



# Version Comparison Table

	Version Comparison			
	5	6	7	8
<b>SeqMan Pro – Sequencing Assembly and Analysis</b>	●	●	●	●
SNP filtering in Reports				●
Codon display in SNP Report				●
Direct annotation capability				●
Faster assembly of large sequence projects				●
Assemble E. coli size genome and large EST and SNP data sets				●
Flowgram for Roche 454 assembly visualization				●
Add new Features by selecting the region or BLASTing				●
Full feature support on sequences and consensus				●
Analyze NextGen sequence assembled with SeqMan Ngen for Roche 454 and Illumina platforms				●
Primer walking system to handle larger number of sequences				●
Assemble E. coli size genomes and large EST and SNP data sets			●	●
Flowspace diagram for 454@ assembly visualization			●	●
Read Roche 454 output files (.sff, .fna, .fas and .qual types)			●	●
Maximum Expected Coverage repeat region analysis			●	●
Enhanced vector trimming			●	●
SNP Discovery			●	●
Advanced scripting ability		●	●	●
Ability to import and edit Sequencher™ assemblies		●	●	●
Pro Assembler for large assemblies of traditional and pyrosequencing data		●	●	●
Import and edit Sequencher assemblies	●	●	●	●
Locate regions of alignments for contig splitting	●	●	●	●
Automatically remove poor quality fragments and vector data	●	●	●	●
<b>MegAlign – Multiple Sequence Alignment</b>	●	●	●	●
Bootstrapping			●	●
ClustalW multiple alignment method	●	●	●	●
Export the majority consensus of alignments	●	●	●	●
Create sub-alignments from multiple sequence alignments	●	●	●	●
Export paup, .pau and .nex	●	●	●	●
Select a subsection of an alignment and clone to new project	●	●	●	●
Export data for further analysis or publication	●	●	●	●
Export sequences as FASTA	●	●	●	●
<b>PrimerSelect – Oligo Primer Design</b>	●	●	●	●
Automatic search for best primer pairs	●	●	●	●
Reports for primer composition, predicted hairpin structures and self and pair dimers	●	●	●	●
Create unique primer catalog	●	●	●	●
Automatic Oligo request form for simplified ordering	●	●	●	●

continued...

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<b>SeqBuilder – Sequence Editor, Feature Annotator, Cloning</b>		●	●	●
Design primers around selected features				●
Enhanced export to GenVision for visualizations				●
Import Vector NTI primers				●
Short-cut compatible enzyme selector				●
Detached feature labels			●	●
Ability to batch import Vector NTI files retaining feature names			●	●
Automated virtual cloning - site-directed, TA, TOPO® and Gateway® protocols			●	●
Copy as picture, export to Adobe Illustrator		●	●	●
Create graphically rich, publication quality linear and circular maps		●	●	●
Display and edit in multiple views simultaneously		●	●	●
Cut/paste sequences and annotations into many views		●	●	●
View ORFs, annotations, translations and restriction cut sites		●	●	●
<b>GeneQuest – Gene Finding</b>	●	●	●	●
Updated Transcription Factor binding sites				●
Enhanced export to GenVision for visualizations				●
Enhanced sorting, Feature display and editing				●
Automatic coding region prediction			●	●
Identify and annotate coding regions		●	●	●
GC content plot	●	●	●	●
Identifies regions where translation matches user specified protein sequence file	●	●	●	●
<b>Protean – Protein Structure Analysis</b>	●	●	●	●
Enhanced export to GenVision for visualizations				●
Implement protein profile pattern searches				●
Update Prosite database				●
Ability to sort features by type, name and position				●
Secondary structural analysis	●	●	●	●
Automatic prediction of proteolytic cleavage site	●	●	●	●
Locate potential antigenic sites determinants and sites from primary sequence data	●	●	●	●
<b>BLAST and ENTREZ Capabilities</b>	●	●	●	●
Text searching		●	●	●
Direct download in module		●	●	●
BLAST/ENTREZ results may be copied, printed and saved as text		●	●	●
BLAST and Entrez searching in all modules	●	●	●	●
Directly enter sequences from NCBI- BLAST or Entrez	●	●	●	●
Supports multiples servers	●	●	●	●
<b>Network License &amp; Platform Compatibility</b>	●	●	●	●
Sassafras Keyserver compatibility			●	●
Dual Platform Support - Windows and Macintosh	●	●	●	●

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