

# BioJS in Action

Biological visualisation with existing components



# BioJS

## VAPoR

## Component examples

Options  
E-value threshold: 1.0e-60

>-example  
ATTTTTCGCAATTTTCGAAATGAGAGATGAGAGTGGGGATGCAAACTGGTGA  
TTTTTTCGCAATTTTCGAAATGAGAGATGAGAGTGGGGATGCAAACTGGTGA  
GGCCCTCGAGGCTCAGGGAGAGCAACTTTTGTGGCTTTGGCTGGAAAC  
TGAGTTGAGATCTGAGGAGGAGGAGGAGCAACTTTTGTGGCTTTGATGATTT

Submit

Log  
Showing expression for AB30G\_ARAT1  
Showing interactions for AB30G\_ARAT1  
Showing interactions for AB43G\_ARAT1

The screenshot displays the VAPoR web interface. At the top, there are input fields for an E-value threshold and a sequence. Below this is a 'Submit' button and a 'Log' section. The main area is divided into four panels: a phylogenetic tree on the left, a sequence alignment matrix in the center, a network diagram on the bottom left, and a plant image on the bottom right. The network diagram shows nodes representing genes like NAP5, ABCA7, GYP702A8, ABCG21, ABCG22, ABCG23, ABCG24, ABCG25, ABCG26, and ABCG30. The plant image shows a green plant with a stem and leaves.

The grid shows nine different BioJS components:
 

- Tree Viewer:** A fan-shaped phylogenetic tree.
- MSA viewer:** A multiple sequence alignment matrix with colored amino acids.
- Proteome:** A circular network diagram representing a proteome.
- 3D structures:** A 3D ribbon model of a protein structure.
- Dot-bracket:** A dot-bracket diagram representing RNA secondary structure.
- Muts-needle plot:** A plot showing mutation rates across a sequence.
- Protein Feature Viewer:** A linear sequence with various features and domains highlighted.
- Plasmids:** A circular plasmid map with a BamHI site and a sequencing region indicated.
- Pathway visualization:** A complex network diagram representing a biological pathway.

<http://vapor.biojs.tgac.ac.uk>



# Component Registry

# Distributed via npm & git

**BIOJS REGISTRY**

Submit Wish a component Stats About us

Search:  130 components found

Component	Stars	Downloads	Modified	Demos
<b>biocider</b> 0.8.8 Carlos Horro Contextualisation INCEX for biological Resources discovery: Contextualised visualisation of ELIXIR training materials, e... ELIXIR   Ann TeSS   conted   bioinformatics   client   util	1		a day ago	
<b>cytoscape</b> 3.8.4 Max Franz Graph theory (a.k.a. network) library for analysis and visualisation... graph   graph-theory   network   node   edge   vertex   link   analysis   visualisation   visualization   requires   and   commonjs   npm   nodejs   bower   jquery	1940		2 days ago	
<b>genomediff</b> 1.7.0 Roland Groza Parses strings from files in the GenomeDiff format generated by the breeq variant caller for haploid microbial organism... genomediff   gd   biology   laboratory   genome   sequencing   parser	1		3 days ago	

**bio-vis-expression-bar**

Single barchart to show expression levels across experiments

npm install bio-vis-expression-bar

Expression unit: count

Legend: study, High level age, Age, High level tissue, Tissue, High level variety, Variety, High level stress-disease, Stress-disease

Bar chart showing expression levels for various studies and conditions.

[www.biojs.io](http://www.biojs.io)

Detail view



[www.biojs.net](http://www.biojs.net)

# Final Result



## 374 Protein Sequence

```

1  | MGTAGKVIKC  KAAVLWGVNQ  PFSIEEIEVA  PPKAKEVRVK  ILATGICRTD  DHIKGSMSVS  KFPVIVGHEA  VGVVESVGE  VTTVRPGDKV  IPLFLPQCRE
101 | CNACLNPEGN  LCIRSDLTGR  GVLADGTTRF  TCKGKPVQHF  MNTSTFTEYT  VLDESSVAKV  DGAAPPEKAC  LIGCGFSTGY  GAAVKTAKVT  PGSTCVVFG
201 | GVGLSVIMG  CKAAGASRII  GIDINKDKFQ  KALAVGATEC  ISPKDSTKPI  SEVLSDMTGN  TIQYTFEVIG  RLETMVDALS  SCHMNYGTSV  VVGAPPSAKM
301 | LTYDPMLLFT  GRTWKGCVFG  GWKSRDDVPK  LVTEFLEKKF  DLDQLITHTL  PFNNINEGFE  LLYSGKSIRT  VLTF

```

# Demo Time



# Thanks for coming!

Stay for pizza and drinks!

