

Pathosystems Resource Integration Center for Bacterial Diseases

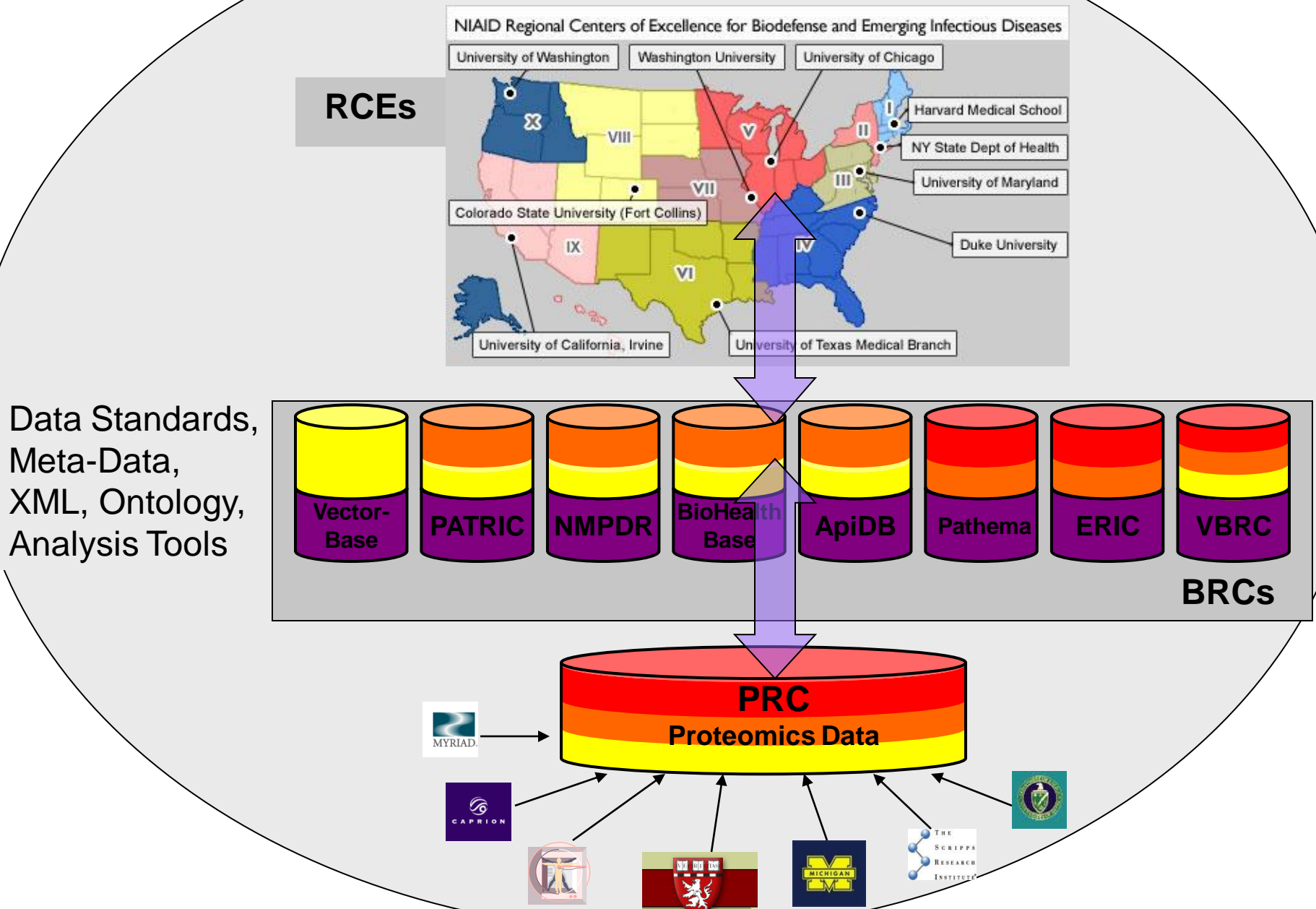
Rebecca Wattam

Bruno Sobral's Cyberinfrastructure Group

17th Annual Microbial Genomics Conference October 11, 2009

Rocky Gap State Park, MD

Original BRC / PRC (& RCE) Programs



Emphasis on NIAID Priority Pathogens...

Category A

- *Bacillus anthracis* (anthrax)
- *Clostridium botulinum* toxin (botulism)
- *Yersinia pestis* (plague)
- *Variola major* (smallpox) and other related pox viruses
- *Francisella tularensis* (tularemia)
- Viral hemorrhagic fevers
- Arenaviruses
 - LCM, Junin virus, Machupo virus, Guanarito virus
 - Lassa Fever
- Bunyaviruses
 - Hantaviruses
 - Rift Valley Fever
- Flaviviruses
 - Dengue
- Filoviruses
 - Ebola
 - Marburg

Category B

- *Burkholderia pseudomallei*
- *Coxiella burnetii* (Q fever)
- *Brucella* species (brucellosis)
- *Burkholderia mallei* (glanders)
- *Chlamydia psittaci* (Psittacosis)
- Ricin toxin (from *Ricinus communis*)
- Epsilon toxin of *Clostridium perfringens*
- *Staphylococcus enterotoxin B*
- Typhus fever (*Rickettsia prowazekii*)
- Food- and Waterborne Pathogens
 - Bacteria
 - Diarrheagenic *E. coli*
 - Pathogenic *Vibrios*
 - *Shigella* species
 - *Salmonella*
 - *Listeria monocytogenes*
 - *Campylobacter jejuni*
 - *Yersinia enterocolitica*

Category C

Emerging infectious disease threats such as Nipah virus and additional hantaviruses.

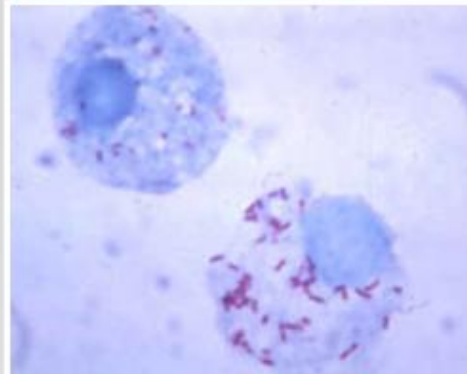
NIAID priority areas:

- Tickborne hemorrhagic fever viruses
 - Crimean-Congo Hemorrhagic fever virus
- Tickborne encephalitis viruses
- Yellow fever
- Multi-drug resistant TB
- Influenza
- Other Rickettsias
- Rabies
- Prions
- Chikungunya virus
- Severe acute respiratory syndrome associated coronavirus (SARS-CoV)
- Antimicrobial resistance, excluding research on sexually transmitted organisms*




News

-  **29 June 2009**
PATRIC Data Release and Website Update.
-  **10 April 2009**
PATRIC Data Release and Website Update.
-  **9 February 2009**
PATRIC Data Release and Website Update.
-  **7 October 2008**
PATRIC Data Release and Website Update.
-  **3 September 2008**
PATRIC Data Release.
-  **11 June 2008**
PATRIC Data Release and Website Update.
-  **18 April 2008**
PATRIC Data Release and Website Update.
-  **31 January 2008**
PATRIC Data Release and Website Update.
-  **More News**






The Organisms We Study







Bacteria

-  *Brucella*
-  *Coxiella*
-  *Rickettsia*



Viruses

-  *Caliciviridae*
-  *Coronavirus*
-  *Hepatitis A Virus*
-  *Hepatitis E Virus*
-  *Lyssavirus*


Assemble & Download Sequences of Interest

-  Perform 9 specialized searches
-  Use custom filters to drill down and narrow search results in feature tables
-  Save and download results with feature cart
-  Manipulate ortholog groups of related proteins for all PATRIC organisms

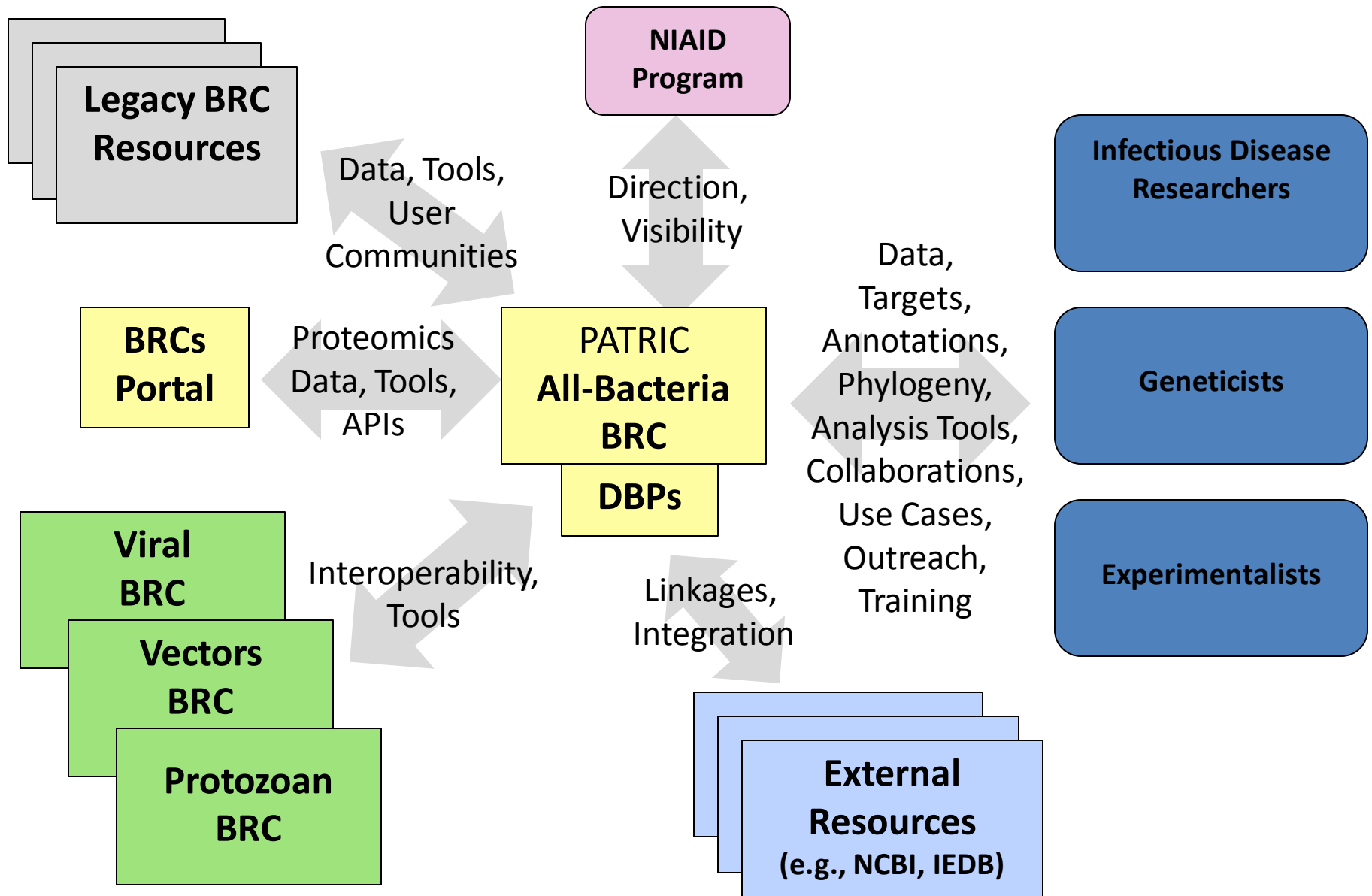
Perform Comparative Genomics

-  Use tools to pinpoint common or unique traits among genes/proteins
-  Compare amino acid sequences across proteins using Multiple Sequence Alignment

Perform Comparative Pathway Analysis

-  Compare PATRIC pathogen genome at pathway level

New PATRIC All-Bacteria BRC



Bacterial Data from Existing BRCs will Migrate to All-Bacterial BRC



[FAQ](#) | [Publications](#) | [Training](#) | [Pathogen Portal](#)

BioHealthBase
BioDefense & Public Health Database

NMPDR
Bioinformatics Resource Center

National Microbial Pathogen Data Resource



Enteropathogen Resource Integration Center

Bioinformatics Resource Center



PATRIC

PathoSystems Resource Integration Center

New All-Bacterial BRC: **PATRIC**
Includes Pathogenic Bacteria and Relatives

Role of 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

The RAST Server -- a public resource for high quality genome annotation

NMPDR

University of Chicago

Argonne National Laboratory

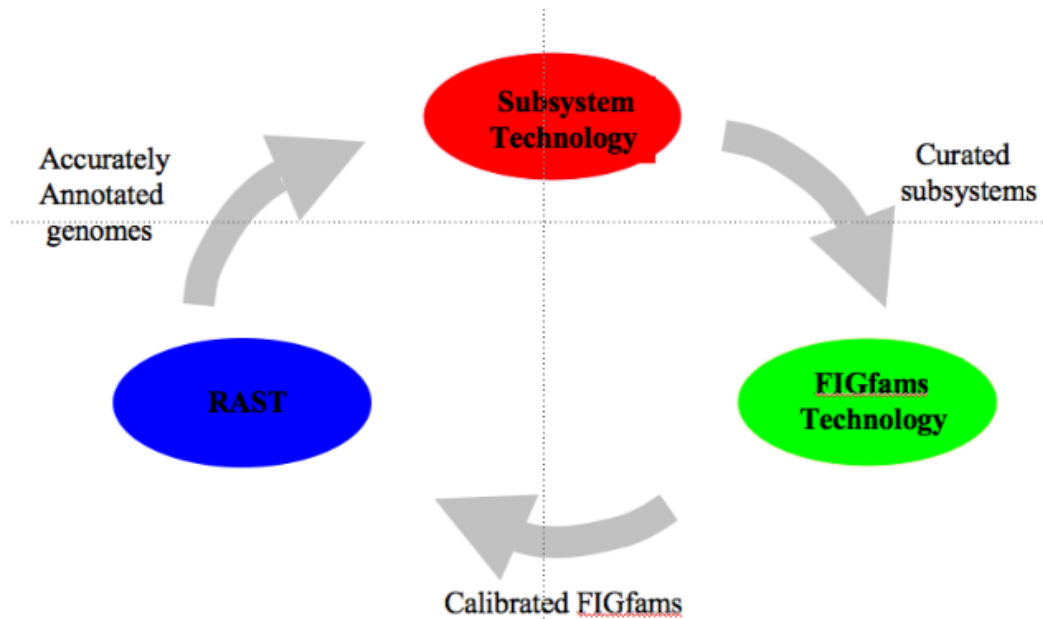
What is RAST?

- 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



What Determines Quality?

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)



Test Case: A large number of closely related genomes

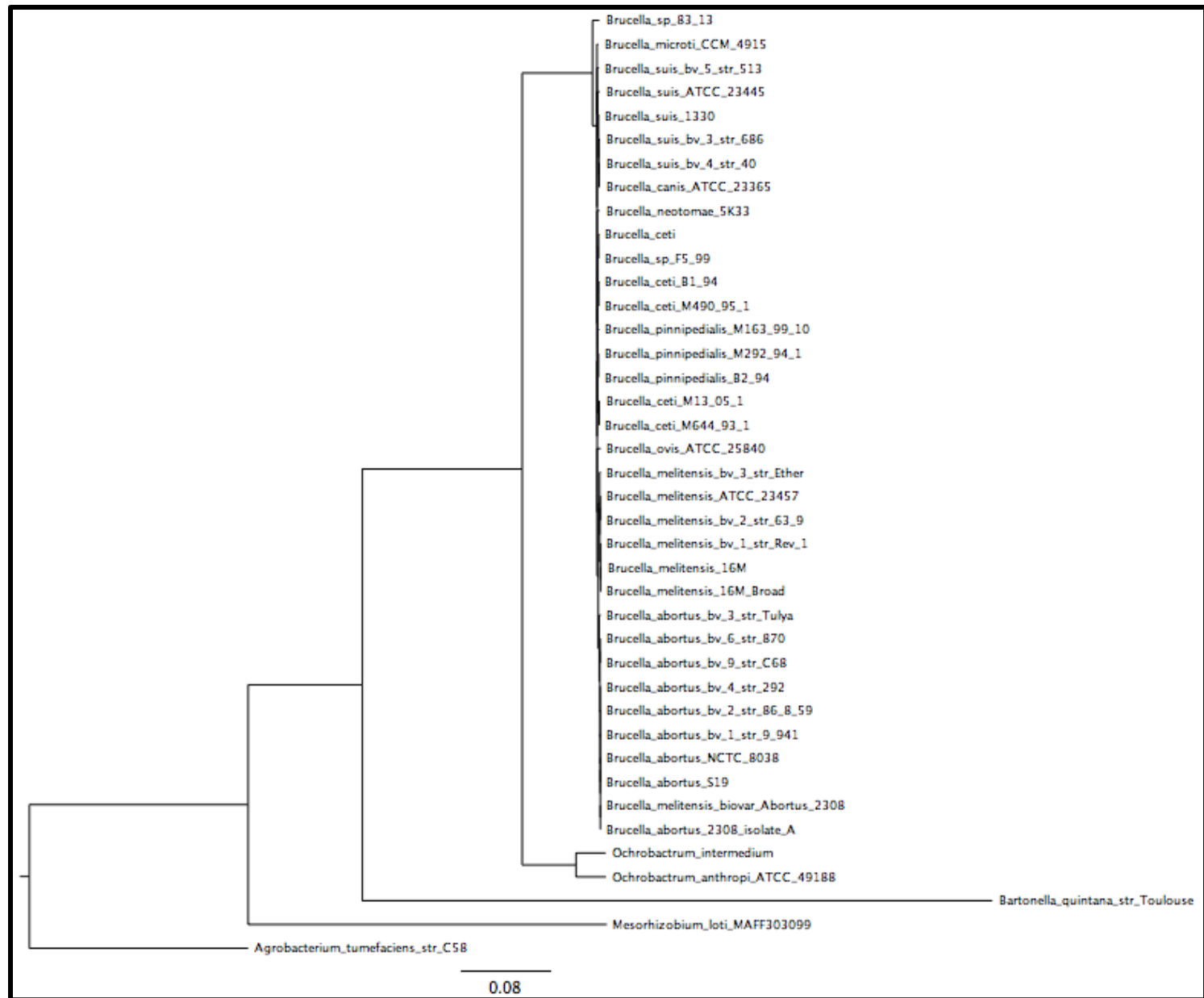


The genus *Brucella*

Workflow for *Brucella* Analysis

- Annotate genomes
- Identify protein families using OrthoMCL
- Create phylogenetic tree using RaxML
- Identify protein families of interest and include pathway associated data if possible
 - Collaborators want clade-specific data that is associated with these genomes

Phylogeny: Members of this Genus are Closely Related



What is a good way to present complex, inter-related data in an easily understandable format?

Protein Family Viewer Prototype

[illegible]

Our collaborators specifically want to know what these clades share, and what differentiates them.

The amount of data can still be overwhelming

Data Shared Across Clades....Analysis Prototype

[illegible]

Data Missing Across Clades...

[illegible]

Driving Software Development and Bioinformatics

Working with Collaborators

PATRIC: Genomics Analysis Resource

PATRIC

- Protein Family Sorter
- Gene Set Explorer
- Pathway Tools
- 2-way genome comparison
- BLAST

New PATRIC

- Dynamic Protein Family Sorter
 - Shows group members
 - Provides multiple sequence alignments
 - Shows instant BLASTP results
- Combination of protein families, phylogeny, and pathway information
 - KEGG pathways
- Gene Set Explorer
- Pathway Tools
- Multi-genome comparison
- BLAST

Transforming Bioinformatics Data to Accessible Data for the Computationally-Challenged Biologist

• Early Design-Protein Family data

>Family 338 -- @locks 238/280 (92%)

BABG_0235270|BABG_02352
BABG_0235670|BABG_02356
BABG_0046670|BABG_00466
BATG_0156870|BATG_01568
BABG_0046470|BABG_00464
BABG_0046170|BABG_00461
BABG_0047170|BABG_00471
BABG_0237870|BABG_02378
[gi|49473703|ref|YP_031745.1|](#)
[fidi|0207042|locus|VBI7202B5191_0163](#)
BABG_0231970|BABG_02319
[fidi|450877|locus|VBI13588AA1_0161](#)
[fidi|489395|locus|VBI10009BA1_0163](#)
BABG_0046670|BABG_00466
BABG_0237970|BABG_02379
[fidi|789443|locus|VBI16890BC1_0163](#)
[fidi|1555505|locus|VBI7639BCe1_0330](#)
BABG_0046570|BABG_00465
BATG_0160370|BATG_01603
[fidi|81264|locus|VBI100106W1_2001|acem|WP_540707.1](#)
[fidi|1104835|locus|VBI186588MAtcc1_0163](#)
[fidi|1501443|locus|VBI100258Mb1_0163](#)
BABG_0285170|BABG_02851
BABG_0124270|BABG_01242
BABG_0289370|BABG_02893
BABG_0045970|BABG_00459
[fidi|823650|locus|VBI16002Bov1_0164](#)
BABG_0178970|BABG_01789
BABG_0144770|BABG_01447
BATG_0237170|BATG_02371
[fidi|1525082|locus|VBI7898B02_0063](#)
[fidi|1632559|locus|VBI1001980210_0141](#)
[fidi|229497|locus|VBI10007B31_0156|acem|NP_697195.1](#)
[fidi|749212|locus|VBI645888Atcc1_0159](#)
[gi|13472789|ref|NP_104356.1|](#)
[gi|153007534|ref|YP_001368729.1|](#)
[fidi|1494583|locus|VBI4212011_0172](#)

nr ABC transporter ATP-binding protein [Brucella abortus bv. 4 str. 292]
nr ABC transporter ATP-binding protein [Brucella abortus bv. 6 str. 870]
nr ABC transporter ATP-binding protein [Brucella ceti M490/95/1]
nr ABC transporter ATP-binding protein [Brucella ceti M644/93/1]
nr ABC transporter ATP-binding protein [Brucella pinnipedialis B2/94]
nr ABC transporter ATP-binding protein [Brucella pinnipedialis M292/94/1]
nr ABC transporter ATP-binding protein [Brucella suis bv. 5 str. 513]
nr ABC transporter ATP-binding protein [Brucella suis bv. 3 str. 686]
nr ABC transporter ATP-binding protein [Bartonella quintana str. Toulouse]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella abortus 819]
nr ABC transporter ATP-binding protein [Brucella abortus bv. 9 str. C68]
nr Uncharacterized ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella abortus 2308 isolate A]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella abortus bv. 1 str. 9-941]
nr ABC transporter ATP-binding protein [Brucella abortus bv. 2 str. 86/8/59]
nr ABC transporter ATP-binding protein [Brucella abortus bv. 3 str. Tulya]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella canis ATCC 23365]
nr ABC transporter related [Brucella ceti]
nr ABC transporter ATP-binding protein [Brucella ceti B1/94]
nr ABC transporter ATP-binding protein [Brucella ceti M13/05/1]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella melitensis 16M]
nr ABC transporter ATP-binding protein [Brucella melitensis ATCC 23457]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella melitensis biovar Abortus 2308]
nr ABC transporter ATP-binding protein [Brucella melitensis bv. 1 str. Rev.1]
nr ATP/GTP-binding site domain-containing protein A [Brucella melitensis bv. 2 str. 63/9]
nr ABC transporter ATP-binding protein [Brucella melitensis bv. 3 str. Ether]
nr ABC transporter ATP-binding protein [Brucella neotoma SR33]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella ovis ATCC 25840]
nr ABC transporter ATP-binding protein [Brucella pinnipedialis M163/99/10]
nr ABC transporter ATP-binding protein [Brucella sp. 83/13]
nr ATP/GTP-binding site domain-containing protein A [Brucella sp. F5/99]
nr ABC transporter [Brucella str. B01]
nr ABC transporter ATP-binding protein [Brucella str. B02]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella suis 1330]
nr Probable ABC transporter ATP-binding protein in ntrA/rpoN Sregion [Brucella suis ATCC 23445]
nr ABC transporter ATP-binding protein (in rpoN upstream) [Mesorhizobium loti MAF303099]
nr ABC transporter related [Ochrobactrum anthropi ATCC 43188]
nr ABC transporter related [Ochrobactrum intermedium]

• Prototype-Protein Family Sorter

Ortholog FASTA Upload

Upload file for Ortholog Processing

Input file

Ortholog Groups Viewer

Project Name:

12102 GROUPS

Include

Exclude

☐ Don't Care

☒ Sat all

☒ Agrobacterium tumefaciens str. C58

☒ Bartonella quintana str. Toulouse

☒ Brucella abortus 2308 isolate A

☒ Brucella abortus NCTC 8038

☒ Brucella abortus S19

☒ Brucella abortus bv. 1 str. 9-941

☒ Brucella abortus bv. 2 str. 86/8/59

☒ Brucella abortus bv. 3 str. Tulya

☒ Brucella abortus bv. 4 str. 292

☒ Brucella abortus bv. 6 str. 870

☒ Brucella abortus bv. 9 str. C68

☒ Brucella canis ATCC 23365

☒ Brucella ceti

☒ Brucella ceti B1/94

☒ Brucella ceti M13/05/1

☒ Brucella ceti M490/95/1

☒ Brucella ceti M644/93/1

☒ Brucella melitensis 16M

☒ Brucella melitensis ATCC 23457

☒ Brucella melitensis biovar Abortus 2308

☒ Brucella melitensis bv. 1 str. Rev.1

☒ Brucella melitensis bv. 2 str. 63/9

☒ Brucella melitensis bv. 3 str. Ether

☒ Brucella microti CCM 4915

☒ Brucella neotoma 5K33

☒ Brucella ovis ATCC 25840

☒ Brucella pinnipedialis B2/94

☒ Brucella pinnipedialis M163/99/10

☒ Brucella pinnipedialis M292/94/1

☒ Brucella sp. 83/13

☒ Brucella sp. F5/99

☒ Brucella suis 1330

☒ Brucella suis ATCC 23445

☒ Brucella suis bv. 3 str. 686

☒ Brucella suis bv. 4 str. 513

☒ Brucella suis bv. 5 str. 513

☒ Mesorhizobium loti MAF303099

☒ Ochrobactrum anthropi ATCC 43188

☒ Ochrobactrum intermedium

Ortholog Groups

Id	Members	Species	Product Description	Min	Max
OG_100	40	40	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	413	423
OG_101	40	40	phosphopyruvate hydratase	422	425
OG_102	40	40	phosphoglucosyltransferase	542	549
OG_103	40	40	preprotein translocase, SecE subunit	66	79
OG_104	40	40	protease II	697	707
OG_105	40	40	16S rRNA processing protein RimM	179	199
OG_106	40	40	30S ribosomal protein S8	132	132
OG_107	40	40	transcription termination/antitermination factor NusG	175	176
OG_108	40	40	N-acetyl-gamma-glutamyl-phosphate reductase	308	311
OG_109	40	40	DNA repair protein RadA	464	468
OG_110	40	40	HSP20 family protein	137	160
OG_111	40	40	ribosomal protein L7/L12	123	125
OG_112	40	40	competence protein F	240	263
OG_113	40	40	outer membrane lipoprotein	177	181
OG_114	40	40	protein TolD	238	239
OG_115	40	40	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	364	431
OG_116	40	40	two component response regulator	227	227
OG_117	40	40	acyl carrier protein	93	94
OG_118	40	40	ribosomal protein L17	141	143
OG_119	40	40	small protein A	159	228
OG_120	40	40	Holliday junction DNA helicase RuvB	345	361
OG_121	40	40	succinate dehydrogenase, flavoprotein subunit	579	630
OG_122	40	40	septum formation initiator	105	120
OG_123	40	40	cross-over junction endonuclease RuvC	169	173
OG_124	40	40	Myosin-14	220	411

Provides information on each protein family

<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella abortus S19	OG_3456	16	16	ABC transporter, ATP binding/permeas	318	3
<input checked="" type="radio"/> <input type="radio"/> <input type="radio"/> Brucella abortus bv. 1 str. 9-941	OG_3457	16	16	AraC family transcriptional regulator	119	1
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<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella abortus bv. 3 str. Tulya	OG_3460	16	16	Hypothetical protein	34	3
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<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella abortus bv. 9 str. C68	OG_3465	16	16	Hypothetical protein	133	1
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella canis ATCC 23365	OG_3466	16	16	ApbE-like lipoprotein	94	9
<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/> Brucella ceti	OG_3467	16	16	sugar ABC transporter, periplasmic sug	147	1
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella ceti B1/94	OG_3469	16	16	multidrug resistance protein	240	2
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella ceti M13/05/1	OG_3470	16	16	sugar ABC transporter, periplasmic sug	115	1
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella ceti M490/95/1						
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella ceti M644/93/1						
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella melitensis 16M						
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella melitensis 16M / Broad						
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella melitensis ATCC 23457						
<input type="radio"/> <input type="radio"/> <input type="radio"/> Brucella melitensis biovar Abortus 2308						

OG_3457: AraC family transcriptional regulator

[Get Group Alignment](#) [EXCEL TABLE](#)

Genome	fid	locus	AA Length	Blast	Protein Product
Brucella abortus S19	2183319	VBI7202BR2_0602	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 1 str. 9-941	219858E	VBI8788BR1_0602	119	NCBI	AraC family transcriptional regulator
Brucella melitensis 16M	2284914	VBI0010BR1_1597	119	NCBI	AraC family transcriptional regulator
Brucella melitensis biovar Abortus 2308	231358C	VBI0025BR1_0604	119	NCBI	AraC family transcriptional regulator
Brucella melitensis ATCC 23457	246203C	VBI13428BR1_0606	119	NCBI	AraC family transcriptional regulator
Brucella abortus 2308 isolate A	2520243	VBI13568BR1_0605	119	NCBI	AraC family transcriptional regulator
Brucella melitensis bv. 3 str. Ether	2823964	VBI8692BR1_2121	119	NCBI	AraC family transcriptional regulator
Brucella melitensis bv. 2 str. 63/9	2890283	VBI8688BR1_2611	119	NCBI	AraC family transcriptional regulator
Brucella abortus NCTC 8038	2997687	VBI14171BR1_1731	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 9 str. C68	3019224	VBI8687BR1_1474	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 6 str. 870	303523C	VBI8690BR1_0290	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 4 str. 292	305311E	VBI8678BR1_0291	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 3 str. Tulya	309822E	VBI8693BR1_0289	119	NCBI	AraC family transcriptional regulator
Brucella melitensis bv. 1 str. Rev.1	3124052	VBI14022BR1_1494	119	NCBI	AraC family transcriptional regulator
Brucella melitensis 16M / Broad	314938E	VBI17030BR1_0949	119	NCBI	AraC family transcriptional regulator
Brucella abortus bv. 2 str. 86/8/59	3173743	VBI8679BR1_2369	119	NCBI	AraC family transcriptional regulator

Multiple sequence alignment provided

OG_3457: AraC family transcriptional regulator

Get Group Alignment EXCEL TABLE

Genome	fid	locus	AA Length	Blast	Protein Product
Brucella abortus S19	21833				
Brucella abortus bv. 1 str. 9-941	21985				
Brucella melitensis 16M	22848				
Brucella melitensis biovar Abortus 2308	23135				
Brucella melitensis ATCC 23457	24620				
Brucella abortus 2308 isolate A	25202				
Brucella melitensis bv. 3 str. Ether	28238				
Brucella melitensis bv. 2 str. 63/9	28902				
Brucella abortus NCTC 8038	29976				
Brucella abortus bv. 9 str. C68	30192				
Brucella abortus bv. 6 str. 870	30352				
Brucella abortus bv. 4 str. 292	30531				
Brucella abortus bv. 3 str. Tulya	30982				
Brucella melitensis bv. 1 str. Rev.1	31240				
Brucella melitensis 16M / Broad	31493				
Brucella abortus bv. 2 str. 86/8/59	31737				

Done

Gblocks 0.91b Results

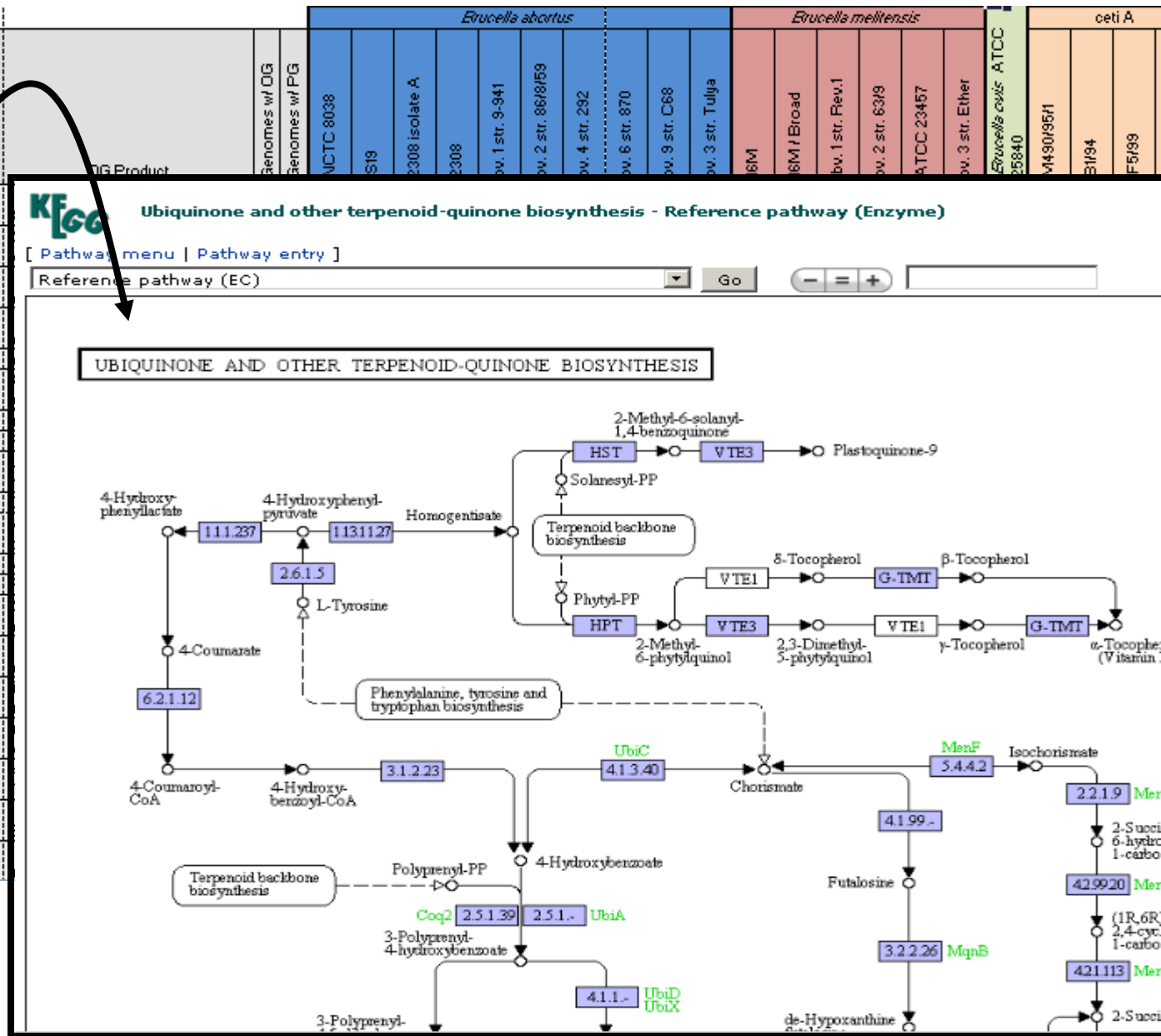
Processed file: OG_3457_align
Number of sequences: 16
Alignment assumed to be: **Protein**
New number of positions: 119 (selected positions are underlined in blue)

	10	20	30	40	50	60
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_melite	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA
Brucella_abortu	MSRSHLYRA	FEPDGGVAKVIR	DKRLDLAYRIL	IDRKGKPTSLKE	IAYCCGFNDRTQ	FTKA

	70	80	90	100	110
Brucella_abortu	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_abortu	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_melite	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_melite	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_abortu	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_melite	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP
Brucella_melite	FKARFELSPKEA	HEIGAPLPQAPSGAL	ILHSHLSEQA	AKIASEHATTSTK	APPSAPVKP

Direct link to KEGG pathway information

Pathway ID	Pathway Name	EC NO	OG ID
72	Synthesis and degradation of ketone bodies	1.1.1.30	OG_1609
72	Synthesis and degradation of ketone bodies	1.1.1.30	OG_3287
72	Synthesis and degradation of ketone bodies	2.3.1.9	OG_1855
72	Synthesis and degradation of ketone bodies	4.1.3.4	OG_2619
100	Steroid biosynthesis	1.14.1.1	OG_2030
120	Primary bile acid biosynthesis	1.1.1.35	OG_2496
120	Primary bile acid biosynthesis	1.14.1.1	OG_2605
120	Primary bile acid biosynthesis	3.5.1.24	OG_976
120	Primary bile acid biosynthesis	5.1.99.4	OG_2520
120	Primary bile acid biosynthesis	5.1.99.4	OG_3370
121	Secondary bile acid biosynthesis	1.1.1.1	OG_2292
121	Secondary bile acid biosynthesis	1.1.1.1	OG_3070
121	Secondary bile acid biosynthesis	3.5.1.24	OG_976
121	Secondary bile acid biosynthesis	4.2.1.1	OG_3078
130	Ubiquinone and other terpenoid-quinone biosynthesis	1.14.1.1	OG_2030
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1083
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1336
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1347
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1671
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1898



Direct link to multiple sequence alignment

Pathway ID	Pathway Name	EC NO	OG ID	EC Description	Genomes w/ OG	Genomes w/ PG	<i>Brucella abortus</i>	<i>Brucella melitensis</i>	<i>Brucella ovis</i> ATCC 5840	<i>Ceti A</i>
72	Synthesis and degradation of ketone bodies	1.1.1.30	OG_160	3-hydroxybutyrate dehydrogenase						
72	Synthesis and degradation of ketone bodies	1.1.1.30	OG_287	2-hydroxy-3-oxobutanoate reductase						
72	Synthesis and degradation of ketone bodies	2.3.1.8	OG_1855	acetyl-CoA synthetase						
72	Synthesis and degradation of ketone bodies	4.1.3.4	OG_2619	hydroxymethylglutaryl-CoA lyase						
100	Steroid biosynthesis	1.14.1.1	OG_2030	heme-thiolate lyase						
120	Primary bile acid biosynthesis	1.1.1.35	OG_2496	3-hydroxyacyl-CoA lyase						
120	Primary bile acid biosynthesis	1.14.1.3	OG_2605	monooxygenase						
120	Primary bile acid biosynthesis	3.5.1.24	OG_376	Penicillinase						
120	Primary bile acid biosynthesis	5.1.99.4	OG_2520	L-carnitine:indole-3-pyruvate transferase						
120	Primary bile acid biosynthesis	5.1.99.4	OG_3370	CAIB/BAIF						
121	Secondary bile acid biosynthesis	1.1.1.1	OG_2292	NADH:flavin oxidoreductase						
121	Secondary bile acid biosynthesis	1.1.1.1	OG_3070	NADH oxidase						
121	Secondary bile acid biosynthesis	3.5.1.24	OG_376	Penicillinase						
121	Secondary bile acid biosynthesis	4.2.1.1	OG_3078	2-oxo-heptanoate hydratase						
130	Ubiquinone and other terpenoid-quinone biosynthesis	1.14.1.1	OG_2030	heme-thiolate lyase						
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1083	ribosomal methyltransferase						
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1336	ubiquinone biosynthesis						
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1347	conserved						
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1671	TIGR00046						
130	Ubiquinone and other terpenoid-quinone biosynthesis	2.1.1.1	OG_1898	Sun						
				methyltransferase						

Gblocks 0.91b Results

Processed file: OG_972_align

Number of sequences: 39

Alignment assumed to be: Protein

New number of positions: 276 (selected positions are underlined in blue)

	10	20	30	40	50	60
Brucella_abortu	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_abortu	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_canis	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_melite	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_melite	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_microt	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_ovis_A	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_suis_1	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_suis_A	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_melite	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_abortu	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_ceti	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Ochrobactrum_in	MAKNDQAQAFDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEDVLRIDPDDH		
Brucella_sp._83	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_suis_b	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_suis_b	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_suis_b	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_sp._F5	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_pinnip	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_pinnip	MISHLIRRLPRPYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_pinnip	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_melite	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_melite	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		
Brucella_ceti_M	MAQSDDKPLDQEQALAEAYNRALAL			EKAGDFFDAAAKAYEEVLQIAPDDH		

PATRIC Prototype Page

Phylogeny
MSA

BLAST

Features

GO Codes

Experiment
Data

BLAST

BLAST selected feature to

NCBI

Brucella

OR

BLAST to this feature

Sequence Similarity

CLUSTAL W	view
Base By Base	view
Phylogenetic Tree	view

Feature Table

Locus Tag	Product Descript...
VBI0007BS1_0611	342 Hypothetical protein
VBI0007BS1_0612	546 Hypothetical protein
VBI0007BS1_0613	633 conserved hypothetical
VBI0007BS1_0614	876 phage conserved hypo
VBI0007BS1_0615	435 putative phage cell wal
VBI0007BS1_0616	20 Hypothetical protein
VBI0007BS1_0618	207 Hypothetical protein
VBI0007BS1_0619	297 Hypothetical protein
VBI0007BS1_0620	690 Transcriptional regulat
VBI0007BS1_0621	1236 Sensor protein phoQ
VBI0007BS1_0622	786 17 kDa surface antigen
VBI0007BS1_0623	1140 Hypothetical protein
VBI0007BS1_0624	498 Cytochrome c-type bio
VBI0007BS1_0625	992 cytochrome c-type bio
VBI0007BS1_0626	477 Cytochrome c-type bio
VBI0007BS1_0627	342 protease Do
VBI0007BS1_0628	708 Transcriptional activato
VBI0007BS1_0629	1404 Probable sensor protei
VBI0007BS1_0630	752 Glutamate-ammonia-li

3325 of 3325 are fet

GO Assignments

GO:0005622	intracellular
GO:0006355	regulation of transcription, DNA-dependent


Experiments

Gene Expression	Z
Protein Interaction	6
Host Interaction	3

Ortholog Group

Ortholog Group	BrOG_1132
Length Min/Max	152/161

Pubmed

Evaluation of three polymerase chain reaction techniques for detection of Brucella DNA in peripheral human blood.
Baddour MM, Alkhalifa DH
Canadian journal of microbiology
PubMed: [18449219](#) 
Abstract

BvrR/BvrS-controlled outer membrane proteins Omp3a and Omp3b are not essential

Orthologs/
Protein
Families

Literature

We're looking for the next generation of
new analysis software...

Driving Biological Projects (DBPs)

Announcement: Late December 2009

DBPs designed to combine Bioinformatics and Experimental Biology

- Generate valuable experimental evidence to the annotation of the genome, proteome or metabolome of the targeted pathogens.
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we'll send you the DBP
announcement when it comes out

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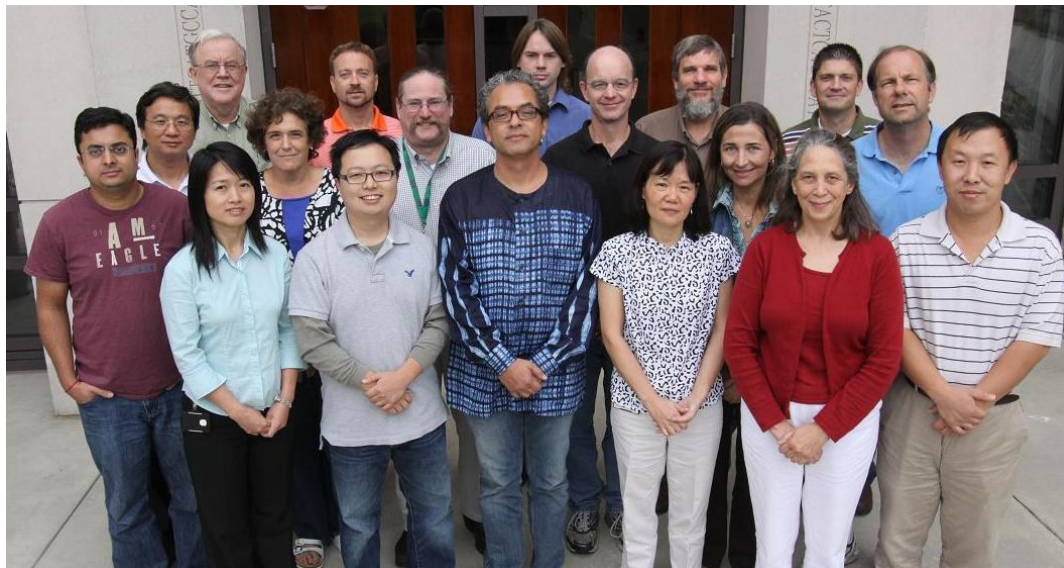
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