



IMMUNOLOGY DATABASE
AND ANALYSIS PORTAL

ImmPort User Community Update

May 30, 2008

Teleconference # 1-866-740-2200

Pass code 5630833



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Agenda

ImmPort 2.3 Feature Enhancements

(July 2008)

- DAIT Minimum Information Standards
- HLA Metadata 'Silver Standard'
- Advanced Queries
- Creating and Using Lists

- Comments



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DAIT Minimum Information Standards

DAIT Program Staff, Principal Investigators from the BISC user community, and other researchers developed a set of minimum information standards to describe:

- Research Subjects and their treatments and
- Selected assay methods
 - ELISPOT
 - MBAA (Multiplex Bead Array Assays)
 - Q-PCR

These revised standards are intended to provide guidance on how to describe research methods and results, encourage consistency and facilitate data interoperability.



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DAIT Minimum Information Standards **Continued**

The revised standards are being incorporated into the ImmPort Data Submission templates.

Changes to expect include:

- Requiring a link to the protocols used for subjects, samples and experiments
- An expanded set of descriptive fields to capture specific details of subjects, samples and assays



ELISPOT Reporting

Cell Isolation

- Cell type used and
- Source - preferably from the Cell Ontology or Foundational Model of Anatomy
- Purification method (with link to protocol)

Assay Conditions (link to assay protocol)

- Control type (positive or negative) and description (PHA, PMA)
- Stimulus (name, concentration)
- Accessory cells (e.g. pDC, B cells)
- Length of culture
- Number of replicates
- Product(s) being measured (e.g. cytokine, chemokine)

Instrumentation Reporting

- Measurement method (manual vs. automated)
- Type of measure (independent or multiplex)
- Type of ELISPOT reader/software (name)
- Units reported (spots/100 cells, etc.)
- Instrument/software settings for spot identification

Data Analysis and Reporting

- Post facto data analysis software (after machine processing)
- Statistical methods (link to protocol)

Data deposition

- Text files containing spot sizes and intensities
- Final analyzed data



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HLA Silver Standard

Glenys Thomson, Steve Mack and HLA Consortium Investigators

Our aim is data validation via a standard reporting of HLA data to include:

- Documentation of the *typing method* used.
For each locus, this includes:
 - Manufacturer of the typing system used (e.g., Luminex, Dynal, etc.).
 - Version of the typing system used (this may include catalog number).
 - Typing approach used to generate the primary data (e.g., SBT, PCR-SSOP, SSP, RSCP, etc.).
 - Exons interrogated (minimally exons 2&3 for class I, and exon 2 for class II loci).
 - A list of the primer and probe sequences used.
 - A list of all alleles detectable using the system.
 - A sublist of all alleles that can be detected unambiguously by the system.
 - A sublist of all allele sets detected ambiguously by the system (i.e., sets of alleles that cannot be distinguished due to polymorphisms that are not detected by the system).
- A listing of *all allele and genotype ambiguities* per individual per locus (given the typing system), formatted to accurately record the ambiguities generated by the typing system.
- Documentation of the *rules* used to assign the two most likely allele “calls.”
- A listing of the two most likely allele “calls.””



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HLA Silver Standard Impact on ImmPort Data Submission

Changes to ImmPort templates will include revised templates for describing HLA typing systems.

BISC currently supports

- QC pipeline for allele name validation
- Mapping of allele names to 'Common and Well Documented' (CWD) alleles

(Common and well-documented HLA alleles: report of the Ad-Hoc committee of the american society for histocompatibility and immunogenetics. Hum Immunol. 2007 May;68(5):392-417. Epub 2007 Feb 15)

- Allele binning



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Advanced Queries

Enable searches of ImmPort submitted data using a user customizable combination of filters.

‘Find all human subjects that have gene expression assay results from the Affymetrix U95 microarray.’

‘Find samples that have genotyping and flow cytometry results.’

- ‘Intuitive’ user interface that allows selection of the data attributes relevant to an investigator.



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List Management

Create Lists from Advanced Query Results

Use Lists in ImmPort gene expression and genetic analysis tools



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Comments and Questions?