# **CYC 2008 and CORUM Information**

**CYC2008**

**CYC2008** provides an **up-to-date reference set of yeast protein complexes** for both experimental biologists who work on yeast protein complexes and **computational biologists** who are interested in **predicting protein-protein interactions and protein complexes in yeast**.

**CORUM**

The CORUM database provides a resource of **manually annotated protein complexes** from **mammalian** **organisms**. Annotation includes **protein complex function, localization, subunit composition, literature references and more.** All information is obtained from individual experiments published in scientific articles, data from high-throughput experiments is excluded.

## **Potential Candidate Databases for Protein-Protein Interaction Data**

* **BioGRID** – mentioned in the tutor meeting and very popularly used database. **Mo** already downloaded **ALL** **human interaction** and **yeast interaction data (RAW) from BioGRID.   
  This might not be the specific subset of CYC2008/CORUM list of complexes we were expected to operate with.**
* **STRING** – Another very popular protein interaction network database used by researchers.
* **MIPS** – “In deriving such networks for the **yeast Saccharomyces cerevisiae** the most widely used ‘**gold standard’** **dataset** has been the manually curated protein complexes catalogued in the **Munich Information Center for Protein Sequences (MIPS) database.**” [2] **CYC2008 list of complexes were downloaded from a MIPS database.**
* **E2D (I believe this is the name)** – Large amount of **annotated proteins** here are from **prediction methods** so making predictions based on other prediction is **not a very wise strategy**. Not recommended to use this database.

**Downloads**

Downloaded the list of **all complexes** in **CYC 2008** (408 heteromeric protein complexes in **S. cerevisiae**) and **CORUM** (2837 protein complexes, 64% **human**).

# **References**

1. <http://wodaklab.org/cyc2008/> - **CYC2008** explanation, **MIPS** and collection of 408 heteromeric **protein complexes** where we **downloaded** from
2. [**https://academic.oup.com/nar/article/37/3/825/1073031**](https://academic.oup.com/nar/article/37/3/825/1073031) **- CYC 2008 complexes** in yeast **research paper** by Yu et al. (Pu, S., Wong, J., Turner, B., Cho, E. and Wodak, S. (2008). Up-to-date catalogues of yeast protein complexes. Nucleic Acids Research, 37(3), pp.825-831.)
3. <https://books.google.co.uk/books?id=tA0mDwAAQBAJ&pg=PA129&lpg=PA129&dq=yeast+cyc2008+string&source=bl&ots=yPgGE4PagL&sig=0_5mmJ3XIIZe4pFRNQKpSOVtuG8&hl=en&sa=X&ved=0ahUKEwiB05bA9-jYAhXhBcAKHZiJAEUQ6AEIOjAE#v=onepage&q=yeast%20cyc2008%20string&f=false> – **Book** on **Computational Prediction of Protein Complexes from Proteins Interaction Networks**, had sentence on **CORUM in humans and CYC 2008 in yeast.** (Srihari, S., Yong, C. and Wong, L. (n.d.). Computational prediction of protein complexes from protein interaction networks.)
4. <http://mips.helmholtz-muenchen.de/corum/> - CORUM data from which we downloaded list of all protein complexes.
5. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2238909/> **- CORUM: the comprehensive resource of mammalian protein complexes, research paper.**(Ruepp, A., Waegele, B., Lechner, M., Brauner, B., Dunger-Kaltenbach, I., Fobo, G., Frishman, G., Montrone, C. and Mewes, H. (2009). CORUM: the comprehensive resource of mammalian protein complexes—2009. Nucleic Acids Research, 38(suppl\_1), pp.D497-D501.)