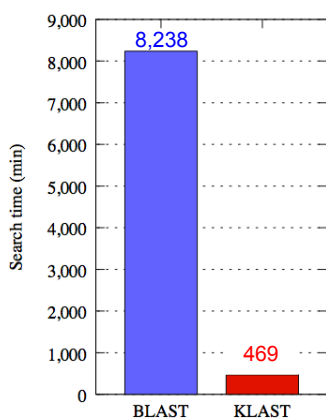


ngKLAST

Next-generation sequence similarity search platform

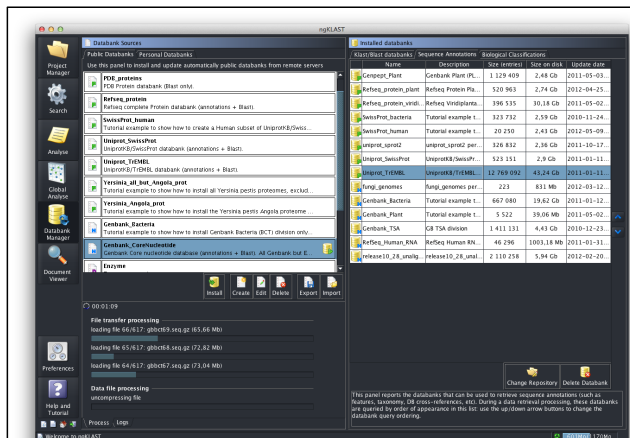
ngKLAST is a graphical platform containing the KLAST high-performance sequence similarity search tool. With an easy-to-use workflow engine and a unified set of data viewers, the ngKLAST platform makes large scale databank exploration accessible to every life science researcher.



KLAST and BLAST benchmark: comparison of 8,245 sequences (translated 454 reads) from *Tara Oceans* metagenomic data against 15 million proteins from Uniprot. Both algorithms ran on 8 Intel Xeon cores.

Benchmark data courtesy of Thomas Vannier and Jean-Marc Aury research team (Genoscope/CEA). [*]

ngKLAST is fully designed to compare query and subject comprised of large sets of DNA, RNA and protein sequences using the new KLAST high-performance sequence similarity search tool (www.klast-search.com).

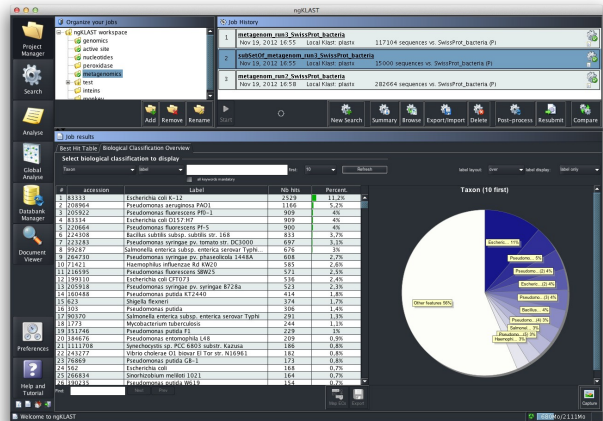
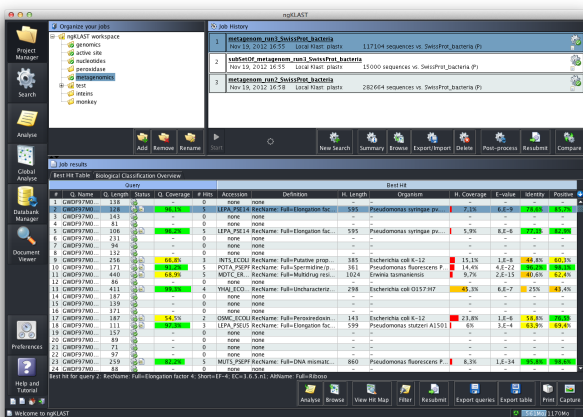


ngKLAST comes with a fully featured *Databank Manager* allowing the automated installation of both public and personal sequence databanks. Taxonomic subsets can also be setup.

NgKLAST's *Project Manager* organizes and keeps a history of all searches done on your NGS data sets over time.

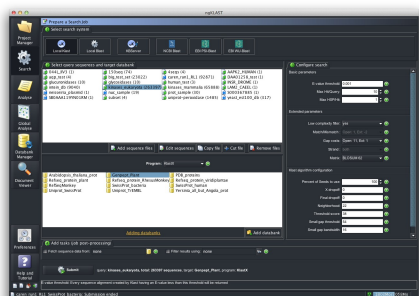


ngKLAST offers numerous graphical tools dedicated to analysing large sets of results combining hits, sequence features and biological classifications.



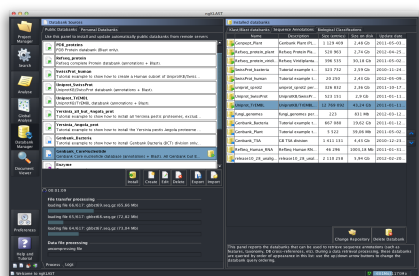
ngKLAST main features

Databank Search (KLAST)



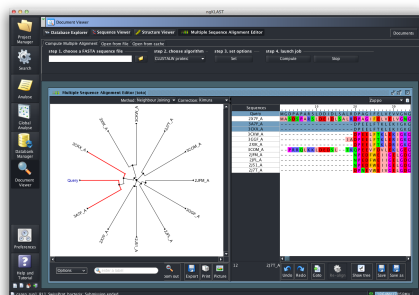
- High-performance comparisons of large sets of sequences using KLAST
- Run local search jobs on your multi-core workstation
- Cluster/Grid enabled using the KLAST Server
- Get fully annotated hits
- Filter results using KLAST and/or annotation data
- Compare results to discover new and common hits

Databank Installation



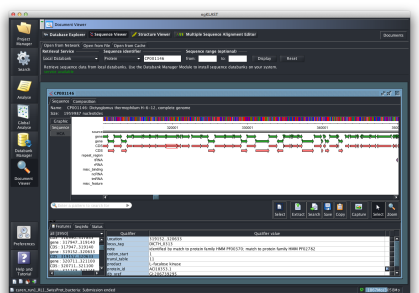
- Automatic deployment from remote servers
- Install public databanks (e.g. NCBI, Uniprot, Silva, DNA Barcodes, etc.)
- Prepare personal databanks
- Manage sequences, annotations and biological classifications
- Prepare taxonomic subsets from public databanks

Data Visualization



- Sequences, Genomes, 3D structures
- Multiple sequence alignments (Clustal/Muscle) viewer and editor
- Phylogenetic trees
- Conserved regions
- Features, annotated Hit 2D plots
- Biological Classification (Taxonomy, Gene Ontology, Enzyme, Interpro)

Data Query and Management



- Query sequence databanks (nucleotides, proteins)
- Query 3D structure databank (PDB)
- Query local and remote (NCBI, RSCB) services
- Batch retrieval of sequences
- Direct KLAST submission
- Analyse data using convenient viewers
- Export data (text, spreadsheet, images, PDF, ...)
- Organize data safely over time
- Share data with other users

Discover more about KLAST
applications on:



System Requirements

- Starter configuration:
- desktop computer
 - Intel 64-bit quad-core
 - 8 Gb RAM
 - Windows, Linux or MacOS X (64-bit required)
 - Java Runtime 1.6 (64-bit required)