

SigPath: Quantitative information management for cell signaling pathways and networks

**Institute for Computational Biomedicine
Weill Medical College of Cornell University
New York, USA**

Fabien Campagne – BOSC – June 2005

The SigPath Team & Sponsors



Sigpath institute for **computational biomedicine**

CORNELL

Members of the Project

Institute for Computational Biomedicine and Department of Physiology and Biophysics (Weill Medical College of Cornell University)

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- ▶ Marko Srdanovic
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- ▶ Ethan Cerami (now cBio/MSKCC)
- ▶ Anat Maoz (now WMC Graduate School)
- ▶ Benjamin Chiang
- ▶ Francois Le Fevre (now Genoscope)
- ▶ Prahlad Ram (now Tulane University)
- ▶ Manda Wilson (now cBio/MSKCC)
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NIH-NHLBI

(Pre-NPEBC P20 program)

NIH-NIDA

(Signaling suppl. to P01 DA12923)

Harel Weinstein

NIH-NCI (R01 CA-81050)

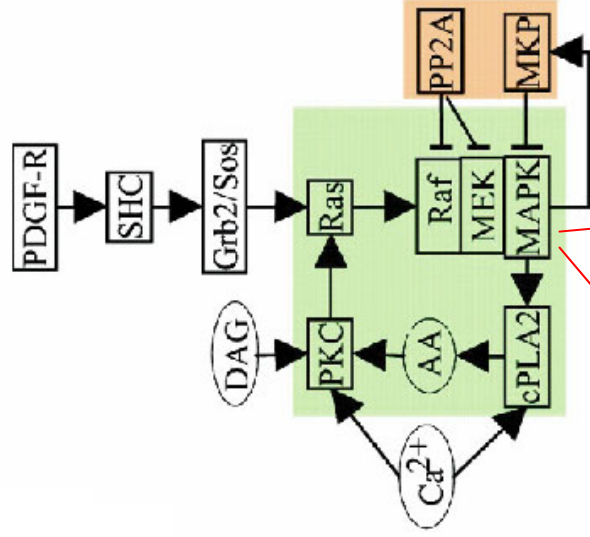
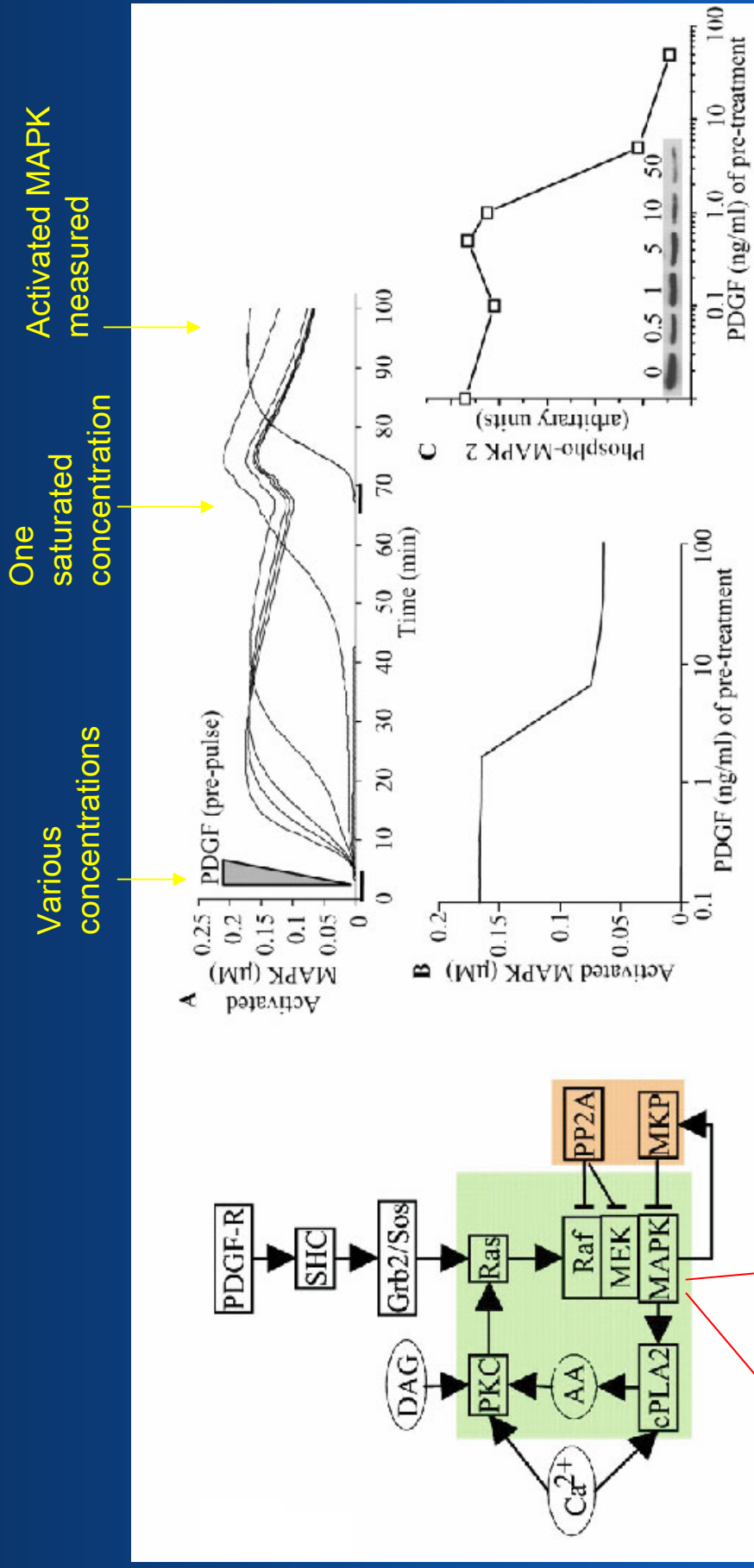
NIH-NIGMS (R01 GM 54-508)

Ravi Iyengar

Frueauff Foundation

Fabien Campagne

Modeling integrated biochemical systems



Bhalla US, Ram PT, Iyengar R. MAP kinase phosphatase as a locus of flexibility in a mitogen-activated protein kinase signaling network. Science. 2002 Aug 9;297(5583):1018-23.

Entry in the cell-cycle

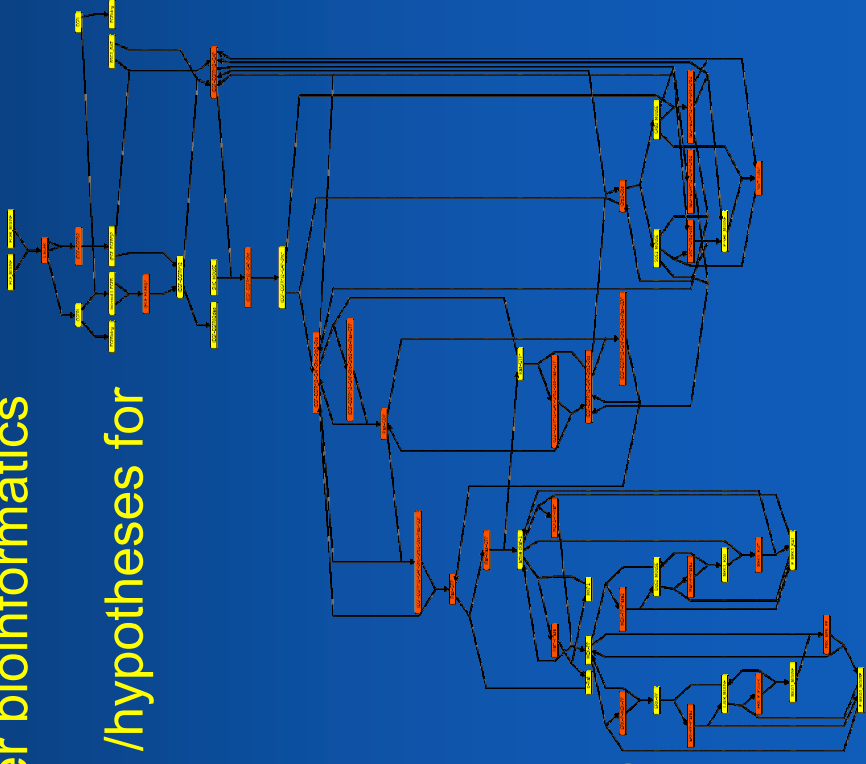
Synthesis of arachidonic acid & Autocrine paracrine systems

History-dependent responses of the MAPK system

Project goals

- Provide means to collaboratively organize biochemical information electronically (w/ links to the primary literature)
- Smoothly integrate with biochemical simulation tools.
- Smoothly integrate with sequence and other bioinformatics databases
- Provide a repository of facts/interpretations /hypotheses for interactions and models
- User-friendly web-based system
- Act as an educational resource

- Going beyond (standard) file formats
- Testing and developing new approaches to help manage biological information





[CRT home](#) > [SigPath Project](#)

[description]

SigPath is a collaborative project of the [Institute for Computational Biomedicine](#) and the [Department of Physiology and Biophysics](#) at the [Weill Medical College of Cornell University](#), and the [Department of Pharmacology & Biological Chemistry](#) at [Mount Sinai School of Medicine](#).

SigPath is an information system designed to support quantitative studies on the signaling pathways and networks of the cell. [More](#)

Campagne F, Neves S, Chang CW, Skrabanek L, Ram PT, Iyengar R, Weinstein H. Quantitative information management for the biochemical computation of cellular networks. *Science* **STKE**. 2004 248:PL11. [[PubMed](#)], [[Full Text](#)]

Srdanovic M, Schenk U, Schwieger M and Campagne F. Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. *BMC Bioinformatics*. 2005. 6:5 [[Abstract](#)] [[Full Text](#)]

[documentation]

Some novel or noteworthy **features** of SigPath include:

- ▶ [Import of background information](#)
- ▶ [Import information through XML submission](#)
- ▶ [Full text search in background information](#)
- ▶ [BioWizard for submission of binding interactions](#)
- ▶ [BioWizard for submission of phosphorylation information](#)
- ▶ [Assemble and export simple quantitative models](#)
- ▶ [Exporting SigPath entities as XML](#)
- ▶ [Reviewing data in SigPath](#)

The following **animated tutorials** highlight some basic uses of SigPath:

- ▶ [Querying SigPath for interactions](#)
- ▶ [Querying SigPath for small molecules](#)
- ▶ [Querying SigPath for proteins](#)
- ▶ [Submitting phosphorylation reactions into SigPath using the BioWizard](#)
- ▶ [Submitting binding reactions into SigPath using the BioWizard](#)
- ▶ [Submitting Interactions into SigPath via XML upload](#)
- ▶ [Assembling a quantitative model using SigPath](#)
- ▶ [Exporting a SigPath model for JSIM](#)
- ▶ [Exporting a SigPath model for Kinetikit](#)
- ▶ [Exporting a SigPath model in SBML format](#)
- ▶ [Exporting a SigPath entity \(models, reactions etc.\) in XML format](#)
- ▶ [Reviewing data in SigPath](#)

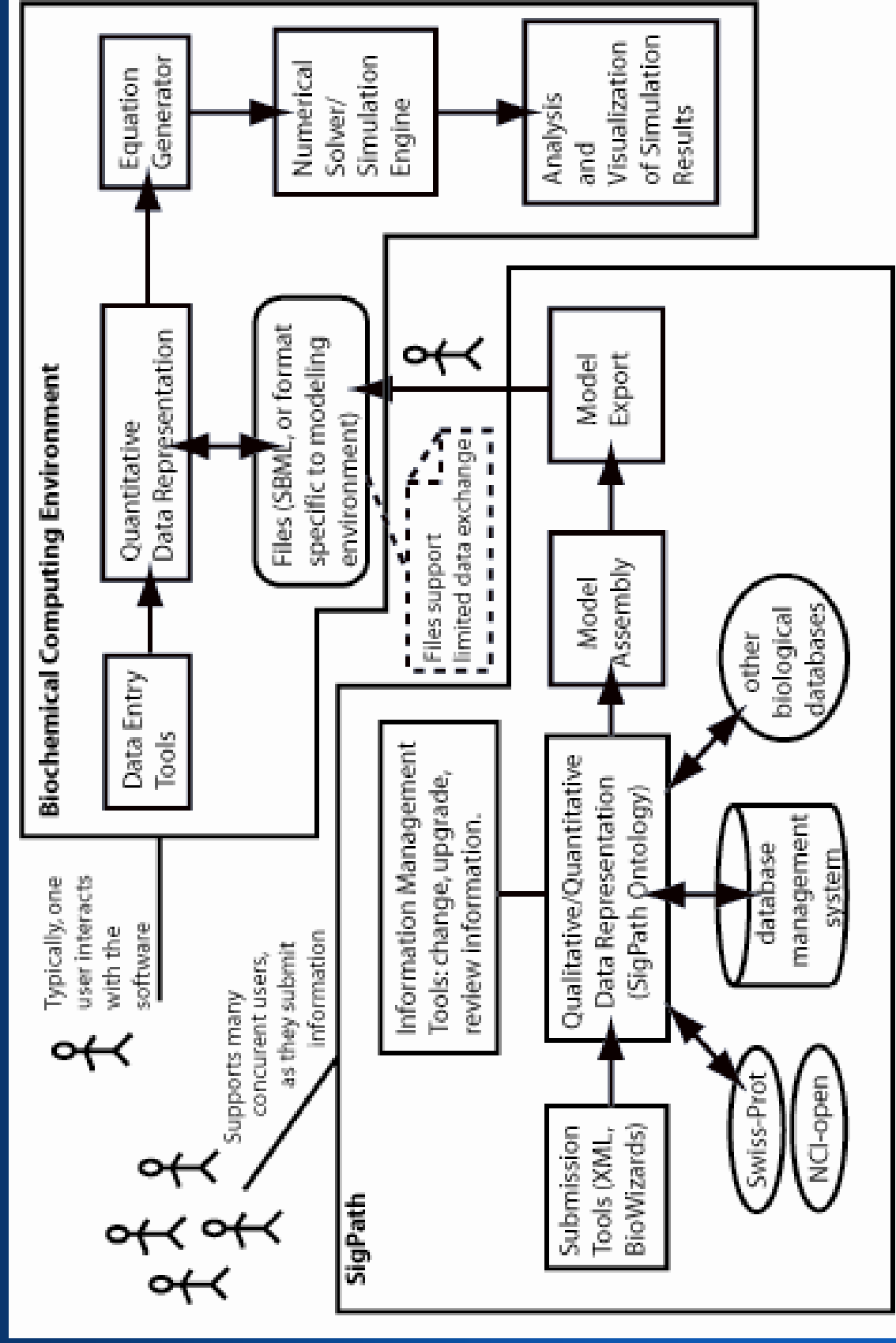
SigPath Production
SigPath Navigator
Project Overview
Contributing to Sigpath
Sigpath XML Schema
Validation Data Set
For Developers
Download SigPath
JDO Benchmark
Bug Tracker
FAQ
Project Members
Sponsors
News Archives

SigPath News

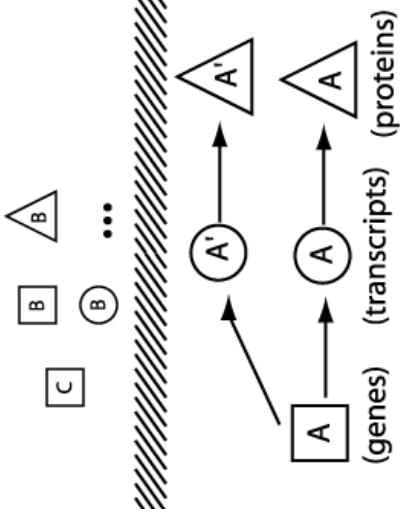
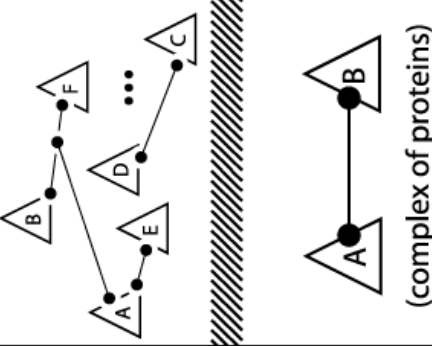
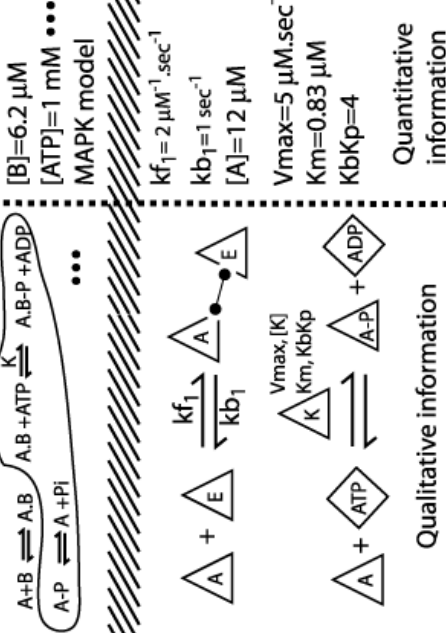
February 9th, 2005; New SigPath production release [[Release info](#)]
December 9-11th, 2004; The [First SigPath workshop](#) was held in New York City. [[Workshop info](#)]
November 3rd, 2004; New SigPath beta release [[Release info](#)]
October 29th, 2004; New SigPath production released [[Release info](#)]
Sept 22nd, 2004; New beta release of SigPath available for preview and testing. [[Release info](#)]
Sep 3rd, 2004; A description of SigPath is now available in *Science* **STKE**. SigPath users may now cite it as Quantitative information management for the biochemical computation of cellular networks; Campagne F, Neves S, Chang CW, Skrabanek L, Ram PT, Iyengar R, Weinstein H. *Science* **STKE** 248:PL11. (2004). [[SigPath](#)]
Mar 2nd, 2004; A new release of SigPath is now available. [[SigPath](#)]
Mar 1st, 2004; SigPath is now released under the GNU General Public License [[download_source](#)]

<http://www.sigpath.org>

SigPath complements biochemical modeling environments



Comparison to other types of data and databases

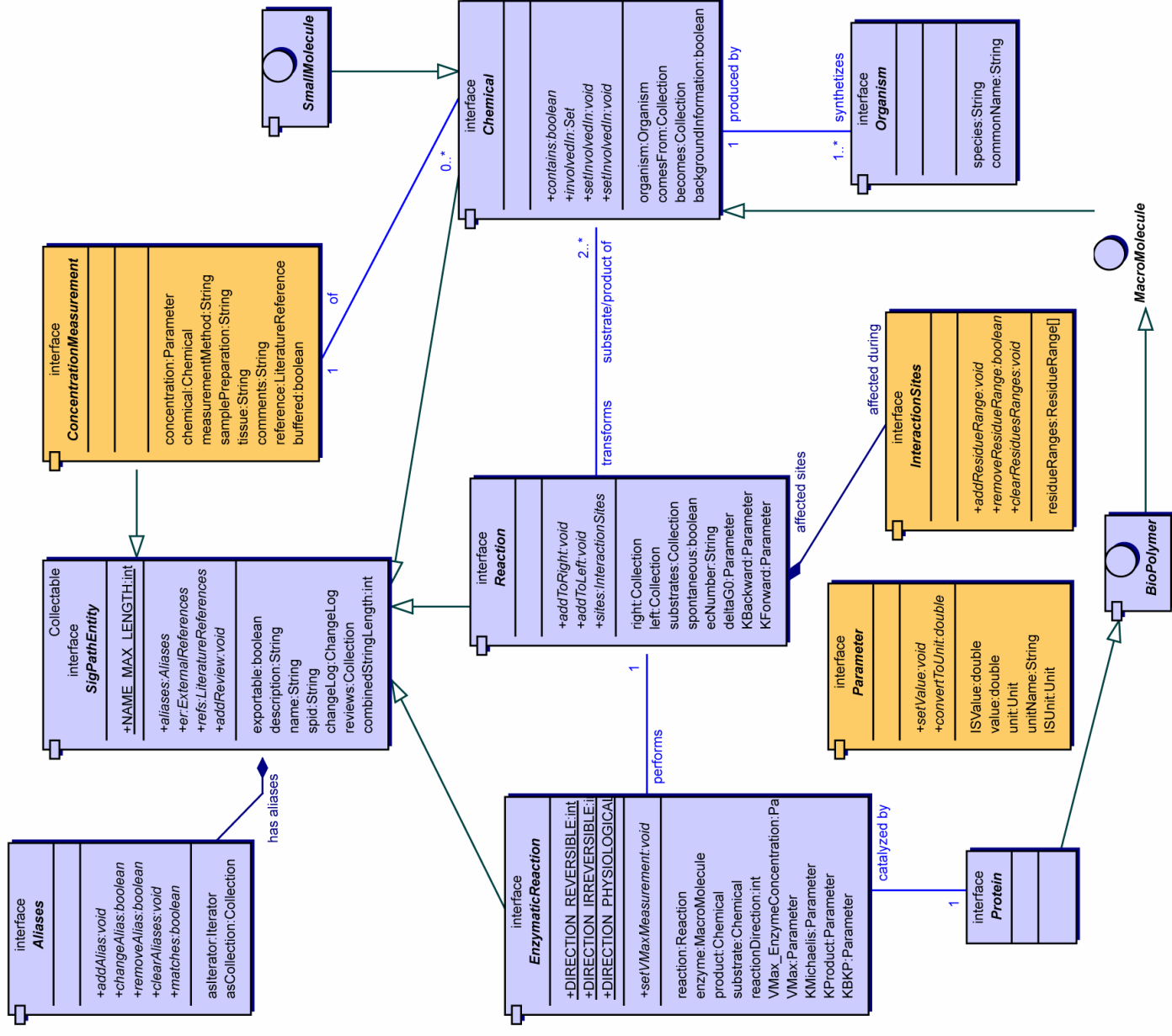
 <p>Genomic and protein databases</p>	 <p>Protein-protein interaction databases</p>	 <p>Quantitative information</p> <p>SigPath information management system</p>
<p>Genomic and protein databases</p>	<p>Protein-protein interaction databases</p>	<p>Quantitative information</p> <p>SigPath information management system</p>

Data generally organized as entries with few connections between entries. (Comparative genomics changes the picture a bit..)

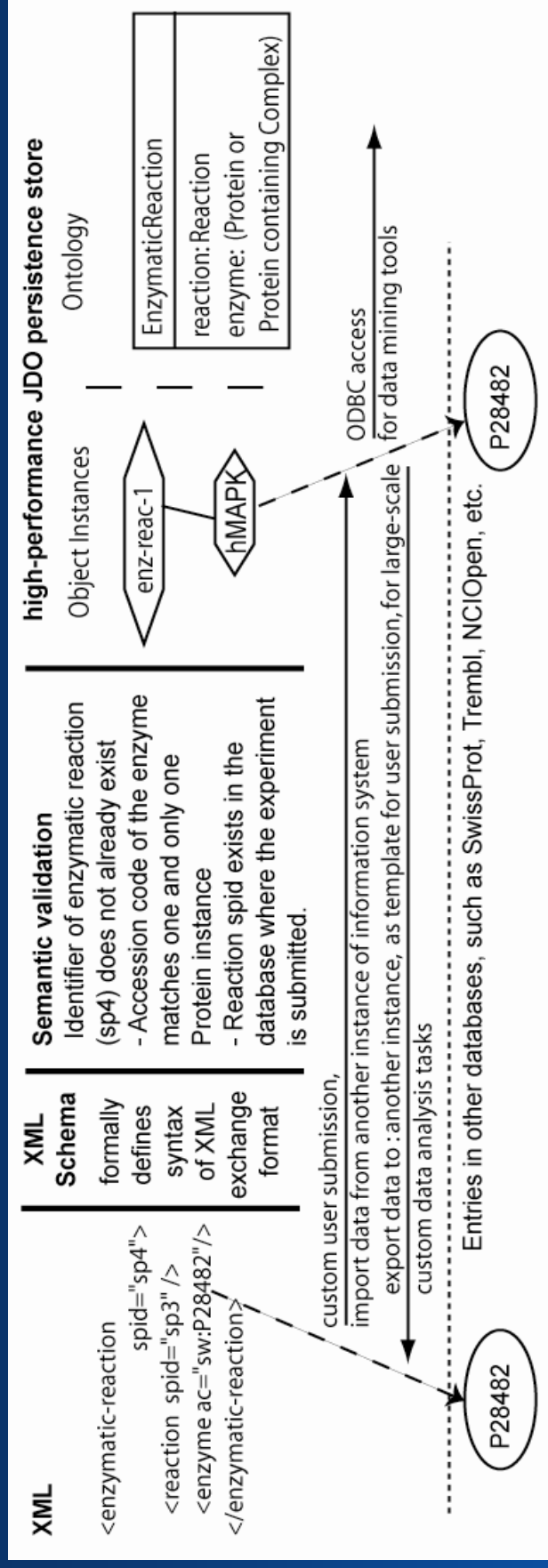
Graph-like data, one or two types of biochemical entities

Graph-like data, many types of biochemical entities, many types of connections (e.g., through interactions, reactions, pathways)

The SigPath ontology is derived from the EcoCyc ontology (Karp P), but includes many extensions. For instance, to represent quantitative features (e.g., rates, concentrations) and context of the measurements. Just a glimpse.. >80 classes in the current ontology



Data integration approach used for SigPath



The ontology is implemented in the semantic validation layer and the Java Data Object-compliant database backend.

(For JDO, see Srdanovic M et al. Critical evaluation of the JDO API for the persistence and portability requirements of complex biological databases. BMC Bioinformatics. 2005 Jan 10;6(1):5.)

The approach is

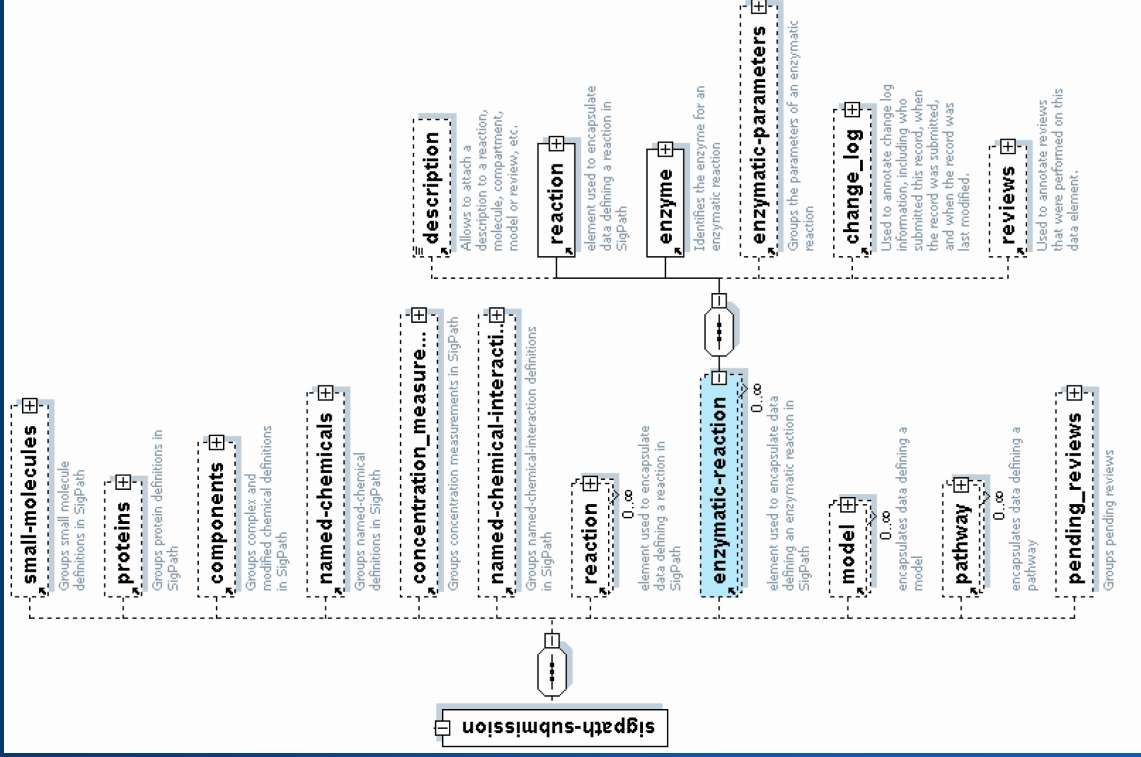
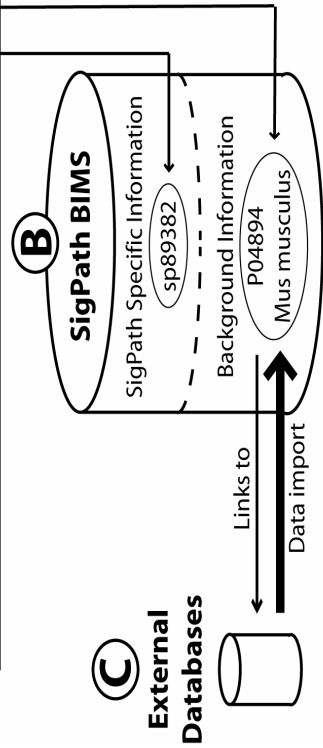
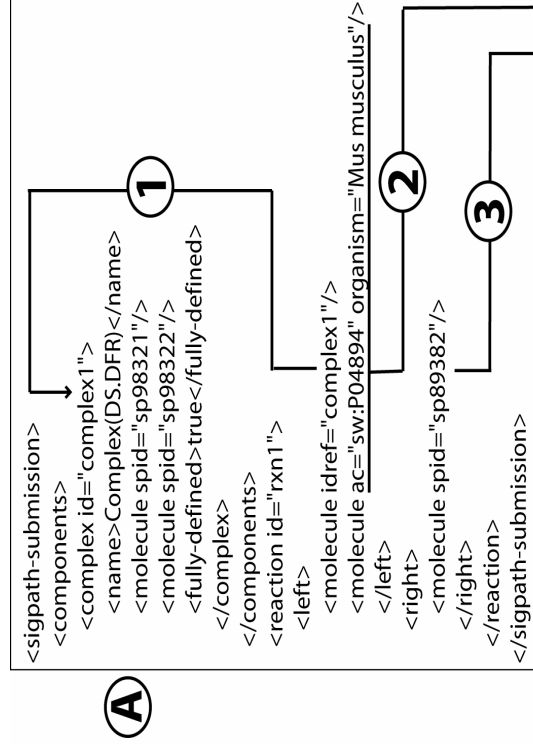
- Scalable (amount of data, # concurrent users)
- Leverages open standards (e.g., XML, JDO)
- Supports customized web-based user interfaces, web services, and batch processes

SigPath XML exchange format

```

<!-- GBB4_MOUSE + GBB2_MOUSE &lt;...&gt; Gbeta4gamma2 -->
<reaction id="rxn221" spid="sp10f">
  <description>Gbeta4 gamma2 dimerization</description>
  <left>
    <molecule spid="bid79997" ac="sw:P29387" organism="Mus musculus">
      <name>GBB4_MOUSE</name>
    </molecule>
    <molecule spid="bid80024" ac="sw:Q9T547" organism="Mus musculus">
      <name>GBG2_MOUSE</name>
    </molecule>
  </left>
  <right>
    <molecule spid="spi102" idref="comp71">
      <name>Gbeta4gamma2</name>
    </molecule>
  </right>
  <parameters/>
  <publications/>
  <change_log>
    <user_name>violechang</user_name>
    <dateSubmitted>2003-03-30T18:01:59.000-05:00</dateSubmitted>
    <dateLastModified>2003-03-30T18:01:59.000-05:00</dateLastModified>
  </change_log>

```



SigPath provides tools for user communities

These users are not curators, they are end-users who submit and edit information in SigPath.

View Users (109)			
name	username	affiliation	
Anja Hartmann	anjaragina	Uni Rostock	View Details
Harvey Florman	hflorman	Univ Massachusetts Medical School	View Details
Chris Brinkerhoff	chrisbrink	Univ of Michigan	View Details
Alasdair Gibb	a.gibb	University College London	View Details
Lily Mirels	mirels	University of California, Berkeley	View Details
Marc Birtwistle	mbirdy857	University of Delaware	View Details
Takako Takai	taka	University of Tokyo	View Details
Jun-ichi Narukawa	nalchan	University of Tokyo	View Details
Joseph mcLaughlin	micreynolds	Vanderbilt	View Details
Lixin Shen	lixin	Vanderbilt University	View Details
Masha Niv	MashaNiv	WCMC	View Details

We designed SigPath to be a tool to manage data about work in progress. This requirement and the type of data managed raise interesting information management questions:

- Is the submitter ownership policy the best option to encourage data sharing and data reuse?
- How to best support different communities of users at different times

SigPath provides tools for user communities

Registered users can track data they submitted

spXXXX values are SigPath identifiers (spids for short).

spids behave like accession codes and can be cited in articles.

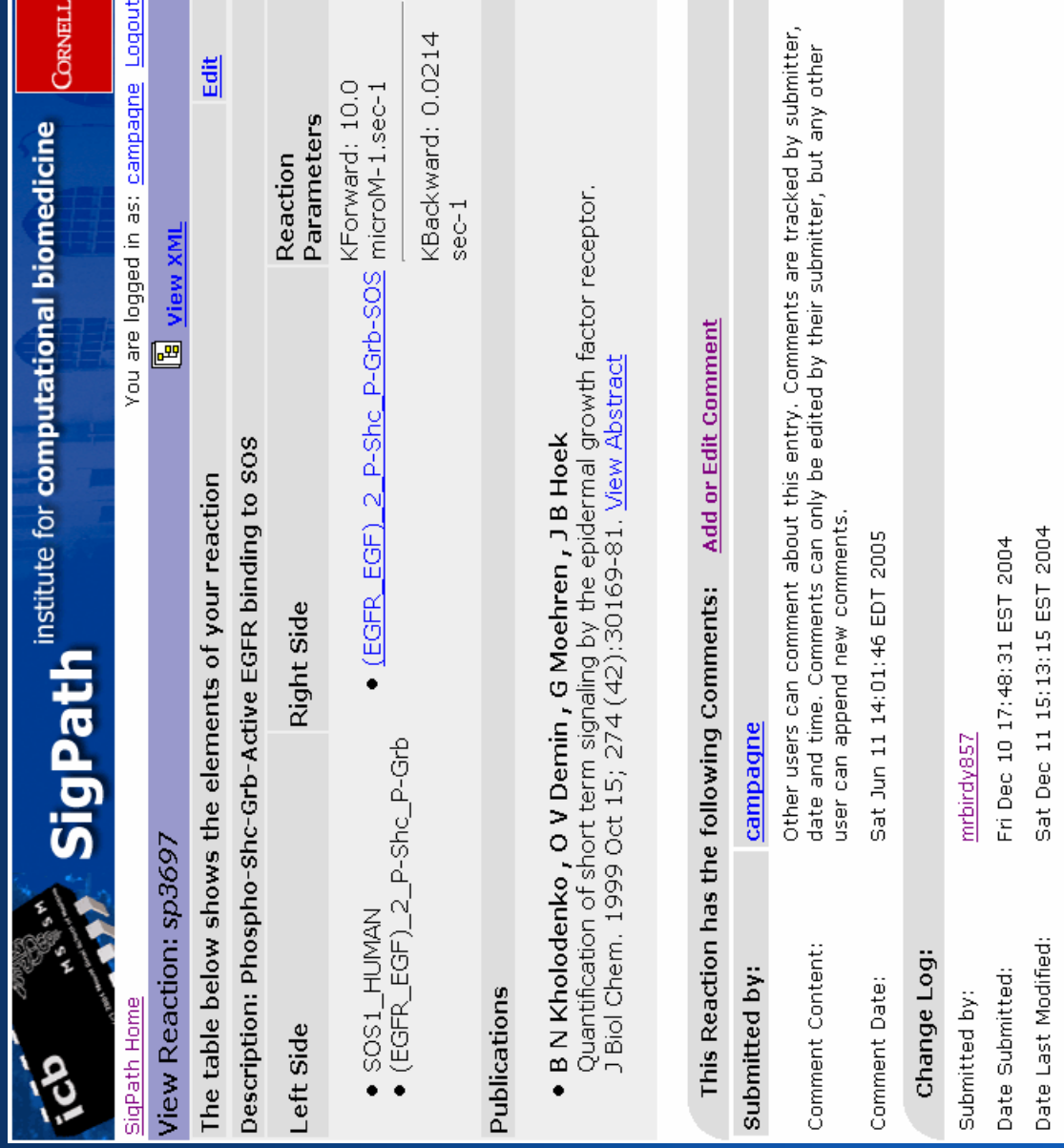


The screenshot displays the SigPath user interface. At the top, there is a navigation bar with the SigPath logo and the text "institute for computational biomedicine". A red "CORNELL" logo is in the top right corner. Below the navigation bar, a message states "You are logged in as: [campaign](#) [Logout](#)".

The main content area shows the user profile for "Marc Birtwistle" at the "University of Delaware". A "View All Users" link is visible. Below the profile information, there is a table of submitted data items.

Submission	Name	Type	Submitted	Modified
sp3490	Generic Tyrosine Phosphatase	NamedChemical	12/11/04 11:08 AM	12/11/04 11:10 AM
sp3506	inositol 1,4,5 triphosphate	NamedChemical	12/11/04 3:28 PM	12/11/04 3:28 PM
sp3513	EGFR_EGF	ComplexImpl	12/10/04 5:36 PM	12/11/04 10:31 AM
sp3518	(EGF_EGFR)_2	ComplexImpl	12/10/04 5:48 PM	12/11/04 10:35 AM
sp3531	DO NOT USE	ComplexImpl	12/11/04 10:18 AM	12/11/04 1:05 PM
sp3539	PLCgamma-(EGFR_EGF)_2_P	ComplexImpl	12/11/04 11:55 AM	12/11/04 11:56 AM
sp3555	Grb2-SOS	ComplexImpl	12/11/04 2:03 PM	12/11/04 2:03 PM
sp3570	Grb-SOS	ComplexImpl	12/11/04 3:20 PM	12/11/04 3:20 PM
sp3571	X1	ComplexImpl	12/14/04 2:45 PM	12/14/04 2:46 PM
sp3572	Complex(EGF_EGFR)	ComplexImpl	12/14/04 2:45 PM	12/14/04 2:45 PM
sp3585	(EGFR_EGF)_2_P	ProteinImpl	12/11/04 12:17 PM	12/11/04 12:17 PM

Web-based Visualization (reaction)



The screenshot shows the SigPath website interface for reaction **sp3697**. The header includes the SigPath logo and the text "institute for computational biomedicine" and "CORNELL". A navigation bar contains "SigPath Home", "You are logged in as: campagne", and "Logout". A "View XML" link is also present.

The main content area displays the reaction details:

- View Reaction: sp3697**
- Description:** Phospho-Shc-Grb-Active EGFR binding to SOS
- Left Side:**
 - SOS1_HUMAN
 - (EGFR_EGF)_2_P-Shc_P-Grb
- Right Side:**
 - (EGFR_EGF)_2_P-Shc_P-Grb-SOS
- Reaction Parameters:**
 - KForward: 10.0 microM-1.sec-1
 - KBackward: 0.0214 sec-1

Below the reaction details is a "Publications" section:

- **B N Kholodenko, O V Demin, G Moehren, J B Hoek**
Quantification of short term signaling by the epidermal growth factor receptor.
J Biol Chem. 1999 Oct 15; 274 (42):30169-81. [View Abstract](#)

A summary box states: "This Reaction has the following Comments: [Add or Edit Comment](#)".

The "Submitted by:" section lists [campagne](#). A note states: "Other users can comment about this entry. Comments are tracked by submitter, date and time. Comments can only be edited by their submitter, but any other user can append new comments."

The "Change Log:" section shows the following entries:

Submitted by:	Date Submitted:	Date Last Modified:
mrbirdv857	Fri Dec 10 17:48:31 EST 2004	Sat Dec 11 15:13:15 EST 2004
	Sat Jun 11 14:01:46 EDT 2005	

Reaction
mechanism
and kinetics

Links to the
literature

User
comments

Change
tracking

SPID: **bid339261**

Name: **RAF1_RAT**

Description: **RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37) (Raf-1) (C-RAF) (cRaf)**

- [Basic Information](#)
- [Comes From](#), [Becomes](#), [Contains](#)
- [Involved in Reactions](#)
- [Concentrations](#)

Basic Information:

Accession Code(s):

- PROSITE: [PS50898](#)

Organism: [Rattus norvegicus \(Rat\)](#)

Aliases:

- [RAF1_RAT](#)

Comes From, Becomes, Contains:

Comes From:

- None

Becomes:

- [sp217675: active cRaf-1](#)
- [sp217735: active cRaf-1](#)

Contains:

- None

Involved in Reactions:

- [sp217980: ATP + RAF1_RAT <...> ADP + active cRaf-1](#)
- [sp3651: RAF1_RAT + Ras.GTP <...> Activated_c_Raf](#)
- [sp217849: GTP-Ras + RAF1_RAT <...> Complex\(GTP-Ras.KRAF_RAT\)](#)
- [sp218019: ATP + active cRaf-1 <...> ADP + RAF1_RAT \[Enzyme: P2AA_CHICK\]](#)
- [sp218018: ATP + active cRaf-1 <...> ADP + RAF1_RAT](#)
- [sp217979: ATP + RAF1_RAT <...> ADP + active cRaf-1 \[Enzyme: active membrane bound PKC\]](#)
- [sp217904: Raf*-p'ase <...> RAF1_RAT + DUS1_RAT](#)
- [sp218104: RAF1_RAT + Ras.GTP <...> Activated_c_Raf](#)
- [sp217901: RAF1_RAT + Ras-GTP <...> Raf-Ras-GTP](#)
- [sp217978: ATP + RAF1_RAT <...> ADP + active cRaf-1](#)
- [sp217981: ATP + RAF1_RAT <...> ADP + active cRaf-1 \[Enzyme: active PKC-DAG-AA\]](#)
- [sp217959: ATP + MPK1_RAT <...> ADP + P-MPK1_RAT \[Enzyme: RAF1_RAT\]](#)

Concentrations

SPID	Concentration	Tissue	Method of Measurement	Sample Preparation	Comments	Pub Med Reference	Action
sp218126	0.0664 micromoles/l	Hela cells	staining with semi-quantitative electrophoresis (western, etc.)	Not Specified	Calculated from molecules per cell, assuming 1e-9 cubic centimeters volume for Hela cells.	Birgit-Schoeberl, Claudia Eichler-Jonsson, Ernst Dieter Gilles, Gertraud Müller	Delete

General Information

Substrate/Product Links

Reactions this molecule is involved in

Concentrations measured for this molecule

Web-based Visualization (molecule)

General Information

Reactions

Initial Concentrations

Exporting to Modeling Environments

Web-based Visualization (model)

Model Schematic (automatically generated)

View Model [View XML](#) | [Edit](#)

Model Information:

Model SPID: sp7
Model Name: MAPK cascade
Model Description: Map kinase cascade. Starting from activated Ra. micromoles/l
Target Unit: micromoles/l

Selected Reactions:

- sp218110 [Enzymatic Reaction: ATP + P-MEK1 <...> ADP + P-P-MEK1 \[Enzyme: Activated_c_Raf\]](#)
- sp218119 [Enzymatic Reaction: P-P-MEK1 <...> P-MEK1 \[Enzyme: P2AA_RAT\]](#)

(details omitted)

• DUS1_RAT_Default_Compartment	4.0E-4 micromoles/l	Default_Compartment	100	no
• P-MAPK1	0.0 mol/l	Default_Compartment	N/A	no

MWP = model will Provide

[Export to Kinetikit](#) [Export to JSim](#) [Export to SBML](#)

[Kinetikit home page](#) from National Center for Biological Sciences (Bangalore, India)
[JSim Documentation](#) from University of Washington (Seattle, USA)
[SBML reference site](#) from the SBML format development group (includes many research groups).

Select Image Format
 Compact enzyme view
 Compact complex view
 Show ATP and ADP (for enzymatic reactions)
[View Model Image](#)

The following options are
Please choose which option to export below to download the model used with modeling environments.
Select options below and click submit

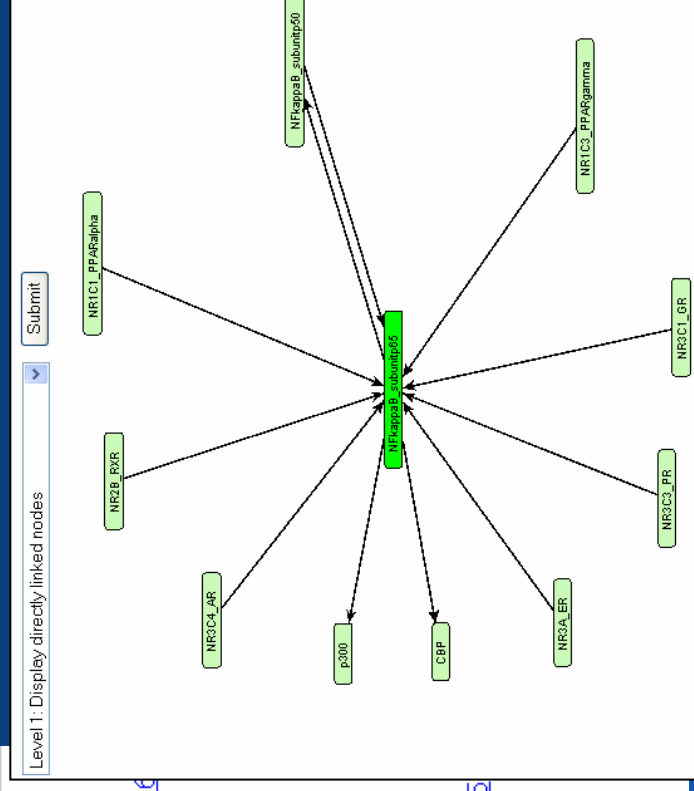
- Level 1 version 1
- Level 1 version 2
- Level 2 version 1
- Include diagram layout (if available)

```
graph TD
    RAF1_RAT[RAF1_RAT] --> Activated_c_Raf[Activated_c_Raf]
    Ras_GTP[Ras GTP] --> Activated_c_Raf
    Activated_c_Raf --> P_MEK1[P-MEK1]
    Activated_c_Raf --> P_P_MEK1[P-P-MEK1]
    P_MEK1 --> P_P_MEK1
    P_P_MEK1 --> P2AA_RAT[P2AA_RAT]
    P_P_MEK1 --> MPK1_RAT[MPK1_RAT]
```

Visualizing interactions is key for the end-user, but is still an open problem..

Involved in Reactions:

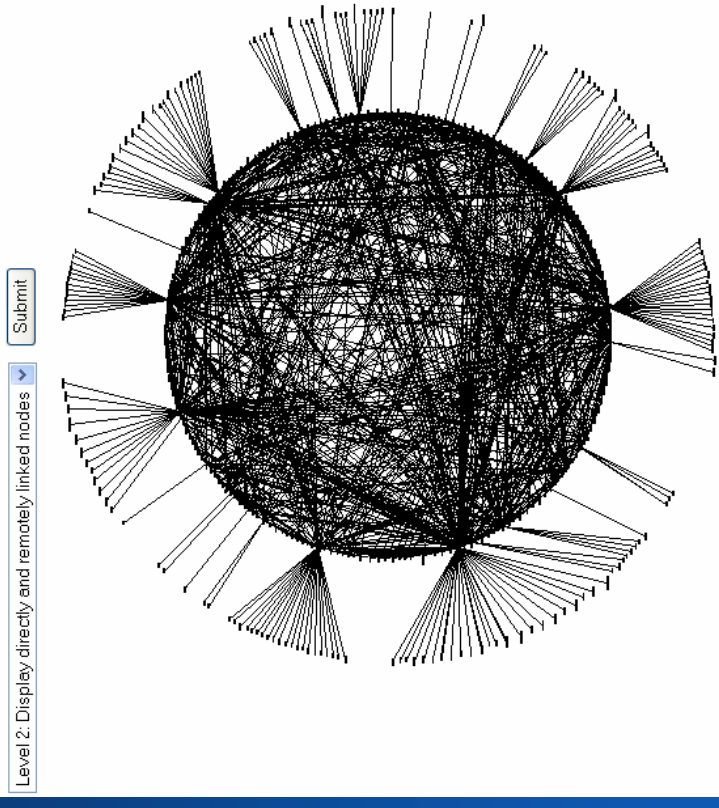
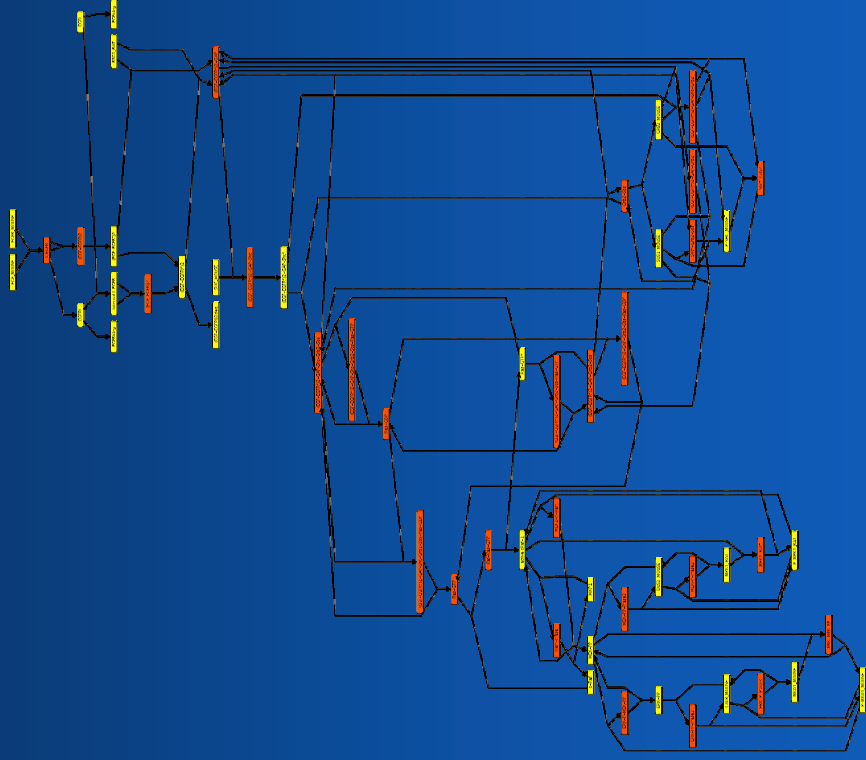
- [View sp2832: NR2B_RXR interacts with NFkappaB_subunitp65](#)
- [View sp3257: NR3C3_PR interacts with NFkappaB_subunitp65](#)
- [View sp1640: NR2B_RXR binds NFkappaB_subunitp65](#)
- [View sp720: NR3C4_AR interacts with NFkappaB_subunitp65](#)
- [View sp639: NFkappaB_subunitp50 forms complex with NFkappaB_subunitp65](#)
- [View sp2566: NR3C1_GR interacts with NFkappaB_subunitp65](#)
- [View sp2624: NR3C1_GR dimerizes with NFkappaB_subunitp65](#)
- [View sp2933: NR3C1_GR links to NFkappaB_subunitp65](#)
- [View sp2282: NR3C1_GR associates with NFkappaB_subunitp65](#)
- [View sp3261: NFkappaB_subunitp65 forms complex with CBP](#)
- [View sp2894: NR3C1_GR precipitates with NFkappaB_subunitp65](#)
- [View sp1571: NR1C3_PPARGamma binds NFkappaB_subunitp65](#)
- [View sp2838: NFkappaB_subunitp50 dimerizes with NFkappaB_subunitp65](#)
- [View sp1207: NFkappaB_subunitp65 has implied interaction with p300](#)
- [View sp896: NR3C1_GR binds NFkappaB_subunitp65](#)
- [View sp1253: NR3C1_GR has implied interaction with NFkappaB_subunitp65](#)
- [View sp1790: NR1C1_PPARGamma interacts with NFkappaB_subunitp65](#)
- [View sp2965: NR3A_ER forms complex with NFkappaB_subunitp65](#)
- [View sp3016: NFkappaB_subunitp65 dimerizes with NFkappaB_subunitp50](#)
- [View sp668: NR3C4_AR forms complex with NFkappaB_subunitp65](#)
- [View sp1972: NR3C4_AR associates with NFkappaB_subunitp65](#)
- [View sp1279: NR3A_ER interacts with NFkappaB_subunitp65](#)



Data reproduced with permission from:

- Sylvie Albert, Sylvain Gaudan, Heidrun Knigge, Andreas Raetsch, Asuncion Delgado, Bettina Huhse, Harald Kirsch, Michael Albers, Dietrich Reholz-Schuhmann, Manfred Koegl
Computer-assisted generation of a protein-interaction database for nuclear receptors. Mol Endocrinol. 2003 Aug; 17 (8): 1555-67. [View Abstract](#)

Visualizing interactions is key for the end-user, but is still an open problem..



SigPath Navigator

Welcome to SigPath Navigator
To get started, click on a SigPath instance in the list below, then click Connect

SigPath Production
SigPath Beta
SigPath Localhost

Name: SigPath Beta
URL: http://icb.med.cornell.edu/betas/sigpath/services/navigatorcastor

SigPath Navigator
SigPath Edit View

SigPath Entities
Models
sp1760: MAPK pathway
Pathways
Interactions
Basic Reactions
sp218104: unnamed
Enzymatic Reactions
sp104: unnamed
sp106: unnamed
sp105: unnamed

Properties
Type: Protein
Spid: sp99
Name: KRAF_RAT
Accession Code: sw:P11345
Organism: Rat

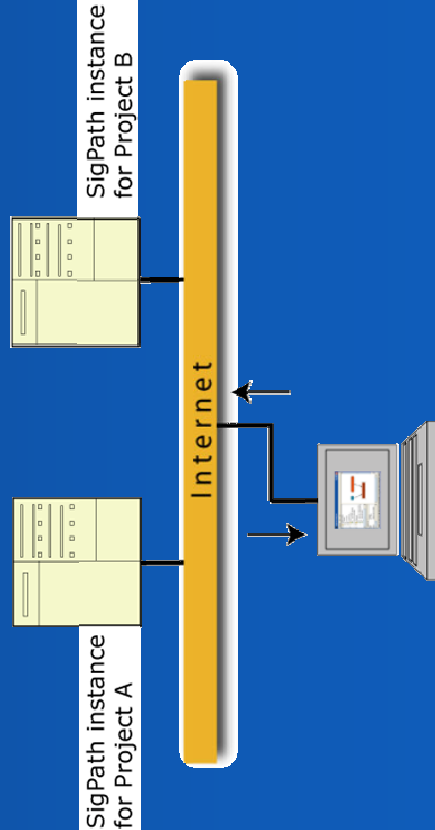
SigPath Instance URL: http://localhost:8080/sigpath/services/navigatorcastor

- Helps users navigate data relationships and create custom views of the data, interactively
- Desktop tool, connects to several SigPath instances
- Cross-platform, Java WebStart (auto install&updates)

SigPath Navigator

- Submit pathways interactively
- Inspect connectivity of entries before deleting or editing data

Submit	Spid	Name	Type	ForwardRef
<input type="checkbox"/>	sp111	unnamed	EnzymaticR...	sp100, sp218118, sp218105, sp218108
<input type="checkbox"/>	sp218104	unnamed	Reaction	sp99, sp102, sp103
<input type="checkbox"/>	sp99	KRAF_RAT	Protein	
<input type="checkbox"/>	sp3	ADP	SmallMolecule	
<input checked="" type="checkbox"/>	tmp1	c_Raf Path...	Pathway	sp104, sp99, sp102, sp103, sp111, sp112, sp113, sp2181...
<input type="checkbox"/>	sp218105	P-MPK1_RAT	Protein	
<input type="checkbox"/>	sp102	Complex(RA...	Complex	
<input type="checkbox"/>	sp218118	unnamed	Reaction	sp218108, sp218105



- Select SigPath entries and transfer to another SigPath instance

SigPath and Open Source

- SigPath is distributed under the GPL
- Leverages the JDO API, an open standard for database portability (object/relational databases, commercial *and* open-source)
- An open-source JDO implementation is on the way (see www.JPOX.org)
- Towards a bio-database framework (reusing the SigPath code base for bio-database projects with similar requirements).
- Interested in the project? Contact us!

(See ISMB
Poster C-37)

Acknowledgments

ICB:

Pharmacology,
MSSM

NCBS:
Upi Bhalla

Harel Weinstein

Eliza Chan

Manuel Martin

Marko Srdanovik

Piali Mukherjee

Ravi Iyengar

Susana Neves

Violet Chang

VCell:

Jim Schaff

SBML:

Mike Hucka,
Andrew Finney

Check out our other open-source bioinformatics projects:

TissueInfo – High-throughput tissue expression profiling with ESTs

Texttractor – Direct protein name dictionary construction from full-text (Poster B-11)

<http://icb.med.cornell.edu>

A few of the tools that help us build SigPath

Open-source



Concurrent Versions System
The open standard for version control

Developed with
IntelliJ IDEA



Logged in as: campagne (Fabien Campagne - administrator)

[Main](#) | [My View](#) | [View Issues](#) | [Report Issue](#) | [Change Log](#) | [Summary](#) | [Docs](#) | [Manage](#) | [Edit News](#) | [My Account](#) | [Logout](#)

04-25-2005 16:33 EDT

Reporter:	Monitored By:	Assigned To:	Category:	Severity:	Resolution:
any	any	any	any	any	any
Status:	Hide Status:	Product Build:	Product Version:	Fixed in Version:	Priority:
any	closed (And Above)	any	any	any	any
Show:	View Status:	Channelled (firs):	Use Data Filters:		
50	any	6	No		

Viewing Issues (1 - 50 / 179) [Print Reports] [CSV Export]

P	ID	#	Category	Severity	Status	Updated
<input type="checkbox"/>	0000862	1	Web Content	crash	assigned (kdorff)	04-25-05
<input type="checkbox"/>	0000791	1	Web Content	minor	assigned (kdorff)	04-22-05
<input type="checkbox"/>	0000861		Code Generation	minor	new	04-22-05
<input type="checkbox"/>	0000860		Documentation	text	assigned (kdorff)	04-21-05
<input type="checkbox"/>	0000859		Navigator	major	new	04-20-05
<input type="checkbox"/>	0000858		Wizard UI	major	new	04-20-05
<input type="checkbox"/>	0000857		Navigator	major	assigned (eliza)	04-20-05
<input type="checkbox"/>	0000844	8	JUnit Test	major	assigned (marko)	04-15-05

icb institute for computational biomedicine
Weill Medical College of Cornell University
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sigpath/mapping

Current directory: [\[Development\]](#) / [sigpath](#) / [mapping](#)
Files shown: 5

File **Rev.** **Age** **Author** **Last log entry**

- [DefaultMapping.xml](#) **1.1** 5 months campagne Adding mapping directory.
- [CastorToDatamodel.xml](#) **1.2** 2 months marko Remove deprecated (and now unused) methods from SigPathEntity, Yippeeel
- [datamodelToCastor.xml](#) **1.22** 3 weeks campagne XML schema changes: - pathway now uses interaction-ref element to reference r...
- [navigatorCastorToDatamodel.xml](#) **1.7** 5 days echan Modified to fix defect 0000857: [head branch]: Pathways not showing.
- [usermapping.xml](#) **1.1** 4 weeks marko Move usermapping file to the mapping directory where it should be.

Show files using tag: [-Branches -]

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Clover coverage report

[Overview](#)
[All Classes](#)

All Packages

Package	0%	2.5%	3%	2%
org.sigpath.tapestry.components.table	0%	3.3%	4.8%	3.4%
org.sigpath.form.review	3%	6.6%	5.7%	5.8%
org.sigpath.tapestry.pages.model	4.3%	7.6%	11.4%	7.2%
org.sigpath.action	3.6%	8.6%	12.5%	8.3%
org.sigpath.task.util	6.7%	10.7%	28%	10.9%
org.sigpath.navigator.memorystore	16.8%	25.6%	27%	23.8%
org.crover.cli	21%	30.8%	20.4%	26.6%
ath.form	19.4%	29.1%	38.8%	27.9%
ath.task	18.5%	34.4%	31.2%	31.4%
ath.tapestry.pages	24.3%	35.6%	44.4%	34.1%
ath.util	32.8%	35.8%	55%	36.8%
ath.task.diagrams	35.3%	43%	36.5%	40.9%
ath.biopimport.xml	28.9%	51%	32.9%	44.5%
ath.database	38.6%	50%	54.3%	49.4%
ath.biopimport	40.6%	56.7%	62.3%	54%
ath.reference	38.5%	65.3%	84%	61.1%
ath.task.edit	50%	67.7%	66.7%	64.3%
ath.biopimport.reaction2.types	50%	73.6%	43.8%	64.3%
ath.task.xml.export	64.6%	70.4%	53%	67.3%
ath.datamodel.reviews	37.5%	74%	65.4%	67.9%
ath.tapestry	70%	70.1%	62.5%	68.8%
ath.task.review	63.2%	71.1%	70.5%	69%
ath.util.xml	59.7%	70.3%	83.8%	68.1%
ath.biopimport.reaction2	65.3%	70.9%	80%	70%
ath.datamodel	66.8%	74.3%	71.7%	73%
ath.datamodel.naming	73.1%	75.3%	80%	73.8%
ath	37.5%	78.9%	55.6%	75.2%
ath.datamodel.models	68.8%	81.3%	75.7%	78.2%
ath.model	65.8%	85.3%	70.7%	80.6%
ath.task.model	71.7%	84.8%	82.7%	82.1%
ath.task.xml	72.9%	84.9%	91%	82.4%
ath.task.navigator.save	51.5%	89.2%	73%	84.6%
ath.model.export	38.9%	90%	88.9%	84.7%
ath.task.navigator	61.3%	94.9%	100%	84.8%
ath.util.formula	87%	87.2%	76.7%	85.3%
ath.datamodel.modifications	-	100%	100%	100%

Show files using tag: [-Branches -]

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ath.util.formula	87%	87.2%	76.7%	85.3%
ath.datamodel.modifications	-	100%	100%	100%

Slides after this are for questions.

Related work

At least three systems share goals similar to SigPath's

- **ProcessDB** Robert Phair and Ann Chason (commercial, free for academia <http://www.integrativebioinformatics.com/processdb.html>)
(Focus is on modeling capabilities, rough UI)
- **Monod** David Soergel, Brian George, Ross Morgan-Linial, Roger Brent, and Drew Endy (open-source <http://monod.molsci.org/docs/Monod-June-2003.pdf>)
(No quantitative data)
- **BioModels.net** Le Novère et al. <http://www.ebi.ac.uk/biomodels/> (April 2005)
(open / closed source?)

These systems differ in their approaches and capabilities