



KODON 3.6: LIST OF NEW FEATURES

Version 3.60 Release – 8 August 2008

Version 3.61 Release – 29 October 2008

Assembler

- Now supporting IUPAC codes for triple degeneracies.
- Option “Show trace names” in consensus view panel.

Feature Matrix and Cluster Analysis

- Version 3.61: Added option <Full sequence> button to select the entire sequences to compare, whatever the composition is. This feature replaces previous <Source> button and makes the tools compatible with composite sequences containing multiple source features.

Annotation

- Improved automatic annotation through BLAST on NCBI/EMBL: optional saving of project after each BLAST to avoid loss of data in case of server time-outs
- Translation of found CDS features now automatically saved with project.

Comparative chromosome analysis

- New option “Optimize alignment of overlapping stretches” to perform a secondary fine alignment for improved matching of stretch ends.

Chromosome Alignment

- Improved and more reliable SNP searches through new option “Optimize alignment of overlapping stretches” (performs a secondary fine alignment to improve matching of stretch ends).
- Assignment of a quality score to SNPs for filtering on SNP significance.
- Addition of Intergenic Mutations to list of mutations to screen for.
- Version 3.61: New function “Export selected sequence as new entry” to save an aligned (chromosome) sequence as a Kodon database entry. This function allows short unassembled sequences directly collected from a high throughput sequencer to be aligned against a full chromosome of a related organism and saved in the database.

Script language

- Large set of new script functions for Annotation, Chromosome alignment and Entry manipulation.