

Viewing your alignment locally



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AliView

About

AliView is yet another alignment viewer and editor, but this is probably one of the fastest and most intuitive to use, not so bloated and hopefully to your liking.

The general idea when designing this program has always been **usability** and **speed**, all new functions are optimized so they do not affect the general performance and capability to work swiftly with large alignments. The speed in rendering even makes it possible to work with large alignments on older hardware.

A need to easily sort, view, remove, edit and merge sequences from large transcriptome datasets initiated the design of the program.

It is of course also working very well with smaller datasets:)

The program is developed at the department of Systematic Biology, [Uppsala University](https://www.uppsala.se), so there is probably a predominance in functionality supporting those working with phylogenies.

Citation: Larsson, A. (2014). AliView: a fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics*30(22): 3276-3278. <http://dx.doi.org/10.1093/bioinformatics/btu531>

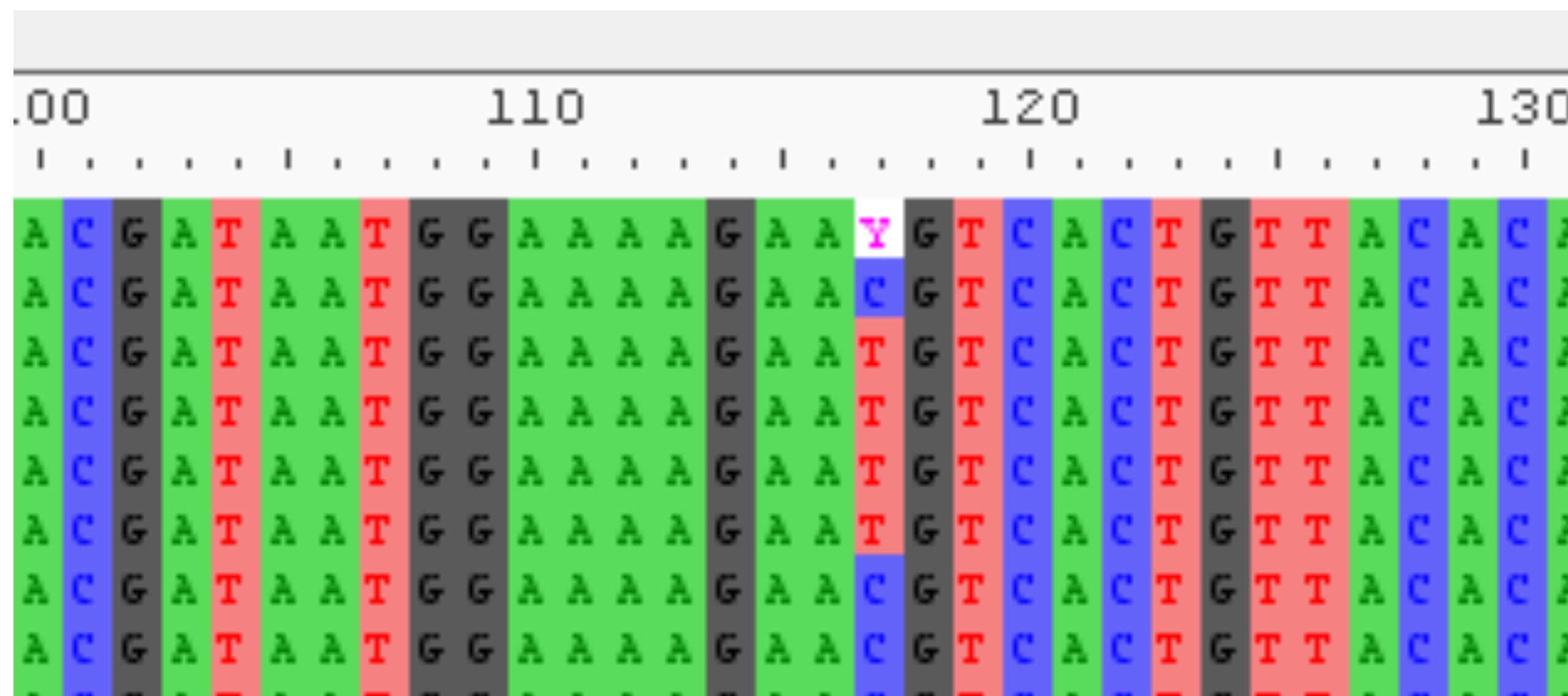
The program is released under the **Open Source** Software License 'GNU General Public License, version 3.0 (GPLv3)'
Source code is available at **GitHub**: <https://github.com/AliView/AliView>

Download the latest stable version: 1.28 (24/Nov/2021) (Mac OS X, Windows, Linux)



Download at <https://ormbunkar.se/aliview/>

Ambiguous bases can disrupt selection analyses



Ambiguous

- **N** Any nucleotide (A or C or G or T or U)
- **R** Purine (A or G)
- **Y** Pyrimidine (T or C)
- **K** Keto (G or T)
- **M** Amino (A or C)
- **S** Strong interaction (3 H bonds) (G or C)
- **W** Weak interaction (2 H bonds) (A or T)
- **B** Not A (C or G or T)
- **D** Not C (A or G or T)
- **H** Not G (A or C or T)
- **V** Not T or U (A or C or G)