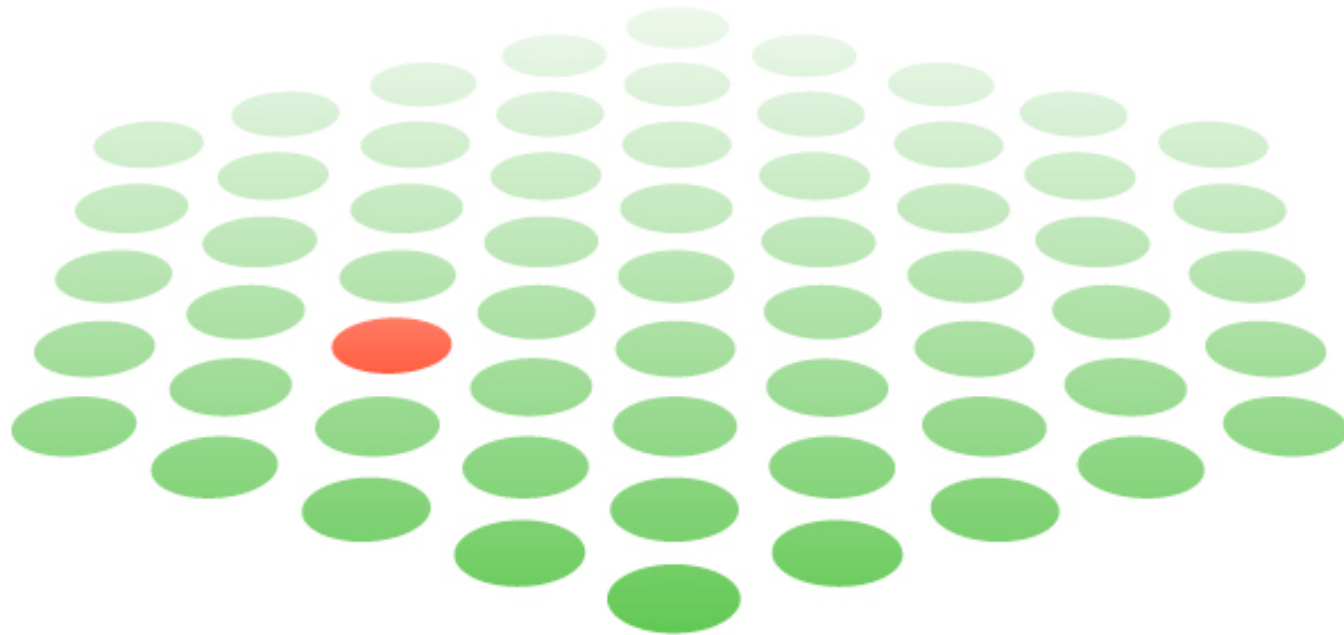


Open access – making the most of biomedical literature mining



Lars Juhl Jensen
EMBL Heidelberg

A cluster of approximately 40 light green circles arranged in a roughly hexagonal pattern. One circle, located slightly to the left of the center, is a different shade of red/pink, making it stand out from the rest.

why open access?

A cluster of approximately 40 light green circles arranged in a roughly hexagonal pattern. One circle, located slightly to the left of the center, is a distinct reddish-pink color.

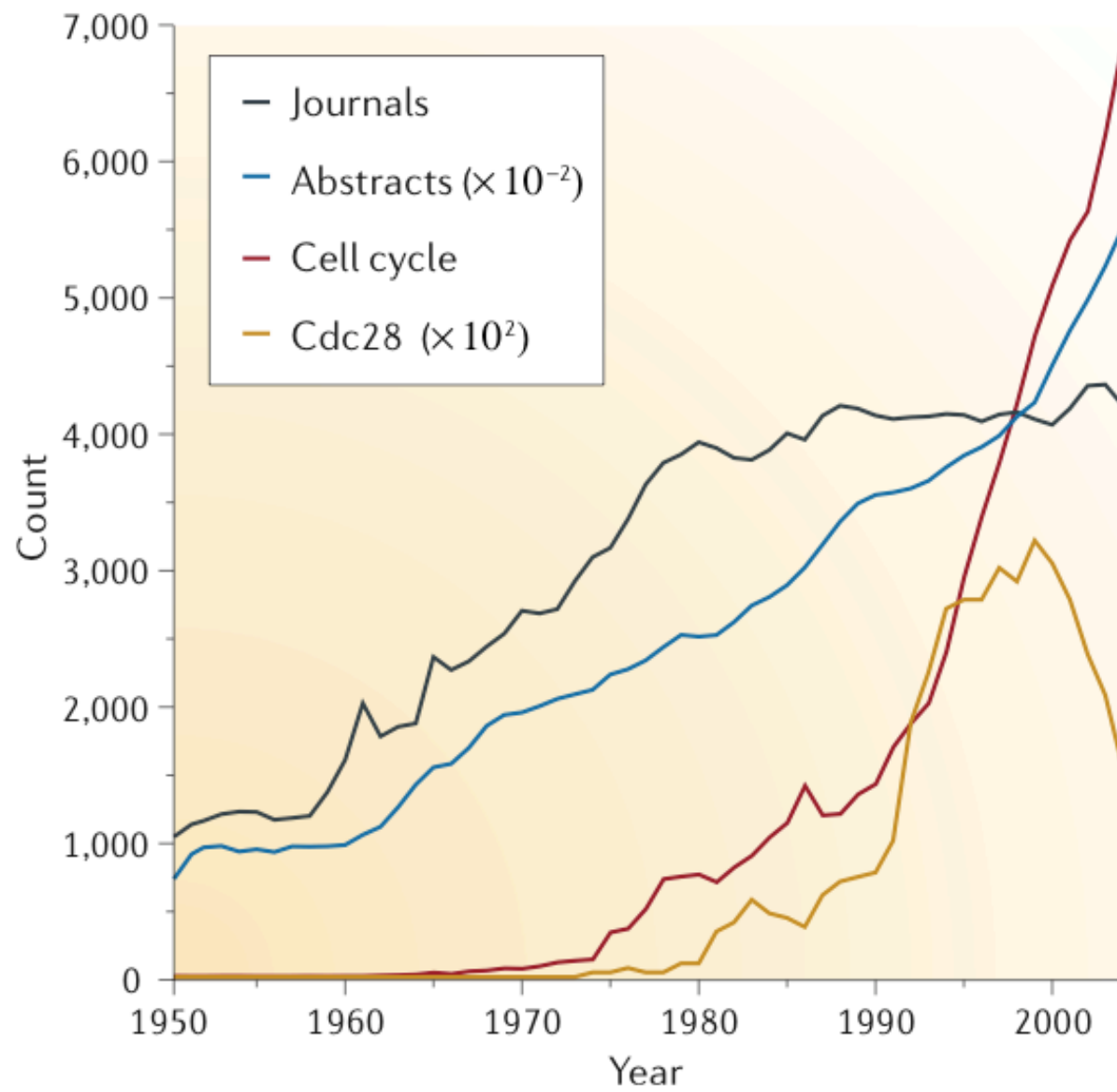
why biomedicine?

A decorative background consisting of a grid of circles. Most circles are light green, while one circle in the center-left area is a slightly different shade of green, appearing more vibrant or red-tinged. The circles are arranged in a pattern that is roughly rectangular but has some irregularities, with some circles missing or overlapping.

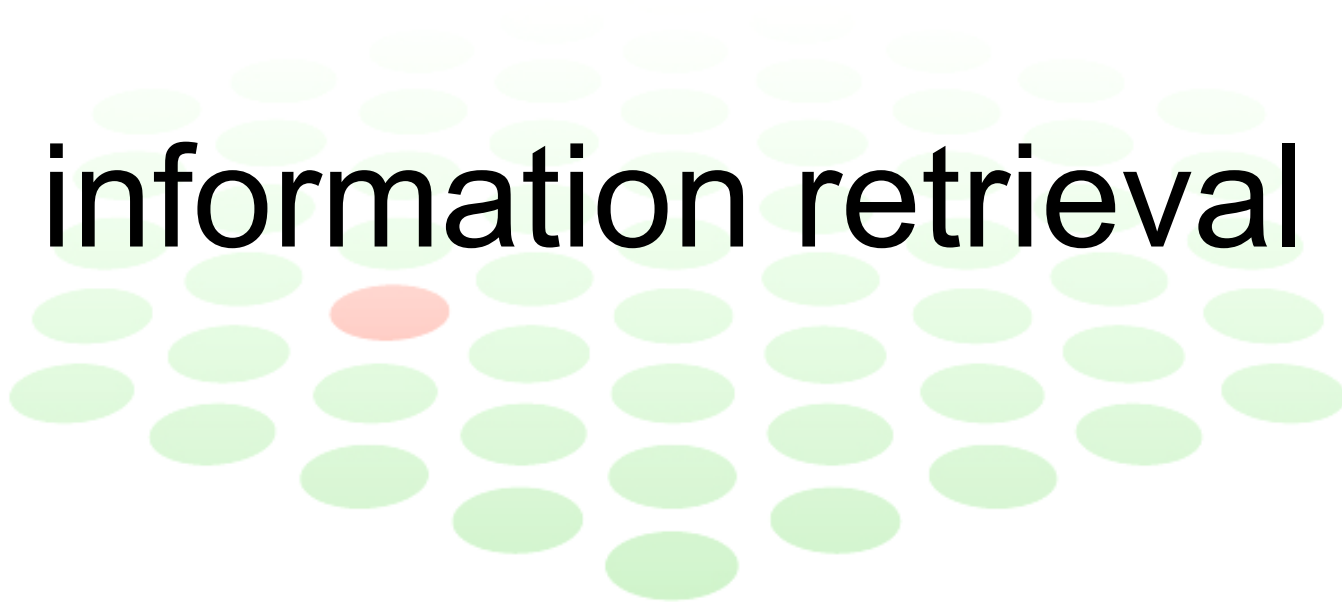
why literature mining?

A cluster of approximately 40 green circles arranged in a roughly hexagonal pattern. One circle, located on the left side of the cluster, is red. The word "MEDLINE" is written in black, bold, uppercase letters across the center of the cluster.

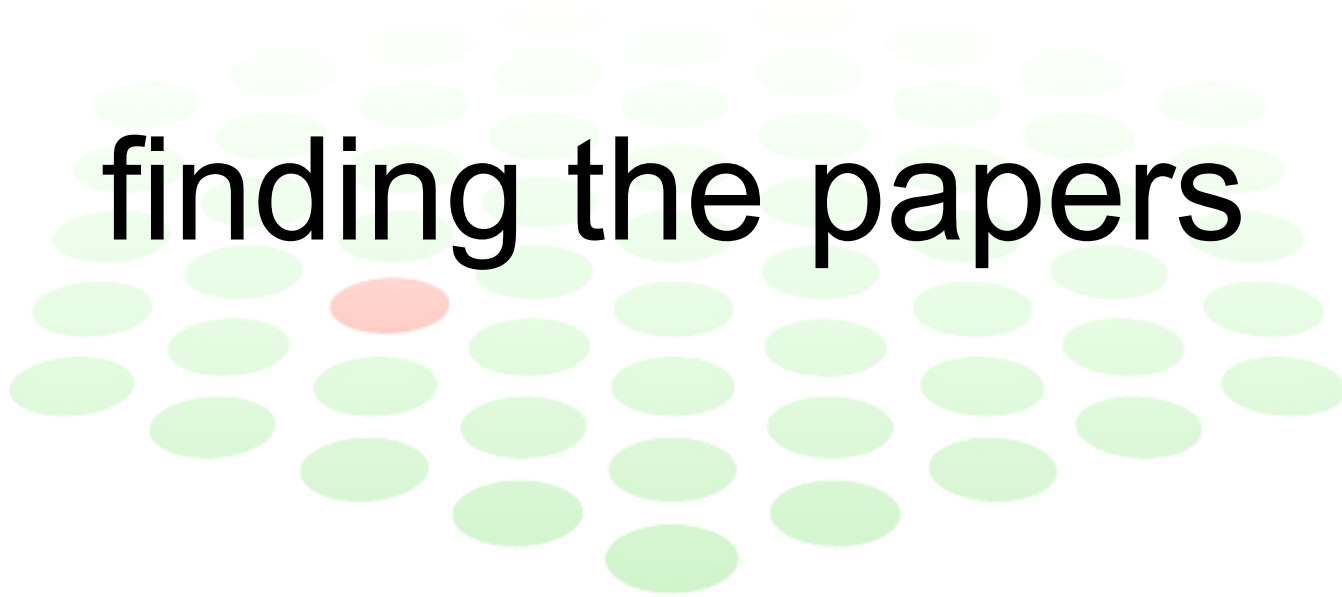
MEDLINE



information retrieval



finding the papers



About Entrez

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MeSH Database

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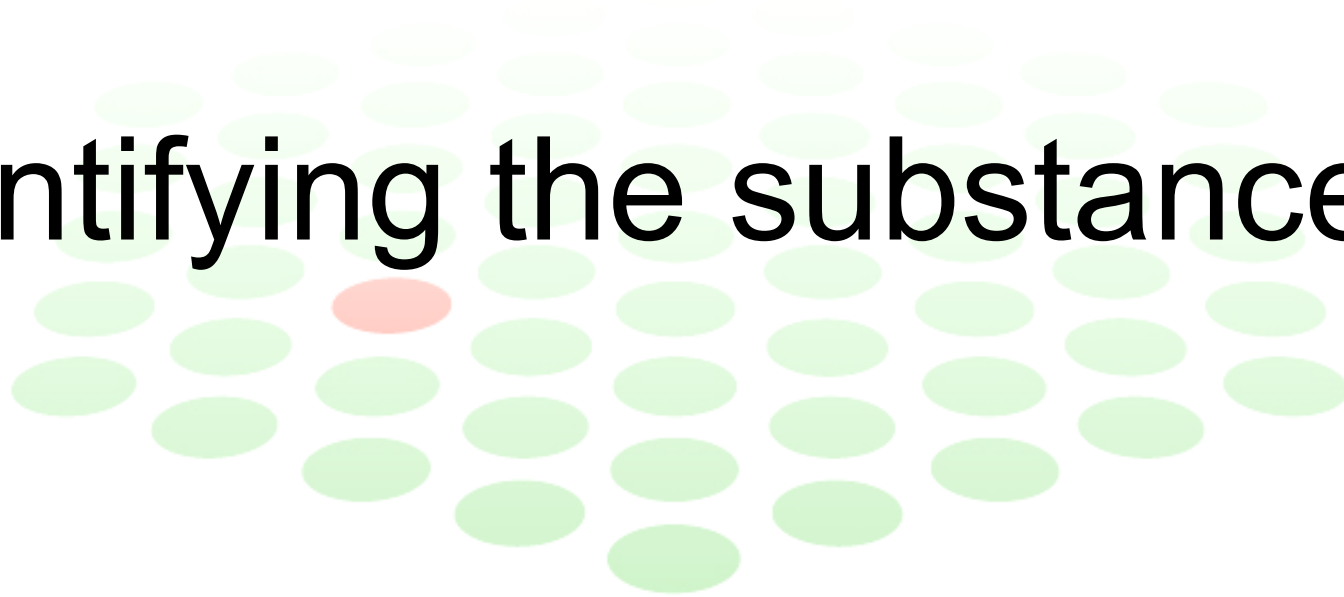
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Mitotic cyclin (Clb2)-bound Cdc28 (Cdk1 homolog) directly phosphorylated Swe1 and this modification served as a priming step to promote subsequent Cdc5-dependent Swe1 hyperphosphorylation and degradation



entity recognition

identifying the substance(s)



Mitotic cyclin (**Clb2**)-bound **Cdc28** (Cdk1 homolog) directly phosphorylated **Swe1** and this modification served as a priming step to promote subsequent **Cdc5**-dependent **Swe1** hyperphosphorylation and degradation

[SEARCH]

Symbol	Name	Synonyms	Organism
CDC28	Cell division control protein 28	CDK1, HSL5, SRM5, YBR1211, YBR160W	Saccharomyces cerevisiae

UniProt [P00546](#)
 IntAct [P00546](#)
 NCBI Gene [852457](#)
 NCBI RefSeq [NP_009718](#)
 NCBI Accession [CAA25065](#), [CAA56509](#), [CAA85119](#)

[Homologues of CDC28 ...](#) **new**

[Definitions for CDC28](#)  ...

[Enhanced PubMed/Google query ...](#) **new**

WARNING: Please keep in mind that gene detection is done automatically and can exhibit a certain error. [Read more.](#)

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Furthermore, SW14 associates with [CLB2](#) protein and is a substrate for the CLB2-associated **CDC28** kinase in vitro.



Furthermore, the [Cks1](#) protein was shown to be physically **associated** with active forms of the **Cdc28 protein kinase**.



The cyclin-dependent kinase **Cdc28p** **associates** with the cyclin [Clb2p](#) to induce mitosis in the yeast *Saccharomyces cerevisiae*.



We find that G1 arrest in the *cdc37-1* mutant is accompanied by a decrease in the **Cdc28** activity **associated** with the G1 **cyclin Cln2**.



We found that [Hct1](#) was **phosphorylated** in vivo at multiple CDK consensus sites during cell cycle stages when activity of the cyclin-dependent kinase **Cdc28** is high and APC activity is low.



It is likely, therefore, that [Cks1](#) mediates a more specialized **function** of the **Cdc28** kinase such as its ability to form specific multimeric complexes or to localize properly in cellular compartments.



[Cdc37](#) **promotes** the stability of protein kinases **Cdc28** and [Cak1](#).



In addition, [Cdc37](#) **promotes** the production of [Cak1](#), but not that of **Cdc28**, when coexpressed in insect cells.



The B-type **cyclins** [Clb5](#) and [Clb6](#) are the primary activators of the S phase **function** of the budding yeast CDK **Cdc28**.



All three [cak1](#) mutants displayed significant synthetic interactions with loss-of-**function** mutations in **CDC28** and [KIN28](#).



A decorative background consisting of a grid of circles. Most circles are light green, while one circle in the center-left area is a slightly different shade of green, possibly representing a selected or active state.

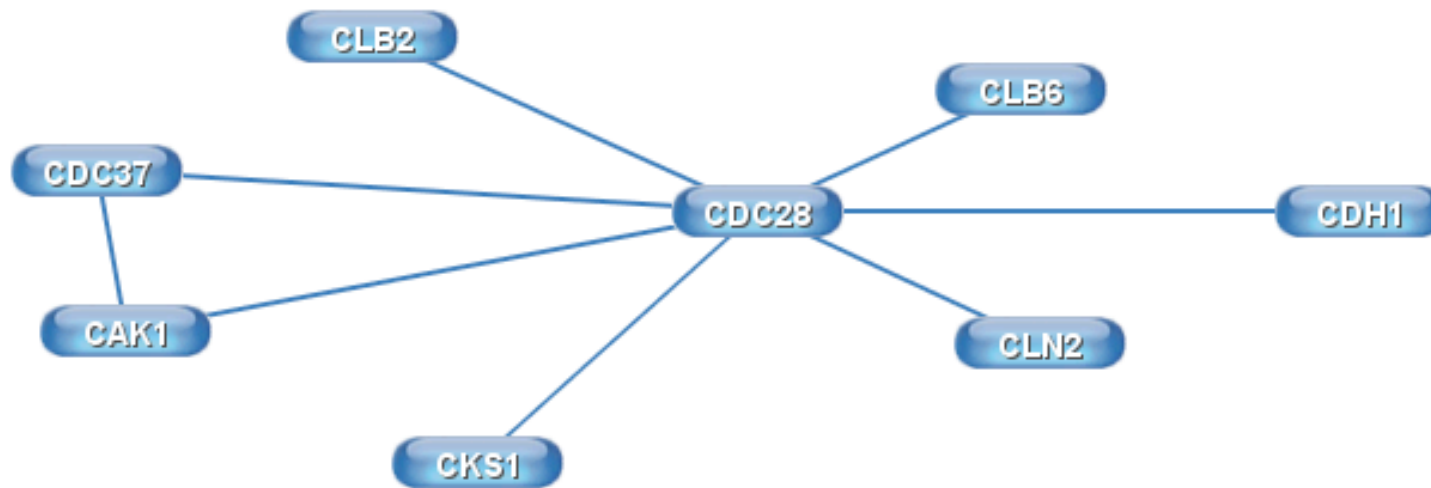
information extraction

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formalizing the facts

A cluster of approximately 40 light green circles arranged in a roughly circular pattern. One circle, located slightly to the left of the center, is a light red color. The text "co-mentioning" is written in a bold, black, sans-serif font, centered over the cluster of circles.

co-mentioning



[Redo graph layout]

The B-type **cyclins** [Clb5 \[CLB5\]](#) and [Clb6 \[CLB6\]](#) are the primary activators of the S phase **function** of the budding yeast CDK [Cdc28 \[CDC28\]](#).

Furthermore, SW14 associates with [CLB2 \[CLB2\]](#) protein and is a substrate for the CLB2-associated [CDC28 \[CDC28\]](#) kinase in vitro.

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In addition, [Cdc37 \[CDC37\]](#) **promotes** the production of [Cak1 \[CAK1\]](#), but not that of [Cdc28 \[CDC28\]](#), when coexpressed in insect cells.

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[Cdc37 \[CDC37\]](#) **promotes** the stability of protein kinases [Cdc28 \[CDC28\]](#) and [Cak1 \[CAK1\]](#).

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NLP

Natural Language Processing

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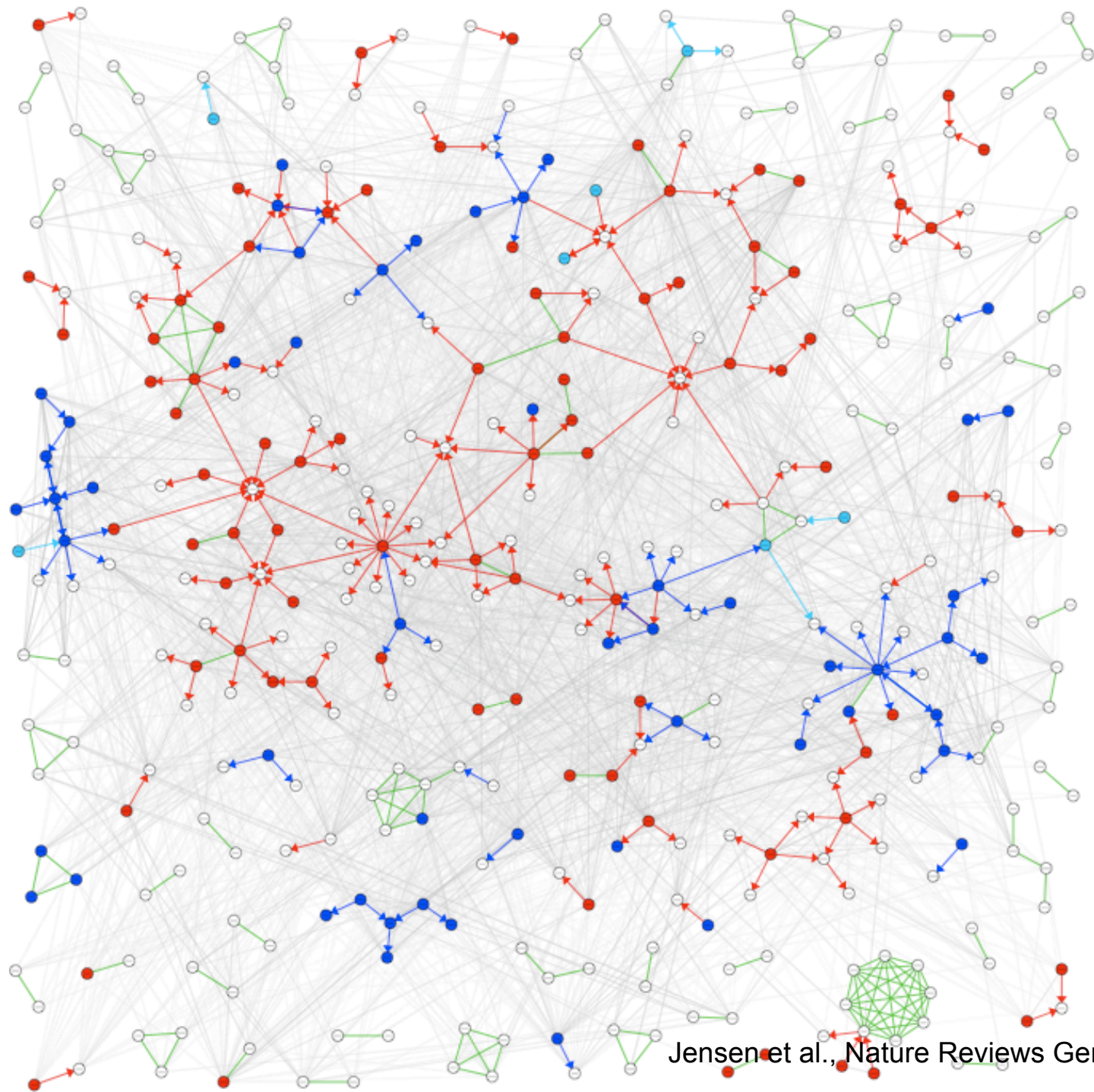
Gene and protein names

Cue words for entity recognition

Verbs for relation extraction

[nxgene The GAL4 gene]

[nxexpr The expression of
[nxgene the cytochrome genes
[nxpg CYC1 and CYC7]]]
is controlled by
[nxpg HAP1]



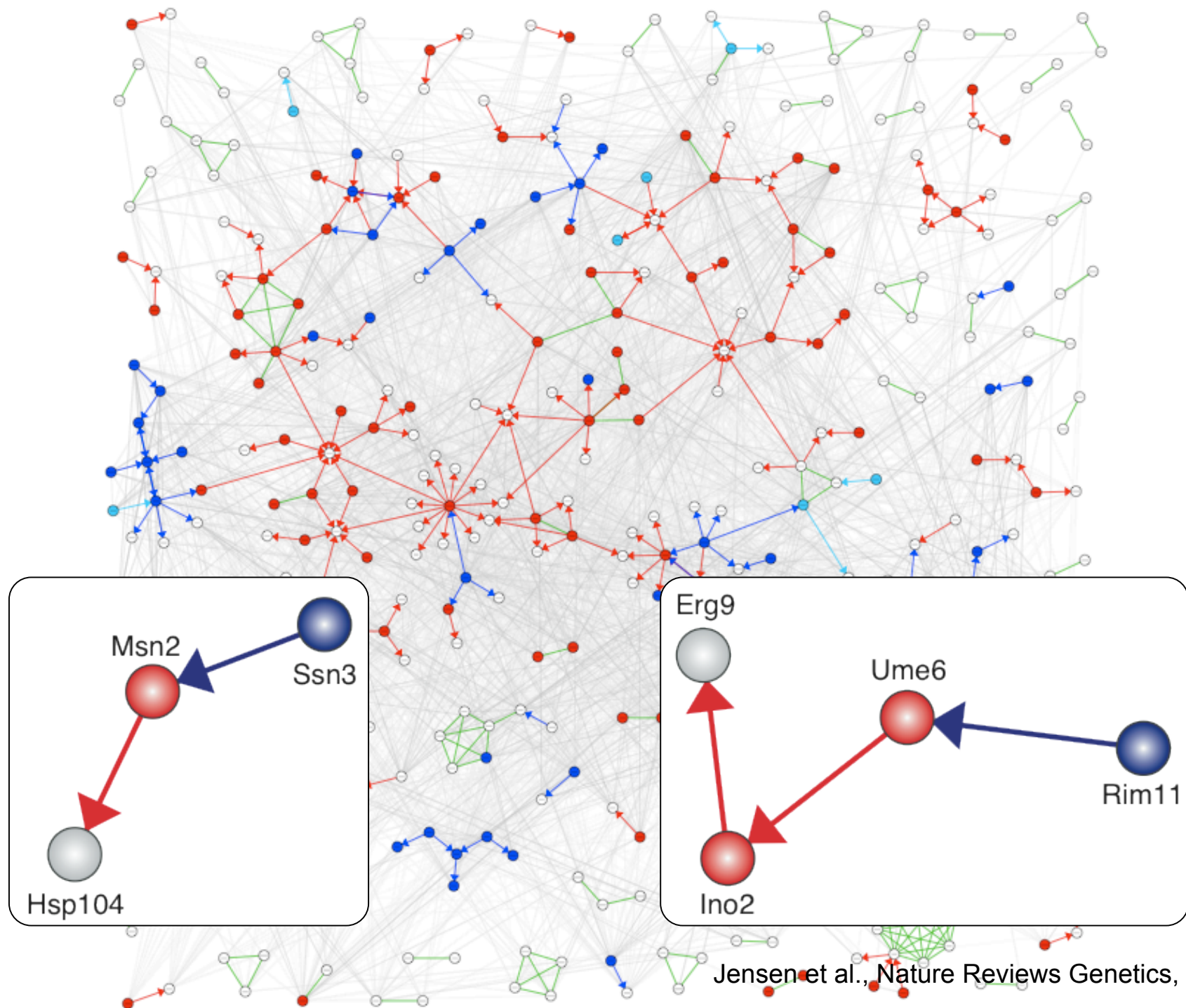
Jensen et al., Nature Reviews Genetics, 2006

A cluster of approximately 40 light green circles arranged in a roughly circular pattern. One circle, located slightly to the left of the center, is a distinct reddish-pink color, standing out from the others. The text "new discoveries" is overlaid in the center of this cluster.

new discoveries



text mining



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integration of text and data

A decorative background consisting of a grid of circles. Most circles are light green, but one circle in the center-left area is a light red color.

open access databases

STRING - Search Tool for the Retrieval of Interacting Genes/Proteins

Enter your gene/protein of interest ...

identifier: e.g. 'trpB', 'ANP1_YEAST', ...
you may also upload a [list](#)

alternatively, paste an amino-acid sequence:

interactors wanted:

GO !

Reset

COGs

☒ Proteins

What it does ...

STRING is a database of known and predicted protein-protein interactions.

The interactions include direct (physical) and indirect (functional) associations; they are derived from four sources:

Genomic
Context



High-throughput
Experiments



(Conserved)
Coexpression



Previous
Knowledge



STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently contains 736429 proteins in 179 species.

References / Info ...

STRING uses orthology information from the excellent [COG database](#) (Ref).

Up-to-date genomes and proteins are maintained at [SWISSPROT](#) and [ENSEMBL](#)

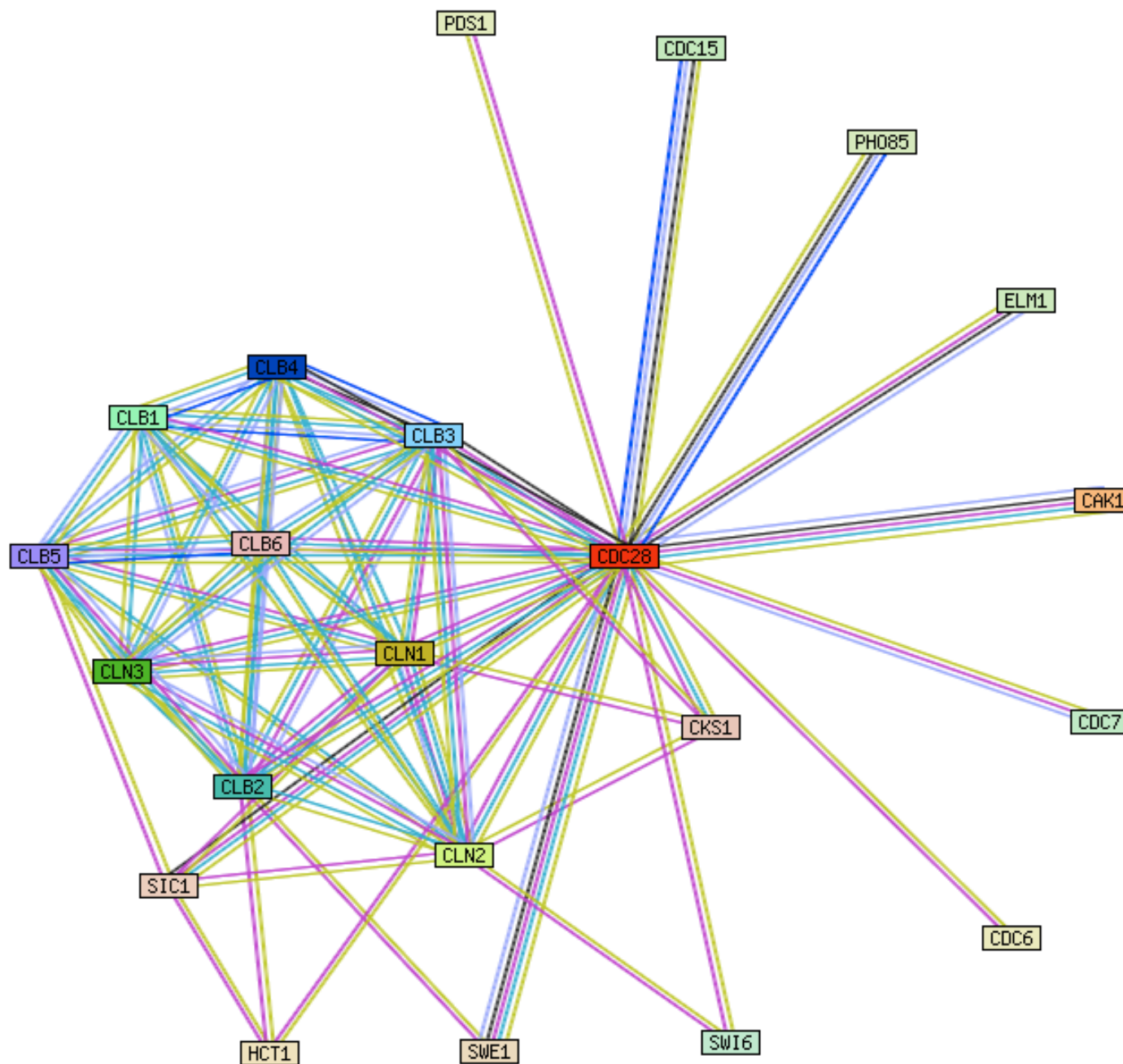
STRING references: [von Mering et.al. 2005](#) / [von Mering et.al. 2003](#) / [Snel et.al. 2000](#).

Miscellaneous: [Access Statistics](#), [Robot Access Guide](#), [Supported Browsers](#).

What's New? You are looking at release 6.2 of STRING - latest additions are the 'HPRD' and 'Reactome' databases.

Previous Releases: Trying to reproduce an earlier finding? Confused? Try our old releases: [version 6.0](#), [version 5.1](#)

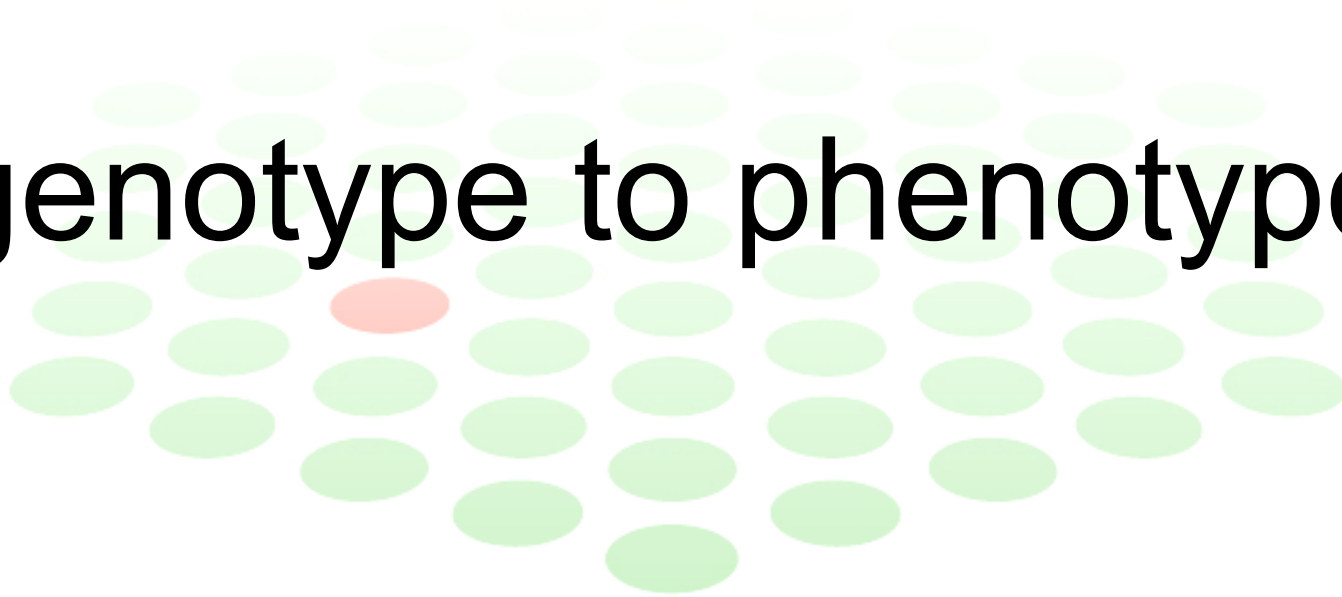


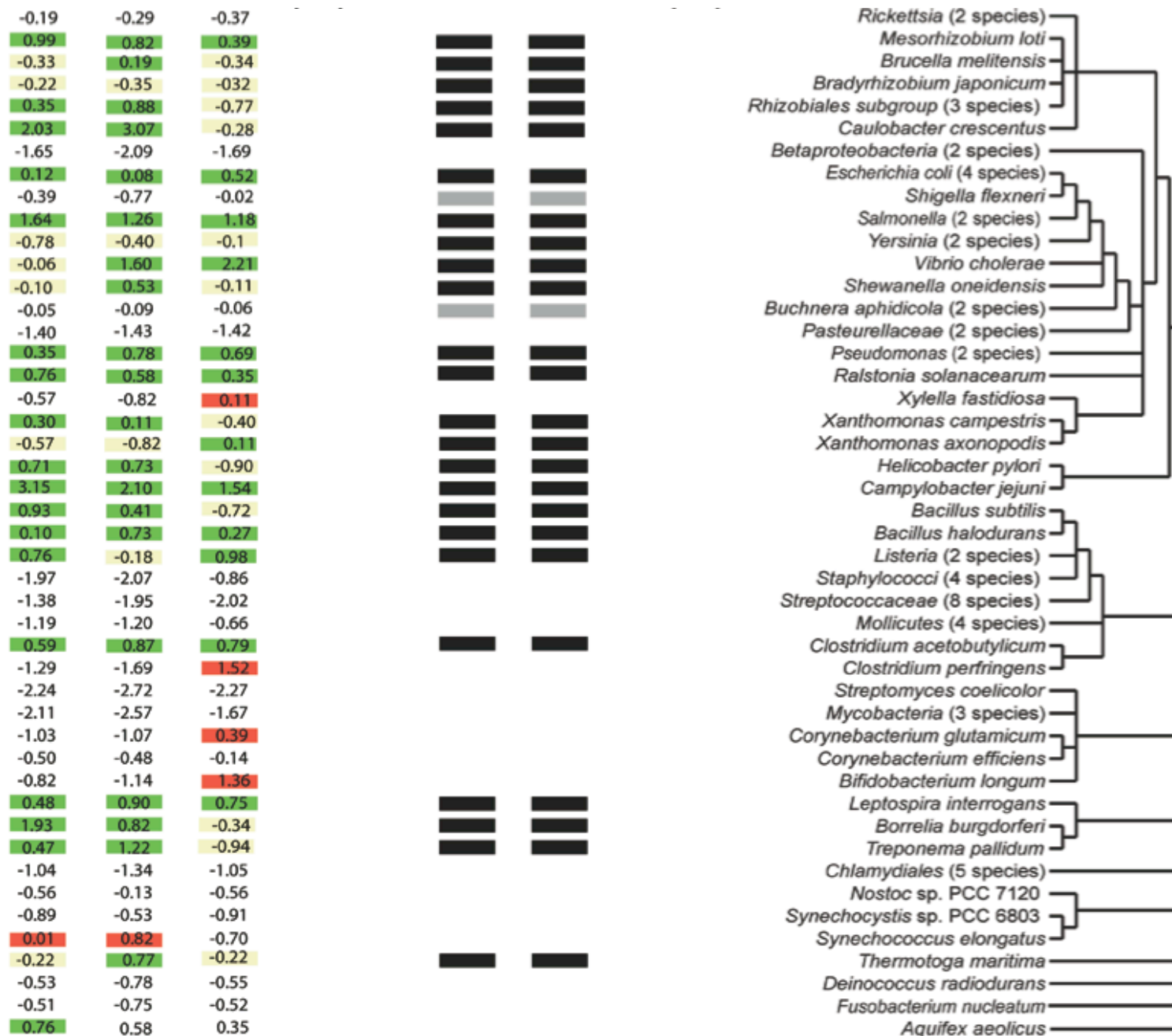


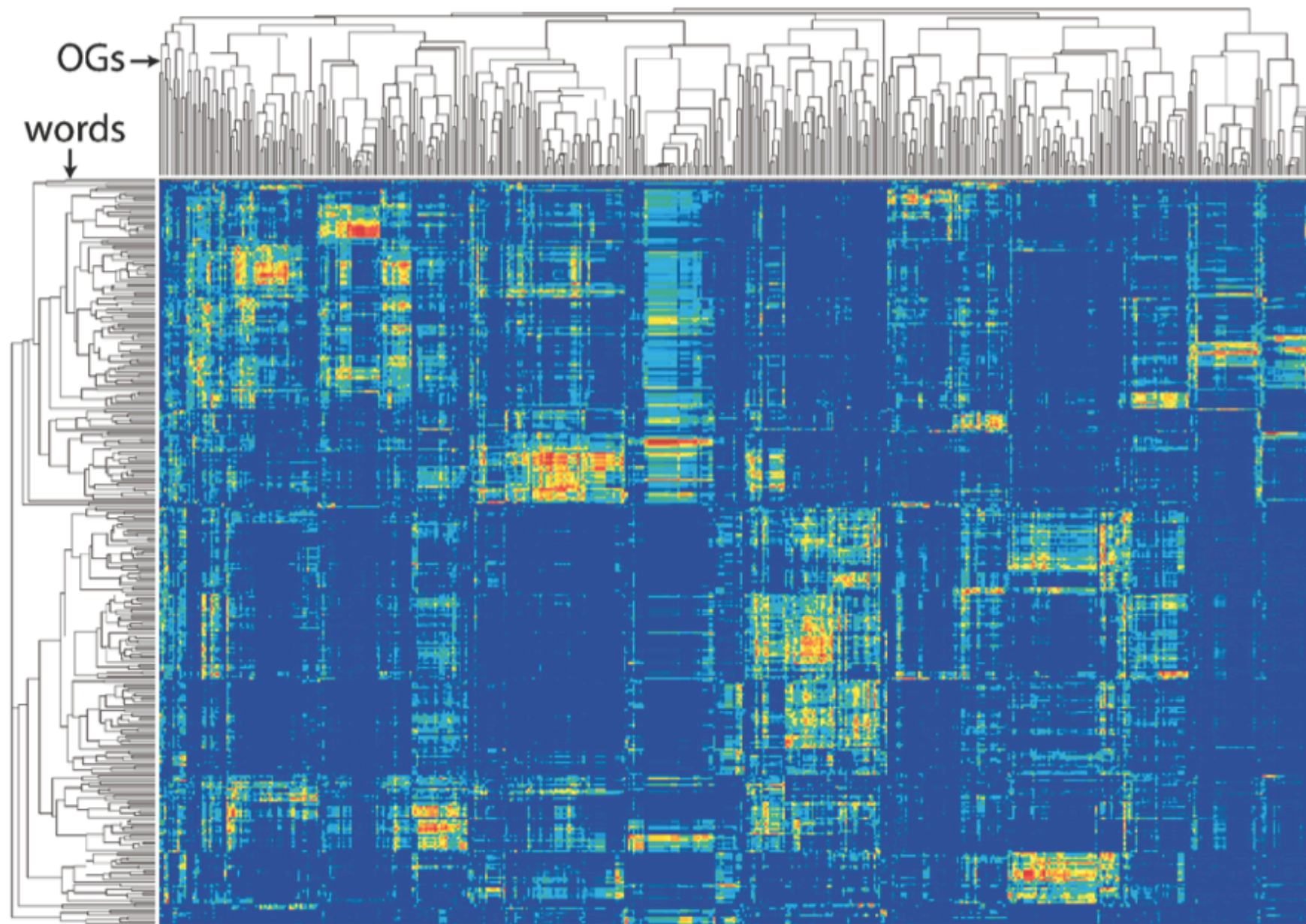
A cluster of approximately 40 green circles arranged in a roughly hexagonal pattern. One circle, located slightly to the left of the center, is red. The text "network mining" is overlaid on the center of the green cluster.

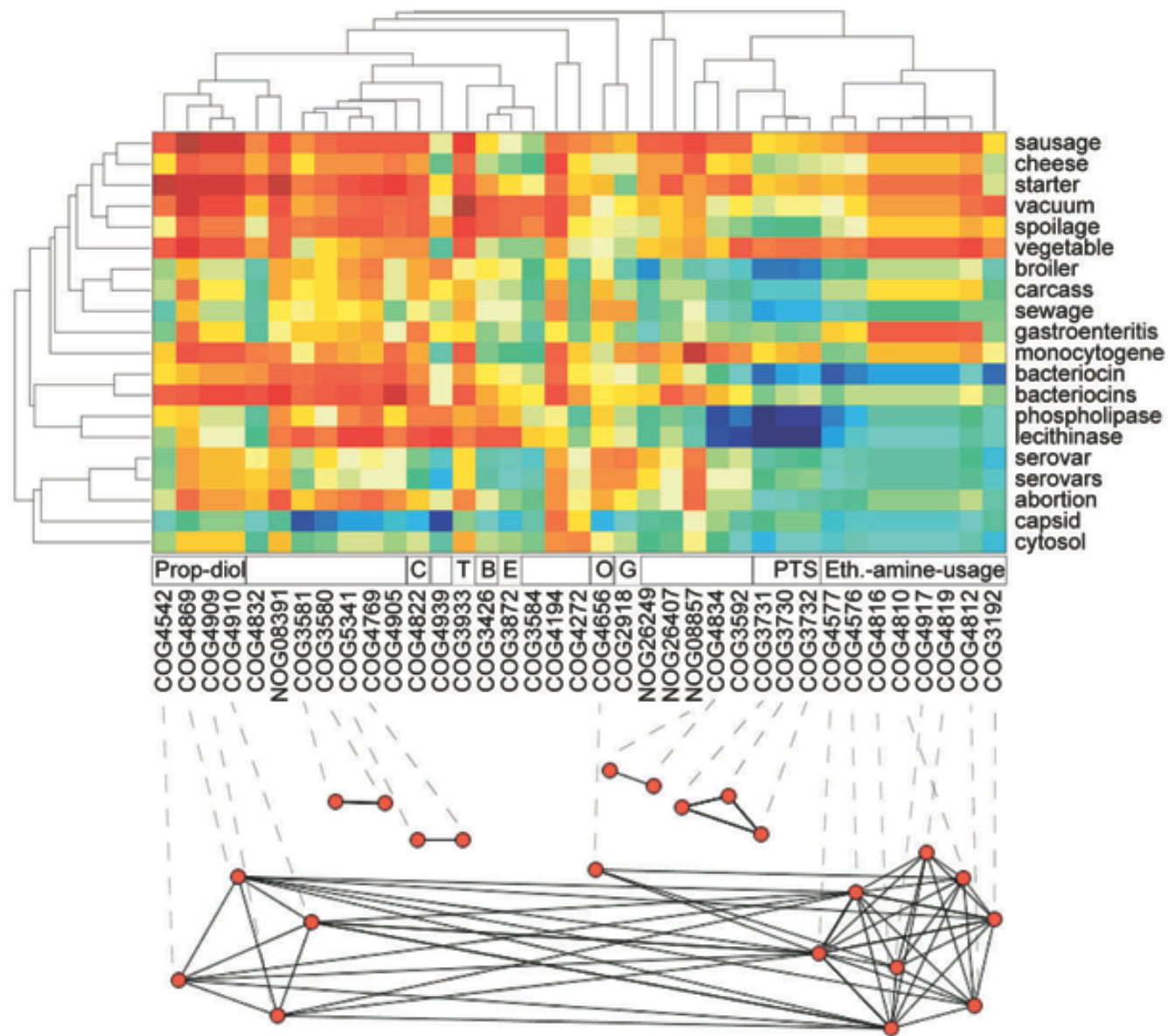
network mining

genotype to phenotype



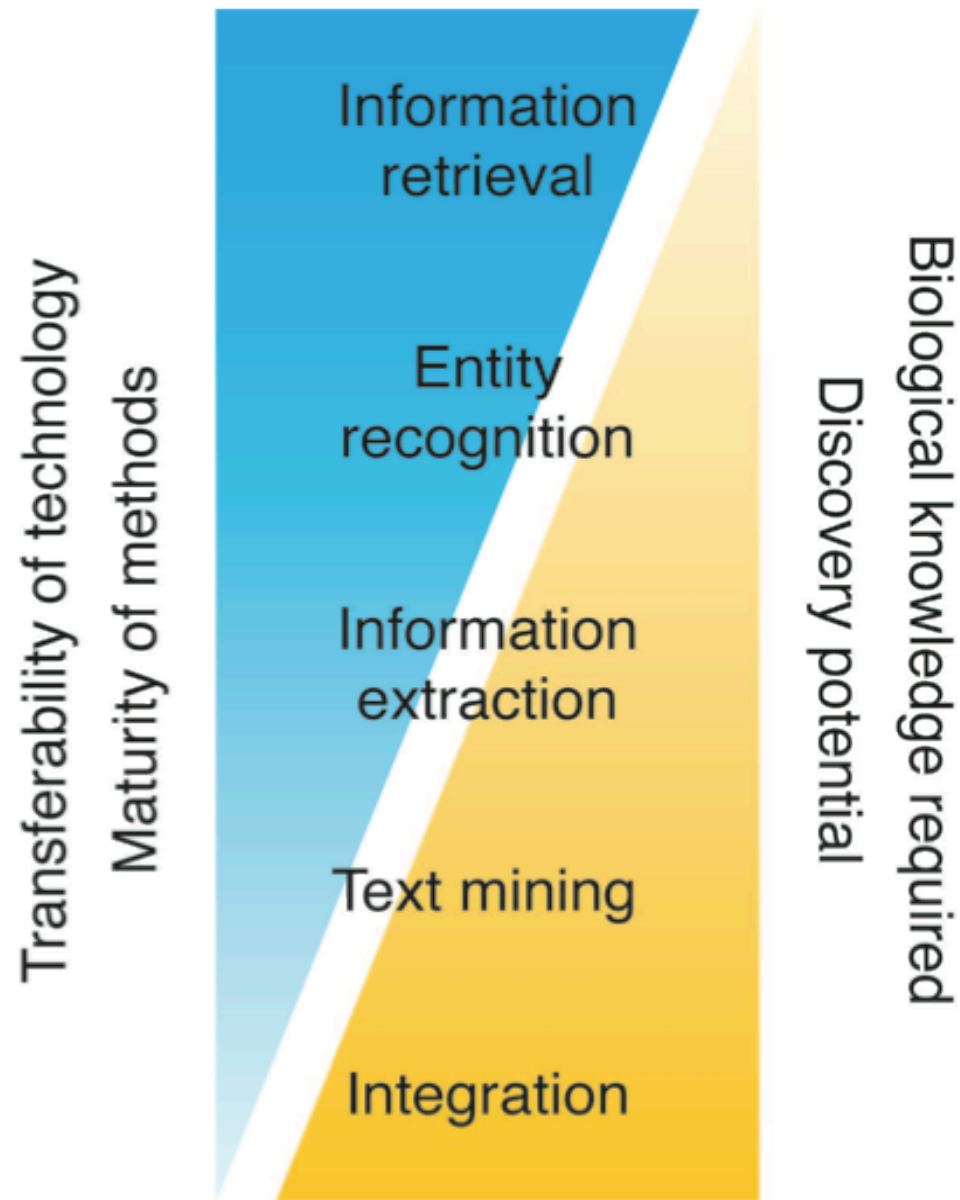






where are we now?





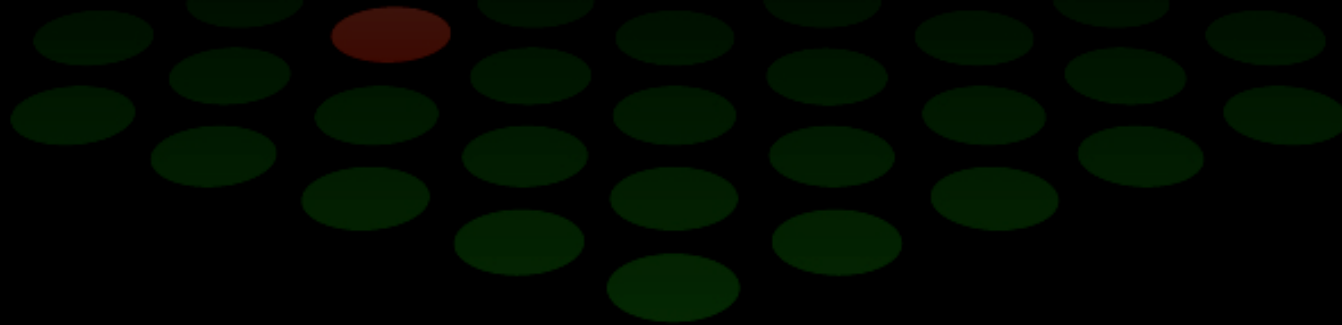
A grid of dark green circles is centered on the page. One circle, located in the middle-left area of the grid, is colored red. The word "abstracts" is written in white text across the center of the grid.

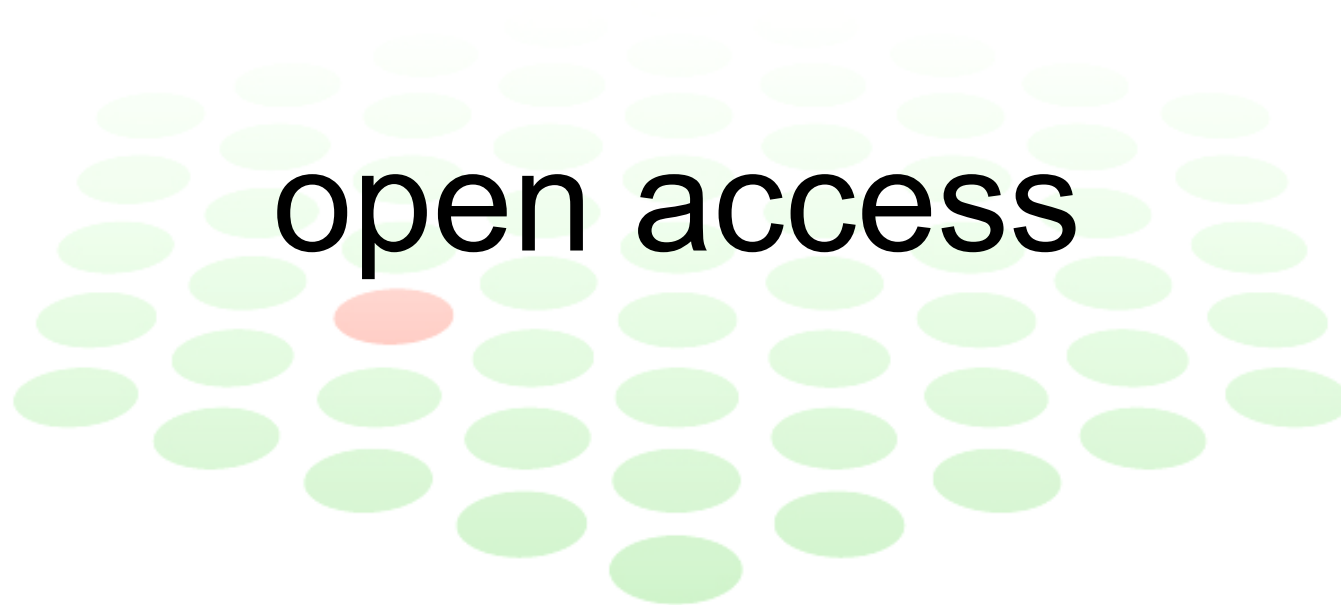
abstracts



complete papers

restricted access





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the tools are there

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now we need the text!

Acknowledgments

Work done in collaboration with

Peer Bork

Jasmin Saric

Rossitza Ouzounova

Michael Kuhn

Isabel Rojas

Presentation style stolen from

Lawrence Lessig

Dick Clarence Hardt

Thank you!

