

Lasergene[®]

SeqMan Pro

FOR USE IN SEQUENCE ASSEMBLY, CONTIG MANAGEMENT AND SNP DISCOVERY

SeqMan Pro enables fragment data assembly from sequencing projects ranging from a few fragments to hundreds of thousands of fragments – at the push of a button. SeqMan Pro removes unreliable data, including poor quality ends, sub-minimal length reads, and vector and contamination host sequences in a single pass, then assembles the trimmed data and calls the consensus.

SeqMan Pro provides two different assembly methods: the Classic assembler, and the Pro assembler. The newer Pro assembler should be used when your data is: 1) large; 2) contains repeated sequences; 3) has noisy ends; or 4) is being used for SNP analysis. The addition of the new SeqMan Pro assembly algorithm provides Lasergene with the tool necessary to assemble bacterial size genomes using Roche 454[®] Life Sciences' pyrosequencing technology.

SeqMan Pro uses DNASTAR's unique trace quality evaluation method to call the most accurate consensus sequence possible. This method reduces the depth of coverage needed for accurate sequence determination, yielding spectacular savings in time and effort. SeqMan Pro also accepts Next Generation Sequencing data assembled on DNASTAR's SeqMan NGen assembly tool. SeqMan NGen can be used with data generated on either Roche 454 or Illumina Next Generation sequencing platforms.

To evaluate the assembly, a single alignment window allows you to view key aspects including:

- Two consensi for the same contig, called by different methods
- Multiple sequences and their underlying trace data
- The six-frame translation
- Candidate SNPs
- Sequence and consensus conflicts

MAIN SeqMan Pro Contig Alignment Window

The screenshot displays the SeqMan Pro interface with three main views highlighted by callouts:

- Translation view:** Shows the consensus sequence and its six-frame translations. The top frame is highlighted, showing the sequence: `D A L L G I I P V V A I T S Q V S A P F I S T D A P`.
- Alignments:** Displays multiple sequence alignments for various contigs (e.g., EBEO3TV04JY00H, EBEO3TV041EH04, etc.) against the consensus sequence. Red arrows indicate mismatches or gaps.
- Flowgram View:** Shows a bar chart representing the signal intensity for each nucleotide (A, C, G, T) at each position, used for quality assessment and SNP discovery.

