



SEQUENCE RESEARCH

SPECIFICATIONS

Description: Ideal for biotechnology pharmaceutical researchers. This report provides solutions and insight for both intellectual property and technical professionals into issues related to biosequences as the core of a research request.

The Report: In accordance with a client's distinct project needs and objectives, a Nerac Analyst merges applicable expertise with relevant research findings to produce this custom report. Principal components of the report typically include:

Executive Summary

Synopsis of research conducted and significant revelations contained in the report

Nerac Methodology

Research is conducted in the Thomson Derwent GeneSeq file (DGENE), STN's PCTGEN, CAS Registry file, and finally the NCBI database run by the BLAST program (National Center for Biotechnological Information). All research is conducted on the STN or NCBI platform, based on client preferences. Both FASTA (Smith-Waterman) or BLAST algorithms are available depending on client needs.

Discussion of Relevant Art

Overview of the patent and literature references found to be most relevant alone or in combination with one another. Each sequence found will create a record with the bioinformatics alignment of the Query-to-Found sequence, Sequence Length, Sequence Location (Claims, Description etc). The basic bibliographic information will also be displayed. Custom reports of any field in any combination are also available.

Tabulated Snapshot of Research Findings

The report will include a patent or literature summary followed by an expanded record of each sequence retrieved.

Nerac Analyst Insight

Views and commentary presented by the Nerac Analyst integrated within the report based on expertise, the relevant findings discovered throughout the course of research and potential implications for the client

