EMERGENCE: A foundation for Synthetic Biology in Europe

WP1: General Networking activities

Fostering a community of knowledge

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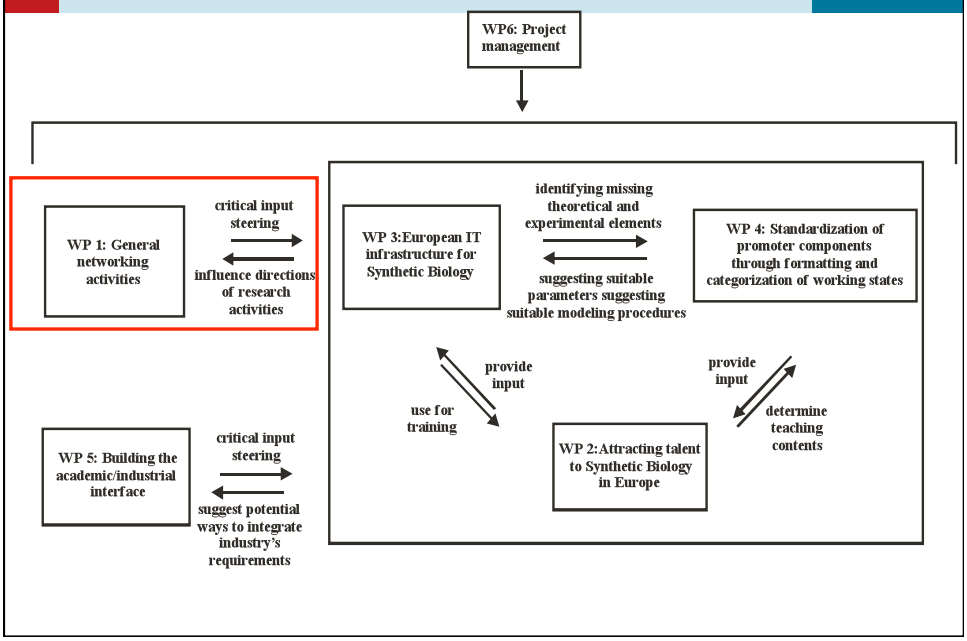
Project Structure



WP1: General Networking Activities

Objectives:

a) To establish a networking platform for current and future synthetic biology projects

b) To rapidly organize workshops for urgent issues in European synthetic biology

c) To implement a Europe-wide, cross-disciplinary framework for discussion on the possibilities, needs, limitations, and implications of synthetic biology.

d) To foster interactions with extra-European initiatives, with special emphasis on US, the Mid-East and Asia: Global knowledge space

Description of Tasks I

Task 1: ***Developing, maintaining, and evaluating a standardized meeting structure*** that allows efficient review and distribution of the conclusions obtained at individual meetings.

Overarching, jointly with WP Management

Task 2: ***Hosting workshops on development of the European IT infrastructure for synthetic biology, design tools for synthetic biology, and/or standardization of biological parts.***

Jointly with WP3 (IT infrastructure), WP4 (Design tools and Biological parts), Standardisation Issues (Overarching)

Description of Tasks II

Task 3: ***Establishment of study groups on specific subjects relevant to synthetic biology***

"Foundational" technologies, including e.g. high-throughput genome minimization,
DNA synthesis),
potential of genetic circuits, modularity in proteins, handling noise & error
propagation in biological systems,
robustness in biological systems,
transferability of engineering foundations
……...

Description of Tasks II

Task 4: ***Platform for organizing thematic workshops/courses/ meetings, resulting from maturation of study groups into specific workshops***, courses, or small scientific meetings, or from initiatives from members of the advisory board or the steering committee.

Task 5: ***EMERGENCE will promote exchange and training visits between European and overseas participants***, in particular with the Middle East and Asia, including:

•invitations for a number of leading scientists in the field to participate in study groups;
•seeking actively to participate in similar initiatives in those countries; and inclusion of Middle Eastern/Asian researchers in the EMERGENCE
•communication and dissemination pipelines.
•The participation of senior European synthetic biology scientists in Asian meetings will be particularly encouraged.

Deliverables Month 1-18

D1.1: Material and rules for standardized meeting structure in place for the first time (month 3). Responsible: HZI

D1.2: Report on the first workshop on development of the European IT infrastructure for synthetic biology (month 8) Responsible: HZI

D1.3: Report on the first workshop for design tools for synthetic biology (month 4) Responsible: CNIO

D1.4. Report on recommendations of the intra-consortium expert group on suitable promoter standardization formats (month 12) Responsible: CNB

Deliverables 18-36 month

D1.5: Updated material for the appropriate section in the quarterly Synthetic Biology Newsletter regarding tasks 2, 3, and 4 (months 3, 6, 9, 12, etc): Responsible ETH (half-yearly)

D1.6. Report on workshop on foundations of measurement statistics in synthetic biology (month 24→ month 36) Responsible CNB (V. de Lorenzo)

D1.7. Document identifying "common European-Asian interests and ways to develop them" or similar document in place and signed by extra-European and European groups/organizations involved in synthetic biology (month 32 → 36)

Milestones and expected results

M1.1. **Recommendations for the European IT infrastructure for synthetic biology** are discussed and recommendations issued (month 3)

M1.2. **Recommendations for design tools on the IT infrastructure** are discussed and recommendations issued (month 4)

M1.3 **First experiences with the study group format** are reviewed by the steering committee after 6 months and by advisory board and steering committee after 12 months and the format is adapted, if necessary (month 6, 12)

M1.4. **Recommendations on standardization of biological parts** are discussed (month 11)

M1.5. **Recommendations on measurement systems in synthetic biology** are discussed (month 24)

M1.6. Steering committee and advisory board decide whether the **critical mass in Europe-Asian relations in synthetic biology** has been reached and drafting a "common interests" document is going to be useful (month 24)

D1.1 - Material and rules for standardized meeting structure

Web-based template document:

Definition of the theme and Scope

The need for the SynBio community and goals

Implementation plan (size, mode, participants

Timeline

Financing possibilities

Process:
Submission to Steering committee (WP-leaders, Coordinator)

Eg. IT: A. Valencia; Teaching: Sven P.; INdustry: L. Pasamontes

D1.1 - Material and rules for standardized meeting structure: examples themes

Tier	Theme	Number of Participants	Length	Contribution to Emergence	Deliverable	Estimated Cost (€)	Financial contribution requested (€)	WP

Tier means 1 - initial, 2 - follow-up or 3 - full meeting
WP means the Work package to which the proposed meeting would contribute

minimal genomes / minimal systems

what to measure / how to measure?

design concepts
how can we handle "systems" (made of parts)?

context-independent biological systems/ modules

microfluidics technologies / single cell measurents

D1.2 -Report on workshop on development of the European IT infrastructure for synthetic biology

Workshop Computational Infrastructure and Methods for Synthetic Biology

The 9th Annual BioPathways Meeting

Vítor Martins dos Santos
Vincent Schachter
Vincent Danos
Joanne Luciano
Aviv Regev
Eric Neumann

July 19-20, 2008
Satellite Meeting ISMB 2008
Toronto, Canada

7:30 – 8:30	**Registration**	
8:30-8:45	VÍtor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig, DE	Opening remarks
Session 1 & Analysis : **Databases & Software Tools** Chair: VÍtor Martins dos Santos		
8:45-09:30	Trey Ideker, University California San Diego, USA	Mapping pathways through integration of physical and genetic interactions
9:30-10:15	Peter Karp, AI.SRI, Menlo Park, USA	The MetaCyc and BioCyc database collection
10:15-10:45	**Coffee Break**	
10:45-11:30	Phillip Bourne, University California San Diego, USA	The role of biopathways in drug repositioning and determining side effects
11:30-12:00	Geoffrey Winsor, Simon Fraser University, CA	InnateDB - Facilitating Systems Level Analyses of the Mammalian Innate Immune Response
12:00-12:30	Jennifer Gardy, Centre for Microbial Diseases & Immunity Research, University of British Columbia, CA	Cerebral 2.0: A Cytoscape plugin for the network-based visualization of datasets from multiple experimental conditions
12:30-13:30	**Lunch**	
Session 2: Network Reconstruction & Analysis Chair: Eric Neumann, Teranode		
13:30-14:10	Rune Linding – Institute for Cancer Reseatrch, London, UK	Constructing in vivo phosphorylation networks
14:10-14:50	Terry Gasterland, University California at San Diego, USA	Examining Cell Cycle Control Networks at Single Cell Resolution
14:50-15:30	Kobi Benenson, Harvard University, Cambridge, USA	Molecular automata: from concepts to applications
15:30-16:00	**Coffee Break**	
16:00-16:35	Ran Kafri, Harvard Medical School, Boston, USA	Functional redundancies - an evolutionarily conserved control element in signal transduction and metabolism
16:35-17:05	Tijana Milenković, Nataša Pržulj, University California Irvine, USA	From network structure to biological function in protein-protein interaction networks
17:05-17:35	Jean Krivine, Harvard Medical School, Boston, USA	Rule-based modeling of large protein networks
17:35-18:15	Peer Bork, EMBL, Heidleberg, DE	Get the most out of your metagenome: computational analysis of environmental sequence data
General Discussion		
18:15-18:30	**Network analysis, Databases & Tools**	

Session 3 : Computational Methods and Infrastructure for Synthetic Biology Chair: Kobi Benenson, Bauer Centre		
8:30-9:00	Vitor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig, DE	EMERGENCE: a Foundation for Synthetic Biology in Europe
9:00-9:40	Randy Rettberg, MIT, Cambridge, USA	Synthetic Biology Based on Standard Parts: Design Competitions and Catalogs
9:40-10:15	Ildefonso Cases, CNIO, Madrid, ES	Bioinformatics tools to help in the design of biological systems
10:15-10:45	**Coffee Break**	
10:45-11:25	Shoshana Wodak, Hospital Sick Children, Toronto, CA	Identifying meaningful pathways in metabolic networks without the help of chemistry
11:25-12:00	David Gilbert, University of Glasgow, UK	A behaviour driven approach to design and implementation in Synthetic Biology
12:00-12:30	Martijn van Iersel, University of Maastricht, NL	WikiPathways, pathway creation and online collaboration
12:30-13:30	**Lunch**	
Session 4: Evolution of pathways and networks Chair: Joanne Luciano, MITRE		
13:30-14:15	Chris Sander, Sloan-Kettering, New York, USA	Systems biology modeling
14:15-14:50	Edwin Wang, National Research Council, McGill University, Montreal, CA	Principles of microRNA regulation of cellular networks
14:50-15:30	Chris Myers, Cornell University, USA	Sloppiness in cellular networks
15:30-16:00	**Coffee Break**	
15:30-16:05	Matthew de Jongh, Hope College, Holland (MI), USA	Generation and Refinement of Metabolic Reaction Networks in the SEED
16:05-16:35	Andrey Ptitsyn, Colorado State University, Fort Collins, USA	The Structure of Biological Pathways in Time
16:35-17:10	Zhenjun Hu, Boston University, USA	Metagraph: a new graph structure for multiple-scale visualization and modeling of biological networks/pathways
17:10-17:45	Pedro Beltrao, University California San Francisco	Evolution of Cellular Networks
Round Table Discussion		
17:45-18:30	**Network Reconstruction, Pathways and Evolution**	

D1.3 - Report on workshop for design tools for synthetic biology (CNB)

Satellite meeting to the ESF – EMBO on SynBio

November 2007

(Alfonso, Jörg, Randy, etc)

Report finished (CNIO)

D1.4 - Report on recommendations of the intra-consortium expert group on suitable promoter standardization formats (CNB)

VDL – Done

Plus: Silva-Rocha R, de Lorenzo V.
Mining logic gates in prokaryotic transcriptional regulation networks.
FEBS Lett. 2008 Apr 9;582(8):1237-44.

Meeting on Promoter standards (Mallorca, October 2009, VDL)

D1.5 -Updated material for the appropriate section in the quarterly Synthetic Biology Newsletter regarding tasks 2, 3, and 4

Frauke Greve / Sven Panke

Newsletters Dec 2006, June 2007, Dec 2008, June & November 2009

Includes list of conferences, research highlights, press releases, funding activities

D1.6. Report on Sandpit on foundations of measurement statistics in synthetic biology

Workshop on Transcription Standards: setting criteria for measuring and exploiting promoter activity in engineered prokaryotic systems

Took place in Mallorca, 21-22 October 2009

Experts on transcription (Virgil Rhodius, Ido Golding Steve Busby, Martin Buck, Hiroshi Aiba)

"vs"

"Parts" school (Ron Weiss, Cristina Smolke, Ron Weiss)

Plus: VDL, SP, VMdS

Workshop on Streamlining and Constructing Genomes

Jointly organised with TARPOL

To take place in Valencia, 16-17 November, 2009

Workshop on Streamlining and Constructing Genomes

Time	16 November	17 November
09:30	A. Moya – V. Martins dos Santos **Introductory remarks**	
	Session 1: Synthetic and Digital Biology Chair: V. Martins dos Santos	**Session 3. Building Genomes** Chair: P. Dennis (? To confirm)
09:30	C. Venter (?)	H. Smith **Making a synthetic cell: building the genome**
10:00	S. Rasmussen **Assembly of a minimal protocell bottom up**	C.A. Hutchison **Making a synthetic cell: installing the genome**
10:30	S. Mansy **Minimal cells from the bottom-up**	I. Itaya **Recombinant genomes produced via novel *Bacillus subtilis* genome vector**
11:00	Coffee break	Coffee break
11:30	A. Danchin **Toward a synthetic cell: information of the program and information of the machine**	B. Wanner **New resources and methods for *E. coli* functional genomics**
12:00	N. Krasnogor **Incremental model building with algorithmic systems biology**	L. Serrano ***M. pneumoniae* systems biology analysis**
13:00	Round table	Round table
14:00	Lunch	Lunch

Workshop on Streamlining and Constructing Genomes

14:00	Lunch	Lunch
	Session 2. Streamlining Genomes Chair: V. de Lorenzo	**Session 4. Circuit Design and Evolution** Chair: L. Serrano
14:30	G. Posfai **Engineering the evolvability of a streamlined genome**	V. Martins dos Santos **Streamlining and re-programming microbial catalysts**
15:00	B. Papp **Systems biology modelling of minimized genomes**	F. de la Cruz **Architecture and design of plasmid transcriptional networks**
15:30	T. Dandekar **Streamlining genomes: several different roads and one goal**	A. Moya **Learning from natural minimal cells**
16:00	Coffee break	Coffee break
16:30	P. Noirot **Model-driven minimization of the *Bacillus subtilis* genome**	T. Gabaldón **Using comparative genomics to study the evolution of cellular metabolisms**
17:00	R. Wagner **Optimized biobricks for functional genomics and industrial applications**	V. de Lorenzo **Minimization of catabolic functions for biodegradation of aromatic pollutants**
18:00	Round table	Round table

What do we need (on setting transcription standards)?

Reference promoters / RBS
(logic gates) characterised over
range of conditions:
Plac
Tac
Ara
Lux
Ps/Pr
T7
Ribosomal promoters

Set of measurable parameters
(strength, robustness, degree of
orthogonality, etc.)

What do we need (on setting transcription standards)?

Basal promoter activity (Broad host-range plasmids for these promoters / logic gates; lamda att, etc.)

Choice and range of chassis (e.coli, pseudomonas, bacillus, mammalian cells, etc.)

Single cell vs population

Set of characterisation assays (including graded outputs):

RNA-sequencing, ChIP-chip, GFP assays, ß-galactosidase, lux, FISH, qRT-PCR, standardised RBS, etc.

Multidimensional calibration curves (GFP, Miller units, PoPS, etc.)

What do we need (on setting transcription standards)?

Beyond transcription

High throughput,

Towards automation, robotics

Activities towards Task 4 (European Networking)

EUROPEAN SCIENCE FOUNDATION
SETTING SCIENCE AGENDAS FOR EUROPE

UNIVERSITAT DE BARCELONA

RESEARCH CONFERENCES

ESF-UB Conference in Biomedicine

European Conference on Synthetic Biology (ECSB): Design, Programming and Optimisation of Biological Systems

Hotel Eden Roc, Sant Feliu de Guixols • Spain
24-29 November 2007

Chair: **Alfonso Valencia**, CNIO Madrid, ES
Co-Chairs: **Natalio Krasnogor**, University of Nottingham, UK
- **Sven Panke**, ETH, Zürich Institute of Process Engineering, CH
- **Victor de Lorenzo**, Centro Nacional de Biotecnologia, Madrid, ES

www.esf.org/conferences/07241

Activities towards Task 4 (European Networking)

Series of Workshops (co-)sponsored on different aspects of SynBio:

-ESF European Conf. SynBio, S. Feliu, Nov 2007, Co-sponsored
-Biofine (Tessy), Freiburg April 10, 2008 and 16/17 April 2009
-Genopole (Jaramillo), 26-27 June, 2008
-IRGC Workshop on the Risk Governance of Synthetic Biology (26 & 27 June 2008, - Geneva, Switzerland)
-Stakeholder meeting Roadmap SynBio (Tessy), 10 June 2008
-Microfluidics Workshop, May 28/29 UCL, London, (co-sponsored)
-Evolution and Design, Mallorca, October 2009 (co-sponsored)
-Transcription Standards, Mallorca, October 2009 (co-sponsored)
-ESF workshop on Minimal Systems (with A. Moya), Nov 2009, Co-organised/ co-sponsored

Activities towards Task 4 (Global Networking)

Series of Workshops (co-)sponsored or attended on different aspects of SynBio:

-Computational design tools in SynBIO: Sattellite to ISMB 2007, 2008, 2009) - Organisation/Sponsoring

- Synthetic Aproaches to Cellular Functions, Tokyo, 13 October 2006,

Organised jointly by D. Kige (JP), H. Ueda (JP), D. Endy (US), Martins dos Santos („EU“)

-Session on Computational design principles in SynBio at SB4.0, Hong Kong, Nov 2008

-New Directions on SynBio: participation on the NSF/EPSRC Sandpit

-National Academies of Sciences in DC, June 2009

- Active Participation from various EMERGENCE participants in a series of Positions papers, strategic planning, conferences, dissemination, etc.

Further networking activities Asia (broadly)

Sino-German Exploratory Workshop on Synthetic Biology, Hangzhou, China, 2009/2010. Couple to Probactys (EU) and perhaps other projects

To be organised jointly with Huanming Yang (Beijing Genome Institute, CN)

Exchange of students/ scientists:

China (2 students 7 month each plus 2 scientists 1 week in 2007)

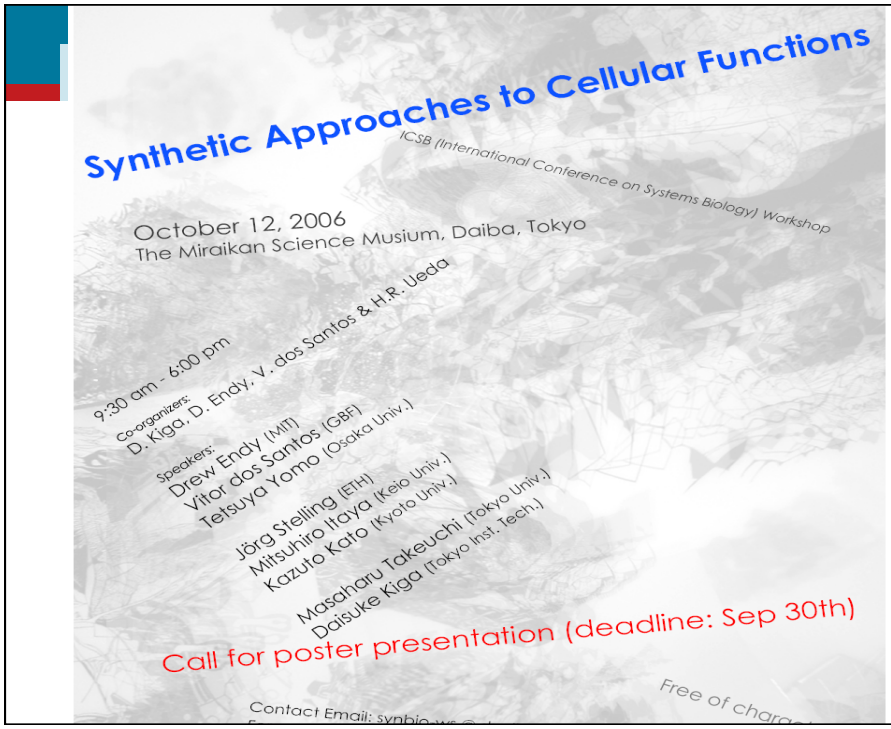
India (2 Students 4 month each, plus scientist 1 week 2008)

Joint HGF-Russia exploratory wokshop Feb 2008

Explorative project in Israel on digital evolving microbial communities

Indian - EU workshop on Synthetic Biology (Early 2010). Meeting brokered at CRG with Minister of Health and Sci Advisore SynBio in July 2008

ESF-JSPS Frontier Science Conference Series for Young Researchers (Synbio tentative for 2011)



Status Deliverables

D1.1: Material and rules for standardized meeting structure in place for the first time (month 3) done

D1.2: Report on the first workshop on development of the European IT infrastructure for synthetic biology (month 9)

D1.3: Report on the first workshop for design tools for synthetic biology (month 12)

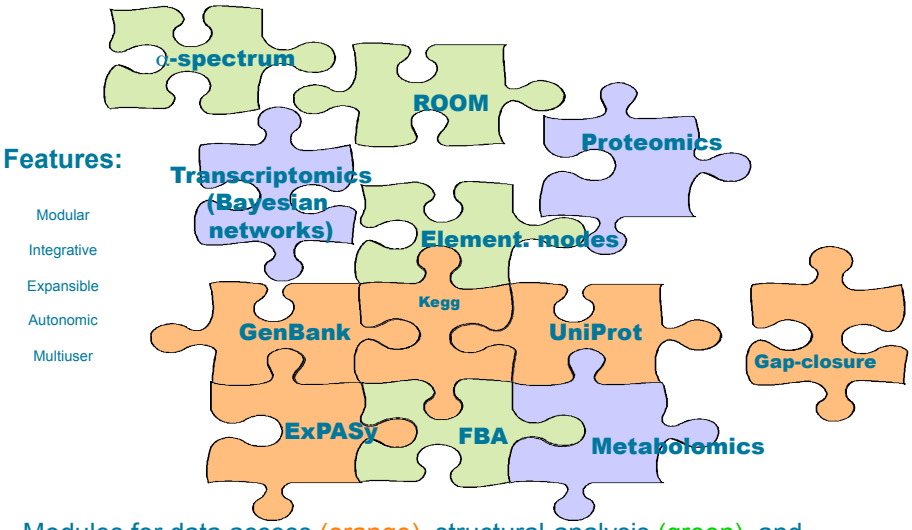
D1.4. Report on recommendations of the intra-consortium expert group on suitable promoter standardization formats (month 15)

D1.5: Updated material for the appropriate section in the quarterly Synthetic Biology Newsletter regarding tasks 2, 3, and 4 (months 3, 6, 9, 12, etc)

D1.6. Report on workshop on foundations of measurement statistics in synthetic biology (month 24) D1.7. Document identifying “common European-Asian interests and ways to develop them” or similar document in place and signin synthetic biology (month 32→ 36). Underway (VDL)

D 1.7 Document identifying “common European-Asian interest and ways to develop them” or similar document in place and signed by extra-European and European groups/organizations involved in synthetic biology. Underway

Contribution to WP3: ToBiN – A Toolbox for Genome-wide Analysis of Biochemical Networks



Features:

Modular

Integrative

Expansible

Autonomic

Multiuser

Modules for data access (orange), structural-analysis (green), and interplay with experiments (violet). PLoS Comp. Biol. 2008

What do we get from the genome sequence?

Central Metabolism (EMP, PPP, TCA cycle, Electron transport)

aceA, aceB, aceE, aceF, ackA, acnA, acnB, acs, adhE, agp, appB, appC, atpA, atpB, atpC, atpD, atpE, atpF, atpG, atpH, atpI, cydA, cydB, cydC, cydD, cyoA, cyoB, cyoC, cyoD, dld, eda, edd, eno, fba, fbp, fdhF, fdnG, fdnH, fdnI, fdoG, fdoH, fdoI, frdA, frdB, frdC, frdD, fumA, fumB, fumC, galM, gapA, gapC_1, gapC_2, glcB, glgA glgC, glgP, glk, glpA, glpB, glpC, glpD, gltA, gnd, gpmA, gpmB, hyaA, hyaB, hyaC, hybA, hybC, hycB, hycE, hycF, hycG, icdA, lctD, ldhA, lpdA, malP, mdh, ndh, nuoA, nuoB, nuoE, nuoF, nuoG, nuoH, nuoI, nuoJ, nuoK, nuoL, nuoM, nuoN, pckA, pfkA, pfkB, pflA, pflB, pflC, pflD, pgi, pgk, pmtA, pmtB, poxB, ppc, ppsA, pta, pur pykA, pykF, rpe, rpiA, rpiB, sdhA, sdhB, sdhC, sdhD, sfcA, sucA, sucB, sucC, sucD, talB, tktA, tktB, tpiA, trxB, zwf, pgl(Fraenkel, 1996*), mae*B(Fraenkel, 1996)

Alternative Carbon Source *adhC, adhE, agaY, agaZ, aldA, aldB, aldH, araA, araB, araD, bglX, cpsG, deoB, deoC, fruK, fucA, fucI, fucK, fucO, galE, galK, galT, galU, gatD, gatY, glk, glpK,gntK, gntV, gpsA, lacZ, manA, melA, mtlD, nagA, nagB, nanA, pfkB, pgi, pgm, rbsK, rhaA, rhaB, rhaD, srlD, treC, xylA, xylB*

Amino Acid Metabolism *adi, aldH, alr, ansA, ansB, argA, argB, argC, argD, argE, argF, argG, argH, argI, aroA, aroB, aroC, aroD, aroE, aroF, aroG, aroH, aroK, aroL, asd, asnA, asnB,aspA, aspC, avtA, cadA, carA, carB, cysC, cysD, cysE, cysH, cysI, cysJ, cysK, cysM, cysN, dadA, dadX, dapA, dapB, dapD, dapE, dapF, dsdA, gabD, gabT, gadA,gadB, gdhA, glk, glnA, gltB, gltD, glyA, goaG, hisA, hisB, hisC, hisD, hisF, hisG, hisH, hisI, ilvA, ilvB, ilvC, ilvD, ilvE, ilvG_1, ilvG_2, ilvH, ilvI, ilvM, ilvN, kbl, ldc leuA, leuB, leuC, leuD, lysA, lysC, metA, metB, metC, metE, metH, metK, metL, pheA, proA, proB, proC, prsA, putA, sdaA, sdaB, serA, serB, serC, speA, speB, speC, speD, speE, speF, tdcB, tdh, thrA, thrB, thrC, tnaA, trpA, trpB, trpC, trpD, trpE, tynA, tyrA, tyrB, ygjG, ygjH, ala*B(Reitzer, 1996*), dapC*(Greene, 1996*), pat*(McFall an Newman, 1996*), prt*(McFall and Newman, 1996*), sad*(Berlyn et al., 1996*), Methylthioadenosine nucleosidase*(Glansdorff, 1996*), 5-Methylthioribose kinase*(Glansdorf 1996*), 5-Methylthioribose-1-phosphate isomerase*(Glansdorff, 1996*), Adenosyl homocysteinase*(Matthews, 1996*), L-Cysteine desulfhydrase*(McFall and Newman, 1996*), Glutaminase* A(McFall and Newman, 1996*), Glutaminase* B(McFall and Newman, 1996)

Purine & Pyrimidine Metabolism *add, adk, amn, apt, cdd, cmk, codA, dcd, deoA, deoD, dgt, dut, gmk, gpt, gsk, guaA, guaB, guaC, hpt, mutT, ndk, nrdA, nrdB, nrdD, nrdE, nrdF, purA, purB, purC,purD, purE, purF, purH, purK, purL, purM, purN, purT, pyrB, pyrC, pyrD, pyrE, pyrF, pyrG, pyrH, pyrI, tdk, thyA, tmk, udk, udp, upp, ushA, xapA, yicP, CMPglycosylase*(Neuhard and Kelln, 1996)

Vitamin & Cofactor Metabolism *acpS, bioA, bioB, bioD, bioF, coaA, cyoE, cysG, entA, entB, entC, entD, entE, entF, epd, folA, folC, folD, folE, folK, folP, gcvH, gcvP, gcvT, gltX, glyA, gor, gshA,gshB, hemA, hemB, hemC, hemD, hemE, hemF, hemH, hemK, hemL, hemM, hemX, hemY, ilvC, lig, lpdA, menA, menB, menC, menD, menE, menF, menG, metF, mutnadA, nadB, nadC, nadE, ntpA, pabA, pabB, pabC, panB, panC, panD, pdxA, pdxB, pdxH, pdxJ, pdxK, pncB, purU, ribA, ribB, ribD, ribE, ribH, serC, thiC, thiE, thiHiG, thiH, thrC, ubiA, ubiB, ubiC, ubiG, ubiH, ubiX, yaaC, ygiG, nadD*(Penfound and Foster, 1996*), nadF*(Penfound and Foster, 1996*), nadG*(Penfound and Foster,1996*), panE*(Jackowski, 1996*), pncA*(Penfound and Foster, 1996*), pncC*(Penfound and Foster, 1996*), thiB*(White and Spenser, 1996*), thiD*(White and Spenser, 1996) *thiK*(White and Spenser, 1996*), thiL*(White and Spenser, 1996*), thiM*(White and Spenser, 1996*), thiN*(White and Spenser, 1996*), ubiE*(Meganathan, 1996*),*

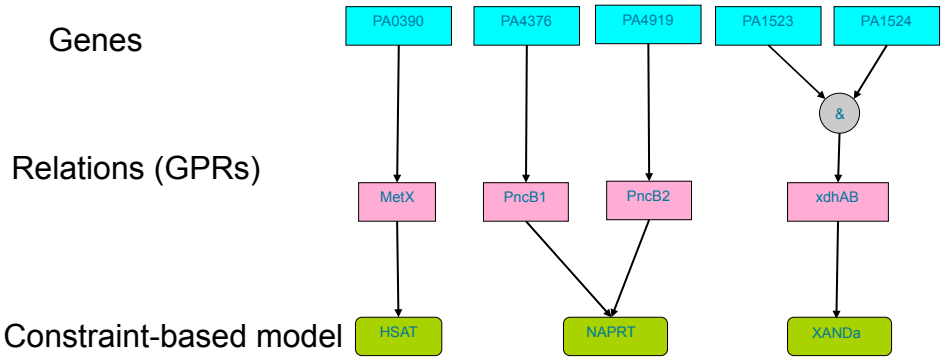
ubiF(Meganathan, 1996*), Arabinose-5-phosphate isomerase*(Karp et al., 1998*), Phosphopantothenate-cysteine ligase*(Jackowski, 1996*), Phosphopantothenate-cystein decarboxylase*(Jackowski, 1996*), Phospho-pantetheine adenylyltransferase*(Jackowski, 1996*), DephosphoCoA kinase*(Jackowski, 1996*), NMN glycohydrolase*(Penfound and Foster, 1996)

Lipid Metabolism *accA, accB, accD, atoB, cdh, cdsA, cls, dgkA, fabD, fabH, fadB, gpsA, ispA, ispB, pgpB, pgsA, psd, pssA, pgpA*(Funk et al., 1992)

Cell Wall Metabolism *ddlA, ddlB, galF, galU, glmS, glmU, htrB, kdsA, kdsB, kdtA, lpxA, lpxB, lpxC, lpxD, mraY, msbB, murA, murB, murC, murD, murE, murF, murG, murI, rfaC, rfaD,rfaF, rfaG, rfaI, rfaJ, rfaL, ushA, glm*M(Mengin-Lecreulx and van Heijenoort, 1996*), lpcA*(Raetz, 1996*), rfaE*(Raetz, 1996*), Tetraacyldisaccharide*

Metabolic reconstruction of an organism

- A combination of:
  - Metabolic and transport genes
  - A constraint-based model
  - Relations that bind genes and reactions

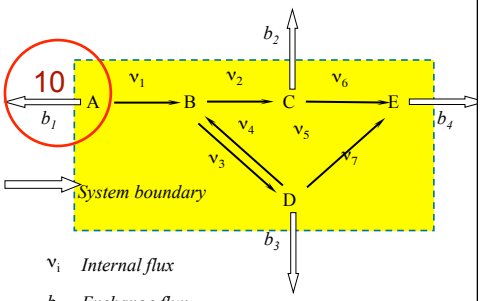


The stoichiometric matrix as a metabolic map

Genetic content

gene	enzyme	flux	rxn
mglA, maglB	galactose transporter	v_1	A ➡ B
galT	uridyl transferase	v_2	B ➡ C
galK	galactokinase	v_3	B ➡ D

Biochemical reaction network



v_i *Internal flux*

b_i *Exchange flux*

Steady state Mass Balance

A: $-v1=-10$
B: $-v1+v4-v2-v3=0$
C: $v2-v5-v6-B_C=0$
D: $v3+v5-v4-v7-B_D=0$
E: $v6+v7-B_E=0$

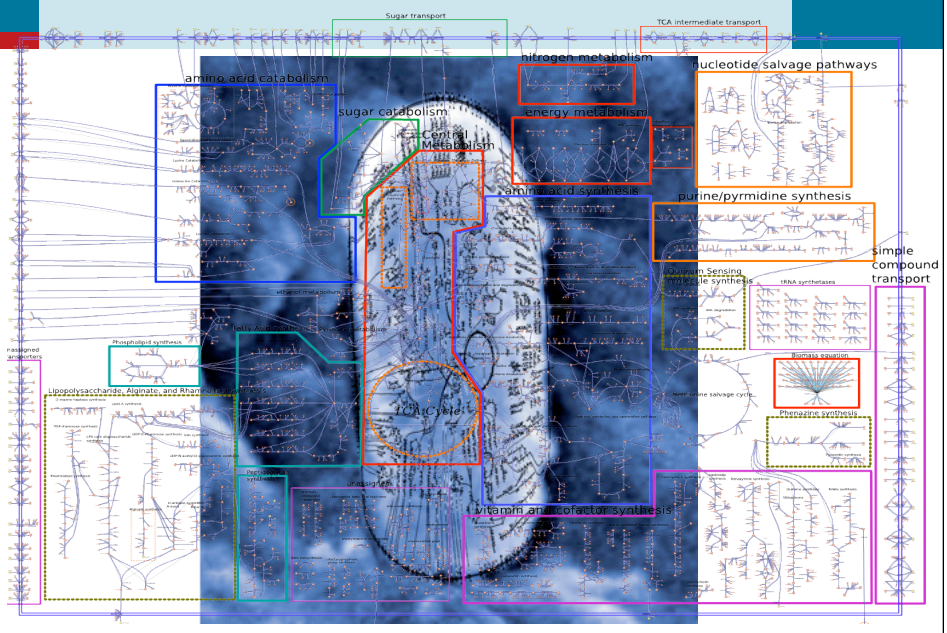
$$\begin{bmatrix} v_1 & v_2 & v_3 & v_4 & v_5 & v_6 & v_7 & B_C & B_D & B_E \end{bmatrix}$$

$$\begin{bmatrix} -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & -1 & -1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & -1 & -1 & 0 & -1 & 0 & 0 \\ 0 & 0 & 1 & -1 & 1 & 0 & -1 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & -1 \end{bmatrix} = \begin{bmatrix} -10 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

10 Unknown fluxes

1 Known fluxes

After Palsson, 2000



P. putida (815 genes, 877 reactions, Puchalka et al., PLoS Comput. Biol, 2008))

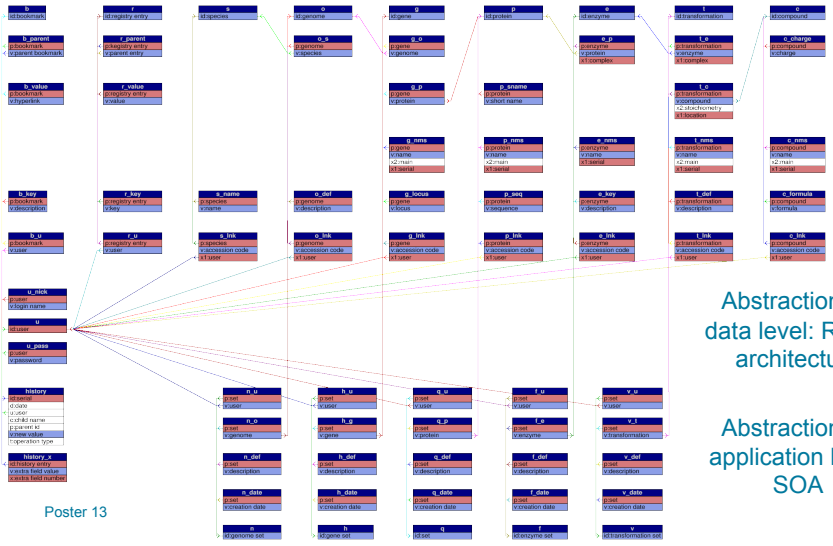
ToBiN is a modular platform based on open-standards

- User management based on OpenID
- The data repository can export/import SBML, JSON, and YAML
- RSS feeds permit the tracking of information that has been updated in the repositories
- The model and data repositories are (web) accessible by means of a REST interface
- Models not to be integrated in the public repository can be ‘plugged in’ and run locally
- 15 genome-scale models with collaborators in 3 continents

7

Relational model underlying ToBiN

Toolbox requires Web, Application and SQL Servers where the biological data, simulation setups and results are processed under a common format



Abstraction at data level: REST architecture

Abstraction at application level: SOA

Poster 13

ToBiN: modules implemented

- ✓ Flux Balance Analysis (FBA)
- ✓ OptKnock - strain optimization
- ✓ ROOM (MOMA)- strain adaptation
- ▸ Genome-Scale Elementary Modes
- ▸ Alpha-Spectrum
- ✓ Biolog - Phenotype Microarrays ™
- ▸ Metabolomics
- ▸ Transcriptomics

➡ Your 'omics' data handling needs

9

ToBiNsupplies an abstraction layer over IT complexity

No IT infrastructure, installations, and configurations are required (web-based)

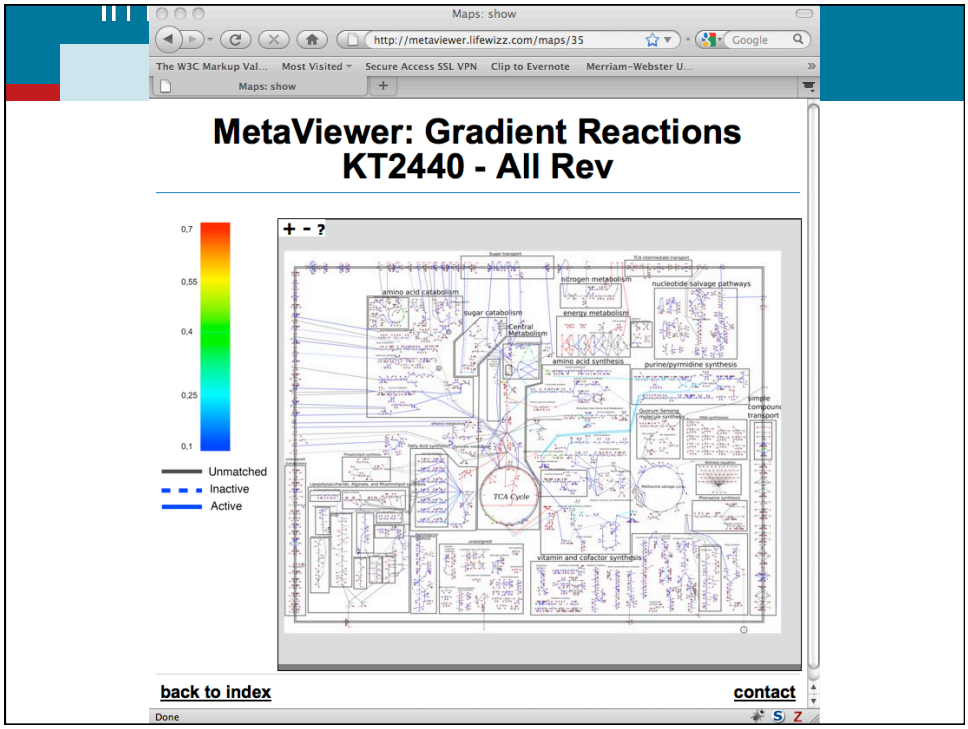
Data are automatically backed up

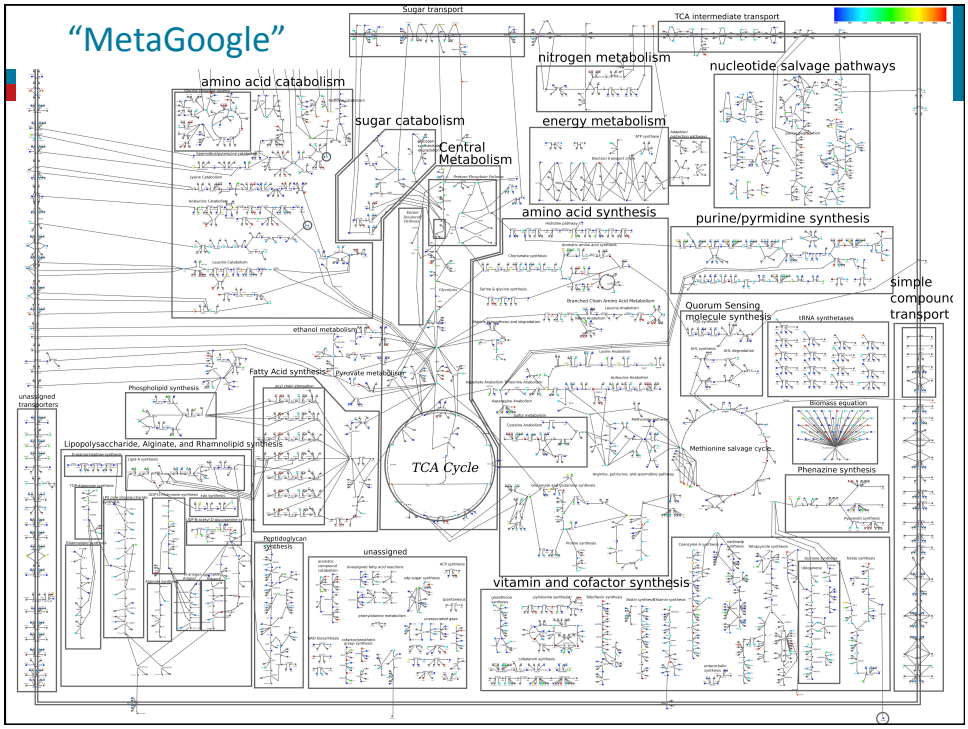
Automatic load-balancing for computationally intensive tasks

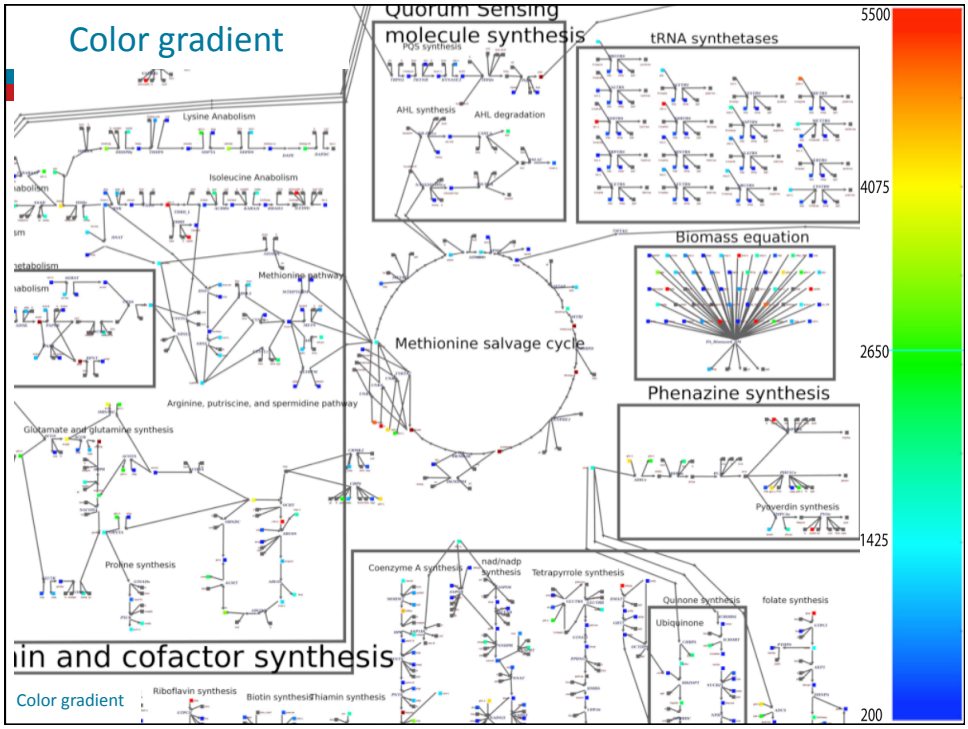
Security is centrally managed with logging, auditing, and roll-back capabilities.

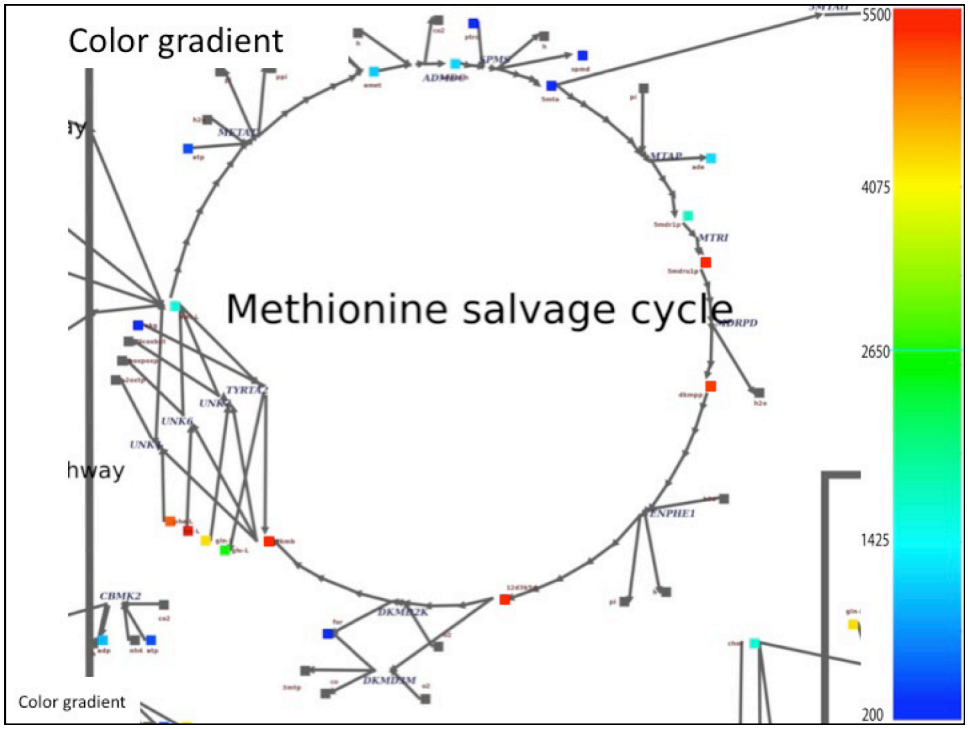
Supports co-existing Individual, Workgroup, Institutional, and Consortium data-share levels

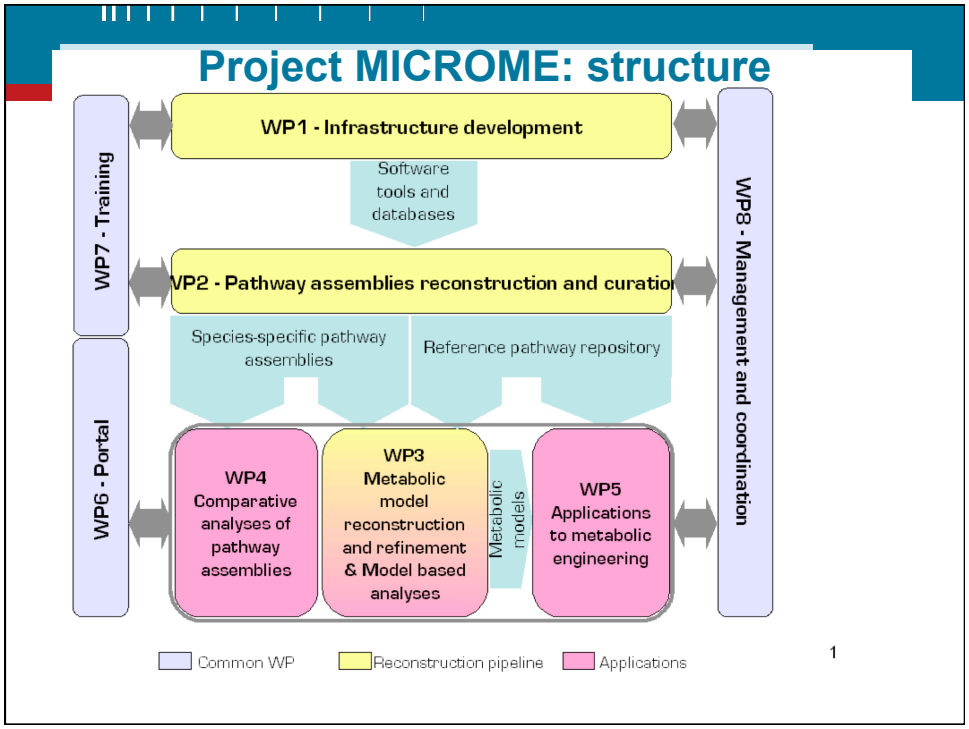
10

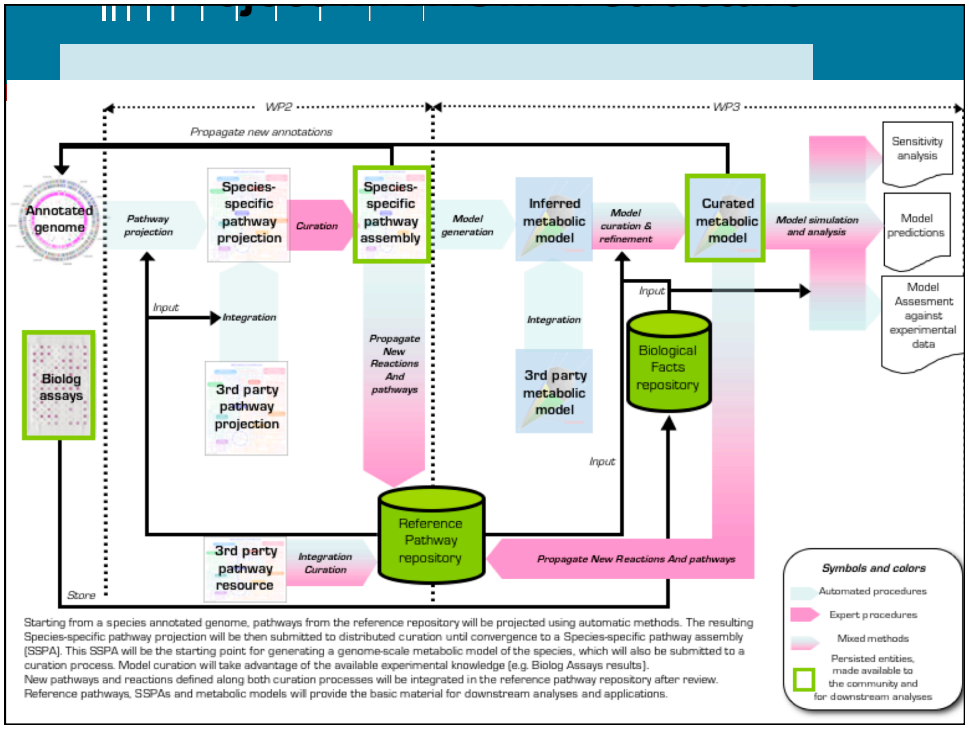

Maps: show
http://metaviewer.lifewizz.com/maps/35
MetaViewer: Gradient Reactions
KT2440 - All Rev
0,7
0,55
0,4
0,25
0,1
Unmatched
Inactive
Active
+ - ?
nitrogen metabolism
nucleotide salvage pathways
amino acid catabolism
sugar catabolism
Central Metabolism
energy metabolism
amino acid synthesis
purine/pyrimidine synthesis
simple compound transport
TCA Cycle
vitamin and cofactor synthesis
back to index
contact
Done


"MetaGoogle"
Sugar transport
TCA intermediate transport
nitrogen metabolism
nucleotide salvage pathways
amino acid catabolism
sugar catabolism
Central Metabolism
energy metabolism
amino acid synthesis
purine/pyrimidine synthesis
simple compound transport
Quorum Sensing molecule synthesis
tRNA synthetases
ethanol metabolism
Fatty Acid synthesis
Pyruvate metabolism
unassigned transporters
Phospholipid synthesis
Lipopolysaccharide, Alginate, and Rhamnolipid synthesis
TCA Cycle
Biomass equation
Methionine salvage cycle
Phenazine synthesis
Peptidoglycan synthesis
unassigned
vitamin and cofactor synthesis


Color gradient
Quorum Sensing
molecule synthesis
PQS synthesis
AHL synthesis
AHL degradation
tRNA synthetases
Lysine Anabolism
Isoleucine Anabolism
Methionine pathway
Arginine, putriscine, and spermidine pathway
Methionine salvage cycle
Biomass equation
Phenazine synthesis
Pyoverdin synthesis
Glutamate and glutamine synthesis
Proline synthesis
Coenzyme A synthesis
nad/nadp synthesis
Tetrapyrrole synthesis
Quinone synthesis
Ubiquinone
folate synthesis
in and cofactor synthesis
Riboflavin synthesis
Biotin synthesis
Thiamin synthesis
Color gradient
5500
4075
2650
1425
200


Color gradient
Methionine salvage cycle
hway
MTAP
MTRI
TYRTA2
UNK6
ENPHE1
CBMK2
DKMPPK
DKMPPM
Color gradient
5500
4075
2650
1425
200


Project MICROME: structure
WP1 - Infrastructure development
Software tools and databases
WP2 - Pathway assemblies reconstruction and curatio
Species-specific pathway assemblies
Reference pathway repository
WP7 - Training
WP6 - Portal
WP8 - Management and coordination
WP4 Comparative analyses of pathway assemblies
WP3 Metabolic model reconstruction and refinement & Model based analyses
Metabolic models
WP5 Applications to metabolic engineering
Common WP
Reconstruction pipeline
Applications
1


WP2
WP3
Propagate new annotations
Annotated genome
Pathway projection
Species-specific pathway projection
Curation
Species-specific pathway assembly
Model generation
Inferred metabolic model
Model curation & refinement
Curated metabolic model
Model simulation and analysis
Sensitivity analysis
Model predictions
Model Assesment against experimental data
Input
Integration
Biolog assays
3rd party pathway projection
Propagate New Reactions And pathways
Integration
3rd party metabolic model
Input
Biological Facts repository
Input
Reference Pathway repository
3rd party pathway resource
Integration Curation
Propagate New Reactions And pathways
Store
Symbols and colors
Automated procedures
Expert procedures
Mixed methods
Persisted entities, made available to the community and for downstream analyses
Starting from a species annotated genome, pathways from the reference repository will be projected using automatic methods. The resulting Species-specific pathway projection will be then submitted to distributed curation until convergence to a Species-specific pathway assembly (SSPA). This SSPA will be the starting point for generating a genome-scale metabolic model of the species, which will also be submitted to a curation process. Model curation will take advantage of the available experimental knowledge (e.g. Biolog Assays results).
New pathways and reactions defined along both curation processes will be integrated in the reference pathway repository after review.
Reference pathways, SSPAs and metabolic models will provide the basic material for downstream analyses and applications.

How shall we proceed?

Report on the identification of scientific & infrastructure bottlenecks in SB (jointly WP4 & WP3)

Study groups: bottom-up, priorital themes?

Possible themes:

- **context-independent biological systems/modules**
- **microfluidics technologies / single cell measurents**
- **minimal genomes / minimal systems**
- **what to measure / how to measure?**
- **design concepts**
- **how can we handle “systems“ (made of parts)?**
- **.....**

Thematic Workshops: IT and Standardization. Time plan?

Exchange visits?

EMERGENCE **WP3**

Information Technology Infrastructure for Synthetic Biology

Victor de la Torre & Alfonso Valencia
Structural and Computational Biology Programme
Spanish National Cancer Research Centre
CNIO Madrid

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Outline

- Introduction.
- Integration between the MIT repository of parts and bioinformatics tools.
- Proposed solution and use cases.
- Adding new annotations.

Contact: vdelatorre@cnio.es

EMERGENCE WP3
Information Technology Infrastructure for Synthetic Biology

- 3.1- Developing the concepts for integrated workflow infrastructure based on the registry
- 3.2- Implementation of the basic software infrastructure and the integration of tools and methods for sequence design and analysis
- 3.3- Development and integration of software for model-based sequence analysis and design
- 3.4- Proof of concept study with integrated system

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Deliverables

- D.3.1 Document describing the concepts for integrated workflow infrastructure based on the registry
- D.3.2 Report describing the implementation of software and the integration of tools and methods for sequence design and analysis
- D.3.3 Report describing the software for model based systems design and analysis, and its integration
- D.3.4 Document describing the proof-of-concept study exploiting the integrated workflow for genetic circuit design

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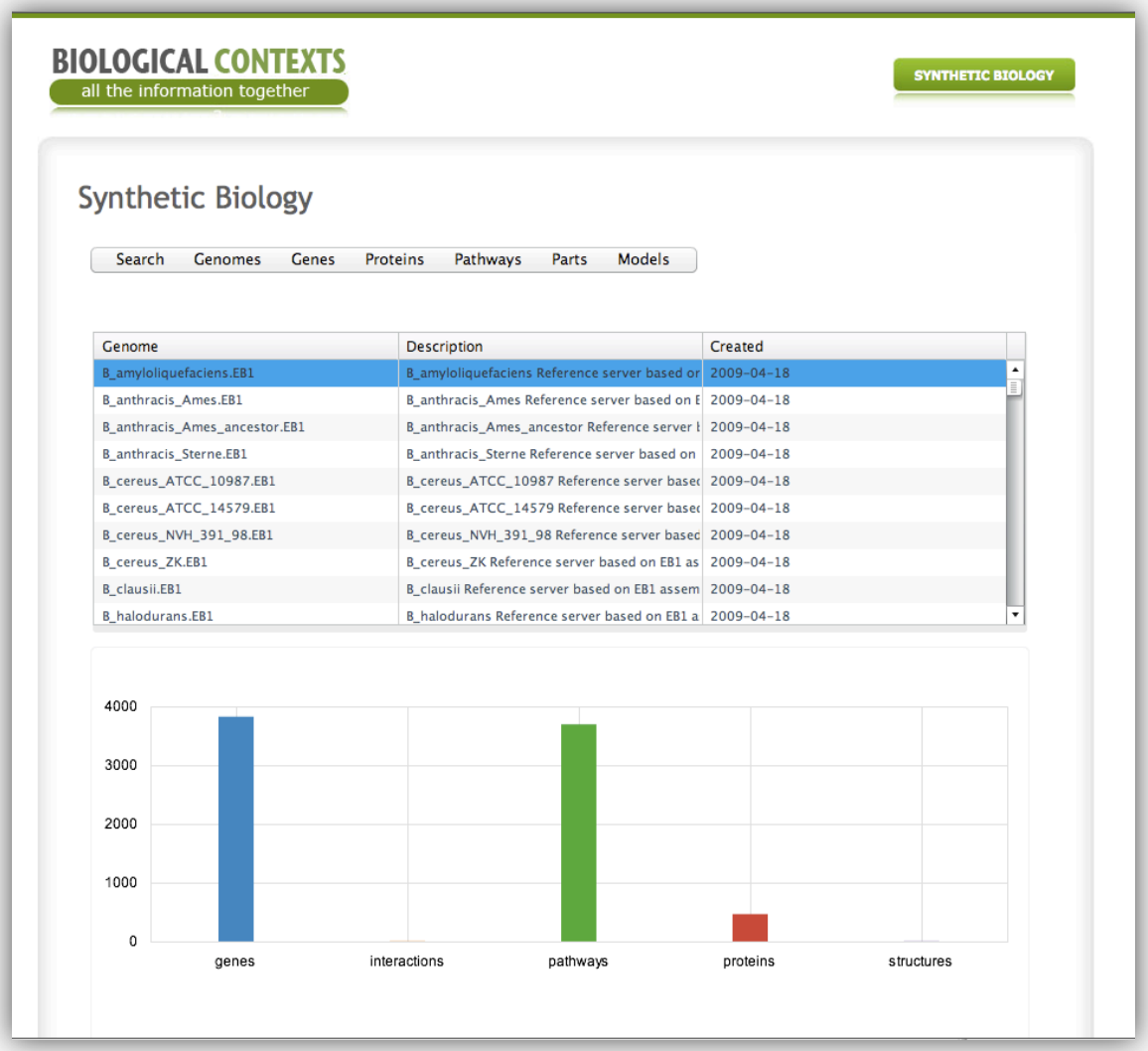
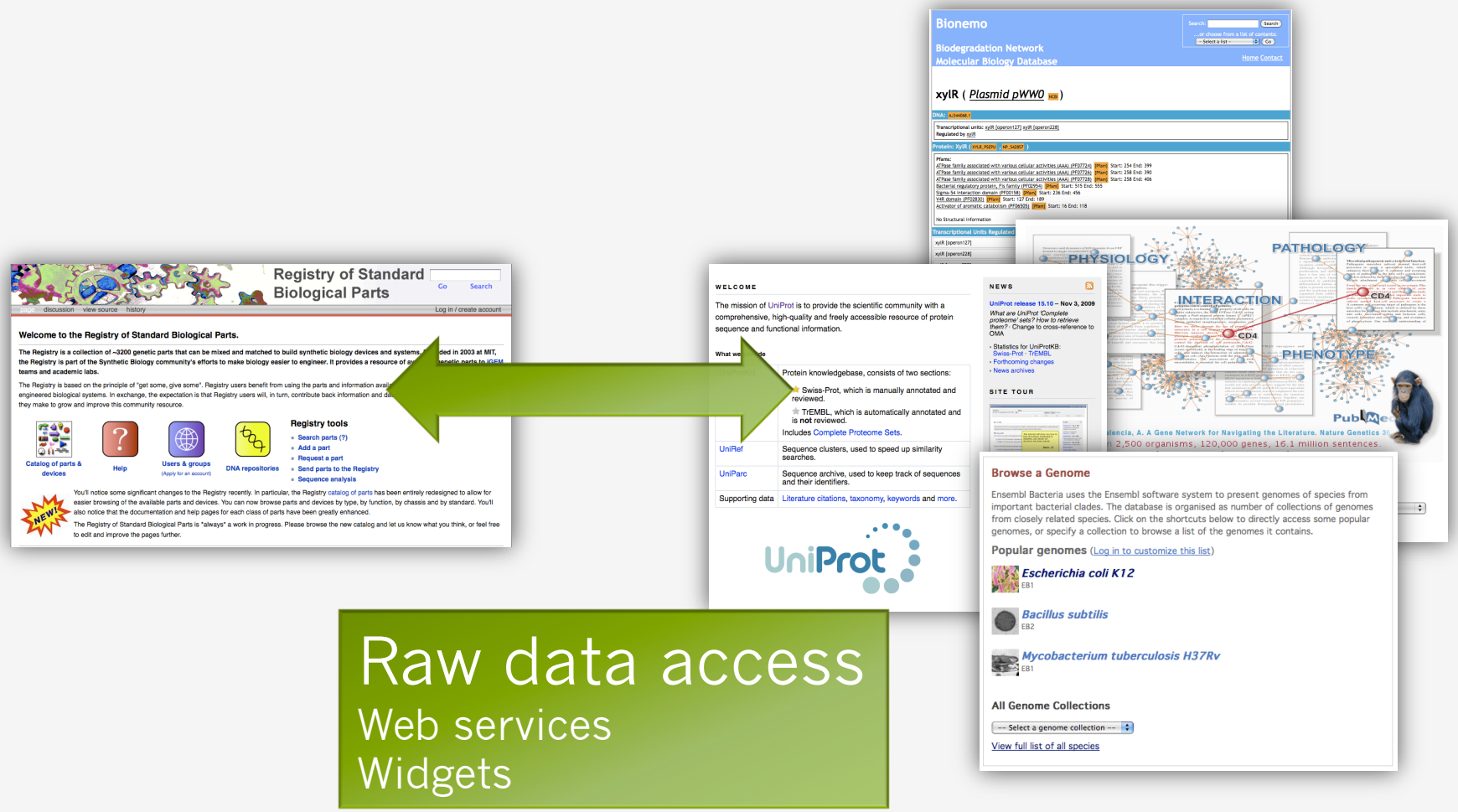
Proposed solution



Biological Contexts is a web client that allows users to connect biological information extracted from different resources.

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Data integration



Raw data access

Web services

Widgets

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Advantages

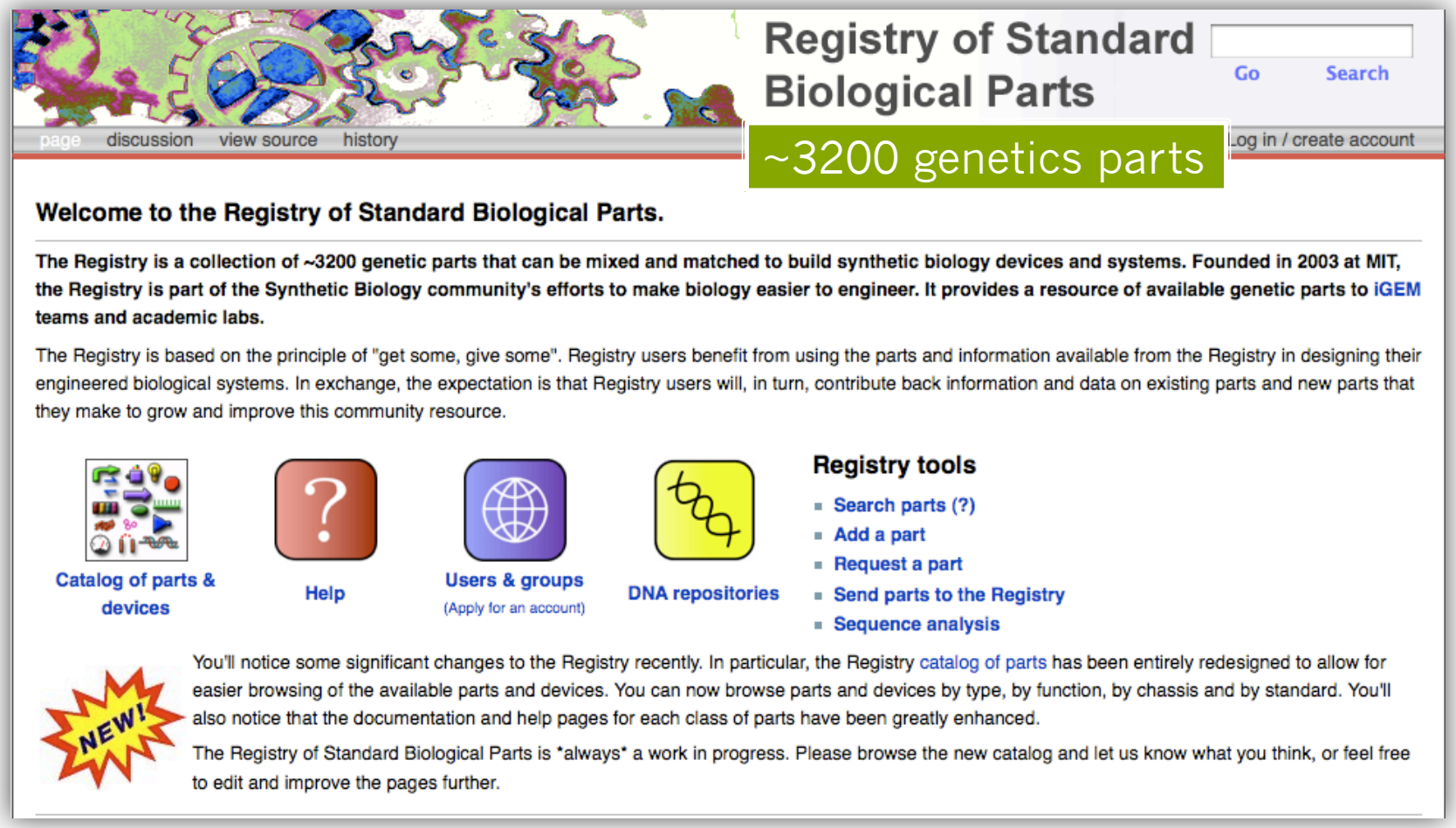
- Data is maintained by each group.
- Web services can exchange data in an efficient way.
- Common visualizations across different sites. (Visualization APIs).
- Setup the basis for exponential expansion of the knowledge.

Contact: vdelatorre@cnio.es

Problems and challenges

- Uncovered genomes.
- Information is not curated in most of the cases.
- Many web pages with information but without raw data access mechanisms.
- Slow services.

Parts Registry



Parts Registry

Biosynthesis: Parts involved in the production or degradation of chemicals and metabolites are listed here.

Cell-cell signaling and quorum sensing: Parts involved in intercellular signaling and quorum sensing between bacteria.

Cell death: Parts involved in killing cells.

Coliroid: Parts involved in taking a bacterial photograph.

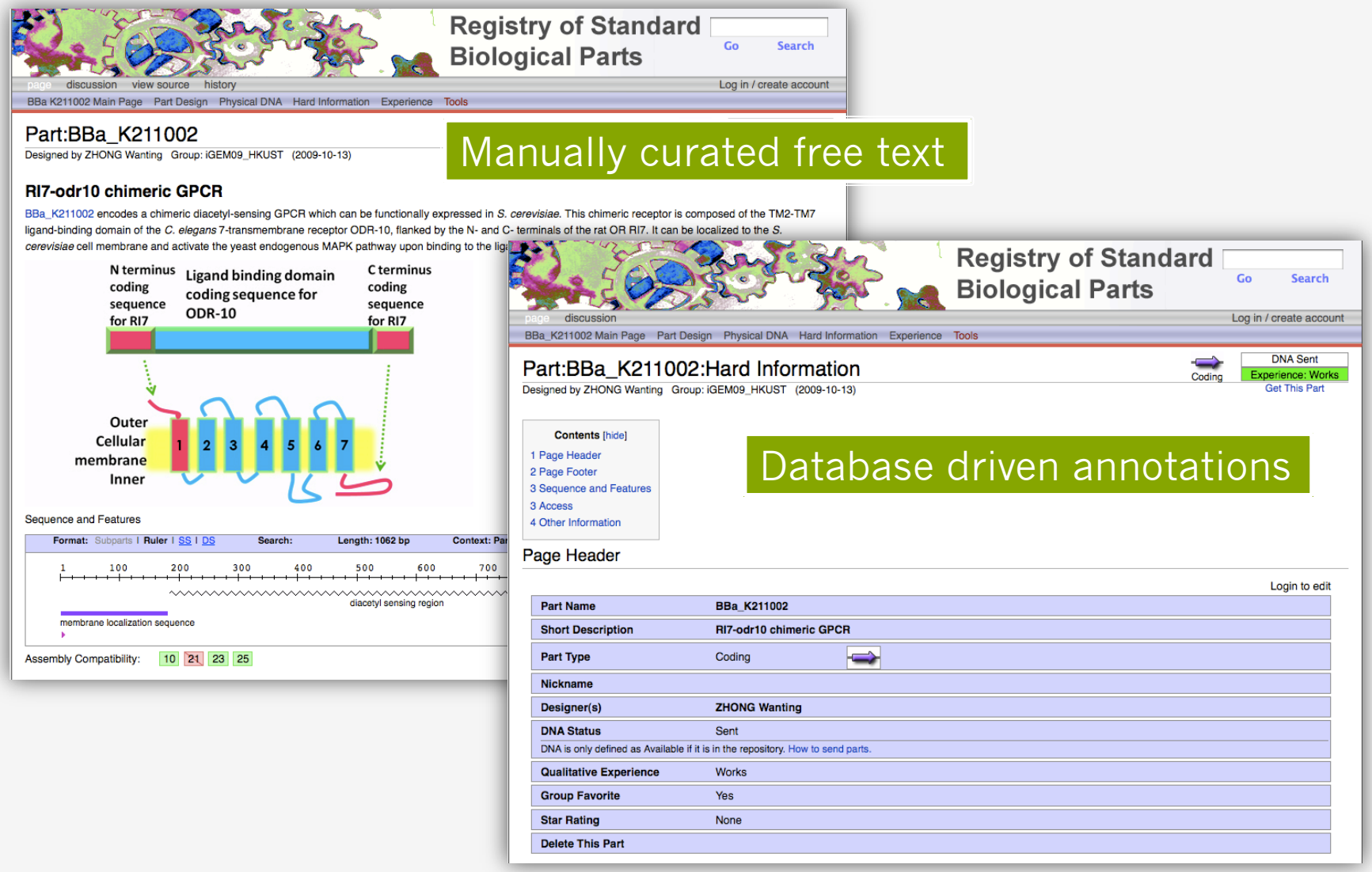
Conjugation: Parts involved in DNA conjugation between bacteria.

Motility and chemotaxis: Parts involved in motility or chemotaxis of cells.

Odor production and sensing: Parts the produce or sense odorants.

DNA recombination: Parts involved in DNA recombination.

Parts Registry

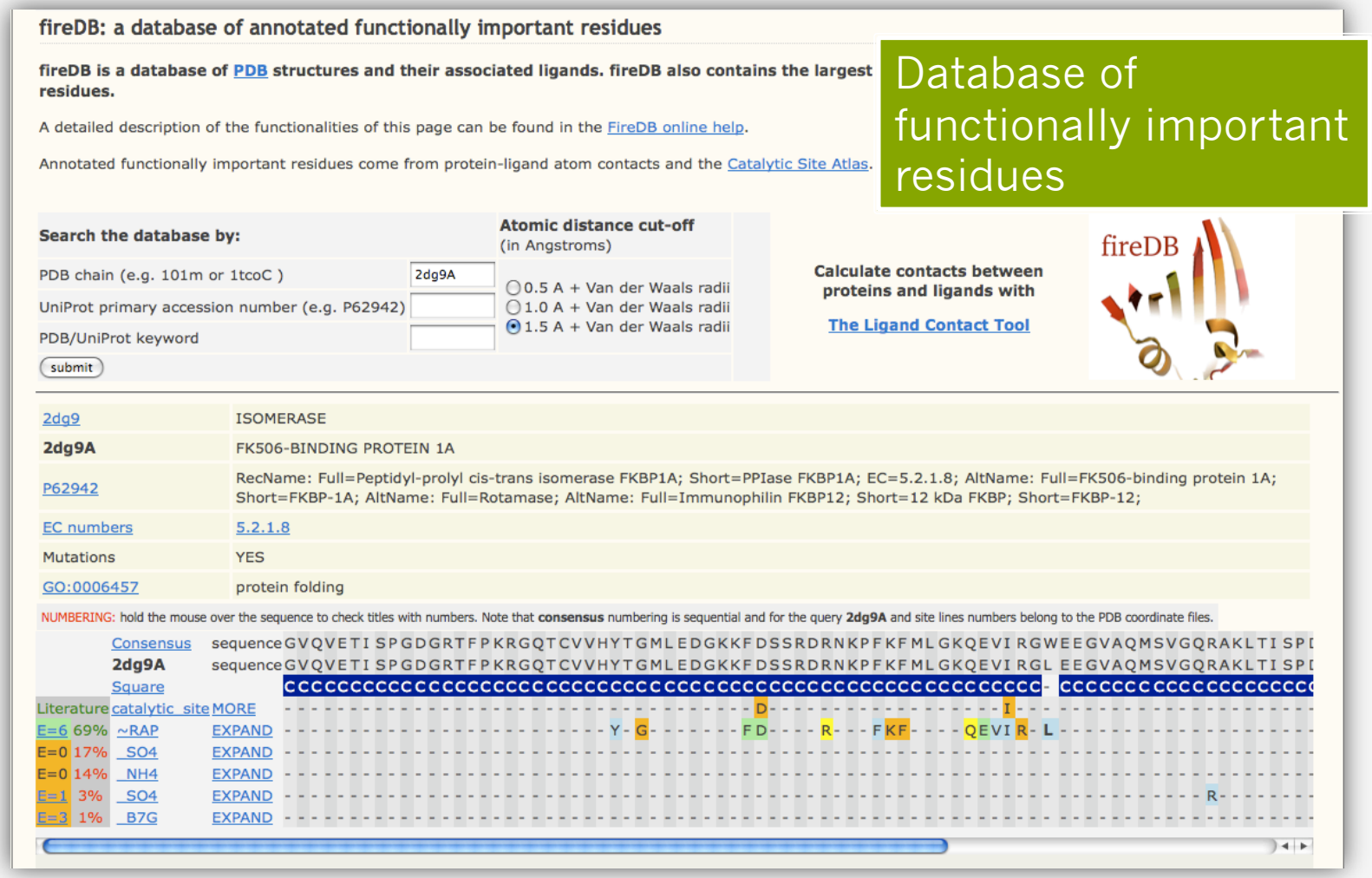


http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Biological databases and tools

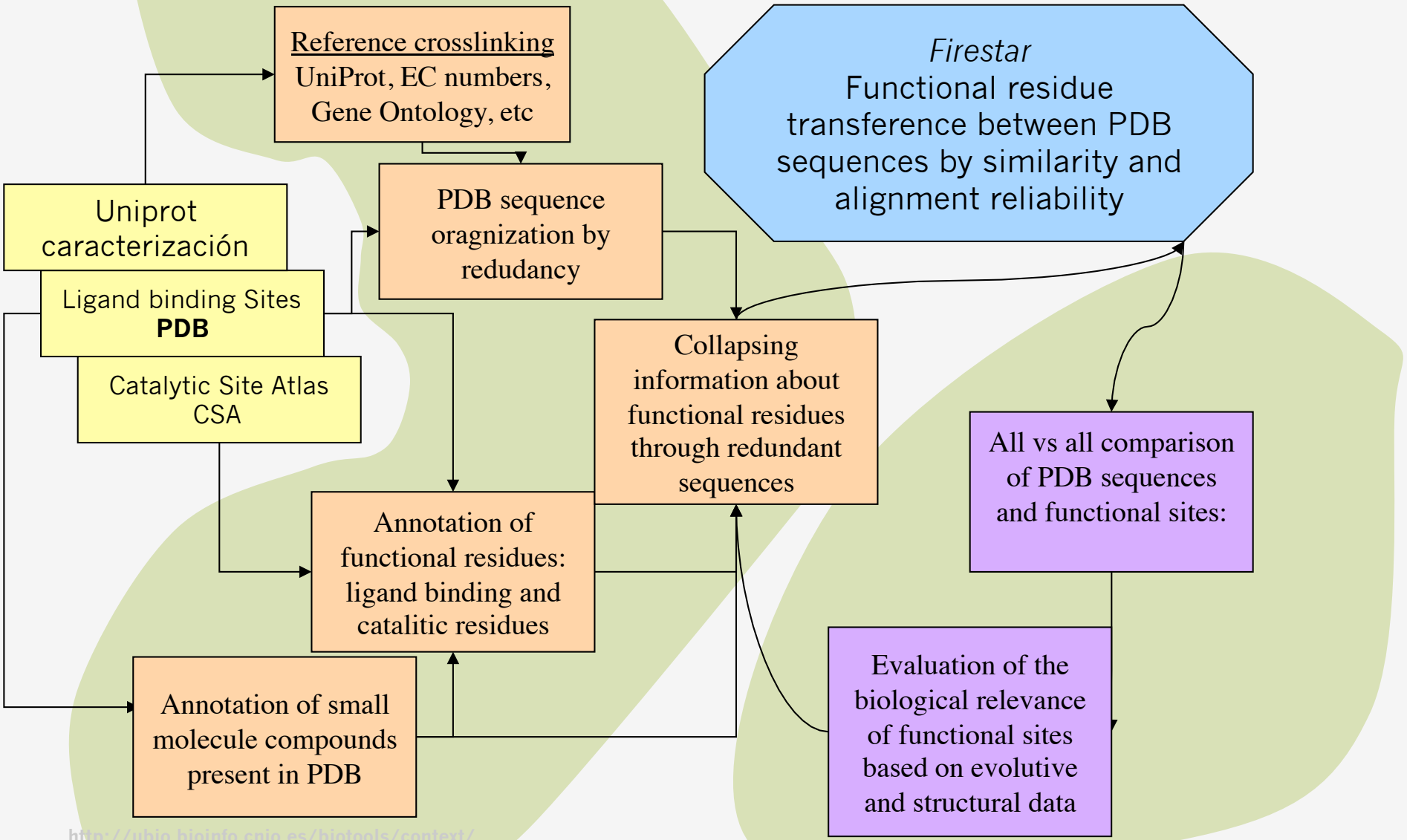
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

FireDB. Functionally residues



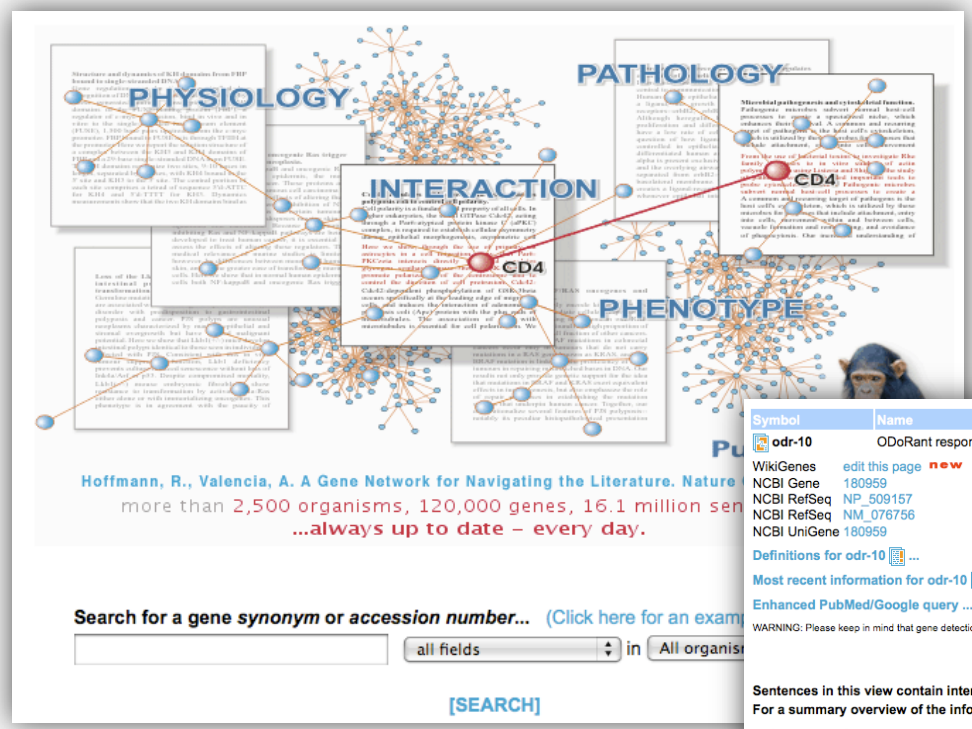
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

FireDB workflow

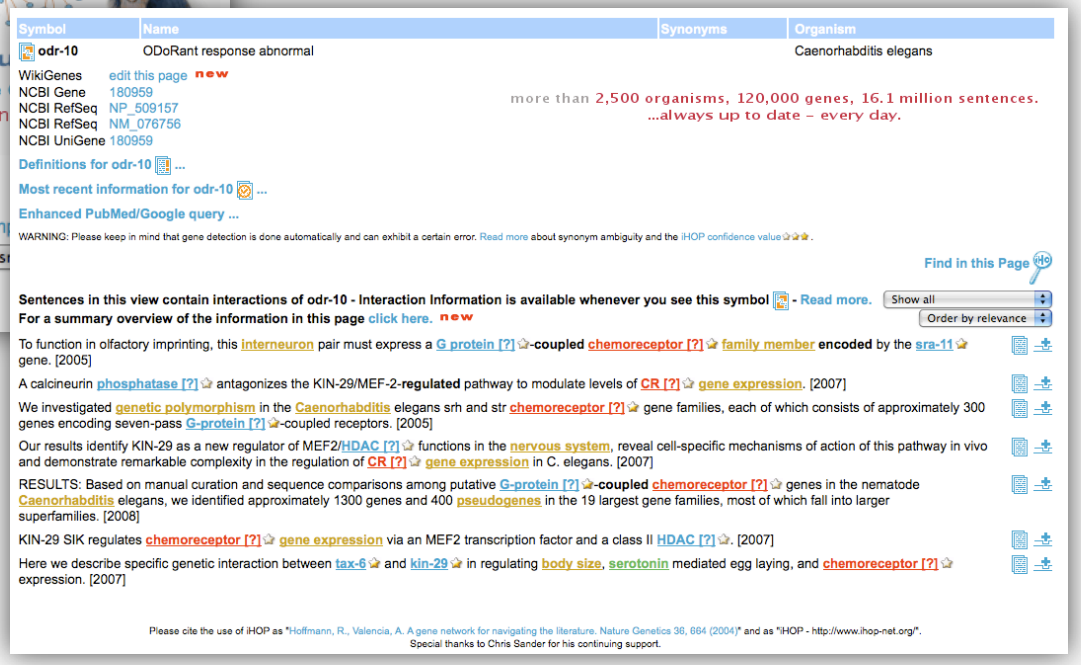


http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

iHOP



Extract interactions from literature



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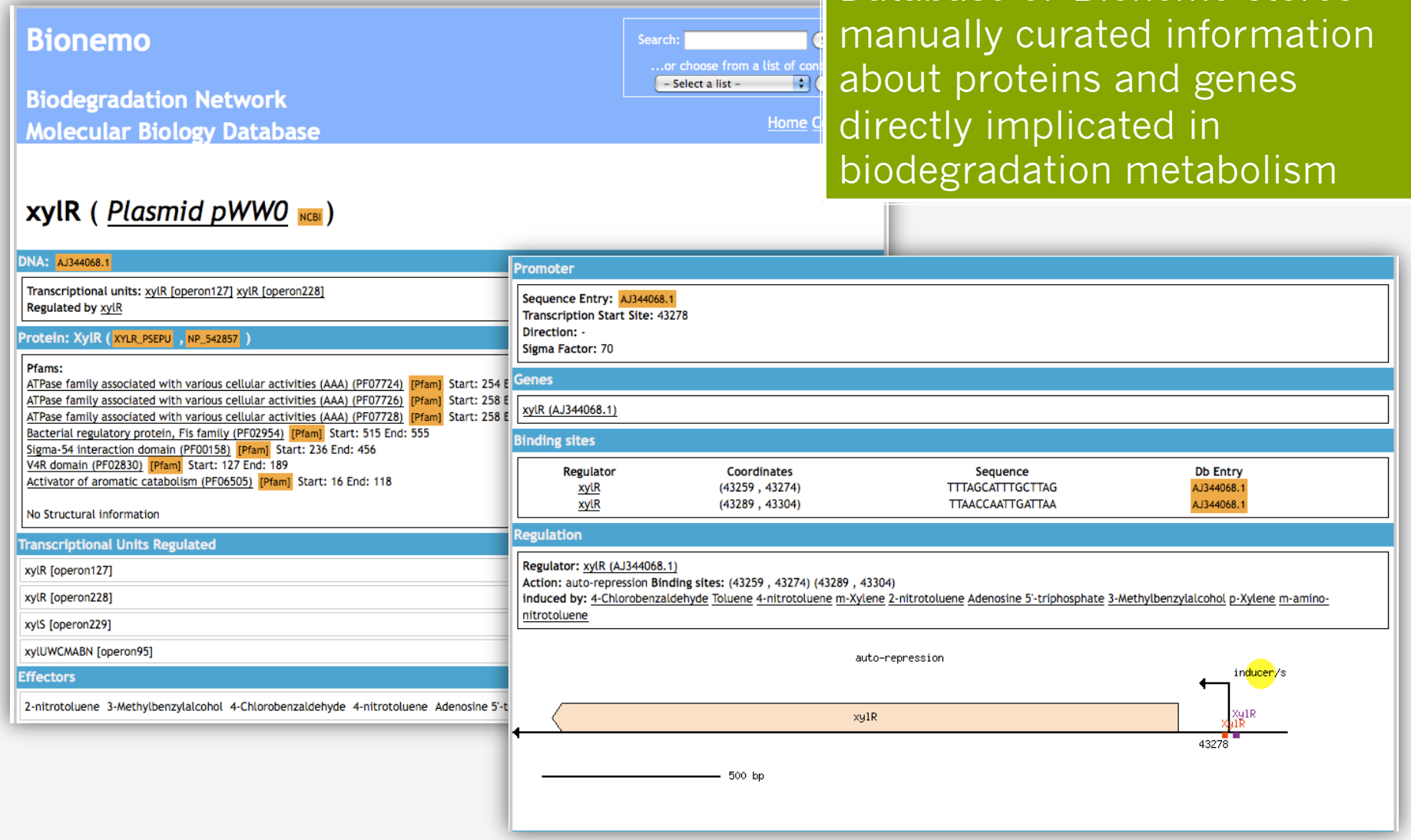
Bionemo

Database of Bionemo stores manually curated information about proteins and genes directly implicated in biodegradation metabolism



http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Web Interface and use cases

http://ubio.bioinfo.cnio.es/biotools/context/

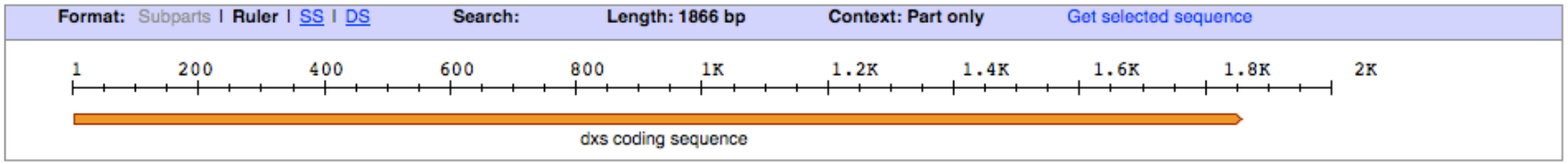
- Get information about parts
- Build new design or redesign composite parts.
- Link to BioModels

BBa_K118000.
dxs coding sequence encoding 1-deoxyxylulose-5-phosphate synthase

dxs coding sequence encoding 1-deoxyxylulose-5-phosphate synthase

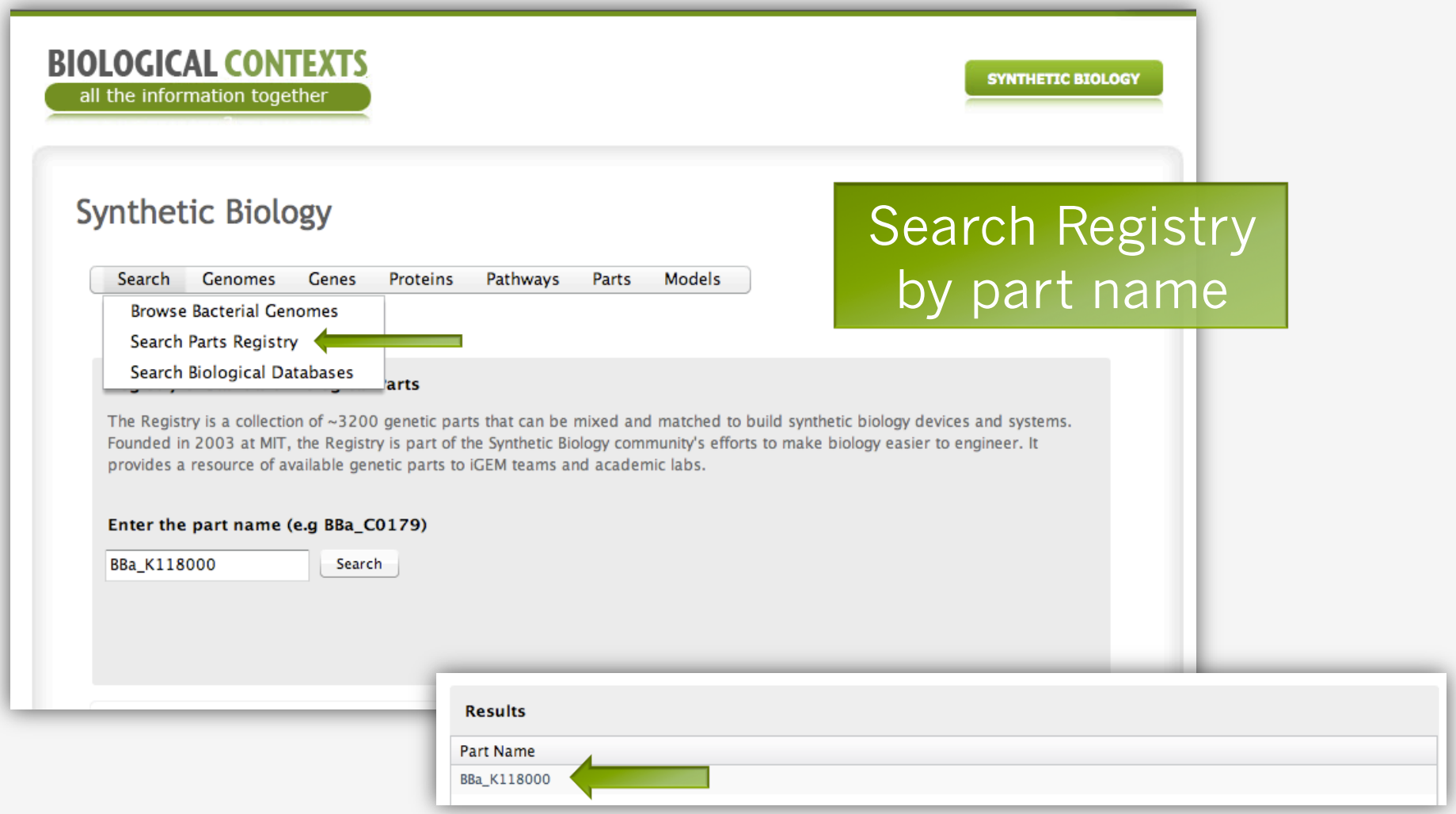
This is the coding sequence of *dxs* from *Escherichia coli* JM109. It encodes 1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, which catalyses the first step in the biosynthesis of terpenoids. Overexpression of dxs has been reported to increase yields of carotenoids and other terpenoids (Kang, M.J., Lee, Y.M., Yoon, S.H., Kim, J.H., Ock, S.W., Jung, K.H., Shin, Y.C., Keasling, J.D., and Kim, S.W. 2005. Identification of genes affecting lycopene accumulation in *Escherichia coli* using a shot-gun method. Biotechnology and Bioengineering **91**, 636-642).

Sequence and Features



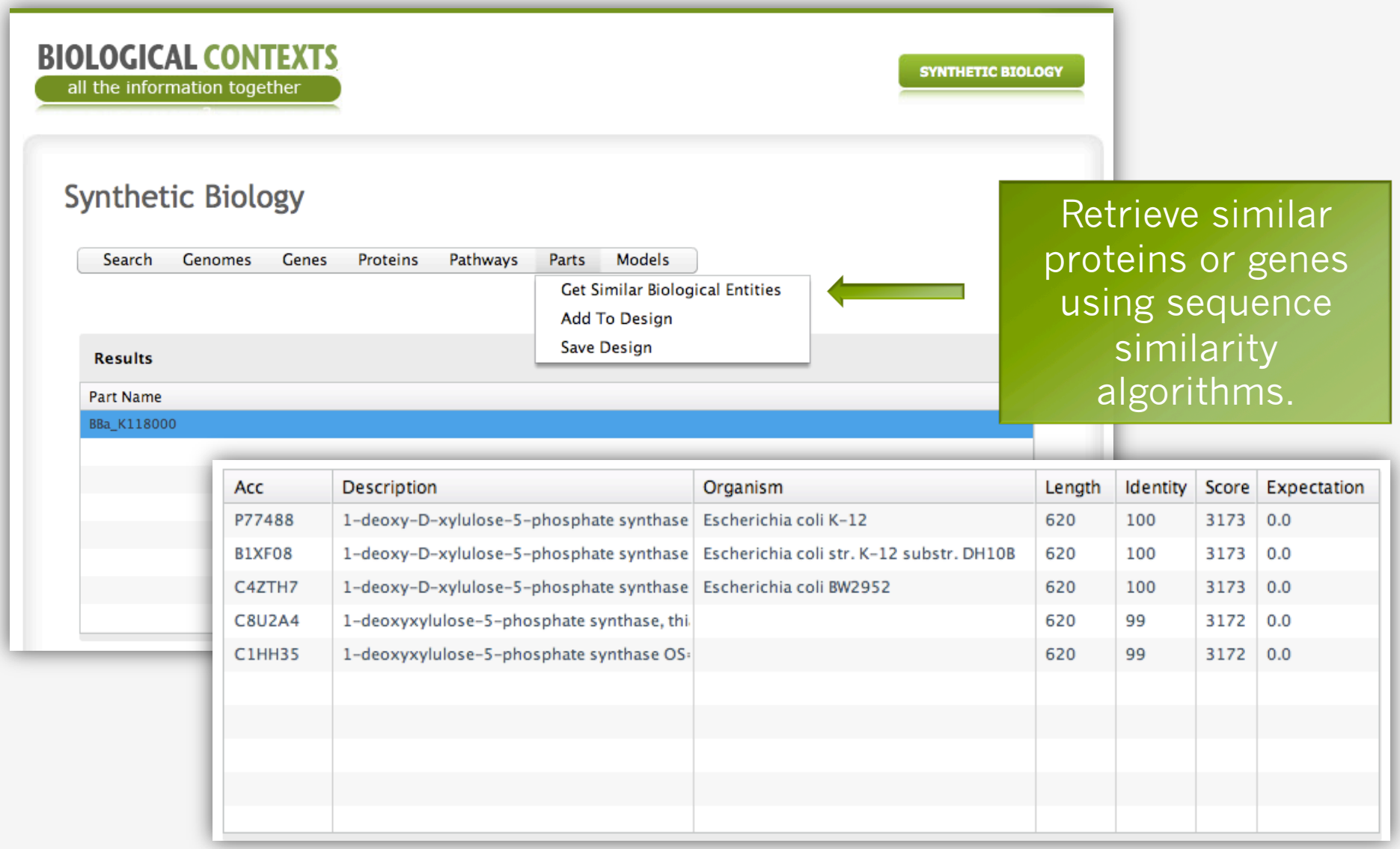
Assembly Compatibility: 10 21 23 25

Start searching



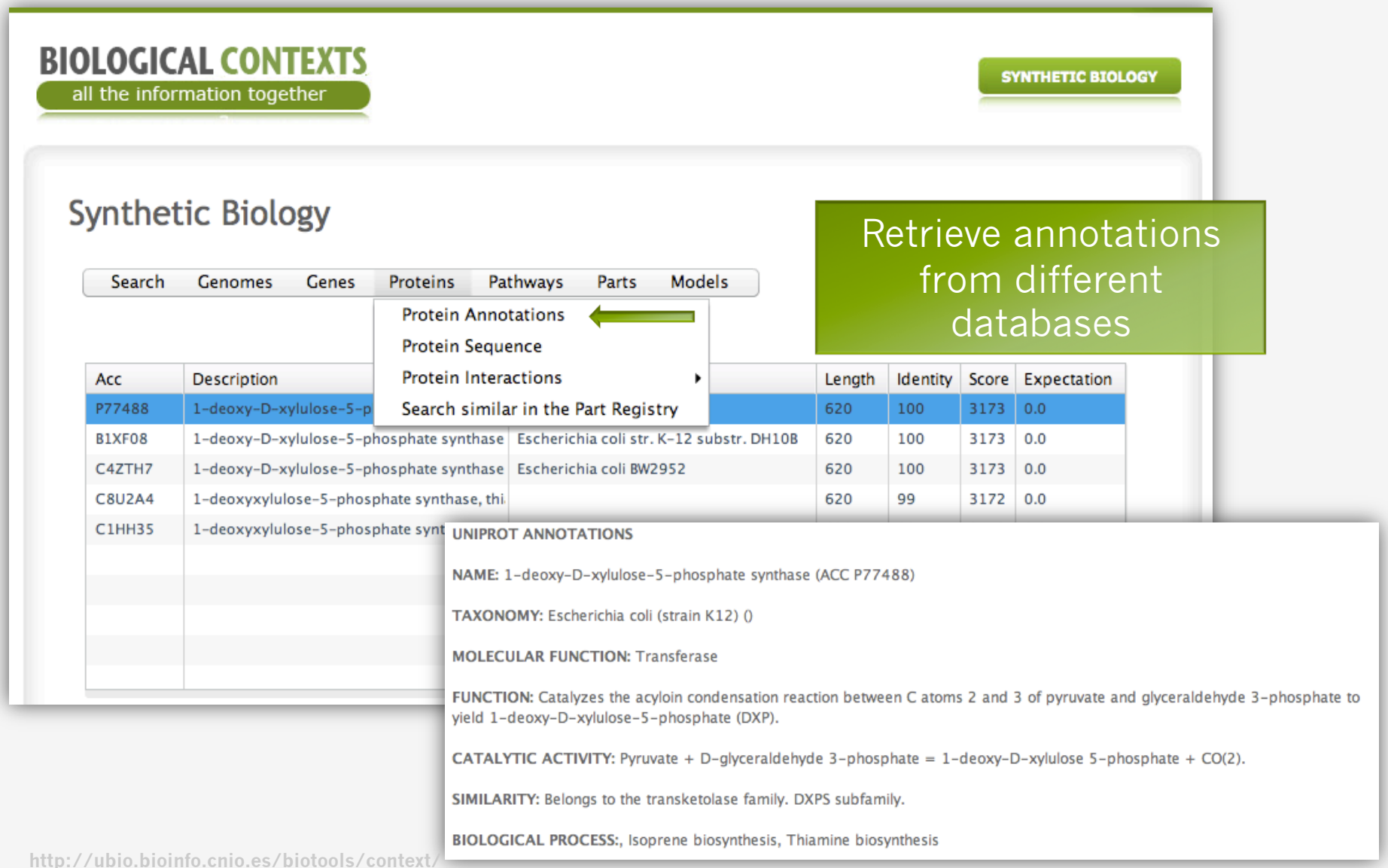
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Getting similar sequences



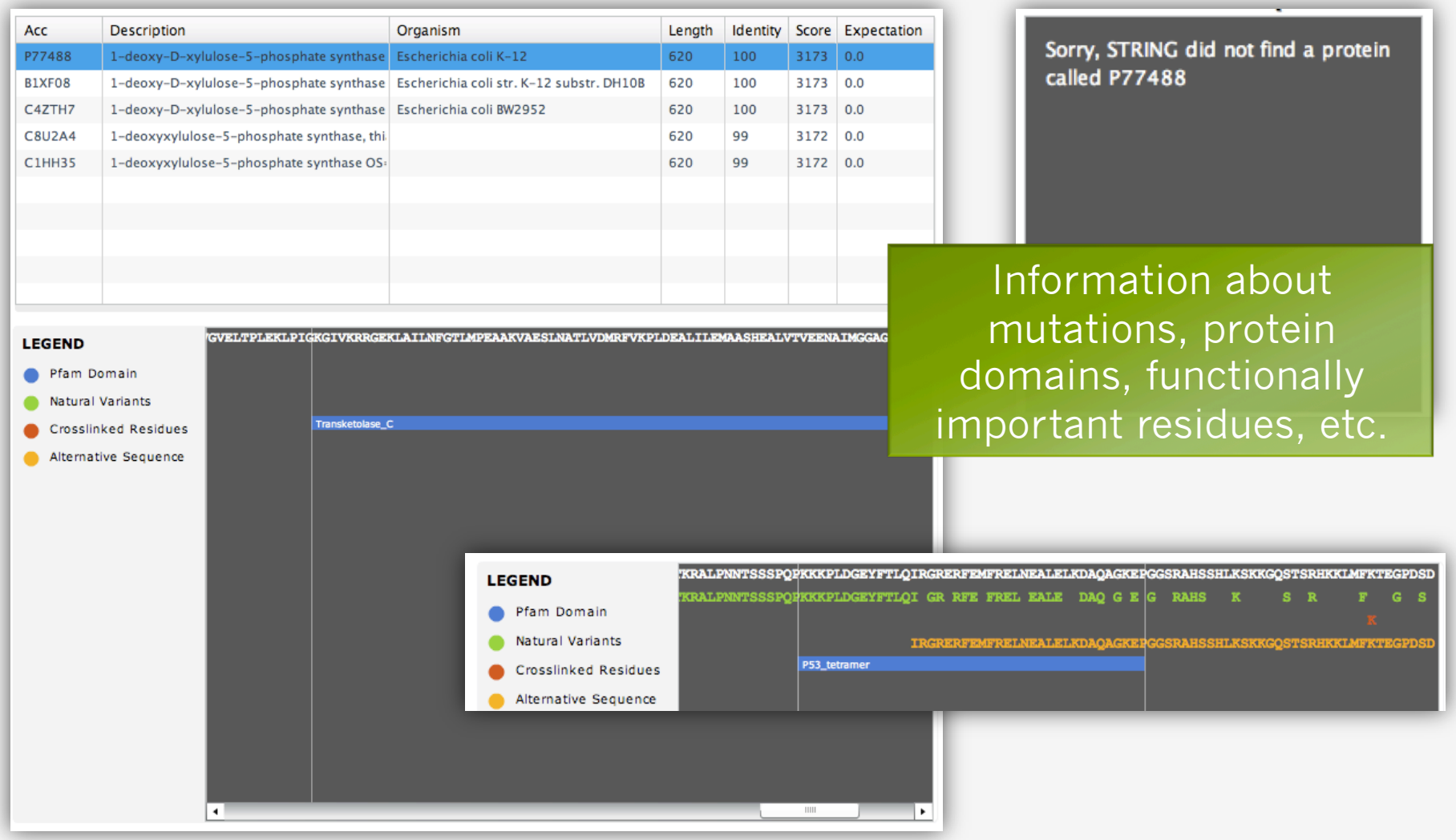
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Retrieving protein annotations



http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Sequence features



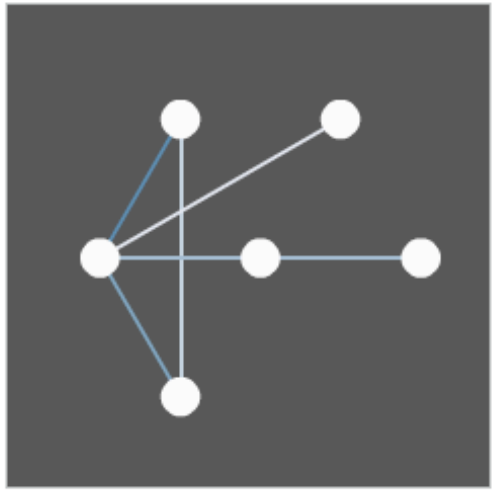
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Protein Interactions

Acc	Description	Organism	Length	Identity	Score	Expectation
Q18807	ODR10 OS=Caenor	Caenorhabditis eleg	339	97	1385	9.9999999999999
C3U4Y0	ODR10 OS=Caenor		342	75	1271	9.9999999999999
C3U4Y6	ODR10 OS=Caenor		342	75	1270	9.9999999999999
C3U4Y1	ODR10 OS=Caenor		342	75	1270	9.9999999999999
C3U4Y2	ODR10 OS=Caenor		342	75	1266	9.9999999999999

Move across the interaction network by clicking on nodes

STRING interactions (Click on a node to see more details)

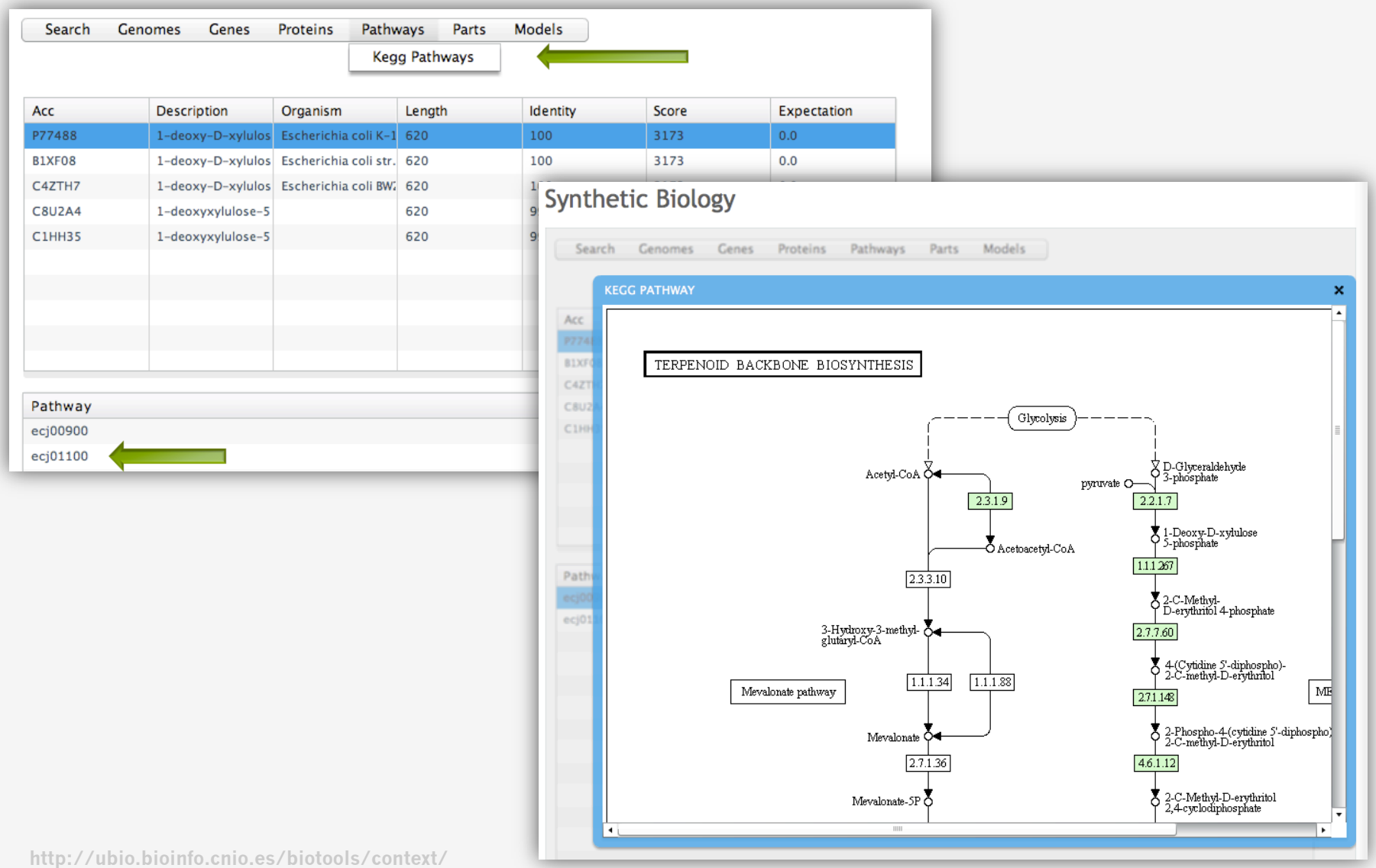


protein odr-10

odr-10 encodes a member of the 7-transmembrane family of odorant receptors which affects chemotaxis to the volatile odorant diacetyl. ODR-10 is strongly expressed in the cilia of the AWA olfactory neurons and, at low levels, in the CEP neurons. expression of odr-10 mRNA and of an odr-10::GFP fusion gene is greatly reduced in odr-7 mutant animals, suggesting that odr-7, which encodes a predicted transcription factor, functions upstream of odr-10 in specifying AWA neuronal cell fate

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Pathways


Search
Genomes
Genes
Proteins
Pathways
Parts
Models
Kegg Pathways
Acc
Description
Organism
Length
Identity
Score
Expectation
P77488
1-deoxy-D-xylulos
Escherichia coli K-1
620
100
3173
0.0
B1XF08
1-deoxy-D-xylulos
Escherichia coli str.
620
100
3173
0.0
C4ZTH7
1-deoxy-D-xylulos
Escherichia coli BW
620
C8U2A4
1-deoxyxylulose-5
620
C1HH35
1-deoxyxylulose-5
620
Pathway
ecj00900
ecj01100
Synthetic Biology
KEGG PATHWAY
TERPENOID BACKBONE BIOSYNTHESIS
Glycolysis
Acetyl-CoA
2.3.1.9
Acetoacetyl-CoA
2.3.3.10
3-Hydroxy-3-methyl-glutaryl-CoA
1.1.1.34
1.1.1.88
Mevalonate pathway
Mevalonate
2.7.1.36
Mevalonate-5P
pyruvate
D-Glyceraldehyde 3-phosphate
2.2.1.7
1-Deoxy-D-xylulose 5-phosphate
1.1.1.267
2-C-Methyl-D-erythritol 4-phosphate
2.7.7.60
4-(Cytidine 5'-diphospho)-2-C-methyl-D-erythritol
2.7.1.148
2-Phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol
4.6.1.12
2-C-Methyl-D-erythritol 2,4-cyclodiphosphate

Build new designs or redesigning composite parts

Lac+RBS+KaiA+Lac+RBS+KaiC

Composite of J36831 and J36834. KaiA and KaiC protein expression in the ratio 1:2 by amount or ~1:4 by mass.

Sequence and Features

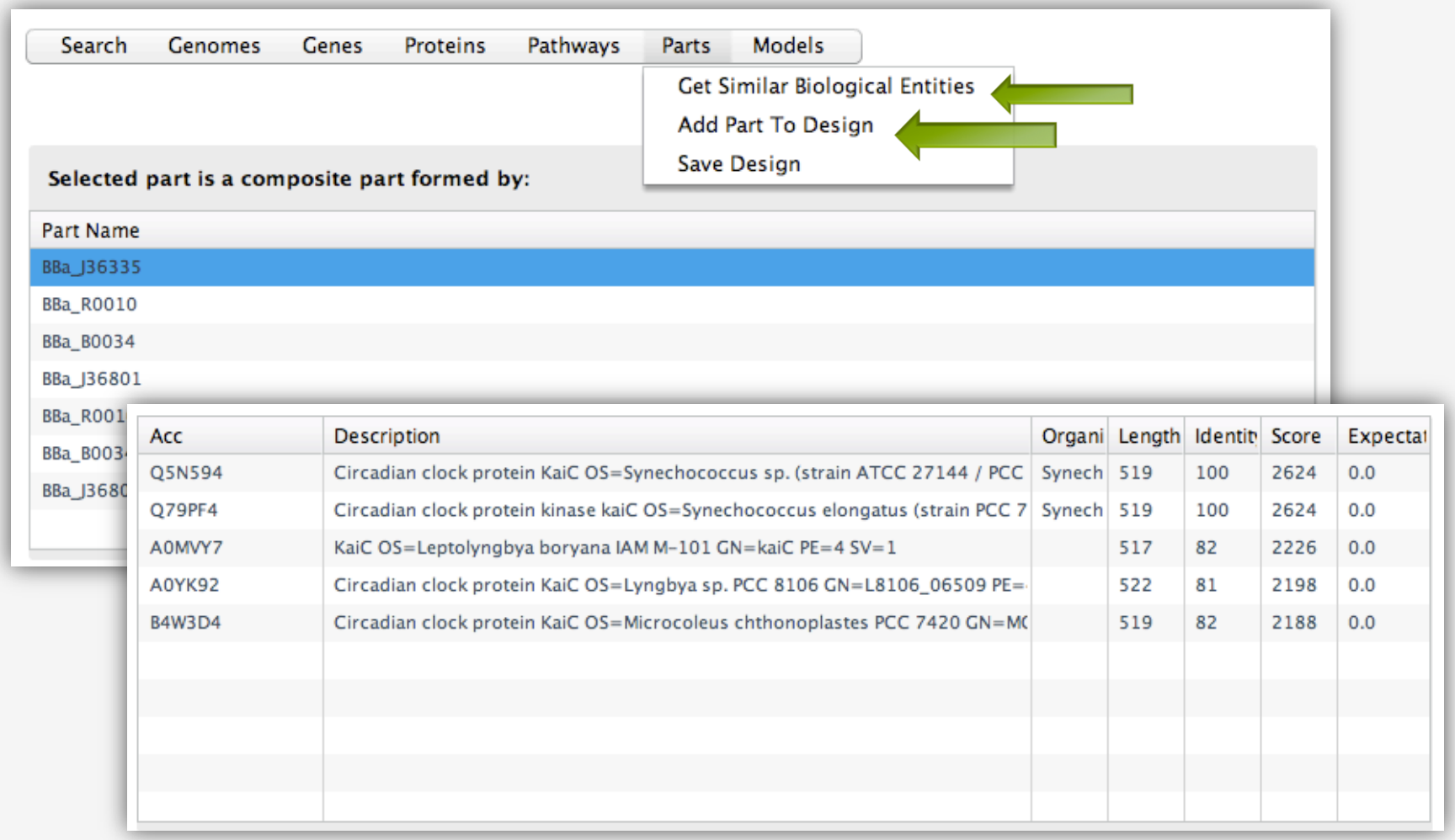
Format: Subparts | Ruler | SS | DS Search: Length: 2883 bp Context: Part only Get selected sequence

Assembly Compatibility: 10 21 23 25

Selected part is a composite part formed by:

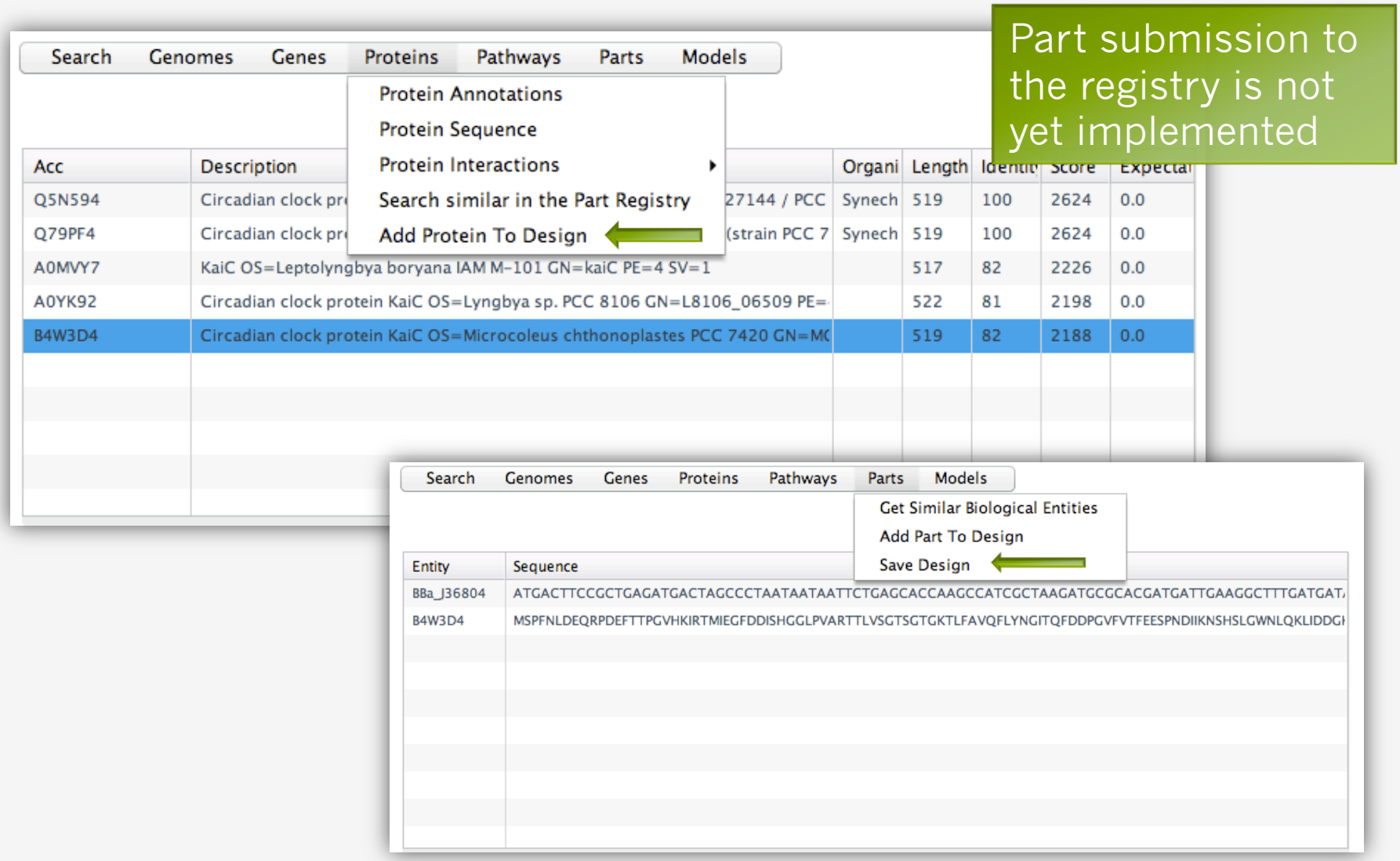
Part Name
BBa_J36335
BBa_R0010
BBa_B0034
BBa_J36801
BBa_R0010
BBa_B0034
BBa_J36804

Adding Parts to a new design



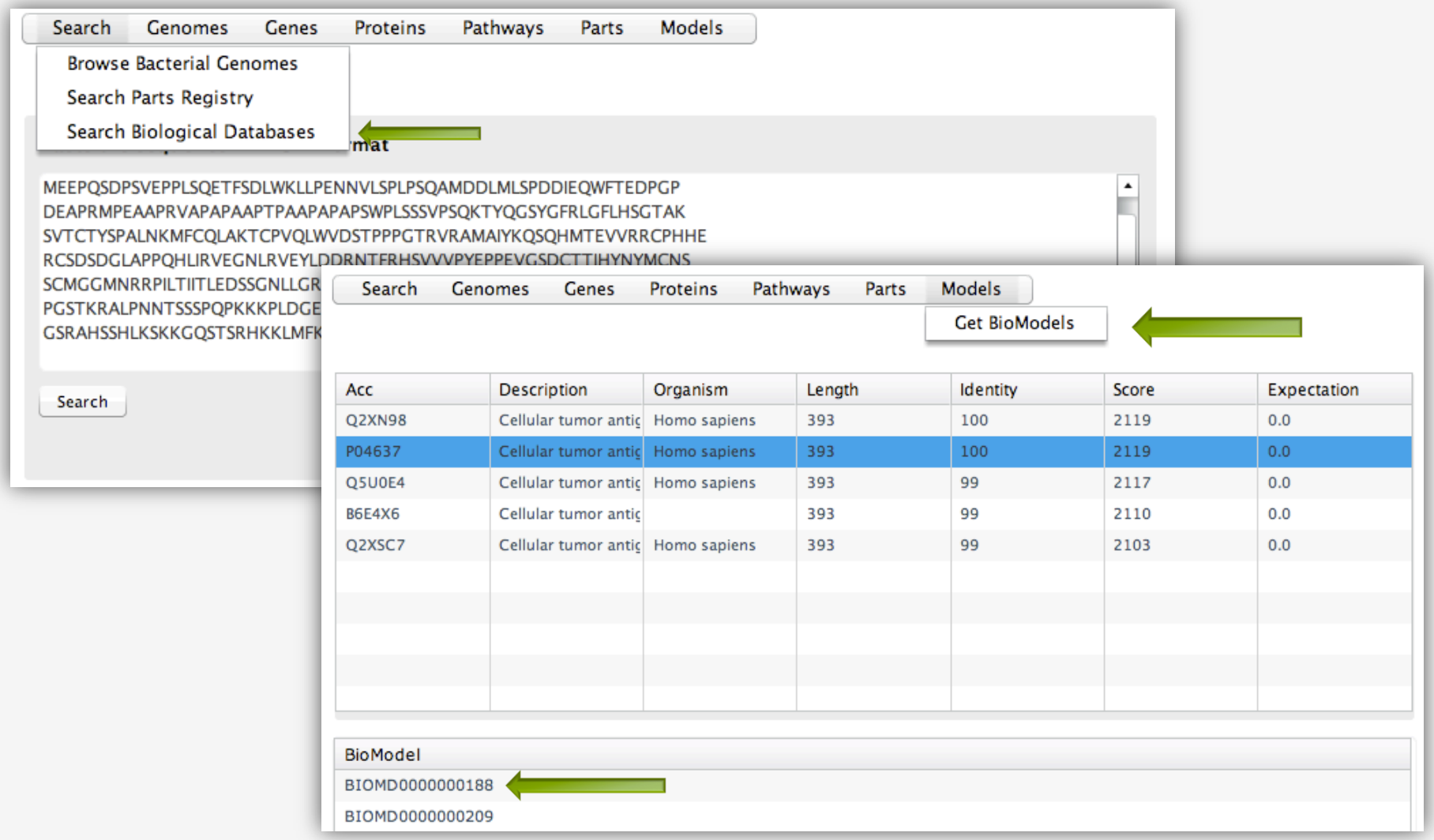
http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Adding other proteins



Part submission to the registry is not yet implemented

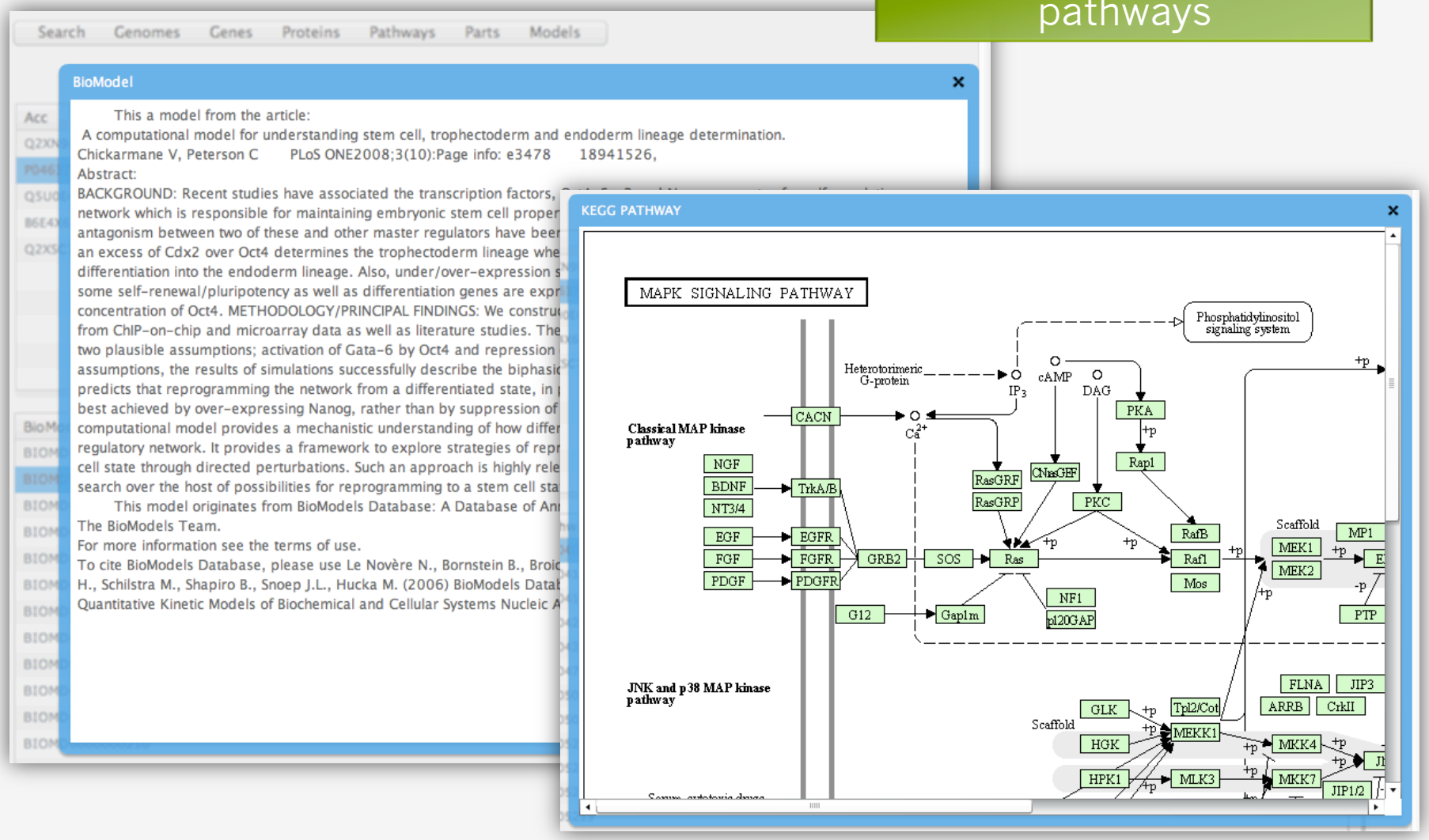
Implement BioModels ?



http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Get BioModel description

Compare models with pathways



http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

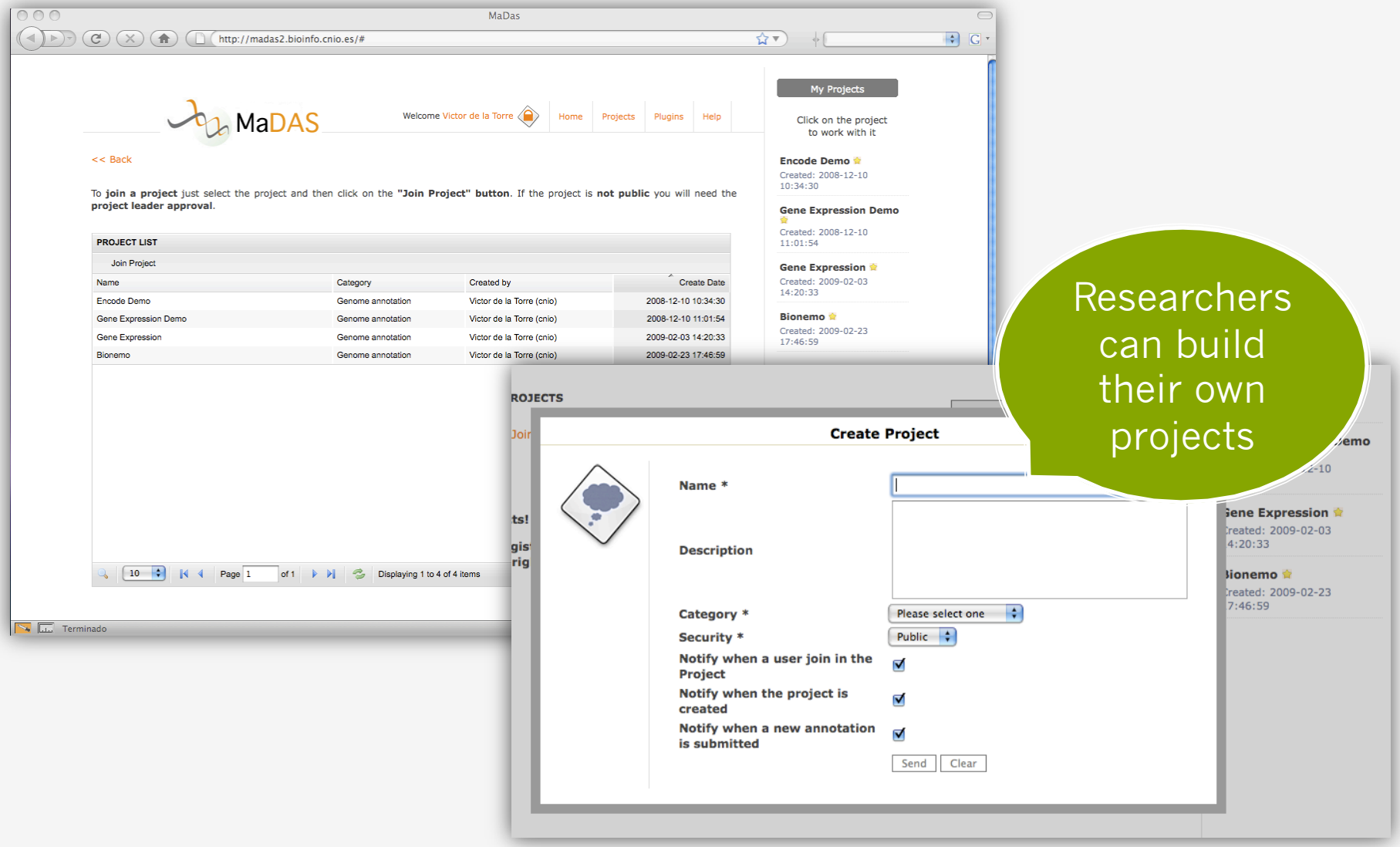
Adding new annotations

- MaDAS system

(http://madas2.bioinfo.cnio.es)

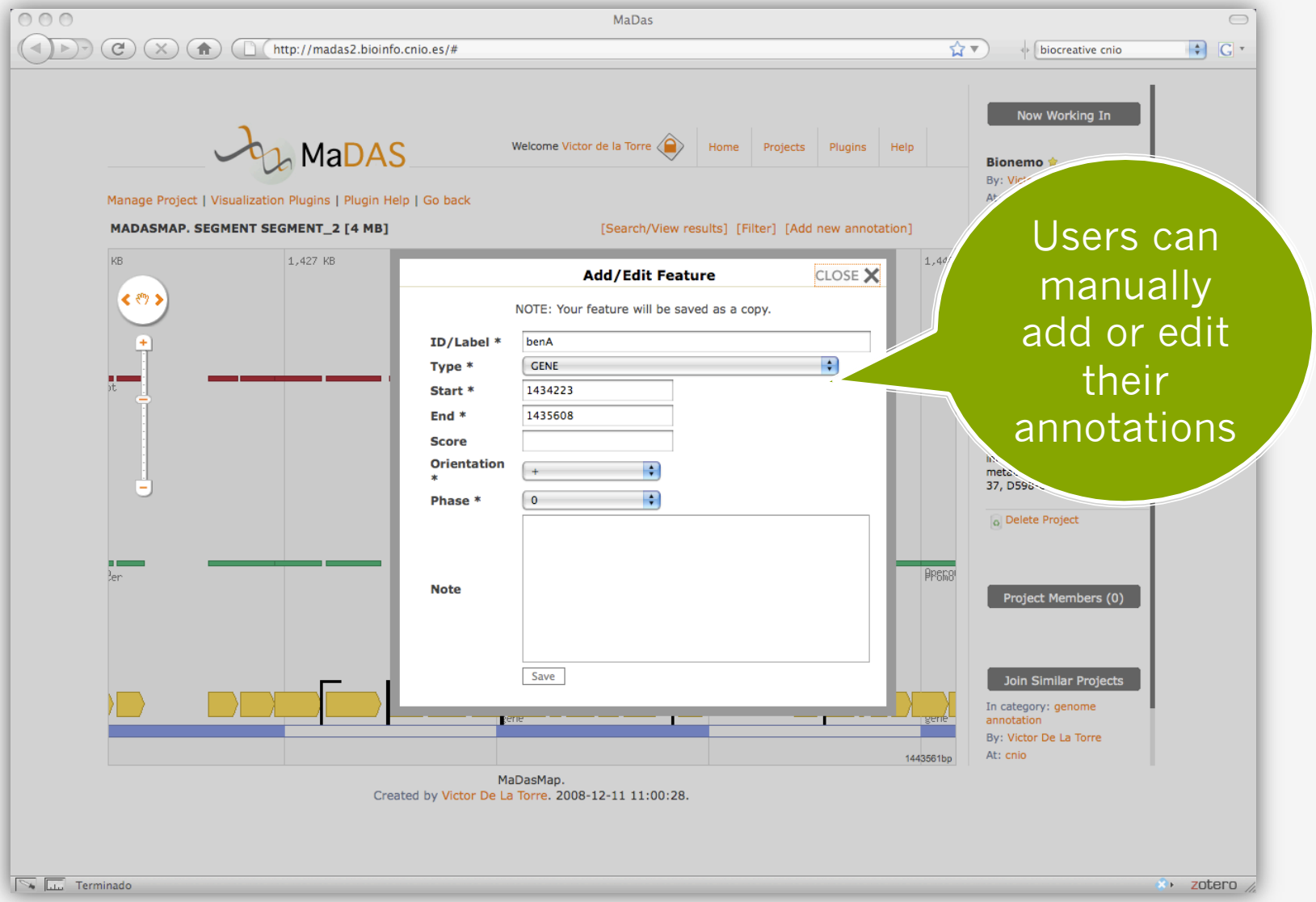
- Submission to the part registry (Not yet implemented)
- Submission to MaDAS (Not yet implemented)

MaDAS. Project based annotation system



http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Adding new annotations



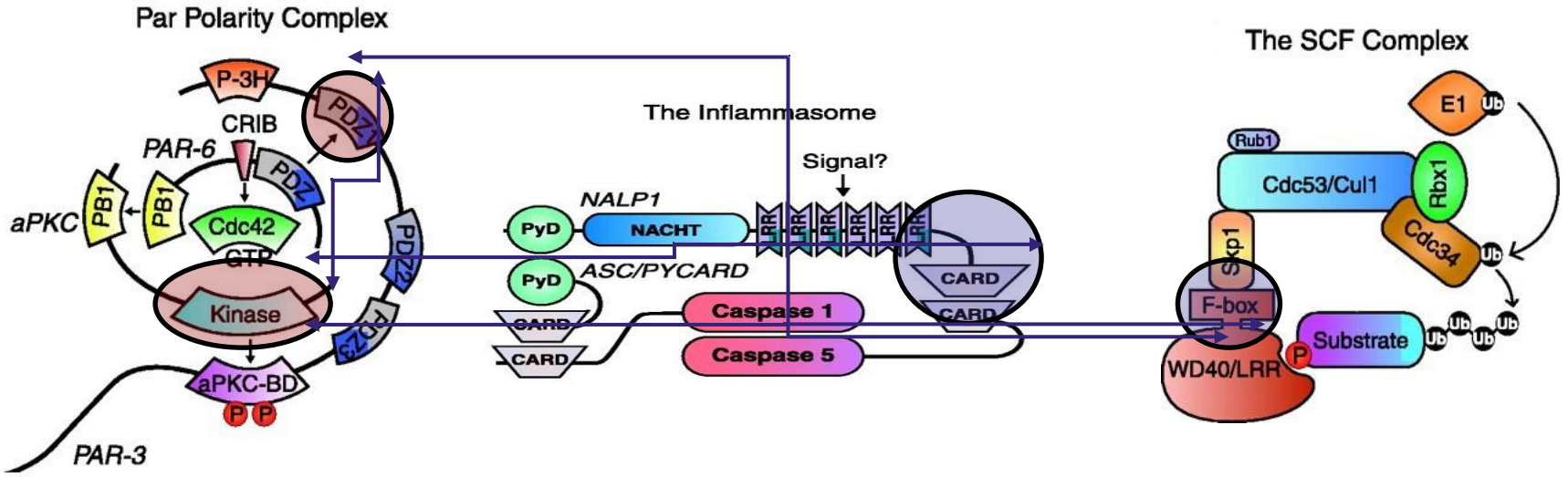
Acknowledgments

- MIT Parts Registry: Randy Rettberg.
- FireDB: Gonzalo López.
- Bionemo: Guillermo Carbajoza, Almudena Trigo.
- iHOP: Robert Hoffmann, Martin Krallinger, Jose M. Fernandez.
- Idelfonso Cases and Alfonso Valencia.

Thanks!

http://ubio.bioinfo.cnio.es/biotools/context/
Contact: vdelatorre@cnio.es

Protein Synthetic Biology



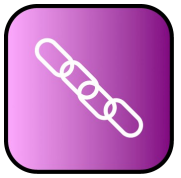
Protein BioBricks

promoter + RBS

- T7 (E. coli)
- ADH1 (yeast)
- GAL S (yeast)
- CUP1 (yeast)

interaction

- Leu Zippers:
  - … parallel
  - … anti-parallel
  - … heterodimer
  - … fast
  - … slow
- FRB / FKBP
- Lov2 / Lov2



linker

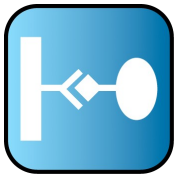
- $(GS)_1$
- $(GS)_3$
- $(GS)_5$
- $(GS)_7$
- $(GS)_{10}$
- P_4
- P_{10}
- P_{15}

measurement

- mCitrine
- mCherry
- mCerulean
- H. Gaussia Luciferase A+B
- b-Lactamase A + B
- B-Lactamase* A + B

cleavage

- TEV site
- preScission



affinity

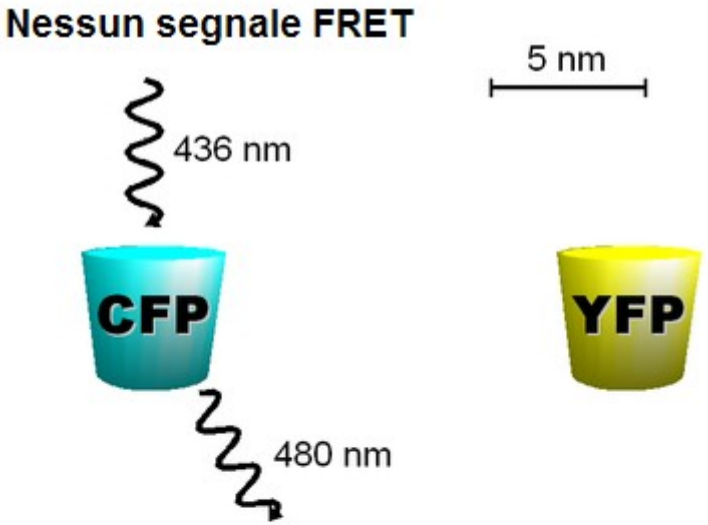
- His
- StrepII
- Gst

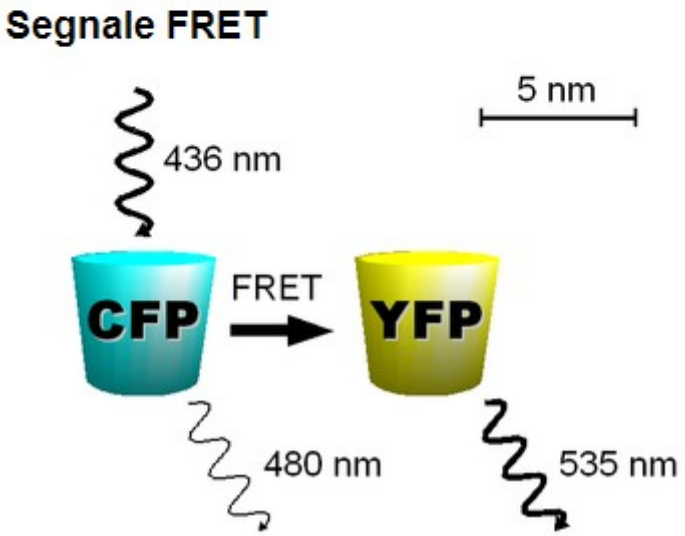
terminator

- T7
- ADH1

* Icons from http://partsregistry.org

FRET Crash Course





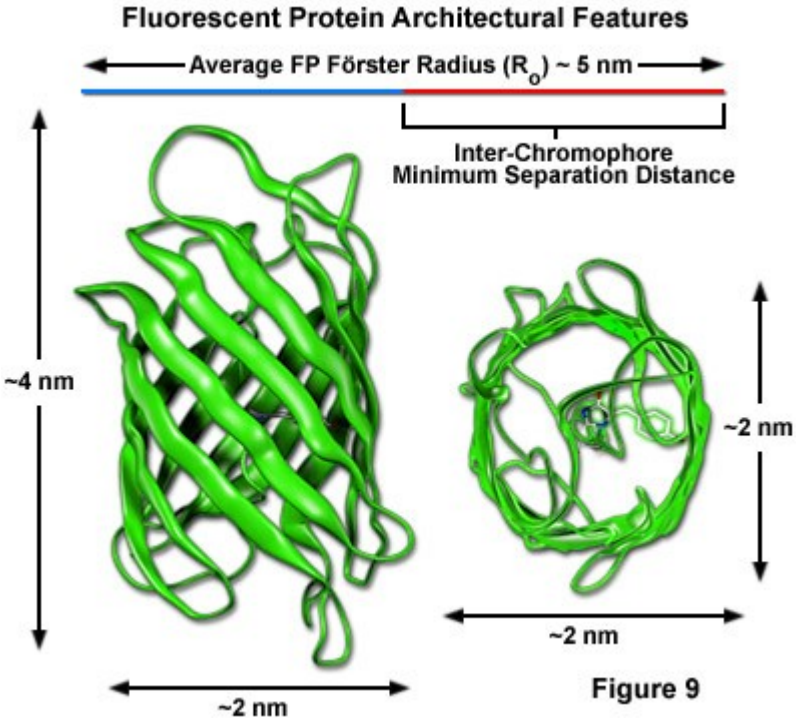
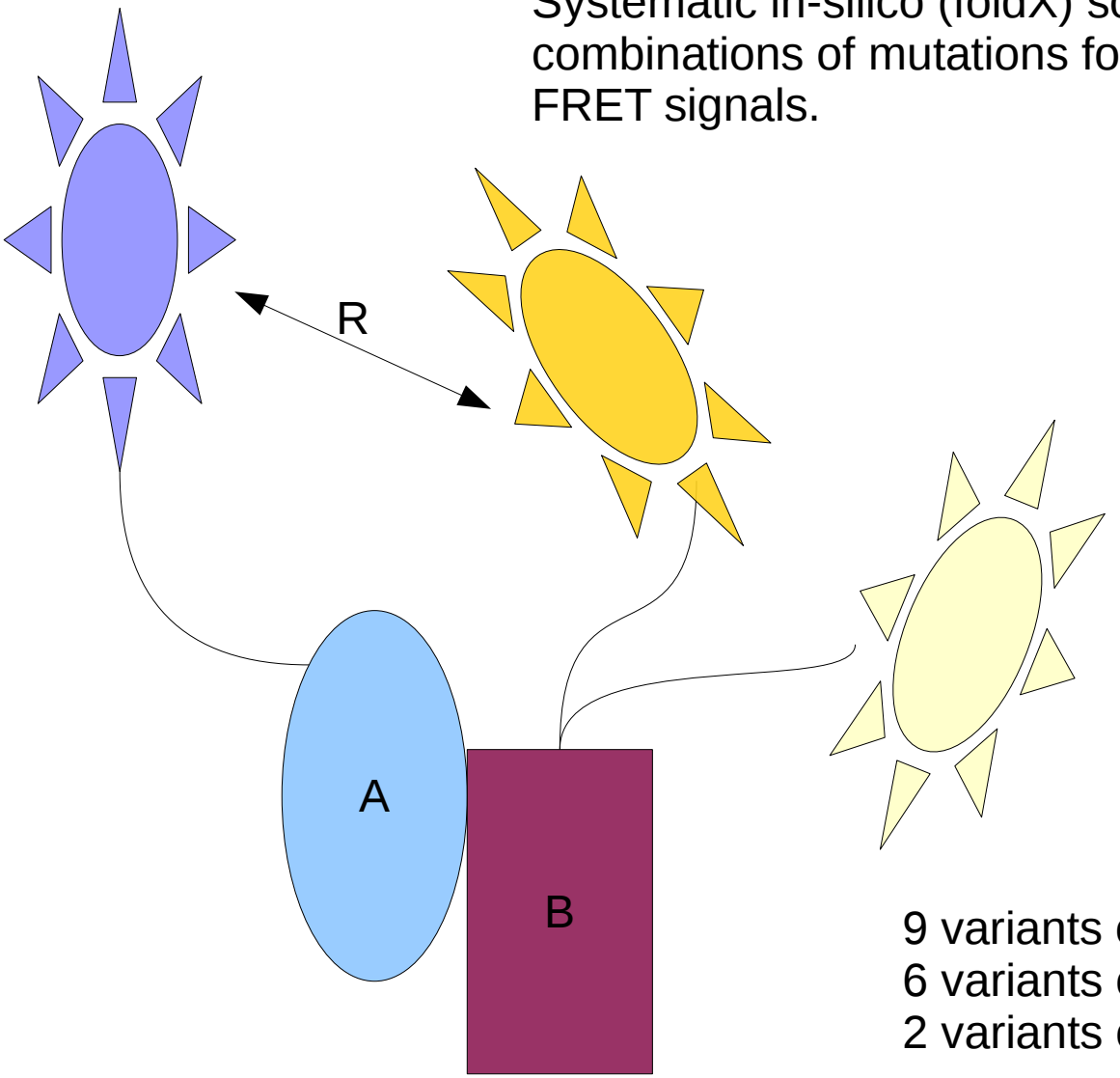


Figure 9

Enhanced FRET

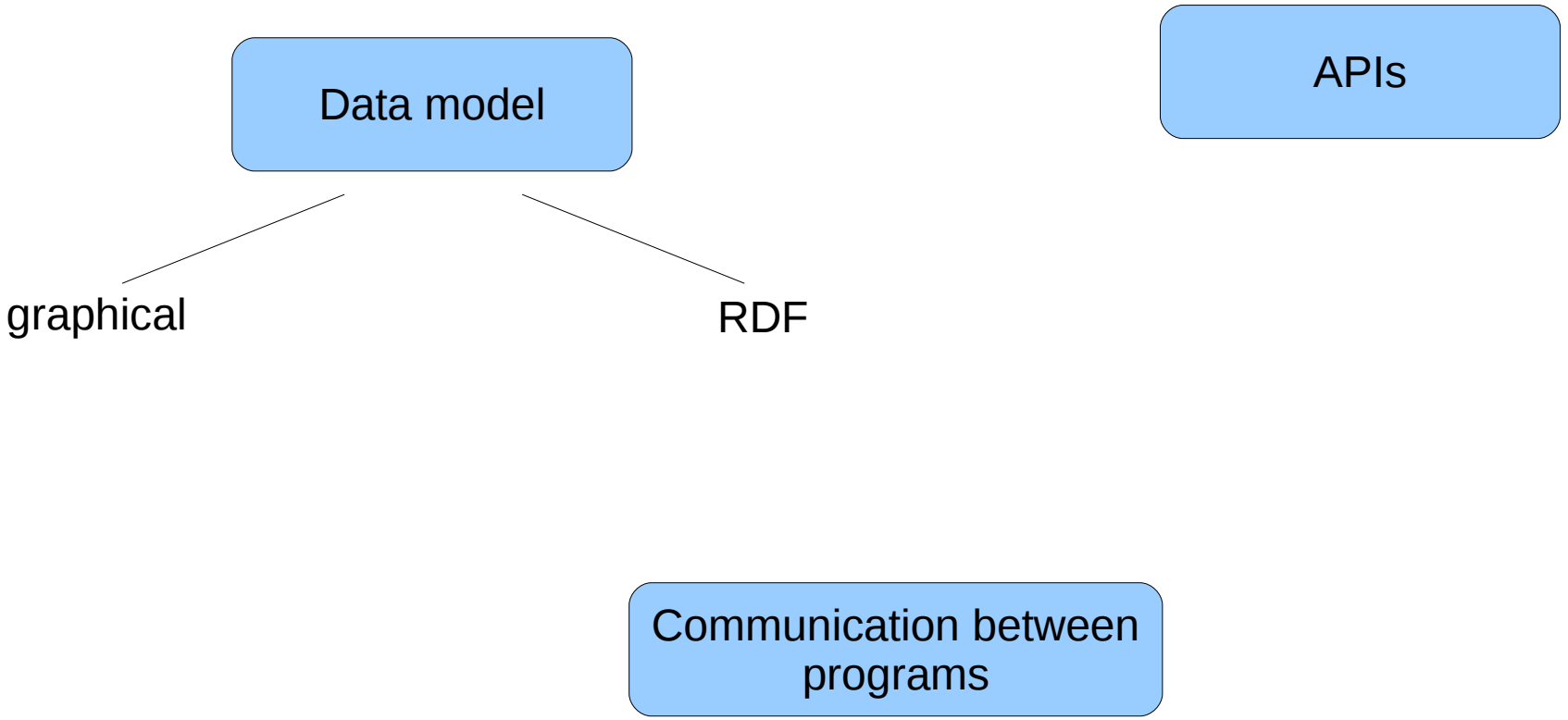
Systematic in-silico (foldX) screen of 100K combinations of mutations for sets that improve FRET signals.



9 variants of cyan (CFP)
6 variants of yellow (YFP)
2 variants of red (RFP)

PoBOL ->SBOL

Synthetic Biology Open Language



Emergence

A foundation for Synthetic Biology in Europe

WP4

(Victor de Lorenzo & Nicolas Szita)

Towards a consensus language for synthetic biology

Esteban Martínez
(CNB, CSIC)

Towards a consensus language for synthetic biology

Deliverables WP4:

4.1: Database on quantitative promoter performance

4.2: Application of design tools on standardized promoters

Towards a consensus language for synthetic biology

Deliverables WP4:

4.1: Database on quantitative promoter performance

Not achieved

Not an adequate format yet!

4.2: Application of design tools on standardized promoters

Why not adequate?

Great variability in promoter data measurements

Not reliable

Database on quantitative promoter performance

Great variability in promoter data measurements

Promoter data obtained with indirect measurements (reporters)

What are reporter genes?

- Structural genes (promoter-less)
- Not present in the organism under study
- Easily measurable and quantifiable products

Variability points:

1- Reporters

2- Genetic tools: vectors & chassis

Review paper project dealing with transcription/reporter systems in BIOESSAYS

Variability in measurements

1-Variability within reporters

1.1- Different type of reporters

- Most used: Enzymatic signal — *lacZ*
  Visual signal — *lux* or *gfp*
- Others: Ice nucleation — *inaZ*
  Enzymatic signal — *gusA*

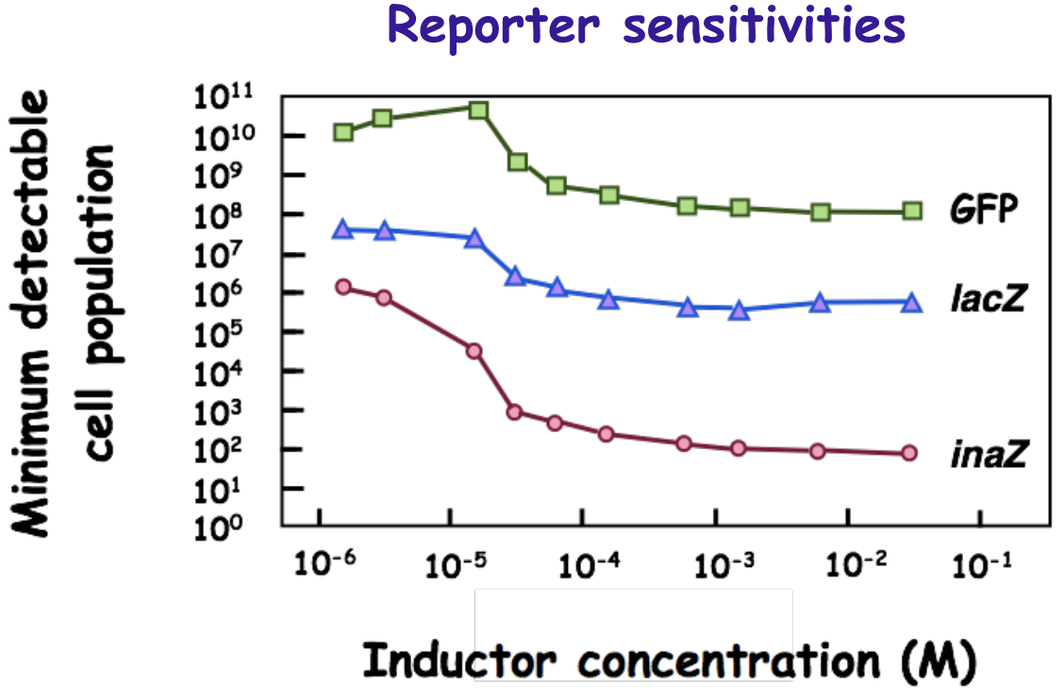
1.2- Differences within the same reporter

Different genetic variants of the same reporter gene

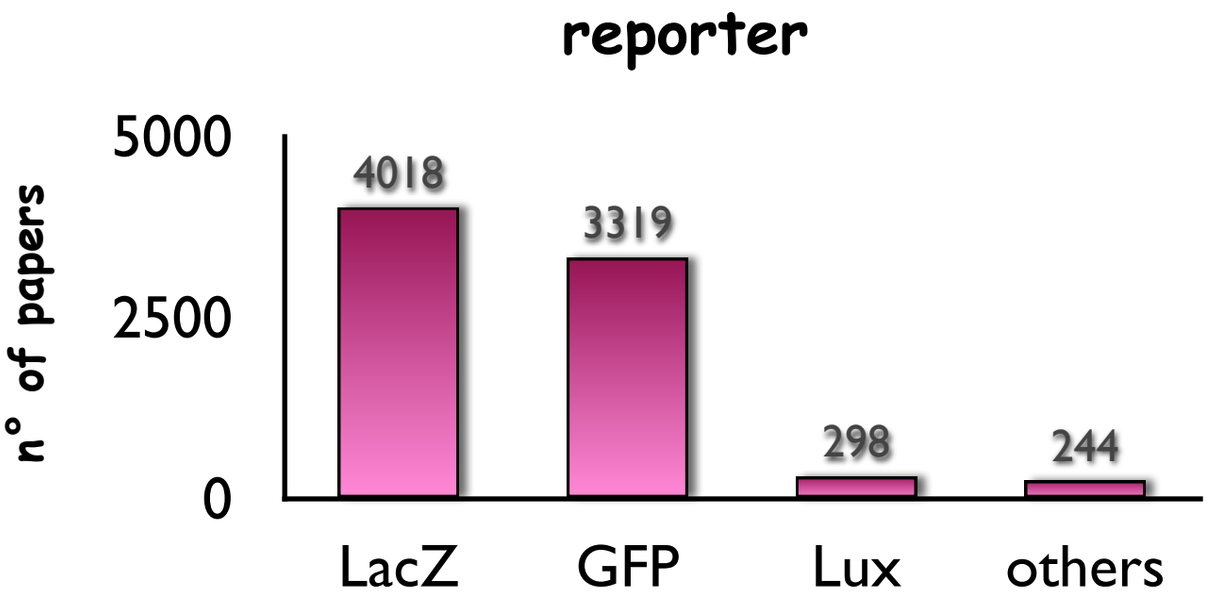
- *lacZ* or *trp-lacZ*
- Many *gfp* versions: *gfp*-WT or *egfp, etc* (differences over 80-fold more fluorescence)
- Complete *lux* operon vs. *luxAB*

So, what reporter is best?

lux	*GFP*	*lacZ*
Non-invasive	Non-invasive	Invasive & Non-invasive
No excitation	Excitation	No excitation
Population	Population & Single cell	Population & Single cell
Costly	Non-costly	Non-costly
Dimer	Monomer	Tetramer



Miller et al. App. Environ. Micro. 2001



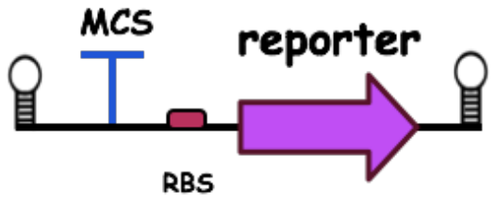
Mostly, depends on the experiment settings

Variability in measurements

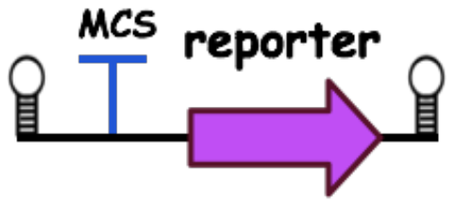
2- Variability in genetic tools

2.1- Type of reporter fusion

- Transcriptional fusions



- Translational fusions



2.2- Type of vectors

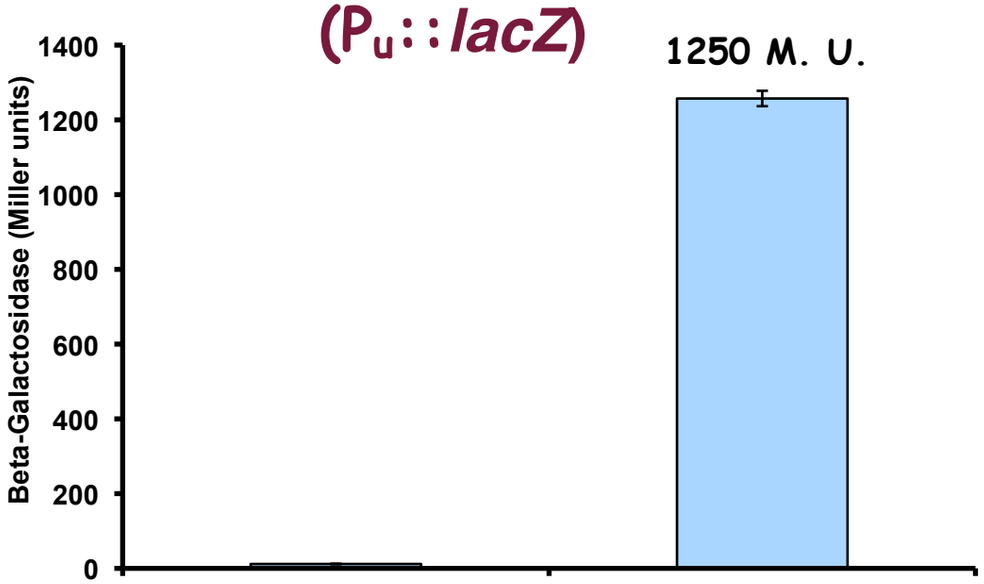
- Copy number: Multi-copy vs. low-copy vs. mono-copy
- Host range (not only for *E. coli*)
- Stability (without antibiotic selection)

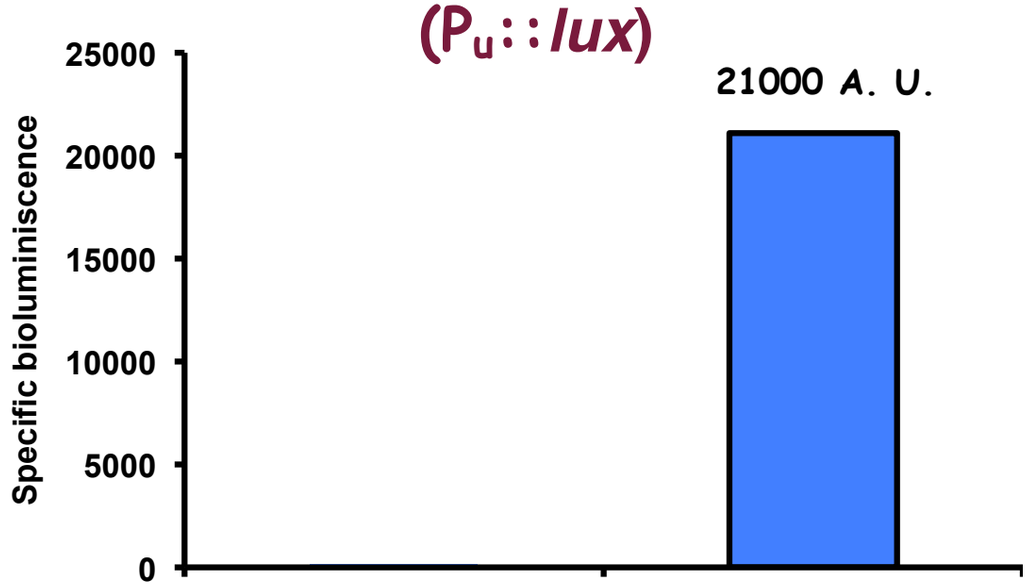
2.3- Chassis

- Genetic repertoire
- Background levels

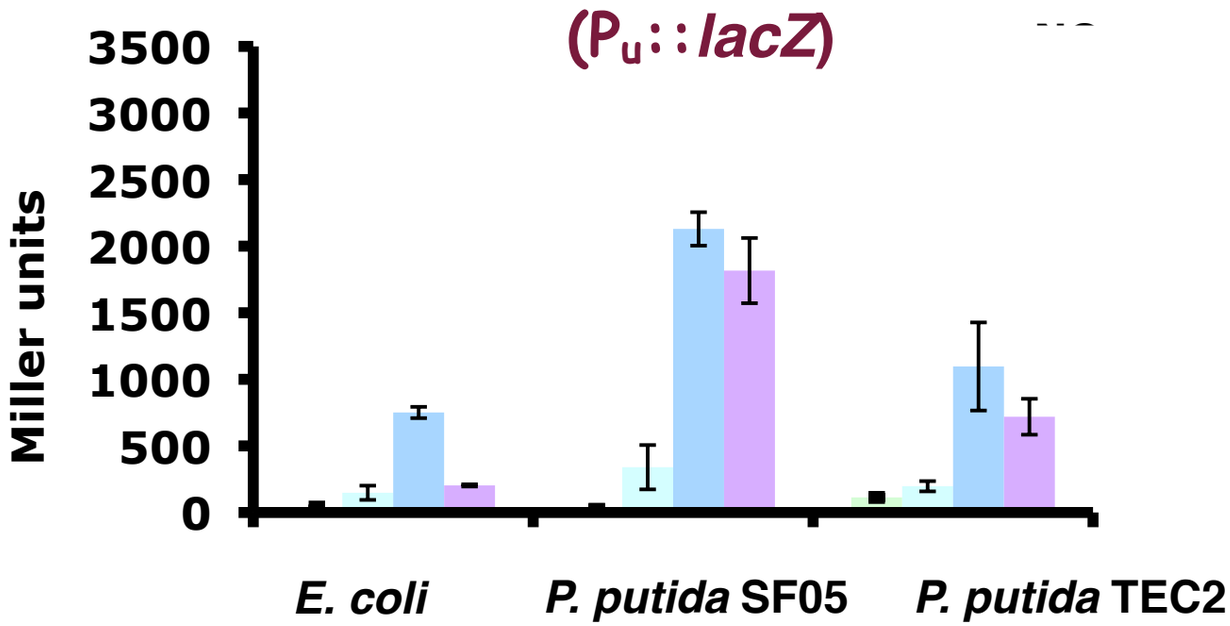
Promoter measurements variability examples

Reporter differences





Strain differences



Towards a consensus language for synthetic biology

Deliverables WP4:

4.1: Database on quantitative promoter performance

Not achieved

Not an adequate format yet!

4.2: Application of design tools on standardized promoters

- **Develop Standard Genetic Tools**

  Plasmids vectors & Genome integration systems

- **Standard measures**

Towards a consensus language for synthetic biology

What do we need to develop SB field further?

Expression systems to build regulatory complex networks

(lacI-P_{lac}, TetR-P_{tet} & CI-P_{RM})

Define promoter activity and regulators in a standard fashion

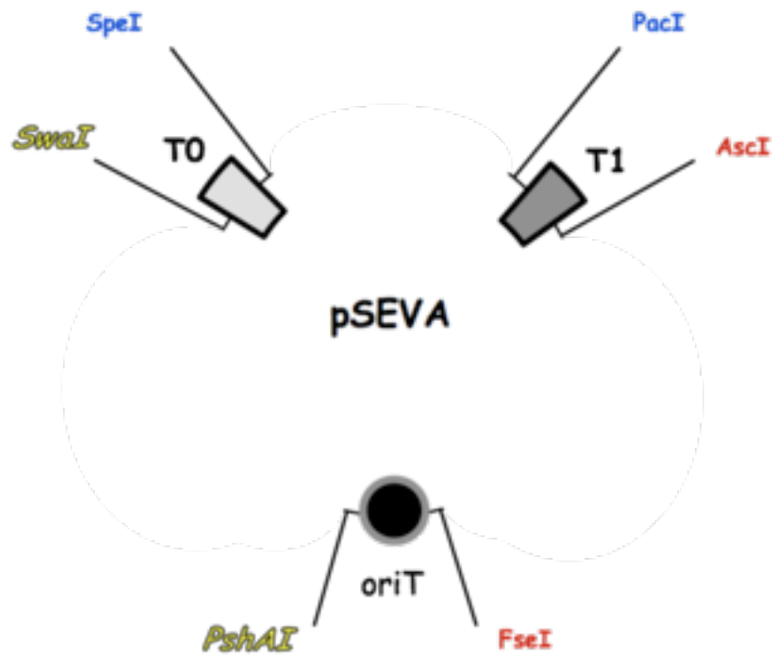
Standard Genetic tools

pStandardEuropeanVectorArchitecture

Backbone

- Minimal origin of transference: oriT-RP4 (260 bp)

- Terminators: T_0
  T_1



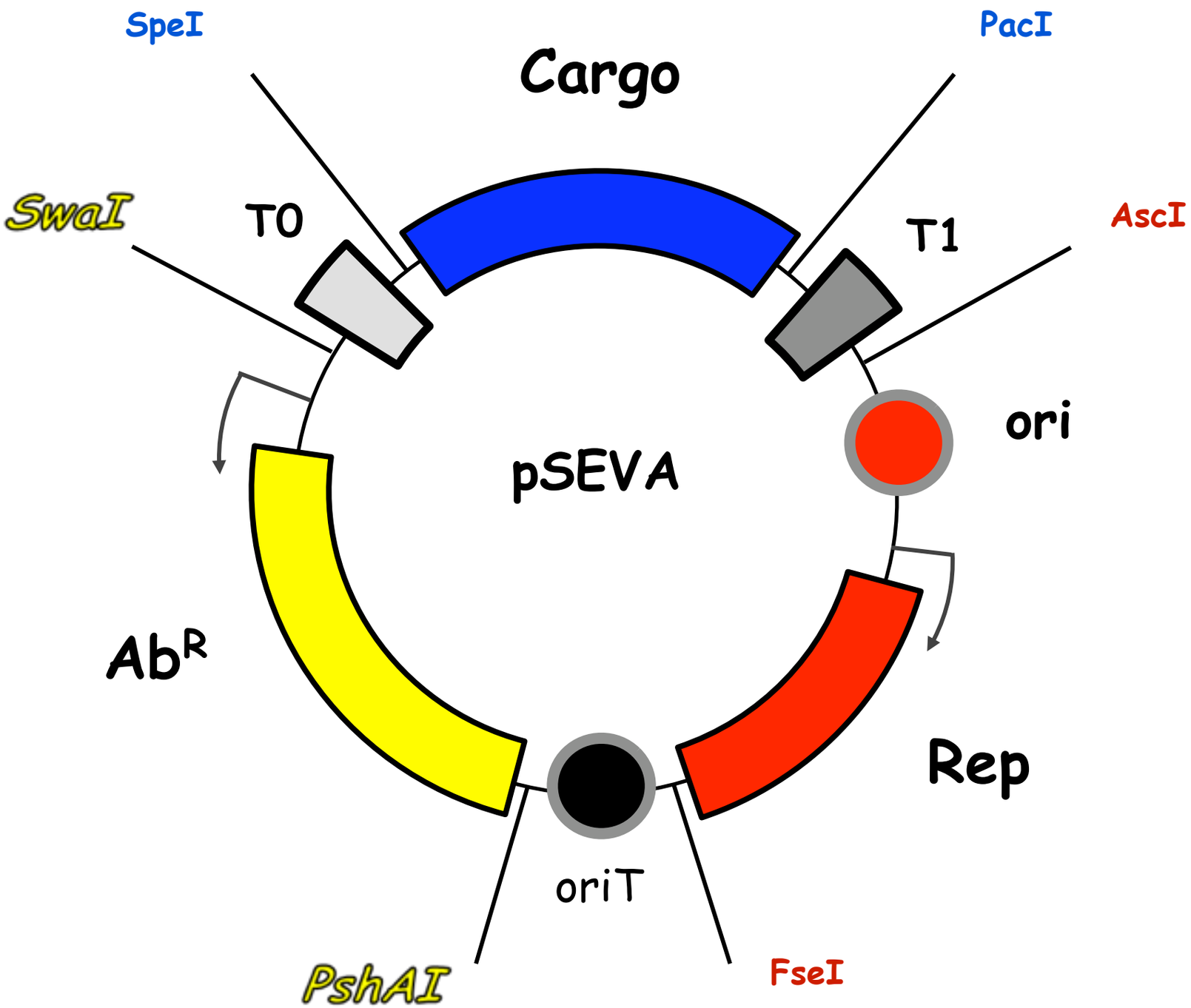
Modules

1) Origin of replication
2) Antibiotic resistance marker
3) Cargo site

- Modules flanked by rare cutting restriction enzymes

Backbone & modules curated of common restriction sites

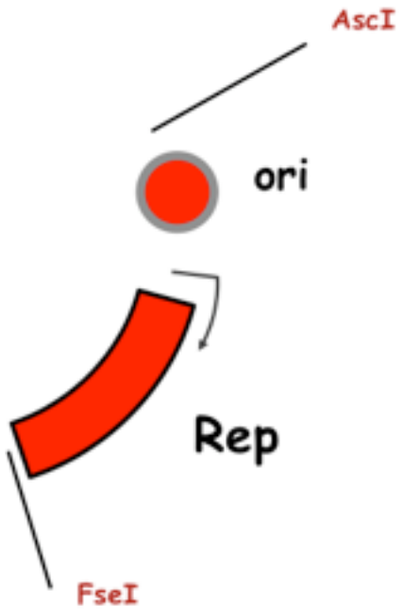
pSEVA


SpeI
PacI
Cargo
SwaI
T0
T1
AscI
ori
pSEVA
Ab^R
Rep
oriT
PshAI
FseI

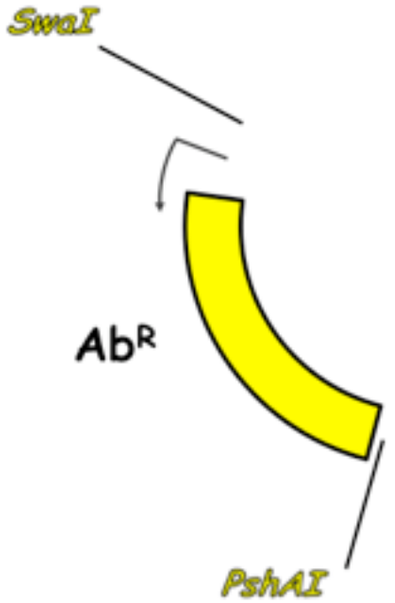
pSEVA modules

1) Origin of replication:

- RK2 (very low copy number)
- RSF1010 (very low copy number)
- pBBR1 (medium copy number)
- pRO1600 (High copy number)
- R6K (Π-dependent replication)



2) Antibiotic resistance marker:

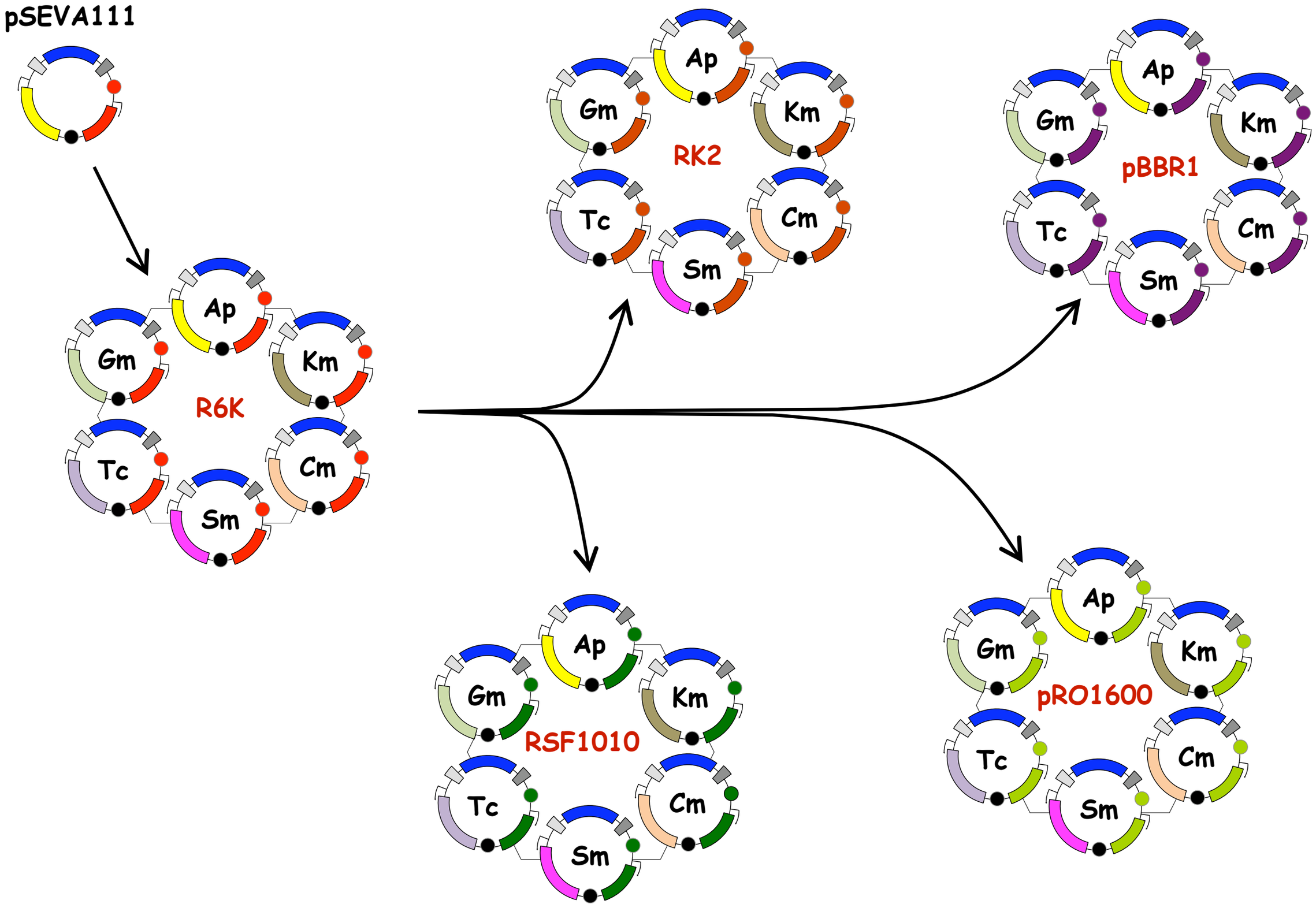


- Ampicillin
- Gentamycin
- Kanamycin
- Streptomycin
- tetracycline
- Chloramphenicol

3) Cargo site:

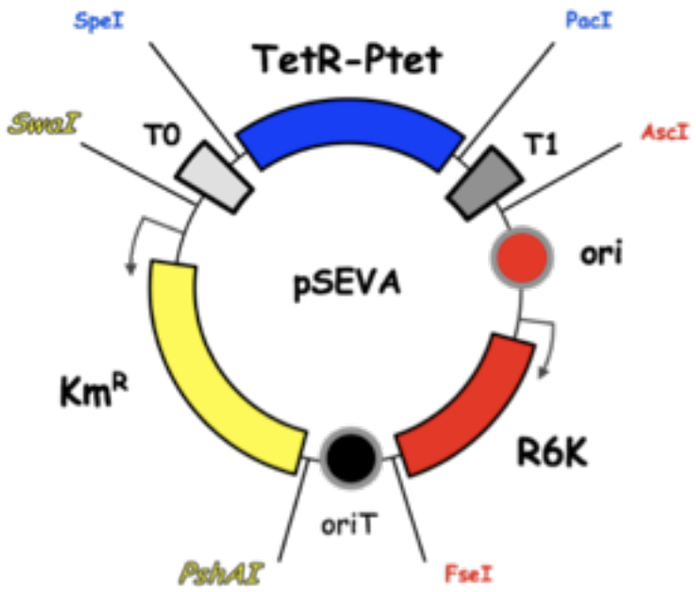
- Cargo polylinker: pUC18 enzymes plus NotI, SfiI & AvrII
- Cloning cargos: lacZα from pUC19 & pUC18
- Transcriptional fusions
- Expression systems

pSEVA collection



pSEVA modules exchange examples

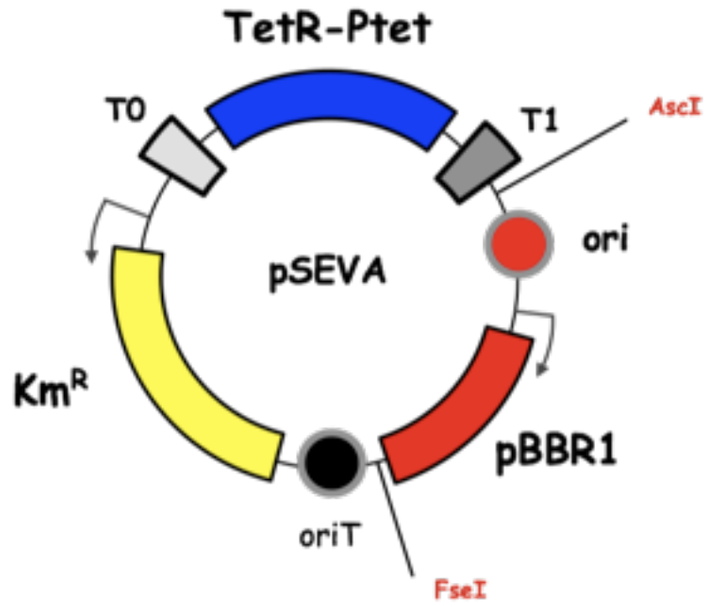
TetR-P_{tet}, Km^R, R6K



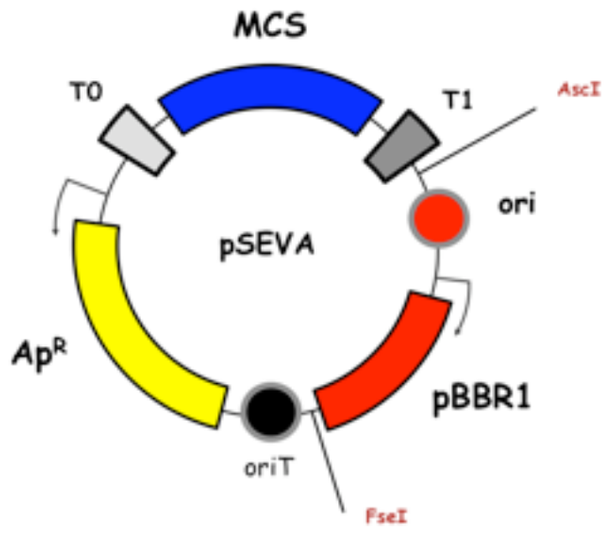
AscI & FseI

Origin of replication exchange

TetR-P_{tet}, Km^R, pBBR1



pBBR1 origin donor

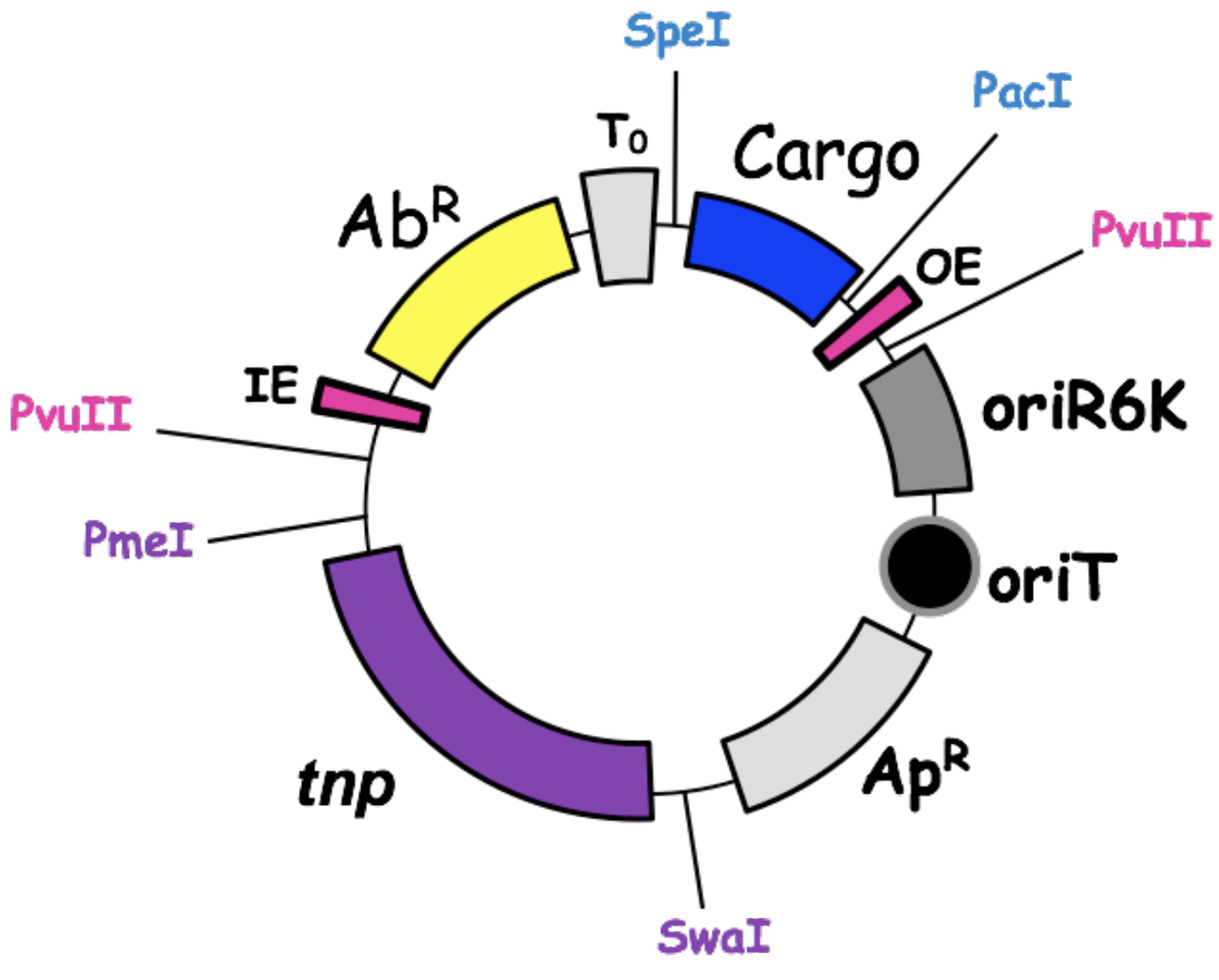


pStandard European Transposon Architecture

Uses:

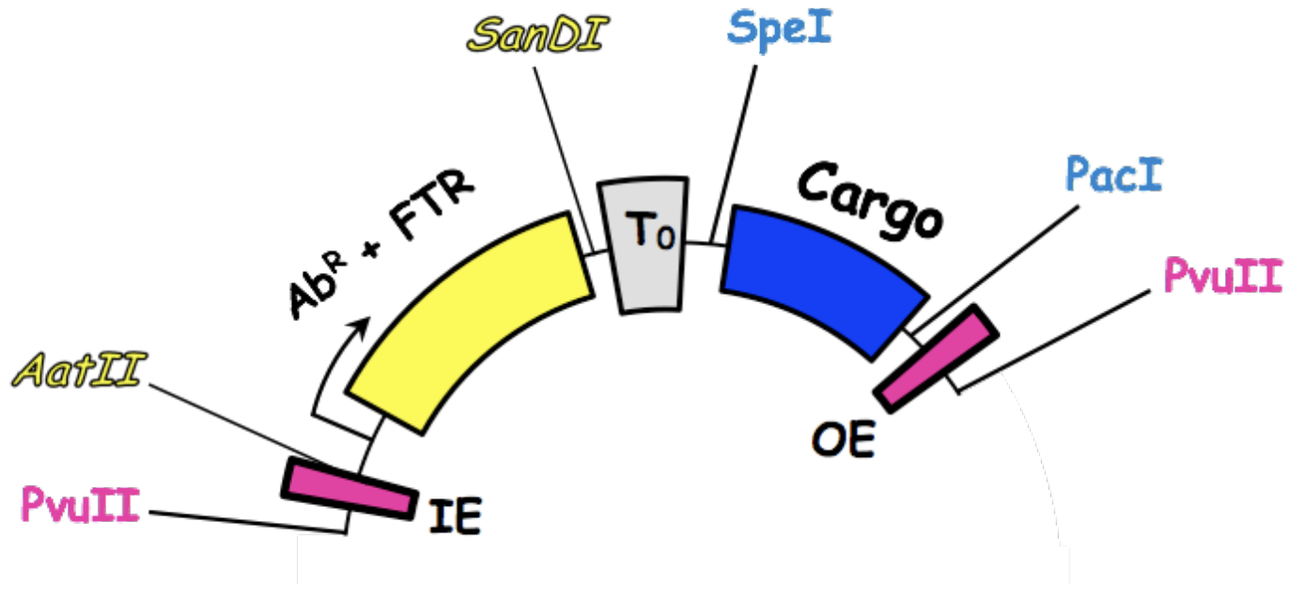
- To integrate cargos into the genome

- Random mutagenesis

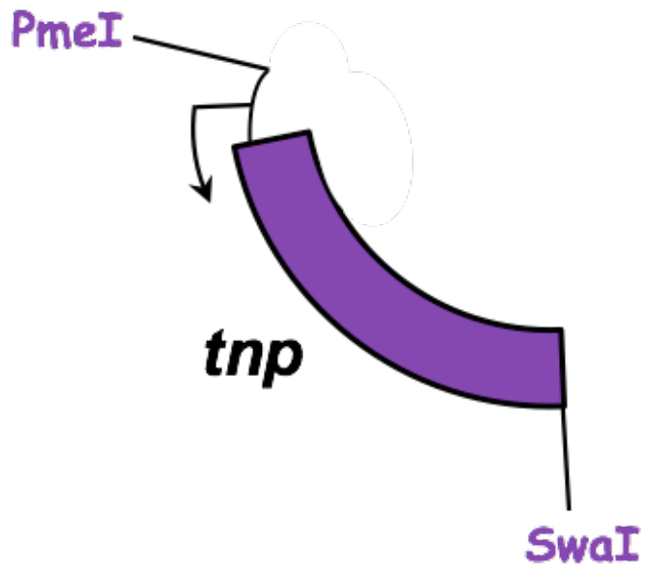


pSETA

The transposon module



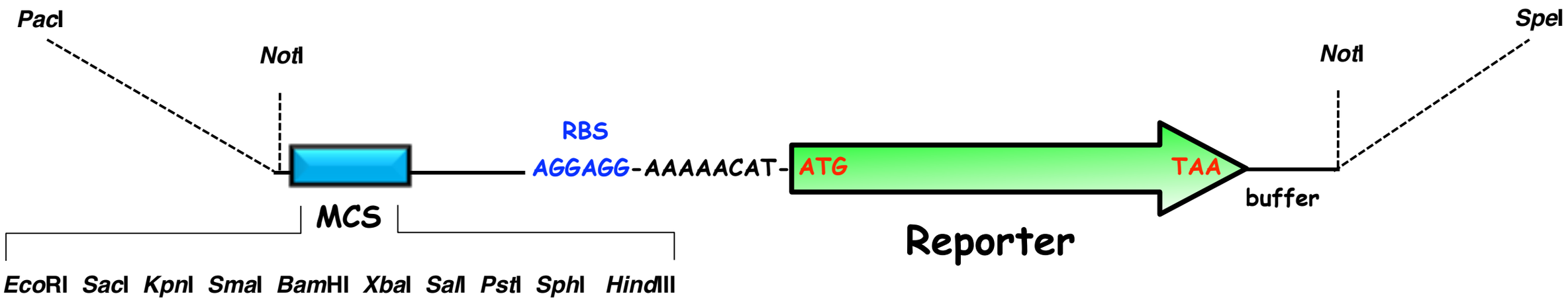
The transposase module



- Tn5
- Tn7
- Mu
- Mariner

pSEVA cargos

Promoter quantification systems



Sequence-edited reporters

- GFP: *gfp* with F64L & S65T mutations (717 bp)
- LacZ: *lacZ* (3075 bp)
- Lux: *luxCDABE* (5798 bp)

Advantages

Same plasmid backbone

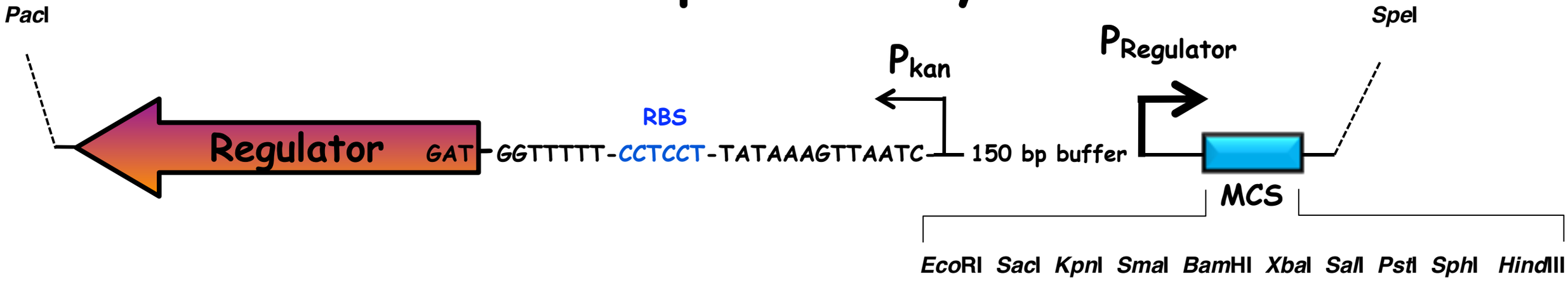
Copy number at choice

Different reporters

Promoter / reporter calibration curves

pSEVA cargos

Gene expression systems



Regulator-P_R edited systems

Promoter	Regulator	Type	Inductor
P_{tet}	TetR	Repressor	Anhydrotetracycline
P_{tac}	$LacI^q$	Repressor	IPTG
P_m	XylS	Activator	Benzoate
P_u	XylR	Activator	Xylene
P_{alkB}	AlkS	Activator	Alkanes
P_{Sal}	NahR	Repressor	Salicylate

Towards a consensus language for synthetic biology

Synthetic edited DNA segments for pSEVA vectors

DNA piece	Function
Tellurite resistance	Non-antibiotic marker
AlkS	Expression system based on alkanoates
Conditional oriV pBR322 TetR	Conditional expression based on Tc
LacZ	Promoter reporter with optimized RBS
LacZα-pUC18	For cargo cloning
TAP/I-SceI	System for TAP tag induction in chromosomal genes
NBP-TNT	Two component sensor (TNT)
TetR-P_{tet}-GFP	GFP expression based on Tc

Towards a consensus language for synthetic biology

Meetings

Microfluidics as analytical tool for SB measurements Nicolas Szita (28^{th}-29^{th} May 2009)

Topics:

Invasive analytical techniques for SB measurement & quantification

Non- Invasive analytical techniques for SB measurement & quantification

Microfluidics for high throughput analytics in SB

Towards a consensus language for synthetic biology

Meetings

Sandpit on defining transcriptional standards Victor de Lorenzo (21^{th}-22^{th} October 2009)

Aim: Position paper to define transcriptional measurements standards

Participants

Engineer	Biology	European Comission
Drew Endy	Steve Busby	Ioannis Economidis
Ron Weiss	Richard Gourse	
Christina Smolke	Fernando de la Cruz	Observers
Ido Golding	Martin Buck	Alistair Elfick
Sven Panke	Virgil Rhodius	Rafael Silva Rocha
Vitor dos Santos	Victor de Lorenzo	Esteban Martínez

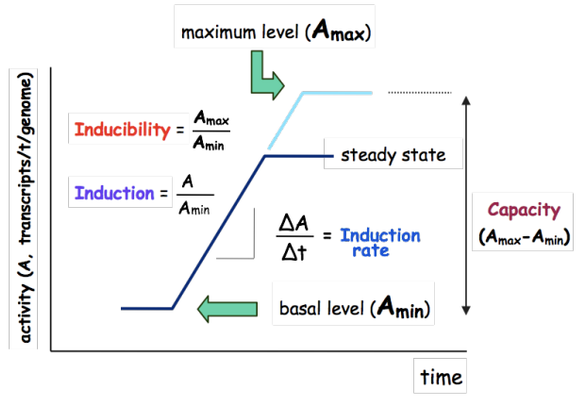
Sandpit on defining transcriptional standards

Topics covered:

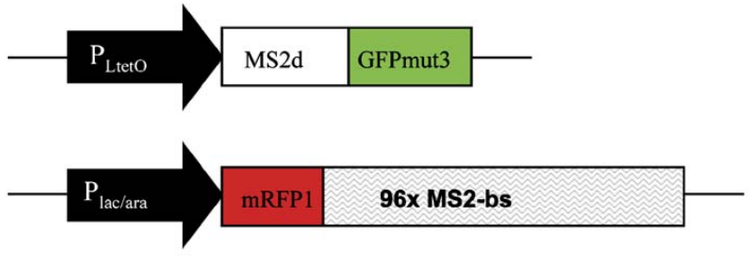
- How to measure promoter strength
- Standard way to perform reporter fusions
- Reporter calibration curves
- Standard reference promoters
- Promoter parameters

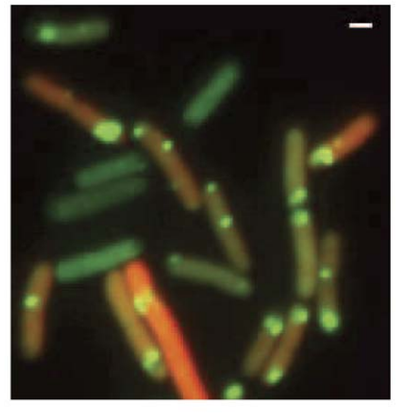
PoPS

RPU



- Indirect vs. Direct measurements*





*: Golding et al. Cell. 2005

Position paper to define transcriptional measurements standards

Towards a consensus language for synthetic biology

Deliverables WP4:

4.1: Database on quantitative promoter performance

Not an adequate format yet!

Review paper project that deals with transcription/reporter systems

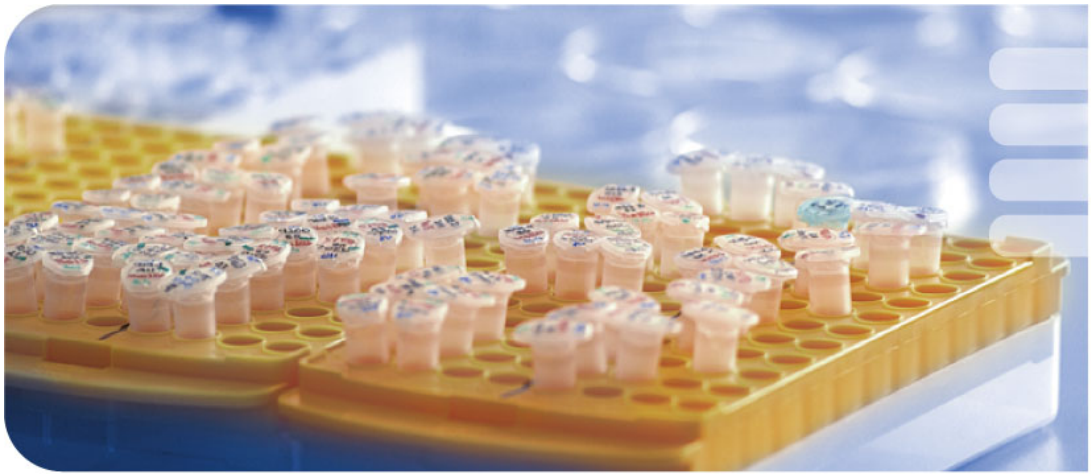
4.2: Application of design tools on standardized promoters

Develop standard plasmid collection (pSEVA & pSETA)

Develop standard promoter quantification plasmids

Develop multiple Regulator-Promoter expression systems

Position paper to define standard measurement procedures



EMERGENCE Meeting; Zürich November 2009

Workpackage 5: Building the Academia-Industry interface

Frank Notka, Ralf Wagner, 13. November 2009

Overview - ACTIVITIES

Workshops/Conference Sessions

- Emergence IP (June 2008)
- Emergence Industry (June 2008)
- SB4.0/ Industrial Biotechnology, Hong Kong (October 2008)
- SATW/acatech, Basel (January 2009)
- DFG Workshop „Synthetic Biology“, Berlin (German Ethic Board) (February 2009)
- Applied industrial Synthetic Biology in Europe, Freiburg (April 2009)
- OECD Workshop, Washington (July 2009)
- DECHEMA/acatech Synthetic Bio(techno)logy, Frankfurt (November 2009)

Industry networks

- DECHEMA **W**orking group Systems Biology and Synthetic Biology (Since February 2009)
- SBIA (Synthetic Biology Industry Association) (est. April 2009)
- BioM-WB – competence cluster White Biotechnology (Since April 2009)
- IGSC (International Gene Synthesis Consortium) (November 2009)

Workpackage 5: Industry Involvement

Priorities:

SynBio in Europe is in a developmental status

Confirmed by industry appearance or better non-appearance of companies at International SB sessions regarding industrial applications

- SB4.0/ “Industrial Biotechnology” (October 2008)
- “Applied industrial Synthetic Biology in Europe” conference (April 2009)
- DECHEMA/acatech “Synthetic Bio(techno)logy” (November 2009)

Highest activity involving companies is found in the field of regulating screening processes to avoid misuse of synthetic genes

- harmonize processes
- in accordance with US government guidelines (to be released in December)

Workpackage 5: Industry Involvement

Public debate and perception:

GENEART
THE GENE OF YOUR CHOICE

Pathways to security

Self-regulation is a good first step — but synthetic-biology companies still need independent oversight.

Regulators have been slow to deal with 'dual use' biological agents such as proteins, DNA or whole organisms that are generally used for benign research, but that could also be used to inflict harm. The reasons are many — not least being the complex way in which these substances behave and interact with their environment — and the result has been a regulatory patchwork.

For example, many countries have tried to regulate the firms that produce made-to-order DNA sequences by requiring permits for export. But the paperwork required is so onerous that the companies often just discard their non-domestic orders — so information about the customers looking to acquire these sequences is lost. And oversight of domestic sales is comparatively lax.

This month, the Industry Association Synthetic Biology (IASB), a consortium of gene-synthesis companies located mainly in Europe, agreed to a series of actions that might provide a more robust solution to the bioterror problem. Several of the US companies in the market have reportedly indicated their willingness to comply. The agreement calls for member companies to develop a database of suspicious or potentially dangerous DNA sequences. The association did note the potential danger of centralizing these data, even though they are already publicly available. But the benefit, argues the IASB, is that an open-source collection will be much easier for experts to keep updated, complete and correct.

Meanwhile, the agreement calls on IASB member companies to share information about the screening processes already in use so that standard practices can be adopted. The firms have said they are willing to cooperate on this effort in a non-competitive way; the report they produced includes ideas for better policing, including a pattern-recognition approach that would be more adaptable to what most predict will be a rise in the number and variety of DNA sequences requested.

These steps, and other proposed elements, are the beginnings of a code of conduct f
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can build

"Industry self-policing can sometimes fail

nature news

Published online 31 August 2009 | Nature | doi:10.1038/461022a

News

Keeping genes out of terrorists' hands

Gene-synthesis industry at odds over how to screen DNA orders.

nature news

Published online 4 November 2009 | Nature | doi:10.1038/news.2009.1065

News

Gene-makers put forward security standards

Workpackage 5: Industry Involvement

History of screening standard:

GENEART
THE GENE OF YOUR CHOICE

Initiative(s) by IASB (International Association Synthetic Biology):

- WS and Report on Biosecurity and Biosafety (September 2008)
- 2nd Workshop on Synthetic Biology (4. November 2009)
  - Code-of-conduct finalization
  - Introduction to ViREP (virolence factor repository data base)

Initiatives by GENEART/IGSC (International Gene Synthesis Consortium):

- Bringing the five leading gene synthesis companies (> ***80% commercial GS***) together to work on solutions for sequence and customer screening (Geneart, DNA2.0, Genscript, Blue Heron, IDT) → press release next week
- Drafting of a best practice protocol for screening → to be published soon
- Assemble a data bank of sequences → combining sequences of concern from all member companies → basis for a public data base with access for all screening companies
- Concerted respond to the guidelines for screening released from the US government

Workpackage 5: Deliverables

Deliverable		Month
5.1	Reports on two industry workshops - to define the priorities of the European industry in the field of synthetic biology, and - to evaluate the fit of the European synthetic biology projects with the industry needs	06/07 & 06/08
5.2	Reports on two workshops (associated to industry-relevant scientific conferences) to teach the industry in synthetic biology concepts and tools	12/07 & 12/08
5.3	Position paper on the priorities of the European industry in the field of synthetic biology, evaluation of fit with current EU synthetic biology projects, and decision on how to address the potential gaps	12/08
5.4	Intermediate and final report on status of discussion regarding IP strategy in the field of synthetic biology, originating from company internal assessments and summarizing the ideas on IP-management (same workshops as in D5.1)	12/07 & 12/09

Workpackage 5

5.1 Reports on two industry workshops

Part 1 : to define the priorities of the European industry in the field of synthetic biology

"Define needs and interests of Industry" EMERGENCE WS (25.06.2008)

→ Report delivered

Part 2: to evaluate the fit of the European synthetic biology projects with the industry needs

→ No report delivered, but activities in different networks started…

Workpackage 5

Industry/Academic Networks

DECHEMA: Gesellschaft für Chemische Technik und Biotechnologie

The major objective is to support and to guide R&D in technical Chemistry and biotechnology.

→ Activities within the Working group Systems Biology and Synthetic Biology

SBIA: Synthetic Biology International Association

Newly founded Industry association with the main focus on education & collaborations and also on social / political regulation

→ GENEART is a board member as the European representative

BioM-WB: competence cluster White Biotechnology, Bavaria

Funded cluster for promoting collaboration between Industry and Academia

Workpackage 5

5.2 Reports on two workshops (associated to industry-relevant scientific conferences)

Example - SB4.0: Industrial Biotechnology (Chair: Ralf Wagner, Geneart)

Example - **Synthetic Bio(techno)logy** (Co-organization: R. Wagner, S. Panke)

Example - Applied industrial Synthetic Biology in Europe conference

Problem: nearly without Industry presence!

The main Industry (showing presence) is the Gene synthesis industry and some international associations (IASB, SBIA)

Workshops to teach the European Industry in Synthetic Biology concepts and tools are difficult to realize in the context of an industry-relevant scientific conference (due to a lack of suitable conferences)

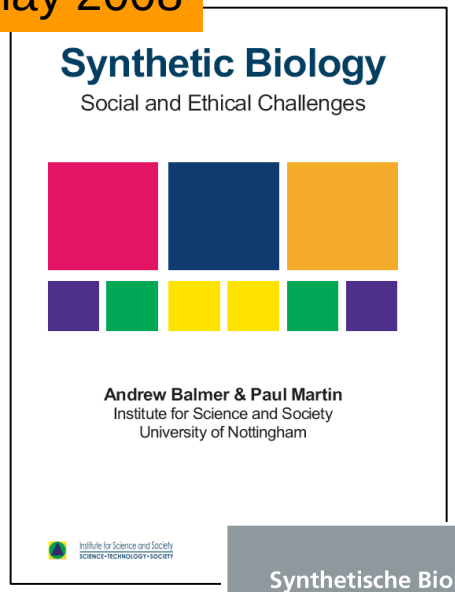
A significant amount of reports dealing with these issues is already available…

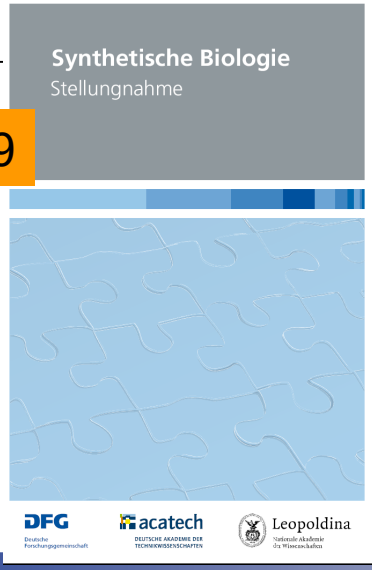
Workpackage 5

5.3 Position paper on the priorities of the European industry in the field of synthetic biology

GENEART
THE GENE OF YOUR CHOICE

May 2008





July 2009

7. Patenting and the Creation of Monopolies

The drive to create a microorganism that can turn biomass into fuels such as ethanol or hydrogen is a major focus of research, which has prompted a concern that patenting may lead to the creation of commercial monopolies or inhibit basic research. In response, there have been moves to develop an open-source movement (based on so called BioBricks) involving creation of a 'commons' that will facilitate open scientific research.

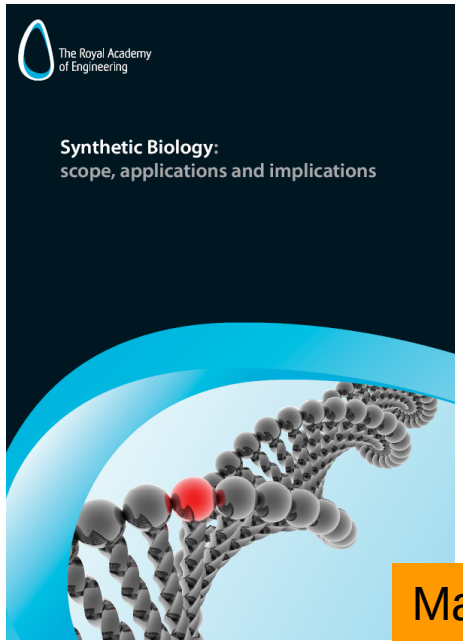
8. Trade and Global Justice

Perhaps the biggest success in synthetic biology to date has been in the production of terpenoids for the manufacture of the antimalarial medicine artemisinin, a drug that holds significant promise for worldwide malaria victims. However, there are concerns that synthetic artemisinin would ensure that no local production of natural *Artemisia* could be sustained in developing countries, thereby maintaining the discrepancy of wealth and health between rich and poor nations.

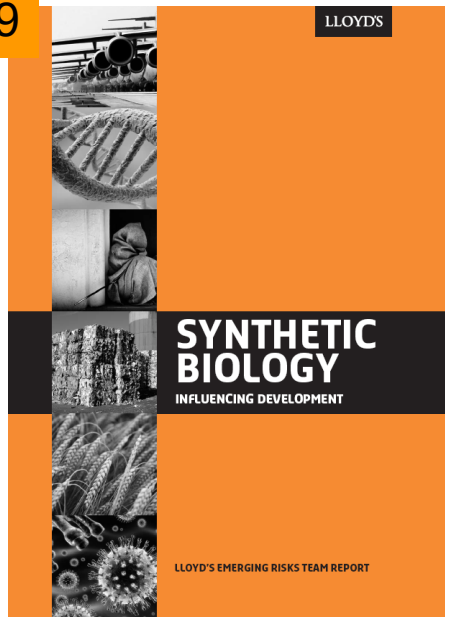
April 2008

Synthetic Biology – Engineering in Biotechnology
Schweizerischen Akademie der Technischen Wissenschaften (SATW)

July 2009



May 2009



Workpackage 5

5.4 Intermediate and final report on status of discussion regarding IP strategy in the field of synthetic biology

"IP issues" EMERGENCE WS (16.06.2008)

→ Report delivered

"Opportunities and Challenges in the Emerging Field of Synthetic Biology"
OECD, US National Academies National Academies and Royal Society
Washington, DC (July 9th 2009)

Richard A. Johnson, Senior Counsel and Senior Partner (Ret.), Arnold & Porter LLP and CEO, Global Helix LLC

→ Transcript available at: http://sites.nationalacademies.org/PGA/stl/PGA_050738

Experts are providing strategic scenarios but persons concerned (potential users) do not really participate or comment on the proposed strategies

→ Practical strategies can be developed only in a real setting

Adjustment of original proposal

- IP regulation turned out to be NOT the critical issue for the acceptance of Synthetic Biology at the moment
- Instead an urged need and some public pressure tightened for ***BioSecurity regulation***
- Neglect of this problem will harm the complete development of Synthetic Biology especially the Industry involvement
- This problem has to be addressed by the responsible Industry player
- Highest attention has been paid to the development of international screening standards (code of conduct) and the harmonization of a screening data base (Regulated Pathogen Database) for all gene synthesis companies (press coverage starting next week)

Conclusion: some of the original objectives have gained less attention in favor of the Biosecurity topic

Open issues: Adjustment of original proposal

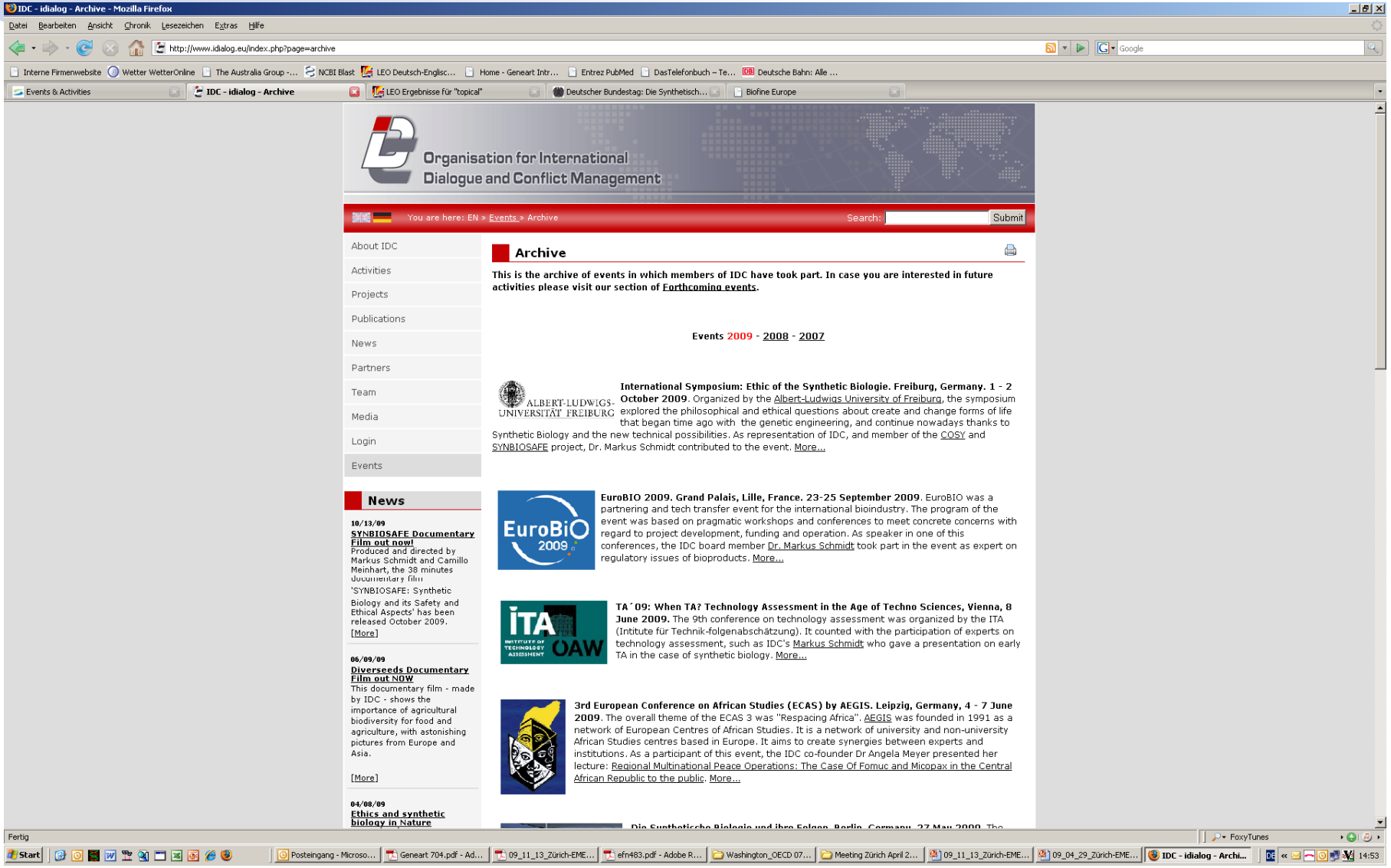
5.1 Second report to evaluate the fit of the European synthetic biology projects with the industry needs → refer to reports/PR on Biosecurity (IGSC, to be released next week), Reports on German Ethikrat regarding SynBio

5.2 Two reports on workshops associated to industry-relevant scientific conferences → refer to public reports or draft short reports on SB4.0 and Synthetic Bio(techno)logie

5.3 Position paper on the priorities of the European industry in the field of synthetic biology
→ refer to other reports e.g. Sven's SATW-report or position report of acatech – DFG – Leopoldina Workshop/Ethikrat Deutscher Bundesrat

5.4 Final report on status of discussion regarding IP strategy
→delayed?

Short reports of activities on the web page!?



Summary

Activities:

The expansion of Academic/Industry networks have been actively supported on regional (BioM-WB), national (DECHEMA) and international (SBIA) levels

The management of Synthetic Biology conferences / workshops has been organized or supported

The international regulation of Biosecurity measures has been promoted to a broad level of acceptance and commitment by the global GS companies

Massages:

In Europe the Industry perceived as involved in Synthetic Biology is nearly exclusively restricted to gene synthesis companies and associated service provider

IP regulation is a highly topical issue. However, attempts to provide legal solutions for handling the SB-related IP-practice may not be successful unless practical experience is available to drive the process

At the moment, the development of regulation processes for the secure use of synthetic DNA has the highest priority

Workpackage 2
University of Cambridge

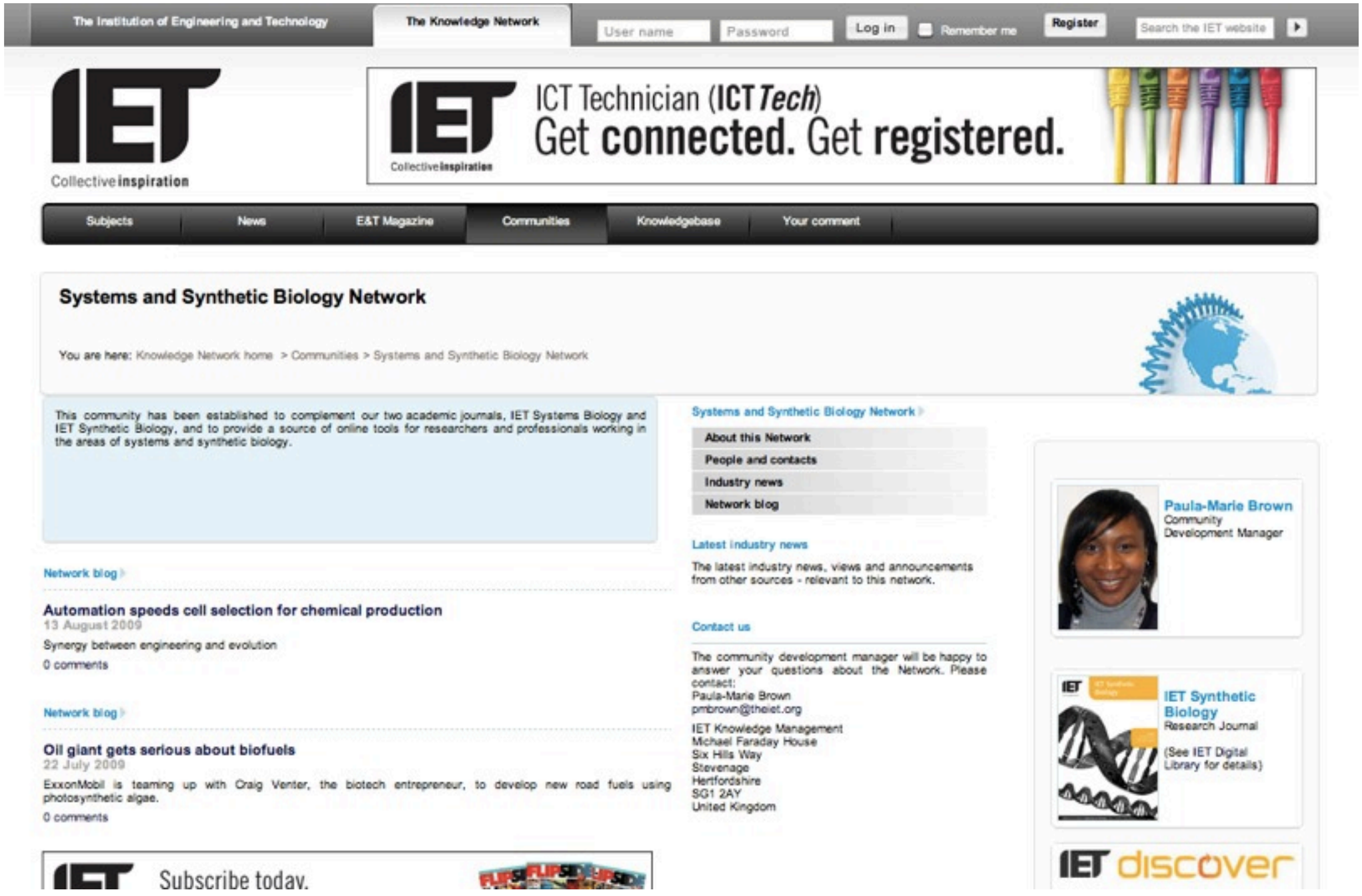
Deliverable 2.5
Educational resource at IET available and continuously available

Workpackage 2: Attracting talent to synthetic biology in Europe
Sven Panke

Deliverable 2.1:	Reports documenting the synthetic biology summer course, including syllabus	8? 20, 32	July 2009	ETH
Deliverable 2.2:	Report on the possibilities and feasibility of implementing a European Master in Synthetic Biology – if considered feasible, then	9	August 2007	EP
Deliverable 2.3:	Report on state of planning affairs at schools intending to participate in the Master	24	December 2008	EP
Deliverable 2.4:	Master studies implemented at the leading and the collaborating schools	34	October 2009	EP
Deliverable 2.5:	Educational resource at IET available and continuously updated.	12	December 2007	UCAM

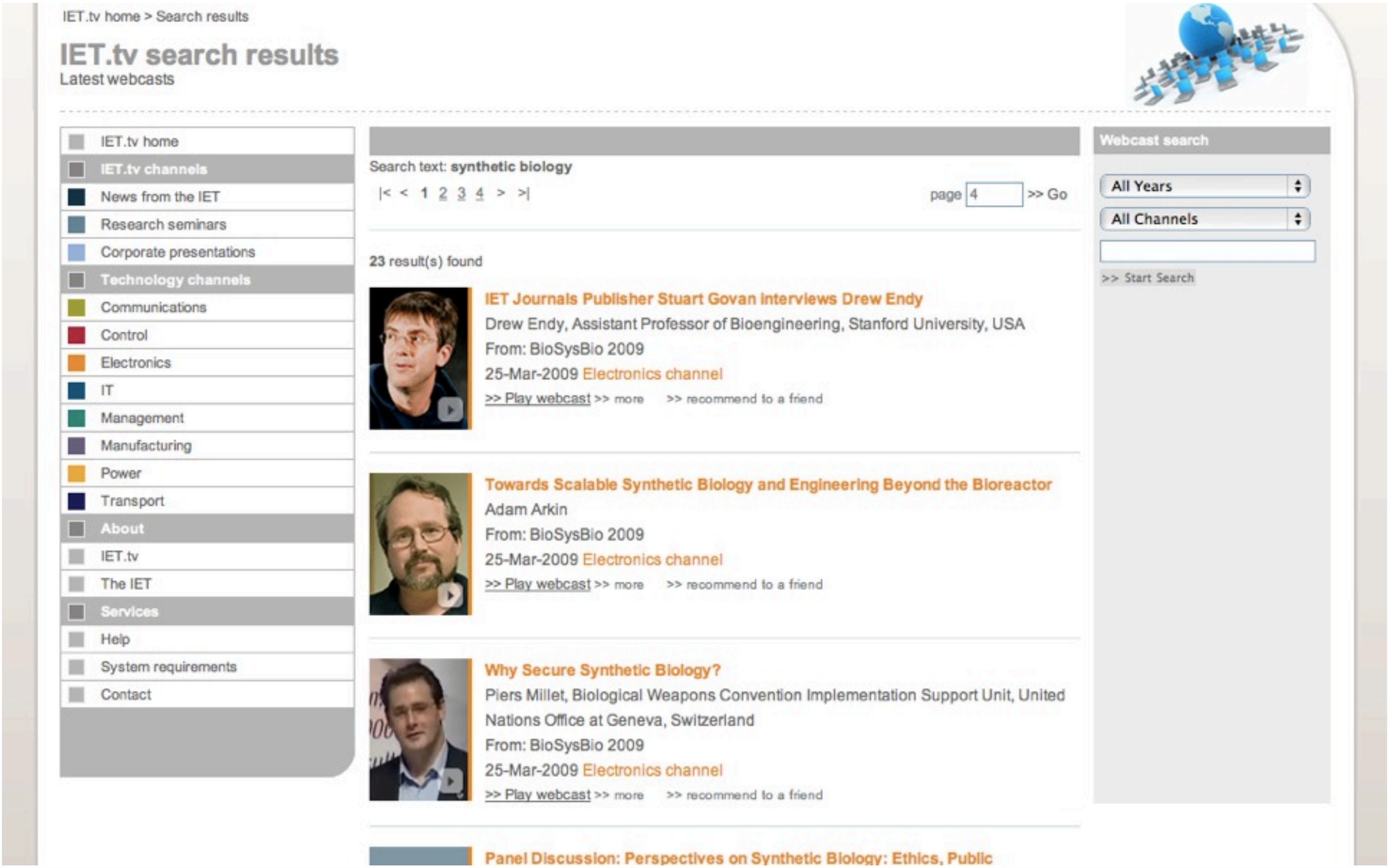
http://www.theiet.org/synbio

With the Institute of Engineering and Technology, we have established a web-based Technical and Professional Network for communication and distribution of information and educational material. This web based resource is hosted by the IET and associated with the IET Synthetic Biology journal.



http://www.iet.tv

The IET web resource includes a video server at http://www.iet.tv, which provides dual screen, streaming video presentations covering Synthetic Biology.



http://www.synbio.org.uk

In addition, we have established a complementary web resource for Synthetic Biology at UCAM. This is a dynamic Web 2.0 site with online access to news articles and links to people and events in the field of Synthetic Biology.

Thursday, November 12, 2009

www.synbio.org.uk
Synthetic Biology Resources

Search...

Synthetic Biology | Cambridge | iGEM | BioBricks | Microbes | Plants | Hardware | Productivity | Misc | Info

SYNTHETIC BIOLOGY MENU

- Synthetic Biology news
- Synthetic Biology Labs
- Jobs
- EU Emergence
- Royal Society Gateway
- SynBioStandards UK
- RoSBNetwork UK
- Synthetic Biology Project
- Community resources
- Developing world
- Education
- IET.tv video channel
- IET Synthetic Biology
- SynBio Journals
- Scientific Journals
- PubMed Search
- Open Innovation

SITE NEWS FEEDS

- Synthetic Biology RSS
- Wetware RSS
- Microbes RSS
- Plants RSS
- Biotechnology RSS
- Scientific Computing RSS
- Instrumentation RSS

LATEST: Computational Biology at Microsoft Research in Cambridge »

Cambridge website for Synthetic Biology Resources

Compiled by Jim Haseloff at the University of Cambridge

This site contains details of recent papers and activity in Synthetic Biology, with particular emphasis on: (i) development of standards in biology and DNA biobricks , (ii) microbial and (iii) plant systems, (iv) hardware for scientific computing and instrumentation, (v) tools for scientific productivity and (vi) collected miscellany.

The site also contains details of Synthetic Biology research and teaching at the University of Cambridge, including the annual iGEM team run by Jim Ajioka, Jim Haseloff and Gos Micklem in Cambridge.

Grand Prize for Cambridge iGEM2009 team

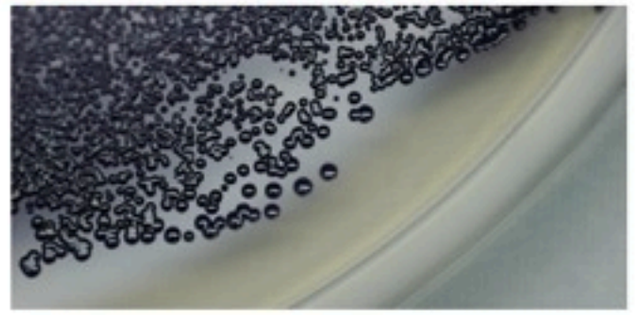
The Cambridge iGEM 2009 team presented their E. chromi project at the iGEM Jamboree at MIT. They described new BioBricks for the production of pigments in bacteria, and sensitivity tuners for the construction of new enviromental biosensors. (1st of November 2009)
The Cambridge iGEM team was awarded the Grand Prize for the iGEM2009 Jamboree - to cap a gold medal and first prize in the Environment track. (Monday 2nd November 2009)

See photos at: http://www.flickr.com/photos/haseloff/sets/72157622587178163/

SYNBIO NEWS

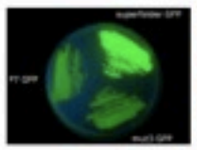
- **Hacking DNA** Hacking DNA Bioengineering technology is maturing, and so is its vocabulary From: http://www.spectrum.ie work/innovation/hackin dna Illustration: Harry Campbell BY PAUL MCFEDRIES // OCTOBER 2009 But the real...
- **Wellcome Trust support for iGEM** UK entries to student synthetic biology competition offered Wellcome Trust support 1 October 2009 UK teams hoping to enter iGEM – the International Genetically Engineered Machine competition – could receive financial support...
- **A life of its own** A LIFE OF ITS OWN Where will synthetic biology lead us? by Michael SpecterThe New Yorker SEPTEMBER 28, 2009 http://www.newyc If the science truly succeeds, it will make it...
- Ginko Bioworks

Synthetic operon for violacein production



The Cambridge iGEM2009 team received sponsorship from DNA2.0 Inc., which allowed them to design and construct a synthetic operon for the biosynthesis of violacein. The operon is 7.5Kb in size, contains 5 genes, and has been submitted to the MIT Registry for Standard Parts in BioBrick format - Part BBa_K274002. Expression of the VioA-E genes results in conversion of L-Tyrosine to an intense violet pigment. Violacein is a hydrophobic compound, and is retained within cells.

New BioBrick encoding an improved fluorescent protein



Green Fluorescent Protein (GFP) offers efficient and convenient means of visualising the dynamic process of gene expression and of obtaining readout of the current state of complex gene regulatory networks - features of major interest for synthetic biology.

Stefan Milde, working in the Haseloff Lab at Cambridge as part of iGEM2008 has constructed BioBrick versions of improved GFP variants and tested their properties (Parts:BBa I746908-I746919). He has compared two recently reported GFP variants to the mut3GFP variant in the Registry of Standard Biological Parts. The two GFP variants chosen were "superfolder GFP", developed and described by Pédelacq et al (2006), which was engineered for improved fluorescence in fusion proteins and P7 GFP ("superfast GFP") which was engineered by Fisher et al (2008) and selected on the basis of its very rapid folding in vitro. Read on for more...

The Registry of Standard Parts at MIT

With BioBrick parts from Cambridge iGEM teams: iGEM2005, iGEM2006, iGEM2007, iGEM2008 and the Haseloff Lab and new Bacillus subtilis strains and key parts (http://partsregistry.org/)

multiprotein complex production. Bieniossek C, Nie Y, Frey D, Olieric N, Schaffitzel C, Collinson I, Romier C, Berger P, Richmond TJ, Steinmetz MO,Berger...

- **Resecting a double-strand break** At loose ends: resecting a double-strand break. Cell. 2009 May 29;137(5):807-10. Bernstein KA, Rothstein R. Columbia University Medical Center, Department of Genetics & Development, New York, NY 10032, USA. Double-strand...
- **Production of difficult-to-express inducer-dependent bacterial repressor proteins** A general strategy for the production of difficult-to-express inducer-dependent bacterial repressor proteins in Escherichia coli. Christen EH, Karlsson M, Kämpf MM, Weber CC, Fussenegger M, Weber W. Protein...
- **Protein sequencing gone awry** Protein sequencing gone awry: 1 sample, 27 labs, 20 results One of the more recent fields to pick up an -omics

www.synbio.org.uk

Synthetic Biology Resources

Search...

SYNTHETIC BIOLOGY MENU

- Synthetic Biology news
- Synthetic Biology Labs
- Jobs
- EU Emergence
- Royal Society Gateway
- SynBioStandards UK
- RoSBNetwork UK
- Synthetic Biology Project
- Community resources
- Developing world
- Education
- IET.tv video channel
- IET Synthetic Biology
- SynBio Journals
- Scientific Journals
- PubMed Search
- Open Innovation

IGEM MENU

- Cambridge iGEM teams
- Photos
- iGEM2009 headquarters
- iGEM2009 teams
- iGEM sponsors
- Techniques
- Resources (private)

CAMBRIDGE MENU

- Cambridge Labs
- Cambridge-KAUST AEA
- Cambridge information

BIOBRICKS MENU

- Wetware news
- BioBrick resources
- DNA assembly software
- Gene synthesis
- Protocols

MICROBES MENU

- Microbiology news
- B. subtilis
- Microbiology

PLANTS MENU

- Plant News
- Biotechnology News
- Arabidopsis
- Brachypodium
- Plant resources
- Review PDFs

HARDWARE MENU

- SciComp group
- SciComp news
- SciComp links
- Instrumentation news
- Physical Computing
- DIY lab equipment
- Microscope construction
- Components

PRODUCTIVITY MENU

- Productivity news
- Productivity links
- Scientific software
- Mac OSX development
- Python
- Scientific illustration
- Design

Emergence: A Foundation for Synthetic Biology in Europe

Emergence

Synthetic biology has emerged as a very recent but highly promising approach to re-organizing the scientific biological endeavor by integrating central elements of engineering design. By applying the tool box of engineering disciplines such as electrical, mechanical, or chemical engineering and computer sciences, including the vigorous application of modeling techniques and organizing the development of novel biological systems along a hierarchical systems architecture with defined and standardized interfaces, synthetic biology aims at no less than revolutionizing the way we do bioengineering today. If successful, synthetic biology will transform bioengineering into a highly successful and sustainable life science industry.

The objective of this coordination action (CA) EMERGENCE is to provide a communication and working platform for the emerging European synthetic biology community in order to strengthen the organizational and conceptual basis of the synthetic biology as a true engineering discipline in biological engineering.

click to see Partner Labs

www.synbio.org.uk

website traffic	last month	last year
visits	36,018	220,662
pages	475,929	2,923,708

Synthetic Biology outreach & research initiatives

- BioSysBio Conference hosted in Cambridge (April 2009)
  Satellite meeting on Standards for Synthetic Biology
  JH raised funding from Microsoft Research and SynBioStandards for Standards Workshop, with invited speakers: Adam Arkin, Berkeley; Herbert Sauro, Seattle; Guy Cochrane, Sanger Institute.

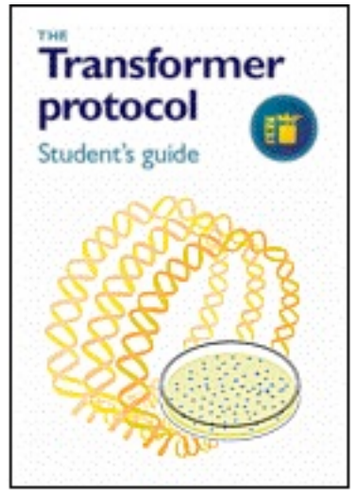
- iGEM2009
  All European finalists: Cambridge, Heidelberg, Freiberg, Imperial, Valencia, Groningen

- iGEM2009
  Collaboration between Cambridge iGEM team and Royal College of Arts

- **Wellcome Trust**: ~ 50 studentships secured for iGEM2010 in UK

- **European Association for Science Events (EUSCEA)** funded Synthetic Biology 2WAYS Project. Public demonstration of Synthetic Biology principles and Youth Parliament: Jim Haseloff, Nicola Buckley (UCAM) & Christophe Godin, Laurent Laplaze (Montpellier)

- **New training materials for Synthetic Biology**
  Seed money for collaboration with Dean Madden, National Centre for Biotechnology Education, University of Reading. Follow on from EU Volvox project



Teaching Resources for Synthetic Biology

Timetable for 2009

Course Assessment

Team Building Exercise

Lecture resources

1. Introduction to Synthetic Biology (Jim Ajioka)
2. Bacterial gene expression (John Archer)
3. Reporter genes (Jim Haseloff)
4. Experimental Design (Gos Micklem)
5. Rhodococcus (John Archer)
6. Sequencing and Synthesis (Gos Micklem)
7. Microbial Diversity (Keith Johnstone)
8. Mol Biol for Syn Biol (Tom Ellis)
9. Synthetic Parts, Genes & Circuits (Jim Ajioka and Jim Haseloff)
10. Stochasticity: Noise in Biological Systems (Lorenz Wernisch)
11. Biological Modelling & SBML (Nicolas Le Novere)
12. Modelling for Synthetic Biology (Andrew Phillips)
13. Quorum Sensing (Rita Monson)
14. Bacterial Mobility (Gillian Fraser)
15. Synthetic Bacterial Communication (James Brown)
16. Microfluidics and microdroplets (Wolfgang Bauer)
17. Chemotaxis (Dennis Bray)
18. Morphogenetic bacteria (Jim Haseloff)
19. Gram positive bacteria (Jim Ajioka)
20. Synthetic Logic (Gos Micklem)
21. Anhydrobiosis (AlanTunnacliffe)
22. Application of Synthetic Biology in plant systems (Jim Haseloff)
23. Biomedical applications of Synthetic Biology (Gos Micklem)

Microbiology 101: resources for microbiology assembled by Duncan Rowe
Molecular Biology 101: resources for molecular Biology assembled by Duncan Rowe

Lab practicals:

1. Scent production (Eau d'Coli)
2. **Quantifiying gene expression**
3. **Repressilator**
4. Noise
5. **Open source hardware: Arduino lab**
6. **Swarming**
7. **Bandpass detector circuit**
8. **Photosensitive Biofilm**
9. **DNA problem solving exercise**

Project Reviews & Mini-Talks
Description
Student teams
Presentations

Dragon's Den
1. Entrepreneurship: a scientist's viewpoint (Alan Tunnacliffe)
2. Entrepreneuship: the University and venture capital (Maher Khaled)
3. Team pitches

Software resources

Documentation; resources & style guide

eBooks

Student participants (contact details)

Logistics

Synthetic Biology consultations (UCAM)

- Royal Society: Synthetic Biology Policy Coordination Group
- Royal Academy of Engineering: Report on Synthetic Biology
- OECD, Royal Society & National Academy of Science USA: Bellagio conference
- BBSRC EPSRC ESRC: Network for Standards in Synthetic Biology
- Wellcome Trust: Synthetic Biology Planning Group.
- Woodrow Wilson Institute: advisor to Synthetic Biology Project
- Cambridge-KAUST Academic Exchange Alliance: establishment of Synthetic Biology curriculum

EPSRC-NSF "Sandpit" on Synthetic Biology 2009

Cyberplasm: An autonomous micro-robot constructed using synthetic biology
Joseph Ayers (Northeastern), Daniel Frankel (Newcastle), Vladimir Parpura (UAB), Christopher Voigt (UCSF)

Programmable Rhizosphere
Kaustubh Bhalerao (UIUC), Hana El Samad (UCSF), Jim Haseloff (Cambridge), Christina Smolke (Stanford), Christopher Voigt (UCSF), Neil Wipat (Newcastle)

Engineering Genetically Augmented Polymers
Andy Ellington (UT Austin), Paula Booth (Bristol), Rachel O'Reilly (Warwick), Michael Jewett (Northwestern)

Synthetic Aesthetics: Connecting Synthetic Biology and Creative Design
Drew Endy (Stanford), Jane Calvert (Edinburgh), Alistair Elfick (Edinburgh)

Synthetic Integrons for Continuous Directed Evolution of Complex Genetic Ensembles
Joshua Leonard (Northwestern), Jay Keasling (UC Berkeley), Susan Rosser (Glasgow), Paul Freemont (UCL), Anne Osbourn (John Innes Centre), Declan Bates (Leicester)

US$12M total
NSF and EPSRC coordinating oversight, and developing plans to strengthen collaborations, build network. UK to host PI meeting in spring 2011