Quick, easy AND powerful sequence analysis

MacVector

Still the leading Macintosh solution after 20 years!

MacVector, the leading sequence analysis package for the Mac, takes full advantage of the Mac's easy to use interface. MacVector makes it simple to import or create sequences, automatically annotate sequences, design primers and store them in a database, subclone into cloning vectors, align, assemble reads, find SNPs, simulate agarose gels, run protein analyses and a wide variety of other functions. All with just a few mouse clicks in a single integrated package.

Our latest release, MacVector 16, makes producing beautiful plasmid maps effortless and accurate de novo assembly easily achievable on your own desktop.

Align to Reference. Assemble sequencing reads against a reference. Quickly spot sequencing and cloning errors. Identify SNPs and other variants. Align cDNA/mRNA sequences against genomic sequences. Screen reads for INDELS or substitutions around CRISPR edits.

Validate CRISPR edits by mapping reads against your original sequence.

Primer Analysis. Design primers for PCR, sequencing and realtime analysis. Test primers before loading the thermal cycler. Maintain primers in your lab's own primer

Analyze your oligo against your template. Watch secondary structure of your primer in realtime. Store in the primer database.
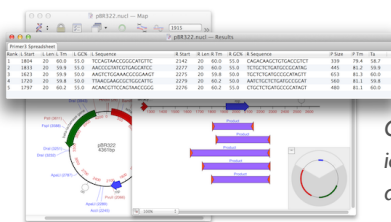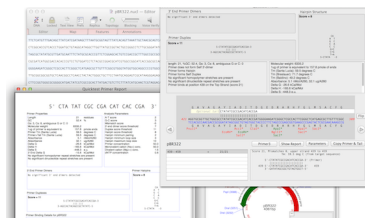
Click on a feature and identify suitable primers with as few as three mouse clicks.

database that can be used to scan any sequence. Add restriction sites and nudge your primer to find the optimal template binding site. Translationally silent sites are color coded.

Simulated Agarose Gel. Drag and drop restriction sites to a gel to see the fragments on a photo realistic agarose gel simulation. Easily design digests to check orientation of a ligation.
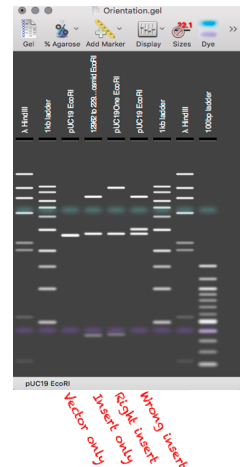
Restriction Mapping. Perform restriction digests using enzymes from a specific supplier or your own lab's freezer drawer.

Beautifully annotated plasmid maps Sequences are automatically scanned and missing features displayed. Even blank sequences will be displayed fully annotated. Keep a curated library of annotated sequences.

Graphical BLAST and Entrez Search the NCBI's Entrez database and run BLAST searches. Retrieve sequences directly to your desktop. Search your own local sequences too.

Multiple Sequence Analysis. Create alignments using ClustalW, Muscle or T-Coffee. Export publication-

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Software for Scientists

quality alignments. Align genes using translated sequences and display both AA and DNA in the resulting alignment. Quickly compare two sequences using Dot Plots.

Open Reading Frames and coding regions. ORFs are automatically displayed whenever you open a DNA sequence. More powerful tools are also available to annotate your gene.

Evolutionary Analysis. Generate customizable, true phylogenetic trees from an alignment and produce publication-quality output.

Click Cloning. Subclone DNA fragments with drag and drop ligations. Compatible cloning sites for are highlighted. Store fragments for later use. Ligations are documented with date, enzymes and and end modifications.

Protein Analysis. Predict protein secondary structure, hydropathy, antigenicity, and flexibility.. Identify potential functional domains with InterProScan.

Generate mRNA from a Genomic Sequence. Use the exon, intron, CDS and RNA features to generate the mRNA associated with a coding region.

MacVector Advantages

Easy to use interface. MacVector takes full advantage of the Mac interface. Open multiple views of your sequence and navigate large sequences with ease.

MacVector's easy to use interface allows you to navigate effortlessly through large feature rich sequences. The Overview keeps you updated on the location of the region shown in the main window.
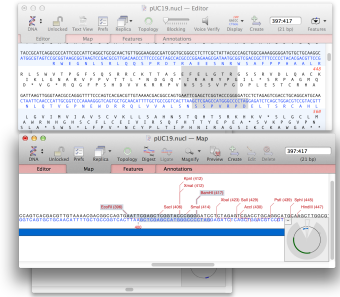
High Quality Graphics. You choose which features and results to display. Easily export graphics into any macOS application for publication by simply copying and pasting.

File Import and Export. Import and export in a wide variety of formats. Never be locked out of your data. Strict adherence to Genbank's Feature Table specification. Import annotation from Genome Browsers.
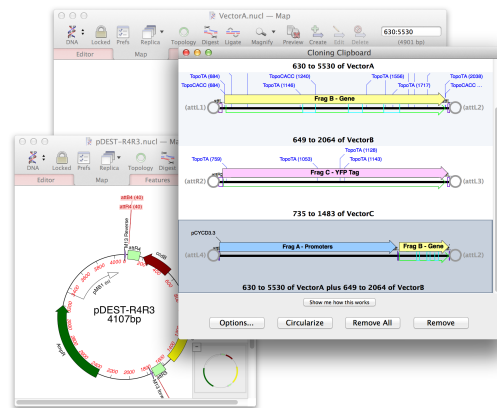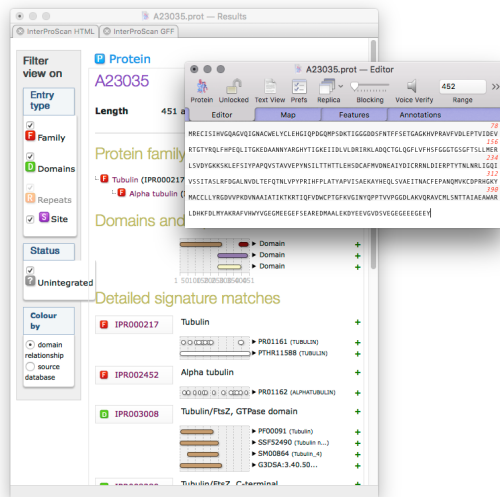
Scan your protein sequence against the InterPro database and annotate functional domains directly on your protein.

Click cloning allows you to easily document your constructs. Each cloning step is annotated as a Genbank compatible feature to document the construct's history.

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http://macvector.com