abYsis

abYsis v5

abYsis is based on 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.

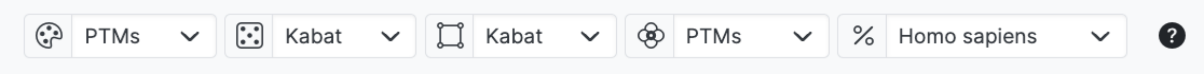
Commercial licencees of abYsis, receive a distribution of the complete, standalone abYsis system so that they can install the system in a location and in a manner of their own choosing.

Licencing is provided through Abysis Ltd

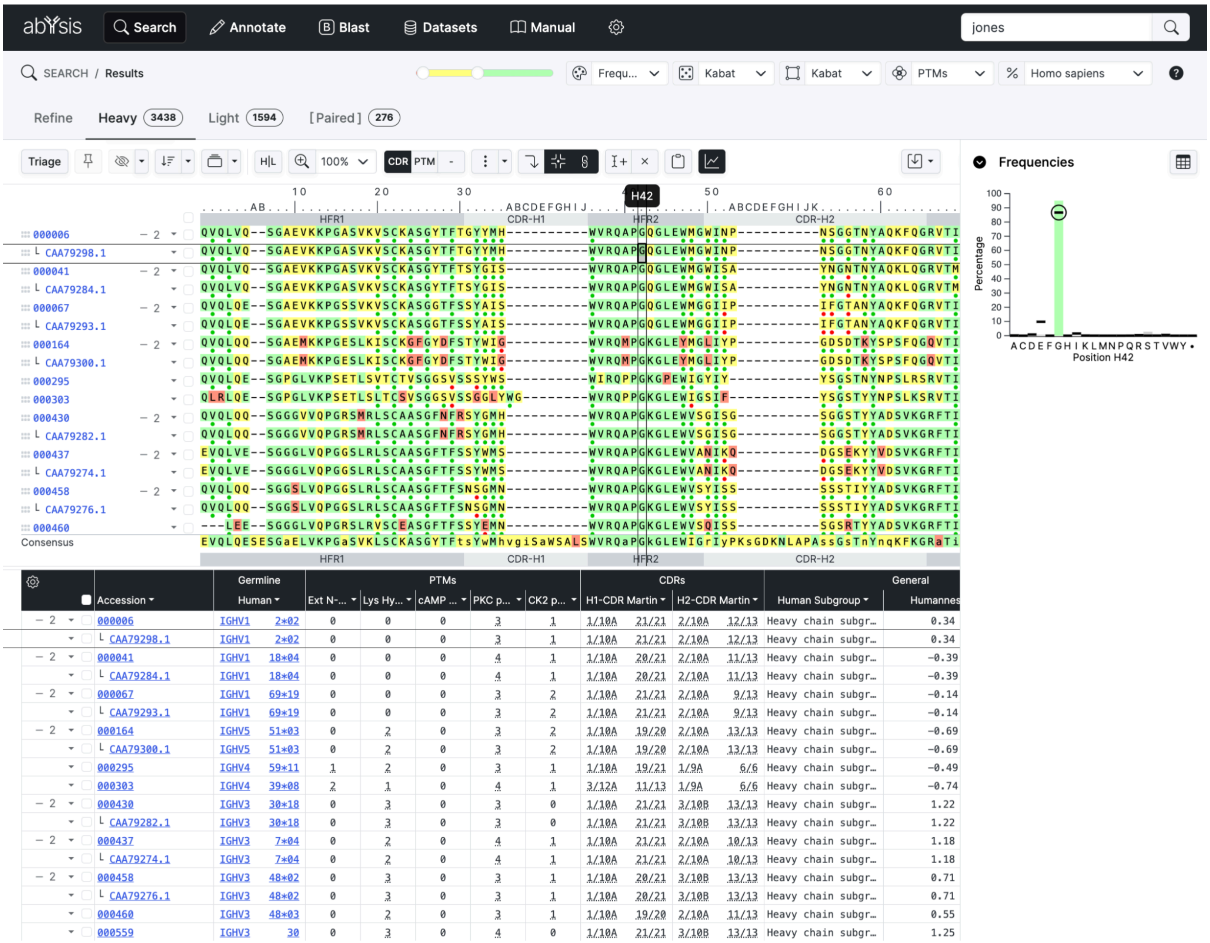
Recent Enhancements

Global settings

A new set of global settings for Numbering, CDRs, Organism preference and additional colouring selections are maintained across all relevant pages.



Multiple sequence display colouring by frequencies (Remember to set frequencies for desired organism in the Global Settings), PTMs, CDR determinants as well as a range of well-known biophysical colouring schemes

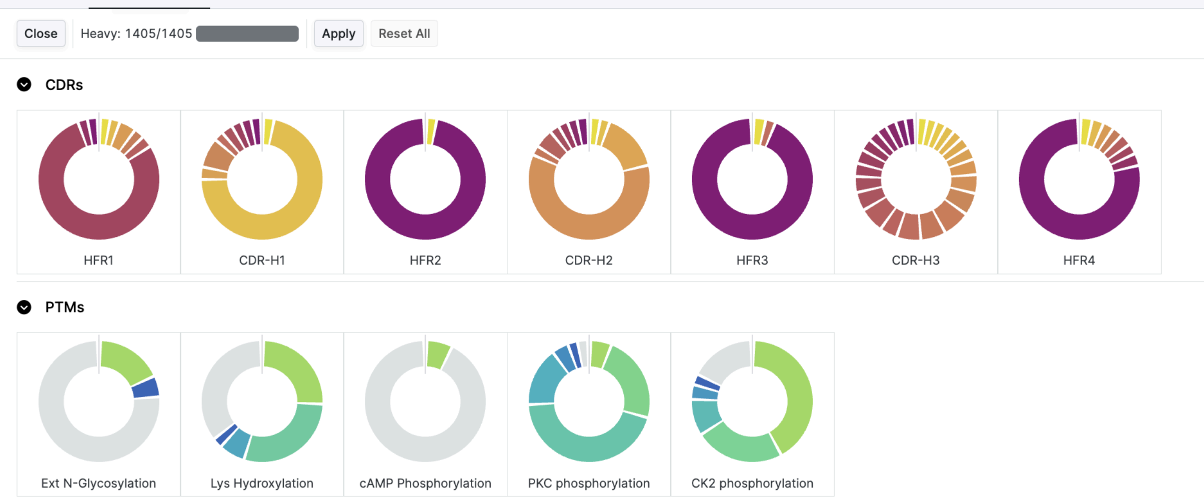


```
                          10        20        30                    H42       50                    60
                    ......AB...|.........|.........|.....ABCDEFGHIJ....|.........|..ABCDEFGHIJK........|.........
                    HFR1                                  CDR-H1          HFR2               CDR-H2
000006        – 2   QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTGYYMH----------WVRQAPGQGLEWMGWINP----------NSGGTNYAQKFQGRVTI
└ CAA79298.1        QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTGYYMH----------WVRQAPGQGLEWMGWINP----------NSGGTNYAQKFQGRVTI
000041        – 2   QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTSYGIS----------WVRQAPGQGLEWMGWISA----------YNGNTNYAQKLQGRVTM
└ CAA79284.1        QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTSYGIS----------WVRQAPGQGLEWMGWISA----------YNGNTNYAQKLQGRVTM
000067        – 2   QVQLQE--SGAEVKKPGSSVKVSCKASGGTFSSYAIS----------WVRQAPGQGLEWMGGIIP----------IFGTANYAQKFQGRVTI
└ CAA79293.1        QVQLQE--SGAEVKKPGSSVKVSCKASGGTFSSYAIS----------WVRQAPGQGLEWMGGIIP----------IFGTANYAQKFQGRVTI
000164        – 2   QVQLQQ--SGAEMKKPGESLKISCKGFGYDFSTYWIG----------WVRQMPGKGLEYMGLIYP----------GDSDTKYSPSFQGQVTI
└ CAA79300.1        QVQLQQ--SGAEMKKPGESLKISCKGFGYDFSTYWIG----------WVRQMPGKGLEYMGLIYP----------GDSDTKYSPSFQGQVTI
000295              QVQLQE--SGPGLVKPSETLSVTCTVSGGSVSSSYWS----------WIRQPPGKGPEWIGYIY-----------YSGSTNYNPSLRSRVTI
000303              QLRLQE--SGPGLVKPSETLSLTCSVSGGSVSSGGLYWG--------WVRQPPGKGLEWIGSIF-----------YSGSTYYNPSLKSRVTI
000430        – 2   QVQLQQ--SGGGVVQPGRSMRLSCAASGFNFRSYGMH----------WVRQAPGKGLEWVSGISG----------SGGSTYYADSVKGRFTI
└ CAA79282.1        QVQLQQ--SGGGVVQPGRSMRLSCAASGFNFRSYGMH----------WVRQAPGKGLEWVSGISG----------SGGSTYYADSVKGRFTI
000437        – 2   EVQLVE--SGGGLVQPGGSLRLSCAASGFTFSSYWMS----------WVRQAPGKGLEWVANIKQ----------DGSEKYYVDSVKGRFTI
└ CAA79274.1        EVQLVE--SGGGLVQPGGSLRLSCAASGFTFSSYWMS----------WVRQAPGKGLEWVANIKQ----------DGSEKYYVDSVKGRFTI
000458        – 2   QVQLQQ--SGGSLVQPGGSLRLSCAASGFTFSNSGMN----------WVRQAPGKGLEWVSYISS----------SSSTIYYADSVKGRFTI
└ CAA79276.1        QVQLQQ--SGGSLVQPGGSLRLSCAASGFTFSNSGMN----------WVRQAPGKGLEWVSYISS----------SSSTIYYADSVKGRFTI
000460              ---LEE--SGGGLVQPGRSLRVSCEASGFTFSSYEMN----------WVRQAPGKGLEWVSQISS----------SGSRTYYADSVKGRFTI
Consensus           EVQLQESESGaELVKPGaSVKLSCKASGYTFtsYwMhvgiSaWSALSWVRQaPGkGLEWIGrIyPKsGDKNLAPAssGsTnYnqKFKGRaTi
                    HFR1                                  CDR-H1          HFR2               CDR-H2
```

		Germline		PTMs					CDRs				General	
	Accession	Human		Ext N-...	Lys Hy...	cAMP ...	PKC p...	CK2 p...	H1-CDR Martin		H2-CDR Martin		Human Subgroup	Humannes
– 2	000006	IGHV1	2*02	0	0	0	3	1	1/10A	21/21	2/10A	12/13	Heavy chain subgr…	0.34
	└ CAA79298.1	IGHV1	2*02	0	0	0	3	1	1/10A	21/21	2/10A	12/13	Heavy chain subgr…	0.34
– 2	000041	IGHV1	18*04	0	0	0	4	1	1/10A	20/21	2/10A	11/13	Heavy chain subgr…	−0.39
	└ CAA79284.1	IGHV1	18*04	0	0	0	4	1	1/10A	20/21	2/10A	11/13	Heavy chain subgr…	−0.39
– 2	000067	IGHV1	69*19	0	0	0	3	2	1/10A	21/21	2/10A	9/13	Heavy chain subgr…	−0.14
	└ CAA79293.1	IGHV1	69*19	0	0	0	3	2	1/10A	21/21	2/10A	9/13	Heavy chain subgr…	−0.14
– 2	000164	IGHV5	51*03	0	2	0	3	2	1/10A	19/20	2/10A	13/13	Heavy chain subgr…	−0.69
	└ CAA79300.1	IGHV5	51*03	0	2	0	3	2	1/10A	19/20	2/10A	13/13	Heavy chain subgr…	−0.69
	000295	IGHV4	59*11	1	2	0	3	1	1/10A	19/21	1/9A	6/6	Heavy chain subgr…	−0.49
	000303	IGHV4	39*08	2	1	0	4	1	3/12A	11/13	1/9A	6/6	Heavy chain subgr…	−0.74
– 2	000430	IGHV3	30*18	0	3	0	3	0	1/10A	21/21	3/10B	13/13	Heavy chain subgr…	1.22
	└ CAA79282.1	IGHV3	30*18	0	3	0	3	0	1/10A	21/21	3/10B	13/13	Heavy chain subgr…	1.22
– 2	000437	IGHV3	7*04	0	2	0	4	1	1/10A	21/21	2/10A	10/13	Heavy chain subgr…	1.18
	└ CAA79274.1	IGHV3	7*04	0	2	0	4	1	1/10A	21/21	2/10A	10/13	Heavy chain subgr…	1.18
– 2	000458	IGHV3	48*02	0	3	0	3	1	1/10A	20/21	3/10B	13/13	Heavy chain subgr…	0.71
	└ CAA79276.1	IGHV3	48*02	0	3	0	3	1	1/10A	20/21	3/10B	13/13	Heavy chain subgr…	0.71
	000460	IGHV3	48*03	0	2	0	3	1	1/10A	19/20	2/10A	11/13	Heavy chain subgr…	0.55
	000559	IGHV3	30	0	3	0	4	0	1/10A	21/21	3/10B	13/13	Heavy chain subgr…	1.25

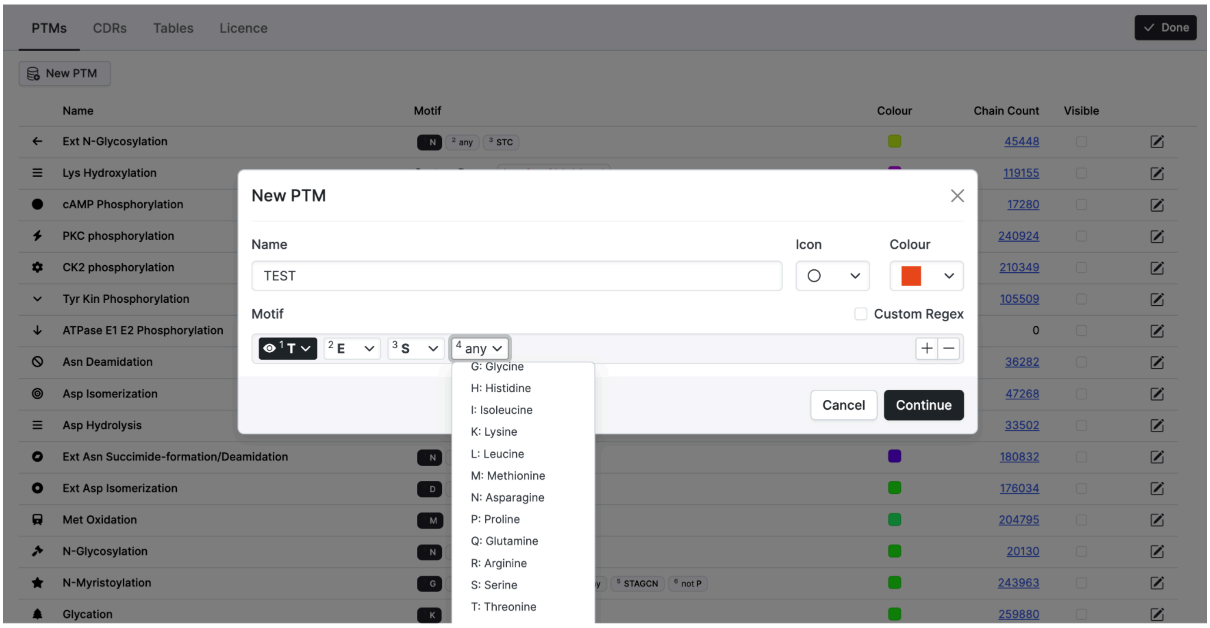
Triage tab

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



PTM Motifs

You can now add your own motifs very simply with our motif builder and search across all sequences in the database



Name	Motif	Colour	Chain Count	Visible
Ext N-Glycosylation	N · 2 any · 3 STC	🟩	45448	☐
Lys Hydroxylation			119155	☐
cAMP Phosphorylation			17280	☐
PKC phosphorylation			240924	☐
CK2 phosphorylation			210349	☐
Tyr Kin Phosphorylation			105509	☐
ATPase E1 E2 Phosphorylation			0	☐
Asn Deamidation			36282	☐
Asp Isomerization			47268	☐
Asp Hydrolysis			33502	☐
Ext Asn Succimide-formation/Deamidation	N	🟪	180832	☐
Ext Asp Isomerization	D	🟩	176034	☐
Met Oxidation	M	🟩	204795	☐
N-Glycosylation	N	🟩	20130	☐
N-Myristoylation	G · …y · 5 STAGCN · 6 not P	🟩	243963	☐
Glycation	K	🟩	259880	☐

New PTM

Name: TEST

Icon: ○

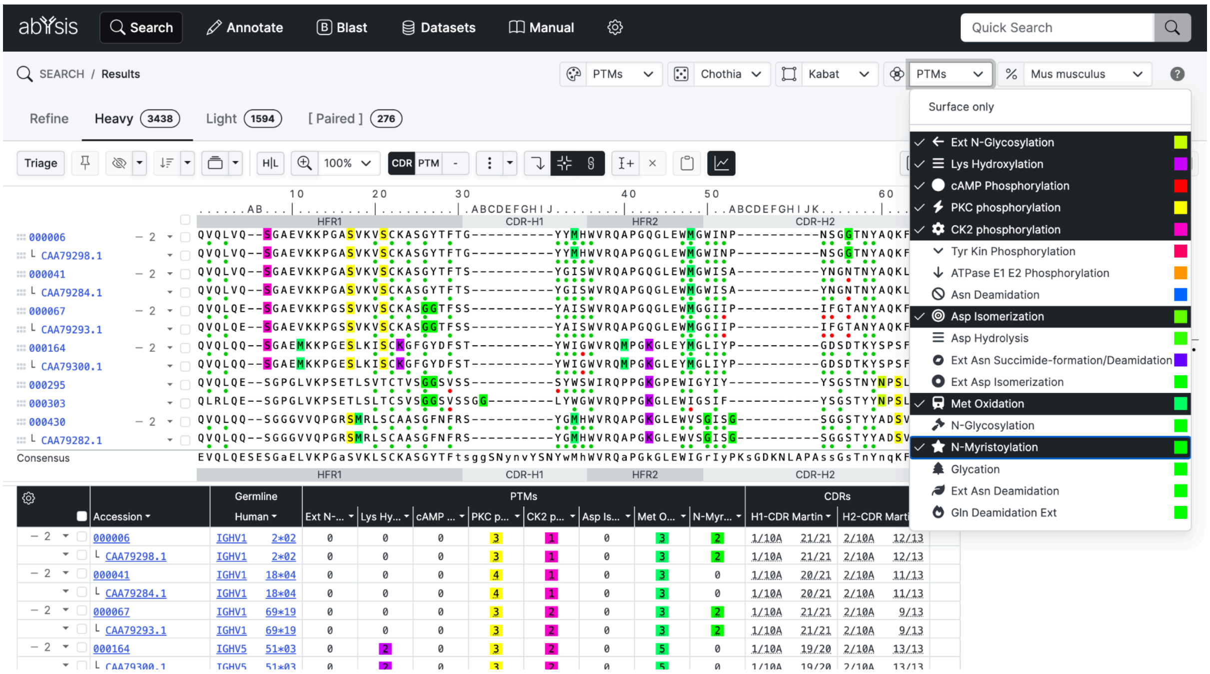
Colour: 🟥

Motif: 1 T · 2 E · 3 S · 4 any

☐ Custom Regex

4 any:
- G: Glycine
- H: Histidine
- I: Isoleucine
- K: Lysine
- L: Leucine
- M: Methionine
- N: Asparagine
- P: Proline
- Q: Glutamine
- R: Arginine
- S: Serine
- T: Threonine

Then PTMs can be displayed flexibly on the interface, just showing those you wish to see:



```
                              10        20        30             40        50              60
                    ......AB...|.........|.........|.ABCDEFGHIJ........|.........|..ABCDEFGHIJK.......|...
                    HFR1                              CDR-H1        HFR2           CDR-H2
000006      — 2     QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTG----------YYMHWVRQAPGQGLEWMGWINP----------NSGGTNYAQKF
└ CAA79298.1        QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTG----------YYMHWVRQAPGQGLEWMGWINP----------NSGGTNYAQKF
000041      — 2     QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTS----------YGISWVRQAPGQGLEWMGWISA----------YNGNTNYAQKL
└ CAA79284.1        QVQLVQ--SGAEVKKPGASVKVSCKASGYTFTS----------YGISWVRQAPGQGLEWMGWISA----------YNGNTNYAQKL
000067      — 2     QVQLQE--SGAEVKKPGSSVKVSCKASGGTFSS----------YAISWVRQAPGQGLEWMGGIIP----------IFGTANYAQKF
└ CAA79293.1        QVQLQE--SGAEVKKPGSSVKVSCKASGGTFSS----------YAISWVRQAPGQGLEWMGGIIP----------IFGTANYAQKF
000164      — 2     QVQLQQ--SGAEMKKPGESLKISCKGFGYDFST----------YWIGWVRQMPGKGLEYMGLIYP----------GDSDTKYSPSF
└ CAA79300.1        QVQLQQ--SGAEMKKPGESLKISCKGFGYDFST----------YWIGWVRQMPGKGLEYMGLIYP----------GDSDTKYSPSF
000295              QVQLQE--SGPGLVKPSETLSVTCTVSGGSVSS----------SYWSWIRQPPGKGPEWIGYIY-----------YSGSTNYNPSL
000303              QLRLQE--SGPGLVKPSETLSLTCSVSGGSVSSGG--------LYWGWVRQPPGKGLEWIGSIF-----------YSGSTYYNPSL
000430      — 2     QVQLQQ--SGGGVVQPGRSMRLSCAASGFNFRS----------YGMHWVRQAPGKGLEWVSGISG----------SGGSTYYADSV
└ CAA79282.1        QVQLQQ--SGGGVVQPGRSMRLSCAASGFNFRS----------YGMHWVRQAPGKGLEWVSGISG----------SGGSTYYADSV
Consensus           EVQLQESESGaELVKPGaSVKLSCKASGYTFTsggSNynvYSNYwMhWVRQaPGkGLEWIGrIyPKsGDKNLAPAssGsTnYnqKF
                    HFR1                              CDR-H1        HFR2           CDR-H2
```

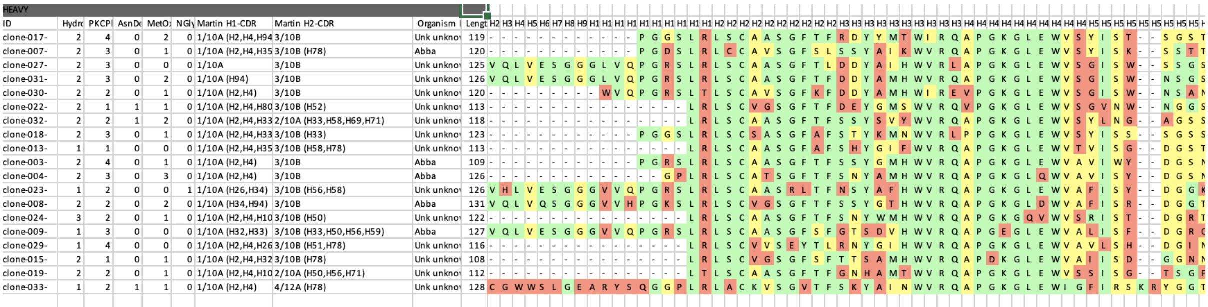
	Accession	Germline Human		PTMs: Ext N-…	Lys Hy…	cAMP …	PKC p…	CK2 p…	Asp Is…	Met O…	N-Myr…	CDRs: H1-CDR Martin		H2-CDR Marti…	
— 2	000006	IGHV1	2*02	0	0	0	3	1	0	3	2	1/10A	21/21	2/10A	12/13
	└ CAA79298.1	IGHV1	2*02	0	0	0	3	1	0	3	2	1/10A	21/21	2/10A	12/13
— 2	000041	IGHV1	18*04	0	0	0	4	1	0	3	0	1/10A	20/21	2/10A	11/13
	└ CAA79284.1	IGHV1	18*04	0	0	0	4	1	0	3	0	1/10A	20/21	2/10A	11/13
— 2	000067	IGHV1	69*19	0	0	0	3	2	0	3	2	1/10A	21/21	2/10A	9/13
	└ CAA79293.1	IGHV1	69*19	0	0	0	3	2	0	3	2	1/10A	21/21	2/10A	9/13
— 2	000164	IGHV5	51*03	0	2	0	3	2	0	5	0	1/10A	19/20	2/10A	13/13
	└ CAA79300.1	IGHV5	51*03	0	2	0	3	2	0	5	0	1/10A	19/20	2/10A	13/13

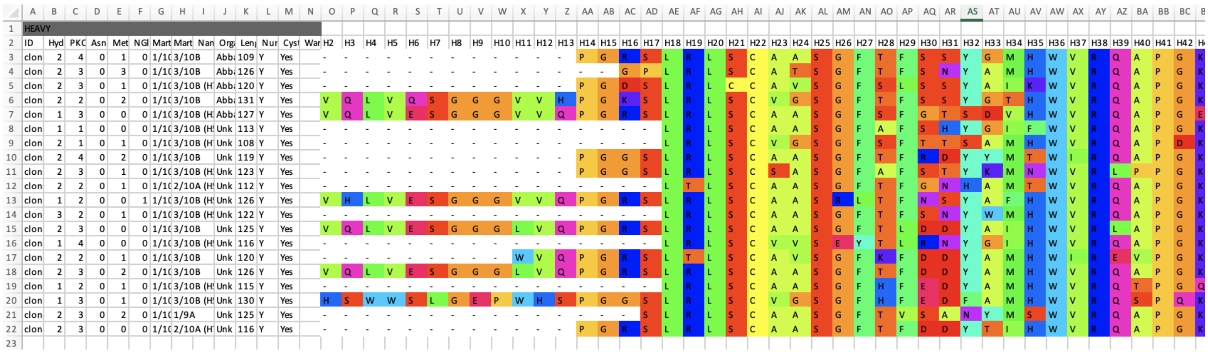
PTMs:

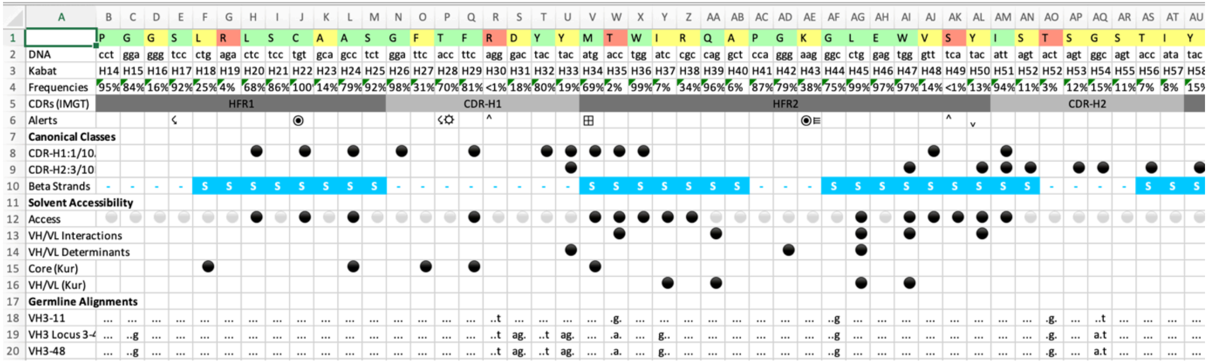
Surface only

	PTM	Colour
✓	Ext N-Glycosylation	🟩
✓	Lys Hydroxylation	🟪
✓	cAMP Phosphorylation	🟥
✓	PKC phosphorylation	🟨
✓	CK2 phosphorylation	🟪
	Tyr Kin Phosphorylation	🟥
	ATPase E1 E2 Phosphorylation	🟧
	Asn Deamidation	🟦
✓	Asp Isomerization	🟩
	Asp Hydrolysis	🟩
	Ext Asn Succimide-formation/Deamidation	🟪
	Ext Asp Isomerization	🟩
✓	Met Oxidation	🟩
	N-Glycosylation	🟩
✓	N-Myristoylation	🟩
	Glycation	🟩
	Ext Asn Deamidation	🟩
	Gln Deamidation Ext	🟩

Excel export from each Tab

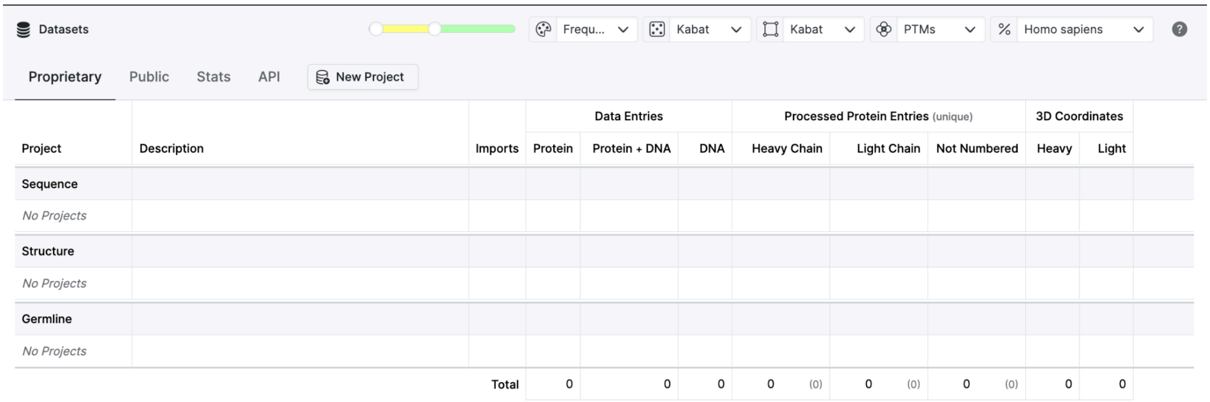






3D Structure

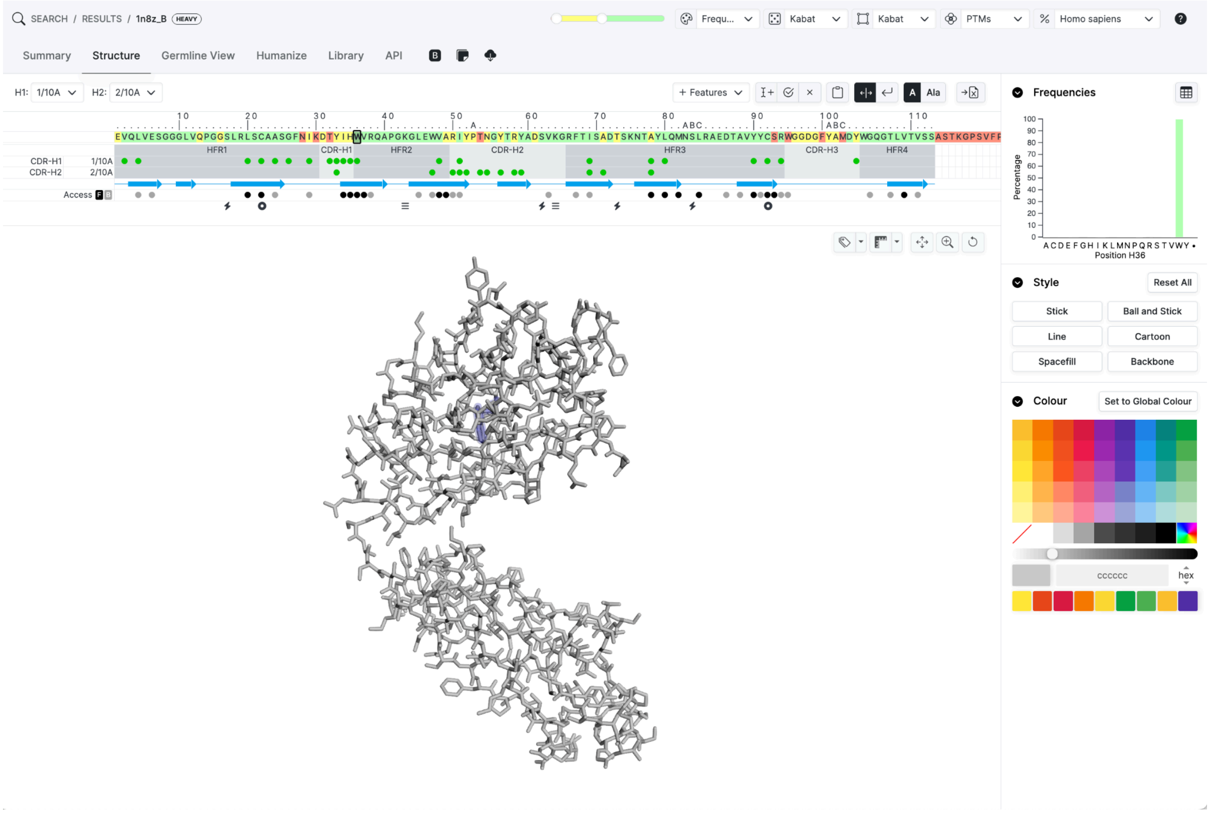
Uploading of PDB coordinates from external sources is not much simpler. Go to Datasets and select New Project > Structure



Project	Description	Imports	Data Entries			Processed Protein Entries (unique)			3D Coordinates	
			Protein	Protein + DNA	DNA	Heavy Chain	Light Chain	Not Numbered	Heavy	Light
Sequence										
No Projects										
Structure										
No Projects										
Germline										
No Projects										
		Total	0	0	0	0 (0)	0 (0)	0 (0)	0	0

Once loaded you can explore sequence positions related to 3D structure marking them for investigation across all tabs.

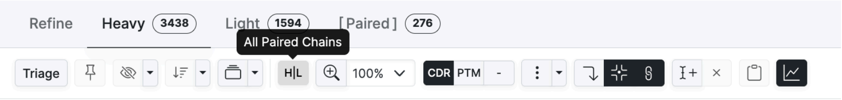
A new viewer is in that latest version which enables two way selections of residues. For antibodies with 3D coordinates, if you select a residue on the sequence display it will be highlighted on the structure and vice versa

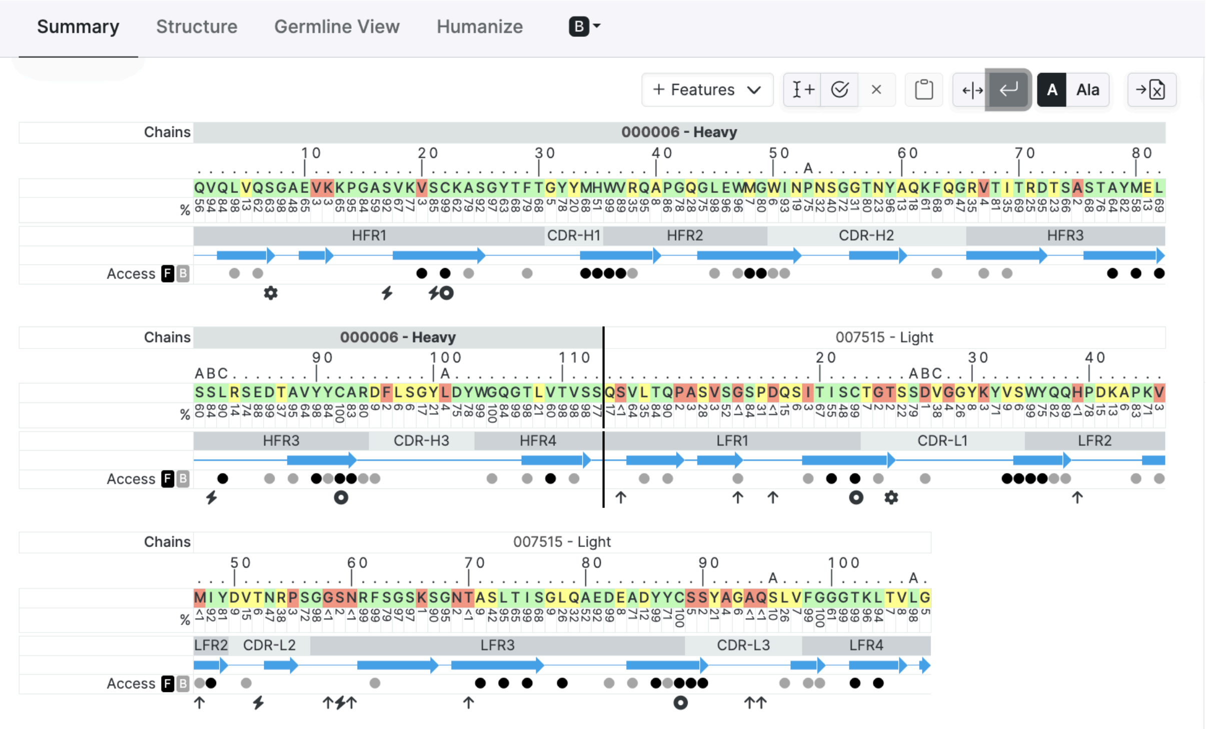


Paired Heavy/Light Analysis

If you have paired Heavy/Light chains and want to view the information together we have improved the system by providing two approaches

The first is to add the corresponding Chain to those which have them

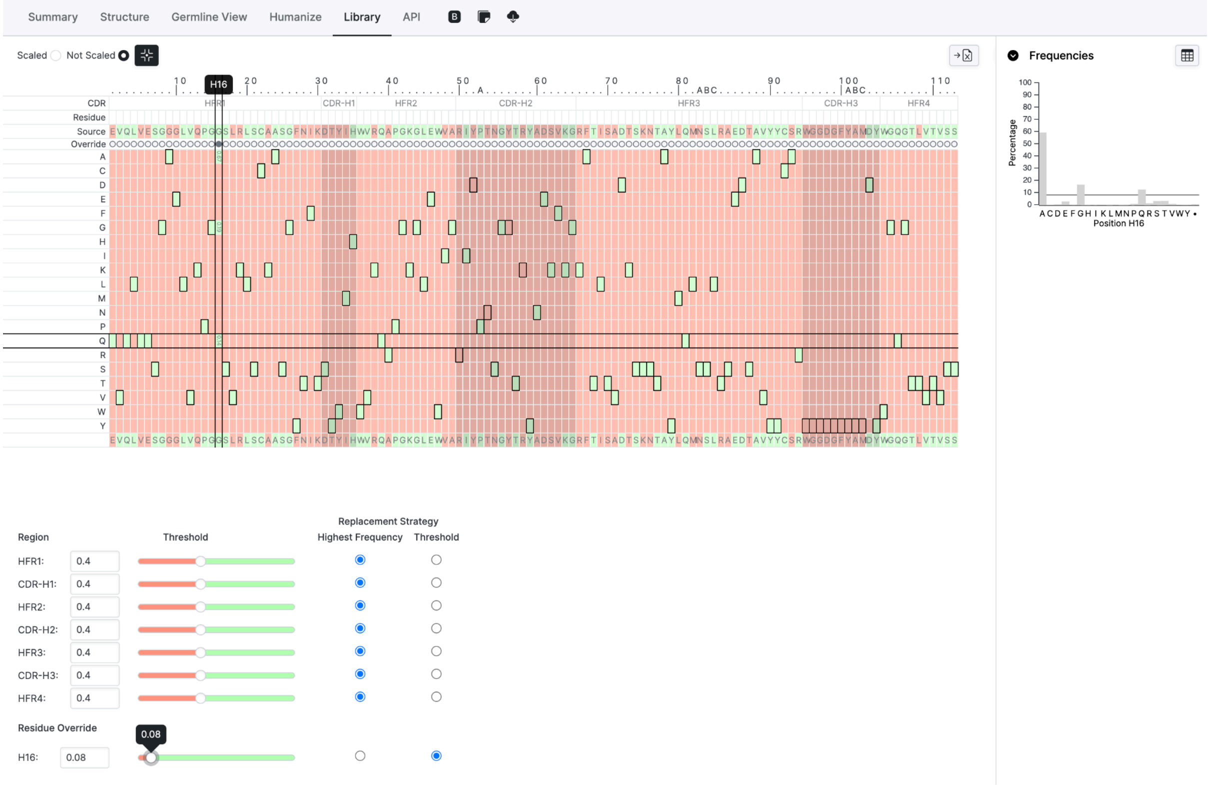




The second approach is to restrict results to just paired chains during the search phase.

Library Module

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



Region	Threshold	Replacement Strategy: Highest Frequency	Replacement Strategy: Threshold
HFR1:	0.4	●	○
CDR-H1:	0.4	●	○
HFR2:	0.4	●	○
CDR-H2:	0.4	●	○
HFR3:	0.4	●	○
CDR-H3:	0.4	●	○
HFR4:	0.4	●	○
Residue Override			
H16:	0.08	○	●