



Integration of Macromolecular Complex Data into the *Saccharomyces* Genome Database



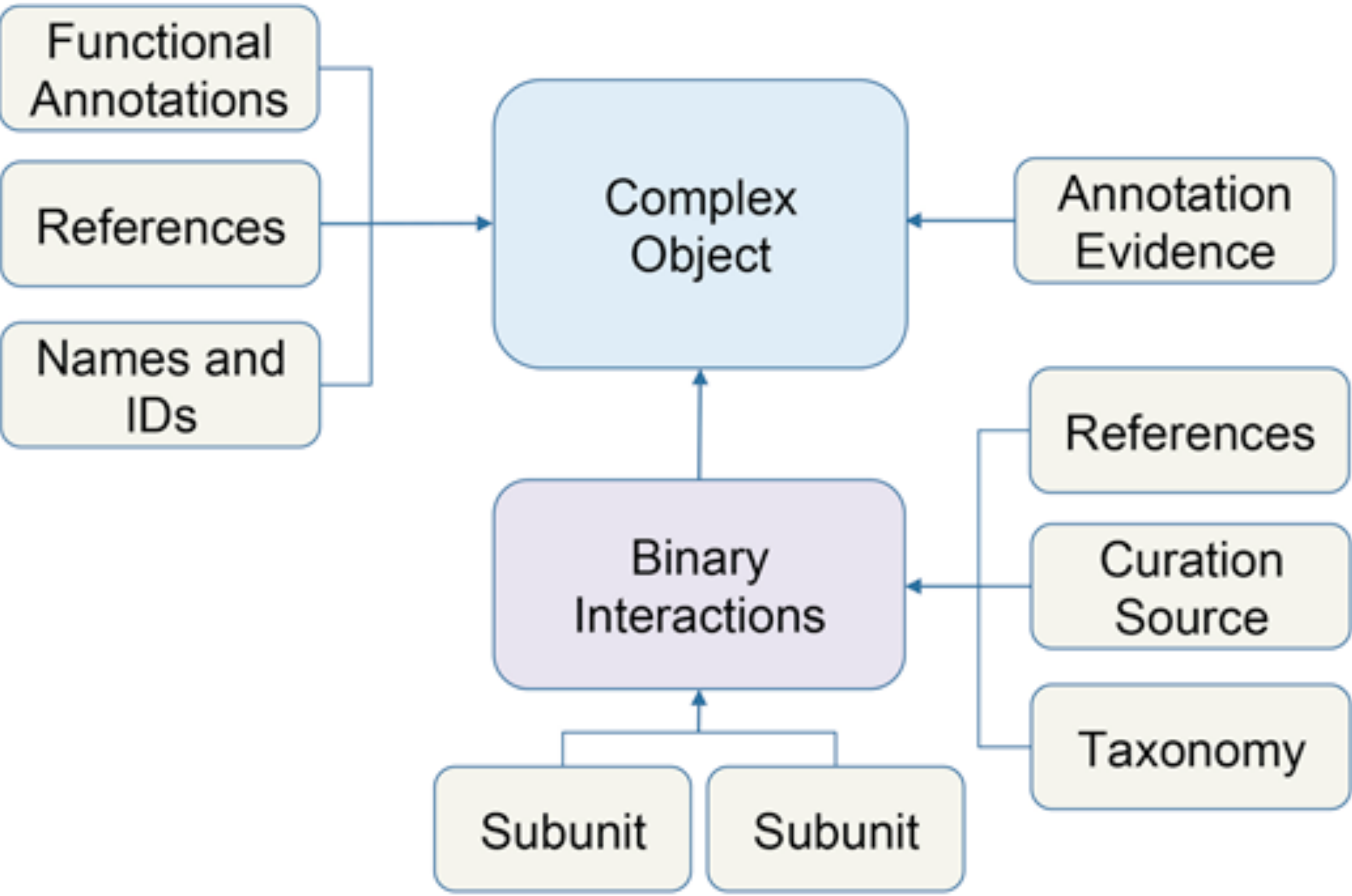
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Proteins seldom function individually. Instead, they interact with other proteins or nucleic acids to form stable macromolecular complexes that play key roles in important cellular processes and pathways. One of the goals of *Saccharomyces* Genome Database (SGD; www.yeastgenome.org) is to provide a complete picture of budding yeast biological processes. To this end, we have collaborated with the Molecular Interactions team that provides the Complex Portal database at EMBL-EBI to manually curate the complete yeast complexome. These data, from a total of 589 complexes, were previously available only in SGD's YeastMine data warehouse (yeastmine.yeastgenome.org) and the Complex Portal (www.ebi.ac.uk/complexportal). We have now incorporated these macromolecular complex data into the SGD core database and designed complex-specific reports to make these data easily available to researchers. These web pages contain referenced summaries focused on the composition and function of individual complexes. In addition, detailed information about how subunits interact within the complex, their stoichiometry, and the physical structure are displayed when such information is available. Finally, we generate network diagrams displaying subunits and Gene Ontology (GO) annotations that are shared between complexes. Information on macromolecular complexes will continue to be updated in collaboration with the Complex Portal team and curated as more data become available. SGD is funded by NIH NHGRI [U41HG001315].

Macromolecular Complex Data



Complex Pages

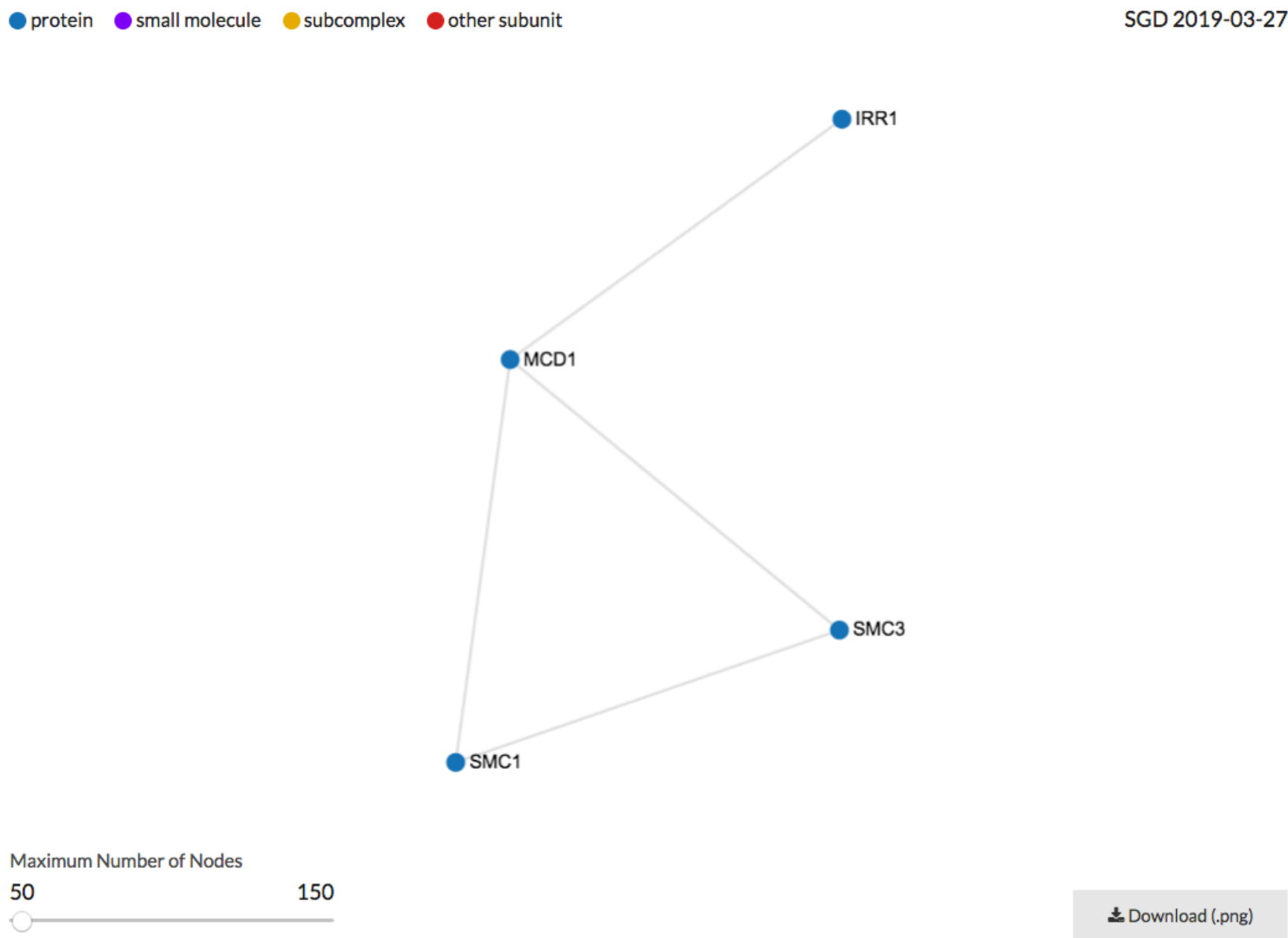
Complex: Nuclear mitotic cohesin complex

Curated by: IntAct
ComplexAc: CPX-1867
Systematic Name: IRR1:MCD1:SMC1:SMC3
Aliases: Cohesin complex

Required for sister chromatid cohesion during cell division, which enables cells to attach sister kinetochores to microtubules with opposing polarity (bi-orientation) and subsequently resists the tendency of these microtubules to pull chromatids toward opposite spindle poles. Before the commencement of replication, the cohesin complex (CPX-1408) is loaded onto DNA. The arms of the SMC1/3 molecules embrace the DNA, thereby forming a ring of approx. 40 nm diameter. The head domains of SMC1 and SMC3 are locked together by Scc1. Cohesion might be generated as the replication fork passes through the ring, entrapping both sister chromatids inside. At the metaphase to anaphase transition, Scc1 is cleaved by separase, thereby opening the lock of the SMC1/3 head domains. The ring opens and sister chromatids can be pulled to opposite spindle poles.

SMC1 and SMC3 form a heterodimer with intramolecular coiled coils. Scc1 bridges the head domains of SMC1 and SMC3 and links them to Scc3.

Complex Diagram



PDB Structure



Subunits

| Subunit | Description |
|---------|--|
| IRR1 | Subunit of the cohesin complex |
| MCD1 | Essential alpha-kleisin subunit of the cohesin complex |
| SMC1 | Subunit of the multiprotein cohesin complex |
| SMC3 | Subunit of the multiprotein cohesin complex |

Gene Ontology

Molecular Function: • chromatin binding
Biological Process: • establishment of mitotic sister chromatid cohesion
Cellular Component: • nuclear mitotic cohesin complex

Function

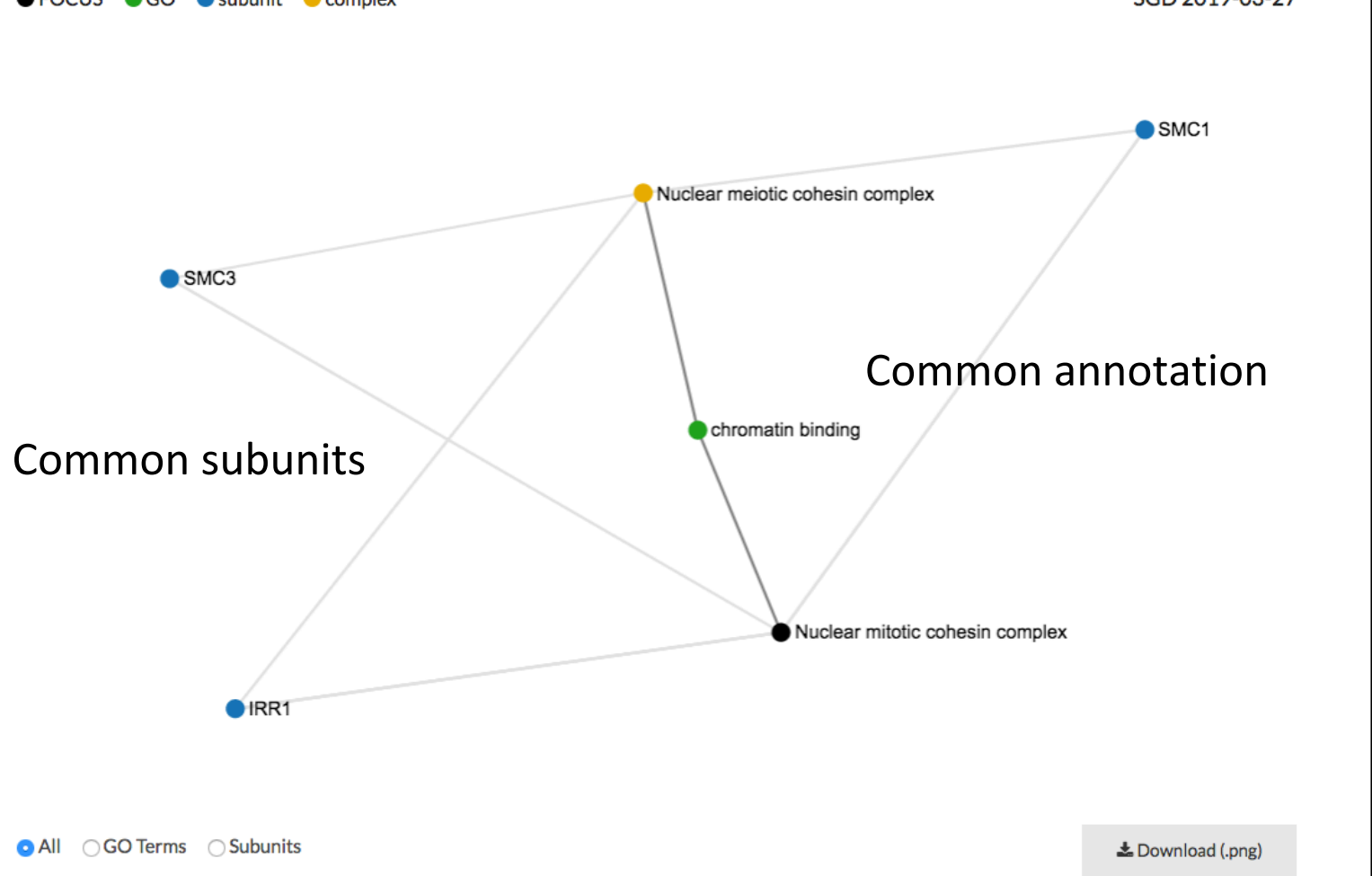
Summary information

Composition and Structure

Related Complexes

Finding Complex Data

Shared Annotations



References

Wong RW (2010) An update on cohesin function as a 'molecular glue' on chromosomes and spindles. Cell Cycle 9(9): 1754-8. PMID: 2054296



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