

Stratagene Pathway Architect

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Literature mining program from Stratagene , based on a proprietary knowledge database. Supports local mysql database to support customers with their own database.

Build Biological Interaction Networks Among Genes/Proteins of Interest

- Build interaction networks with multiple algorithms including direct interactions, shortest path, putative targets and putative regulators
- Multiple filter options to view pertinent interactions and simplify your BIN
 - Visualize Interaction Networks
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- Supports hundreds of visual elements that can be moved and highlighted for easy comprehension
- Modify, remove or add interactions to validate associations
- Export publication quality graphics in variety of file formats
- Overlay microarray gene expression data onto BIN/RINs
- Export and share BIN/RINs as HTML Web pages with full links to gene annotations and supporting references
- New visualization components including resizable pictures of organelles and localization compartments
- View larger image

PathwayArchitect Interaction Database

- Gene/Protein annotations include: Entrez gene annotations, alias (synonyms), subcellular locations, gene ontology terms and microarray IDs
- Repository of over two million biological findings on your desktop derived from the current literature
- Curated data sources included are BIND and MINT
- Import your own biological interaction data in a simple tab-delimited text format ideal for yeast two-hybrid or genetic screen data
 - Advanced Biological Text-Mining with Fact Curation Tool
- Next generation natural language processing (NLP) engine reads biological literature to extract facts
- Secondary manual curation ensures fact quality
- PathwayArchitect software includes the PathwayArchitect Interaction Database and a local NLP engine
- An enterprise text-mining system with a custom curation engine is also available
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 - Keep Current with the Literature

- Easily update your BINs with information from the most current literature
 - Interactions in a BIN/RIN include hyperlinks to supporting references and abstracts
 - All references supporting interactions depicted in a BIN can be easily exported as an EndNote® reference library
 - Extract biological interactions from PubMed abstracts, full-text journal articles (text or PDF), and internal documents
- Relevance Interaction Network Analysis
- Relevance Interaction Networks (RINs) start with the result from a BIN and calculate the significance of your pathway
 - A RIN is built after first determining if addition of a new biological object improves the statistical significance of the pathway
 - The Relevance Network can expand the BIN to maximize the relevance statistic
 - Provides a relevance metric for every node and increases confidence in your pathways