

## NEW FEATURES IN KODON VERSION 2.0

### **GeneBuilder contig assembler:**

- Two-level sequence cleanup function: trimming of bad quality areas and disabling of poor quality areas. Quality estimation based on chromatograms. Disabled areas are still aligned, but not used for contig determination.
- Improved automatic trim function
- Search function for subsequences with optional mismatches
- Possibility to trim contig to primers or other signature subsequences. Primer sequences can be saved.
- Possibility to screen and remove vectors using EMVEC (EMBL vector database)
- All colors user-adjustable
- Improved overall stability

### **Import-Export**

- Easier direct import from downloaded GenBank or EMBL sequence batch files
- Direct import from public websites using Kodon's internal web browser
- Import and export of FASTA formatted sequences
- Import of GeneBase files

### **Database**

- New powerful relational database system: choice between Oracle, SQL Server, Access, or the Jet engine driven by Kodon
- Automatic launch of BLAST searches on NCBI or any other public or private database
- Improved subsequence search with allowance of mismatches and gaps
- Easy *Sort by selected field* button

### **Sequence editor**

- New graphical overview of sequence in text editor
- Advanced subsequence search with allowance of mismatches and/or gaps in search and target sequence
- Export as FASTA/EMBL-GENBANK format
- New search tool for subsequences: gaps, mismatches, strand differentiation
- Fast and easy mapping of CDS from selected sequence
- Possibility to edit layout of sequence out of the Sequence Editing view
- New graphical overview within the Sequence Editing view: easy selection of sequence on the plot, easy selection of features

### **Direct & Inverted repeats**

- Automated search for optimal settings by starting up the module

### **Primer design**

- Screens primers for possible hairpin structures
- Improved control of parameters

- New graphical overview: easy selection of sequence on the plot, easy selection of features
- Easy selection of sense and antisense primer by clicking on the display
- Additional settings (such as salt-, DNA-concentrations)

### **Frame analysis**

- Direct annotation of CDS features from Frame analysis window
- Direct launch of Motif search from Frame analysis window
- New graphical overview: easy selection of sequences on the plot, easy selection of features
- Direct mapping of new CDS features on the sequence
- Launching primer design, motif search and protein property modules on the selected CDS

### **Restriction mapping**

- New graphical overview: easy selection of sequence on the plot, easy selection of features

### **Gel Window**

- Possibility to mark positions of gel marker

### **Cloning window**

- Undo function
- Deletion of clones

### **New applications and features in Molecular Analysis module**

- Analysis of RNA secondary structure (folding)
- Analysis of protein properties: amino acid composition, alpha helices, Leucine zippers and coiled coils
- Advanced search for multiple short repeats, e.g. for VNTR or PCR fragment analysis

### **Multiple alignment editor**

- Possibility to superimpose multiple alignment of protein sequences on corresponding DNA sequences
- New Maximum likelihood clustering
- New display of unrooted trees for maximum parsimon and maximum likelihood methods