

Sequence contribution analysis and graphical representation

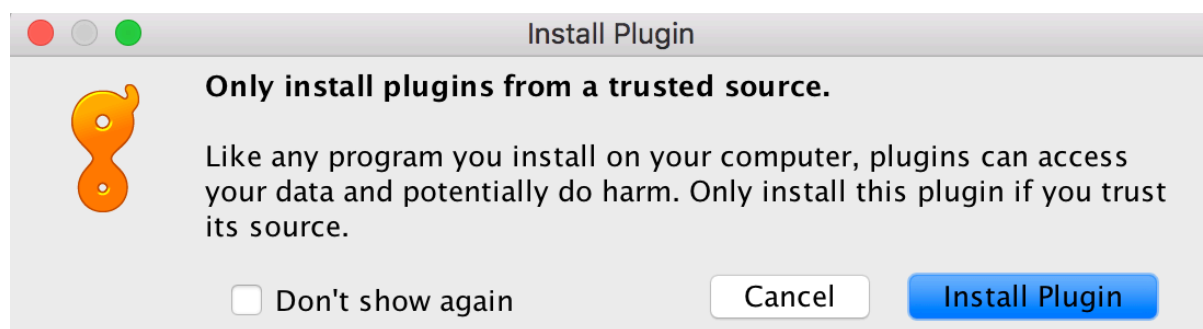
Background:

For Background information refer to Materials and Methods section of the manuscript:

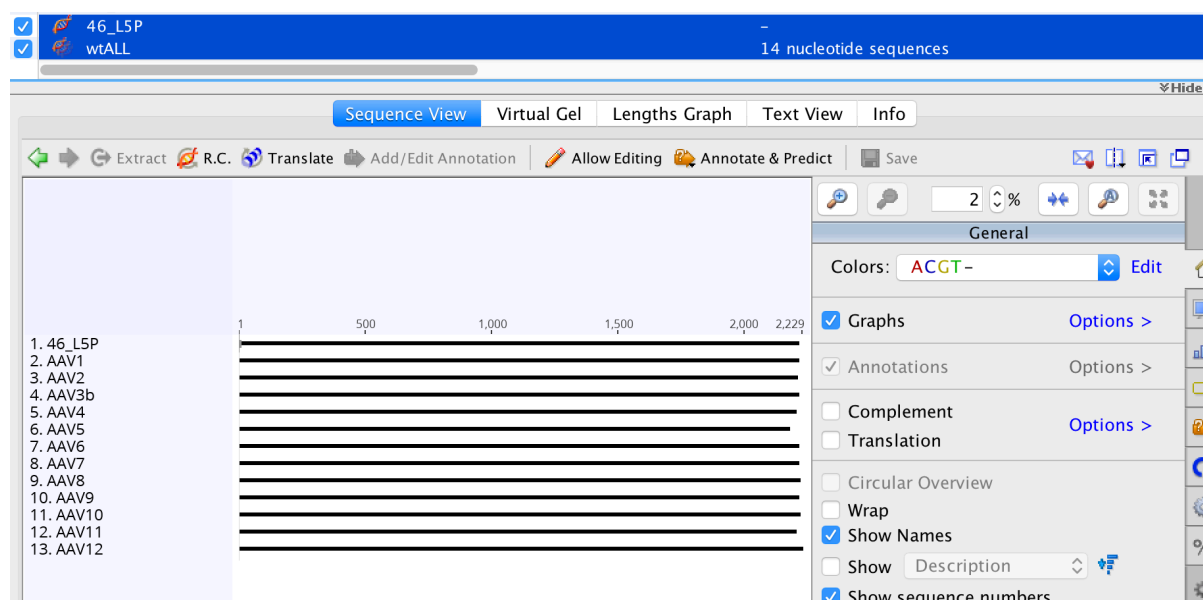
Cabanes-Creus M et al, Codon-Optimization of Wild-Type Adeno-Associated Virus Capsid Sequences Enhances DNA Family Shuffling while Conserving Functionality. Mol Ther Methods Clin Dev. 2018 Nov 1;12:71-84.

Step by step guide

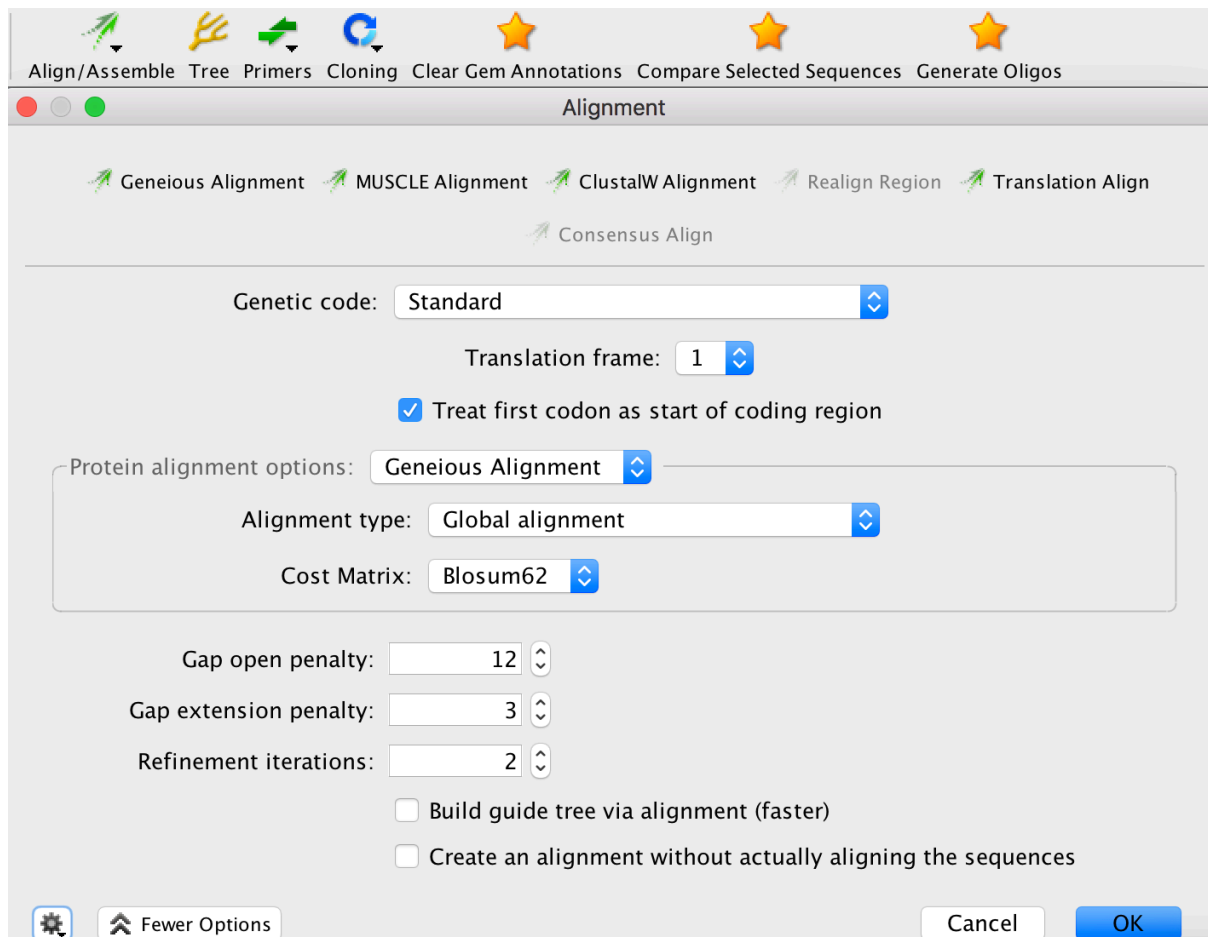
1. Download the 'Sequence contribution analysis.gplugin' from <https://github.com/CMRI-TVG/AAVcodons>
2. Install plugin on Geneious.



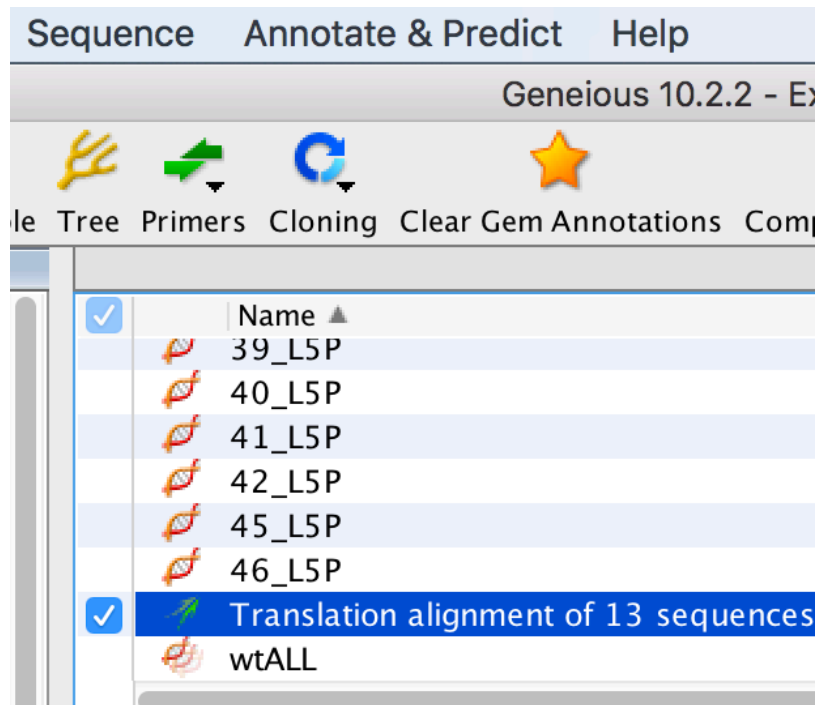
3. In order to use the plugin, first generate a Geneious FASTA file with all the parental AAV serotypes used in library construction (in this example wtALL).



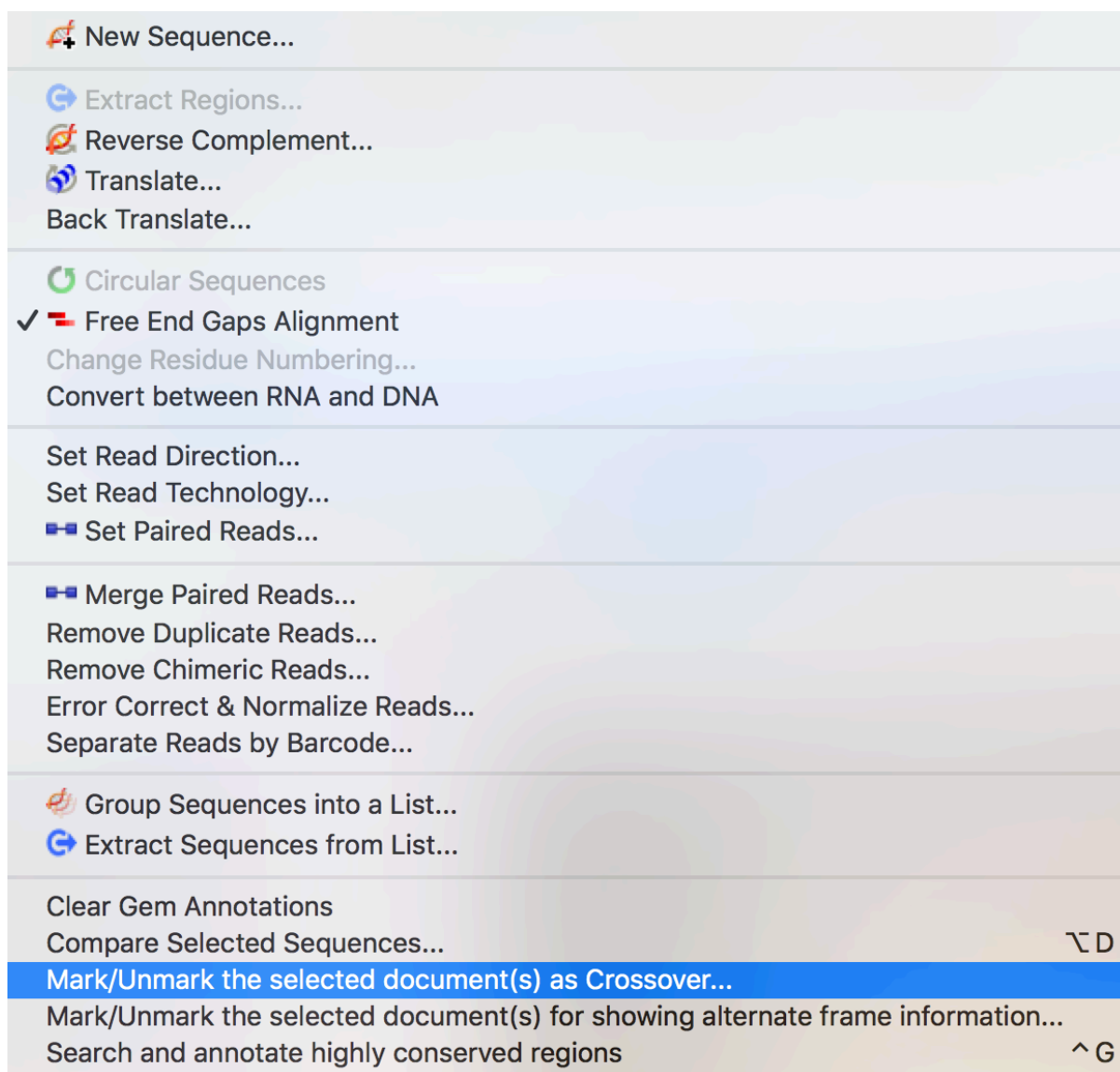
4. Select then your chimera of interest (in this example 46_L5P) and perform a Translation based Multiple sequence alignment by clicking on Align/Assemble in the main menu -> Multiple Align... -> Translation align. Use the following settings and click OK.



5. With the alignment selected, click on Sequence (top Menu).



6. Finally, click on Mark/Unmark the selected document(s) as Crossover...



- The crossover should appear on the Alignment view window. Statistics can be found on the right panel.

