



geneIOUS

Research software for Biologists, not computer scientists!

Geneious Pro™ is an integrated and extendable software platform for the organization and analysis of biological data. Geneious Pro™ is revolutionary software that combines major DNA and protein analysis tools into a single package that is both powerful and easy to use. Geneious Pro™ has a comprehensive set of technical features, superb visualizations, specialized functionality through numerous plugins and runs on all major operating systems.







Technical Features of Geneious Pro

- NEW Ultra-fast *de novo* assembler
- NEW Primer extension support
- NEW Primer design on alignment and assemblies
- NEW Map primer to sequence
- NEW Trim by primers
- NEW Batch export
- NEW Import FastQ, CsFasta, Qual file formats
- NEW Add, remove and combine enzymes from lists
- NEW Find in translated sequence
- NEW Bundled EMBOSS Tools
-  Automated *Smart Agent* searching
-  Advanced alignment (ClustalW, MUSCLE, MAUVE)
-  Sequence detection (2° structure, heterozygosity, ORFs, antigenic regions, motifs, tandem repeats, transmembrane regions & recombination)
-  Phylogenetics (PhyML, ModelTest, PAUP*, NJ)
-  Contig viewing, editing & assembly
-  Primer design (using Primer3)
-  Restriction analysis
-  *in silico* cloning and Gateway® cloning
-  Keyboard preferences for any function
-  Sassafras K2 license server support
-  Bioinformatics teaching tutorials
-  Geneious Public API












Visualization Features

- NEW Genome-capable dotplot
- NEW Color by annotation color-scheme
- NEW Side-ways panning in the sequence view
- NEW Change the residue numbering on circular sequence

View, edit, annotate and publish:

-  Sequences (up to mammalian chromosomes)
-  Circular sequences (plasmids & vectors)
-  Alignments
-  Phylogenetic trees
-  Chromatograms & contigs
-  Restriction sites

Plugins

-  Phobos tandem repeat search tool
-  PAUP*
-  MrBayes
-  PhyML
-  DeCypher (FPGA technology)
-  Green Button (supercomputing)
-  Dual Brothers Recombination Detection
-  MAUVE genome alignment
-  Heterozygotes, CpG Islands
-  Transmembrane Prediction
-  Coiled Coils

