Managing Projects and Data with B-Fabric

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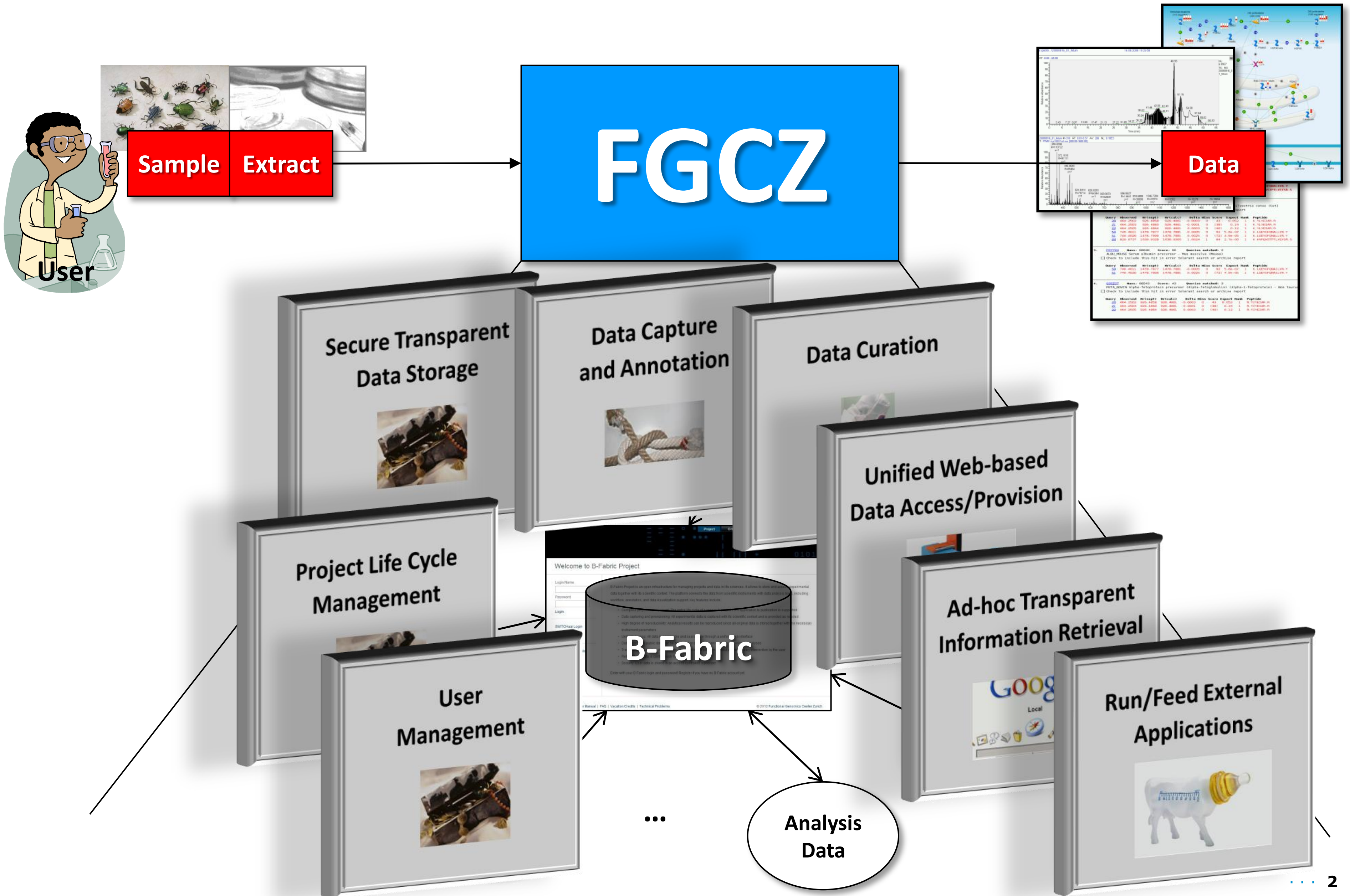
November 16th, 2012

B-Fabric - The FGCZ Approach to Managing Projects and Data



User

Sample

Extract

FGCZ

Data

Secure Transparent Data Storage

Data Capture and Annotation

Data Curation

Unified Web-based Data Access/Provision

Project Life Cycle Management

User Management

Ad-hoc Transparent Information Retrieval

Run/Feed External Applications

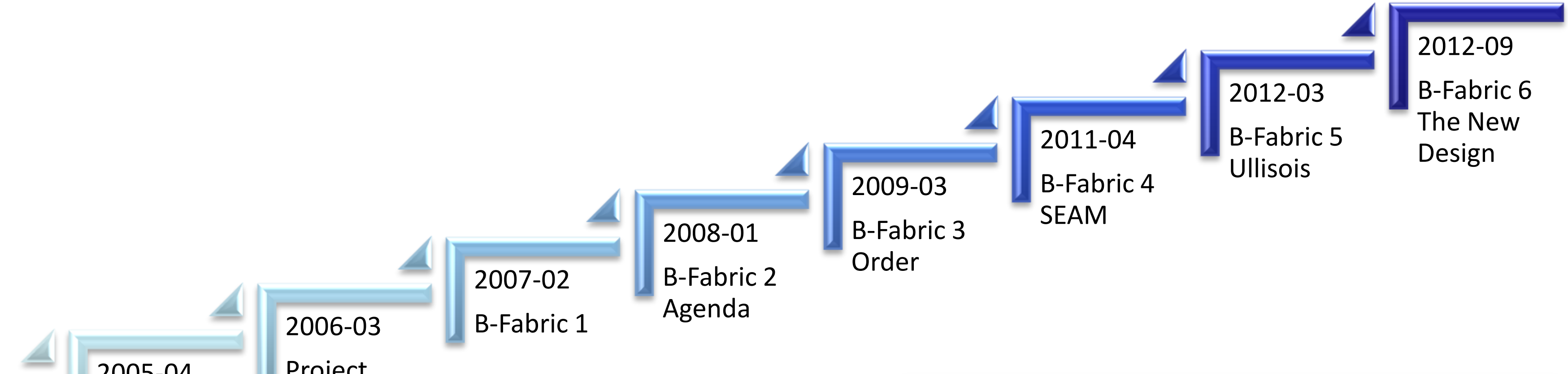
Welcome to B-Fabric Project

B-Fabric

...

Analysis Data

B-Fabric History



2005-02
B-Fabric Implementation Start

2005-04
Project Request Tool Implementation Start

2006-03
Project Request Tool

2007-02
B-Fabric 1

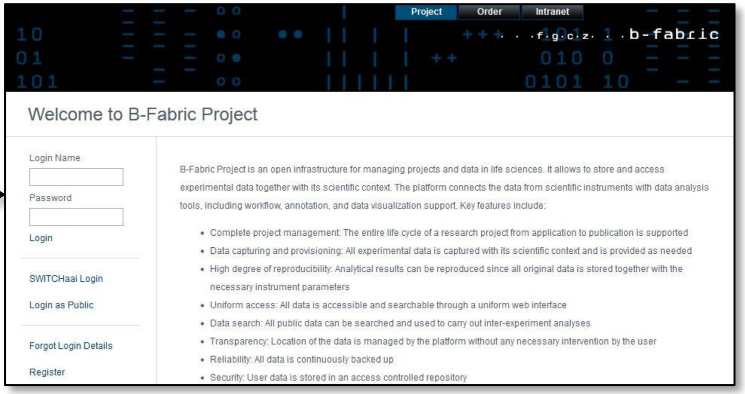
2008-01
B-Fabric 2
Agenda

2009-03
B-Fabric 3
Order

2011-04
B-Fabric 4
SEAM

2012-03
B-Fabric 5
Ullisois

2012-09
B-Fabric 6
The New Design



Welcome to B-Fabric Project

Login Name
Password
Login

SWITCHaai Login

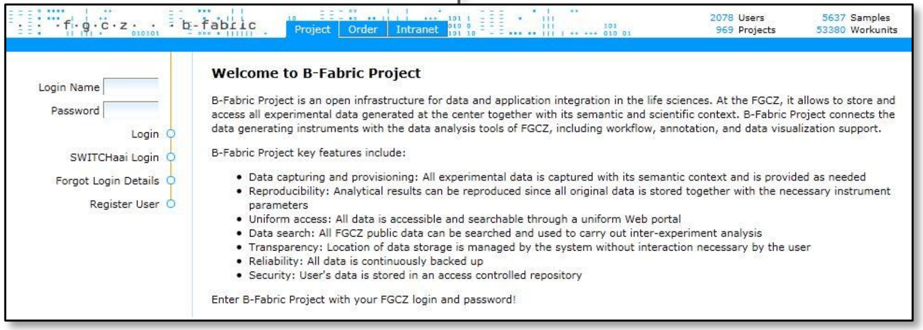
Login as Public

Forgot Login Details

Register

B-Fabric Project is an open infrastructure for managing projects and data in life sciences. It allows to store and access experimental data together with its scientific context. The platform connects the data from scientific instruments with data analysis tools, including workflow, annotation, and data visualization support. Key features include:

- Complete project management: The entire life cycle of a research project from application to publication is supported
- Data capturing and provisioning: All experimental data is captured with its scientific context and is provided as needed
- High degree of reproducibility: Analytical results can be reproduced since all original data is stored together with the necessary instrument parameters
- Uniform access: All data is accessible and searchable through a uniform web interface
- Data search: All public data can be searched and used to carry out inter-experiment analyses
- Transparency: Location of the data is managed by the platform without any necessary intervention by the user
- Reliability: All data is continuously backed up
- Security: User data is stored in an access controlled repository



2078 Users
969 Projects
5637 Samples
53380 Workunits

Login Name
Password
Login
SWITCHaai Login
Forgot Login Details
Register User

Welcome to B-Fabric Project

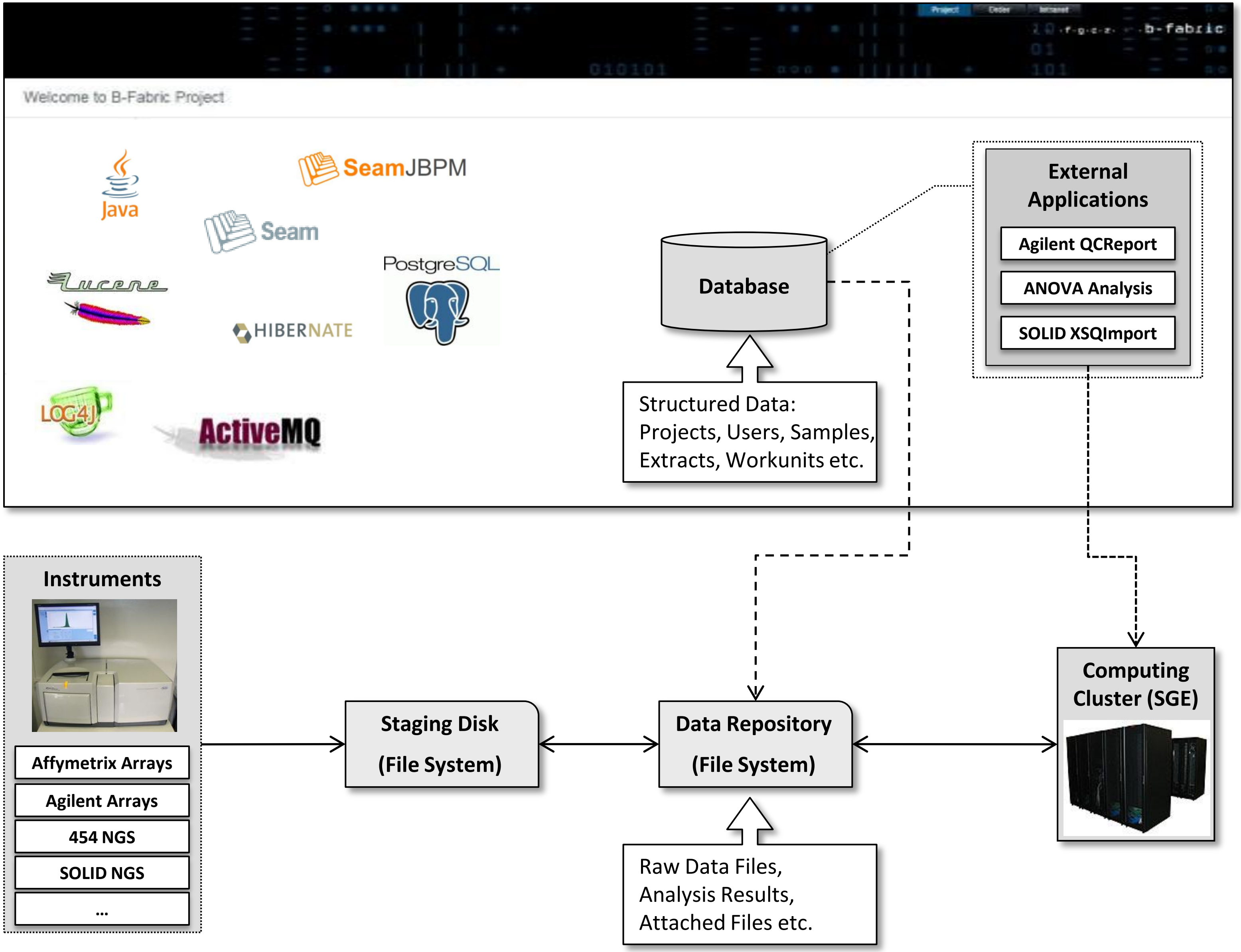
B-Fabric Project is an open infrastructure for data and application integration in the life sciences. At the FGCZ, it allows to store and access all experimental data generated at the center together with its semantic and scientific context. B-Fabric Project connects the data generating instruments with the data analysis tools of FGCZ, including workflow, annotation, and data visualization support.

B-Fabric Project key features include:

- Data capturing and provisioning: All experimental data is captured with its semantic context and is provided as needed
- Reproducibility: Analytical results can be reproduced since all original data is stored together with the necessary instrument parameters
- Uniform access: All data is accessible and searchable through a uniform Web portal
- Data search: All FGCZ public data can be searched and used to carry out inter-experiment analysis
- Transparency: Location of data storage is managed by the system without interaction necessary by the user
- Reliability: All data is continuously backed up
- Security: User's data is stored in an access controlled repository

Enter B-Fabric Project with your FGCZ login and password!

B-Fabric Architecture



Welcome to B-Fabric Project

External Applications

- Agilent QCReport
- ANOVA Analysis
- SOLID XSQImport

Database

Structured Data: Projects, Users, Samples, Extracts, Workunits etc.

Instruments

- Affymetrix Arrays
- Agilent Arrays
- 454 NGS
- SOLID NGS
- ...

Staging Disk

(File System)

Data Repository

(File System)

Raw Data Files, Analysis Results, Attached Files etc.

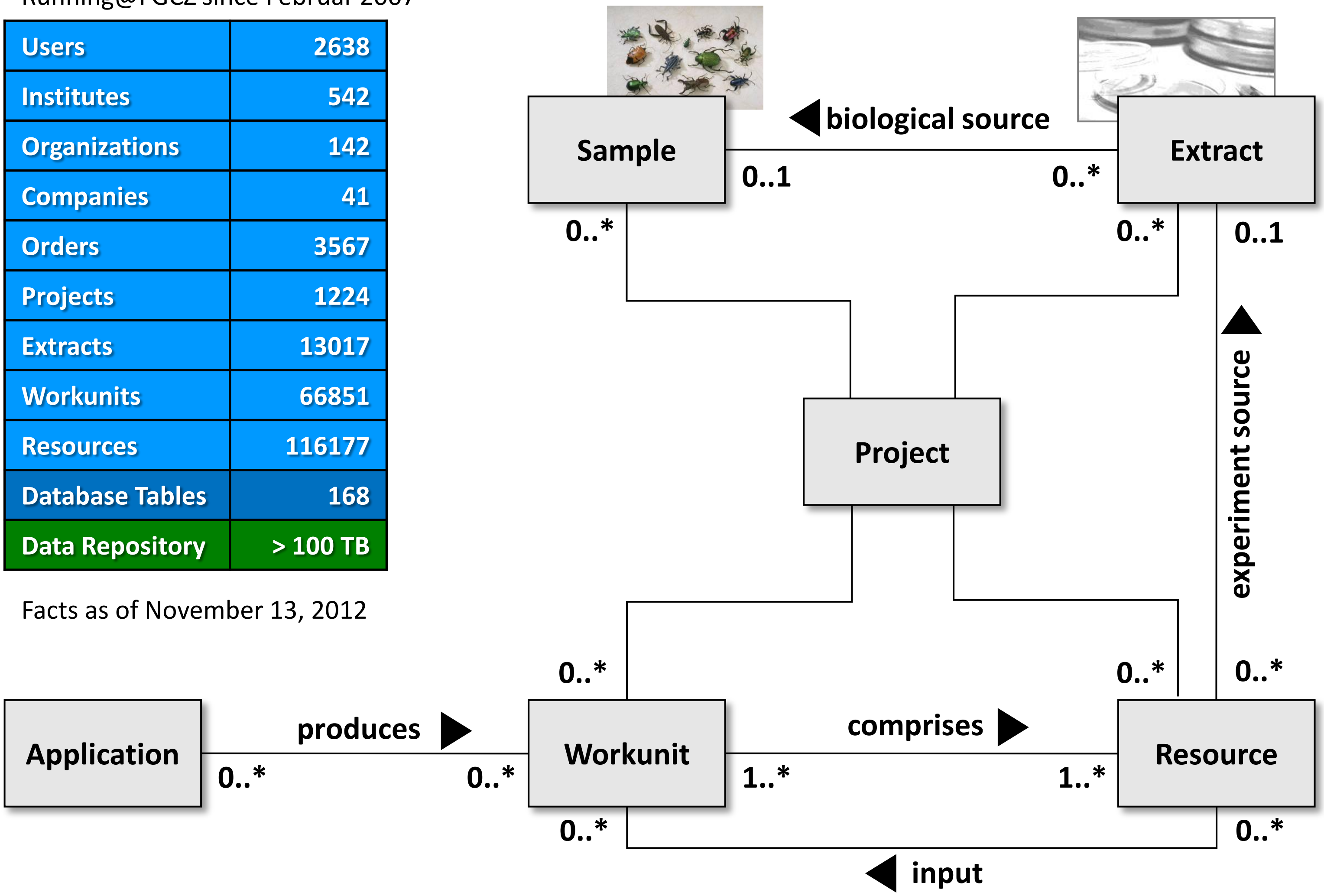
Computing Cluster (SGE)

Core B-Fabric Objects

Running@FGCZ since Februar 2007

Users	2638
Institutes	542
Organizations	142
Companies	41
Orders	3567
Projects	1224
Extracts	13017
Workunits	66851
Resources	116177
Database Tables	168
Data Repository	> 100 TB

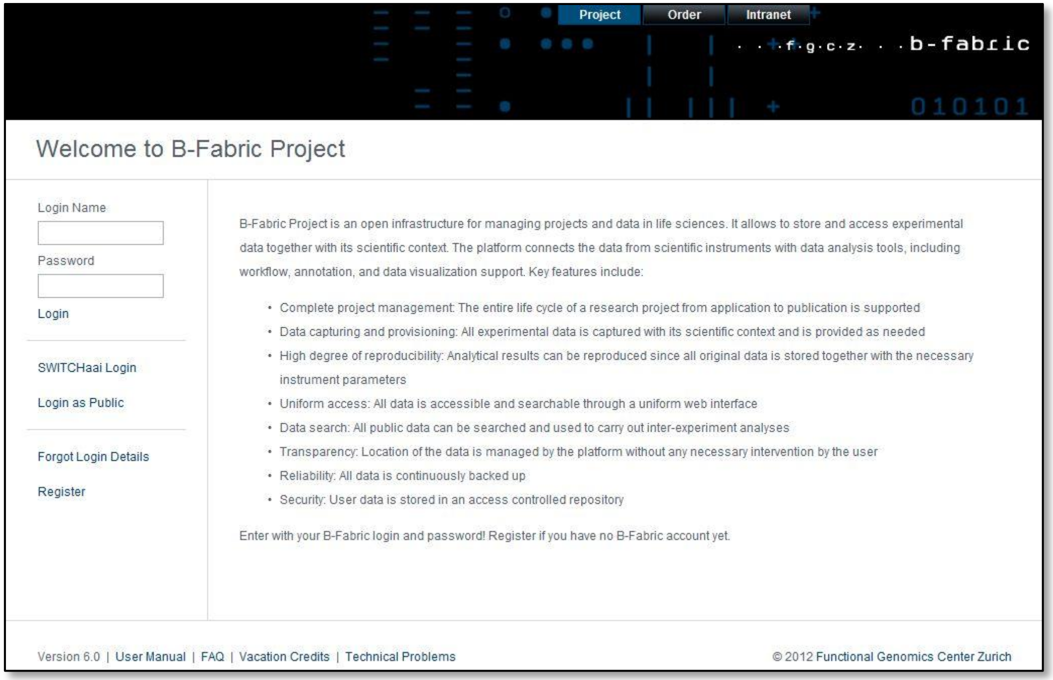
Facts as of November 13, 2012



B-Fabric Project

Functionality

- Submit/Review/Coach/Publish Projects
- Manage Project Members
- Import/Annotate Data Files
- One-click Access to “My” Data
- Browse Data Network
- Quick/Advanced Search
- Export/Download Data
- Create/Run External Applications
- Manage Annotations
- Manage Services
- Submit/Process/Track Project Orders
- Charge/Invoice Projects/Orders
- Reserve/Charge Instruments
- …



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Enter with your B-Fabric login and password! Register if you have no B-Fabric account yet.

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Goals

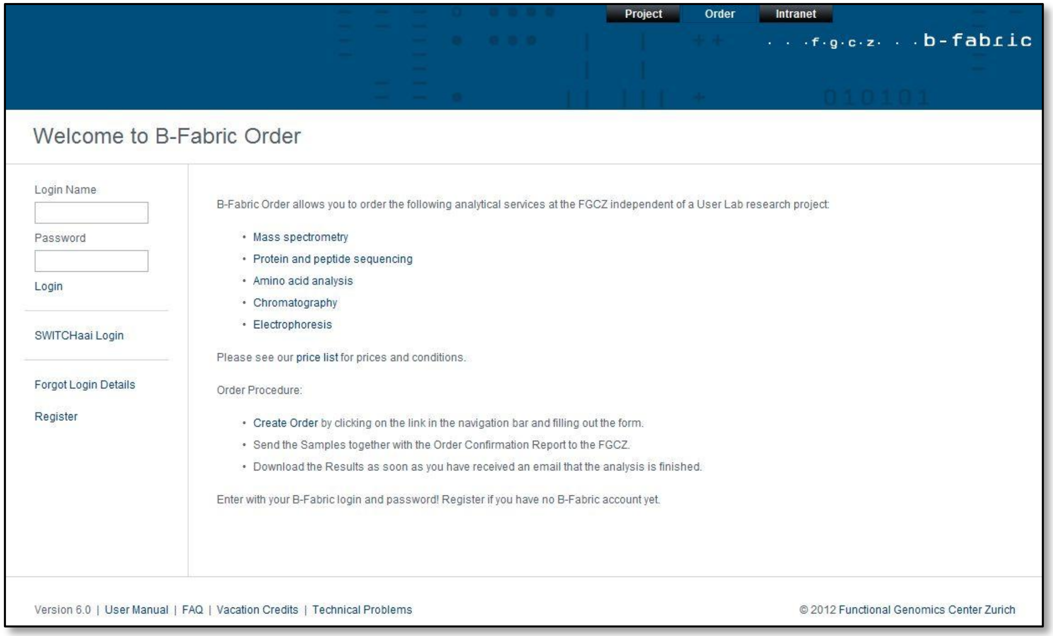
- Reduce Time/Costs for Project/Order Application/Management
- Track Entire Project/Order Life Cycle
- Capture/Manage/Provide Data
- Allow Access-Controlled Data Sharing
- Dynamically Add/Revise Services/Functionality
- Generate Statistics/Reports

B-Fabric Order

Functionality

- Edit Orders
- Upload Sequence Files
- Browse Orders
- Upload/Download Results
- Invoice Orders

* Orders are here Service Orders addressed to the FGCZ Protein Analysis Group



Welcome to B-Fabric Order

Login Name

Password

Login

SWITCHaai Login

Forgot Login Details

Register

B-Fabric Order allows you to order the following analytical services at the FGCZ independent of a User Lab research project:

- Mass spectrometry
- Protein and peptide sequencing
- Amino acid analysis
- Chromatography
- Electrophoresis

Please see our price list for prices and conditions.

Order Procedure:

- Create Order by clicking on the link in the navigation bar and filling out the form.
- Send the Samples together with the Order Confirmation Report to the FGCZ.
- Download the Results as soon as you have received an email that the analysis is finished.

Enter with your B-Fabric login and password! Register if you have no B-Fabric account yet.

Version 6.0 | User Manual | FAQ | Vacation Credits | Technical Problems

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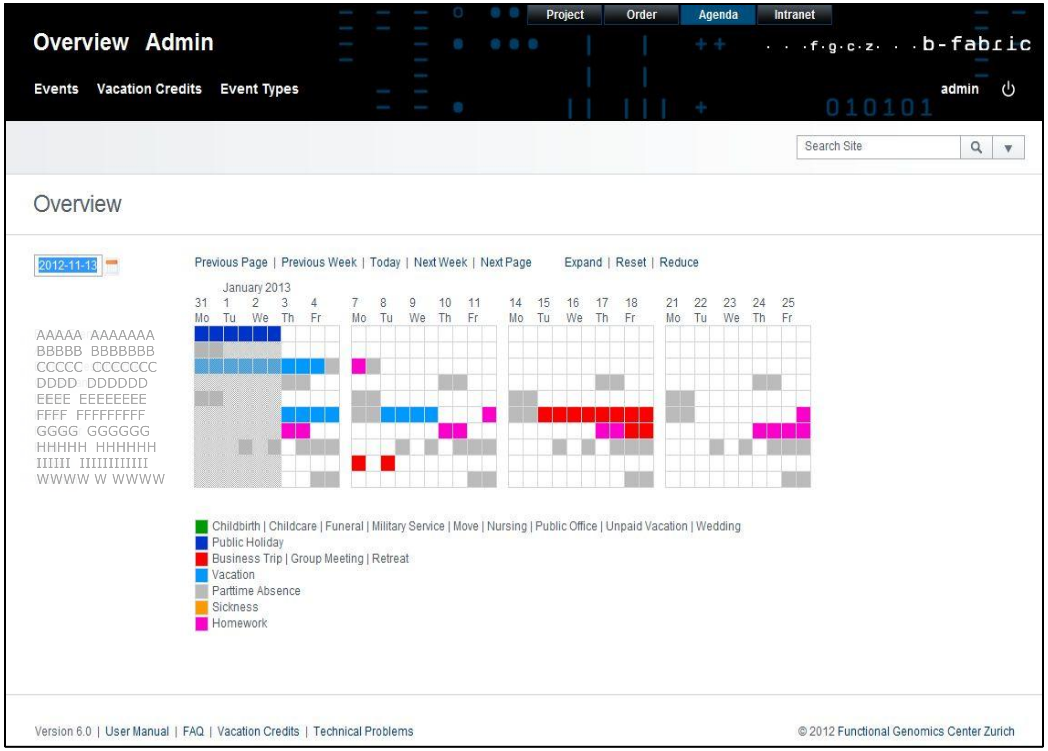
Goals

- Ease Ordering/Managing FGCZ services
- Track Entire Order Management Process (Communication, Results, Invoices etc.)
- Reduce Time/Costs for Order Management
- Improve Support and Automate FGCZ Services
- Generate Reports

B-Fabric Agenda

Functionality

- Edit Events/Vacation Credits
- Browse Events/Vacation Credits
- Overview Events
- Generate Reports



🟩 Childbirth | Childcare | Funeral | Military Service | Move | Nursing | Public Office | Unpaid Vacation | Wedding
🟦 Public Holiday
🟥 Business Trip | Group Meeting | Retreat
🟦 Vacation
⬜ Parttime Absence
🟧 Sickness
🟪 Homework

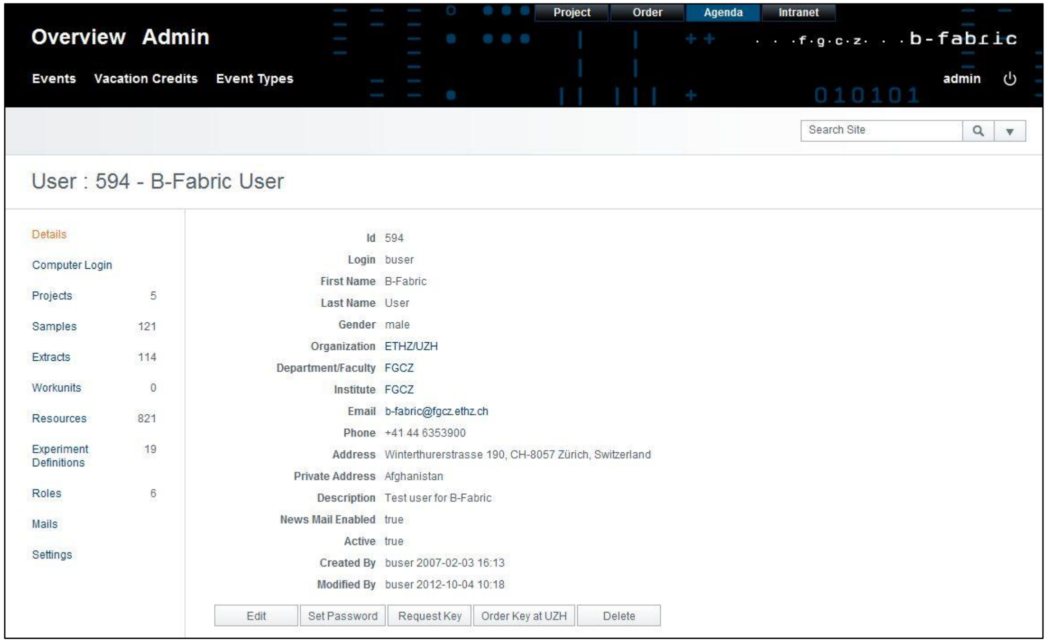
Goals

- Managing Employee Absences
- Managing Vacation Credits
- Vacation Calculation/Reporting
- Adjustable Events Overview

B-Fabric Common Features

Functionality

- Registering users
- Managing user accounts
- Managing roles
- Browsing mails
- Merging duplicates
- Cleaning unassigned objects
- Sending messages to selected users
- Request access to the FGCZ lab
- …



User : 594 - B-Fabric User

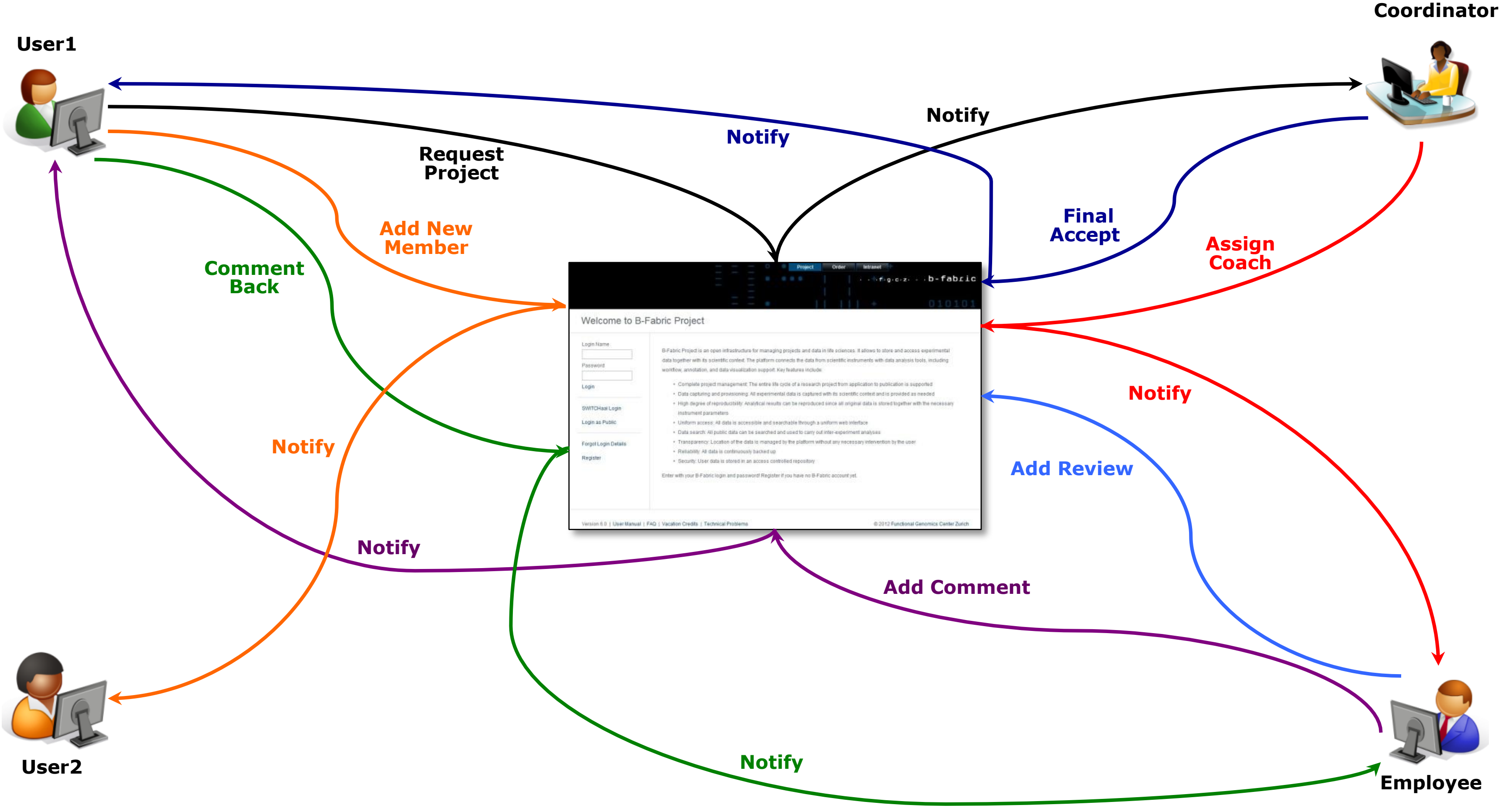
Id	594
Login	buser
First Name	B-Fabric
Last Name	User
Gender	male
Organization	ETHZ/UZH
Department/Faculty	FGCZ
Institute	FGCZ
Email	b-fabric@fgcz.ethz.ch
Phone	+41 44 6353900
Address	Winterthurerstrasse 190, CH-8057 Zürich, Switzerland
Private Address	Afghanistan
Description	Test user for B-Fabric
News Mail Enabled	true
Active	true
Created By	buser 2007-02-03 16:13
Modified By	buser 2012-10-04 10:18

Goals

- Transparent login generation
- FGCZ-wide password management (automatic password push to relevant FGCZ services)
- Event-driven email notifications
- Task management

Project Management

Application, Reviewing, Communication, State Tracking, Member Mgmt., Data Mgmt., Reporting



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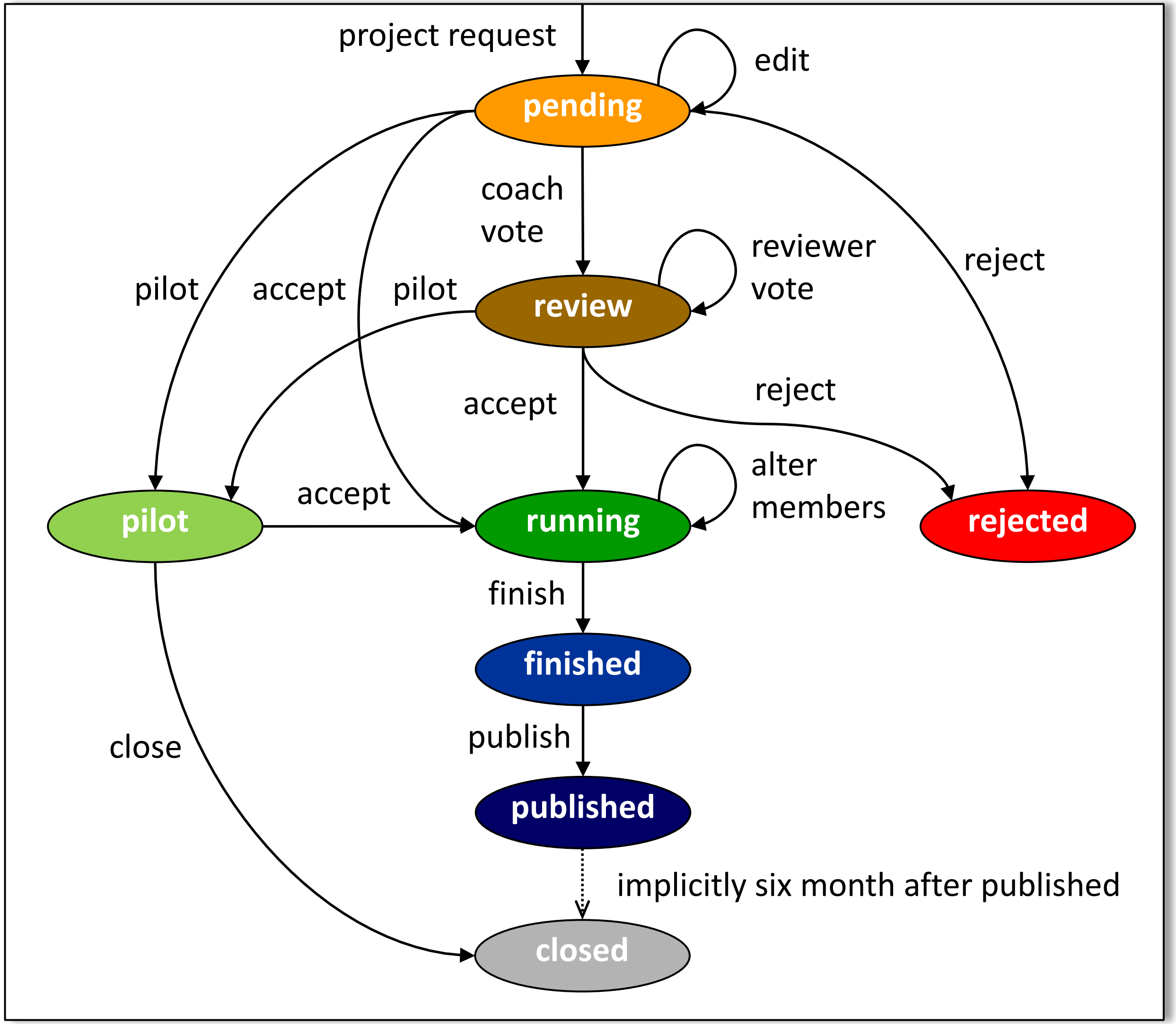
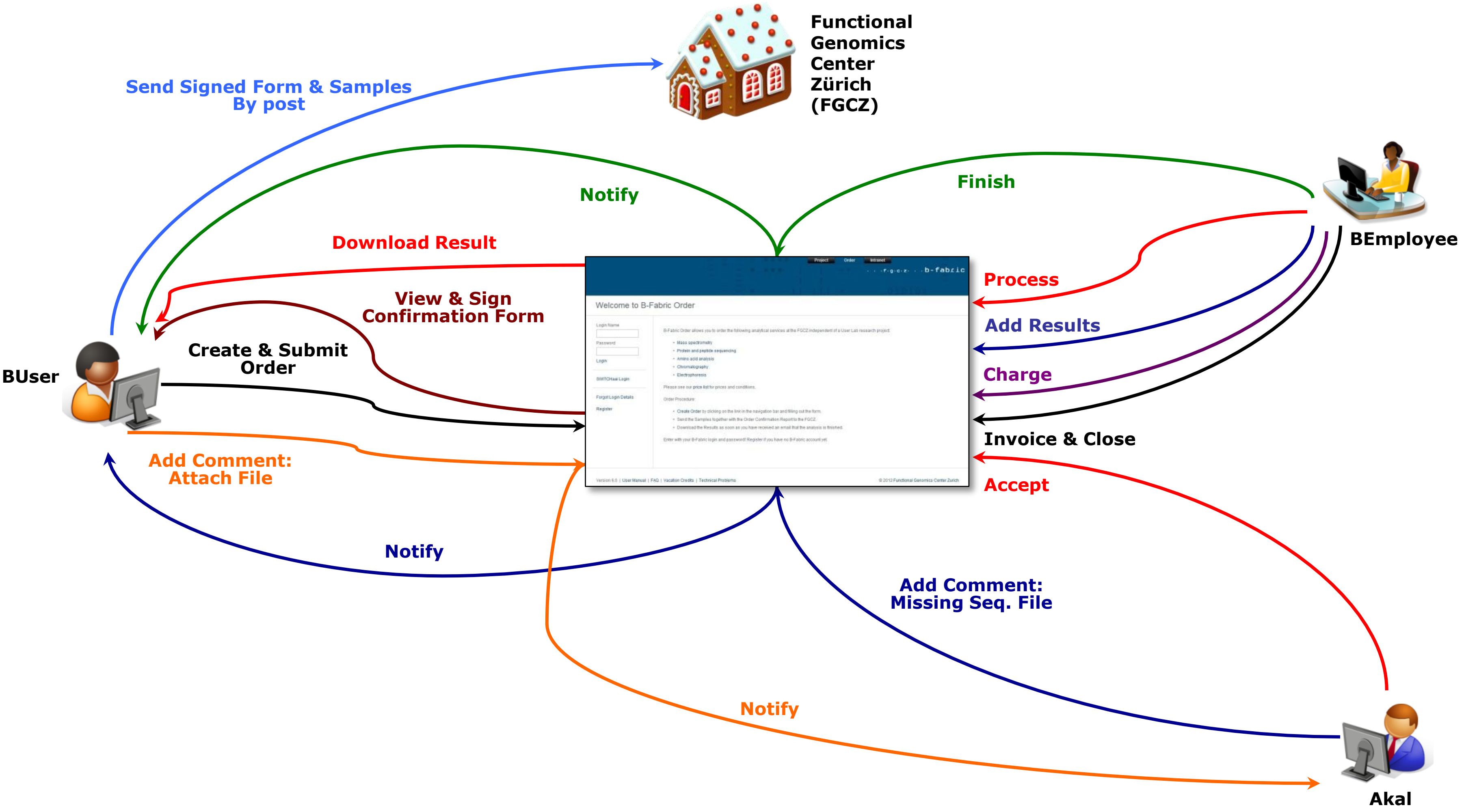
Project States



Order Management

Submission, Communication, State Tracking, Result Provision, Charging, Invoicing



Functional Genomics Center Zürich (FGCZ)

Send Signed Form & Samples
By post

Notify

Finish

Download Result

View & Sign
Confirmation Form

Create & Submit
Order

BUser

BEmployee

Process

Add Results

Charge

Invoice & Close

Accept

Add Comment:
Attach File

Notify

Add Comment:
Missing Seq. File

Notify

Akal

Welcome to B-Fabric Order

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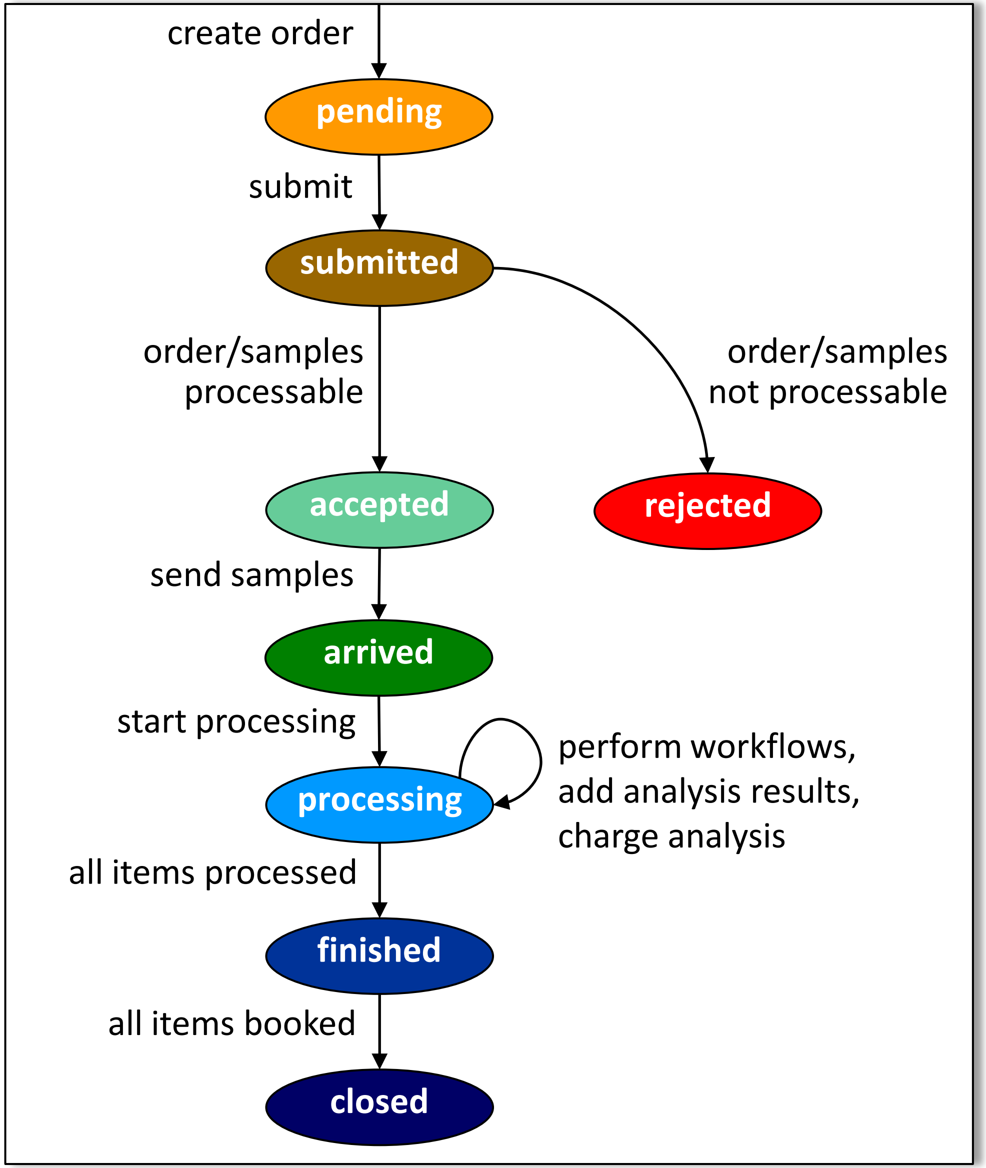
Order States



create order

pending

submit

submitted

order/samples processable

order/samples not processable

accepted

rejected

send samples

arrived

start processing

processing

perform workflows, add analysis results, charge analysis

all items processed

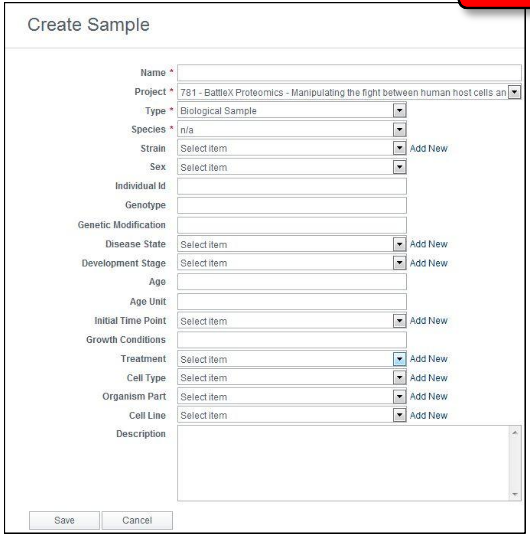
finished

all items booked

closed

Scientific Data Management

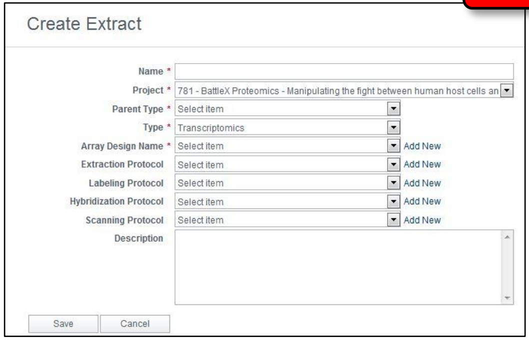
1. Register Sample(s)



Create Sample

Name *		
Project *	781 - BattleX Proteomics - Manipulating the fight between human host cells an	
Type *	Biological Sample	
Species *	n/a	
Strain	Select item	Add New
Sex	Select item	
Individual Id		
Genotype		
Genetic Modification		
Disease State	Select item	Add New
Development Stage	Select item	Add New
Age		
Age Unit		
Initial Time Point	Select item	Add New
Growth Conditions		
Treatment	Select item	Add New
Cell Type	Select item	Add New
Organism Part	Select item	Add New
Cell Line	Select item	Add New
Description		

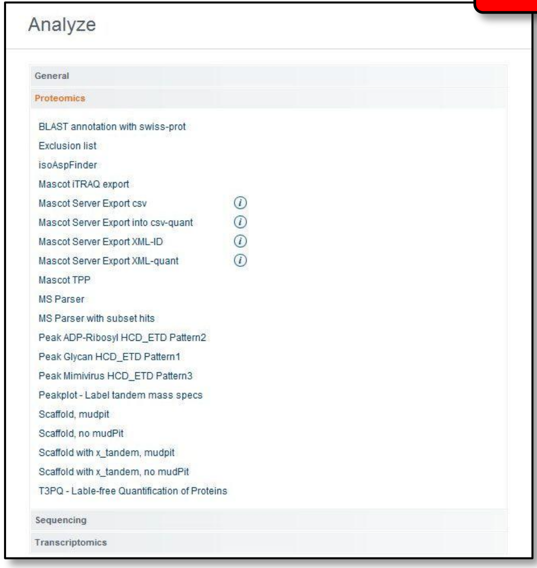
2. Register Extract(s)



Create Extract

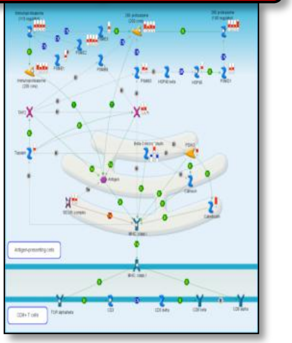
Name *		
Project *	781 - BattleX Proteomics - Manipulating the fight between human host cells an	
Parent Type *	Select item	
Type *	Transcriptomics	
Array Design Name *	Select item	Add New
Extraction Protocol	Select item	Add New
Labeling Protocol	Select item	Add New
Hybridization Protocol	Select item	Add New
Scanning Protocol	Select item	Add New
Description		

4. Analyze Data

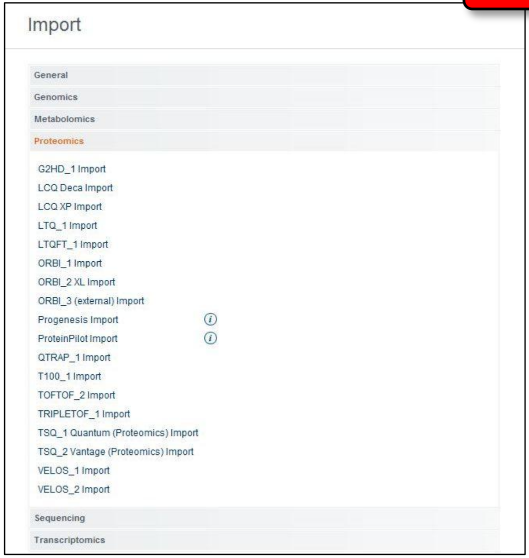


Analyze

- BLAST annotation with swiss-prot
- Exclusion list
- isoAspFinder
- Mascot iTRAQ export
- Mascot Server Export csv
- Mascot Server Export into csv-quant
- Mascot Server Export XML-ID
- Mascot Server Export XML-quant
- Mascot TPP
- MS Parser
- MS Parser with subset hits
- Peak ADP-Ribosyl HCD_ETD Pattern2
- Peak Glycan HCD_ETD Pattern1
- Peak Mimivirus HCD_ETD Pattern3
- Peakplot - Label tandem mass specs
- Scaffold, mudpit
- Scaffold, no mudPit
- Scaffold with x_tandem, mudpit
- Scaffold with x_tandem, no mudPit
- T3PQ - Lable-free Quantification of Proteins

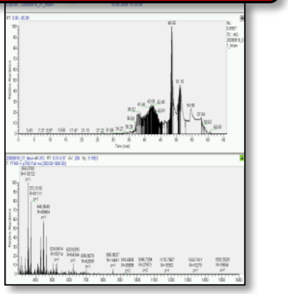


3. Import Data



Import

- G2HD_1 Import
- LCQ Deca Import
- LCQ XP Import
- LTQ_1 Import
- LTQFT_1 Import
- ORBI_1 Import
- ORBI_2 XL Import
- ORBI_3 (external) Import
- Progenesis Import
- ProteinPilot Import
- QTRAP_1 Import
- T100_1 Import
- TOFTOF_2 Import
- TRIPLETOF_1 Import
- TSQ_1 Quantum (Proteomics) Import
- TSQ_2 Vantage (Proteomics) Import
- VELOS_1 Import
- VELOS_2 Import

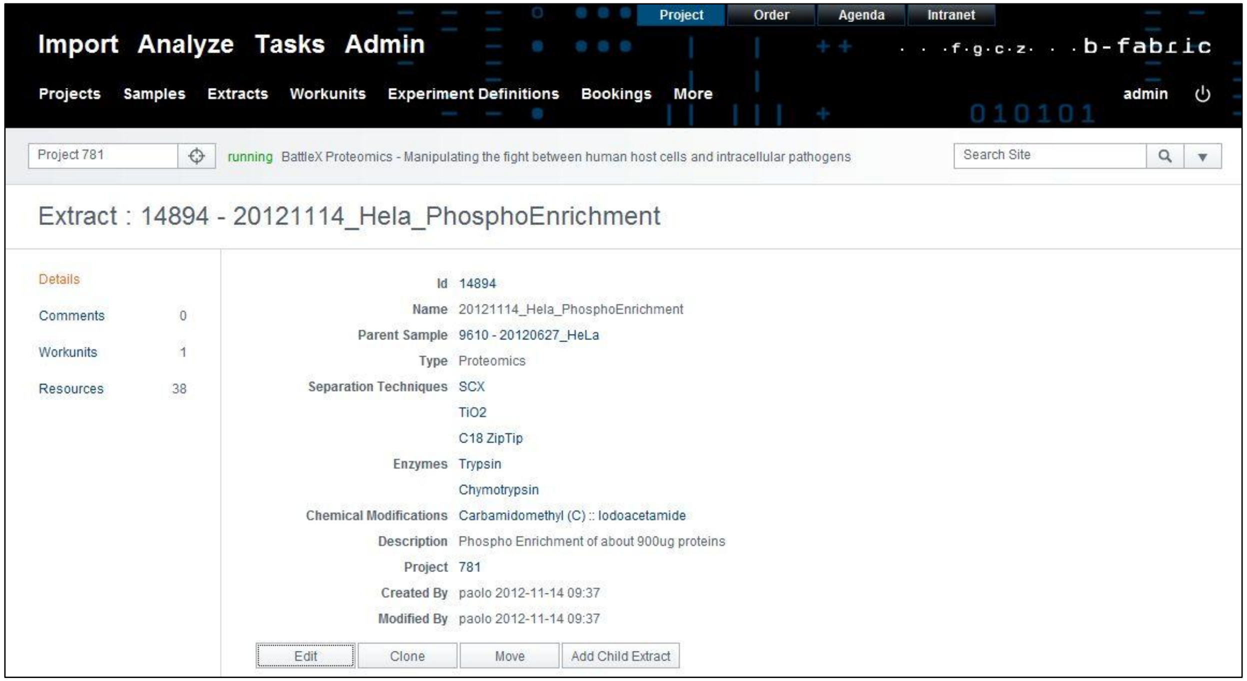


Data Import and Annotation

- Capture experimental data together with its semantic context

- Import Workflow:

1. Describe samples and extracts
2. Select data import application
3. Select resources (data files) for import
4. Describe the resulting workunit
5. Assign extracts to the workunit resources



running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogens

Extract : 14894 - 20121114_Hela_PhosphoEnrichment

Id	14894
Name	20121114_Hela_PhosphoEnrichment
Parent Sample	9610 - 20120627_HeLa
Type	Proteomics
Separation Techniques	SCX TiO2 C18 ZipTip
Enzymes	Trypsin Chymotrypsin
Chemical Modifications	Carbamidomethyl (C) :: Iodoacetamide
Description	Phospho Enrichment of about 900ug proteins
Project	781
Created By	paolo 2012-11-14 09:37
Modified By	paolo 2012-11-14 09:37

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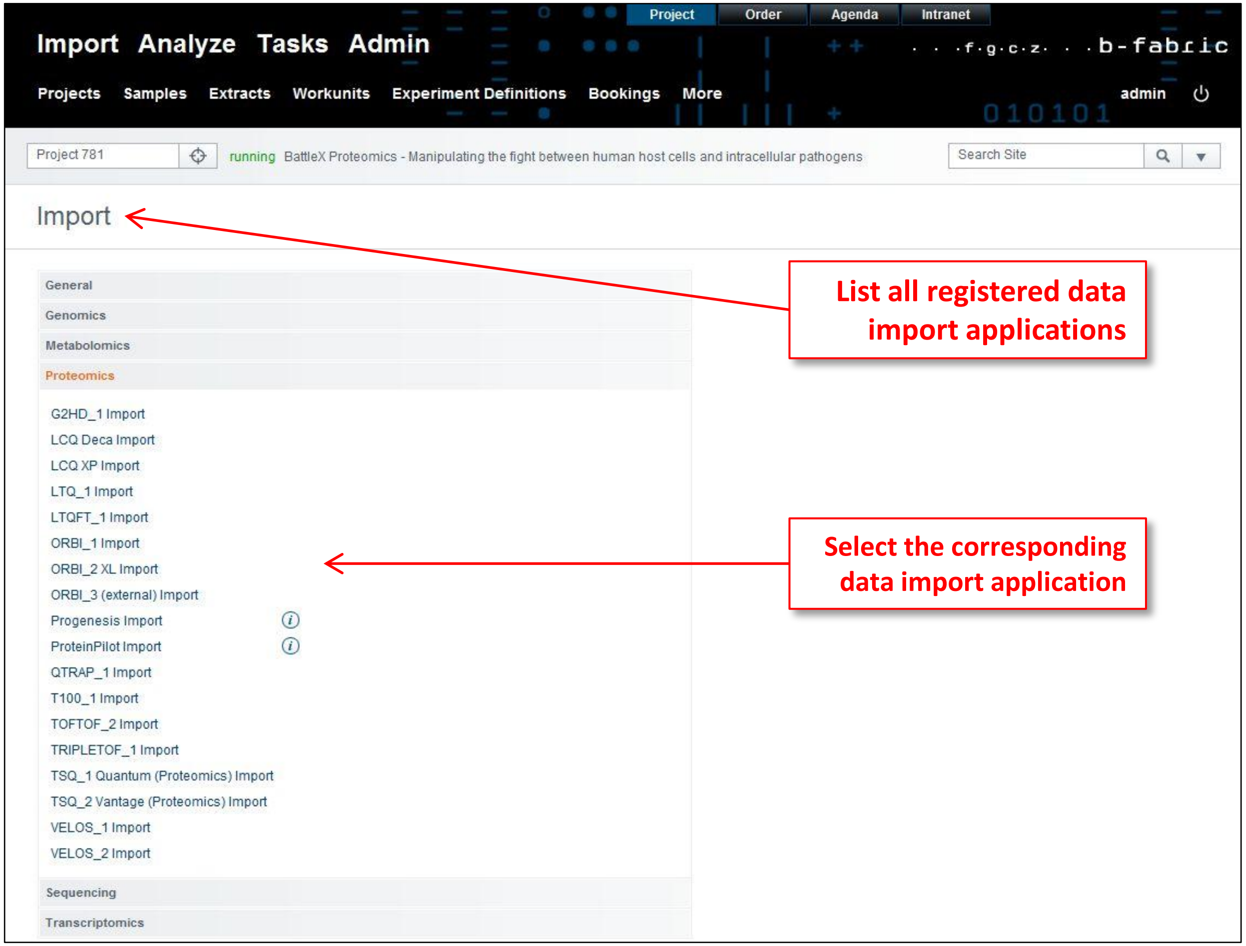

running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogens

Import

General
Genomics
Metabolomics
Proteomics

G2HD_1 Import
LCQ Deca Import
LCQ XP Import
LTQ_1 Import
LTQFT_1 Import
ORBI_1 Import
ORBI_2 XL Import
ORBI_3 (external) Import
Progenesis Import ⓘ
ProteinPilot Import ⓘ
QTRAP_1 Import
T100_1 Import
TOFTOF_2 Import
TRIPLETOF_1 Import
TSQ_1 Quantum (Proteomics) Import
TSQ_2 Vantage (Proteomics) Import
VELOS_1 Import
VELOS_2 Import

Sequencing
Transcriptomics

List all registered data import applications

Select the corresponding data import application

Data Import and Annotation

- Capture experimental data together with its semantic context

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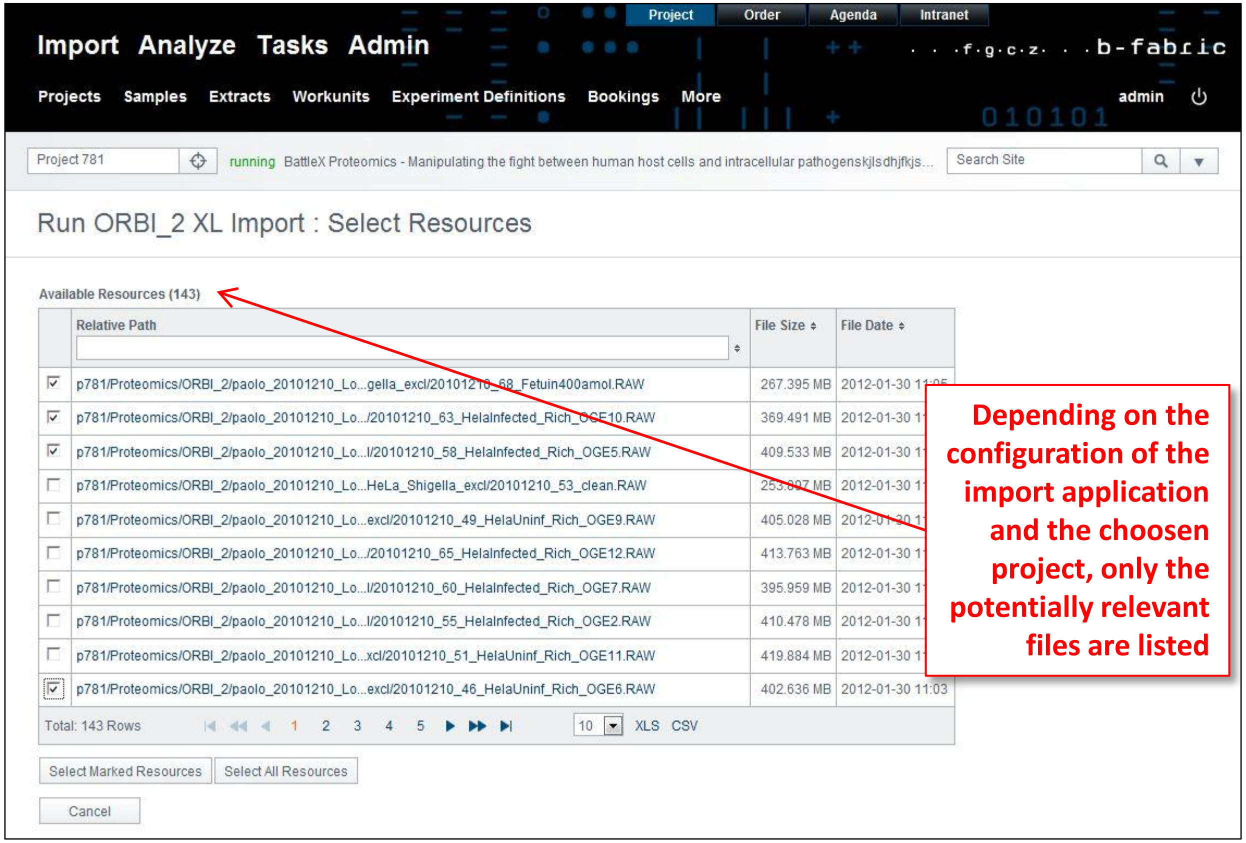


Project 781 running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjs...

Run ORBI_2 XL Import : Select Resources

Available Resources (143)

	Relative Path	File Size	File Date
☑	p781/Proteomics/ORBI_2/paolo_20101210_Lo...gella_excl/20101210_68_Fetuin400amol.RAW	267.395 MB	2012-01-30 11:05
☑	p781/Proteomics/ORBI_2/paolo_20101210_Lo.../20101210_63_HelaInfected_Rich_OGE10.RAW	369.491 MB	2012-01-30 1
☑	p781/Proteomics/ORBI_2/paolo_20101210_Lo...l/20101210_58_HelaInfected_Rich_OGE5.RAW	409.533 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo...HeLa_Shigella_excl/20101210_53_clean.RAW	253.897 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo...excl/20101210_49_HelaUninf_Rich_OGE9.RAW	405.028 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo.../20101210_65_HelaInfected_Rich_OGE12.RAW	413.763 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo...l/20101210_60_HelaInfected_Rich_OGE7.RAW	395.959 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo...l/20101210_55_HelaInfected_Rich_OGE2.RAW	410.478 MB	2012-01-30 1
☐	p781/Proteomics/ORBI_2/paolo_20101210_Lo...xcl/20101210_51_HelaUninf_Rich_OGE11.RAW	419.884 MB	2012-01-30 1
☑	p781/Proteomics/ORBI_2/paolo_20101210_Lo...excl/20101210_46_HelaUninf_Rich_OGE6.RAW	402.636 MB	2012-01-30 11:03

Total: 143 Rows

10

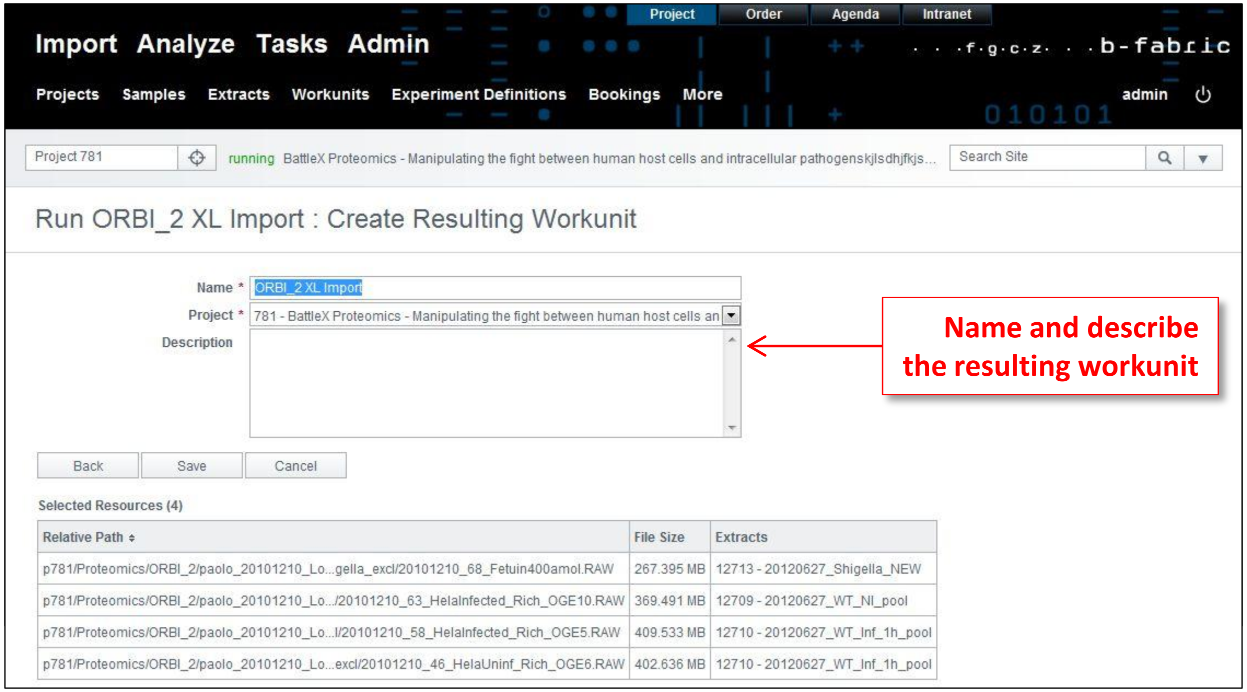
Depending on the configuration of the import application and the choosen project, only the potentially relevant files are listed

Data Import and Annotation

- Capture experimental data together with its semantic context

- Import Workflow:

1. Describe samples and extracts
2. Select data import application
3. Select resources (data files) for import
4. Describe the resulting workunit
5. Assign extracts to the workunit resources



Project 781 running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjs...

Run ORBI_2 XL Import : Create Resulting Workunit

Name * ORBI_2 XL Import
Project * 781 - BattleX Proteomics - Manipulating the fight between human host cells an
Description

Name and describe the resulting workunit

Selected Resources (4)

Relative Path ⬍	File Size	Extracts
p781/Proteomics/ORBI_2/paolo_20101210_Lo...gella_excl/20101210_68_Fetuin400amol.RAW	267.395 MB	12713 - 20120627_Shigella_NEW
p781/Proteomics/ORBI_2/paolo_20101210_Lo.../20101210_63_HelaInfected_Rich_OGE10.RAW	369.491 MB	12709 - 20120627_WT_NI_pool
p781/Proteomics/ORBI_2/paolo_20101210_Lo...l/20101210_58_HelaInfected_Rich_OGE5.RAW	409.533 MB	12710 - 20120627_WT_Inf_1h_pool
p781/Proteomics/ORBI_2/paolo_20101210_Lo...excl/20101210_46_HelaUninf_Rich_OGE6.RAW	402.636 MB	12710 - 20120627_WT_Inf_1h_pool

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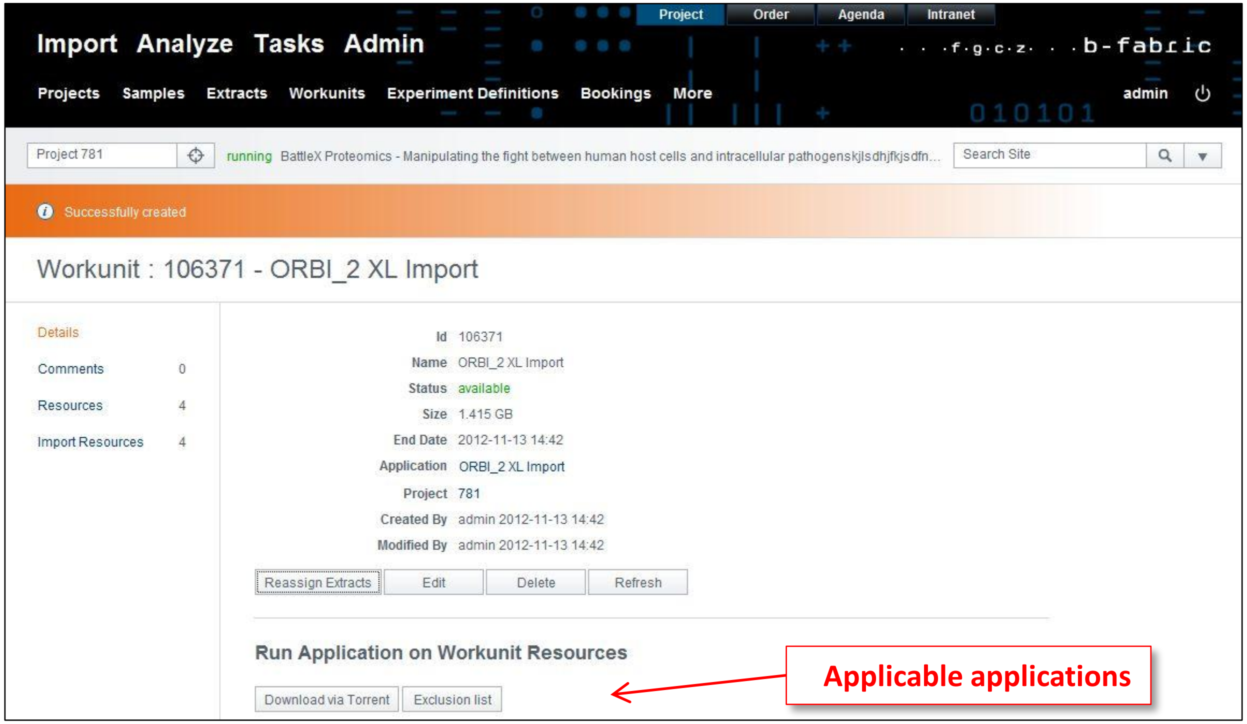
4. Describe the resulting workunit
5. Assign extracts to the workunit resources



running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjsdfn...

Successfully created

Workunit : 106371 - ORBI_2 XL Import

Id 106371
Name ORBI_2 XL Import
Status available
Size 1.415 GB
End Date 2012-11-13 14:42
Application ORBI_2 XL Import
Project 781
Created By admin 2012-11-13 14:42
Modified By admin 2012-11-13 14:42

Run Application on Workunit Resources

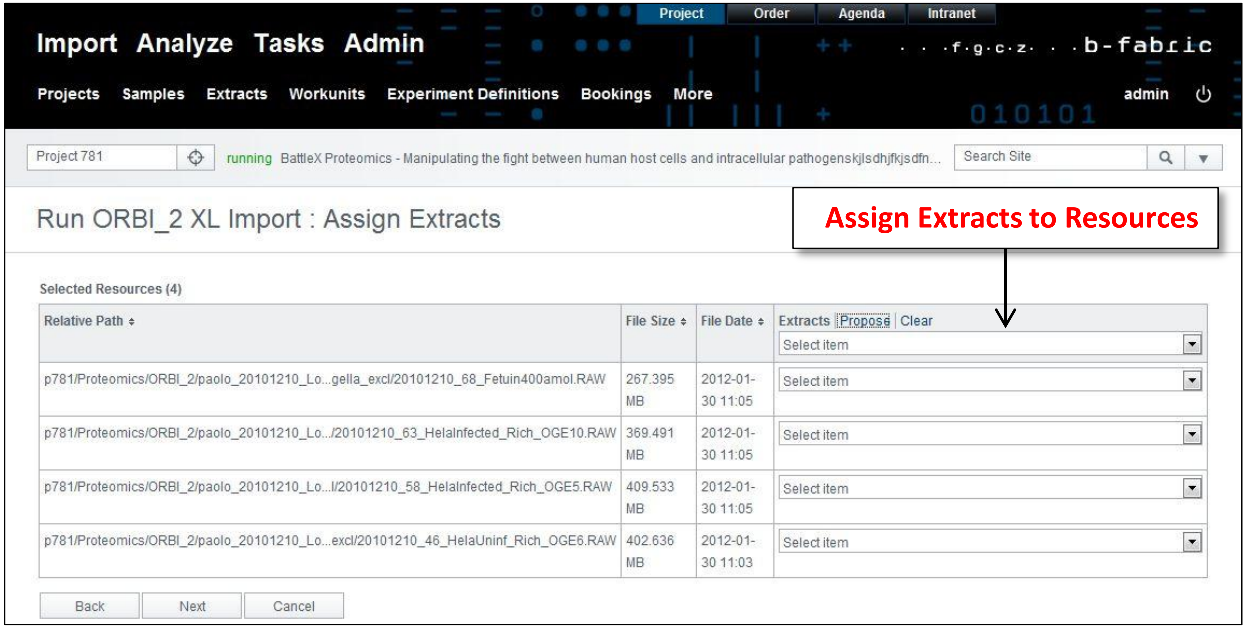
Applicable applications

Data Import and Annotation

- Capture experimental data together with its semantic context

- Import Workflow:

1. Describe samples and extracts
2. Select data import application
3. Select resources (data files) for import
4. Describe the resulting workunit
5. Assign extracts to the workunit resources



Project 781 running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjsdfn...

Run ORBI_2 XL Import : Assign Extracts

Assign Extracts to Resources

Selected Resources (4)

Relative Path	File Size	File Date	Extracts Propose | Clear Select item
p781/Proteomics/ORBI_2/paolo_20101210_Lo...gella_excl/20101210_68_Fetuin400amol.RAW	267.395 MB	2012-01-30 11:05	Select item
p781/Proteomics/ORBI_2/paolo_20101210_Lo.../20101210_63_HelaInfected_Rich_OGE10.RAW	369.491 MB	2012-01-30 11:05	Select item
p781/Proteomics/ORBI_2/paolo_20101210_Lo...l/20101210_58_HelaInfected_Rich_OGE5.RAW	409.533 MB	2012-01-30 11:05	Select item
p781/Proteomics/ORBI_2/paolo_20101210_Lo...excl/20101210_46_HelaUninf_Rich_OGE6.RAW	402.636 MB	2012-01-30 11:03	Select item

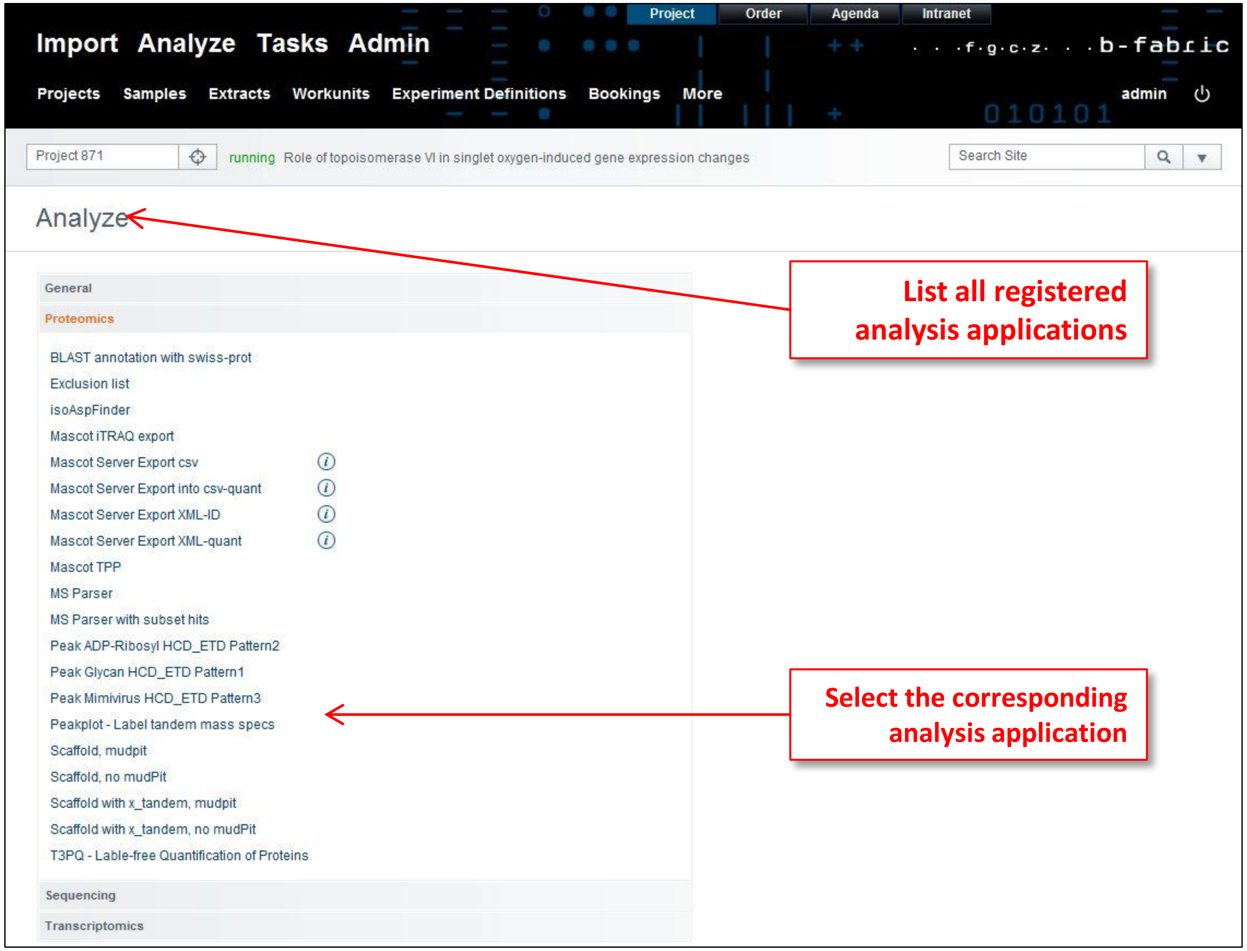
Data Analysis

- Support for robust, widely applicable analyses that are runnable by users

- Remaining analyses are manually run and results are registered in B-Fabric

- Analysis Workflow:

1. Select analysis application
2. Select input resources
3. Describe the resulting workunit
4. Optionally rerun the analysis application with adapted parameters



Project 871 running Role of topoisomerase VI in singlet oxygen-induced gene expression changes

Analyze

General

Proteomics

- BLAST annotation with swiss-prot
- Exclusion list
- isoAspFinder
- Mascot iTRAQ export
- Mascot Server Export csv
- Mascot Server Export into csv-quant
- Mascot Server Export XML-ID
- Mascot Server Export XML-quant
- Mascot TPP
- MS Parser
- MS Parser with subset hits
- Peak ADP-Ribosyl HCD_ETD Pattern2
- Peak Glycan HCD_ETD Pattern1
- Peak Mimivirus HCD_ETD Pattern3
- Peakplot - Label tandem mass specs
- Scaffold, mudpit
- Scaffold, no mudPit
- Scaffold with x_tandem, mudpit
- Scaffold with x_tandem, no mudPit
- T3PQ - Lable-free Quantification of Proteins

Sequencing

Transcriptomics

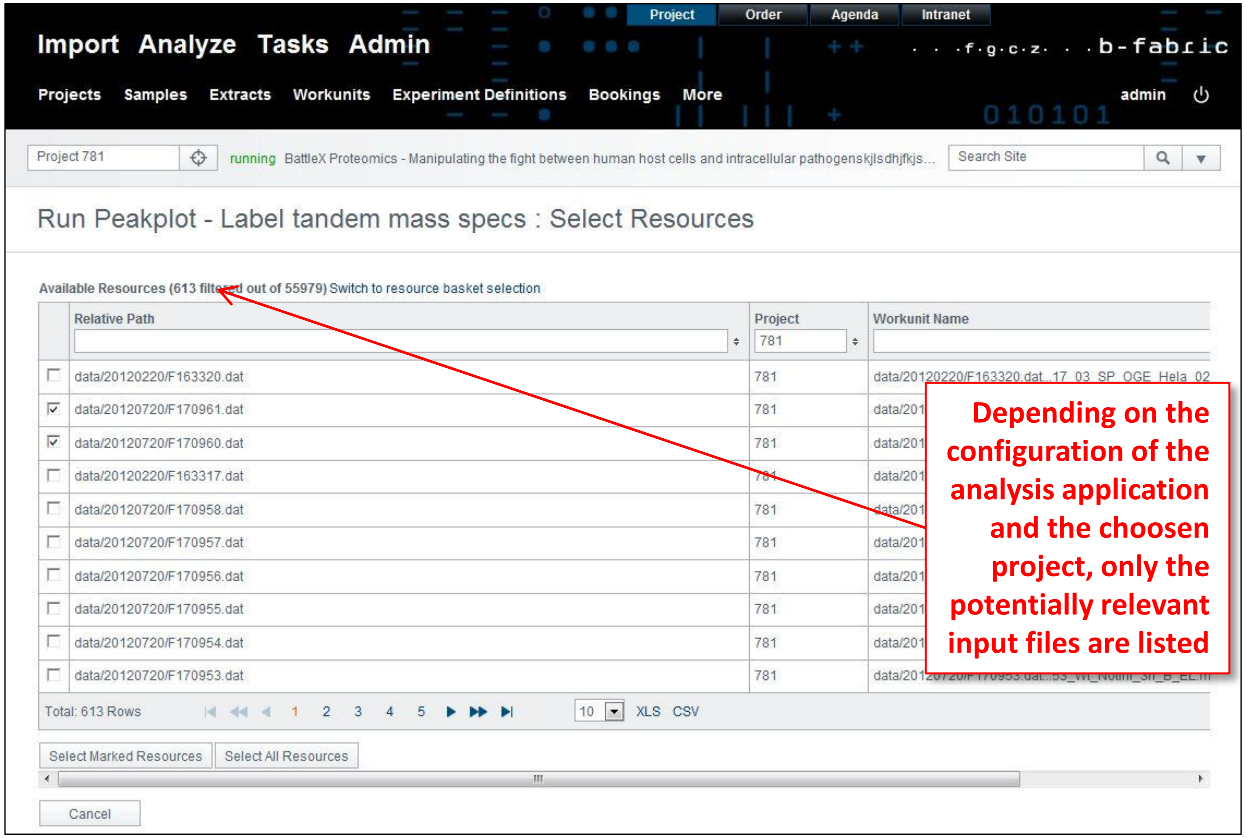
List all registered analysis applications

Select the corresponding analysis application

Data Analysis

- Support for robust, widely applicable analyses that are runnable by users
- Remaining analyses are manually run and results are registered in B-Fabric
- Analysis Workflow:

1. Select analysis application
2. Select input resources
3. Describe the resulting workunit
4. Optionally rerun the analysis application with adapted parameters



Project 781 running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjs...

Run Peakplot - Label tandem mass specs : Select Resources

Available Resources (613 filtered out of 55979) Switch to resource basket selection

	Relative Path	Project	Workunit Name
		781	
☐	data/20120220/F163320.dat	781	data/20120220/F163320.dat...17_03_SP_OGE_Hela_02
☑	data/20120720/F170961.dat	781	data/201
☑	data/20120720/F170960.dat	781	data/201
☐	data/20120220/F163317.dat	781	data/201
☐	data/20120720/F170958.dat	781	data/201
☐	data/20120720/F170957.dat	781	data/201
☐	data/20120720/F170956.dat	781	data/201
☐	data/20120720/F170955.dat	781	data/201
☐	data/20120720/F170954.dat	781	data/201
☐	data/20120720/F170953.dat	781	data/201

Total: 613 Rows 1 2 3 4 5 10 XLS CSV

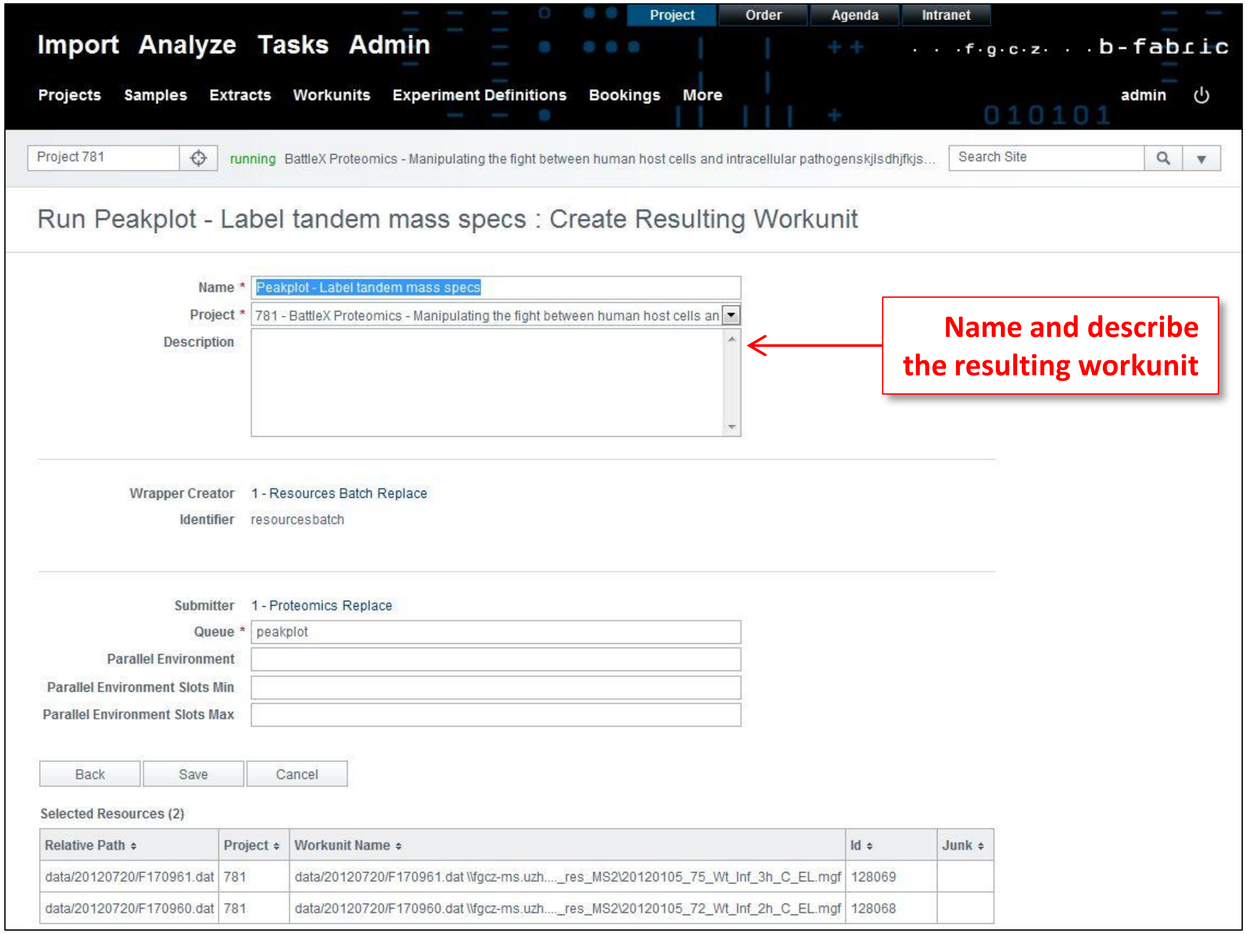
Depending on the configuration of the analysis application and the choosen project, only the potentially relevant input files are listed

Data Analysis

- Support for robust, widely applicable analyses that are runnable by users

- Remaining analyses are manually run and results are registered in B-Fabric

- Analysis Workflow:
1. Select analysis application
2. Select input resources
3. Describe the resulting workunit
4. Optionally rerun the analysis application with adapted parameters



Run Peakplot - Label tandem mass specs : Create Resulting Workunit

Name * Peakplot - Label tandem mass specs
Project * 781 - BattleX Proteomics - Manipulating the fight between human host cells an
Description

Wrapper Creator 1 - Resources Batch Replace
Identifier resourcesbatch

Submitter 1 - Proteomics Replace
Queue * peakplot
Parallel Environment
Parallel Environment Slots Min
Parallel Environment Slots Max

Selected Resources (2)

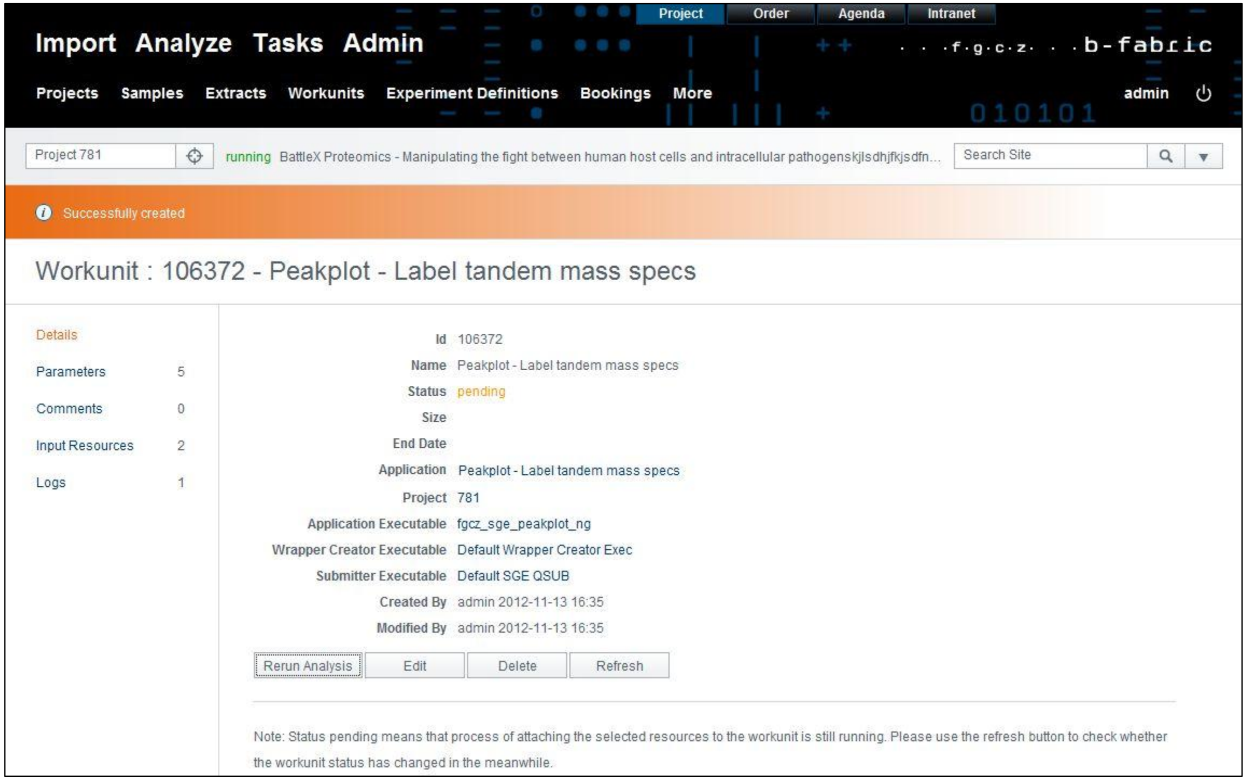
Relative Path	Project	Workunit Name	Id	Junk
data/20120720/F170961.dat	781	data/20120720/F170961.dat \\fgcz-ms.uzh...._res_MS2\20120105_75_Wt_Inf_3h_C_EL.mgf	128069	
data/20120720/F170960.dat	781	data/20120720/F170960.dat \\fgcz-ms.uzh...._res_MS2\20120105_72_Wt_Inf_2h_C_EL.mgf	128068	

Name and describe the resulting workunit

Data Analysis

- Support for robust, widely applicable analyses that are runnable by users
- Remaining analyses are manually run and results are registered in B-Fabric
- Analysis Workflow:

1. Select analysis application
2. Select input resources
3. Describe the resulting workunit
4. Optionally rerun the analysis application with adapted parameters



running BattleX Proteomics - Manipulating the fight between human host cells and intracellular pathogenskjlsdhjfkjsdfn...

Successfully created

Workunit : 106372 - Peakplot - Label tandem mass specs

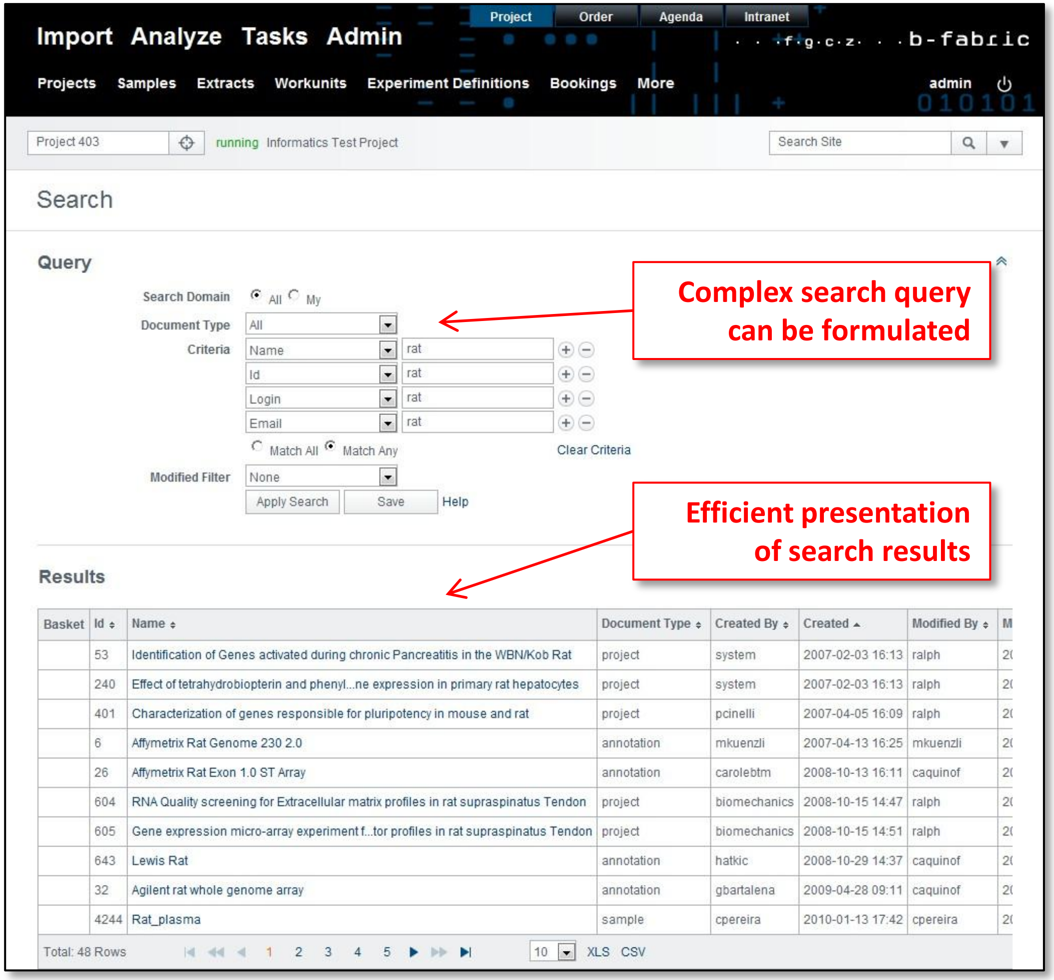
Details	
Parameters	5
Comments	0
Input Resources	2
Logs	1

Id	106372
Name	Peakplot - Label tandem mass specs
Status	pending
Size	
End Date	
Application	Peakplot - Label tandem mass specs
Project	781
Application Executable	fgcz_sge_peakplot_ng
Wrapper Creator Executable	Default Wrapper Creator Exec
Submitter Executable	Default SGE QSUB
Created By	admin 2012-11-13 16:35
Modified By	admin 2012-11-13 16:35

Note: Status pending means that process of attaching the selected resources to the workunit is still running. Please use the refresh button to check whether the workunit status has changed in the meanwhile.

Data Search

- Quick vs. Advanced Search
- Sortable data tables with filters



Project 403 running Informatics Test Project

Search

Query

Search Domain ● All ○ My

Document Type: All

Criteria:
Name: rat
Id: rat
Login: rat
Email: rat

○ Match All ● Match Any

Clear Criteria

Modified Filter: None

Apply Search | Save | Help

Complex search query can be formulated

Results

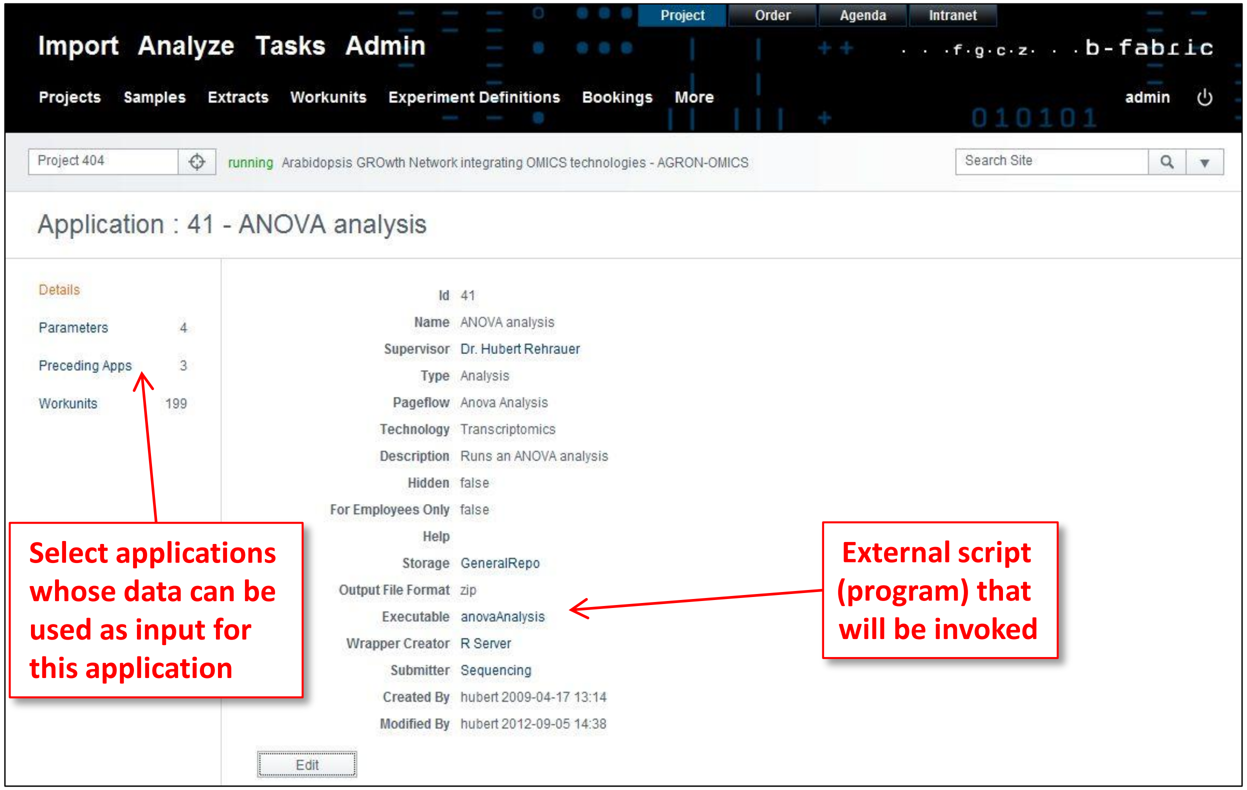
Efficient presentation of search results

Basket	Id	Name	Document Type	Created By	Created	Modified By	M
	53	Identification of Genes activated during chronic Pancreatitis in the WBN/Kob Rat	project	system	2007-02-03 16:13	ralph	2
	240	Effect of tetrahydrobiopterin and phenyl...ne expression in primary rat hepatocytes	project	system	2007-02-03 16:13	ralph	2
	401	Characterization of genes responsible for pluripotency in mouse and rat	project	pcinelli	2007-04-05 16:09	ralph	2
	6	Affymetrix Rat Genome 230 2.0	annotation	mkuenzli	2007-04-13 16:25	mkuenzli	2
	26	Affymetrix Rat Exon 1.0 ST Array	annotation	carolebtm	2008-10-13 16:11	caquinof	2
	604	RNA Quality screening for Extracellular matrix profiles in rat supraspinatus Tendon	project	biomechanics	2008-10-15 14:47	ralph	2
	605	Gene expression micro-array experiment f...tor profiles in rat supraspinatus Tendon	project	biomechanics	2008-10-15 14:51	ralph	2
	643	Lewis Rat	annotation	hatkic	2008-10-29 14:37	caquinof	2
	32	Agilent rat whole genome array	annotation	gbartalena	2009-04-28 09:11	caquinof	2
	4244	Rat_plasma	sample	cpereira	2010-01-13 17:42	cpereira	2

Total: 48 Rows 1 2 3 4 5 10 XLS CSV

External Applications

- Framework with generic workflows to invoke and connect external applications
- Ad-hoc coupling without compiling and restarting the system
- External applications hide complexity and technical details of the analysis



running Arabidopsis GROwth Network integrating OMICS technologies - AGRON-OMICS

Application : 41 - ANOVA analysis

Id	41
Name	ANOVA analysis
Supervisor	Dr. Hubert Rehrauer
Type	Analysis
Pageflow	Anova Analysis
Technology	Transcriptomics
Description	Runs an ANOVA analysis
Hidden	false
For Employees Only	false
Help	
Storage	GeneralRepo
Output File Format	zip
Executable	anovaAnalysis
Wrapper Creator	R Server
Submitter	Sequencing
Created By	hubert 2009-04-17 13:14
Modified By	hubert 2012-09-05 14:38

Select applications whose data can be used as input for this application

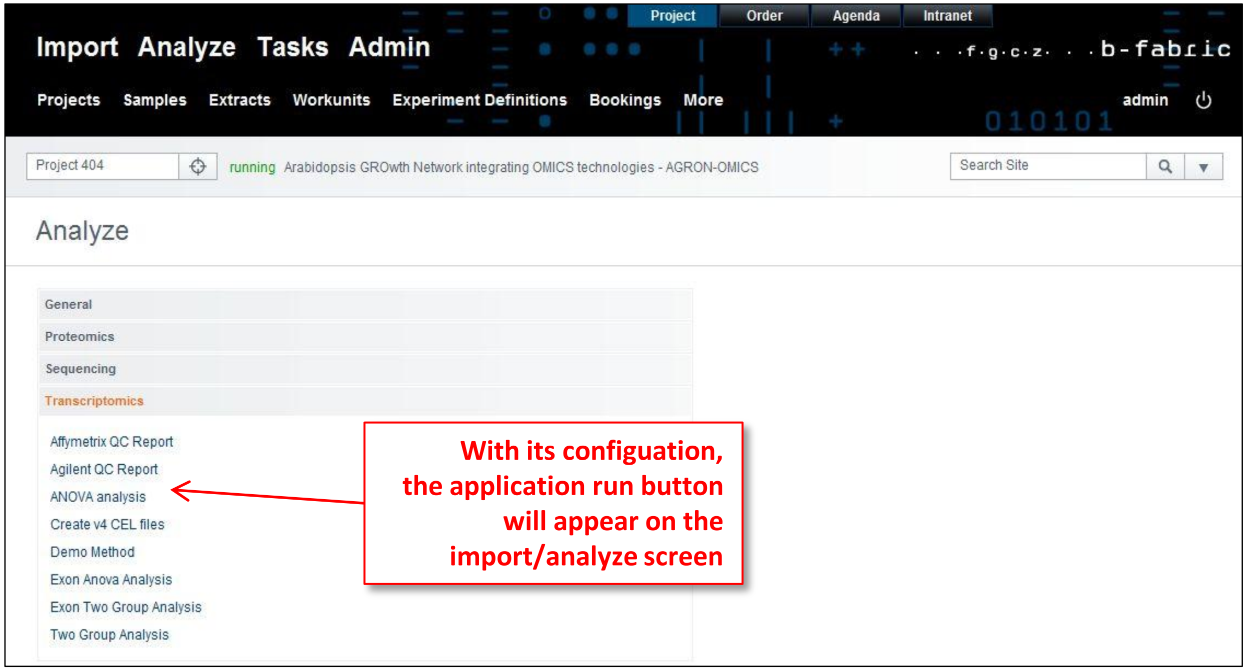
External script (program) that will be invoked

External Applications

- Framework with generic workflows to invoke and connect external applications

- Ad-hoc coupling without compiling and restarting the system

- External applications hide complexity and technical details of the analysis



Project 404 running Arabidopsis GROwth Network integrating OMICS technologies - AGRON-OMICS

Analyze

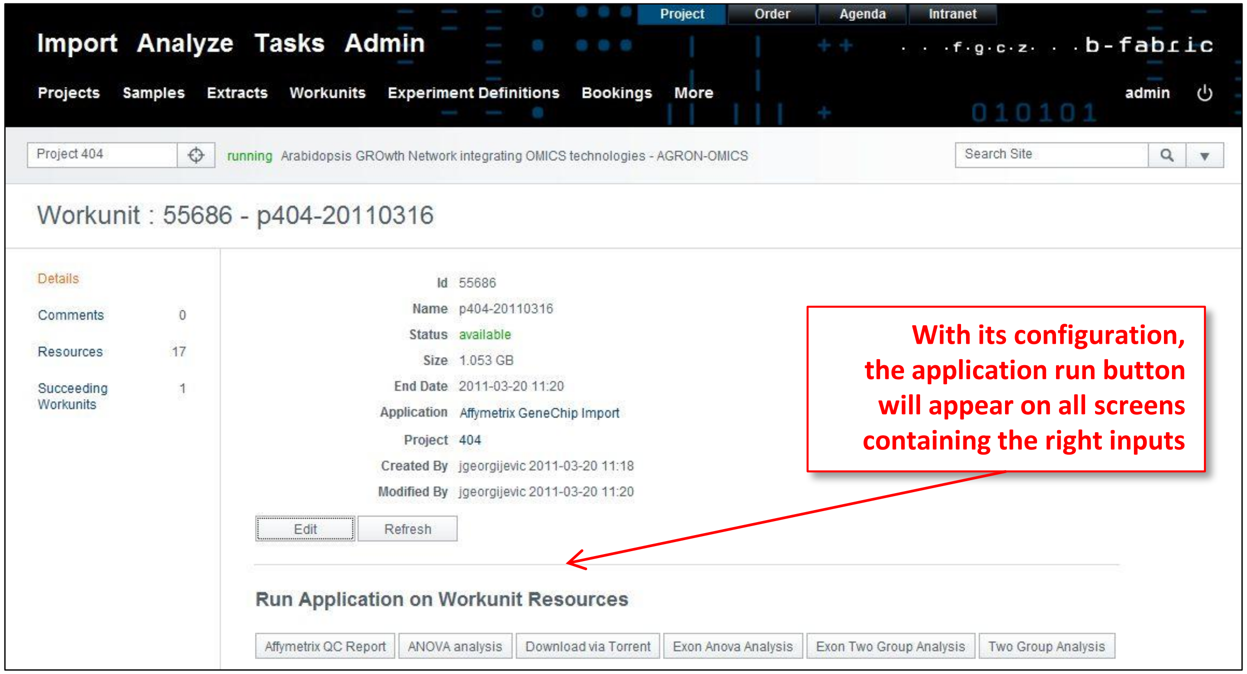
General
Proteomics
Sequencing
Transcriptomics

Affymetrix QC Report
Agilent QC Report
ANOVA analysis
Create v4 CEL files
Demo Method
Exon Anova Analysis
Exon Two Group Analysis
Two Group Analysis

With its configuation, the application run button will appear on the import/analyze screen

External Applications

- Framework with generic workflows to invoke and connect external applications
- Ad-hoc coupling without compiling and restarting the system
- External applications hide complexity and technical details of the analysis



running Arabidopsis GROwth Network integrating OMICS technologies - AGRON-OMICS

Workunit : 55686 - p404-20110316

Id	55686
Name	p404-20110316
Status	available
Size	1.053 GB
End Date	2011-03-20 11:20
Application	Affymetrix GeneChip Import
Project	404
Created By	jgeorgijevic 2011-03-20 11:18
Modified By	jgeorgijevic 2011-03-20 11:20

Run Application on Workunit Resources

With its configuration, the application run button will appear on all screens containing the right inputs

Summary: B-Fabric Benefits

- Secure, long-term data storage
- Easy web-based data access
- Fast access to relevant data
- Sophisticated data search
- Data reuse
- Reduced annotation work through automatic export to external marts
- Access-controlled data sharing
- Communication tracking
- Easy application/analysis invocation
- Workflow tracking (→ basis for reproducibility of research results)
- Increased data (research) quality

- Transparent management of users, projects, …
- Ad-hoc addition of new services
- Generation of reports etc.
- Charging / Invoicing
- Task management (user guidance)
- Event-driven email notifications
- Tracking centers resources/capacities
- Major administration tasks automated (user registration, FGCZ-wide password management, FGCZ access request, …)
- …

Many Thanks to all B-Fabric Developers, Testers, Users, and Supporters

Current Developers

- Fuat Akal
- Aleksander Markovic
- Can Türker

Alumni Developers

- David Altorfer
- Christian Decker
- Michael Fetzer
- Felix Knecht
- Dieter Joho
- Lucas Marti
- Haissam Mouhasseb
- Giacomo Pati
- Benedikt Thelen

External Application Developers

- Simon Barkow-Oesterreicher
- Tanguy Le Carrour
- Jonas Grossmann
- Christian Panse
- Weihong Qi
- Hubert Rehrauer
- Marco Schmidt

Sponsors

- UZH / ETHZ (financiers of the FGCZ)
- SWITCH: «Generalizing B-Fabric towards an Infrastructure for Collaborative Research in Switzerland» (June 2009-May 2011)
- SYBIT: «Infrastructure for BATTLEX» (June 2010-December 2011)
- HP: «HP Sequence Services» (August 2011-April 2012) for using and supporting B-Fabric adaptations within the HP Sequence Services project which won the Pistoia Alliance competition

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