 369 743 413">VARIANT</td><td data-bbox="743 369 781 413"></td></tr> <tr> <td data-bbox="634 413 743 457">REGION</td><td data-bbox="743 413 781 457"></td></tr> </table>	GENE		VARIANT		REGION		transcriptId <i>String</i>	Transcript ID.	geneName <i>String</i>	Gene name.	xrefs <i>List<Xref></i>	List of synonymous. <table border="1"> <tr> <td data-bbox="634 709 802 800"> id <i>String</i> </td><td data-bbox="802 709 980 800"> ID. </td></tr> <tr> <td data-bbox="634 800 802 890"> dbName <i>String</i> </td><td data-bbox="802 800 980 890"> DB name. </td></tr> <tr> <td data-bbox="634 890 802 980"> dbDisplayName <i>String</i> </td><td data-bbox="802 890 980 980"> DB display name. </td></tr> <tr> <td data-bbox="634 980 802 1071"> description <i>String</i> </td><td data-bbox="802 980 980 1071"> Description. </td></tr> </table>	id <i>String</i>	ID.	dbName <i>String</i>	DB name.	dbDisplayName <i>String</i>	DB display name.	description <i>String</i>	Description.				
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