PATRIC – Bacterial Bioinformatics Resource Center

www.patricbrc.org

Stephen Cammer
**Virginia Bioinformatics Institute**

Role in BRC Program

- Provide publicly accessible database to

  - store, update, integrate and display genome sequence data, annotation and associated data for human pathogens
  - allow users to query and examine such information with user friendly interfaces and computational analyses tools.
  - serve as the public repository for NIAID-supported genomics programs
  - collaborate on experimental research projects via Driving Biological Projects

PATRIC All-Bacteria BRC
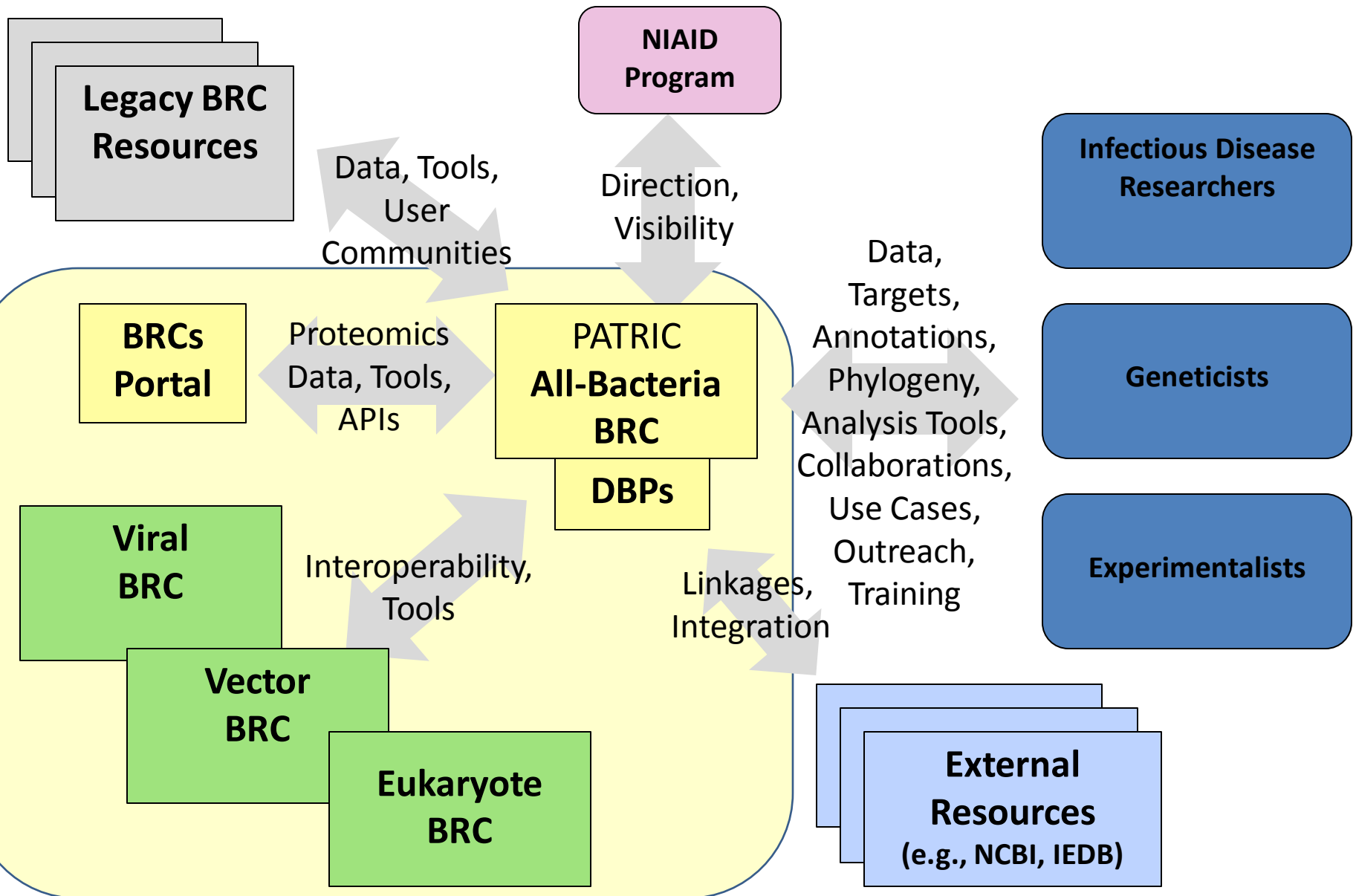
Pathogen Portal Concept
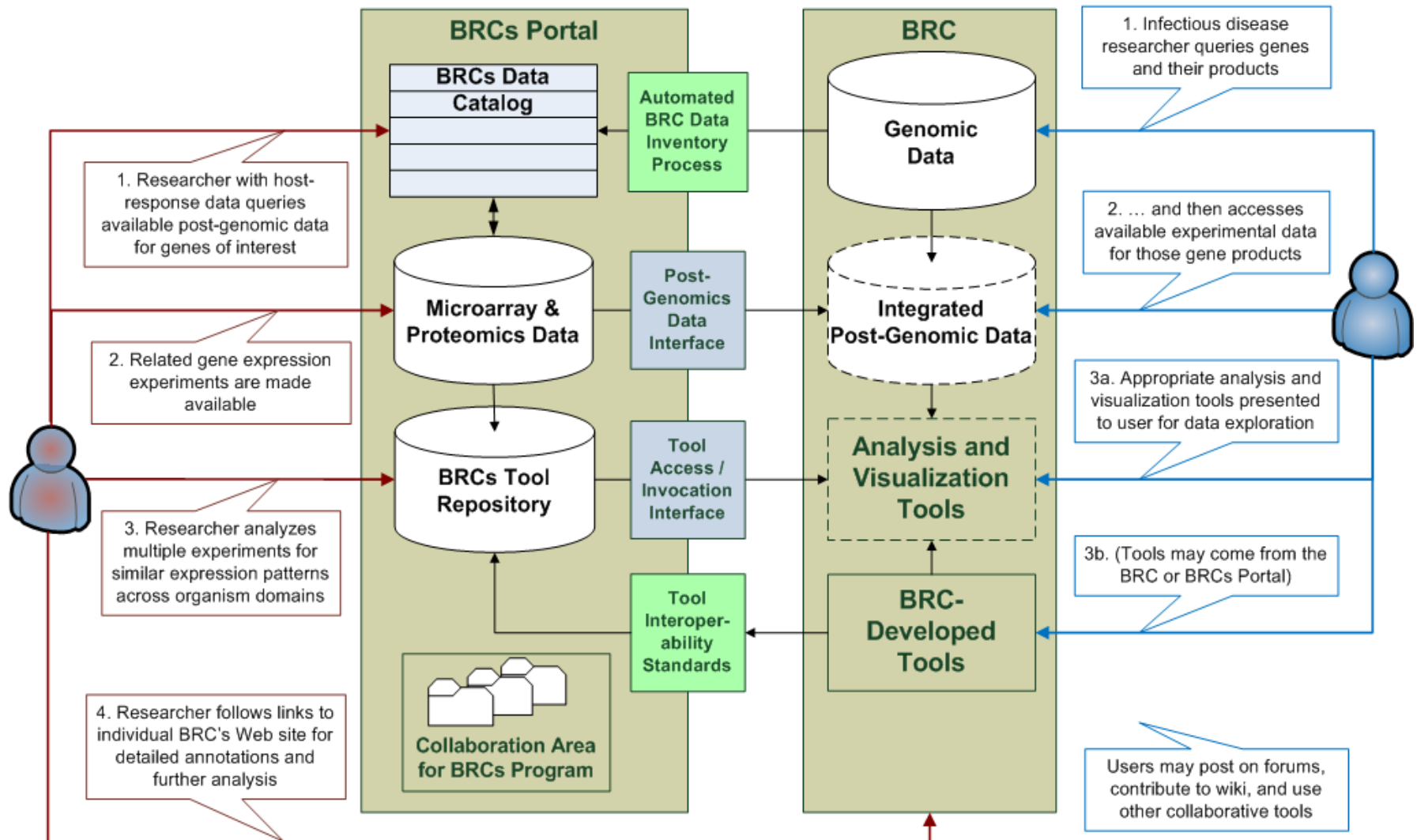
PATRIC Organisms

Bacillus	Francisella	**A, B, C Priority Bacteria**
Bartonella	Helicobacter	
Borrelia	Listeria	**Genome Annotations**
Brucella	Mycobacterium	
Burkholderia	Rickettsia	**Phylogenetic Analysis**
Campylobacter	Salmonella	
Chlamydophila	Shigella	**Comparative Analysis**
Clostridium	Staphylococcus	
Coxiella	Streptococcus	**Pathogens**
Ehrlichia	Vibrio	**Non-Pathogens**
Escherichia	Yersinia	
		Analysis Tools

RAST Server - high quality genome annotation

NMPDR

University of Chicago
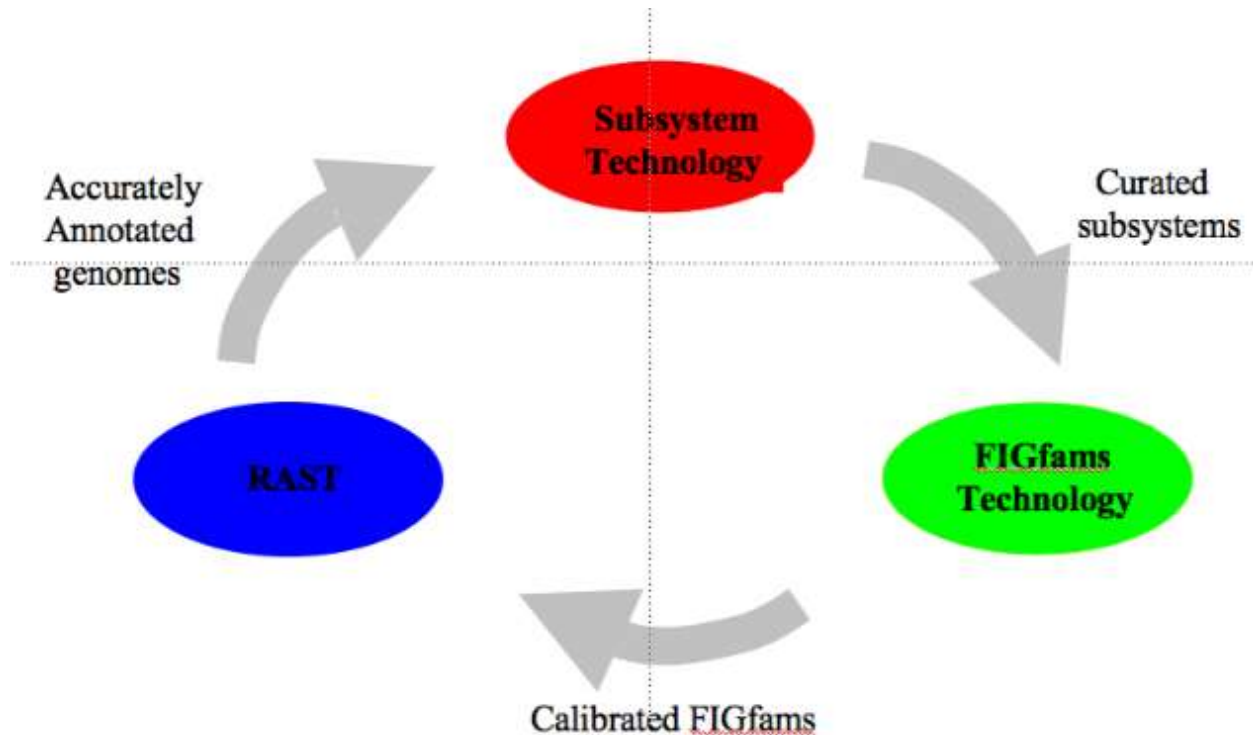
Argonne National Laboratory

RAST

- RAST is a completely open annotation service for prokaryotes
  - open-source
- **Input**: either a fasta file of contigs or a GenBank entry
- **Output**:
  - called genes (protein-encoding, rRNAs, and tRNAs)
  - functions assigned to genes
  - genes placed in subsystems
  - an initial metabolic reconstruction

RAST **Rapid Annotation using Subsystem Technology** version 2.0

The NMPDR, SEED-based, prokaryotic genome annotation service.
For more information about The SEED please visit theSEED.org.
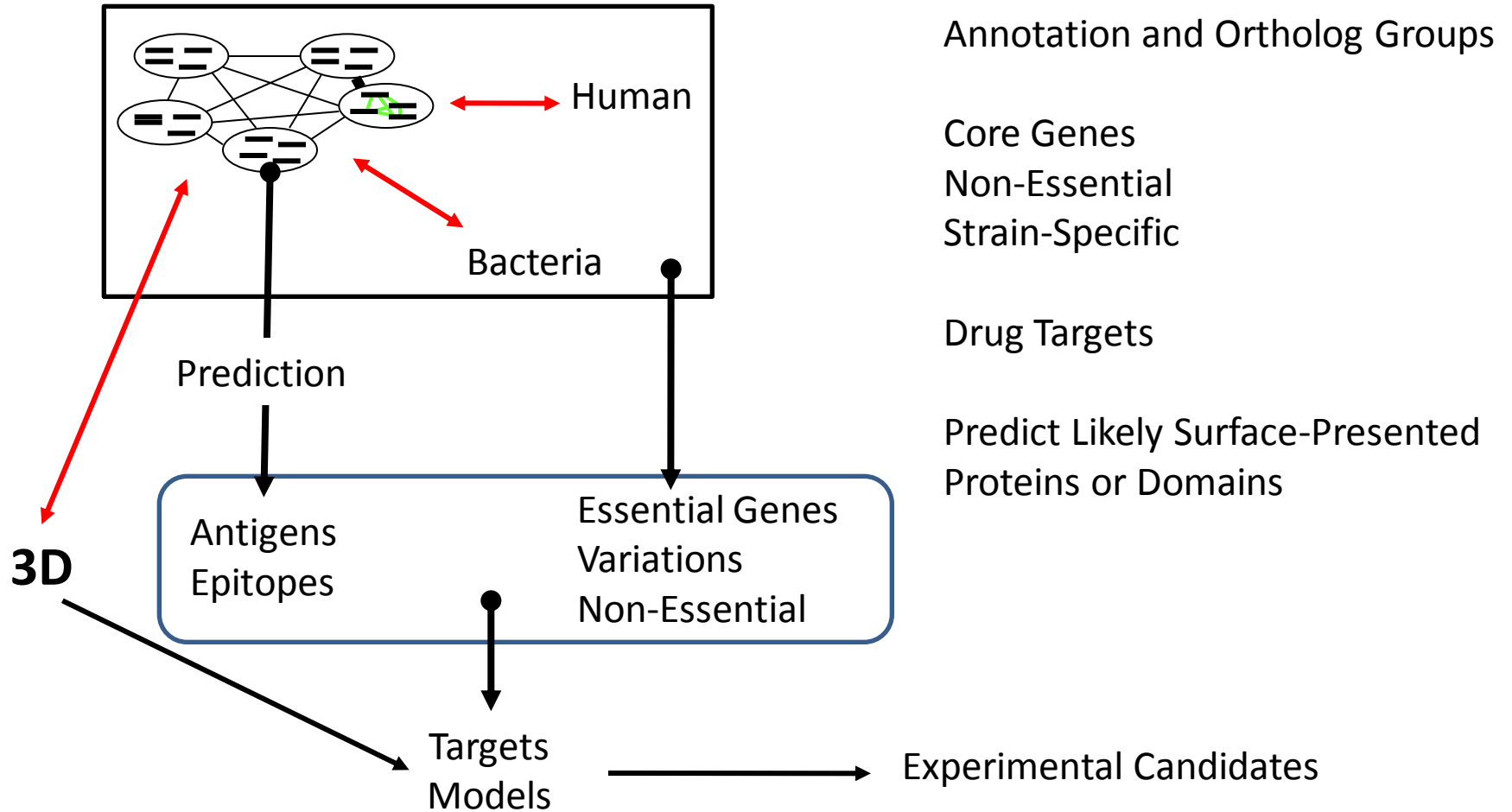
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Quality Determination

1. Accurately annotated core of **diverse genomes**
2. **Subsystems** that are manually curated across the entire collection of genomes, are also **computable objects**
3. **Protein families** that accurately characterize difficult cases (guided by the subsystems)
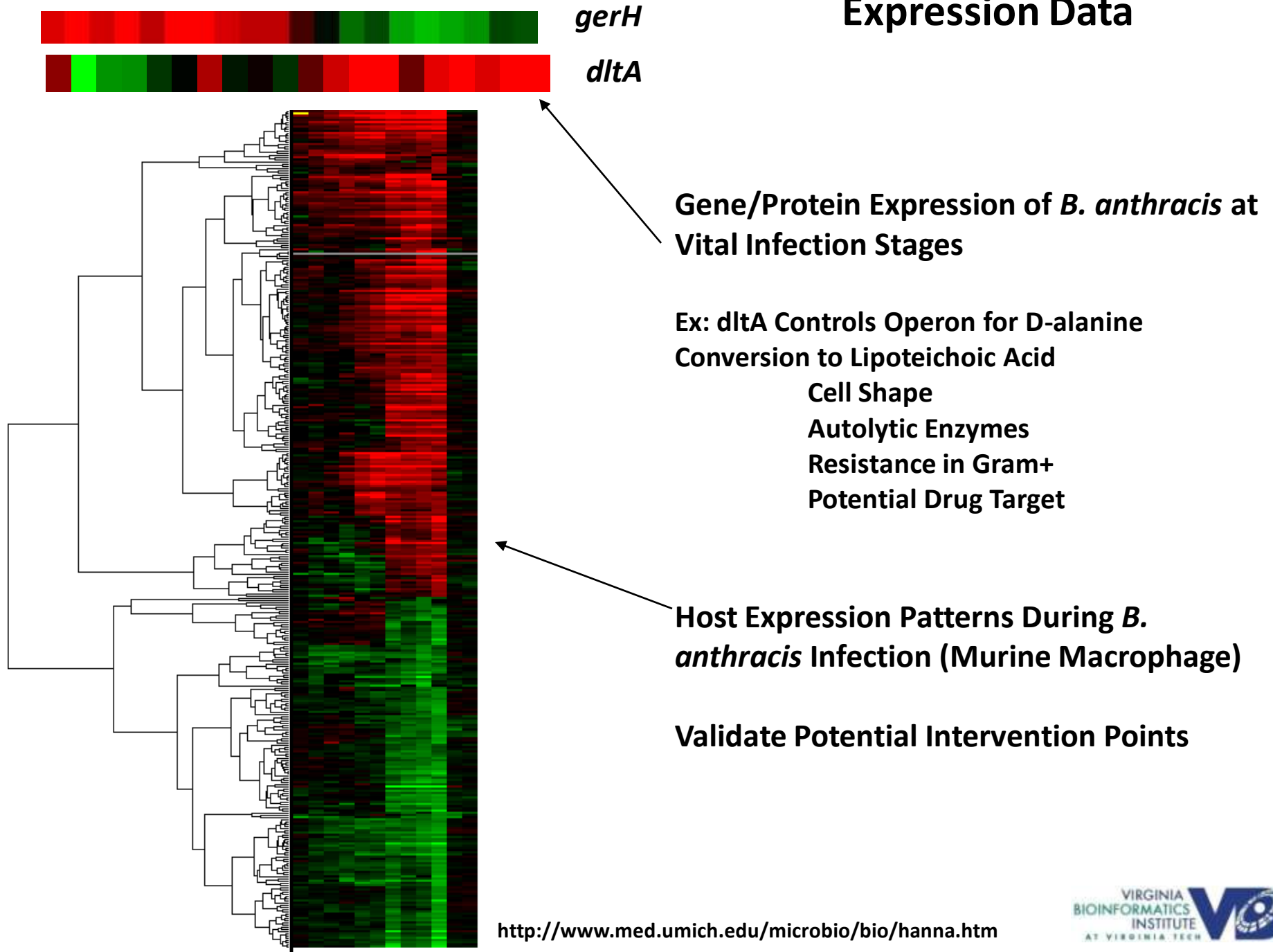
Pan-Genomic Approach

Annotation and Ortholog Groups

Core Genes
Non-Essential
Strain-Specific

Drug Targets

Predict Likely Surface-Presented
Proteins or Domains

Post-Genomic Data
PATRIC/Pathogen Portal

Expression Data

gerH

dltA

Gene/Protein Expression of *B. anthracis* at Vital Infection Stages

Ex: dltA Controls Operon for D-alanine Conversion to Lipoteichoic Acid
          Cell Shape
          Autolytic Enzymes
          Resistance in Gram+
          Potential Drug Target

Host Expression Patterns During *B. anthracis* Infection (Murine Macrophage)

Validate Potential Intervention Points

http://www.med.umich.edu/microbio/bio/hanna.htm

Mass Spec. Data

Mass and Time Tag Database for *Salmonella typhimurium* strain 14208

Protein ID	Protein name	Master Protein Directory
PSLT046	Putative carbonic anhydrase	Q7DAP2

Peptide
K.GSNYDFVDAVAR.K
K.HDYLAQK.R
K.IVGSMYHLTGGK.V
R.DGMTPDAVIEHFK.Q
R.KGSNYDFVDAVAR.K
R.KNSPVLK.Q
R.KNVELTIENIR.K
R.KNVELTIENIRK.N

XCorr

Validation

MS Data Forthcoming

Salmonella typhi strain TY2
Vaccinia Virus Western Reserve
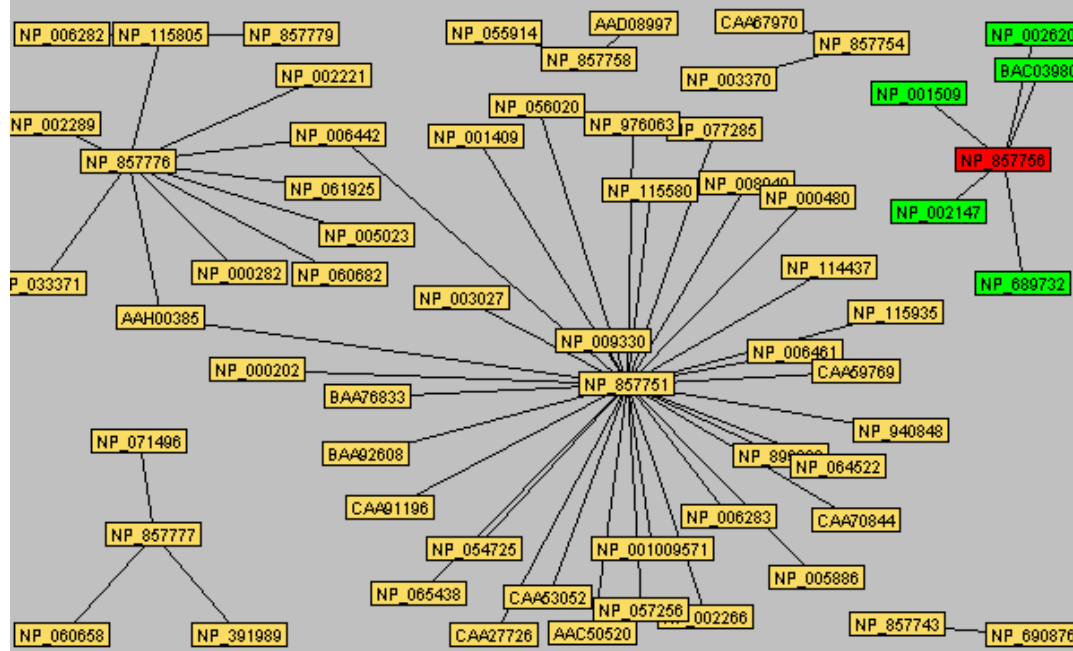Monkey Pox strain Zaire
Vaccinia Infected HELA cells
Vaccinia Infected THP-1

Low Expression   **High Expression**

Heat Map Using Protein Abundances

BIOINFORMATICS INSTITUTE AT VIRGINIA TECH

Protein-Protein Interaction Data
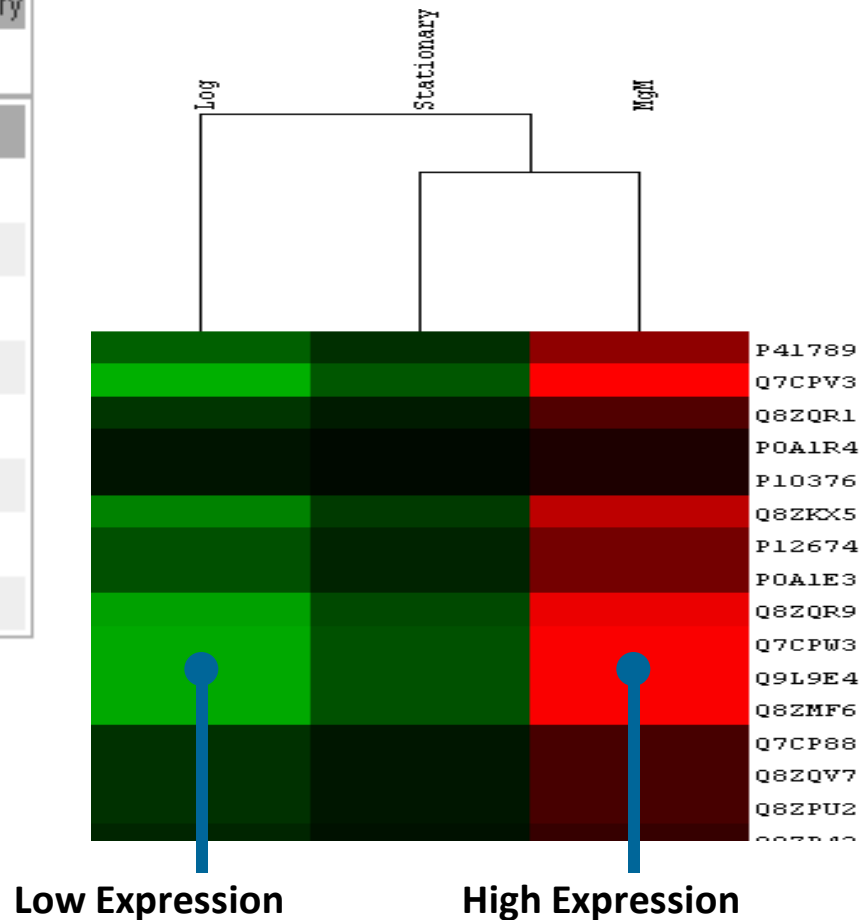
Interaction ID	Activation domain protein accession	Activation domain gene ID	Activation domain nucleotide accession	Activation domain protein GI	Binding domain protein accession	Binding domain gene ID	Binding domain nucleotide accession	Binding domain protein GI	Protein interaction detail
15369832	NP_005023	251	NM_005032	7549809	NP_857776	66945	NC_004836	31795319	View
15369833	NP_002289	153	NM_002298	4504965	NP_857776	66945	NC_004836	31795319	View
15369834	NP_060682	12251	NM_018212	39930375	NP_857776	66945	NC_004836	31795319	View
15369847	CAA53052	2409	X75304	405715	NP_857751	66912	NC_004836	31795291	View
15369850	NP_005886	956	NM_005895	5174441	NP_857751	66912	NC_004836	31795291	View
15369851	NP_008949	8297	NM_007018	38158018	NP_857751	66912	NC_004836	31795291	View
15369882		23342		0	NP_857751	66912	NC_004836	31795291	View
15369883	NP_001009571	39847	NM_001009571	57546902	NP_857751	66912	NC_004836	31795291	View
15369884	NP_000480	236	NM_000489	20336209	NP_857751	66912	NC_004836	31795291	View
15369886	NP_003027	238	NM_003036	4506967	NP_857751	66912	NC_004836	31795291	View
15369887	CAA70844	8492	Y09631	3925685	NP_857751	66912	NC_004836	31795291	View
15369888	BAA92608	10638	AB037791	7243121	NP_857751	66912	NC_004836	31795291	View
15369891	NP_115580	33255	NM_032204	20270253	NP_857751	66912	NC_004836	31795291	View
15369892	NP_006283	310	NM_006292	5454140	NP_857751	66912	NC_004836	31795291	View
15369893	CAA27726	2904	X04106	35328	NP_857751	66912	NC_004836	31795291	View

High Throughput Yeast Two-Hybrid Technology

Host/Pathogen Interactions

Biochemical Pathways

Proteins Binding to Membrane Proteins
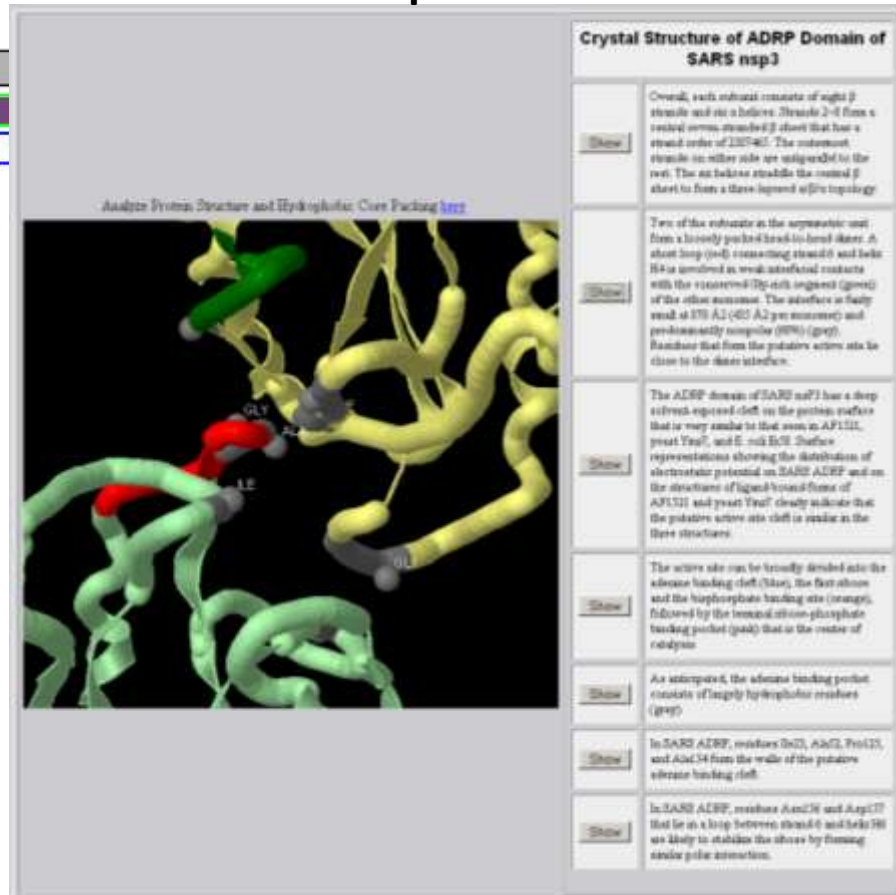

http://www.myriad.com/index.php

VIRGINIA BIOINFORMATICS INSTITUTE AT VIRGINIA TECH

SARS Proteome 3D Structures
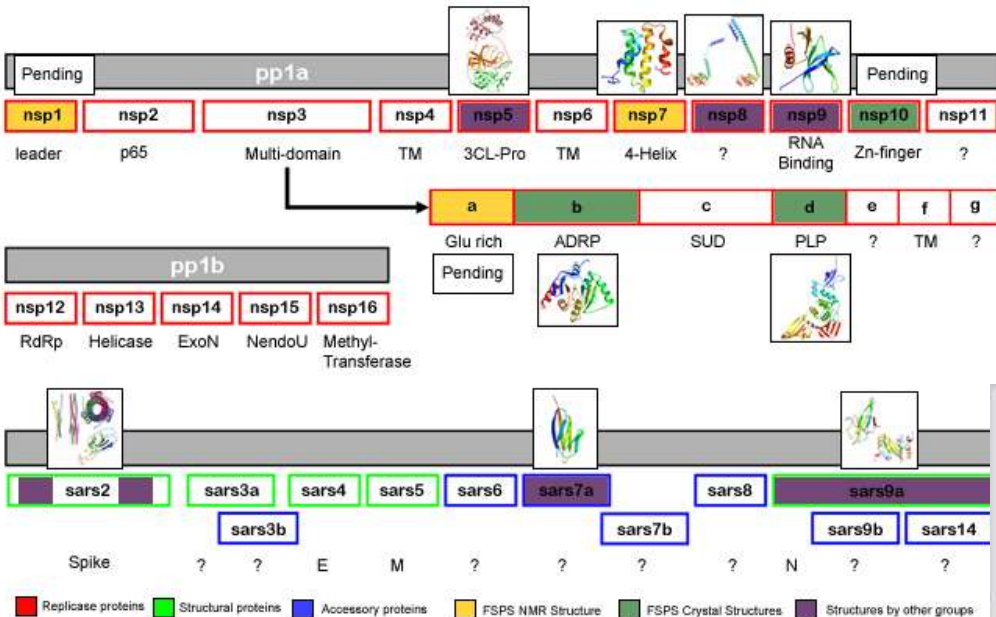
— **Proteome Via Crystallography, NMR, Microscopy**

SARS nsp3 ADRP

Annotations Derived from Published Manuscripts

Illustrate Features Described in Paper

Fully Interactive 3D Graphics

http://sars.scripps.edu/

PATRIC 3-D Structure Viewer

Structure Analysis at PATRIC

1D:

Identify What Structures are Available for All Sequences

Identify Homologues for All Sequences – 30% Identity

3D:

Compare Two Different Structures

Compare Conformations of a Structure

Compare a Structure to a Database of Structures

Find All structures With a Motif

Find All Similarities (Motifs) in All Structures

PATRIC Project Team

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