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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; <u>http://info.abysis.org</u> 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)

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Heavy chain alignment Frequencies Lower limit: 0.05 Upper limit: 0.45 0.06 70 80 90 100 CDRs 000006 0 VOLVOSGAEVKKPGASVKVSCKASGYTFTGYNH WVRQAPGOGLEWMGWINPNSGGTNYAOKFGGRVTITRDTS & TAYNELSS LRSEDTAVYYCARD FLSGYL	Refine	Triage Alignment	1-20 / 4688 🔇 🎸	< >> > 20 ~ _	🚣 🔮 Frequ	uencies 🗸 🍫 Kabat	V [] IMGT V	Homo sapiens	✓ Apply Ø
All/None 10 20 30 40 50 60 70 80 90 100 CDRs CDRs	Heavy	chain alignment		Frequencies Lower lin	nit: 0.05 Upper limi	t: 0.45	0	- 17 Ø O	I .
CDRs CDRs CDRs CVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYNH WVRQAPGQGLEWMGNINPNSGTNYAQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGYL CVQQQAEVKKPGASVKVSCKASGYTFTSYGIS WVRQAPGQGLEWMGNINANGGTNYAQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGYL CVQQQAEVKKPGASVKVSCKASGYTFTSYGIS WVRQAPGQGLEWMGNINANAQKQGRVTITRDTSTSTAYMELSSLRSDDTAVYCARDFLSGYL CVQQQAEVKKPGASVKVSCKASGYTFTSYGIS WVRQAPGQGLEWMGNISAYNGNTNYAQKLQGRVTITRDTSTSTAYMELSSLRSDDTAVYCARDFLSGYVF, CVQQQAEVKKPGASVKVSCKASGYTFTSYGIS WVRQAPGQGLEWMGNISAYNGNTNYAQKLQGRVTITRDTSTSTAYMELSSLRSDDTAVYCARDFLSGYVF, CVQQQAEVKKPGSVKVSCKASGYTFSYNIG WVRQAPGQGLEWMGNISAYNGNTYASDKSISTAVHELSSLRSDDTAVYCARDFLSGY CVQYYYYH	All/None	0 1	0 20	30 40	50 6	0 70	80 	90 100	HIJKLMNO
0000006 0V0LV0SGAEVKKPGASVKVSCKASGYTFTSYNHWYRQAPG0GLEWMGVNPSGTNYAQKF0GRVTITRDTSTSTAYHELSSLRSEDTAVYYCAADFLSGYL 000061 0V0LV0SGAEVKKPGASVKVSCKASGYTFTSYGISWYRQAPG0GLEWMGVISAYNGNTNYAQKL0GRVTITRDTSTSTAYHELSSLRSEDTAVYYCAADFLSGYL 000067 0V0L0SGAEVKKPGSVKVSCKASGGTFSSYAISWYRQAPG0GLEWMGVISAYNGNTNYAQKL0GRVTITRDTSTSTAYHELSSLRSEDTAVYYCAADFLSGYL 000068 0V0L0SGAEVKKPGSVKVSCKASGGTFSYAISWYRQAPG0GLEWMGVISAYNGNTNYAQKF0GRVTITRDTSTSTAYHELSSLRSEDTAVYYCAADFLRGVCVYYYH 000069 0V0L0SGAEVKKPGSVKVSCKASGGTFSSYAISWYRQAPG0GLEWMGVIFYDDSDTKYSPSF0G0VTISADSXISTAVL0KSSLSRSEDTAVYYCAADFLXGVYYYHDV 000295 0V0L0SGAEVKKPGSVKVSCKASGGTFSSYAND WYRQAPG0GLEWAGSLFYGDSVKYSTAVDSVKRSTISVDSTNAPSLSKSVTISVDTKNPSLKSVTUSVTSVGNFVUVSKTSVSVVVVVSKSVSVVV 000330 0LRL0ESGPLVRPSETLSTCTVSGVSGSVSSVS-WS-WYRQAPG6GLEWVSGISGSGGSTYVADSVKGRFTISRDNSKNTLVL0NNSLRBEDTAVYCARGSNIVARYF	CDRs								
000041 0V0LVQSGAEVKKPGASVKVSCKASGYTFTSGISWVRQAPGQGLEMMGGIPTGTANVAQKQGRVTHTIDTSTSTAYHELSLRSDDTAVYYCARDDPKGVHFDYGQQ 000067 0V0LQESGAEVKKPGSVKVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIPTGTANVAQKFGGRVTITADESTSTAYHELSSLRSDDTAVYYCARVGPRGVCTGAVGYYYYHDYGGQ 000164 0V0LQESGAEVKKPGSSLKISCKASGGTFSSYAISWVRQAPGQGLEMMGGIPTGTANVAQKFGGRVTITADESTSTAYHELSSLRSDTAVYYCARVGVGYSSTSSSVGYYYHHOW 000265 0V0LQESGAEVKKPGSSLKISCKASGGTFSSYAISWVRQAPGKGLEYGIYYSGSTNYAPSLRSRVTISVDTKNOFSLKLGSVTAADTAVYYCARVUVSRTSOVSTSSSVGYSYM	000006	Q V Q L V Q S G A E	V K K P G A S V K V S C K A S	G <mark>YTFTGYYMH</mark> WVRQAPG <mark>Q</mark> I	G L E W M G W I N P N S G <mark>G</mark> T N Y A	QKFQGRVTITRDTSAST	AYMELSSLRSEDTA	VYYCARDFLSGYL	D <mark>Y</mark> WGQGT
000067 0V10_05SGAEWKKPGSSVKVSCKASGGTFSSVISWRQAPPGGLEWMGLIYPEGTANYAQKPGCRVTITADESTSTAVHELSSLRSEDTAVYYCARCPLEGVDYYYYH	000041	QVQLVQSGAE	V K K P G A S V K V S C K A S (G <mark>YTFTSYGIS</mark> WVRQAPG <mark>Q</mark> I	G L E W <mark>M G W I S A Y N</mark> G <mark>N T N</mark> Y A	QKLQGRVTMTTDTSTST	AYMELRSLRSDDTA	VYYCAADTGRIDDFWSGYN	F D Y W G Q G T
000140 0V01_00SGAE_MKKPGESLKISCKGFGYPESTYNIG WRQMPGKGLEYMGLIYPGDSDTKYSPSFGG0YTISADSKISTATL0WSSLKASDTAMYYCARVSGYSSTSSYDYYYYMDW 0002959 0V01_00SGGCVV0PGKSMLSCASSGFTSSYGMT-WRQMPGKGLEWIGSIF-YSGSTYNAPSLKSSYTTISVDTKNPSLKLSSYTAADTAVYCARGFUVGSYSYM	000067	QVQLQESGAE	<mark>VK</mark> KPG <mark>SSVKV</mark> SC <mark>K</mark> AS	G <mark>GTFSSYAIS</mark> WVRQAPG <mark>Q</mark> I	GLEW <mark>M G G I I P I F</mark> G T A N Y A	QKFQGRVTITADESTST	AYMELSSLRSEDTA	VYYCARGPLRGYDYYYYM	– – – – – – – <mark>D V W G K</mark> – –
000205 0 V01 0 ESGPELUKPSETLSUTCTVSGGSVSSSYMS	000164	QVQLQQSGAE	M <mark>KKPGESLKISCKGF</mark>	G <mark>YD</mark> FS <mark>TYWIG</mark> WVRQ <mark>M</mark> PGK(G L E <mark>Y M G L I Y P G D S D T K</mark> Y S	PSFQGQVTISADKSIST	T <mark>aylqwsslkas</mark> dta	MYYCARVSGYCSSTSSYDY	<u>Y Y Y Y M D V W</u>
0000030 0 LR U DESGPEULVKPSETLSTT SVSGGSVSSGL YNGWROPPGKGLEWYASTSF YSGSTYNPSLKSRVTTSVDT KNMFSLKLSSVTAADTAVYYCTAPGYGDTSVKRRWMNDWGOG 000430 0 VQL 00SGGGVU OPGGSLRLSCAASGFTFSSYMMSWVROAPGKGLEWYASTSGSGSTYTADSVKRFTTSRDNAKNTLYL 0MNSLRAEDTAVYYCAKOS MIYUASTYC 000437 EVOL VESGGGL VOPGGSLRLSCAASGFTFSSYMMSWVROAPGKGLEWYATSSSSSTTYADSVKGRFTTSRDNAKNTLYL 0MNSLRAEDTAVYYCAKOS MIYUASTYC 000438 0 VQL 00SGGSU VOPGGSLRLSCAASGFTFSSYMMSWVROAPGKGLEWYATSSSSSTTYADSVKGRFTTSRDNAKNSLYL 0MNSLRAEDTAVYYCAKOPTCSMRRLVTFGGVYSGG 000460	000295	Q V Q L Q E S G P G	L V K P S E T L S V T C T V S (G <mark>GSVSSSYWS</mark> – – <mark>WIRQP</mark> PGK	G <mark>P</mark> EWIGYIY-YSGSTNYN	IPSLRSRVTISVDTSKN(FSLKLGSVTAADTA	VYYCARVLVSRTISQYSYY	M – – – – – – – D <mark>V W G K</mark> G T
00040 0004005666/VV0PGRSML5CAAS6FFFRSYGMH - WVR0APGKGLEWVAIXSGSGGSTYVADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAKGSMIVVARFF	000303	Q L R L Q E S G P G	LVKP <mark>SETLSLTC</mark> SVS(G <mark>G S V S S <mark>G G L</mark> Y W <mark>G</mark> W V R Q P P G K (</mark>	GLEW <mark>IGSI<mark>F</mark>-YSGSTYYN</mark>	IPSLKSRVTISVDTLKNN	FSLKLSSVTAADTA	VYYC <mark>TRPGYGDTS</mark> VRKRVW	<mark>N M</mark> – – – – – – D <mark>L</mark> W G Q G T
000437 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMSWYRQAPGKGLEWVALIKYDGGSEYYYDGSVKGRFTISRDNAKNTLYLQMNSLREDTAVYYCAKNPRDSGSYYFDYWGGK 000458 QVQLOSGGSLVQPGGSLRLSCAASGFTFSSYMMSWYRQAPGKGLEWVSQISSSGSRTYYADSVKGRFTISRDNAKNLYLQMNSLRAEDTAVYYCARBGGLH	000430	Q V Q L Q Q S G G G	V V Q P G <mark>R </mark> S M R L S C A A S I	G F <mark>N</mark> F <mark>R S Y G M H</mark> – – W V R Q A P G K I	GLEW <mark>VSGISGSGGSTY</mark> YA	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCAKGSMIVVARYF	– – – – – – – – D <mark>Y</mark> W G Q G T
000460 0 VQL 005GGSLV 00FGGSLRLSCAASGFTFSNGMN - WVRQAPGKGLEWVSLISSSSTITYADSVKGRTTISRDNAKNSLVLOMNSLRBEDTAVYYCAREGGLM	000437		L	G F T F S <mark>S Y W M S</mark> – – W V R Q A P G K I	G L E W V A <mark>N</mark> I K Q D G S E K Y Y V	D S V K G R F T I S R D N A K N 1	T <mark>lylqmnslr</mark> dedta	VYYCAKNPRDSGSYYYF	D <mark>YWGQG</mark> -
000400 LEESGGGUVQPGRSLRVSCEASGFTFSSYEMNWYRQAPGKGLEWYAVISSGSRTYYADSVKGRFTISRDNAKNSLYLEMTSLRVDDTAVYYCARGRLVTFGGVVSGGPIWGGV 000559 0VQLVESGGGVVQPGRSLRVSCAASGETTSSYAMHWYRQAPGKGLEWYAVISSGSNKYYADSVKGRFTISRDNSKNTLYLQMDLRAEDTAVYYCARGRLVTGKEVYNYYYHDVWGK 000579 0VQLVESGGGVVQPGRSLRVSCAASGETTSSYAMHWYRQAPGKGLEWYAVISSDGSNKYYADSVKGRFTISRDNSKNTLYLQMDLRAEDTAVYYCARGPTSGSCYSYYYHYHDVWGK 000579 0VQLVESGGGVVQPGRSLRVSCAASGETFSSYAMHWYRQAPGKGLEWYAVISSDGSNKYYADSVKGRFTISRDNSKNTLYLQMDSLRAEDTAVYYCARGPTSGSCYSYYYHYHDVWGK 000580 0VQLVESGGSVVQPGRSLRVSCAASGETFSSYAMHWYRQAPGKGLEWYAVISSDGSNKYYADSVKGRFTISRDNSKNTLYLQMDSLRAEDTAVYYCARGPTSNSSNSVTYYTYTHDVWGK 000581 0VQLVESGGSVVQPGRSLRVSCAASGFTFSSYGMHWYRQAPGKGLEWYAVISSDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDSVHTAPYYYTHDVWGK 000582 EVQLVESGGGLVQPGGSLRVSCAASGFTFSSYGMHWYRQAPGKGLEWYAFTKSDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDSVHTAPYYYTHDVWGK 000582 EVQLVESGGLVQPGGSLRVSCAASGFTFSYYMHWYRQAPGKGLEWYAFTKYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDSVTGRFNYYMHDVWGK 000582 LEESGEAVVQPGRSLRVSCAASGFTFRYAMHWYRQAPGKGLEWYAFTKYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCARDDGVKGRFNITAGFDYWGQU 000583 LEESGEAVVQPGRSLRVSCAASGFTFRYAMHWYRQAPGKGLEWYALTKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDGVKGEHVDLTAYGPDYWGQU 000589 LEESGEAVVQPGRSLRVSCAASGFTFRYAMHWYRQAPGKGLEWYALTKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDJGVKGEHYDILTAYGPDYWGQU	000458	Q V Q L Q Q S G G S	L V <mark>Q</mark> P G <mark>G</mark> S L R L S C A A S I	G F T F S <mark>N S G</mark> M <mark>N </mark> – – W V R Q A P G K I	GLEW <mark>VSYISSSSSTIY</mark> YA	D S V K G R F T I S R D N A K N S	SLYLQMNSLR <mark>D</mark> EDTA	VYYCAREEGGLM	– – – – – – – – <mark>D V W G K</mark> G –
000559 0 VQL VESGGG VVQ PG KSLRLSCAASGFTFSSYAMH WVRQAP KGLEW VAJTSVG SNKYYAD SVKGRFTISRDNSKNTLSLQNNSLRAEDTAVYYCARGFCSGGSCYSYYYYY - DVWG K 000579 0 VQL VESGGG VVQ PG KSLRLSCAASGFTFSSYAMH WVRQ PG KGLEW VAJTSVD GSNKYYAD SVKGRFTISRDNSKNTLYLQNDSLRAEDTAVYYCKED VYTG KFYYMH DVWG K 000580 0 VQL VESGG VVQ PG KSLRLSCAASGFTFSSYG H WVRQ PG KGLEW VAJTSVD GSNKYYAD SVKGRFTISRDNSKNTLYLQND SLR TEDTAVYYCAKGY VCSSSS CYSYYY HYH DVWG K 000580 0 VQL VESGG VVQ PG KSLRLSCAASGFTFSYG H WVRQ PG KGLEW VAJTSD GSNKYYAD SVKGRFTISRDNSKNTLYLQND SLR TEDTAVYYCAKD JSVKGVYSSSS CYSYYY HYH DVWG K 000582 C VQL 0 ESGG SVVQ PG KSLRLSCAASGFTFSYG H WVRQ PG KGLEW VAJTSD GGY EY VAD SVKGR TISRDNSKNTLYLQND SLRAEDTAVYYCKEDHVITTG KHYMYH DVWG K 000582 E VQL VESGG CVVQ PG KSLRLSCAASGFTFS SYG H WVRQ AP G KGLEW VAJTSVG GNKYYAD SVKGR FTISRDNSKNTLYLQND SLRAEDTAVYYCKEDHVITTG KHYMYH DVWG K 000586 L ESG G AVVQ PG KSLRLSCAASGFTFRNYAMH WVRQ AP G KGLEW VAJTSVD G NKYYAD SVKGR FTISRDNSKNTLYLQND SLRAEDTAVYYCARD G LKG CHYD LTAYGP DYWG Q 000588 L ESG G AVVQ PG KSLRLSCAASGFTFRNYAMH WVRQ AP G KGLEW VAJTKYD G NKYYAD SVKGR FTISRDNSKNTLYLQND SLRAEDTAVYYCARD G LKG CHYD LTAYGP DYWG Q 000589 L EESG G AVVQ PG KSLRLSCAASGFTFRNYAMH WVRQ AP G KGLEW VAJTKYD G NKYYAD SVKGR FTISRDNSKNTLYLQND SLRAEDTAVYYCARD G LKG CHYD LTAYGP DYWG Q 000589 L EESG G AVVQ PG KSLRLSCAASGFTFRNYAMH WVRQ AP G KGLEW VAJTKYD G NKYYAD SVKGR FTISRDNSKNTLYLQND SLRAEDTAVYYCARD G LKG CHYD LTAYGP DYWG Q	000460	LEESGGG	L V <mark>Q</mark> P G <mark>R</mark> S L R <mark>V</mark> S C <mark>E</mark> A S I	G F T F S <mark>S Y <mark>E</mark>MN – – W V R Q A P G K (</mark>	G L E W <mark>V S Q</mark> I S S S G S <mark>R</mark> T Y Y A	D S V K G R F T I S R D N A K N S	E Y L EMTSLR <mark>V</mark> DDTA	VYYCARGRRLVTFGGVVSG	<mark>G N I W G Q G T</mark>
000579 QVQLQESGGGLVQPGGSLRLSCAASGLTFSSYAMHWYRQAPGKGLEWVAVISDQGSNKYYADSVKGRFTISRDNSKNTLYLQMDLRAEDTAVYYCVREDYVITSGFYYHMDYWGGK 000580 QVQLVESGGGVVQPGGSLRLSCAASGFFSSYGMHWYRQPPGKGLEWVAVISDQGSNKYYADSVKGRFTISRDNSKNTLYLQMDSLRAEDTAVYYCARDYCSSSCYSYYYYHYHDYWGGK 000581 QVQLVESGGGVVQPGGSLRLSCAASGFFFSYGMHWYRQAPGKGLEWVAVISDQGSNKYYADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYYCARDASVHTAFYYHDYWGGK 000582 EVQLVESGGGLVQPGGSLRLSCAASGFFFSYGMHWYRQAPGKGLEWVALISYDGGNKYYADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHVTTGRYHYH	000559	QVQLVESGGG	<mark>V V Q P G R</mark> S L R L S C A A S I	GFTFS <mark>SYAMH</mark> WVRQAPGK	G L E W <mark>V A V I S Y D G S N K Y Y</mark> A	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>LS</mark> LQM <mark>N</mark> SLRAEDTA	VYYCARGRECSGGSCYSYY	<mark>YYYYM</mark> DVWG <mark>K</mark> GT
000580 0 VQL VESGGG VVQ PG KSLRLSCAASGF5F5SYGMH WVRQ PC KGLEW AV ISD 0GSNY YAD SVKGRFTISRDNSKTL VLQM SLREDTAVYYCAKGWYCSSSCYSYYY HYM DVWGK 000581 0 VQL VESGGG VVQ PG KSLRLSCAASGF1FSNYIM WVRQ PC KGLEW AV ISD 0GSNY YAD SVKGRFTISRDNSKTL VLQMNSLRAEDTAVYYCARDD SVHTAFYNYT DVWGK 000582 EVQL VESGGGLVQ PG GSLRLSCAASGF1FSNYIM WVRQ PG KGLEW AV ISD 0GSNY YAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARDD SVHTAFYNT DVWGK 000582 EVQL VESGGGLVQ PG GSLRLSCAASGF1FSNYAM WVRQ APG KGLEW AFI RYDG SNKYYAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARDD GLKGEH VDILTAGF DVWGK 000586 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW AFI KYDG SNKYYAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARD GLKGEH VDILTAGF DYWG 0L 000587 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW VALIKYDG RNKYYAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARD IG LKGEH VDILTAYGF DYWG 0L 000588 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW VALIKYDG RNKY YAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARD IG LKGEH VDILTAYGF DYWG 0L 000589 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW VALIKYDG RNKY YAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARD IG LKGEH VDILTAYGF DYWG 0L 000589 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW VALIKYDG KNKY YAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYYCARD IG LKGEH VDILTAYGF DYWG 0L 000590 L EESG EAVVQ PG KSLRLSCAASGF1FRNYAM WVRQ APG KGLEW VALIKYDG KNKY YAD SVKGRFTISRDNSKNTL VLQMNSLRAEDTAVYCARD IG LKGEH VDILTAYGF DYWG 0L 000590	000579	QVQLQESGGG	L	GLTFSSYAMHWVRQAPGK	GLEW <mark>VAVISYDGSNKYYA</mark>	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>lylqm</mark> dnlraedta	VYYCVREDYVITSGFYYYH	M D V W G K
000581 0 VQL 0 ES GG VV QP GRSLRLS CAAS GFTFS NAIH WVR QAP GKGLEW VALTS VG GGY EV YAD SV KGR TIS RON SKNTL VL QNNSLRAEDT AVY YCARDAS VHTAPY YY H	000580		<mark>V V Q P G R </mark> S L R L S C A A S I	G F <mark>S F S S Y GMH</mark> – – W V R Q <mark>C</mark> P G K I	G L E W V A V I S <mark>D</mark> D G S N K Y Y A	DSVKGRFTISRD <mark>N</mark> SK <mark>K</mark> T	T <mark>LYLQMD</mark> SLR <mark>T</mark> EDTA	VYYCAKGVYCSSSSCYSYY	YYHYMDVWG <mark>K</mark> GT
000582 EVQLVESGGLVQPGGSLRLSCAASGFTFSSYGMHWVQAPGKGLEWVALIKYQGNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGHYPTGR/HYYMDYWGQI 000586 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYQGNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGHYDILTAYGPDYWGQI 000587 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGHYDILTAYGPDYWGQI 000588 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000589 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000580 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000580 LEESGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000580 LEGSGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000580 LEGSGGAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000580 LEGSGGAVVQPGRSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVALIKYDGRNKYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQI COnsensus QVQLqESGggVVQPGYSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVALISYDGSNKYGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQI	000581	Q V Q L Q E S G G S	<mark>V V Q P G R</mark> S L R L S C A A S I	GFTFS <mark>NYAIH</mark> WVRQAPGK	GLEW <mark>VAVISYDGGY</mark> EYYA	DSVKGR <mark>S</mark> TISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCARDASVHTAPYYYM-	DVWG <mark>K</mark> G-
000586 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALLKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCABDIGLKGEHYDILTAYGPDYWGQI 000587 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALLKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000588 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000589 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000590 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000590 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI 000590 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWYRQAPGKGLEWYALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQI COnsensus QVQLqESGGgVVQPGrSLRLSCAASGFTFRNYAMHWYRQAPGKGLEWYALIKYDGSNKYADSSKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQI COR QVQLqESGGgVVQPGrSLRLSCAASGFTFSSYAHHWYRQAPGKGLEWYALISYDGSNKYADSSKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLAASGFTFSSYAHHWYRQAPGKGLEWYALISYDGSNKYADSSKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDGYNYCARDIGLKAEHYDGYNYCARDIGLAASGFTFSSYAHHWYRQAPGKGLEWYALISYDGSNKYADSSKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDGYNYCARDIGLAASGFTFSSYAHHWYRQAPGKGLEWYALISYDGSNKYADSSYGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLAEHYDGY	000582	EVQLVESGGG	L	GFTFS <mark>SYGMH</mark> WV <mark>L</mark> QAPGKI	GLEWVA FIRYDGSNKYYA	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCVREDHVITTGRYHYY	M D V W G <mark>K</mark>
000587 LEESGEAVVQPGRSLRLSCAASGFIFRNYAMHWVRQAPPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQU 000588 LEESGEAVVQPGRSLRLSCAASGFIFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQU 000589 LEESGEAVVQPGRSLRLSCAASGFIFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQU 000589 LEESGEAVVQPGRSLRLSCAASGFIFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKGEHYDILTAYGPDYWGQU 000590 LEGSGEAVVQPGRSLRLSCAASGFIFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQU 000590 LEGSGEAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQU COnsensus QVQLqESGggVVQPGrSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVALIKYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQU CORs GVSQLqESGggVVQPGrSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVALISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQU CORs GVSQLqESGggVVQPGrSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVALISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQU	000586	LEESGEA	<mark>V V Q P G R </mark> S L R L S C A A S I	GF <mark>IFRNYAMH</mark> WVRQAPGK	GLEW <mark>VAL</mark> IKYDG <mark>RNKYYA</mark>	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCARDIGLKGEHYDILT	AYGPDYWGQGT
000580 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWVRQAPGKGLEWVALLKYDGRNYYADSVKGRFTJSRDNSKNTLYLQNNSLRAEDTAVYYCARDJGLKGEHVDILTAYGPDYWGQU 000589 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWVRQAPGKGLEWVALLKYDGRNKYYADSVKGRFTJSRDNSKNTLYLQNNSLRAEDTAVYYCARDJGLKGEHVDILTAYGPDYWGQU 000580 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWVRQAPGKGLEWVALLKYDGRNKYYADSVKGRFTJSRDNSKNTLYLQNNSLRAEDTAVYYCARDJGLKAEHVDILTAYGPDYWGQU 000580 LEESGEAVVQPGRSLRLSCAASGFJFRNYAMHWVRQAPGKGLEWVALLKYDGRNKYYADSVKGRFTJSRDNSKNTLYLQNNSLRAEDTAVYYCARDJGLKAEHVDILTAYGPDYWGQU COnsensus QVQLqESGggVVQPGrSLRLSCAASGFJFSSYaMHWVRQAPGKGLEWVALISYDGSnKYYADSVKGRFTJSRDNSKNTLYLQNNSLRAEDTAVYYCARDJGLKAEHVDILTAYGPDYWGQU COns SortAegion	000587	OLEESGEA	V V Q P G <mark>R</mark> S L R L S C A A S (GF <mark>IFRNYAMH</mark> WVRQAPGKI	G L E W V A L I K Y D G <mark>R</mark> N K Y Y A	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCARDIGLKGEHYDILT	AYGPDYWGQGT
000590LEESGEAVVQPGRSLRLSCAASGFFFRYAMHWYRQAPGKGLEWVALLKYDGRNYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCABDGLKKGENYDILTAYGPDYWGQU 000590LEGSGEAVVQPGRSLRLSCAASGFFFRYAMHWYRQAPGKGLEWVALLKYDGRNYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCABDGLKKAENDILTAYGPDYWGQU Consensus QVQLqESGggVVQPGrSLRLSCAASGFFFSYAMHWYRQAPGKGLEWVALISyDGsnkYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARdiglkgehyyjytDYWGQU CORs SOTRegion Sotregion Sotregi	000588	—LEESGEA	<mark>V V Q P G R</mark> S L R L S C A A S I	G F <mark>I F RN Y AMH W V R Q A P G K (</mark>	G L E W V A L I K Y D G <mark>R</mark> N K Y Y A	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCARDIGLKGEHYDILT	AYGPDYWGQGT
000500 LEQSGEAVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVALIKYDGRNKYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARDIGLKAEHYDILTAYGPDYWGQ Consensus QVQLqESGggVVQPGrSLRLSCAASGFTFSSYaMHWVRQAPGKGLEWVALIsyDGsnkYYADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCARdiglkgehyyiytDYWGQ CORs SortRegion	000589	OLEESGEA	<u> </u>	GF <mark>IFRNYAMH</mark> WVRQAPGK	G L E W V A L I K Y D G R N K Y Y A	D S V K G R F T I S R D N S K N 1	LYLQM <mark>N</mark> SLRAEDTA	VYYCARDIGLKGEHYDILT	AYGPDYWGQGT
Consensus QVQLqESGggVVQPGrSLRLSCAASGFTFSSYaMHWVRQAPGKGLEWVAlIsyDGsnkYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARdiglkgehyyiytDyWGQU CDRs SortRegion	000590	DLEQSGEA	V V Q P G <mark>R</mark> S L R L S C A A S (G F T F <mark>R N Y A M H</mark> – – W V R Q A P G K I	G L E W V A L I K Y D G <mark>R</mark> N K Y Y A	DSVKGRFTISRD <mark>N</mark> SKN1	T <mark>L</mark> YLQM <mark>N</mark> SLRAEDTA	VYYCARDIGLKAEHYDILT	<mark>A Y G P</mark> D <mark>Y</mark> W G Q G T
CDRs Sort Region	Consensus	Q V Q L q E S G g g	VVQPGrSLRLSCAAS	GFTFSSYaMHWVRQAPGK	GLEWVAlIsyDGsnkYYA	DSVKGRFTISRDNSKNT	LYLQMNSLRAEDTA	VYYCARdiglkgehyyiyt	D y W G Q G T
Sort Region	CDRs								
	Sort Region								

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.

Refine Triage	Alignment	¥						Frequence	ies 🗸 🌗	Kabat	~ []	IMGT	~ %	Homo sapie	ns N	Apply	•
Heavy: 3397/3397		Light: 1554/15	54	P	aired: 263/	263		Total: 4688/4	688		Show	partners: [Extra	PTMs:	Triage	eset All	
Heavy CDR & PT	M Total																
C)						C							
Q HFR1	ים פ מ	CDR-H1 🕤	с н	FR2 🕤	۹	CDR-H2	5 Q	HFR3	5 Q	CDR-H3	C	۹	HFR4	5 Q	PTMs	C	
Heavy PTM Deta	il																
	cAMP pho:	sphorylation 1	l motif/sequ	ience							120						
Hydrox												C					
cAMPPhos												C					
PKCPhos												C					
CK2Phos												C					
TyrKinPhos												C					
AsnDeam												C					
Asplsom												C					
AspHyd												C					

Improved Excel export from each Tab

abĭfsis



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.



ab¥sis

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.

리아비SIS Q. Search - 🖍 Annotate 🕊 Paired 🧭 Blast 🚯 Import 🖌 Tools - 🚯 Manual	
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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).

Summary	Canonical Classes	Germline View	Humanize	Structure	Library @	í 🕹		
Scaled 🔵 Not sca	aled • +							
	10	20	30 	4 0 	50 A	60 	70	80 ABC
CDR	HFR	1	CDR-H1	HFR2	CDR-I	H2	I	HFR3
Residue								
Source	EVQLVESGGGLVQ	P G <mark>G</mark> S L R L S C A A S C	FNIKDTYIH	WVRQAPGKGI	LEWVARIYPTN	GYTRYADSVKO	RFTISADTSK	NTAYLQMNSLRAEDTAV
Override	00000000000000		000000000000000000000000000000000000000	000000000000000000000000000000000000000	00000000000	000000000000000000000000000000000000000	000000000000000000000000000000000000000	000000000000000000000000000000000000000
VH3 Locus 3-66 VH3 Locus 3-66 VH3-53	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · ·	T V S S N . M S T V S S N . M S T V S S N . M S		S V S G S V S G S V S G	. S . Y	R . N 	· · L · · · · · · · · · · · · · · · · ·
A								
С								
D								
E								
F								

In the following image you can see the extra slider for the selected H16



