

MIPS DATABASE:

1. The MIPS mammalian protein-protein interaction database (MPPI) is a new resource of high-quality experimental protein interaction data in mammals.
2. Protein-protein interactions (PPI) determine biological processes at many levels of cellular complexity from basic metabolism to cell differentiation. Their importance is reflected by the number of protein interaction experiments described in the life science literature and the increasing interest in high-throughput techniques such as yeast two-hybrid and large-scale mass spectroscopy of protein complexes .
3. Computational analyses of experimental data as well as insilico predictions are important tools in the effort to increase our understanding of cellular architecture. In addition to the necessity of a complete and in-depth knowledge of protein-protein interaction networks for the understanding of cellular biology, they are highly interesting for target selection aiming for pharmaceutical application.
4. large scale experiments on protein-protein interactions were derived from microorganisms, most prominently *S. cerevisiae*.
5. The first and foremost principle of our MPPI database is to favour quality over completeness.

STRING DATABASE:

1. The STRING database aims to integrate all known and predicted associations between proteins, including both physical interactions as well as functional associations. To achieve this, STRING collects and scores evidence from a number of sources:
 - (i) automated text mining of the scientific literature,
 - (ii) databases of interaction experiments and annotated complexes/pathways,
 - (iii) computational interaction predictions from co-expression and from conserved genomic context and
 - (iv) systematic transfers of interaction evidence from one organism to another.
2. The entire database content of STRING is pre-computed, stored in a relational database and available for separate download. All interaction evidence that contributes to a given network is benchmarked and scored and the scores are integrated into a final ‘combined score’.
3. This score is scaled between zero and one and provides an estimate of STRING’s confidence on whether a proposed association is biologically meaningful given all the contributing evidence.
4. Each association is provided as a connection between two non-identical proteins, each from a different protein-coding gene locus.
5. STRING does not differentiate between splicing variants or post-translationally modified protein isoforms encoded from the same locus—instead, all such isoforms are collapsed and represented by a single, canonical protein