



Sequence search for biological patent intelligence

Derwent Sequence Search helps IP teams to search and analyze biological sequences described in global patent publications



Find, analyze and understand biological sequences data from around the world.



Identify prior art and establish freedom to operate and patentability.



Understand the global patent landscape and competitor activities.

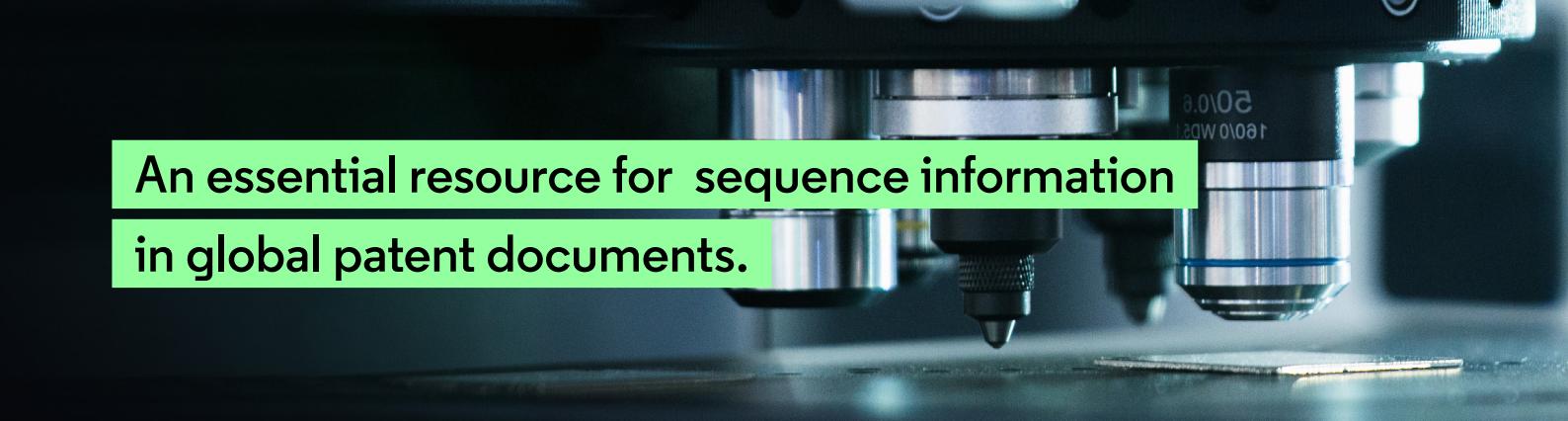


Quickly assess the context of the sequence in the patent.



Surface potential patent infringements.

Understand the
global biological
sequence
landscape
across patent
documents



An essential resource for sequence information in global patent documents.

GENESEQ: Spend less time searching and make faster, better informed decisions.

Comprehensive, timely, annotated coverage

GENESEQ

GENESEQ is a proprietary database used to easily search and identify biological sequences (DNA, RNA, protein sequences) covered in patents from 58 issuing authorities. Manually annotated to highlight IP context and biological significance, GENESEQ allows IP professionals and biologic scientists to spend less time searching and understanding sequence data and more time assessing patentability, identifying potential infringing patents and tracking competitor activities.

GENESEQ delivers the entire patent landscape surrounding the biological sequence under investigation with coverage beginning in 1981 from worldwide patent issuing authorities including WO, US, EP, JP, DE, IN, KR, and CN.

Find context faster with annotated analysis

Our editorial team of more than 40 biology and life sciences experts provides written summaries that clarify and explain sequence novelty and utility of a given sequence, including:

- Enhanced patent titles that are more intuitive
- Record detail includes organism name, gene/protein name, sequence modification or other highlighted biologically significant regions of the sequence, and associated disease information
- Sequence location within the patent document
- Standardized, full bibliographic data
- Links to identical records from NCBI and SWISSPROT, Gene Ontology (GO) when provided in the patent
- GENESEQ covers 110+ million of sequences from more than hundreds of thousands of unique patents.

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

- 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

GENESEQ is available through Derwent Sequence Search or can be accessed through an API for organizations that want enterprise-wide access to conduct sequence searching and analysis on their in-house platforms.

GENESEQ: Enhanced and curated for more accurate results.

Example 1: WO2024259656A1

Patent Title: Formulation of an anti-il-4 receptor alpha mab or an antigen-binding fragment thereof comprising 2hpbetacd and leucine

Sequence Listing with 11 sequences provided as part of the specification but NO indication of presence of CDRs.

Example GENESEQ record

 **WO2025201418 A1**
Published: 2025-10-02 Total Document Sequences: 73 

[Bibliography](#) [Abstract](#) [Family](#) [Sequences](#)

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FAAGGAVHTRGLDFACDIYIWAPIACTCGVLLSLIVITLYCKRGRKKLLYIFKQPFMRFV  
QTQEEDGCSRFFEEEGCCELRVKFERSADAPAYQQQNQLYNELNLRREEYDVLDR  
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SDEQLKSGTASVVCCLNNFYFREAKQWQKVVDNALQSGNSQESVTEQDSKDSTYSLSSLT  
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SKYGFPCFPCCPAPEFLGGPSVFLFPFPKPKDTLMISRTPEVICVVVDVSQE...
```

Feature table

KEY	LOCATION	FEATURE
Peptide	1..21	note: "Signal peptide"
Peptide	376..397	note: "P2A"
Peptide	398..416	note: "Signal peptide"
Region	440..454	label: complementarity_determining_region_1
Region	470..476	label: complementarity_determining_region_2
Region	509..517	label: complementarity_determining_region_3
Peptide	635..662	note: "T2A"
Peptide	663..681	note: "Signal peptide"
Region	712..716	label: complementarity_determining_region_1
Region	731..747	label: complementarity_determining_region_2
Region	780..790	label: complementarity_determining_region_3
Region	795..1128	note: "Fc region"

Manually curated Feature Table highlighting CDRs

Comprehensive global patented sequence coverage

USGENE

A trusted resource for life science intellectual property professionals, providing unrivaled searchable access to all available peptide and nucleotide sequences from the published applications and issued patents of the United States Patent and Trademark Office.

With over 292 million biological sequences from more than 436K unique U.S. patents and published patent applications, it contains a wealth of essential sequence information not available anywhere else. With coverage beginning in 1981, the database is continually growing with hundreds of documents containing biological sequences added twice per week and within 24 hours of patent publication.

WOGENE

Providing comprehensive coverage from international published patent applications containing nucleic acid and protein sequences from: the World Intellectual Property Organization, the European Patent Office, the Japanese Patent Office, and the Korean Intellectual Property office.

With coverage dating back to 1979, contains a wealth of essential sequence information not available anywhere else. Additional documents containing biological sequences are added twice per week and within 24 hours of publication.

Coverage in USGENE and WOGENE includes:

- 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
- Sequence information, including organism name, molecule type, and modifications

Database annotation includes:

- Patent title
- Sequence identity number (SEQ ID NO) within the sequence listing
- Original source organism
- Standardized bibliographic data

GenBank

NIH's genetic sequence database is an annotated collection of all publicly available DNA sequences. GenBank is part of the International Nucleotide Sequence Database Collaboration, which comprises the DNA DataBank of Japan (DDBJ), the European Nucleotide Archive (ENA), and GenBank at NCBI.

With over 1 trillion nucleotide bases from more than 486 million individual sequences, GenBank provides access within the scientific community to the most up-to-date and wide-ranging DNA sequence information.



Derwent Sequence Search

Complete search algorithm suite to match your use case



BLAST

Heuristics-based Basic Local Alignment Search Tool from NCBI finds regions of local similarity between sequences.



MOTIF

Search using regular expressions for specific pattern searching or search specific substitutions.



Antibody

Find patents using CDRs as queries optionally combined with heavy/light chains to filter results.

- CDR Variation Tables
- Robust Filtering & Subsearching



Smith-Waterman

Aligns sequences using dynamic programming to find mathematically optimal local alignment.



Multiple Sequence Search

Search for multiple sequences using the Smith-Waterman algorithm, with specialized result analysis capabilities.



Keyword

Search for sequences by keywords, patents bibliographic information and sequences annotations.



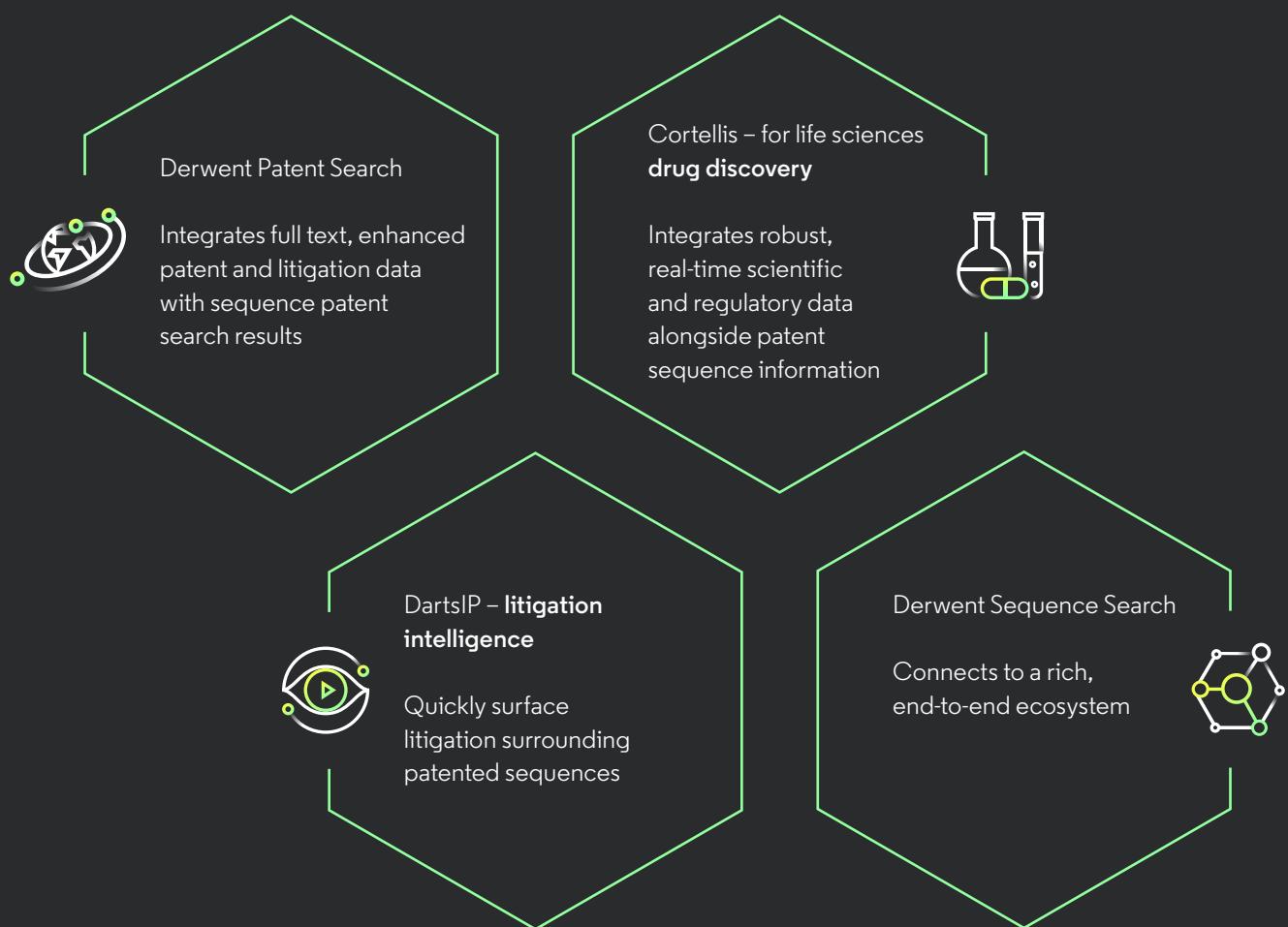
BestSeq

Proprietary search algorithm based on a speed optimization of Smith-Waterman for patent searching.

The screenshot shows the Derwent Sequence Search interface. At the top, there are tabs for 'Projects', 'My Folders', 'My Queries', and 'Monitor'. The 'My Projects' section shows a single project named 'SequenceVariation' (created on Oct 23, 2025). Below this is the 'Search' tab, which is active. The search interface includes a 'Search name:' input field, a 'Templates' dropdown, and a 'Query' input field. The 'Database' section lists several options: 'Select all' (checked), 'Clear all', 'GENESEQ, a Clarivate brand' (checked), 'USGENE' (checked), 'WOGENE' (checked), 'GenBank' (unchecked). There are checkboxes for 'Exclude mega published applications (10,000 or more sequences)' and 'Exclude publication folder documents', both of which are unchecked. The 'Target Sequence Length' section has 'Min:' and 'Max:' fields, and a 'Subsequence From:' field. There are also 'Low-complexity filter' and 'Automatically adjust parameters for short input sequences' checkboxes. At the bottom, there are sections for 'Algorithm parameters' and 'Additional search options', both with a 'Defaults' button. A 'Search' button is located at the very bottom left.

Derwent Sequence Search integrations

Integrated with these solutions to make it easy to incorporate patent data for biologic sequences into your current workflows



About Clarivate

Clarivate is a leading global provider of transformative intelligence. We offer enriched data, insights & analytics, workflow solutions and expert services in the areas of Academia & Government, Intellectual Property and Life Sciences & Healthcare. For more information, please visit clarivate.com.

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