

BINDplus

THE FOREMOST BIOMOLECULAR INTERACTION RESOURCE



WHAT IT INCLUDES

- Accurate, manually-captured information
- More than 200,000 documented interactions and complexes
- Biomolecules and corresponding binding partners
- Relevant biological relationships for your molecule of interest
- Comprehensive, high quality interaction information

WHO CAN BENEFIT

- Pharmaceutical researchers
- Biochemists
- Molecular biologists
- Bioinformatics specialists supporting molecular research efforts

THE LEADING EDGE OF MOLECULE-BASED DISCOVERY

Public biological data are often fragmented and isolated, using inconsistent molecular identifiers and non-standardized terms. Thomson Reuters solves all these problems with *BINDplus*.

BINDplus builds on the high regard of BIND (Biomolecular Interaction Network Database), the foremost interaction database in science since its development in 1999. Used in over 120 countries by more than 3,000 organizations, BIND is endorsed by the scientific community, and its IDs have been published in world-renowned journals including *Science*, *Nature* and *Cell*.

With *BINDplus*, Thomson Reuters is identifying, extracting, and curating all interactions published in over 120 journals. *BINDplus* records derive only from peer-reviewed published data of observed physical interactions. Its records are chosen and edited by postgraduate level curators.

With each new curated interaction, *BINDplus* grows as the definitive biomolecular resource.

UNRIVALLED CONTENT

BINDplus contains historic as well as the latest published low- and high-throughput interactions documented according to rigorous data curation standards.

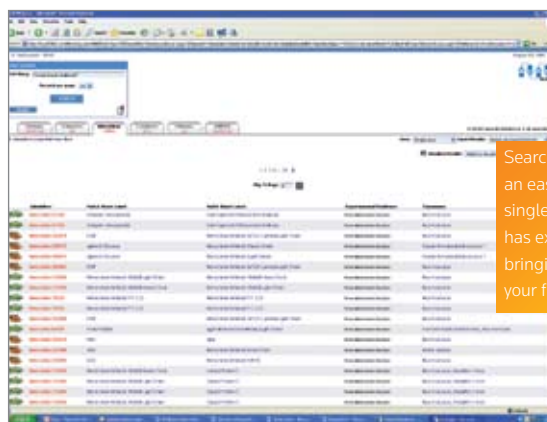
BINDplus includes a diversity of interaction types including protein-protein (44%), protein-DNA (28%), and protein-small molecule (16%) with data compiled into a single, standardized, scalable and comprehensive database specification.

The growing data in *BINDplus* include more than 60,000 unique gene identifiers, over 1,500 unique organisms, and 7,555 gene ontology terms derived from peer-reviewed scientific data extracted from over 23,800 journal articles and over 9,000 corresponding authors.

BINDplus also accommodates information obtained by a wide range of experimental methods, and describes a variety of biological processes in a consistent, computer-readable format.



BINDplus is searchable via free text and identifier search. You can also build complex queries using a field-specific search engine.



Search results are returned in an easy-to-read tabbed and single-line format. Each record has expandable data fields, bringing specific information to your fingertips.



The comprehensive BIND data specification allows for storage of human-curated interaction data in over 2,000 data fields including:

- Experimental descriptions
- Changes in molecule configuration or conformation
- Descriptions of binding site and residue topology
- Chemical reactions resulting from the interaction
- Descriptions of the pre-determined chemical states of the interacting molecules
- Kinetic parameters of the interaction
- Links to molecular object databases such as Entrez Gene and Gene Ontology
- Sub-cellular localization
- The publication supporting the interaction

To ensure you get the most current information, *BINDplus* releases data in a 'real-time' system, with database updates available through *BONDplus* immediately upon public release. The *BINDplus* flat-file is produced via FTP every week.

ASSURANCE OF QUALITY

BINDplus data derive from peer-reviewed scientific publications. Qualified *BINDplus* curators read the abstract, main text and supporting materials of each publication. They then identify experimental evidence detailing a biomolecular interaction, and catalogue all interactions and complexes into *BINDplus* using proven curation standards and controlled vocabularies.

CUSTOMER VALUE AND SUPPORT

BINDplus assembles a dynamic, computable resource of related molecular interaction data. It can facilitate your scientific efforts to identify important biological molecules and complexes, such as drug targets and diagnostic biomarkers, and metabolic processes critical to healthcare, agriculture, food, materials, and environmental science.

New information is added every day, ensuring your research will be at the absolute forefront of discovery.

BINDplus meets specific research interests by presenting dedicated datasets-delineated taxonomy, organism and gene ontology. New analytical tools and datasets will be delivered on a rolling basis. You will also receive comprehensive service through easy-to-follow product manuals, and dedicated telephone and email helpdesk support.

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