FAIRDOMHub for storing, finding, sharing, and reusing of data, models, operations

Olga Krebs

Heidelberg Institute for Theoretical Studies

EmPowerPutida project meeting and practical workshop on data management, Bruxselles, 30-23 November 2016

Agenda

- 40 minutes
  - What is data and model management ?
  - What do we offer?
- 40 minutes step by step powerpoint demo
- 40 minutes hands on
- Questions

FAIRDOM

FAIRDOM

NWO

BBSRC
bioscience for the future

Federal Ministry of Education and Research

ERASysAPP
ERA-Net for Applied Systems Biology

ISBE
Infrastructure for Systems Biology Europe

SystemsX.ch
The Swiss Initiative in Systems Biology

ETH Zürich

Carole Goble

Jacky Snoep

Wolfgang Mueller

Rostyslav Kuzyakiv

Natalie Stanford

Olga Krebs

Bernd Rinn

MANCHESTER 1824
The University of Manchester

Stuart Owen

Quyen Nguyen

Katy Wolstencroft

also contributing:
UK SEEK team

also contributing:
SDBV team

FAIRDOM PALs

- Post-docs, Postgrads
- **Co-designers**,
- **Advocates**
- Seed knowledge network
- Bridge modellers-experimentalists

- Training
- Workshops, meetings,
- Kick-offs, Visits……

FAIRDOM project funding

SystemsX.ch
The Swiss Initiative in Systems Biology

NWO
Netherlands Organisation
for Scientific Research

Bundesministerium
für Bildung
und Forschung

ptj
Projektträger Jülich
Forschungszentrum Jülich

Funding set aside **independent of projects**
For centralized

- Data&models management
- Services
- Community development
- Outreach

FAIRDOM

Experience with big project DMM

13 consortia
9 European countries
> 300 people

SysMO
Systems Biology of Microorganisms

SystemsX.ch
The Swiss Initative in System Biology

virtual liver network

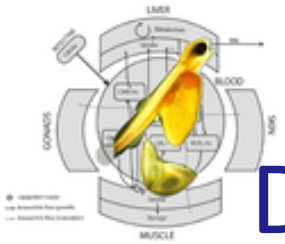
1 country
> 100 projects
> 300 groups

1 country
44 organisations
45 subprojects
> 250 people

ERASysAPP
ERA-Net for Applied Systems Biology

12 consortia

SEEK



DigiSal

Systems Science for Health (SSfH)

eagle genomics ElasticAP

SynthSys
SYNTHETIC & SYSTEMS BIOLOGY

unicellsys

SYNBIOCHEM
Manchester Synthetic Biology Research Centre for Fine and Speciality Chemicals

EMSL
Pacific Northwest
NATIONAL LABORATORY

EVIMalaR

Host–pathogen interactions

SBCancer.

RosAge
Reactive oxygen species and the dynamics of ageing

ERASysBio Plus

FORSYS
MACS

JENAGE
JENA CENTRE FOR SYSTEMS BIOLOGY OF AGEING

CISBIC

livSYSiPS

GLYCON

Consensus model of Yeast Glycolysis

sybacol

FAIRDOM

Findable

Accessible

Interoperable

Reusable

Data

S **O** Ps

Models

} Assets

http://www.fair-dom.org

http://www.fairdomhub.org

FAIRDOM

Why data management?

https://scholarlykitchen.sspnet.org/2016/11/11/a-painful-but-true-to-life-look-at-data-availability-and-reuse/

FAIRDOM

The FAIRDOM Platform

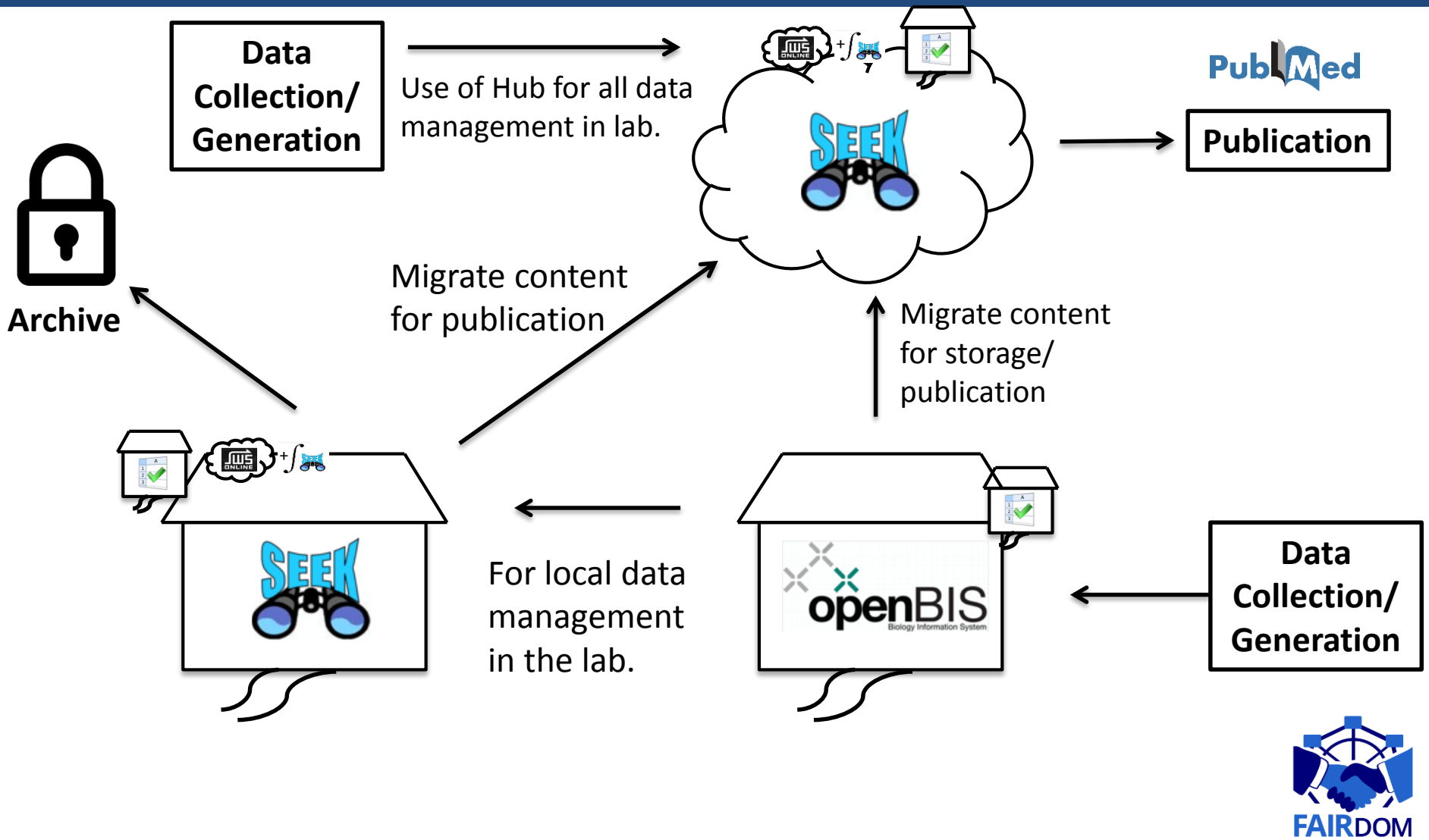
Front end: Science Commons

Web-based Cataloguing and Rich web interface for describing, finding, linking and promoting ongoing research and outcomes. Small files, aggregates across data archives.

Back end: Scaled local Data Mgt. (incl. LIMS/ELN) and analysis integration

Ingest and transformation directly from the instruments or a web app, link with data analysis pipelines. Automatic archiving support. Very scriptable. Handles also large data.

How to use FAIRDOM



FAIRDOM hub:
A catalogue for project outcomes

Standards

SEEK

SBML W3C

SED ML

isatools MIBBI

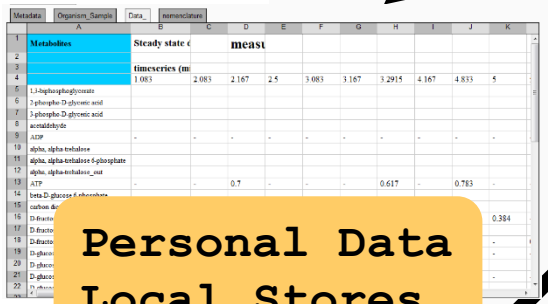
External Databases

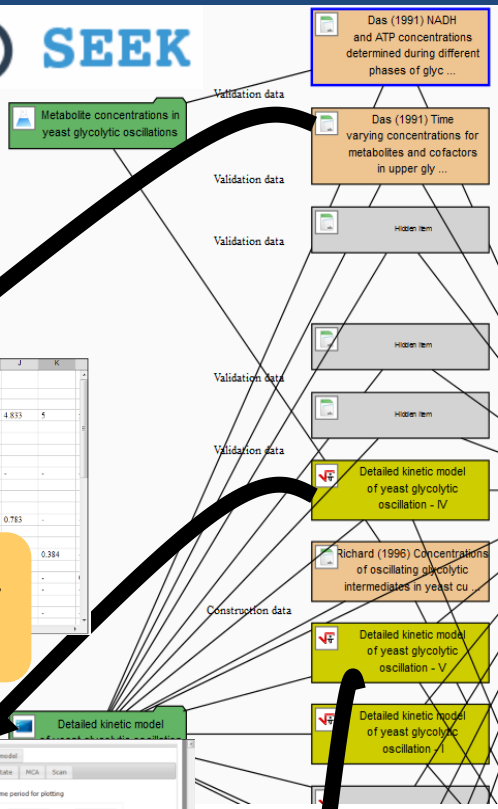
SABIO-RK

ChEBI

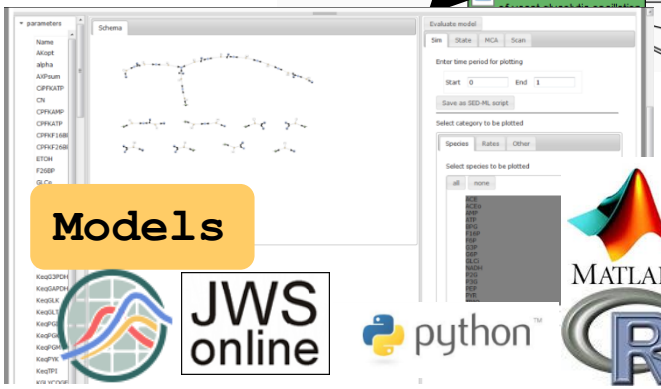
PRIDE

Personal Data Local Stores





Models



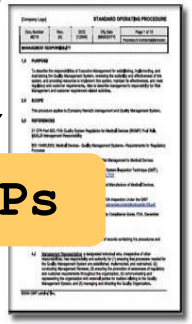
JWS online

python

MATLAB

R

SOPs



Articles

FAIRDOM

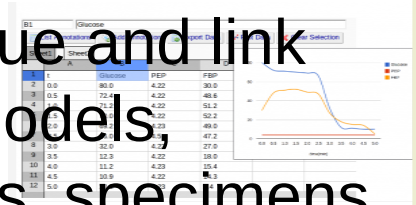
FAIRDOMHub: Platform Features

yellow pages of peers projects, experts

project mgt, access control reporting, citation governance & policies

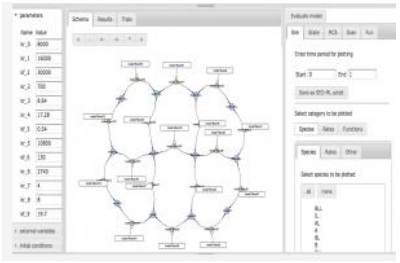
integrate local tools and data systems

catalogue and link data, models, samples, specimens, sops, experiments, publications using standards



manage, store and exchange different types and scales of data

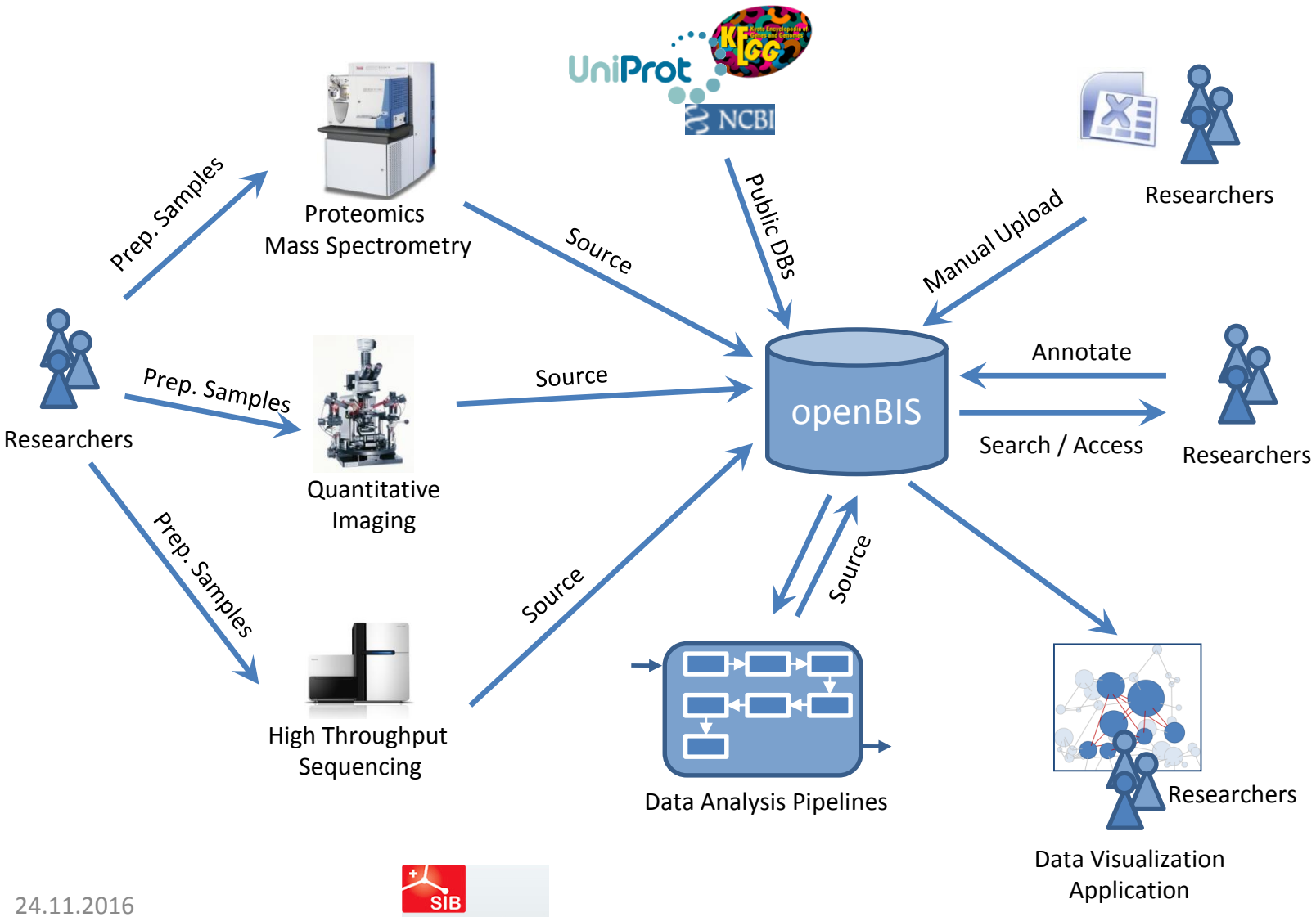
simulate models



curate & annotate data and models using standards

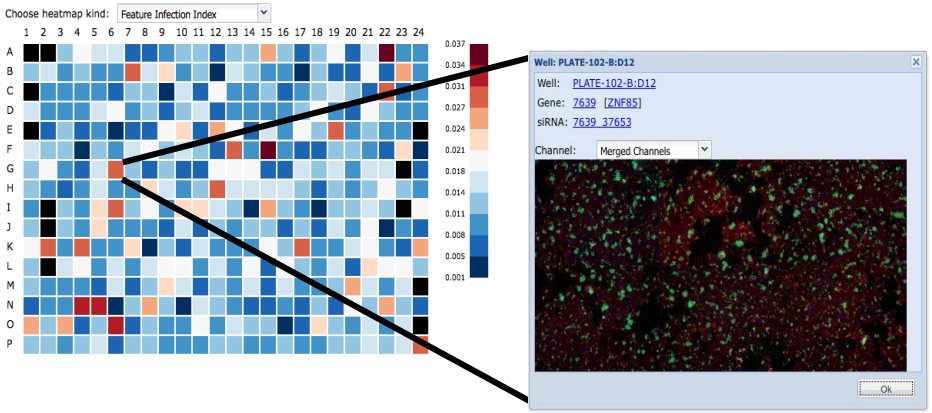
scaled-out collection & processing

openBIS in a nutshell

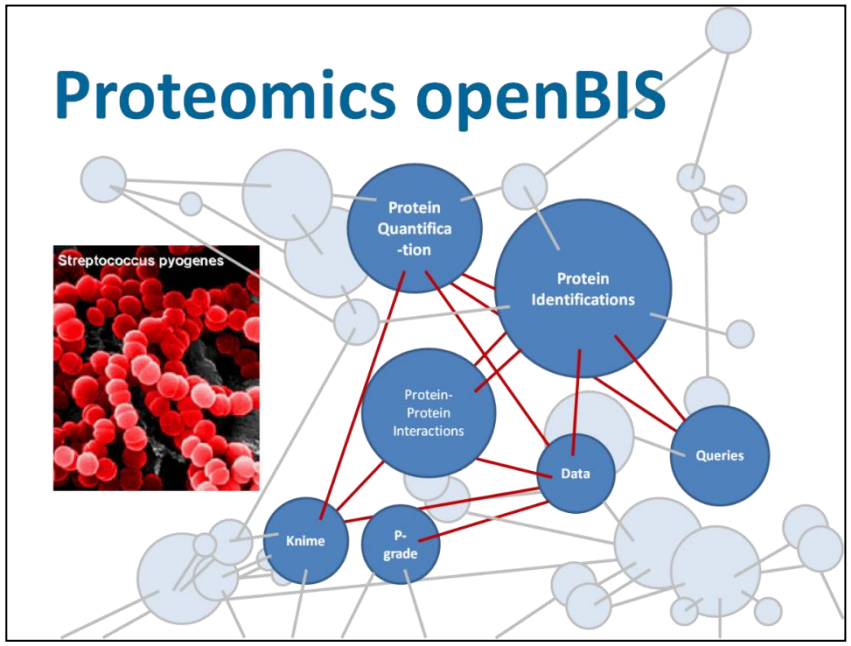


openBIS is used for…

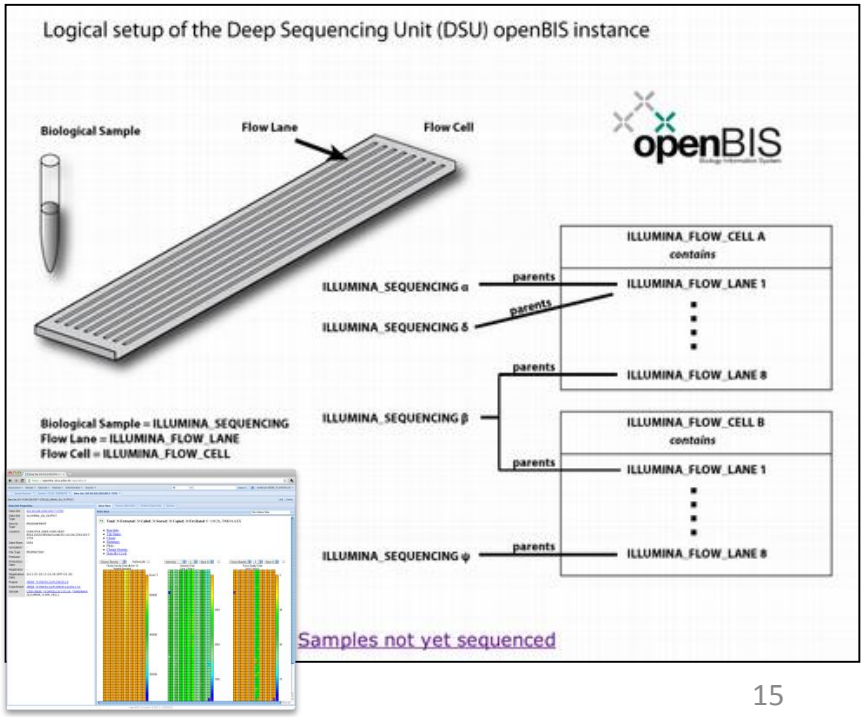
High Content Screening & Microscopy



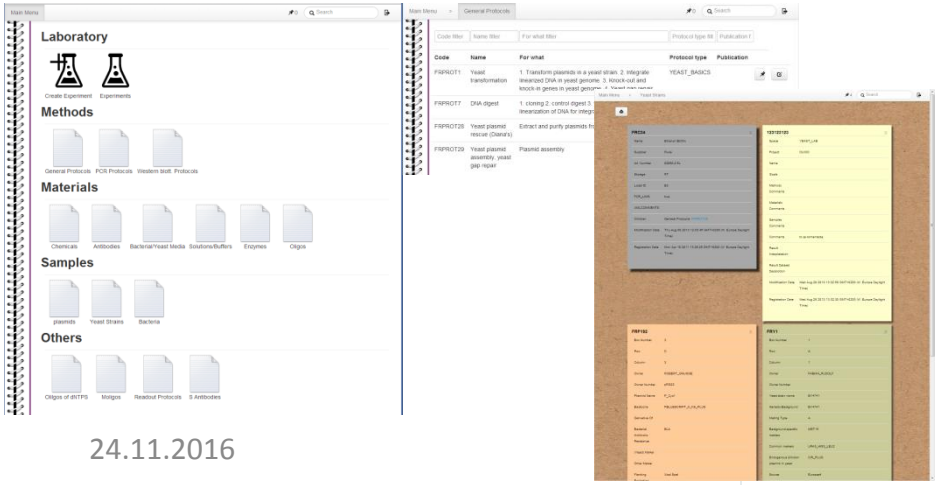
Proteomics openBIS



Next Generation Sequencing

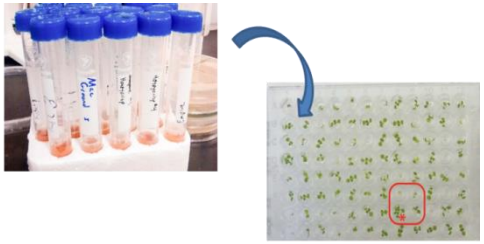


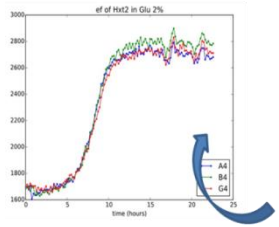
Electronic Lab Notebook



openBIS LIMS

metadata extraction
data relationship/linking
data processing
minimal user input





PS_GROUP » GROWTH_RATE » 187992378900 » PL13 » Data Set 187992378900 [PS_PLATE_READER]

Data Set Properties

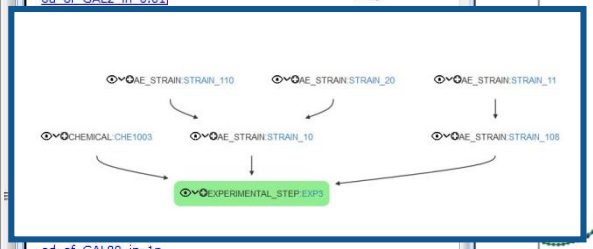
Sample	/PS_GROUP/PL13 [PS_IMG_PLATE]
Measurement date	2012-12-16
Measurement time	19:20:40
.mth file	March2012_2EmWL_1gain_M2_80c
Wsp file	2012_12_16.wsp
Instrument	infinite 200
Serial Nr	907001834
Plate desc.	[BD96ft_FluoroBlok] - BD Falcon 96 Flat Transparent/Black
Plate Cell Range	A1:H12
Temperature [C]	29.5
Min Temp. [C]	29.0
Max Temp. [C]	30.0
Shaking	Duration: 1000 sec; Mode: Linear; Amplitude: 6 mm; Frequency: 57.9 rpm;
Run Time	1days 45min 16s
Channels	OD 485-525mGain 485-585mGain
Channel1	OD Absorbance 595 nm reads:15
Channel2	485-525mGain

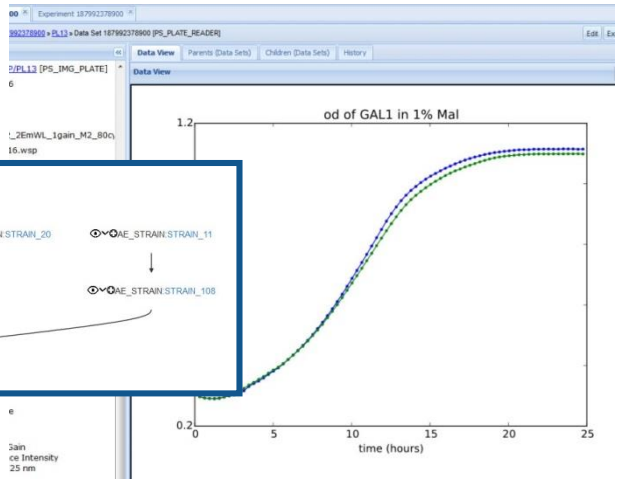
Data View | Parents ([

Data View

Folder:

..
2012_12_16_GALgen
GALgenes_contents_
od_of_GAL10_in_0.0
od_of_GAL10_in_0.1
od_of_GAL10_in_1p
od_of_GAL10_in_2p
od_of_GAL1_in_0.01
od_of_GAL1_in_0.1p
od_of_GAL1_in_1p_M
od_of_GAL1_in_2p_R
od_of_GAL2_in_0.01
od_of_GAL80_in_1p
od_of_GAL80_in_2p
od_of_null_in_0.01p
od_of_null_in_0.1p_M
od_of_null_in_1p_Ma
od_of_null_in_2p_Ra
od_of_WT_in_0.01p

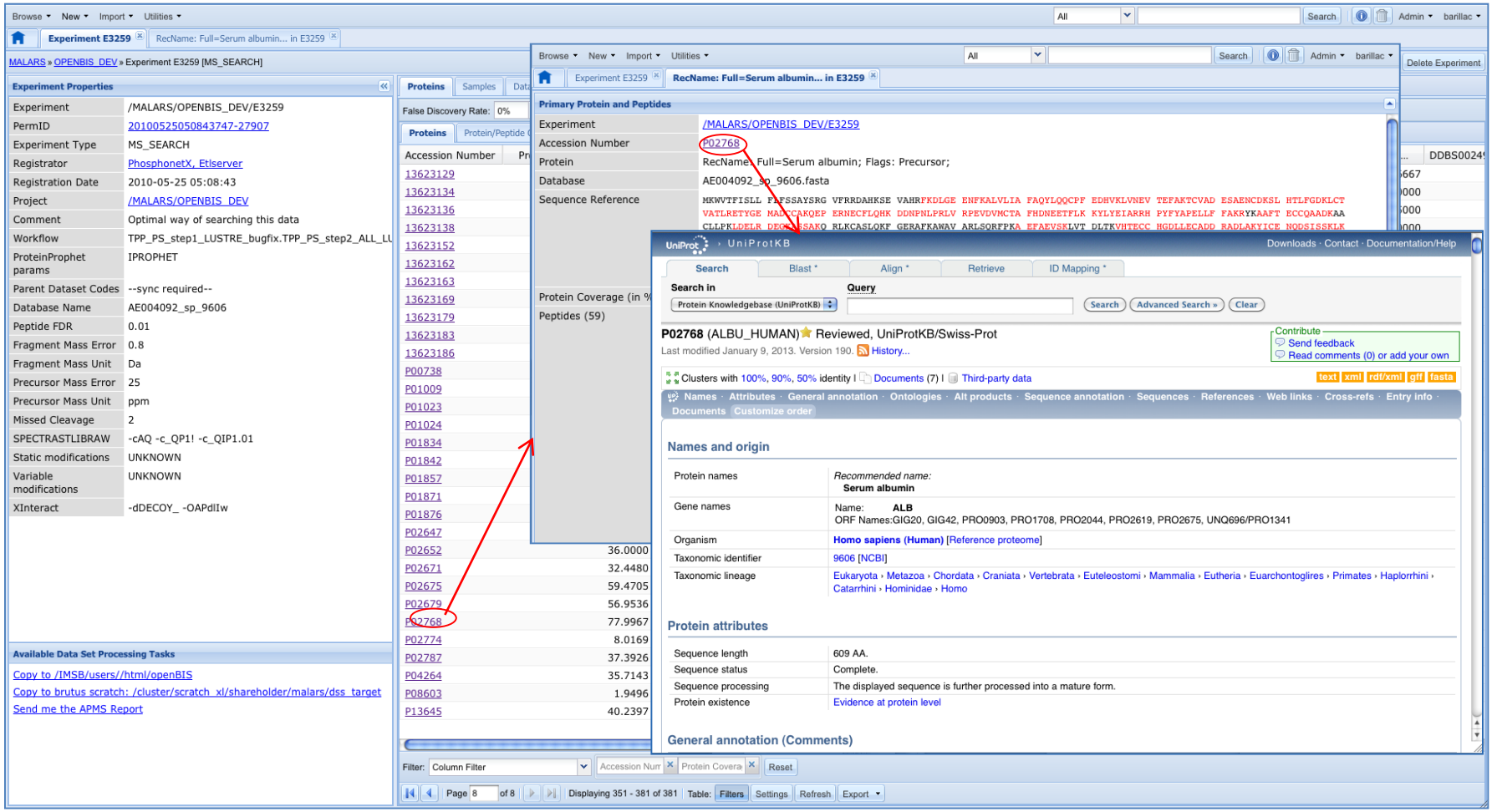




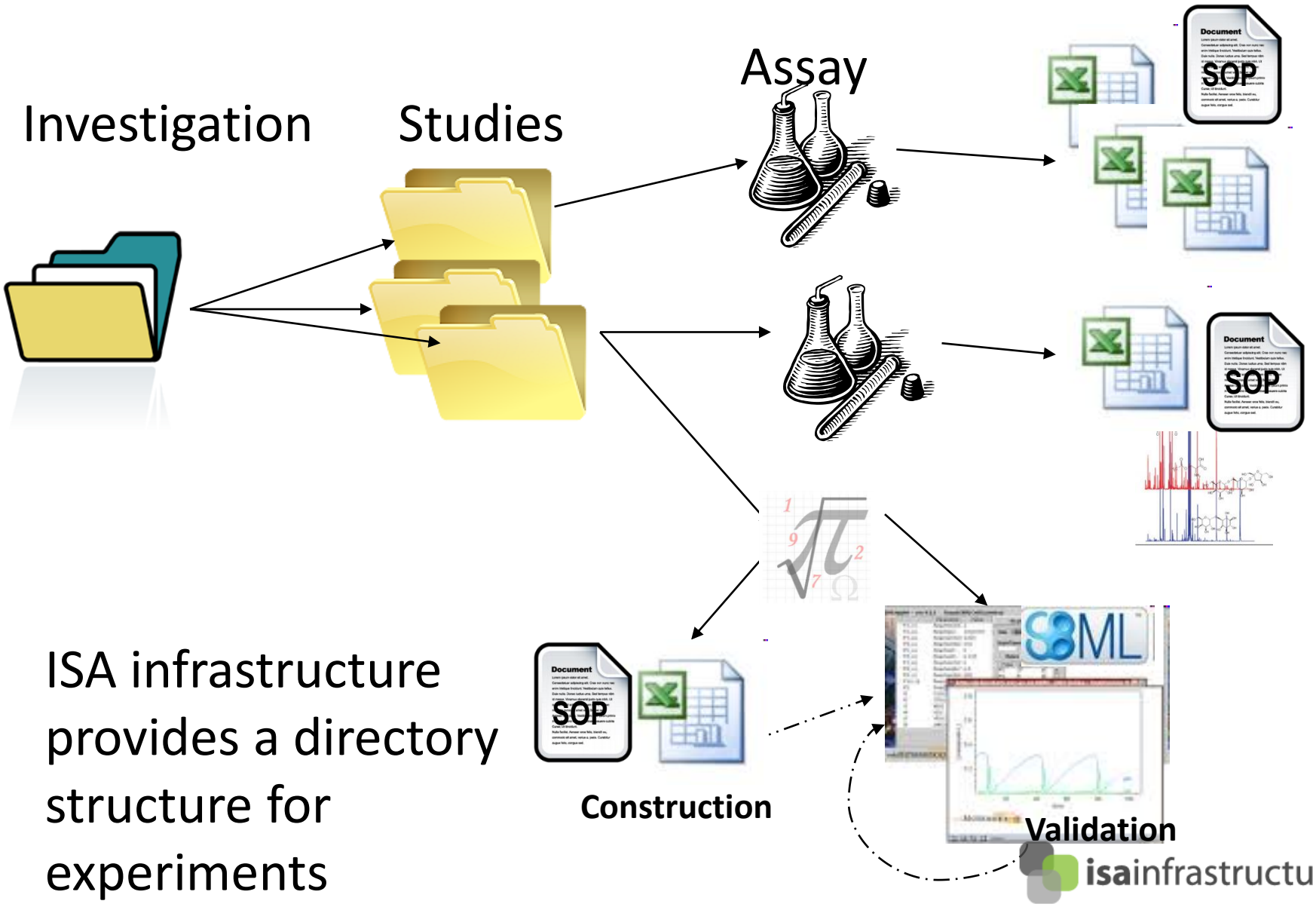
*Troup, E.; Clark, I; Swain, P; Millar, AJ; **Zielinski, T** (2015) Practical evaluation of SEEK and openBIS for biological data management in SynthSys http://hdl.handle.net/1842/12236

openBIS : Platform for High-throughput Proteomics

Proteomics data in openBIS

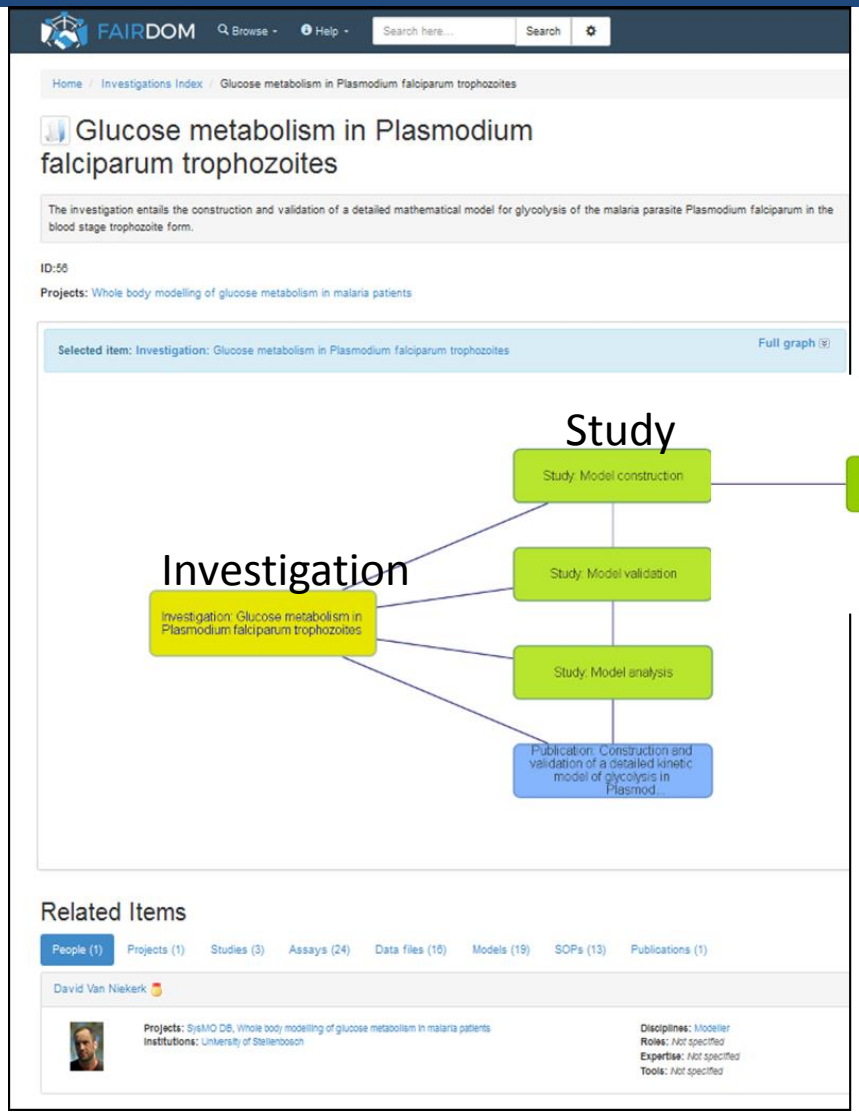


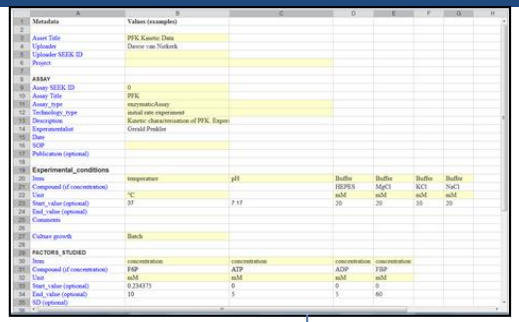
Organising and Linking Assets

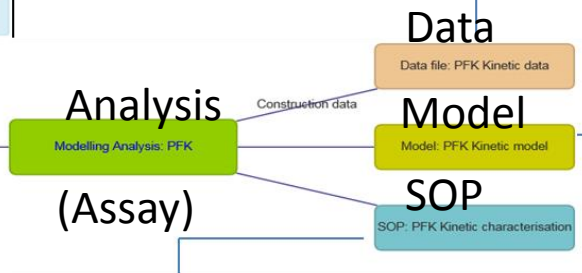


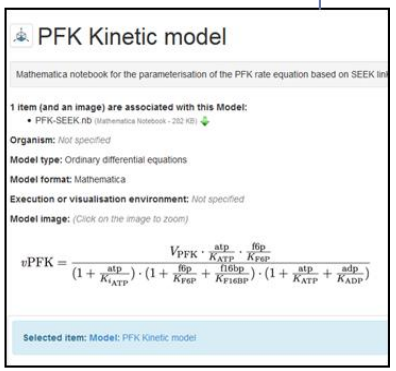
ISA infrastructure provides a directory structure for experiments

….organised in an ISA (Investigation, Study, Assay/Analysis) format.

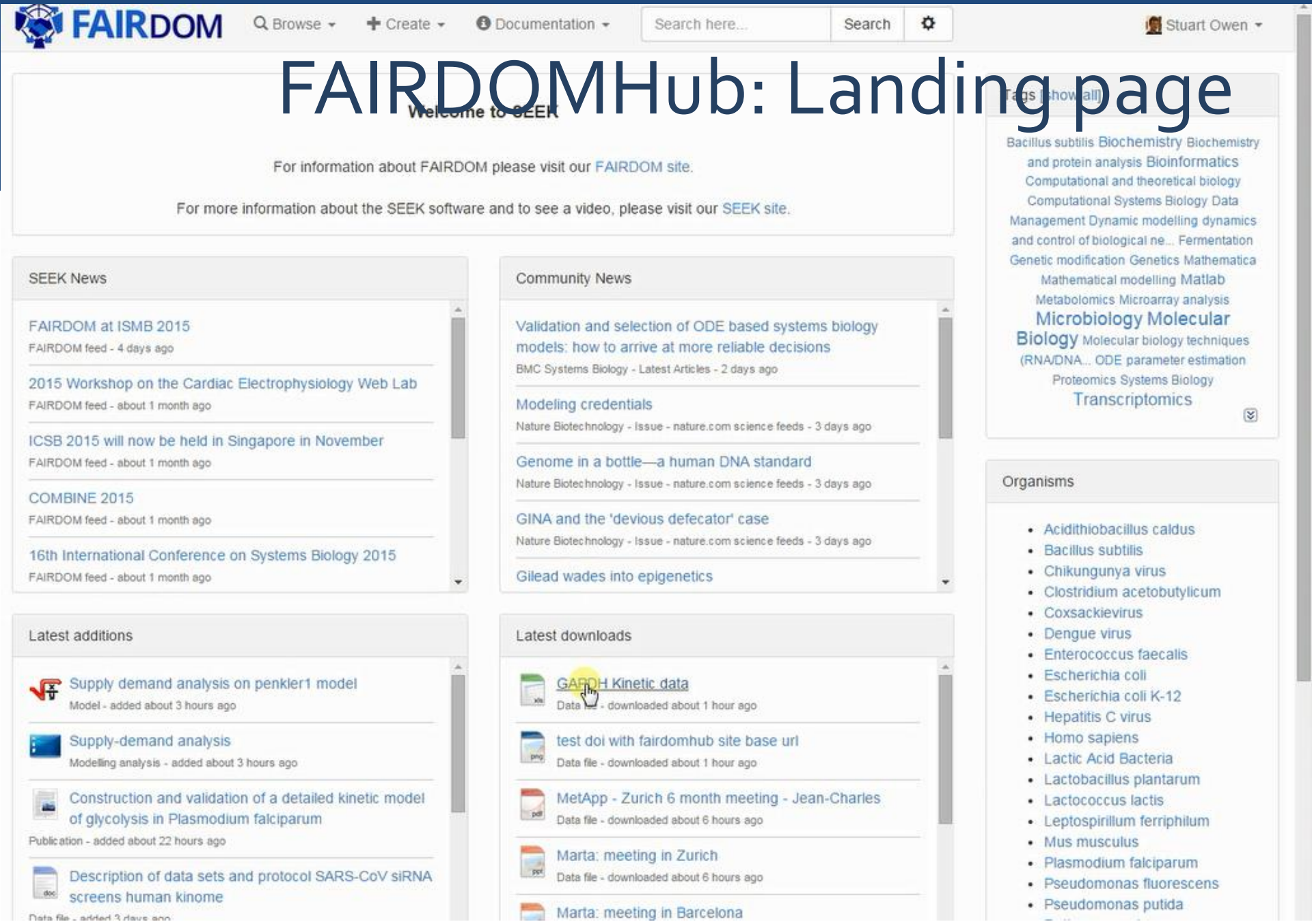




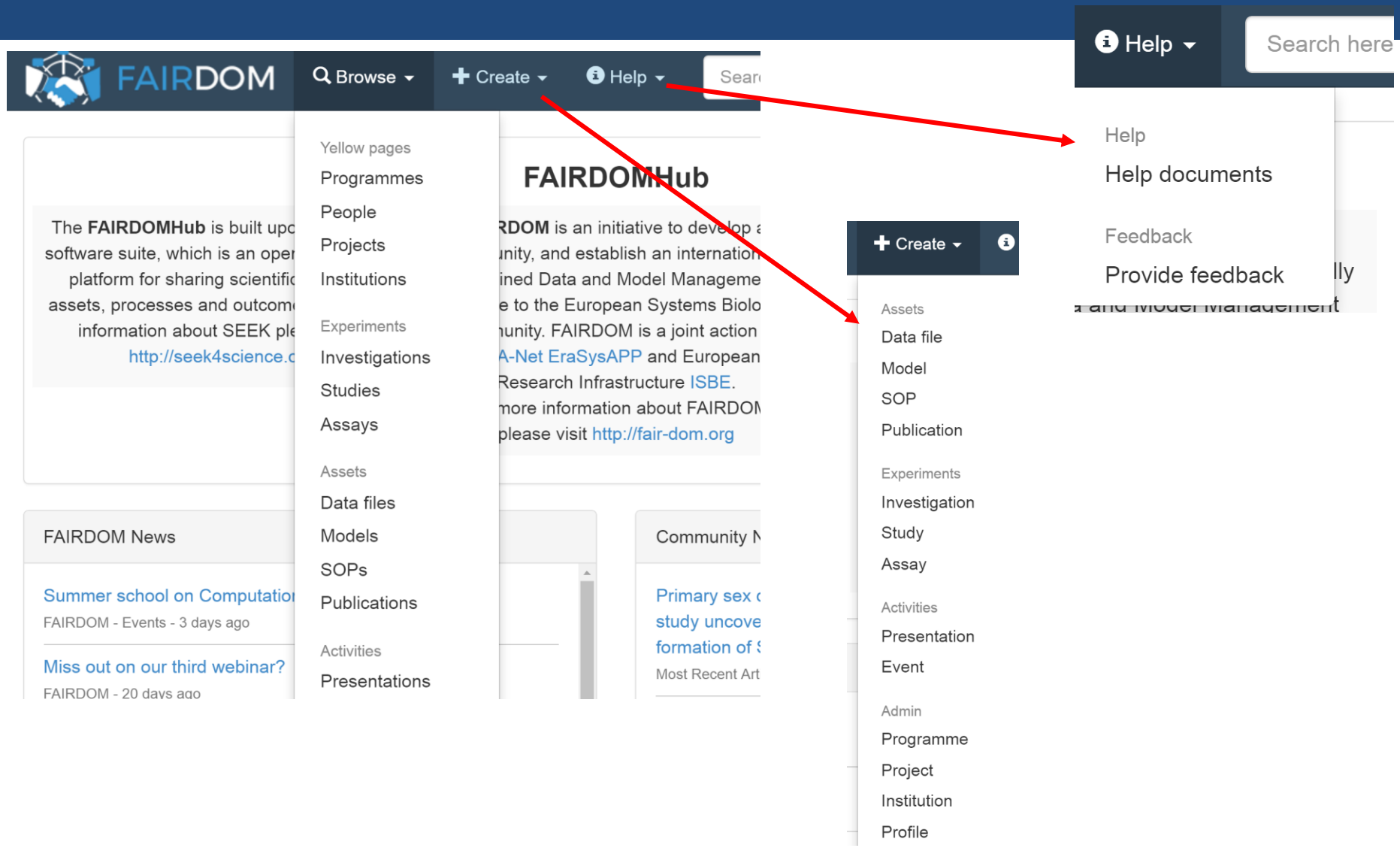




FAIRDOMHub: Landing page



FAIRDOMHub: Landing page



Project centric approach

Home > Projects Index > MOSES

MOSES (Micro Organism Systems biology: Energy and Saccharomyces cerevisiae) develops a new Systems Biology approach, which is called 'domino systems biology'. It uses this to unravel the role of cellular free energy ('ATP') in the control and regulation of cell function. MOSES operates though continuous iterations between partner groups through a new systems-biology driven data-management workflow. MOSES also tries to serve as a substrate for three or more other SYSMO programs.

Programme: SysMO

Public web page: http://www.moses.sys-bio.net/

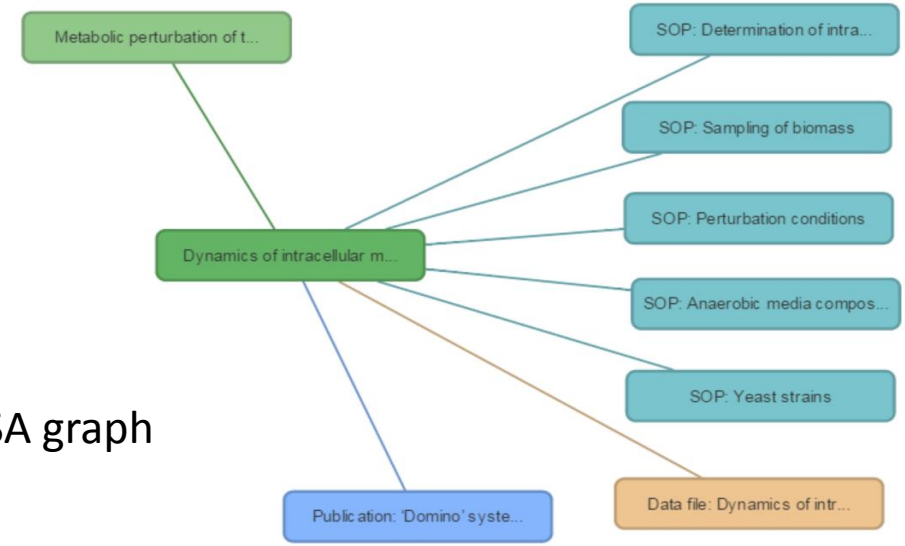
Organisms: Saccharomyces cerevisiae

FAIRDOM PALs: Femke Mensonides, Maksim Zakhartsev, Walter Glaser

Related items

People (20) | Institutions (6) | Investigations (3) | Studies (8) | Assays (12+1) | Samples (0+4) | Cell cultures (0+4) | Strains (1) | Data files (9+1) | Models (1+2) | SOPs (7+4) | Publications (5)

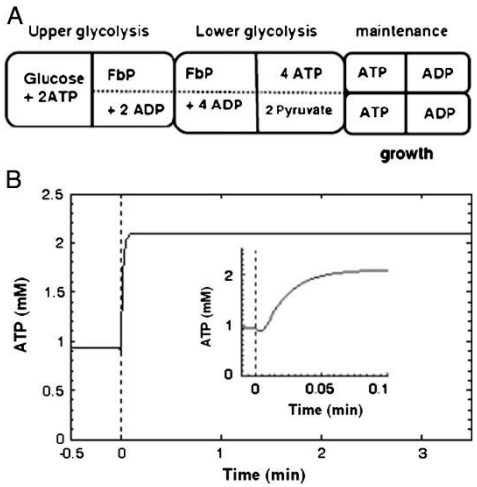
ISA graph



Experimental Assay: Dynamics of intracellular metabolites during glucose pulse

Connected items

Data file: Dynamics of intracellular metabolites during glucose pulse
SOP: Yeast strains
SOP: Anaerobic media composition
SOP: Perturbation conditions
SOP: Sampling of biomass



https://fairdomhub.org/projects/58

Apps ★ Bookmarks Erste Schritte Aus Firefox imp Watch Submarin Excelфункций V wiki instruction wiki.deutsch Anmeldung am http://www.redh » Other bookmar

FAIRDOM HUB | Browse | Create | Help | Search here... | Search | Olga Krebs

Home / Projects Index / EmPowerPutida

EmPowerPutida

Asset report | Administration

Exploiting native endowments by re-factoring, re-programming and implementing novel control loops in Pseudomonas putida for bespoke biocatalysis. The EmPowerPutida project aims to engineer the lifestyle of Pseudomonas putida to generate a tailored, re-factored chassis for the production of so far non-accessible biological compounds. Pseudomonas putida is a bacterium with a highly versatile metabolism, including the capability to degrade or produce organic chemicals.

EMPOWER PUTIDA

Change picture

Programme: Independent Projects

Public web page: http://www.empowerputida.eu/

Internal web page: *Not specified*

Organisms: Pseudomonas putida

FAIRDOM PALs: *No PALs for this Project*

Storage Usage

The total size of all project assets is: **0 Bytes**

Related items

People (16) | Institutions (9)

Ruben Van Heck

Projects: EmPowerPutida
Institutions: University of Wageningen
Email: rubenvanheck@gmail.com
Web page: *Not specified*
Phone: *Not specified*
Skype: *Not specified*

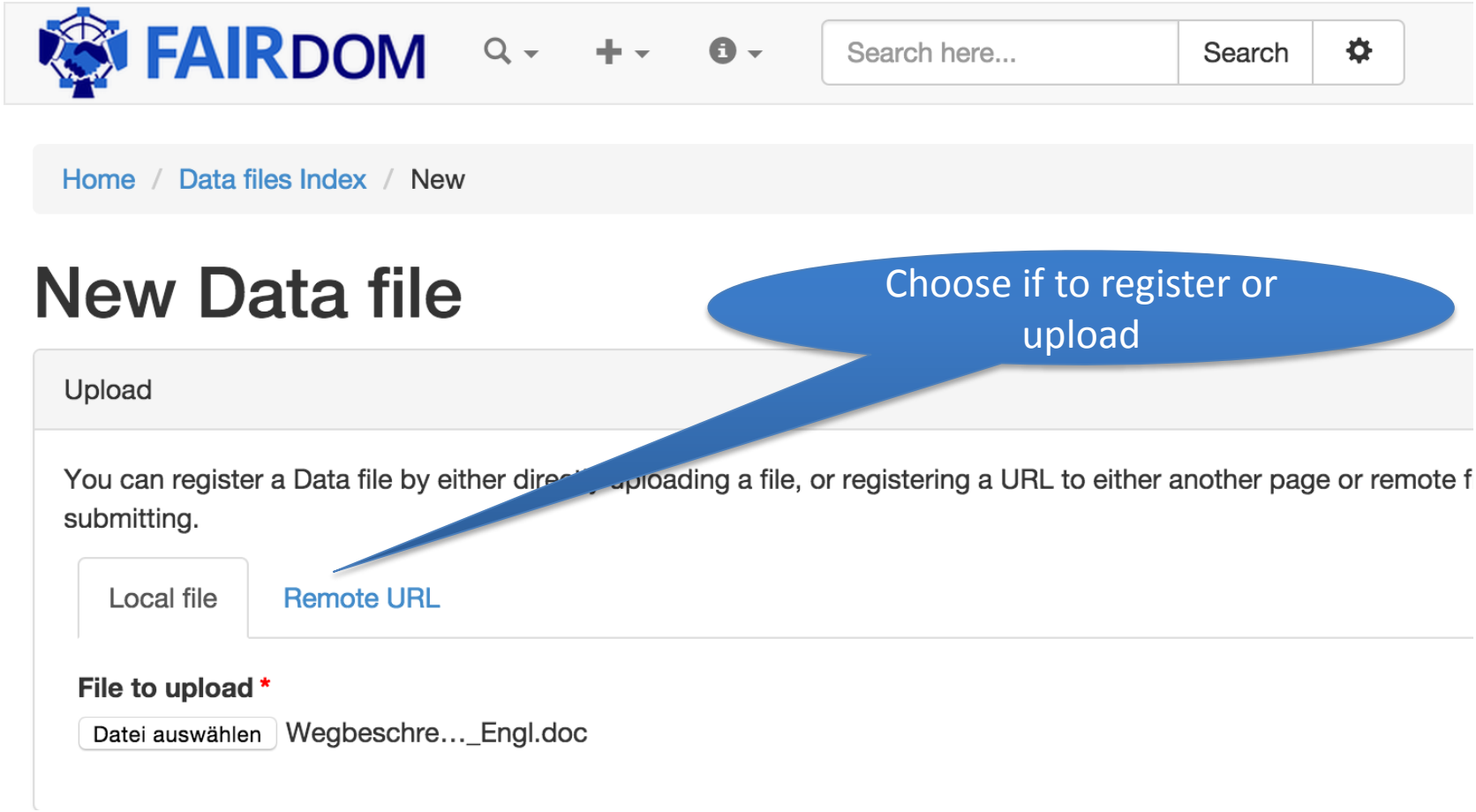
Disciplines: *Not specified*
Roles: *Not specified*
Expertise: *Not specified*
Tools: *Not specified*

Victor De Lorenzo

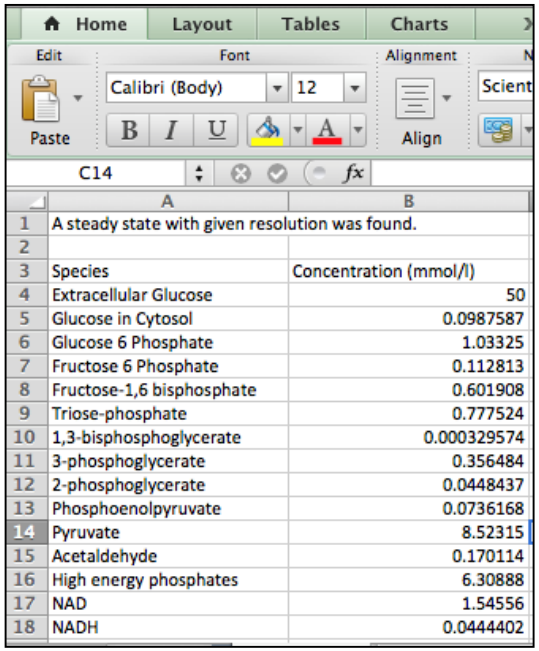
Projects: PSYSMO, EmPowerPutida
Institutions: CSIC Madrid, CSIC
Email: vdlorenzo@cnb.csic.es
Web page: *Not specified*
Phone: *Not specified*
Skype: *Not specified*

Disciplines: *Not specified*
Roles: *Not specified*
Expertise: *Not specified*
Tools: *Not specified*

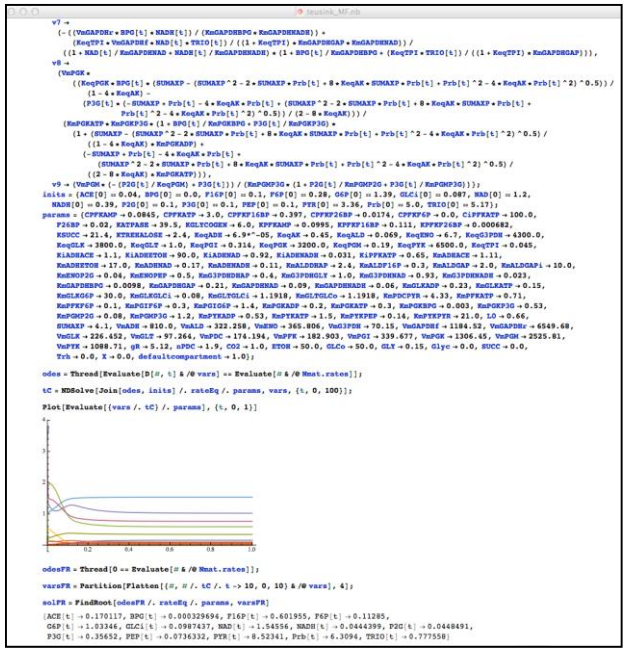
Data file - Register vs. Upload

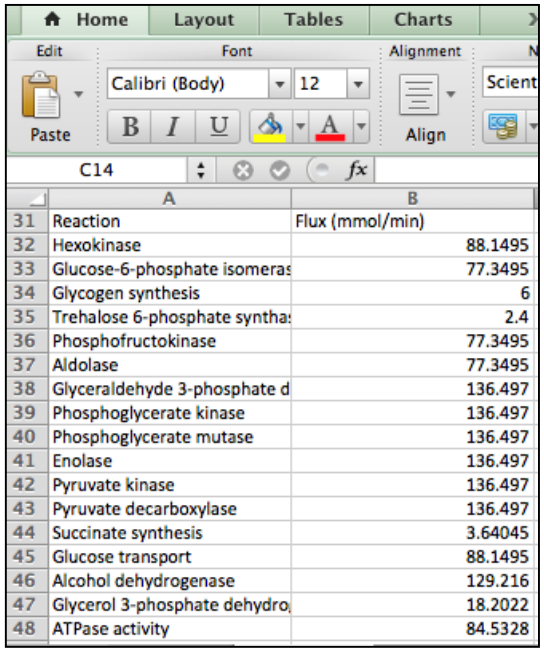


The data contained within the files can be very ambiguous.



	A	B
1	A steady state with given resolution was found.	
2		
3	Species	Concentration (mmol/l)
4	Extracellular Glucose	50
5	Glucose in Cytosol	0.0987587
6	Glucose 6 Phosphate	1.03325
7	Fructose 6 Phosphate	0.112813
8	Fructose-1,6 bisphosphate	0.601908
9	Triose-phosphate	0.777524
10	1,3-bisphosphoglycerate	0.000329574
11	3-phosphoglycerate	0.356484
12	2-phosphoglycerate	0.0448437
13	Phosphoenolpyruvate	0.0736168
14	Pyruvate	8.52315
15	Acetaldehyde	0.170114
16	High energy phosphates	6.30888
17	NAD	1.54556
18	NADH	0.0444402



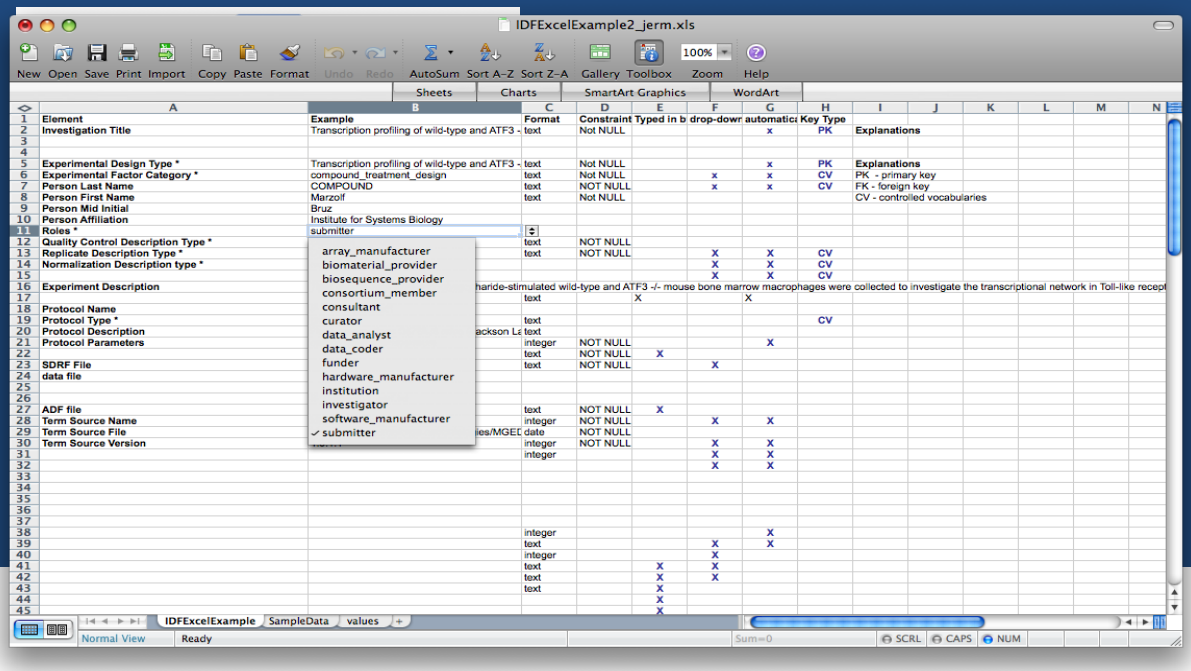


	A	B
31	Reaction	Flux (mmol/min)
32	Hexokinase	88.1495
33	Glucose-6-phosphate isomeras	77.3495
34	Glycogen synthesis	6
35	Trehalose 6-phosphate synthas	2.4
36	Phosphofructokinase	77.3495
37	Aldolase	77.3495
38	Glyceraldehyde 3-phosphate d	136.497
39	Phosphoglycerate kinase	136.497
40	Phosphoglycerate mutase	136.497
41	Enolase	136.497
42	Pyruvate kinase	136.497
43	Pyruvate decarboxylase	136.497
44	Succinate synthesis	3.64045
45	Glucose transport	88.1495
46	Alcohol dehydrogenase	129.216
47	Glycerol 3-phosphate dehydro	18.2022
48	ATPase activity	84.5328

Standardisation helps understanding and exchange

RightField

Capture & Curate Data: Spreadsheet tools

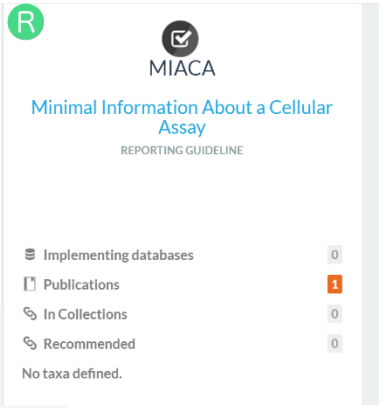


- Admins create spreadsheet with ontology-annotated selection lists
- Users helped in providing annotated data

Instrument Excel template sheets to annotate with **controlled vocabulary terms**

Self-contained data package

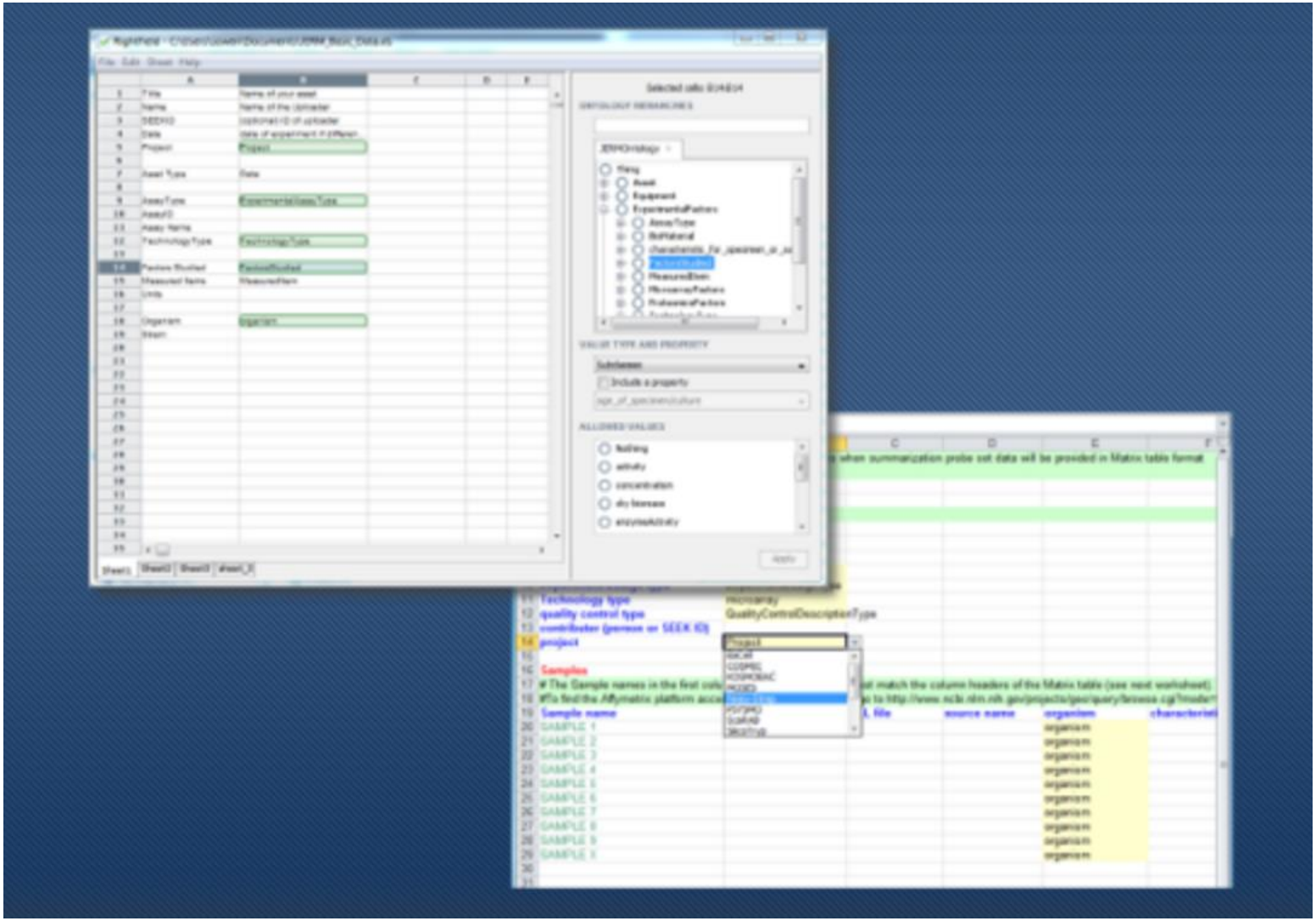
Upload, index, discover, process, compare in SEEK



http://www.rightfield.org.uk

biosharing.org
Information Resources

Biosamples can be defined according to Minimum Information Models either directly in SEEK (with output of Rightfield annotated spreadsheet), or Through input of Rightfield annotated spreadsheets.



Chip-chip Excel data

Unsubscribe | View samples | Download | Explore

Metadata Template | Matrix | Metadata Example | Samples | Matrix Example

	A	B	C	D	E	F	G	H	I
1	Sample name	title	raw data file 1	raw data file 2	ch1: source name	ch1: organism	ch1: char	ch1: char	ch
2	Sample 1	RAG H3K4me2	RAG_H3K4me2_Cy5.pair	RAG_H3K4me2_Cy3.pair	H3K4me2 ChIP DNA from Rag2-/- pro-B cells	Mus musculus	Rag2-/-	pro-B cell	C5
3	Sample 2	RAG H3K4me3	RAG_H3K4me3_Cy5.pair	RAG_H3K4me3_Cy3.pair	H3K4me3 ChIP DNA from H3K9ac ChIP DNA from F	Mus musculus	Rag2-/-	pro-B cell	C5
4	Sample 3	RAG H3K9ac	RAG_H3K9ac_Cy5.pair	RAG_H3K9ac_Cy3.pair	H3K9ac ChIP DNA from Pax5-/- Rag2-/- pro-B cells	Mus musculus	Pax5-/- R	pro-B cell	C5
5	Sample 4	P5R2 H3K4me3	P5R2_H3K4me3_Cy5.pair	P5R2_H3K4me3_Cy3.pair	H3K4me3 ChIP DNA from Pax5-/- Rag2-/- pro-B cell	Mus musculus	Pax5-/- R	pro-B cell	C5
6	Sample 5	P5R2 H3K4me2	P5R2_H3K4me2_Cy5.pair	P5R2_H3K4me2_Cy3.pair	H3K4me2 ChIP DNA from Pax5-/- Rag2-/- pro-B cell	Mus musculus	Pax5-/- R	pro-B cell	C5
7	Sample 6	RAG H3K9ac	RAG_H3K9ac_Cy5.pair	RAG_H3K9ac_Cy3.pair	H3K9ac ChIP DNA from Rag2-/- pro-B cells	Mus musculus	Rag2-/-	pro-B cell	C5
8									

Sample 1

Sample type: Chip-chip Excel

Source data: Chip-chip Excel data

Sample name: Sample 1

title: RAG H3K4me2

raw data file 1: RAG_H3K4me2_Cy5.pair

raw data file 2: RAG_H3K4me2_Cy3.pair

ch1: source name: H3K4me2 ChIP DNA from Rag2-/- pro-B cells

ch1: organism: Mus musculus

ch1: characteristics: Genotype: Rag2-/-

ch1: characteristics: Cell type: pro-B cells

ch1: characteristics: Strain: C57BL/6J

ch1: characteristics: ChIP Antibody: H3K4me2

ch1: molecule: genomic DNA

ch1: label: Cy5

ch1: treatment protocol: Rag2-/- pro-B cells were MACs sorted from the bone

Samples

Show 5 entries

Sample name	title	raw data file 1	raw data file 2	ch1: source name	ch1: organism
Sample 1	RAG H3K4me2	RAG_H3K4me2_Cy5.pair	RAG_H3K4me2_Cy3.pair	H3K4me2 ChIP DNA from Rag2-/- pro-B cells	Mus musculus
Sample 2	RAG H3K4me3	RAG_H3K4me3_Cy5.pair	RAG_H3K4me3_Cy3.pair	H3K4me3 ChIP DNA from H3K9ac ChIP DNA from Rag2-/- pro-B cells	Mus musculus
Sample 3	RAG H3K9ac	RAG_H3K9ac_Cy5.pair	RAG_H3K9ac_Cy3.pair	H3K9ac ChIP DNA from Pax5-/- Rag2-/- pro-B cells	Mus musculus
Sample 6	RAG H3K9ac	RAG_H3K9ac_Cy5.pair	RAG_H3K9ac_Cy3.pair	H3K9ac ChIP DNA from Rag2-/- pro-B cells	Mus musculus
Search Sample name	RAG	Search raw data file 1	Search raw data file 2	Search ch1: source name	Search ch1: organism

Chip-chip Excel

No description specified

Template

GA_ChIP_chip_w_platf_SEEKJERM_edited.xls - Download

Attributes

- Sample name (String) *
- title (String) *
- raw data file 1 (String) *
- raw data file 2 (String) *
- ch1: source name (String) *
- ch1: organism (String) *
- ch1: characteristics: Genotype (String) *
- ch1: characteristics: Cell type (String) *
- ch1: characteristics: Strain (String) *
- ch1: characteristics: ChIP Antibody (String) *
- ch1: molecule (String) *
- ch1: label (String) *
- ch1: treatment protocol (String) *
- ch1: growth protocol (String)
- ch2: source name (String) *
- ch2: organism (String) *
- ch2: characteristics: Genotype (String) *
- ch2: characteristics: Cell type (String) *
- ch2: characteristics: Strain (String) *
- ch2: characteristics: ChIP Antibody (String) *
- ch2: molecule (String) *
- ch2: label (String) *
- ch2: treatment protocol (String) *

Biosample instance (type based)

Biosample type

Related items

People (1) | Investigations (1) | Studies (1) | Assays (1) | Data files (1)

Standard Operating Procedures

Home > SOPs Index > Introduction of shRNAs, miRNAs or anti-microRNAs into primary human hepatocytes with lentivirus

Introduction of shRNAs, miRNAs or anti-microRNAs into primary human hepatocytes with lentivirus

Download SOP | View content

Here we used VSV-G-pseudotyped, EGFP-expressing lentiviral vectors to develop an efficient gene transfer protocol to modify gene expression in primary human hepatocytes (by RNAi). The protocol comprises the production of recombinant viruses as well as the steps for efficient delivery of short-hairpin RNA (shRNAs), microRNAs or anti-microRNAs to human hepatocytes. On average infection efficiencies of over 95% are achieved at relatively low multiplicity of infection (MOI), which effectively reduces the amount of preparative work required per experiment. Depending on the laboratory equipment available, we provide here two alternative workflows, which can be easily adapted in the lab. The procedure of virus production with subsequent titer determination takes approx. 6 to 10 working days. The procedure of viral infection of hepatocytes until effects can be measured takes approx. 3 to 5 days. This protocol should be helpful to study many aspects of functional genomics in primary human hepatocytes.

Contributors
[Maria Thomas]

Attributions
None

Scales
Not Specified

Filename: Lentiviral production and infection_SOP_04042011.pdf

Format: PDF document

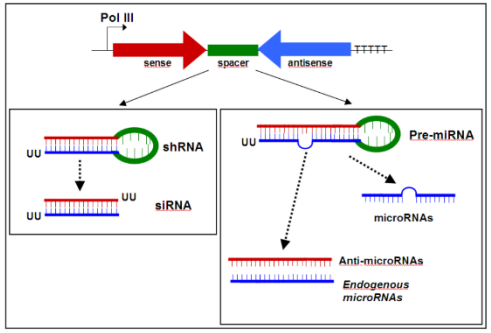


Fig.1: Schematic presentation of designed template sequences which are processed intracellularly into short hairpin RNAs, microRNAs or anti-microRNAs. The stem-loop structures consisting of both the sense and anti-sense strands of the targeted sequence are separated by a loop sequence.

MATERIALS

REAGENTS/KITS

BLOCK-iT™ Lentiviral RNAi Expression Kit (Invitrogen#49-4400)

ViraPower™ Lentiviral Gateway Expression Kit (Invitrogen#K49-6000)

miRZip™ Lentivector-based Anti- MicroRNAs (System Biosciences#MZIPxxxPA/AA-1)

ed microRNAs (System Biosciences#PMIRHxxxPA/AA-1)

PROCEDURE

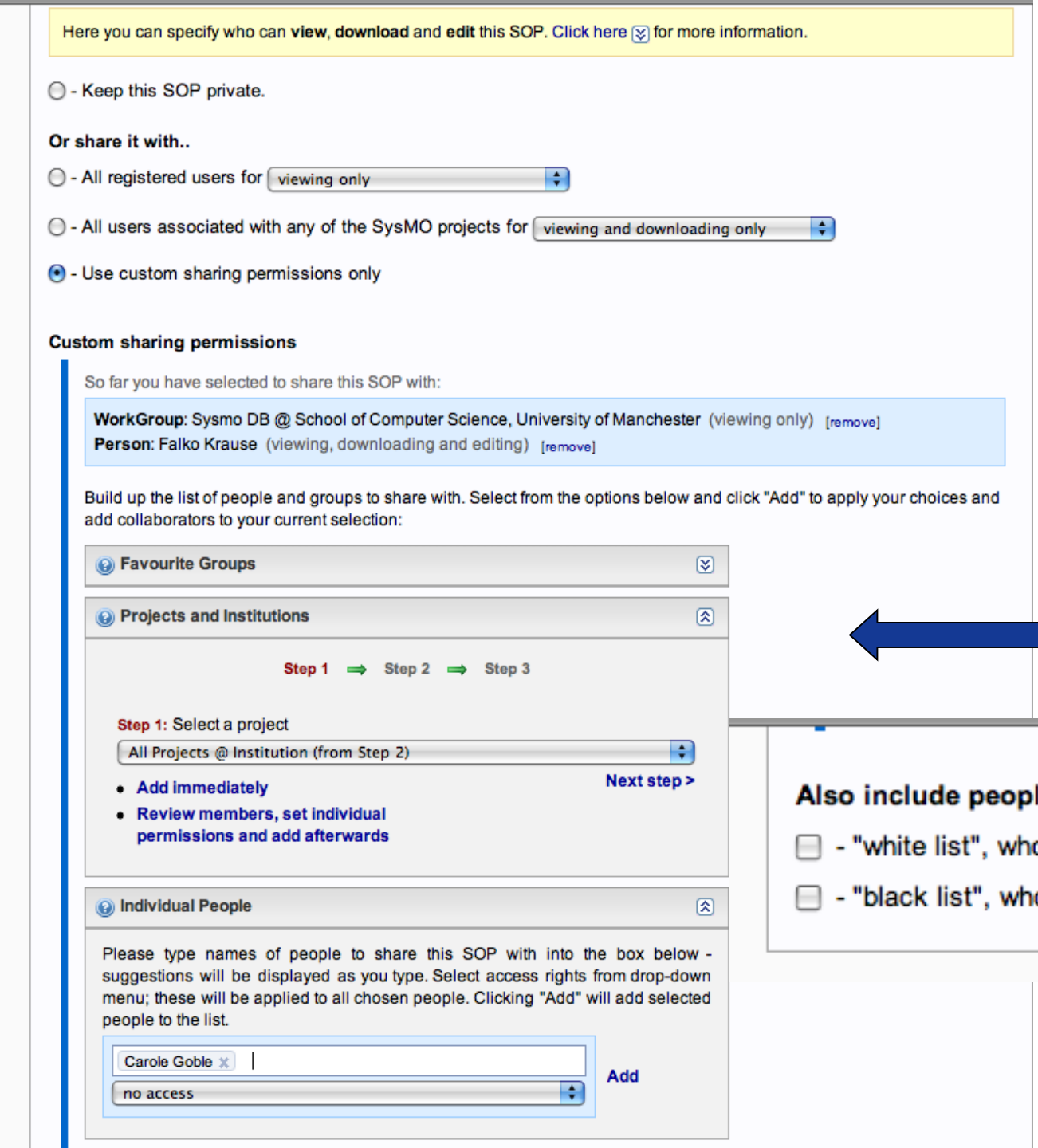
NOTE: all the steps marked with "S" should be performed following recommended guidelines for working with BL-2 organisms (Germany: S2 lab).

1. Preparation of HEK293FT cells.

For cultivating HEK293FT cells, add G148 (Geneticin, final concentration 500 µg/ml) to the DMEM culture medium with components (see Reagent Setup). The cells should be passaged at least 1-2 times after thawing to adapt to the culture conditions. Three days prior to transfection, plate out the cells at a density of approximately $3{,}5*10^6$ cells/per 1 T175 flask in 30 ml of medium with components and G148 to achieve optimal phase of cellular growth.

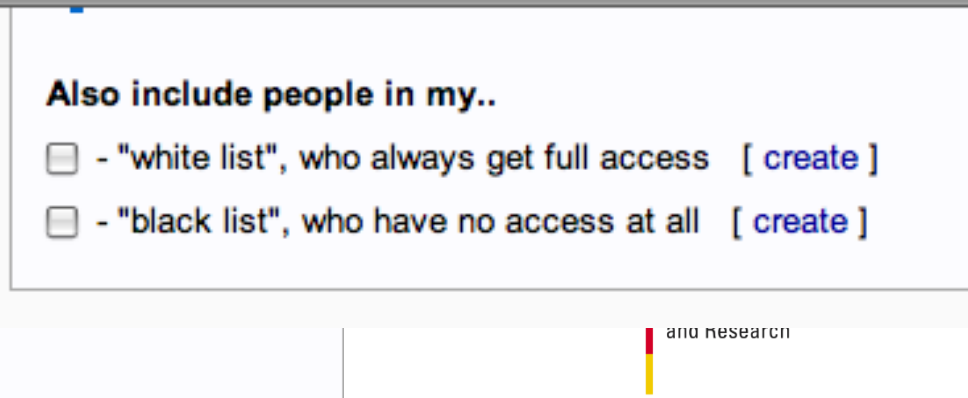
virtual liver network

Federal Ministry of Education and Research



Just Enough Sharing

Access Permissions



and Research

Kinetic model for incubation (penkler2) Version 7

Simulate Model on JWS | Find related Data files | Subscribe | Download

- Version 7 (latest)
- Version 6
- Version 5
- Version 4
- Version 3
- Version 2
- Version 1 (earliest)

Glycolytic model for Plasm… system

3 items are associated wi… ge icon

Filename	Format	…ion
penkler2.xml	XML docu…	
penkler2.nb	Mathemat…	
penkler2.dat	uuencode…	

Organism: *Not specified*

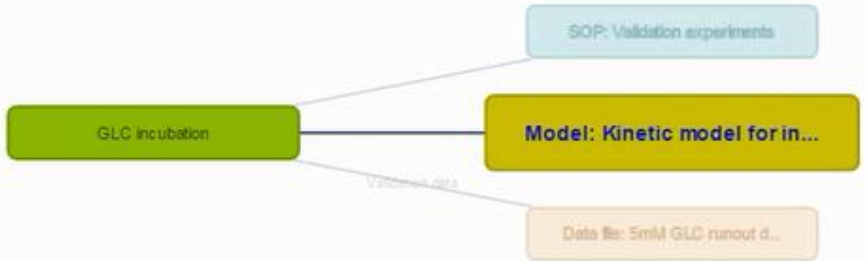
Model type: Ordinary differential equations

Model format: SBML

Execution or visualisation environment: JWS Online

Model image: *No image specified*

Selected item: Model: Kinetic model for incubation (penkler2)



Contributors

Activity

Views: 258 **Downloads:** 31

Created: 11th Aug 2014 at 09:58
Last updated: 1st Jul 2015 at 10:19
Last used: 10th Jul 2015 at 15:53

Tags

plasmodium

Update your tags

Attributions

None

Double-click to go to fullscreen,

Integration of Modelling Platforms

Kinetic model for steady state (penkler1) Version 8 -

Glycolytic model for Plasmodium falciparum; open system

3 items are associated with this Model:
- penkler1.xml (XML document - 101 KB)
- penkler1.nb (Mathematica Notebook - 58.4 KB)
- penkler1.dat (uuencoded file - 11.4 KB)

Organism: *Not specified*

Model type: Ordinary differential equations

Model format: SBML

Execution or visualisation environment: JWS Online

Model image: *No image specified*

Contributors

JWS ONLINE

Kinetic model incorporating glucose transport inhibition (vanniekerk1) - JWS Online Model Simulation

Selected item: Model: Kinetic model for steady state (penkle

Modelling Analysis: Supply-demand analysis

Modelling Analysis: Inhibition of lactate flux

Modelling Analysis: Steady state

vanniekerk1

vanniekerk1

Detail

Download

Reactions

Parameters

Fixed species

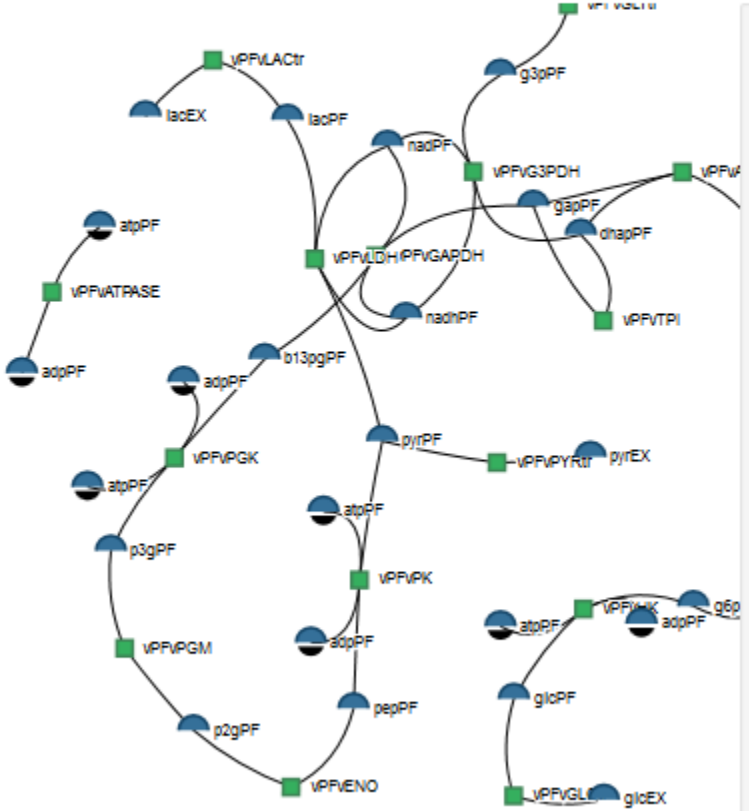
Initial values

Functions and Rules

Events

Constraints

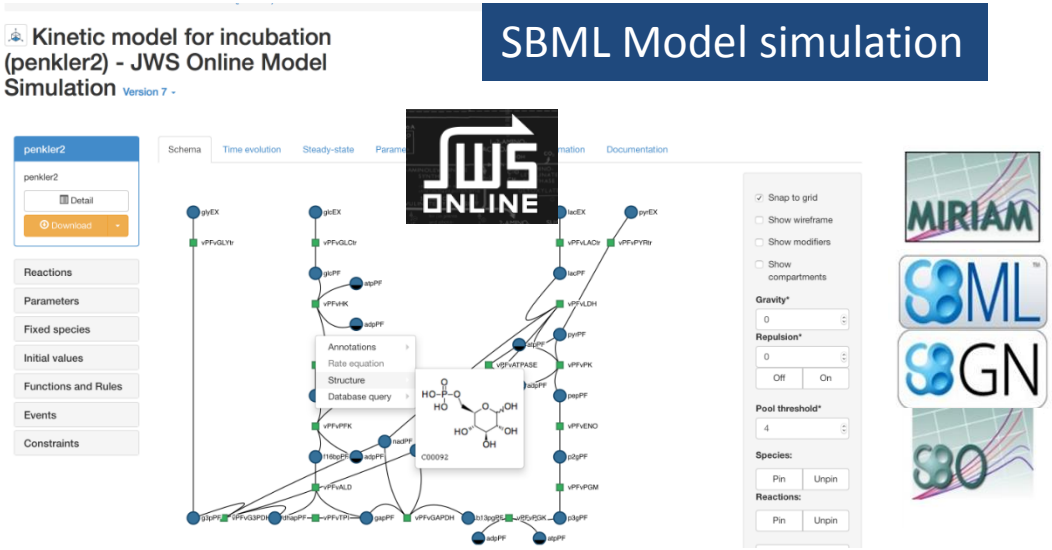
Schema | Time evolution | Steady-state | Parameter scan | Reaction plots | Information



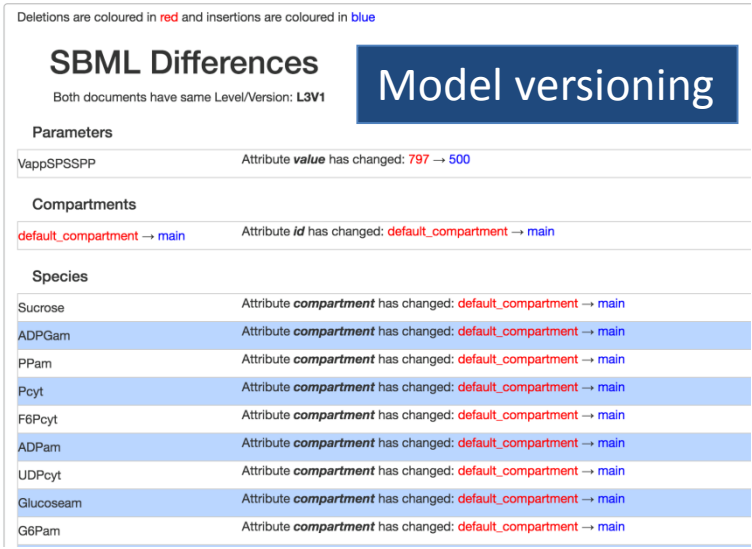
Plugin Tools

… with integrated tooling

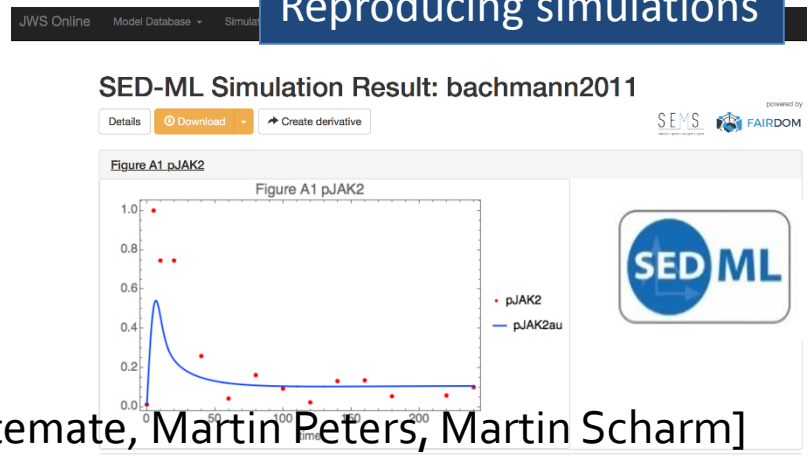
SBML Model simulation



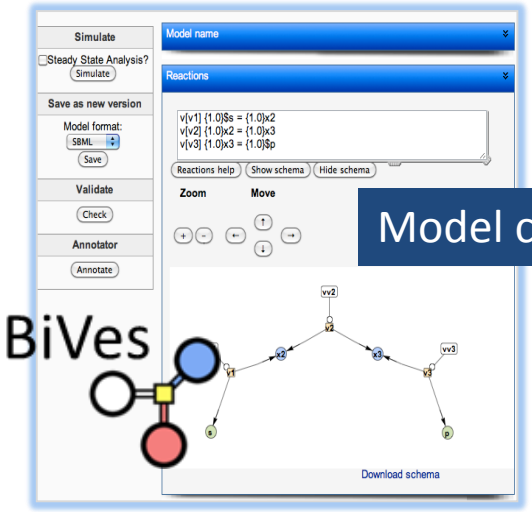
Model versioning



Reproducing simulations



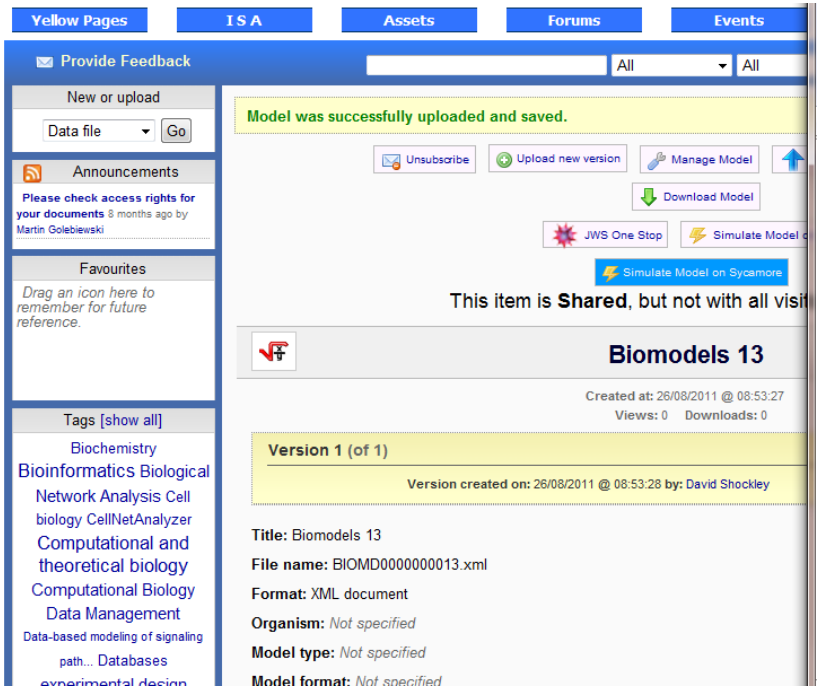
Model comparison

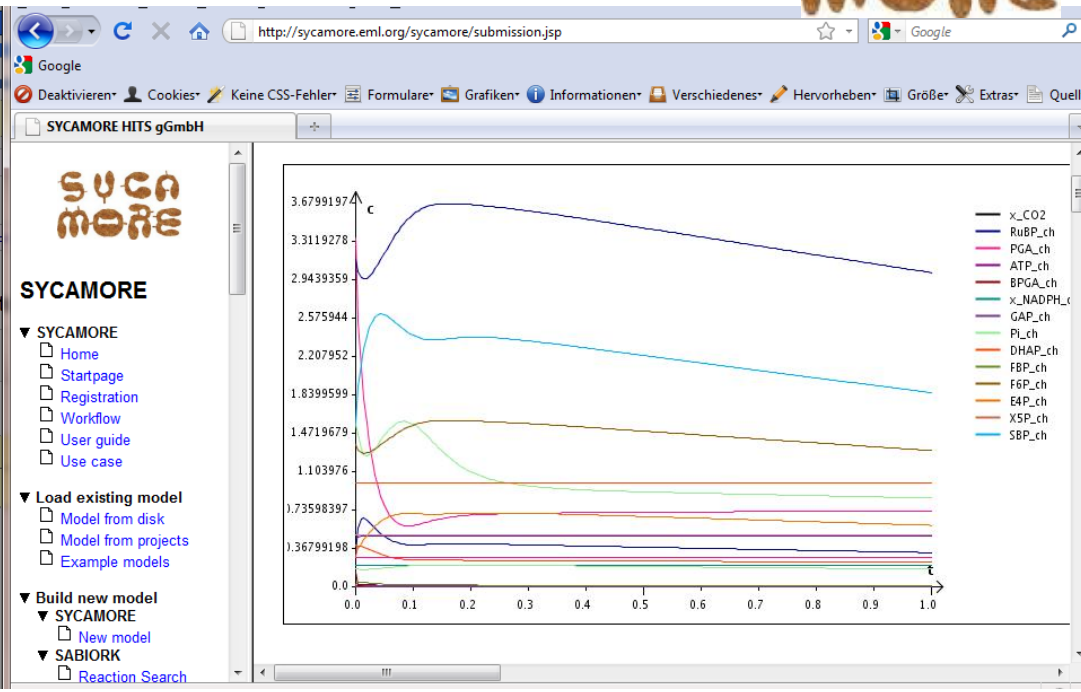


[Jacky Snoep, Dagmar Waltemate, Martin Peters, Martin Scharm]

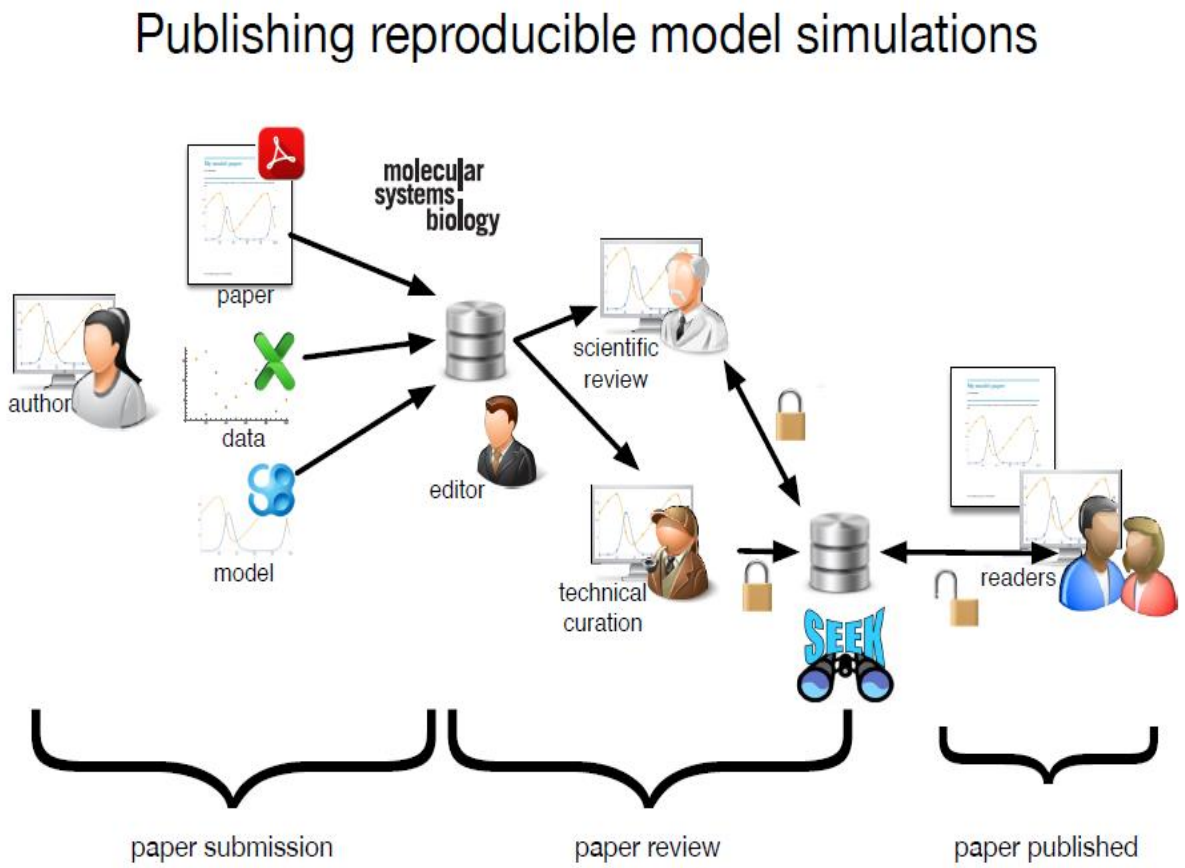
Integration of Modelling Platforms

Models in SEEK can be directly transferred to and subsequently edited, processed and simulated in JWS online, SYCAMORE or Cytoscape Web





Reproducible model simulations in papers using SED-ML



Three tiered service

+ store DOI citable supplementary files on FAIRDOMHub

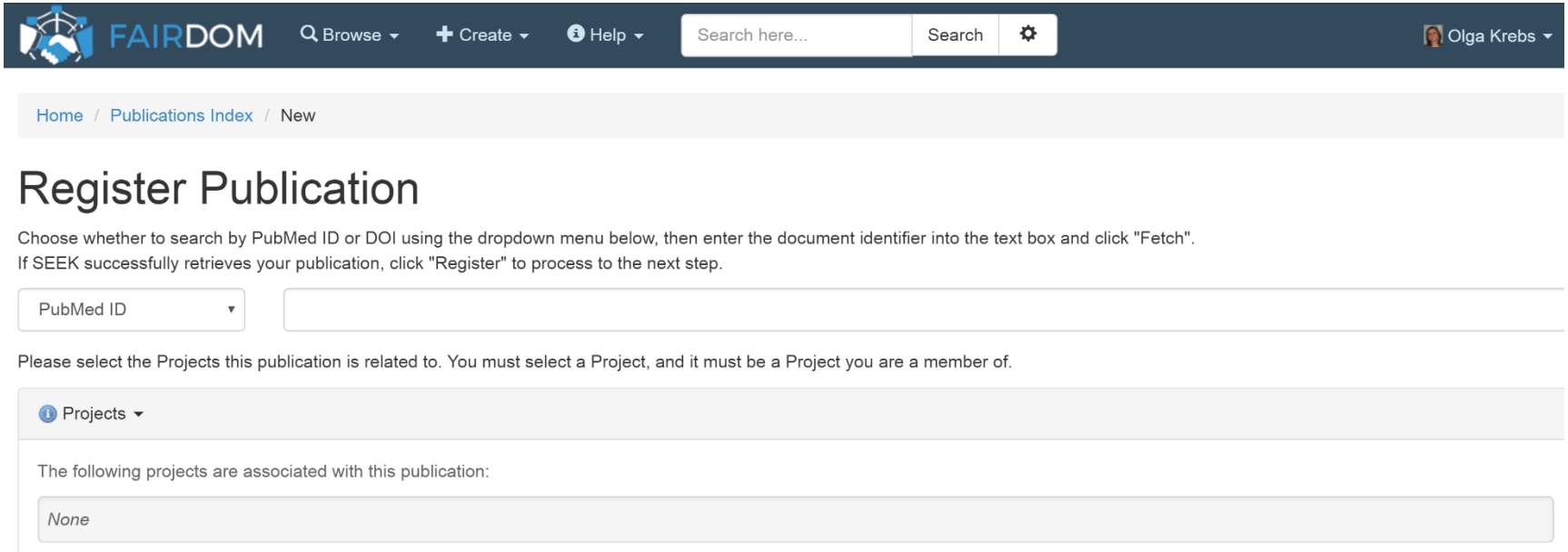
++ model and data curation

+++ reproducible clickable figures in papers using SED-ML

[Jacky Snoep, Dagmar Waltemath]

FAIRDOM

Register publication in SEEK



Create snapshot and get DOI for your reaseach asset

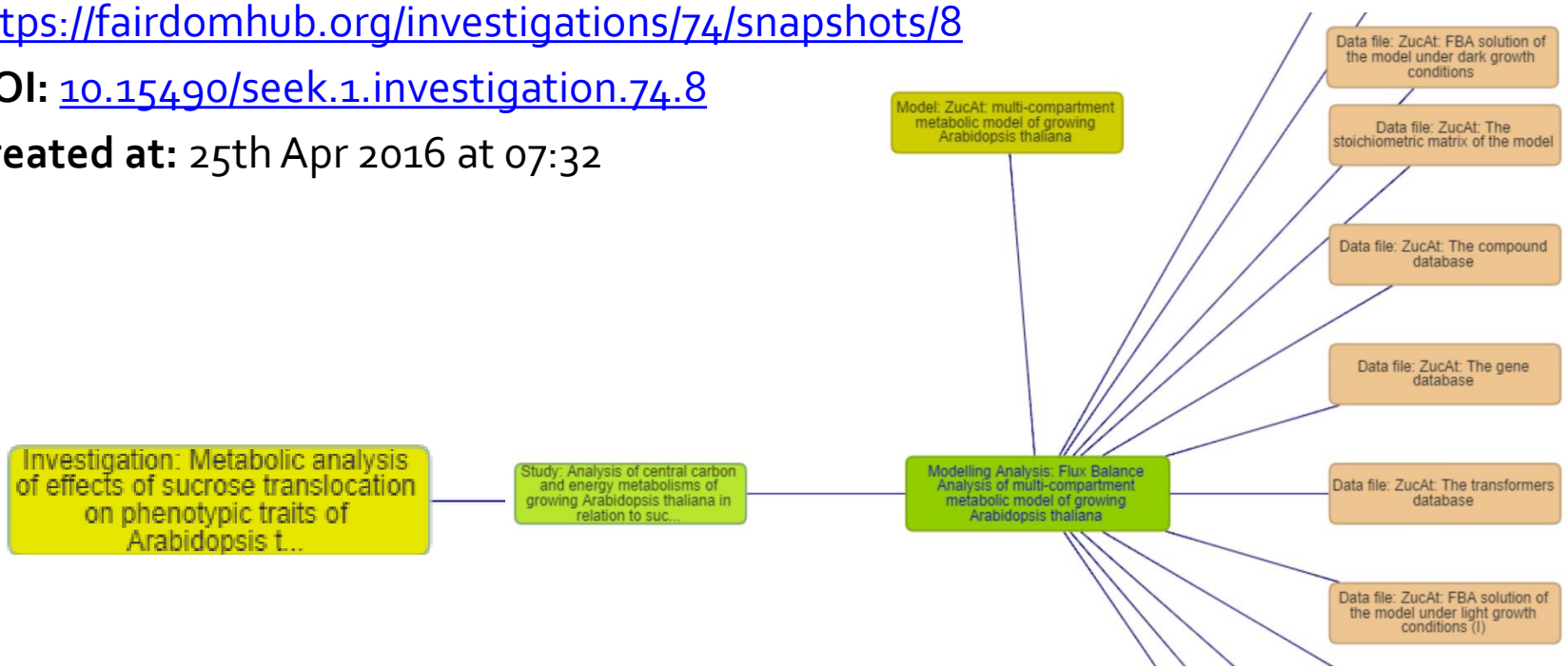
Snapshot 8 (25th Apr 2016)

DOI: 10.15490/seek.1.investigation.74

https://fairdomhub.org/investigations/74/snapshots/8

DOI: 10.15490/seek.1.investigation.74.8

Created at: 25th Apr 2016 at 07:32



the FEBS Journal

Construction and validation of a detailed kinetic model of glycolysis in *Plasmodium falciparum*

Gerald Penkler[1,2], Francois du Toit[1], Waldo Adams[1], Marina Rautenbach[1], Daniel C. Palm[1], David D. van Niekerk[1] and Jacky L. Snoep[1,2,3]

1 Department of Biochemistry, Stellenbosch University, Matieland, South Africa
2 Molecular Cell Physiology, Vrije Universiteit Amsterdam, The Netherlands
3 MIB, University of Manchester, UK

https://doi.org/10.15490/seek.1.investigation.56

Keywords
enzyme kinetics; glucose metabolism; model workflow; mathematical model; systems biology

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(Received 19 August 2014, revised 7 February 2015, accepted 13 February 2015)

doi:10.1111/febs.13237

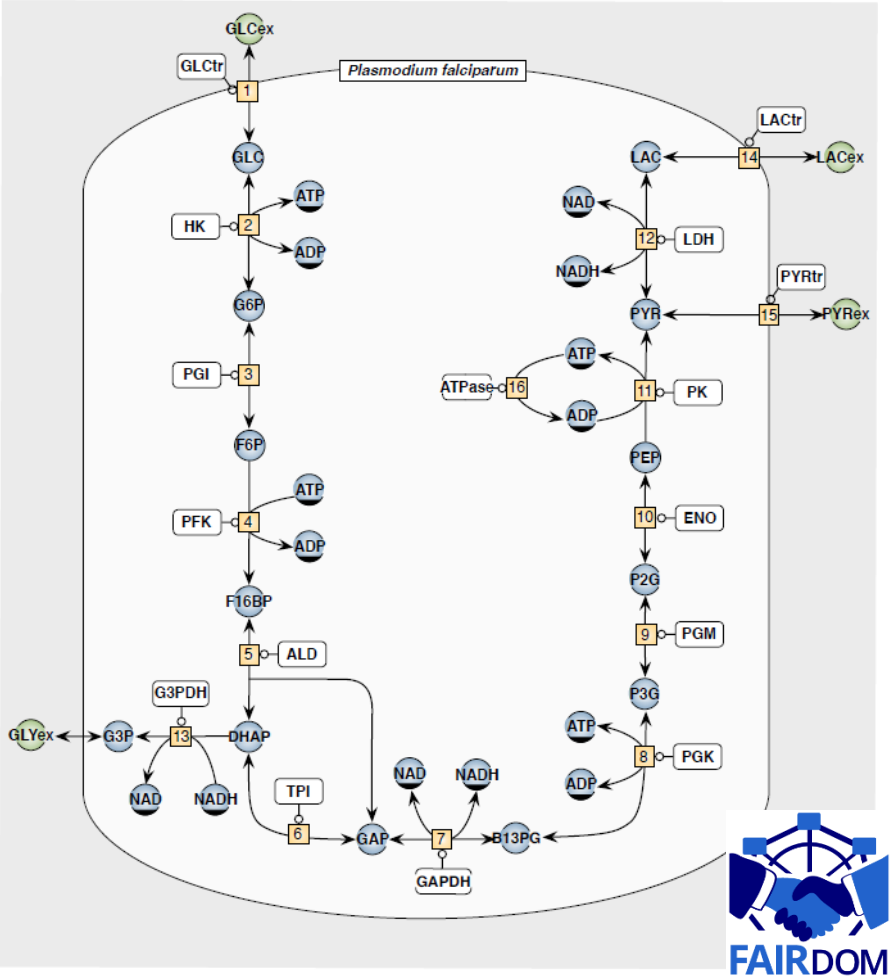
The enzymes in the Embden–Meyerhof–Parnas pathway of *Plasmodium falciparum* trophozoites were kinetically characterized and their integrated activities analyzed in a mathematical model. For validation of the model, we compared model predictions for steady-state fluxes and metabolite concentrations of the hexose phosphates with experimental values for intact parasites. The model, which is completely based on kinetic parameters that were measured for the individual enzymes, gives an accurate prediction of the steady-state fluxes and intermediate concentrations. This is the first detailed kinetic model for glucose metabolism in *P. falciparum*, one of the most prolific malaria-causing protozoa, and the high predictive power of the model makes it a strong tool for future drug target identification studies. The modelling workflow is transparent and reproducible, and completely documented in the SEEK platform, where all experimental data and model files are available for download.

Database
The mathematical models described in the present study have been submitted to the JWS Online Cellular Systems Modelling Database (http://jjj.bio.vu.nl/database/penkler). The investigation and complete experimental data set is available on SEEK (10.15490/seek.1.investigation.56).

Introduction

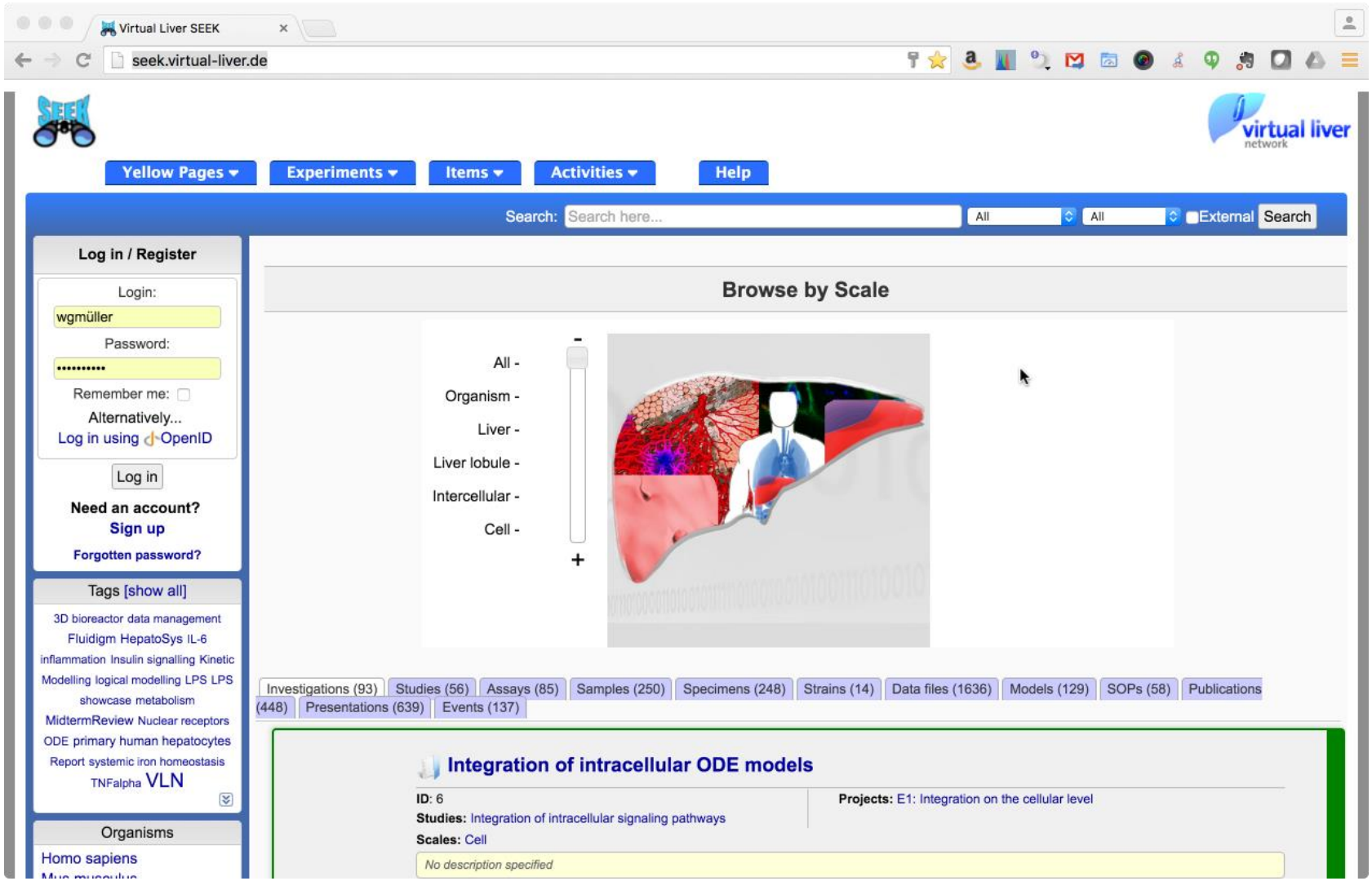
Despite several attempts at a complete eradication of the disease, malaria is still killing more than half a million people per year, mostly small children in sub-saharan Africa (World Health Organisation Malaria report 2013, http://www.who.int/malaria/publications/world_malaria_report_2013/en/). The disease is caused by parasitic protozoa of the *Plasmodium* genus, which have a complicated life cycle consisting of an insect vector and vertebrate host [1]. In the human host, parasite sporozoites first invade liver cells, but the malaria disease symptoms manifest only at a later stage during multiplication of the asexual stages of the parasite in red blood cells (RBCs). The blood life cycle consists of ring, trophozoite and schizont stages, and subsequent

Abbreviations
2PG, 2-phosphoglycerate; 3PG, 3-phosphoglycerate; ALD, fructose-bisphosphate aldolase; B13PG, 1,3-bisphosphoglycerate; DHAP, glycerone phosphate; ENO, phosphopyruvate hydratase; F16BP, fructose 1,6-bisphosphate; F6P, fructose 6-phosphate; G3P, glycerol 3-phosphate; G3PDH, glycerol 3-phosphate dehydrogenase; G6P, glucose 6-phosphate; GAP, D-glyceraldehyde 3-phosphate; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; GLC, glucose; GLY, glycerol; HK, hexokinase; LAC, lactate; LDH, lactate dehydrogenase; MCT, monocarboxylate transporter; ODE, ordinary differential equation; PEP, phosphoenolpyruvate; PFK, 6-phosphofructokinase; PGI, glucose 6-phosphate isomerase; PGK, phosphoglycerate kinase; PGM, phosphoglycerate mutase; PK, pyruvate kinase; PYR, pyruvate; RBC, red blood cell; TCA, tricarboxylic acid; TPI, triose-phosphate isomerase.

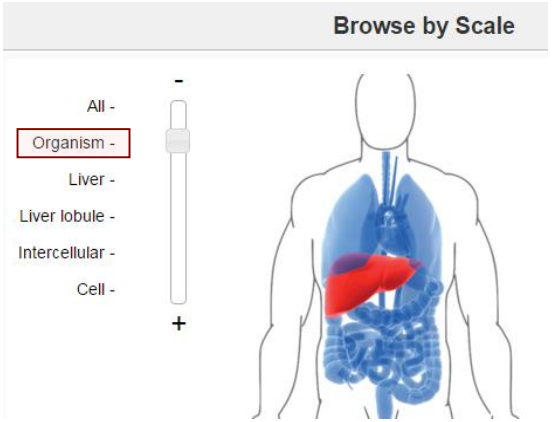


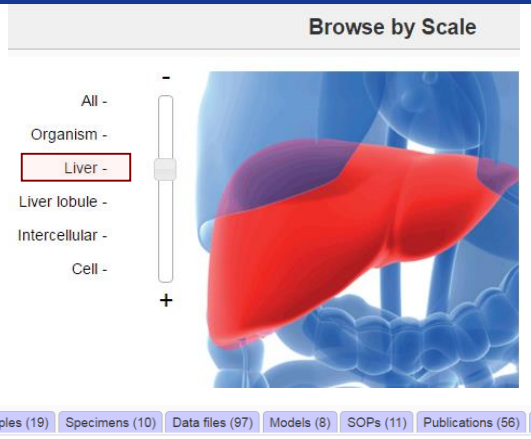
Penkler et al (2015) FEBSJ 282:1481-1511.

Example: Virtual Liver SEEK



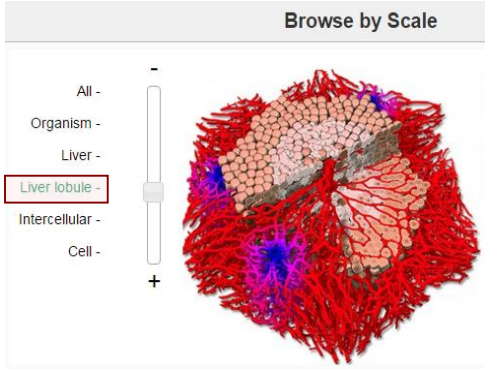
Virtual Liver Data - browse by scale

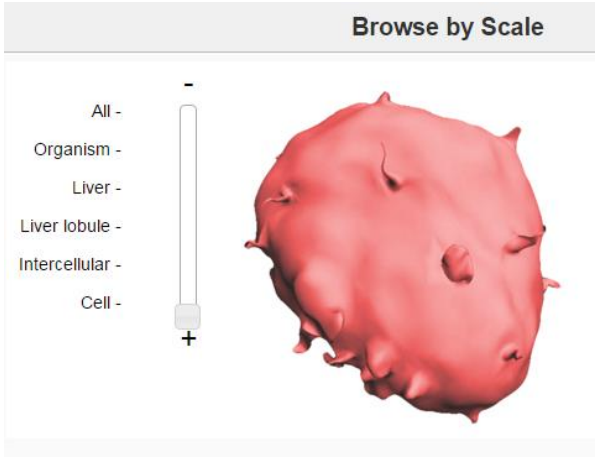




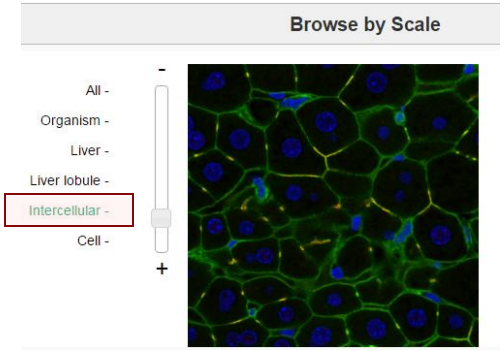
Investigations (8) | Studies (12) | Assays (14) | Samples (19) | Specimens (10) | Data files (97) | Models (8) | SOPs (11) | Publications (56) | Presentations (99)

Investigations (3) | Studies (1) | Specimens (26) | Data files (19) | Models (9) | SOPs (7) | Publications (28) | Presentations (64)





Investigations (25) | Studies (35) | Assays (45) | Samples (32) | Specimens (16) | Data files (284) | Models (86) | SOPs (26) | Publications (158) | Presentations (210)



SEEK for NMTrypI

Ulrike Wittig

New Medicines
for Trypanosomatidic Infections

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NEWS

Drug Development for Neglected Parasitic Diseases Funded projects, Modena, June 2016

Location: UNIMORE, Modena, Italy
Start day: 15-06-16
End Day: 16-06-16
For more information please click here

1 2

PRESS & PUBLICATIONS

NMTrypI communication and dissemination activities

The complete list of communication and dissemination activities of NMTrypI project is available here. For additional information, please visit the "news and events" session.

NMTRYPI PROJECT

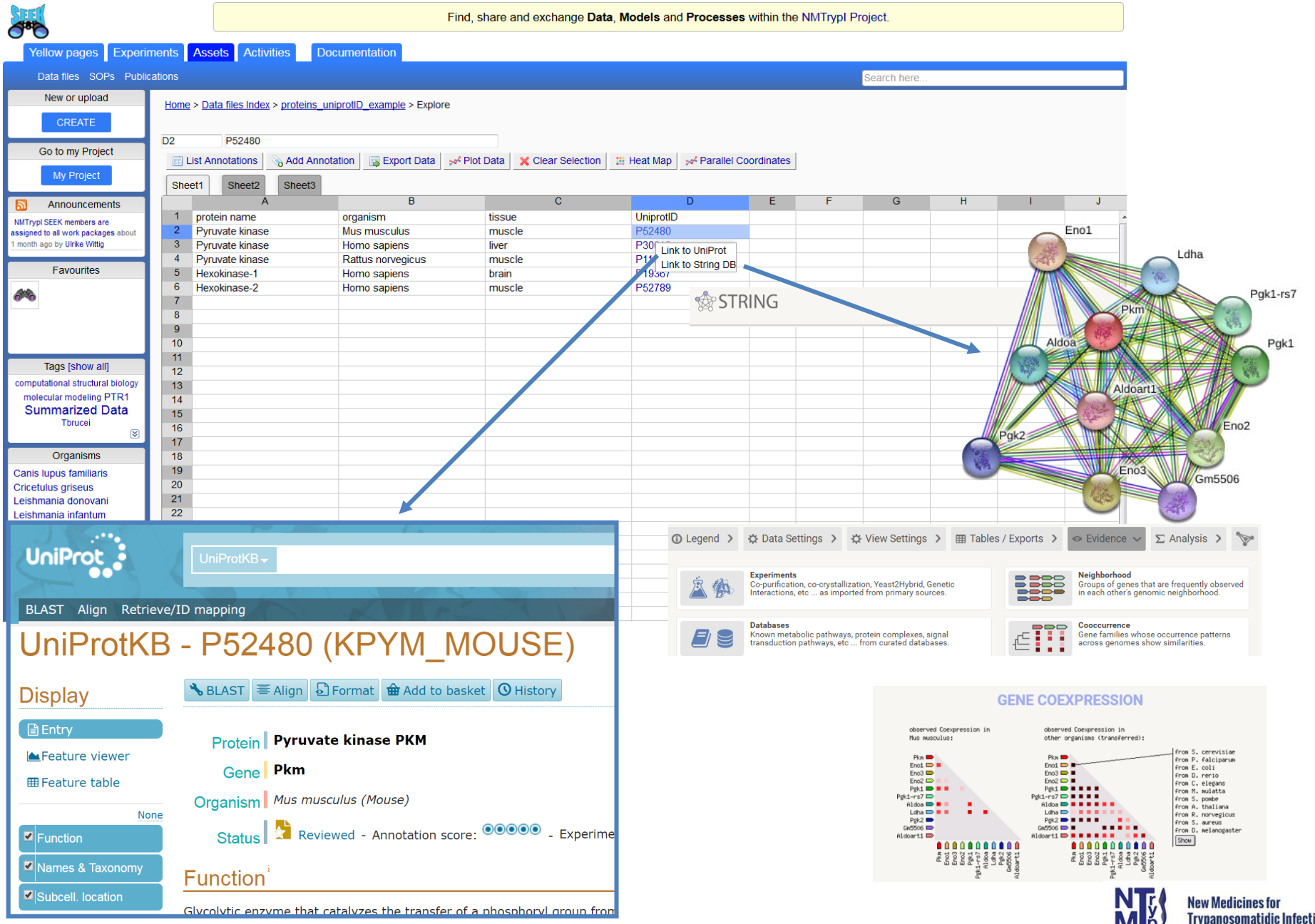
ABSTRACT

The **NMTrypI concept** is based on the development of **innovative drug leads** including a mechanism-based combination of a known and investigational drug and dual targets inhibitionby using a **common drug discovery platform.** The platform is established by experts in their respective fields from SMEs and the public research sector in Europe and in disease-endemic countries.

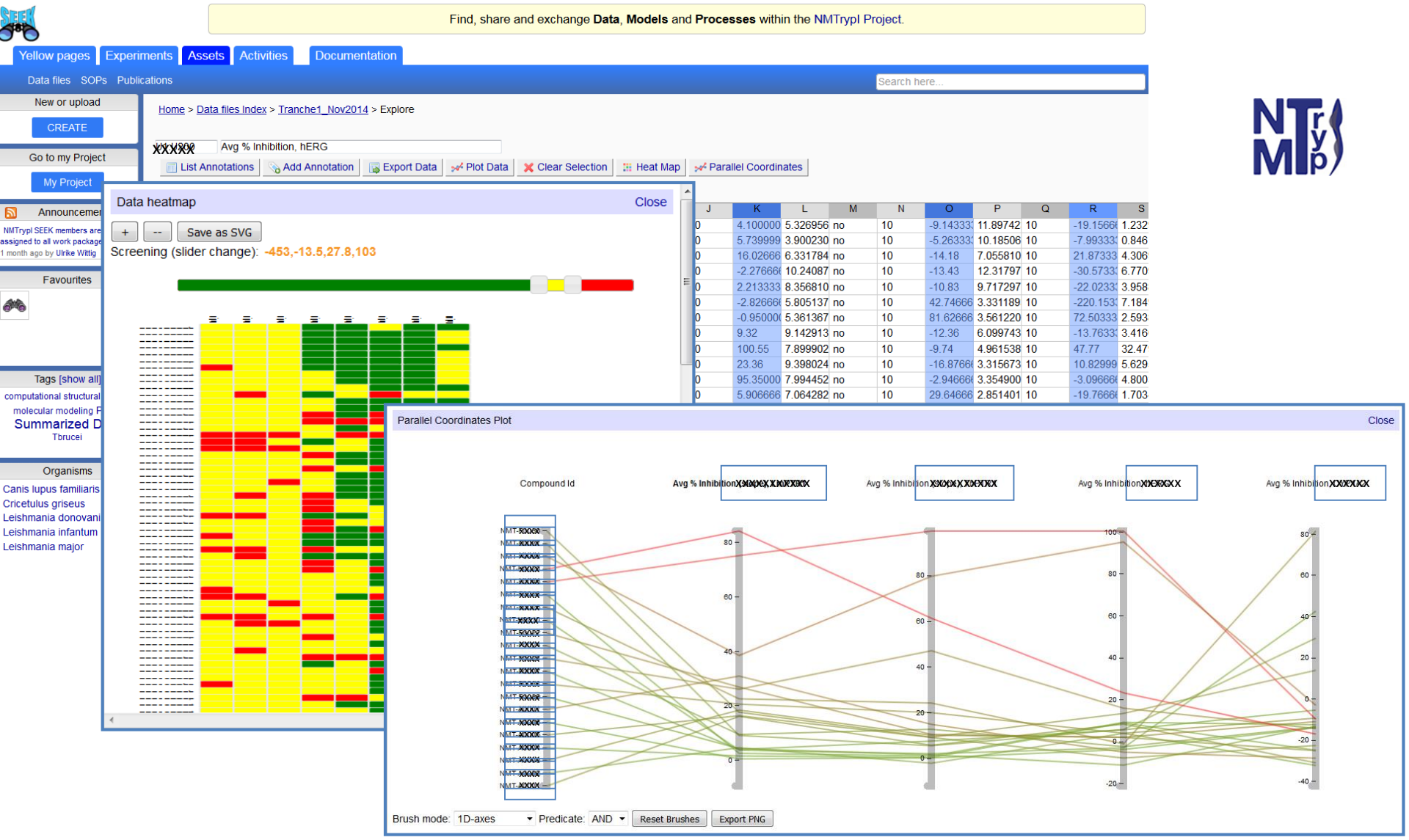
The innovative concept is reinforced by the identification of preclinical **biomarkers** enabling the proteomic profiling of the compound to understand the mechanism of action (MoA biomarker) and to detect the efficacy of the lead candidate (pharmacodynamic biomarkers).

The new NMTrypI platform will perform the screening of compound libraries, lead development, testing in mice, hamsters and dogs as a reservoir of the visceral leishmaniasis disease as well as **toxicology** and **safety testing** (*in vitro* against cellular types and *in vivo* in animals) to overcome current limitations in

Automatic detection of protein IDs and link to UniprotKB and StringDB



Visualization of enzyme inhibition by different compounds (in %)
Heat map + Parallel coordinates plot



J	K	L	M	N	O	P	Q	R	S
0	4.100000	5.326956	no	10	-9.14333	11.89742	10	-19.1566	1.232
0	5.739999	3.900230	no	10	-5.26333	10.18506	10	-7.99333	0.846
0	16.02666	6.331784	no	10	-14.18	7.055810	10	21.87333	4.306
0	-2.27666	10.24087	no	10	-13.43	12.31797	10	-30.5733	6.770
0	2.213333	8.356810	no	10	-10.83	9.717297	10	-22.0233	3.958
0	-2.82666	5.805137	no	10	42.74666	3.331189	10	-220.153	7.184
0	-0.95000	5.361367	no	10	81.62666	3.561220	10	72.50333	2.593
0	9.32	9.142913	no	10	-12.36	6.099743	10	-13.7633	3.416
0	100.55	7.899902	no	10	-9.74	4.961538	10	47.77	32.47
0	23.36	9.398024	no	10	-16.8766	3.315673	10	10.82999	5.629
0	95.35000	7.994452	no	10	-2.94666	3.354900	10	-3.09666	4.800
0	5.906666	7.064282	no	10	29.64666	2.851401	10	-19.7666	1.703

We help to build/judge DMM plans

FAIRDOM

Data management checklist

ERASysAPP DMMcore checklist document

The goal of this checklist is to help facilitate the planning and writing of the Data and Model Management part of an ERASysAPP proposal.
For any questions, please contact ptj-dmmcore@fz-juelich.de or participate in the DMMcore webinars (go to registration for webinars).

There will be a centrally funded DMMCore project which plans to offer the following facilities to all projects:

Data management

- Management facilities for project data
- Secure and private storage and management of your data
- First-class management of spreadsheet data
- Permanent storage and management of large scale data up to 1.5TB/Project (for dedicated storage of data beyond 1.5TB/Project, please contact ptj-dmmcore@fz-juelich.de. The data is kept 10 years beyond the project lifetime.

Metadata management

- Linking to data stored at outside resources
- Interlinking and management of SOPs, data, models, people, projects, publications
- Cataloguing and metadata management of data, models and SOPs
- Support with use of standards and vocabularies.

Curation support

DMM checklist

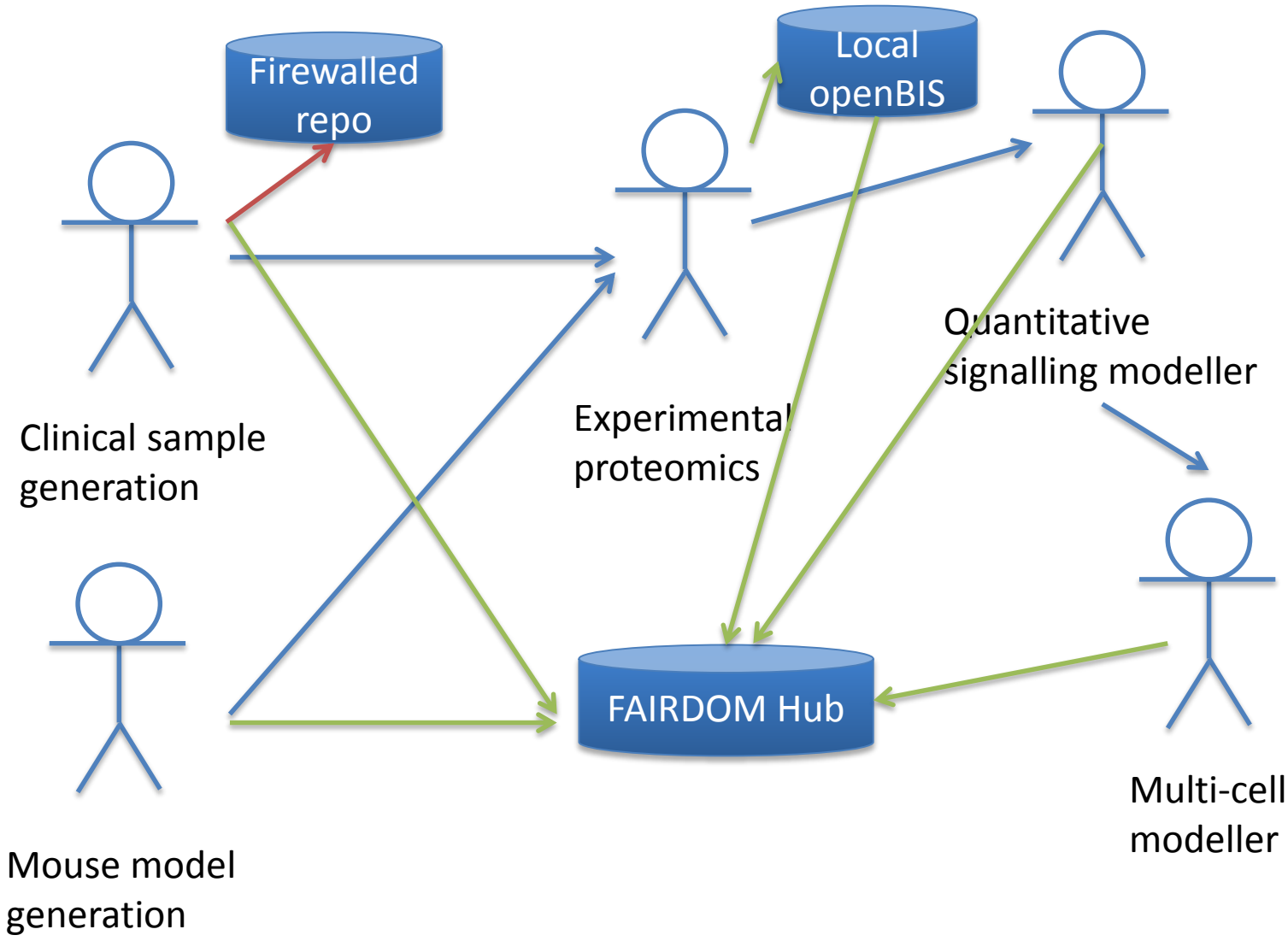
Questions about

- Amount of Data/Model/SOP **storage**
- About data **flows**
- About **Meta** data needs
- About **sequence** of needs
- About people responsible (contacts) for DMM

- Needs judges with experience

FAIRDOM

Example: How is the data flow?

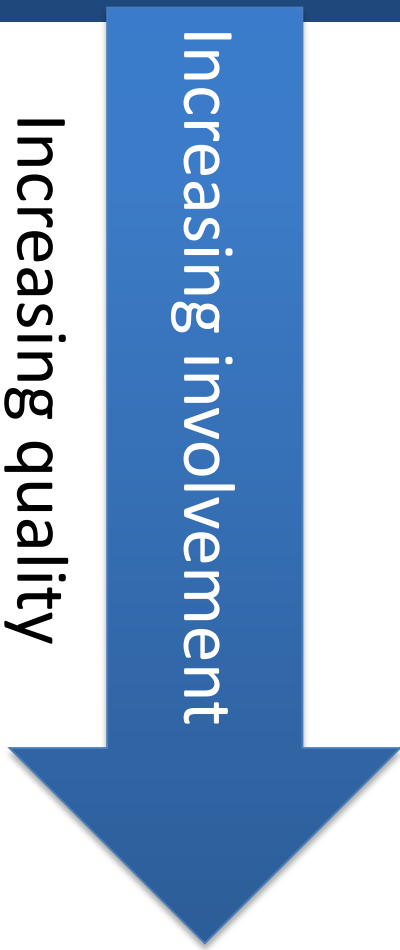


Tiers of possible support

FAIRDOM

Three tiers of possible support

- **Best effort** tier:
  - Feasible with current resources
  - In completely line with our remit
  - No specific support
- **Subcontract** tier: Requires Subcontract
  - Close to our remit
  - Not feasible with our current resources
  - Short-term/punctual
- **Partnership** tier: Requires Partnership
  - Not feasible with our current resources
  - Long-term/continuous



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Tiers software platform

Tier	Proposed
Best effort	• Get and install software from GitHub repository • Use FAIRDOM Hub • Suggestions/Extensions exactly fitting our roadmap
Subcontract	• Small modifications to FAIRDOM Hub • Small extensions
Partnership	• Continuous development support (as above, but all the time)

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Tiers FAIRDOM Hub

Tier	Proposed
Best effort	• Use FAIRDOM Hub with small storage requirement • Few support requests (not realistic)
Subcontract	• Extension for disk space & backup • Support requests beyond „best effort“
Partnership	• Continuous support

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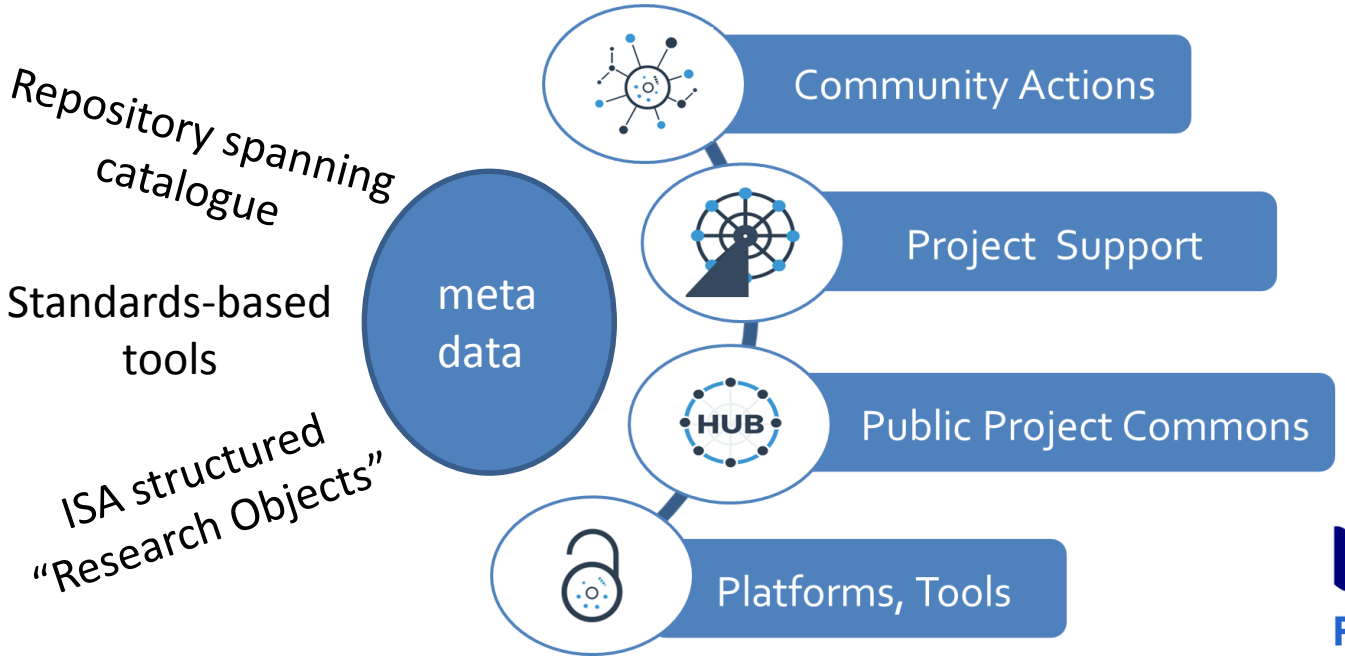
Tiers Community / Service

Tier	Proposed
Best effort	• Participate in FAIRDOM events on own cost • Proposal of topics for FAIRDOM events • Receiving best effort basis support (limited resources)
Subcontract	• Pre-call data management webinars • Proposal support • Organise events geared towards ERACoSysMed
Partnership	• Building PALs program • Collecting requirements • Help in curation • Proposing solutions • Helping with plans • Make plans work • Wider community activities

FAIRDOM

In summary…Pragmatic FAIR support for projects *people, assets, processes*

- *Multiple, interrelated assets*
- *Multiple, dispersed repositories*
- *Multi-partner, -discipline projects*
- *Multiple community tools*
- *Team science practices*
- *Experiment – Asset lifecycles*
- *Academic innovation drivers*



FAIRDOM

Developers Foundry Meeting

- **Time:**
  December 1st, 10:00
  December 2nd, 15:00

- **Location:** **Next to Frankfurt Main Station**

- **Contact:** **wolfgang.mueller@h-its.org**

FAIRDOM

Working together

Contact mail

- fairdom@fair-dom.org

Web site

- http://fair-dom.org

FAIRDOM Hub

- http://www.fairdomhub.org

Let’s try it - Hands On