








# Immunological\_screening

Entity: Cluster

<b>Concept description:</b>		<b>Identification:</b>			
unknown		<i>Id:</i> openEHR-EHR-CLUSTER.immunological_screening.v0 <i>Reference model:</i> openEHR_EHR			
<b>Purpose</b>	<b>Use</b>	<b>Misuse</b>	<b>Copyright</b>	<b>References</b>	<b>Contact</b>

Concept	Description	Constraints	Values
 <b>Screening</b>	*	<b>Cluster</b> 0..1	
 <b>Screening Date</b>	*	<b>DateTime</b> 0..1	Allow all
<b>T</b> <b>Technique</b>	*	<b>Text</b> 0..1	Internal; 'Luminex', 'Elisa', 'DTT', 'CDC', 'Other'
 <b>Antibodies</b>	*	<b>Cluster</b> 0..*	
<b>T</b> <b>Locus</b>	Locus (ex: "HLA-A", "HLA-DRB1")	<b>Text</b> 1..1	Internal; 'HLA-A', 'HLA-B', 'HLA-C', 'HLA-DR', 'HLA-DQA', 'HLA-DQB', 'HLA-DPA', 'HLA-DPB'
<b>T</b> <b>Method</b>	Typing method used e.g. DNA or Serology	<b>Text</b> 1..1	Internal; 'DNA', 'Serology'
<b>T</b> <b>Type</b>	Allele/code level type (ex: "01:01", "01:AB")	<b>Text</b> 1..1	Text;
	*	<b>Quantity</b>	Property = Qualified real

<b>Q</b> PRA		0..1	Units = %; >=0; <=100;
<b>T</b> Auto antibodies detected	*	<i>Text</i> 0..1	Internal; 'Yes', 'No', 'Not Tested'
<b>T</b> Non cytotoxic/complement fixing antibodies detected	*	<i>Text</i> 0..1	Internal; 'Yes', 'No', 'Unknown', 'Not Tested'
 <i>Cumulative Antibodies</i>	*	<i>Cluster</i> 0..*	
<b>T</b> Locus	Locus (ex: "HLA-A", "HLA- DRB1")	<i>Text</i> 1..1	Internal; 'HLA-A', 'HLA-B', 'HLA- C', 'HLA-DR', 'HLA-DQA', 'HLA- DQB', 'HLA-DPA', 'HLA-DPB'
<b>T</b> Type	Allele/code level type (ex: "01:01", "01:AB")	<i>Text</i> 1..1	Text;
 <i>Unacceptable antigens</i>	*	<i>Cluster</i> 0..*	
<b>T</b> Locus	Locus (ex: "HLA-A", "HLA- DRB1")	<i>Text</i> 1..1	Internal; 'HLA-A', 'HLA-B', 'HLA- C', 'HLA-DR', 'HLA-DQA', 'HLA- DQB', 'HLA-DPA', 'HLA-DPB'
<b>T</b> Type	Allele/code level type (ex: "01:01", "01:AB")	<i>Text</i> 1..1	Text;
<b>T</b> Interpretation	Interpretation of the repeated mismatches. To enable removing some antigens from the set of unacceptable antigens but still marking them as risk for evaluation during cross-matching or after transplantation	<i>Text</i> 1..1	Internal; 'Unacceptable', 'Risk antigen'
 <i>Acceptable antigens</i>	*	<i>Cluster</i> 0..*	
<b>T</b> Locus	Locus (ex: "HLA-A", "HLA- DRB1")	<i>Text</i> 1..1	Internal; 'HLA-A', 'HLA-B', 'HLA- C', 'HLA-DR', 'HLA-DQA', 'HLA- DQB', 'HLA-DPA', 'HLA-DPB'

<b>T</b> Type	Allele/code level type (ex: "01:01", "01:AB")	<i>Text</i> 1..1	Text;
 <i>Donor frequency</i>	*	<i>Cluster</i> 0..*	
<b>T</b> Type	*	<i>Text</i> 1..1	Internal; 'cPRA', 'Kidney', 'Heart'
<b>Q</b> Frequency	*	<i>Quantity</i> 1..1	Property = Qualified real Units = 1; >=0; <=1; Units = %; >=0; <=100;