A complete list of the model elements and their description.

| **Element: sub-elements and description** | **Overall description** |
| --- | --- |
| **orderID**   |  |  | | --- | --- | | order identifier | alpha-numeric identifier for lab result | | Order identifier for the lab result |
| **author**   |  |  | | --- | --- | | firstName | author’s first name | | lastName | author’s last name | | id | author identifier | | authoringDateandTime | time the document was created | | Provides information on the author of the document |
| **patient**   |  |  | | --- | --- | | firstName | patient’s first name | | lastName | patient’s last name | | id | patient identifier | | dateOfBirth | patient’s birthday | | gender | patient’s gender | | Describes the patient |
| **orderingClinician**   |  |  | | --- | --- | | firstName | clinician’s first name | | lastName | clinician’s last name | | id | clinician’s identifier | | specialty | clinician’s practice specialty | | orderingDate | Date and time the order request created | | Describes the clinician |
| **reasonForTesting** | Why the test was ordered if known |
| **relevantDiagnosis** | Diagnosis if known |
| **sample**   |  |  | | --- | --- | | anatomicLocation | Location the sample analyte was collected, e.g. breast | | analyte | Specimen collected e.g. tissue sample | | samplingDateTime | Date and time the specimen was collected | | receivedDate | Date and time the specimen was collected by lab | | tumorSize | Size in cm3 or inch3 if relevant and known | | nodeStatus | Lymph node involvement (whether positive or negative) if relevant and known | | notes | Provide a place holder for additional information about the sample in free text form | | Provides sample specific information |
| test:platform   |  |  | | --- | --- | | platformName | Sequencing platform name, e.g. Illumina HiSeq | | platformVersion | Version of the platform, e.g. 2000 | | sequencingLocation | Address and contact for the sequencing location if available |   test:analysis   |  |  | | --- | --- | | typeOfAnalysis | Describes if the results being reported are “absolute” or “differential” (compared to other control sample) gene expression | | rawDataReferce | Provides a url to reference genome data used for the results if available | | analysisMethos | Contains information on either the analysis pipeline with version or includes various individual tools and their corresponding versions used in the analysis | | referenceGenome | Describes reference genome name, version and gene annotation name and version used for analysis | | analysisBy | Describes the person performing the analysis by providing full name and id | | analysisDateTime | Date and time when the analysis was done |   test:results   |  |  | | --- | --- | | gene | Provides ‘geneId’ and ‘normalizedExpression’ values with corresponding units. HGNC symbol, HGNC ID, ENTREZ ID or ENSEMBL IDs are accommodated and at least one must be provided in ‘geneId’.  ‘Value’ is to present the gene expression values that are normalized and ‘logBase’ can be used when the ‘Value ’ is logged and the number specified here indicate the base of log used for the value. ‘logBase’ is optional. | | numberOfGenesReported | This element is to show the total number of genes shown in the results. |   test: notes is to provide any additional information that could not be conveyed in the structured element but important for analysis. | Provides information on sequencing platform, analysis pipeline, and presents results |