













# Histoimmunogenetic typing

Entity: Cluster

|  |   |   |  |  |                |
|--|---|---|--|--|----------------|
| <b>Concept description:</b>  |   |   | <b>Identification:</b>   |  |                |
| unknown  |   |   | <i>Id:</i> openEHR-EHR-CLUSTER.histoimmunogenetic_typing.v0<br><i>Reference model:</i> openEHR_EHR |  |                |
| <b>Purpose</b>   | <b>Use</b>  | <b>Misuse</b>                                       | <b>Copyright</b>   | <b>References</b>  | <b>Contact</b> |
| For registering an HLA (Human Leukocyte Antigens) based on the Histoimmunogenetic typing Markup Language (HML) | Should be used with the Lab result observation archetype to register the specific sample and date/time collection of that sample. | Should not be used for Antibody screening purposes. |  | <a href="https://bioinformatics.bethematchclinical.org/hla-resources/hml/">https://bioinformatics.bethematchclinical.org/hla-resources/hml/</a> <a href="https://schemas.nmdp.org/">https://schemas.nmdp.org/</a><br><a href="https://www.ncbi.nlm.nih.gov/pubmed/23849068">https://www.ncbi.nlm.nih.gov/pubmed/23849068</a> |                |

| Concept   | Description  | Constraints             | Values            |
|---|--|-------------------------|-------------------|
|  <b>Gene family</b>      | Represents the gene evaluated in this typing report, e.g. "HLA" or "KIR"   | <i>Text</i><br>1..1     | Internal;         |
|  <b>Typing date</b>      | Typing/testing date for this sample  | <i>DateTime</i><br>1..1 | Allow all         |
|  <b>Slot</b>             | Typing method [Cluster]  | Include : Cluster       | Exclude : Cluster |
|  <b>Allel-Assignment</b> | Specifies the genotyping call at the most specific level possible. This call can be represented within haploid elements or using gl-resources. When reporting data | <i>Cluster</i><br>1..1  |                   |

|   |  |   |                   |
|---|--|---|-------------------|
|   | using haploid, typical use is one or two haploid elements for a particular locus, but possibly more if multiple loci are covered (ex: two DRB1 haploids + one DRB3 haploid). |   |                   |
|  <b>Haploid</b>        | *  | <b>Cluster</b><br>1..*                                  |                   |
|  <b>Antigen</b>        | Slot<br>Antigen [Cluster]  | Include : Cluster<br>antigen(-[a-zA-Z0-9_+])*\.v0       | Exclude : Cluster |
|  <b>glstring</b>       | Genotype List String (GL String) format for the interpretation of a typing result, or a URI identifying a resource in GL String format.                                      | <b>URI</b><br><hr/> <b>Text</b><br>0..1                 | <hr/> Text;       |
|  <b>Allele DB</b>      | Database or other source for nomenclature used in the interpretation. (ex: "IMGT-HLADB")   | <b>Text</b><br>0..1                                     | Text;             |
|  <b>Allele Version</b> | A specific version of the allele-db (ex: "3.18.0")   | <b>Text</b><br>0..1                                     | Text;             |
|  <b>Date</b>           | *  | <b>DateTime</b><br>0..1                                 | Allow all         |
|  <b>Antigen</b>       | Slot<br>Consensus sequence [Cluster]   | Include : Cluster                                       | Exclude : Cluster |
|  <b>Antigen</b>      | Slot<br>Property [Cluster]   | Include : Cluster<br>hla_phenotype(-[a-zA-Z0-9_+])*\.v0 | Exclude : Cluster |