

Systems Biology & BiGCaT

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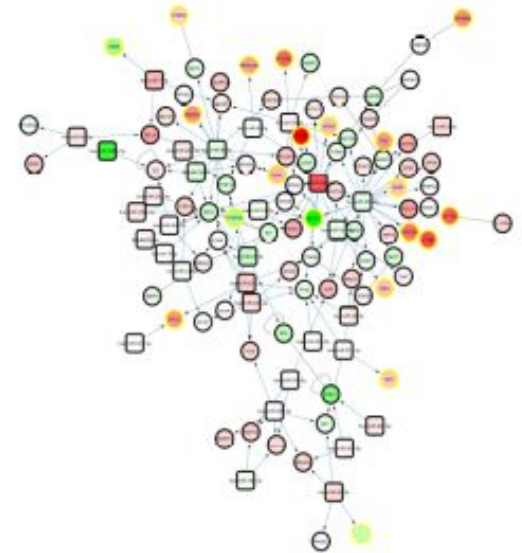
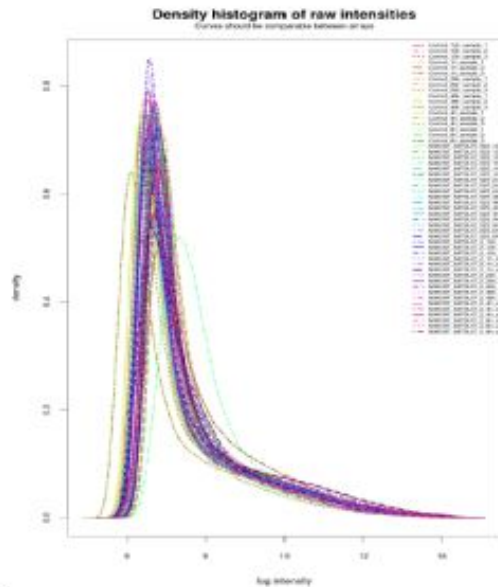
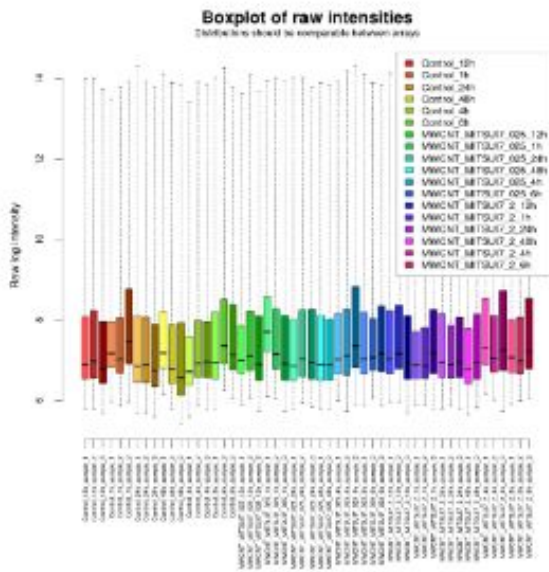
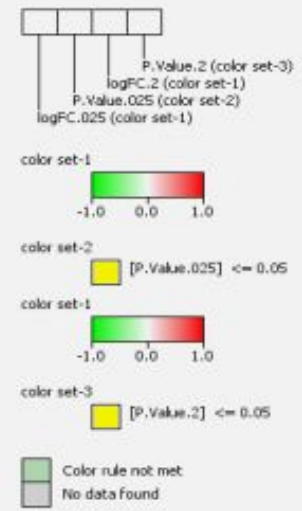
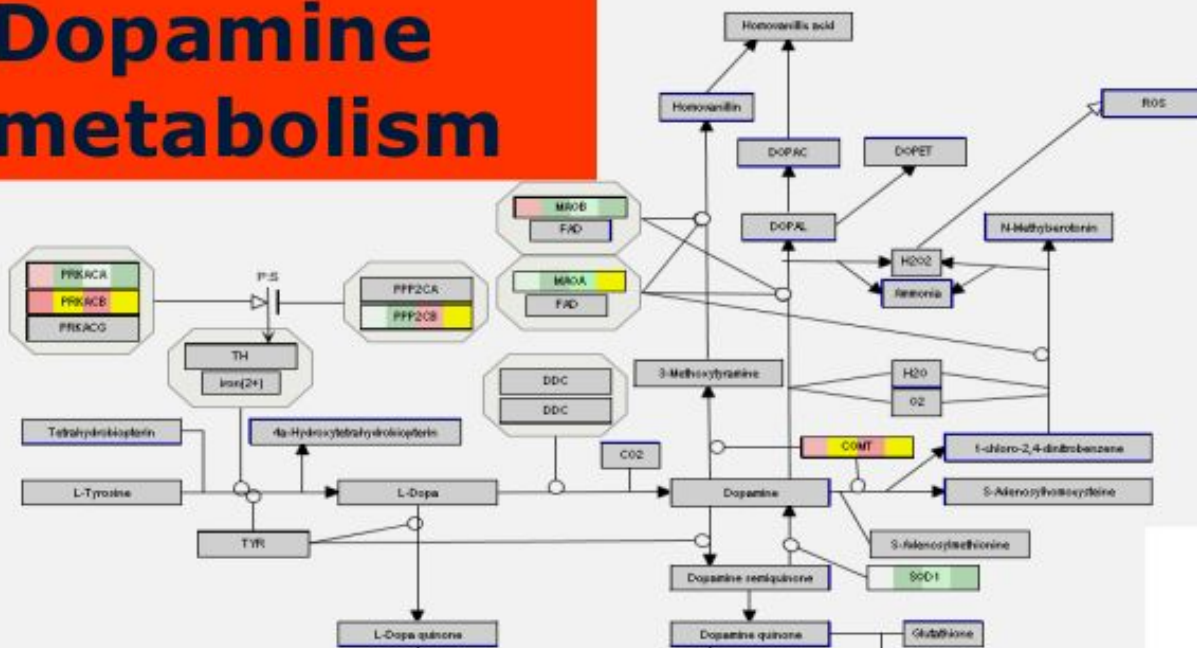
Nuno Nunes



A decorative graphic consisting of a 4x4 grid of squares. The top row has a purple square in the first column and a dark purple square in the second column. The second row has a purple square in the first column, a white square in the second column, and an orange square in the third column. The third row has a purple square in the first column, a white square in the second column, and a pink square in the third column. The fourth row has a purple square in the first column, a white square in the second column, and a dark red square in the third column.

FAIRplus

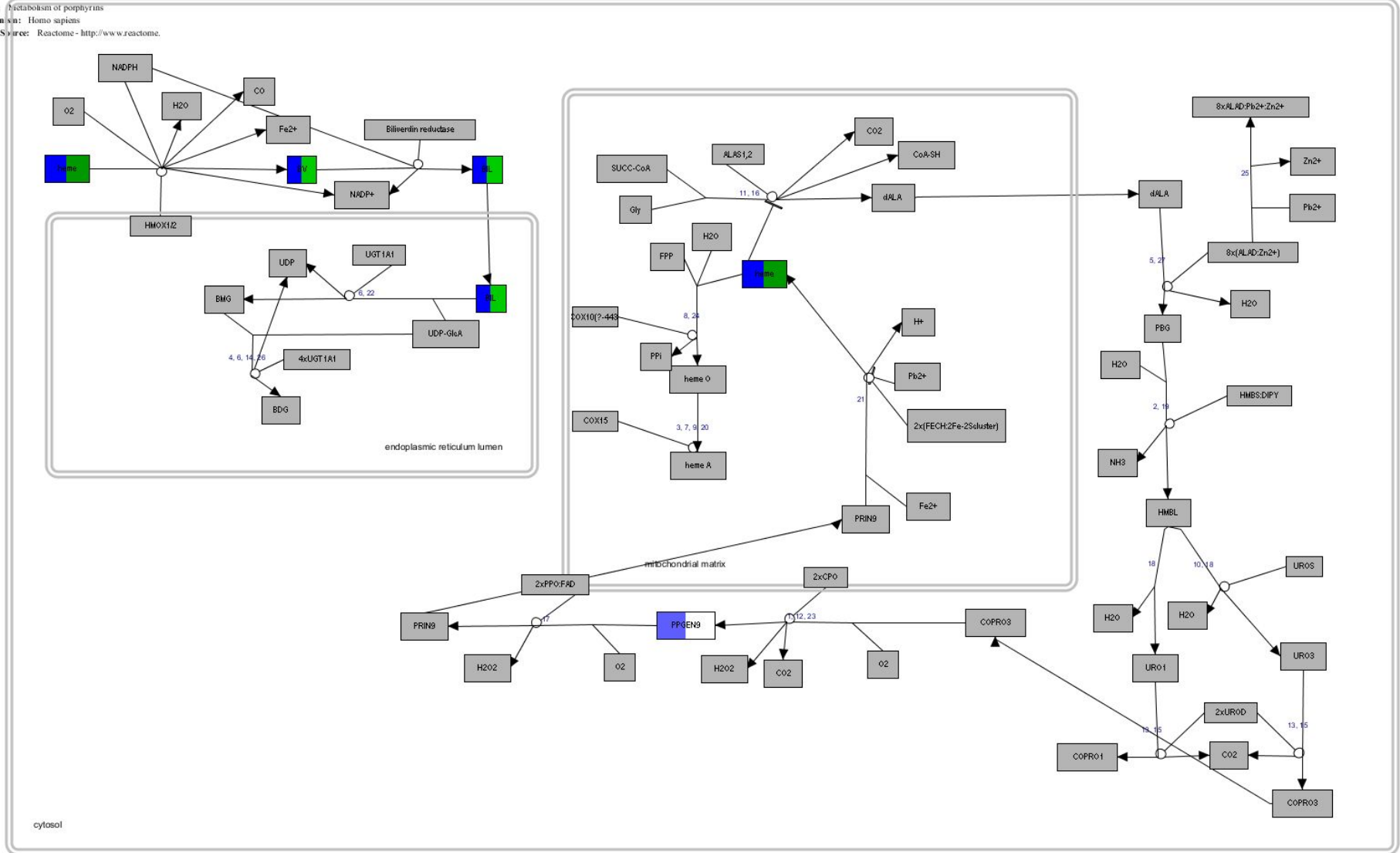
Dopamine metabolism



Marloes Poort

The effect of troglitazone on heme biosynthesis

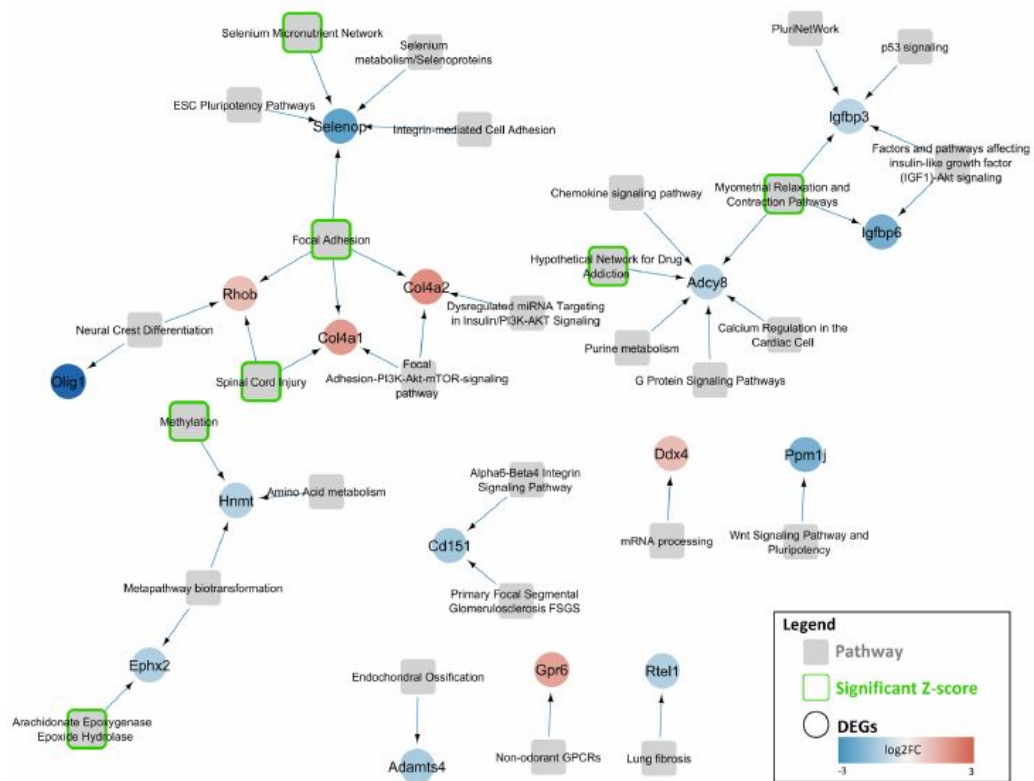
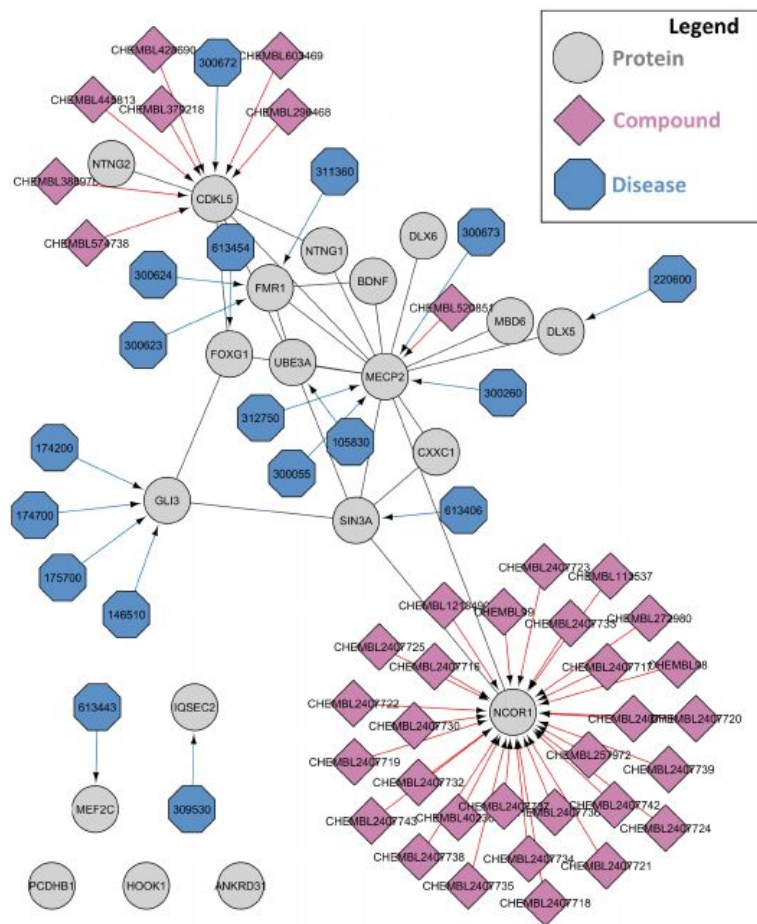
Title: Metabolism of porphyrins
Organism: Homo sapiens
Data Source: Reactome - <http://www.reactome.org>



Metabolism of porphyrins (Homo sapiens), 2018, Reactome Team, Anwesha Bohler, Egon Willighagen, Martijn van Iersel,

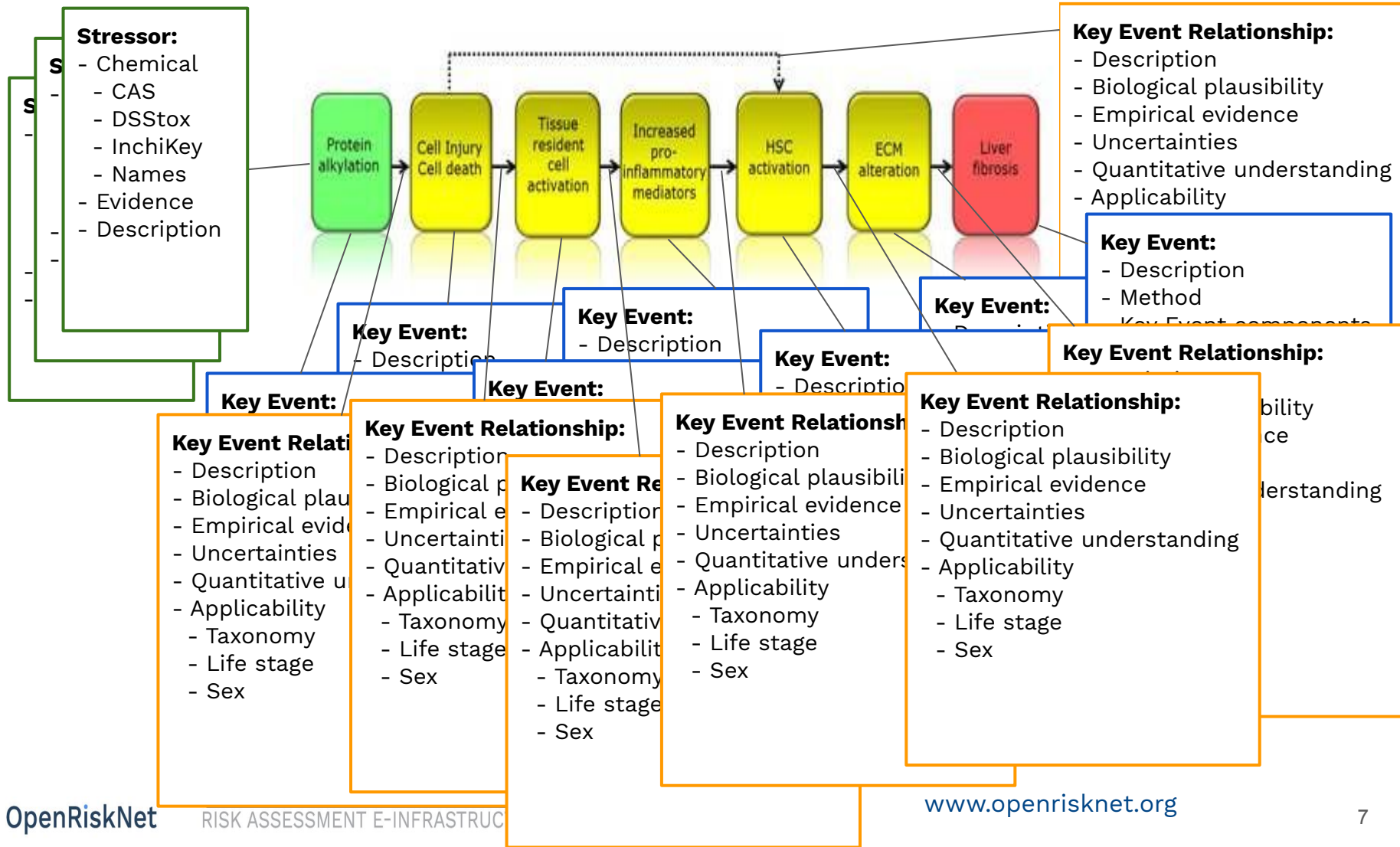
<http://identifiers.org/wikipathways/WP1852>

CyTargetLinker



CyTargetLinker app update: A flexible solution for network extension in Cytoscape. 2018. F1000Research. 7. 743.
10.12688/f1000research.14613.1

AOPs in AOP-Wiki contain diverse types of info



WikiPathways: a multifaceted pathway database bridging metabolomics to other omics research

Denise N Slenter, Martina Kutmon, Kristina Hanspers, Anders Riutta, Jacob Windsor, Nuno Nunes, Jonathan Mélius, Elisa Cirillo, Susan L Coort, Daniela Digles ... Show more

Nucleic Acids Research, Volume 46, Issue D1, 4 January 2018, Pages D661–D667, <https://doi.org/10.1093/nar/gkx1064>

Published: 10 November 2017 Article history ▼

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Abstract

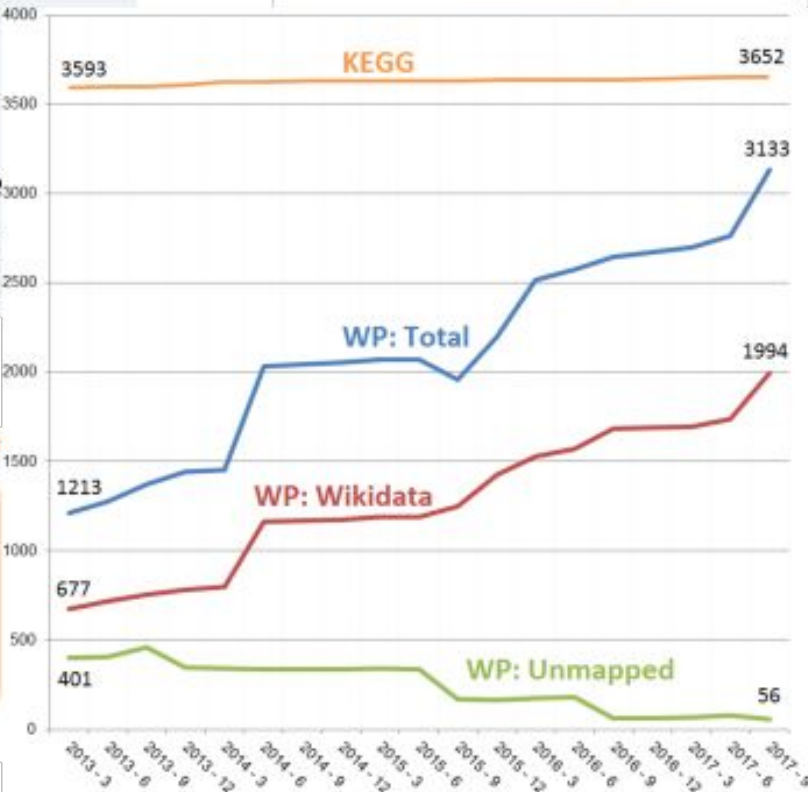
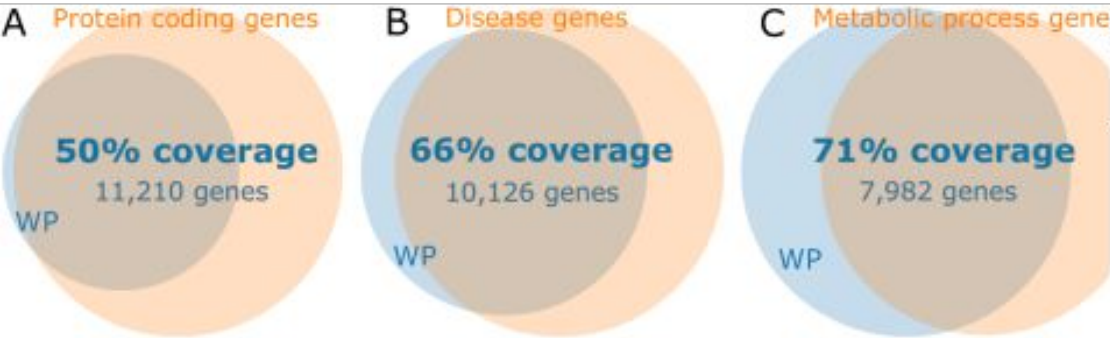
WikiPathways ([wikipathways.org](http://www.wikipathways.org)) captures the collective knowledge represented in biological pathways. By providing a database in a curated, machine readable way, omics data analysis and visualization is enabled. WikiPathways and other pathway databases are used to analyze experimental data by research groups in many fields. Due to the open and collaborative nature of the WikiPathways platform, our content keeps growing and is growing



View Metrics

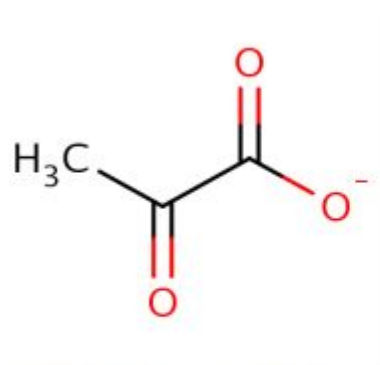
Email alerts

- New issue alert
- Advance article alerts
- Article activity alert

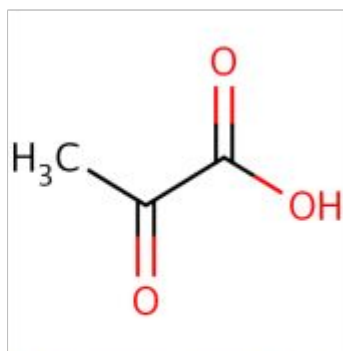


Chemistry in metabolic pathways

CHEBI:15361 (Pyruvate) -> Ce:CHEBI:32816 (conjugate) -> Ck:C00022 -> [WP2456 HIF1A and PPARG regulation of glycolysis, WP2453 TCA Cycle and PDHc]

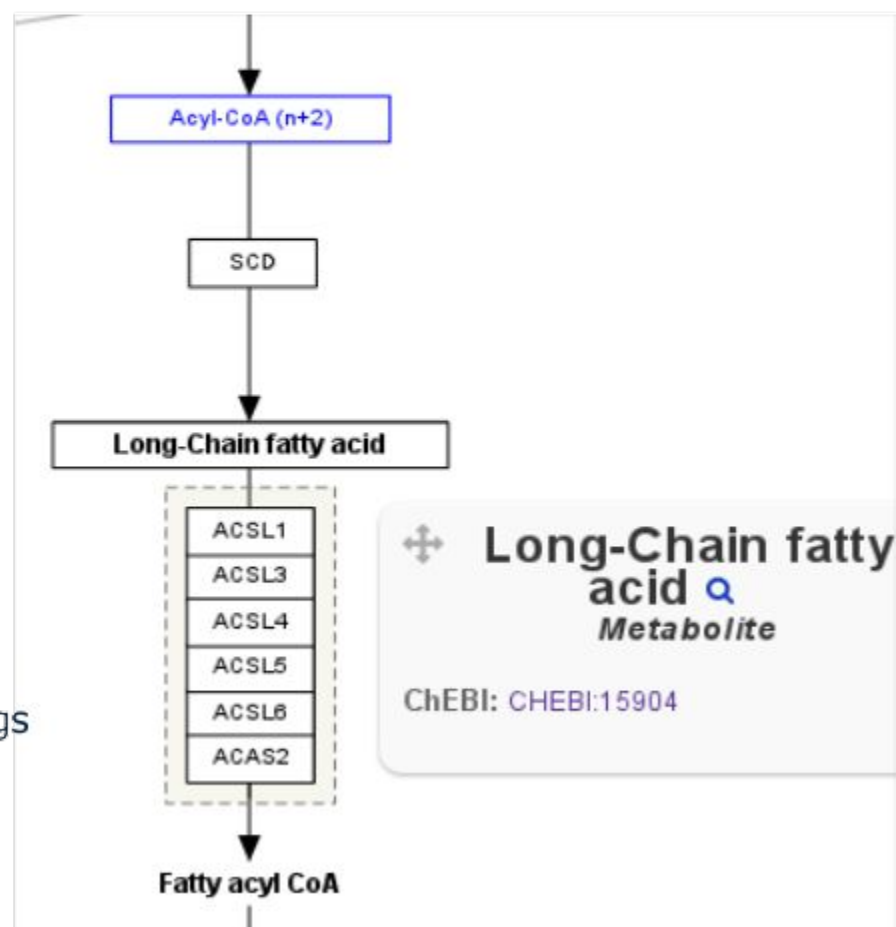


CHEBI:15361



CHEBI:32816

Brenninkmeijer, CYA, et al. "Scientific Lenses over Linked Data: An approach to support task specific views of the data. A vision." Proceedings of 2nd International Workshop on Linked Science. 2012.



So, what IDs are used in WikiPathways? 2019

2017

datasource	numberEntries
ChEBI	1923
HMDB	623
CAS	299
KEGG Compound	251
PubChem-compound	245
Chemspider	174
PubChem-substance	33
LIPID MAPS	10
Reactome	4
Wikidata	3
ChEMBL compound	2

+ Reactome

2015

source	count
HMDB	56
ChEBI	49
KEGG Compound	40
CAS	29
PubChem-compound	21
Chemspider	15
PubChem-substance	24
LIPID MAPS	11
Wikipedia	9
ChemIDplus	7
Reactome	4
ChEMBL compound	2
Other	1
CTD Chemical	1
ChemSpider	1

datasource	numberEntries
ChEBI	2428
HMDB	931
KEGG Compound	397
PubChem-compound	357
CAS	293
Wikidata	273
Chemspider	202
LIPID MAPS	148
KNAPSAcK	112
ChEMBL compound	7
Reactome	2
KEGG Glycan	2
PubChem-substance	2
TTD Drug	1



(What about reactions (- identifiers)? In progress

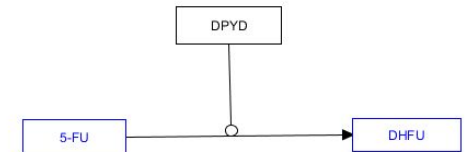
source	count
Reactome	11320
KEGG Reaction	61
Rhea	59
WikiPathways	13
KEGG Pathway	8
XMetDB	2
SPIKE	1
WormBase	1

	Interaction Type	Interaction Count
0	Interaction	15228
1	DirectedInteraction	11586
2	Conversion	1362
3	Catalysis	1169
4	Inhibition	1081
5	ComplexBinding	889
6	Binding	889
7	Stimulation	721
8	TranscriptionTranslation	256

WikiPathways Interaction Types

Catalysis

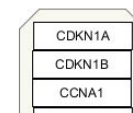
Title: Catalysis
Organism: Homo sapiens



- [GPML](#)
- [Expected results](#)

Complex binding

Title: Binding
Organism: Homo sapiens



Portal:Semantic Web

The WikiPathways Semantic Web Portal

edit

Welcome to the WikiPathways Semantic Web Portal!

This portal describes the Semantic Web features of the WikiPathways databases, such as the [Resource Description Framework](#) (RDF) translation, the ontology, and the new nanopublications.

The WikiPathways RDF is provided as part of the monthly releases and contains the [Curated](#) and [Reactome](#) pathways. The RDF is split in two parts, the GPMLRDF part which contains a direct translation of the content in the GPML files, and a WPRDF part which contains the biology represented in the GPML.

The WikiPathways Vocabularies

The [WikiPathways vocabularies](#) are for the semantic information about the pathway, data nodes, and interactions and the GPML vocabulary is for the graphical information about how the pathway diagram is laid out and represented.

How to cite

If you use the RDF, vocabularies, or nanopublication, please cite the following paper:

- Waagmeester, A., Kutmon, M., Riutta, A., Miller, R., Willighagen, E. L., Evelo, C. T., Pico, A. R., Jun. 2016. Using the semantic web for rapid integration of WikiPathways with other biological online data resources. PLoS Comput Biol 12 (6), e1004989+. doi:10.1371/journal.pcbi.1004989

For the pathway content, please follow these [How to cite WikiPathways](#) instructions.



search

- [Help](#)
- [About us](#)
- [Contact us](#)
- [Report a bug](#)
- [How to cite](#)

download

- [Download files](#)
- [Web service API](#)
- [WikiPathways RDF](#)
- [Embed code](#)

activity

- [Browse pathways](#)
- [Recent changes](#)
- [New pathways](#)
- [Edit pathways](#)
- [Create pathway](#)
- [Statistics](#)

tools

- [PathwayWidget](#)
- [Pathway Finder](#)
- [Software tools](#)

community

- [Quality control](#)
- [Development](#)
- [WikiPathways Blog](#)
- [AOP portal](#)

News

edit

2018-11-18 - Five species have been [added](#) to the RDF: *Equus caballus*, *Mycobacterium tuberculosis*, *Plasmodium falciparum*, *Populus trichocarpa*, and *Solanum lycopersicum*.

2018-10-12 - Paper about how [WikiPathways RDF](#) is used to expose interactions via [Open PHACTS](#)

2018-01-01 - The RDF is being used to expose [facts from WikiPathways as nanopublications](#)

2017-05-04 - This portal was created

2016-06-23 - Andra Waagmeester's [Using the Semantic Web for Rapid Integration of WikiPathways with Other Biological Online Data Resources](#) paper is published

SPARQL

edit

We provide a [SPARQL endpoint](#) where data queries can be done.

WikiPathways Example SPARQL Queries

We have a large collection of [general example queries](#) and [metabolite related example queries](#).

For example, to list all pathways per instance of a particular gene or protein (wp:GeneProduct), you can use the following SPARQL:

```
PREFIX wp:      <http://vocabularies.wikipathways.org/wp#>
```

SPARQL endpoint

Virtuoso SPARQL Query Editor

Default Data Set Name (Graph IRI)

Query Text

```
select ?KeyEventID ?KeyName ?AssayText
where {
  ?KeLook a aopo:KeyEvent ;
  rdfs:label ?KeyName ;
  dc:title ?KeyName ;
  dcterms:isPartOf ?aop1 ;
  mmo:0000000 ?AssayText .
  ?aop1 dc:identifier ?AopAssoc .
  values ?aop1 {aop:38}
}
```

(Security restrictions of this server do not allow you to retrieve remote RDF data, see [details](#).)

Results Format:

Execution timeout: milliseconds (values less than 1000 are ignored)

Options:

- ☒ Strict checking of void variables
- ☐ Log debug info at the end of output (has no effect on some queries and output formats)
- ☐ Generate SPARQL compilation report (instead of executing the query)

(The result can only be sent back to browser, not saved on the server, see [details](#))

grlc REST API

GET

/get-methods-for-aop-simple Get measurement methods for all Key Events of an Adverse Outco
is "3".

```
#+ endpoint_in_url: False
#+ tags:
#+ - Methods
#+ defaults:
#+ - aopfilter: 3

prefix dc: <http://purl.org/dc/elements/1.1/>
prefix dcterms: <http://purl.org/dc/terms/>
prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#>
prefix aop: <http://identifiers.org/aop/>
prefix aopo: <http://aopkb.org/aop_ontology#>
prefix mmo: <http://purl.obolibrary.org/obo/MMO_>

select ?AopLabel ?KeyEventID (?KeLook AS ?KeyEventURL) ?AssayText ?_aopfilter_integer
where {
  ?KeLook a aopo:KeyEvent ;
  rdfs:label ?KeyEventID ;
  dcterms:isPartOf ?aop;
  mmo:0000000 ?AssayText .
  ?aop rdfs:label ?AopLabel .
  BIND(IRI(CONCAT("http://identifiers.org/aop/",?_aopfilter_integer)) AS ?Aopf )
  FILTER (?aop = ?Aopf)
}
```

Parameters

Name	Description
------	-------------

aopfilter * required

string
(query)

A value of type string that will substitute ?_aopfilter_integer in the orig

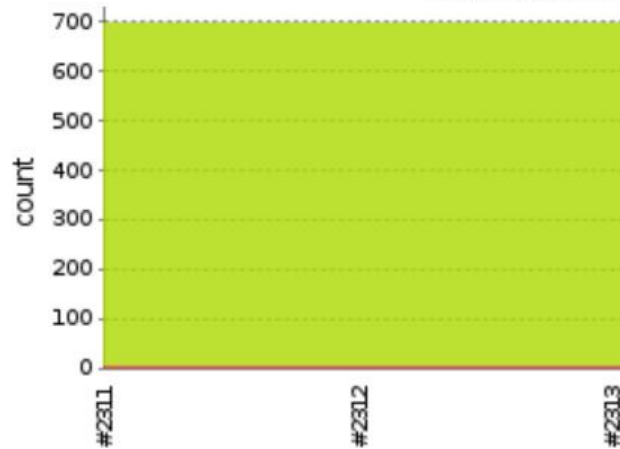
38

Execute

Computer assisted Curation (SPARQL++)

		Wikidata Checks for Metabolomics	6 hr 29 min - #63
		WikiPathways Curation (SPARQL endpoint)	6 days 13 hr - #5510
		WikiPathways Curation (WP2RDF Curation)	33 min - #5605
		WikiPathways Curation (WP2RDF Curation)_(all)	5 hr 32 min - #2315
		WikiPathways Curation (WP2RDF Curation)_(all, dev)	5 hr 10 min - #1483
		WikiPathways Curation Events	5 hr 10 min - #710

Test Result Trend



Test Result

2 failures (+1)

693 tests (± 0)
[Took 8 min 42 sec.](#)

All Failed Tests



Test Name	Duration	Age
+ nl.unimaas.bigcat.wikipathways.curator.ChEBIMetabolites.secondaryChEBIIdentifiers	0.26 sec	1
+ nl.unimaas.bigcat.wikipathways.curator.Metabolites.ChEBIIDsNotMarkedAsMetabolite	43 ms	1

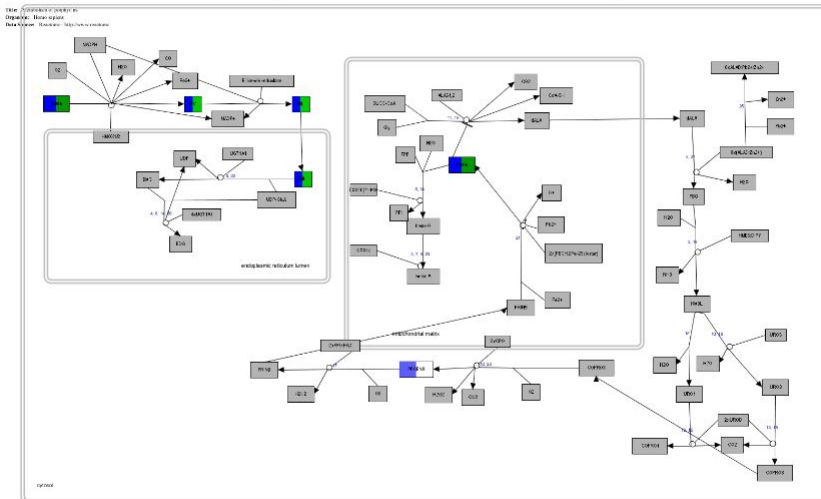
All Tests

Package	Duration	Fail (diff)	Skip (diff)	Pass (diff)	Total (diff)
nl.unimaas.bigcat.wikipathways.curator	1 min 13 sec	2 +1	0	691 -1	693



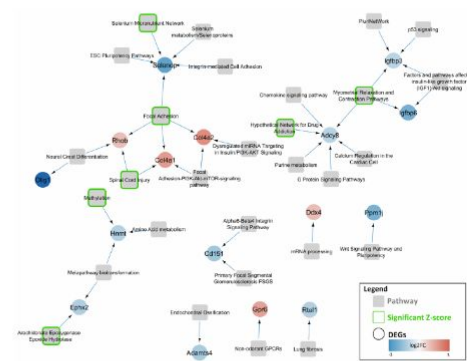
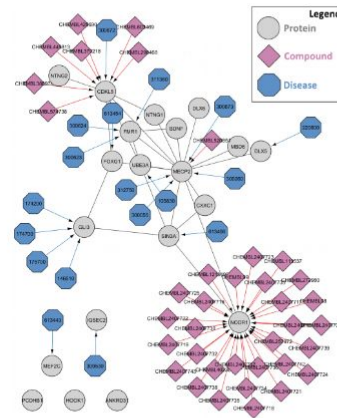
From individual entities to huge networks

The effect of troglitazone on heme biosynthesis



Metabolism of porphyrins (Homo sapiens), 2018, Reactome Team, Anwesha Bohler, Egon Willighagen, Martijn van Iersel, <http://identifiers.org/kegg/pathway/HMP1852>

CyTargetLinker



CyTargetLinker app update: A flexible solution for network extension in Cytoscape. 2018. F1000Research. 7. 743. 10.12688/f1000research.14613.1

Wikidata / Scholia



Redirecting

If you know the identifier then Scholia can make a lookup based on the identifier:

cas/50-00-0

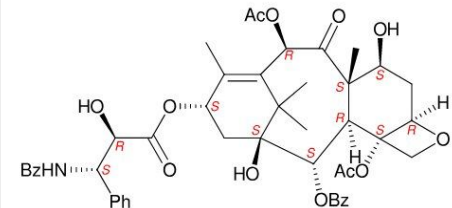
Lookup CAS 50-00-0. This will identify formaldehyde and redirect to its Scholia page.

inchikey/QTBSBXVTEAMEQO-UHFFFAOYSA-N

Redirect also works for InChIKeys, here for acetic acid.

paclitaxel (Q423762)

Paclitaxel (PTX), sold under the brand name Taxol among others, is a chemotherapy medication used to treat a number of types of cancer. This includes ovarian cancer, breast cancer, lung cancer, Kaposi sarcoma, cervical cancer, and pancreatic cancer. It is given by injection into a vein. ... (from the [English Wikipedia](#))



Identifiers

Show entries

Search:

IDpred	Id
ATC code	L01CD01
CAS Registry Number	33069-62-4

2019: 10.3897/rio.5.e35820
2017: 10.6084/m9.figshare.6356027.v1

Wikidata / Scholia

DSSTOX substance identifier  DTXSID30678817

▼ 1 reference

stated in

Mapping file of InChIStrings, InChIKeys and DTXSIDs for the EPA CompTox Dashboard

IDpred	IDpredLabel	count
 wd:P235	InChIKey	152393
 wd:P233	canonical SMILES	152233
 wd:P234	InChI	149944
 wd:P662	PubChem CID	145798
 wd:P661	ChemSpider ID	125510
 wd:P2017	isomeric SMILES	84844
 wd:P683	ChEBI ID	84011
 wd:P231	CAS Registry Number	72475
 wd:P652	UNII	59293
 wd:P592	ChEMBL ID	49622
 wd:P3117	DSSTOX substance identifier	36373
 wd:P232	EC ID	20335
 wd:P1579	Beilstein Registry Number	19083
 wd:P665	KEGG ID	15065
 wd:P2566	ECHA InfoCard ID	12362
 wd:P715	Drugbank ID	7786
 wd:P595	Guide to Pharmacology Ligand ID	5950
	HMDB ID	5705
	KNAPSAcK ID	4272

Show entries

Search:

Mol	InChIKey	CAS	ChemSpider	PubChem CID
acetic acid	QTBSBXVTEAMEQO-UHFFFAOYSA-N	64-19-7	171	176
deuterated acetic acid	QTBSBXVTEAMEQO-GUEYOVJQSA-N	1186-52-3	2006083	2723903
acetic acid c-14	QTBSBXVTEAMEQO-HQMMCQRPSA-N	2845-03-6	144444	164769
acetic acid c-13	QTBSBXVTEAMEQO-VQEHIDDOSA-N	1563-79-7	8329490	10153982
acetic acid c-11	QTBSBXVTEAMEQO-JVVVGQRLSA-N	78887-71-5	396653	450349
acetate ion	QTBSBXVTEAMEQO-UHFFFAOYSA-M	71-50-1	170	175

[Edit on query.Wikidata.org](#)

Showing 1 to 6 of 6 entries

Previous Next

Wikidata / Scholia

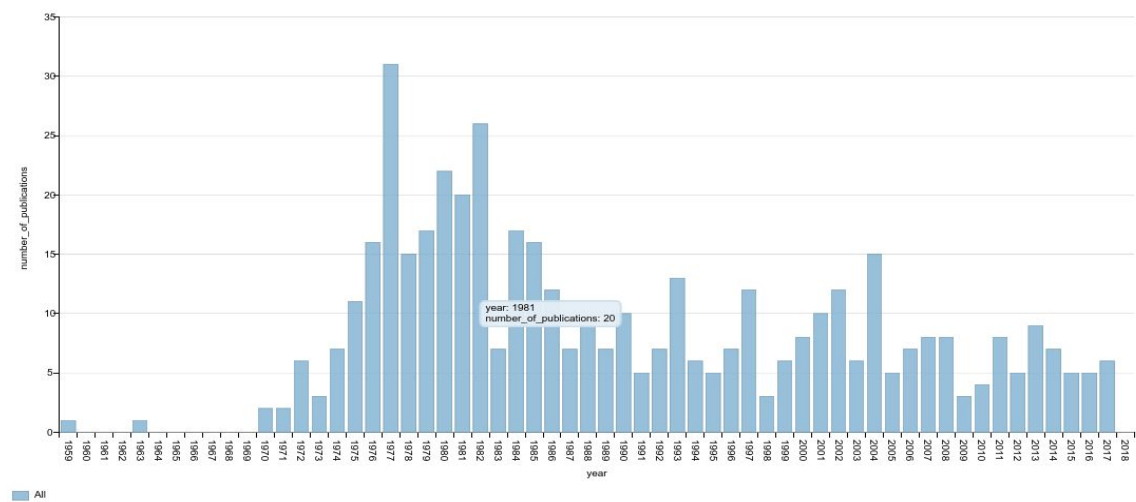
Physchem Properties

Show entries

Search:

PropEntity	Value	Units	Qualifiers	Source	Doi
acid dissociation constant	4.74	1		Small Scale Determination of the pKa Values for Organic Acids	10.1021/ED071PA6
mass	60.021129	atomic mass unit		PubChem	
acid dissociation constant	4.756	1	temperature: 25	CRC Handbook of Chemistry and Physics (95th edition)	
boiling point	117.9	degrees Celsius	pressure: 101325	CRC Handbook of Chemistry and Physics (95th edition)	
density	1.0446	gram per cubic centimetre	temperature: 25	CRC Handbook of Chemistry and Physics (95th edition)	

Publications per year



Recently published works on the chemical

Show entries

Date	Work	Type	Topics
2017-08-09	In vitro human skin permeation of benzene in gasoline: effects of concentration, multiple dosing and skin preparation	scholarly article	oil and gas extraction // benzene
2017-04-27	Nicotine, aerosol particles, carbonyls and volatile organic compounds in tobacco- and menthol-flavored e-cigarettes	scholarly article	toluene // benzene

Automation / repeating

The screenshot shows the BioCypse web application interface. The interface is divided into several panels:

- BioCypse Navigator:** A file tree on the left showing various molecular files, including "C00020.mol", "polycarpol_3d.mol", "polycarpol.mol", "0017_3d.mol", "0017.cml", "broken.cvv", "CHEBI_complete.sdf", "dix+trouch.cvv", "fragments_2_3d.sdf", "fragments2.sdf", "jmolExample.js", "mymol2.cml", "polycarpol_3d_2.mol", "polycarpol_3d.mol", "substructureSearch.js", "text.png", "unnamed_3d.cml", "unnamed.cml", and "unnamed.cml".
- Properties:** A panel below the navigator showing properties for the selected molecule. It includes fields for "Has 2D Coords" (yes), "Has 3D Coords" (no), "Molecular Formula" (C10H16O2), "Molecular Mass" (168.2332), "Charge" (0), "CHEBI ID" (CHEBI:25), "CHEBI Name" ((+)-isodolal), "Formulae" (C10H16O2), "SMILES" (CC1=C(C(=O)O)C1=O), "Molecular Weight" (168.2332), "PubChem Database Links" (8346238), "SMILES" (CC1=C(C(=O)O)C1=O), "Molecular Weight" (168.2332), and "Synonyms" ((+)-isodolal).
- Table:** A table with columns "2D-structure", "Last Modified", and "Formulae". It contains two entries:

2D-structure	Last Modified	Formulae
	23 May 2008	C10H16
	23 Apr 2007	C10H16O2
- 3D Model:** A large 3D molecular model of the selected molecule, showing atoms as spheres and bonds as sticks.
- Outline:** A panel on the right showing a list of models, including "Model 0", "Model 1", "Model 2", "Model 3", and "Model 4".
- Chemical Structure:** A chemical structure diagram of a molecule, showing a central carbon atom bonded to two hydroxyl groups and two other groups.

Software | [OPEN](#) | [Published: 03 December 2009](#)

Bioclipse 2: A scriptable integration platform for the life sciences

[Ola Spjuth](#) , [Jonathan Alvarsson](#), [Arvid Berg](#), [Martin Eklund](#), [Stefan Kuhn](#), [Carl Mäsak](#), [Gilleain Torrance](#), [Johannes Wagener](#), [Egon L Willighagen](#), [Christoph Steinbeck](#) & [Jarl ES Wikberg](#)

BMC Bioinformatics 10, Article number: 397 (2009) | [Download Citation](#)

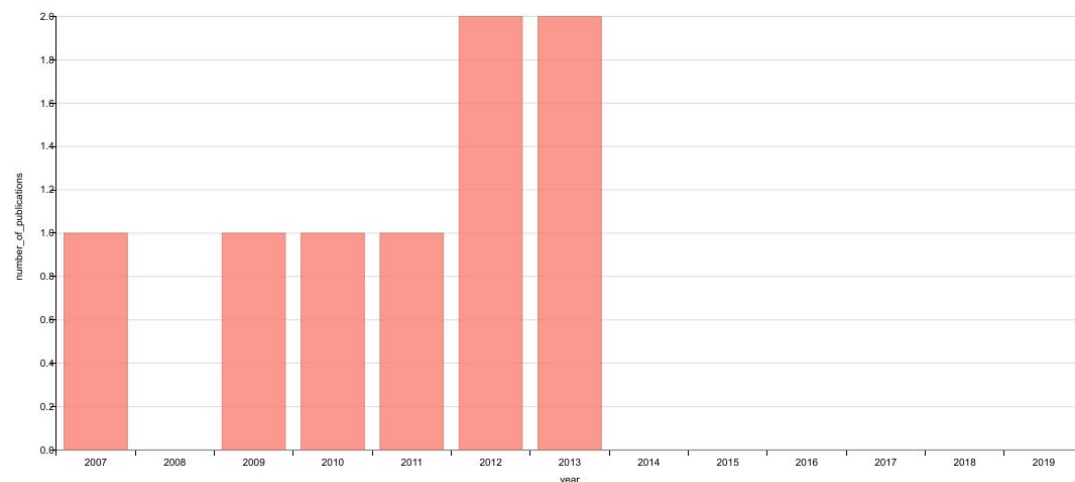
Abstract

Background

Contemporary biological research integrates neighboring scientific domains to answer complex questions in fields such as systems biology and drug discovery. This calls for tools that are intuitive to use, yet flexible to adapt to new tasks.

Results

Publications per year



topic

Bioclipse (Q1769726)

The Bioclipse project is a Java-based, open-source, visual platform for chemo- and bio-scripting functionality in 2009. Like any RCP application, Bioclipse uses a plugin architecture, such as help system, software updates, preferences, cross-platform deployment, and extension points that easily can be extended by other, possibly proprietary (Wikipedia)

Recently published works on the topic

Show entries

Date	Work
2013-01-15	Bioclipse-R: integrating management and visualization of life science data with statistical analysis
2013-01-01	Applications of the InChI in cheminformatics with the CDK and Bioclipse
2012-01-01	Interactive predictive toxicology with Bioclipse and OpenTox
2012-01-01	Open source drug discovery with bioclipse.
2011-01-01	Computational toxicology using the OpenTox application programming interface and Bioclipse
2010-01-01	Use of historic metabolic biotransformation data as a means of anticipating metabolic sites using MetaPrint2D and Bioclipse
2009-01-01	Bioclipse 2: a scriptable integration platform for the life sciences
2007-	Bioclipse: an open source workbench for chemo- and bioinformatics

Bacting := acting as the Bioclipse TNG

egonw / **bacting** Unwatch 1 Star 0 Fork 0

Code Issues 1 Pull requests 0 Security Insights Settings

Branch: master **bacting** / README.md Find file Copy path

egonw Updated the Zenodo link 1086f4e 3 days ago

1 contributor

71 lines (46 sloc) 2.56 KB

bacting

License EPL 1.0 DOI 10.5281/zenodo.3334372

Bacting := acting as the Bioclipse TNG

How to cite

If you use this software, please cite the [Bioclipse 2 paper](#).

Install

<https://bioclipse.github.io/bioclipse.scripting/>

bioclipse.scripting

FromSMILES.groovy

Source code

The source code may use or refer to content in a local workspace. This Bioclipse workspace used can be found [on GitHub](#).

Bioclipse 2.6

```
mol = cdk.fromSMILES("COC")
println mol
```

Bacting

To run this code, you first need to install [Bacting](#).

```
@Grab(group='io.github.egonw.bacting', module='managers-cdk', version='0.0.5')

workspaceRoot = "../ws"
cdk = new net.bioclipse.managers.CDKManager(workspaceRoot);

mol = cdk.fromSMILES("COC")
println mol
```

Output

```
CDKMolecule:C2H6O
```



[Home](#) » [Bioconductor 3.10](#) » [Software Packages](#) » BridgeDbR (development version)

BridgeDbR

platforms **all** rank **708 / 1728** posts **0** in Bioc **4.5 years**
build **ok** updated **before release**

DOI: [10.18129/B9.bioc.BridgeDbR](https://doi.org/10.18129/B9.bioc.BridgeDbR) [f](#) [t](#)

This is the **development** version of BridgeDbR; to use it, please install the [development version](#) of Bioconductor.

Code for using BridgeDb identifier mapping framework within R

- 1 Introduction
- 2 Concepts
- 3 Mapping Identifiers
- 4 Metabolomics
- References

```
<script type="application/ld+json">
```

```
{
  "@context": "http://schema.org/",
  "@type": "CreativeWork",
  "about": "This tutorial describes how to use the BridgeDbR package for mapping.",
  "audience": [
    "http://edamontology.org/topic_3070",
    "http://edamontology.org/topic_3314"
  ],
  "genre": [
    "http://edamontology.org/topic_0605",
    "http://edamontology.org/operation_3282",
    "http://edamontology.org/data_1025",
    "http://edamontology.org/data_0982"
  ],
  "name": "BridgeDbR Tutorial",
  "author": [{
    "@type": "Person",
    "name": "Egon Willighagen",
    "identifier": "0000-0001-7542-0286"
  }],
  "difficultyLevel": "beginner",
  "keywords": "ELIXIR RIR, BridgeDb",
}
```

Documentation »

Bioconductor

- Package [vignettes](#) and manuals.
- [Workflows](#) for learning and use.
- [Course and conference](#) material.
- [Videos](#).
- Community [resources](#) and [tutorials](#).

BridgeDbR Tutorial

Egon Willighagen

2 May 2019

Package

BridgeDbR 1.19.0

1 Introduction

BridgeDb is a combination of an application programming interface (API), library, and set of data files for mapping identifiers for identical objects [1]. Because BridgeDb is used by projects in bioinformatics, like [WikiPathways](#) [2] and [PathVisio](#) [3], identifier mapping databases are available for gene products and metabolites.

Questions can be directed to the [BridgeDb Google Group](#).

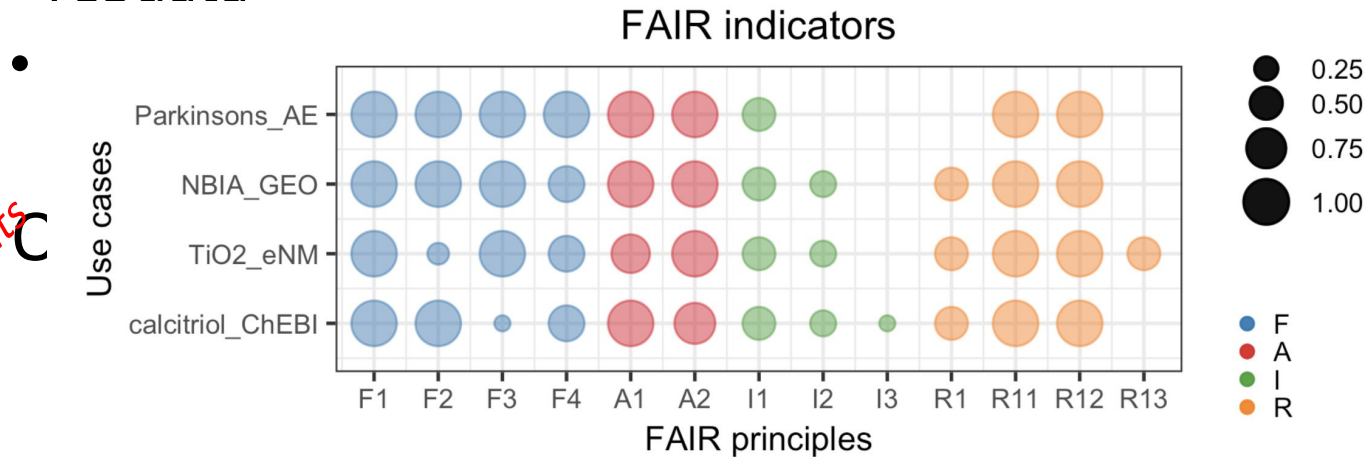
The [Bioconductor BridgeDbR package](#) page describes how to install the package. After installation, the library can be loaded with the following command:

```
library(BridgeDbR)
```

```
## Loading required package: rJava
```

Implementation

1. Research question via API □ Data ID and metadata
2. Calculation of metrics:
 - Findability in a searchable resource : Google Dataset Search
 - About repository (e.g. persistent identifier, license): re3data



3. C

Not final results

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Funded projects



Maastricht University



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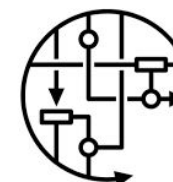
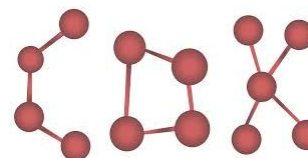


<https://www.bigcat.unimaas.nl/>

<https://tools.wmflabs.org/scholia/organization/Q19845644>



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WIKIPATHWAYS
Pathways for the People