

EMERGENCE: A foundation for Synthetic Biology in Europe

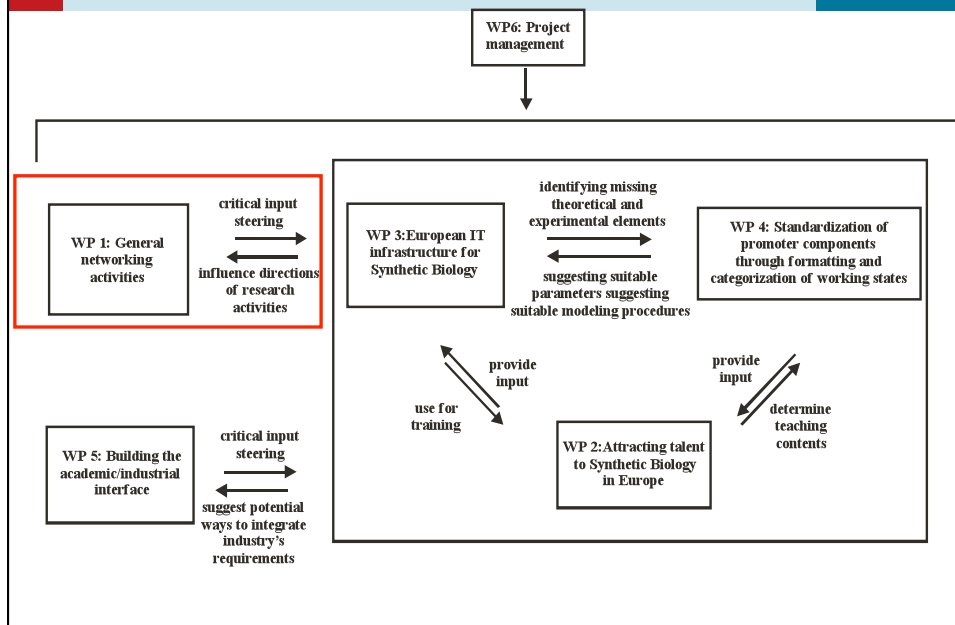
WP1: General Networking activities

Fostering a community of knowledge

Vitor Martins dos Santos

Systems and Synthetic Biology Group
Division of Microbiology
Helmholtz Centre for Infection Research
Braunschweig, Germany

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

context-independent biological systems/
modules

what to measure / how to measure?

microfluidics technologies / single cell
measurements

design concepts

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

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	Vitor Martins dos Santos, Helmholtz Center for Infection Research, Braunschweig, DE	Opening remarks
Session 1 & Analysis : Databases & Software Tools		
Chair: Vitor 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
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 Research, 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, Heidelberg, 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 Pletsyn, 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		

**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 <i>Bacillus subtilis</i> 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 <i>E. coli</i> functional genomics
12:00	N. Krasnogor Incremental model building with algorithmic systems biology	L. Serrano <i>M. pneumoniae</i> systems biology analysis
13:00	Round table	Round table
14:00	Lunch	Lunch
	Session 2. Streamlining Genomes	Session 4. Circuit Design and Evolution

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 <i>Bacillus subtilis</i> 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, β -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)



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 Biotecnología, 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 Approaches 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/EPSCRC 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 Probiactys (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)

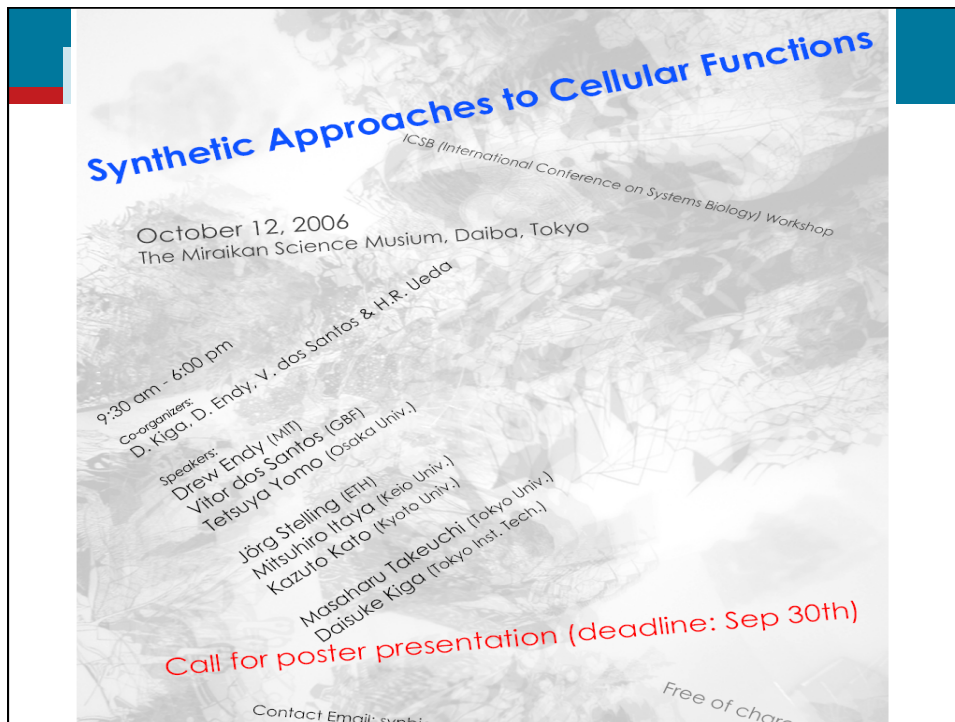
India (2 Students 4 month each, plus scientist 1 week 2008)

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 Advimore SynBio in July 2008

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

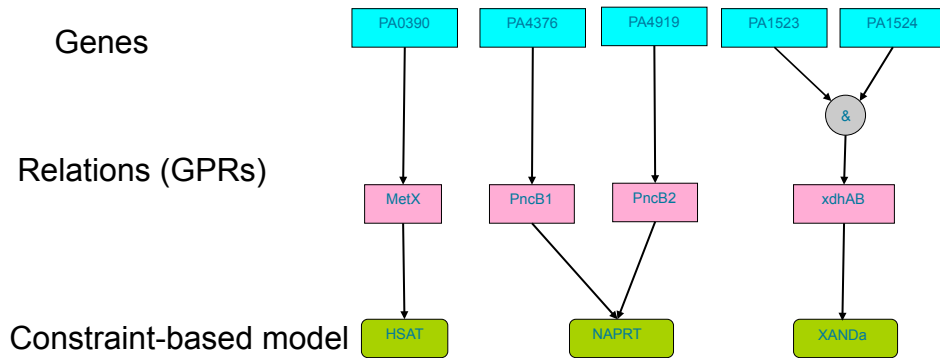


Status Deliverables
D1.1: Material and rules for standardized meeting structure in place for the first time (month 3) done
D1.2: Report on the first workshop on development of the European IT infrastructure for synthetic biology (month 9)
D1.3: Report on the first workshop for design tools for synthetic 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 signed by 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

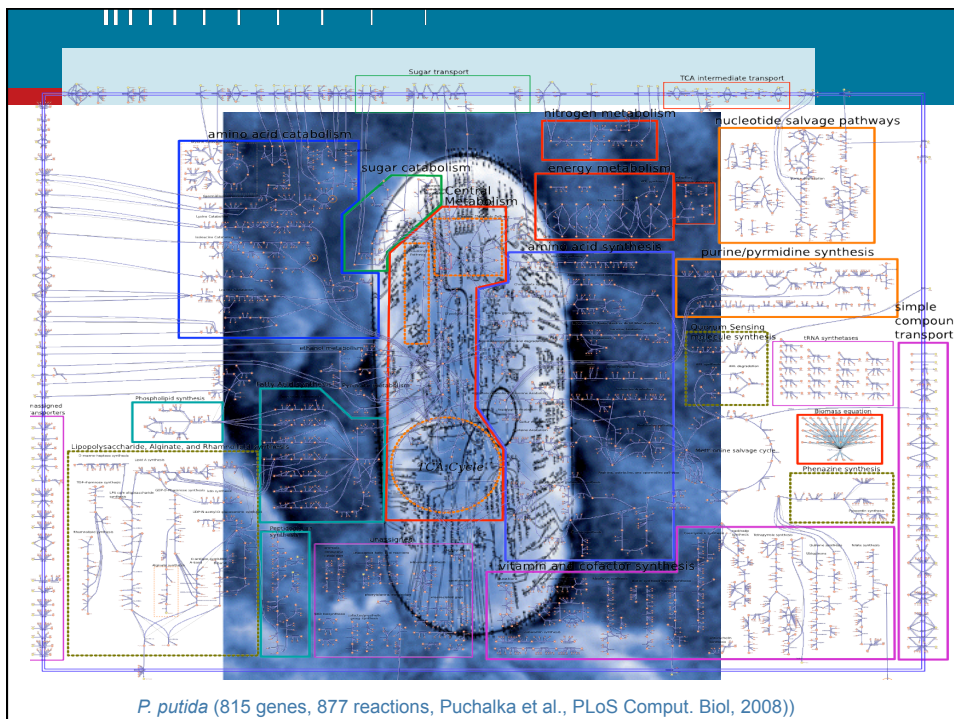
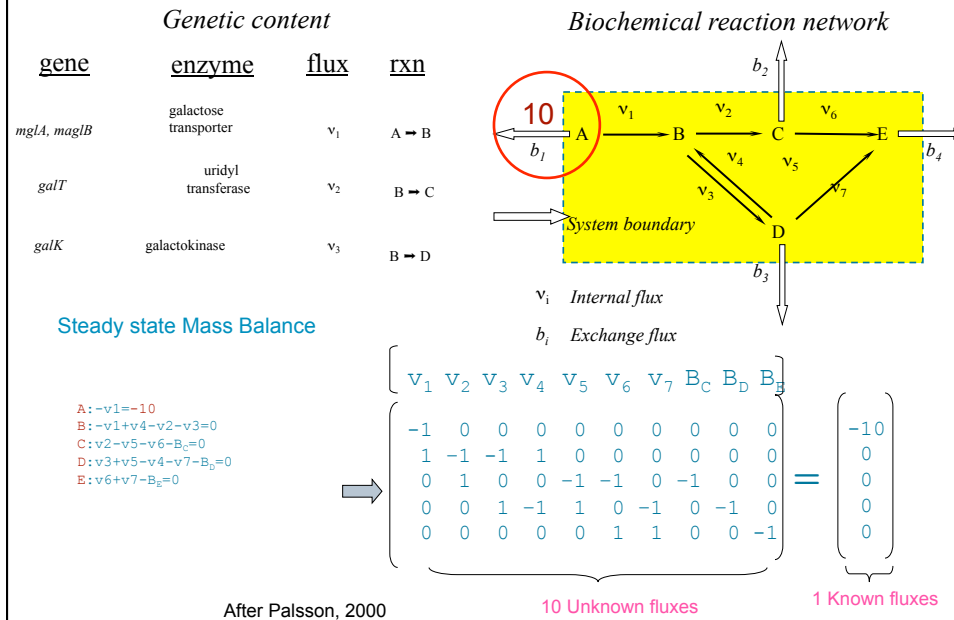


Metabolic reconstruction of an organism

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



The stoichiometric matrix as a metabolic map



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

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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



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

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ToBiN supplies an abstraction layer over IT complexity

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

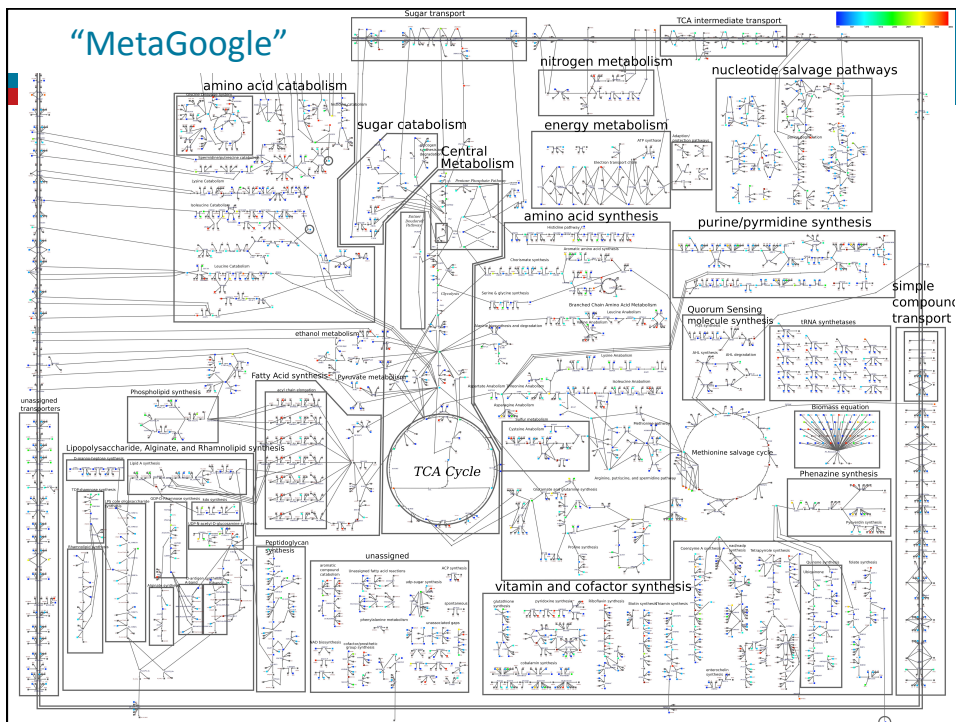
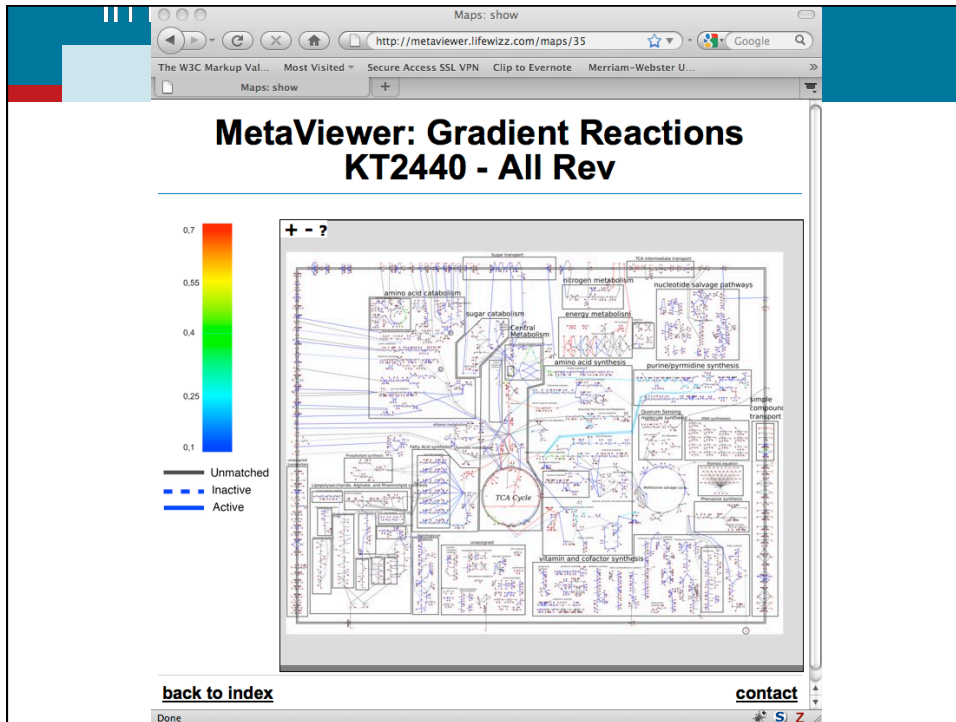
Data are automatically backed up

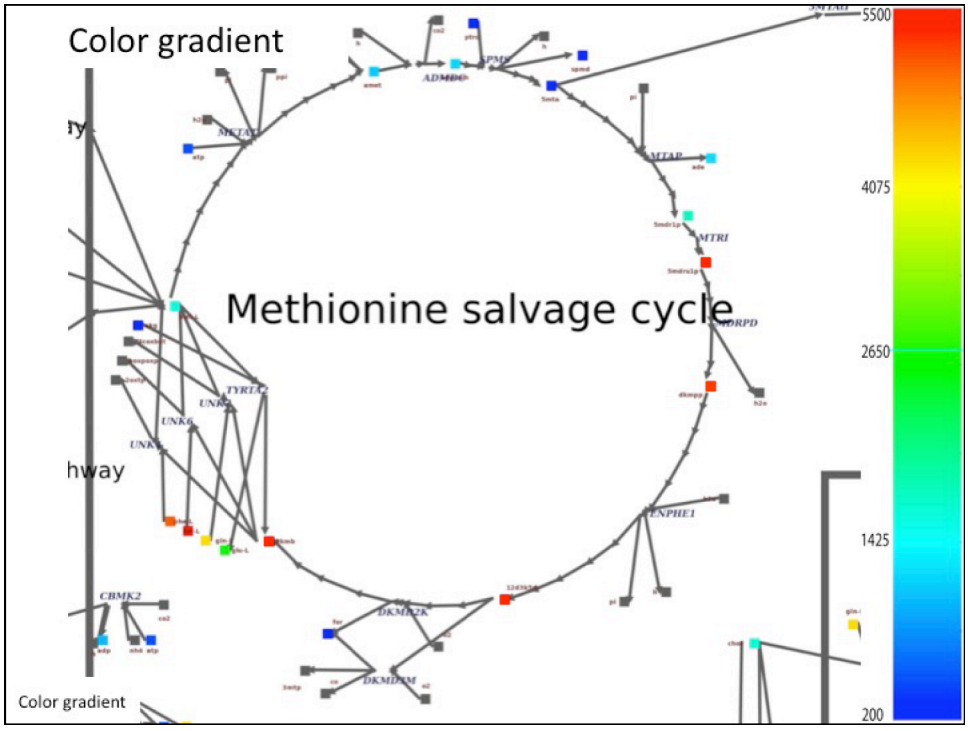
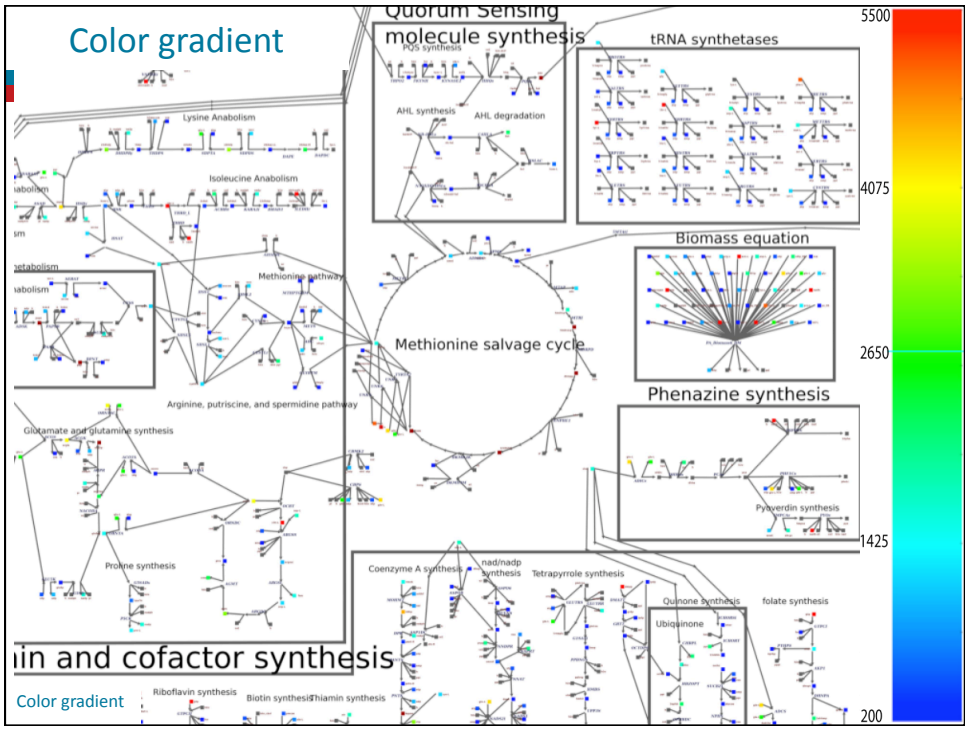
Automatic load-balancing for computationally intensive tasks

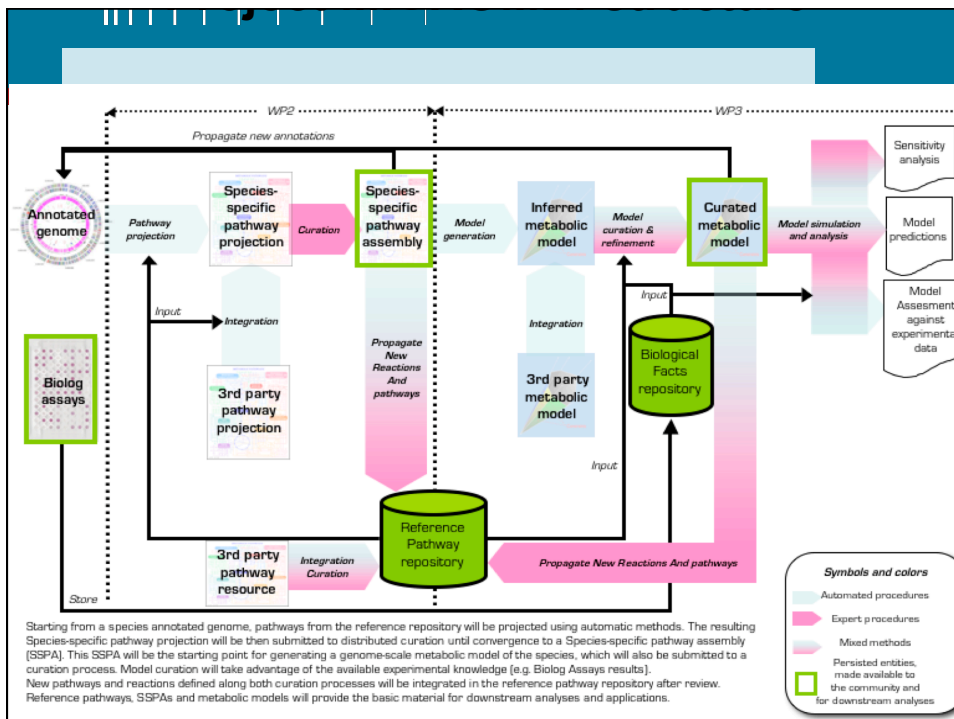
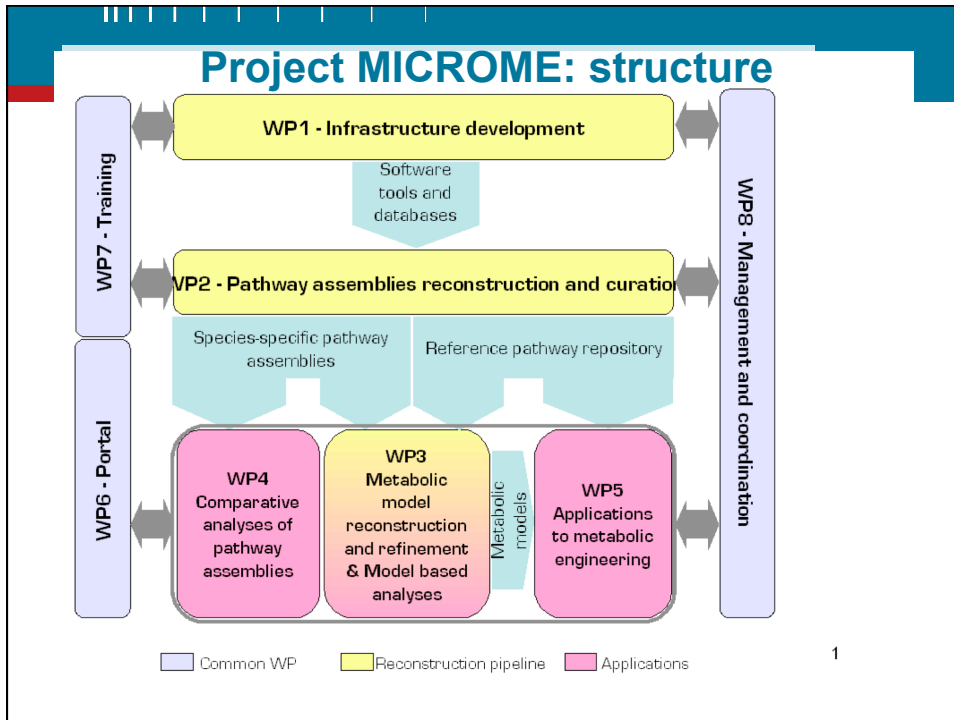
Security is centrally managed with logging, auditing, and roll-back capabilities.

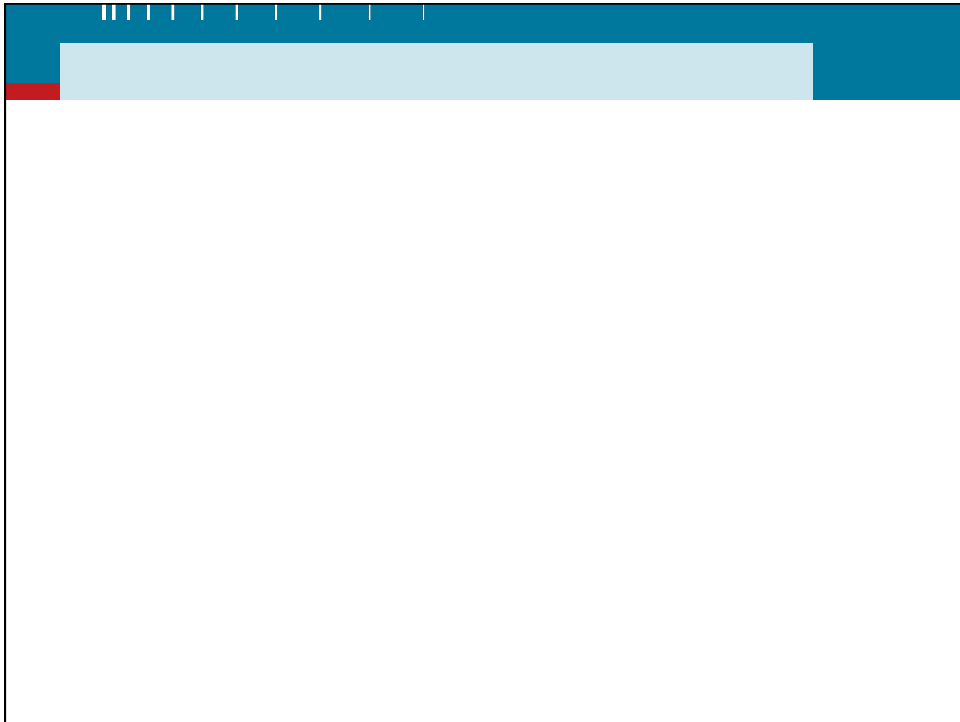
Supports co-existing Individual, Workgroup, Institutional, and Consortium data-share levels

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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 measurements
- 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

Outline

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

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

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

Proposed solution

BIOLOGICAL CONTEXTS
all the information together

SYNTHETIC BIOLOGY

Synthetic Biology

Search Genomes Genes Proteins Pathways Parts Models

Genome	Description	Created
B_amyloliquefaciens.EB1	B_amyloliquefaciens Reference server based on	2009-04-18
B_anthraxis_Ames.EB1	B_anthraxis_Ames Reference server based on E	2009-04-18
B_anthraxis_Ames_ancestor.EB1	B_anthraxis_Ames_ancestor Reference server l	2009-04-18
B_anthraxis_Sterne.EB1	B_anthraxis_Sterne Reference server based on	2009-04-18
B_cereus_ATCC_10987.EB1	B_cereus_ATCC_10987 Reference server base	2009-04-18
B_cereus_ATCC_14579.EB1	B_cereus_ATCC_14579 Reference server base	2009-04-18
B_cereus_NVH_391_98.EB1	B_cereus_NVH_391_98 Reference server base	2009-04-18
B_cereus_ZK.EB1	B_cereus_ZK Reference server based on EB1 as	2009-04-18
B_clausii.EB1	B_clausii Reference server based on EB1 assem	2009-04-18
B_halodurans.EB1	B_halodurans Reference server based on EB1 a	2009-04-18

Category	Count
genes	3800
interactions	0
pathways	3700
proteins	400
structures	0

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

Data integration

Registry of Standard Biological Parts

Welcome to the Registry of Standard Biological Parts.

The Registry is a collection of ~3200 genetic parts that can be mixed and matched to build synthetic biology devices and systems.

Registry tools

- Search parts (7)
- Add a part
- Request a part
- Send parts to the Registry
- Sequence analysis

WELCOME

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we do

- Protein knowledgebase, consists of two sections:
 - Swiss-Prot, which is manually annotated and reviewed.
 - TrEMBL, which is automatically annotated and is not reviewed.
- Includes Complete Proteome Sets.

UniRef: Sequence clusters, used to speed up similarity searches.

UniParc: Sequence archive, used to keep track of sequences and their identifiers.

Supporting data: Literature citations, taxonomy, keywords and more.

UniProt

Bionemo

Biodegradation Network
Molecular Biology Database

xyIR (Plasmid pWWO)

DNA: **xyR**

Transcriptional unit: xyR (open127) xyR (open228)
(required by xyR)

Protein: **xyR** (P18, P20, P4, S040)

Transcriptional Units Regulation

PHYSIOLOGY

PATHOLOGY

INTERACTION

PHENOTYPE

CD4

PubMed

Browse a Genome

Ensembl Bacteria uses the Ensembl software system to present genomes of species from important bacterial clades. The database is organised as number of collections of genomes from closely related species. Click on the shortcuts below to directly access some popular genomes, or specify a collection to browse a list of the genomes it contains.

Popular genomes (Log in to customize this list)

- Escherichia coli K12
- Bacillus subtilis
- Mycobacterium tuberculosis H37Rv

All Genome Collections

Select a genome collection

View full list of all species

Raw data access
Web services
Widgets


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.

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



Registry of Standard Biological Parts

Go Search

page discussion view source history


~3200 genetics parts

Log in / create account


Welcome to the Registry of Standard Biological Parts.

The Registry is a collection of ~3200 genetic parts that can be mixed and matched to build synthetic biology devices and systems. Founded in 2003 at MIT, the Registry is part of the Synthetic Biology community's efforts to make biology easier to engineer. It provides a resource of available genetic parts to iGEM teams and academic labs.


The Registry is based on the principle of "get some, give some". Registry users benefit from using the parts and information available from the Registry in designing their engineered biological systems. In exchange, the expectation is that Registry users will, in turn, contribute back information and data on existing parts and new parts that they make to grow and improve this community resource.




Catalog of parts & devices



Help



Users & groups
(Apply for an account)



DNA repositories

Registry tools

- [Search parts \(?\)](#)
- [Add a part](#)
- [Request a part](#)
- [Send parts to the Registry](#)
- [Sequence analysis](#)

NEW! You'll notice some significant changes to the Registry recently. In particular, the Registry [catalog of parts](#) has been entirely redesigned to allow for easier browsing of the available parts and devices. You can now browse parts and devices by type, by function, by chassis and by standard. You'll also notice that the documentation and help pages for each class of parts have been greatly enhanced.

The Registry of Standard Biological Parts is "always" a work in progress. Please browse the new catalog and let us know what you think, or feel free to edit and improve the pages further.

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.



Colioid: 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 that produce or sense odorants.



DNA recombination: Parts involved in DNA recombination.

Parts Registry

Registry of Standard Biological Parts

page discussion view source history

BBa_K211002 Main Page Part Design Physical DNA Hard Information Experience Tools

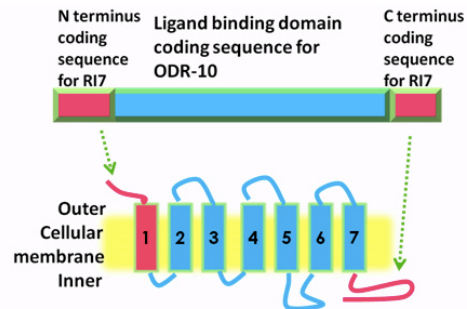
Log in / create account

Part:BBa_K211002

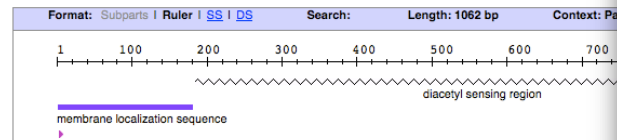
Designed by ZHONG Wanting Group: iGEM09_HKUST (2009-10-13)

RI7-odr10 chimeric GPCR

BBa_K211002 encodes a chimeric diacetyl-sensing GPCR which can be functionally expressed in *S. cerevisiae*. This chimeric receptor is composed of the TM2-TM7 ligand-binding domain of the *C. elegans* 7-transmembrane receptor ODR-10, flanked by the N- and C-terminals of the rat OR RI7. It can be localized to the *S. cerevisiae* cell membrane and activate the yeast endogenous MAPK pathway upon binding to the ligand.



Sequence and Features



Assembly Compatibility: [10](#) [21](#) [23](#) [25](#)

Manually curated free text

Registry of Standard Biological Parts

page discussion

BBa_K211002 Main Page Part Design Physical DNA Hard Information Experience Tools

Log in / create account

Part:BBa_K211002:Hard Information

Designed by ZHONG Wanting Group: iGEM09_HKUST (2009-10-13)

Coding [DNA Sent](#)
Experience: [Works](#)
[Get This Part](#)

Contents [hide]

- [1 Page Header](#)
- [2 Page Footer](#)
- [3 Sequence and Features](#)
- [3 Access](#)
- [4 Other Information](#)

Database driven annotations

Page Header

Part Name	BBa_K211002	Login to edit
Short Description	RI7-odr10 chimeric GPCR	
Part Type	Coding	
Nickname		
Designer(s)	ZHONG Wanting	
DNA Status	Sent	
	DNA is only defined as Available if it is in the repository. How to send parts.	
Qualitative Experience	Works	
Group Favorite	Yes	
Star Rating	None	
Delete This Part		

Biological databases and tools

FireDB. Functionally residues

fireDB: a database of annotated functionally important residues

fireDB is a database of [PDB](#) structures and their associated ligands. fireDB also contains the largest residues.

A detailed description of the functionalities of this page can be found in the [FireDB online help](#).

Annotated functionally important residues come from protein-ligand atom contacts and the [Catalytic Site Atlas](#).

Database of functionally important residues

Search the database by:

PDB chain (e.g. 101m or 1tcoC)	<input type="text" value="2dg9A"/>
UniProt primary accession number (e.g. P62942)	<input type="text"/>
PDB/UniProt keyword	<input type="text"/>

Atomic distance cut-off
(in Angstroms)

0.5 A + Van der Waals radii
 1.0 A + Van der Waals radii
 1.5 A + Van der Waals radii

Calculate contacts between proteins and ligands with

[The Ligand Contact Tool](#)

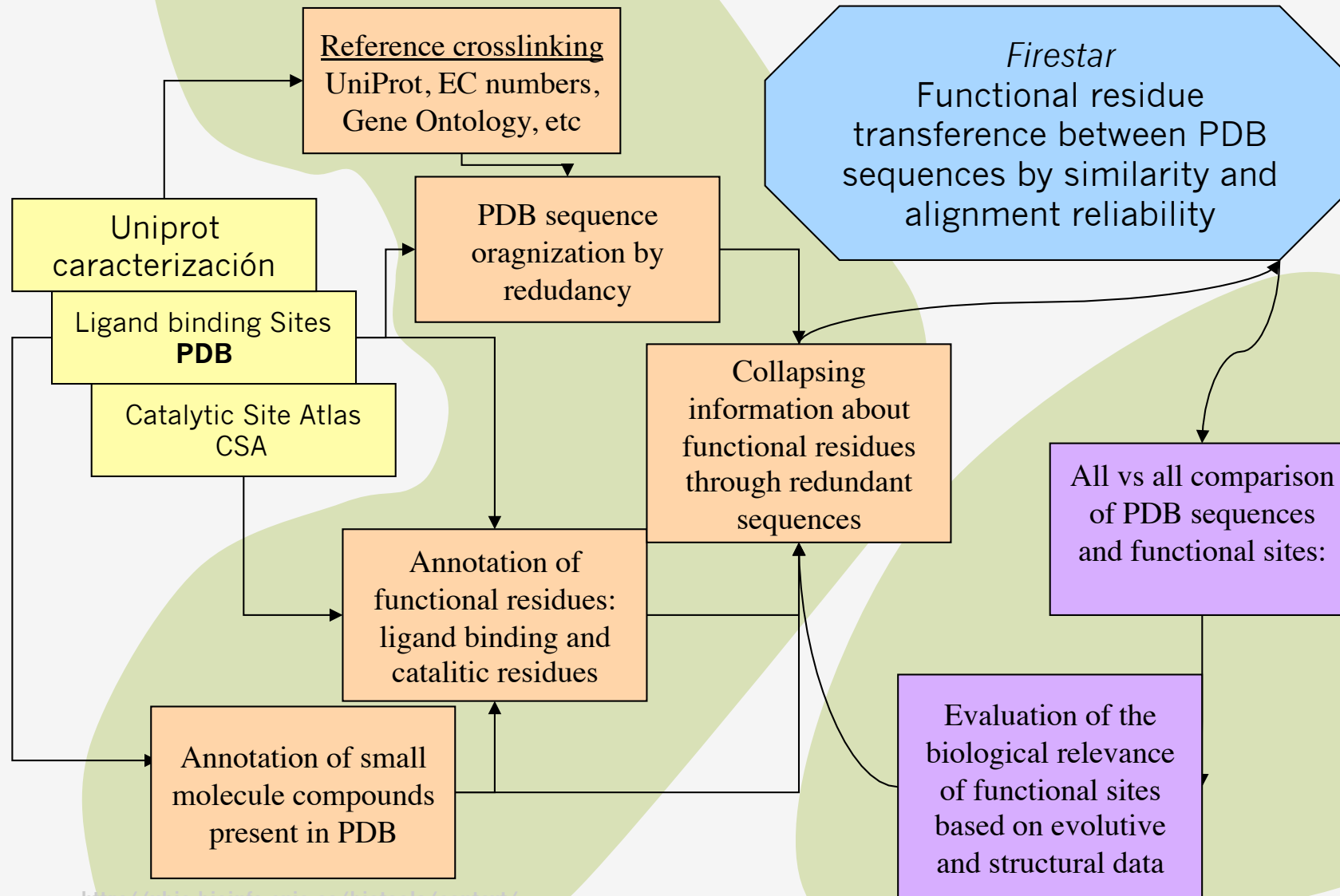


2dg9	ISOMERASE
2dg9A	FK506-BINDING PROTEIN 1A
P62942	RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP1A; Short=PPIase FKBP1A; EC=5.2.1.8; AltName: Full=FK506-binding protein 1A; Short=FKBP-1A; AltName: Full=Rotamase; AltName: Full=Immunophilin FKBP12; Short=12 kDa FKBP; Short=FKBP-12;
EC numbers	5.2.1.8
Mutations	YES
GO:0006457	protein folding

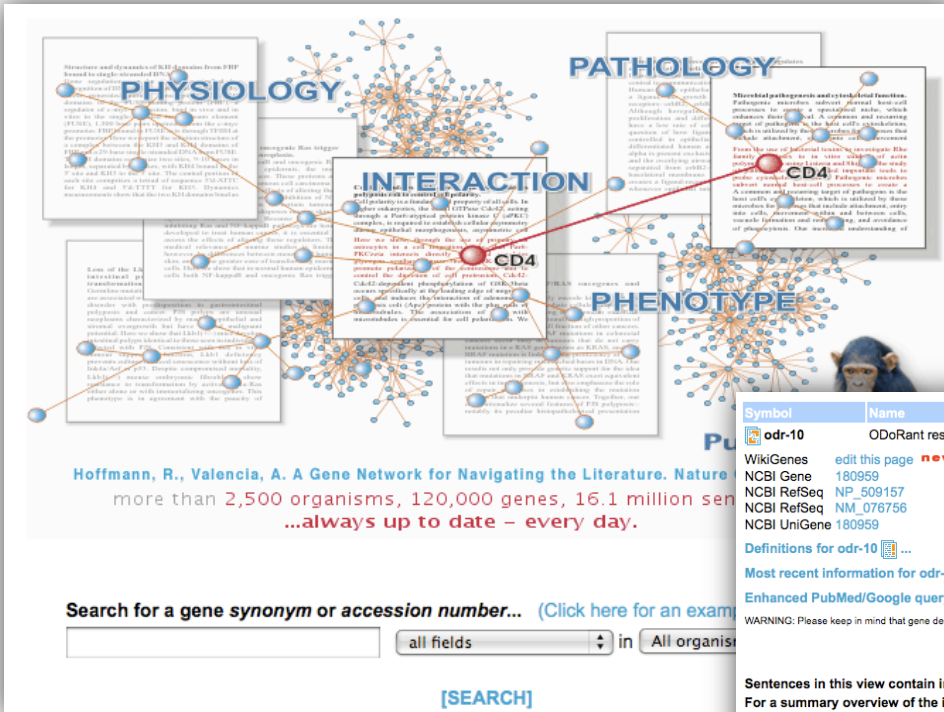
NUMBERING: hold the mouse over the sequence to check titles with numbers. Note that **consensus** numbering is sequential and for the query **2dg9A** and site lines numbers belong to the PDB coordinate files.

Consensus	sequence	GVQVETI SPGDGRTFP KRGGT CVVHYTG MLEDGKKF DSSRD RNKPF KML GKQ EVI R G WEE GVA QMSV GQRA KLT I SP	
2dg9A	sequence	GVQVETI SPGDGRTFP KRGGT CVVHYTG MLEDGKKF DSSRD RNKPF KML GKQ EVI RGL EEGVA QMSV GQRA KLT I SP	
Square		CC	
Literature	catalytic site	MORE	
E=6 69%	~RAP	EXPAND	Y G D R F K F Q E V I R L
E=0 17%	SO4	EXPAND	
E=0 14%	NH4	EXPAND	
E=1 3%	SO4	EXPAND	
E=3 1%	B7G	EXPAND	R

FireDB workflow



iHOP



Extract interactions from literature

Hoffmann, R., Valencia, A. A Gene Network for Navigating the Literature. *Nature*
 more than 2,500 organisms, 120,000 genes, 16.1 million sentences
 ...always up to date – every day.

Search for a gene synonym or accession number... (Click here for an example)

all fields in All organisms

[SEARCH]

Symbol	Name	Synonyms	Organism
odr-10	ODO-Rant response abnormal		Caenorhabditis elegans

[WikiGenes edit this page](#) **new**
[NCBI Gene 180959](#)
[NCBI RefSeq NP_509157](#)
[NCBI RefSeq NM_076756](#)
[NCBI UniGene 180959](#)

[Definitions for odr-10](#) ...
[Most recent information for odr-10](#) ...
[Enhanced PubMed/Google query](#) ...

WARNING: Please keep in mind that gene detection is done automatically and can exhibit a certain error. [Read more about synonym ambiguity and the iHOP confidence value](#) ⭐⭐⭐.

[Find in this Page](#) ⓘ

Sentences in this view contain interactions of odr-10 - Interaction Information is available whenever you see this symbol ⓘ - Read more. [Show all](#)

For a summary overview of the information in this page click here. **new** [Order by relevance](#)

To function in olfactory imprinting, this **interneuron** pair must express a **G-protein** [?] **↔-coupled chemoreceptor** [?] **↔ family member encoded by the sra-11** **↔** gene. [2005]

A calcineurin **phosphatase** [?] **↔** antagonizes the KIN-29/MEF-2-regulated pathway to modulate levels of **CR** [?] **↔ gene expression**. [2007]

We investigated **genetic polymorphism** in the **Caenorhabditis elegans** srr and str **chemoreceptor** [?] **↔** gene families, each of which consists of approximately 300 genes encoding seven-pass **G-protein** [?] **↔-coupled receptors**. [2005]

Our results identify KIN-29 as a new regulator of MEF2/**HDAC** [?] **↔** functions in the **nervous system**, reveal cell-specific mechanisms of action of this pathway in vivo and demonstrate remarkable complexity in the regulation of **CR** [?] **↔ gene expression** in C. elegans. [2007]

RESULTS: Based on manual curation and sequence comparisons among putative **G-protein** [?] **↔-coupled chemoreceptor** [?] **↔** genes in the nematode **Caenorhabditis elegans**, we identified approximately 1300 genes and 400 **pseudogenes** in the 19 largest gene families, most of which fall into larger superfamilies. [2008]

KIN-29 SIK regulates **chemoreceptor** [?] **↔ gene expression** via an MEF2 transcription factor and a class II **HDAC** [?] **↔**. [2007]

Here we describe specific genetic interaction between **tax-6** **↔** and **kin-29** **↔** in regulating **body size**, **serotonin** mediated egg laying, and **chemoreceptor** [?] **↔** expression. [2007]

Please cite the use of iHOP as "Hoffmann, R., Valencia, A. A gene network for navigating the literature. *Nature Genetics* 38, 684 (2004)" and as "iHOP - <http://www.iHop-net.org>".
 Special thanks to Chris Sander for his continuing support.

Bionemo

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

Bionemo
Biodegradation Network
Molecular Biology Database

Search: ...or choose from a list of cont...
- Select a list -

Home

xylR (*Plasmid pWWO* NCBI)

DNA: [AJ344068.1](#)

Transcriptional units: [xylR \[operon127\]](#) [xylR \[operon228\]](#)
Regulated by [xylR](#)

Protein: [XylR \(XYL_R_PSEPU , NP_542857 \)](#)

Pfams:
[ATPase family associated with various cellular activities \(AAA\) \(PF07724\)](#) [Pfam] Start: 254 End: 258
[ATPase family associated with various cellular activities \(AAA\) \(PF07726\)](#) [Pfam] Start: 258 End: 258
[ATPase family associated with various cellular activities \(AAA\) \(PF07728\)](#) [Pfam] Start: 258 End: 258
[Bacterial regulatory protein, Fis family \(PF02954\)](#) [Pfam] Start: 515 End: 555
[Sigma-54 interaction domain \(PF00158\)](#) [Pfam] Start: 236 End: 456
[V4R domain \(PF02830\)](#) [Pfam] Start: 127 End: 189
[Activator of aromatic catabolism \(PF06505\)](#) [Pfam] Start: 16 End: 118

No Structural Information

Transcriptional Units Regulated

[xylR \[operon127\]](#)
[xylR \[operon228\]](#)
[xylS \[operon229\]](#)
[xylUWCMABN \[operon95\]](#)

Effectors

[2-nitrotoluene](#) [3-Methylbenzylalcohol](#) [4-Chlorobenzaldehyde](#) [4-nitrotoluene](#) [Adenosine 5'-triphosphate](#)

Promoter

Sequence Entry: [AJ344068.1](#)
 Transcription Start Site: 43278
 Direction: -
 Sigma Factor: 70

Genes

[xylR \(AJ344068.1\)](#)

Binding sites

Regulator	Coordinates	Sequence	Db Entry
xylR	(43259 , 43274)	TTAGCATTGCTTAG	AJ344068.1
xylR	(43289 , 43304)	TTAACCAATTGATTAA	AJ344068.1

Regulation

Regulator: [xylR \(AJ344068.1\)](#)
 Action: auto-repression
 Binding sites: (43259 , 43274) (43289 , 43304)
 induced by: 4-Chlorobenzaldehyde Toluene 4-nitrotoluene m-Xylene 2-nitrotoluene Adenosine 5'-triphosphate 3-Methylbenzylalcohol p-Xylene m-amino-nitrotoluene

500 bp

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

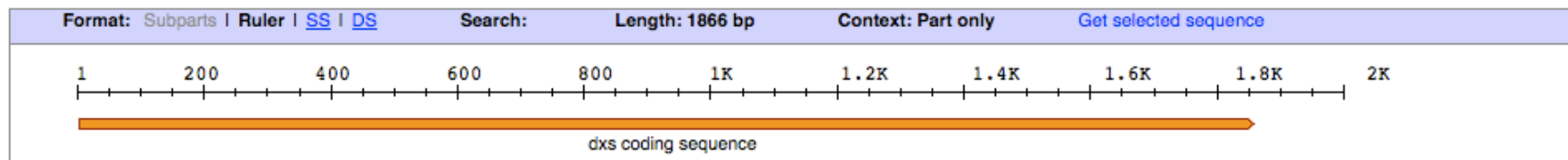
BBa_K118000.

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

BIOLOGICAL CONTEXTS

all the information together

SYNTHETIC BIOLOGY

Synthetic Biology

Search Genomes Genes Proteins Pathways Parts Models

Browse Bacterial Genomes

Search Parts Registry

Search Biological Databases

Search Registry
by part name

The Registry is a collection of ~3200 genetic parts that can be mixed and matched to build synthetic biology devices and systems. Founded in 2003 at MIT, the Registry is part of the Synthetic Biology community's efforts to make biology easier to engineer. It provides a resource of available genetic parts to iGEM teams and academic labs.

Enter the part name (e.g BBa_C0179)

BBa_K118000

Search

Results

Part Name

BBa_K118000

Getting similar sequences

BIOLOGICAL CONTEXTS

all the information together

SYNTHETIC BIOLOGY

Synthetic Biology

Search Genomes Genes Proteins Pathways Parts Models

Get Similar Biological Entities
Add To Design
Save Design

Results

Part Name

BBa_K118000

Acc	Description	Organism	Length	Identity	Score	Expectation
P77488	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli K-12	620	100	3173	0.0
B1XF08	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli str. K-12 substr. DH10B	620	100	3173	0.0
C4ZTH7	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli BW2952	620	100	3173	0.0
C8U2A4	1-deoxyxylulose-5-phosphate synthase, thi		620	99	3172	0.0
C1HH35	1-deoxyxylulose-5-phosphate synthase OS:		620	99	3172	0.0

Retrieve similar proteins or genes using sequence similarity algorithms.

Retrieving protein annotations

BIOLOGICAL CONTEXTS

all the information together

SYNTHETIC BIOLOGY

Synthetic Biology

Search Genomes Genes Proteins Pathways Parts Models

- Protein Annotations ←
- Protein Sequence
- Protein Interactions ▶
- Search similar in the Part Registry

Acc	Description		Length	Identity	Score	Expectation
P77488	1-deoxy-D-xylulose-5-p		620	100	3173	0.0
B1XF08	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli str. K-12 substr. DH10B	620	100	3173	0.0
C4ZTH7	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli BW2952	620	100	3173	0.0
C8U2A4	1-deoxyxylulose-5-phosphate synthase, thi		620	99	3172	0.0
C1HH35	1-deoxyxylulose-5-phosphate synt					

Retrieve annotations
from different
databases

UNIPROT ANNOTATIONS

NAME: 1-deoxy-D-xylulose-5-phosphate synthase (ACC P77488)

TAXONOMY: Escherichia coli (strain K12) ()

MOLECULAR FUNCTION: Transferase

FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP).

CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

SIMILARITY: Belongs to the transketolase family. DXPS subfamily.

BIOLOGICAL PROCESS: Isoprene biosynthesis, Thiamine biosynthesis

Sequence features

Acc	Description	Organism	Length	Identity	Score	Expectation
P77488	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli K-12	620	100	3173	0.0
B1XF08	1-deoxy-D-xylulose-5-phosphate synthase	Escherichia coli str. K-12 substr. DH10B	620	100	3173	0.0
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C8U2A4	1-deoxyxylulose-5-phosphate synthase, thi		620	99	3172	0.0
C1HH35	1-deoxyxylulose-5-phosphate synthase OS		620	99	3172	0.0

Sorry, STRING did not find a protein called P77488

Information about mutations, protein domains, functionally important residues, etc.

LEGEND

- Pfam Domain
- Natural Variants
- Crosslinked Residues
- Alternative Sequence

IGVELTPLEKLP I G K G I V K R R G E K L A I L N F G T L M P E A A K V A E S L N A T L V D M R F V K P L D E A L I L E M A A S H E A L V T V E E N A I M G G A G

Transketolase_C

LEGEND

- Pfam Domain
- Natural Variants
- Crosslinked Residues
- Alternative Sequence

KRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD

KRALPNNTSSSPQPKKKPLDGEYFTLQI GR RFE FREL EALE DAQ G E G RAHS K S R F G S

IRGRERFEMFRELNEALELKDAQAGKEPGGSRRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD

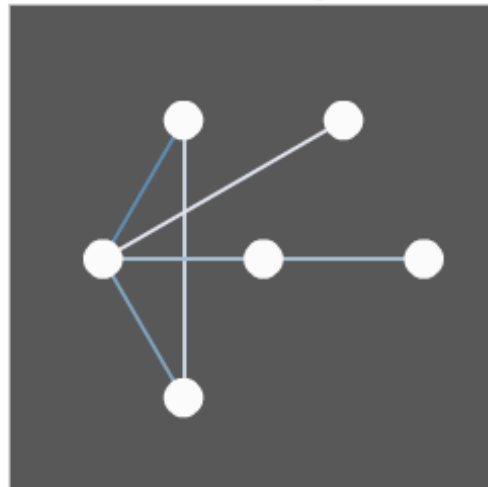
P53_tetramer

Protein Interactions

Acc	Description	Organism	Length	Identity	Score	Expectation
Q18807	ODR10 OS=Caenor	Caenorhabditis eleg	339	97	1385	9.999999999999999!
C3U4Y0	ODR10 OS=Caenor		342	75	1271	9.999999999999999!
C3U4Y6	ODR10 OS=Caenor		342	75	1270	9.999999999999999!
C3U4Y1	ODR10 OS=Caenor		342	75	1270	9.999999999999999!
C3U4Y2	ODR10 OS=Caenor		342	75	1266	9.999999999999999!

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

Pathways

Search Genomes Genes Proteins Pathways Parts Models

Kegg Pathways ←

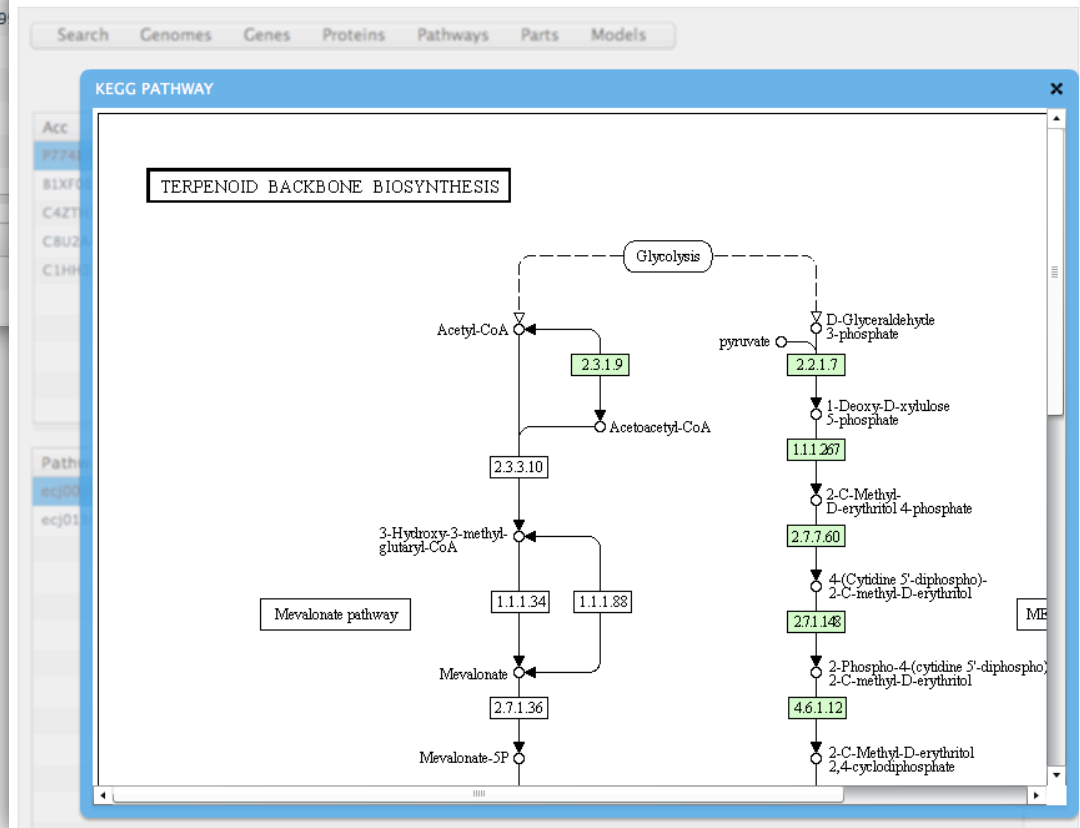
Acc	Description	Organism	Length	Identity	Score	Expectation
P77488	1-deoxy-D-xylulos	Escherichia coli K-1	620	100	3173	0.0
B1XF08	1-deoxy-D-xylulos	Escherichia coli str.	620	100	3173	0.0
C4ZTH7	1-deoxy-D-xylulos	Escherichia coli BW	620	100	3173	0.0
C8U2A4	1-deoxyxylulose-5		620			
C1HH35	1-deoxyxylulose-5		620			

Pathway

ecj00900 ←

ecj01100 ←

Synthetic Biology

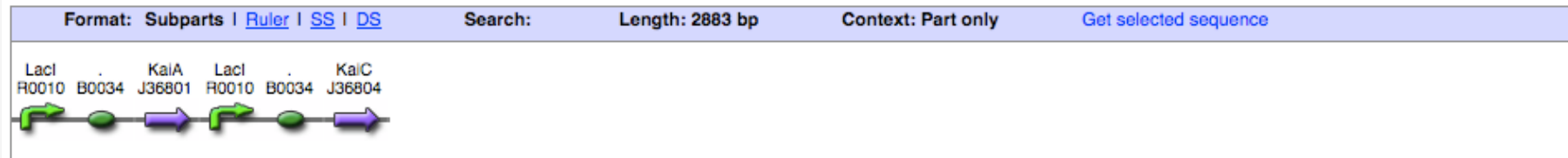


Build new designs or redesigning composite parts

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



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

Search Genomes Genes Proteins Pathways **Parts** Models

Get Similar Biological Entities
Add Part To Design
Save Design

Selected part is a composite part formed by:

Part Name

- BBa_J36335
- BBa_R0010
- BBa_B0034
- BBa_J36801
- BBa_R0010
- BBa_B0034
- BBa_J36801

Acc	Description	Organi	Length	Identit	Score	Expecta
Q5N594	Circadian clock protein KaiC OS=Synechococcus sp. (strain ATCC 27144 / PCC	Synech	519	100	2624	0.0
Q79PF4	Circadian clock protein kinase kaiC OS=Synechococcus elongatus (strain PCC 7	Synech	519	100	2624	0.0
A0MVY7	KaiC OS=Leptolyngbya boryana IAM M-101 GN=kaiC PE=4 SV=1		517	82	2226	0.0
A0YK92	Circadian clock protein KaiC OS=Lyngbya sp. PCC 8106 GN=L8106_06509 PE=		522	81	2198	0.0
B4W3D4	Circadian clock protein KaiC OS=Microcoleus chthonoplastes PCC 7420 GN=MC		519	82	2188	0.0

Adding other proteins

Search Genomes Genes **Proteins** Pathways Parts Models

Protein Annotations
Protein Sequence
Protein Interactions
Search similar in the Part Registry
Add Protein To Design ←

Acc	Description	Organism	Length	Identity	Score	Expectation
Q5N594	Circadian clock protein KaiC OS=Leptolyngbya boryana IAM M-101 GN=kaiC PE=4 SV=1	27144 / PCC Synech	519	100	2624	0.0
Q79PF4	Circadian clock protein KaiC OS=Leptolyngbya boryana IAM M-101 GN=kaiC PE=4 SV=1	(strain PCC 7 Synech	519	100	2624	0.0
A0MVY7	KaiC OS=Leptolyngbya boryana IAM M-101 GN=kaiC PE=4 SV=1		517	82	2226	0.0
A0YK92	Circadian clock protein KaiC OS=Lyngbya sp. PCC 8106 GN=L8106_06509 PE=4 SV=1		522	81	2198	0.0
B4W3D4	Circadian clock protein KaiC OS=Microcoleus chthonoplastes PCC 7420 GN=MC		519	82	2188	0.0

Part submission to the registry is not yet implemented

Search Genomes Genes Proteins Pathways **Parts** Models

Get Similar Biological Entities
Add Part To Design
Save Design ←

Entity	Sequence
BBa_J36804	ATGACTTCCGCTGAGATGACTAGCCCTAATAATAATTCTGAGCACCAAGCCATCGCTAAGATGCCGACGATGATTGAAGCCTTTGATGAT,
B4W3D4	MSPFNLDEQRPDEFTHPGVHKIRTMIEGFDDISHGGLPVARTTLVSGTSGTKLFAVQFLYNGITQFDDPGVFVTFEESPNDIIKNSHSLGWNLQKLIDG,

Implement BioModels ?

Search Genomes Genes Proteins Pathways Parts Models

Browse Bacterial Genomes
Search Parts Registry
Search Biological Databases

mat

MEE PQSDPSVEPPLSQETFSDLWKLLPENNVLSPLSQAMDDLMLSPDDIEQWFTEDPGP
DEAPRMPEAAAPRVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRGLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTDEVVRRCPHHE
RCSDDGLAPPQHILRVEGNLRVEYLDDRNTERHSVVVPEPPEVGSDDCTTIHYNMCNS
SCMGGMNRRPILTIITLEDSSGNLLGR
PGSTKRALPNNTSSSPQPKKKPLDGE
GSRHSSHLKSKKGQSTSRHKKLMFK

Search

Search Genomes Genes Proteins Pathways Parts Models

Get BioModels

Acc	Description	Organism	Length	Identity	Score	Expectation
Q2XN98	Cellular tumor antigen	Homo sapiens	393	100	2119	0.0
P04637	Cellular tumor antigen	Homo sapiens	393	100	2119	0.0
Q5U0E4	Cellular tumor antigen	Homo sapiens	393	99	2117	0.0
B6E4X6	Cellular tumor antigen		393	99	2110	0.0
Q2XSC7	Cellular tumor antigen	Homo sapiens	393	99	2103	0.0

BioModel

BIOMD0000000188
BIOMD0000000209

Get BioModel description

Compare models with pathways

Search Genomes Genes Proteins Pathways Parts Models

BioModel

This a model from the article:
A computational model for understanding stem cell, trophectoderm and endoderm lineage determination.
Chickarmane V, Peterson C PLoS ONE2008;3(10):Page info: e3478 18941526,
Abstract:
BACKGROUND: Recent studies have associated the transcription factors, network which is responsible for maintaining embryonic stem cell proper antagonism between two of these and other master regulators have been an excess of Cdx2 over Oct4 determines the trophectoderm lineage when differentiation into the endoderm lineage. Also, under/over-expression of some self-renewal/pluripotency as well as differentiation genes are expression concentration of Oct4. METHODOLOGY/PRINCIPAL FINDINGS: We constructed from ChIP-on-chip and microarray data as well as literature studies. The two plausible assumptions; activation of Gata-6 by Oct4 and repression assumptions, the results of simulations successfully describe the biphasic predicts that reprogramming the network from a differentiated state, in best achieved by over-expressing Nanog, rather than by suppression of computational model provides a mechanistic understanding of how differential regulatory network. It provides a framework to explore strategies of reprogramming cell state through directed perturbations. Such an approach is highly relevant search over the host of possibilities for reprogramming to a stem cell state.
This model originates from BioModels Database: A Database of Annotated and Reusable Computational Models for Systems Biology.
The BioModels Team.
For more information see the terms of use.
To cite BioModels Database, please use Le Novère N., Bornstein B., Broic H., Schilstra M., Shapiro B., Snoep J.L., Hucka M. (2006) BioModels Database: A Free, Open-Access, High-Quality Resource for the Quantitative Kinetic Models of Biochemical and Cellular Systems Nucleic Acids Res 34:D659-663.

KEGG PATHWAY

MAPK SIGNALING PATHWAY

Phosphatidylinositol signaling system

Heterotrimeric G-protein

IP₃

cAMP

DAG

PKA

Rap1

PKC

RafB

Raf1

Mos

Scaffold

MEK1

MEK2

MP1

ERK1

ERK2

PTP

Classical MAP kinase pathway

NGF

BDNF

NT3/4

EGF

FGF

PDGF

TykA/B

EGFR

FGFR

PDGFR

GRB2

SOS

Ras

Raf1

RafB

Mos

G12

Gap1m

NF1

p120GAP

JNK and p38 MAP kinase pathway

GLK

HGK

HPK1

Tpl2/Cot

MEK1

MLK3

MKK4

MKK7

JIP1/2

FLNA

ARRB

CytII

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

The screenshot shows the MaDAS web application interface. At the top, there is a navigation bar with the MaDAS logo, a welcome message for 'Victor de la Torre', and links for Home, Projects, Plugins, and Help. Below the navigation bar, there is a section for joining a project, followed by a table listing existing projects. To the right, there is a 'My Projects' section showing details for several projects.

Name	Category	Created by	Create Date
Encode Demo	Genome annotation	Victor de la Torre (cnio)	2008-12-10 10:34:30
Gene Expression Demo	Genome annotation	Victor de la Torre (cnio)	2008-12-10 11:01:54
Gene Expression	Genome annotation	Victor de la Torre (cnio)	2009-02-03 14:20:33
Bionemo	Genome annotation	Victor de la Torre (cnio)	2009-02-23 17:46:59

Researchers can build their own projects

The screenshot shows the 'Create Project' form in the MaDAS web application. The form includes fields for Name, Description, and Category. It also has a Security dropdown menu set to 'Public' and three checkboxes for notifications: 'Notify when a user join in the Project', 'Notify when the project is created', and 'Notify when a new annotation is submitted'. The form has 'Send' and 'Clear' buttons at the bottom.

Adding new annotations

The screenshot displays the MaDas web application interface. At the top, the browser address bar shows <http://madas2.bioinfo.cnio.es/#>. The page header includes the MaDAS logo, a welcome message for Victor de la Torre, and navigation links for Home, Projects, Plugins, and Help. Below the header, there are links for Manage Project, Visualization Plugins, Plugin Help, and Go back. The main content area shows a genomic map for 'MADASMAP. SEGMENT SEGMENT_2 [4 MB]' with a scale of 1,427 KB. A central dialog box titled 'Add/Edit Feature' is open, containing the following fields and options:

- NOTE: Your feature will be saved as a copy.
- ID/Label *: benA
- Type *: GENE
- Start *: 1434223
- End *: 1435608
- Score: (empty)
- Orientation *: +
- Phase *: 0
- Note: (empty text area)
- Save button

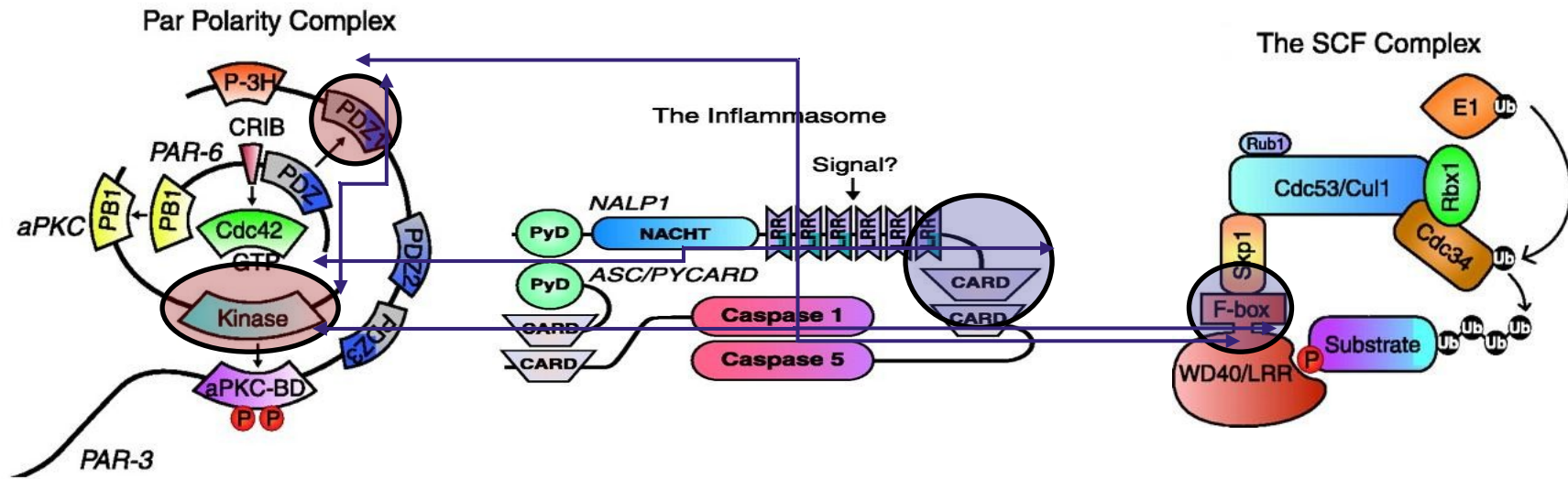
A green callout bubble on the right side of the dialog contains the text: "Users can manually add or edit their annotations". The background shows a genomic map with various colored bars representing features. The bottom of the page includes the text "MaDasMap. Created by Victor De La Torre. 2008-12-11 11:00:28." and a Zotero logo.

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!

Protein Synthetic Biology



Protein BioBricks



promoter +
RBS

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



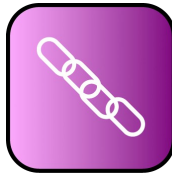
interactio
n

Leu Zippers:

... parallel
... anti-parallel
... heterodimer
... fast
... slow

FRB / FKBP

Lov2 / Lov2



linke
r

(GS)₁

(GS)₃

(GS)₅

(GS)₇

(GS)₁₀

P₄

P₁₀

P₁₅



measureme
nt

mCitrine

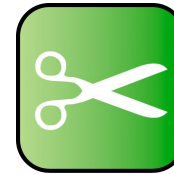
mCherry

mCerulean

H. Gaussia Luciferase A+B

β-Lactamase A + B

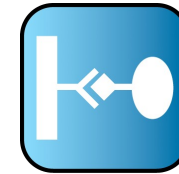
B-Lactamase* A + B



cleavag
e

TEV site

preScission



affinity

His

StrepII

Gst



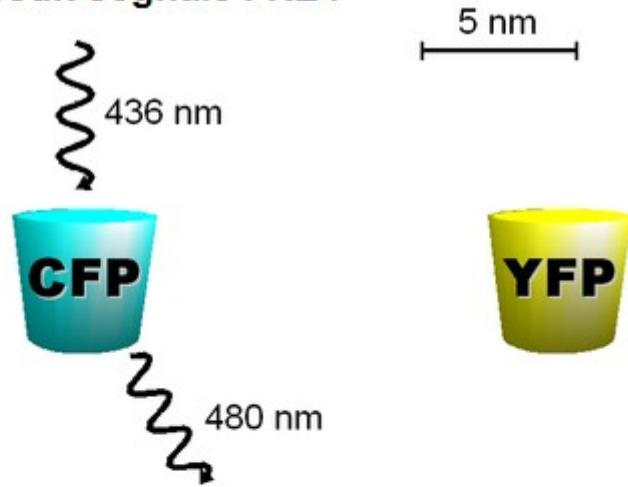
terminat
or

T7

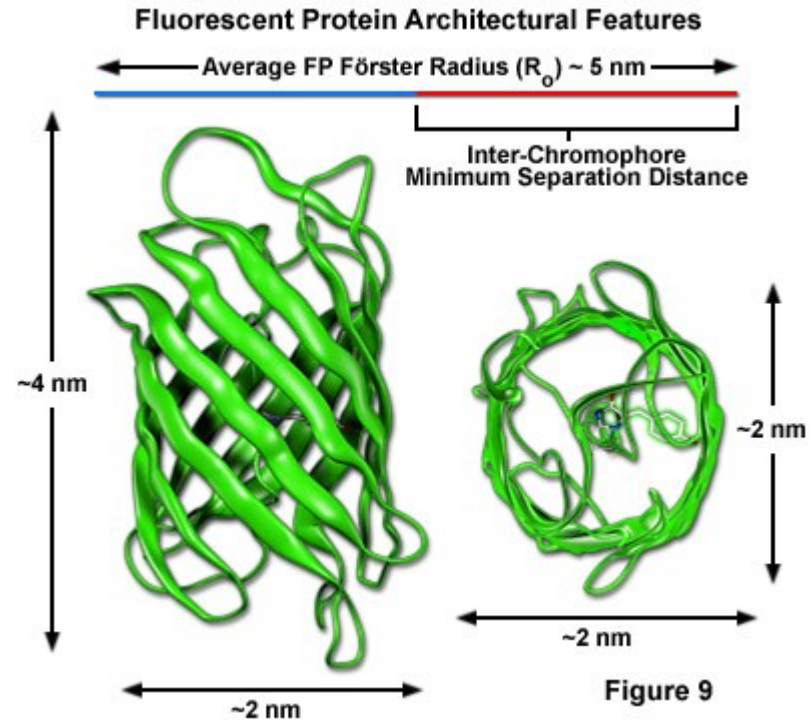
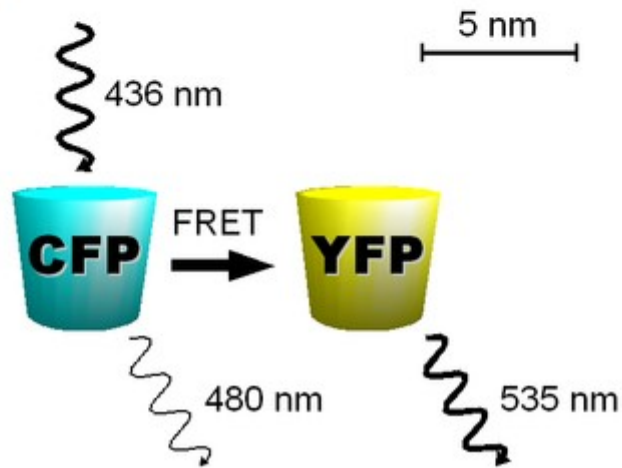
ADH1

FRET Crash Course

Nessun segnale FRET

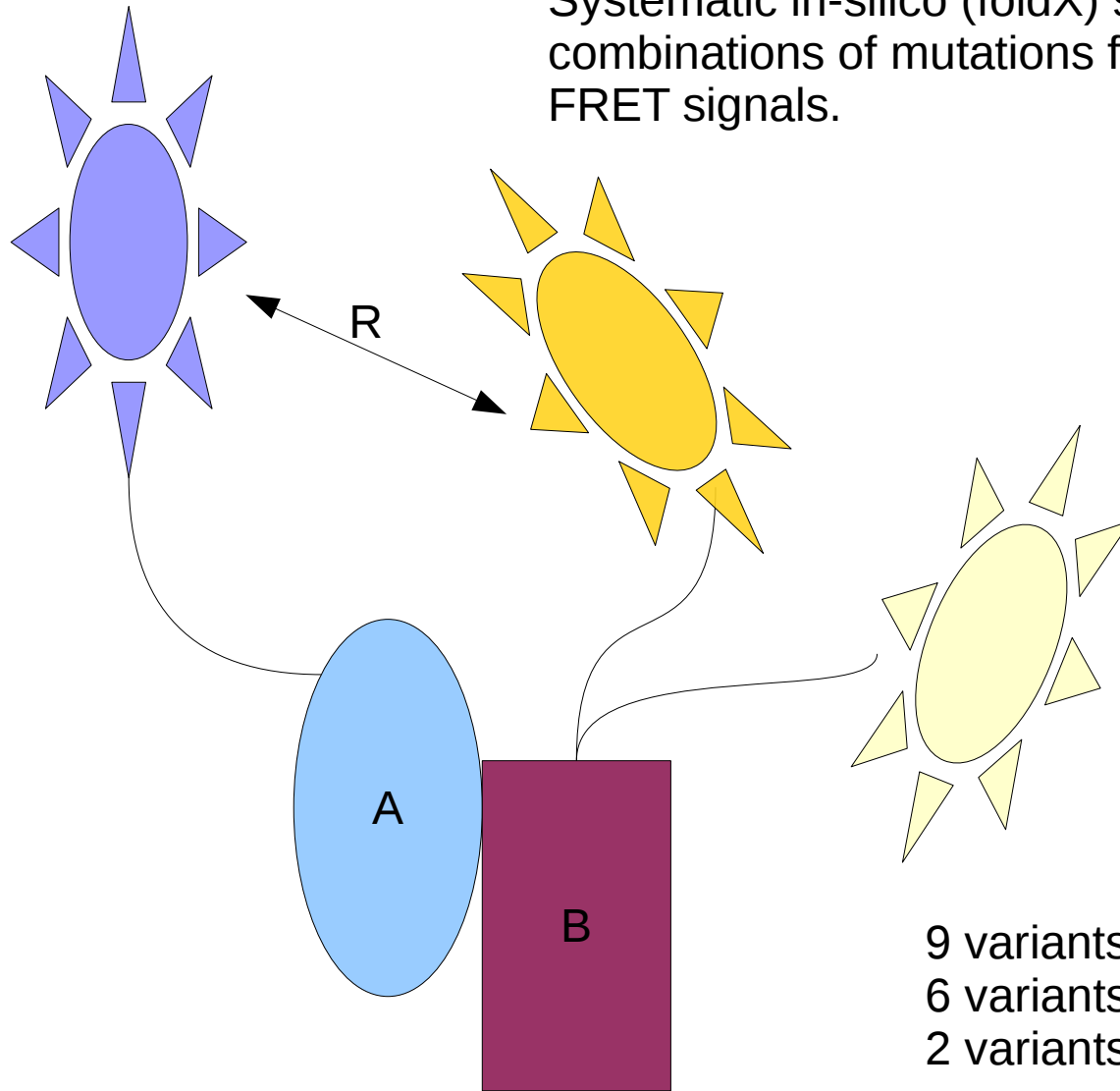


Segnale FRET



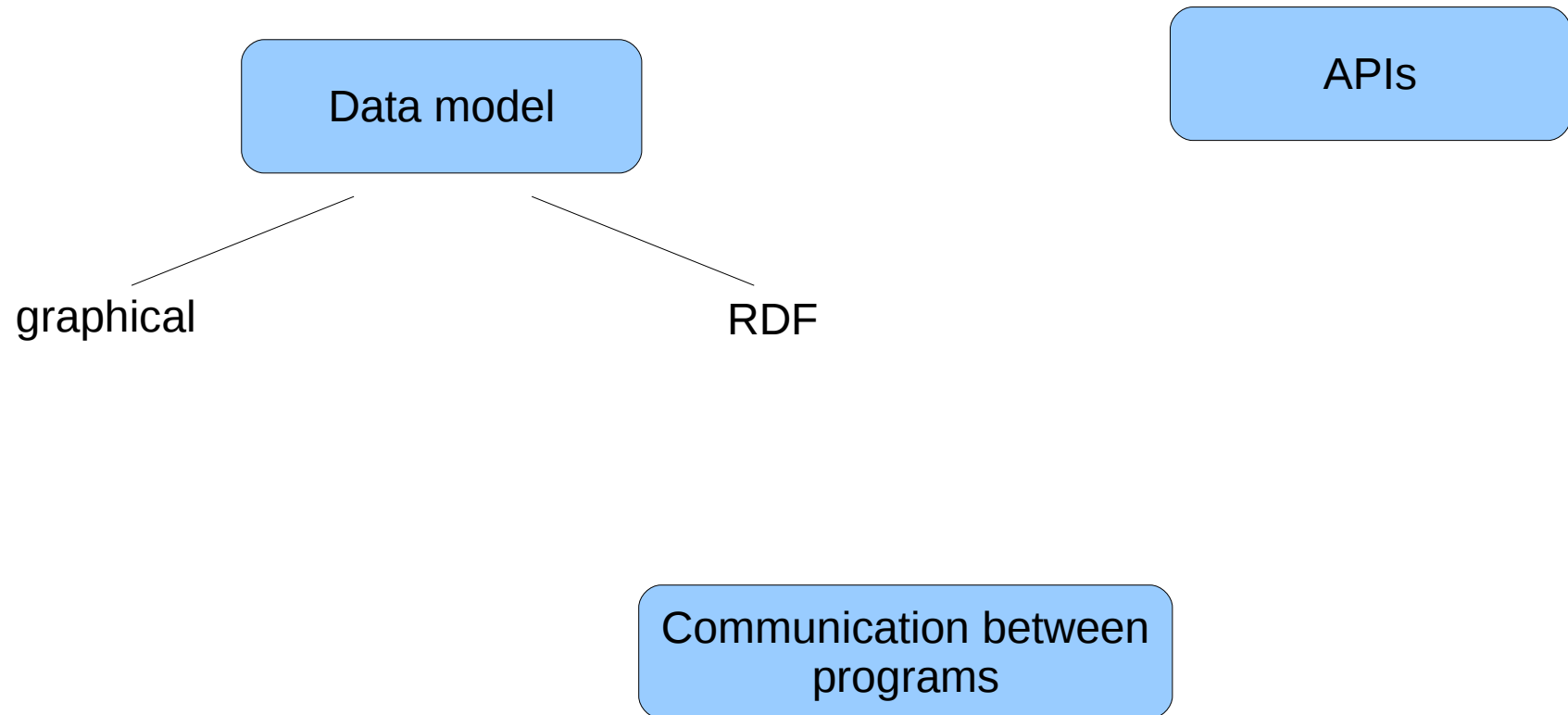
Enhanced FRET

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



PoBOL -> SBOL

Synthetic Biology Open Language



The logo for 'Emergence' features a stylized, golden, wavy line that resembles a DNA double helix or a musical staff with notes. It starts from the top left and curves downwards and to the right, ending near the letter 'E'.

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

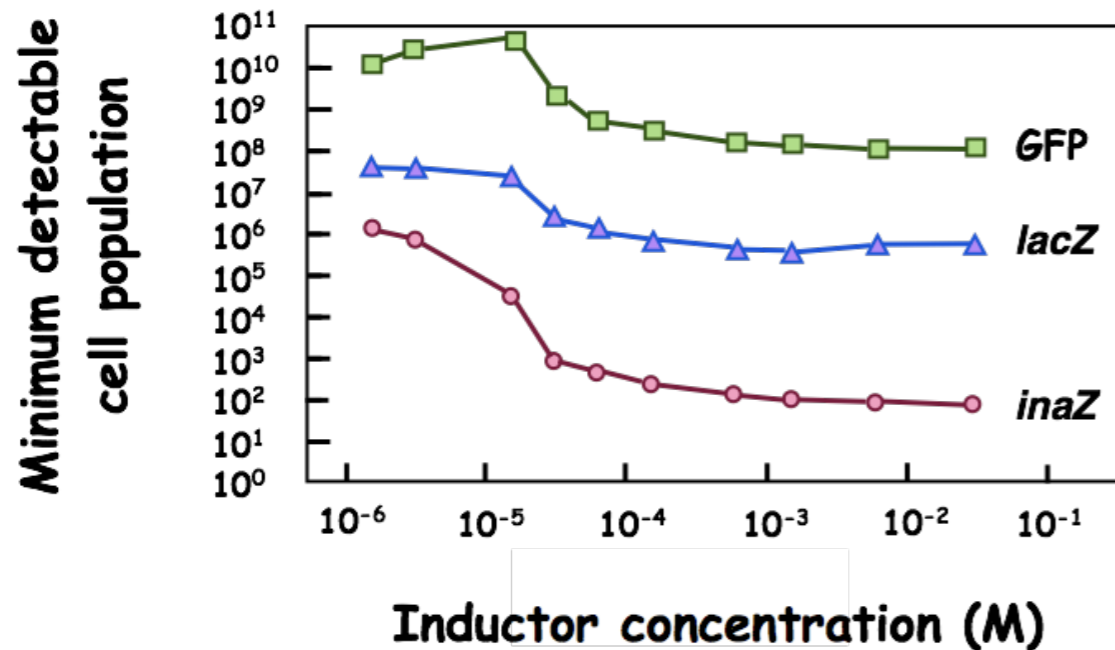
Different genetic variants of the same reporter gene

- *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?

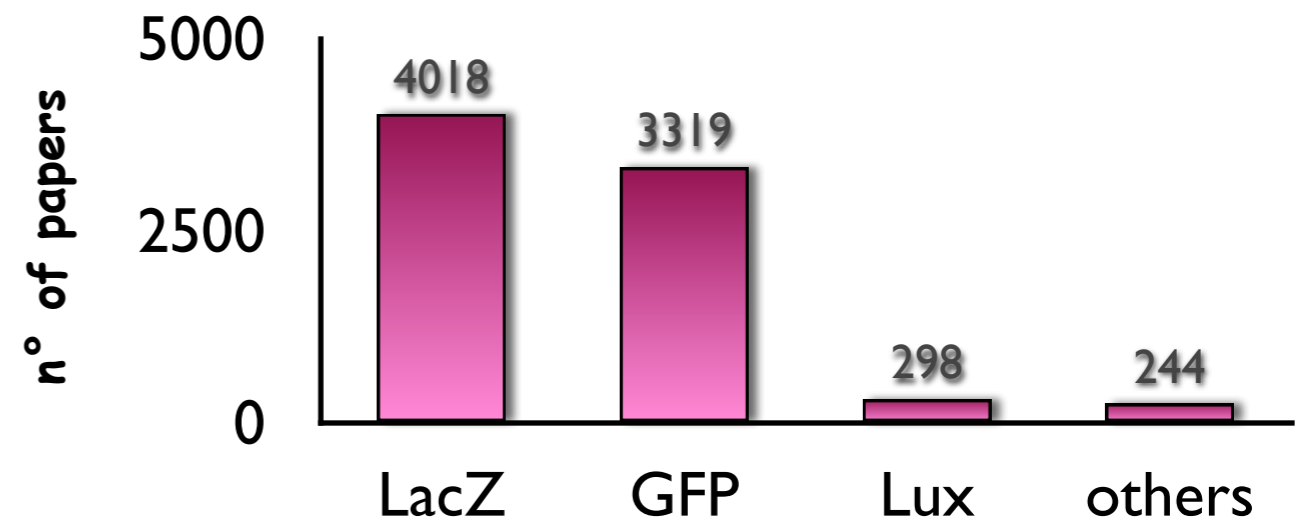
<i>lux</i>	<i>GFP</i>	<i>lacZ</i>
Non-invasive	Non-invasive	Invasive & Non-invasive
No excitation	Excitation	No excitation
Population	Population & Single cell	Population & Single cell
Costly	Non-costly	Non-costly
Dimer	Monomer	Tetramer

Reporter sensitivities



Miller et al. App. Environ. Micro. 2001

reporter



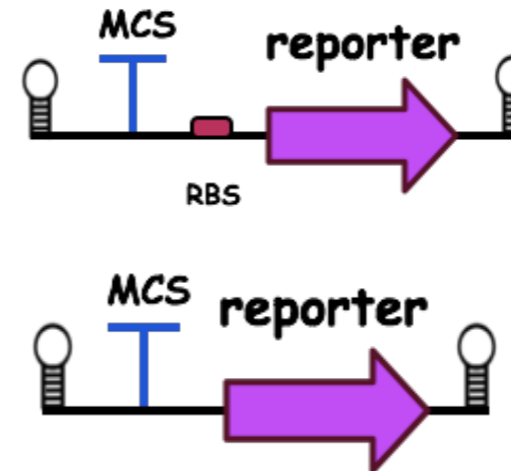
Mostly, depends on the experiment settings

Variability in measurements

2- Variability in genetic tools

2.1- Type of reporter fusion

- Transcriptional fusions
- Translational fusions



2.2- Type of vectors

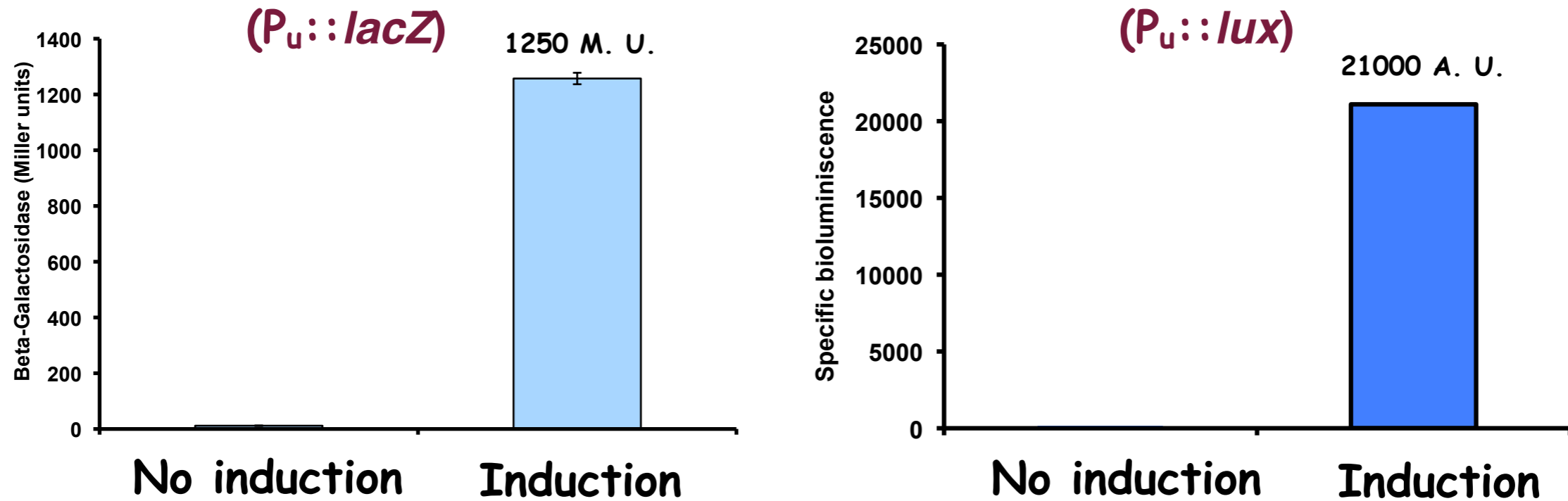
- Copy number: Multi-copy vs. low-copy vs. mono-copy
- Host range (not only for *E. coli*)
- Stability (without antibiotic selection)

2.3- Chassis

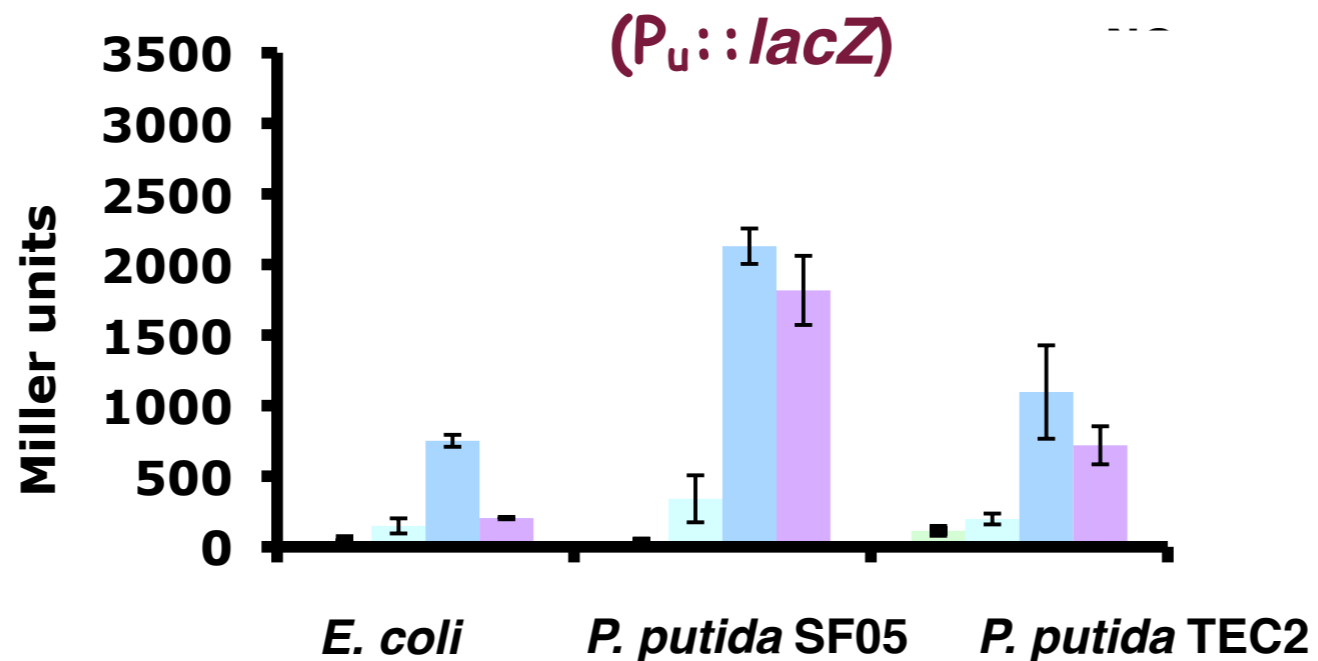
- Genetic repertoire
- Background levels

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

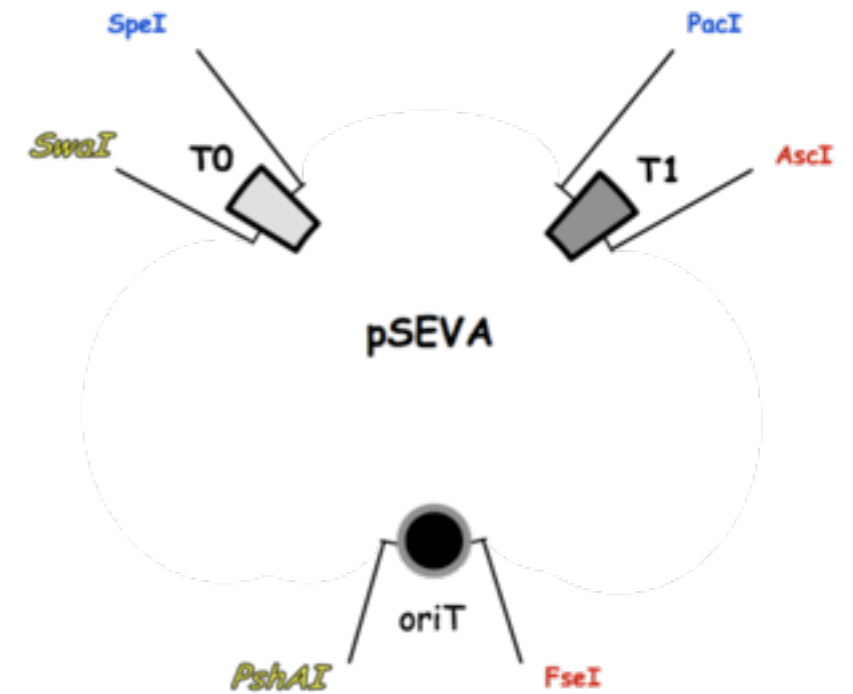
Standard Genetic tools



pStandard European Vector Architecture

Backbone

- Minimal origin of transference: oriT-RP4 (260 bp)
- Terminators: T₀
T₁



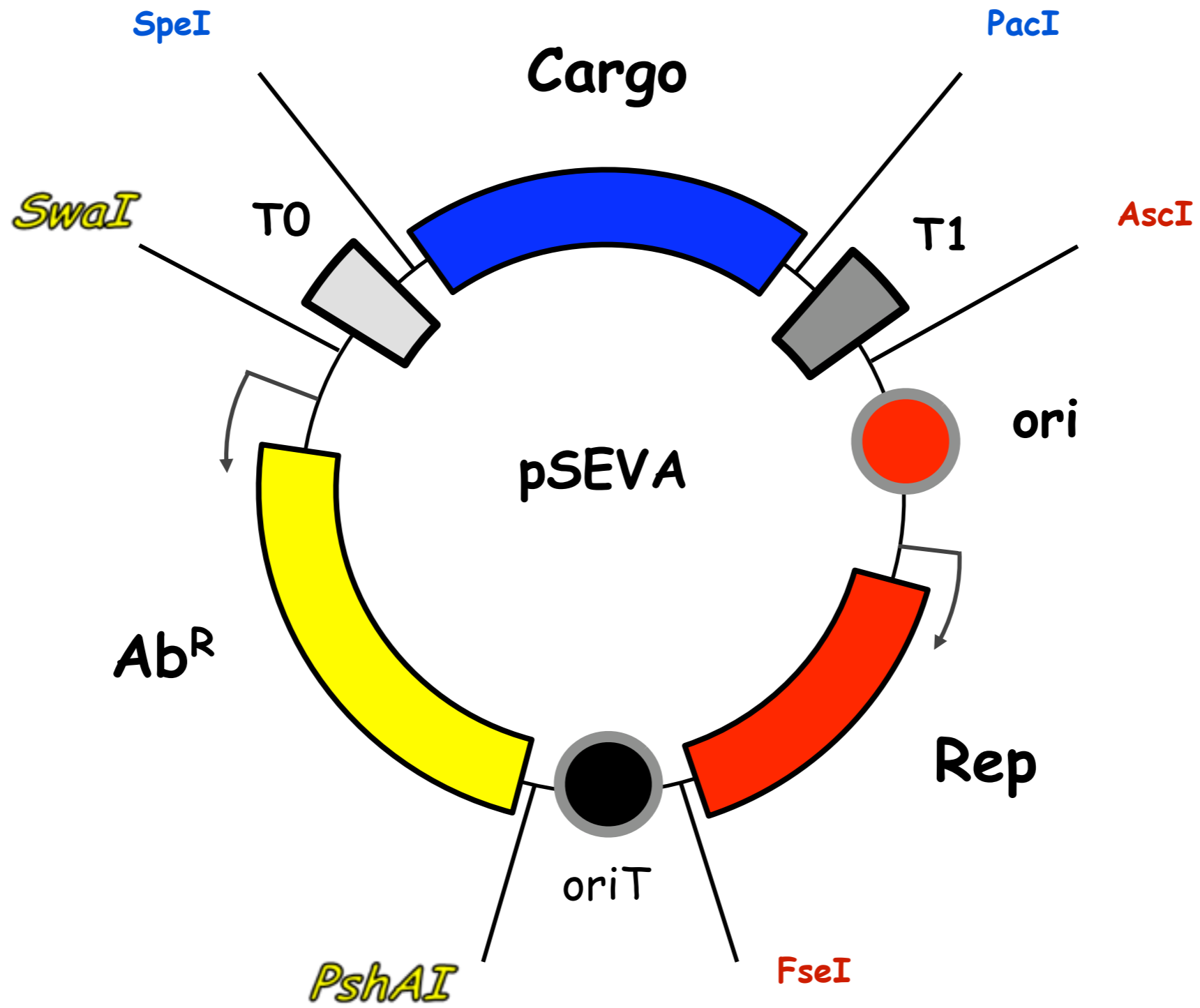
Modules

- 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

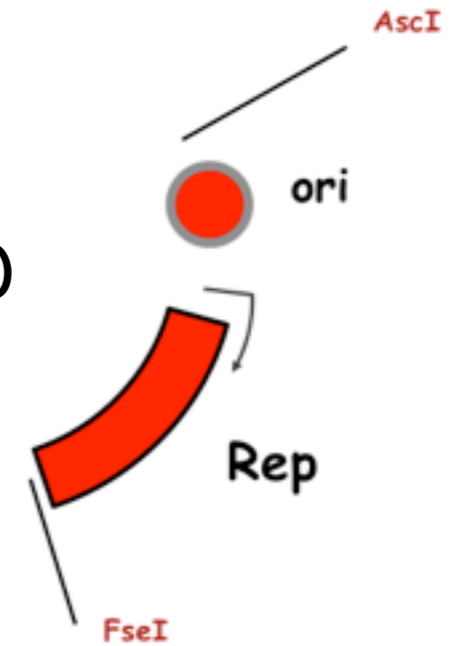




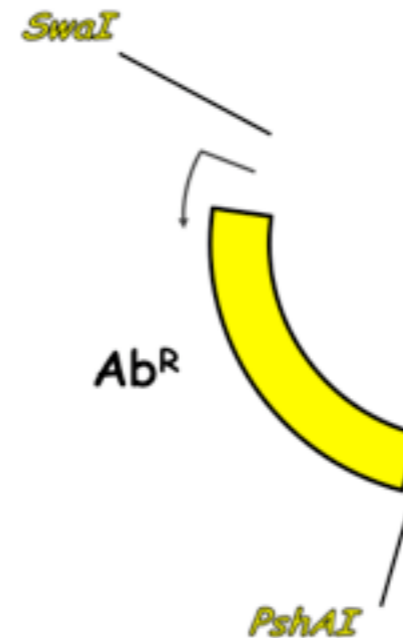
pSEVA modules

1) Origin of replication:

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



2) Antibiotic resistance marker:



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

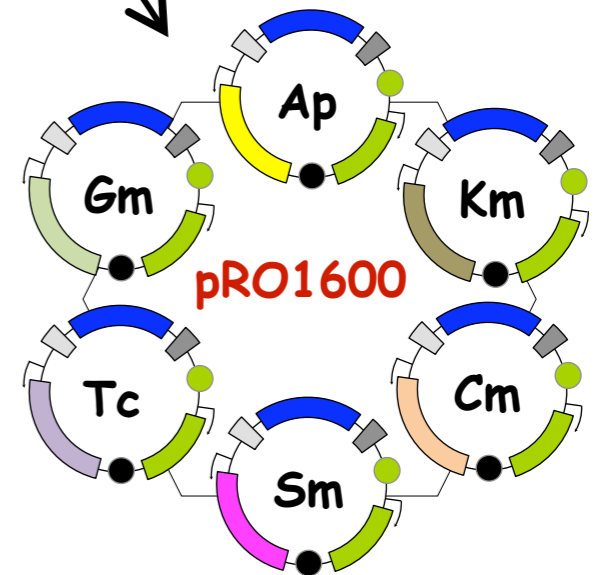
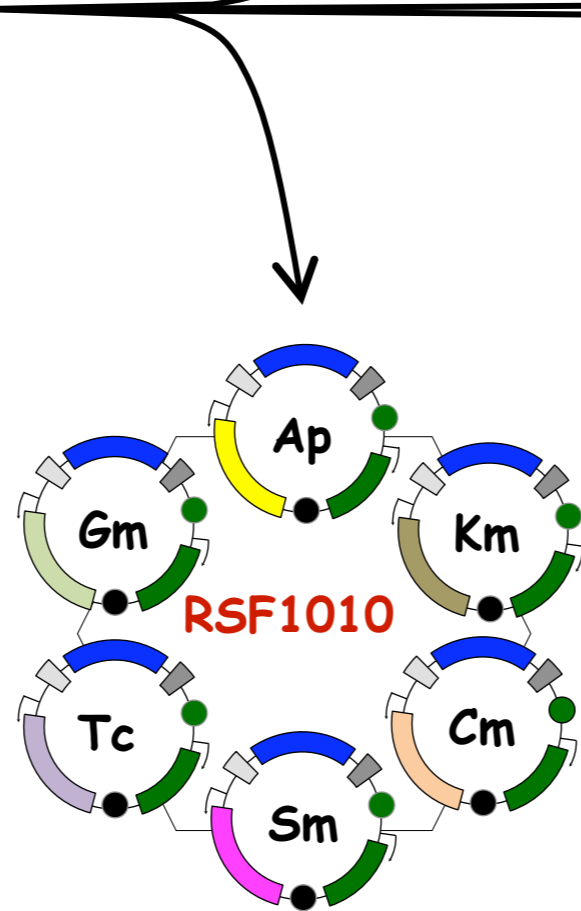
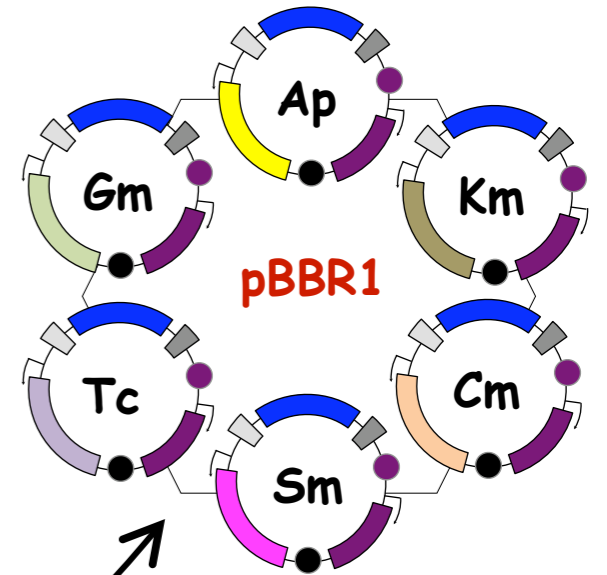
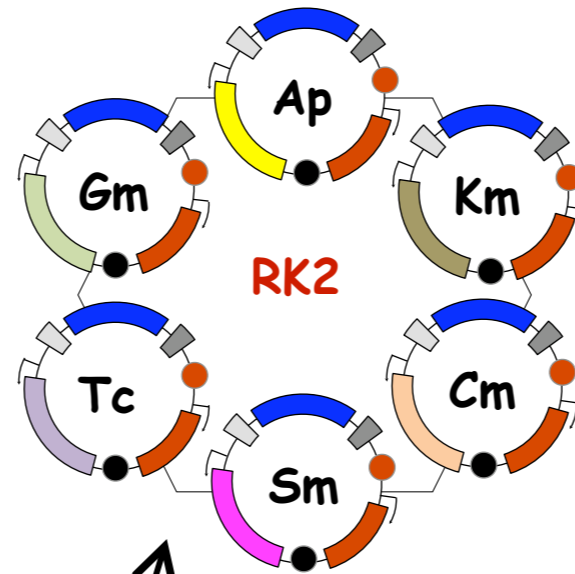
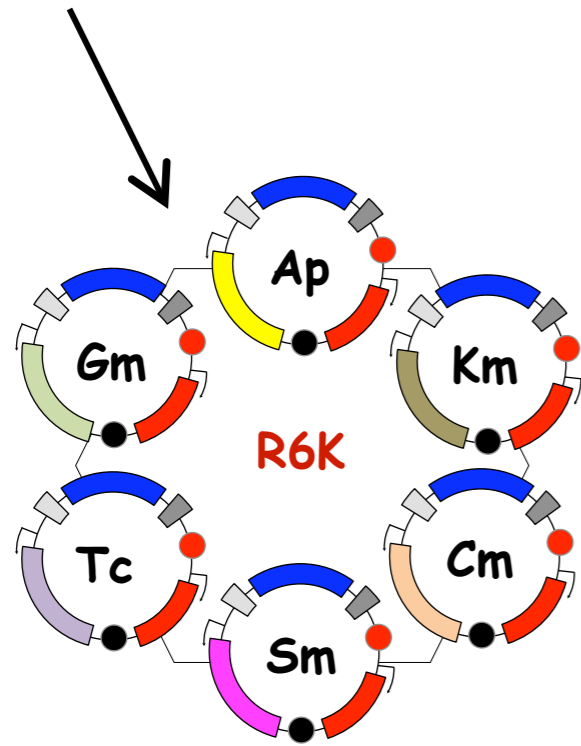
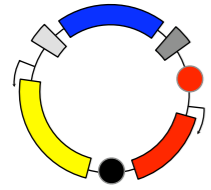
3) Cargo site:



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

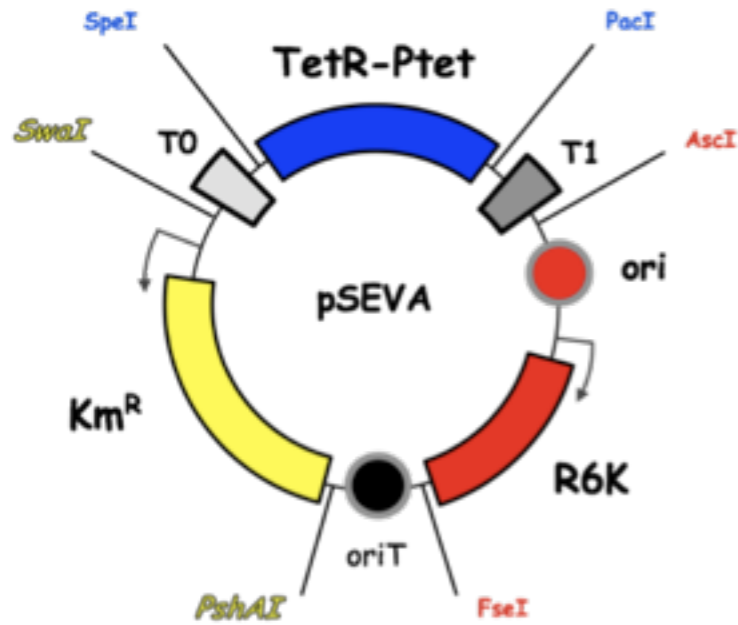
pSEVA collection

pSEVA111

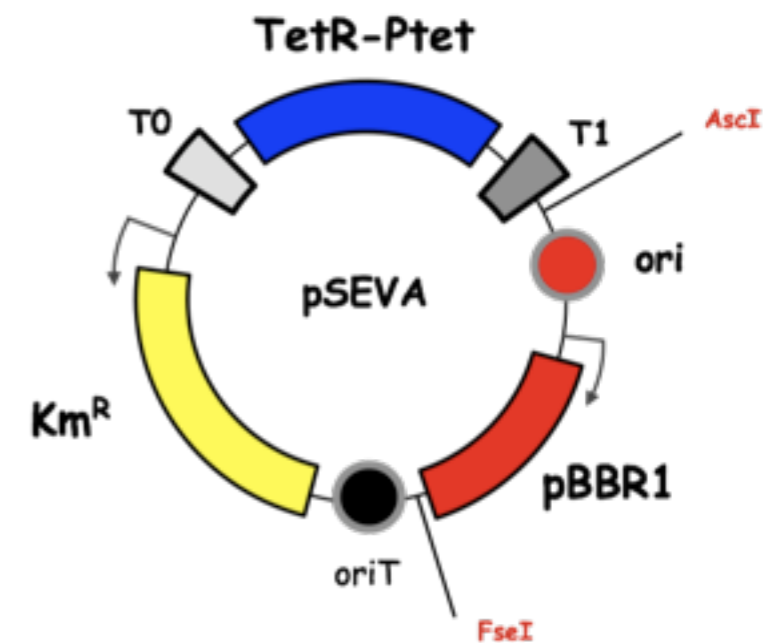


pSEVA modules exchange examples

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



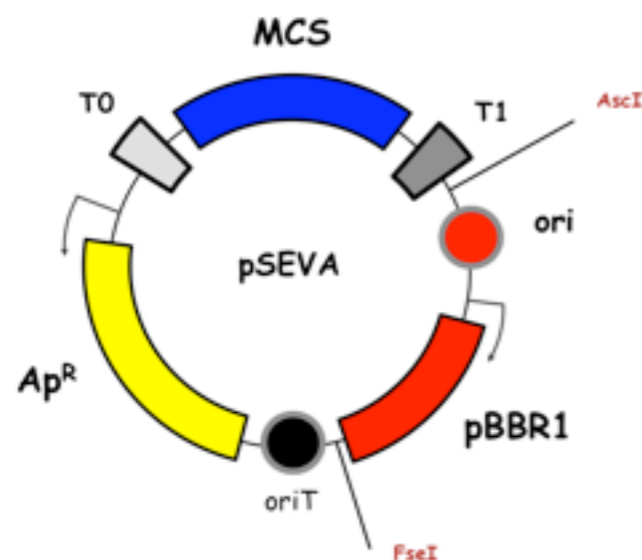
TetR- P_{tet} , Km^R , pBBR1




AscI & FseI

Origin of replication
exchange

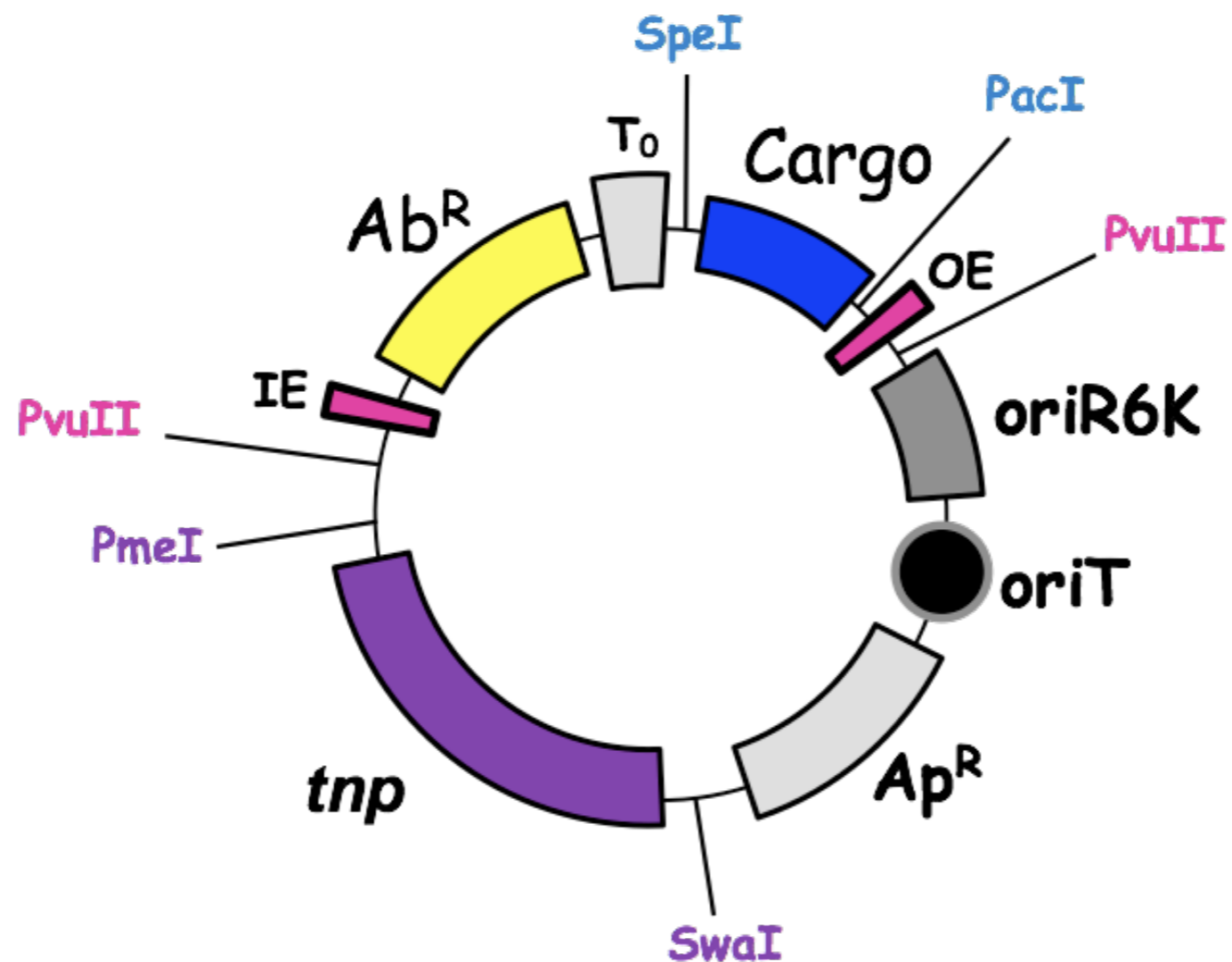
pBBR1 origin donor



 **pS** standard **E**uropean **T**ransposon **A**rchitecture

Uses:

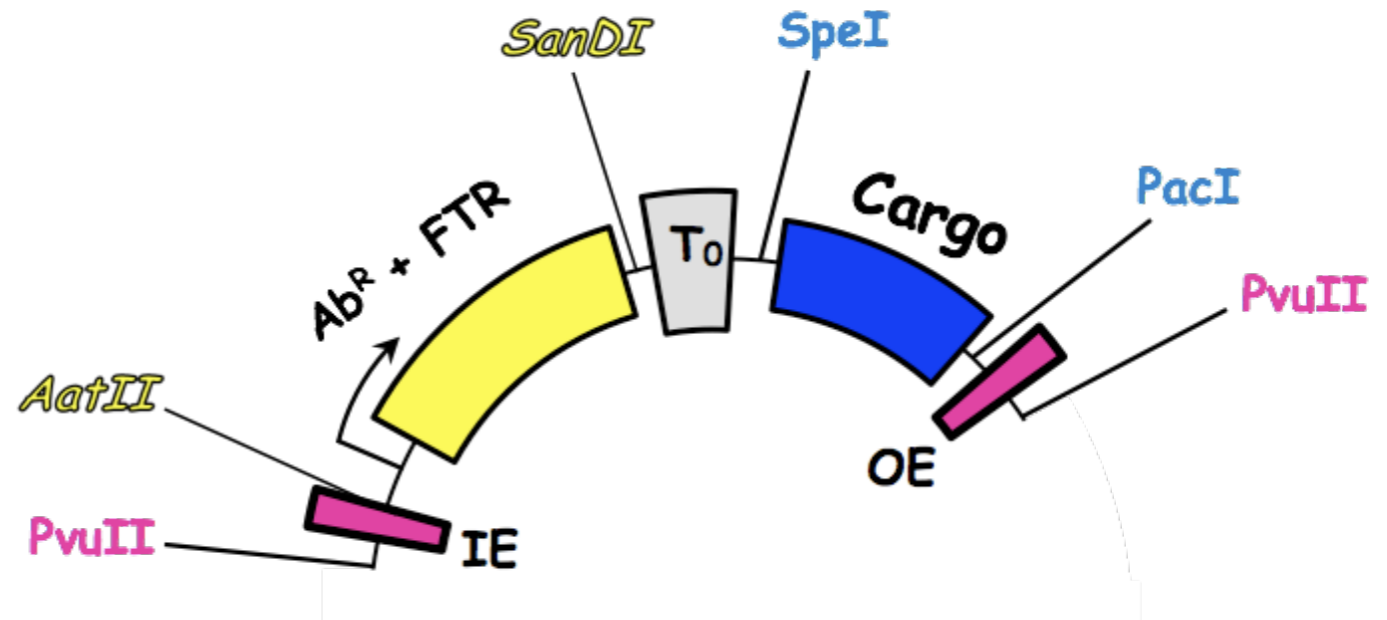
- To integrate cargos into the genome
- Random mutagenesis



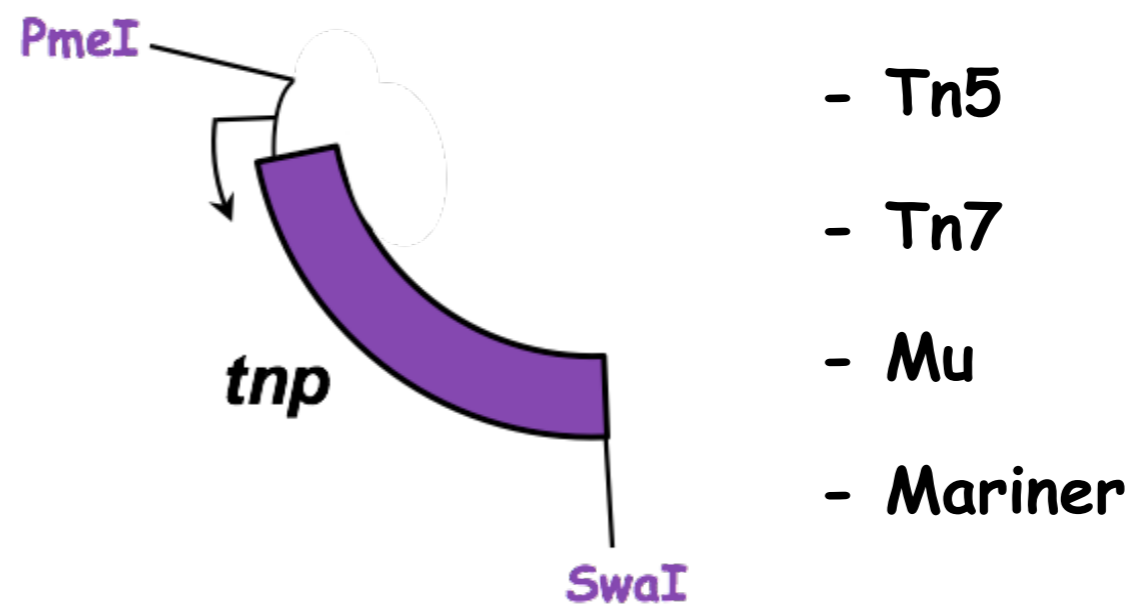


pSETA

The transposon module



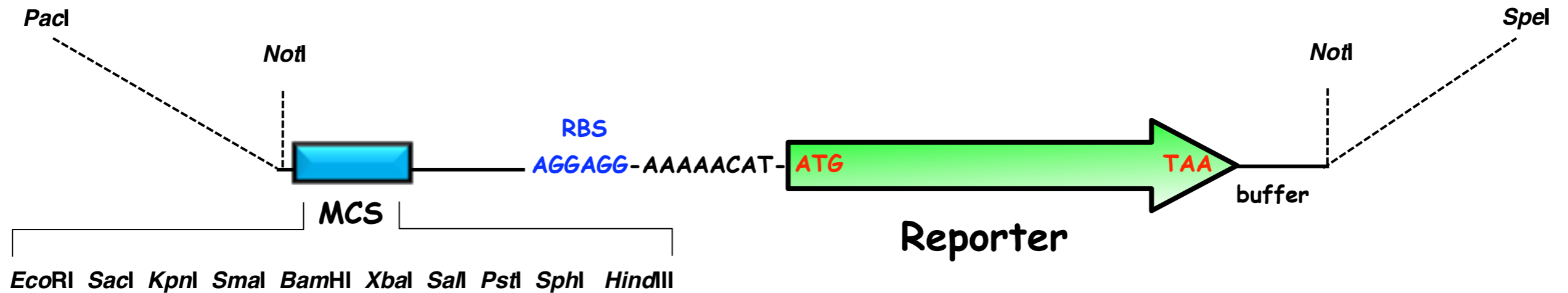
The transposase module





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

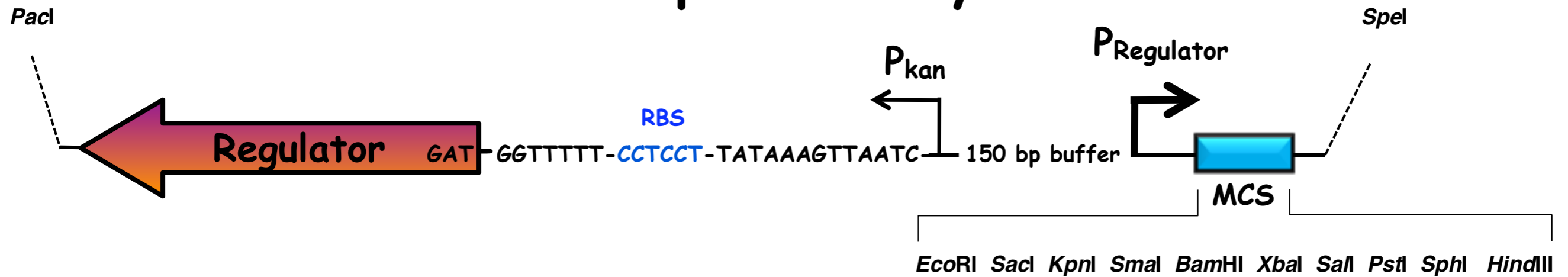
- Same plasmid backbone
- Copy number at choice
- Different reporters

Promoter / reporter calibration curves



pSEVA cargos

Gene expression systems



Regulator- P_R edited systems

<u>Promoter</u>	<u>Regulator</u>	<u>Type</u>	<u>Inductor</u>
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 alkanolates

Conditional oriV pBR322 TetR

Conditional expression based on Tc

LacZ

Promoter reporter with optimized RBS

LacZ α -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](#) (28th-29th 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](#) (21th-22th October 2009)

Aim: Position paper to define transcriptional measurements standards

Participants

Engineer

Drew Endy

Ron Weiss

Christina Smolke

Ido Golding

Sven Panke

Vitor dos Santos

Biology

Steve Busby

Richard Gourse

Fernando de la Cruz

Martin Buck

Virgil Rhodius

Victor de Lorenzo

European Comission

Ioannis Economidis

Observers

Alistair Elfick

Rafael Silva Rocha

Esteban Martínez

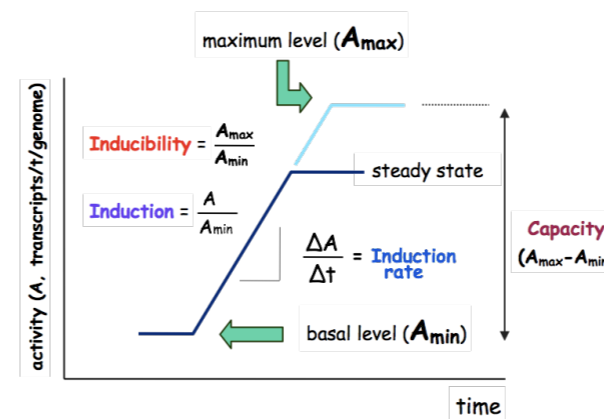
Sandpit on defining transcriptional standards

Topics covered:

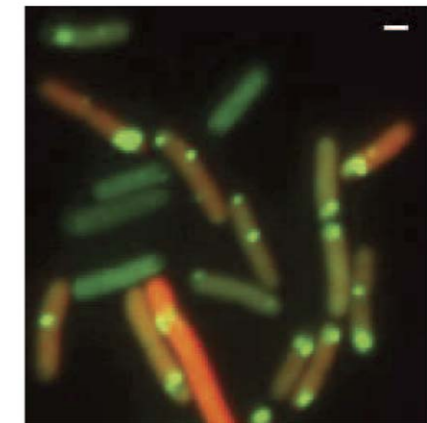
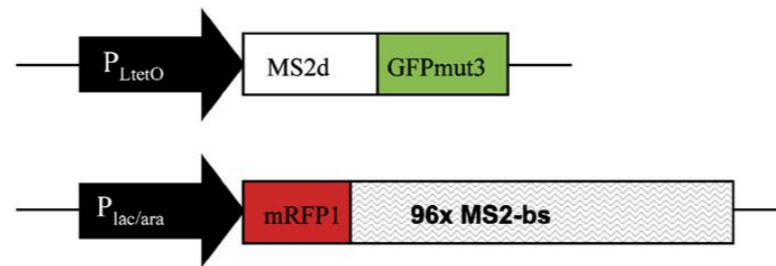
- How to measure promoter strength
- Standard way to perform reporter fusions
- Reporter calibration curves
- Standard reference promoters
- Promoter parameters

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

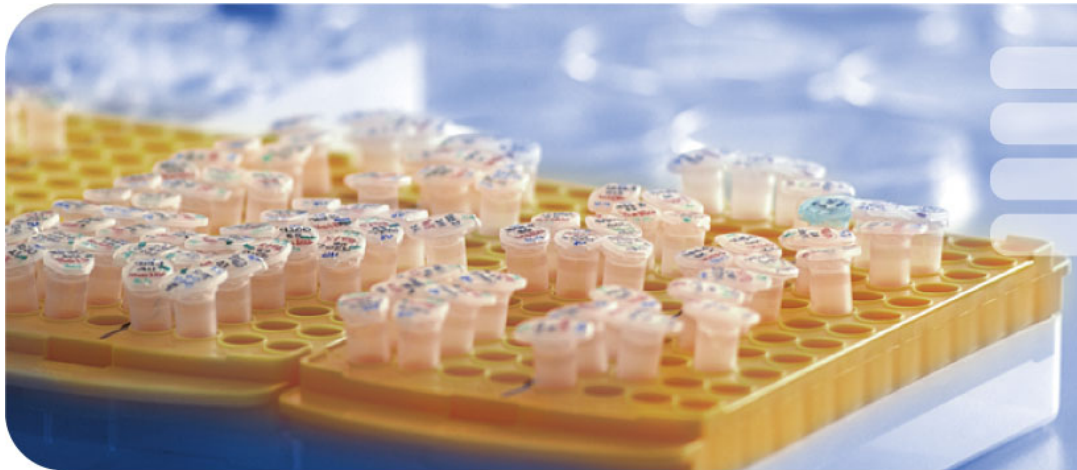
4.2: Application of design tools on standardized promoters

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

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:

EDITORIALS

NATURE | Vol 455 | 25 September 2008

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 beginning of a road of

"Industry self-policing can sometimes fail"



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.

432

© 2008 Macmillan Publishers Limited, All



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:



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 (violence 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	<p>Reports on two industry workshops</p> <ul style="list-style-type: none"> ■ 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

May 2008

Synthetic Biology

Social and Ethical Challenges



Andrew Balmer & Paul Martin
Institute for Science and Society
University of Nottingham

Institute for Science and Society
SCIENCE-TECHNOLOGY-SOCIETY

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.

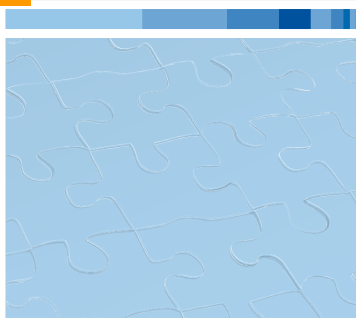
April 2008

Synthetic Biology – Engineering in Biotechnology

Schweizerischen Akademie der Technischen Wissenschaften (SATW)

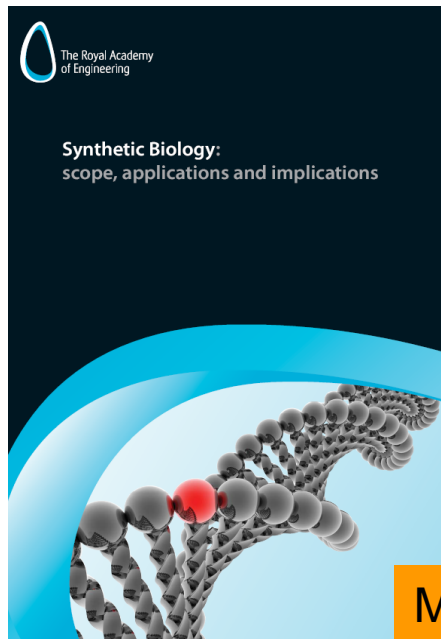
July 2009

Synthetische Biologie Stellungnahme



DFG Deutsche Forschungsgemeinschaft
acatech DEUTSCHE AKADEMIE DER TECHNISCHEN WISSENSCHAFTEN
Leopoldina Nationale Akademie der Wissenschaften

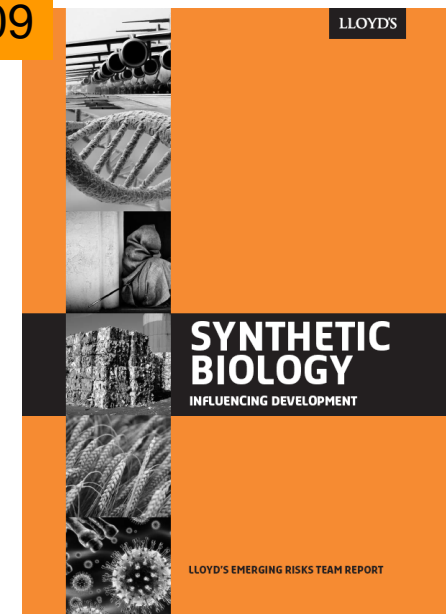
July 2009



The Royal Academy of Engineering

Synthetic Biology: scope, applications and implications

May 2009



LLOYDS

SYNTHETIC BIOLOGY INFLUENCING DEVELOPMENT

LLOYD'S EMERGING RISKS TEAM REPORT

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!?

Organisation for International Dialogue and Conflict Management

You are here: EN > Events > Archive

Archive

This is the archive of events in which members of IDC have took part. In case you are interested in future activities please visit our section of [Earthcomina events](#).

Events **2009 - 2008 - 2007**

International Symposium: Ethic of the Synthetic Biologie. Freiburg, Germany. 1 - 2 October 2009. Organized by the [Albert-Ludwigs University of Freiburg](#), the symposium explored the philosophical and ethical questions about create and change forms of life that began time ago with the genetic engineering, and continue nowadays thanks to Synthetic Biology and the new technical possibilities. As representation of IDC, and member of the [COSY](#) and [SYNBIOSAFE](#) project, Dr. Markus Schmidt contributed to the event. [More...](#)

EuroBio 2009. Grand Palais, Lille, France. 23-25 September 2009. EuroBio was a partnering and tech transfer event for the international bioindustry. The program of the event was based on pragmatic workshops and conferences to meet concrete concerns with regard to project development, funding and operation. As speaker in one of this conferences, the IDC board member [Dr. Markus Schmidt](#) took part in the event as expert on regulatory issues of bioproducts. [More...](#)

TA '09: When TA? Technology Assessment in the Age of Techno Sciences, Vienna, 8 June 2009. The 9th conference on technology assessment was organized by the ITA (Institute für Technik-folgenabschätzung). It counted with the participation of experts on technology assessment, such as IDC's [Markus Schmidt](#) who gave a presentation on early TA in the case of synthetic biology. [More...](#)

3rd European Conference on African Studies (ECAS) by AEGIS. Leipzig, Germany, 4 - 7 June 2009. The overall theme of the ECAS 3 was "Respacing Africa". [AEGIS](#) was founded in 1991 as a network of European Centres of African Studies. It is a network of university and non-university African Studies centres based in Europe. It aims to create synergies between experts and institutions. As a participant of this event, the IDC co-founder Dr Angela Meyer presented her lecture: [Regional Multinational Peace Operations: The Case Of Fomuc and Micopax in the Central African Republic to the public](#). [More...](#)

News

10/13/09
SYNBIOSAFE Documentary Film out now!
Produced and directed by Markus Schmidt and Camillo Meinhart, the 38 minutes Documentary film 'SYNBIOSAFE: Synthetic Biology and its Safety and Ethical Aspects' has been released October 2009. [\[More\]](#)

06/09/09
Diverseeds Documentary Film out NOW!
This documentary film - made by IDC - shows the importance of agricultural biodiversity for food and agriculture, with astonishing pictures from Europe and Asia. [\[More\]](#)

04/08/09
Ethics and synthetic biology in Nature

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

Messages:

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

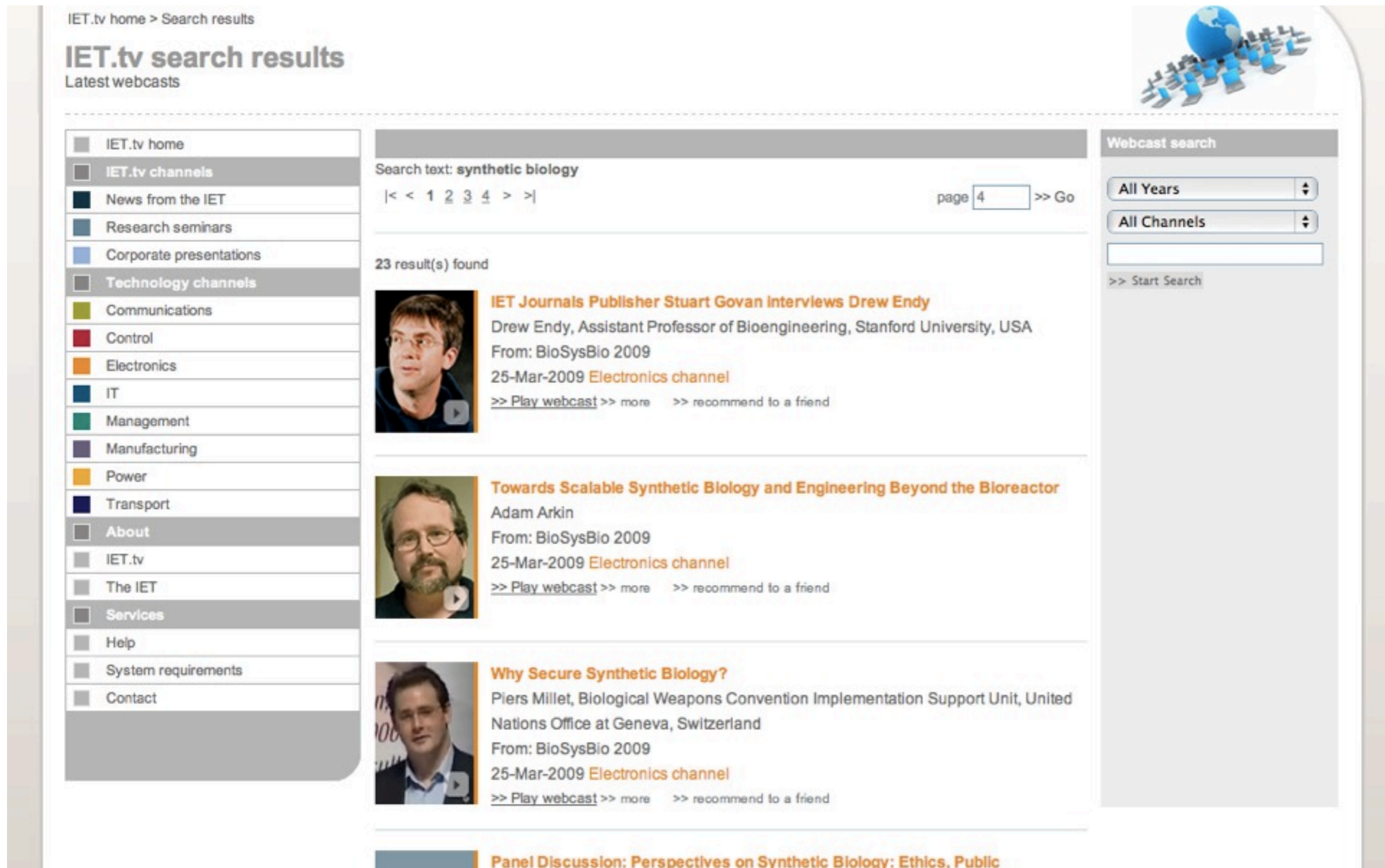
http://www.theiet.org/synbio

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.

The screenshot shows the website for the Systems and Synthetic Biology Network. At the top, there is a navigation bar with the IET logo and the text 'Collective inspiration'. Below this is a search bar and a navigation menu with options like 'Subjects', 'News', 'E&T Magazine', 'Communities', 'Knowledgebase', and 'Your comment'. The main content area is titled 'Systems and Synthetic Biology Network' and includes a breadcrumb trail: 'You are here: Knowledge Network home > Communities > Systems and Synthetic Biology Network'. A blue globe icon is visible on the right. The main text describes the community's purpose: 'This community has been established to complement our two academic journals, IET Systems Biology and IET Synthetic Biology, and to provide a source of online tools for researchers and professionals working in the areas of systems and synthetic biology.' Below this, there are two network blog entries. The first is titled 'Automation speeds cell selection for chemical production' dated 13 August 2009, with the subtitle 'Synergy between engineering and evolution' and 0 comments. The second is titled 'Oil giant gets serious about biofuels' dated 22 July 2009, with the subtitle 'ExxonMobil is teaming up with Craig Venter, the biotech entrepreneur, to develop new road fuels using photosynthetic algae.' and 0 comments. On the right side, there is a sidebar with a section titled 'Systems and Synthetic Biology Network' containing links for 'About this Network', 'People and contacts', 'Industry news', and 'Network blog'. Below these links is a 'Latest industry news' section with a brief description. A 'Contact us' section follows, providing contact information for Paula-Marie Brown, Community Development Manager, including her email (pmbrown@theiet.org) and address (IET Knowledge Management, Michael Faraday House, Six Hills Way, Stevenage, Hertfordshire, SG1 2AY, United Kingdom). A profile picture of Paula-Marie Brown is shown next to her name and title. At the bottom right, there is a section for the 'IET Synthetic Biology Research Journal' with a DNA helix image and a link to the IET Digital Library. The footer contains the IET logo, the text 'Subscribe today.', and the 'IET discover' logo.

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.



IET.tv home > Search results

IET.tv search results

Latest webcasts

Search text: **synthetic biology**

|< < 1 2 3 4 > >| page 4 >> Go

23 result(s) found

IET Journals Publisher Stuart Govan interviews Drew Endy
Drew Endy, Assistant Professor of Bioengineering, Stanford University, USA
From: BioSysBio 2009
25-Mar-2009 **Electronics channel**
>> [Play webcast](#) >> more >> [recommend to a friend](#)

Towards Scalable Synthetic Biology and Engineering Beyond the Bioreactor
Adam Arkin
From: BioSysBio 2009
25-Mar-2009 **Electronics channel**
>> [Play webcast](#) >> more >> [recommend to a friend](#)

Why Secure Synthetic Biology?
Piers Millet, Biological Weapons Convention Implementation Support Unit, United Nations Office at Geneva, Switzerland
From: BioSysBio 2009
25-Mar-2009 **Electronics channel**
>> [Play webcast](#) >> more >> [recommend to a friend](#)

Panel Discussion: Perspectives on Synthetic Biology: Ethics, Public

Webcast search

All Years
All Channels
>> Start Search

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- Transport
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- IET.tv
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- Help
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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
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- 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 Ajjoka**, **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 environmental 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)

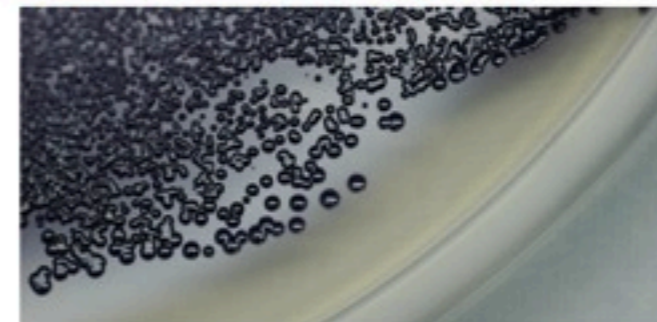
See photos at: <http://www.flickr.com/photos/haseloff/sets/72157622587178163/>



SYNBIO NEWS

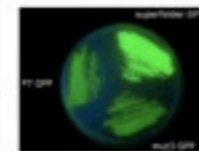
- Hacking DNA**
Hacking DNA Bioengineering technology is maturing, and so is its vocabulary. From: <http://www.spectrum.ie/innovation/hackingdna> Illustration: Harry Campbell BY PAUL MCFEDRIES // OCTOBER 2009 But the real...
- Wellcome Trust support for iGEM**
UK entries to student synthetic biology 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 Specter The New Yorker SEPTEMBER 28, 2009 <http://www.newyorker.com> If the science truly succeeds, it will make it...

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 Pedelacq 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 T.J, 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



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

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- ▶ Brachypodium
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- ▶ Review PDFs

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- ▶ Components

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Thursday, November 12, 2009



Synthetic Biology Cambridge iGEM BioBricks Microbes Plants Hardware Productivity

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- Miscellany RSS

LATEST: Cambridge iGEM2009 team

Synthetic Biology EU Emergence

PARTICIPANTS IN EU EMERGENCE PROGRAMME

Search on directory Title and intro Ordering by...

Results 1 - 11 of 11



1. Alfonso Jaramillo Lab
<http://www.enseignement.polytechnique.fr/profs/biochimie>
 We are developing a research plan in Synthetic Biology a foundations for this new engineering discipline. We will ap focusing in concrete engineering projects, involving each level...
 | 304 hits



2. Alfonso Valencia Lab
<http://www.cnio.es/ing/grupos/plantillas/curriculum.asp?pag=1002>
 The main interest of our group is understanding the organisation and evolution of gene/protein networks, and in particular the relation between protein/gene specific interactions with cancer related processes.
 | 316 hits



3. Jim Ajioka Lab
<http://www.path.cam.ac.uk/pages/ajioka/>
 Microbial and protozoan biology Jim Ajioka's lab studies genetic circuits and genomics in Bacillus subtilis and Toxoplasma.
 | 325 hits



4. Jim Haseloff Lab
<http://www.plantsci.cam.ac.uk/Haseloff/Home.html>
 Engineering plant form. This site for Jim Haseloff's laboratory at the University of Cambridge describes the growing set of methods for visualising and manipulating cell fates in intact plant tissues. We are using these as tools for reprogramming...
 | 315 hits



5. Jorg Stelling Lab
<http://www.csb.ethz.ch/about/index>
 Computational Methods for Studying Complex Networks The group develops computational methods for studying complex networks that establish cellular

Emergence: A Foundation for Synthetic Biology in Europe



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](#)

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.newyorker.com> If the science truly succeeds, it will make it...

Ginko Bloworks From: Technology

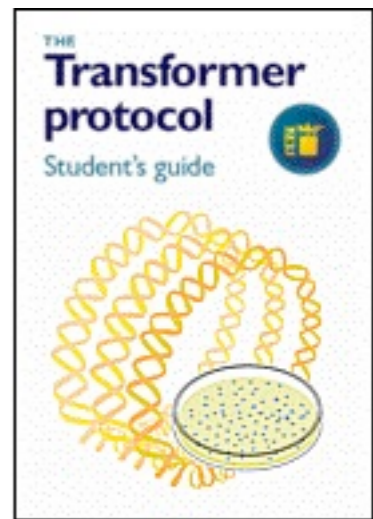
www.synbio.org.uk

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. [Quantifying 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. [Entrepreneurship: 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