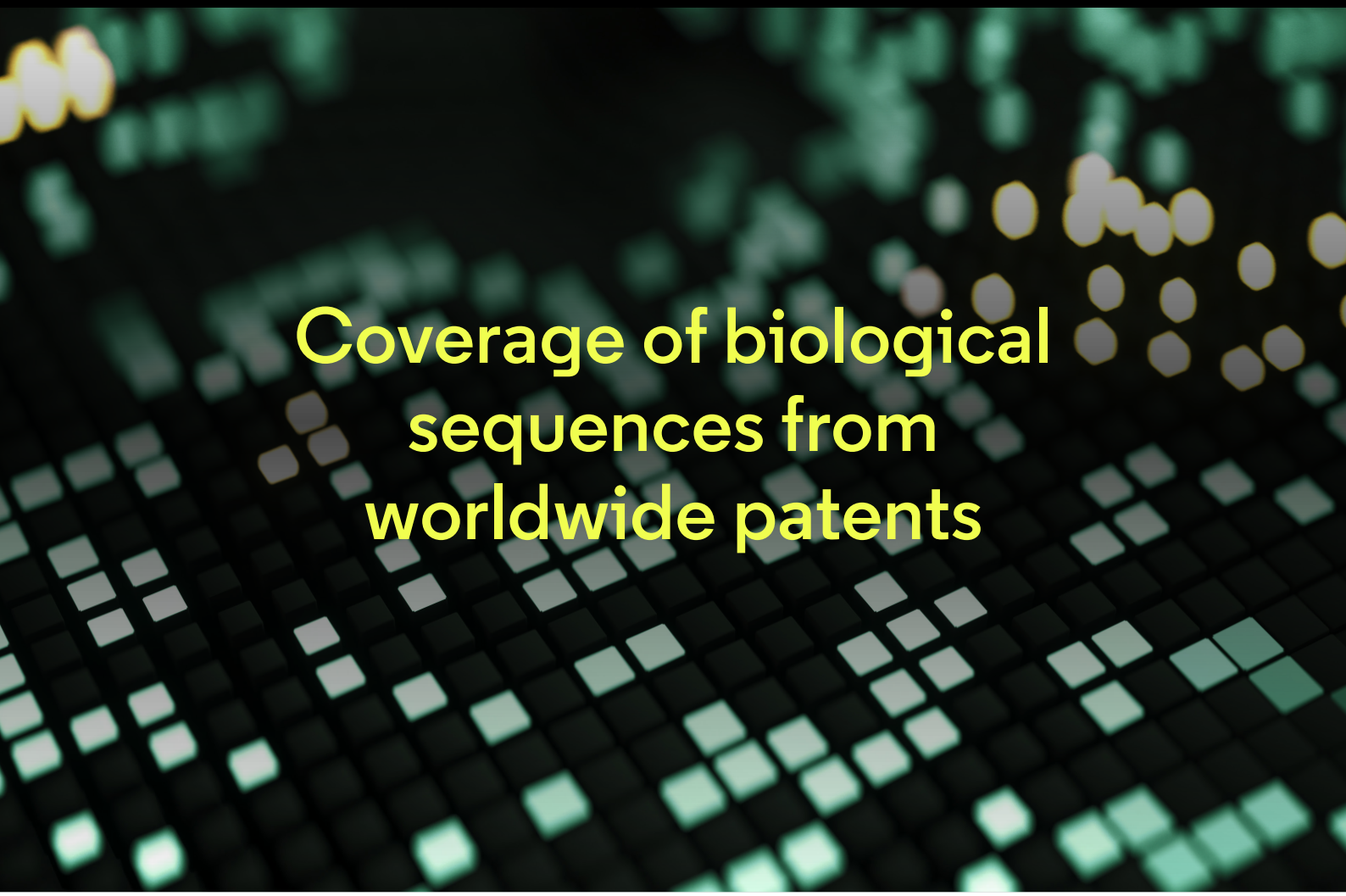

Coverage of biological sequences from worldwide patents

Unravel the complex strands of biological sequence patents

GENESEQ ensures you are seeing the entire patent landscape surrounding the biological sequence under investigation.

Manually curated and professionally annotated, it covers all biological sequences patented since 1981 from 57 worldwide patent-issuing authorities — including WO, US, EP, JP, DE, IN, KR, and CN.

With over 87 million biological sequences from more than 443,000 unique patents, GENESEQ contains a wealth of essential sequence information not available anywhere else.

The database is continually growing with an average of 1400 unique patents containing biological sequences added every two weeks.

IP professionals can be sure they don't miss any potential infringements or competitor activities, and biological scientists can spend less time searching for sequence data and more time on research and development.

Clarivate

GENESEQ contains genetic sequences from worldwide patents, manually annotated tohighlight IP context and biological significance.

What you can do

Find biological sequences not available in other databases

- Identify highly relevant prior art
- Establish freedom to operate and patentability
- Quickly assess the location and context of the sequence in the patent
- Understand the global patent landscape
- Uncover the activities of your competitors
- Reveal potential patent infringements

Who can benefit

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

Complete, timely annotated analysis with global coverage

Our dedicated team of scientific editors provides thorough coverage of all biological sequence information from patents including:

- Nucleic acid sequences 10 or more bases in length
- Amino acid sequences 4 or more residues in length
- All PCR primers and probes of any length

Uniquely, we go beyond what is available in electronic sequence submissions to bring you all sequences – even 'hard-to-find' sequences in figures and tables so that you have the complete picture.

In addition to manual capture of sequences, the team adds detailed annotations and indexing. This enables accurate search and retrieval, and speeds up review and prioritization of search results. Every record is fully indexed in English, irrespective of its location within a patent, or the language of the original patent document.

This annotation includes:

- Unique commentary, clarifying sequence novelty and the actual utility underlying each invention.
- Enhanced patent titles
- Sequence location within the patent document
- Organism name, gene/protein name, sequence modification or other highlighted biologically significant regions of the sequence, associated disease information
- Standardized, full bibliographic data
- Links to identical records from NCBI and SWISSPROT, Gene Ontology (GO) where provided in the patent

57

Issuing authorities, including all US family members

How GENESEQ aids IP professionals

GENESEQ provides manually-captured sequence information not available in any other sequence database, nor in patent office databases. Many biological sequence patents do not have electronically available or machine-readable sequence information — the only way to capture this information is manually. GENESEQ captures up to three million characters of this sequence data every week.

Manual indexing standardizes terminology, enabling you to narrow your results quickly and accurately to the relevant disease, technology, or sequence itself. You can search all sequences in a patent, irrespective of their location (in figures, disclosure, claims, and so on) and identify key sequences by putting each sequence into context. GENESEQ is used by major patent issuing authorities — so you can be sure you're checking the same information that your examiners are.

How GENESEQ aids biological scientists

GENESEQ enables you to understand the context of each sequence in the patent, quickly identifying new disease, gene, or target associations, and sequence modifications. Its standardized terminology makes it easy to map GENESEQ into your in-house bioinformatics systems.

GENESEQ contains raw sequence information for:

- Gene/protein disease association
- Target identification
- Biotherapeutic creation
- Biomedical technology creation
- Gene/protein families enrichment

Comprehensive access and release options

GENESEQ is available through leading sequence search and data management solutions including:

- GENESEQ is available on Derwent Sequence Search — search GENESEQ, GENESEQ FASTAlert and the USPTO sequence database ('USGene') with online BLAST search.
- Analyze integrated results from patents across 57 issuing authorities, including all US family members
- GENESEQ is available on GenomeQuest — search GENESEQ on the same web platform as GQ-Pat
- DGENE is available on STN International — suitable for advanced information searchers
- GENESEQ is also available to licence for inclusion within in-house information systems. The EMBLlike flat file, is delivered via ftp every two weeks

GENESEQ FASTAlert

An additional option is the companion database GENESEQ FASTAlert that enables rapid searching of new sequences. It is released as a rolling FASTA database on Tuesday and Thursday every week. GENESEQ FASTAlert is available via Derwent Sequence Search or to licence for inclusion within in-house systems.

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About Clarivate

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