

GENESEQ™

COMPREHENSIVE PATENT SEQUENCE DATABASE



WHAT YOU CAN DO

- Access more than 9 million patented sequences
- Review detailed commercial summaries
- Check sequences for existing patent obligations
- Search for prior art before patenting
- Interrogate potential patent infringements
- Obtain data in advance of your competitors, with greater, earlier sequence coverage

WHO CAN BENEFIT

- IP professionals
- Bioinformatics specialists
- Biochemists
- Molecular biologists
- Licensing and business development professionals

UNRAVEL THE COMPLEX STRANDS OF BIOLOGICAL SEQUENCES

GENESEQ™ contains high quality, easy-to-understand annotated biological sequences from worldwide patents — an essential tool for any organization that needs to know what's happening in genomic-based life science discovery.

It contains millions of patented sequences from more than 120,000 unique patents spanning 41 patent offices worldwide (including WO, US, EP, IP, DE, IN and CN), covering genetic discovery back to 1981. As many as 40,000 new records are added every two weeks, with each record annotated by highly-trained editorial staff.

GENESEQ enables you to search sequence information from around the world in a single database. Foreign patents compose over 20% of the database — and English language titles are provided for each foreign patent.

Patents can appear in *GENESEQ* years before other sequence databases, putting you far ahead of the competition and ensuring that your IP professionals will not miss any potential infringements or competitor activities.

COMPLETE, TIMELY, ANNOTATED ANALYSIS WITH GLOBAL COVERAGE

Our dedicated editorial team provides thorough, up-to-the-minute coverage of all relevant patent information sources. In addition, the team adds unique commentary to each sequence record, clarifying sequence novelty and the actual application underlying each invention.

This analysis includes:

- Bibliographic data (enhanced titles, English language abstract from non-English sources, translations)
- Sequence location within the disclosure
- Original source organism
- Highlighted biologically significant regions of the sequence
- Sequence provided in EMBL-like format to ease integration into in-house systems
- Consistently applied, searchable keywords based on controlled vocabularies

GENESEQ includes the biological context of each sequence, including links to identical records from NCBI, SWISSPROT, *BINDplus* (Biomolecular Interaction Network Database Plus), Gene Ontology (GO) annotation, and sequence aliases.

```
FILE GENESQ 01/03/01 /home/pd
#####
### title: cycline receptor ligand; aliases: ligand; tumor
### desc: ligand; colon tumor; breast tumor; rectal tumor; cytostatic; cancer
### seqfeat: nucleic acid; gene; si
### name: ligand
###
### key            location/qualifiers
### chs            121..173
### feat          /frame 5
### seqfeat       /product "cycline receptor ligand H02320"
### mat_seqfeat   /tag 5
### mat_seqfeat   /tag 6
###
### 01/03/01/1739-01.
### 25-SEP-2002.
### 16-SEP-2002; 200209-0604654.
###
### 13-NOV-2002; 200209-0115151.
### 13-NOV-2002; 200209-0350438.
### 13-NOV-2002; 200209-0350438.
### 13-NOV-2002; 200209-0350438.
###
### (c) 2002 Thomson Scientific Inc.
###
###
### no gene encoding the
### act or structure.
### tumors in mammals, e.g.,
###
### polypeptide, which is a
### nucleic acid polypeptide or
### nucleic acid polypeptide or
### nucleic acid polypeptide or
```

Data are provided in an EMBL-like flat-file format. Each record includes a wealth of annotation on each sequence, including bibliographic information, precise sequence location, and biological context.

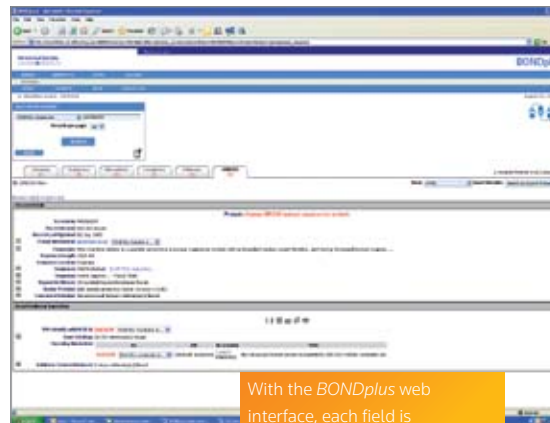
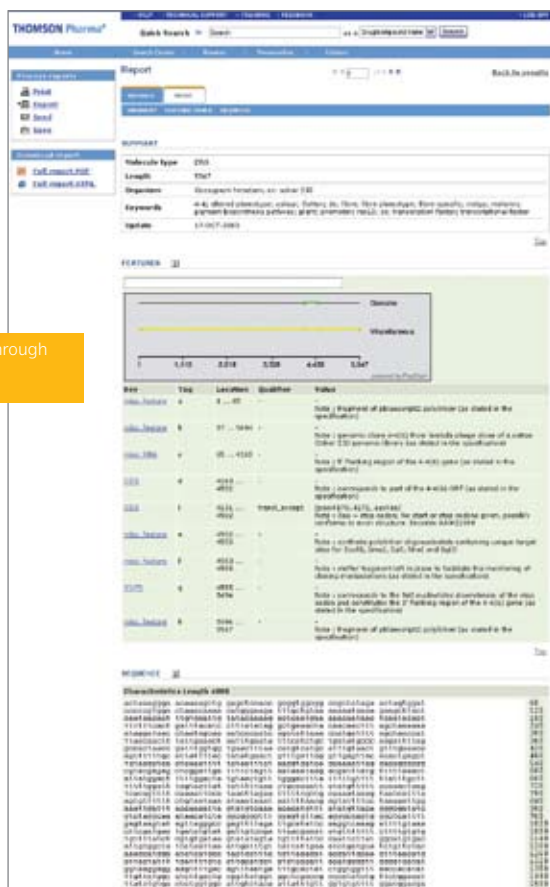
COMPREHENSIVE ACCESS AND RELEASE OPTIONS

GENESEQ is released via an EMBL-like flat file every two weeks, with GENESEQ FASTAlert released as a rolling FASTA database every Tuesday and Thursday. GENESEQ data are also available through:

- STN
- Thomson Pharma®

By visiting GENESEQ through Thomson Pharma, you can create guided searches, and explore the relationships with your sequence of interest. Thomson Pharma provides a comprehensive view of each record, including a sequence view and details on related patents. You can use the customization features of Thomson Pharma to save your searches or receive alerts on new records.

Accessing GENESEQ through Thomson Pharma®.



With the BONDplus web interface, each field is expandable, providing an easy-to-view summary of the information, or a comprehensive 'drill-down' into the record.

- BONDplus platform. BONDplus is a molecule-focused interface delivering effective bioinformatics support for the bench researcher. GENESEQ sequence and patent information are completely integrated into the BONDplus warehouse of over 80 million sequences and 200,000 biomolecular interactions, including pre-computed homology links to public databases, RPS-BLAST domain annotation, and integrated BLAST search capabilities. BONDplus also includes a robust API, enabling in-house applications to benefit from its broad scope of data.

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