


# ClustalW

**Purpose:** Bioinformatics

**Latest version:** 2.1

**Licence:**  Free of use for academics users  
Mixed

**Website:** [http://www.clustal.org/omega/\\_ext-link](http://www.clustal.org/omega/_ext-link)

**Clustal** is a series of widely used computer programs used in Bioinformatics for multiple sequence alignment.

**ClustalW** is the third generation, released in 1994, greatly improved upon the previous versions. It improved upon the progressive alignment algorithm in various ways, including allowing individual sequences to be weighted down or up according to similarity or divergence respectively in a partial alignment. It also included the ability to run the program in batch mode from the command line.

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