

# Introduction to Bioinformatics

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Director of Informatics

JCVI



**ViPR**  
Virus Pathogen Resource



Influenza Research Database

**J. Craig Venter**<sup>®</sup>  
I N S T I T U T E

# Outline

- What is Bioinformatics?
  - Some definitions
  - Data types and analysis objectives
- Big Data
  - The Big Data value proposition
- The Power of Bioinformatics
  - Extracting knowledge from data
  - DMID Systems Biology data in the Bioinformatics Resource Centers

# What is Bioinformatics?

- And related terms – biomedical informatics, computational biology, systems biology
- Wikipedia
  - Bioinformatics: an interdisciplinary field that develops and improves on methods for storing, retrieving, organizing and analyzing biological data. A major activity in bioinformatics is to develop software tools to generate useful biological knowledge.
- NIH Biomedical Information Science and Technology Initiative Consortium (BISTIC)
  - Bioinformatics: Research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize, archive, analyze, or visualize such data.
  - Computational Biology: The development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems.

# What is Bioinformatics?

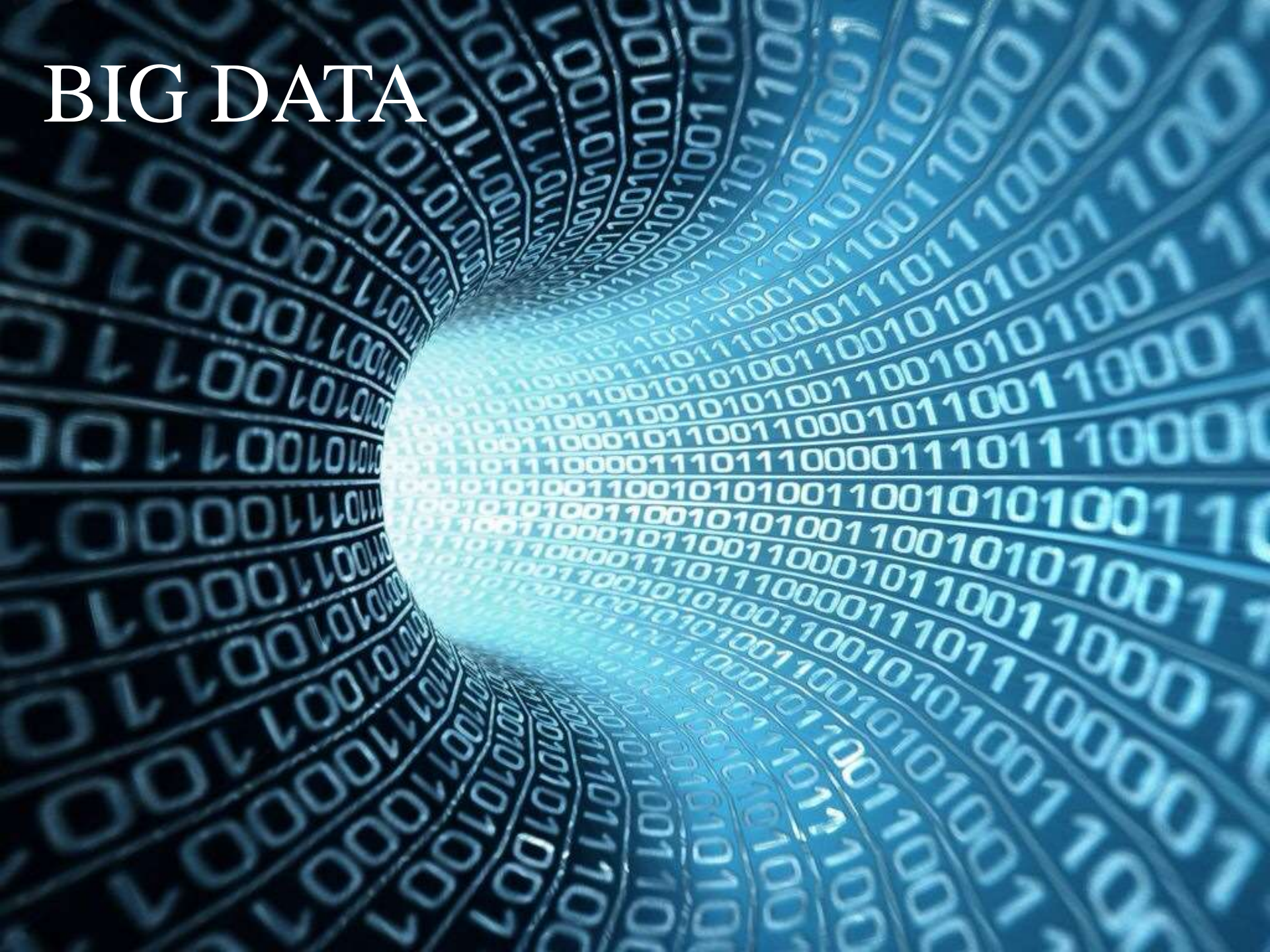
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# Biological data types and analysis objectives

- Genomics
  - Nucleotide genome sequences, metagenomic sequences
  - Gene finding, functional annotation, sequence alignment, homology determination, comparative analysis, phylogenetic inferencing, association analysis, mutation functional prediction, species distribution analysis
- Transcriptomics
  - RNA expression levels, transcription factor binding, chromatin structure information
  - Differential expression, clustering, functional enrichment, transcriptional regulation/causal reasoning
- Proteomics
  - Proteins levels, protein structures, protein interactions
  - Protein identification, protein functional predictions, structural predictions, structural comparison, molecular dynamic simulation, mutation functional prediction, docking predictions, network analysis
- Metabolomics
  - Metabolite/small molecule levels
  - Pathway/network analysis
- Imaging
  - Microscopy images, MRI images, CT scans
  - Feature extraction, high content screening
- Cytometry
  - Cell levels, cell phenotypes
  - Cell population clustering, cell biomarker discovery
- Systems biology
  - All of the above
  - Network analysis, causal reasoning, reverse causal reasoning, drug target prediction, regulatory network analysis, information flow, population dynamics, modeling and simulation



# BIG DATA







FUNDING OPPORTUNITIES & NOTICES

WORKSHOPS

NEWS

ABOUT BD2K

FAQs



The NIH Big Data to Knowledge (BD2K) announces funding opportunity for

## CENTERS OF EXCELLENCE FOR BIG DATA COMPUTING IN THE BIOMEDICAL SCIENCES

[LEARN MORE](#)

The mission of the **NIH Big Data to Knowledge (BD2K)** initiative is to enable biomedical scientists to capitalize more fully on the Big Data being generated by those research communities. With advances in technologies, these investigators are increasingly generating and using large, complex, and diverse datasets. Consequently, the biomedical research enterprise is increasingly becoming data-intensive and data-driven. However, the ability of researchers to locate, analyze, and use Big Data (and more generally all biomedical and behavioral data) is often limited for reasons related to access to relevant software and tools, expertise, and other factors. BD2K aims to develop the new approaches, standards, methods, tools, software, and competencies that will enhance the use of biomedical Big Data by supporting research, implementation, and training in data science and other relevant fields that will lead to: [Read more](#)

## WORKSHOPS



**Frameworks for Community-Based Standards Efforts**

September 25 - 26, 2013

[More Workshops >](#)

## NEWS HIGHLIGHT

- **NIH Names Dr. Philip E. Bourne First Associate Director for Data Science**  
December 9, 2013
- **NIH commits \$24 million annually for Big Data Centers of Excellence**  
July 22, 2013
- **NIH to recruit Associate Director for Data Science**  
January 10, 2013
- **NIH proposes critical initiatives to sustain future of U.S. biomedical research**  
December 7, 2012

[More News >](#)

## FUNDING OPPORTUNITIES & NOTICES

- **Development of an NIH BD2K Data Discovery Index Coordination Consortium(U24)**  
December 17, 2013
- **BD2K-LINCS-Perturbation Data Coordination and Integration Center (DCIC) (U54)**  
December 4, 2013
- **Input on Development of Analysis Methods and Software for Big Data (RFI)**  
August 8, 2013
- **Centers of Excellence for Big Data Computing in the Biomedical Sciences (U54)**  
July 22, 2013

## CONNECT WITH US



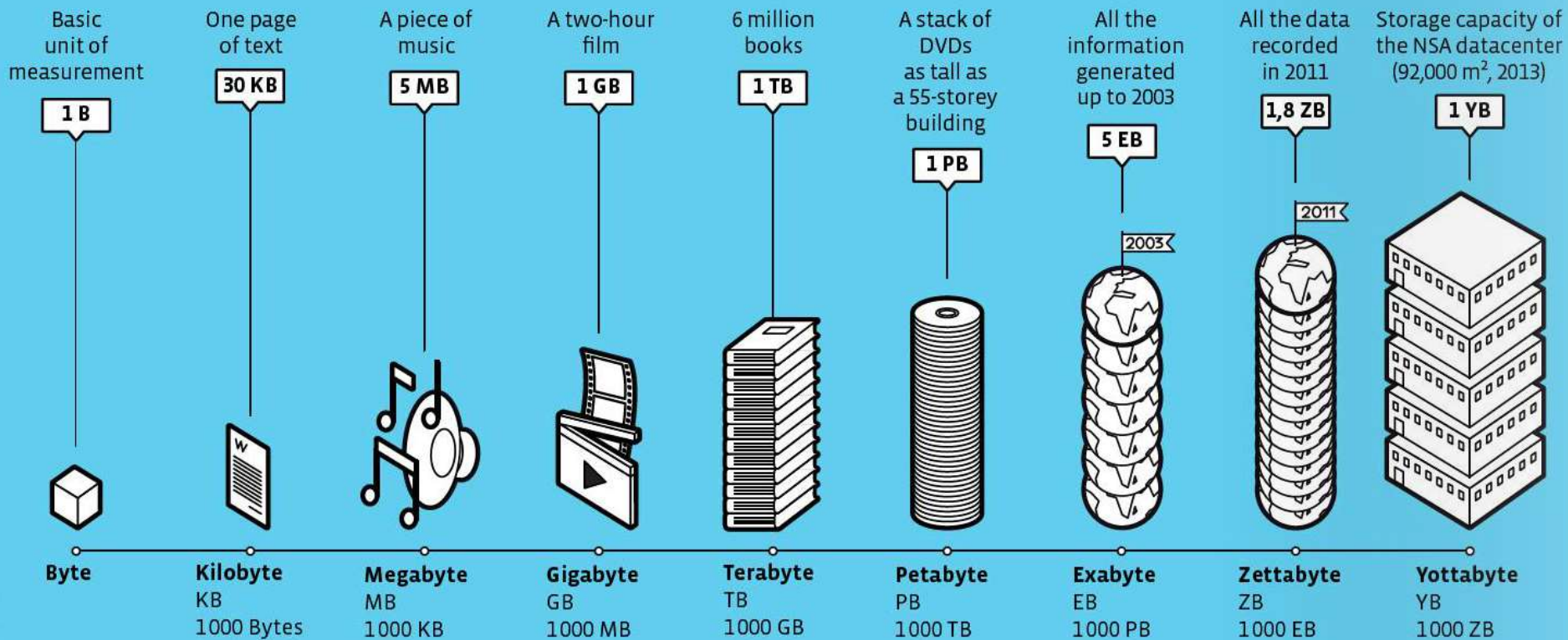
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Follow us on Twitter

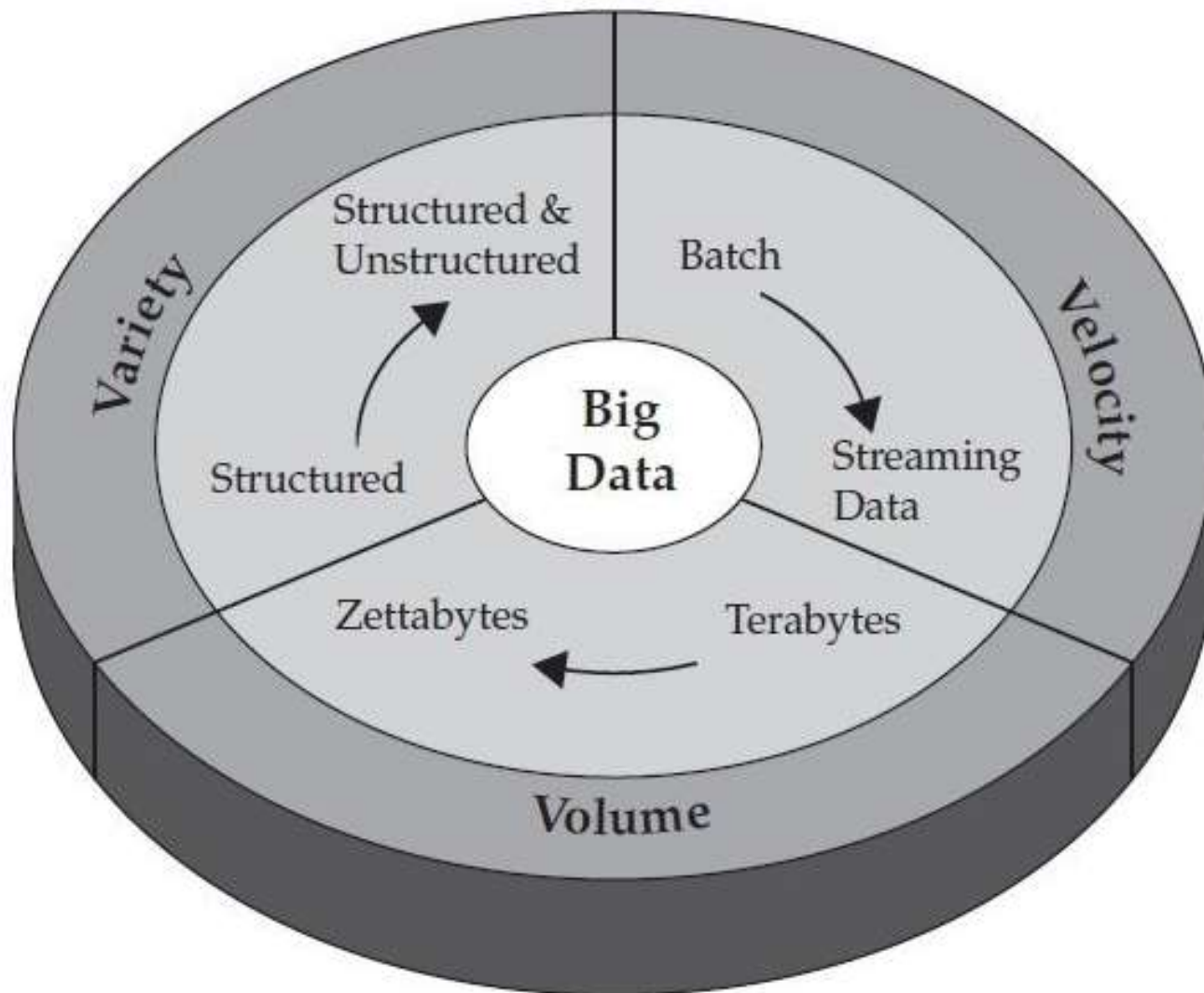
# Big Data Volumes

## COMPARATIVE SCALE OF BYTES

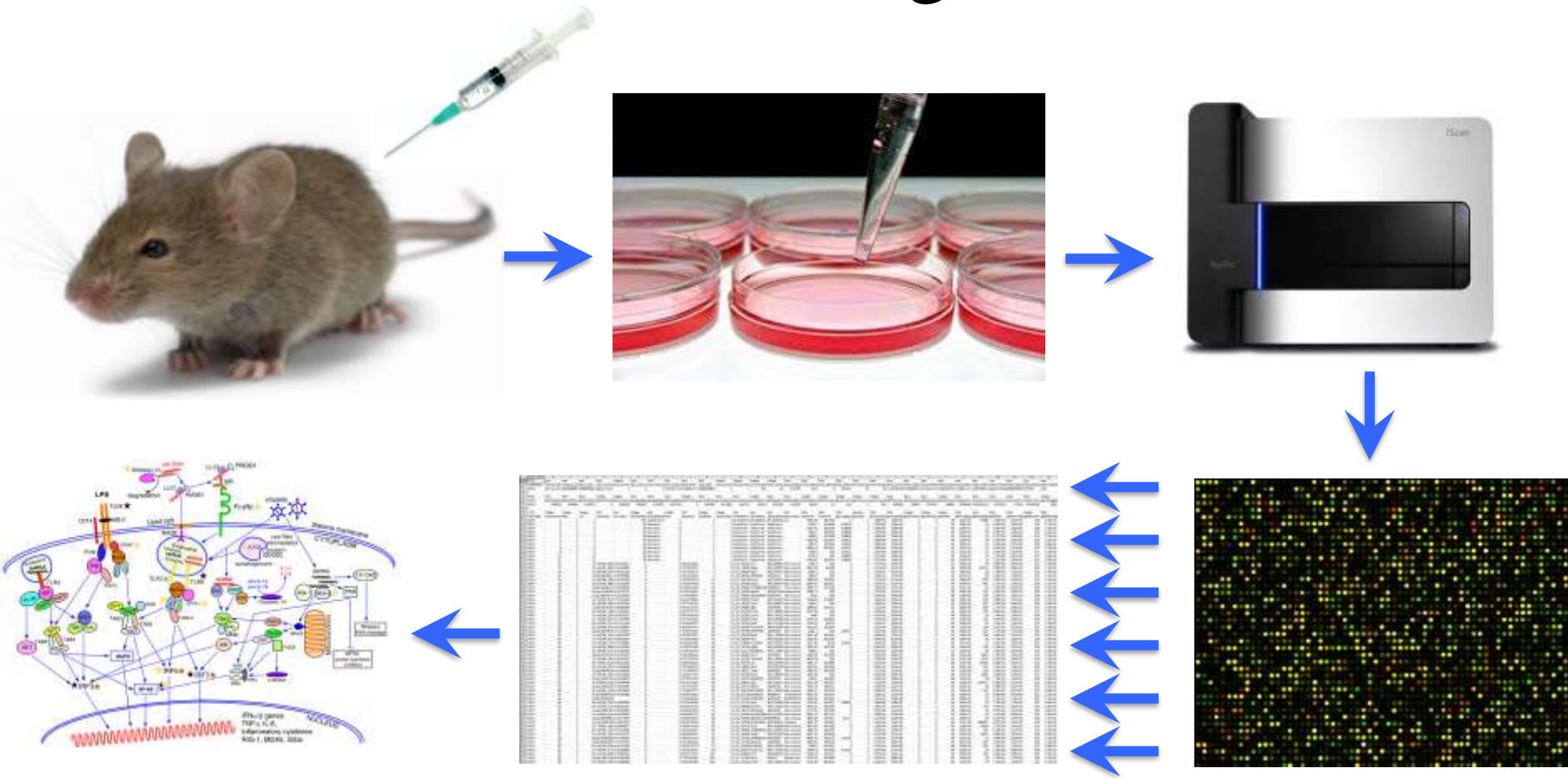




# Big Data 3 V's



# Data Levels in Biological Research

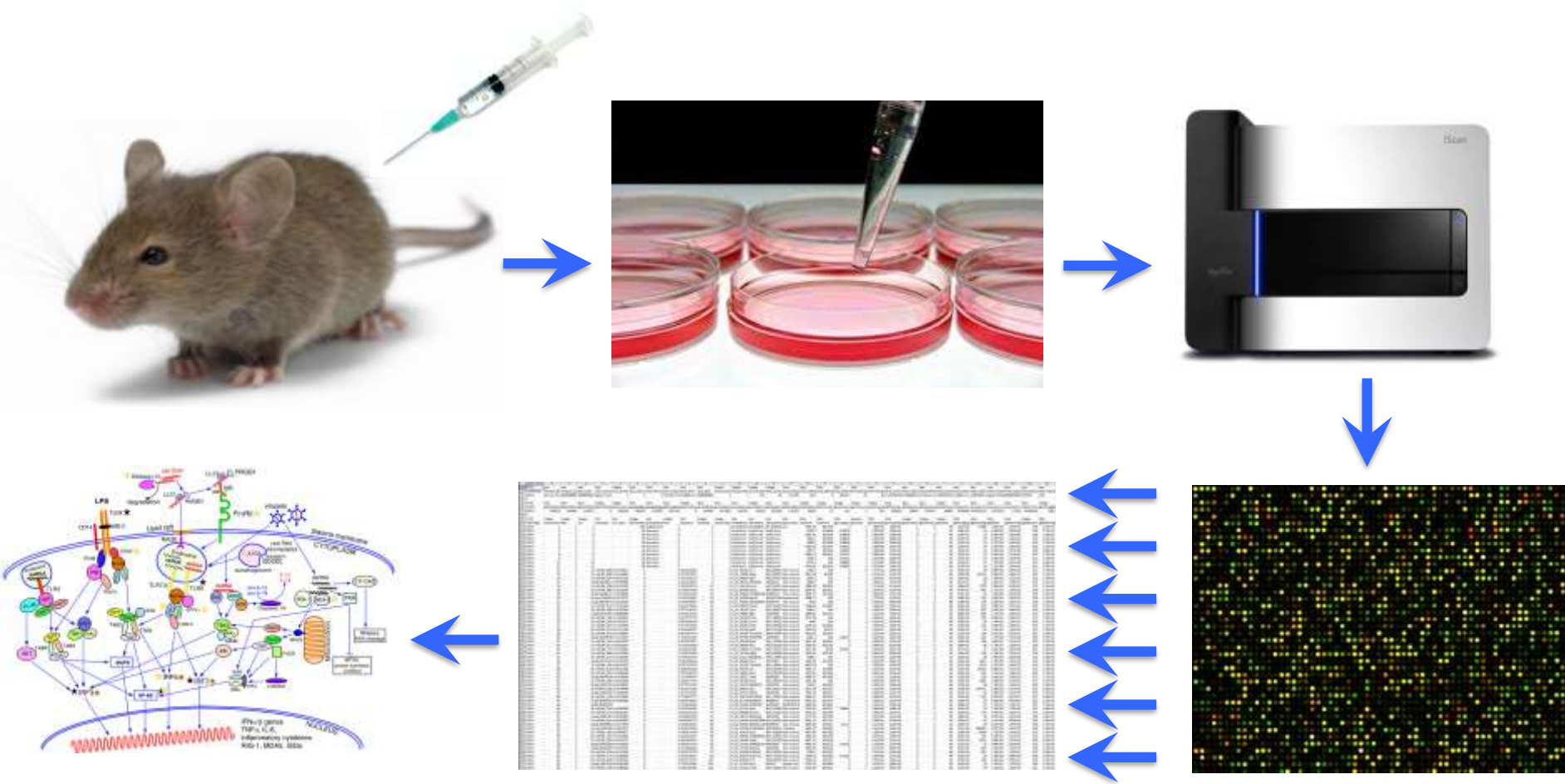


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INSTITUTE

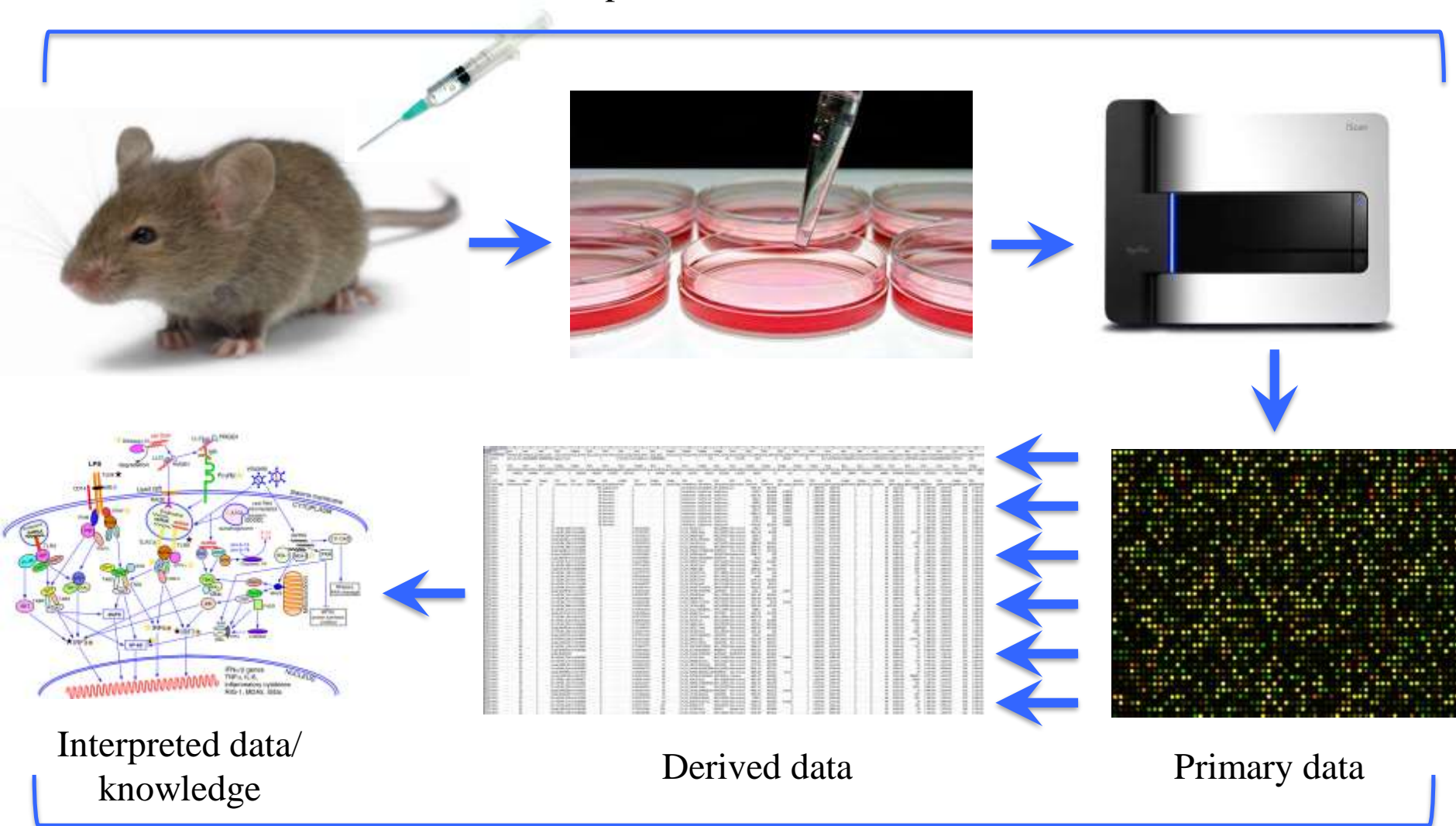


Derived data

Primary data



## Experimental metadata



## Analytical metadata



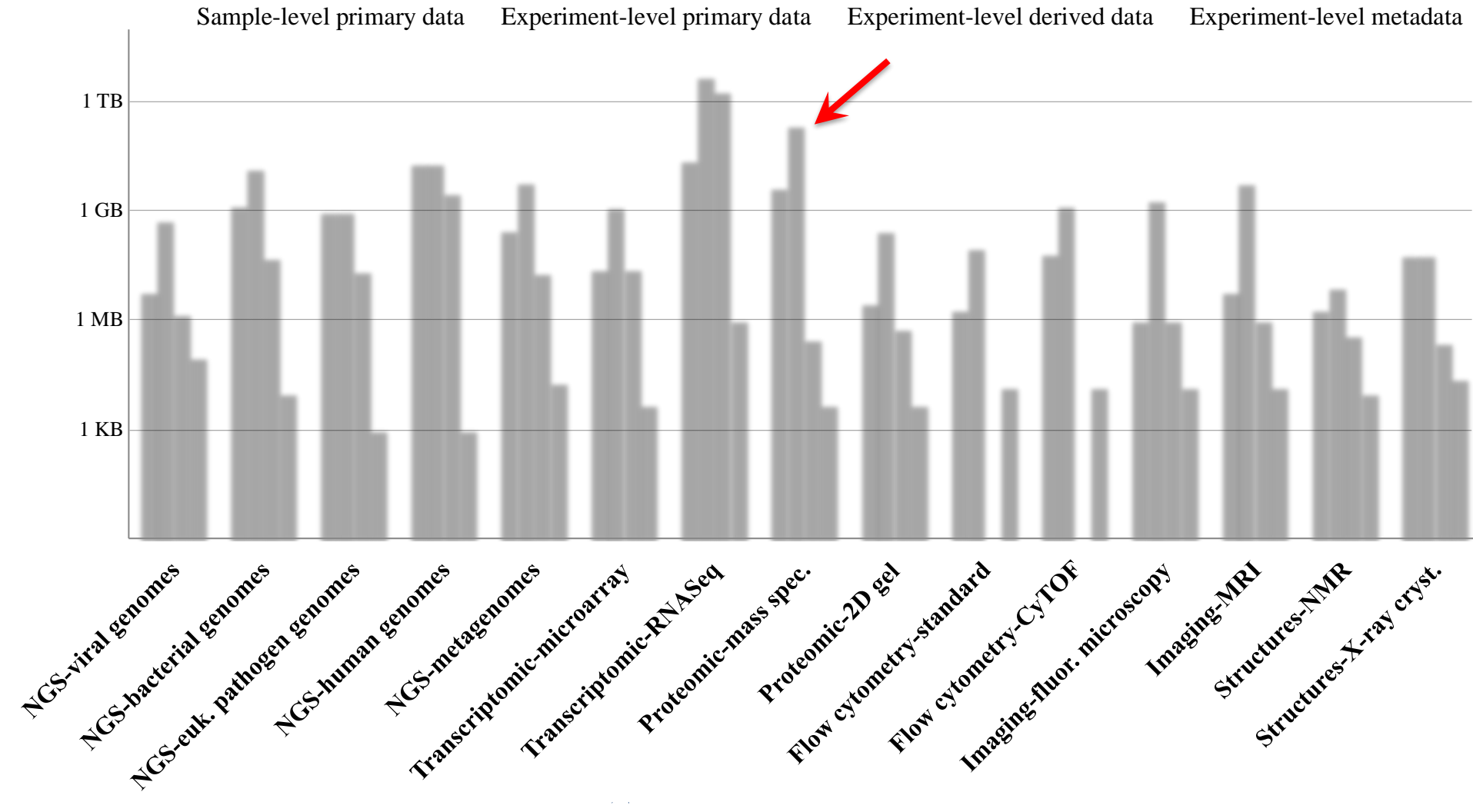
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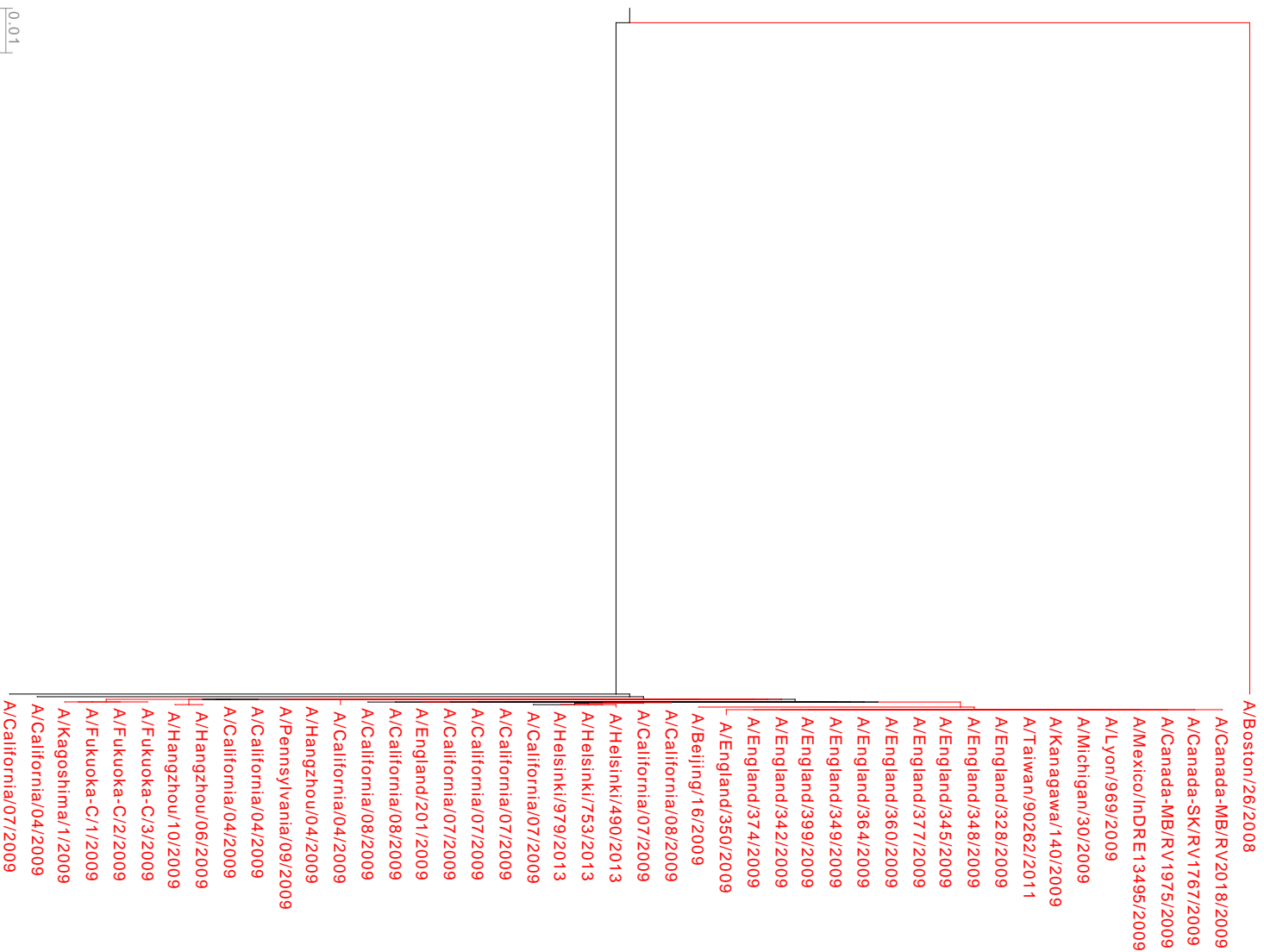
# Big Data in Biology







# No Variety



0.01

# Big Data

Volume + Variety = Value

Variety = Metadata

# \* NIAID/DMID Genomics Program

## Sequencing

Genomic  
Sequencing  
Centers

## Functional Genomics

Functional  
Genomic  
Research  
Centers

## Proteomics

Clinical  
Proteomics  
Centers

## Structural Genomics

Structural  
Genomics  
Centers

## Systems Biology

Systems  
Biology  
Centers

Bioinformatics  
Resource  
Centers

## Genomic Research Resources

Genomic/Omics Data Sets, Databases, Bioinformatics Tools, Biomarkers, 3D Structures, Protein Clones, Predictive Models

To address key questions in  
microbiology and infectious  
disease

To identify new targets and develop  
new strategies for vaccines,  
diagnostics and therapeutics



# Bioinformatics Resource Centers (BRCs)





## Resources for Researchers

[DMID Resources for Researchers](#)

[Systems Biology](#)

[News Releases](#)

[Related Resources](#)

[Systems Biology Working Group](#)

[Data Sharing Guidelines](#)

## Systems Biology for Infectious Diseases Research

### What services do the programs provide?

The NIAID program in Systems Biology for Infectious Diseases Research utilizes a combination of computational and experimental methodologies to conduct research projects to analyze, identify, quantify, model, and predict the overall dynamics of the network of cellular molecular components of microbial organisms and their interactions with the host cells. The knowledge generated from the research projects, including research data, analytical software tools, computational models, experimental protocols, and reagents, is widely disseminated to the scientific community through publicly accessible databases and reagent repositories. The research findings will provide a deeper understanding of the overall complexity of the biological, biochemical and biophysical molecular processes in microbial organisms as well as how the molecular events within the pathogen lead to the initiation and progression of infectious disease.

### Where are services provided?

The research activities are carried out by

- [Battelle—Pacific Northwest National Laboratory \(Systems Biology for Enteropathogens\)](#)
- [Institute for Systems Biology \(Systems Influenza\)](#)
- [Stanford University and the Broad Institute \(TB Systems Biology\)](#)
- [University of Washington \(Systems Virology\)](#)

### Access

Research and associated data, protocols, and computational and statistical models will be made freely and publicly available to the scientific community through the research centers websites within 4 weeks of publication, or within 1 year of generation, whichever comes first and as agreed upon by the Project Officer.

Reagents will be made available through the [BEI Resources Repository \(BEI\)](#).

### Related Resources and Information

- [Data Sharing Guiding Principles](#)
- [News and Announcements](#)
- [Related NIAID-Supported Services](#)

## Website Tools

- [Email this page](#)
- [Print this page](#)
- [Get email updates](#)
- [Get plug-ins and viewers](#)
- [Order publications](#)
- [Bookmark & share](#)

## Stay Connected



[Social media privacy policy and disclaimers.](#)

## Contact Info

Valentina Di Francesco

**E-mail:**  
[vdifrancesco@niaid.nih.gov](mailto:vdifrancesco@niaid.nih.gov)

## Highlight

Funding Opportunity:  
"OMICS" Technologies For  
Predictive Modeling of  
Infectious Diseases (U19)

[Building on a Decade of  
Accomplishments: Report of  
the 2010 Blue Ribbon Panel  
on Genomics \(PDF\)](#)

[A Systems Biology Approach  
to Infectious Disease  
Research: Innovating the  
Pathogen-Host Research  
Paradigm](#), Feb 2011

[New class of biomolecules  
triggered in response to  
respiratory virus infection](#),  
October 25, 2010

[What is systems biology?](#),  
Feb. 2010

# Systems Biology of Viral Infection

- Systems Virology (Michael Katze group, Univ. Washington)
  - Influenza H1N1 and H5N1 and SARS Coronavirus
  - Statistical models, algorithms and software, raw and processed gene expression data, and proteomics data
- Systems Influenza (Alan Aderem group, Institute for Systems Biology/Seattle Biomed)
  - Various influenza viruses
  - Microarray, mass spectrometry, and lipidomics data

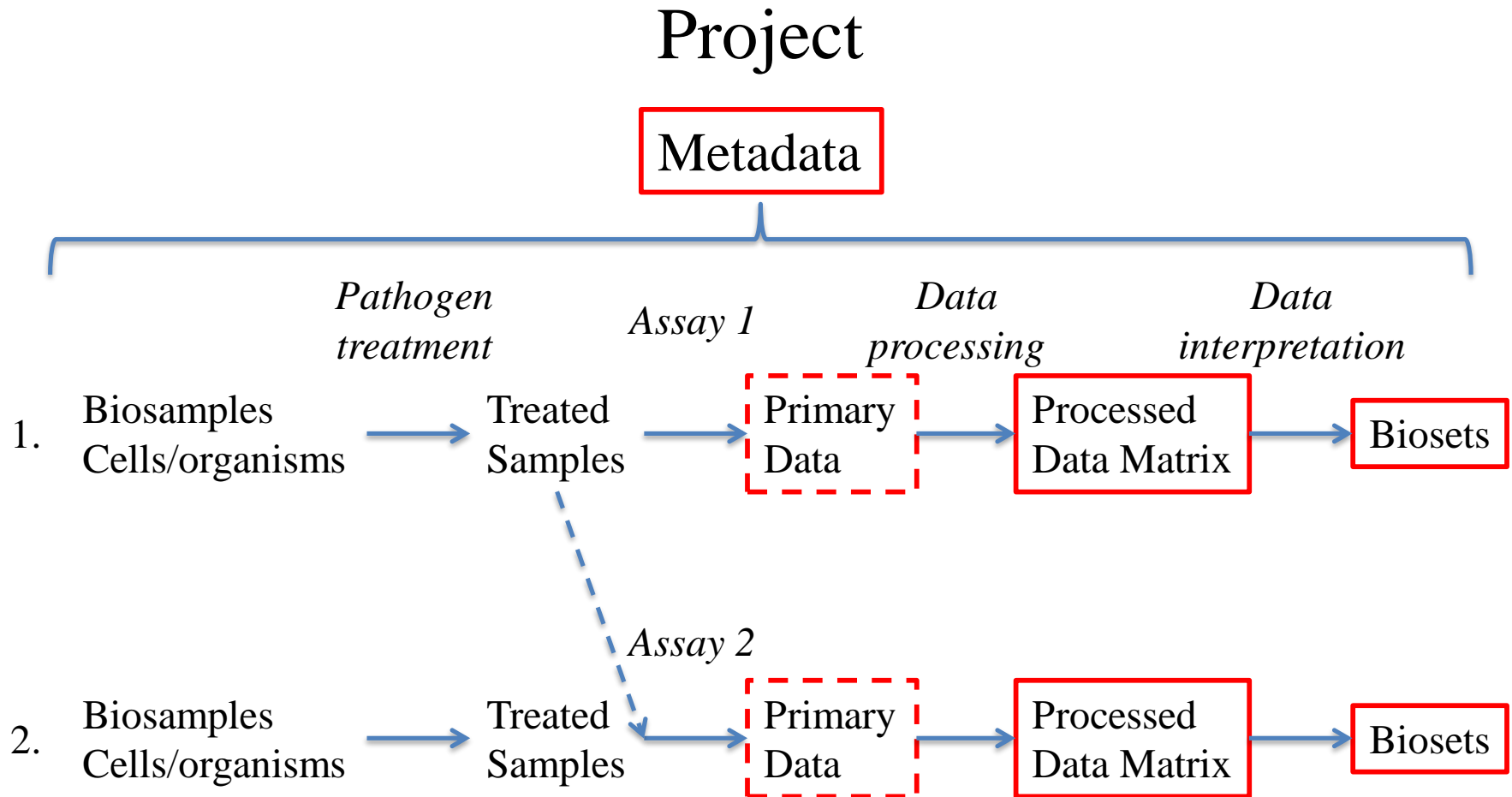


# Data Dissemination Working Group

- Representatives from SysBio programs and relevant BRCs
- Jeremy Zucker



# “Omics” Data Management

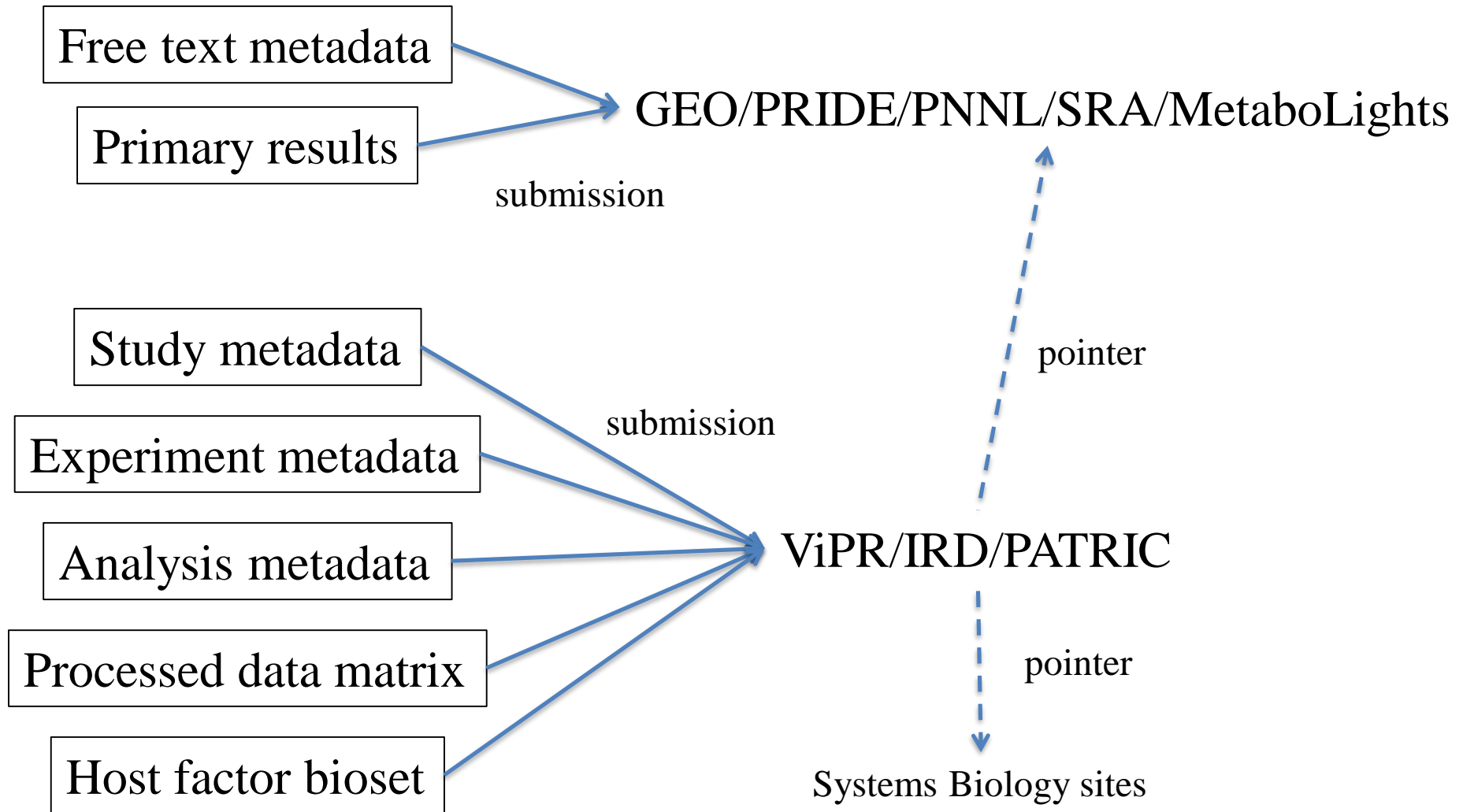


# Strategy for Handling “Omics” Data

- “Omics” data management (MIBBI)
  - Project metadata (1 template)
    - Title, PI, abstract, publications
  - Experiment metadata (~6 templates)
    - Biosamples, treatments, reagents, protocols, subjects
  - Primary results data
    - Raw expression values
  - Processed data
    - Data matrix of fold changes and p-values
  - Data processing metadata (1 template)
    - Normalization and summarization methods
  - Interpreted results (Host factor biosets)
    - Interesting gene, protein and metabolite lists
  - Data interpretation metadata (1 template)
    - Fold change and p-value cutoffs used
- Visualize biosets in context of biological pathways and networks
- Statistical analysis of pathway/sub-network overrepresentation



# Data Submission Workflows



[SEARCH DATA](#)[ANALYZE & VISUALIZE](#)[WORKBENCH](#)[SUBMIT DATA](#)

## Search

Search our comprehensive database for:

- ▲ Influenza segment and protein sequences
- ▲ Avian and non-human mammalian surveillance data
- ▲ Virus phenotypic characteristics
- ▲ Host Factor Data (Prototype)
- ▲ Immune epitope data
- ▲ 3D protein structures

[Browse All Search Types](#)

## Analyze

Analyze data online:

- ▲ Align sequences
- ▲ Identify similar sequences (BLAST)
- ▲ Identify short peptides in flu proteins
- ▲ Identify point mutations in flu proteins
- ▲ Analyze Sequence Variation (SNP)
- ▲ Generate a phylogenetic tree

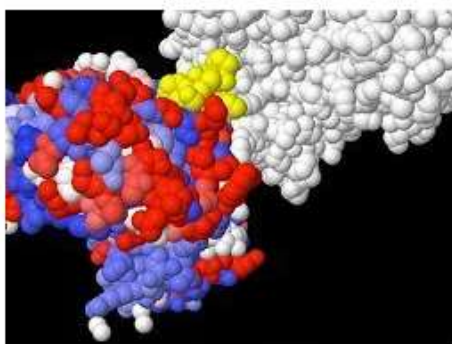
[Browse All Tools](#)

## Save to Workbench

Use your **workbench** to:

- ▲ Store sequences or other data in working sets for future analysis
- ▲ Combine working sets
- ▲ Integrate IRD data with your laboratory data
- ▲ Store analysis results
- ▲ Share results

## Highlights



### 3D Protein Structure

Visualize protein structures in 3D. Users can display sequence conservation score on a structure and highlight experimentally determined epitopes as well.

#### Key Highlights:

- Visualize protein structure in 3D
- Display sequence conservation heat map on the structure
- Highlight sequence features (epitopes, etc.)
- Download highlighted protein structure image

[View 3D Structure](#)[Start Search](#)[Tutorial](#)

### Comparative Analysis of MERS-CoV Sequences

We have recently completed a [comparative genomics analysis](#) of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) whole genome sequences, with implications for viral evolution, performed using the suite of bioinformatics tools available in ViPR. Also see a digest of recent events concerning MERS-CoV [here](#).

### What's New with Flu

An article in *Cell* says that a single amino acid change enhances **H7N9** binding to lung receptors, but no new human H7N9 cases reported in a month. WHO implements a new 4-phase pandemic alert system, and issues a new H7N9 risk assessment. Find these and other flu developments in the latest [IRD Influenza Digest](#) ([View Archive](#)).

And be sure to see a [sequence analysis](#) with implications for H7N9 evolution, carried out by IRD scientists using IRD comparative genomics analysis tools.

### Announcements

- St. Jude Children's Research Hospital CEIRS

### Community Spotlight

[View Archive](#)

We would like to recognize the contribution of all our

# Live Demo



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I N S T I T U T E



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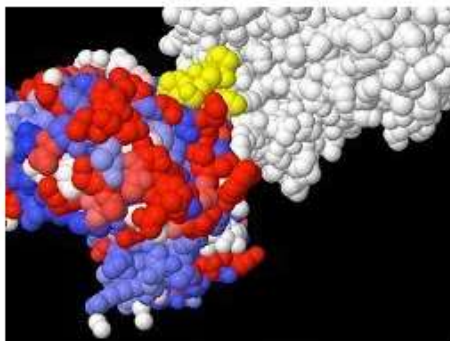
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[View Archive](#)

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### Host Factor Experiments

Listed below are experiments from NIAID funded studies of viral infection. A given study may be divided into multiple experiments based commonly on the type of biological measurement.

### Search Help

- Keyword Search uses an exact match to fields Entrez Gene ID, Gene Accession, Symbol, Product Name
- Selection of checkboxes will use a "or" for checkboxes in a category and "and" for groups of categories.

Displaying 55 of 55 records.

Data sorted by Experiment ID in ascending order

☐ Select all 55 records (including those not displayed)

**KEYWORD**

**FAMILY (55)**

- ☐ Coronaviridae (21)
- ☐ Orthomyxoviridae (33)

**VIRAL AGENT (92)**

- ☐ Bris/59/07 (H1N1) (1)
- ☐ CA04 (H1N1) (10)
- ☐ HKx31\_RG (H3N2) (3)
- ☐ Interferon alpha (1)
- ☐ Interferon gamma (1)
- ☐ MA-CA/04 (H1N1) (1)
- ☐ MERS-CoV (1)
- ☐ Mex/4482/09 (H1N1) (1)
- ☐ NJB/76 (H1N1) (1)
- ☐ NL602 (H1N1) (2)
- ☐ PR8 (H1N1) (5)
- ☐ SARS CoV MA15 (11)
- ☐ VN1203 (H5N1) (9)
- ☐ VN1203(6+2)\_RG (H5N1 ... (1)
- ☐ VN1203-CIP048\_RG1 (... (1)
- ☐ VN1203-CIP048\_RG2 (... (4)
- ☐ VN1203-CIP048\_RG3 (... (8)
- ☐ VN1203-CIP048\_RG4 (... (1)
- ☐ VN1203\_CIP048\_RG5 (... (1)
- ☐ VN1203\_CIP048\_RG6 (... (1)
- ☐ icSARS Bat (1)
- ☐ icSARS CoV (1)
- ☐ icSARS CoV Urbani (1)
- ☐ icSARS ExoNI (2)
- ☐ icSARS nNSP18 (3)
- ☐ icSARS gORF6 (6)
- ☐ r1918 (H1N1) (1)

**ANALYTE TYPE (55)**

- ☐ Lipid Quantification (4)
- ☐ Protein Quantification (16)
- ☐ Transcript Quantification (35)

**HOST (55)**

- ☐ Human (21)
- ☐ Mouse (34)

**TIME POST INFECTION (291)**

- ☐ 0 days (20)
- ☐ 3 hours (14)
- ☐ 6 hours (4)

**Your Selected Items: 0 items selected**

View Associated Biosets Save Search Download

Experiment ID	Study Name	Analyte Type	Viral Agent	Viral
<input checked="" type="checkbox"/> CAD4M001-P	CAD4M001 :A/CA/04/09 (H1N1) infection in C57BL/6 mice with variable doses and times post infection.	Protein Quantification	CA04 (H1N1)	10 <sup>4</sup> , 10 <sup>5</sup>
<input checked="" type="checkbox"/> CA04M001-R	CAD4M001 :A/CA/04/09 (H1N1) infection in C57BL/6 mice with variable doses and times post infection.	Transcript Quantification	CA04 (H1N1)	10 <sup>3</sup> , 10 <sup>4</sup> , PFU
<input type="checkbox"/> ECL001-R	ECL001: MERS-CoV infection in Calu3 cells: A time course	Transcript Quantification	MERS-CoV	5 MOI
<input type="checkbox"/> ICL004-P	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Protein Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/> ICL004-R	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Transcript Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/> ICL006-P	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Protein Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/> ICL006-R	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Transcript Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/> ICL010-P	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Protein Quantification	NL602 (H1N1)	3 MOI
<input type="checkbox"/> ICL010-R	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Transcript Quantification	CA04 (H1N1), NL602 (H1N1)	3 MOI
<input type="checkbox"/> ICL011-P	ICL011: VN1203 PB2-627E and PB1-F2del infection in Calu3 cells: A time course	Protein Quantification	VN1203 (H5N1), VN1203-CIP048_RG2 (H5N1), VN1203-CIP048_RG3 (H5N1)	1 MOI
<input type="checkbox"/> ICL011-R	ICL011: VN1203 PB2-627E and PB1-F2del infection in Calu3 cells: A time course	Transcript Quantification	VN1203 (H5N1), VN1203-CIP048_RG2 (H5N1), VN1203-CIP048_RG3 (H5N1)	1 MOI
<input type="checkbox"/> ICL012-P	ICL012: Vietnam/1203/2004 (H5N1) and Vietnam/1203-NS1-trunc124/2004 (H5N1) infection in Calu3 cells: A time course	Protein Quantification	VN1203 (H5N1), VN1203-CIP048_RG4 (H5N1)	1 MOI
<input type="checkbox"/> ICL012-R	ICL012: Vietnam/1203/2004 (H5N1) and Vietnam/1203-NS1-trunc124/2004 (H5N1) infection in Calu3 cells: A time course	Transcript Quantification	VN1203 (H5N1), VN1203-CIP048_RG4 (H5N1)	1 MOI

The H5N1 VN1203-PB2627E mutant possesses an amino acid substitution (Lys-to-Glu) at position 627 in the PB2 polymerase subunit. This mutation is known to confer increased polymerase activity in mammalian cells, and also modulates anti-viral activity, apoptosis, and viral clearance.

- 35 transcriptomic, 16 proteomic, 4 lipidomic experiments
- 2845 experiment samples
- 590 biosets
- 24 viral (flu, SARS, MERS) and 2 non-viral agents

# Host Factor Experiment [ICL004-R]

[Search Host Factor Experiments](#)[Result Matrix](#)[Previous Experiment](#) **Browse** [Next Experiment](#)[Experiment Information](#) | [Experiment Sample Summary](#) | [Host Factor Bioset Information](#) | [Host Factor Bioset Summary](#) | [Host Factor Bioset Patterns](#) | [Host Factor Results](#)

## Experiment Information

<b>Study Name:</b>	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course
<b>Experiment Name:</b>	ICL004-R: Calu-3 infections with A/Vietnam/1203-CIP048_RG1/2004(H5N1)
<b>PI:</b>	Michael Katze
<b>Point of Contact:</b>	Lynn Law, University of Washington, Department of Microbiology, Seattle, WA, gllaw@u.washington.edu; Michael Katze, University of Washington, Department of Microbiology, Seattle, WA, honey@u.washington.edu
<b>Experiment Type:</b>	Transcript Quantification
<b>Measurement Technique:</b>	Array, Agilent Techno_G4112F, geo   GPL6480-26599_Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
<b>Description:</b>	Purpose: To obtain samples from Calu-3 cells infected with A/Vietnam/1203/2004 (H5N1) for both transcriptional and proteomics analyses. Details: Time Points = 0*, 3*, 7, 12, 18*, and 24* hours post infection (*note: for proteomics the 0 and 3 hour samples were pooled and the 18 and 24h samples were pooled); Done in triplicate for both RNA and Protein; Triplicates are defined as 3 different wells, plated at the same time using the same cell stock for all replicates; Time matched mocks done in triplicate from same cell stock as rest of samples; Inoculation medium for mock infection was the same as the medium used for virus infection. Infection done at an MOI of 1.
<b>Experimenters:</b>	Yoshi Kawaoka, Dick Smith, Michael Katze, Shannon McWeeney, Katrina Waters
<b>PubMed ID:</b>	21865398 <a href="#">↗</a> 22074594 <a href="#">↗</a>
<b>Conditional Variables:</b>	Time points
<b>Host Species Used:</b>	Human
<b>Geo Accession:</b>	GSE28166 <a href="#">↗</a>
<b>Protocols Used:</b>	T003.0P_Nanochip_Bioanalyzer_protocol TCL001.0P - Preparation of Samples from Calu-3 cells for Isolation of RNA T002.0P Qiagen_RNeasy_Mini_Protocol SCL002.0P - Maintenance, Plating and Virus Infection of Calu-3 cells T006.0P Operating_the_Agilent_Microarray_Scanner T005.0P 4X44K_Hyb_only_protocol T004.1P cRNA_Probe_Synthesis
<b>Viral Agent:</b>	VN1203 (H5N1) High level of pathogenicity

## Experiment Sample Summary

# Animal Subjects	Subject Species	Subject Strain/Line	Strain/Line Characteristics	# Biological Samples	Biological Sample Source	Viral Agent	Viral Dose	Time Post Infection	# Experiment Samples
1	Homo sapiens	Calu-3 cells		36	Cell Line	VN1203 (H5N1)	1 MOI	0,3,7,12,18,24 hours	36

Display Settings: ☒ Abstract

Send to:

BMC Syst Biol. 2011 Nov 11;5:190. doi: 10.1186/1752-0509-5-190.

**Conserved host response to highly pathogenic avian influenza virus infection in human cell culture, mouse and macaque model systems.**

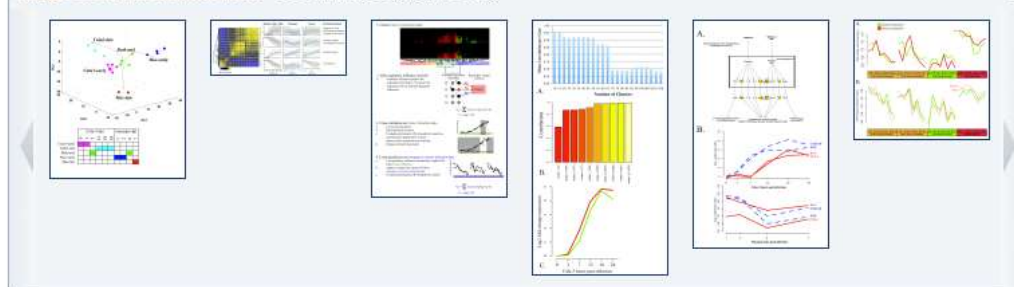
McDermott JE, Shankaran H, Einfeld AJ, Belisle SE, Neuman G, Li C, McWeeney S, Sabourin C, Kawaoka Y, Katze MG, Waters KM.

**Author information****Abstract**

**BACKGROUND:** Understanding host response to influenza virus infection will facilitate development of better diagnoses and therapeutic interventions. Several different experimental models have been used as a proxy for human infection, including cell cultures derived from human cells, mice, and non-human primates. Each of these systems has been studied extensively in isolation, but little effort has been directed toward systematically characterizing the conservation of host response on a global level beyond known immune signaling cascades.

**RESULTS:** In the present study, we employed a multivariate modeling approach to characterize and compare the transcriptional regulatory networks between these three model systems after infection with a highly pathogenic avian influenza virus of the H5N1 subtype. Using this approach we identified functions and pathways that display similar behavior and/or regulation including the well-studied impact on the interferon response and the inflammasome. Our results also suggest a primary response role for airway epithelial cells in initiating hypercytokinemia, which is thought to contribute to the pathogenesis of H5N1 viruses. We further demonstrate that we can use a transcriptional regulatory model from the human cell culture data to make highly accurate predictions about the behavior of important components of the innate immune system in tissues from whole organisms.

**CONCLUSIONS:** This is the first demonstration of a global regulatory network modeling conserved host response between in vitro and in vivo models.

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Systems-level comparison of host-responses elicited by avian H5N1 and sw [PLoS One. 2009]

Highly pathogenic avian influenza H5N1 viruses elicit an attenuated type I interferon [J Virol. 2007]

Host regulatory network response to infection with highly pathogenic H5N1 avian [J Virol. 2011]

**Review** New strategies for the development of H5N1 subtype influenza vaccine [BioDrugs. 2011]**Review** Innate immune responses to influenza A H5N1: friend or foe? [Trends Immunol. 2009][See reviews...](#)[See all...](#)[Click here to read article using PubReader](#)**Cited by 7 PubMed Central articles**

A semiautomated framework for integrating expert knowledge into disease [Dis Markers. 2013]

Old world monkeys and new age science: the evolution of nonhuman primate sy [ILAR J. 2013]

A network integration approach to predict conserved regulators related to [PLoS One. 2013]

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# Host Factor Experiment [ICL004-R]

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[Experiment Information](#) | [Experiment Sample Summary](#) | [Host Factor Bioset Information](#) | [Host Factor Bioset Summary](#) | [Host Factor Bioset Patterns](#) | [Host Factor Results](#)

## Experiment Information

<b>Study Name:</b>	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course
<b>Experiment Name:</b>	ICL004-R: Calu-3 infections with A/Vietnam/1203-CIP048_RG1/2004(H5N1)
<b>PI:</b>	Michael Katze
<b>Point of Contact:</b>	Lynn Law, University of Washington, Department of Microbiology, Seattle, WA, gllaw@u.washington.edu; Michael Katze, University of Washington, Department of Microbiology, Seattle, WA, honey@u.washington.edu
<b>Experiment Type:</b>	Transcript Quantification
<b>Measurement Technique:</b>	Array, Agilent Techno_G4112F, geo   GPL6480-26599_Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
<b>Description:</b>	Purpose: To obtain samples from Calu-3 cells infected with A/Vietnam/1203/2004 (H5N1) for both transcriptional and proteomics analyses. Details: Time Points = 0*, 3*, 7, 12, 18*, and 24* hours post infection (*note: for proteomics the 0 and 3 hour samples were pooled and the 18 and 24h samples were pooled); Done in triplicate for both RNA and Protein; Triplicates are defined as 3 different wells, plated at the same time using the same cell stock for all replicates; Time matched mocks done in triplicate from same cell stock as rest of samples; Inoculation medium for mock infection was the same as the medium used for virus infection. Infection done at an MOI of 1.
<b>Experimenters:</b>	Yoshi Kawaoka, Dick Smith, Michael Katze, Shannon McWeeney, Katrina Waters
<b>PubMed ID:</b>	21865398 <a href="#">↗</a> 22074594 <a href="#">↗</a>
<b>Conditional Variables:</b>	Time points
<b>Host Species Used:</b>	Human
<b>Geo Accession:</b>	GSE28166 <a href="#">↗</a>
<b>Protocols Used:</b>	T003.0P_Nanochip_Bioanalyzer_protocol TCL001.0P - Preparation of Samples from Calu-3 cells for Isolation of RNA T002.0P Qiagen_RNeasy_Mini_Protocol SCL002.0P - Maintenance, Plating and Virus Infection of Calu-3 cells T006.0P Operating_the_Agilent_Microarray_Scanner T005.0P 4X44K_Hyb_only_protocol T004.1P cRNA_Probe_Synthesis
<b>Viral Agent:</b>	VN1203 (H5N1) High level of pathogenicity

## Experiment Sample Summary

# Animal Subjects	Subject Species	Subject Strain/Line	Strain/Line Characteristics	# Biological Samples	Biological Sample Source	Viral Agent	Viral Dose	Time Post Infection	# Experiment Samples
1	Homo sapiens	Calu-3 cells		36	Cell Line	VN1203 (H5N1)	1 MOI	0,3,7,12,18,24 hours	36



## Experiment Sample Details [ICL004-R]

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Row	Experiment Sample User-Defined ID	Subject Species Name	Subject Strain/Line	Biological Sample Source	Treatment 1	Treatment 1 Dose	Treatment 1 Duration	Biological Sample Type	Source
1	251485048466_1_1_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697564</a>
2	251485048495_1_1_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697566</a>
3	251485048496_1_2_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697583</a>
4	251485048496_1_4_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697582</a>
5	251485048497_1_2_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697584</a>
6	251485048498_1_3_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	0 hours	RNA	<a href="#">GSM697565</a>
7	251485048465_1_1_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697568</a>
8	251485048468_1_2_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697569</a>
9	251485048468_1_3_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697567</a>
10	251485048469_1_3_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697585</a>
11	251485048497_1_4_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697586</a>
12	251485048498_1_1_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	3 hours	RNA	<a href="#">GSM697587</a>
13	251485048467_1_1_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	7 hours	RNA	<a href="#">GSM697570</a>
14	251485048469_1_2_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	7 hours	RNA	<a href="#">GSM697589</a>
15	251485048495_1_4_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	7 hours	RNA	<a href="#">GSM697571</a>
16	251485048497_1_3_ES	Homo sapiens	Calu-3 cells	Cell Line	VN1203 (H5N1)	1 MOI	7 hours	RNA	<a href="#">GSM697590</a>

GEO help: Mouse over screen elements for information.

Scope: [Self](#) Format: [HTML](#) Amount: [Quick](#) GEO accession: [GSM697564](#) [View](#)

**Sample GSM697564** [Query DataSets for GSM697564](#)

Status	Public on Sep 02, 2011
Title	Mock_OH_1
Sample type	RNA
Source name	calu3, mock, OH
Organism	<a href="#">Homo sapiens</a>
Characteristics	cell line: Calu-3 cell type: lung adenocarcinoma infection: mock infection duration: 0h
Treatment protocol	For RNA isolation, Calu-3 cells were seeded in 6-well plates (1 x 10 <sup>6</sup> cells/well) two days prior to infection. Immediately preceding infection, monolayers were washed twice with DF12 supplemented with 0.3% bovine serum albumin (DF12-BSA), and inoculated with VN1203 (multiplicity of infection [MOI] of 1 plaque forming unit per cell) in DF12-BSA for 50 minutes at 37°C. Mock-infected controls were inoculated with DF12-BSA only. Following inoculation, monolayers were washed once with DF12-BSA and incubated in DF12-BSA containing 0.5 µg/ml of TPCK-treated trypsin (Worthington Biochemical Corporation, Lakewood, NJ) for the times indicated.
Growth protocol	Calu-3 cells, a human lung adenocarcinoma cell line, were kindly provided by Dr. Raymond Pickles (University of North Carolina, Chapel Hill, NC) and were maintained in a 1:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 nutrient medium (DF12; Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum. All cells were grown at 37°C in an atmosphere of 5% CO <sub>2</sub> , with an antibiotic/antimycotic mixture (Invitrogen).
Extracted molecule	total RNA
Extraction protocol	At 0, 3, 7, 12, 18 and 24 hours post-infection (hpi), triplicate wells of mock-infected and VN1203-infected Calu-3 monolayers were washed with 5 ml cold phosphate-buffered saline (PBS) and lysed directly with 1 ml of TRIzol (Invitrogen), according to the manufacturer's recommendation. The resulting lysates were stored at -80°C until further processing. All TRIzol lysates were processed simultaneously: they were phase-separated, and RNA was isolated from the aqueous phase (diluted 2 fold with RLT buffer) using Qiagen RNeasy Mini columns and the manufacturer's recommended protocol (Qiagen Inc., Valencia, CA). RNA quality was assessed on an Agilent 2100 Bioanalyzer using the nanochip format, and only intact RNA was used for quantitative real-time PCR (qPCR) and microarray analyses.
Label	Cy3
Label protocol	The Agilent One-Color Microarray-Based Gene Expression Analysis Protocol was followed for all processing steps, including Cy3-cDNA probe preparation.
Hybridization protocol	The Agilent One-Color Microarray-Based Gene Expression Analysis Protocol was followed for all processing steps, including hybridization and array washing.
Scan protocol	Dry slides were scanned on an Agilent DNA microarray scanner (Model G2505B) using the XDR setting.
Description	251485048466_1_1 Mock host response OH.
Data processing	Raw images were analyzed using the Agilent Feature Extraction software (version 9.5.3.1) and the GE1-v5_95_Feb07 extraction protocol. Data were normalized using RMA.
Submission date	Mar 24, 2011
Last update date	Sep 02, 2011
Contact name	Armand Bankhead III
Organization name	Oregon Health and Science University
Department	Department of Medical Informatics and Clinical Epidemiology
Street address	3181 SW Sam Jackson Park Rd.
City	Portland
State/province	OR
ZIP/Postal code	97080
Country	USA



Virus

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ITUTE

## Host Factor Bioset Information

<b>Bioset Type:</b>	Differentially expressed genes
<b>Protocol Used:</b>	M001.0P - Statistical Protocol - Normalization, QAQC and Differential Expression Analysis for Agilent Arrays
<b>Description:</b>	This is a results matrix that lists all DE genes compared to time matched mock samples for Calu-3 cell samples infected with A/Vietnam/1203-CIP048_RG1/2004(H5N1) at an MOI of 1. Time points are 0, 3, 7, 12, 18, and 24 h post infection. Differential Expression Criteria: passes Agilent QC flag and $ FC  > 1.5$ and $q\text{-value} < .05$ .
<b>Analysis Method:</b>	Agilent Preprocess 44x4K/LIMMA
<b>Normalization Method:</b>	quantile
<b>Differential Expression Criteria Used:</b>	passes Agilent QC flag and $ \log_2 FC  > 1.5$ and $q\text{-value} < .05$

## Host Factor Bioset Summary

Bioset Name	Host Factors	Viral Agent	Viral Dose	Time Post Infection	Strain/Line	Host
ICL004-R_0	0	VN1203 (H5N1)	1 MOI	0 hours	Calu-3 cells	Human
ICL004-R_3	0	VN1203 (H5N1)	1 MOI	3 hours	Calu-3 cells	Human
ICL004-R_7	5,277	VN1203 (H5N1)	1 MOI	7 hours	Calu-3 cells	Human
ICL004-R_12	13,030	VN1203 (H5N1)	1 MOI	12 hours	Calu-3 cells	Human
ICL004-R_18	12,944	VN1203 (H5N1)	1 MOI	18 hours	Calu-3 cells	Human
ICL004-R_24	17,324	VN1203 (H5N1)	1 MOI	24 hours	Calu-3 cells	Human



## Host Factor Bioset Patterns

Your Selected Items: 0 items selected

Host Factor Results

Download

The Host Factor Results button will create a union of the selected items and build a [table](#) below Host Factor Bioset Patterns.

### Significant Host Factors as Compared to Control

"+" up-regulated, "-" down-regulated, blank: no change

Find expression pattern:

SYMBOL

Use comma to separate multiple entries.  
Ex. DDX58

Find

Your search returned **55** records.

Data sorted by **Number of Probes** in descending order

	Pattern	Virus Time Post Infection Viral Dose Strain/Line	VN1203 (H5N1), 0 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 3 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 12 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 18 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 24 hours, 1 MOI, Calu-3 cells
<input type="checkbox"/>		Host Factors	0	0	<input type="checkbox"/> 5277	<input type="checkbox"/> 13030	<input type="checkbox"/> 12944	<input type="checkbox"/> 17324
<input type="checkbox"/>	0,0,0,+,+,+	2921				+	+	+
<input type="checkbox"/>	0,0,0,-,-,-	2764				-	-	-
<input type="checkbox"/>	0,0,0,0,0,+	2105						+
<input type="checkbox"/>	0,0,0,0,0,-	1974						-
<input type="checkbox"/>	0,0,-,-,-,-	1643			-	-	-	-
<input type="checkbox"/>	0,0,0,0,-,-	1621					-	-
<input type="checkbox"/>	0,0,+,+,+,+	1094			+	+	+	+
<input type="checkbox"/>	0,0,0,0,+,+	931					+	+
<input type="checkbox"/>	0,0,0,+,0,0	919				+		
<input type="checkbox"/>	0,0,0,-,0,0	746				-		
<input type="checkbox"/>	0,0,0,-,0,-	487				-		-
<input type="checkbox"/>	0,0,0,+,0,+	452				+		+
<input type="checkbox"/>	0,0,+,0,0,0	433			+			
<input type="checkbox"/>	0,0,0,+,+,0	433				+	+	
<input type="checkbox"/>	0,0,0,-,-,0	402				-	-	
<input type="checkbox"/>	0,0,-,0,0,0	275			-			
<input type="checkbox"/>	0,0,0,0,-,0	230					-	



# Host Factor Experiments

Listed below are experiments from NIAID funded studies of viral infection. A given study may be divided into multiple experiments based commonly on the type of biological measurement.

Search Help:

- Keyword Search uses an exact match to fields Entrez Gene ID, Gene Accession, Symbol, Product Name.
- Selection of checkboxes will use a "or" for checkboxes in a category and "and" for groups of categories.

Displaying **55 of 55** records.

Data sorted by **Experiment ID** in ascending order

☐ **Select all 55 records** (including those not displayed)

KEYWORD

FAMILY ( 55 )

- ☐ Coronaviridae ( 21 )
- ☐ Orthomyxoviridae ( 33 )

VIRAL AGENT ( 92 )

- ☐ Bris/59/07 (H1N1) ( 1 )
- ☐ CA04 (H1N1) ( 10 )
- ☐ HKx31\_RG (H3N2) ( 3 )
- ☐ Interferon alpha ( 1 )
- ☐ Interferon gamma ( 1 )
- ☐ MA-CA/04 (H1N1) ( 1 )
- ☐ MERS-CoV ( 1 )
- ☐ Mex/4482/09 (H1N1) ( 1 )
- ☐ NJ/8/76 (H1N1) ( 1 )
- ☐ NL602 (H1N1) ( 2 )
- ☐ PR8 (H1N1) ( 5 )
- ☐ SARS CoV MA15 ( 11 )
- ☐ VN1203 (H5N1) ( 9 )
- ☐ VN1203(6+2)\_RG (H5N1 ...

( 1 )

- ☐ VN1203-CIP048\_RG1 ( ... ( 1 )
- ☐ VN1203-CIP048\_RG2 ( ... ( 4 )
- ☐ VN1203-CIP048\_RG3 ( ... ( 6 )
- ☐ VN1203-CIP048\_RG4 ( ... ( 4 )
- ☐ VN1203\_CIP048\_RG1(H5 ...

( 1 )

- ☐ icSARS Bat SRBD ( 6 )
- ☐ icSARS CoV ( 1 )
- ☐ icSARS CoV Urbani ( 9 )
- ☐ icSARS ExoNI ( 2 )
- ☐ icSARS dNSP16 ( 3 )
- ☐ icSARS dORF6 ( 6 )
- ☐ r1918 (H1N1) ( 1 )

Your Selected Items: 2 items selected | [Deselect All](#)

[View Associated Biosets](#)

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<input type="checkbox"/>	Experiment ID	Study Name	Analyte Type	Viral Agent	Viral
<input type="checkbox"/>	CA04M001-P	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Protein Quantification	CA04 (H1N1)	10 <sup>4</sup> , 10 <sup>5</sup>
<input type="checkbox"/>	CA04M001-R	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Transcript Quantification	CA04 (H1N1)	10 <sup>3</sup> , 10 <sup>4</sup> , PFU
<input type="checkbox"/>	ECL001-R	ECL001: MERS-CoV infection in Calu3 cells: A time course	Transcript Quantification	MERS-CoV	5 MOI
<input type="checkbox"/>	ICL004-P	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Protein Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/>	ICL004-R	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Transcript Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/>	ICL006-P	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Protein Quantification	CA04 (H1N1)	3 MOI
<input checked="" type="checkbox"/>	ICL006-R	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Transcript Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/>	ICL010-P	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Protein Quantification	NL602 (H1N1)	3 MOI
<input checked="" type="checkbox"/>	ICL010-R	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Transcript Quantification	CA04 (H1N1), NL602 (H1N1)	3 MOI

# Host Factor Biosets

Search Help:

- Keyword Search uses an exact match to fields Entrez Gene ID, Gene Accession, Symbol, Product Name.
- Selection of checkboxes will use a "or" for checkboxes in a category and "and" for groups of categories.
- If no checkbox is shown for a bioset, no host factors are currently available.

Displaying **22** of **22** records.

Data sorted by **Bioset Name** in ascending order

☐ Select all **22** records (including those not displayed)

KEYWORD

EXPERIMENT NAME (22)

- ☐ CA04M001-P: A/CA/04/ ... (0)
- ☐ CA04M001-R: Mouse in ... (0)
- ☐ ECL001-R: MERS-CoV ... (0)
- ☐ ICL004-P: A/Vietnam/ ... (0)
- ☐ ICL004-R: Calu-3 inf ... (0)
- ☐ ICL006-P: A/CA/04/09 ... (0)
- ☒ ICL006-R: Calu-3 inf ... (9)
- ☐ ICL010-P: A/Netherla ... (0)
- ☒ ICL010-R: A/Netherla ... (13)
- ☐ ICL011-P: VN1203 PB2 ... (0)
- ☐ ICL011-R: VN1203 PB2 ... (0)
- ☐ ICL012-P: Vietnam/12 ... (0)
- ☐ ICL012-R: Vietnam/12 ... (0)
- ☐ IM001-P: A/Vietnam/1 ... (0)
- ☐ IM001-R: Mouse infec ... (0)
- ☐ IM002-R: Influenza A ... (0)
- ☐ IM004-P: VN1203 HA a ... (0)
- ☐ IM004-R: Mouse infec ... (0)
- ☐ IM005-P: Vietnam/120 ... (0)
- ☐ IM005-R: Vietnam/120 ... (0)
- ☐ IM006A-P: Vietnam/12 ... (0)
- ☐ IM006A-R: Vietnam/12 ... (0)
- ☐ IM006B-P: Vietnam/12 ... (0)
- ☐ IM006B-R: Vietnam/12 ... (0)
- ☐ IM007-P: Vietnam/120 ... (0)
- ☐ IM007-R: Vietnam/120 ... (0)
- ☐ IM009-R: Influenza A ... (0)
- ☐ IM010-R: Vietnam/120 ... (0)
- ☐ IM015-R: Influenza A ... (0)
- ☐ SBRI\_AA: Transcripto ... (0)
- ☐ SBRI\_LAE: BALF lipid ... (0)
- ☐ SBRI\_LI: BALF lipid ... (0)
- ☐ SBRI\_LN: BALF lipid ... (0)
- ☐ SBRI\_LV: BALF lipid ... (0)

Your Selected Items: 2 items selected | Deselect All

Patterns

Save Search

Set Operations ▼

Host Factor Results

Download

Find shared factors (Intersect, AND)

Find all factors (Union, OR)

Find unique factors (XOR)

Find exclusive factors (Subtract)

<input type="checkbox"/>	Bioset Name	Host	Strain/Line	Host
<input type="checkbox"/>	ICL006_0hr_H1N1	0	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_12hr_H1N1	1141	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_18hr_H1N1	1948	Calu-3 cells	Human
<input checked="" type="checkbox"/>	ICL006_24hr_H1N1	1546	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_30hr_H1N1	1326	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_36hr_H1N1	1255	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_3hr_H1N1	0	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_48hr_H1N1	1190	Calu-3 cells	Human
<input type="checkbox"/>	ICL006_7hr_H1N1	360	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_Cal_0h_array_DE	0	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_Cal_12h_array_DE	459	Calu-3 cells	Human
<input checked="" type="checkbox"/>	ICL010_Cal_24h_array_DE	756	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_Cal_48h_array_DE	734	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_NL_0h_array_DE	0	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_NL_12h_array_DE	105	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_NL_18h_array_DE	226	Calu-3 cells	Human
<input type="checkbox"/>	ICL010_NL_24h_array_DE	580	Calu-3 cells	Human



# Boolean Analysis Result for Derived Bioset

Search Help:

- Keyword Search uses an exact match to fields Entrez Gene ID, Gene Accession, Symbol, Product Name.
- Selection of checkboxes will use a "or" for checkboxes in a category and "and" for groups of categories.

Displaying 200 of 502 records.

Data sorted by Gene Symbol, Probe Id in ascending order

## SET TYPE

Intersect

## EXPERIMENT NAME ( 2 )

- ☐ CA04M001-P: A/CA/04/ ... ( 0 )
- ☐ CA04M001-R: Mouse in ... ( 0 )
- ☐ ECL001-R: MERS-CoV i ... ( 0 )
- ☐ ICL004-P: A/Vietnam/ ... ( 0 )
- ☐ ICL004-R: Calu-3 inf ... ( 0 )
- ☐ ICL006-P: A/CA/04/09 ... ( 0 )
- ☒ ICL006-R: Calu-3 inf ... ( 1 )
- ☐ ICL010-P: A/Netherla ... ( 0 )
- ☒ ICL010-R: A/Netherla ... ( 1 )
- ☐ ICL011-P: VN1203 PB2 ... ( 0 )
- ☐ ICL011-R: VN1203 PB2 ... ( 0 )
- ☐ ICL012-P: Vietnam/12 ... ( 0 )
- ☐ ICL012-R: Vietnam/12 ... ( 0 )
- ☐ IM001-P: A/Vietnam/1 ... ( 0 )
- ☐ IM001-R: Mouse infec ... ( 0 )
- ☐ IM002-R: Influenza A ... ( 0 )
- ☐ IM004-P: VN1203 HA a ... ( 0 )
- ☐ IM004-R: Mouse infec ... ( 0 )
- ☐ IM005-P: Vietnam/120 ... ( 0 )
- ☐ IM005-R: Vietnam/120 ... ( 0 )
- ☐ IM006A-P: Vietnam/12 ... ( 0 )
- ☐ IM006A-R: Vietnam/12 ... ( 0 )
- ☐ IM006B-P: Vietnam/12 ... ( 0 )
- ☐ IM006B-R: Vietnam/12 ... ( 0 )
- ☐ IM007-P: Vietnam/120 ... ( 0 )
- ☐ IM007-R: Vietnam/120 ... ( 0 )
- ☐ IM009-R: Influenza A ... ( 0 )
- ☐ IM010-R: Vietnam/120 ... ( 0 )
- ☐ IM015-R: Influenza A ... ( 0 )
- ☐ SBRI\_AA: Transcripto ... ( 0 )
- ☐ SCL005-P: icSARS ORF ...

Your Selected Items: 0 items selected




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	Host Factor	Entrez Gene ID	Symbol	Genbank Accession	Name	Import	ICL
<input type="checkbox"/>	A_24_P263878	27	abl2	NM_007314	v-abl abelson murine leukemia viral oncogene homolog 2 (arg, abelson-related gene)		1.8
<input type="checkbox"/>	A_24_P46130	55	acpp	NM_001099	acid phosphatase, prostate		-3.
<input type="checkbox"/>	A_23_P1102	58	acta1	NM_001100	actin, alpha 1, skeletal muscle		2.6
<input type="checkbox"/>	A_23_P126363	11085	adam30	NM_021794	adam metalloproteinase domain 30		1.9
<input type="checkbox"/>	A_23_P137786	54507	adamts14	AK023606	adamts-like 4		2.0
<input type="checkbox"/>	A_23_P49816	55803	adap2	NM_018404	arfgap with dual ph domains 2		1.5
<input type="checkbox"/>	A_23_P51787	270	ampd1	NM_000036	adenosine monophosphate deaminase 1 (isoform m)		4.2
<input type="checkbox"/>	A_23_P159325	51129	angptl4	NM_139314	angiopoietin-like 4		3.5
<input type="checkbox"/>	A_24_P357572	338699	ankrd42	NM_182603	ankyrin repeat domain 42		1.5
<input type="checkbox"/>	A_23_P155049	80830	apol6	NM_030641	apolipoprotein I, 6		2.8
<input type="checkbox"/>	A_24_P941167	80830	apol6	NM_030641	apolipoprotein I, 6		1.7
<input type="checkbox"/>	A_24_P380061	83478	arhgap24	NM_001025616	rho gtpase activating protein 24		-2.
<input type="checkbox"/>	A_24_P414553	57561	arrdc3	NM_020801	arrestin domain containing 3		1.9
<input type="checkbox"/>	A_23_P155265	142686	asb14	NM_130387	ankyrin repeat and soxs box-containing 14		3.1
<input type="checkbox"/>	A_23_P302750	83858	atad3b	AB033099	atpase family, aaa domain containing 3b		2.3
<input type="checkbox"/>	A_23_P118894	79170	atad4	NM_024320	atpase family, aaa domain containing 4		-1.
<input type="checkbox"/>	A_24_P405205	493	atp2b4	NM_001001396	atpase, ca++ transporting, plasma membrane 4		-1.
<input type="checkbox"/>	A_23_P53257	10677	avil	BX647344	advillin		2.5

	Genbank Accession	Name		ICL010_Cal_24h_array_DE		ICL006_24hr_H1N1		
				Import	Log2 FC	Q-Value	Log2 FC	P-Value
	NM_007314	v-abl abelson murine leukemia viral oncogene homolog 2 (arg, abelson-related gene)		1.8	1.3E-2	1.9	1.0E-3	<input type="checkbox"/>
	NM_001099	acid phosphatase, prostate		-3.0	4.1E-3	-1.9	8.3E-4	<input type="checkbox"/>
	NM_001100	actin, alpha 1, skeletal muscle		2.6	1.6E-3	3.0	2.5E-3	<input type="checkbox"/>
	NM_021794	adam metallopeptidase domain 30		1.9	2.4E-2	2.3	7.2E-3	<input type="checkbox"/>
	AK023606	adamts-like 4		2.0	3.2E-2	1.9	4.4E-2	<input type="checkbox"/>
	NM_018404	arfgap with dual ph domains 2		1.5	6.9E-3	1.7	9.3E-3	<input type="checkbox"/>
	NM_000036	adenosine monophosphate deaminase 1 (isoform m)		4.2	2.1E-3	4.0	6.4E-3	<input type="checkbox"/>
	NM_139314	angiopoietin-like 4		3.5	1.5E-3	1.9	5.3E-4	<input type="checkbox"/>
	NM_182603	ankyrin repeat domain 42		1.5	4.2E-2	1.8	9.8E-3	<input type="checkbox"/>
	NM_030641	apolipoprotein I, 6		2.8	4.9E-3	1.5	8.7E-3	<input type="checkbox"/>
	NM_030641	apolipoprotein I, 6		1.7	3.5E-3	2.2	5.0E-3	<input type="checkbox"/>
	NM_001025616	rho gtpase activating protein 24		-2.1	3.6E-3	-1.5	2.0E-2	<input type="checkbox"/>
	NM_020801	arrestin domain containing 3		1.9	2.2E-3	1.5	3.6E-3	<input type="checkbox"/>
	NM_130387	ankyrin repeat and socs box-containing 14		3.1	3.8E-3	2.9	2.1E-2	<input type="checkbox"/>
	AB033099	atpase family, aaa domain containing 3b		2.3	5.0E-3	1.7	4.1E-2	<input type="checkbox"/>
	NM_024320	atpase family, aaa domain containing 4		-1.9	2.7E-3	-2.6	2.7E-4	<input type="checkbox"/>
	NM_001001396	atpase, ca++ transporting, plasma membrane 4		-1.5	2.1E-3	-2.0	5.3E-3	<input type="checkbox"/>
	BX647344	advillin		2.5	5.3E-4	1.7	1.6E-3	<input type="checkbox"/>
	NM_004655	axin 2		-1.9	3.2E-3	-1.5	1.6E-2	<input type="checkbox"/>
	AK022379	beta-2-microglobulin		2.9	2.0E-3	2.9	1.9E-3	<input type="checkbox"/>
	NM_138456	basic leucine zipper transcription factor, atf-like 2		4.2	7.0E-4	3.3	3.1E-4	<input type="checkbox"/>





<input type="checkbox"/>	Experiment ID	Study Name	Analyte Type	Viral Agent	Viral
<input type="checkbox"/>	CA04M001-P	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Protein Quantification	CA04 (H1N1)	$10^4, 10^5$
<input type="checkbox"/>	CA04M001-R	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Transcript Quantification	CA04 (H1N1)	$10^3, 10^4$ , PFU
<input type="checkbox"/>	ECL001-R	ECL001: MERS-CoV infection in Calu3 cells: A time course	Transcript Quantification	MERS-CoV	5 MOI
<input type="checkbox"/>	ICL004-P	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Protein Quantification	VN1203 (H5N1)	1 MOI
<input checked="" type="checkbox"/>	ICL004-R	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Transcript Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/>	ICL006-P	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Protein Quantification	CA04 (H1N1)	3 MOI
<input checked="" type="checkbox"/>	ICL006-R	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Transcript Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/>	ICL010-P	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Protein Quantification	NL602 (H1N1)	3 MOI
<input type="checkbox"/>	ICL010-R	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Transcript Quantification	CA04 (H1N1), NL602 (H1N1)	3 MOI

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Patterns

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Host Factor Results

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<input type="checkbox"/>	<u>Bloset Name</u>	<u>Host Factors</u>	<u>Viral Agent</u>	<u>Viral Dose</u>	<u>Time Post Infection</u>	<u>Strain/Line</u>	<u>Host</u>	<input type="checkbox"/>
<input type="checkbox"/>	ICL004-R_0	0	VN1203 (H5N1)	1 MOI	0 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL004-R_12	13030	VN1203 (H5N1)	1 MOI	12 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL004-R_18	12944	VN1203 (H5N1)	1 MOI	18 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input checked="" type="checkbox"/>	ICL004-R_24	17324	VN1203 (H5N1)	1 MOI	24 hours	Calu-3 cells	Human	<input checked="" type="checkbox"/>
<input type="checkbox"/>	ICL004-R_3	0	VN1203 (H5N1)	1 MOI	3 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL004-R_7	5277	VN1203 (H5N1)	1 MOI	7 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_0hr_H1N1	0	CA04 (H1N1)	3 MOI	0 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_12hr_H1N1	1141	CA04 (H1N1)	3 MOI	12 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_18hr_H1N1	1948	CA04 (H1N1)	3 MOI	18 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input checked="" type="checkbox"/>	ICL006_24hr_H1N1	1546	CA04 (H1N1)	3 MOI	24 hours	Calu-3 cells	Human	<input checked="" type="checkbox"/>
<input type="checkbox"/>	ICL006_30hr_H1N1	1326	CA04 (H1N1)	3 MOI	30 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_36hr_H1N1	1255	CA04 (H1N1)	3 MOI	36 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_3hr_H1N1	0	CA04 (H1N1)	3 MOI	3 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_48hr_H1N1	1190	CA04 (H1N1)	3 MOI	48 hours	Calu-3 cells	Human	<input type="checkbox"/>
<input type="checkbox"/>	ICL006_7hr_H1N1	360	CA04 (H1N1)	3 MOI	7 hours	Calu-3 cells	Human	<input type="checkbox"/>





## SET TYPE

Intersect

## EXPERIMENT NAME (2)

- ☐ CA04M001-P: A/CA/04/ ... (0)
- ☐ CA04M001-R: Mouse in ... (0)
- ☐ ECL001-R: MERS-CoV I ... (0)
- ☐ ICL004-P: A/Vietnam/ ... (0)
- ☒ ICL004-R: Calu-3 inf ... (1)
- ☐ ICL006-P: A/CA/04/09 ... (0)
- ☒ ICL006-R: Calu-3 inf ... (1)
- ☐ ICL010-P: A/Netherla ... (0)
- ☐ ICL010-R: A/Netherla ... (0)
- ☐ ICL011-P: VN1203 PB2 ... (0)
- ☐ ICL011-R: VN1203 PB2 ... (0)
- ☐ ICL012-P: Vietnam/12 ... (0)
- ☐ ICL012-R: Vietnam/12 ... (0)
- ☐ IM001-P: A/Vietnam/1 ... (0)
- ☐ IM001-R: Mouse infec ... (0)
- ☐ IM002-R: Influenza A ... (0)
- ☐ IM004-P: VN1203 HA a ... (0)
- ☐ IM004-R: Mouse infec ... (0)
- ☐ IM005-P: Vietnam/120 ... (0)
- ☐ IM005-R: Vietnam/120 ... (0)
- ☐ IM006A-P: Vietnam/12 ... (0)
- ☐ IM006A-R: Vietnam/12 ... (0)
- ☐ IM006B-P: Vietnam/12 ... (0)
- ☐ IM006B-R: Vietnam/12 ... (0)
- ☐ IM007-P: Vietnam/120 ... (0)
- ☐ IM007-R: Vietnam/120 ... (0)
- ☐ IM009-R: Influenza A ... (0)
- ☐ IM010-R: Vietnam/120 ... (0)
- ☐ IM015-R: Influenza A ... (0)
- ☐ SBRI\_AA: Transcripto ... (0)

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	Host Factor	Entrez Gene ID	Symbol	Genbank Accession	Name	Immpotlog2 FC	ICL006_2
<input type="checkbox"/>	A_23_P9415	48	aco1	NM_002197	aconitase 1, soluble	<a href="#">🔗</a>	-2.6
<input type="checkbox"/>	A_23_P9416	48	aco1	NM_002197	aconitase 1, soluble	<a href="#">🔗</a>	-14.7
<input type="checkbox"/>	A_23_P317756	6296	acsm3	NM_202000	acyl-coa synthetase medium-chain family member 3	<a href="#">🔗</a>	-2.3
<input type="checkbox"/>	A_23_P1102	58	acta1	NM_001100	actin, alpha 1, skeletal muscle	<a href="#">🔗</a>	2.6
<input type="checkbox"/>	A_23_P137786	54507	adamtsl4	AK023606	adamts-like 4	<a href="#">🔗</a>	12.6
<input type="checkbox"/>	A_23_P49816	55803	adap2	NM_018404	arfgap with dual ph domains 2	<a href="#">🔗</a>	1.5
<input type="checkbox"/>	A_23_P126313	55811	adcy10	NM_018417	adenylate cyclase 10 (soluble)	<a href="#">🔗</a>	19.6
<input type="checkbox"/>	A_23_P145024	154	adrb2	NM_000024	adrenergic, beta-2-, receptor, surface	<a href="#">🔗</a>	-1.9
<input type="checkbox"/>	A_23_P76823	122622	adssl1	NM_199165	adenylosuccinate synthase like 1	<a href="#">🔗</a>	-1.7
<input type="checkbox"/>	A_23_P214897	9590	akap12	NM_144497	a kinase (prka) anchor protein 12	<a href="#">🔗</a>	2.7
<input type="checkbox"/>	A_23_P257971	1645	akr1c1	NM_001353	aldo-keto reductase family 1, member c1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	<a href="#">🔗</a>	-1.7
<input type="checkbox"/>	A_24_P220947	1645	akr1c1	NM_001353	aldo-keto reductase family 1, member c1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	<a href="#">🔗</a>	-8.0

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<input type="checkbox"/>	Experiment ID	Study Name	Analyte Type	Viral Agent	Viral
<input type="checkbox"/>	CA04M001-P	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Protein Quantification	CA04 (H1N1)	$10^4, 10^5$
<input type="checkbox"/>	CA04M001-R	CA04M001 :A/CA/04/09 (H1N1) infection in C57BL6 mice with variable doses and times post infection.	Transcript Quantification	CA04 (H1N1)	$10^3, 10^4$ , PFU
<input type="checkbox"/>	ECL001-R	ECL001: MERS-CoV infection in Calu3 cells: A time course	Transcript Quantification	MERS-CoV	5 MOI
<input checked="" type="checkbox"/>	ICL004-P	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Protein Quantification	VN1203 (H5N1)	1 MOI
<input checked="" type="checkbox"/>	ICL004-R	ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course	Transcript Quantification	VN1203 (H5N1)	1 MOI
<input type="checkbox"/>	ICL006-P	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Protein Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/>	ICL006-R	ICL006: A/CA/04/09 (H1N1) infection in Calu3 cell: A time course	Transcript Quantification	CA04 (H1N1)	3 MOI
<input type="checkbox"/>	ICL010-P	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Protein Quantification	NL602 (H1N1)	3 MOI
<input type="checkbox"/>	ICL010-R	ICL010: A/Netherlands/602/2009 (H1N1) and A/CA/04/2009 (H1N1) infection in Calu3 cells: A time course	Transcript Quantification	CA04 (H1N1), NL602 (H1N1)	3 MOI



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Host Factor Results

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Find shared factors (Intersect, AND)



Find all factors (Union, OR)



Find unique factors (XOR)



Find exclusive factors (Subtract)

<input type="checkbox"/>	Bloset Name					Post Infection	Strain/Line
	ICL004-R_0						Calu-3 cells
<input type="checkbox"/>	ICL004-R_12	13030	VN1203 (H5N1)	1 MOI	12 hours		Calu-3 cells
<input type="checkbox"/>	ICL004-R_18	12944	VN1203 (H5N1)	1 MOI	18 hours		Calu-3 cells
<input checked="" type="checkbox"/>	ICL004-R_24	17324	VN1203 (H5N1)	1 MOI	24 hours		Calu-3 cells
	ICL004-R_3	0	VN1203 (H5N1)	1 MOI	3 hours		Calu-3 cells
<input type="checkbox"/>	ICL004-R_7	5277	VN1203 (H5N1)	1 MOI	7 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_0/3h_proteomics	179	VN1203 (H5N1)	1 MOI	0/3 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_12h_proteomics	417	VN1203 (H5N1)	1 MOI	12 hours		Calu-3 cells
<input checked="" type="checkbox"/>	ICL004_VN1203_18/24h_proteomics	737	VN1203 (H5N1)	1 MOI	18/24 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_7h_proteomics	60	VN1203 (H5N1)	1 MOI	7 hours		Calu-3 cells

## SET TYPE

Intersect

## EXPERIMENT NAME ( 2 )

- ☐ CA04M001-P: A/CA/04/ ... ( 0 )
- ☐ CA04M001-R: Mouse in ... ( 0 )
- ☐ ECL001-R: MERS-CoV i ... ( 0 )
- ☒ ICL004-P: A/Vietnam/ ... ( 1 )
- ☒ ICL004-R: Calu-3 inf ... ( 1 )
- ☐ ICL006-P: A/CA/04/09 ... ( 0 )
- ☐ ICL006-R: Calu-3 inf ... ( 0 )
- ☐ ICL010-P: A/Netherla ... ( 0 )
- ☐ ICL010-R: A/Netherla ... ( 0 )
- ☐ ICL011-P: VN1203 PB2 ... ( 0 )
- ☐ ICL011-R: VN1203 PB2 ... ( 0 )
- ☐ ICL012-P: Vietnam/12 ... ( 0 )
- ☐ ICL012-R: Vietnam/12 ... ( 0 )
- ☐ IM001-P: A/Vietnam/1 ... ( 0 )
- ☐ IM001-R: Mouse infec ... ( 0 )
- ☐ IM002-R: Influenza A ... ( 0 )
- ☐ IM004-P: VN1203 HA a ... ( 0 )
- ☐ IM004-R: Mouse infec ... ( 0 )
- ☐ IM005-P: Vietnam/120 ... ( 0 )
- ☐ IM005-R: Vietnam/120 ... ( 0 )
- ☐ IM006A-P: Vietnam/12 ... ( 0 )
- ☐ IM006A-R: Vietnam/12 ... ( 0 )
- ☐ IM006B-P: Vietnam/12 ... ( 0 )
- ☐ IM006B-R: Vietnam/12 ... ( 0 )
- ☐ IM007-P: Vietnam/120 ... ( 0 )
- ☐ IM007-R: Vietnam/120 ... ( 0 )
- ☐ IM009-R: Influenza A ... ( 0 )
- ☐ IM010-R: Vietnam/120 ... ( 0 )
- ☐ IM015-R: Influenza A ... ( 0 )
- ☐ SBRI\_AA: Transcripto ... ( 0 )
- ☐ SCL005-P: IcSARS ORF ... ( 0 )
- ☐ SCL005-R: Calu3 cell ... ( 0 )
- ☐ SCL006-P: IcSARS urb ... ( 0 )
- ☐ SCL006-R: Calu3 cell ... ( 0 )
- ☐ SCL008-P: IcSARS CoV ... ( 0 )

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<input type="checkbox"/>	HID	Bioset Name	Host Factor	Entrez Gene ID	Symbol
<input type="checkbox"/>	5	ICL004_VN1203_18/24h_proteomics ICL004-R_24	<input type="checkbox"/> ACADV_HUMAN <input type="checkbox"/> A_23_P207650	37 37	acadvl acadvl
<input type="checkbox"/>	84	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P111835 <input type="checkbox"/> DLDH_HUMAN	1738 1738	dld dld
<input type="checkbox"/>	100	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_24_P53080 <input type="checkbox"/> ETFA_HUMAN	2108 2108	etfa etfa
<input type="checkbox"/>	145	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_24_P108451 <input type="checkbox"/> G6PI_HUMAN	2821 2821	gpi gpi
<input type="checkbox"/>	147	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P255884 <input type="checkbox"/> GELS_HUMAN	2934 2934	gsn gsn
<input type="checkbox"/>	148	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P210920 <input type="checkbox"/> GSHB_HUMAN	2937 2937	gss gss
<input type="checkbox"/>	149	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P102202 <input type="checkbox"/> MSH6_HUMAN	2956 2956	msh6 msh6
<input type="checkbox"/>	152	ICL004-R_24 ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_24_P242688 <input type="checkbox"/> A_24_P353964 <input type="checkbox"/> ECHA_HUMAN	3030 3030 3030	hadha hadha hadha
<input type="checkbox"/>	153	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P79703 <input type="checkbox"/> ECHB_HUMAN	3032 3032	hadhb hadhb
<input type="checkbox"/>	191	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P86012 <input type="checkbox"/> LAMB3_HUMAN	3914 3914	lamb3 lamb3
<input type="checkbox"/>	227	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P140256 <input type="checkbox"/> PNPH_HUMAN	4860 4860	np pnp
<input type="checkbox"/>	335	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_24_P38815 <input type="checkbox"/> TPP1_HUMAN	1200 1200	tpp1 tpp1
<input type="checkbox"/>	358	ICL004-R_24 ICL004_VN1203_18/24h_proteomics	<input type="checkbox"/> A_23_P92954 <input type="checkbox"/> DHB4_HUMAN	3295 3295	hsd17b hsd17b



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Patterns


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Host Factor Results

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Find shared factors (Intersect, AND) 

Find all factors (Union, OR) 

Find unique factors (XOR) 

Find exclusive factors (Subtract) 

<input type="checkbox"/>	Bloset Name					Post Infection	Strain/Line
	ICL004-R_0						Calu-3 cells
<input type="checkbox"/>	ICL004-R_12	13030	VN1203 (H5N1)	1 MOI	12 hours		Calu-3 cells
<input type="checkbox"/>	ICL004-R_18	12944	VN1203 (H5N1)	1 MOI	18 hours		Calu-3 cells
<input checked="" type="checkbox"/>	ICL004-R_24	17324	VN1203 (H5N1)	1 MOI	24 hours		Calu-3 cells
	ICL004-R_3	0	VN1203 (H5N1)	1 MOI	3 hours		Calu-3 cells
<input type="checkbox"/>	ICL004-R_7	5277	VN1203 (H5N1)	1 MOI	7 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_0/3h_proteomics	179	VN1203 (H5N1)	1 MOI	0/3 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_12h_proteomics	417	VN1203 (H5N1)	1 MOI	12 hours		Calu-3 cells
<input checked="" type="checkbox"/>	ICL004_VN1203_18/24h_proteomics	737	VN1203 (H5N1)	1 MOI	18/24 hours		Calu-3 cells
<input type="checkbox"/>	ICL004_VN1203_7h_proteomics	60	VN1203 (H5N1)	1 MOI	7 hours		Calu-3 cells

## Boolean "Subtract"

Select one bioset from column A. Select one or more biosets from column B (hold down the shift key while selecting multiple values). Biosets selected from column B will be subtracted from the bioset selected in column A. The maximum sets that can be subtracted from column A is 4.

**A**

- ☐ ICL004-R\_24
- ☒ ICL004\_VN1203\_18/24h\_proteomics

**B**

ICL004-R\_12  
ICL004-R\_18  
**ICL004-R\_24**  
ICL004-R\_7

Cancel

Submit





## SET TYPE

Minus

## EXPERIMENT NAME ( 2 )

- ☐ CA04M001-P: A/CA/04/ ... ( 0 )
- ☐ CA04M001-R: Mouse in ... ( 0 )
- ☐ ECL001-R: MERS-CoV i ... ( 0 )
- ☒ ICL004-P: A/Vietnam/ ... ( 1 )
- ☒ ICL004-R: Calu-3 inf ... ( 1 )
- ☐ ICL006-P: A/CA/04/09 ... ( 0 )
- ☐ ICL006-R: Calu-3 inf ... ( 0 )
- ☐ ICL010-P: A/Netherla ... ( 0 )
- ☐ ICL010-R: A/Netherla ... ( 0 )
- ☐ ICL011-P: VN1203 PB2 ... ( 0 )
- ☐ ICL011-R: VN1203 PB2 ... ( 0 )
- ☐ ICL012-P: Vietnam/12 ... ( 0 )
- ☐ ICL012-R: Vietnam/12 ... ( 0 )
- ☐ IM001-P: A/Vietnam/1 ... ( 0 )
- ☐ IM001-R: Mouse infec ... ( 0 )
- ☐ IM002-R: Influenza A ... ( 0 )
- ☐ IM004-P: VN1203 HA a ... ( 0 )
- ☐ IM004-R: Mouse infec ... ( 0 )
- ☐ IM005-P: Vietnam/120 ... ( 0 )
- ☐ IM005-R: Vietnam/120 ... ( 0 )
- ☐ IM006A-P: Vietnam/12 ... ( 0 )
- ☐ IM006A-R: Vietnam/12 ... ( 0 )
- ☐ IM006B-P: Vietnam/12 ... ( 0 )
- ☐ IM006B-R: Vietnam/12 ... ( 0 )
- ☐ IM007-P: Vietnam/120 ... ( 0 )
- ☐ IM007-R: Vietnam/120 ... ( 0 )
- ☐ IM009-R: Influenza A ... ( 0 )
- ☐ IM010-R: Vietnam/120 ... ( 0 )
- ☐ IM015-R: Influenza A ... ( 0 )
- ☐ SBRI\_AA: Transcripto ... ( 0 )
- ☐ SCL005-P: icSARS ORF ...

Your Selected Items: 0 items selected

Set Operations ▾

Save Search

Add to Working Set

Download

<input type="checkbox"/>	HID	Bloset Name	Host Factor	Entrez Gene ID	Symbol
<input type="checkbox"/>	347	ICL004_VN1203_18/24h_proteomics	GALE_HUMAN	2582	gale
<input type="checkbox"/>	658	ICL004_VN1203_18/24h_proteomics	GSTM3_HUMAN	2947	gstm3
<input type="checkbox"/>	726	ICL004_VN1203_18/24h_proteomics	PPIB_HUMAN	5479	ppib
<input type="checkbox"/>	779	ICL004_VN1203_18/24h_proteomics	RS3_HUMAN	6188	rps3
<input type="checkbox"/>	803	ICL004_VN1203_18/24h_proteomics	RS27_HUMAN	6232	rps27
<input type="checkbox"/>	980	ICL004_VN1203_18/24h_proteomics	CIRBP_HUMAN	1153	cirbp
<input type="checkbox"/>	1038	ICL004_VN1203_18/24h_proteomics	DOPD_HUMAN	1652	ddt
<input type="checkbox"/>	1039	ICL004_VN1203_18/24h_proteomics	DHX9_HUMAN	1660	dhx9
<input type="checkbox"/>	1174	ICL004_VN1203_18/24h_proteomics	HNRPL_HUMAN	3191	hnmpl
<input type="checkbox"/>	1180	ICL004_VN1203_18/24h_proteomics	HSPB1_HUMAN	3315	hspb1
<input type="checkbox"/>	1194	ICL004_VN1203_18/24h_proteomics	CYR61_HUMAN	3491	cyr61
<input type="checkbox"/>	1250	ICL004_VN1203_18/24h_proteomics	COPD_HUMAN	372	arcn1
<input type="checkbox"/>	1275	ICL004_VN1203_18/24h_proteomics	AT5F1_HUMAN	515	atp5f1
<input type="checkbox"/>	1327	ICL004_VN1203_18/24h_proteomics	CPNS1_HUMAN	826	capns1
<input type="checkbox"/>	1568	ICL004_VN1203_18/24h_proteomics	GNS_HUMAN	2799	gns
<input type="checkbox"/>	1660	ICL004_VN1203_18/24h_proteomics	REXO4_HUMAN	57109	rexo4
<input type="checkbox"/>	1707	ICL004_VN1203_18/24h_proteomics	IMB1_HUMAN	3837	kpnb1
<input type="checkbox"/>	1855	ICL004_VN1203_18/24h_proteomics	MYPT1_HUMAN	4659	ppp1r12a
<input type="checkbox"/>	1933	ICL004_VN1203_18/24h_proteomics	PA1B3_HUMAN	5050	pafah1b3
<input type="checkbox"/>	1945	ICL004_VN1203_18/24h_proteomics	PCNA_HUMAN	5111	pcna

## Significant Host Factors as Compared to Control

"+" up-regulated, "-" down-regulated, blank: no change

Find expression pattern:

SYMBOL

Find

Use comma to separate multiple entries.  
Ex. DDX58

Your search returned **55** records.

Data sorted by **Number of Probes** in descending order

	Pattern	Virus Time Post Infection Viral Dose Strain/Line	VN1203 (H5N1), 0 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 3 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 12 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 18 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 24 hours, 1 MOI, Calu-3 cells
		<b>Host Factors</b>	0	0	<input type="checkbox"/> 5277	<input type="checkbox"/> 13030	<input type="checkbox"/> 12944	<input type="checkbox"/> 17324
<input type="checkbox"/>	0,0,0,+,+,+	2921				+	+	+
<input type="checkbox"/>	0,0,0,-,-,-	2764				-	-	-
<input type="checkbox"/>	0,0,0,0,0,+	2105						+
<input type="checkbox"/>	0,0,0,0,0,-	1974						-
<input type="checkbox"/>	0,0,-,-,-,-	1643			-	-	-	-
<input type="checkbox"/>	0,0,0,0,-,-	1621					-	-
<input type="checkbox"/>	0,0,+,+,+,+	1094			+	+	+	+
<input type="checkbox"/>	0,0,0,0,+,+	931					+	+
<input type="checkbox"/>	0,0,0,+,0,0	919				+		
<input type="checkbox"/>	0,0,0,-,0,0	746				-		
<input type="checkbox"/>	0,0,0,-,0,-	487				-		-
<input type="checkbox"/>	0,0,0,+,0,+	452				+		+
<input type="checkbox"/>	0,0,+,0,0,0	433			+			
<input type="checkbox"/>	0,0,0,+,+,0	433				+	+	
<input type="checkbox"/>	0,0,0,-,-,0	402				-	-	
<input type="checkbox"/>	0,0,-,0,0,0	275			-			
<input type="checkbox"/>	0,0,0,0,-,0	230					-	
<input type="checkbox"/>	0,0,-,-,0,0	222			-	-		
<input type="checkbox"/>	0,0,-,-,-,0	195			-	-	-	
<input type="checkbox"/>	0,0,+,0,0,+	192			+			+
<input type="checkbox"/>	0,0,-,-,0,-	180			-	-		-
<input type="checkbox"/>	0,0,0,0,+,0	152					+	
<input type="checkbox"/>	0,0,+,0,+,+	133			+		+	+
<input type="checkbox"/>	0,0,0,+,0,-	115				+		-
<input type="checkbox"/>	0,0,+,+,0,0	110			+	+		
<input type="checkbox"/>	0,0,-,0,-,-	102			-		-	-
<input type="checkbox"/>	0,0,-,0,0,-	102			-			-

Displaying 500 of 1,094 records.

Data sorted by Symbol, Host Factor ID in ascending order

☐ Select all 1,094 records (including those not displayed)

Your Selected Items: 0 items selected

Add to Working Set

Save Search

Download

Download Reactome Data

Pathway View

HOST FACTOR ID OR SYMBOL

Find data for

Find

Reset

Use comma to separate multiple entries.  
Ex. DDX58

Study Name

Experiment Name

Bioset Criteria

Associated Bioset Information 1

ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course

ICL004-R: Calu-3 infections with A/Vietnam/1203-CIP048\_RG1/2004(H5N1)

passes Agilent QC flag and  $|\log_2 FC| > 1.5$  and  $q\text{-value} < .05$

	Symbol	Name	Import	Host Factor ID	Entrez Gene ID	Public Identifier	Bioset Information Key	ICL004-R VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells		
								Log2 FC	P-Value	Log
<input type="checkbox"/>	ABCA11P	atp-binding cassette, sub-family a (abc1), member 11 (pseudogene)	<a href="#">🔗</a>	A_23_P92602	79963	NR_002451	1	2.0	2.2E-2	2.7
<input type="checkbox"/>	ABT1	activator of basal transcription 1	<a href="#">🔗</a>	A_23_P30784	29777	NM_013375	1	1.6	1.8E-2	1.9
<input type="checkbox"/>	ACRC	acidic repeat containing	<a href="#">🔗</a>	A_23_P171237	93953	NM_052957	1	2.2	1.3E-2	3.0
<input type="checkbox"/>	ACTA1	actin, alpha 1, skeletal muscle	<a href="#">🔗</a>	A_23_P1102	58	NM_001100	1	31.2	2.8E-3	79.
<input type="checkbox"/>	ACTA2	actin, alpha 2, smooth muscle, aorta	<a href="#">🔗</a>	A_23_P150053	59	NM_001613	1	6.2	3.2E-2	5.7
<input type="checkbox"/>	ACTC1	actin, alpha, cardiac muscle 1	<a href="#">🔗</a>	A_23_P205894	70	NM_005159	1	4.1	1.2E-2	9.5
<input type="checkbox"/>	ACTG2	actin, gamma 2, smooth muscle, enteric	<a href="#">🔗</a>	A_23_P39955	72	NM_001615	1	6.1	1.6E-2	49.
<input type="checkbox"/>	ACYP2	acylphosphatase 2, muscle type	<a href="#">🔗</a>	A_24_P336848	98	NM_138448	1	1.7	2.1E-2	2.8
<input type="checkbox"/>	AGAP1	arfgap with gtpase domain, ankyrin repeat and ph domain 1	<a href="#">🔗</a>	A_32_P55161	116987	NM_001037131	1	1.9	2.1E-2	2.7
<input type="checkbox"/>	AGAP7	arfgap with gtpase domain, ankyrin repeat and ph domain 7	<a href="#">🔗</a>	A_24_P729905	653268	NM_001077685	1	2.0	5.9E-3	4.9
<input type="checkbox"/>	AGBL2	atp/gtp binding protein-like 2	<a href="#">🔗</a>	A_32_P167705	79841	NM_024783	1	2.8	1.2E-2	3.6



## Analysis results, per pathway

This table provides an overview of your expression data in a pathway context. For each Reactome pathway, the total number of proteins is shown, plus of the pathway, where your expression levels are represented as coloration of proteins.

Select format to download this table:

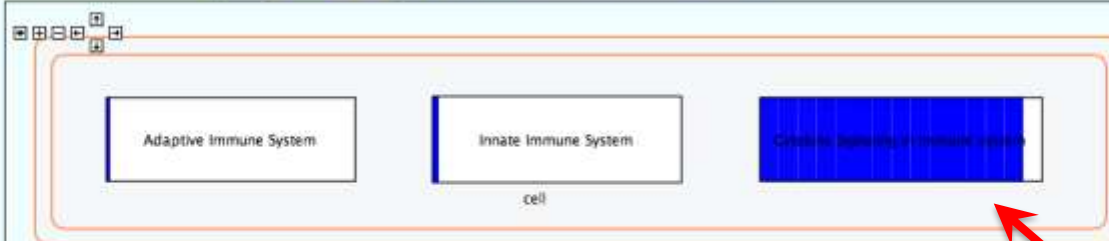
Pathway	Species	IDs in pathway (%)	ICL004_R_VN1203_H5N1_7_hours_1_00E_00_MOI_Calu_3_cells	ICL004_R_VN1203_H5N1_12_hours_1_00E_00_M
Not assigned	Not known	483 (0%)	9.6	25.6
Apoptosis	Homo sapiens	1 (0%)	2.1	1.7
Binding and Uptake of Ligands by Scaveng	Homo sapiens	3 (1%)	12.3	28.8
Cell Cycle	Homo sapiens	9 (2%)	1.8	2.8
Cell-Cell communication	Homo sapiens	0 (0%)		
Cellular responses to stress	Homo sapiens	1 (0%)	1.6	1.6
Chromatin organization	Homo sapiens	4 (4%)	1.9	3.1
Circadian Clock	Homo sapiens	0 (0%)		
Developmental Biology	Homo sapiens	7 (1%)	2.8	4.5
Disease	Homo sapiens	23 (2%)	5.4	13.8
DNA Repair	Homo sapiens	1 (0%)	1.6	2.8
DNA Replication	Homo sapiens	2 (2%)	1.9	3.3
Extracellular matrix organization	Homo sapiens	5 (2%)	5.4	17.7
Gene Expression	Homo sapiens	24 (3%)	2.4	4.2
Homeostasis	Homo sapiens	16 (3%)	6.2	32.0
Immune System	Homo sapiens	36 (3%)	9.6	22.0





Event Hierarchy:

- Apoptosis
- Binding and Uptake of Ligands by S
- Cell Cycle
- Cell-Cell communication
- Cellular responses to stress
- Chromatin organization
- Circadian Clock
- Developmental Biology
- Disease
- DNA Repair
- DNA Replication
- Extracellular matrix organization
- Gene Expression
- Hemostasis
- Immune System**
- Meiosis
- Membrane Trafficking
- Metabolism
- Metabolism of proteins
- Muscle contraction
- Neuronal System
- Reproduction
- Signal Transduction
- Transmembrane transport of small t



702.71

352.14

Stable Identifier

REACT\_6900.5

Summation

Humans are exposed to millions of potential pathogens daily, through contact, ingestion, and inhalation. Our ability to avoid infection depends on the adaptive immune system and during the first critical hours and days of exposure to a new pathogen, our innate immune system.

**REACTOME**

Event Hierarchy:

- Apoptosis
- Binding and Uptake of Ligands by S
- Cell Cycle
- Cell-Cell communication
- Cellular responses to stress
- Chromatin organization
- Circadian Clock
- Developmental Biology
- Disease
- DNA Repair
- DNA Replication
- Extracellular matrix organization
- Gene Expression
- Hemostasis
- Immune System**
  - Adaptive Immune System
  - Innate Immune System
  - Cytokine Signaling in Immune System**
- Meiosis
- Membrane Trafficking
- Metabolism
- Metabolism of proteins
- Muscle contraction
- Neuronal System
- Reproduction
- Signal Transduction
- Transmembrane transport of small molecules

Pathways for: **Homo sapiens**

[Click here for a tour of this pathway viewer.](#) [Hide](#)

Protein ☐ Small molecule ☐ Complex ☐

cell

Interleukin signaling

Signaling by Interleukins

Growth hormone receptor signaling






































Prolactin receptor signaling

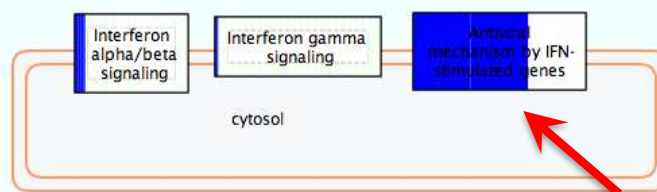
702.71

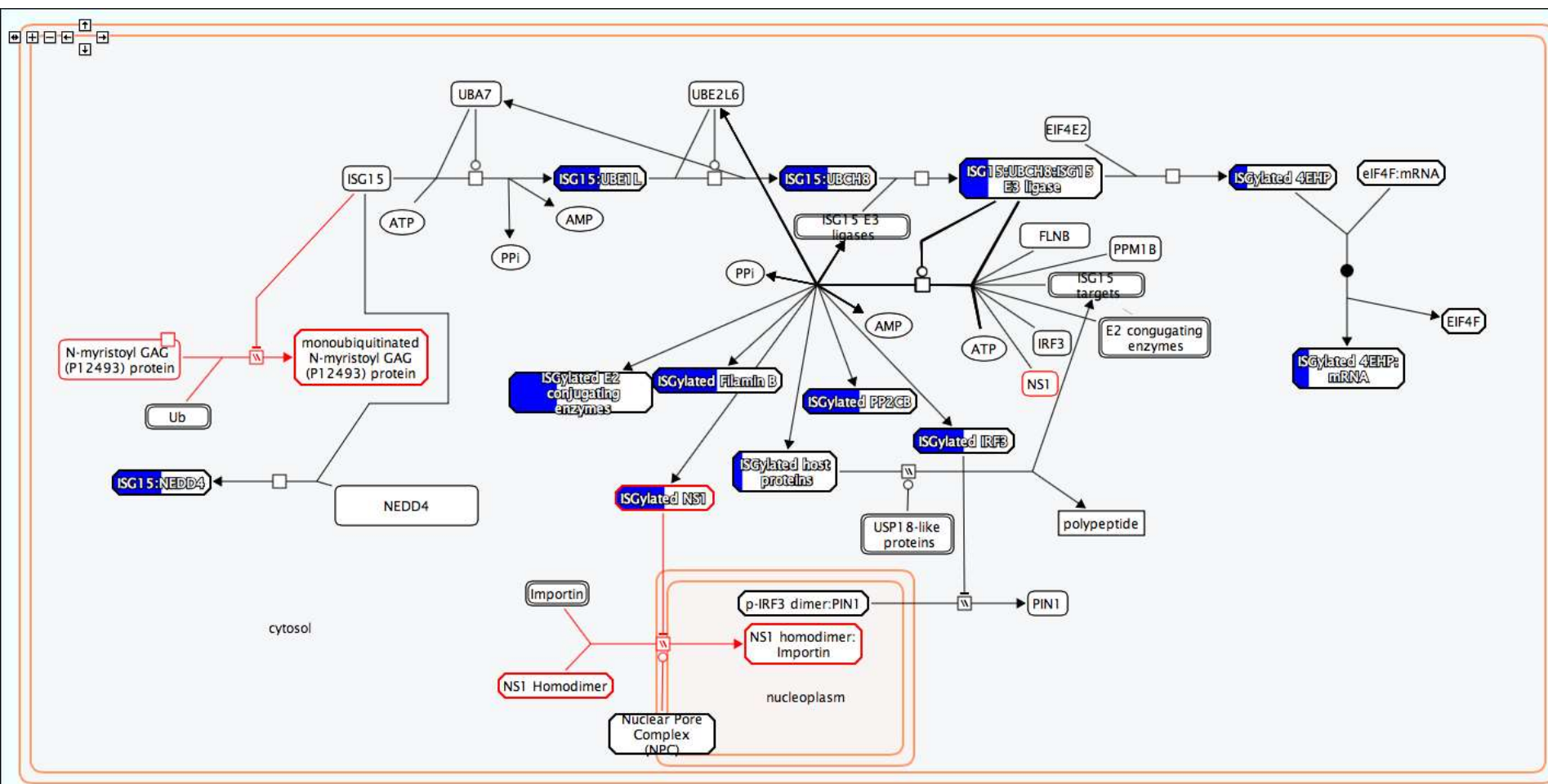
352.14



### Event Hierarchy:

- ⊕  Apoptosis
- ⊕  Binding and Uptake of Ligands by S
- ⊕   Cell Cycle
- ⊕  Cell-Cell communication
- ⊕   Cellular responses to stress
- ⊕   Chromatin organization
- ⊕  Circadian Clock
- ⊕  Developmental Biology
- ⊕  Disease
- ⊕  DNA Repair
- ⊕  DNA Replication
- ⊕  Extracellular matrix organization
- ⊕  Gene Expression
- ⊕   Hemostasis
- ☐  **Immune System**
  - ⊕  Adaptive Immune System
  - ⊕  Innate Immune System
- ☐  **Cytokine Signaling in Immu**
  - ⊕  Interferon Signaling
  - ⊕  Signaling by Interleukins
  - ⊕  Growth hormone receptor sign
  - ⊕  Prolactin receptor signaling
- ⊕  Meiosis
- ⊕  Membrane Trafficking
- ⊕  Metabolism
- ⊕   Metabolism of proteins
- ⊕  Muscle contraction
- ⊕  Neuronal System
- ⊕  Reproduction
- ⊕   Signal Transduction
- ⊕  Transmembrane transport of small i







## Significant Host Factors as Compared to Control

"+" up-regulated, "-" down-regulated, blank: no change

Find expression pattern:

SYMBOL

RNAseL

Find

Use comma to separate multiple entries.  
Ex. DDX58

Your search returned **55** records.

Data sorted by **Number of Probes** in descending order

	Pattern	Virus Time Post Infection Viral Dose Strain/Line	VN1203 (H5N1), 0 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 3 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 12 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 18 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 24 hours, 1 MOI, Calu-3 cells
		<b>Host Factors</b>	0	0	<input type="checkbox"/> 5277	<input type="checkbox"/> 13030	<input type="checkbox"/> 12944	<input type="checkbox"/> 17324
<input type="checkbox"/>	0,0,0,+,+,+	2921				+	+	+
<input type="checkbox"/>	0,0,0,-,-,-	2764				-	-	-
<input type="checkbox"/>	0,0,0,0,0,+	2105						+
<input type="checkbox"/>	0,0,0,0,0,-	1974						-
<input type="checkbox"/>	0,0,-,-,-,-	1643			-	-	-	-
<input type="checkbox"/>	0,0,0,0,-,-	1621					-	-
<input type="checkbox"/>	0,0,+,+,+,+	1094			+	+	+	+
<input type="checkbox"/>	0,0,0,0,+,+	931					+	+
<input type="checkbox"/>	0,0,0,+,0,0	919				+		
<input type="checkbox"/>	0,0,0,-,0,0	746				-		
<input type="checkbox"/>	0,0,0,-,0,-	487				-		-
<input type="checkbox"/>	0,0,0,+,0,+	452				+		+
<input type="checkbox"/>	0,0,+,0,0,0	433			+			
<input type="checkbox"/>	0,0,0,+,+,0	433				+	+	
<input type="checkbox"/>	0,0,0,-,-,0	402				-	-	
<input type="checkbox"/>	0,0,-,0,0,0	275			-			
<input type="checkbox"/>	0,0,0,0,-,0	230					-	
<input type="checkbox"/>	0,0,-,-,0,0	222			-	-		
<input type="checkbox"/>	0,0,-,-,-,0	195			-	-	-	
<input type="checkbox"/>	0,0,+,0,0,+	192			+			+
<input type="checkbox"/>	0,0,-,-,0,-	180			-	-		-
<input type="checkbox"/>	0,0,0,0,+,0	152					+	
<input type="checkbox"/>	0,0,+,0,+,+	133			+		+	+
<input type="checkbox"/>	0,0,0,+,0,-	115				+		-
<input type="checkbox"/>	0,0,+,+,0,0	110			+	+		
<input type="checkbox"/>	0,0,-,0,-,-	102			-		-	-
<input type="checkbox"/>	0,0,-,0,0,-	102			-			-

## Significant Host Factors as Compared to Control

"+" up-regulated, "-" down-regulated, blank: no change

Find expression pattern:

SYMBOL

Find

Use comma to separate multiple entries.  
Ex. DDX58

Your search returned **1** record.

Data sorted by **Number of Probes** in descending order

	Pattern	Virus Time Post Infection Viral Dose Strain/Line	VN1203 (H5N1), 0 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 3 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 12 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 18 hours, 1 MOI, Calu-3 cells	VN1203 (H5N1), 24 hours, 1 MOI, Calu-3 cells
		<b>Host Factors</b>	0	0	<input type="checkbox"/> 5277	<input type="checkbox"/> 13030	<input type="checkbox"/> 12944	<input type="checkbox"/> 17324
<input type="checkbox"/>	0,0,-,- ,0,-	180			-	-		-



**ViPR**  
Virus Pathogen Resource



Influenza Research Database

**J. Craig Venter**  
INSTITUTE

☐ Select all 1,094 records (including those not displayed)

Your Selected Items: 0 items selected

Add to Working Set

Save Search

Download

Download Reactome Data

Pathway View

## HOST FACTOR ID OR SYMBOL

Find data for

Find

Reset

Use comma to separate multiple entries.  
Ex. DDX58

Study Name

Experiment Name

Bioset Criteria

## Associated Bioset Information 1

ICL004: A/Vietnam/1203/2004(H5N1) infection in Calu3 cell: A time course

ICL004-R: Calu-3 infections with A/Vietnam/1203-CIP048\_RG1/2004(H5N1)

passes Agilent QC flag and  $|\log_2 FC| > 1.5$  and  $q\text{-value} < .05$ 

								ICL004-R VN1203 (H5N1), 7 hours, 1 MOI, Calu-3 cells	VN	
<input type="checkbox"/>	Symbol	Name	Import	Host Factor ID	Entrez Gene ID	Public Identifier	Bioset Information Key	Log2 FC	P-Value	Log
<input type="checkbox"/>	ABCA11P	atp-binding cassette, sub-family a (abc1), member 11 (pseudogene)	<a href="#">🔗</a>	A_23_P92602	79963	NR_002451	1	2.0	2.2E-2	2.7
<input type="checkbox"/>	ABT1	activator of basal transcription 1	<a href="#">🔗</a>	A_23_P30784	29777	NM_013375	1	1.6	1.8E-2	1.9
<input type="checkbox"/>	ACRC	acidic repeat containing	<a href="#">🔗</a>	A_23_P171237	93953	NM_052957	1	2.2	1.3E-2	3.0
<input type="checkbox"/>	ACTA1	actin, alpha 1, skeletal muscle	<a href="#">🔗</a>	A_23_P1102	58	NM_001100	1	31.2	2.8E-3	79.
<input type="checkbox"/>	ACTA2	actin, alpha 2, smooth muscle, aorta	<a href="#">🔗</a>	A_23_P150053	59	NM_001613	1	6.2	3.2E-2	5.7
<input type="checkbox"/>	ACTC1	actin, alpha, cardiac muscle 1	<a href="#">🔗</a>	A_23_P205894	70	NM_005159	1	4.1	1.2E-2	9.5
<input type="checkbox"/>	ACTG2	actin, gamma 2, smooth muscle, enteric	<a href="#">🔗</a>	A_23_P39955	72	NM_001615	1	6.1	1.6E-2	49.
<input type="checkbox"/>	ACYP2	acylphosphatase 2, muscle type	<a href="#">🔗</a>	A_24_P336848	98	NM_138448	1	1.7	2.1E-2	2.8
<input type="checkbox"/>	AGAP1	arfgap with gtpase domain, ankyrin repeat and ph domain 1	<a href="#">🔗</a>	A_32_P55161	116987	NM_001037131	1	1.9	2.1E-2	2.7
<input type="checkbox"/>	AGAP7	arfgap with gtpase domain, ankyrin repeat and ph domain 7	<a href="#">🔗</a>	A_24_P729905	653268	NM_001077685	1	2.0	5.9E-3	4.9
<input type="checkbox"/>	AGBL2	atp/gtp binding protein-like 2	<a href="#">🔗</a>	A_32_P167705	79841	NM_024783	1	2.8	1.2E-2	3.6

3	Experiment variable value 1	log2 Fold Change	Adjusted p- value	Experiment variable value 1	log2 Fold Change	Adjusted p- value	Experiment variable value 1	log2 Fold Change	Adjusted p- value	Experiment variable value 1	log2 Fold Change	Adjusted p- value	Experiment variable value 1	log2 Fold Change	Adjusted p- value
11813	3	-1.131153886	0.811597139	7	1.564843454	0.053754389	12	2.045130419	0.04537852	18	2.098974965	0.063960151	24	1.758797907	0.002917
11814	3	-1.004883272	0.987697131	7	-1.686246762	0.004212621	12	-1.760109848	0.009058148	18	-2.85109639	0.070304281	24	-6.338681279	0.020403
11815	3	-1.127237747	0.639828379	7	-1.038181834	0.877468486	12	-1.520819821	0.030117971	18	1.390211743	0.132987206	24	2.472705842	0.023203
11816	3	-1.132914897	0.804156099	7	1.110272302	0.869699135	12	2.408836912	0.037394034	18	2.469927467	0.251833771	24	5.483019801	0.018734
11817	3	1.113506963	0.485327841	7	-1.324509552	0.104280784	12	-1.914464291	0.012503302	18	-1.522732301	0.098559408	24	-1.769301005	0.033294
11818	3	-1.228789891	0.284346617	7	-1.498997532	0.062885106	12	-1.75233759	0.012899142	18	-1.516841556	0.091982819	24	-2.112064909	0.035343
11819	3	1.002137203	0.992041697	7	-1.102622134	0.662929877	12	-1.761783745	0.009011575	18	1.020812186	0.853205672	24	2.446585731	0.001137
11820	3	-1.168668591	0.537514164	7	1.668169818	0.225966254	12	-2.326971916	0.014047249	18	-2.643219438	0.316178618	24	-9.223953805	0.007485
11821	3	1.209027519	0.413739971	7	-1.819234161	0.041904688	12	-4.056013998	0.029811136	18	-8.550235918	0.075582847	24	-9.165251603	0.008939
11822	3	-1.097699367	0.618458938	7	1.531791165	0.14542335	12	1.638863123	0.019141701	18	1.092643552	0.806111263	24	-1.658466032	0.039107
11823	3	1.06914455	0.527936013	7	-1.312241892	0.072980309	12	-1.559867295	0.012568074	18	-1.069599722	0.858047926	24	-1.54511637	0.035452
11824	3	1.130611447	0.633790421	7	-1.900459964	0.029976993	12	-2.468589581	0.023690888	18	-12.59293969	0.053867539	24	-17.95333397	0.000419
11825	3	1.098535732	0.909402419	7	1.453425509	0.135134607	12	2.042578599	0.02670337	18	4.473426677	0.050539179	24	8.956037481	0.005123
11826	3	1.090593643	0.808766528	7	-2.555013274	0.010278205	12	-4.161120859	0.004358051	18	-6.203653108	0.112976889	24	-21.96429584	0.000899
11827	3	1.08654734	0.648306248	7	-1.533209381	0.063091572	12	-2.227653343	0.047516398	18	-10.81450906	0.067059062	24	-26.04841199	0.008638
11828	3	-1.617772682	0.325873477	7	-2.557499535	0.014259769	12	-7.185046268	0.023849116	18	-6.073874347	0.050403426	24	-26.92780274	0.006341
11829	3	-1.045038213	0.975752662	7	1.342812942	0.148028276	12	2.051808141	0.00262082	18	1.518148851	0.298996804	24	3.1993322	0.003295
11830	3	-1.599270411	0.349883277	7	-3.921198424	0.046013075	12	-2.431202577	0.004957721	18	-2.623164974	0.056005091	24	-4.711879967	0.032704
11831	3	1.021859105	0.962661537	7	1.259118526	0.189597341	12	1.749884772	0.023677065	18	2.174157429	0.125668602	24	4.485621874	0.000691
11832	3	-1.158952352	0.913298374	7	1.206971838	0.595342968	12	-2.371287468	0.030042671	18	-1.832819169	0.562190483	24	-3.4809188	0.013807
11833	3	-1.116677039	0.762525075	7	-1.314959666	0.119090741	12	-1.982368986	0.028192209	18	-2.802748916	0.053649918	24	-6.408424269	0.003045
11834	3	-1.094689556	0.959393828	7	-1.51784673	0.171560128	12	-1.509503638	0.037470011	18	-6.925109377	0.084255225	24	-18.60189989	0.004385





# Summary of “Omics” Data Support in IRD/ViPR

- Structured metadata about study, experiments, analysis methods
- Series of derived biosets
- Boolean analysis of biosets from different experiments
- Biosets based on expression patterns
- Search for expression patterns of specific genes
- Access to complete data matrix
- Data linkout to pathway knowledgebase

# Big Data to Knowledge

Volume + Variety = Value

Variety = Metadata

Data + Metadata + Interpretation =  
Knowledge

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