

The (new) MINT Database.

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Introduction

Scientists recognize that a complete description of cell physiology requires an understanding of the “global” protein interaction network. Thus, a database that collects this information, which is presently dispersed in the scientific literature (or accumulated by high throughput experiments), is an essential post genomic tool. MINT was conceived a couple of years ago, as a collaborative effort between the group of Molecular Genetics and the students of the PhD program of Molecular and Cellular Biology of the University of Rome Tor Vergata, MINT is a relational database designed to store data on functional interactions between proteins, and aims at being exhaustive in the description of the interaction including information, whenever available, about kinetic and binding constants and about the domains participating in the interaction. Presently MINT focuses on experimentally verified interactions extracted from the scientific literature by curators, with special emphasis on mammalian organisms. The MINT protein interaction database offers to the scientific community, a unique bioinformatic tool to design and interpret their experiments.

Recent developments

Two years after its conception MINT[1], with its 2500 curated mammalian interactions, although still largely incomplete, contains the largest publicly available dataset of curated entries. The database can be freely accessed at <http://mint.bio.uniroma2.it/mint>. Scientists that require assistance in the use of this informatic tool, or want to make suggestions, can contact us at cesareni@uniroma2.it.

In the past year we have worked in several directions to improve the service for the scientific community and to integrate our effort into equivalent efforts that are carried out in the world [2].

- We have added more than 700 new curated interactions and we have uploaded more than 30000 interactions obtained by high-throughput experiments in model organisms.
- We have improved the structure of MINT and its graphical interface to meet the user’s requirements. In this respect we have linked the database to the OMIM database.
- We have enhanced the capability of the MINT viewer applet for visualization of the interaction network. Namely the user can now freely edit the network by adding and removing interactions.
- We have actively participated to the Protein Standard Initiative aimed at a collaborative effort for interaction data exchange[3].
- We have developed appropriate software tools to facilitate the exchange, in XML format, of the interaction information between the major public databases.
- We have enhanced the search and analysis tools available from the WEB site.

- We have developed HomoMINT an inferred interaction network obtained by extending to the human orthologs the interactions observed in model systems

Finally all the data stored in MINT can be freely downloaded from the WEB site in the PSI format.

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References

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