

# LifeQuest

Take your prior art searches beyond keywords

## INTEGRATE TEXT AND SEQUENCE SEARCHES

Prior art searching in the life sciences is complicated. With over 13 million worldwide patent applications, and many different platforms for both sequence and keyword searching, finding the most accurate, relevant hits is challenging. Different user interfaces & output formats, weak cross-platform integration, and the limitations of strict Boolean search algorithms mean valuable time is spent cross-checking and re-analyzing the same pieces of information. With **LifeQuest**, you can leverage the power of the only patent search platform that is specific for the life sciences.

## YOU KNOW GENOMEQUEST AS A LEADER IN SEQUENCE SEARCHING

GenomeQuest's **GQ-Pat Platinum** collection comprises non-ST.25 documents from major authorities such as US, EP, WO, JP, KR, BR, IN, CN, and RU - for a total of over 620,000 patent documents. This means over 285 million sequences at your fingertips: from sequence listings, as well as abstracts, descriptions, tables, figures, and examples. Customers not requiring emerging countries can still leverage the same powerful algorithms with **GQ-Pat Gold+**, which includes US, WO, EPO, and JP non-ST.25 documents. Each sequence is manually curated for the highest accuracy, and leverages GenomeQuest's exclusive inclusion of extended legal status, legal status national phase, unique family sequence, normalized patent assignee, and normalized parent statuses, to create the most meaningful results for your reports.

## INTRODUCING LIFEQUEST - THE SOLUTION FOR SEMANTIC KEYWORD AND LIFE SCIENCE ONTOLOGY SEARCHING

### Specific for Life Sciences

Relevant documents & search strategies that avoid false hits in unrelated fields

### Accurate

Dynamic access to the ontology search terms and synonyms in life science patents

### Efficient

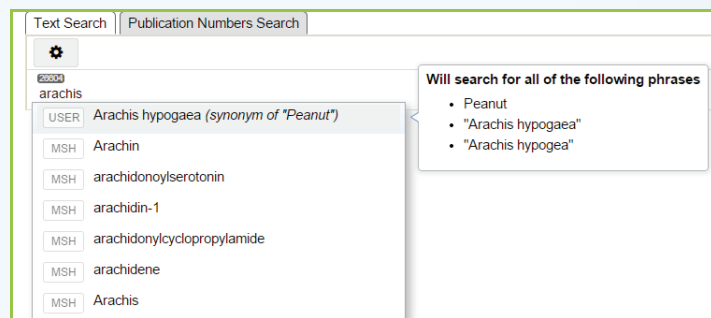
Elegant, fast, user-centered experience designed to save time & resources in searching

### Non-Redundant

Tight integration of keyword, synonym, ontology, and sequence searching

### Cost Effective

Fewer platforms (and subscriptions) needed to get the most relevant, accurate information



As you begin typing your query, suggested matching terms appear based on the ontologies you choose. Synonym phrases are included, and you can even create customized terms for your specific needs.

# CASE STUDY

Obstacles in prior art searches in the life sciences include variable spellings, life science-specific ontological terms, false positives, and irrelevant results. With variable patent authority coverage and lack of life science specificity, other platforms can return irrelevant or incomplete results.

For example, different sequence and keyword searches for prior art on “transgenic hypoallergenic peanuts via modification of *ara h 1* genes” across multiple platforms yields a range of 28 to >1000 sequence hits, and 13 to 53,700 keyword hits. **LifeQuest + GenomeQuest** return accurate results:

Text Search | Publication Numbers Search

288  
all: ( **Arachis hypogaea** AND **Plants Transgenic** AND **allerg\*^5** ) AND pd: [ 1995-03-05 TO \* ]

Leverage ontology terms in query

By utilizing life science specific ontologies (such as “transgenic plants”) and developing custom synonym lists (for the genus and species of peanut - often misspelled, often with aliases) that are significant for your specific search, you can create a highly specific query that will return the most pertinent prior art documents. You can further refine by boosting a term’s importance (e.g., “allergenic” and its variants are five times more important than “transgenic plants”). A preview of the number of hits appears above the query in real time, so you can quickly determine which search strategies are most effective.

Color code results based on your own criteria, rank hits for relevance, preview documents, link out to USPTO and other authorities, view the PDF, and produce reports in multiple formats.

LifeQuest [Arachis hypogaea]

Q Search Workfile Operations...

US 8217228 B2

Down-regulation and silencing of allergen genes in transgenic peanut seeds

An allergen-free transgenic peanut seed is produced by recombinant methods. Peanut plants are transformed with multiple copies of each of the allergen genes, or fragments thereof, to suppress gene expression and allergen protein production. Alternatively, peanut plants are transformed with peanut allergen antisense genes introduced into the peanut genome as antisense fragments, sense fragments, or combinations of both antisense and sense fragments. Peanut transgenes are under the control of the 35S promoter, or the promoter of the Ara h2 gene to produce antisense RNAs, sense RNAs, and double-stranded RNAs for suppressing allergen protein production in peanut plants. A full length genomic clone for allergen Ara h2 is isolated and sequenced. The ORF is 622 nucleotides long. The predicted encoded protein is 207 amino acids long and includes a putative transit peptide of 21 residues. One polyadenylation signal is identified at position 951. Six additional stop codons are observed. A promoter region was revealed containing a putative TATA box located at position -72. Homologous regions were identified between Ara h2, h6, and h7, and between Ara h3 and h4, and between Ara h1P41B and Ara h1P17. The homologous regions will be used for the screening of peanut genomic library to isolate all peanut allergen genes and for down-regulation and silencing of multiple peanut allergen genes.

Hits in Claims

...A transgenic seed of the plant of claim 1 having reduced or undetectable levels of at least one of the said more than one allergen protein content compared to wild-type. 8. An **Arachis hypogaea** cell comprising a gene operably linked to a promoter, the gene comprising an antisense sequence selected from the group consisting of: the antisense sequence of SEQ ID NO. 3, the antisense sequence of SEQ ID NO. 4, the antisense sequence of SEQ ID NO. 5, the antisense sequence of SEQ ID NO. 6, and a fragment of any of the foregoing, wherein the cell has reduced or undetectable levels of at least one allergen protein selected from the group consisting of Ara h1, h2, h3, h4, h5, h6, and h7 compared to wild-type when the gene is expressed. ...

...The cell of claim 9, wherein the cell displays reduced or eliminated expression of each of the more than one Ara h allergens, to which the region is common compared to wild-type. 16. A **transgenic plant** comprising the cell of claim 8. 17. A transgenic seed of the plant of claim 16 wherein the seed has reduced or undetectable levels of at least one allergen protein selected from the group consisting of Ara h1, h2, h3, h4, h5, h6, and h7 compared to wild-type. ...

30 claims total

Efficiently review & categorize results

GenomeQuest

Home >

Result View Export Applications

Filtering Grouping Sorting Sharing Export To LifeQuest

Integrate with the GQ Platform

Sequence hits for the *Arachis hypogaea* *ara h 1* gene CDS on the **GenomeQuest** platform can easily be exported to **LifeQuest**, for workfile comparison with text search queries.

The Union set operation between the text and sequence search workfiles creates a single, complete framework for analysis.

Union Intersect Subtract Symmetric Difference

Name	Items	Date	Compare
[Arachis hypogaea] AND [Plants Trasngenic] AND allerg*^5 AND pd:[19950301 TO *]	288	February 9, 2015	A B
peanut AND "transgenic plant" AND allerg*	1592	February 9, 2015	A B
GQ sequence hit query	216	February 6, 2015	A B
peanuts allerg mutants	13967	February 6, 2015	A B
[Arachis hypogaea] AND [Transgene] AND allerg*	373	February 3, 2015	A B

Prior art searching in the life sciences requires more than simple keywords and Boolean syntax. Leverage the life science specific semantic and ontology capabilities of **LifeQuest**.