

BONDplus

INTEGRATED PUBLIC AND PROPRIETARY SEQUENCE, INTERACTION,
AND PATENT DATABASES



WHAT YOU CAN DO

- Search *GENESEQ*[™], *BINDplus* and public life science data on a single platform
- Integrate external and internal information silos
- Accelerate your work with pre-computed datasets and cross-references
- Access data via a rich web interface
- Enable your biological applications with robust data retrieval API

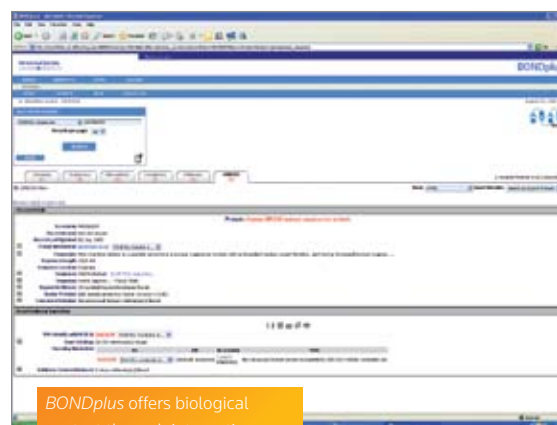
WHO CAN BENEFIT

- Pharmaceutical researchers
- IP professionals
- Bioinformatics specialists
- Biochemists
- Molecular biologists
- Life science researchers

AN INTEGRATED APPROACH TO DISCOVERY FOR BIOLOGY

BONDplus (Biomolecular Object Network Databank plus) is a life science data management platform that leverages public and proprietary data to help drive discovery across your organization. Integrating *GENESEQ*[™] and *BINDplus*, *BONDplus* takes you beyond the genome to take full account of all the relevant biological and IP relationships surrounding your molecule of interest.

BONDplus delivers a powerful range of data to your desktop, including sequence, interaction, patent, taxonomy, publication, annotation, domain, and cross-reference data from 15 assembled information sources.



BONDplus offers biological context through integration of *GENESEQ* records with publicly-available sequence, taxonomy, and interaction information.

PUBLIC DATA

- More than 80 million public domain sequences, originating GenBank, RefSeq, Entrez Gene, and UniProt/SWISSPROT

GENESEQ[™]

- The definitive source of annotated genetic sequences from worldwide patents
- Integration with public sequence data provides more biological context on patented sequences, making it easy to find prior art or potential infringement
- Includes links to identifiers from NCBI, UniProt/SWISS-PROT, *BINDplus*, additional synonyms and Gene Ontology (GO) terms
- Visualize *GENESEQ* records using accession, patent, and sequence-centric views
- Precomputed homology and RPS-BLAST results for *GENESEQ* records
- Comprehensive and continuously updated

BINDplus

- The largest manually curated molecular interaction database available
- 60,000 unique Gene Identifiers (GIs), over 1,500 unique organisms, and 7,555 GO terms derived from peer-reviewed scientific data extracted from over 23,800 journal articles and over 9,000 corresponding authors
- Over 200,000 molecular interactions
- Comprehensive and continually updated

No other resource integrates sequence, interaction, and patent data in such a way to leverage new insight.



SCALABLE TO MEET YOUR SPECIFIC REQUIREMENTS

- Web-based platform delivers insight from any location through a simple, secure log-in process
- Designed for modularized content display, *BONDplus* ensures you receive only content relevant to your requirements
- The rapidly expanding platform will result in frequent releases of new data and analytics

TIMELY AND EXPERTLY-ANNOTATED DATA

- Discover relationships that span disparate databases
- Constantly updated to ensure timely information delivery
- Never miss new and important information relevant to your research
- Pre-computed data by Thomson Reuters saves analytical resources and enables immediate insight

POWERFUL, EASY-TO-USE SEARCH CAPABILITIES

- All databases fully searchable via free text, identifier, or BLAST search
- Easy to use for developer, researchers, and educators
- Web interface supports full text queries and even field specific queries, enabling users to search across all *BONDplus* data in a matter of seconds
- Each search result returned can be viewed in one integrated layout
- Batch search results can be exported in a variety of common file formats
- With a full-featured query language and powerful filters, users can refine their search and narrow down results

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