abYsis v4

abYsis was created from the academic work of Prof. Andrew Martin's group at UCL (University College London). The public version of abYsis is one of the world's most popular systems for investigating antibody sequences.

Commercial licencees of abYsis, receive a distribution of the complete, standalone abYsis system so that they can install the system in a location and in a manner of their own choosing.

Licencing is provided through the university commercialisation subsidiary, UCL Business Ltd. Commercial licencing of abYsis helps fund and facilitate academic research for the benefit of the wider community.

IT/TECHNICAL/COMPUTE INFORMATION

In addition to the information below please refer to the other files at; http://info.abysis.org which cover Installation and Data Loading, plus an introduction to using hosted servers which are increasingly popular. AWS is used as the exemplar.

Of note in the new version are the following enhancements and improvements:

Licence Key Assignment

The Licence Key to activate usage – typically renewed each year – can now be uploaded by users through a dedicated page rather than requiring IT team involvement. Go to Tools/Licence & Info
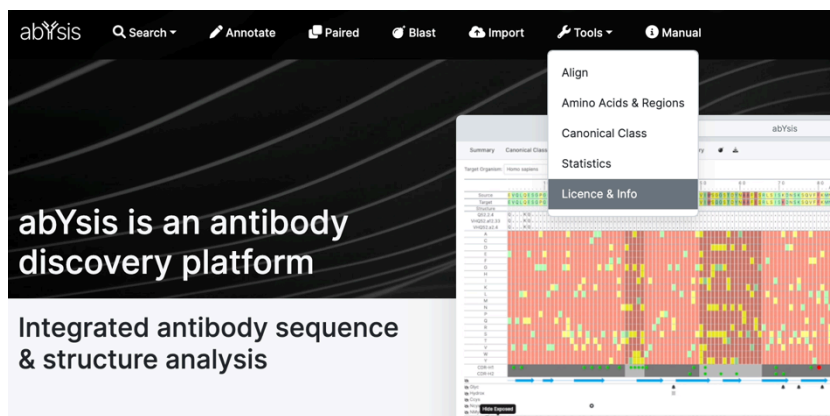
Installation Process

Reduction in external library dependencies especially HTML::Mason module, simplifying installation.

Increased checks including
- presence/absence of files starting from a minimal OS
- differences resulting from hardened variants.

User preferences

Simple cookies enable each user to set and maintain preferences especially; Antibody numbering scheme, CDR definition scheme, Organism and Sequence Display format. This removes the previous requirement to constantly reset manually.

Libraries
The following were removed and replaced with "Bootstrap v5.0.2":
- OverLib – Tooltips and Popovers
- jQueryUI – Tooltips, Dialog boxes and Accordions

Display Improvements
- Adjustments to the cascading style sheets
- Layout to better support HDPI screens and windows resizing.
- Menus work on "click" rather than on "hover" enabling better support of touch screens.
- A new help system using an "in window" display rather than "popup windows", removes previous issues with popup blockers.

USER/SCIENTIFIC ENHANCEMENTS

Global settings

Global settings for Numbering, CDRs, Organism preference and colouring maintained across all pages. Select preferred strategy and click Apply
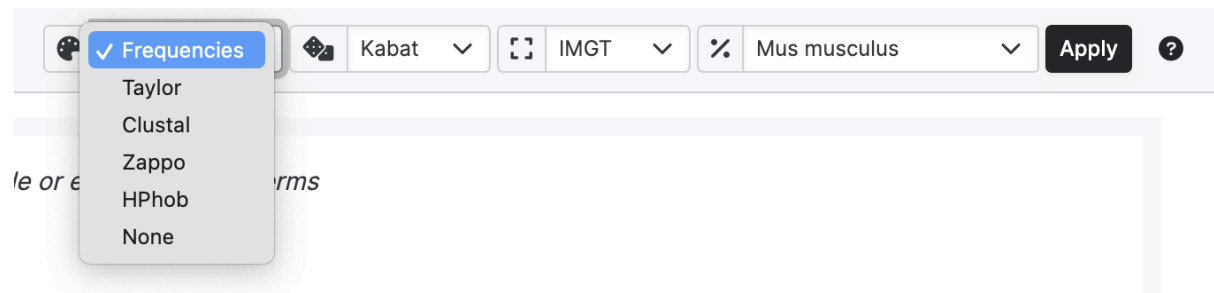
Multiple sequence display colouring by frequencies (Remember to set frequencies for desired organism in the Global Settings)

Triage tab

This enhancement allows you to prioritise sequences from large datasets based on CDR length & PTMs before viewing in detail.

Note: To use the Triage Tab your sequences MUST have been loaded into the database using the Import function. Triage will NOT appear if just using the interactive Annotate option.

Improved Excel export from each Tab

3D Structure

For the first time we have introduced a way to interrogate your own sequences with 3D structure annotation. At the current time, for this to work, you must have built a homology model using an external 3rd party program and loaded it using the new PDB Import option. In the future we will introduce our own modelling capability – this is the first step towards that goal.

Once loaded you can explore sequence positions with characteristics of interest by selecting them on the humanise tab and seeing their positions reflected in the 3D tab.
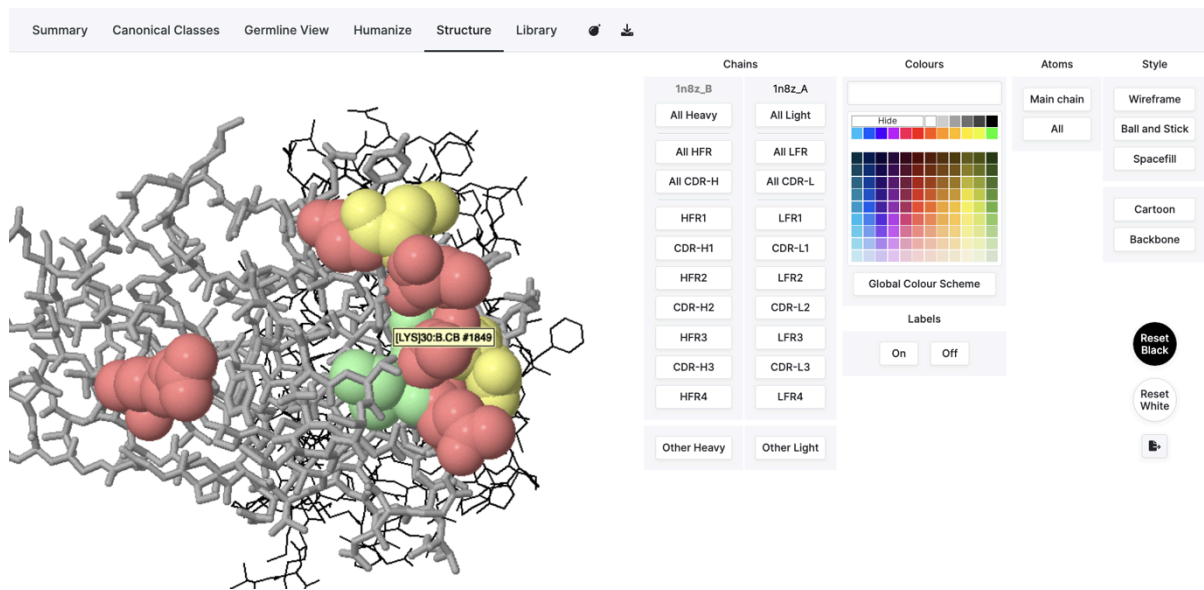
Paired Heavy/Light Analysis

Historically, abYsis was designed as a means to interrogate one chain (heavy or light) individually. If you have paired Heavy/Light chains and want to view the information together we have improved the system by providing a new Paired facility from the top menu.

This will give you the humanise tab layout which contains most data, for both chains on a single web page (but without the individual detailed tabs). If you also want the Tab detail simply open separate browser Tabs and additionally load each chain individually (so you'd have three Tabs in total; heavy, light and Paired).

Library Module

For those with Library module access. A new position-specific override so that you can select the frequency threshold per position, not just per region.
In the first image we have selected H16 to over-ride (first you must select the residue and then click override).
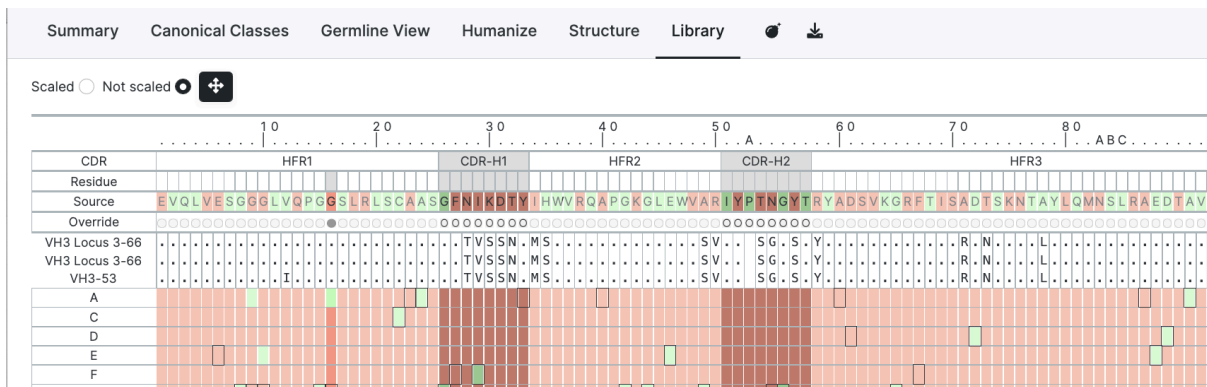
In the following image you can see the extra slider for the selected H16

H16 (Kabat) Mus musculus (Source)
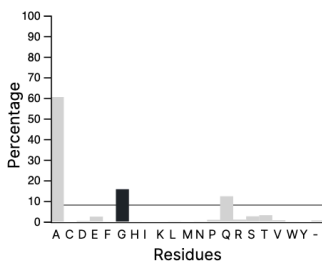
AA	Sequences	f	AA	Sequences	f
A	14425	60%	M	3	<1%
C	0	<1%	N	22	<1%
D	81	<1%	P	195	<1%
E	567	2%	Q	2929	12%
F	10	<1%	R	225	<1%
G	3746	16%	S	604	3%
H	15	<1%	T	733	3%
I	3	<1%	V	153	<1%
K	7	<1%	W	9	<1%
L	22	<1%	Y	0	<1%
			-	128	<1%

HFR1:	0.4
CDR-H1:	0.4
HFR2:	0.4
CDR-H2:	0.4
HFR3:	0.4
CDR-H3:	0.4
HFR4:	0.4
Override:	
H16:	0.08