



# geneIOUS

Geneious Pro™ is the 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 familiar, email like interface, data is presented in a consistent manner and runs on Windows, Mac OS X, Linux and Solaris. Geneious Pro™ combines all the major bioinformatic tools providing a comprehensive set of technical features, superb visualization features and specialized functionality through numerous plugins. By bringing all of these tools together, Geneious Pro™ eliminates the need for task specific applications, saving you time and money.

## Technical Features of Geneious Pro

- \*\*NEW in 4.7\*\* Ultra-fast reference assembler
- \*\*NEW in 4.7\*\* Contig Express Importer (Vector NTI)
- \*\*NEW in 4.7\*\* Query-centric alignment of BLAST results
- \*\*NEW in 4.7\*\* Primer database
- \*\*NEW in 4.7\*\* 454 import and handling
- \*\*NEW in 4.7\*\* Keyboard preferences for any function
- \*\*NEW in 4.7\*\* Multi-region sequence selection
- \*\*NEW in 4.7\*\* Structure prediction on alignments

Automated **search agents** (NCBI, Pfam, Uniprot, PubMed)  
DNA/Protein Sequence Alignment (MUSCLE, ClustalW)  
Phylogenetic tree building (UPGMA, NJ, PhyML, PAUP\*)  
Primer Design (utilizing Primer 3) & restriction analysis  
Contig viewing, editing & assembly  
Support for cloning and Invitrogen's Gateway® Cloning  
Sassafras K2 license server support  
Free editable tutorials

## Visualization Features

- \*\*NEW in 4.7\*\* Dynamic DNA to protein translation
- \*\*NEW in 4.7\*\* Color nucleotide triplets by translated AA
- \*\*NEW in 4.7\*\* Automated chromatogram scaling
- \*\*NEW in 4.7\*\* MacClade color scheme

**Annotated sequence viewing and editing** for: Mammalian chromosomes, Bacterial genomes, Chromatograms, Circular sequences, Plasmid mapping & Restriction sites  
**Publication ready images** in pdf format for: Nucleotide and protein sequences, Plasmids and vectors (including restriction sites), Alignments, Chromatograms, Phylogenetic trees, 3D Protein Structures

## Plugins

- PAUP\*
- Mr. Bayes
- PhyML
- DeCypher
- Green Button
- Dual Brothers Recombination Detection
- Mauve Genome Alignment
- CpG Islands
- Heterozygotes
- Transmembrane Prediction
- Coiled Coils (prediction)
- EMBOSS Tools

## Compatibility

Geneious can import all non-proprietary file formats from other major software packages.

- Clustal \*.aln
- DNASTar \*.seq, \*.pro
- DNA Strider \*.str
- Embl/UniProt \*.embl, \*.swp
- Endnote (8.0) XML \*.xml
- Fasta \*.fasta, \*.fas, etc.
- GCG \*.seq
- GenBank \*.gb, \*.xml
- Geneious \*.xml, \*.geneious
- Geneious Education \*.tutorial.zip
- GFF \*.gff
- MEGA \*.meg
- Molecular structure \*.pdb”, \*.mol, \*.xyz, \*.cml, \*.gpr, \*.hin, \*.nwo
- Newick \*.tre, \*.tree, etc.
- Nexus \*.nxs, \*.nex
- PDB \*.pdb
- PDF \*.pdf
- Phrap ACE \*.ace
- PileUp \*.msf
- PIR/NBRF \*.pir
- Raw sequence text \*.seq
- Rich Sequence Format \*.rsf
- Sequence Chromatograms \*.ab1, \*.scf
- Vector NTI sequence \*.gb, \*.gp
- Vector NTI/AlignX alignment \*.apr
- Vector NTI Archive \*.ma4, \*.pa4, \*.oa4, \*.ea4, \*.ca6
- Vector NTI database
- Vector NTI Contig Express .cep