

Information about Sequence

Context information about a sequence can be found on the *Statistics* tab in the *Options Panel*. All information is contextual, i.e. it shows statistics about the currently selected region (on the selected sequence). The tab includes information about:

- Common statistics
 - Length - number of bases in the analyzed sequence
 - GC content - the molar percentage of guanine and cytosine bases in an oligonucleotide sequence
 - Molar weight - is the sum of the atomic masses of the constituent atoms for 1 mole of oligonucleotide
 - Molar ext. coefficient - the molar extinction coefficient is a physical constant that is unique for each sequence and describes the amount of absorbance at 260nm (A_{260}) of 1 mole/L DNA solution measured in 1 cm path-length cuvette
 - Melting T_M - melting temperature is the temperature at which an oligonucleotide duplex is 50% in single-stranded form and 50% in double-stranded form
 - nmole/ OD_{260} - the amount of oligonucleotide in nanomoles that, when dissolved in 1 mL volume, results in 1 unit of absorbance at 260 nm with a standard 1 cm path-length cuvette
 - g/ OD_{260} - the amount of oligonucleotide in micrograms that, when dissolved in 1 mL volume, results in 1 unit of absorbance at 260 nm with a standard 1 cm path-length cuvette
- Characters occurrence
- Dinucleotides occurrence (for sequences with the standard DNA and RNA alphabets)

The screenshot shows a bioinformatics software interface. The main window displays a sequence alignment with various annotations. A statistics panel on the right provides detailed metrics for the selected region.

Statistics

▼ Common Statistics

- Length:** 589
- GC Content:** 52.12%
- Molar Weight:** 181766.49 Da
- Molat Ext. Coef:** 6352900 I/mol
- Melting T_M :** 85.13 C
- nmole/ OD_{260} :** 0.16
- μ g/ OD_{260} :** 28.61

▼ Characters Occurrence

- A:** 151 25.6%
- C:** 163 27.7%
- G:** 144 24.4%
- T:** 131 22.2%

▼ Dinucleotides

- AA:** 50
- AC:** 28
- AG:** 44
- AT:** 29
- CA:** 41
- CC:** 54
- CG:** 27
- CT:** 41
- GA:** 37
- GC:** 38
- GG:** 37
- GT:** 32
- TA:** 22

Name | **Value**

- Auto-annotations [murine.gb | NC_001363]
- NC_001363 features [murine.gb]
 - CDS (0, 4)
 - CDS: 1042..2658
 - CDS: join(2970..3413,3412..3873)
 - CDS: 3875..4999
 - CDS: 5048..5203
 - misc_feature (0, 2)
 - misc_feature: 2..590
 - misc_feature: 5245..5833
 - source (0, 1)

To copy the statistical information about a sequence select it on the *Options Panel* and choose the copy item in the context menu, or use the Ctrl+C shortcut.