# Pypath & Omnipath: integrate, analyze and extract signaling networks from literature curated resources

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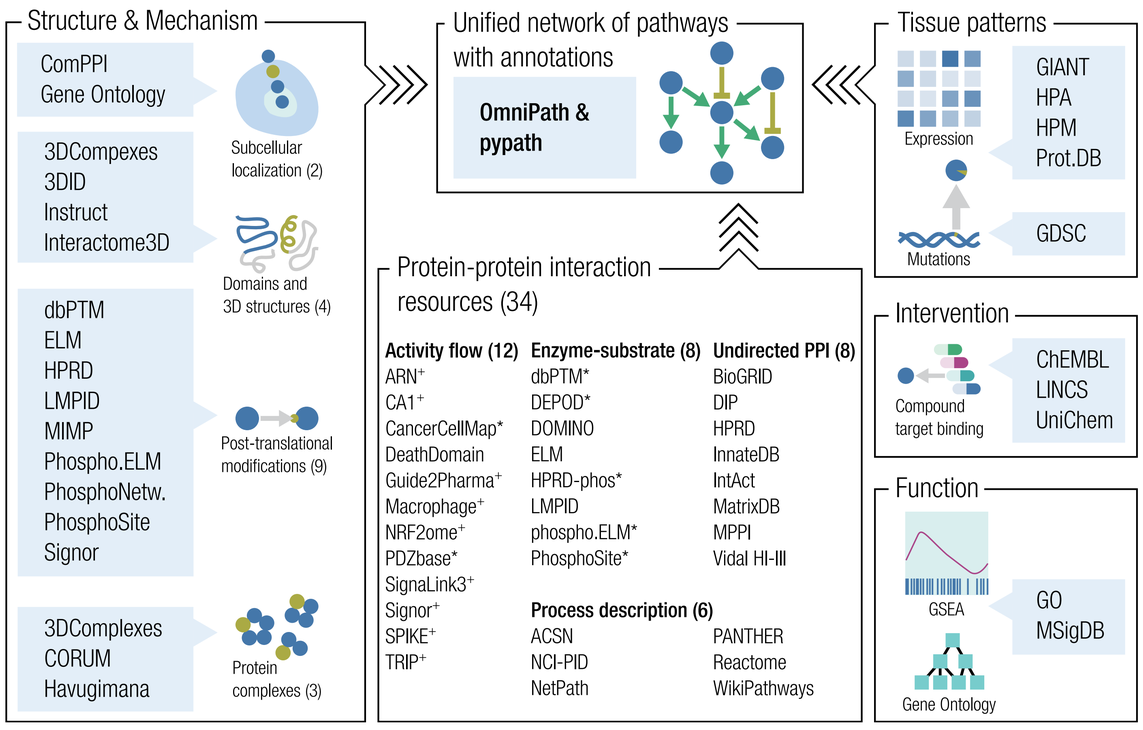
## Motivation

Literature curated information on signaling pathways is an extremely valuable resource for researchers studying different biological questions. These resources can help in the generation of hypothesis to explain experimental data and they provide support for the building of computational models.

The existing curated information is currently distributed throughout a large number of online resources. Gathering and retrieving this information in a consistent manner is a non-trivial endeavour.

Omnipath and Pypath greatly facilitate the integration and extraction of biological prior knowledge for analysis and model building, and they can be incorporated into wider data processing pipelines.




## Available at http://omnipathdb.org

## Quick start

```
import pypath
pa = pypath.main.PyPath()
pa.init_network()
```

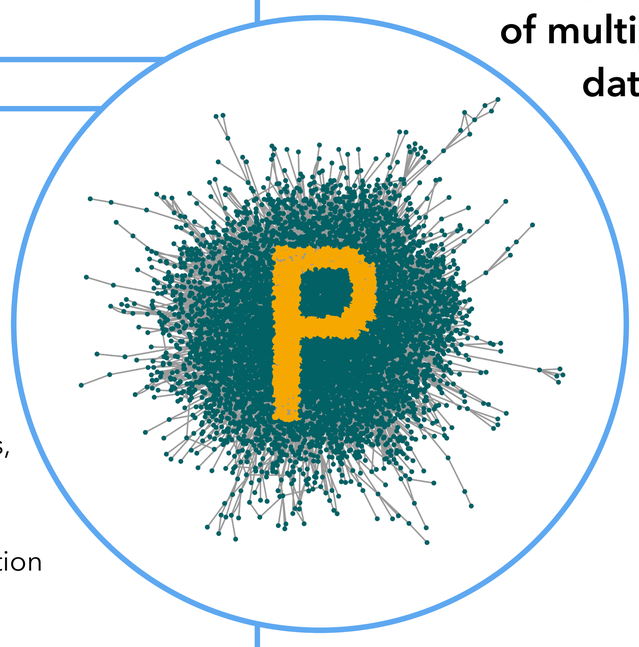
## Features

Pypath is the Python package that gives full access to the Omnipath database:

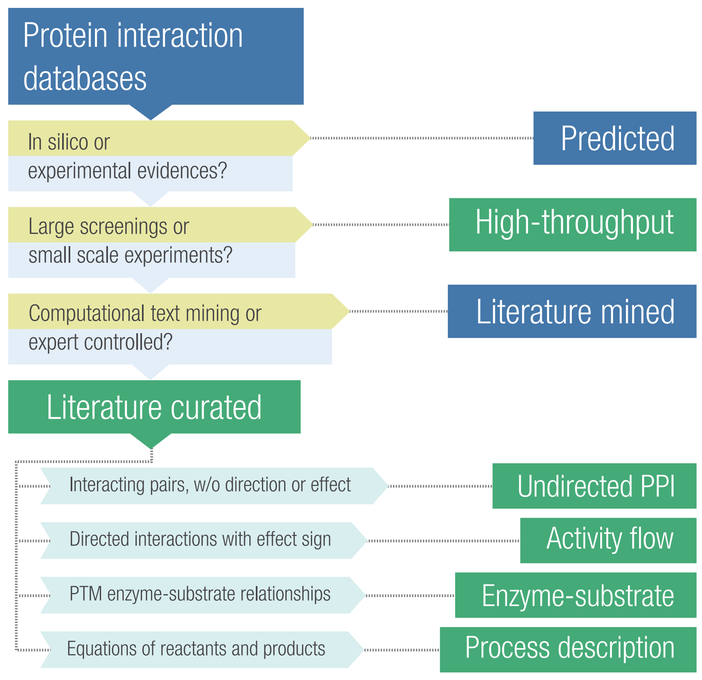
- Easy protein ID conversion to gene IDs
- Ready integration of dozens of bioinformatics resources directly from the original source
- Incorporate new databases or your own networks and compare information between different databases
- Efficient handling of annotations: sources, literature references, directions, effect signs (stimulation/inhibition) and enzyme-substrate interactions
- Extract information on pathways, protein complexes, transcription factors and more
- Plot networks

The network is represented as an *igraph* object, giving access to plenty of graph analysis methods with excellent computational performance:

- complex node/edge queries
- shortest path searches
- statistical graph analysis (centrality, betweenness, community detection, and more)




**Curated integration of multiple databases**




## Usage in PrECISE

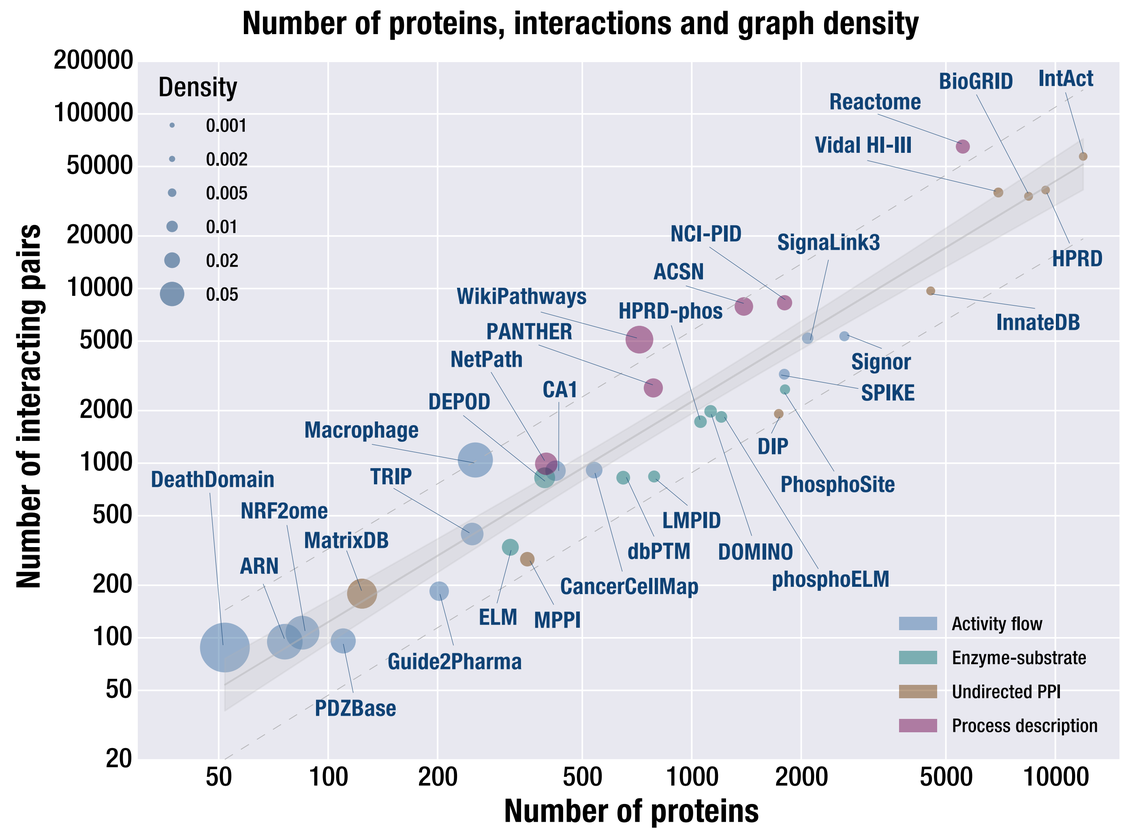
PrECISE (Personalized Engine for Cancer Integrative Study and Evaluation) is a European H2020 project focused on prostate cancer, an international collaboration that aims to translate into clinical advances many of the technical and methodological developments achieved during the last years.

PrECISE

We will build interaction networks for increasing our understanding of prostate cancer tumours. The wealth of data generated will be encoded into mathematical models, both qualitative and quantitative.

The incorporation of prior biological knowledge into these models is eased by the usage of Omnipath and Pypath. Among other things, Omnipath helps in the definition of logic models that can later be simulated and used to make predictions about cell signalling pathways relevant to the biology of prostate cancer.

**Number of proteins, interactions and graph density**




## References

D Turei, T Korcsmaros and J Saez-Rodriguez: Guidelines for literature curated signaling pathway resources (under revision)

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