



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2026 – 04:57 PM EDT

PDB ID : 12UV / pdb_000012uv
EMDB ID : EMD-76773
Title : The AAV2 capsid in complex with IgA-Fab#3-4
Authors : Zachery, J.; Mietzsch, M.; McKenna, R.
Deposited on : 2026-04-20
Resolution : 2.68 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

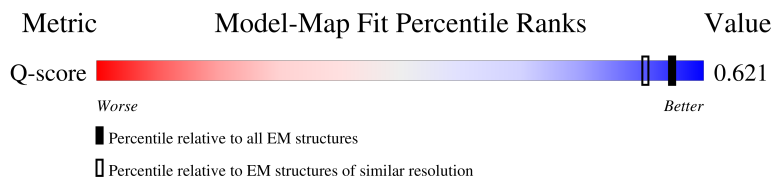
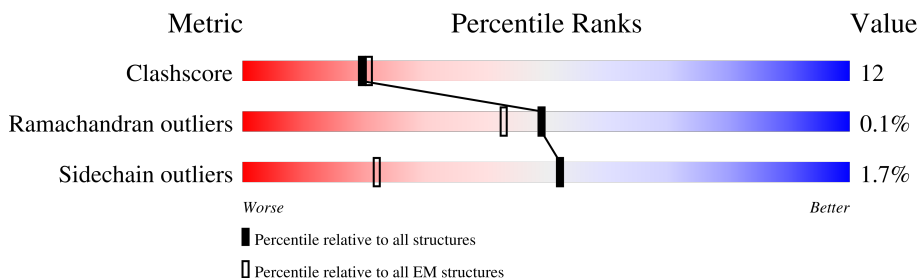
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



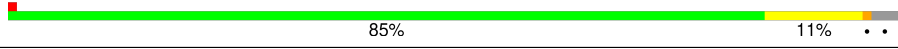
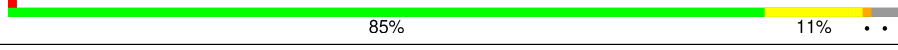
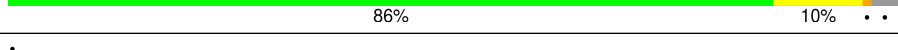
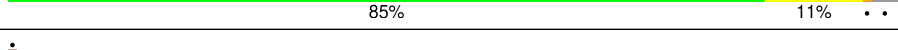
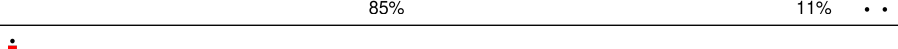
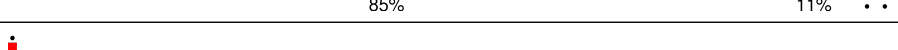
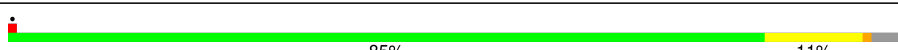
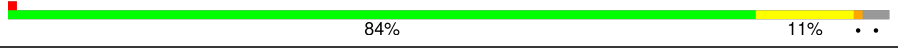
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9255 (2.18 - 3.18)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	533	
1	2	533	
1	3	533	
1	4	533	

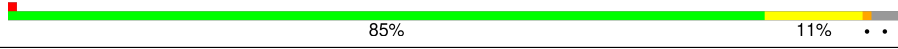
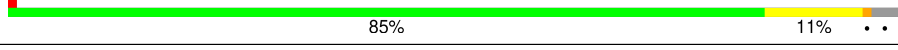
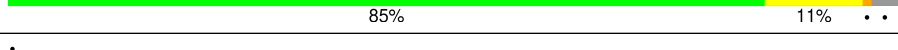
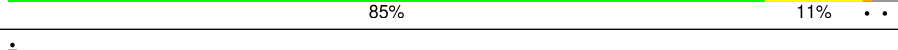
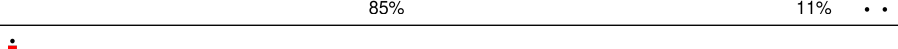
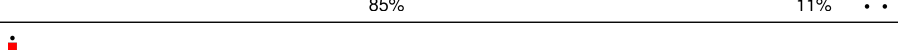
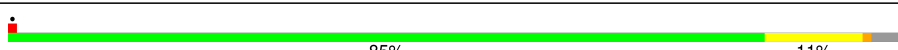
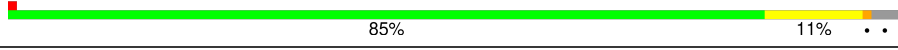
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Mol	Chain	Length	Quality of chain
1	5	533	
1	6	533	
1	7	533	
1	8	533	
1	A	533	
1	B	533	
1	C	533	
1	D	533	
1	E	533	
1	F	533	
1	G	533	
1	H	533	
1	I	533	
1	J	533	
1	K	533	
1	L	533	
1	M	533	
1	N	533	
1	O	533	
1	P	533	
1	Q	533	
1	R	533	
1	S	533	
1	T	533	
1	U	533	

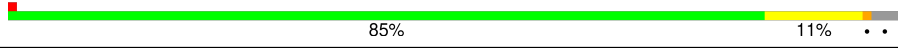
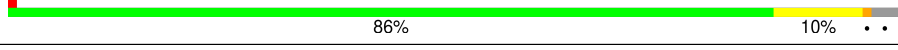
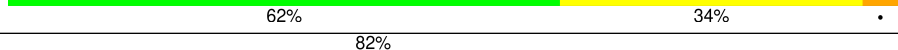
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Mol	Chain	Length	Quality of chain
1	V	533	
1	W	533	
1	X	533	
1	Y	533	
1	Z	533	
1	a	533	
1	b	533	
1	c	533	
1	d	533	
1	e	533	
1	f	533	
1	g	533	
1	h	533	
1	i	533	
1	j	533	
1	k	533	
1	l	533	
1	m	533	
1	n	533	
1	o	533	
1	p	533	
1	q	533	
1	r	533	
1	s	533	
1	t	533	

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Mol	Chain	Length	Quality of chain
1	u	533	
1	v	533	
1	w	533	
1	x	533	
1	y	533	
1	z	533	
2	1h	125	
2	2h	125	
2	3h	125	
2	4h	125	
2	5h	125	
2	6h	125	
2	7h	125	
2	8h	125	
2	Ah	125	
2	Bh	125	
2	Ch	125	
2	Dh	125	
2	Eh	125	
2	Fh	125	
2	Gh	125	
2	Hh	125	
2	Ih	125	
2	Jh	125	
2	Kh	125	

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Mol	Chain	Length	Quality of chain
2	Lh	125	83% 61% 35% .
2	Mh	125	83% 62% 34% .
2	Nh	125	81% 62% 34% .
2	Oh	125	83% 62% 34% .
2	Ph	125	81% 62% 34% .
2	Qh	125	82% 62% 34% .
2	Rh	125	83% 62% 34% .
2	Sh	125	83% 61% 35% .
2	Th	125	82% 61% 35% .
2	Uh	125	83% 62% 34% .
2	Vh	125	82% 61% 35% .
2	Wh	125	81% 62% 34% .
2	Xh	125	83% 62% 34% .
2	Yh	125	81% 61% 35% .
2	Zh	125	83% 61% 35% .
2	ah	125	82% 62% 34% .
2	bh	125	83% 62% 34% .
2	ch	125	81% 62% 34% .
2	dh	125	81% 62% 34% .
2	eh	125	82% 62% 34% .
2	fh	125	83% 62% 34% .
2	gh	125	82% 61% 35% .
2	hh	125	82% 61% 35% .
2	ih	125	83% 62% 34% .
2	jh	125	82% 61% 35% .

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Mol	Chain	Length	Quality of chain
2	kh	125	83% 62% 34%
2	lh	125	83% 61% 35%
2	mh	125	83% 62% 34%
2	nh	125	83% 62% 34%
2	oh	125	82% 62% 34%
2	ph	125	82% 61% 35%
2	qh	125	83% 62% 34%
2	rh	125	82% 62% 34%
2	sh	125	82% 62% 34%
2	th	125	83% 61% 35%
2	uh	125	83% 62% 34%
2	vh	125	83% 62% 34%
2	wh	125	82% 62% 34%
2	xh	125	82% 61% 35%
2	yh	125	81% 62% 34%
2	zh	125	81% 61% 35%
3	1l	106	70% 61% 38%
3	2l	106	70% 60% 39%
3	3l	106	70% 62% 37%
3	4l	106	70% 62% 37%
3	5l	106	70% 62% 37%
3	6l	106	70% 61% 38%
3	7l	106	69% 61% 38%
3	8l	106	71% 61% 38%
3	Al	106	67% 61% 38%

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Mol	Chain	Length	Quality of chain
3	B1	106	69% 62% 37% .
3	C1	106	71% 62% 37% .
3	D1	106	69% 62% 37% .
3	E1	106	71% 62% 37% .
3	F1	106	70% 61% 38% .
3	G1	106	71% 61% 38% .
3	H1	106	69% 62% 37% .
3	I1	106	71% 60% 39% .
3	J1	106	69% 62% 37% .
3	K1	106	71% 62% 37% .
3	L1	106	69% 61% 38% .
3	M1	106	71% 62% 37% .
3	N1	106	69% 62% 37% .
3	O1	106	71% 61% 38% .
3	P1	106	69% 62% 37% .
3	Q1	106	71% 62% 37% .
3	R1	106	69% 61% 38% .
3	S1	106	69% 62% 37% .
3	T1	106	71% 62% 37% .
3	U1	106	69% 61% 38% .
3	V1	106	71% 61% 38% .
3	W1	106	69% 62% 37% .
3	X1	106	71% 62% 37% .
3	Y1	106	69% 61% 38% .
3	Z1	106	71% 60% 39% .

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Mol	Chain	Length	Quality of chain
3	al	106	71% 62% 37% .
3	bl	106	71% 62% 37% .
3	cl	106	69% 62% 37% .
3	dl	106	69% 62% 37% .
3	el	106	69% 61% 38% .
3	fl	106	71% 61% 38% .
3	gl	106	71% 62% 37% .
3	hl	106	70% 61% 38% .
3	il	106	71% 62% 37% .
3	jl	106	71% 62% 37% .
3	kl	106	69% 62% 37% .
3	ll	106	69% 62% 37% .
3	ml	106	69% 61% 38% .
3	nl	106	71% 62% 37% .
3	ol	106	71% 61% 38% .
3	pl	106	70% 61% 38% .
3	ql	106	71% 62% 37% .
3	rl	106	71% 62% 37% .
3	sl	106	70% 61% 38% .
3	tl	106	69% 61% 38% .
3	ul	106	69% 62% 37% .
3	vl	106	69% 62% 37% .
3	wl	106	70% 61% 38% .
3	xl	106	71% 62% 37% .
3	yl	106	69% 62% 37% .

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Mol	Chain	Length	Quality of chain
3	zl	106	69% 61% 38%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 354120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	B	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	C	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	D	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	E	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	F	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	G	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	H	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	I	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	J	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	K	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	L	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	M	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	N	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	O	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	P	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		
1	Q	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	S	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	T	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	U	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	V	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	W	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	X	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	Y	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	Z	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	1	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	2	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	3	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	4	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	5	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	6	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	a	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	b	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	c	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	d	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	e	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	f	516	Total 4135	C 2603	N 722	O 797	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	h	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	i	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	j	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	k	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	l	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	m	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	n	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	o	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	p	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	q	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	r	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	s	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	t	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	u	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	v	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	w	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	x	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	y	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	z	516	Total 4135	C 2603	N 722	O 797	S 13	0	0
1	7	516	Total 4135	C 2603	N 722	O 797	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	516	Total	C	N	O	S	0	0
			4135	2603	722	797	13		

- Molecule 2 is a protein called IgA-Fab3-4 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ah	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Bh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Ch	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Dh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Eh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Fh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Gh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Hh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Ih	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Jh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Kh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Lh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Mh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Nh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Oh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Ph	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Qh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		
2	Rh	125	Total	C	N	O	S	0	0
			989	632	165	187	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Sh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Th	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Uh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Vh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Wh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Xh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Yh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	Zh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	1h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	2h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	3h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	4h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	5h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	6h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	ah	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	bh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	ch	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	dh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	eh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	fh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	gh	125	Total 989	C 632	N 165	O 187	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	hh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	ih	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	jh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	kh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	lh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	mh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	nh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	oh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	ph	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	qh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	rh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	sh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	th	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	uh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	vh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	wh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	xh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	yh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	zh	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	7h	125	Total 989	C 632	N 165	O 187	S 5	0	0
2	8h	125	Total 989	C 632	N 165	O 187	S 5	0	0

- Molecule 3 is a protein called IgA-Fab3-4 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Al	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Bl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Cl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Dl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	El	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Fl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Gl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Hl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Il	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Jl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Kl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Ll	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Ml	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Nl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Ol	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Pl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Ql	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Rl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Sl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Tl	106	Total	C	N	O	S	0	0
			778	477	134	165	2		
3	Ul	106	Total	C	N	O	S	0	0
			778	477	134	165	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Vl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	Wl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	Xl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	Yl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	Zl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	1l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	2l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	3l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	4l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	5l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	6l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	al	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	bl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	cl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	dl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	el	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	fl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	gl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	hl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	il	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	jl	106	Total 778	C 477	N 134	O 165	S 2	0	0

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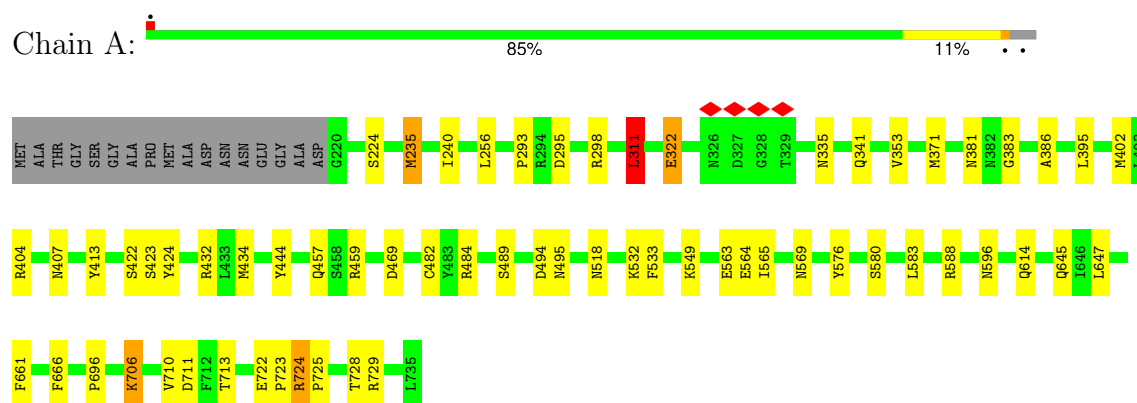
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Mol	Chain	Residues	Atoms					AltConf	Trace
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3	ll	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	ml	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	nl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	ol	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	pl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	ql	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	rl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	sl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	tl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	ul	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	vl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	wl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	xl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	yl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	zl	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	7l	106	Total 778	C 477	N 134	O 165	S 2	0	0
3	8l	106	Total 778	C 477	N 134	O 165	S 2	0	0

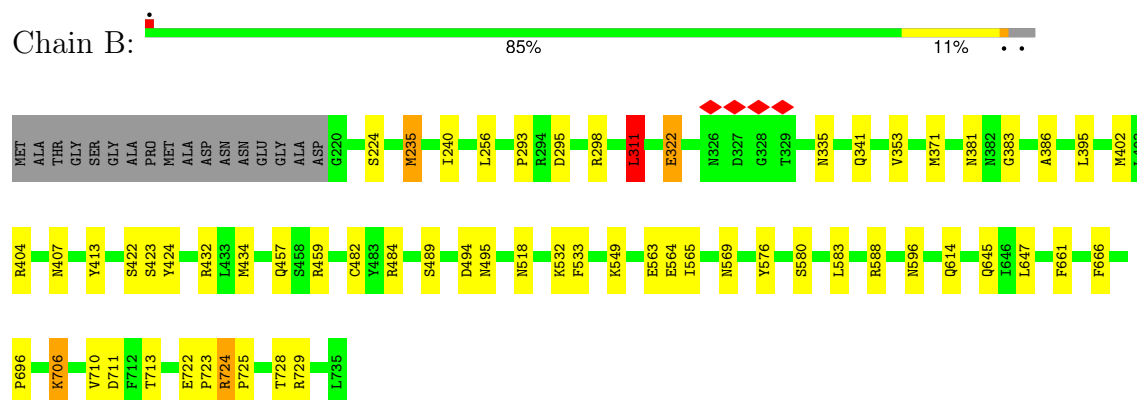
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

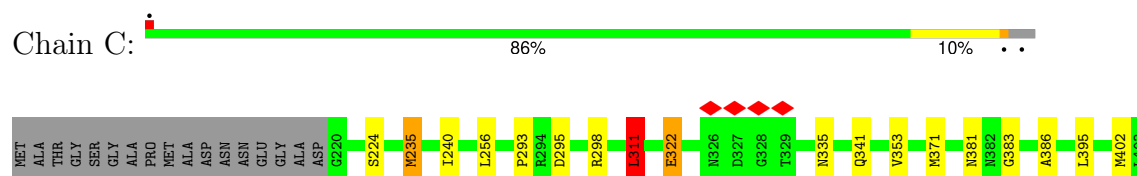
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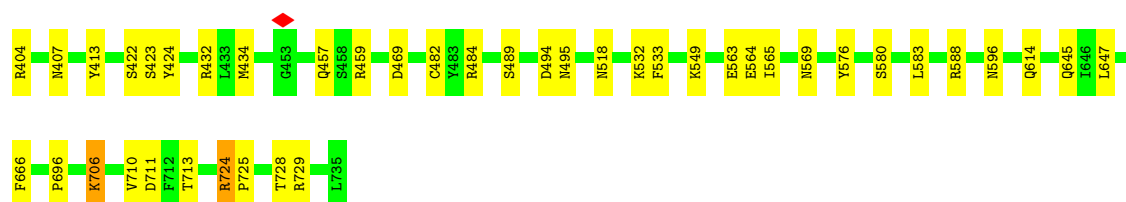


• Molecule 1: Capsid protein VP1



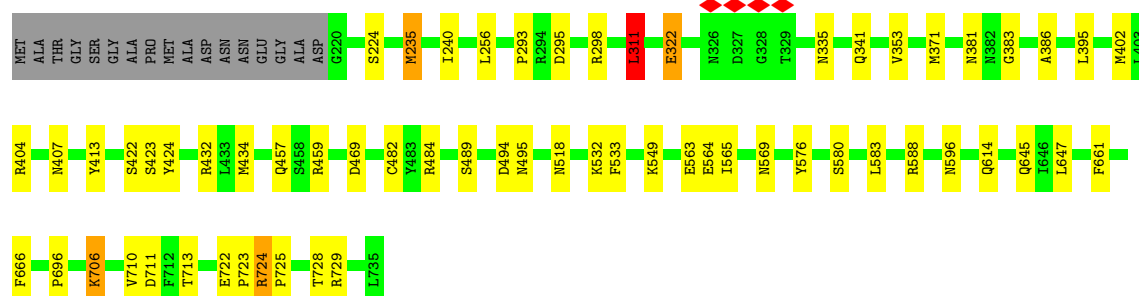
• Molecule 1: Capsid protein VP1





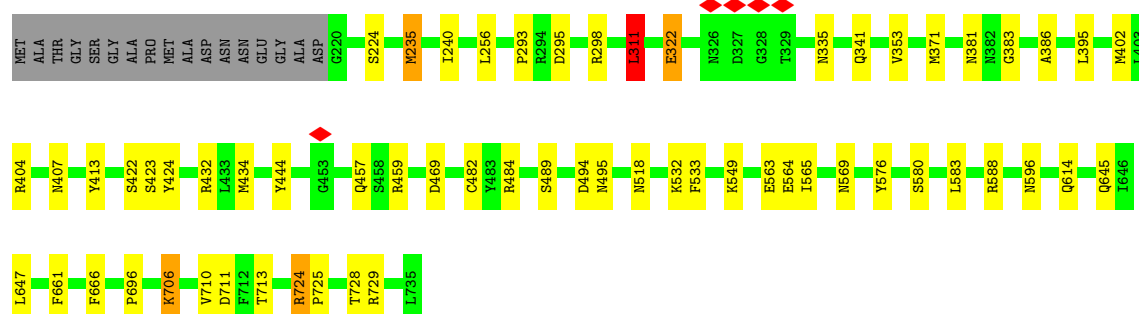
- Molecule 1: Capsid protein VP1

Chain D: 85% 11% . .



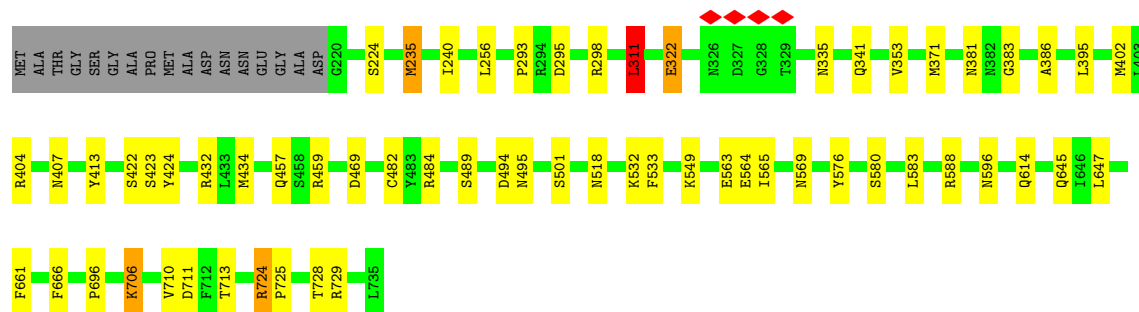
- Molecule 1: Capsid protein VP1

Chain E: 85% 11% . .

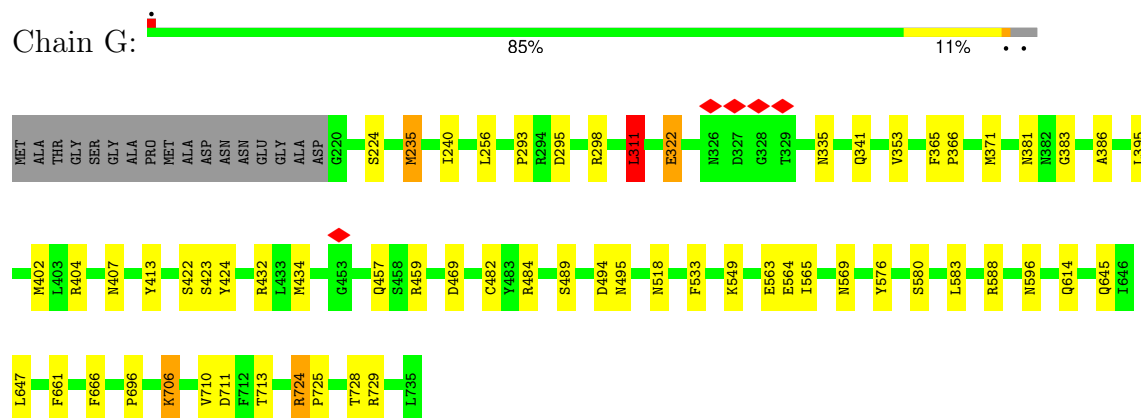


- Molecule 1: Capsid protein VP1

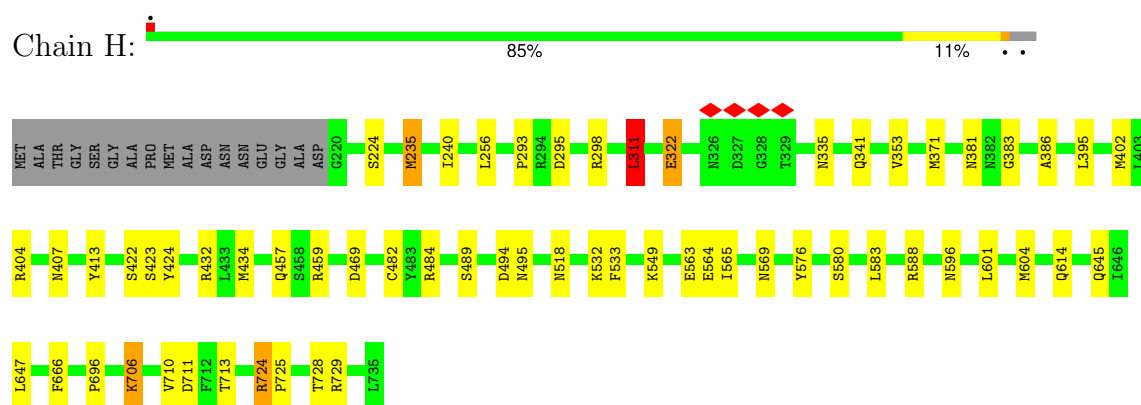
Chain F: 85% 11% . .



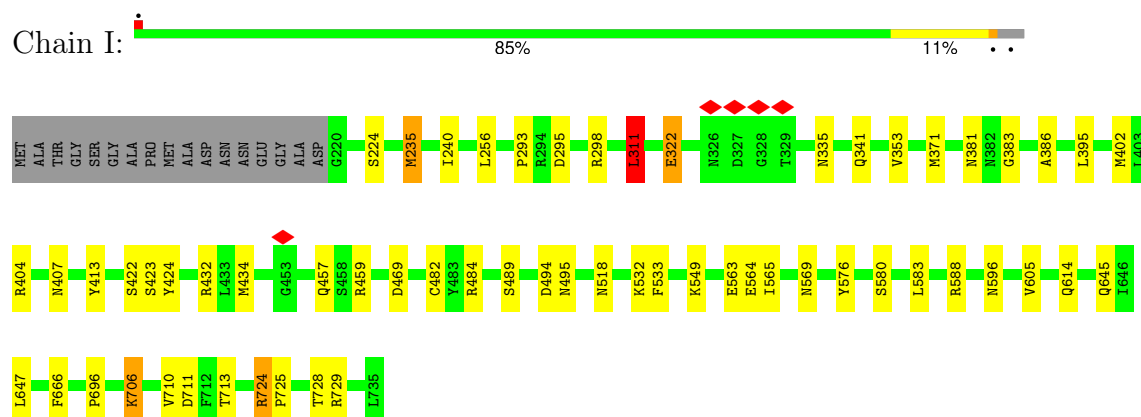
- Molecule 1: Capsid protein VP1



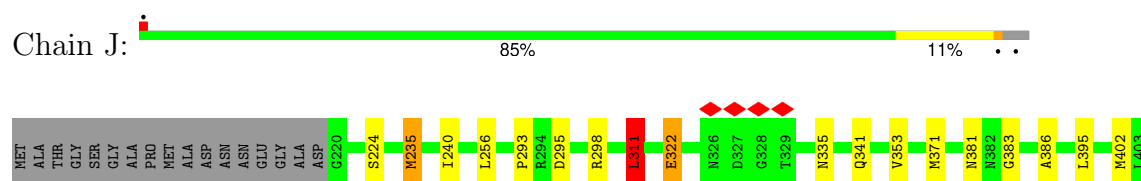
- Molecule 1: Capsid protein VP1



- Molecule 1: Capsid protein VP1



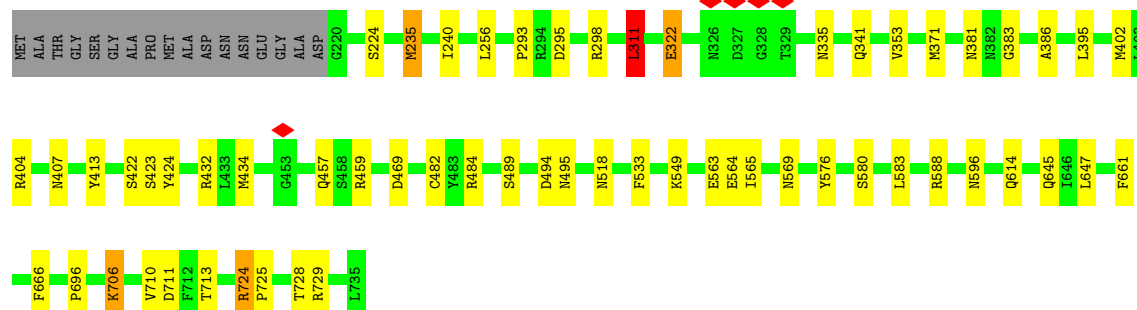
- Molecule 1: Capsid protein VP1





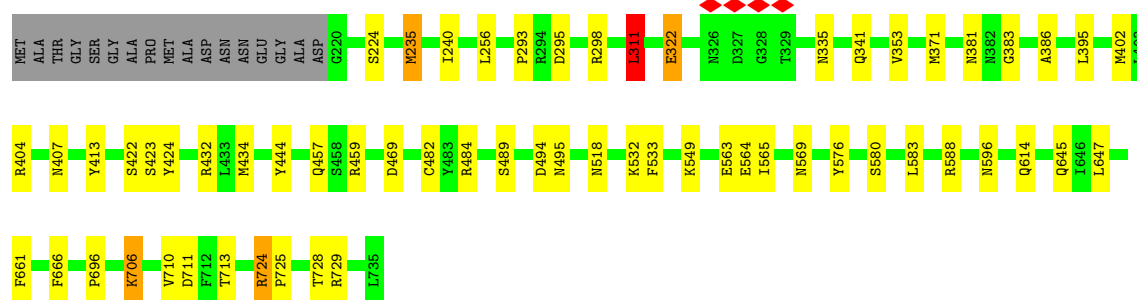
• Molecule 1: Capsid protein VP1

Chain K: 86% 10% ..



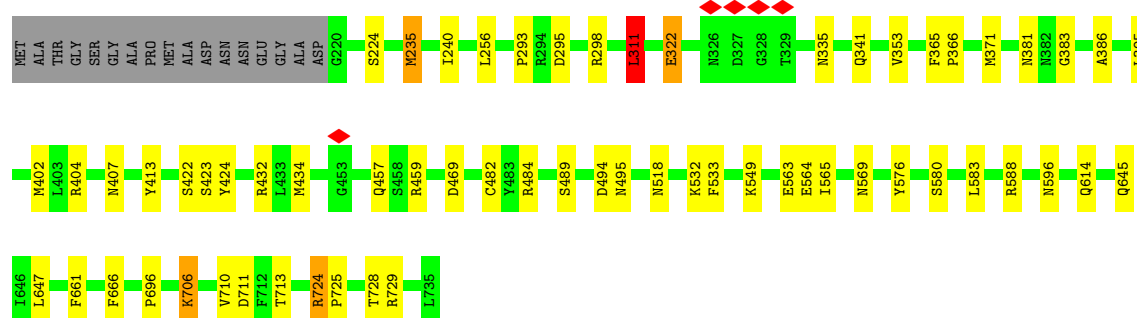
• Molecule 1: Capsid protein VP1

Chain L: 85% 11% ..

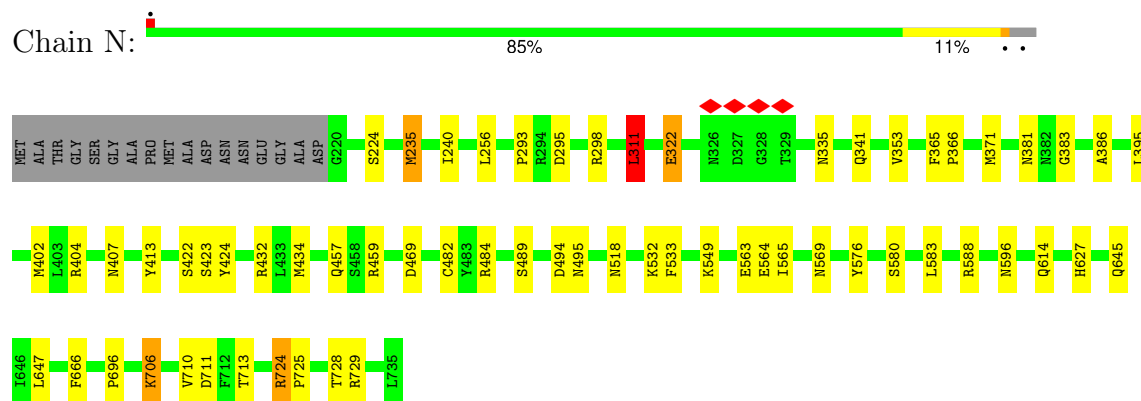


• Molecule 1: Capsid protein VP1

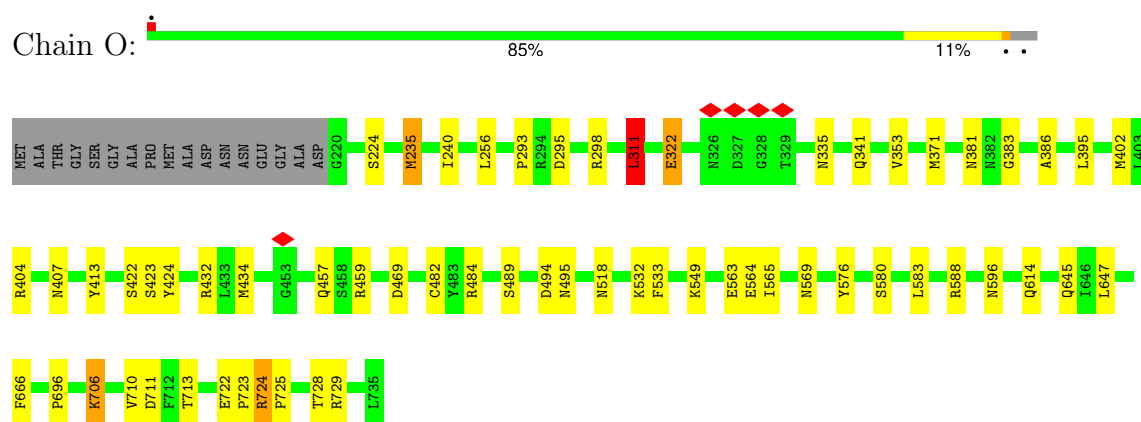
Chain M: 85% 11% ..



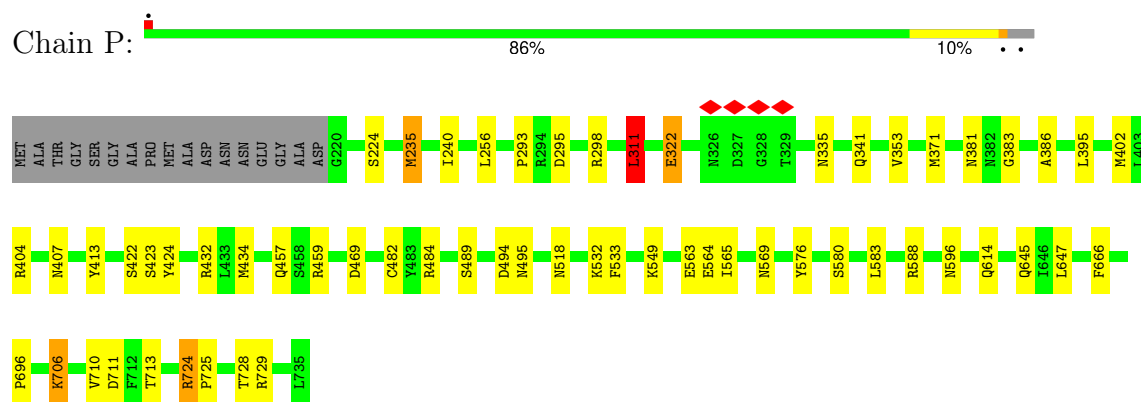
• Molecule 1: Capsid protein VP1



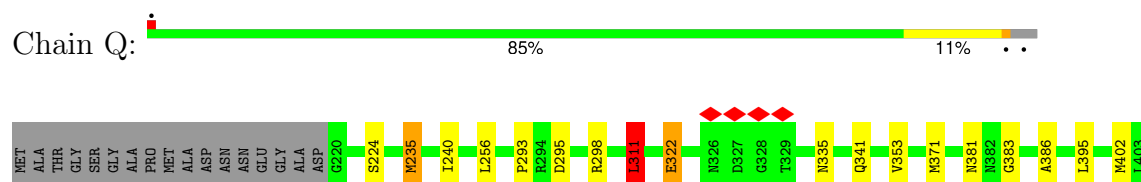
• Molecule 1: Capsid protein VP1

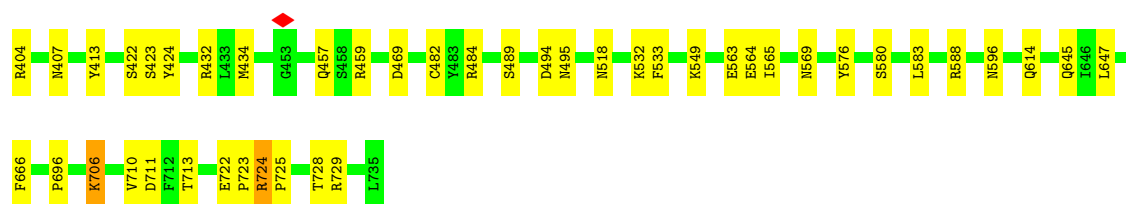


• Molecule 1: Capsid protein VP1



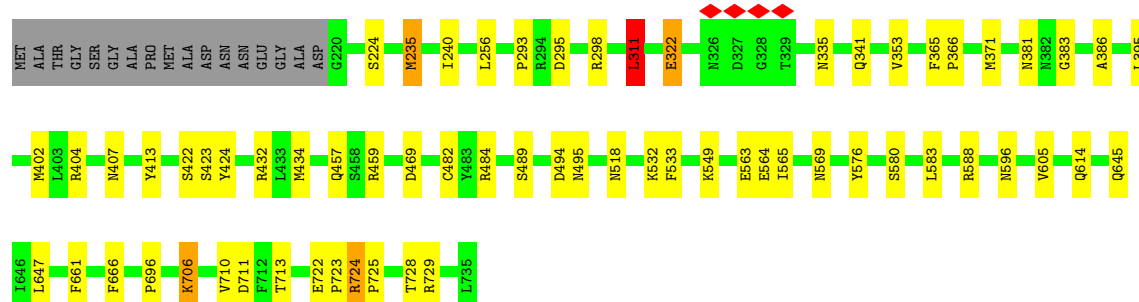
• Molecule 1: Capsid protein VP1





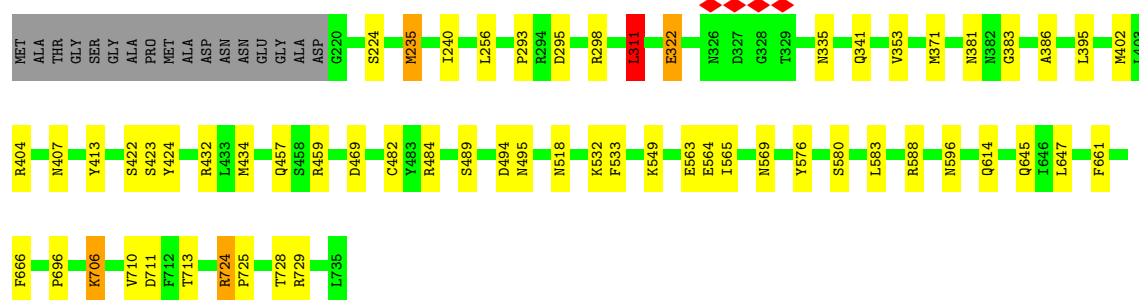
- Molecule 1: Capsid protein VP1

Chain R: 84% 11% ..



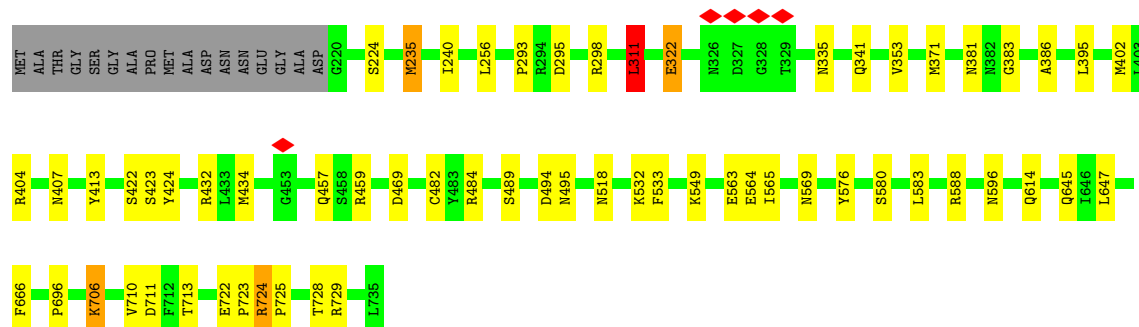
- Molecule 1: Capsid protein VP1

Chain S: 85% 11% ..

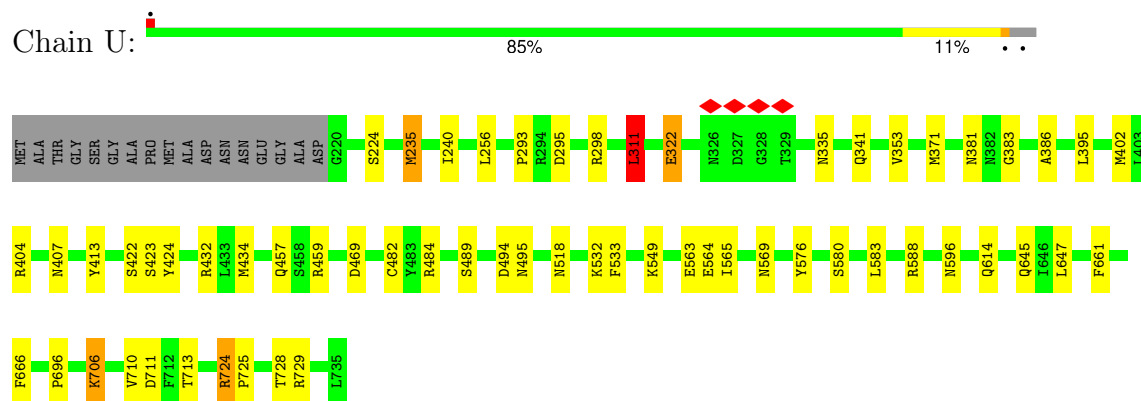


- Molecule 1: Capsid protein VP1

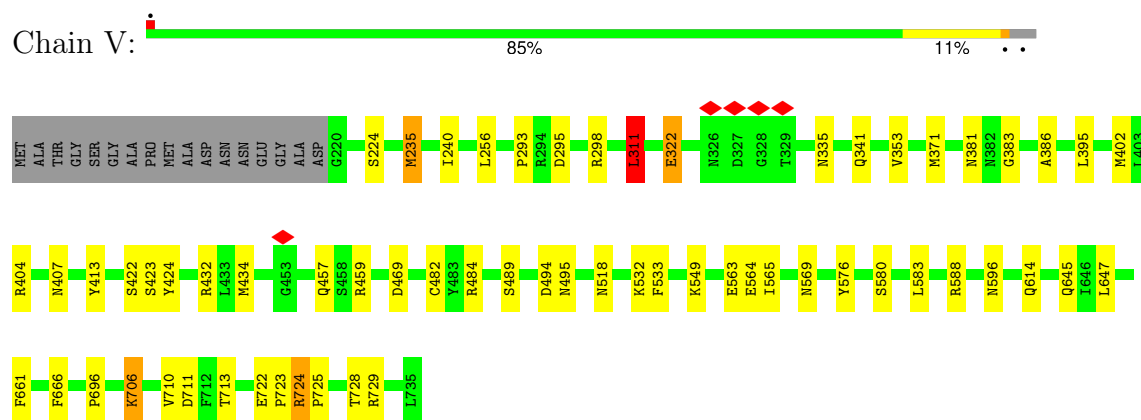
Chain T: 85% 11% ..



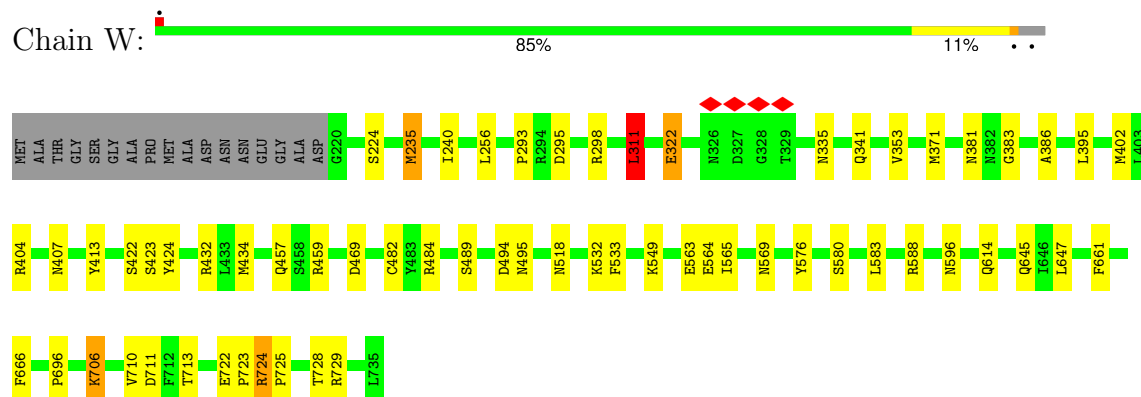
- Molecule 1: Capsid protein VP1



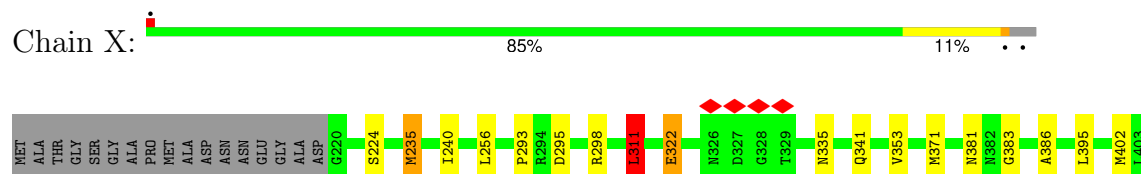
• Molecule 1: Capsid protein VP1

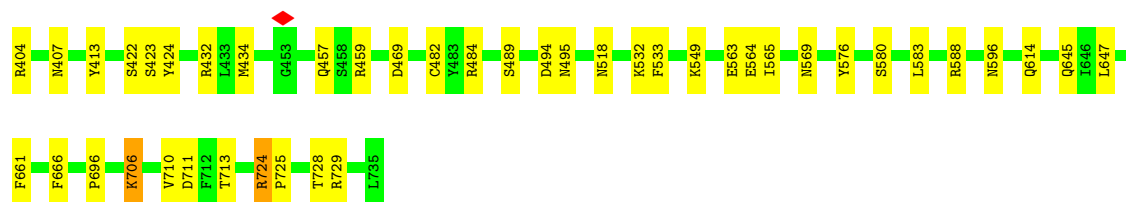


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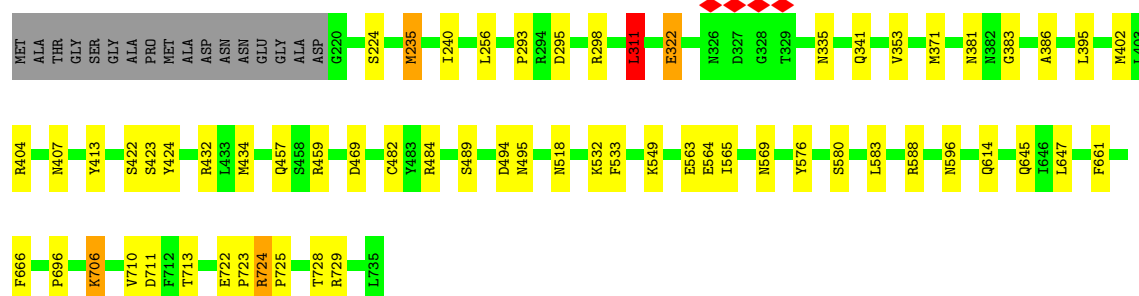
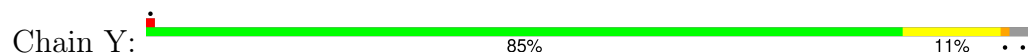


• Molecule 1: Capsid protein VP1

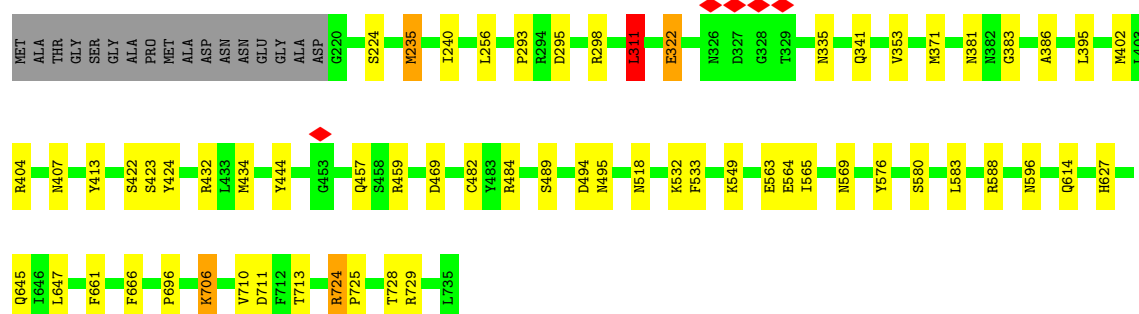
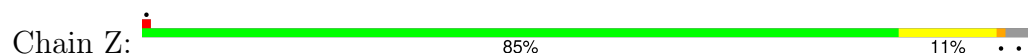




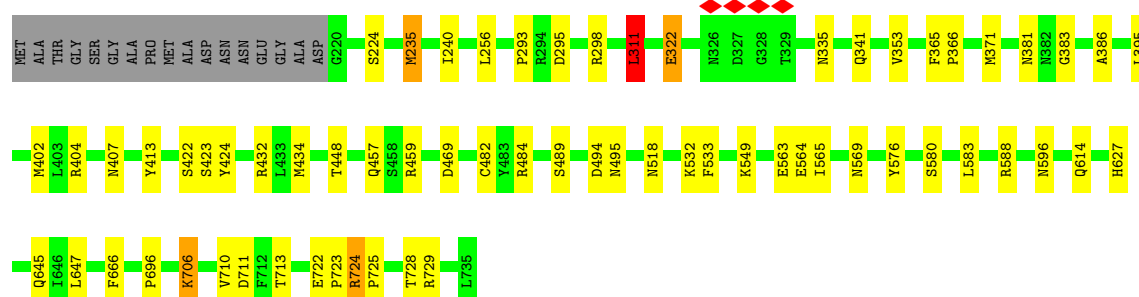
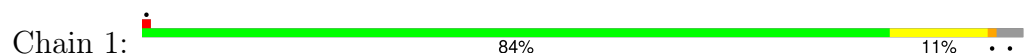
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

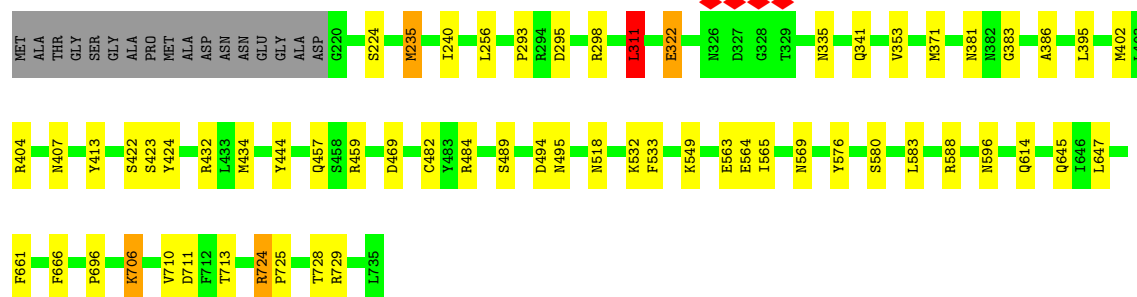


• Molecule 1: Capsid protein VP1



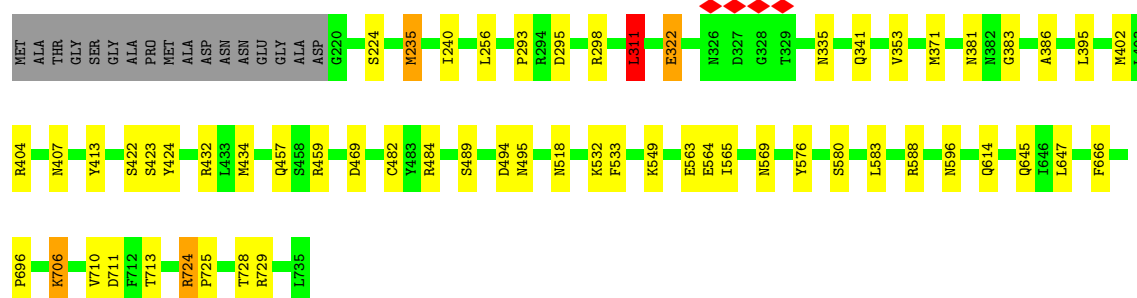
• Molecule 1: Capsid protein VP1

Chain 2:  85% 11% ..



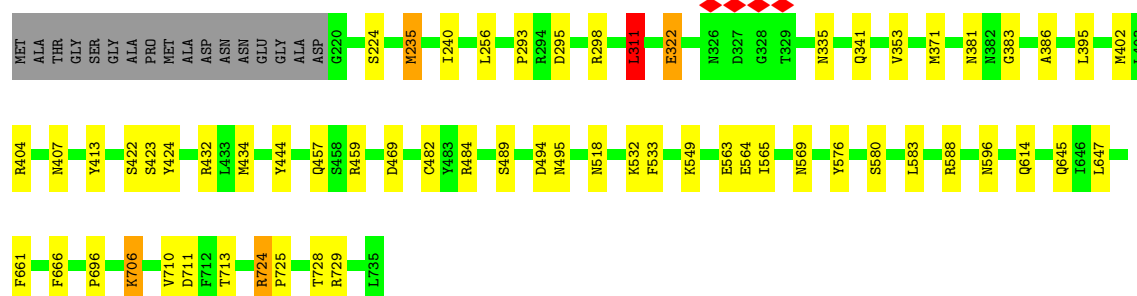
• Molecule 1: Capsid protein VP1

Chain 3:  86% 10% ..



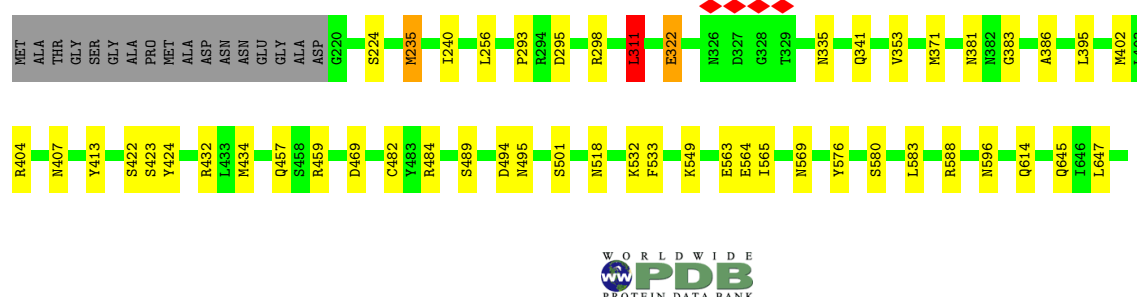
• Molecule 1: Capsid protein VP1

Chain 4:  85% 11% ..



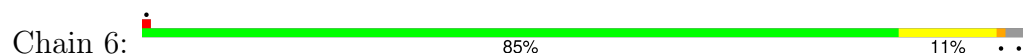
• Molecule 1: Capsid protein VP1

Chain 5:  85% 11% ..

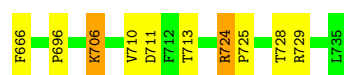
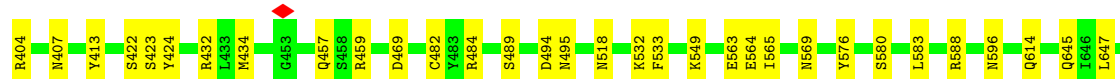
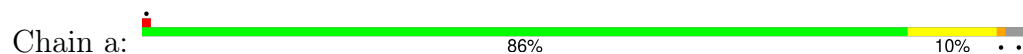




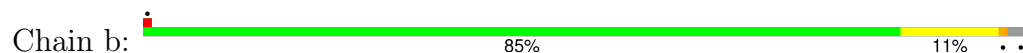
• Molecule 1: Capsid protein VP1



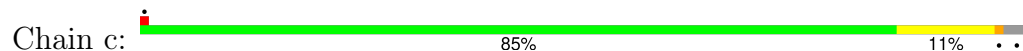
• Molecule 1: Capsid protein VP1

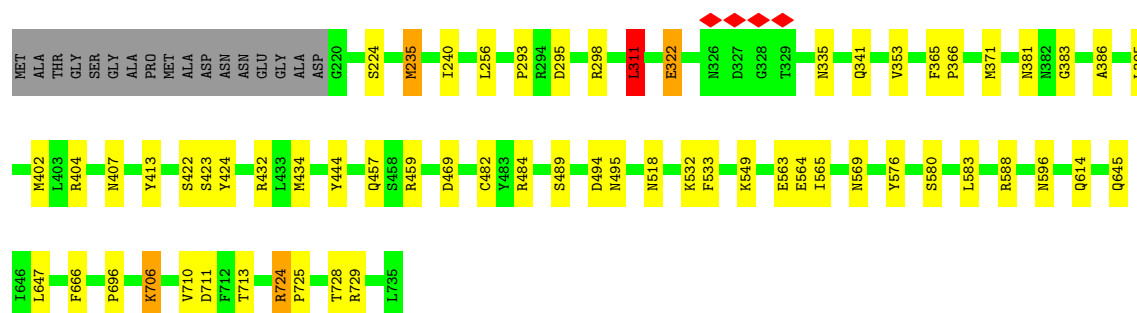


• Molecule 1: Capsid protein VP1

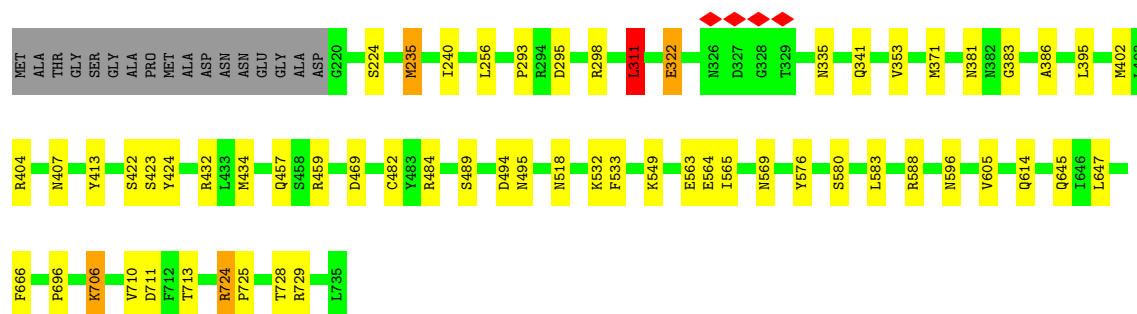
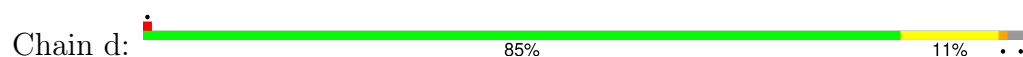


• Molecule 1: Capsid protein VP1

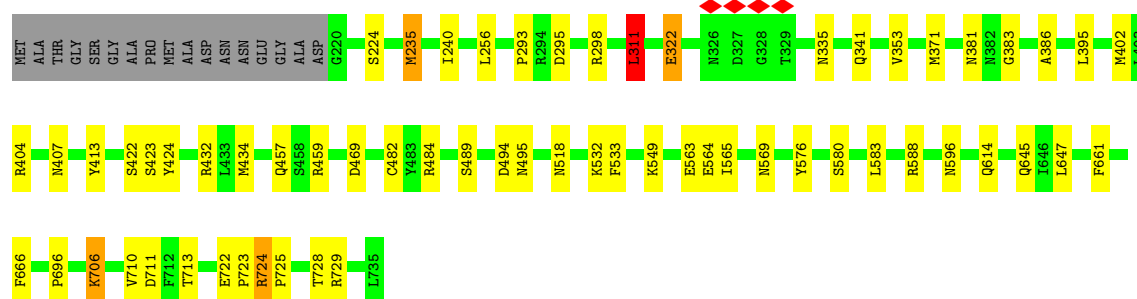
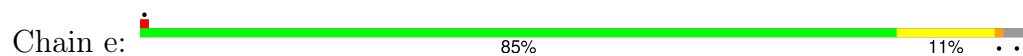




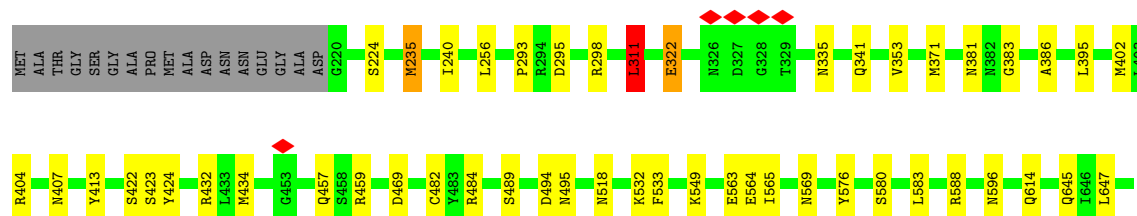
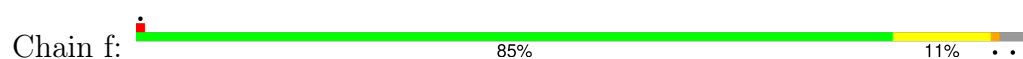
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



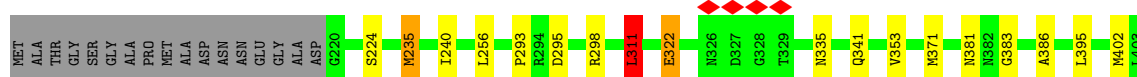
• Molecule 1: Capsid protein VP1





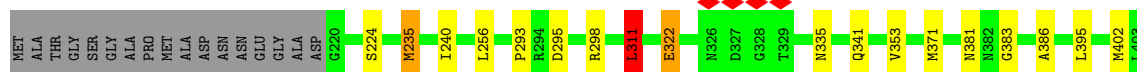
• Molecule 1: Capsid protein VP1

Chain g: 86% 10% ..



• Molecule 1: Capsid protein VP1

Chain h: 85% 11% ..



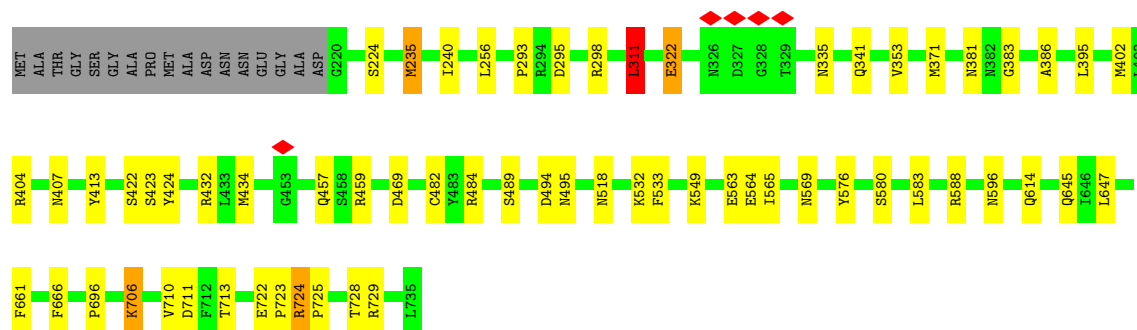
• Molecule 1: Capsid protein VP1

Chain i: 85% 11% ..



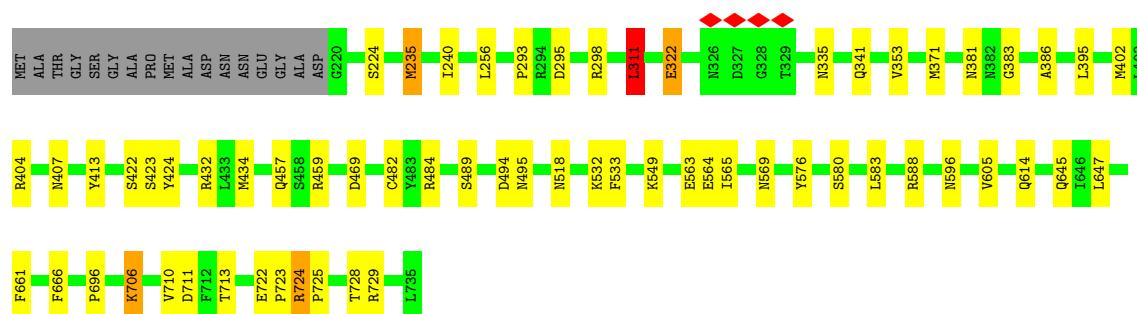
• Molecule 1: Capsid protein VP1

Chain j: 85% 11% ..



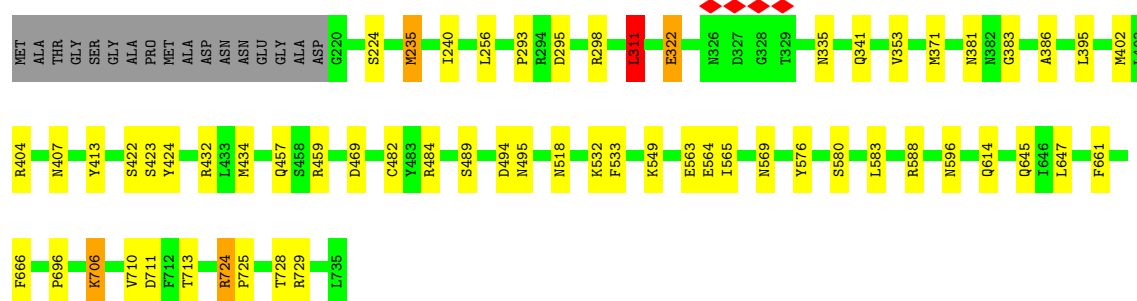
- Molecule 1: Capsid protein VP1

Chain k: 85% 11% ..



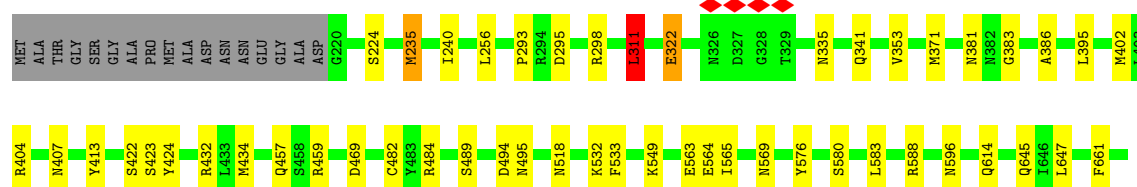
- Molecule 1: Capsid protein VP1

Chain l: 85% 11% ..



- Molecule 1: Capsid protein VP1

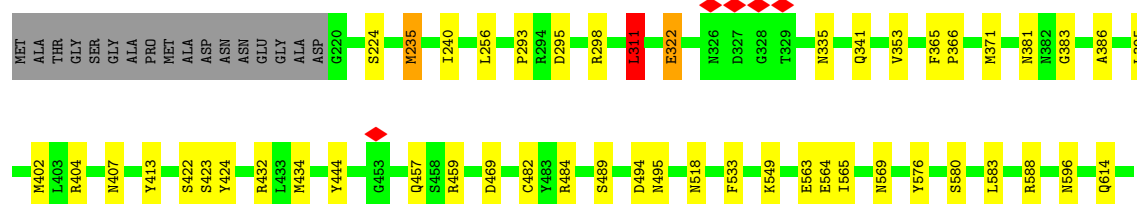
Chain m: 85% 11% ..





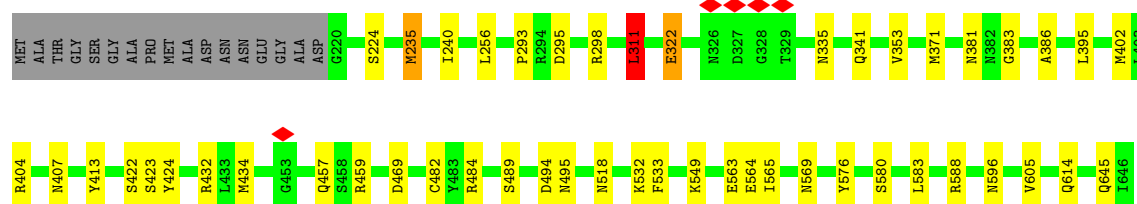
• Molecule 1: Capsid protein VP1

Chain n: 85% 11% ..



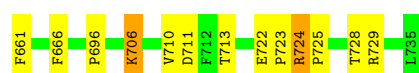
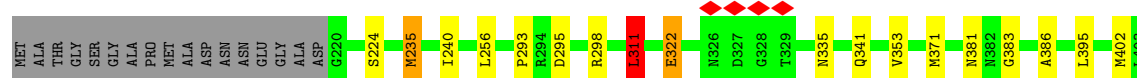
• Molecule 1: Capsid protein VP1

Chain o: 85% 11% ..



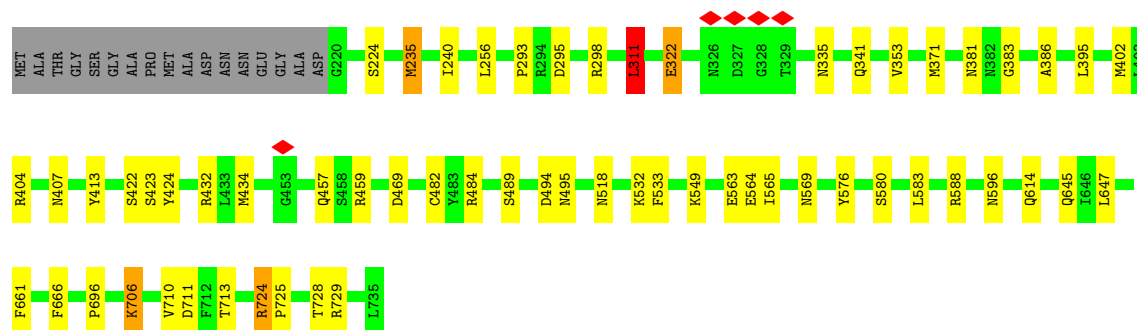
• Molecule 1: Capsid protein VP1

Chain p: 85% 11% ..

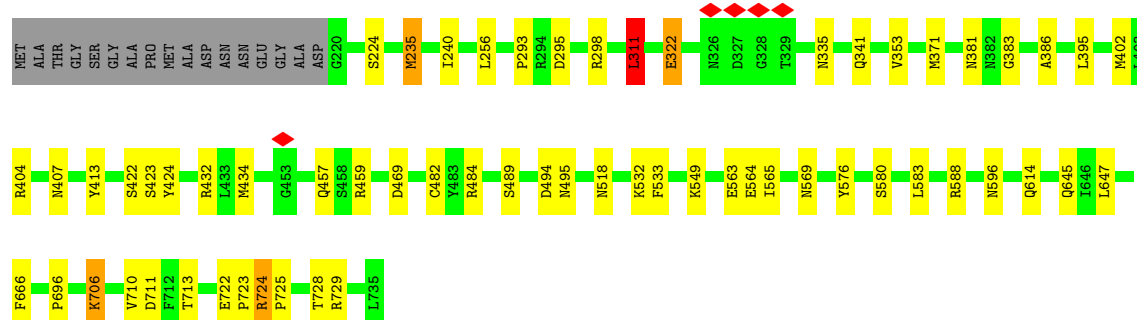
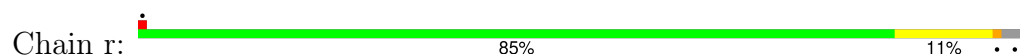


• Molecule 1: Capsid protein VP1

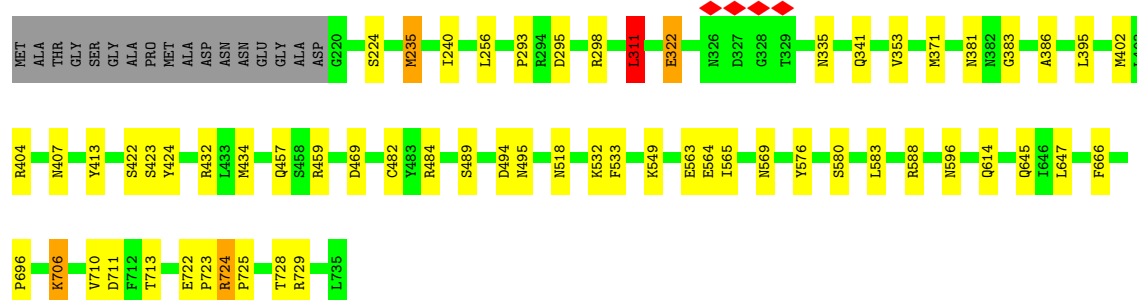
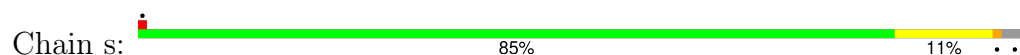
Chain q: 85% 11% ..



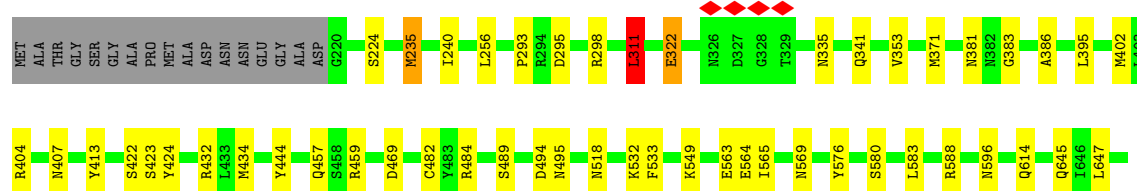
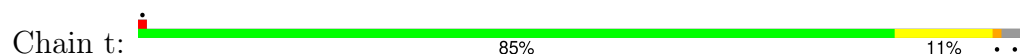
• Molecule 1: Capsid protein VP1

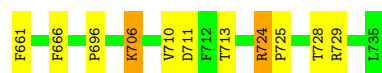


• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1





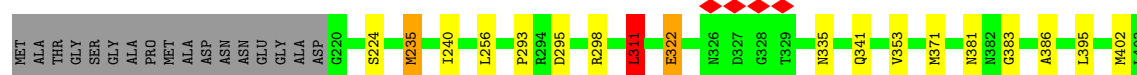
• Molecule 1: Capsid protein VP1

Chain u: 85% 11% ..



• Molecule 1: Capsid protein VP1

Chain v: 85% 11% ..



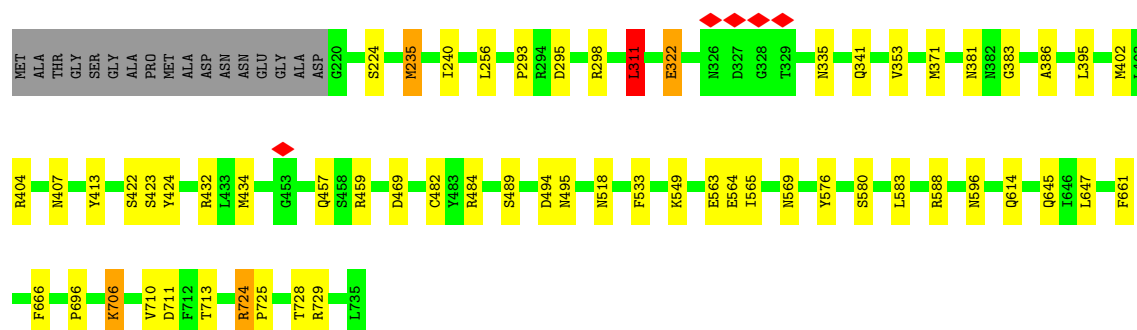
• Molecule 1: Capsid protein VP1

Chain w: 85% 11% ..

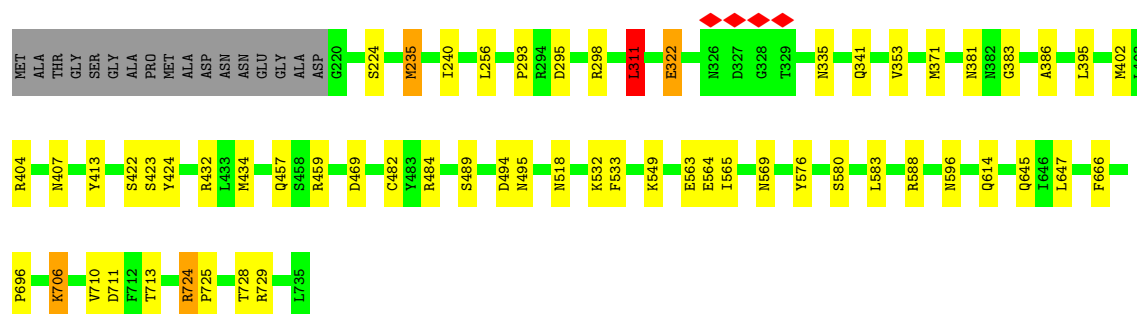
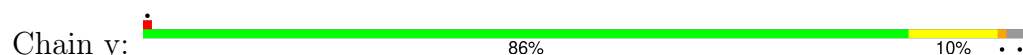


• Molecule 1: Capsid protein VP1

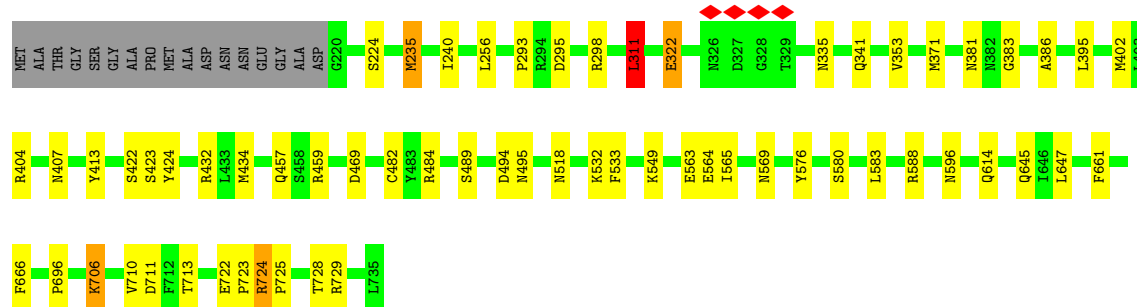
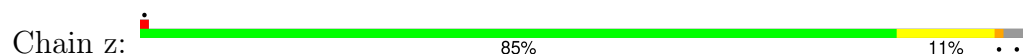
Chain x: 86% 10% ..



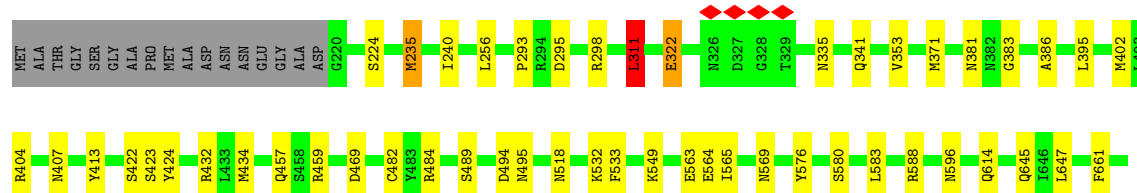
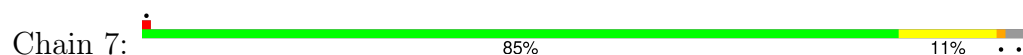
• Molecule 1: Capsid protein VP1



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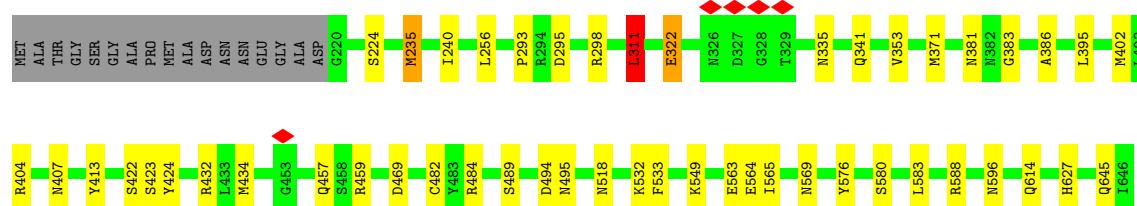
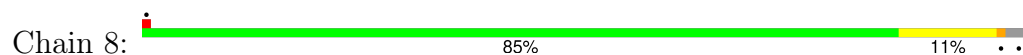


• Molecule 1: Capsid protein VP1

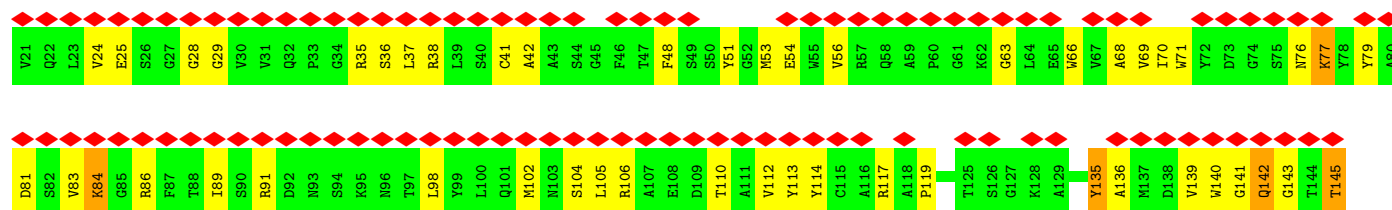
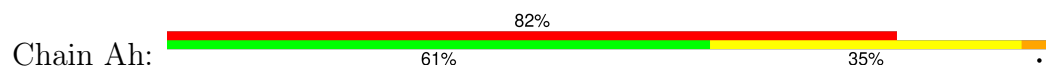




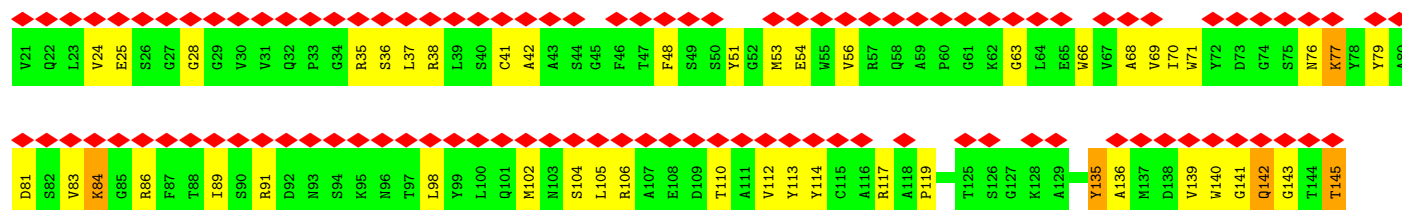
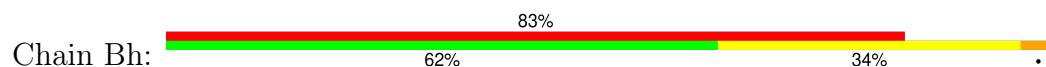
• Molecule 1: Capsid protein VP1



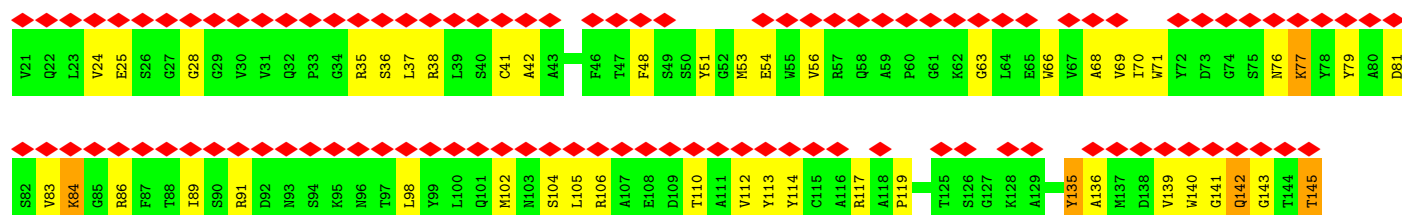
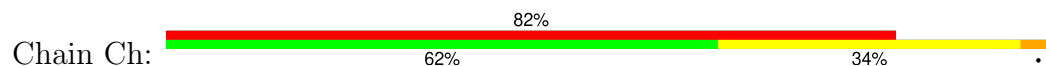
• Molecule 2: IgA-Fab3-4 heavy chain



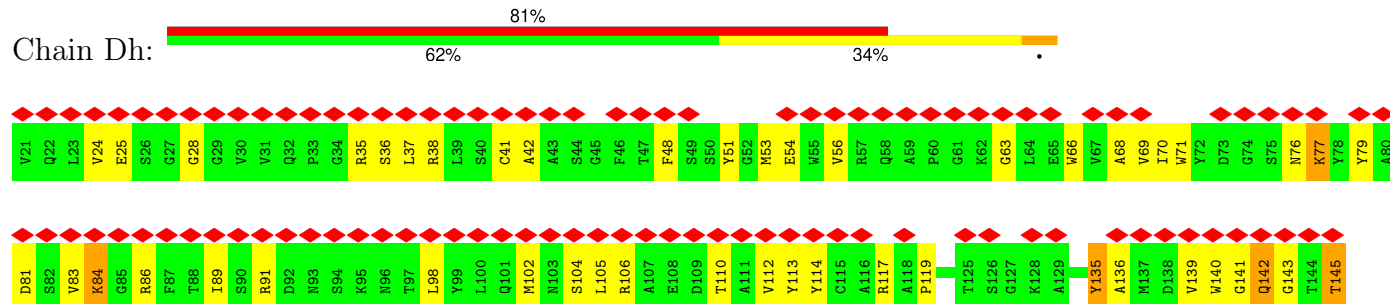
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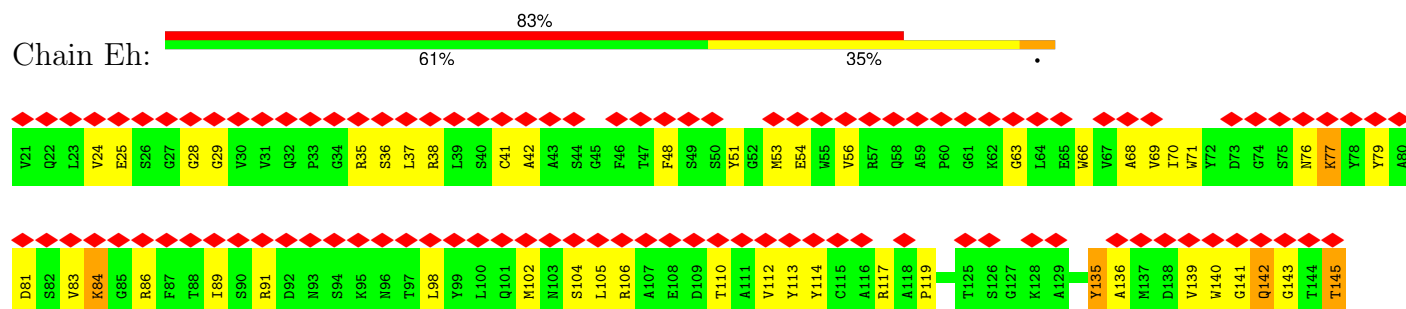
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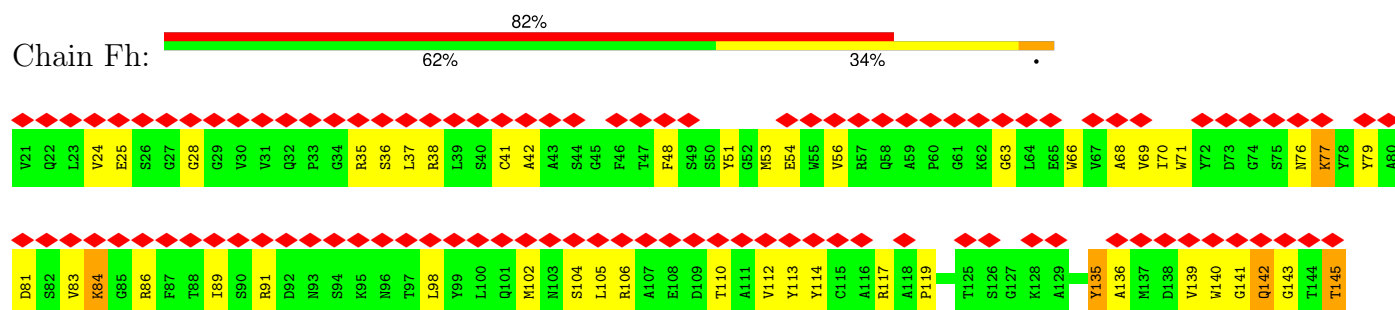
- Molecule 2: IgA-Fab3-4 heavy chain



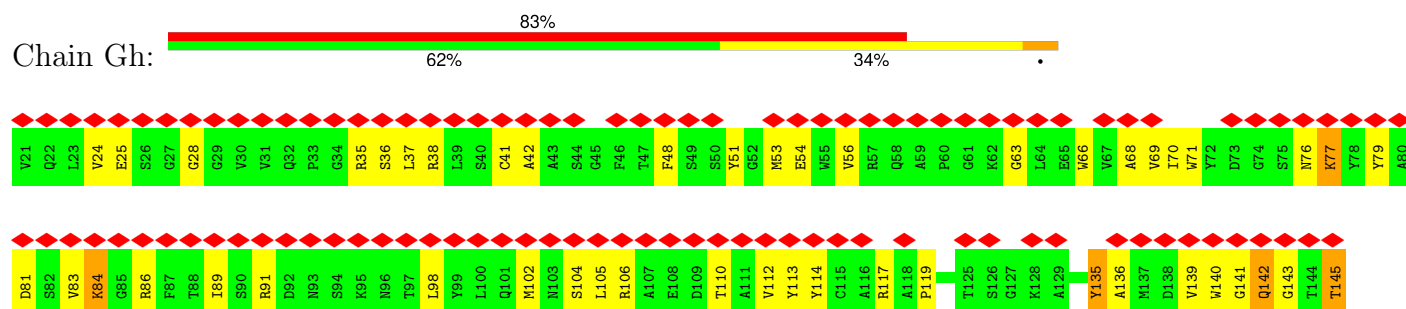
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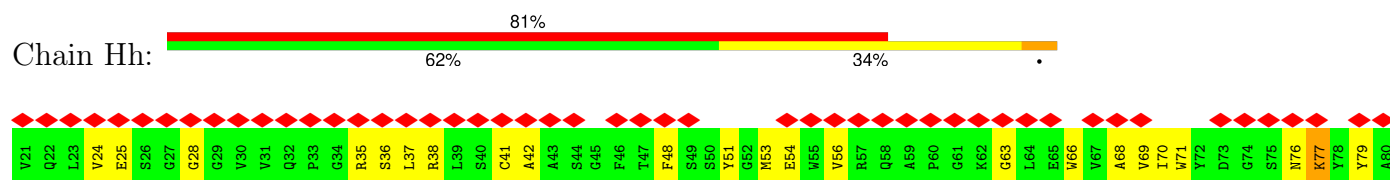
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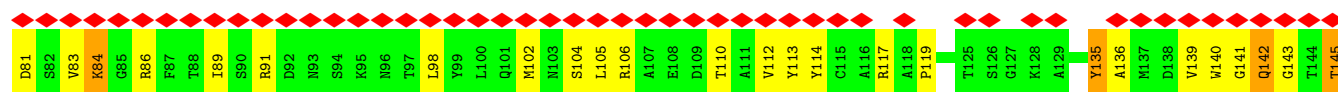


- Molecule 2: IgA-Fab3-4 heavy chain

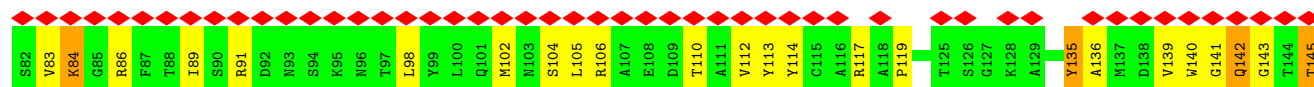
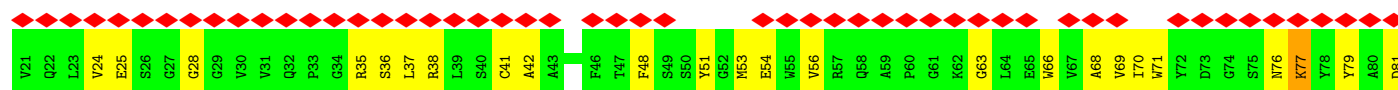
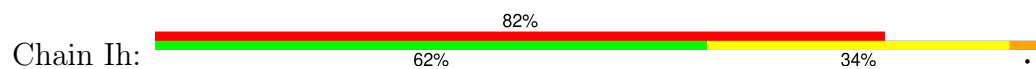


- Molecule 2: IgA-Fab3-4 heavy chain

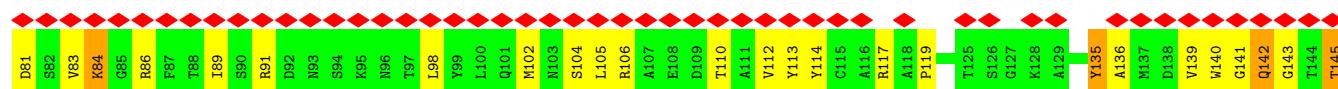
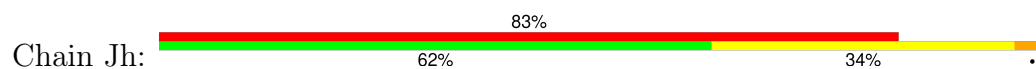




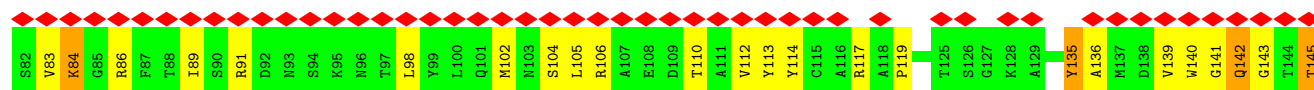
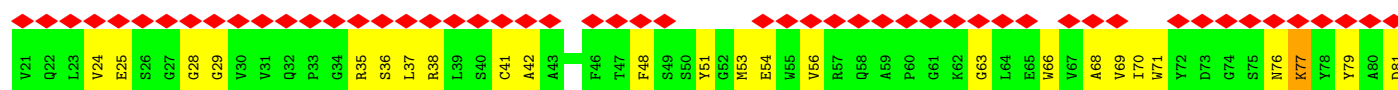
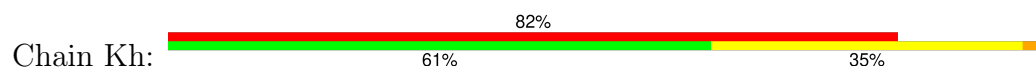
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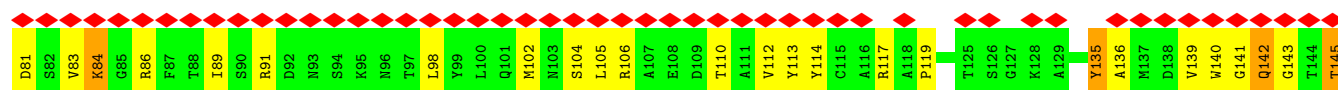
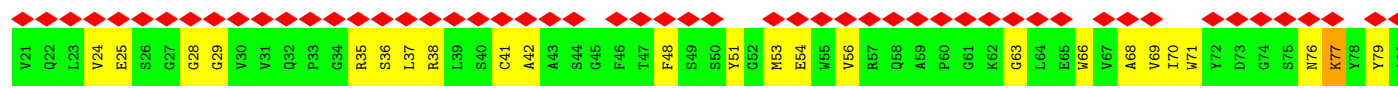
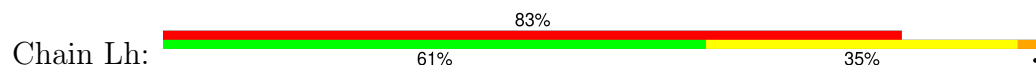
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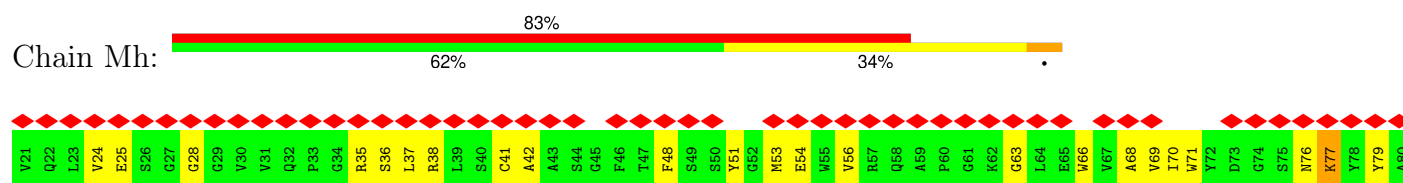
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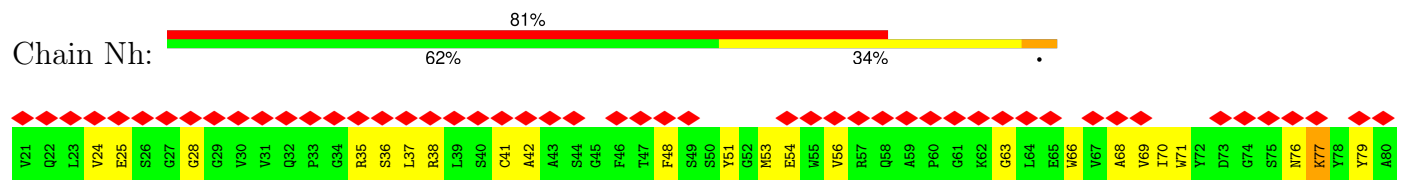
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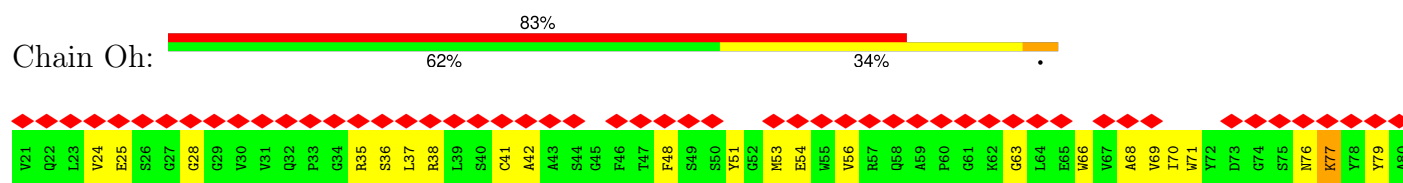
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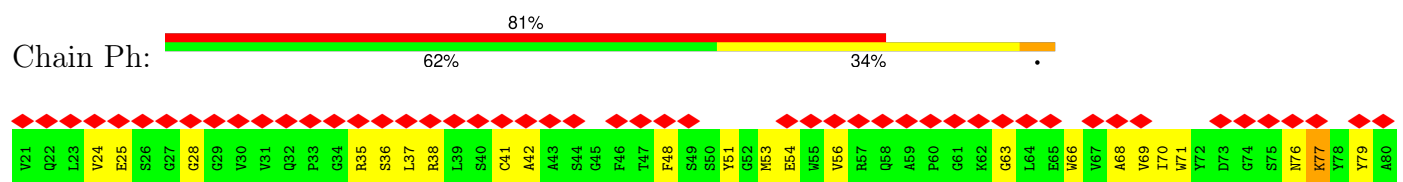
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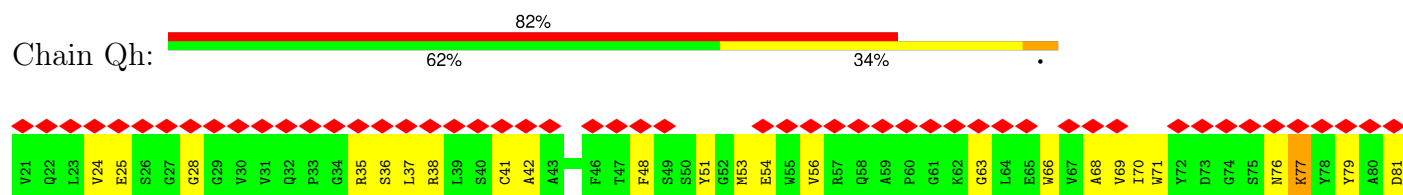
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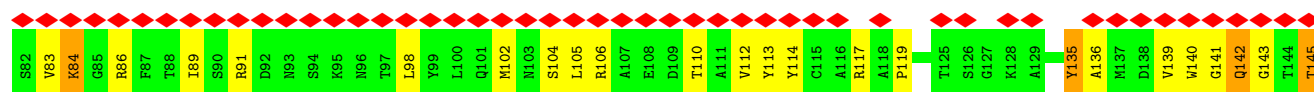


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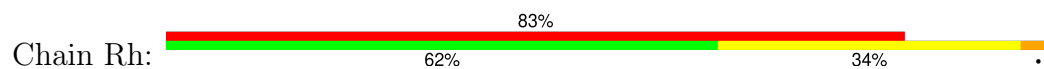


• Molecule 2: IgA-Fab3-4 heavy chain

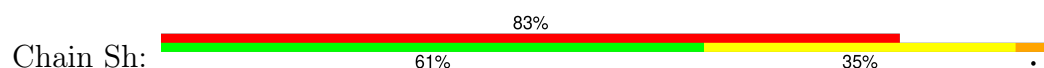




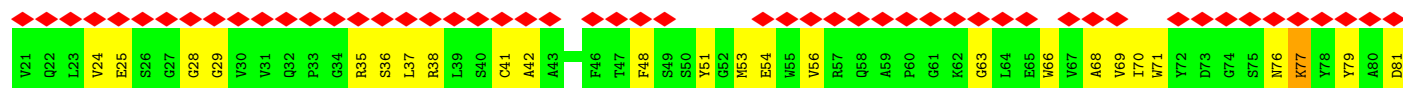
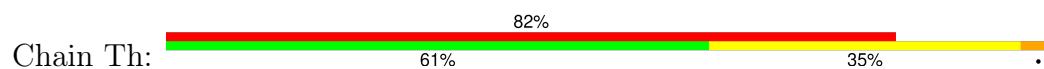
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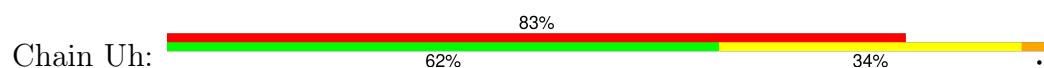
• Molecule 2: IgA-Fab3-4 heavy chain



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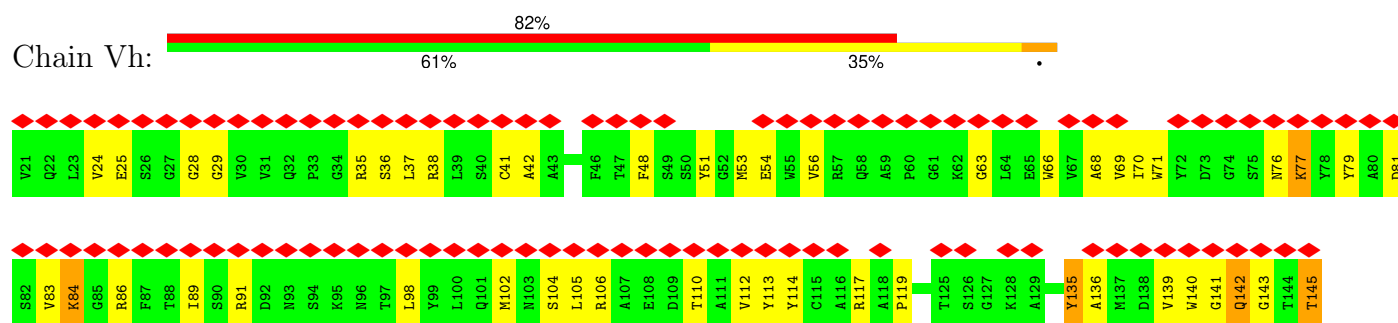


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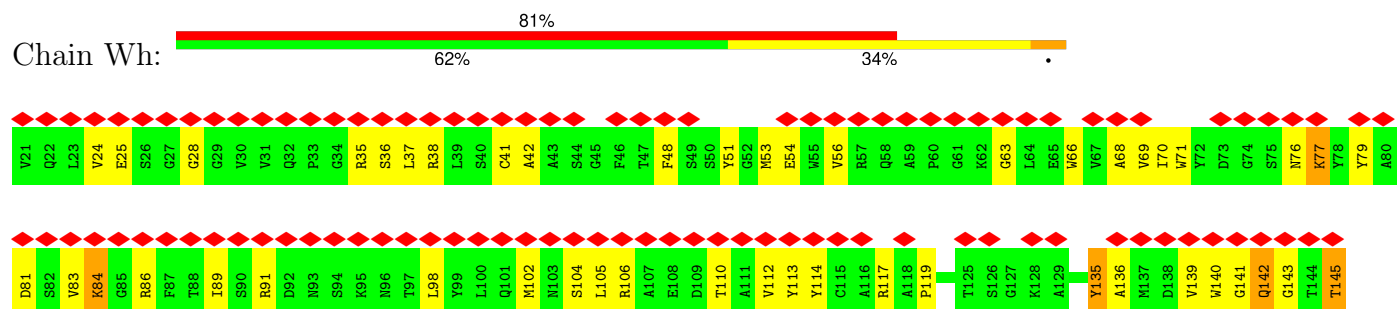


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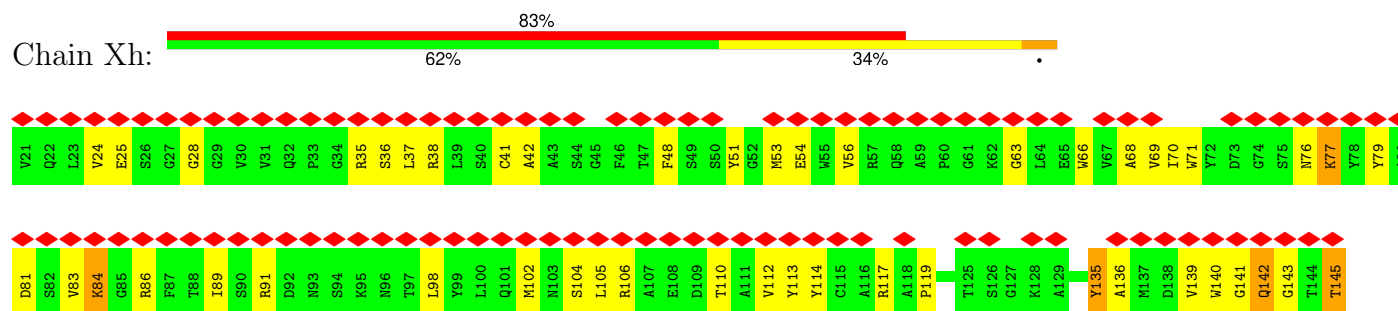




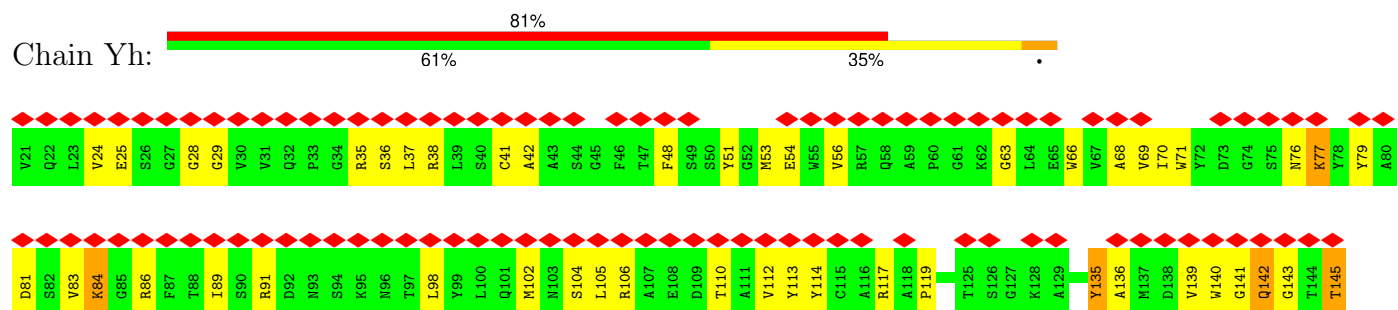
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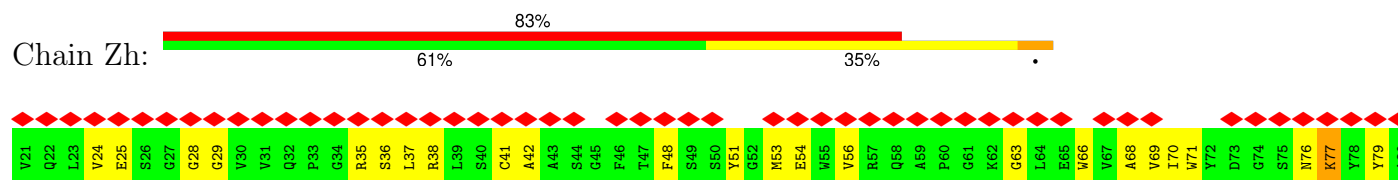
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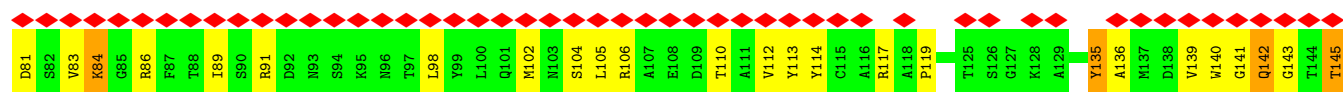


• Molecule 2: IgA-Fab3-4 heavy chain

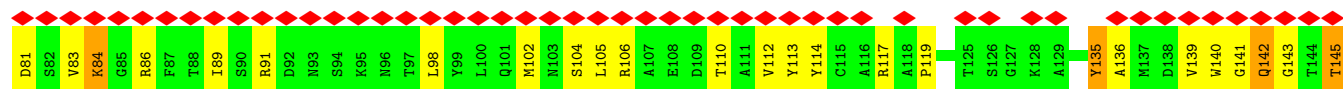
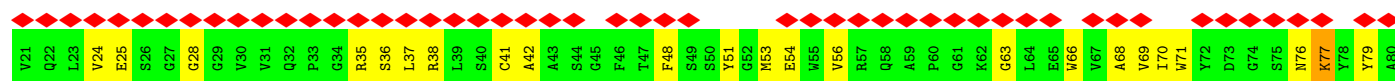
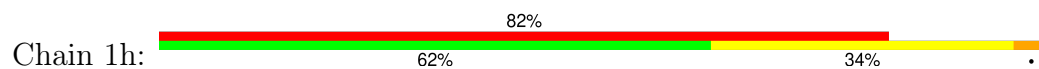


• Molecule 2: IgA-Fab3-4 heavy chain

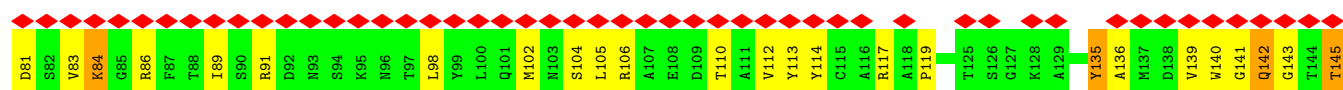
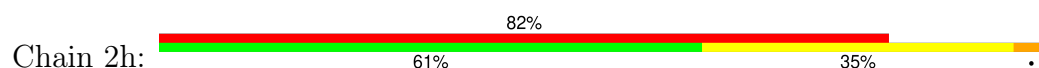




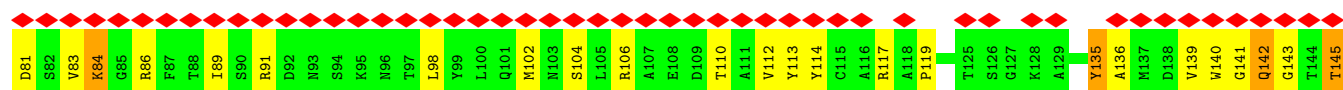
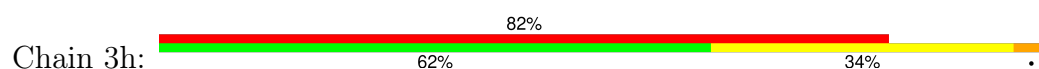
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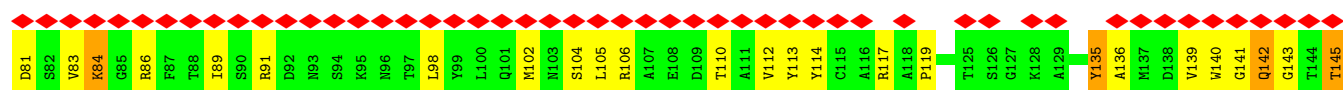
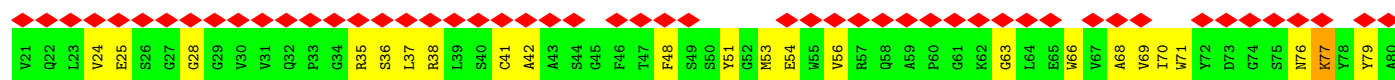
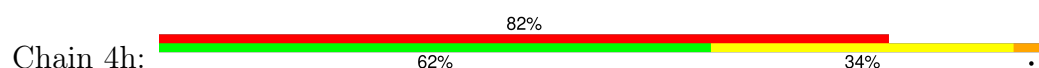
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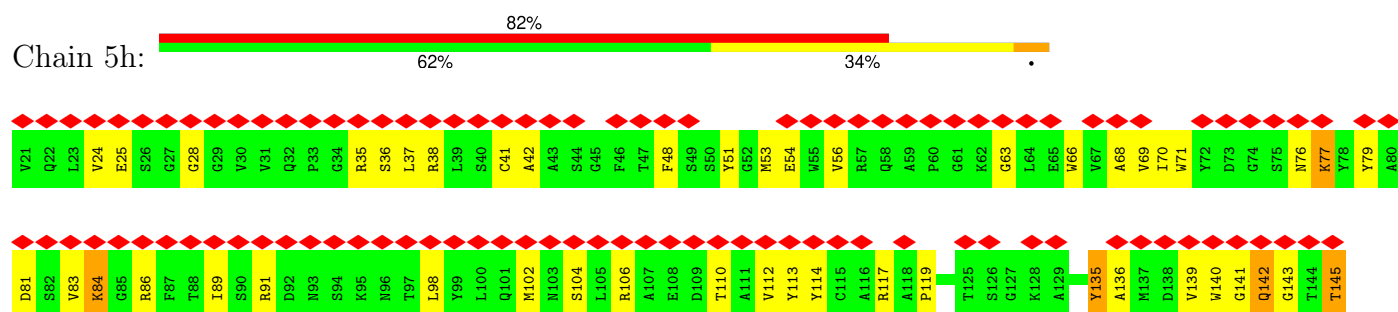
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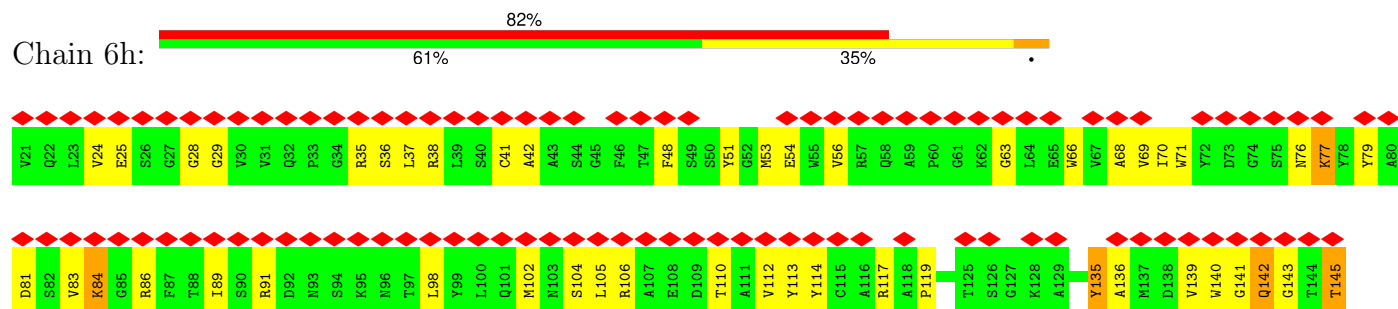
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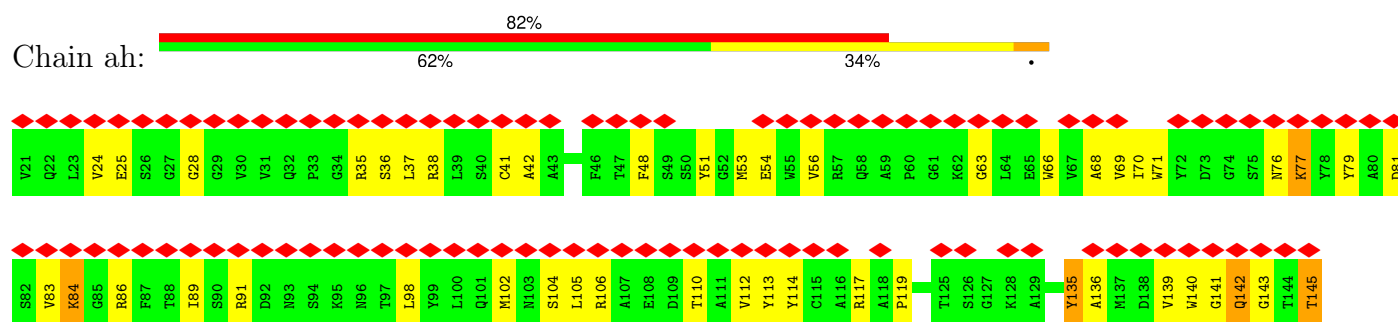
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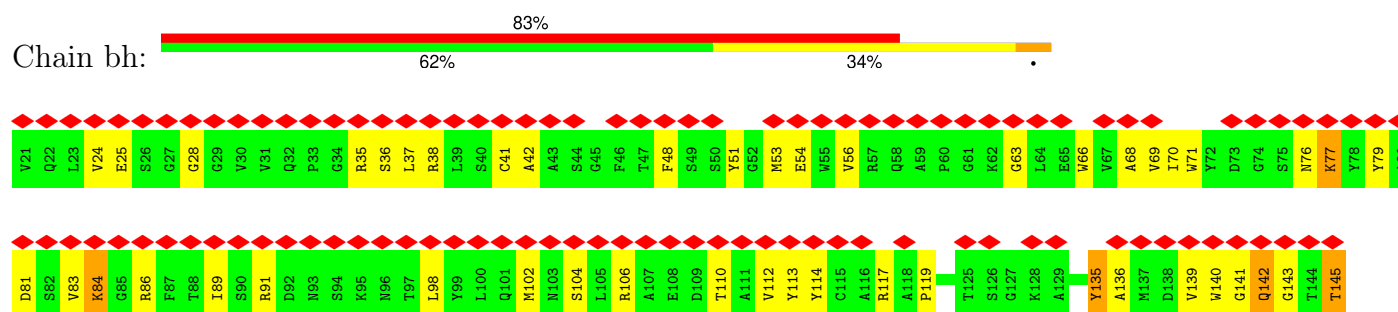
- Molecule 2: IgA-Fab3-4 heavy chain



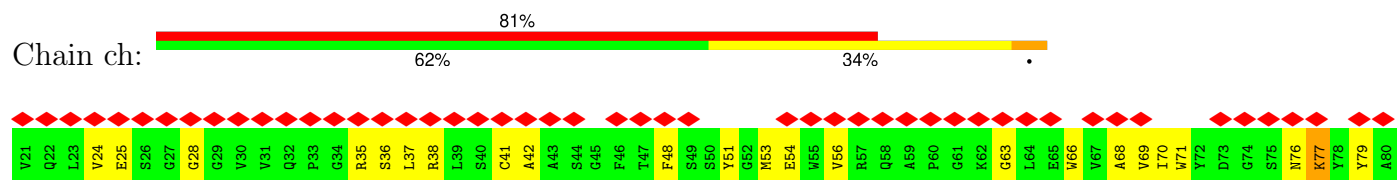
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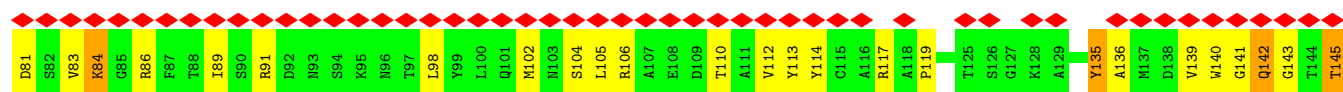


- Molecule 2: IgA-Fab3-4 heavy chain

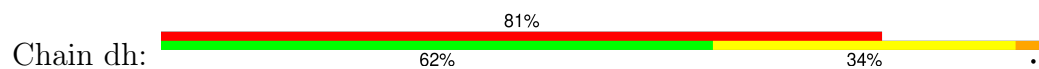


- Molecule 2: IgA-Fab3-4 heavy chain

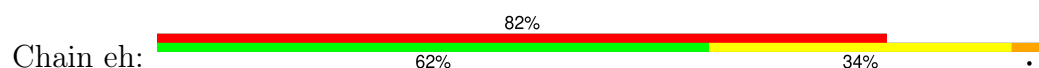




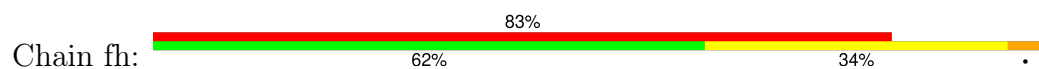
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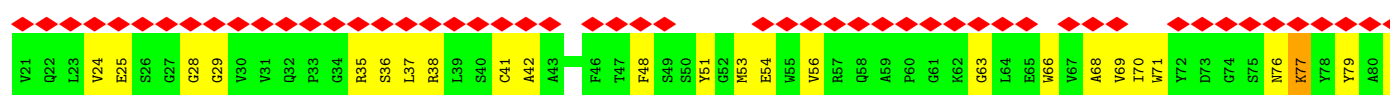
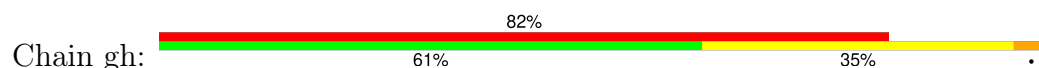
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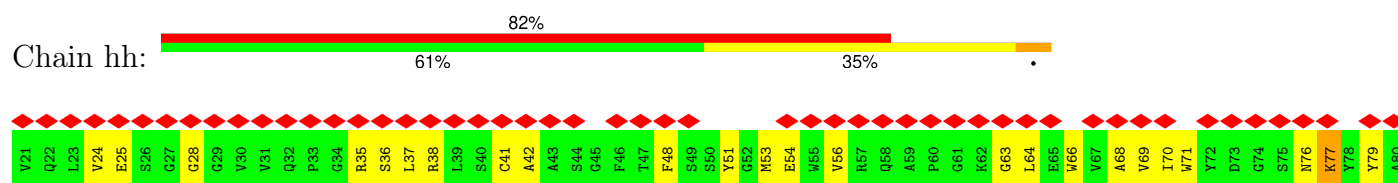
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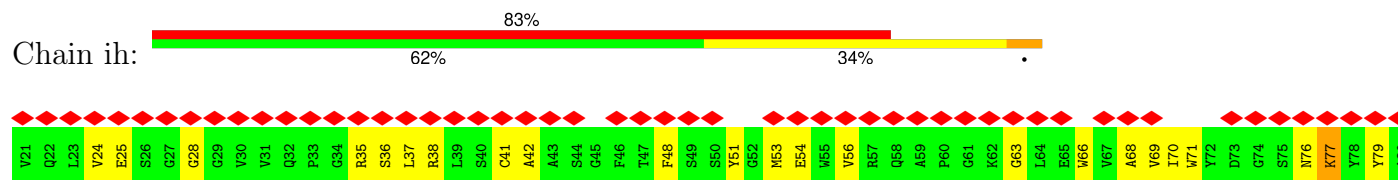
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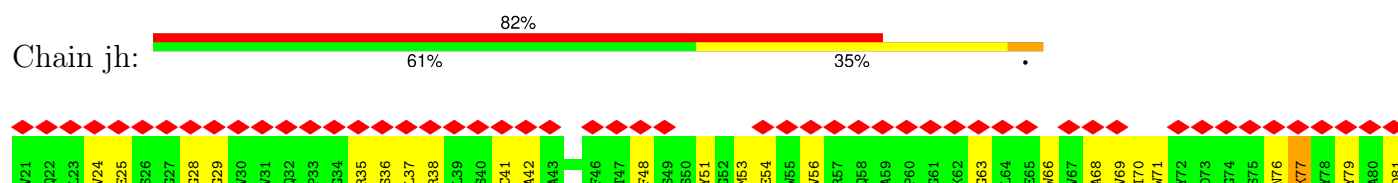
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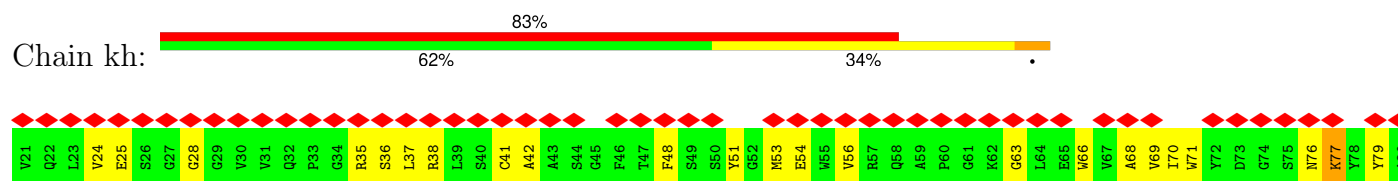
• Molecule 2: IgA-Fab3-4 heavy chain



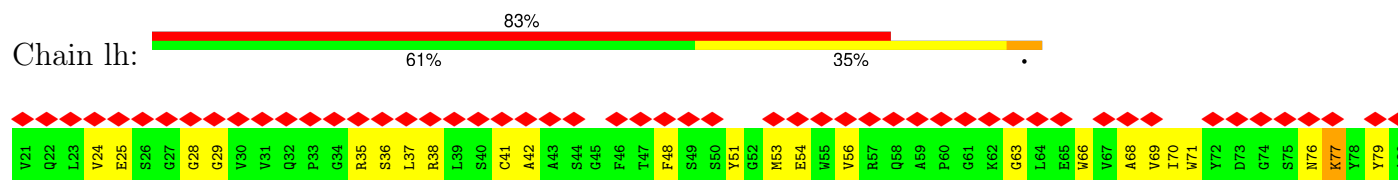
• Molecule 2: IgA-Fab3-4 heavy chain



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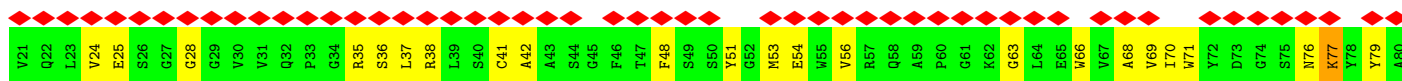
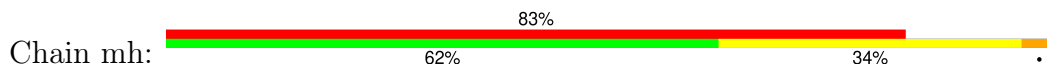


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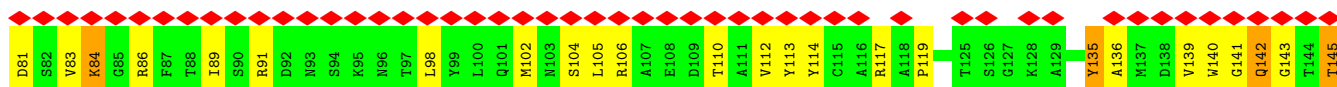
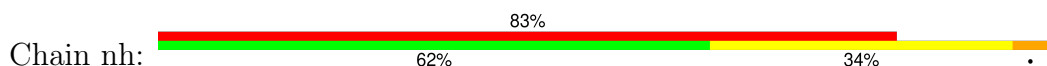




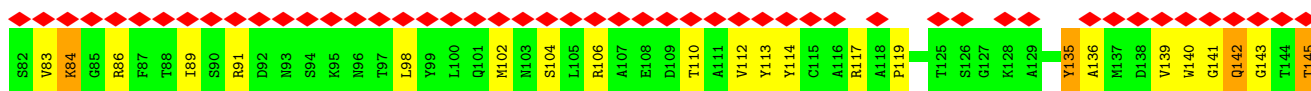
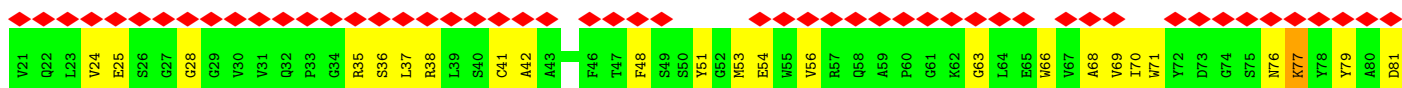
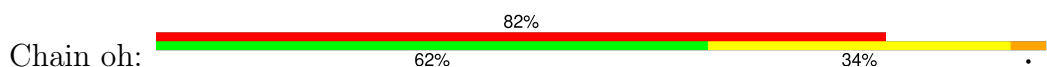
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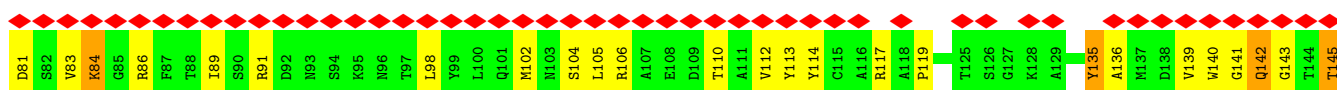
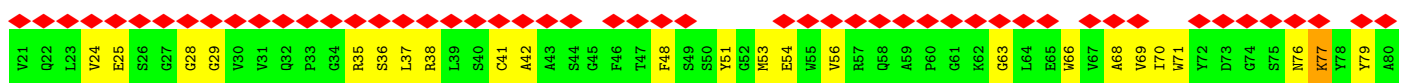
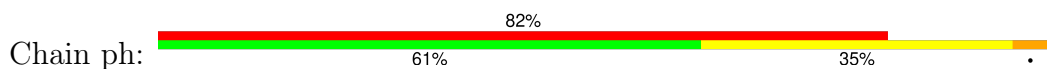
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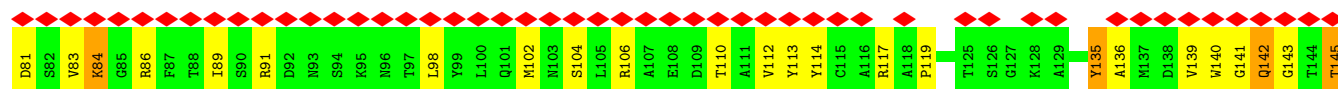
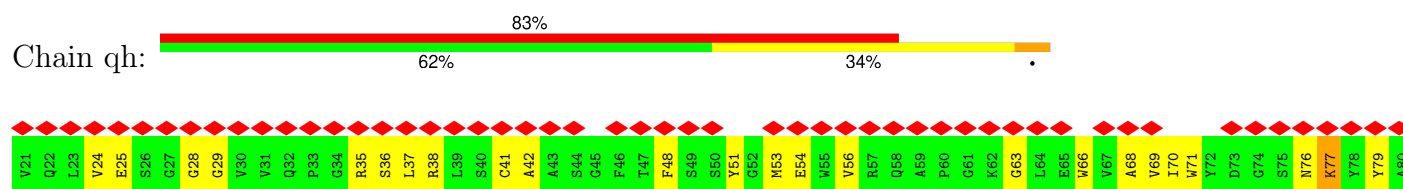
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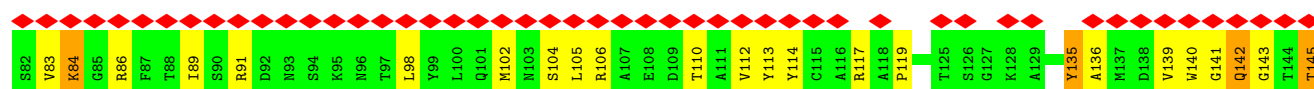
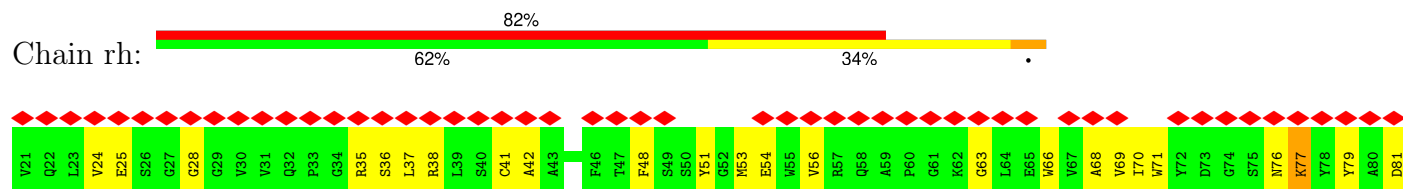
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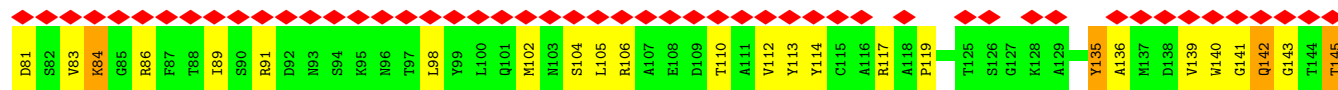
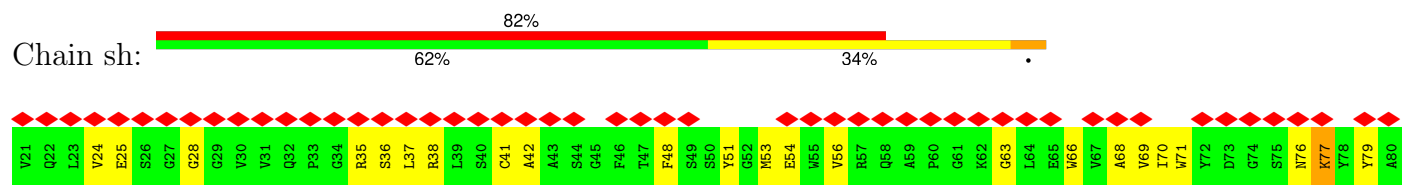
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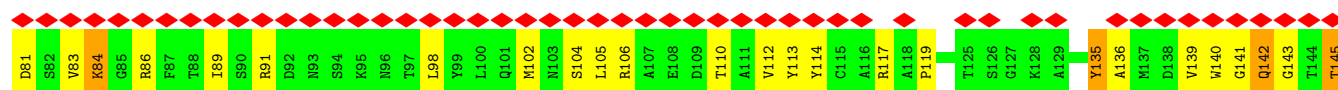
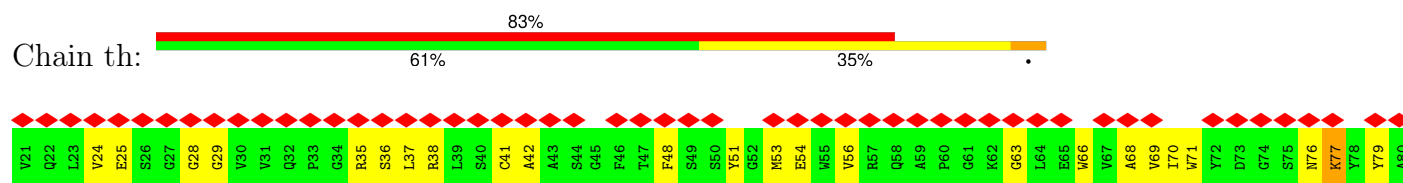
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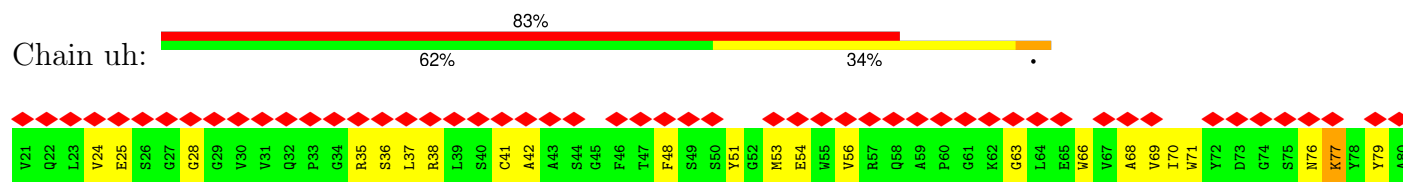
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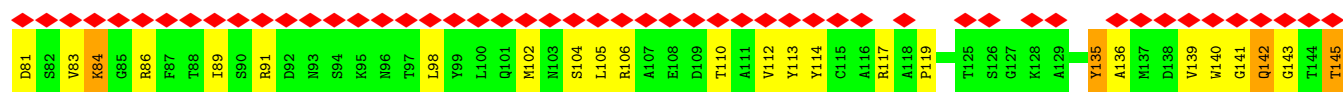


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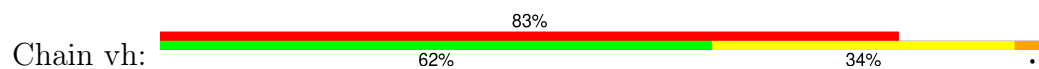


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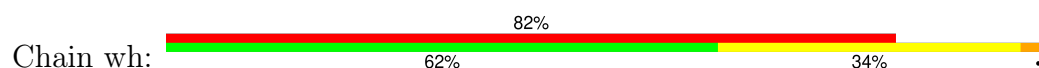




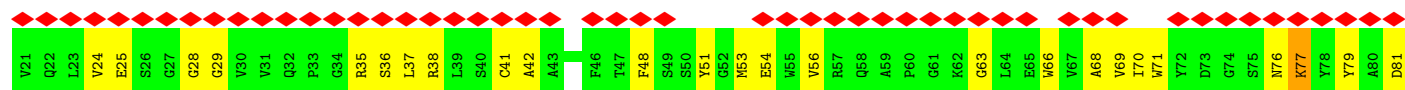
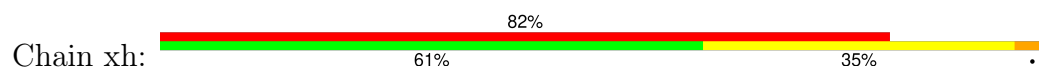
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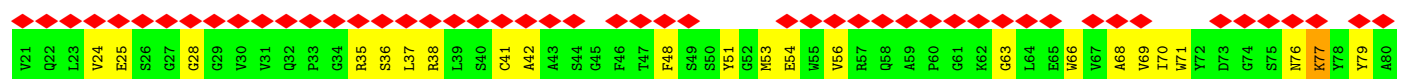
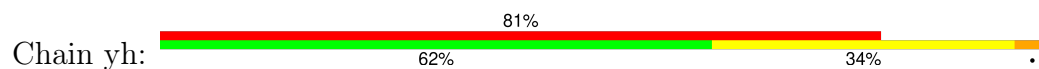
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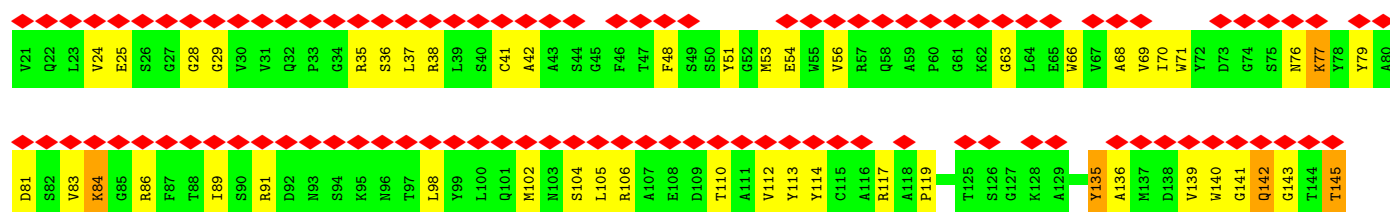
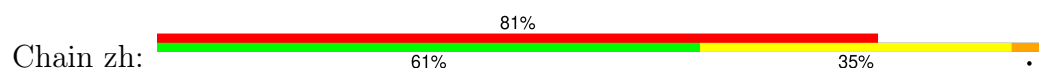


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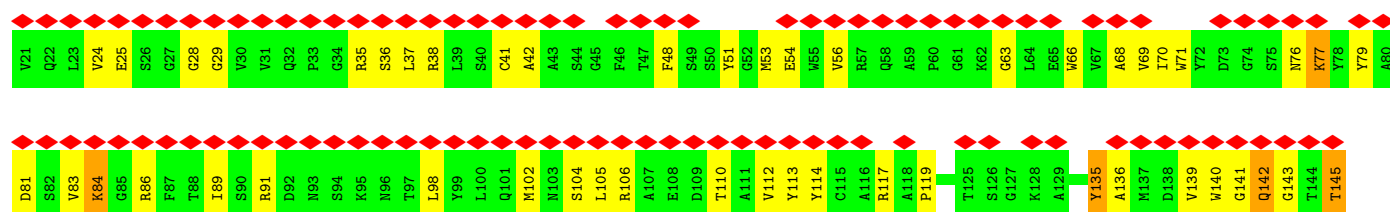
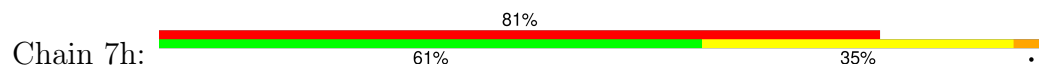


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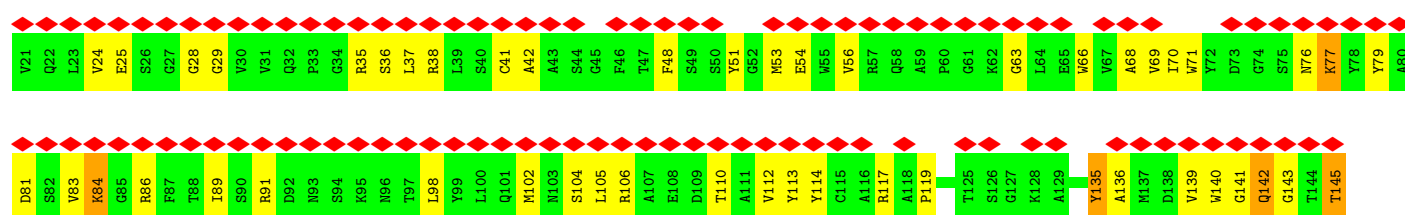
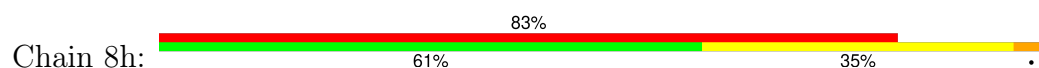




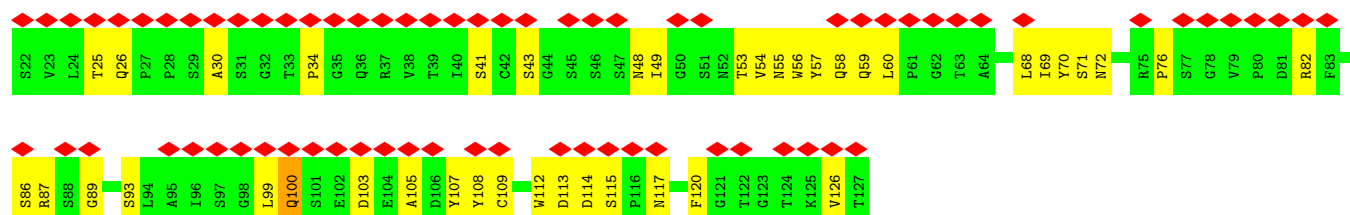
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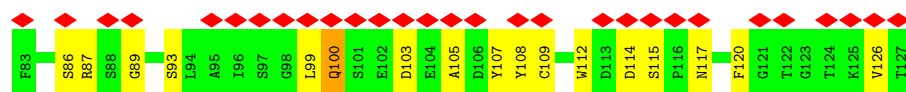


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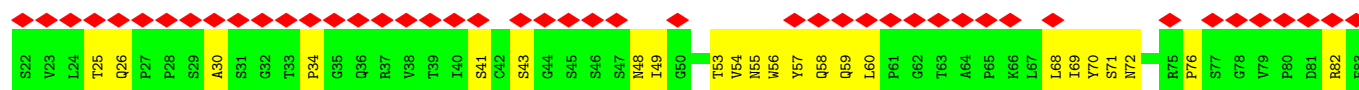
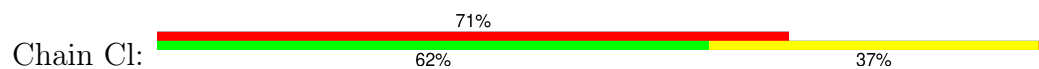


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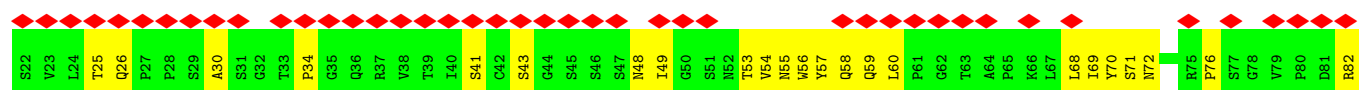




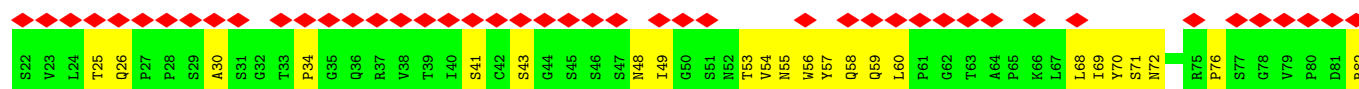
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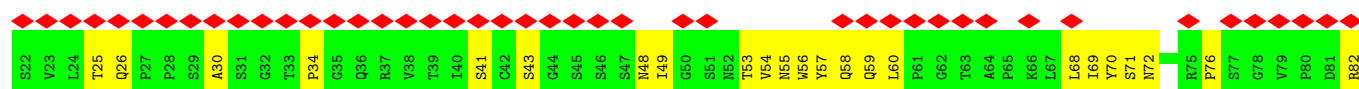
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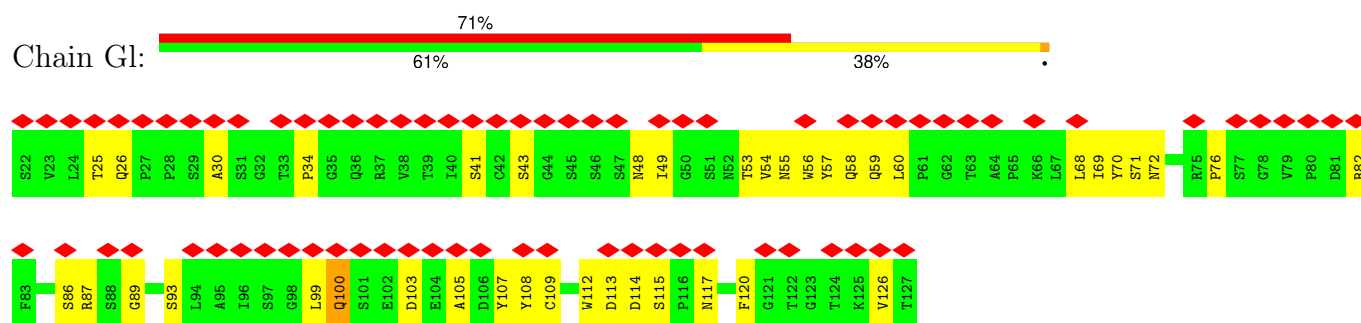
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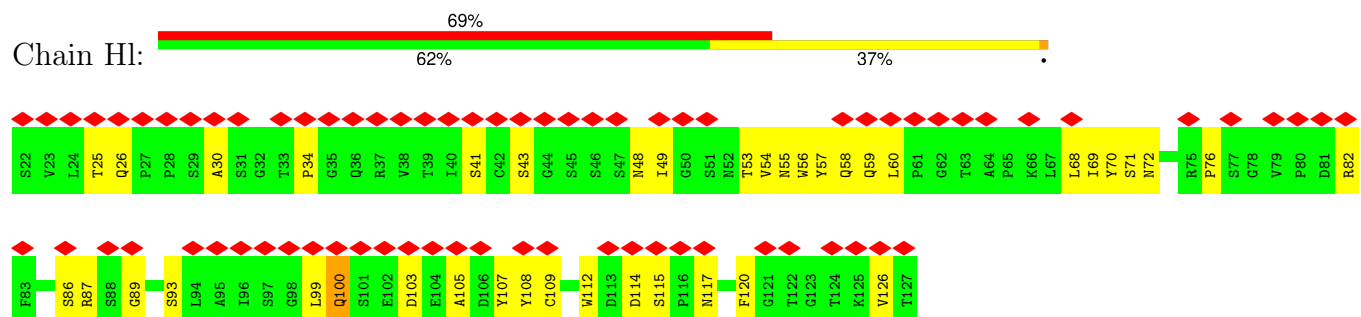
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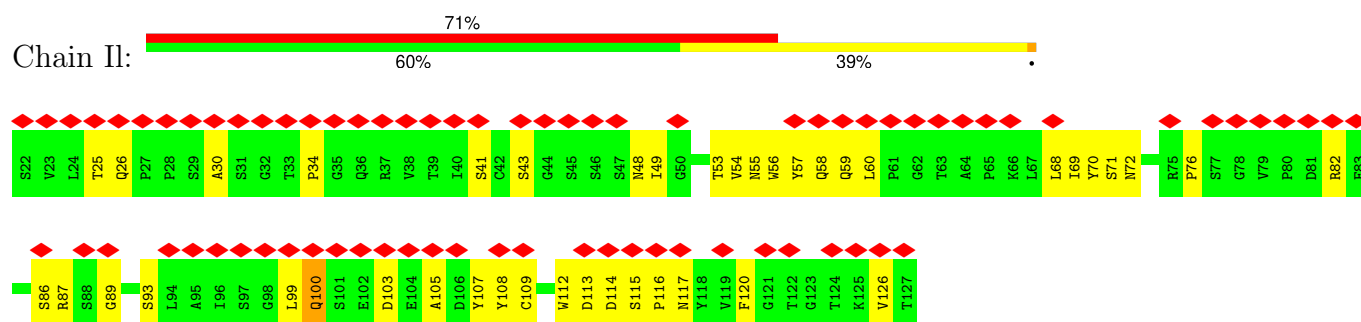
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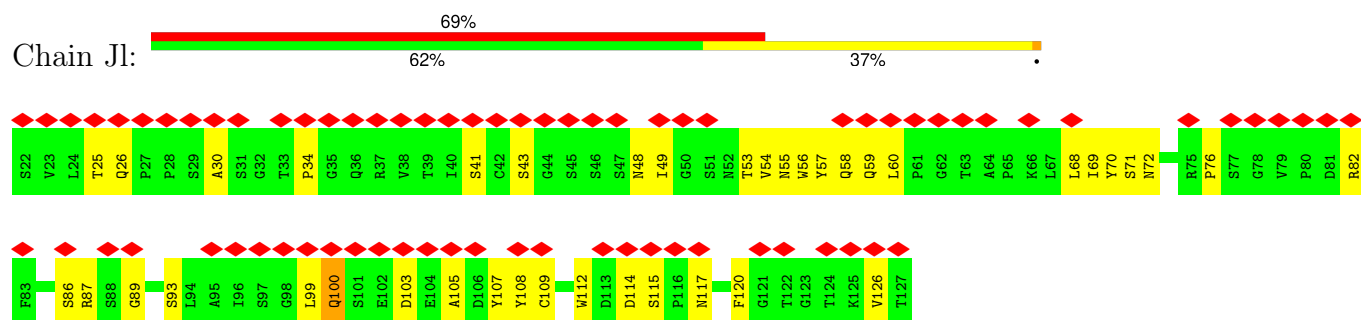
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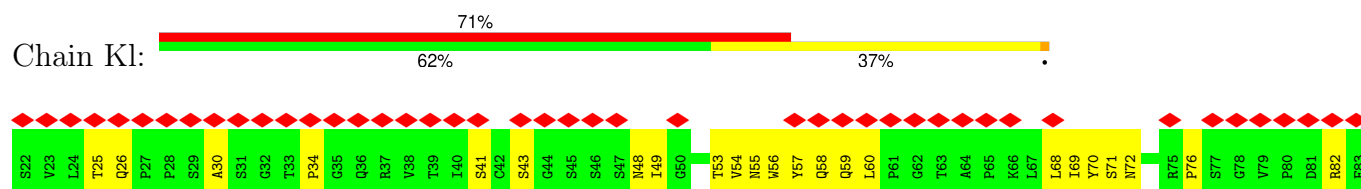
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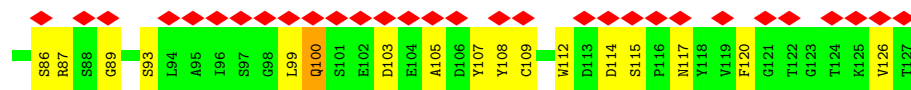


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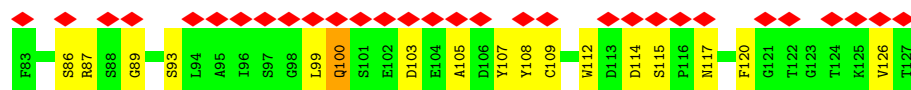
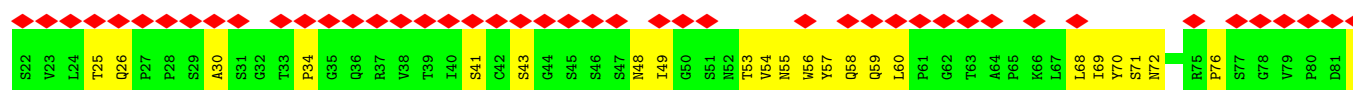
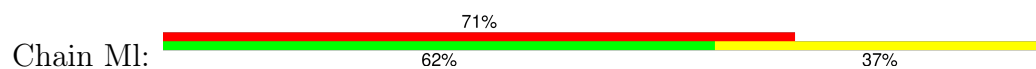




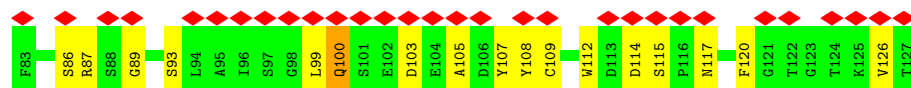
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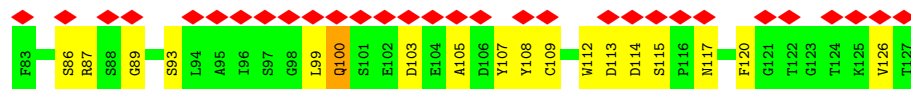
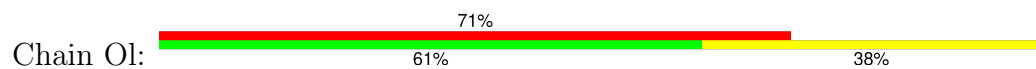
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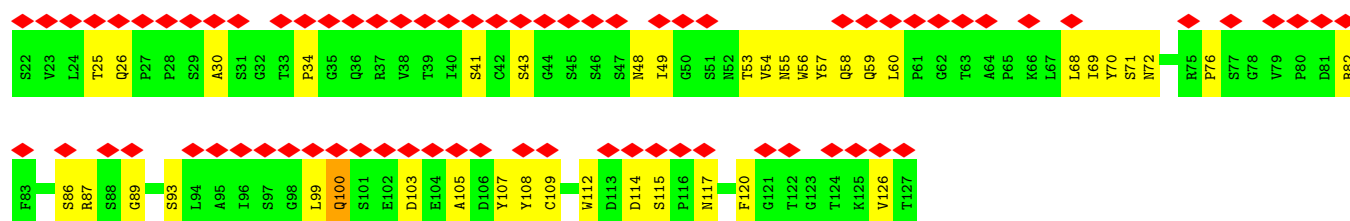
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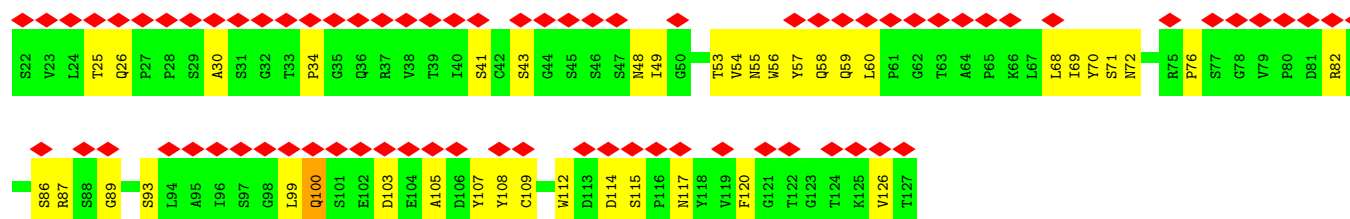
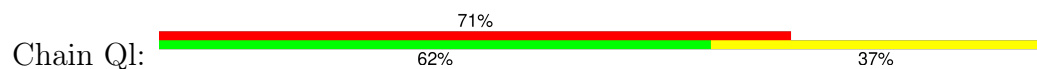
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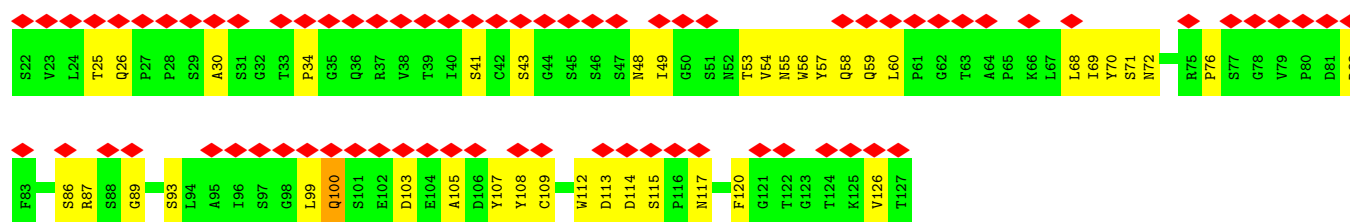
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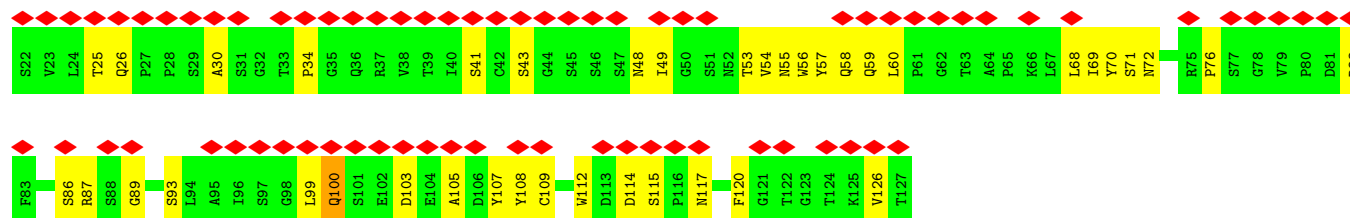
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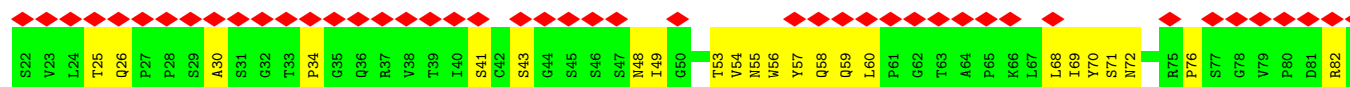
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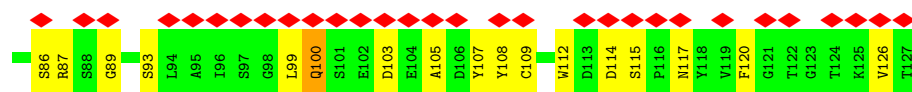


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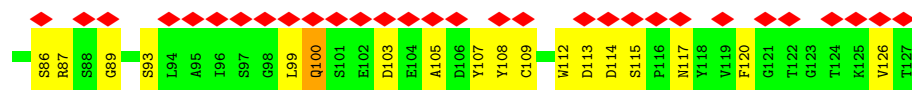
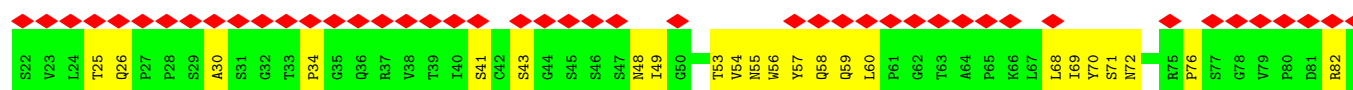




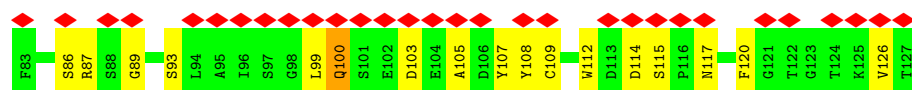
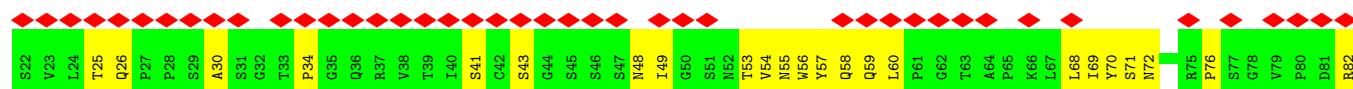
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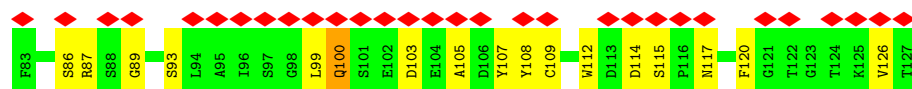
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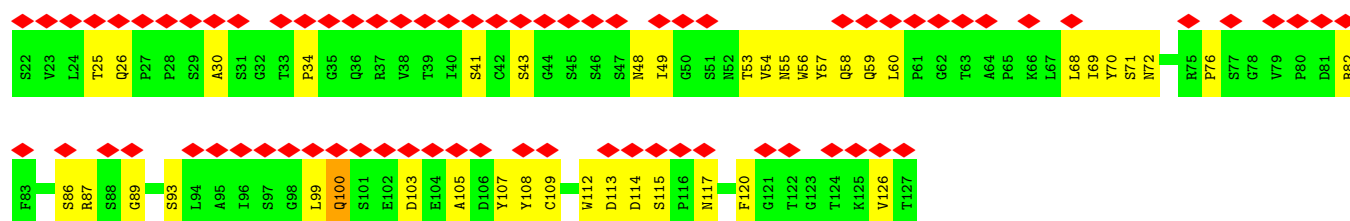
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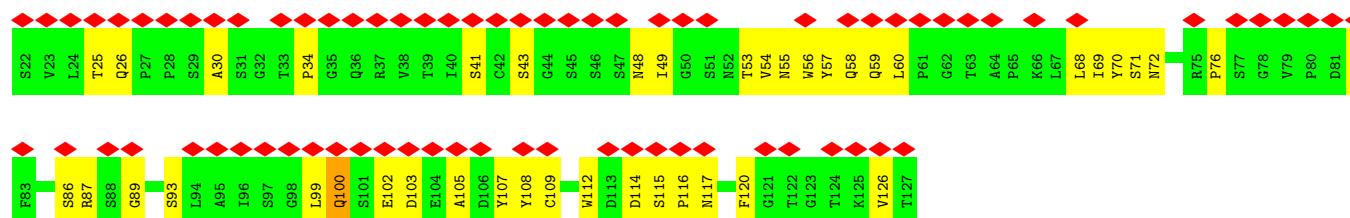
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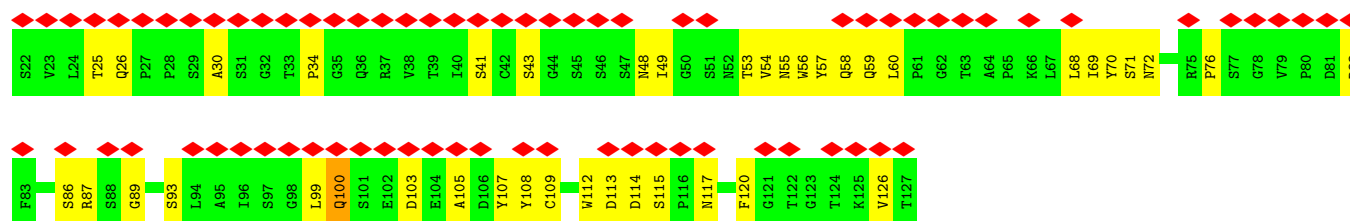
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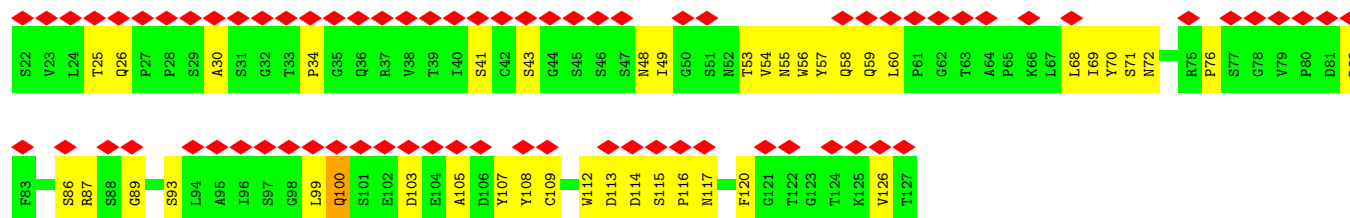
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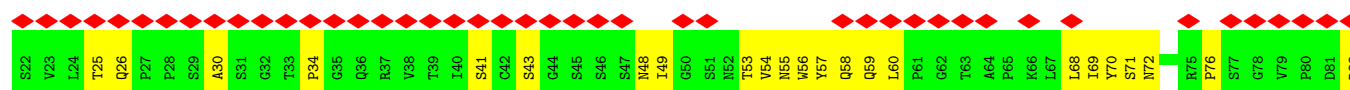
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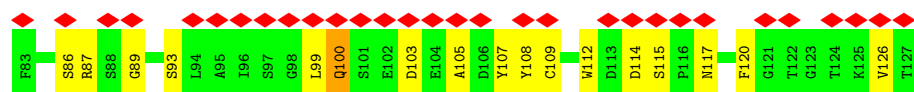


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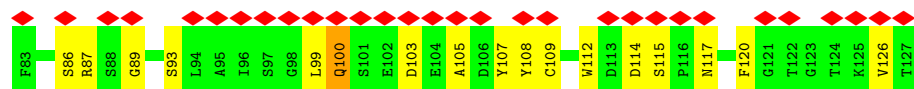
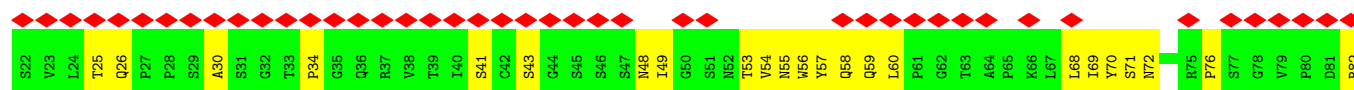


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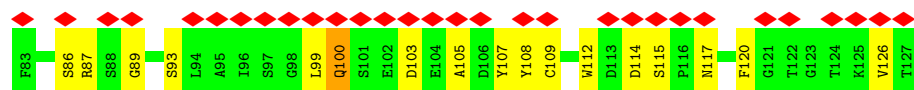
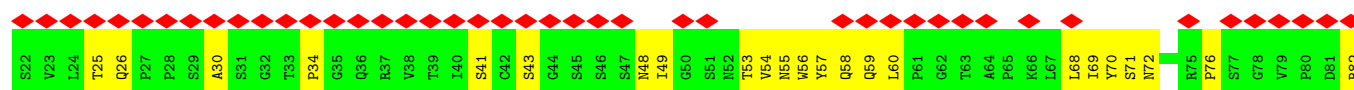




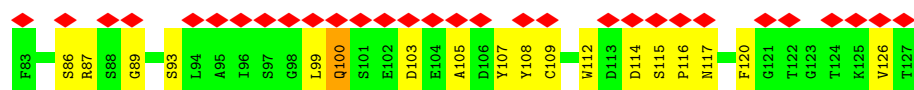
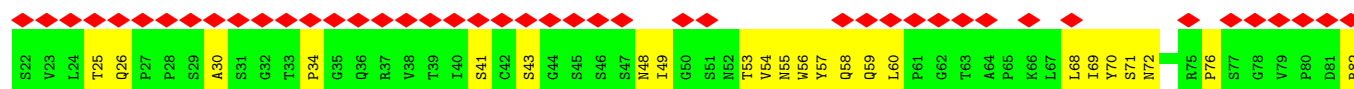
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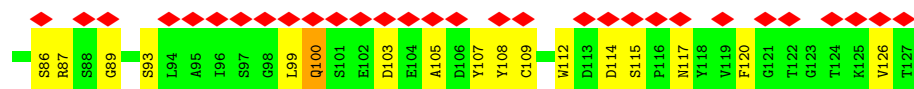
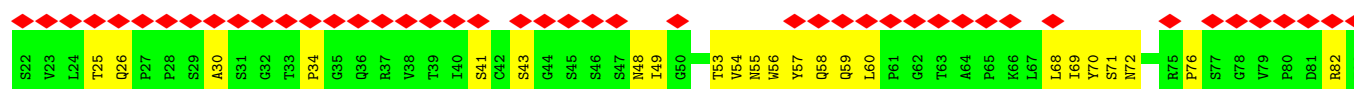
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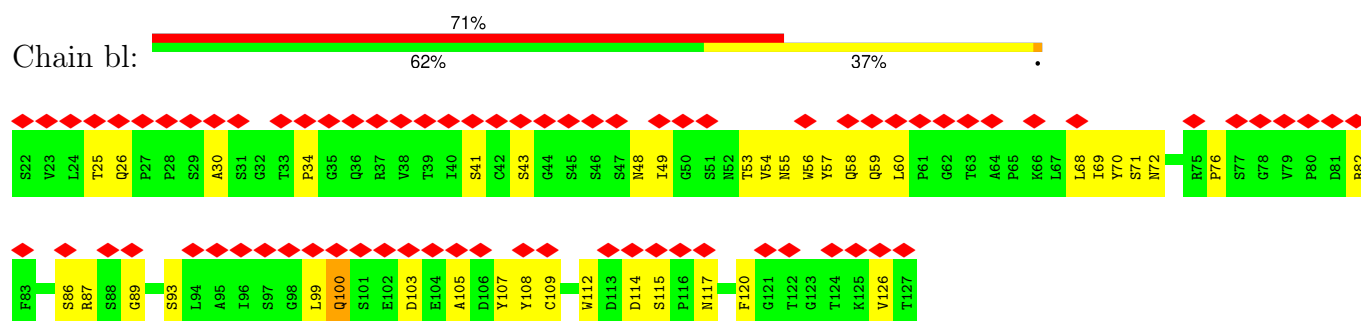
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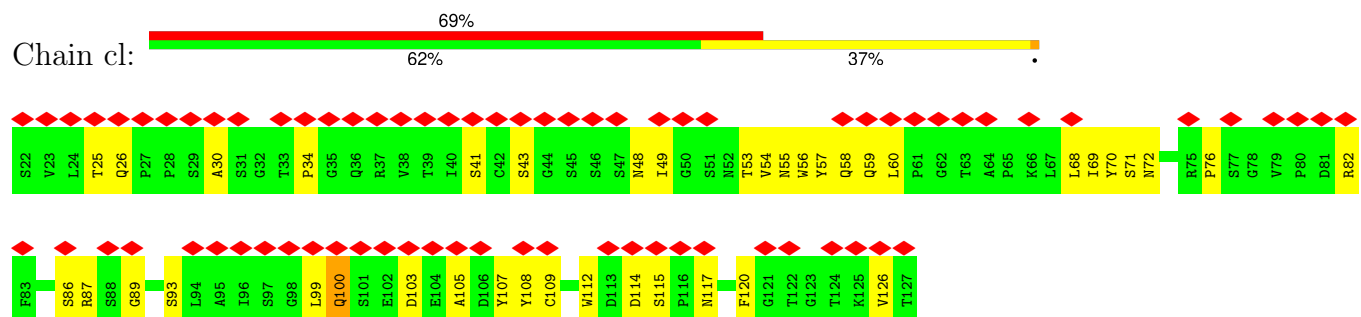
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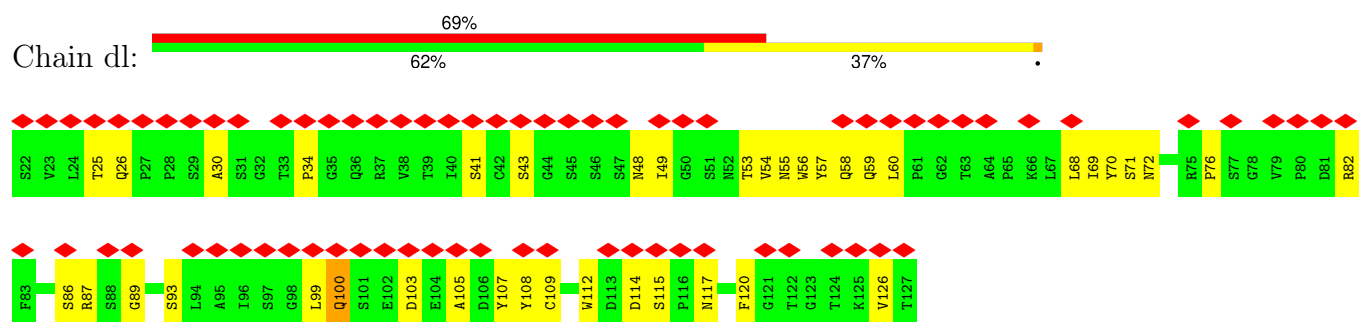
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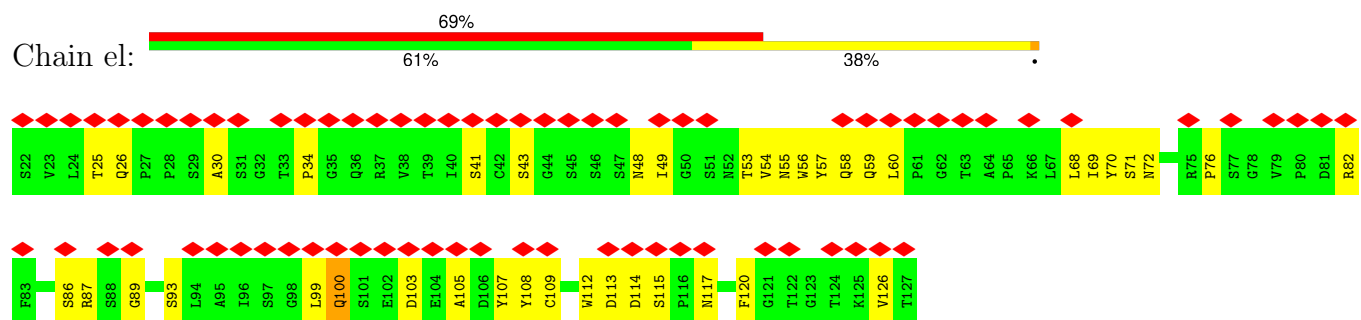
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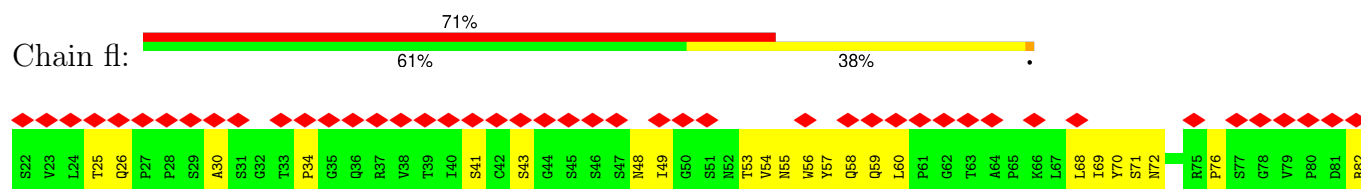
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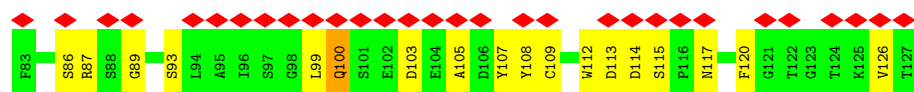


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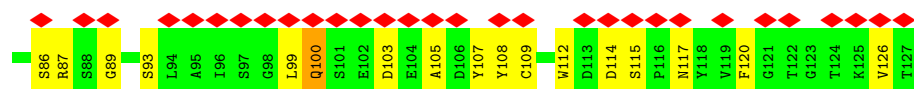
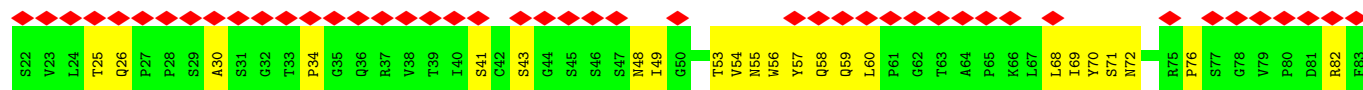


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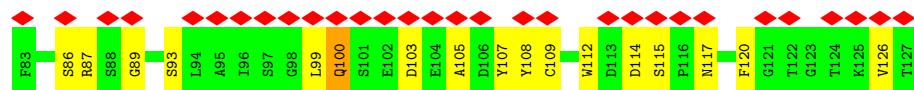
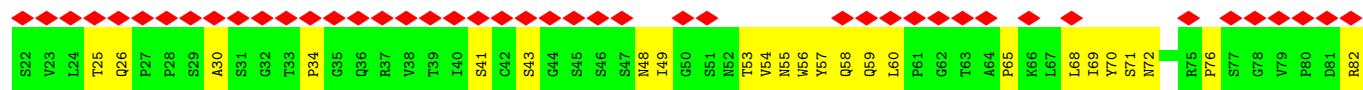




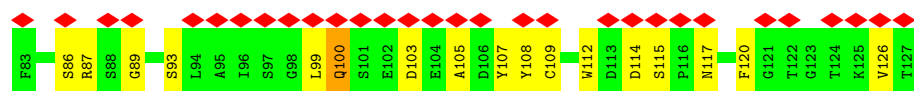
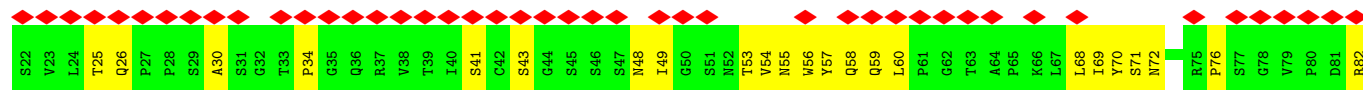
• Molecule 3: IgA-Fab3-4 light chain



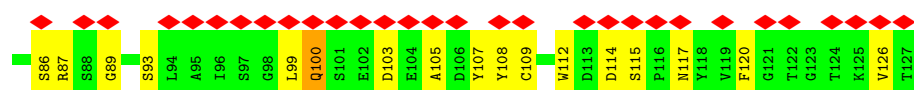
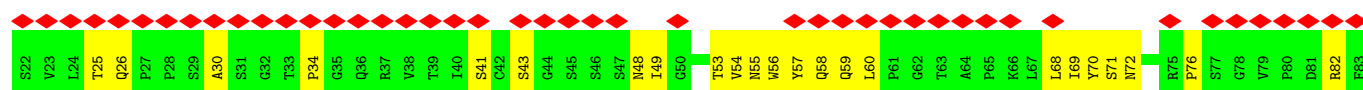
• Molecule 3: IgA-Fab3-4 light chain



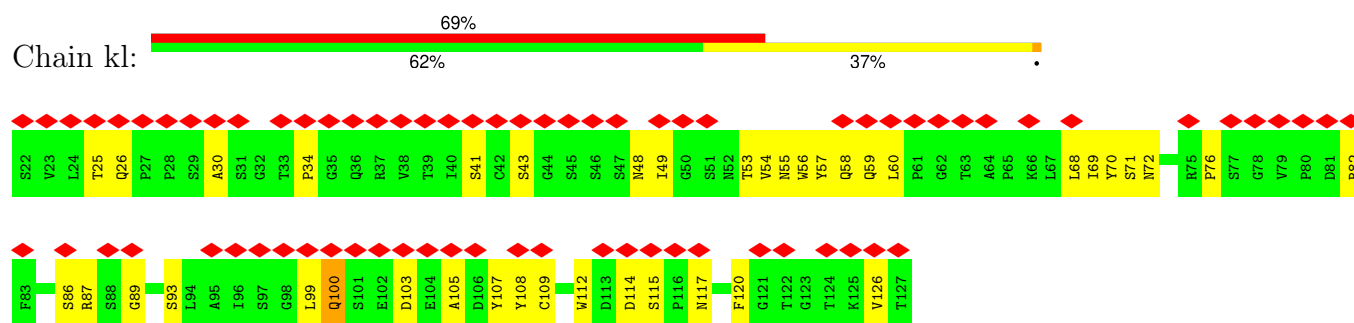
• Molecule 3: IgA-Fab3-4 light chain



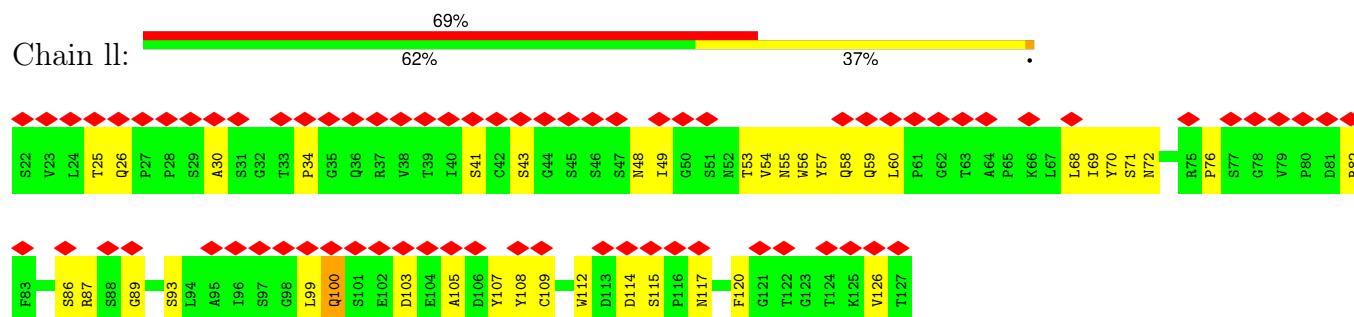
• Molecule 3: IgA-Fab3-4 light chain



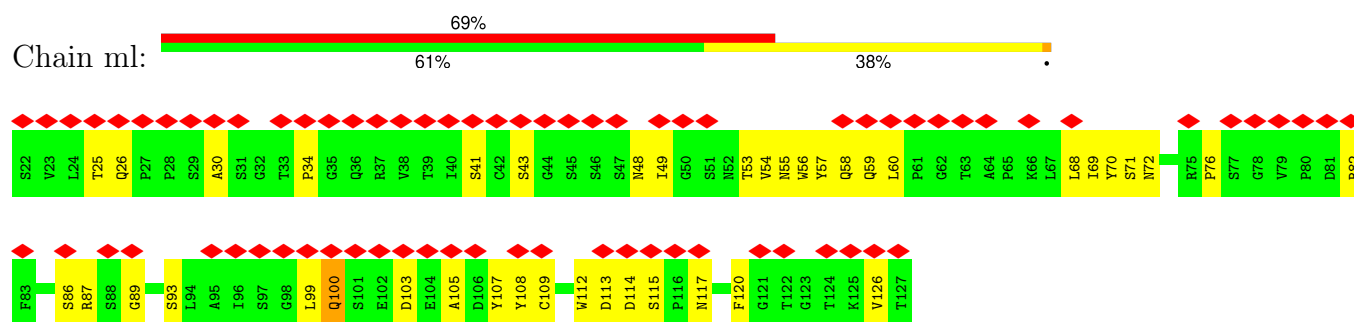
• Molecule 3: IgA-Fab3-4 light chain



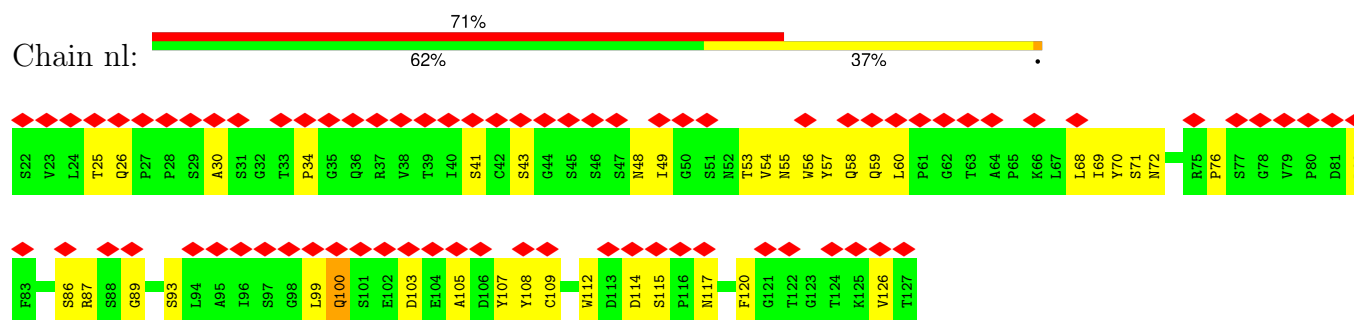
- Molecule 3: IgA-Fab3-4 light chain



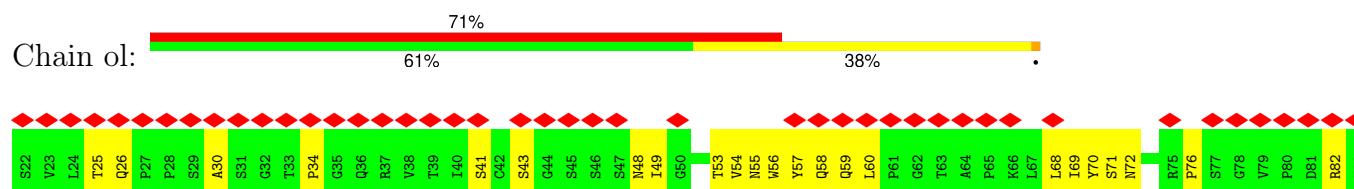
- Molecule 3: IgA-Fab3-4 light chain



- Molecule 3: IgA-Fab3-4 light chain

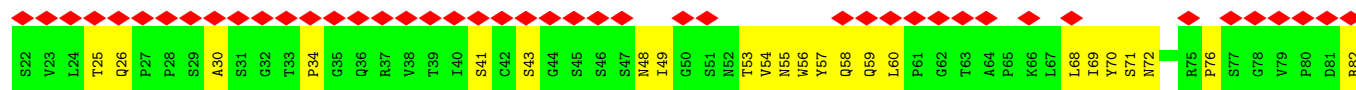


- Molecule 3: IgA-Fab3-4 light chain

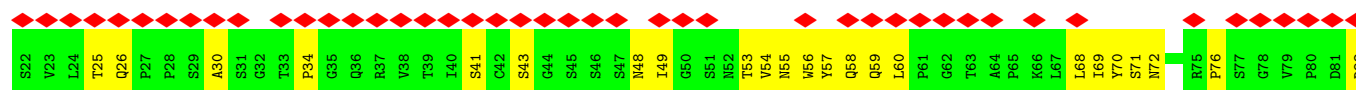




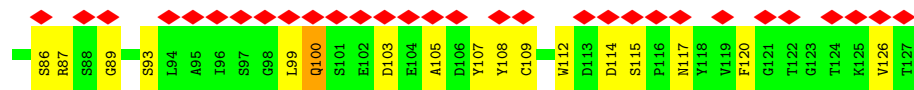
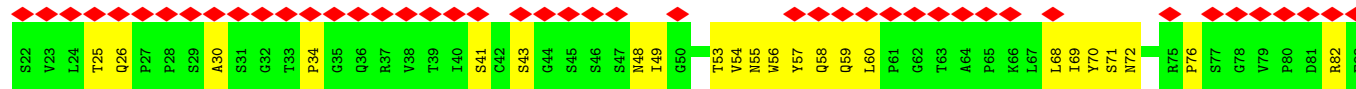
• Molecule 3: IgA-Fab3-4 light chain



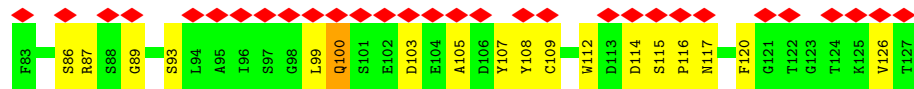
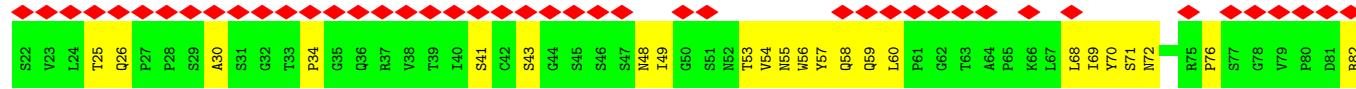
• Molecule 3: IgA-Fab3-4 light chain



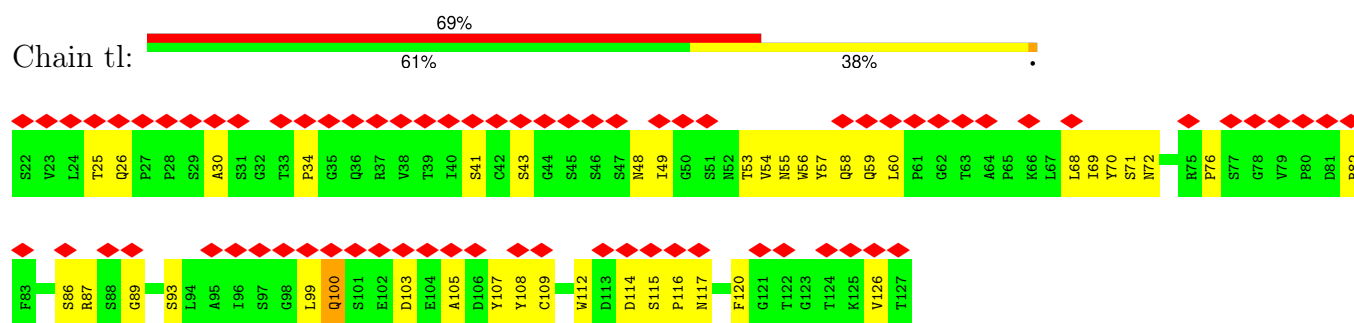
• Molecule 3: IgA-Fab3-4 light chain



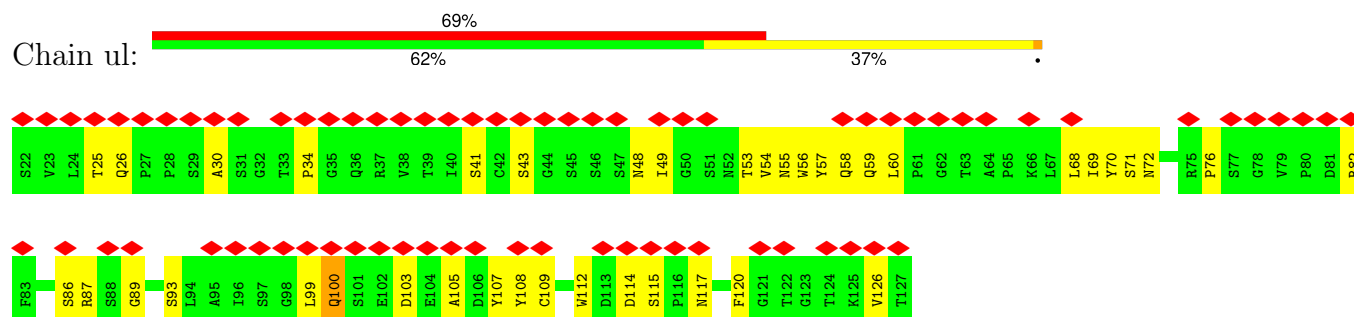
• Molecule 3: IgA-Fab3-4 light chain



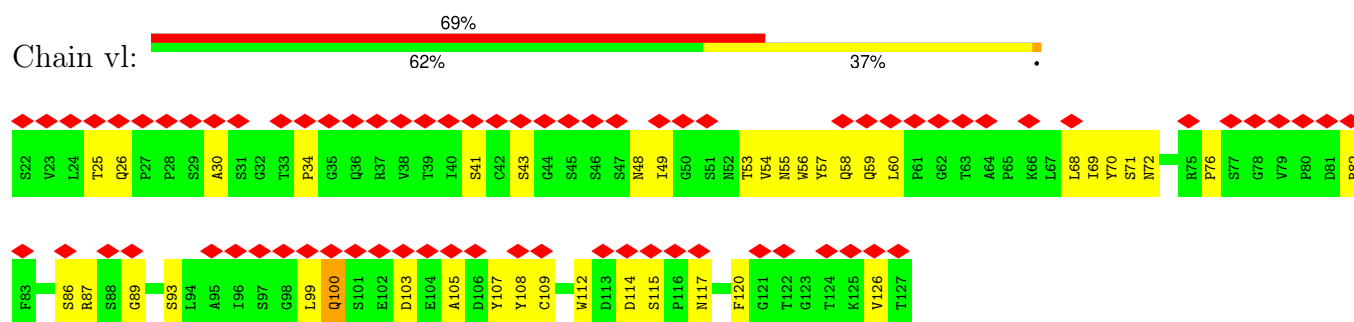
• Molecule 3: IgA-Fab3-4 light chain



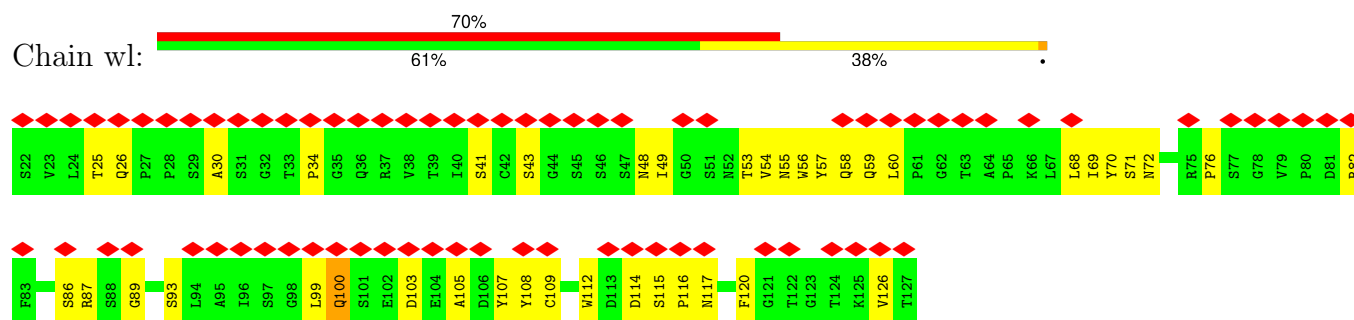
• Molecule 3: IgA-Fab3-4 light chain



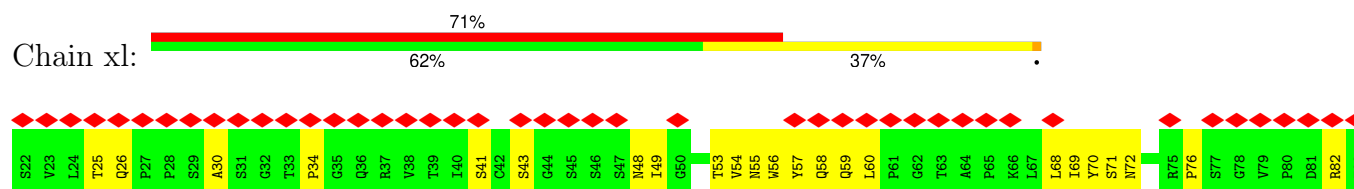
• Molecule 3: IgA-Fab3-4 light chain

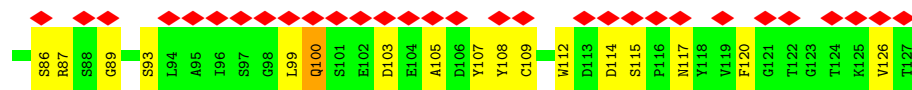


• Molecule 3: IgA-Fab3-4 light chain



• Molecule 3: IgA-Fab3-4 light chain

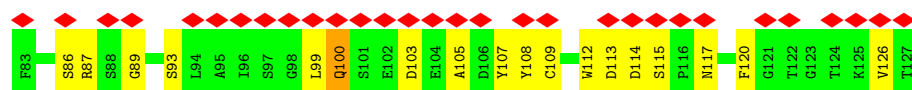




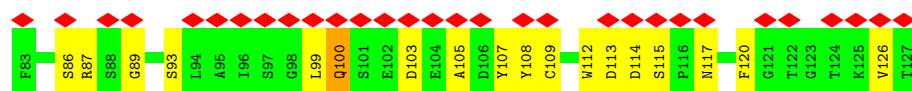
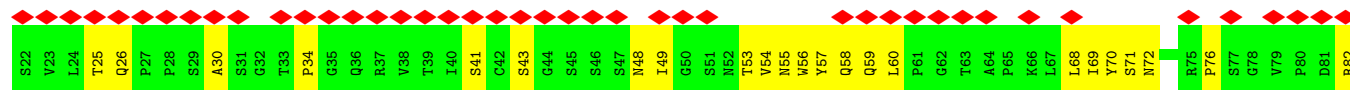
• Molecule 3: IgA-Fab3-4 light chain



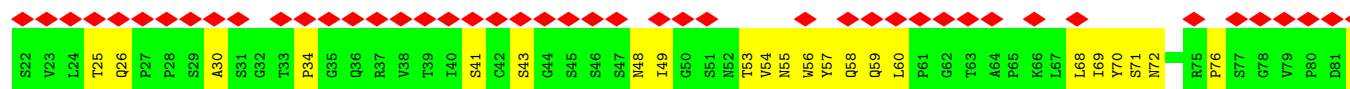
• Molecule 3: IgA-Fab3-4 light chain



• Molecule 3: IgA-Fab3-4 light chain



• Molecule 3: IgA-Fab3-4 light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10090	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32.44	Depositor
Minimum defocus (nm)	320	Depositor
Maximum defocus (nm)	2450	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	18.592	Depositor
Minimum map value	-12.340	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	439.8, 439.8, 439.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.733, 0.733, 0.733	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	2	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	3	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	4	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	5	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	6	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	7	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	8	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	A	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	B	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	C	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	D	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	E	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	F	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	G	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	H	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	I	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	J	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	K	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	L	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	M	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	N	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	O	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	P	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	Q	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	R	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	S	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	T	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	U	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	V	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	W	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	X	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	Y	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	Z	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	b	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	c	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	d	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	e	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	f	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	g	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	h	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	i	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	j	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	k	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	l	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	m	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	n	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	o	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	p	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	q	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	r	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	s	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	t	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	u	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	v	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	w	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	x	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	y	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
1	z	0.73	1/4258 (0.0%)	0.80	4/5804 (0.1%)
2	1h	0.42	0/1018	0.70	0/1383
2	2h	0.42	0/1018	0.70	0/1383
2	3h	0.42	0/1018	0.70	0/1383
2	4h	0.42	0/1018	0.71	0/1383
2	5h	0.42	0/1018	0.70	0/1383
2	6h	0.42	0/1018	0.70	0/1383
2	7h	0.42	0/1018	0.70	0/1383
2	8h	0.42	0/1018	0.70	0/1383
2	Ah	0.42	0/1018	0.70	0/1383
2	Bh	0.42	0/1018	0.70	0/1383
2	Ch	0.42	0/1018	0.70	0/1383
2	Dh	0.42	0/1018	0.70	0/1383
2	Eh	0.42	0/1018	0.70	0/1383
2	Fh	0.42	0/1018	0.70	0/1383
2	Gh	0.42	0/1018	0.70	0/1383
2	Hh	0.42	0/1018	0.70	0/1383
2	Ih	0.42	0/1018	0.70	0/1383

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Jh	0.42	0/1018	0.70	0/1383
2	Kh	0.42	0/1018	0.70	0/1383
2	Lh	0.42	0/1018	0.70	0/1383
2	Mh	0.42	0/1018	0.70	0/1383
2	Nh	0.42	0/1018	0.70	0/1383
2	Oh	0.42	0/1018	0.70	0/1383
2	Ph	0.42	0/1018	0.70	0/1383
2	Qh	0.42	0/1018	0.70	0/1383
2	Rh	0.42	0/1018	0.70	0/1383
2	Sh	0.42	0/1018	0.70	0/1383
2	Th	0.42	0/1018	0.70	0/1383
2	Uh	0.42	0/1018	0.70	0/1383
2	Vh	0.42	0/1018	0.70	0/1383
2	Wh	0.42	0/1018	0.70	0/1383
2	Xh	0.42	0/1018	0.70	0/1383
2	Yh	0.42	0/1018	0.70	0/1383
2	Zh	0.42	0/1018	0.70	0/1383
2	ah	0.42	0/1018	0.70	0/1383
2	bh	0.42	0/1018	0.70	0/1383
2	ch	0.42	0/1018	0.70	0/1383
2	dh	0.42	0/1018	0.70	0/1383
2	eh	0.42	0/1018	0.70	0/1383
2	fh	0.42	0/1018	0.70	0/1383
2	gh	0.42	0/1018	0.70	0/1383
2	hh	0.42	0/1018	0.70	0/1383
2	ih	0.42	0/1018	0.70	0/1383
2	jh	0.42	0/1018	0.70	0/1383
2	kh	0.42	0/1018	0.70	0/1383
2	lh	0.42	0/1018	0.70	0/1383
2	mh	0.42	0/1018	0.70	0/1383
2	nh	0.42	0/1018	0.70	0/1383
2	oh	0.42	0/1018	0.70	0/1383
2	ph	0.42	0/1018	0.70	0/1383
2	qh	0.42	0/1018	0.70	0/1383
2	rh	0.42	0/1018	0.70	0/1383
2	sh	0.42	0/1018	0.70	0/1383
2	th	0.42	0/1018	0.70	0/1383
2	uh	0.42	0/1018	0.70	0/1383
2	vh	0.42	0/1018	0.70	0/1383
2	wh	0.42	0/1018	0.71	0/1383
2	xh	0.42	0/1018	0.70	0/1383
2	yh	0.42	0/1018	0.70	0/1383
2	zh	0.42	0/1018	0.70	0/1383

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	1l	0.33	0/796	0.64	0/1088
3	2l	0.33	0/796	0.64	0/1088
3	3l	0.33	0/796	0.64	0/1088
3	4l	0.33	0/796	0.64	0/1088
3	5l	0.33	0/796	0.64	0/1088
3	6l	0.33	0/796	0.64	0/1088
3	7l	0.33	0/796	0.64	0/1088
3	8l	0.33	0/796	0.64	0/1088
3	Al	0.33	0/796	0.64	0/1088
3	Bl	0.33	0/796	0.64	0/1088
3	Cl	0.33	0/796	0.64	0/1088
3	Dl	0.33	0/796	0.64	0/1088
3	El	0.33	0/796	0.64	0/1088
3	Fl	0.33	0/796	0.63	0/1088
3	Gl	0.33	0/796	0.64	0/1088
3	Hl	0.33	0/796	0.64	0/1088
3	Il	0.33	0/796	0.64	0/1088
3	Jl	0.33	0/796	0.64	0/1088
3	Kl	0.33	0/796	0.64	0/1088
3	Ll	0.33	0/796	0.64	0/1088
3	Ml	0.33	0/796	0.64	0/1088
3	Nl	0.33	0/796	0.64	0/1088
3	Ol	0.33	0/796	0.64	0/1088
3	Pl	0.33	0/796	0.64	0/1088
3	Ql	0.33	0/796	0.64	0/1088
3	Rl	0.33	0/796	0.64	0/1088
3	Sl	0.33	0/796	0.64	0/1088
3	Tl	0.33	0/796	0.64	0/1088
3	Ul	0.33	0/796	0.64	0/1088
3	Vl	0.33	0/796	0.64	0/1088
3	Wl	0.33	0/796	0.64	0/1088
3	Xl	0.33	0/796	0.64	0/1088
3	Yl	0.33	0/796	0.64	0/1088
3	Zl	0.33	0/796	0.64	0/1088
3	al	0.33	0/796	0.64	0/1088
3	bl	0.33	0/796	0.64	0/1088
3	cl	0.33	0/796	0.64	0/1088
3	dl	0.33	0/796	0.64	0/1088
3	el	0.33	0/796	0.64	0/1088
3	fl	0.33	0/796	0.64	0/1088
3	gl	0.33	0/796	0.64	0/1088
3	hl	0.33	0/796	0.64	0/1088
3	il	0.33	0/796	0.64	0/1088

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	jl	0.33	0/796	0.64	0/1088
3	kl	0.33	0/796	0.64	0/1088
3	ll	0.33	0/796	0.64	0/1088
3	ml	0.33	0/796	0.64	0/1088
3	nl	0.33	0/796	0.64	0/1088
3	ol	0.33	0/796	0.64	0/1088
3	pl	0.33	0/796	0.64	0/1088
3	ql	0.33	0/796	0.64	0/1088
3	rl	0.33	0/796	0.64	0/1088
3	sl	0.33	0/796	0.64	0/1088
3	tl	0.33	0/796	0.64	0/1088
3	ul	0.33	0/796	0.64	0/1088
3	vl	0.33	0/796	0.64	0/1088
3	wl	0.33	0/796	0.64	0/1088
3	xl	0.33	0/796	0.64	0/1088
3	yl	0.33	0/796	0.64	0/1088
3	zl	0.33	0/796	0.64	0/1088
All	All	0.65	60/364320 (0.0%)	0.76	240/496500 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	2	0	1
1	3	0	1
1	4	0	1
1	5	0	1
1	6	0	1
1	7	0	1
1	8	0	1
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
1	Y	0	1
1	Z	0	1
1	a	0	1
1	b	0	1
1	c	0	1
1	d	0	1
1	e	0	1
1	f	0	1
1	g	0	1
1	h	0	1
1	i	0	1
1	j	0	1
1	k	0	1
1	l	0	1
1	m	0	1
1	n	0	1
1	o	0	1
1	p	0	1
1	q	0	1
1	r	0	1
1	s	0	1
1	t	0	1
1	u	0	1
1	v	0	1
1	w	0	1
1	x	0	1
1	y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	z	0	1
All	All	0	60

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	706	LYS	C-N	-7.07	1.25	1.33
1	I	706	LYS	C-N	-7.07	1.25	1.33
1	Q	706	LYS	C-N	-7.07	1.25	1.33
1	o	706	LYS	C-N	-7.07	1.25	1.33
1	r	706	LYS	C-N	-7.07	1.25	1.33

The worst 5 of 240 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	563	GLU	N-CA-C	6.03	117.93	111.36
1	Y	563	GLU	N-CA-C	6.03	117.93	111.36
1	c	563	GLU	N-CA-C	6.03	117.93	111.36
1	7	563	GLU	N-CA-C	6.03	117.93	111.36
1	B	563	GLU	N-CA-C	6.00	117.90	111.36

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	518	ASN	Peptide
1	B	518	ASN	Peptide
1	C	518	ASN	Peptide
1	D	518	ASN	Peptide
1	E	518	ASN	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4135	0	3892	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	4135	0	3892	47	0
1	3	4135	0	3892	46	0
1	4	4135	0	3892	47	0
1	5	4135	0	3892	47	0
1	6	4135	0	3892	48	0
1	7	4135	0	3892	47	0
1	8	4135	0	3892	50	0
1	A	4135	0	3892	49	0
1	B	4135	0	3892	48	0
1	C	4135	0	3892	47	0
1	D	4135	0	3892	47	0
1	E	4135	0	3892	49	0
1	F	4135	0	3892	48	0
1	G	4135	0	3892	48	0
1	H	4135	0	3892	46	0
1	I	4135	0	3892	48	0
1	J	4135	0	3892	47	0
1	K	4135	0	3892	46	0
1	L	4135	0	3892	48	0
1	M	4135	0	3892	49	0
1	N	4135	0	3892	47	0
1	O	4135	0	3892	48	0
1	P	4135	0	3892	46	0
1	Q	4135	0	3892	47	0
1	R	4135	0	3892	49	0
1	S	4135	0	3892	47	0
1	T	4135	0	3892	48	0
1	U	4135	0	3892	48	0
1	V	4135	0	3892	47	0
1	W	4135	0	3892	49	0
1	X	4135	0	3892	46	0
1	Y	4135	0	3892	47	0
1	Z	4135	0	3892	49	0
1	a	4135	0	3892	46	0
1	b	4135	0	3892	49	0
1	c	4135	0	3892	47	0
1	d	4135	0	3892	46	0
1	e	4135	0	3892	47	0
1	f	4135	0	3892	48	0
1	g	4135	0	3892	47	0
1	h	4135	0	3892	46	0
1	i	4135	0	3892	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	j	4135	0	3892	47	0
1	k	4135	0	3892	48	0
1	l	4135	0	3892	47	0
1	m	4135	0	3892	48	0
1	n	4135	0	3892	48	0
1	o	4135	0	3892	48	0
1	p	4135	0	3892	49	0
1	q	4135	0	3892	47	0
1	r	4135	0	3892	47	0
1	s	4135	0	3892	48	0
1	t	4135	0	3892	49	0
1	u	4135	0	3892	48	0
1	v	4135	0	3892	47	0
1	w	4135	0	3892	46	0
1	x	4135	0	3892	46	0
1	y	4135	0	3892	45	0
1	z	4135	0	3892	50	0
2	1h	989	0	930	72	0
2	2h	989	0	930	72	0
2	3h	989	0	930	71	0
2	4h	989	0	930	73	0
2	5h	989	0	930	71	0
2	6h	989	0	930	72	0
2	7h	989	0	930	72	0
2	8h	989	0	930	73	0
2	Ah	989	0	930	72	0
2	Bh	989	0	930	70	0
2	Ch	989	0	930	69	0
2	Dh	989	0	930	69	0
2	Eh	989	0	930	74	0
2	Fh	989	0	930	72	0
2	Gh	989	0	930	71	0
2	Hh	989	0	930	71	0
2	Ih	989	0	930	72	0
2	Jh	989	0	930	71	0
2	Kh	989	0	930	72	0
2	Lh	989	0	930	71	0
2	Mh	989	0	930	69	0
2	Nh	989	0	930	70	0
2	Oh	989	0	930	70	0
2	Ph	989	0	930	72	0
2	Qh	989	0	930	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Rh	989	0	930	72	0
2	Sh	989	0	930	73	0
2	Th	989	0	930	71	0
2	Uh	989	0	930	71	0
2	Vh	989	0	930	73	0
2	Wh	989	0	930	72	0
2	Xh	989	0	930	70	0
2	Yh	989	0	930	72	0
2	Zh	989	0	930	72	0
2	ah	989	0	930	69	0
2	bh	989	0	930	70	0
2	ch	989	0	930	70	0
2	dh	989	0	930	72	0
2	eh	989	0	930	69	0
2	fh	989	0	930	70	0
2	gh	989	0	930	71	0
2	hh	989	0	930	73	0
2	ih	989	0	930	70	0
2	jh	989	0	930	73	0
2	kh	989	0	930	72	0
2	lh	989	0	930	73	0
2	mh	989	0	930	71	0
2	nh	989	0	930	71	0
2	oh	989	0	930	71	0
2	ph	989	0	930	71	0
2	qh	989	0	930	73	0
2	rh	989	0	930	69	0
2	sh	989	0	930	72	0
2	th	989	0	930	73	0
2	uh	989	0	930	71	0
2	vh	989	0	930	71	0
2	wh	989	0	930	71	0
2	xh	989	0	930	73	0
2	yh	989	0	930	71	0
2	zh	989	0	930	73	0
3	1l	778	0	730	36	0
3	2l	778	0	730	38	0
3	3l	778	0	730	35	0
3	4l	778	0	730	36	0
3	5l	778	0	730	35	0
3	6l	778	0	730	37	0
3	7l	778	0	730	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	8l	778	0	730	37	0
3	Al	778	0	730	36	0
3	Bl	778	0	730	35	0
3	Cl	778	0	730	35	0
3	Dl	778	0	730	35	0
3	El	778	0	730	35	0
3	Fl	778	0	730	37	0
3	Gl	778	0	730	37	0
3	Hl	778	0	730	36	0
3	Il	778	0	730	38	0
3	Jl	778	0	730	35	0
3	Kl	778	0	730	35	0
3	Ll	778	0	730	36	0
3	Ml	778	0	730	35	0
3	Nl	778	0	730	36	0
3	Ol	778	0	730	36	0
3	Pl	778	0	730	35	0
3	Ql	778	0	730	36	0
3	Rl	778	0	730	36	0
3	Sl	778	0	730	35	0
3	Tl	778	0	730	35	0
3	Ul	778	0	730	37	0
3	Vl	778	0	730	37	0
3	Wl	778	0	730	36	0
3	Xl	778	0	730	35	0
3	Yl	778	0	730	36	0
3	Zl	778	0	730	38	0
3	al	778	0	730	35	0
3	bl	778	0	730	35	0
3	cl	778	0	730	36	0
3	dl	778	0	730	35	0
3	el	778	0	730	36	0
3	fl	778	0	730	36	0
3	gl	778	0	730	35	0
3	hl	778	0	730	37	0
3	il	778	0	730	35	0
3	jl	778	0	730	36	0
3	kl	778	0	730	35	0
3	ll	778	0	730	35	0
3	ml	778	0	730	37	0
3	nl	778	0	730	36	0
3	ol	778	0	730	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	pl	778	0	730	36	0
3	ql	778	0	730	35	0
3	rl	778	0	730	36	0
3	sl	778	0	730	37	0
3	tl	778	0	730	36	0
3	ul	778	0	730	35	0
3	vl	778	0	730	35	0
3	wl	778	0	730	37	0
3	xl	778	0	730	35	0
3	yl	778	0	730	36	0
3	zl	778	0	730	37	0
All	All	354120	0	333120	8578	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 8578 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6h:63:GLY:HA2	3:6l:108:TYR:OH	1.50	1.11
2:5h:63:GLY:HA2	3:5l:108:TYR:OH	1.50	1.10
2:2h:63:GLY:HA2	3:2l:108:TYR:OH	1.50	1.10
2:3h:63:GLY:HA2	3:3l:108:TYR:OH	1.50	1.10
2:Fh:63:GLY:HA2	3:Fl:108:TYR:OH	1.52	1.09

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	1	514/533 (96%)	500 (97%)	14 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	3	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	4	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	5	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	6	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	7	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	8	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	A	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	B	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	C	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	D	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	E	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	F	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	G	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	H	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	I	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	J	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	K	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	L	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	M	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	N	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	O	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	P	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	Q	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	R	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	S	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	T	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	U	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	V	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	W	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	X	514/533 (96%)	500 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	Z	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	a	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	b	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	c	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	d	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	e	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	f	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	g	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	h	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	i	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	j	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	k	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	l	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	m	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	n	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	o	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	p	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	q	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	r	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	s	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	t	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	u	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	v	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	w	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	x	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	y	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
1	z	514/533 (96%)	500 (97%)	14 (3%)	0	100	100
2	1h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	2h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	3h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	5h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	6h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	7h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	8h	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Ah	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Bh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Ch	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Dh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Eh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Fh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Gh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Hh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Ih	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Jh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Kh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Lh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Mh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Nh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Oh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Ph	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Qh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Rh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Sh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Th	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Uh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Vh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Wh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Xh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Yh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	Zh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	ah	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	bh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	ch	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	dh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	eh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	fh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	gh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	hh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	ih	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	jh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	kh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	lh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	mh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	nh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	oh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	ph	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	qh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	rh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	sh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	th	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	uh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	vh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	wh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	xh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	yh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
2	zh	123/125 (98%)	119 (97%)	3 (2%)	1 (1%)	16	34
3	1l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	2l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	3l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	4l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	5l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	6l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	7l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	8l	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Al	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Bl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Cl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Dl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	El	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Fl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Gl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Hl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Il	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Jl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Kl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Ll	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Ml	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Nl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Ol	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Pl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Ql	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Rl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Sl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Tl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Ul	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Vl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Wl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Xl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Yl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	Zl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	al	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	bl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	cl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	dl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	el	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	fl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	gl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	hl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	il	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	jl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	kl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	ll	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	ml	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	nl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	ol	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	pl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	ql	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	rl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	sl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	tl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	ul	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	vl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	wl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	xl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	yl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
3	zl	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
All	All	44460/45840 (97%)	43140 (97%)	1260 (3%)	60 (0%)	49	71

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ah	135	TYR
2	Bh	135	TYR
2	Ch	135	TYR
2	Dh	135	TYR
2	Eh	135	TYR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	2	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	3	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	4	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	5	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	6	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	7	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	8	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	A	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	B	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	C	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	D	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	E	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	F	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	G	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	H	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	I	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	J	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	K	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	L	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	M	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	N	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	O	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	P	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	Q	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	R	458/468 (98%)	453 (99%)	5 (1%)	65	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	T	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	U	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	V	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	W	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	X	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	Y	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	Z	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	a	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	b	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	c	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	d	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	e	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	f	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	g	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	h	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	i	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	j	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	k	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	l	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	m	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	n	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	o	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	p	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	q	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	r	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	s	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	t	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	u	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	v	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	w	458/468 (98%)	453 (99%)	5 (1%)	65	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	y	458/468 (98%)	453 (99%)	5 (1%)	65	83
1	z	458/468 (98%)	453 (99%)	5 (1%)	65	83
2	1h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	2h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	3h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	4h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	5h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	6h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	7h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	8h	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Ah	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Bh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Ch	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Dh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Eh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Fh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Gh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Hh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Ih	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Jh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Kh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Lh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Mh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Nh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Oh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Ph	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Qh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Rh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Sh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Th	101/101 (100%)	96 (95%)	5 (5%)	22	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Uh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Vh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Wh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Xh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Yh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	Zh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	ah	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	bh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	ch	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	dh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	eh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	fh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	gh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	hh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	ih	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	jh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	kh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	lh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	mh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	nh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	oh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	ph	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	qh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	rh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	sh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	th	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	uh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	vh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	wh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	xh	101/101 (100%)	96 (95%)	5 (5%)	22	45
2	yh	101/101 (100%)	96 (95%)	5 (5%)	22	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	zh	101/101 (100%)	96 (95%)	5 (5%)	22	45
3	1l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	2l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	3l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	4l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	5l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	6l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	7l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	8l	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Al	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Bl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Cl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Dl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	El	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Fl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Gl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Hl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Il	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Jl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Kl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Ll	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Ml	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Nl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Ol	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Pl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Ql	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Rl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Sl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Tl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Ul	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Vl	88/88 (100%)	87 (99%)	1 (1%)	65	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Wl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Xl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Yl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	Zl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	al	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	bl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	cl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	dl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	el	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	fl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	gl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	hl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	il	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	jl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	kl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	ll	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	ml	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	nl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	ol	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	pl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	ql	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	rl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	sl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	tl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	ul	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	vl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	wl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	xl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	yl	88/88 (100%)	87 (99%)	1 (1%)	65	83
3	zl	88/88 (100%)	87 (99%)	1 (1%)	65	83
All	All	38820/39420 (98%)	38160 (98%)	660 (2%)	52	77

5 of 660 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	ah	142	GLN
2	wh	142	GLN
2	dh	84	LYS
2	ah	110	THR
2	mh	77	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1301 such sidechains are listed below:

Mol	Chain	Res	Type
1	s	457	GLN
2	2h	142	GLN
1	t	641	HIS
1	s	426	HIS
1	y	496	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

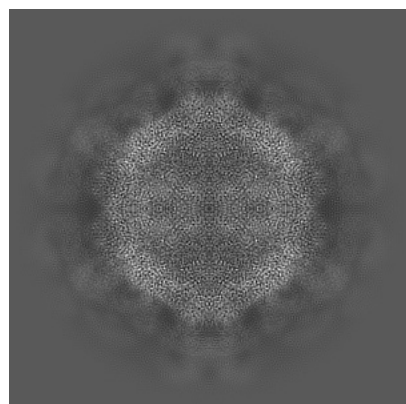
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76773. These allow visual inspection of the internal detail of the map and identification of artifacts.

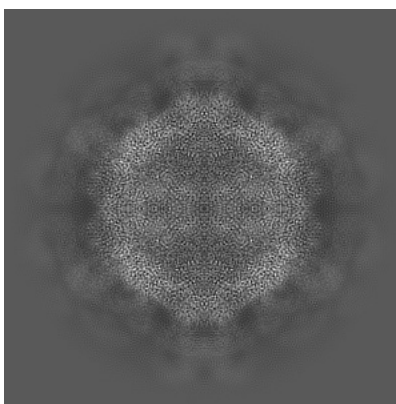
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

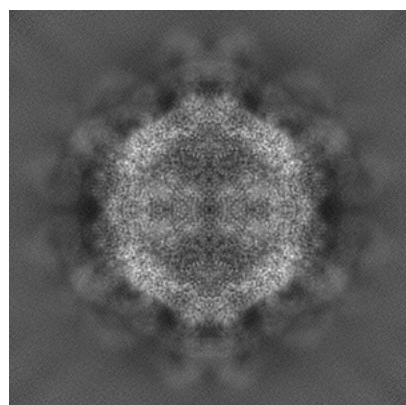


Y

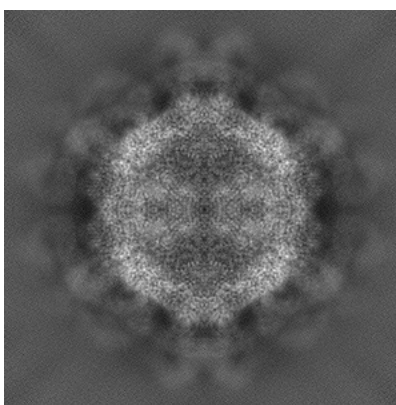


Z

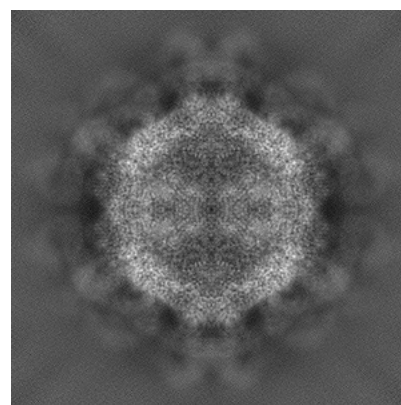
6.1.2 Raw map



X



Y

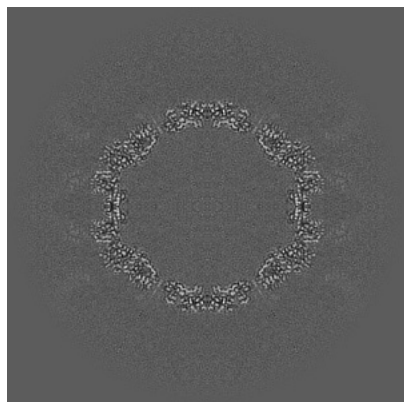


Z

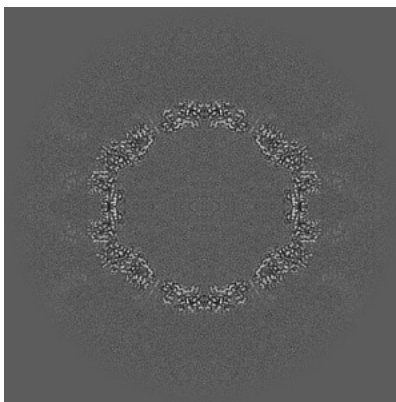
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

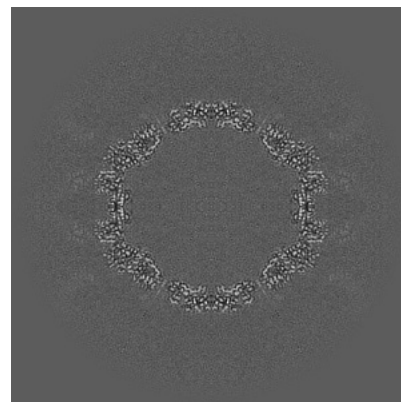
6.2.1 Primary map



X Index: 300

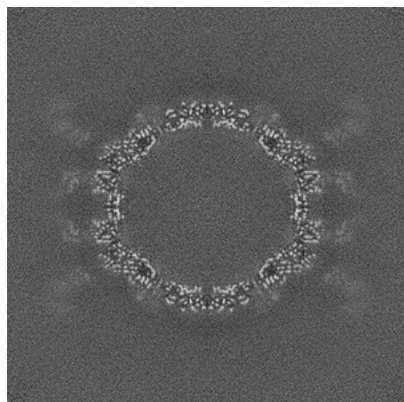


Y Index: 300

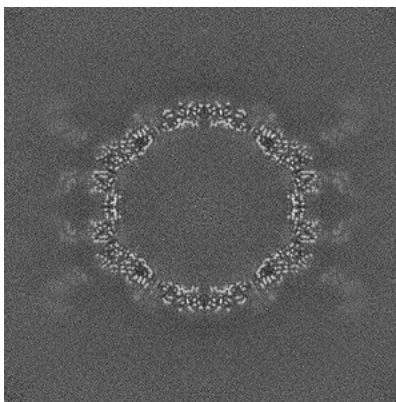


Z Index: 300

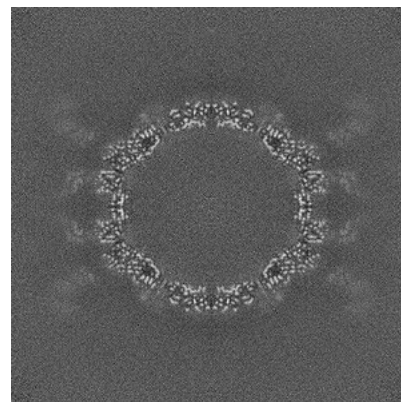
6.2.2 Raw map



X Index: 300



Y Index: 300

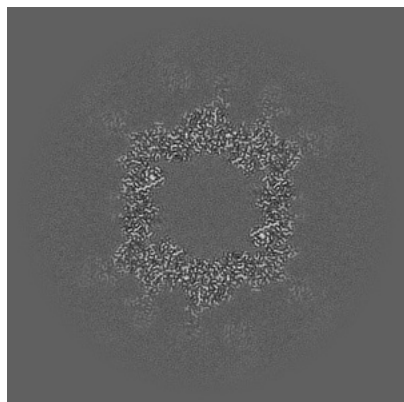


Z Index: 300

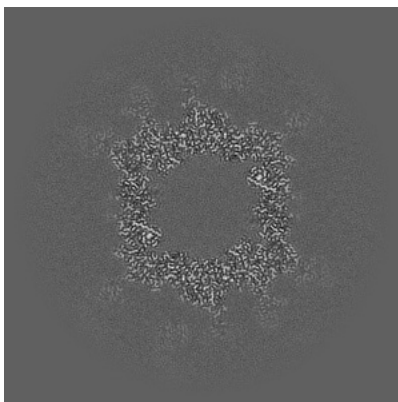
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

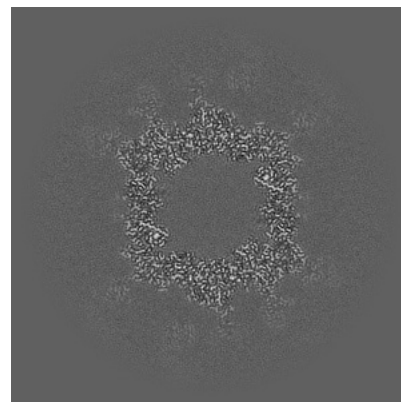
6.3.1 Primary map



X Index: 391

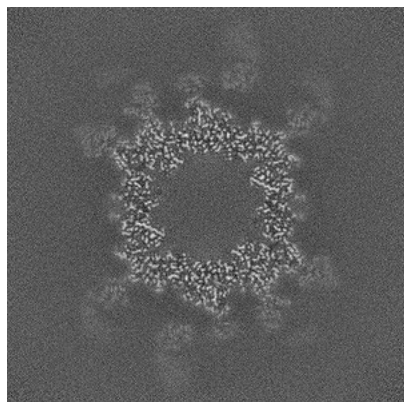


Y Index: 209

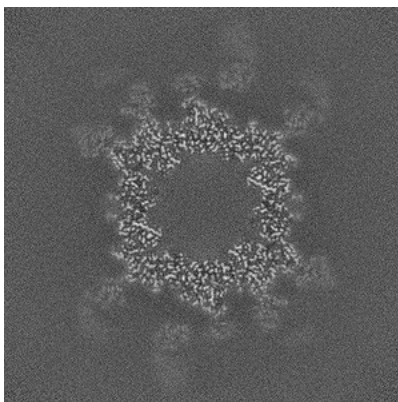


Z Index: 209

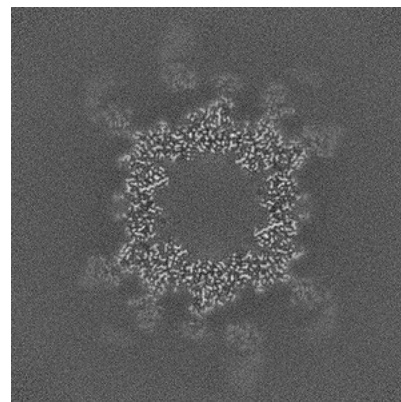
6.3.2 Raw map



X Index: 209



Y Index: 209

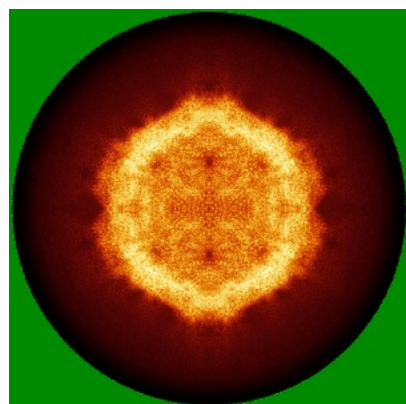


Z Index: 391

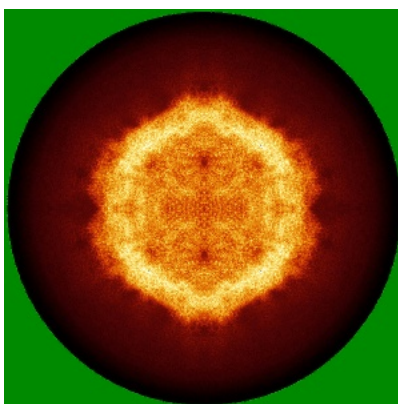
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

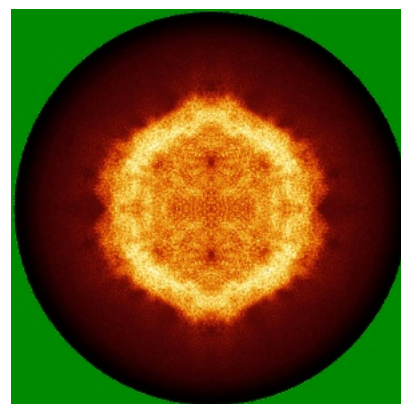
6.4.1 Primary map



X

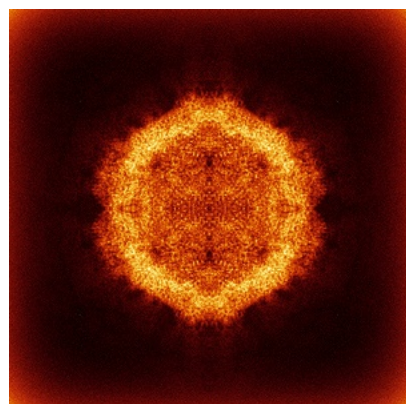


Y

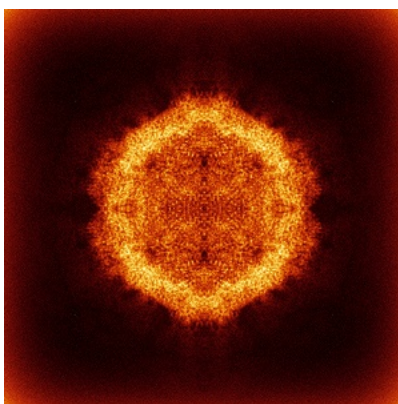


Z

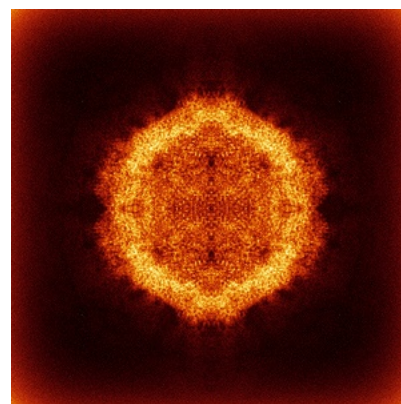
6.4.2 Raw map



X



Y

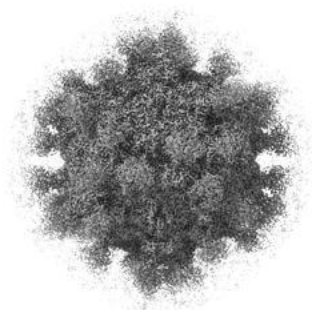


Z

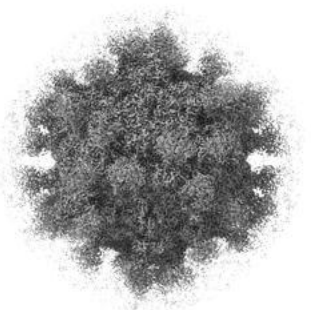
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

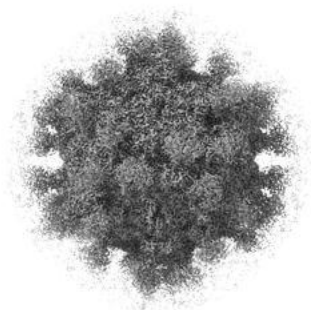
6.5.1 Primary map



X



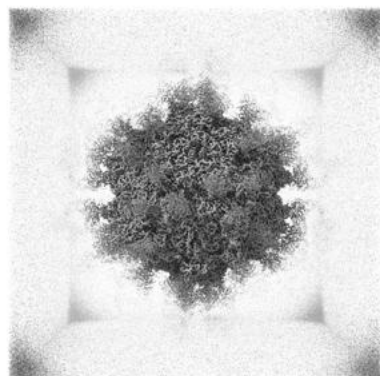
Y



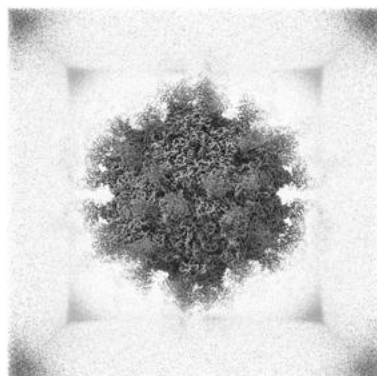
Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

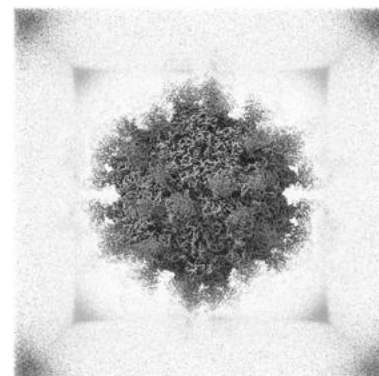
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

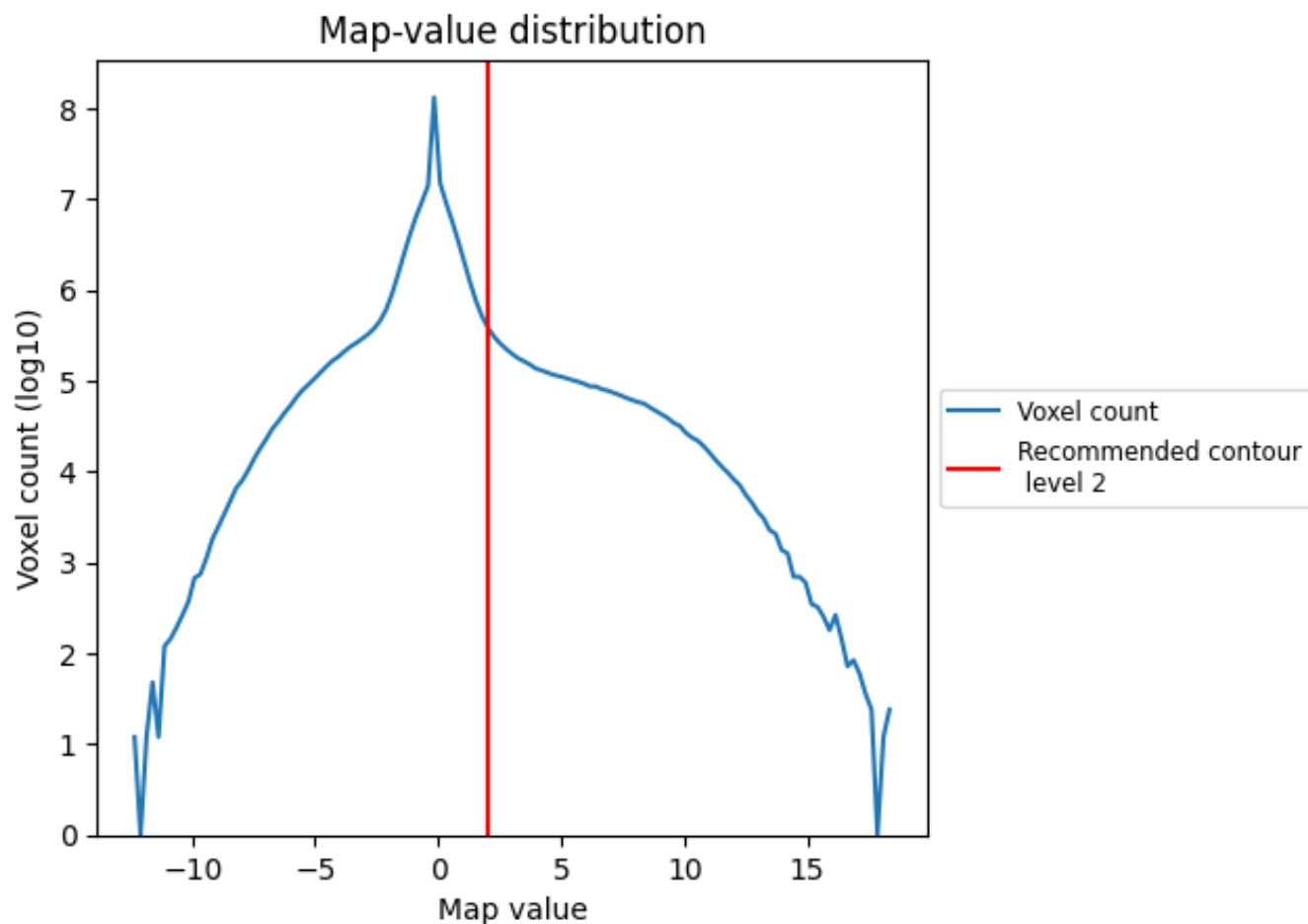
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

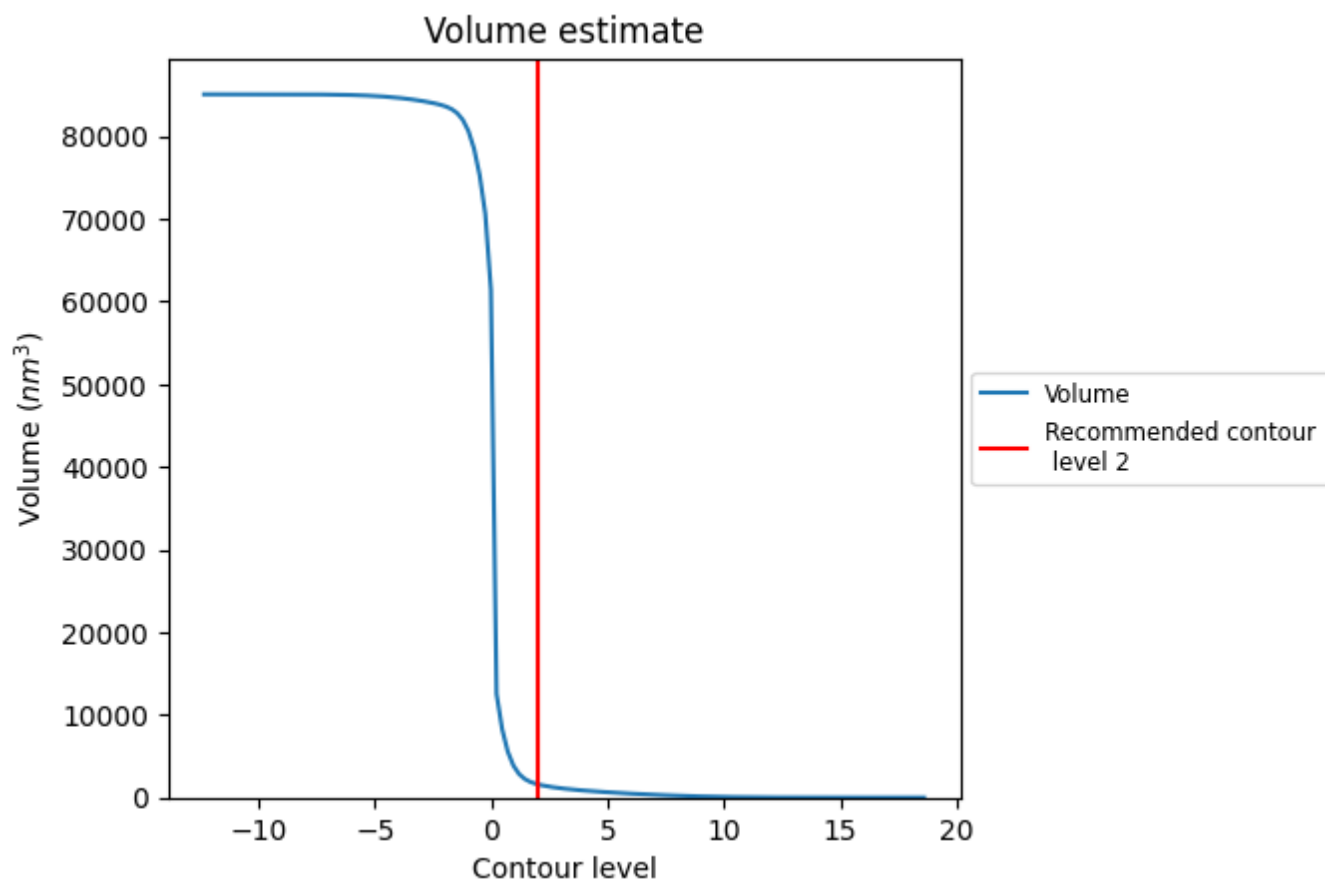
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

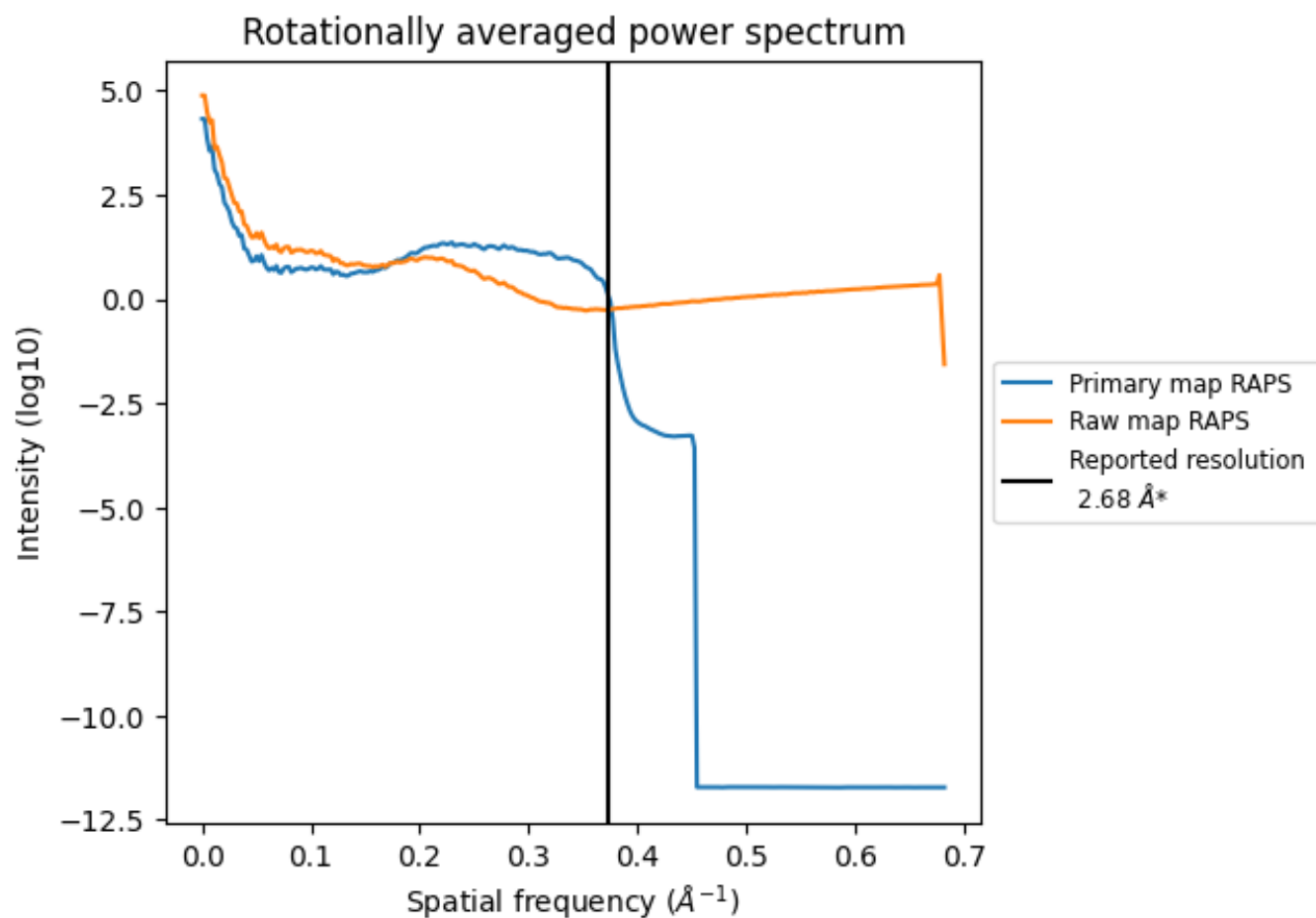
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1606 nm³; this corresponds to an approximate mass of 1450 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

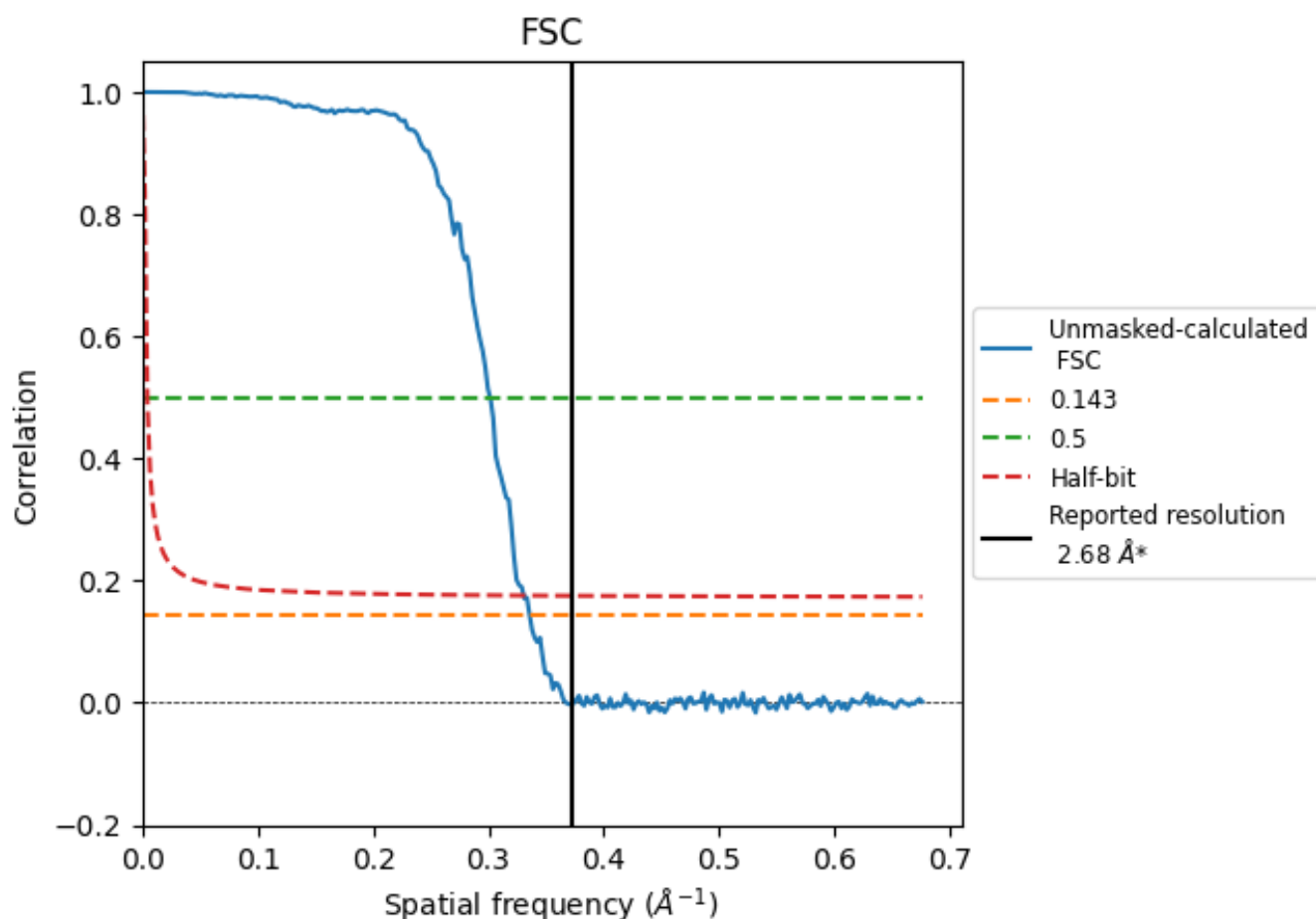


*Reported resolution corresponds to spatial frequency of 0.373 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.373 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

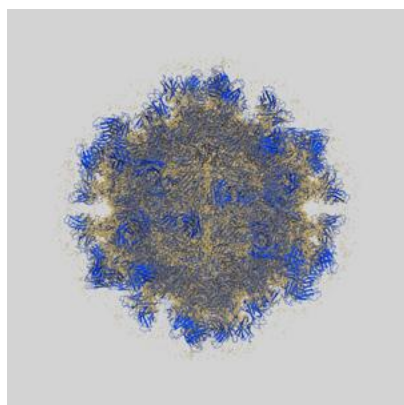
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.68	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.98	3.32	3.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.98 differs from the reported value 2.68 by more than 10 %

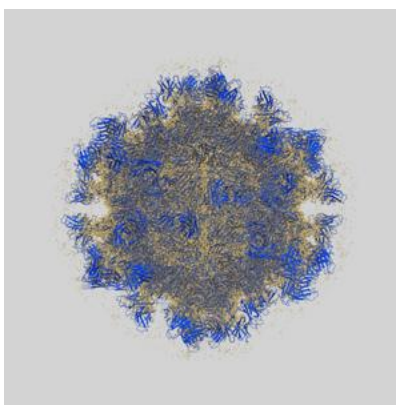
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-76773 and PDB model 12UV. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

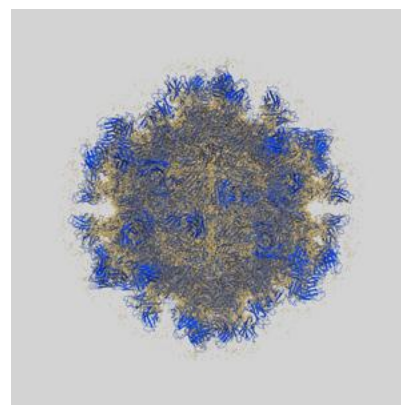
9.1 Map-model overlay [i](#)



X



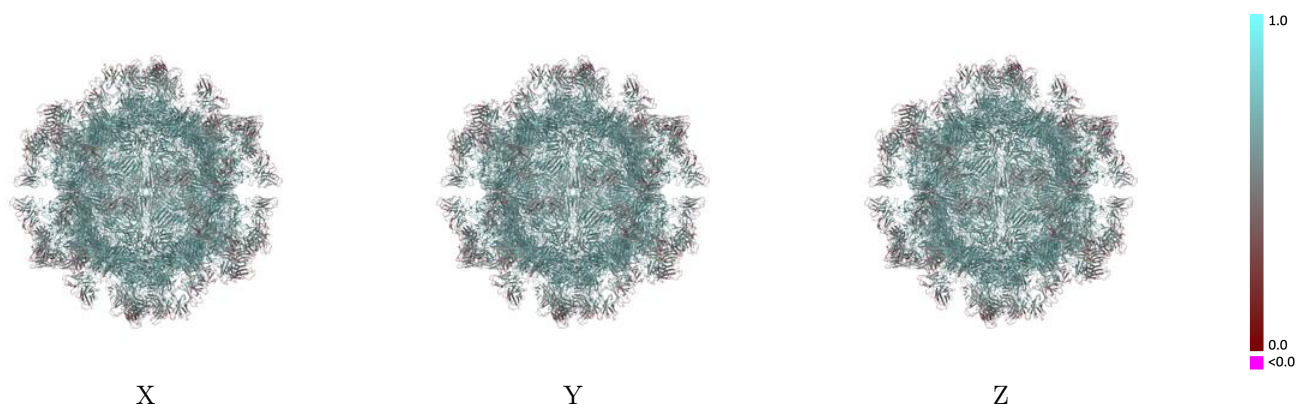
Y



Z

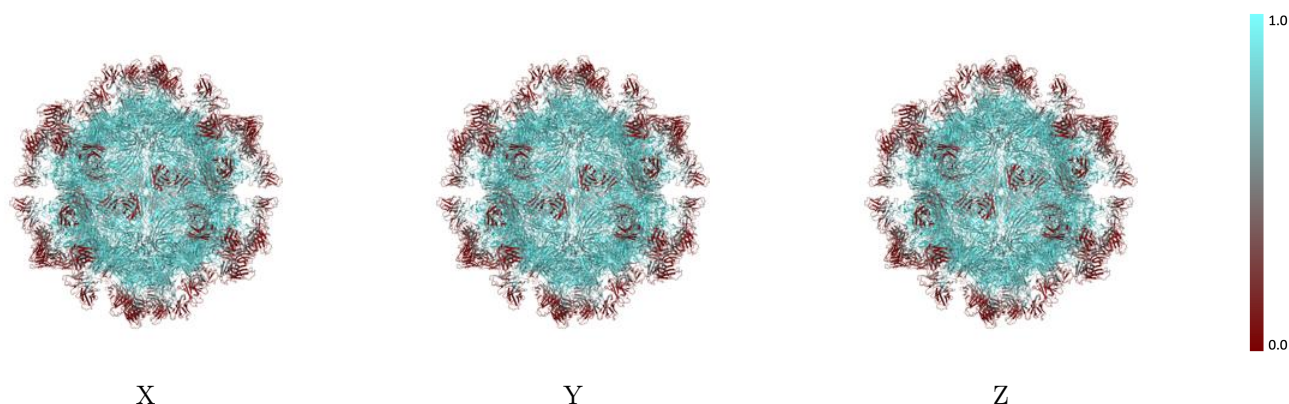
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



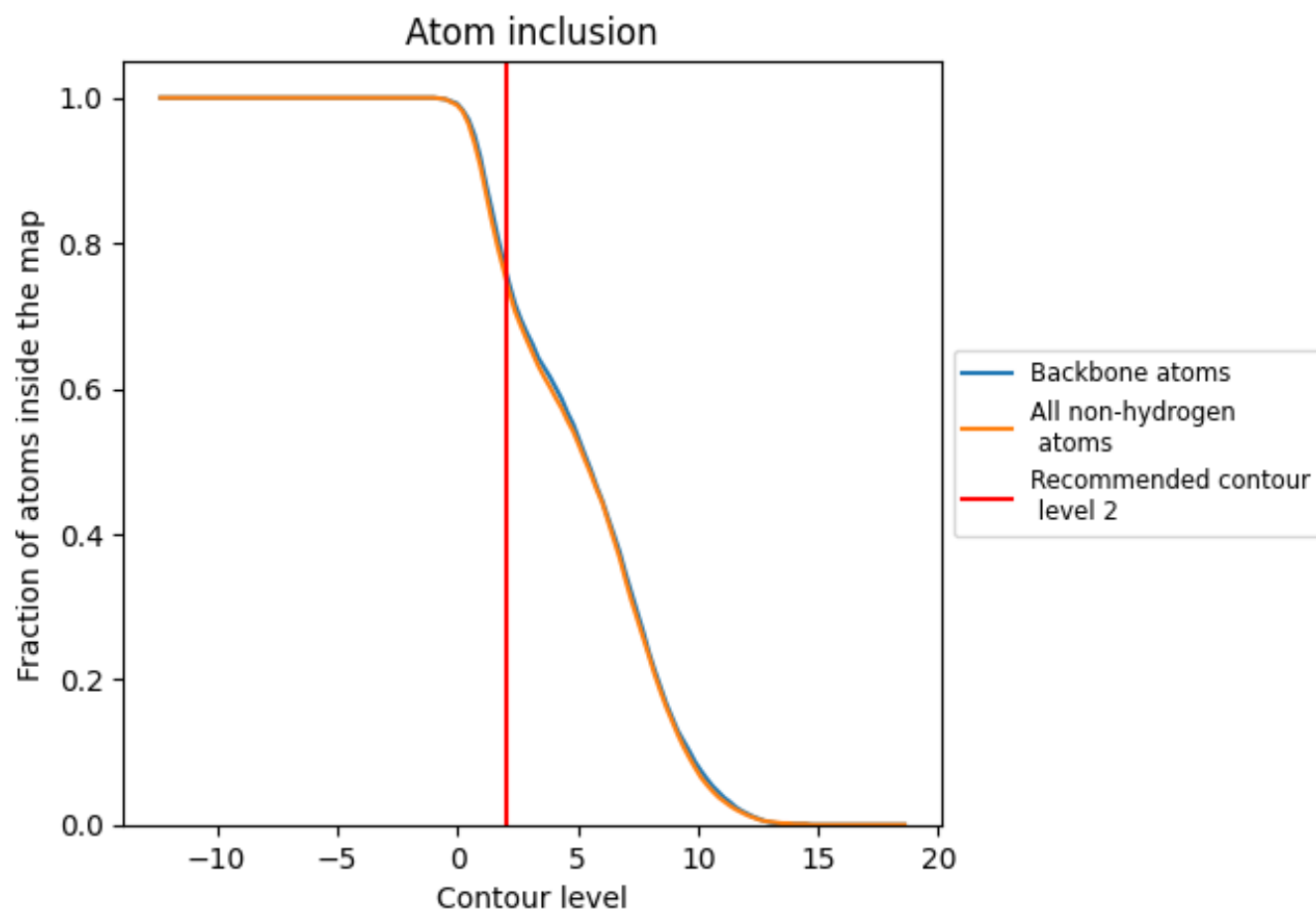
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.6210
1	 0.9660	 0.6760
1h	 0.2210	 0.5000
1l	 0.2950	 0.4920
2	 0.9660	 0.6760
2h	 0.2240	 0.4980
2l	 0.2920	 0.4870
3	 0.9660	 0.6760
3h	 0.2240	 0.4980
3l	 0.2920	 0.4910
4	 0.9660	 0.6760
4h	 0.2210	 0.4980
4l	 0.2950	 0.4880
5	 0.9660	 0.6760
5h	 0.2240	 0.4970
5l	 0.2920	 0.4890
6	 0.9660	 0.6760
6h	 0.2230	 0.4970
6l	 0.2910	 0.4900
7	 0.9660	 0.6760
7h	 0.2260	 0.5000
7l	 0.2960	 0.4900
8	 0.9650	 0.6760
8h	 0.2160	 0.5040
8l	 0.2810	 0.4920
A	 0.9660	 0.6760
Ah	 0.2230	 0.4990
Al	 0.2910	 0.4920
B	 0.9640	 0.6750
Bh	 0.2170	 0.4960
Bl	 0.2940	 0.4840
C	 0.9650	 0.6750
Ch	 0.2280	 0.4940
Cl	 0.2950	 0.4910
D	 0.9660	 0.6760



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Chain	Atom inclusion	Q-score
Dh	 0.2270	 0.5030
DI	 0.2960	 0.4880
E	 0.9650	 0.6760
Eh	 0.2170	 0.5070
El	 0.2810	 0.4900
F	 0.9660	 0.6760
Fh	 0.2210	 0.4970
Fl	 0.2830	 0.4910
G	 0.9650	 0.6760
Gh	 0.2170	 0.5040
Gl	 0.2810	 0.4890
H	 0.9660	 0.6760
Hh	 0.2280	 0.4990
HI	 0.2960	 0.4870
I	 0.9650	 0.6760
Ih	 0.2280	 0.4930
Il	 0.2940	 0.4880
J	 0.9640	 0.6760
Jh	 0.2170	 0.4980
JI	 0.2950	 0.4850
K	 0.9650	 0.6760
Kh	 0.2310	 0.4940
KI	 0.2950	 0.4870
L	 0.9640	 0.6760
Lh	 0.2200	 0.4950
LI	 0.2940	 0.4840
M	 0.9650	 0.6760
Mh	 0.2170	 0.5020
MI	 0.2810	 0.4890
N	 0.9660	 0.6770
Nh	 0.2260	 0.5000
NI	 0.2960	 0.4890
O	 0.9650	 0.6760
Oh	 0.2160	 0.5020
OI	 0.2810	 0.4910
P	 0.9660	 0.6760
Ph	 0.2280	 0.5000
PI	 0.2960	 0.4890
Q	 0.9650	 0.6760
Qh	 0.2280	 0.4920
QI	 0.2940	 0.4870
R	 0.9640	 0.6760

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Chain	Atom inclusion	Q-score
Rh	 0.2170	 0.4970
Rl	 0.2950	 0.4880
S	 0.9640	 0.6760
Sh	 0.2170	 0.4980
Sl	 0.2950	 0.4850
T	 0.9650	 0.6760
Th	 0.2310	 0.4950
Tl	 0.2950	 0.4910
U	 0.9640	 0.6760
Uh	 0.2200	 0.4950
Ul	 0.2940	 0.4830
V	 0.9650	 0.6760
Vh	 0.2280	 0.4980
Vl	 0.2950	 0.4900
W	 0.9660	 0.6760
Wh	 0.2270	 0.5040
Wl	 0.2960	 0.4880
X	 0.9650	 0.6770
Xh	 0.2170	 0.5030
Xl	 0.2810	 0.4880
Y	 0.9660	 0.6760
Yh	 0.2260	 0.4990
Yl	 0.2960	 0.4880
Z	 0.9650	 0.6750
Zh	 0.2160	 0.5040
Zl	 0.2810	 0.4920
a	 0.9650	 0.6750
ah	 0.2280	 0.4960
al	 0.2950	 0.4890
b	 0.9650	 0.6760
bh	 0.2170	 0.5010
bl	 0.2810	 0.4870
c	 0.9660	 0.6770
ch	 0.2260	 0.4990
cl	 0.2960	 0.4890
d	 0.9660	 0.6750
dh	 0.2280	 0.5000
dl	 0.2960	 0.4870
e	 0.9660	 0.6750
eh	 0.2260	 0.5040
el	 0.2960	 0.4890
f	 0.9650	 0.6750

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Chain	Atom inclusion	Q-score
fh	 0.2160	 0.5010
fl	 0.2810	 0.4920
g	 0.9650	 0.6760
gh	 0.2310	 0.4930
gl	 0.2950	 0.4880
h	 0.9660	 0.6760
hh	 0.2180	 0.5000
hl	 0.2950	 0.4890
i	 0.9650	 0.6770
ih	 0.2170	 0.5020
il	 0.2810	 0.4880
j	 0.9650	 0.6750
jh	 0.2280	 0.4960
jl	 0.2950	 0.4910
k	 0.9640	 0.6750
kh	 0.2170	 0.4960
kl	 0.2940	 0.4820
l	 0.9640	 0.6760
lh	 0.2170	 0.4990
ll	 0.2950	 0.4840
m	 0.9640	 0.6770
mh	 0.2200	 0.4940
ml	 0.2940	 0.4840
n	 0.9650	 0.6760
nh	 0.2170	 0.5070
nl	 0.2810	 0.4900
o	 0.9650	 0.6770
oh	 0.2280	 0.4930
ol	 0.2940	 0.4890
p	 0.9660	 0.6760
ph	 0.2210	 0.4960
pl	 0.2920	 0.4870
q	 0.9650	 0.6760
qh	 0.2170	 0.5030
ql	 0.2810	 0.4900
r	 0.9650	 0.6760
rh	 0.2280	 0.4920
rl	 0.2940	 0.4880
s	 0.9660	 0.6760
sh	 0.2210	 0.5000
sl	 0.2920	 0.4880
t	 0.9640	 0.6750

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Chain	Atom inclusion	Q-score
th	 0.2200	 0.4970
tl	 0.2940	 0.4860
u	 0.9640	 0.6750
uh	 0.2170	 0.4980
ul	 0.2940	 0.4860
v	 0.9640	 0.6760
vh	 0.2170	 0.4970
vl	 0.2950	 0.4860
w	 0.9660	 0.6760
wh	 0.2210	 0.4980
wl	 0.2950	 0.4890
x	 0.9650	 0.6750
xh	 0.2310	 0.4950
xl	 0.2950	 0.4870
y	 0.9660	 0.6770
yh	 0.2280	 0.4980
yl	 0.2960	 0.4870
z	 0.9660	 0.6760
zh	 0.2270	 0.5030
zl	 0.2960	 0.4890