



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2026 – 05:09 PM EDT

PDB ID : 12US / pdb_000012us
EMDB ID : EMD-76770
Title : The AAV2 capsid in complex with IgG-Fab#3-2
Authors : Zachery, J.; Mietzsch, M.; McKenna, R.
Deposited on : 2026-04-20
Resolution : 3.28 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

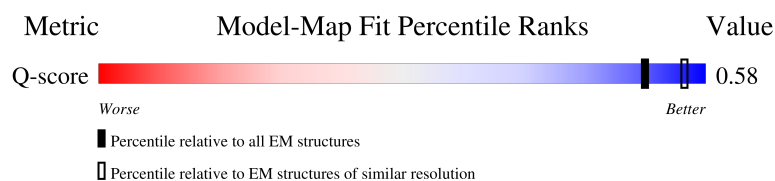
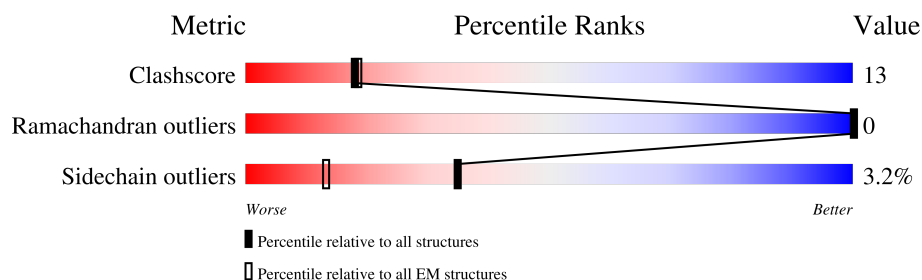
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.28 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.



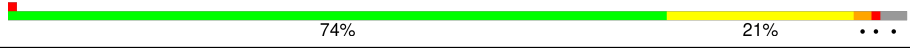
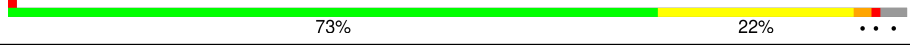
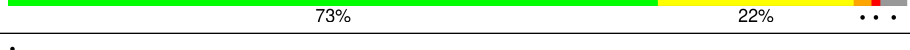
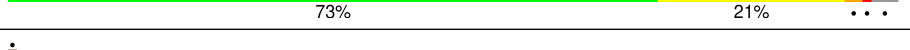
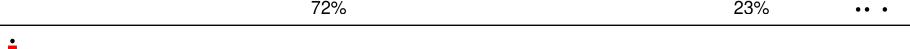
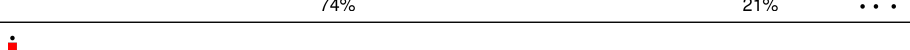
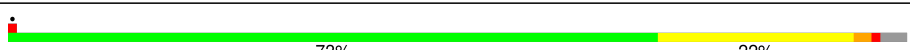
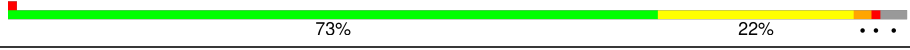
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14492 (2.78 - 3.78)

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	 73% 22% ...
1	2	533	 74% 21% ...
1	3	533	 74% 21% ...
1	4	533	 73% 21% ...

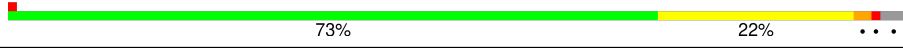
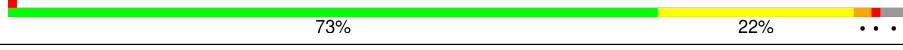
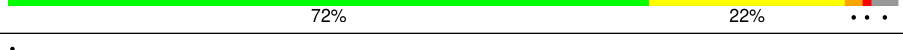
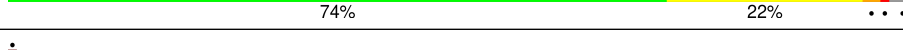
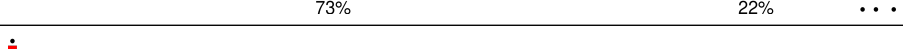
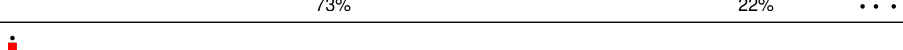
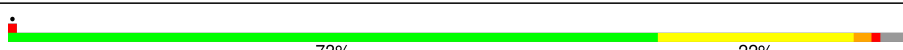
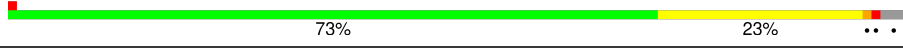
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Mol	Chain	Length	Quality of chain
1	5	533	
1	6	533	
1	7	533	
1	8	533	
1	A	533	
1	B	533	
1	C	533	
1	D	533	
1	E	533	
1	F	533	
1	G	533	
1	H	533	
1	I	533	
1	J	533	
1	K	533	
1	L	533	
1	M	533	
1	N	533	
1	O	533	
1	P	533	
1	Q	533	
1	R	533	
1	S	533	
1	T	533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

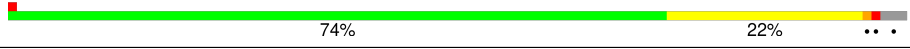
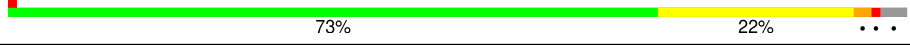
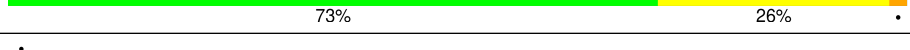
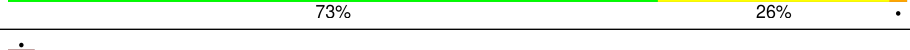
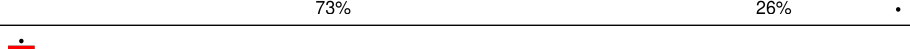
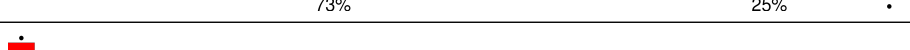
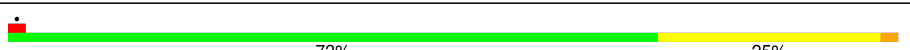
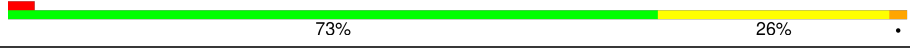
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Mol	Chain	Length	Quality of chain
1	V	533	
1	W	533	
1	X	533	
1	Y	533	
1	Z	533	
1	a	533	
1	b	533	
1	c	533	
1	d	533	
1	e	533	
1	f	533	
1	g	533	
1	h	533	
1	i	533	
1	j	533	
1	k	533	
1	l	533	
1	m	533	
1	n	533	
1	o	533	
1	p	533	
1	q	533	
1	r	533	
1	s	533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

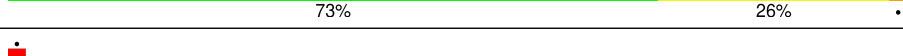
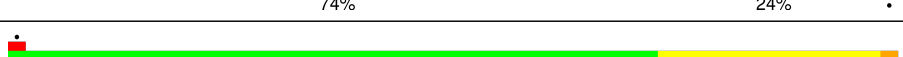
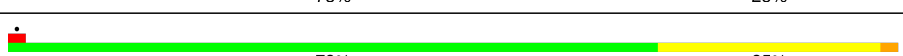
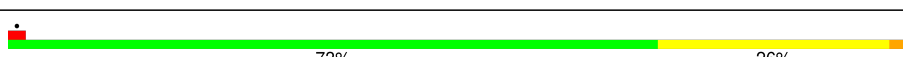
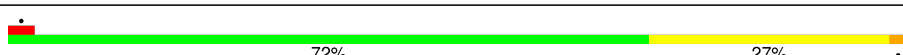
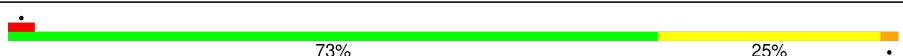
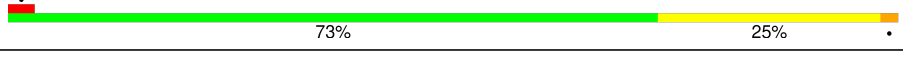
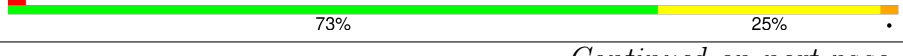
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Mol	Chain	Length	Quality of chain
1	u	533	
1	v	533	
1	w	533	
1	x	533	
1	y	533	
1	z	533	
2	1h	132	
2	2h	132	
2	3h	132	
2	4h	132	
2	5h	132	
2	6h	132	
2	7h	132	
2	8h	132	
2	Ah	132	
2	Bh	132	
2	Ch	132	
2	Dh	132	
2	Eh	132	
2	Fh	132	
2	Gh	132	
2	Hh	132	
2	Ih	132	
2	Jh	132	
2	Kh	132	

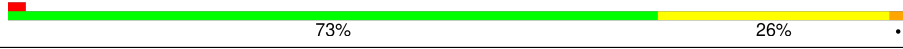
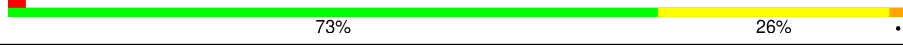
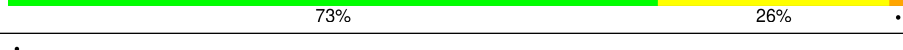
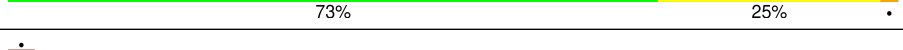
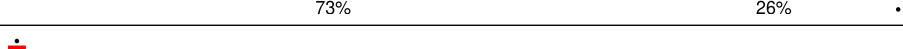
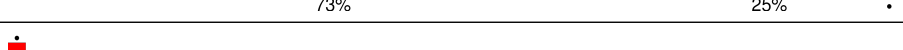
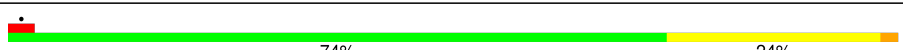
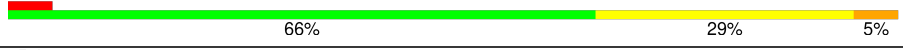
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Mol	Chain	Length	Quality of chain
2	Lh	132	
2	Mh	132	
2	Nh	132	
2	Oh	132	
2	Ph	132	
2	Qh	132	
2	Rh	132	
2	Sh	132	
2	Th	132	
2	Uh	132	
2	Vh	132	
2	Wh	132	
2	Xh	132	
2	Yh	132	
2	Zh	132	
2	ah	132	
2	bh	132	
2	ch	132	
2	dh	132	
2	eh	132	
2	fh	132	
2	gh	132	
2	hh	132	
2	ih	132	
2	jh	132	

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Mol	Chain	Length	Quality of chain
2	kh	132	
2	lh	132	
2	mh	132	
2	nh	132	
2	oh	132	
2	ph	132	
2	qh	132	
2	rh	132	
2	sh	132	
2	th	132	
2	uh	132	
2	vh	132	
2	wh	132	
2	xh	132	
2	yh	132	
2	zh	132	
3	1l	110	
3	2l	110	
3	3l	110	
3	4l	110	
3	5l	110	
3	6l	110	
3	7l	110	
3	8l	110	
3	A1	110	

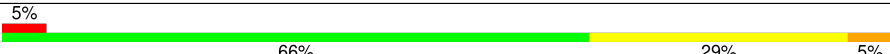
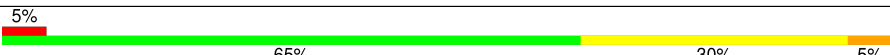
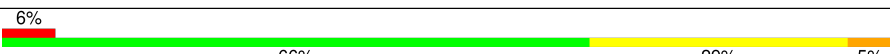
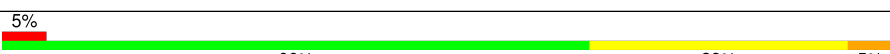
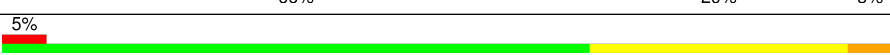
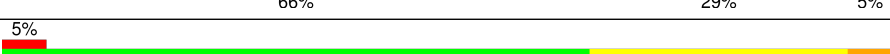
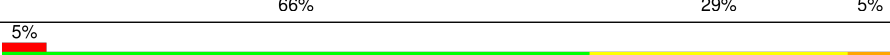
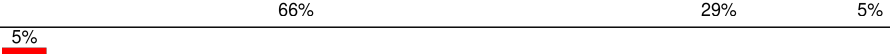
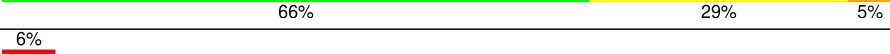
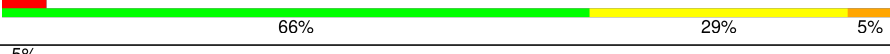
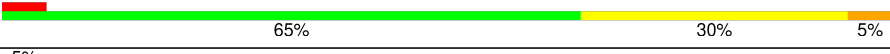
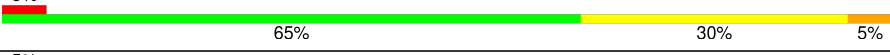
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Mol	Chain	Length	Quality of chain
3	B1	110	
3	C1	110	
3	D1	110	
3	E1	110	
3	F1	110	
3	G1	110	
3	H1	110	
3	I1	110	
3	J1	110	
3	K1	110	
3	L1	110	
3	M1	110	
3	N1	110	
3	O1	110	
3	P1	110	
3	Q1	110	
3	R1	110	
3	S1	110	
3	T1	110	
3	U1	110	
3	V1	110	
3	W1	110	
3	X1	110	
3	Y1	110	
3	Z1	110	

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Mol	Chain	Length	Quality of chain
3	al	110	
3	bl	110	
3	cl	110	
3	dl	110	
3	el	110	
3	fl	110	
3	gl	110	
3	hl	110	
3	il	110	
3	jl	110	
3	kl	110	
3	ll	110	
3	ml	110	
3	nl	110	
3	ol	110	
3	pl	110	
3	ql	110	
3	rl	110	
3	sl	110	
3	tl	110	
3	ul	110	
3	vl	110	
3	wl	110	
3	xl	110	
3	yl	110	

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Mol	Chain	Length	Quality of chain
3	zl	110	5% 65% 30% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 358740 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	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	B	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	C	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	D	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	E	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	F	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	G	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	H	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	I	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	J	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	K	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	L	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	M	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	N	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	O	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	P	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		
1	Q	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	S	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	T	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	U	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	V	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	W	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	X	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	Y	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	Z	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	1	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	2	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	3	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	4	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	5	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	6	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	a	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	b	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	c	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	d	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	e	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	f	518	Total 4148	C 2610	N 724	O 801	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	h	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	i	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	j	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	k	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	l	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	m	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	n	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	o	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	p	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	q	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	r	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	s	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	t	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	u	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	v	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	w	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	x	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	y	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	z	518	Total 4148	C 2610	N 724	O 801	S 13	0	0
1	7	518	Total 4148	C 2610	N 724	O 801	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	518	Total	C	N	O	S	0	0
			4148	2610	724	801	13		

- Molecule 2 is a protein called Fab3-2 IgG Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ah	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Bh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Ch	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Dh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Eh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Fh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Gh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Hh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Ih	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Jh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Kh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Lh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Mh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Nh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Oh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Ph	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Qh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Rh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Sh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Th	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Uh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Vh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Wh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Xh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Yh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	Zh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	1h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	2h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	3h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	4h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	5h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	6h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	ah	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	bh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	ch	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	dh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	eh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	fh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	gh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	hh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	ih	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	jh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	kh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	lh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	mh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	nh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	oh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	ph	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	qh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	rh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	sh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	th	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	uh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	vh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	wh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	xh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	yh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	zh	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	7h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		
2	8h	132	Total	C	N	O	S	0	0
			1028	659	169	198	2		

- Molecule 3 is a protein called Fab3-2 IgG Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Al	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Bl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Cl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Dl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	El	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Fl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Gl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Hl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Il	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Jl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Kl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Ll	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Ml	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Nl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Ol	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Pl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Ql	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Rl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Sl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Tl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Ul	110	Total 803	C 496	N 135	O 168	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Vl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Wl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Xl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Yl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	Zl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	1l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	2l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	3l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	4l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	5l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	6l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	al	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	bl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	cl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	dl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	el	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	fl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	gl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	hl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	il	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	jl	110	Total 803	C 496	N 135	O 168	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	kl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	ll	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	ml	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	nl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	ol	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	pl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	ql	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	rl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	sl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	tl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	ul	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	vl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	wl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	xl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	yl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	zl	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	7l	110	Total 803	C 496	N 135	O 168	S 4	0	0
3	8l	110	Total 803	C 496	N 135	O 168	S 4	0	0

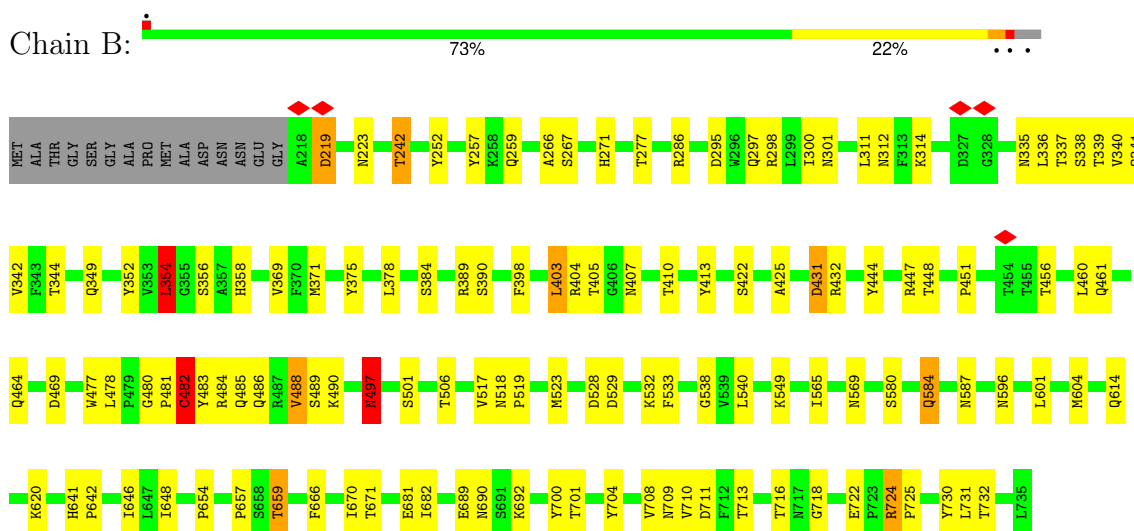
3 Residue-property plots

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.

• Molecule 1: Capsid protein VP1

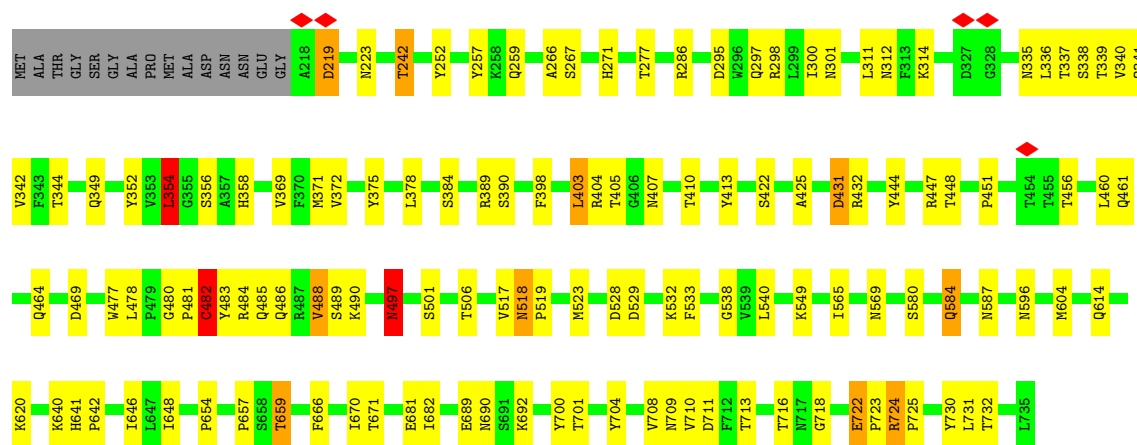


• Molecule 1: Capsid protein VP1

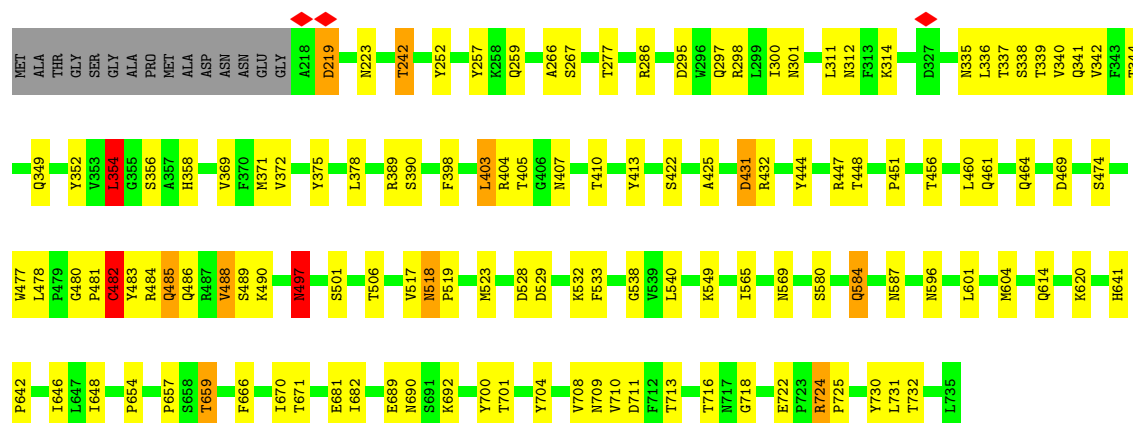


• Molecule 1: Capsid protein VP1

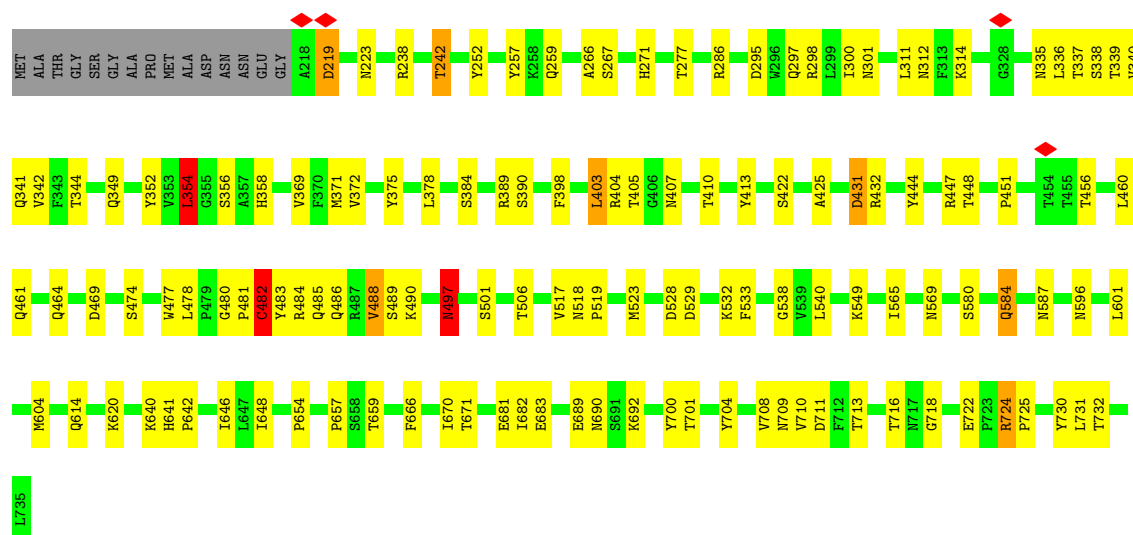




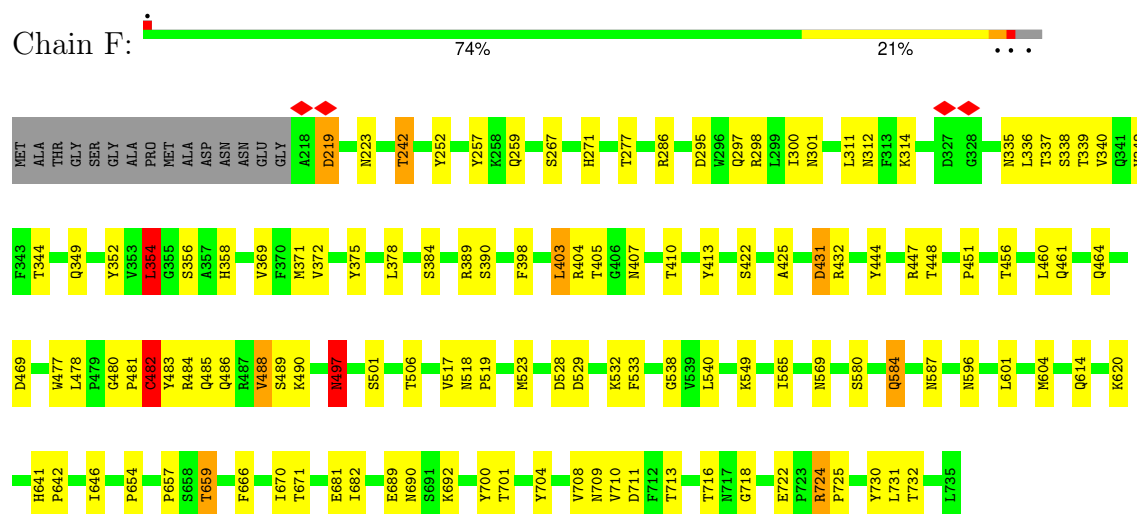
• Molecule 1: Capsid protein VP1



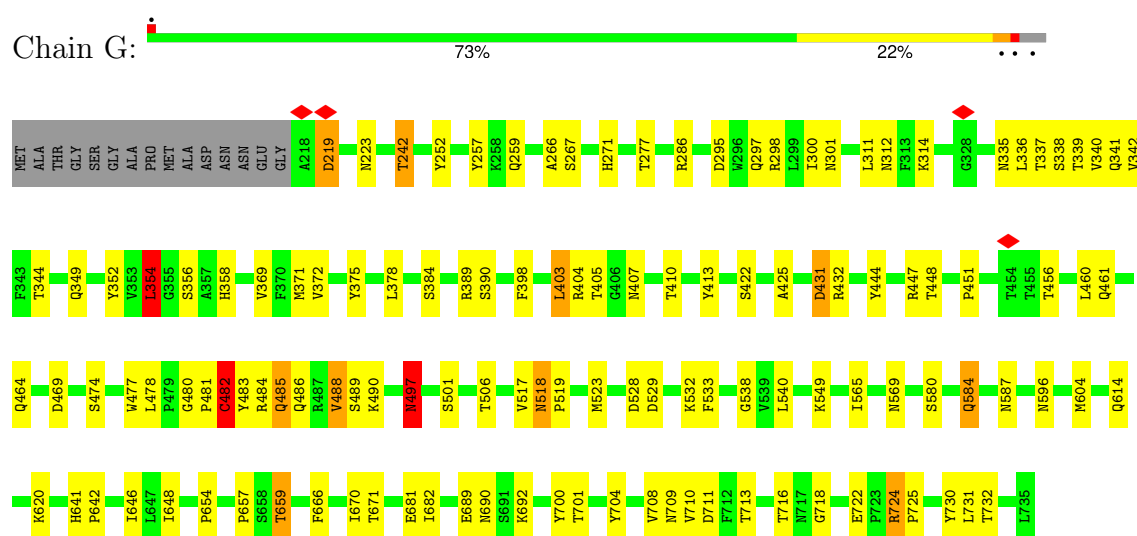
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

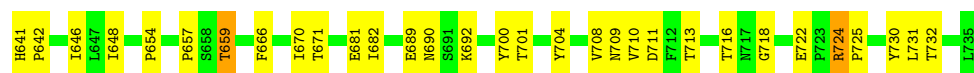


• Molecule 1: Capsid protein VP1

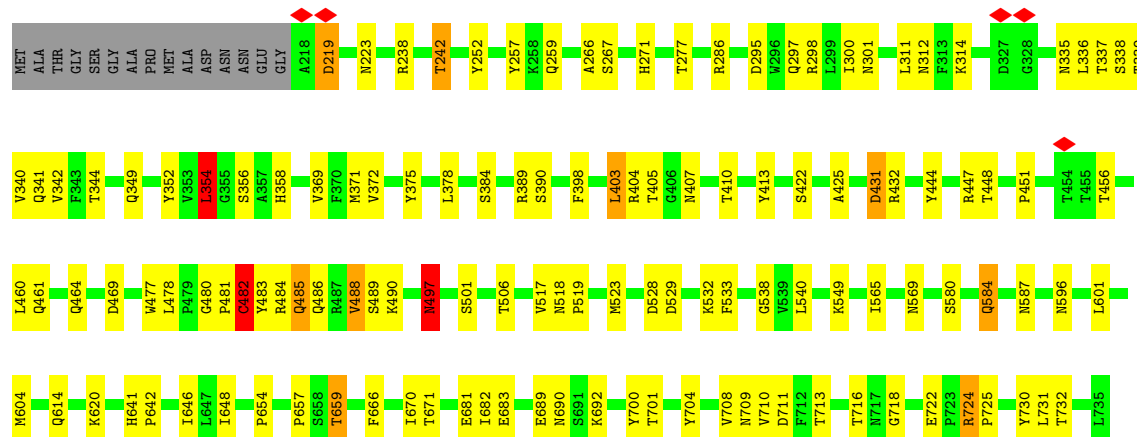


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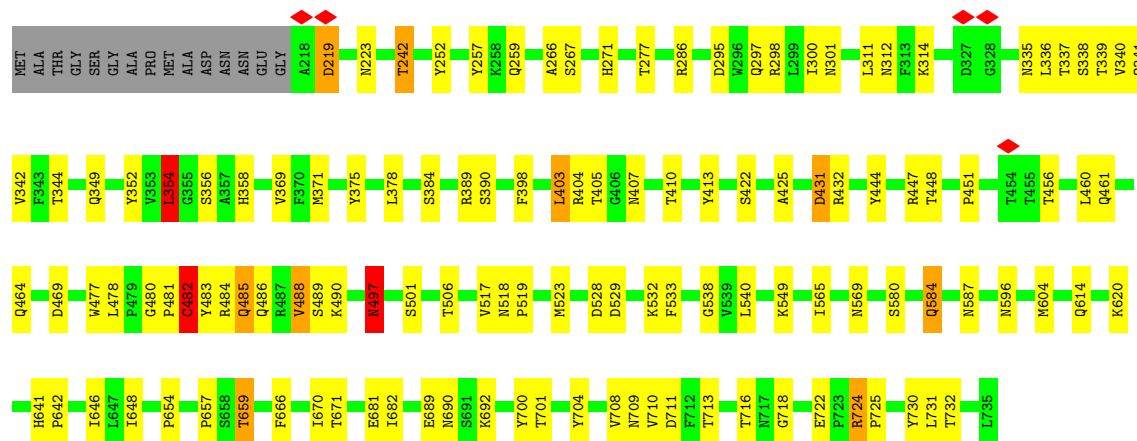




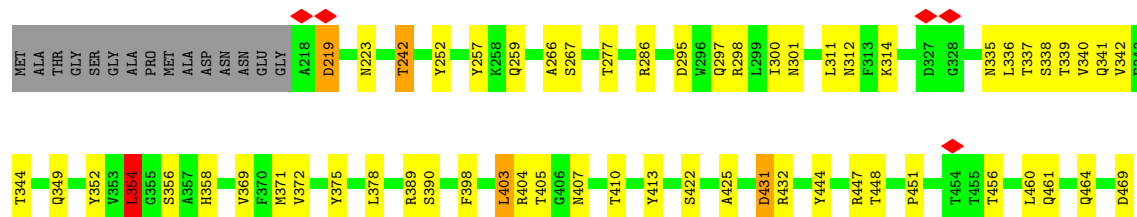
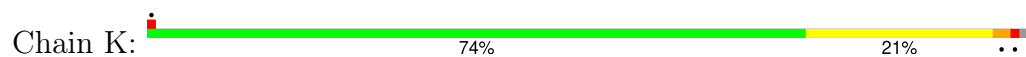
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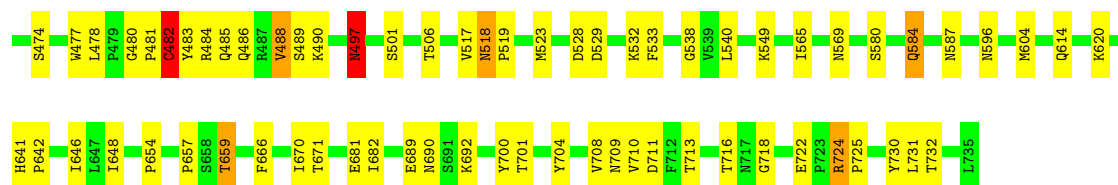


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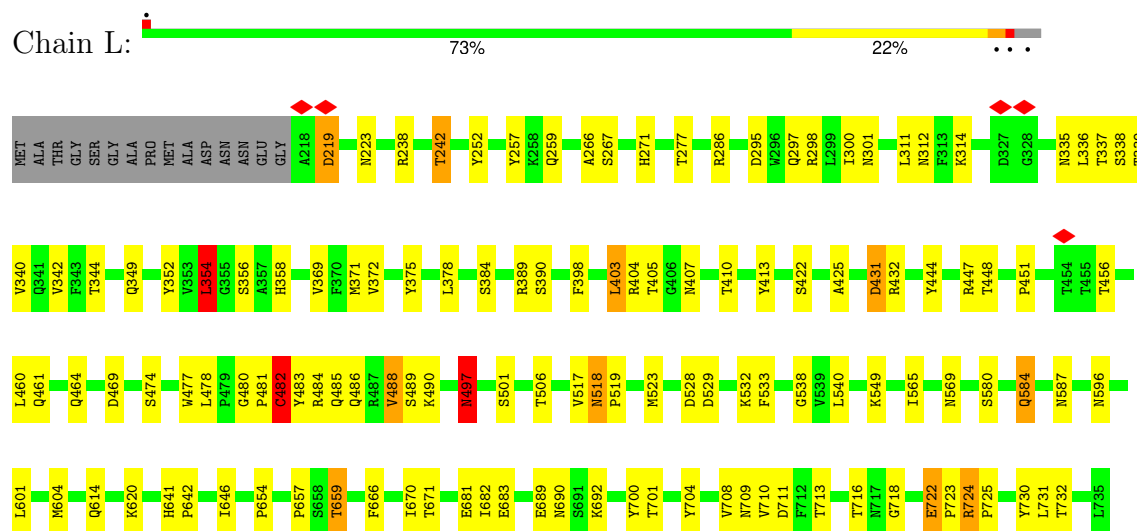


• Molecule 1: Capsid protein VP1

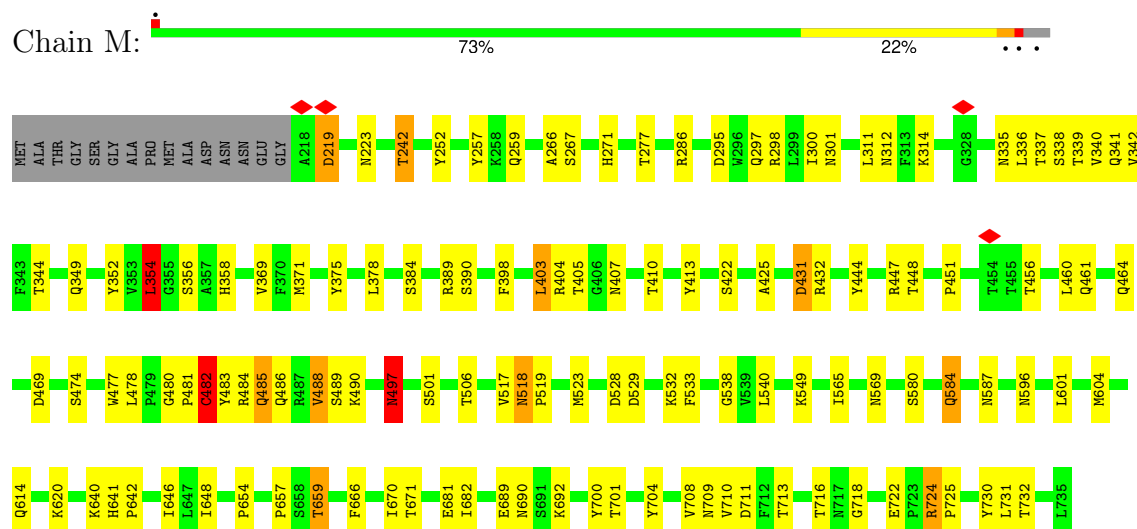




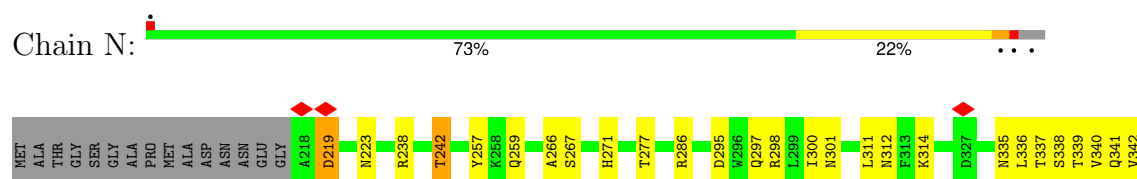
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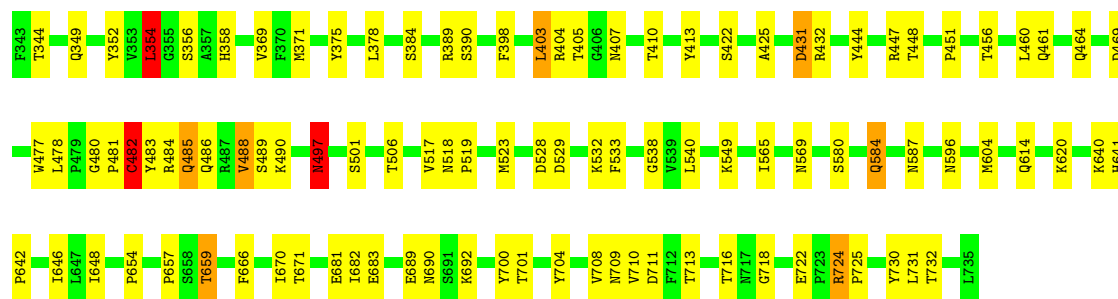


• Molecule 1: Capsid protein VP1

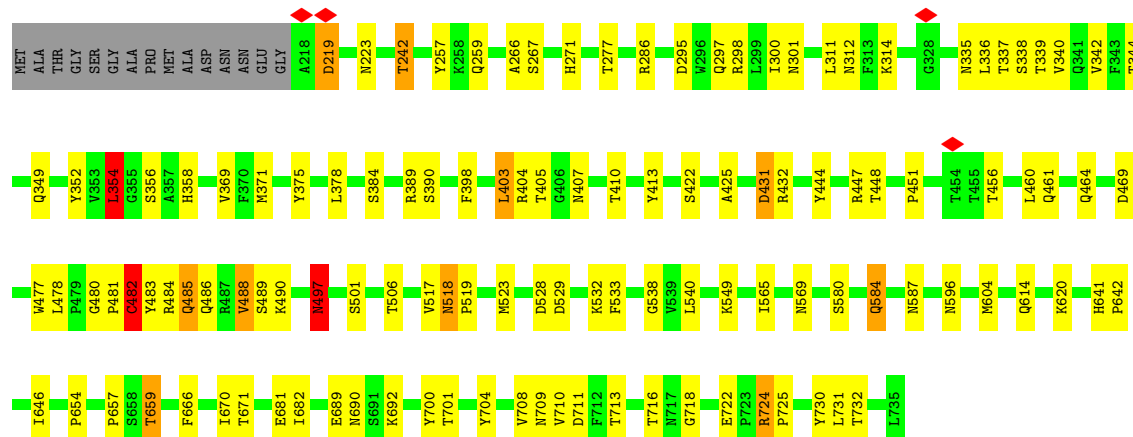


• Molecule 1: Capsid protein VP1

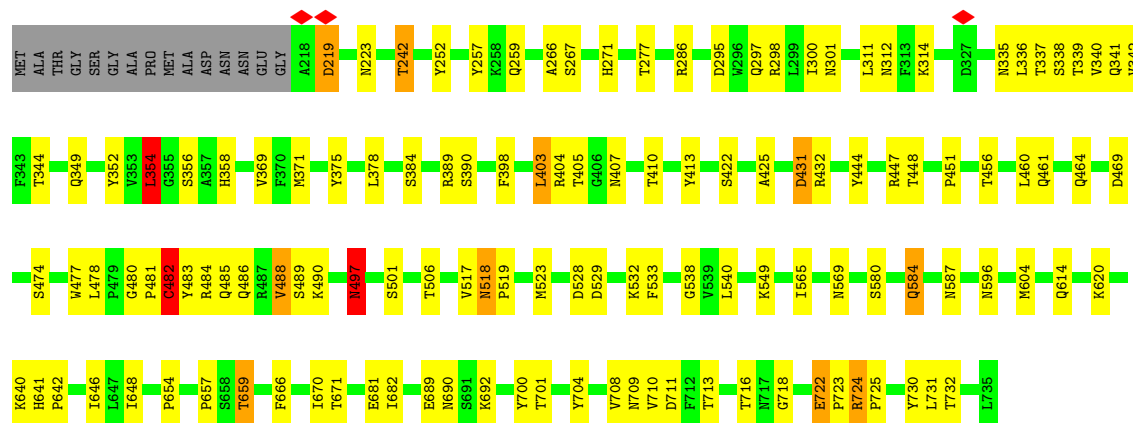




● Molecule 1: Capsid protein VP1

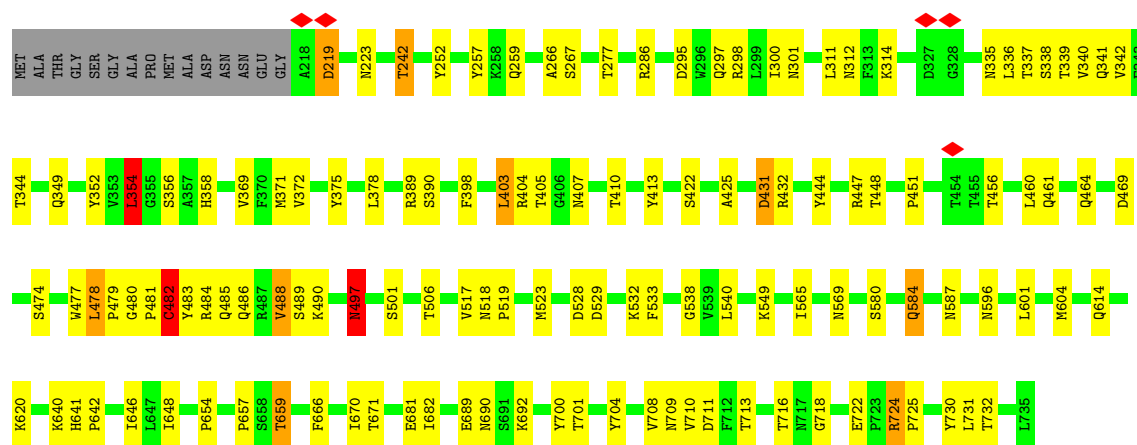


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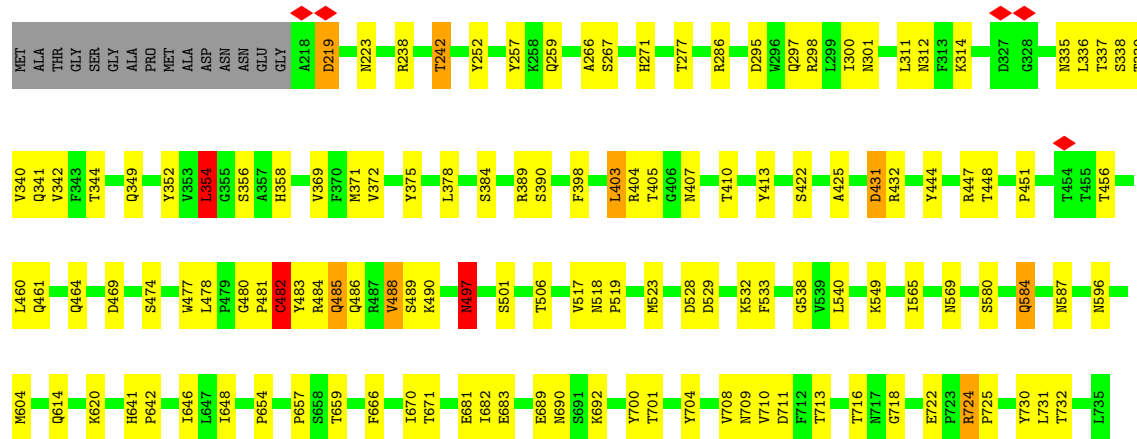


● Molecule 1: Capsid protein VP1

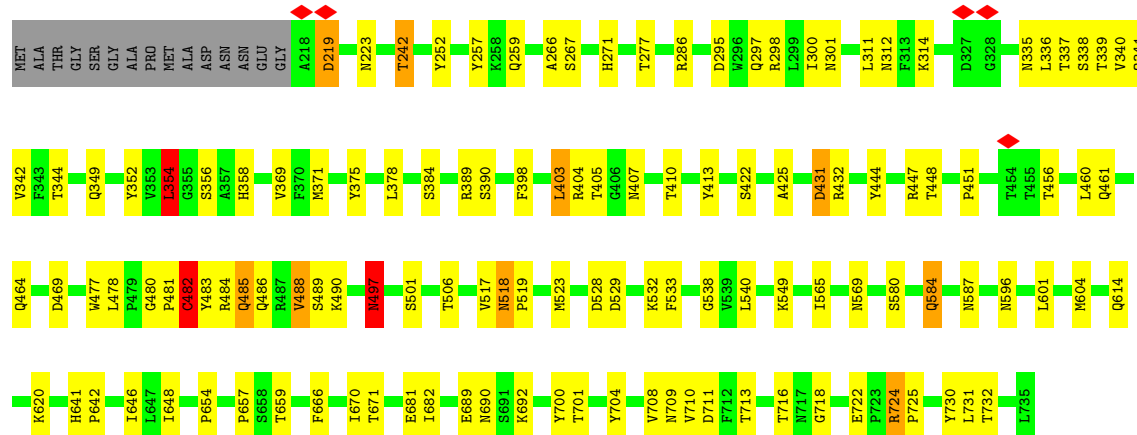




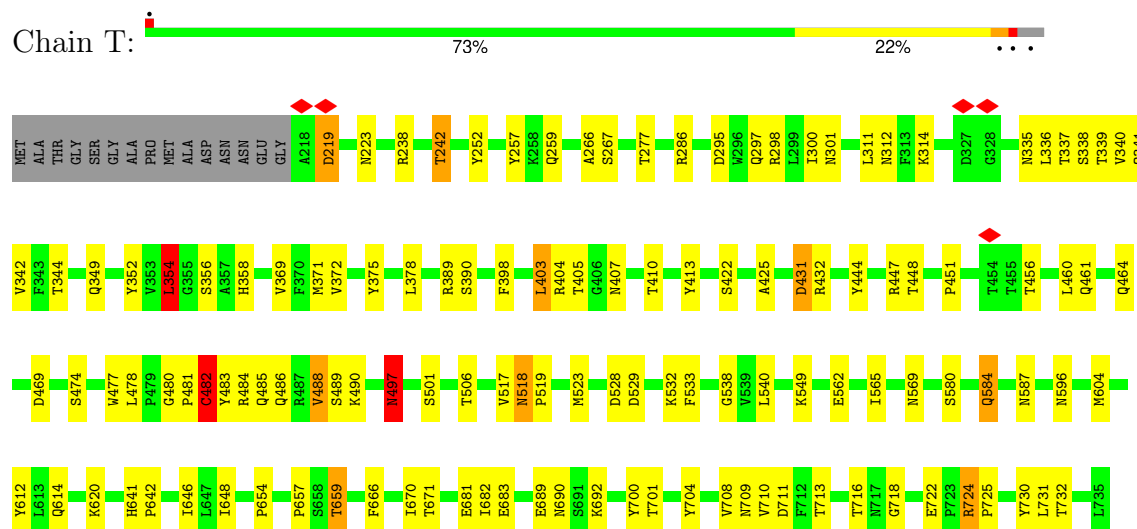
• Molecule 1: Capsid protein VP1



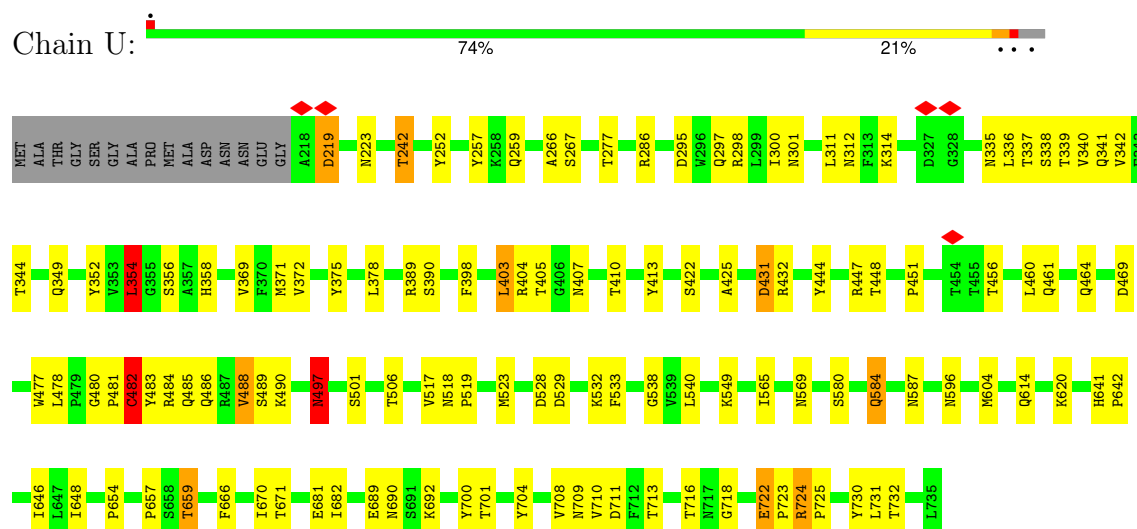
• Molecule 1: Capsid protein VP1



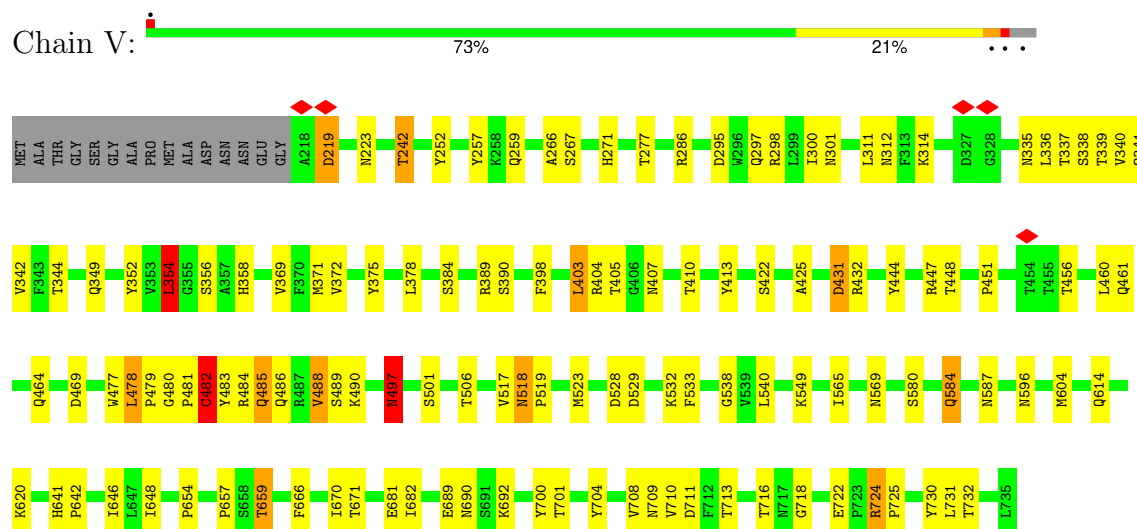
• Molecule 1: Capsid protein VP1



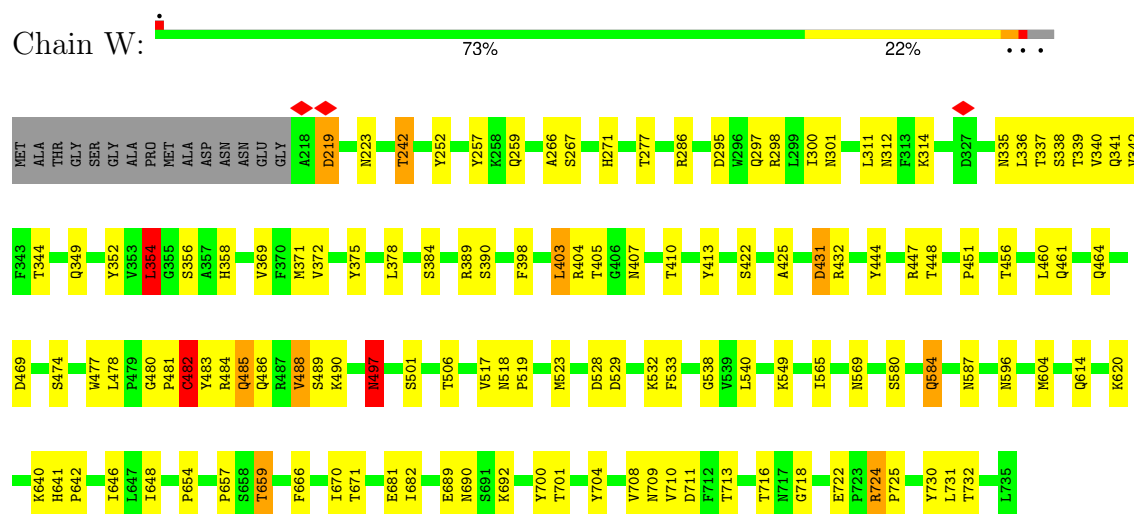
• Molecule 1: Capsid protein VP1



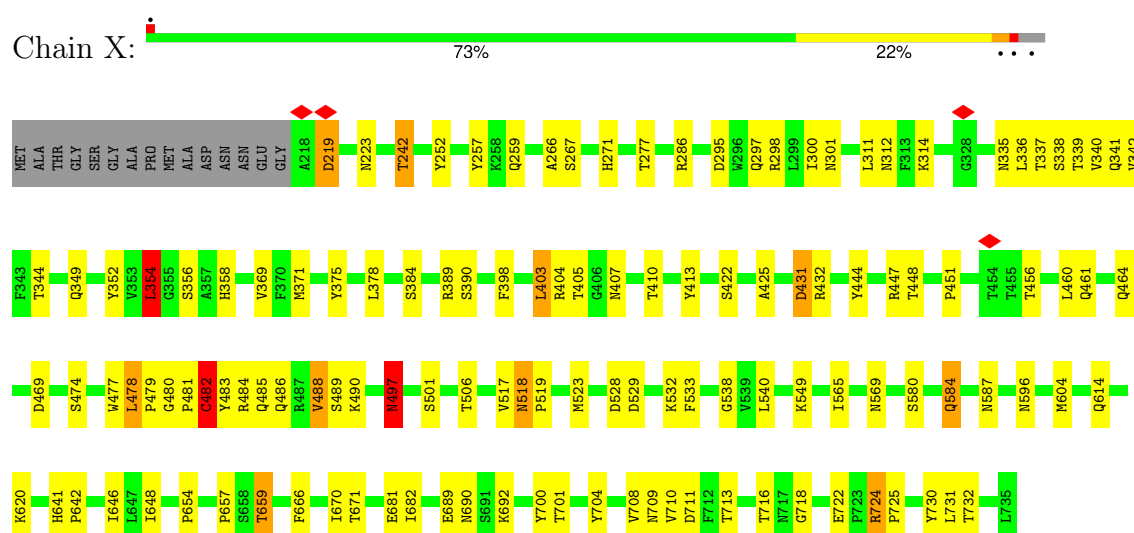
• Molecule 1: Capsid protein VP1



- Molecule 1: Capsid protein VP1



- Molecule 1: Capsid protein VP1

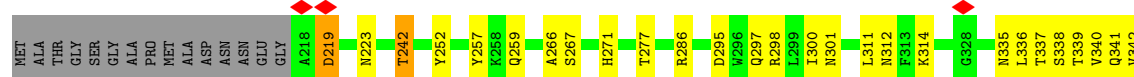


- Molecule 1: Capsid protein VP1

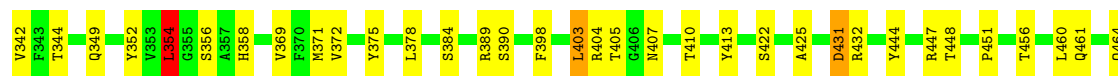




• Molecule 1: Capsid protein VP1

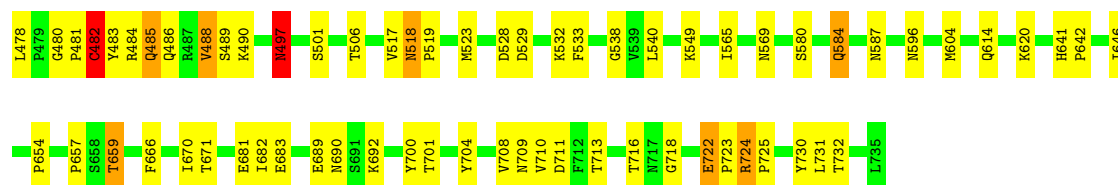


• Molecule 1: Capsid protein VP1

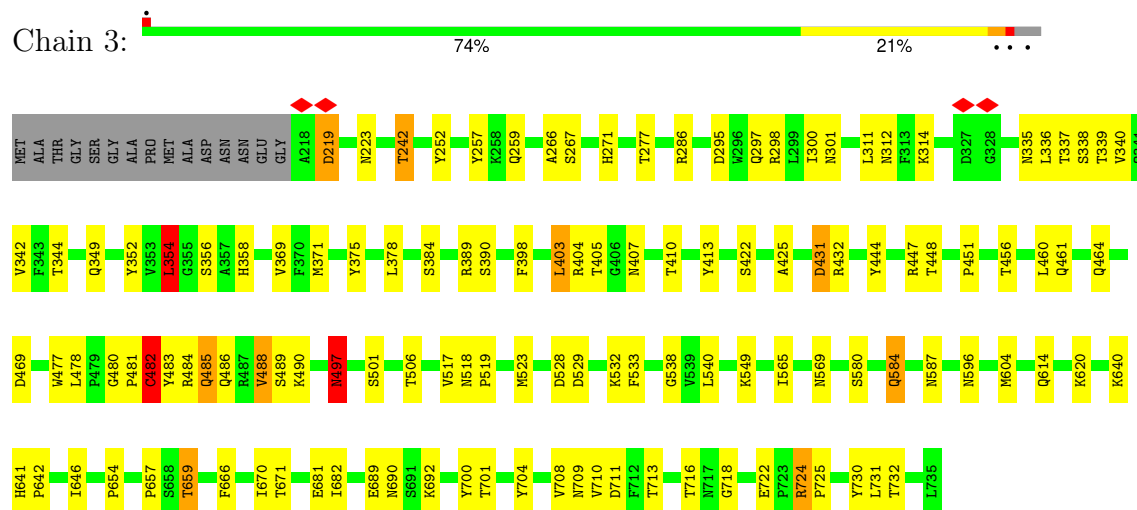


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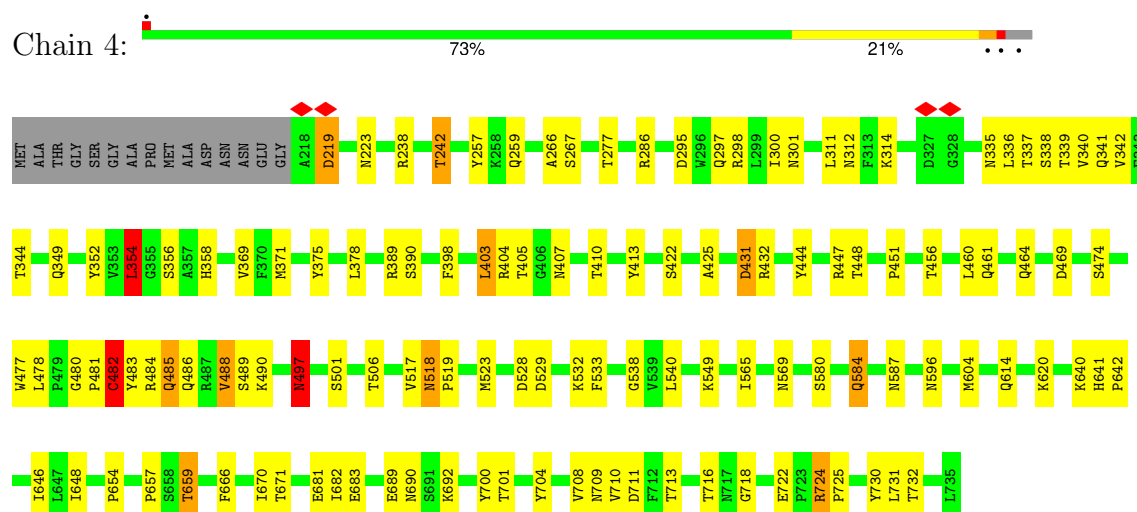




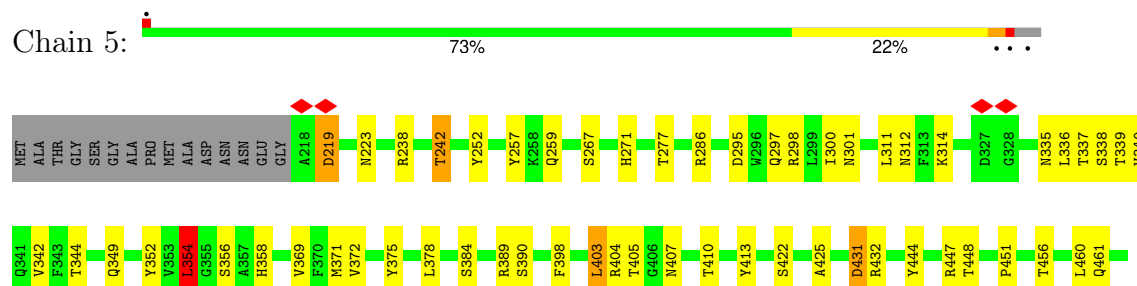
• Molecule 1: Capsid protein VP1

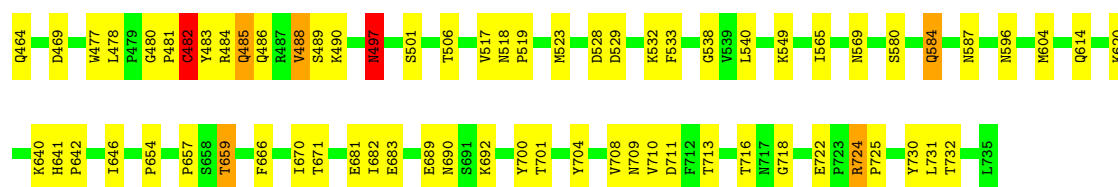


• Molecule 1: Capsid protein VP1

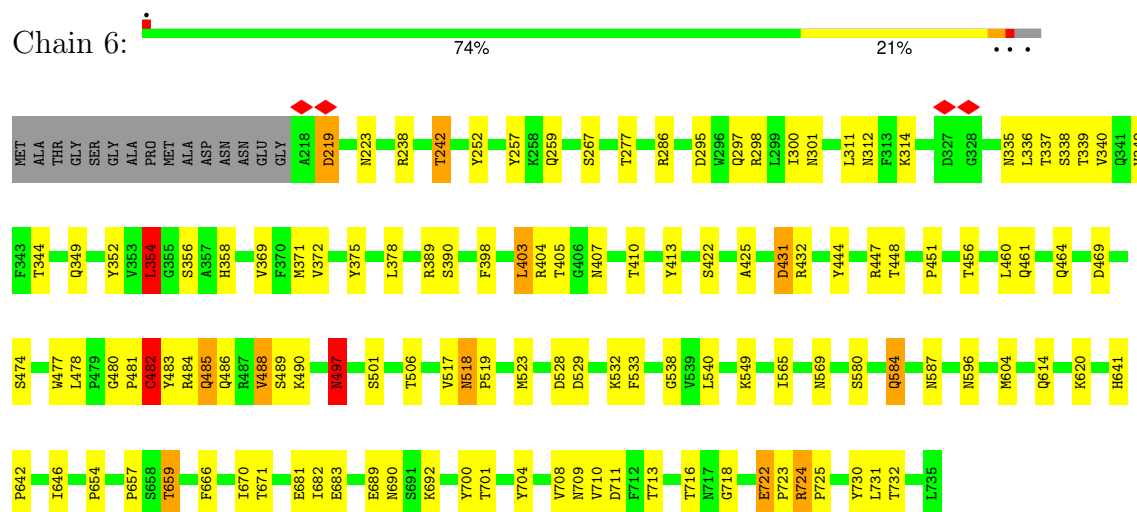


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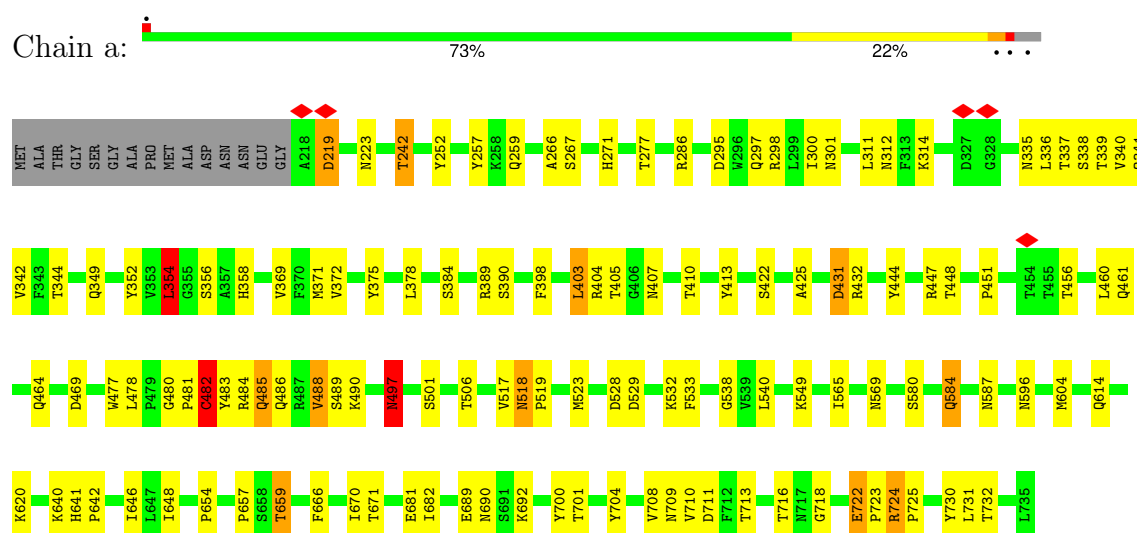




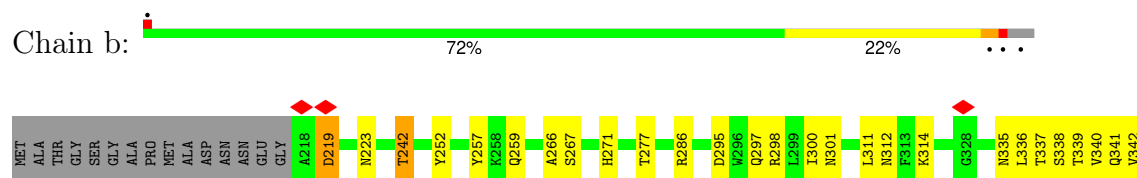
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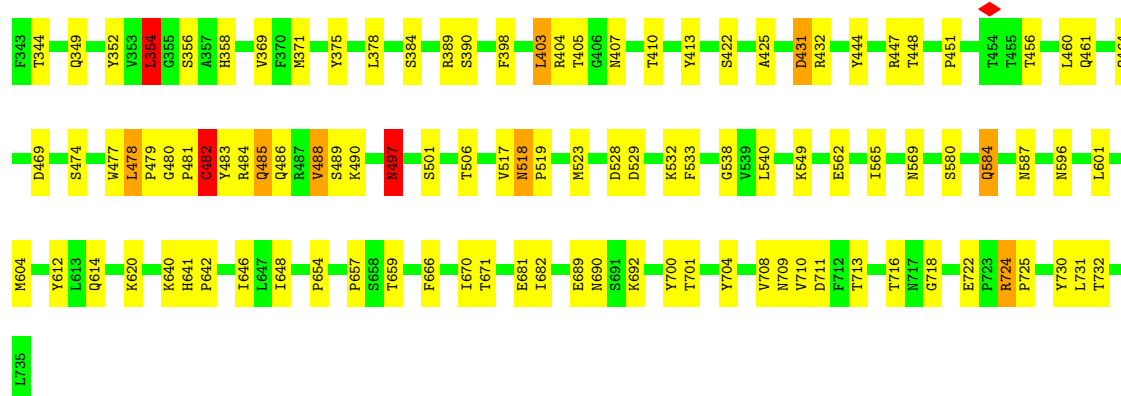


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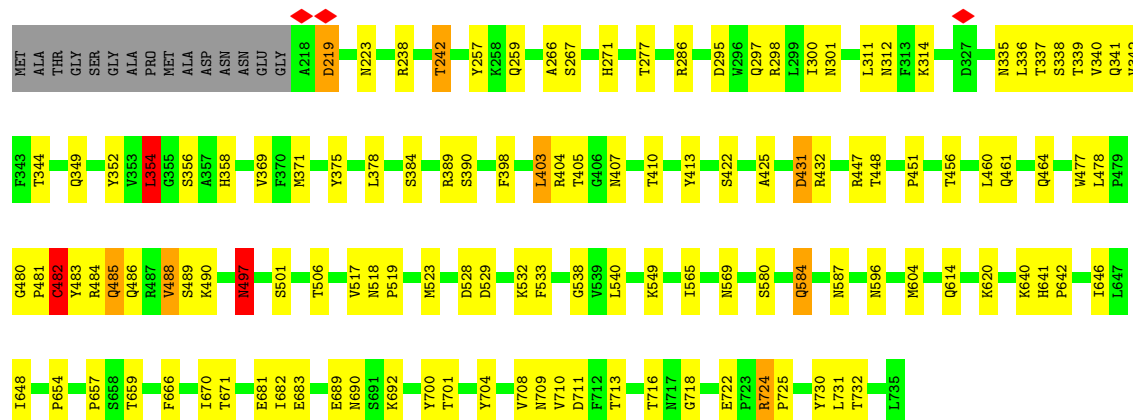
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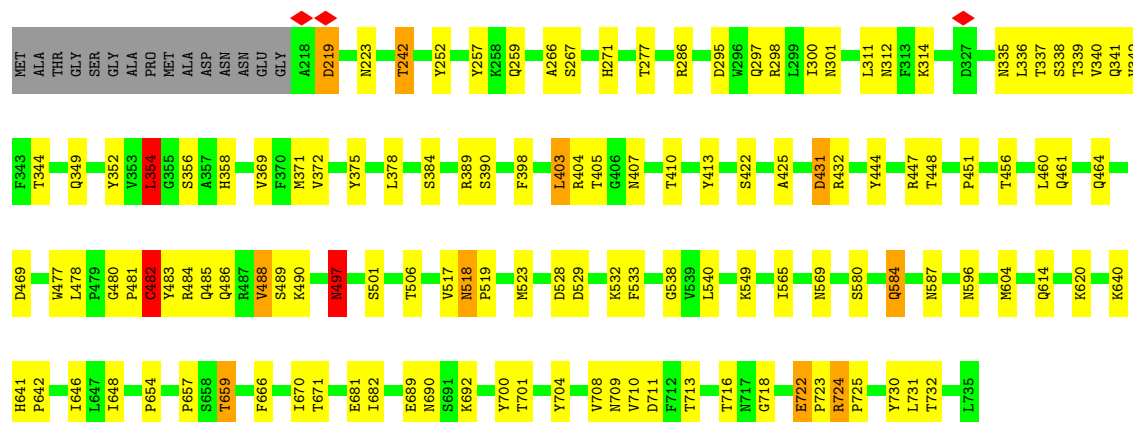
• Molecule 1: Capsid protein VP1

Chain c: 74% 22%



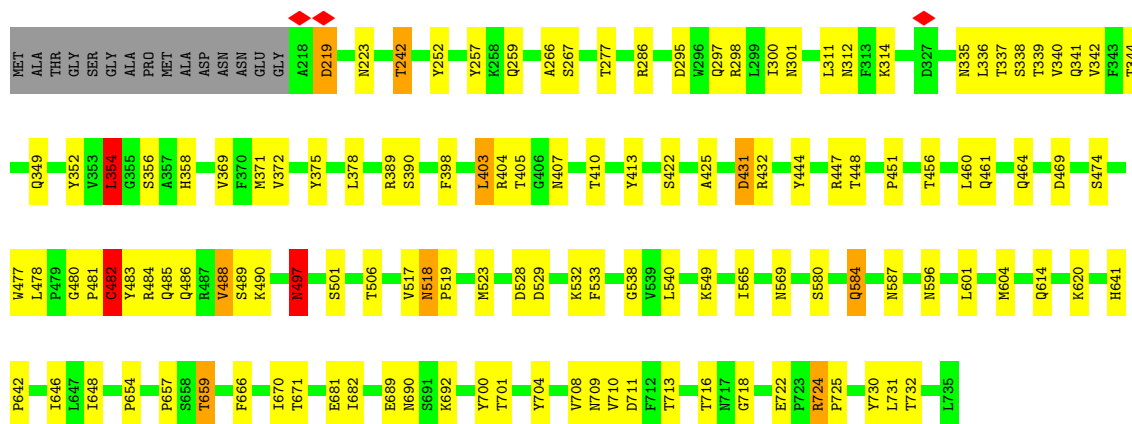
• Molecule 1: Capsid protein VP1

Chain d: 73% 22%

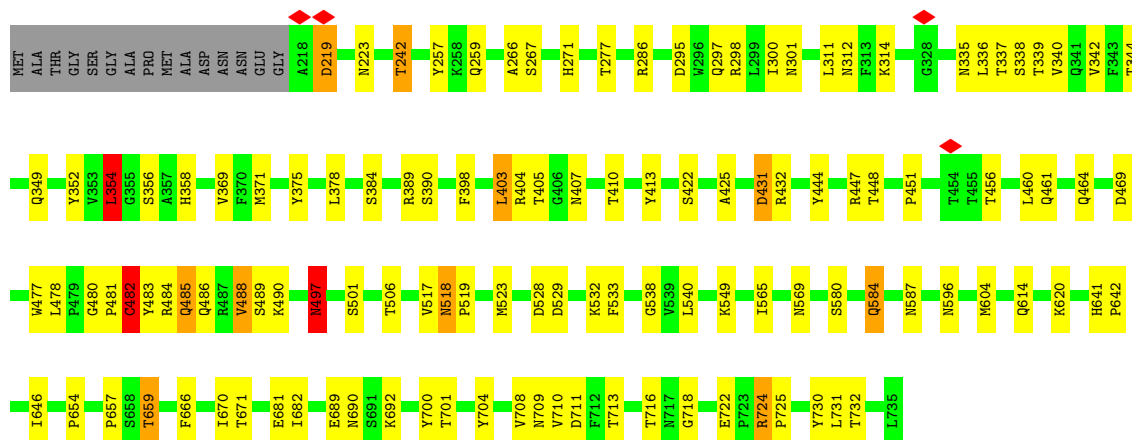


• Molecule 1: Capsid protein VP1

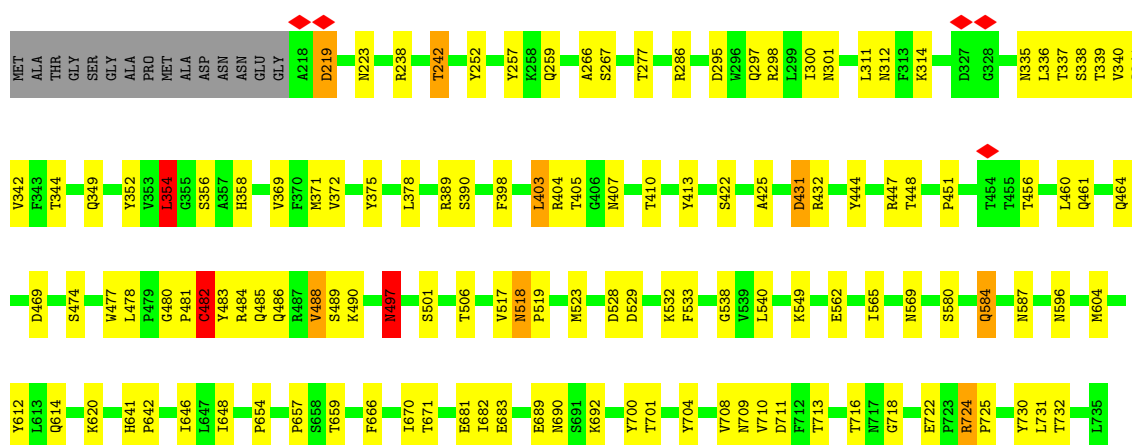
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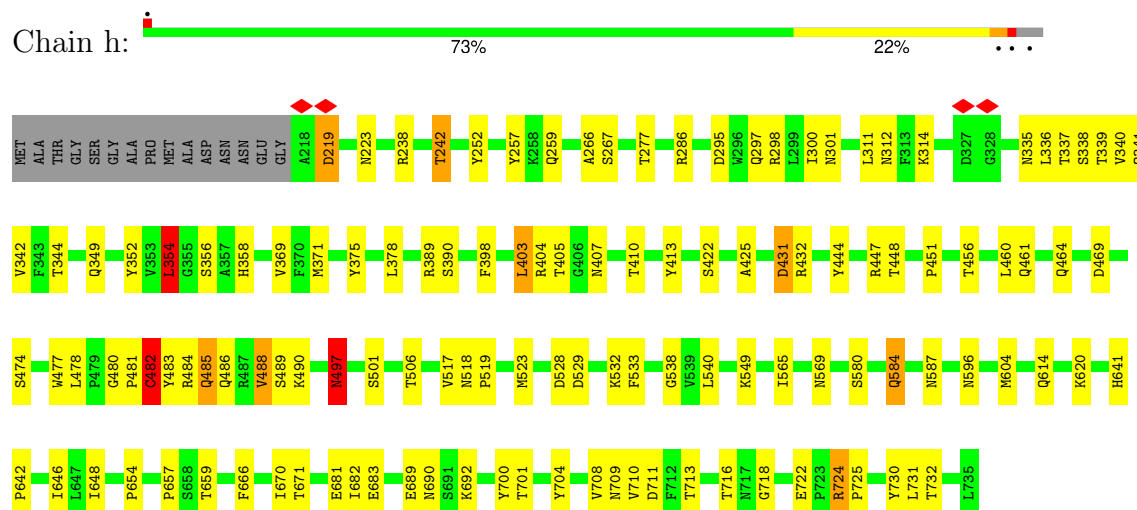
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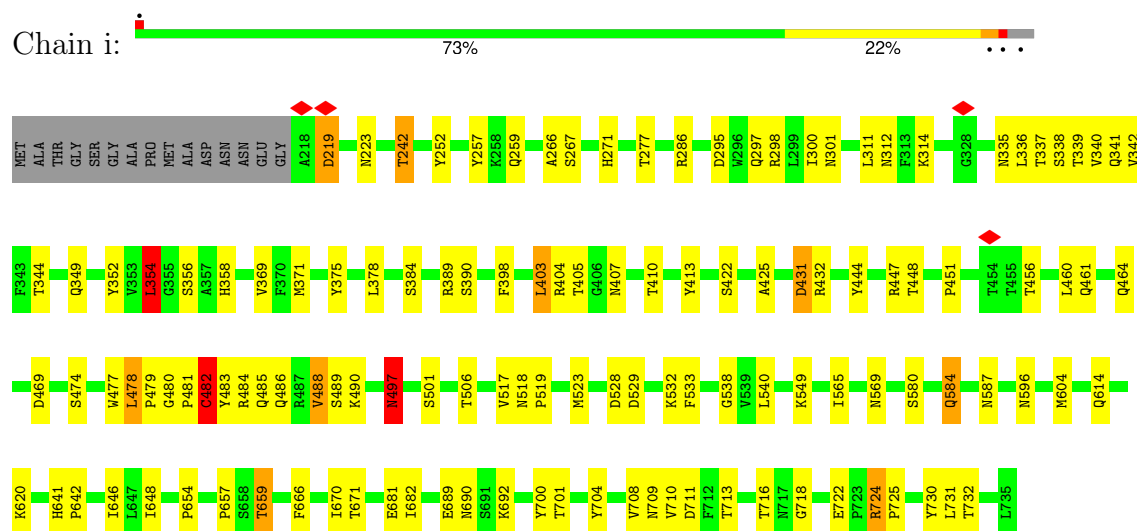
• Molecule 1: Capsid protein VP1



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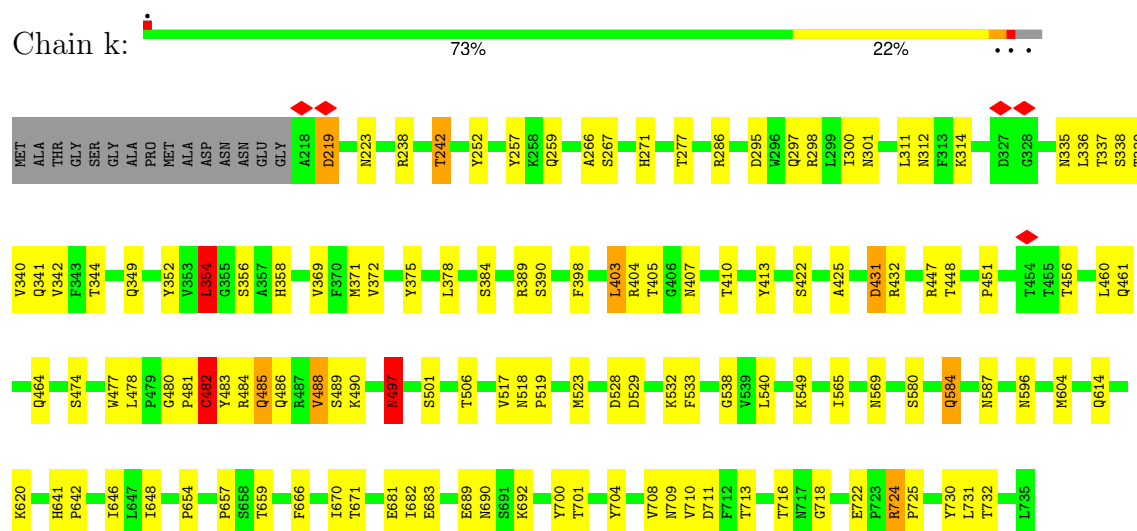
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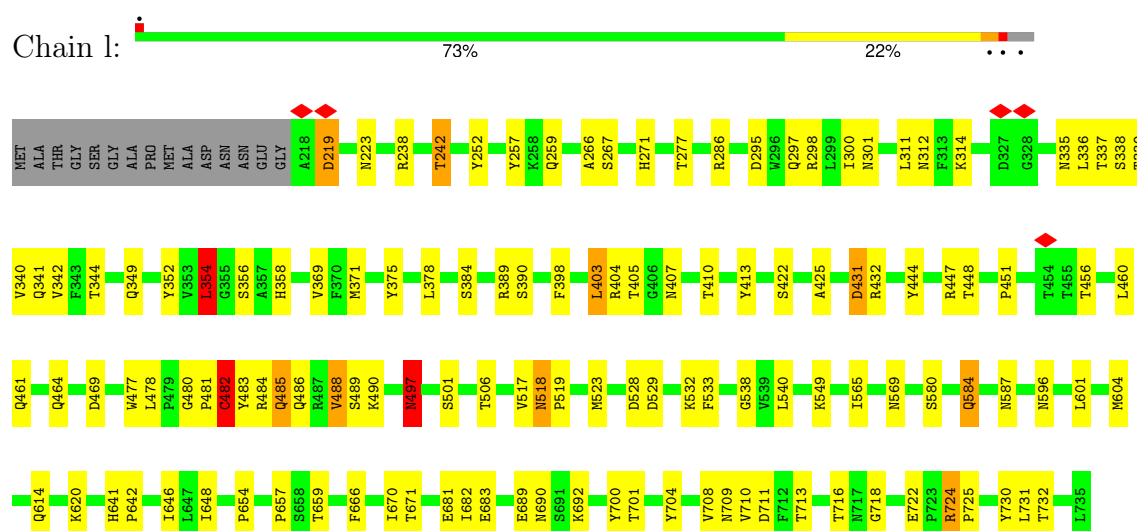
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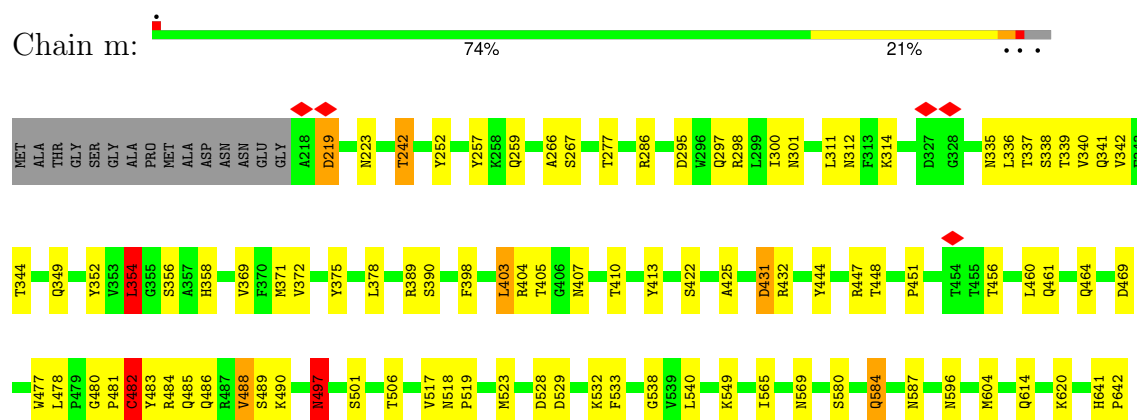
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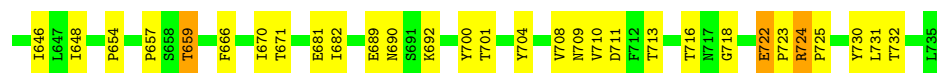


- Molecule 1: Capsid protein VP1



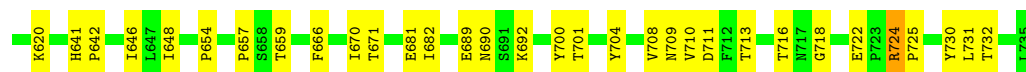
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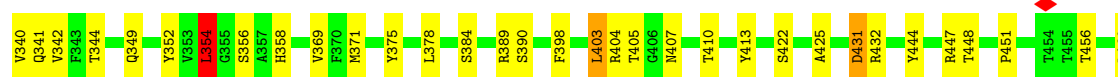
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Chain n: 73% 22%



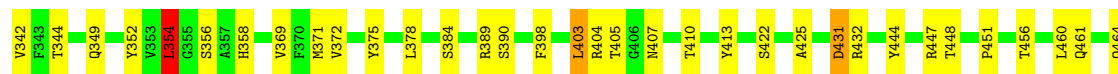
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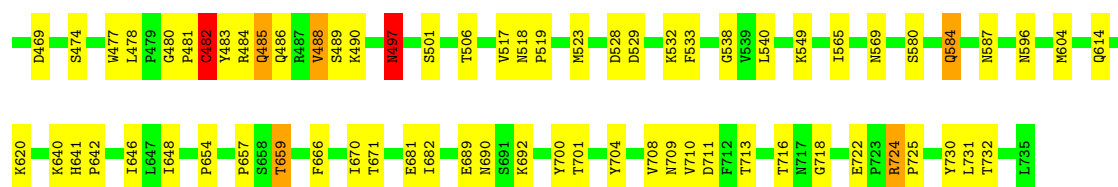
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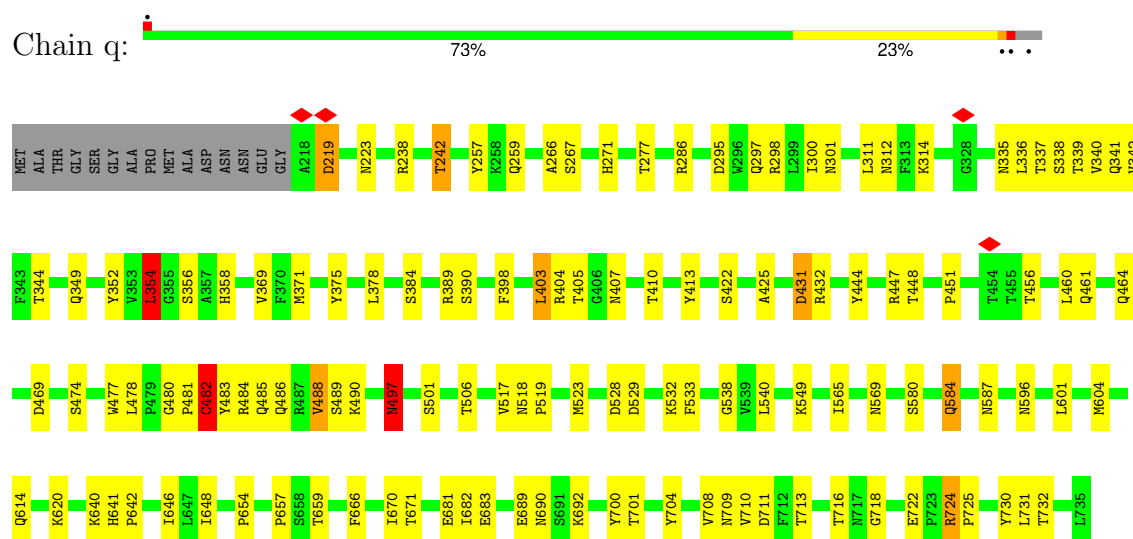
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Chain p: 73% 22%

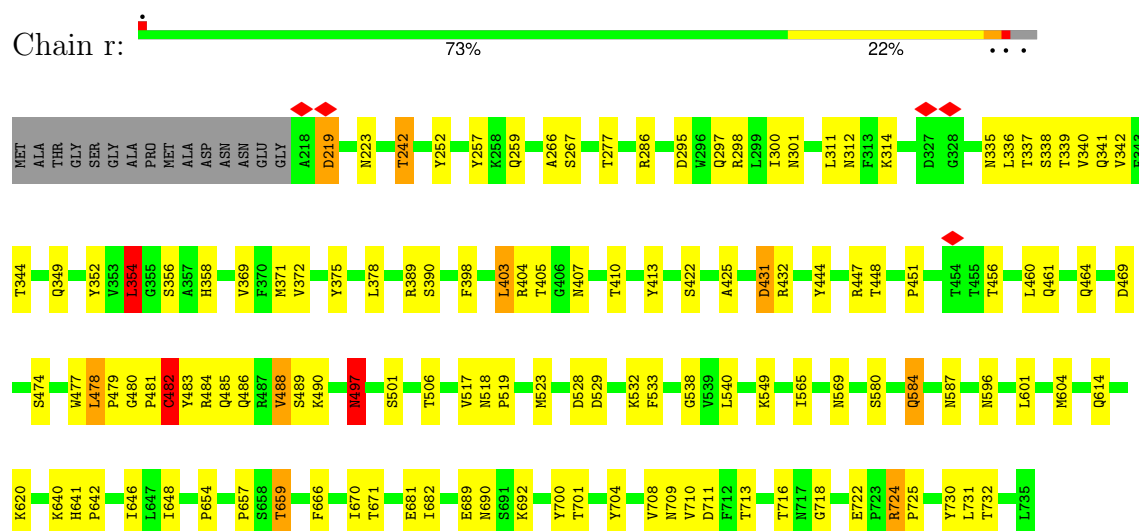




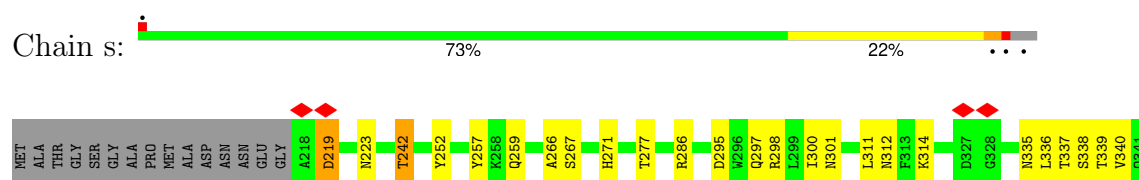
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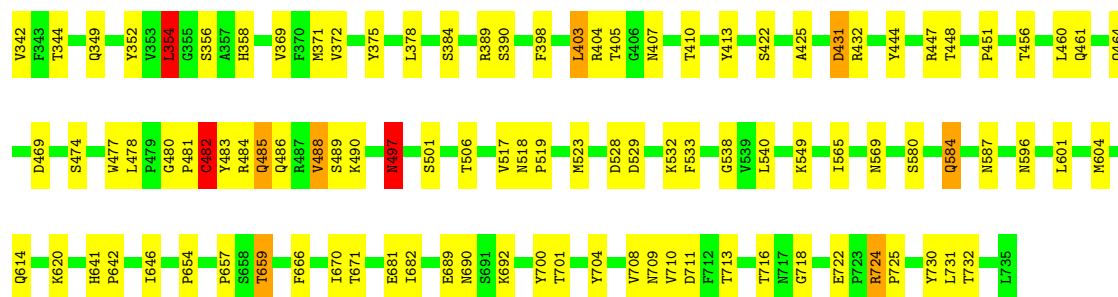


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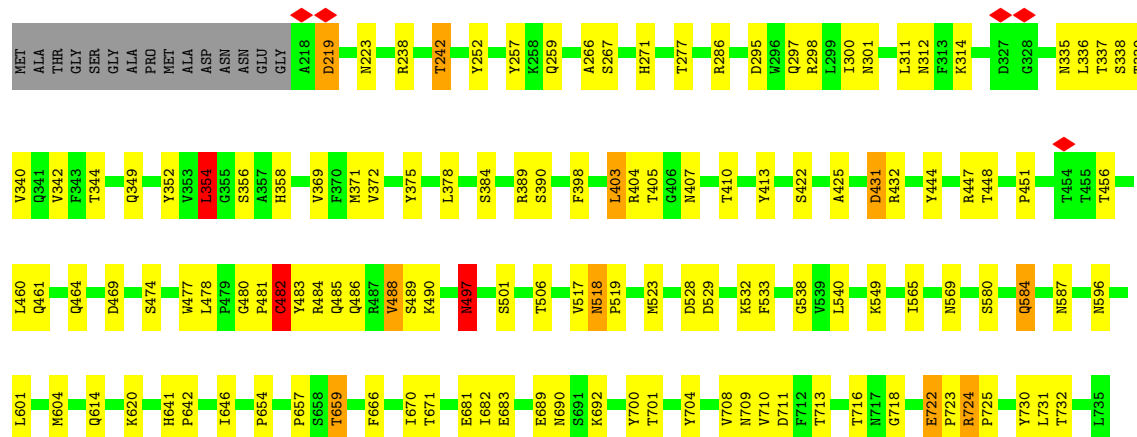


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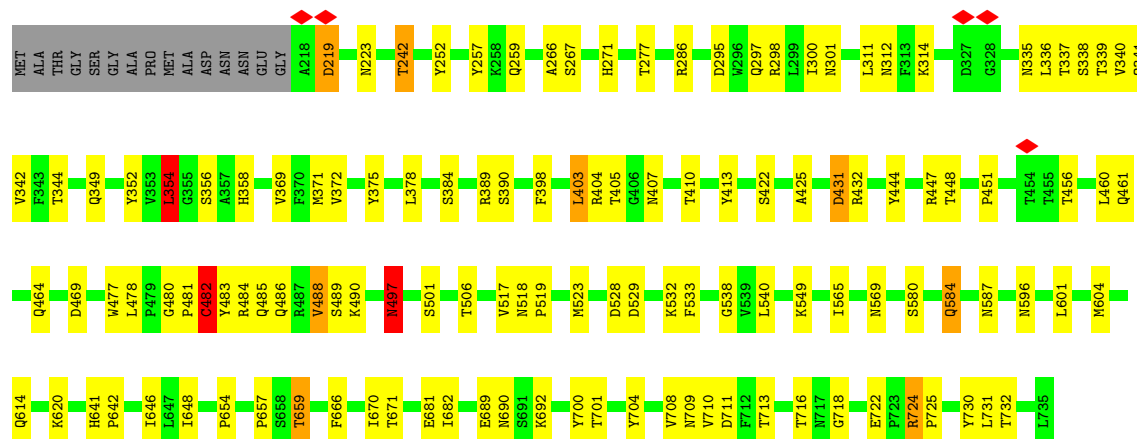




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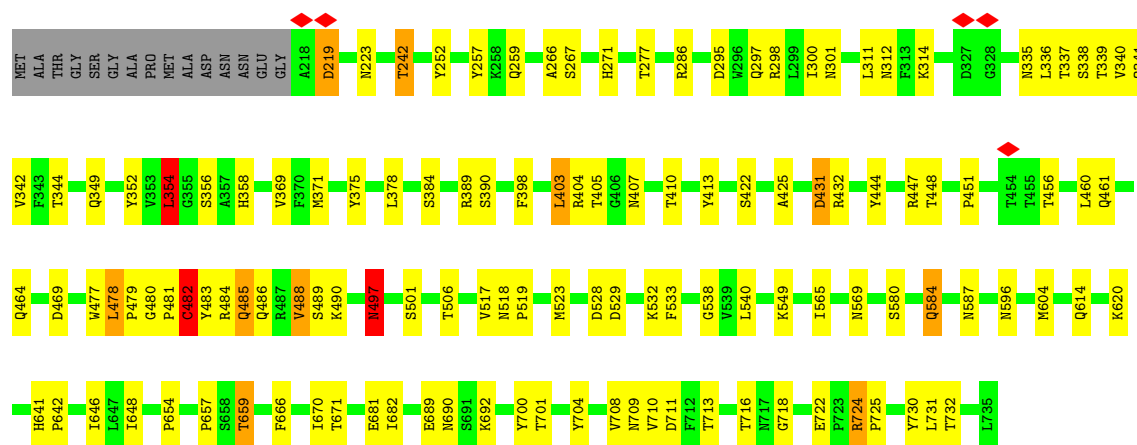


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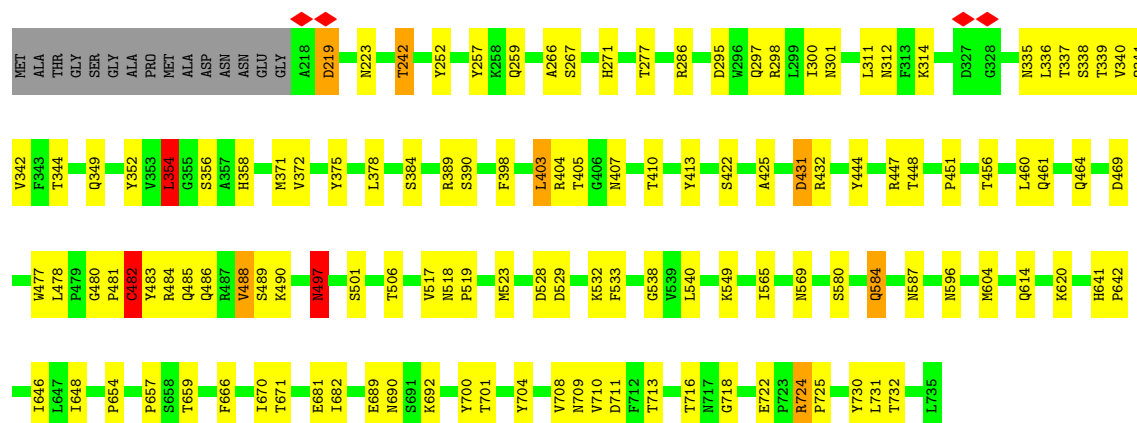


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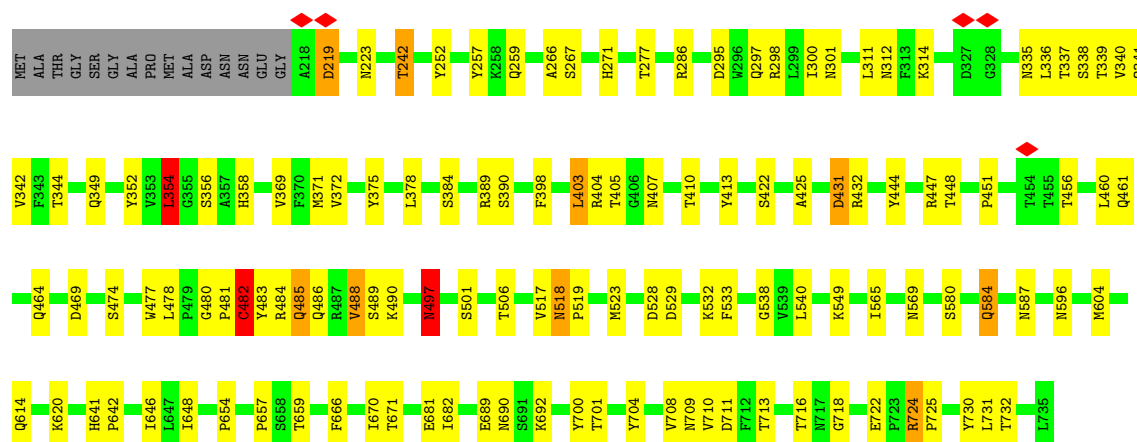




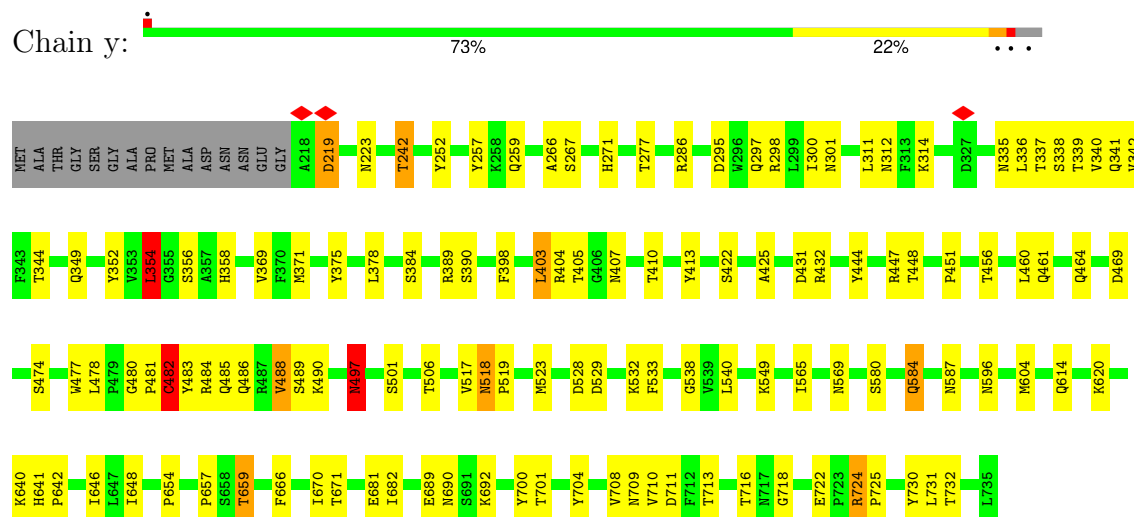
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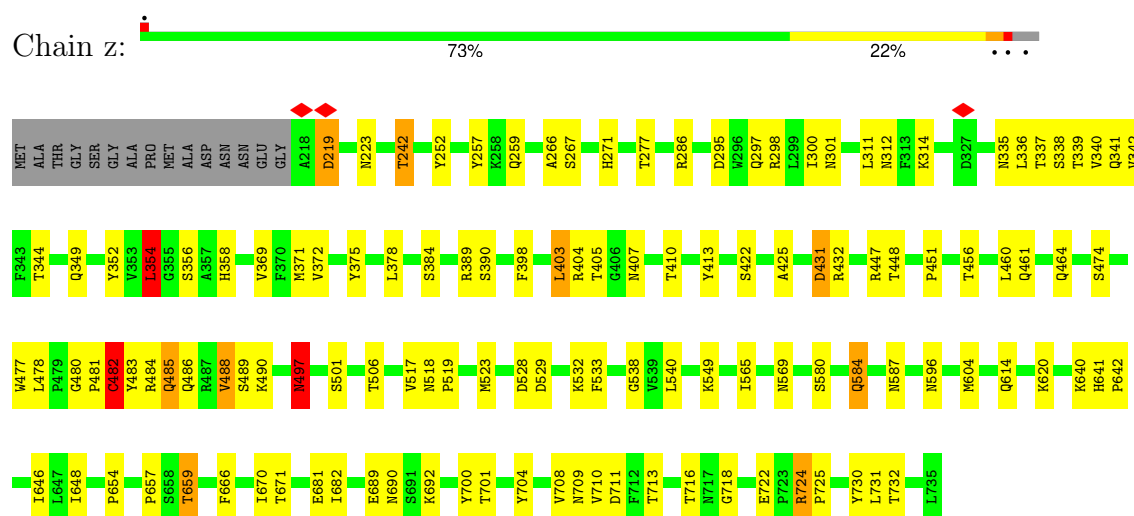
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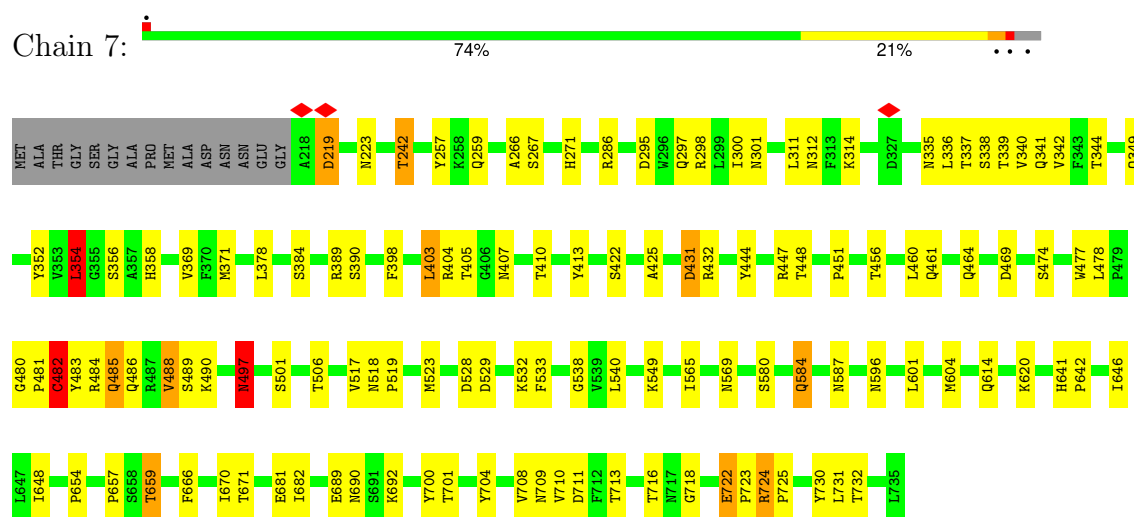
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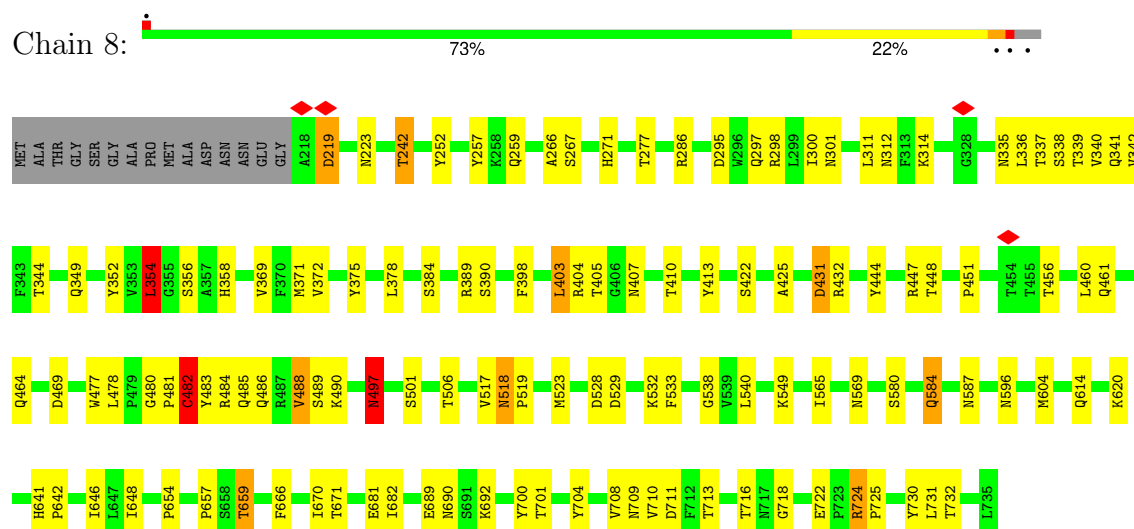
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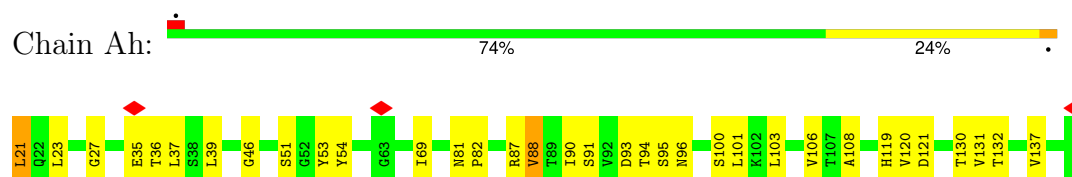
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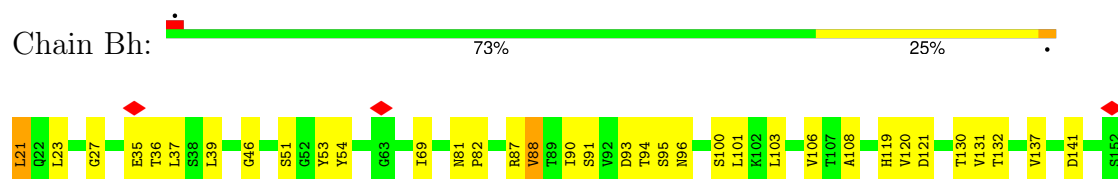
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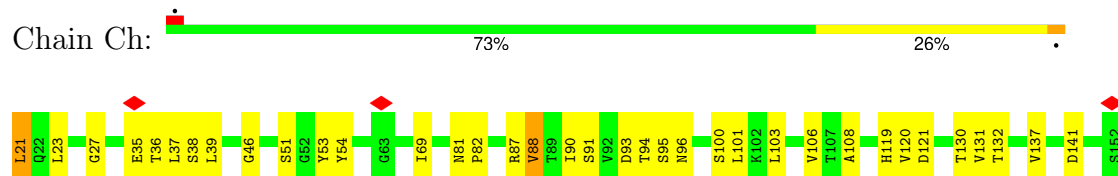
- Molecule 2: Fab3-2 IgG Heavy chain



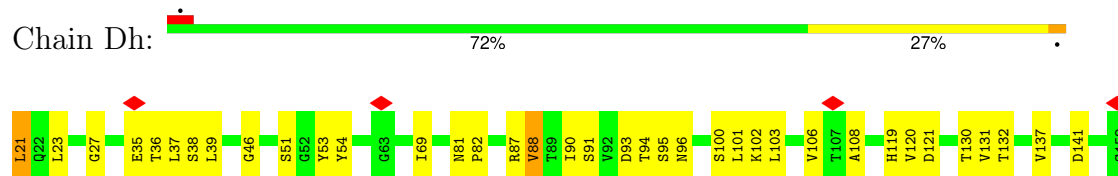
- Molecule 2: Fab3-2 IgG Heavy chain



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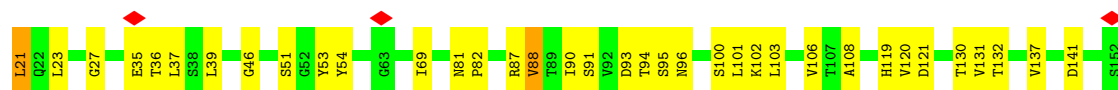


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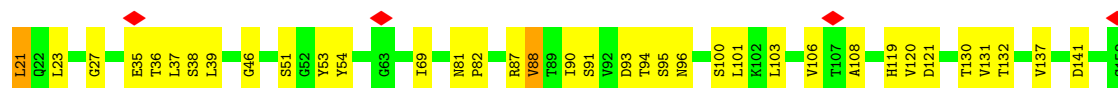


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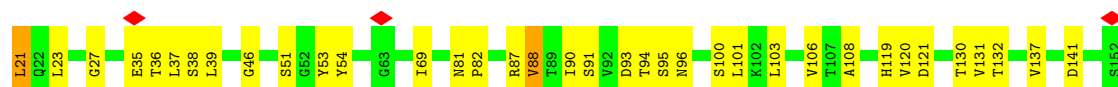




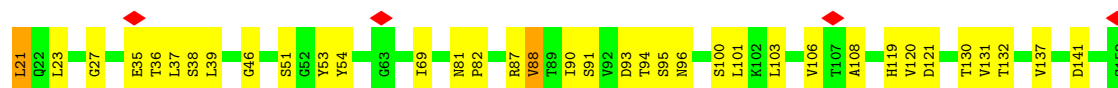
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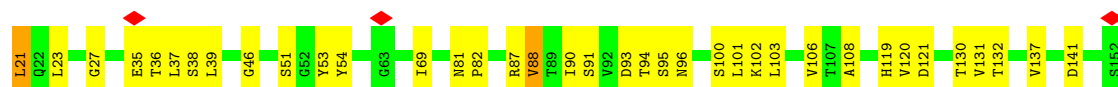
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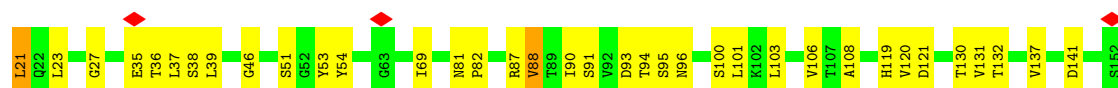
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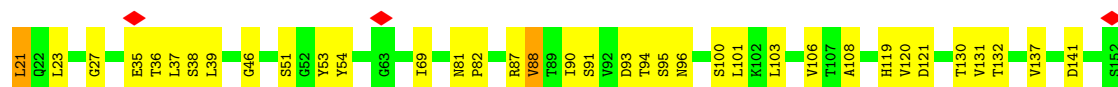
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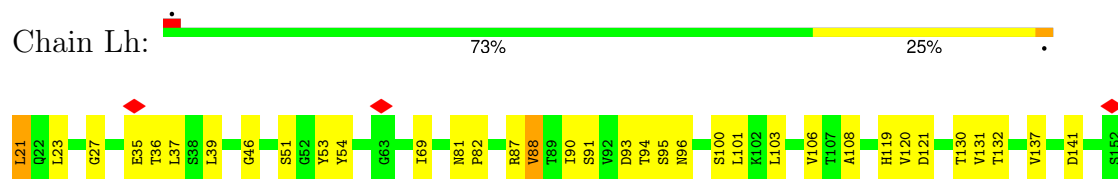
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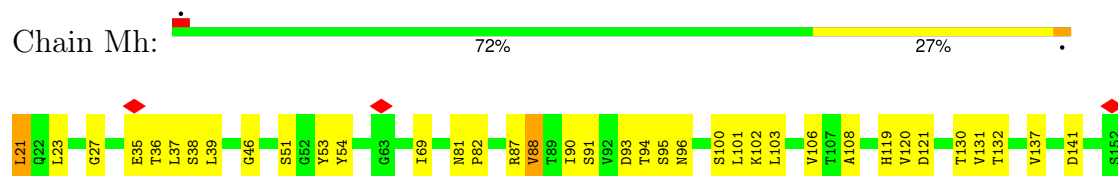
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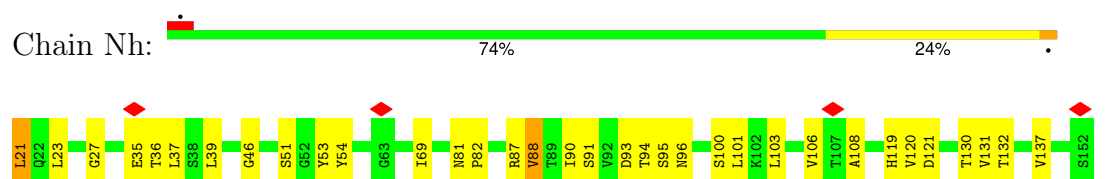
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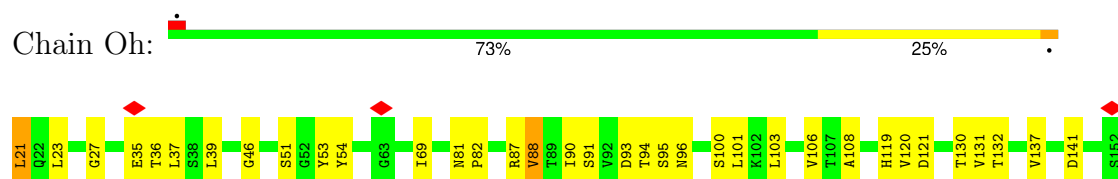
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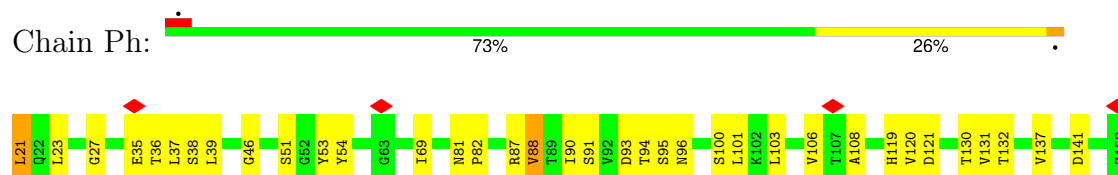
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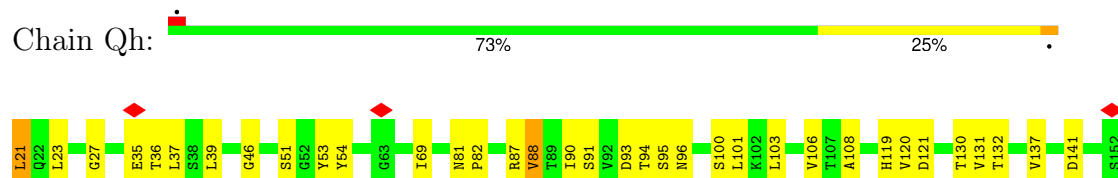
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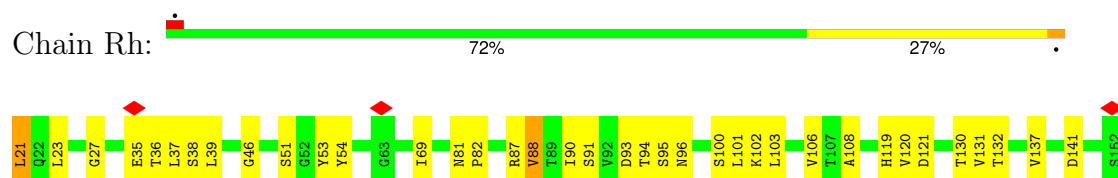
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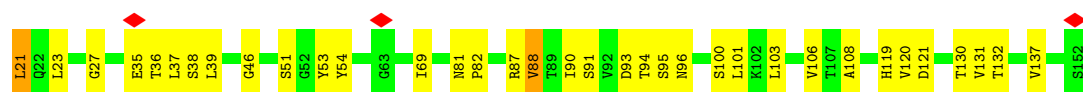
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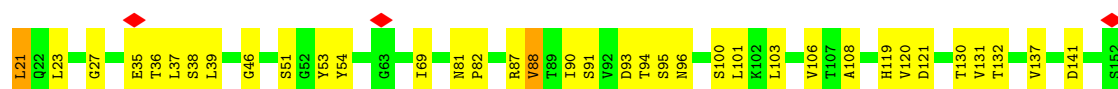
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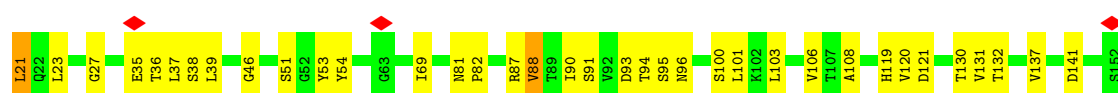
● Molecule 2: Fab3-2 IgG Heavy chain

Chain Sh:  73% 25%

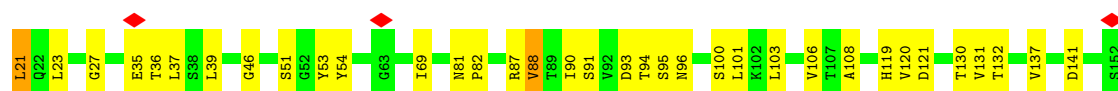
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Chain Th:  73% 26%

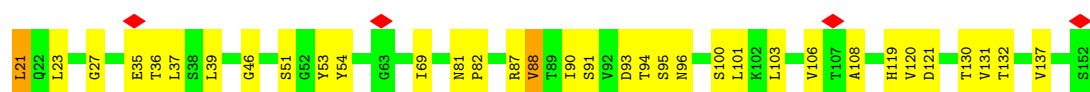
● Molecule 2: Fab3-2 IgG Heavy chain

Chain Uh:  73% 26%

● Molecule 2: Fab3-2 IgG Heavy chain

Chain Vh:  73% 25%

● Molecule 2: Fab3-2 IgG Heavy chain

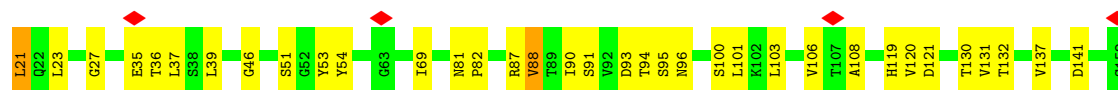
Chain Wh:  74% 24%

● Molecule 2: Fab3-2 IgG Heavy chain

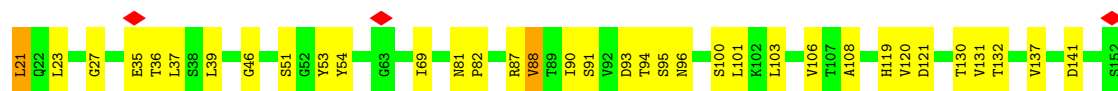
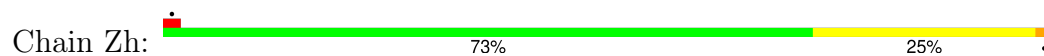
Chain Xh:  73% 25%

● Molecule 2: Fab3-2 IgG Heavy chain

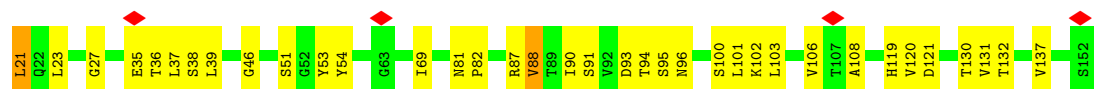
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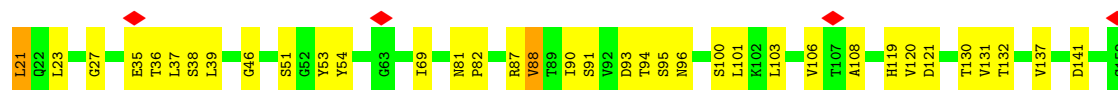
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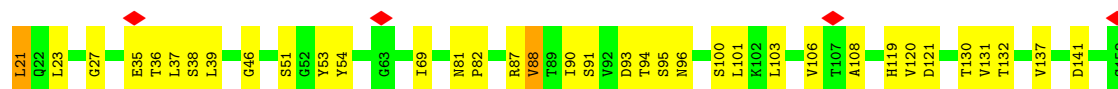
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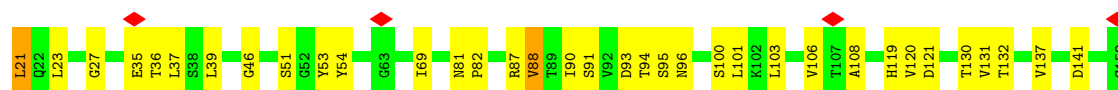
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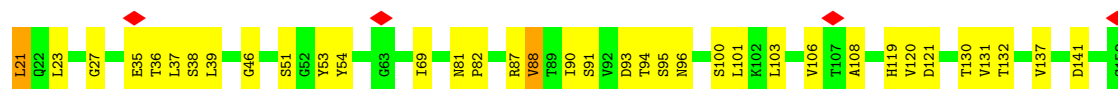
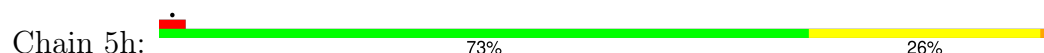
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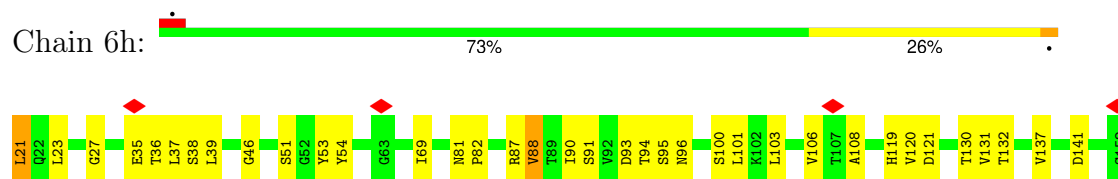
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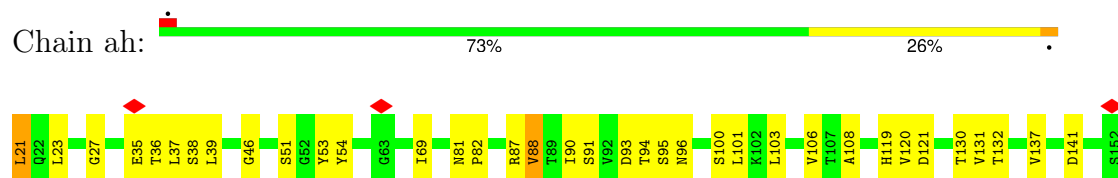
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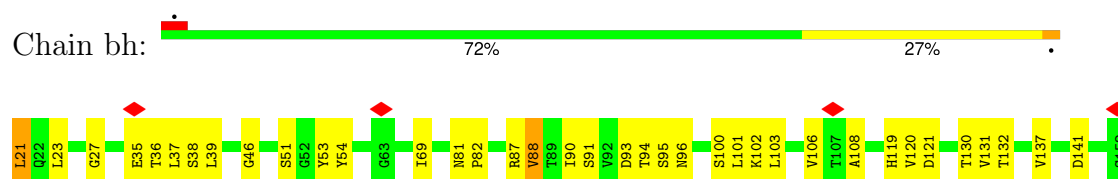
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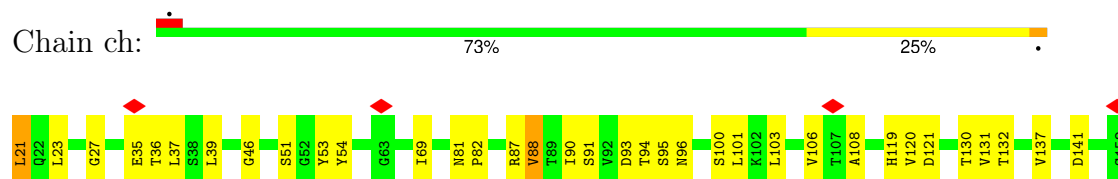
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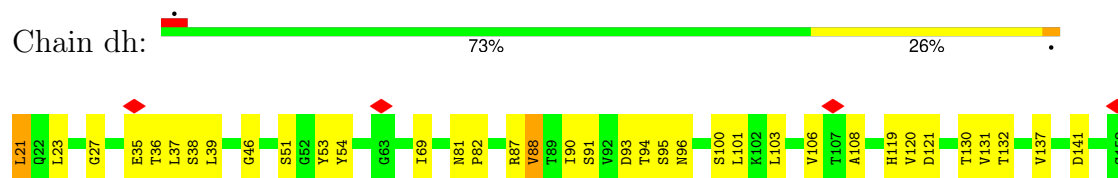
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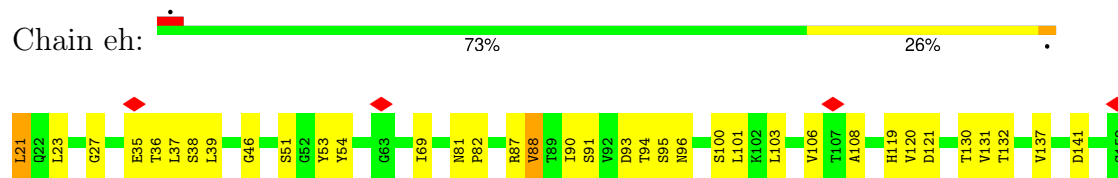
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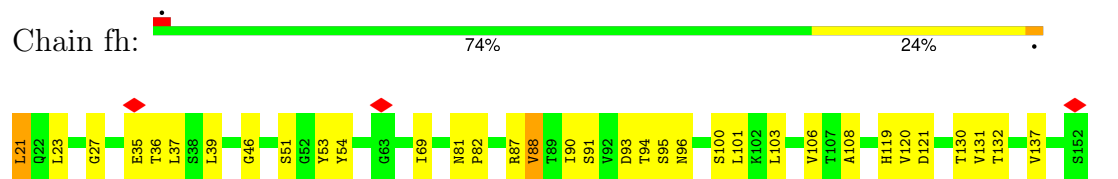
- Molecule 2: Fab3-2 IgG Heavy chain



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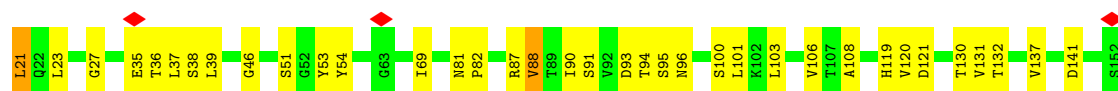


- Molecule 2: Fab3-2 IgG Heavy chain



- Molecule 2: Fab3-2 IgG Heavy chain

Chain gh: 



- Molecule 2: Fab3-2 IgG Heavy chain

Chain hh: 



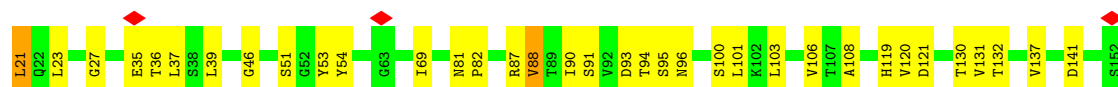
- Molecule 2: Fab3-2 IgG Heavy chain

Chain ih: 



- Molecule 2: Fab3-2 IgG Heavy chain

Chain jh: 



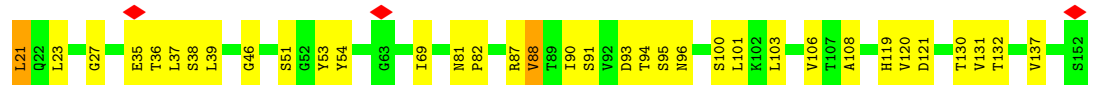
- Molecule 2: Fab3-2 IgG Heavy chain

Chain kh: 



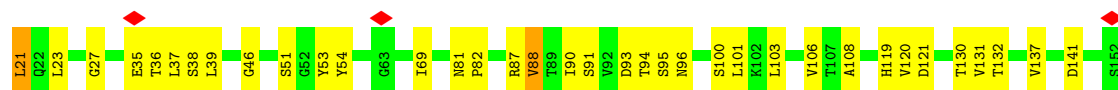
- Molecule 2: Fab3-2 IgG Heavy chain

Chain lh: 

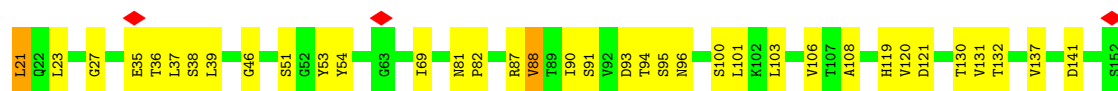


- Molecule 2: Fab3-2 IgG Heavy chain

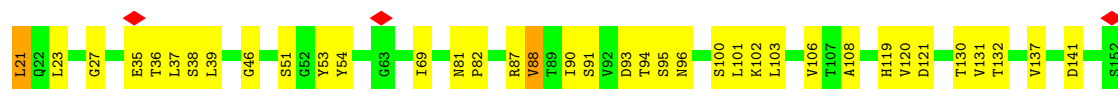
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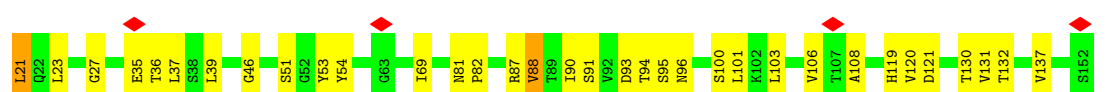
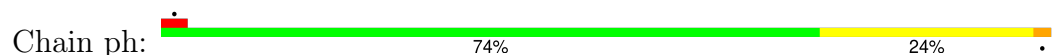
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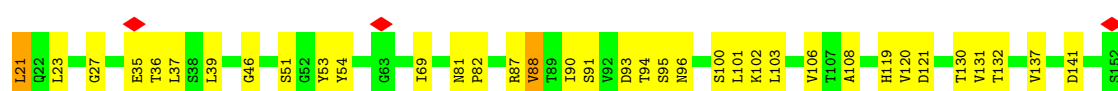
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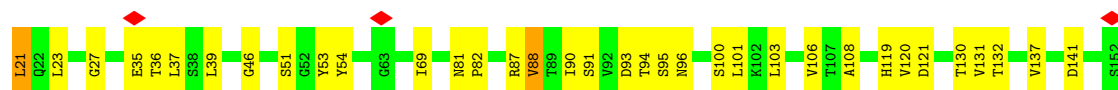
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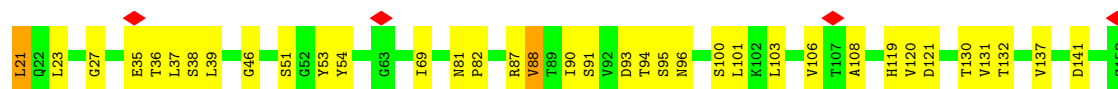
- Molecule 2: Fab3-2 IgG Heavy chain



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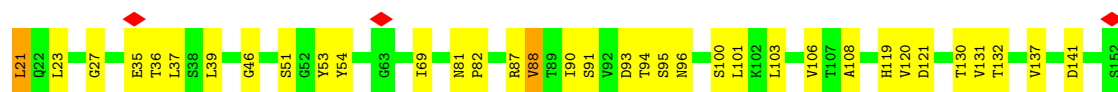


- Molecule 2: Fab3-2 IgG Heavy chain



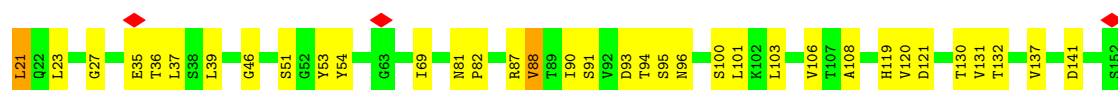
- Molecule 2: Fab3-2 IgG Heavy chain

Chain th:  73% 25%



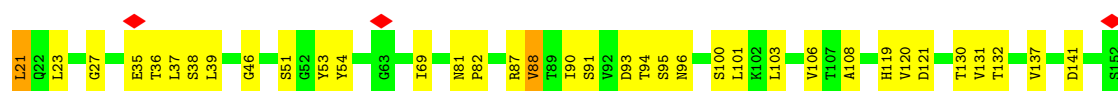
- Molecule 2: Fab3-2 IgG Heavy chain

Chain uh:  73% 25%



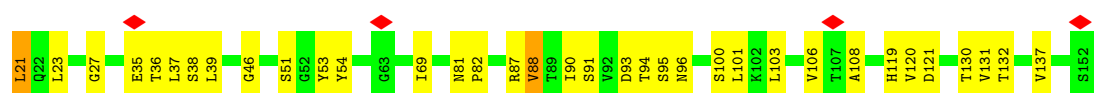
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Chain vh:  73% 26%



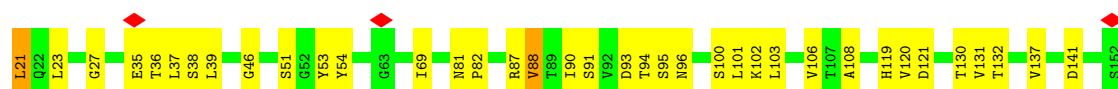
- Molecule 2: Fab3-2 IgG Heavy chain

Chain wh:  73% 25%



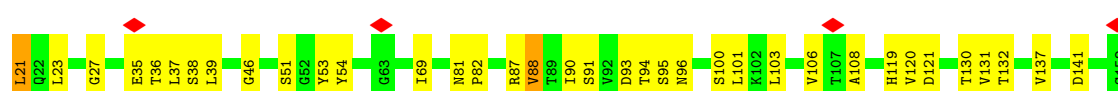
- Molecule 2: Fab3-2 IgG Heavy chain

Chain xh:  72% 27%



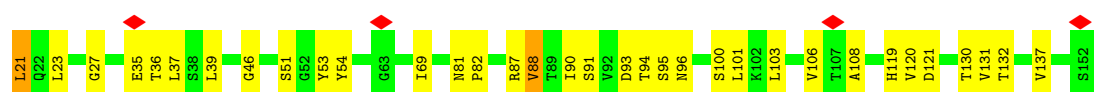
- Molecule 2: Fab3-2 IgG Heavy chain

Chain yh:  73% 26%

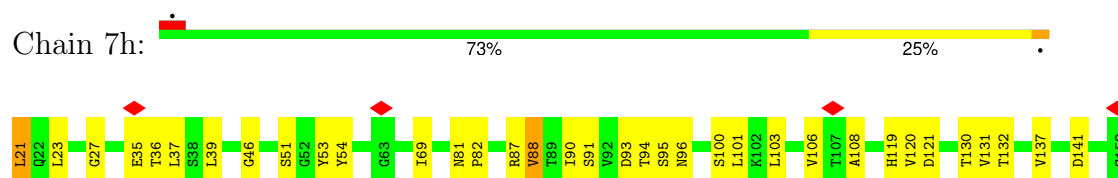


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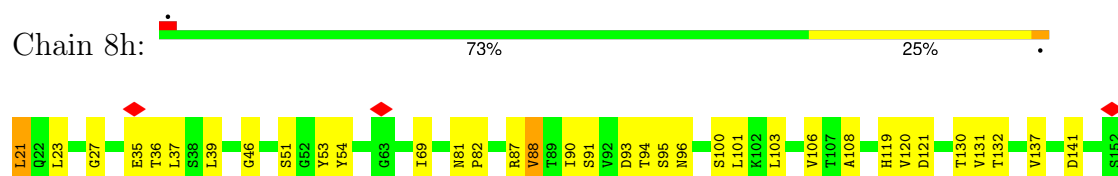
Chain zh:  74% 24%



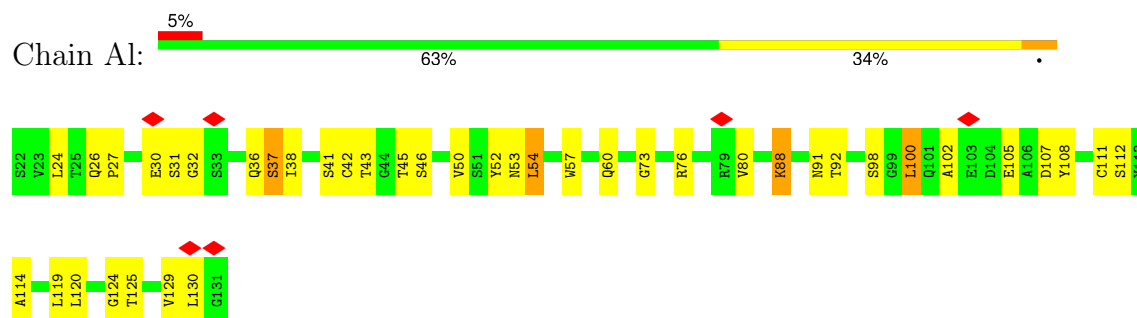
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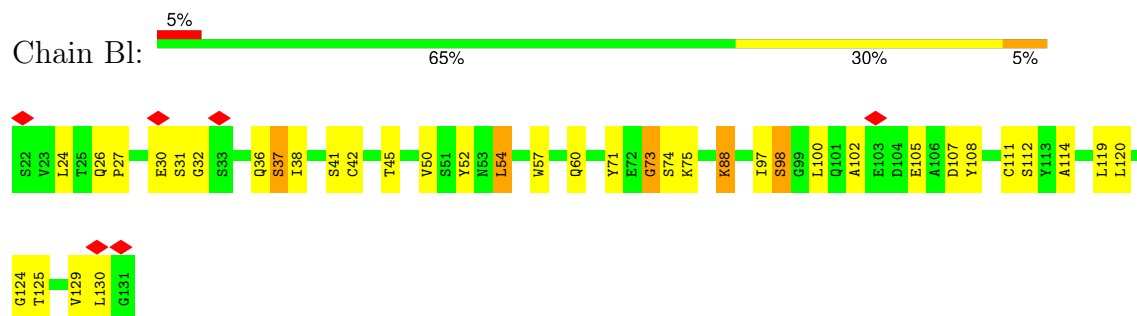
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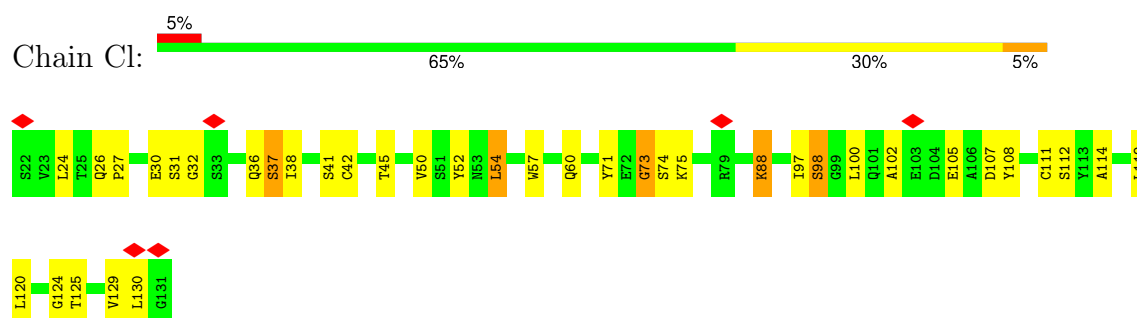
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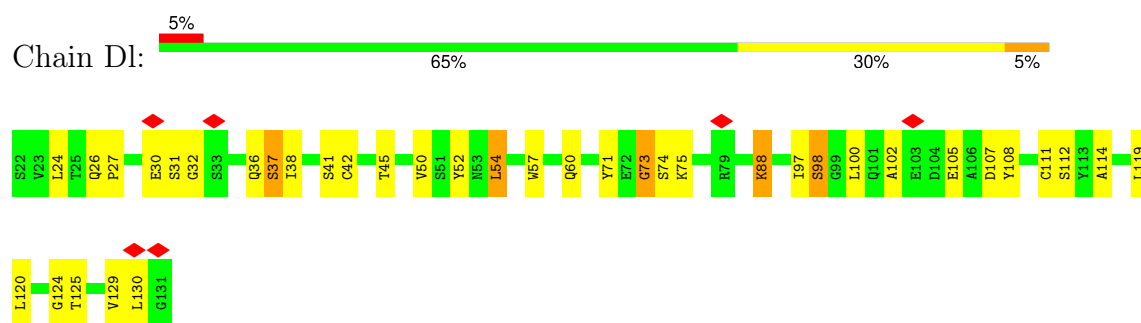
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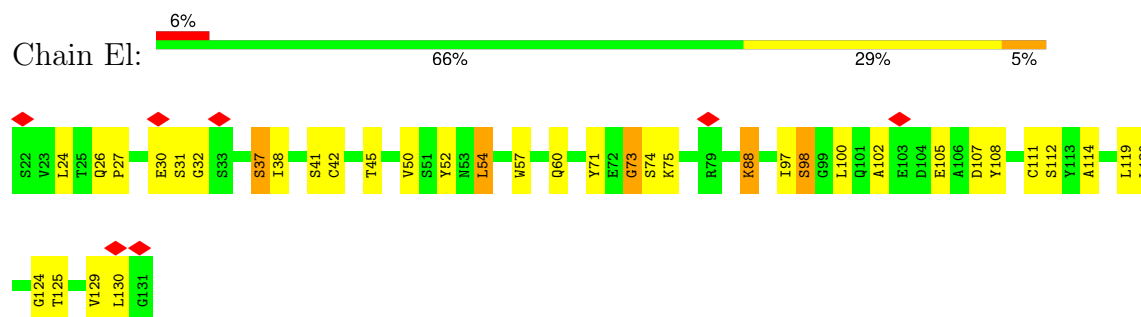
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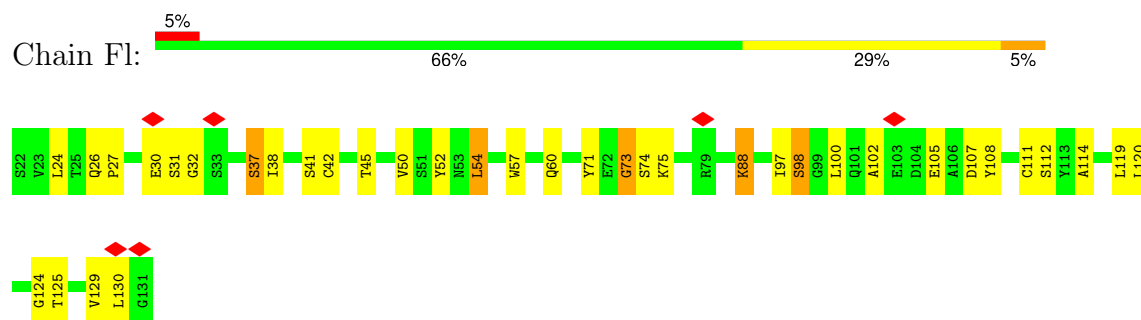
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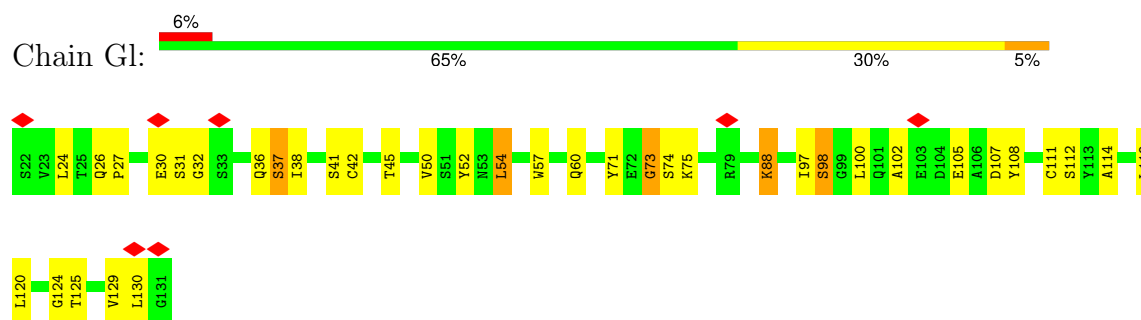
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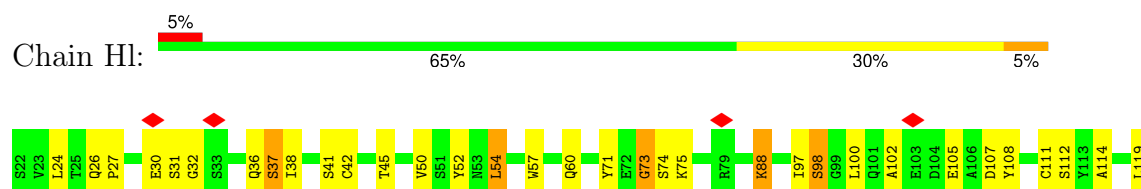
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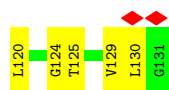


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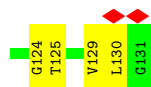


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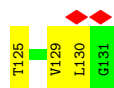




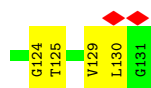
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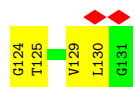
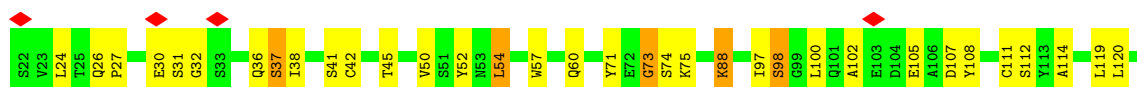
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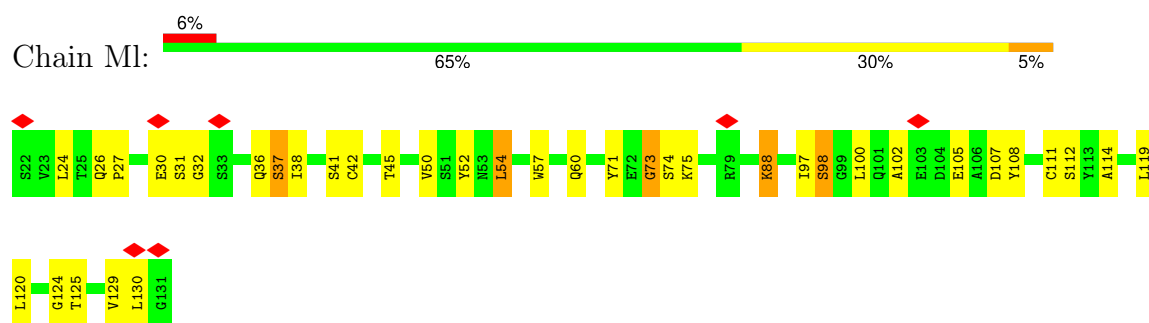
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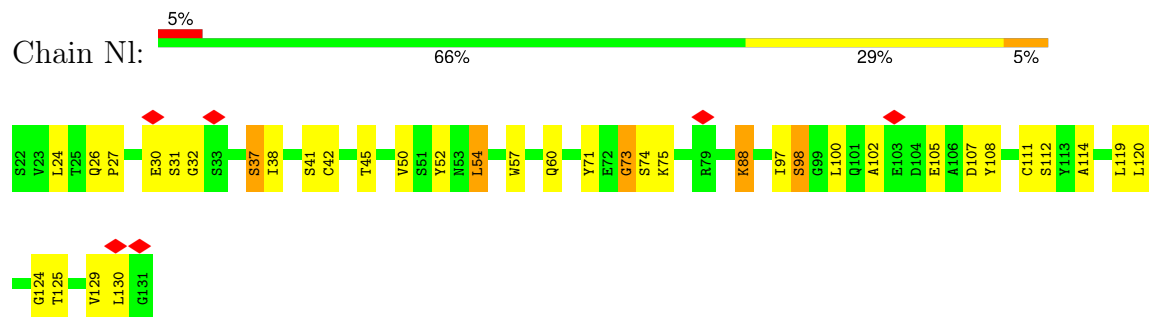
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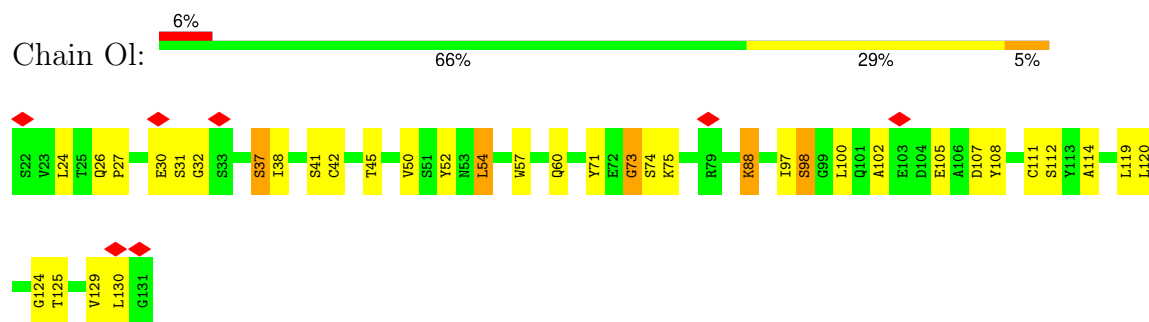
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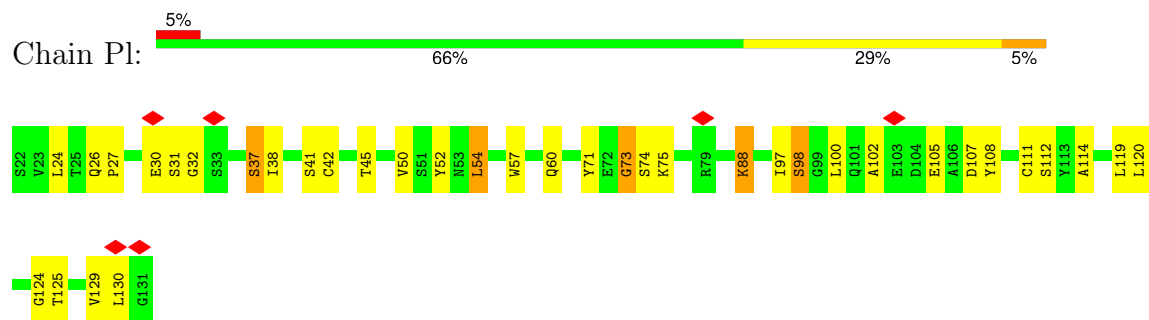
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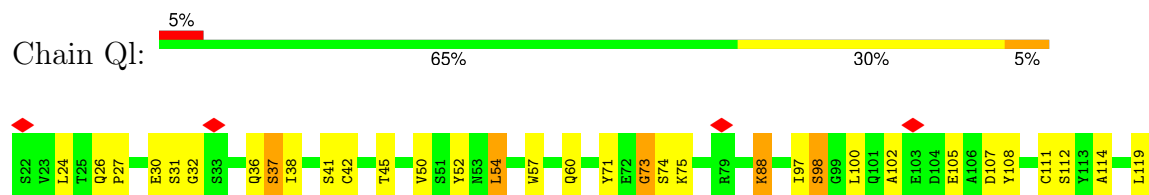
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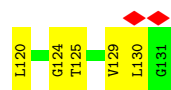


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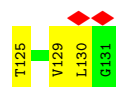
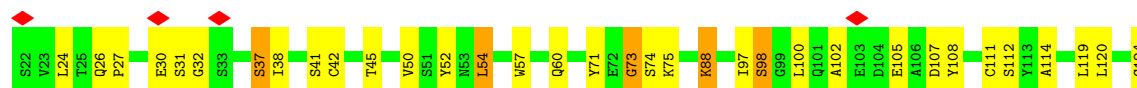


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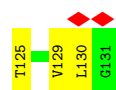
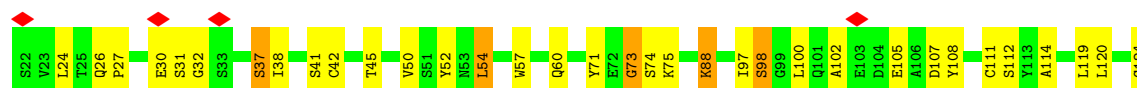




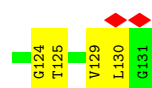
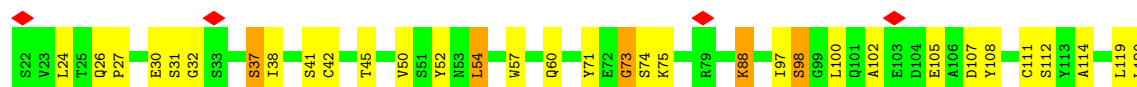
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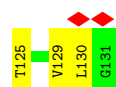
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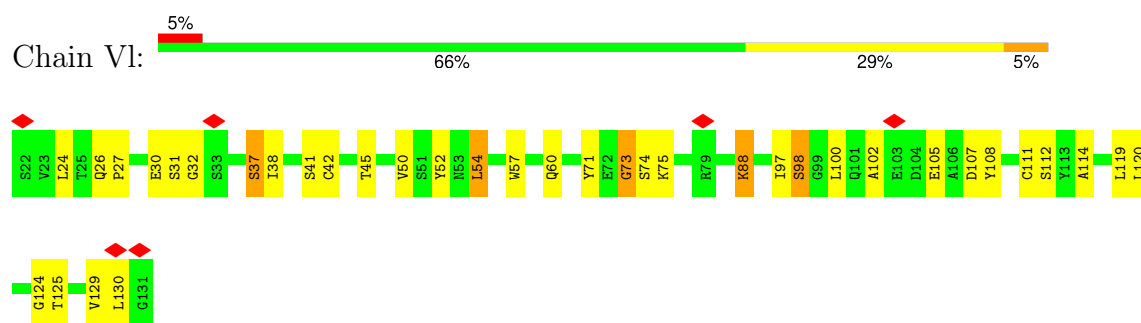
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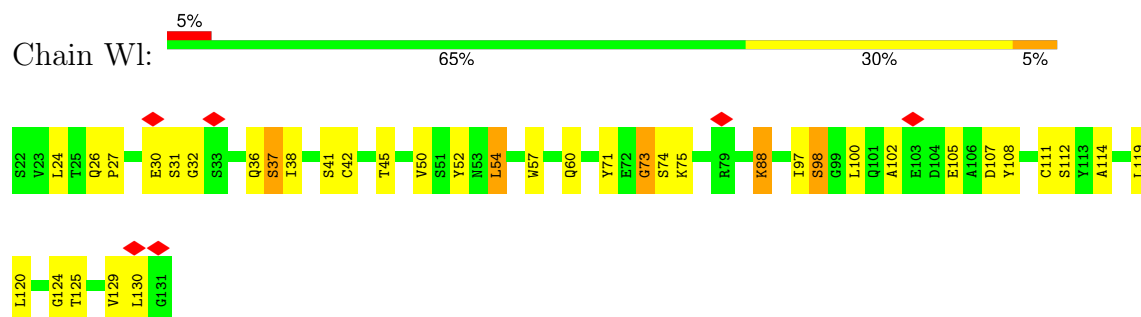
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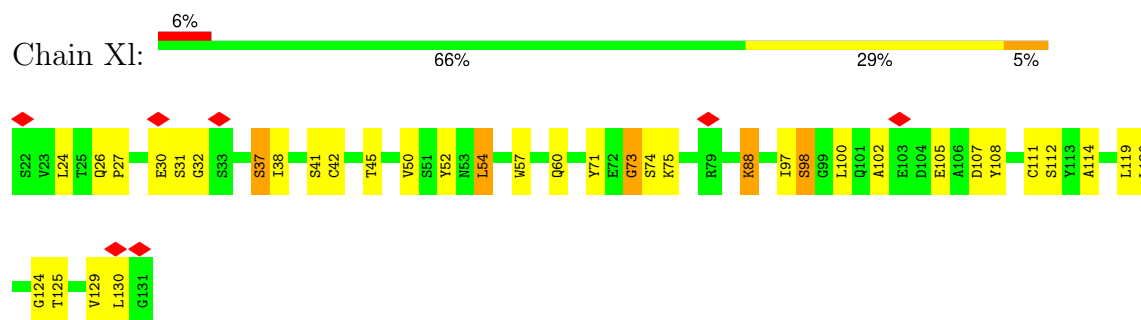
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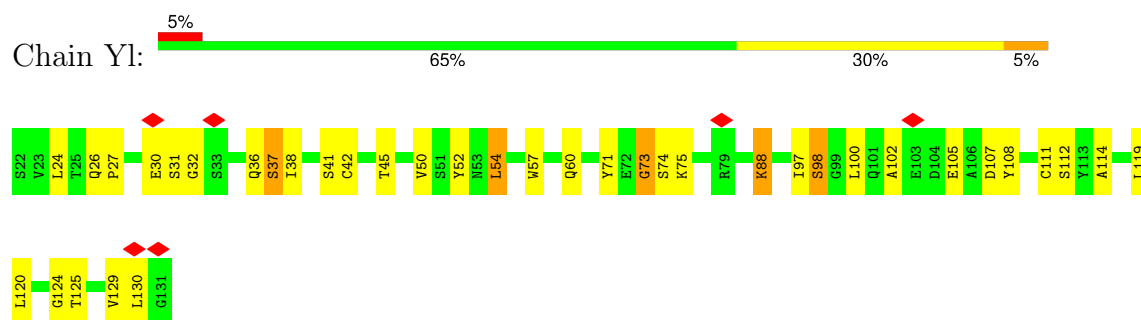
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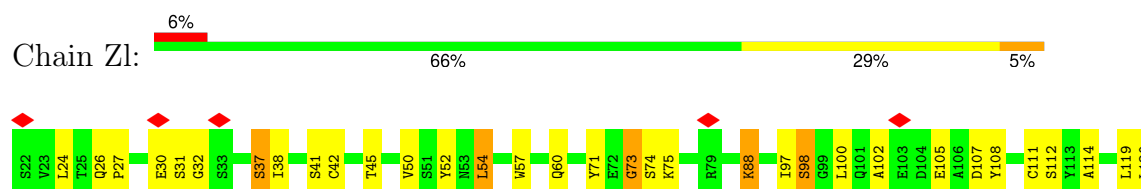
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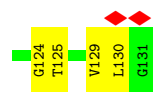


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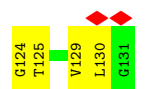


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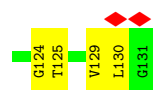




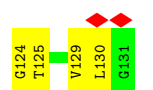
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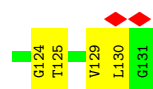
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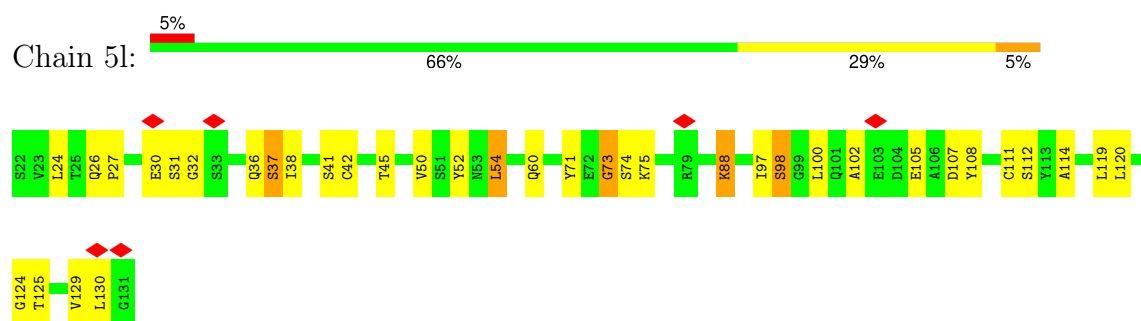
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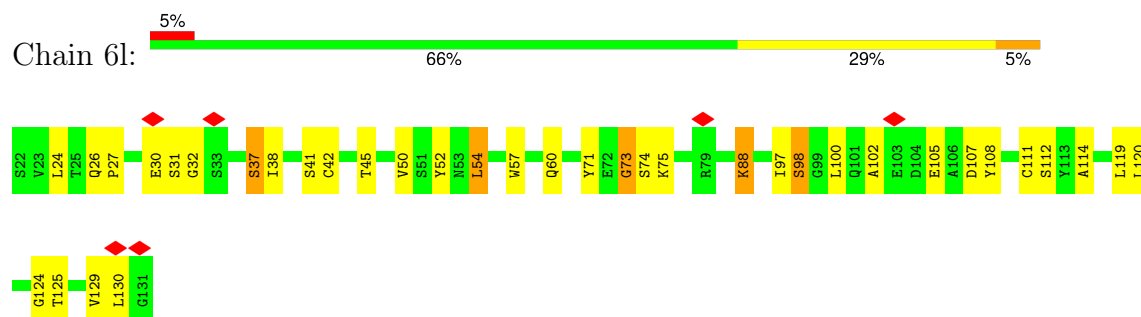
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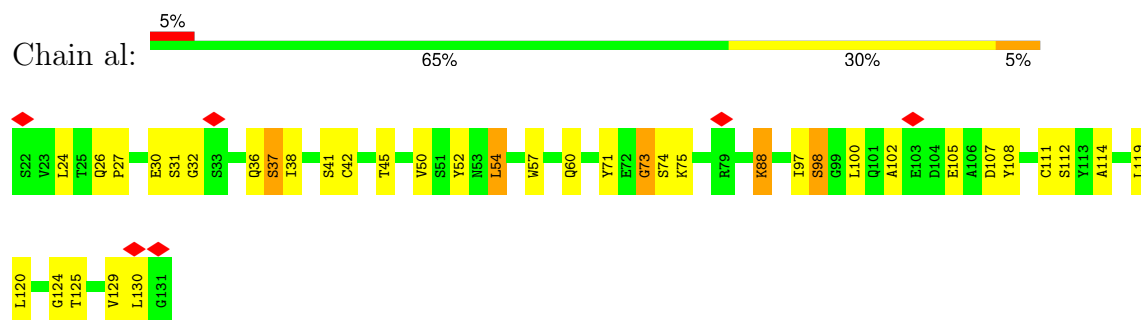
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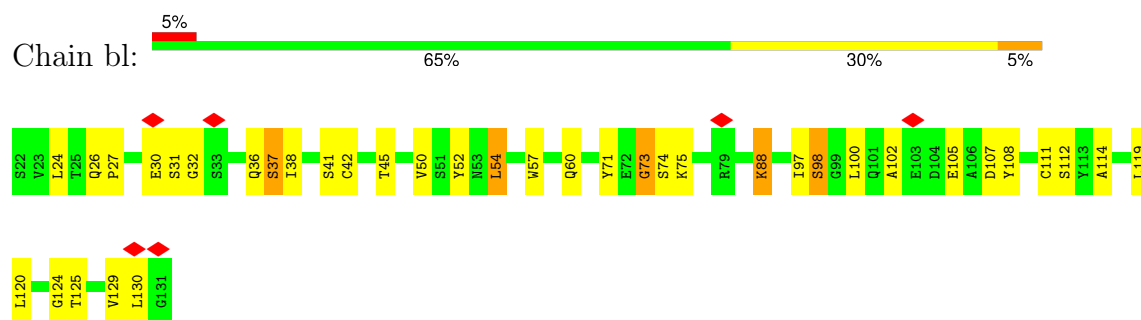
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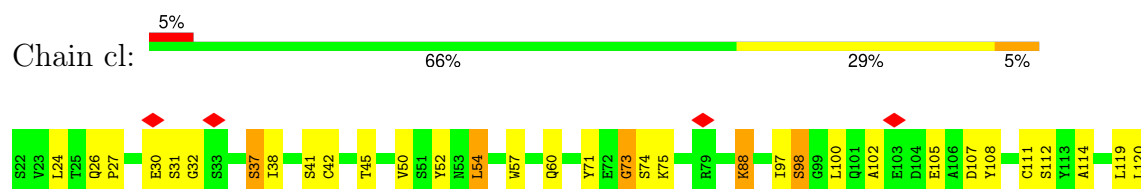
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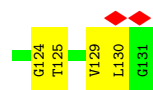


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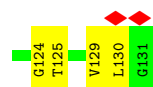
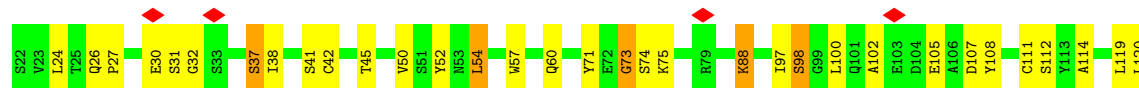


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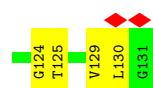
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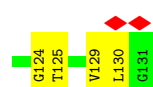
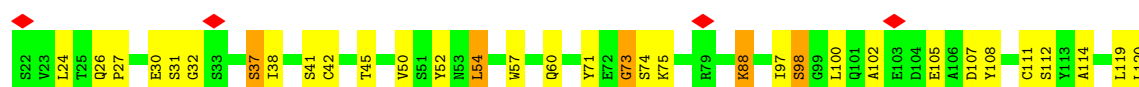
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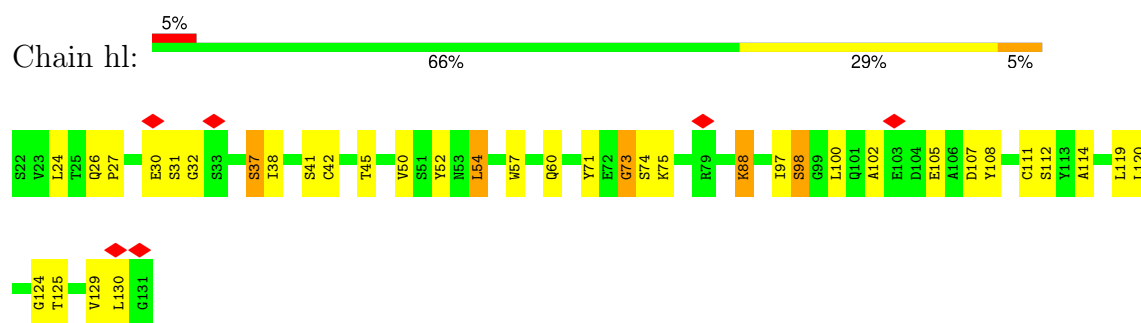
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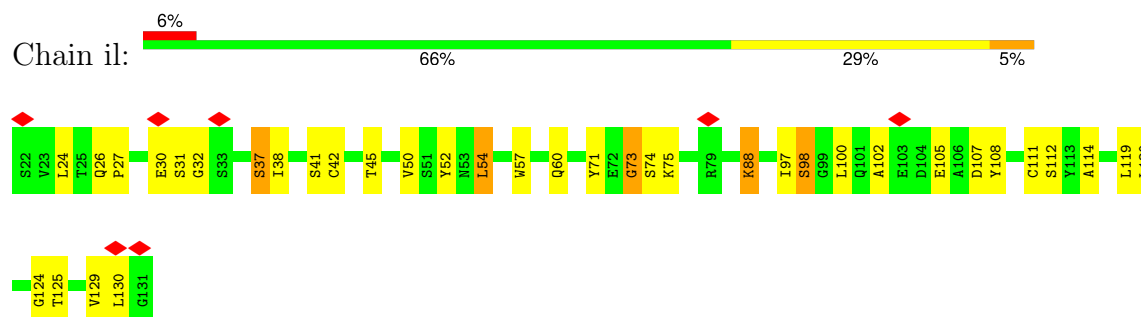
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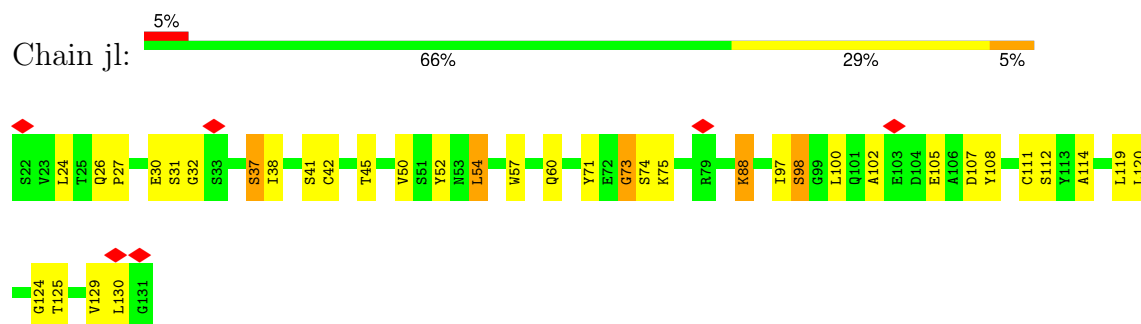
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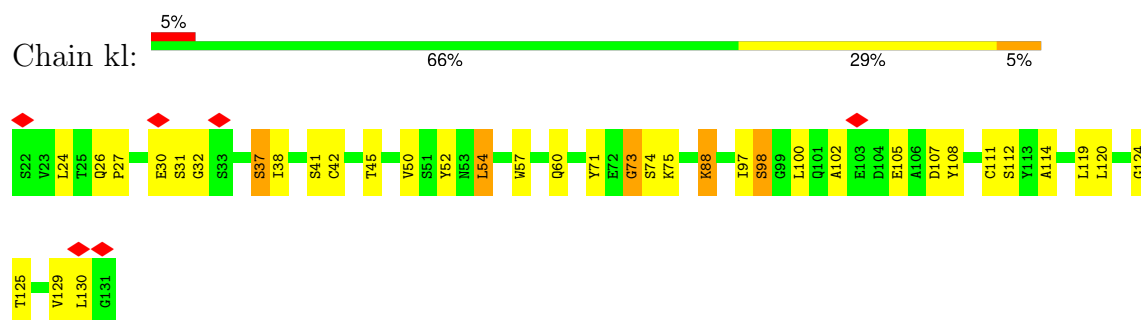
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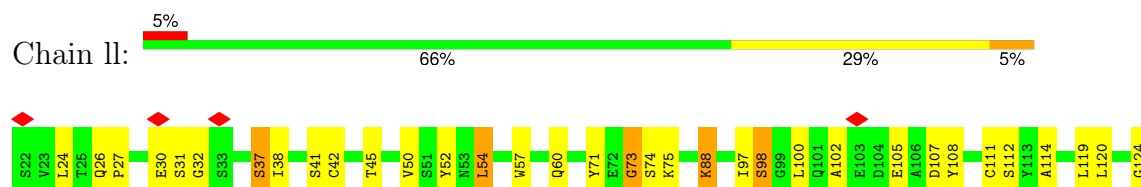
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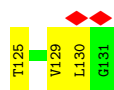


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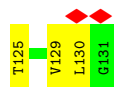
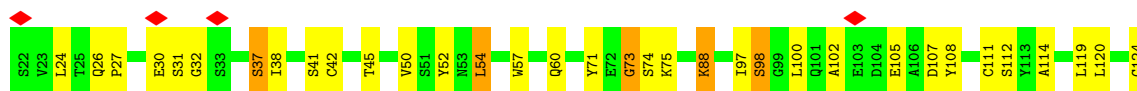


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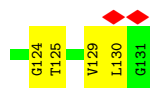




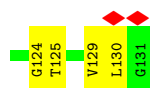
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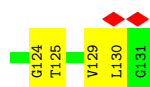
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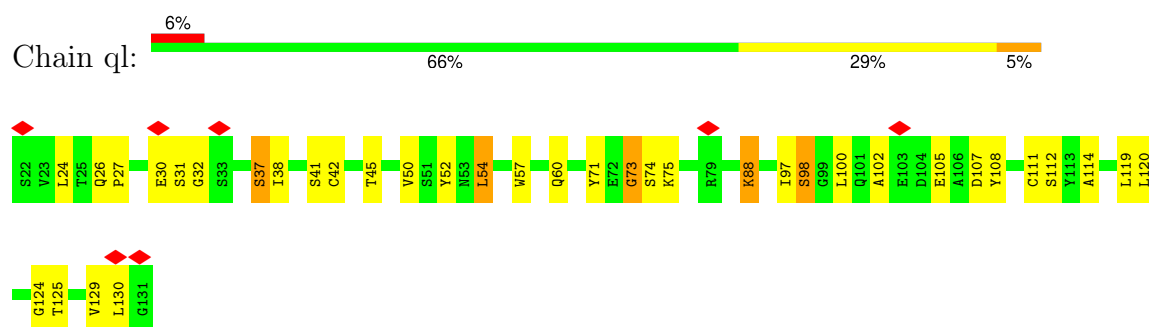
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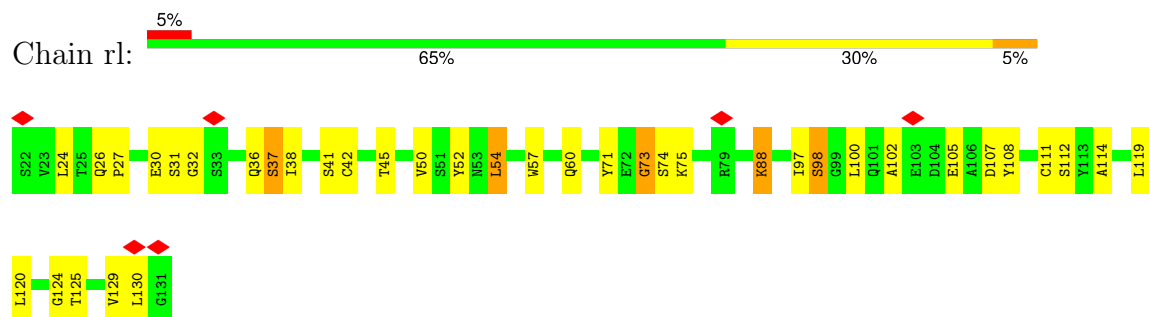
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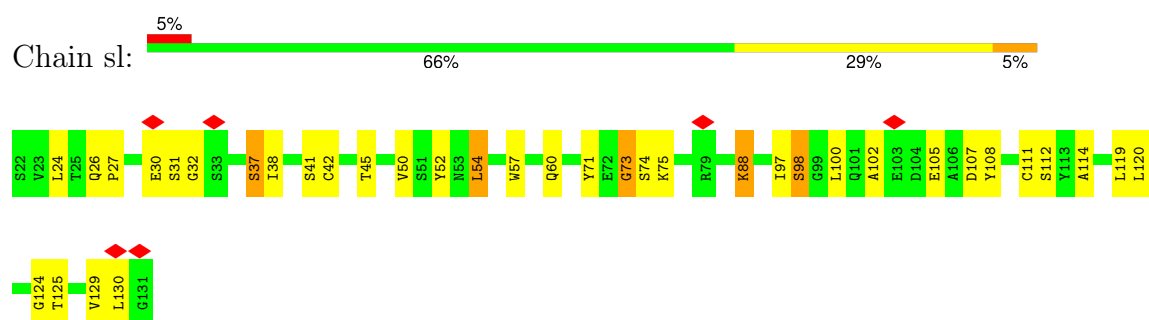
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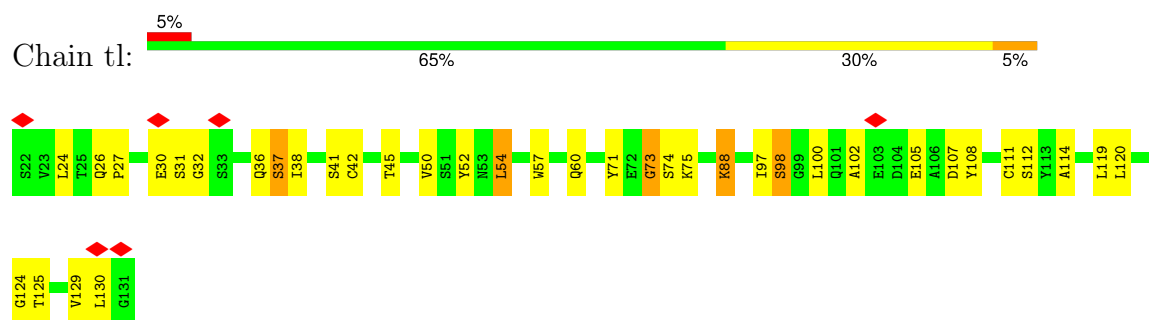
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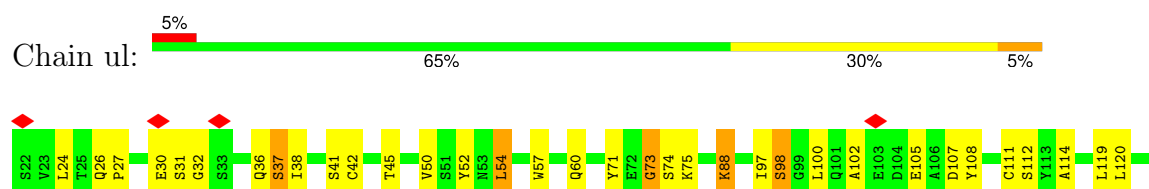
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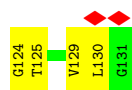


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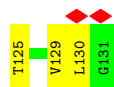
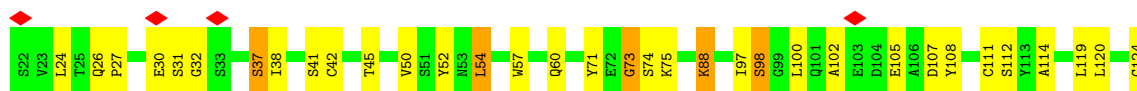


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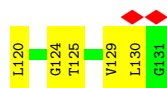




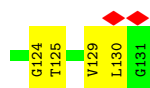
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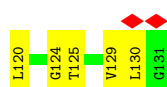
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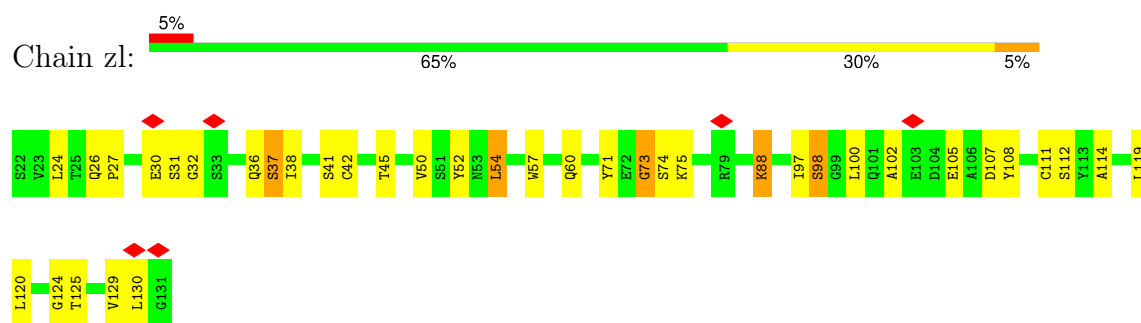
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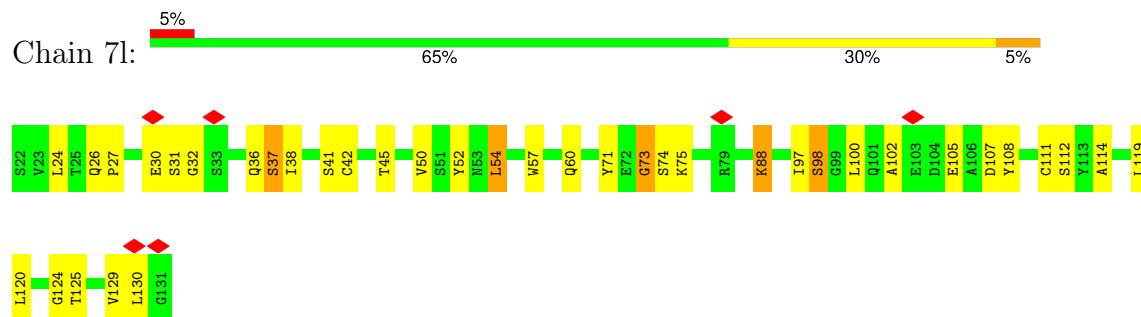
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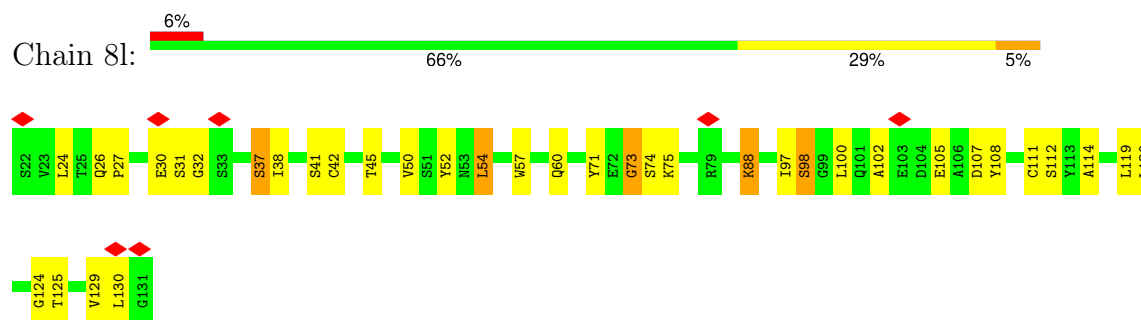
- Molecule 3: Fab3-2 IgG Light Chain



- Molecule 3: Fab3-2 IgG Light Chain



- Molecule 3: Fab3-2 IgG Light Chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35713	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	16.535	Depositor
Minimum map value	-12.543	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	439.19998, 439.19998, 439.19998	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.732, 0.732, 0.732	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	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	2	0.57	2/4271 (0.0%)	0.84	14/5822 (0.2%)
1	3	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	4	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	5	0.57	2/4271 (0.0%)	0.84	14/5822 (0.2%)
1	6	0.57	2/4271 (0.0%)	0.84	14/5822 (0.2%)
1	7	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	8	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	A	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	B	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	C	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	D	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	E	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	F	0.57	2/4271 (0.0%)	0.84	14/5822 (0.2%)
1	G	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	H	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	I	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	J	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	K	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	L	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	M	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	N	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	O	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	P	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	Q	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	R	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	S	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	T	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	U	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	V	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	W	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	X	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	Y	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	Z	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	b	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	c	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	d	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	e	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	f	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	g	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	h	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	i	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	j	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	k	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	l	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	m	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	n	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	o	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	p	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	q	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	r	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	s	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	t	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	u	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	v	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	w	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	x	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	y	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
1	z	0.57	3/4271 (0.1%)	0.84	14/5822 (0.2%)
2	1h	0.54	0/1058	0.84	3/1445 (0.2%)
2	2h	0.54	0/1058	0.84	3/1445 (0.2%)
2	3h	0.54	0/1058	0.84	3/1445 (0.2%)
2	4h	0.54	0/1058	0.84	3/1445 (0.2%)
2	5h	0.54	0/1058	0.84	3/1445 (0.2%)
2	6h	0.54	0/1058	0.84	3/1445 (0.2%)
2	7h	0.54	0/1058	0.84	3/1445 (0.2%)
2	8h	0.54	0/1058	0.84	3/1445 (0.2%)
2	Ah	0.54	0/1058	0.84	3/1445 (0.2%)
2	Bh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Ch	0.53	0/1058	0.84	3/1445 (0.2%)
2	Dh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Eh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Fh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Gh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Hh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Ih	0.54	0/1058	0.84	3/1445 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Jh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Kh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Lh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Mh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Nh	0.53	0/1058	0.84	3/1445 (0.2%)
2	Oh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Ph	0.54	0/1058	0.84	3/1445 (0.2%)
2	Qh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Rh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Sh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Th	0.54	0/1058	0.84	3/1445 (0.2%)
2	Uh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Vh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Wh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Xh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Yh	0.54	0/1058	0.84	3/1445 (0.2%)
2	Zh	0.54	0/1058	0.84	3/1445 (0.2%)
2	ah	0.54	0/1058	0.84	3/1445 (0.2%)
2	bh	0.54	0/1058	0.84	3/1445 (0.2%)
2	ch	0.53	0/1058	0.84	3/1445 (0.2%)
2	dh	0.54	0/1058	0.85	3/1445 (0.2%)
2	eh	0.54	0/1058	0.84	3/1445 (0.2%)
2	fh	0.54	0/1058	0.84	3/1445 (0.2%)
2	gh	0.54	0/1058	0.84	3/1445 (0.2%)
2	hh	0.54	0/1058	0.84	3/1445 (0.2%)
2	ih	0.54	0/1058	0.84	3/1445 (0.2%)
2	jh	0.54	0/1058	0.84	3/1445 (0.2%)
2	kh	0.54	0/1058	0.84	3/1445 (0.2%)
2	lh	0.54	0/1058	0.84	3/1445 (0.2%)
2	mh	0.54	0/1058	0.84	3/1445 (0.2%)
2	nh	0.54	0/1058	0.84	3/1445 (0.2%)
2	oh	0.54	0/1058	0.84	3/1445 (0.2%)
2	ph	0.54	0/1058	0.84	3/1445 (0.2%)
2	qh	0.54	0/1058	0.84	3/1445 (0.2%)
2	rh	0.54	0/1058	0.84	3/1445 (0.2%)
2	sh	0.54	0/1058	0.84	3/1445 (0.2%)
2	th	0.54	0/1058	0.84	3/1445 (0.2%)
2	uh	0.53	0/1058	0.84	3/1445 (0.2%)
2	vh	0.54	0/1058	0.84	3/1445 (0.2%)
2	wh	0.54	0/1058	0.84	3/1445 (0.2%)
2	xh	0.54	0/1058	0.84	3/1445 (0.2%)
2	yh	0.54	0/1058	0.84	3/1445 (0.2%)
2	zh	0.54	0/1058	0.84	3/1445 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	1l	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	2l	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	3l	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	4l	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	5l	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	6l	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	7l	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	8l	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Al	0.61	1/818 (0.1%)	0.79	0/1108
3	Bl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Cl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Dl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	El	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Fl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Gl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Hl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Il	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Jl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Kl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Ll	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Ml	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Nl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Ol	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Pl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Ql	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Rl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Sl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Tl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Ul	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Vl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Wl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Xl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Yl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	Zl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	al	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	bl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	cl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	dl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	el	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	fl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	gl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	hl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	il	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	jl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	kl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	ll	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	ml	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	nl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	ol	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	pl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	ql	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	rl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	sl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	tl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	ul	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	vl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	wl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	xl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	yl	0.85	5/818 (0.6%)	0.92	4/1108 (0.4%)
3	zl	0.86	5/818 (0.6%)	0.92	4/1108 (0.4%)
All	All	0.61	472/368820 (0.1%)	0.85	1256/502500 (0.2%)

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
3	1l	0	1
3	2l	0	1
3	3l	0	1
3	4l	0	1
3	5l	0	1
3	6l	0	1
3	7l	0	1
3	8l	0	1
3	Bl	0	1
3	Cl	0	1
3	Dl	0	1
3	El	0	1
3	Fl	0	1
3	Gl	0	1
3	Hl	0	1
3	Il	0	1
3	Jl	0	1
3	Kl	0	1
3	Ll	0	1
3	Ml	0	1
3	Nl	0	1
3	Ol	0	1
3	Pl	0	1
3	Ql	0	1
3	Rl	0	1
3	Sl	0	1
3	Tl	0	1
3	Ul	0	1
3	Vl	0	1
3	Wl	0	1
3	Xl	0	1
3	Yl	0	1
3	Zl	0	1
3	al	0	1
3	bl	0	1
3	cl	0	1
3	dl	0	1
3	el	0	1
3	fl	0	1
3	gl	0	1
3	hl	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	il	0	1
3	jl	0	1
3	kl	0	1
3	ll	0	1
3	ml	0	1
3	nl	0	1
3	ol	0	1
3	pl	0	1
3	ql	0	1
3	rl	0	1
3	sl	0	1
3	tl	0	1
3	ul	0	1
3	vl	0	1
3	wl	0	1
3	xl	0	1
3	yl	0	1
3	zl	0	1
All	All	0	119

The worst 5 of 472 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2l	97	ILE	C-N	-11.15	1.19	1.33
3	6l	97	ILE	C-N	-11.15	1.19	1.33
3	Rl	97	ILE	C-N	-11.13	1.19	1.33
3	kl	97	ILE	C-N	-11.13	1.19	1.33
3	ul	97	ILE	C-N	-11.13	1.19	1.33

The worst 5 of 1256 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	d	584	GLN	N-CA-C	13.55	125.78	111.14
1	h	584	GLN	N-CA-C	13.54	125.77	111.14
1	E	584	GLN	N-CA-C	13.54	125.76	111.14
1	G	584	GLN	N-CA-C	13.54	125.76	111.14
1	q	584	GLN	N-CA-C	13.54	125.76	111.14

There are no chirality outliers.

5 of 119 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

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	4148	0	3901	120	0
1	2	4148	0	3901	120	0
1	3	4148	0	3901	119	0
1	4	4148	0	3901	120	0
1	5	4148	0	3901	122	0
1	6	4148	0	3901	121	0
1	7	4148	0	3901	119	0
1	8	4148	0	3901	120	0
1	A	4148	0	3901	120	0
1	B	4148	0	3901	120	0
1	C	4148	0	3901	123	0
1	D	4148	0	3901	121	0
1	E	4148	0	3901	124	0
1	F	4148	0	3901	120	0
1	G	4148	0	3901	122	0
1	H	4148	0	3901	120	0
1	I	4148	0	3901	121	0
1	J	4148	0	3901	121	0
1	K	4148	0	3901	120	0
1	L	4148	0	3901	120	0
1	M	4148	0	3901	120	0
1	N	4148	0	3901	121	0
1	O	4148	0	3901	117	0
1	P	4148	0	3901	122	0
1	Q	4148	0	3901	121	0
1	R	4148	0	3901	121	0
1	S	4148	0	3901	119	0
1	T	4148	0	3901	123	0
1	U	4148	0	3901	116	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	4148	0	3901	122	0
1	W	4148	0	3901	123	0
1	X	4148	0	3901	118	0
1	Y	4148	0	3901	123	0
1	Z	4148	0	3901	118	0
1	a	4148	0	3901	125	0
1	b	4148	0	3901	123	0
1	c	4148	0	3901	119	0
1	d	4148	0	3901	122	0
1	e	4148	0	3901	121	0
1	f	4148	0	3901	117	0
1	g	4148	0	3901	123	0
1	h	4148	0	3901	117	0
1	i	4148	0	3901	117	0
1	j	4148	0	3901	124	0
1	k	4148	0	3901	119	0
1	l	4148	0	3901	119	0
1	m	4148	0	3901	118	0
1	n	4148	0	3901	123	0
1	o	4148	0	3901	121	0
1	p	4148	0	3901	122	0
1	q	4148	0	3901	122	0
1	r	4148	0	3901	123	0
1	s	4148	0	3901	122	0
1	t	4148	0	3901	119	0
1	u	4148	0	3901	120	0
1	v	4148	0	3901	121	0
1	w	4148	0	3901	118	0
1	x	4148	0	3901	122	0
1	y	4148	0	3901	120	0
1	z	4148	0	3901	123	0
2	1h	1028	0	988	33	0
2	2h	1028	0	988	33	0
2	3h	1028	0	988	34	0
2	4h	1028	0	988	31	0
2	5h	1028	0	988	34	0
2	6h	1028	0	988	34	0
2	7h	1028	0	988	32	0
2	8h	1028	0	988	33	0
2	Ah	1028	0	988	30	0
2	Bh	1028	0	988	33	0
2	Ch	1028	0	988	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Dh	1028	0	988	37	0
2	Eh	1028	0	988	32	0
2	Fh	1028	0	988	33	0
2	Gh	1028	0	988	36	0
2	Hh	1028	0	988	35	0
2	Ih	1028	0	988	36	0
2	Jh	1028	0	988	33	0
2	Kh	1028	0	988	34	0
2	Lh	1028	0	988	32	0
2	Mh	1028	0	988	37	0
2	Nh	1028	0	988	32	0
2	Oh	1028	0	988	33	0
2	Ph	1028	0	988	35	0
2	Qh	1028	0	988	32	0
2	Rh	1028	0	988	37	0
2	Sh	1028	0	988	32	0
2	Th	1028	0	988	33	0
2	Uh	1028	0	988	33	0
2	Vh	1028	0	988	34	0
2	Wh	1028	0	988	31	0
2	Xh	1028	0	988	32	0
2	Yh	1028	0	988	32	0
2	Zh	1028	0	988	33	0
2	ah	1028	0	988	35	0
2	bh	1028	0	988	37	0
2	ch	1028	0	988	33	0
2	dh	1028	0	988	36	0
2	eh	1028	0	988	36	0
2	fh	1028	0	988	31	0
2	gh	1028	0	988	34	0
2	hh	1028	0	988	31	0
2	ih	1028	0	988	33	0
2	jh	1028	0	988	34	0
2	kh	1028	0	988	38	0
2	lh	1028	0	988	33	0
2	mh	1028	0	988	33	0
2	nh	1028	0	988	36	0
2	oh	1028	0	988	36	0
2	ph	1028	0	988	31	0
2	qh	1028	0	988	32	0
2	rh	1028	0	988	32	0
2	sh	1028	0	988	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	th	1028	0	988	33	0
2	uh	1028	0	988	33	0
2	vh	1028	0	988	33	0
2	wh	1028	0	988	32	0
2	xh	1028	0	988	35	0
2	yh	1028	0	988	35	0
2	zh	1028	0	988	31	0
3	1l	803	0	777	26	0
3	2l	803	0	777	26	0
3	3l	803	0	777	26	0
3	4l	803	0	777	26	0
3	5l	803	0	777	26	0
3	6l	803	0	777	26	0
3	7l	803	0	777	27	0
3	8l	803	0	777	26	0
3	Al	803	0	777	37	0
3	Bl	803	0	777	27	0
3	Cl	803	0	777	27	0
3	Dl	803	0	777	27	0
3	El	803	0	777	26	0
3	Fl	803	0	777	26	0
3	Gl	803	0	777	27	0
3	Hl	803	0	777	27	0
3	Il	803	0	777	26	0
3	Jl	803	0	777	26	0
3	Kl	803	0	777	26	0
3	Ll	803	0	777	27	0
3	Ml	803	0	777	27	0
3	Nl	803	0	777	26	0
3	Ol	803	0	777	26	0
3	Pl	803	0	777	26	0
3	Ql	803	0	777	27	0
3	Rl	803	0	777	26	0
3	Sl	803	0	777	26	0
3	Tl	803	0	777	26	0
3	Ul	803	0	777	26	0
3	Vl	803	0	777	26	0
3	Wl	803	0	777	27	0
3	Xl	803	0	777	26	0
3	Yl	803	0	777	27	0
3	Zl	803	0	777	26	0
3	al	803	0	777	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	bl	803	0	777	27	0
3	cl	803	0	777	26	0
3	dl	803	0	777	26	0
3	el	803	0	777	27	0
3	fl	803	0	777	26	0
3	gl	803	0	777	26	0
3	hl	803	0	777	26	0
3	il	803	0	777	26	0
3	jl	803	0	777	26	0
3	kl	803	0	777	26	0
3	ll	803	0	777	26	0
3	ml	803	0	777	26	0
3	nl	803	0	777	26	0
3	ol	803	0	777	26	0
3	pl	803	0	777	26	0
3	ql	803	0	777	26	0
3	rl	803	0	777	27	0
3	sl	803	0	777	26	0
3	tl	803	0	777	27	0
3	ul	803	0	777	27	0
3	vl	803	0	777	26	0
3	wl	803	0	777	27	0
3	xl	803	0	777	26	0
3	yl	803	0	777	27	0
3	zl	803	0	777	28	0
All	All	358740	0	339960	9269	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 13.

The worst 5 of 9269 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)
3:Al:46:SER:HB3	3:Al:91:ASN:HD21	0.96	1.07
3:Al:46:SER:HB3	3:Al:91:ASN:ND2	1.72	1.02
1:3:614:GLN:HE22	1:3:725:PRO:HA	1.32	0.94
1:5:614:GLN:HE22	1:5:725:PRO:HA	1.32	0.94
1:v:614:GLN:HE22	1:v:725:PRO:HA	1.32	0.94

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	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	2	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	3	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	4	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	5	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	6	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	7	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	8	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	A	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	B	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	C	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	D	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	E	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	F	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	G	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	H	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	I	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	J	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	K	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	L	516/533 (97%)	497 (96%)	19 (4%)	0	100	100
1	M	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	N	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	O	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	P	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	Q	516/533 (97%)	498 (96%)	18 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	S	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	T	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	U	516/533 (97%)	497 (96%)	19 (4%)	0	100	100
1	V	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	W	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	X	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	Y	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	Z	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	a	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	b	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	c	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	d	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	e	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	f	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	g	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	h	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	i	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	j	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	k	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	l	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	m	516/533 (97%)	497 (96%)	19 (4%)	0	100	100
1	n	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	o	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	p	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	q	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	r	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	s	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	t	516/533 (97%)	497 (96%)	19 (4%)	0	100	100
1	u	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	v	516/533 (97%)	498 (96%)	18 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	x	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	y	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
1	z	516/533 (97%)	498 (96%)	18 (4%)	0	100	100
2	1h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	2h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	3h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	4h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	5h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	6h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	7h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	8h	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Ah	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Bh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Ch	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Dh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Eh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Fh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Gh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Hh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Ih	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Jh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Kh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Lh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Mh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Nh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Oh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Ph	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Qh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Rh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Sh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Th	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Uh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Vh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Wh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Xh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Yh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	Zh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	ah	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	bh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	ch	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	dh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	eh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	fh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	gh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	hh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	ih	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	jh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	kh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	lh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	mh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	nh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	oh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	ph	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	qh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	rh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	sh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	th	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	uh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	vh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	wh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	xh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	yh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
2	zh	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
3	1l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	3l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	4l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	5l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	6l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	7l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	8l	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Al	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
3	Bl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Cl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Dl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	El	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Fl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Gl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Hl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Il	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Jl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Kl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Ll	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Ml	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Nl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Ol	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Pl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Ql	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Rl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Sl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Tl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Ul	108/110 (98%)	104 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Vl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Wl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Xl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Yl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	Zl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	al	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	bl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	cl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	dl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	el	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	fl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	gl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	hl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	il	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	jl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	kl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	ll	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	ml	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	nl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	ol	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	pl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	ql	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	rl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	sl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	tl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	ul	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	vl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	wl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	xl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	yl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	zl	108/110 (98%)	104 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	45240/46500 (97%)	43737 (97%)	1503 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	2	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	3	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	4	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	5	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	6	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	7	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	8	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	A	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	B	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	C	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	D	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	E	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	F	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	G	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	H	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	I	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	J	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	K	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	L	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	M	459/468 (98%)	443 (96%)	16 (4%)	32	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	O	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	P	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	Q	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	R	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	S	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	T	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	U	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	V	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	W	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	X	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	Y	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	Z	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	a	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	b	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	c	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	d	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	e	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	f	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	g	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	h	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	i	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	j	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	k	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	l	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	m	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	n	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	o	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	p	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	q	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	r	459/468 (98%)	443 (96%)	16 (4%)	32	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	s	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	t	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	u	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	v	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	w	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	x	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	y	459/468 (98%)	443 (96%)	16 (4%)	32	58
1	z	459/468 (98%)	443 (96%)	16 (4%)	32	58
2	1h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	2h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	3h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	4h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	5h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	6h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	7h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	8h	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Ah	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Bh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Ch	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Dh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Eh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Fh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Gh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Hh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Ih	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Jh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Kh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Lh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Mh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Nh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Oh	114/114 (100%)	111 (97%)	3 (3%)	40	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ph	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Qh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Rh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Sh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Th	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Uh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Vh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Wh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Xh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Yh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	Zh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	ah	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	bh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	ch	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	dh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	eh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	fh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	gh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	hh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	ih	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	jh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	kh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	lh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	mh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	nh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	oh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	ph	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	qh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	rh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	sh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	th	114/114 (100%)	111 (97%)	3 (3%)	40	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	uh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	vh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	wh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	xh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	yh	114/114 (100%)	111 (97%)	3 (3%)	40	64
2	zh	114/114 (100%)	111 (97%)	3 (3%)	40	64
3	1l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	2l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	3l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	4l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	5l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	6l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	7l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	8l	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Al	91/91 (100%)	88 (97%)	3 (3%)	33	59
3	Bl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Cl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Dl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	El	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Fl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Gl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Hl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Il	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Jl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Kl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Ll	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Ml	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Nl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Ol	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Pl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Ql	91/91 (100%)	89 (98%)	2 (2%)	45	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Rl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Sl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Tl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Ul	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Vl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Wl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Xl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Yl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	Zl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	al	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	bl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	cl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	dl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	el	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	fl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	gl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	hl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	il	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	jl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	kl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	ll	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	ml	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	nl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	ol	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	pl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	ql	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	rl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	sl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	tl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	ul	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	vl	91/91 (100%)	89 (98%)	2 (2%)	45	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	wl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	xl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	yl	91/91 (100%)	89 (98%)	2 (2%)	45	66
3	zl	91/91 (100%)	89 (98%)	2 (2%)	45	66
All	All	39840/40380 (99%)	38579 (97%)	1261 (3%)	35	60

5 of 1261 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	z	716	THR
3	Cl	88	LYS
1	8	497	ASN
1	z	701	THR
2	1h	95	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1248 such sidechains are listed below:

Mol	Chain	Res	Type
1	t	288	HIS
2	7h	96	ASN
1	u	545	GLN
1	t	259	GLN
1	z	496	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	Dl	2
3	Ll	2
3	Ul	2
3	Wl	2
3	Yl	2
3	2l	2
3	6l	2
3	al	2
3	dl	2
3	el	2
3	jl	2
3	ml	2
3	tl	2
3	Bl	2
3	Cl	2
3	El	2
3	Fl	2
3	Gl	2
3	Hl	2
3	Il	2
3	Jl	2
3	Kl	2
3	Ml	2
3	Nl	2
3	Ol	2
3	Pl	2
3	Ql	2
3	Rl	2
3	Sl	2
3	Tl	2

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Mol	Chain	Number of breaks
3	Vl	2
3	Xl	2
3	Zl	2
3	1l	2
3	3l	2
3	4l	2
3	5l	2
3	bl	2
3	cl	2
3	fl	2
3	gl	2
3	hl	2
3	il	2
3	kl	2
3	ll	2
3	nl	2
3	ol	2
3	pl	2
3	ql	2
3	rl	2
3	sl	2
3	ul	2
3	vl	2
3	wl	2
3	xl	2
3	yl	2
3	zl	2
3	7l	2
3	8l	2

The worst 5 of 118 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Dl	73:GLY	C	74:SER	N	1.20
1	Ll	73:GLY	C	74:SER	N	1.20
1	Ul	73:GLY	C	74:SER	N	1.20
1	Wl	73:GLY	C	74:SER	N	1.20
1	Yl	73:GLY	C	74:SER	N	1.20

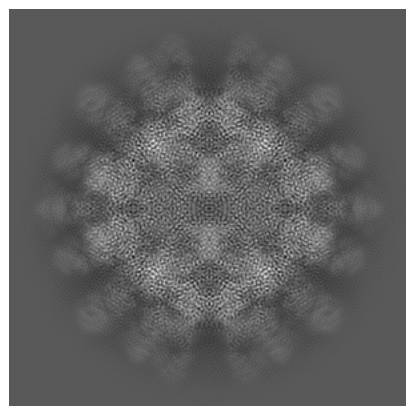
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76770. These allow visual inspection of the internal detail of the map and identification of artifacts.

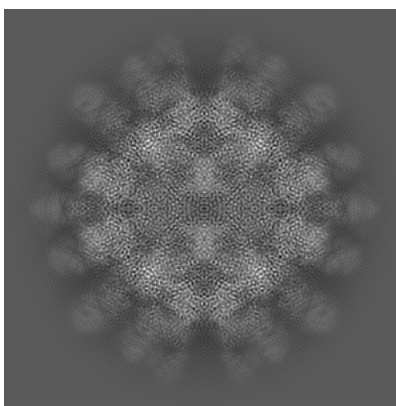
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

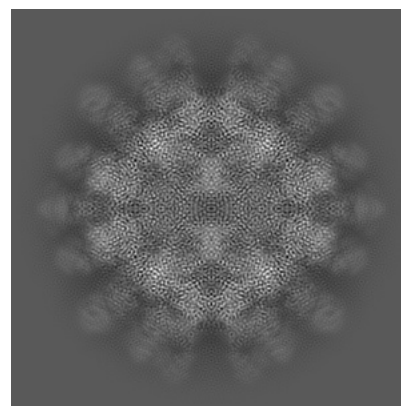
6.1.1 Primary map



X

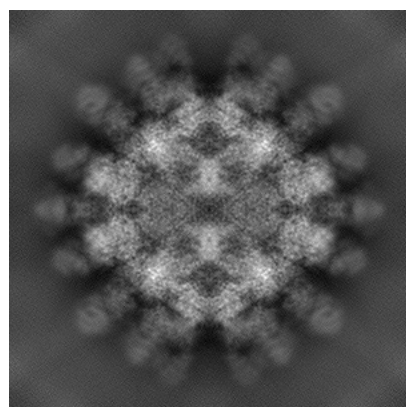


Y

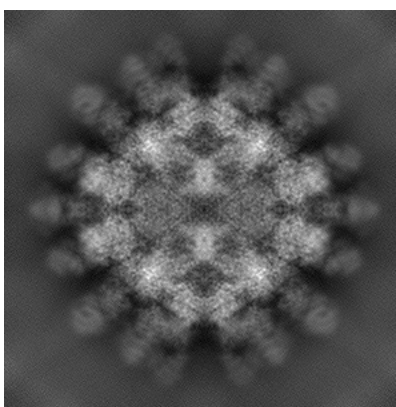


Z

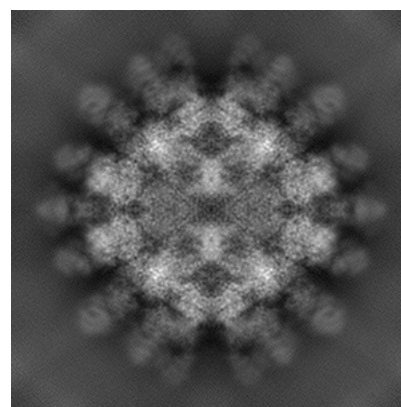
6.1.2 Raw map



X



Y

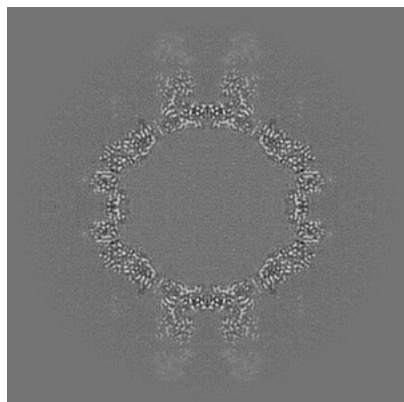


Z

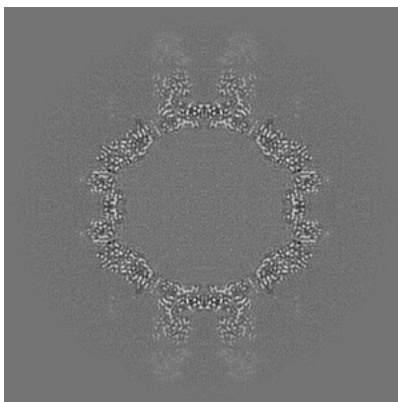
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

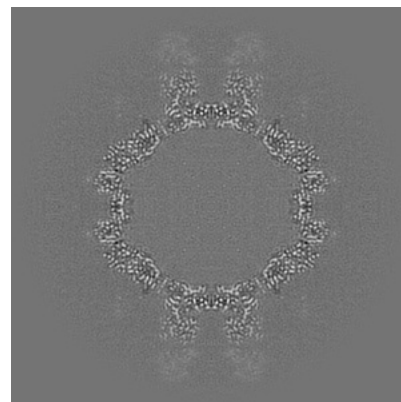
6.2.1 Primary map



X Index: 300

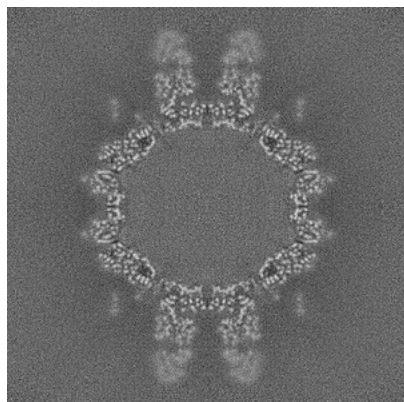


Y Index: 300

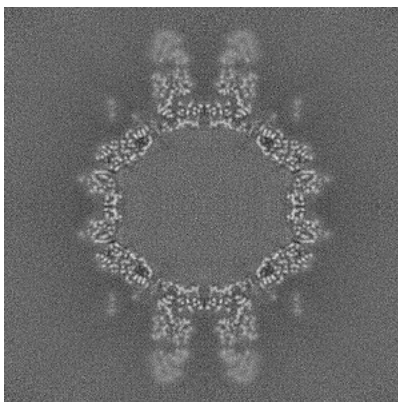


Z Index: 300

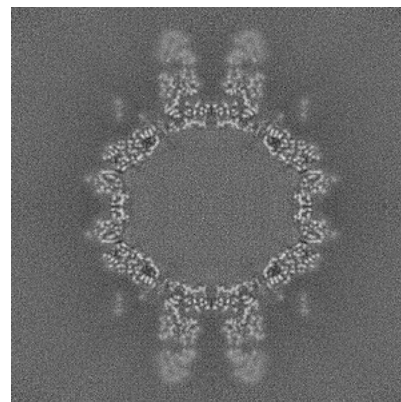
6.2.2 Raw map



X Index: 300



Y Index: 300

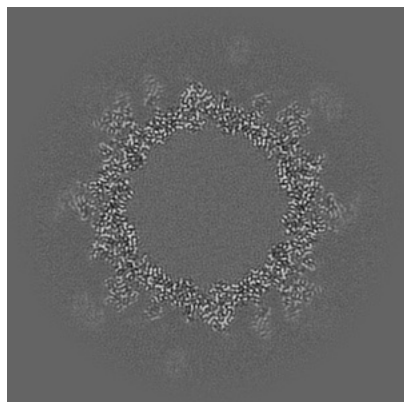


Z Index: 300

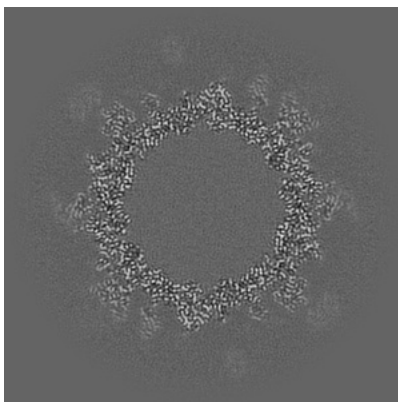
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

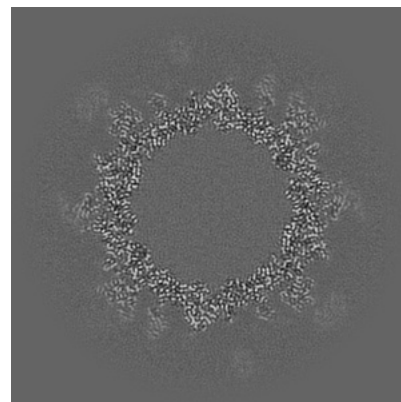
6.3.1 Primary map



X Index: 271

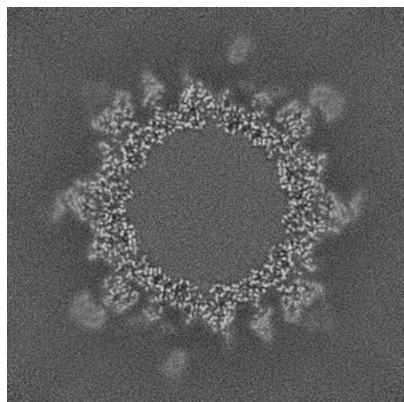


Y Index: 329

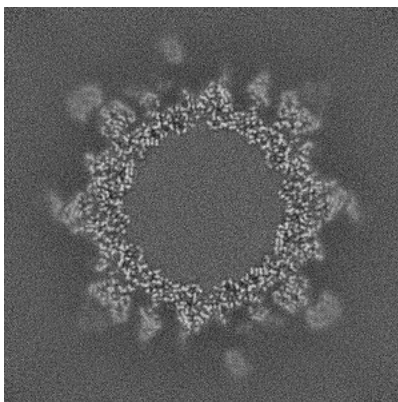


Z Index: 329

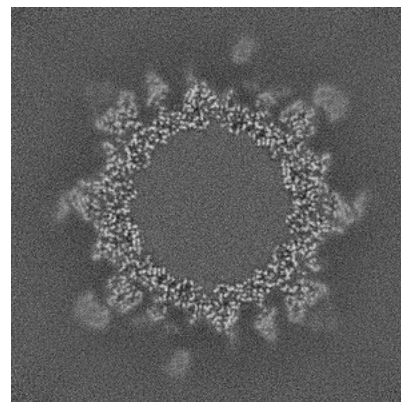
6.3.2 Raw map



X Index: 271



Y Index: 329

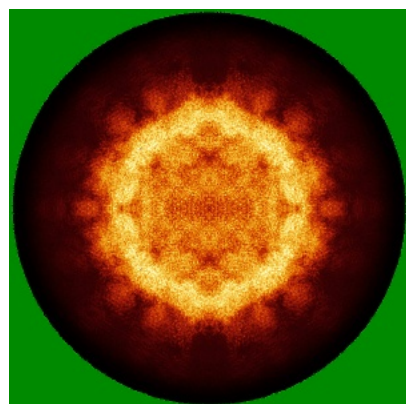


Z Index: 271

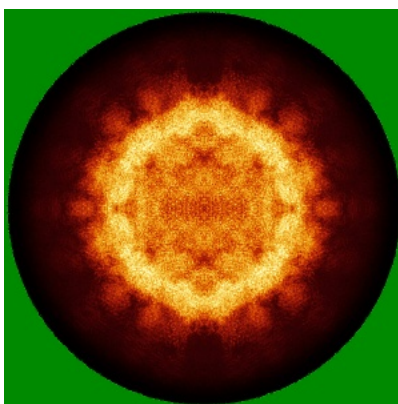
The images above show the largest variance slices of the map in three orthogonal directions.

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

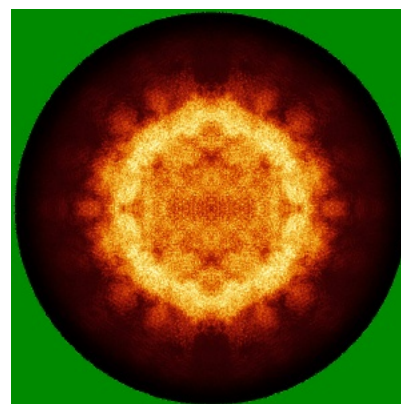
6.4.1 Primary map



X

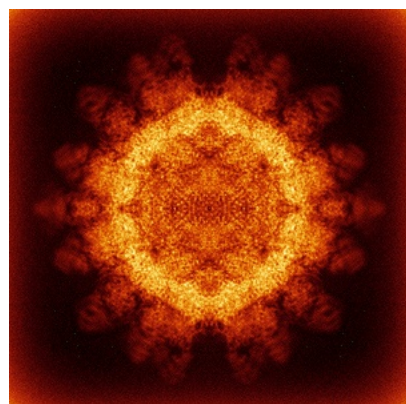


Y

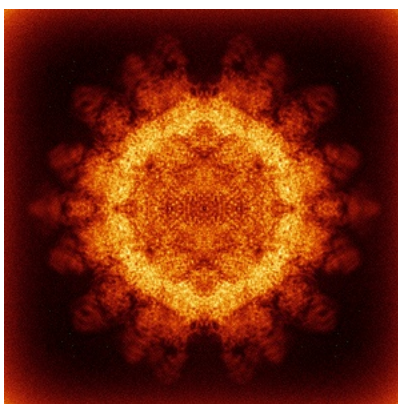


Z

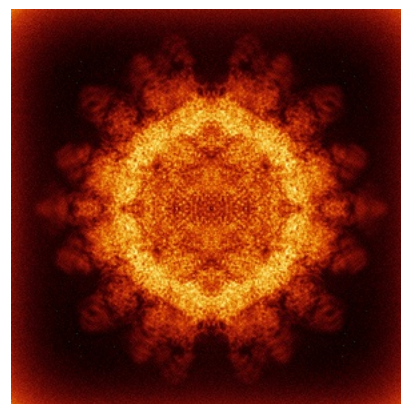
6.4.2 Raw map



X



Y

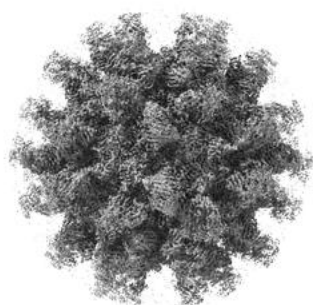


Z

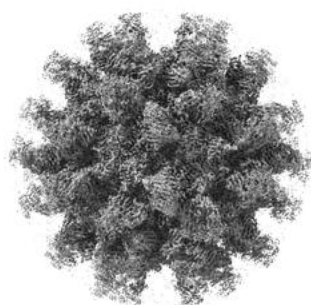
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

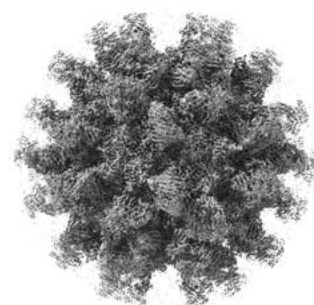
6.5.1 Primary map



X



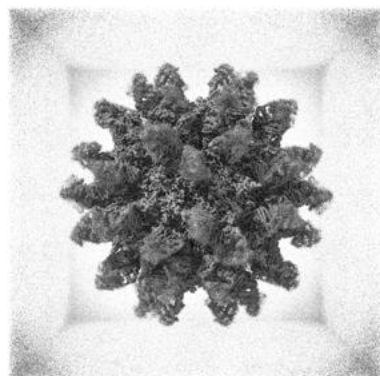
Y



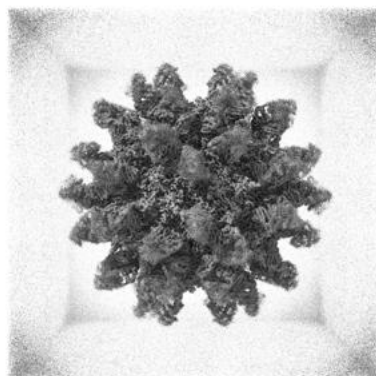
Z

The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

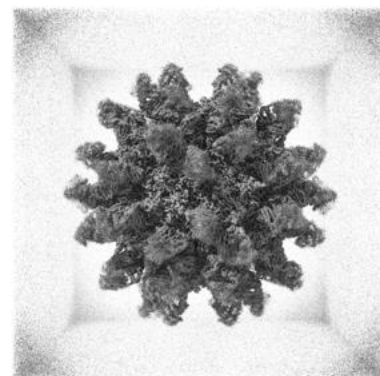
6.5.2 Raw map



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.

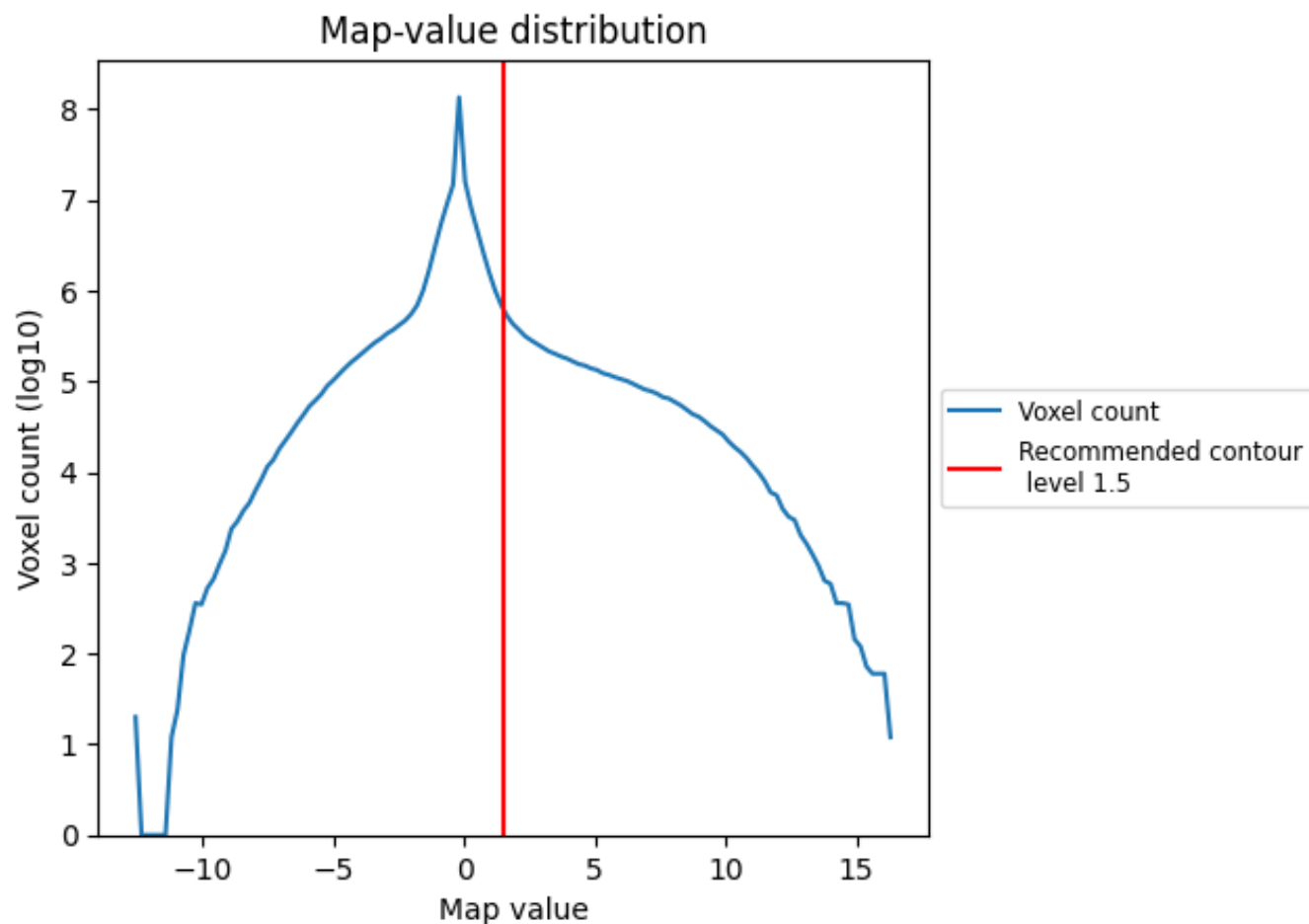
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

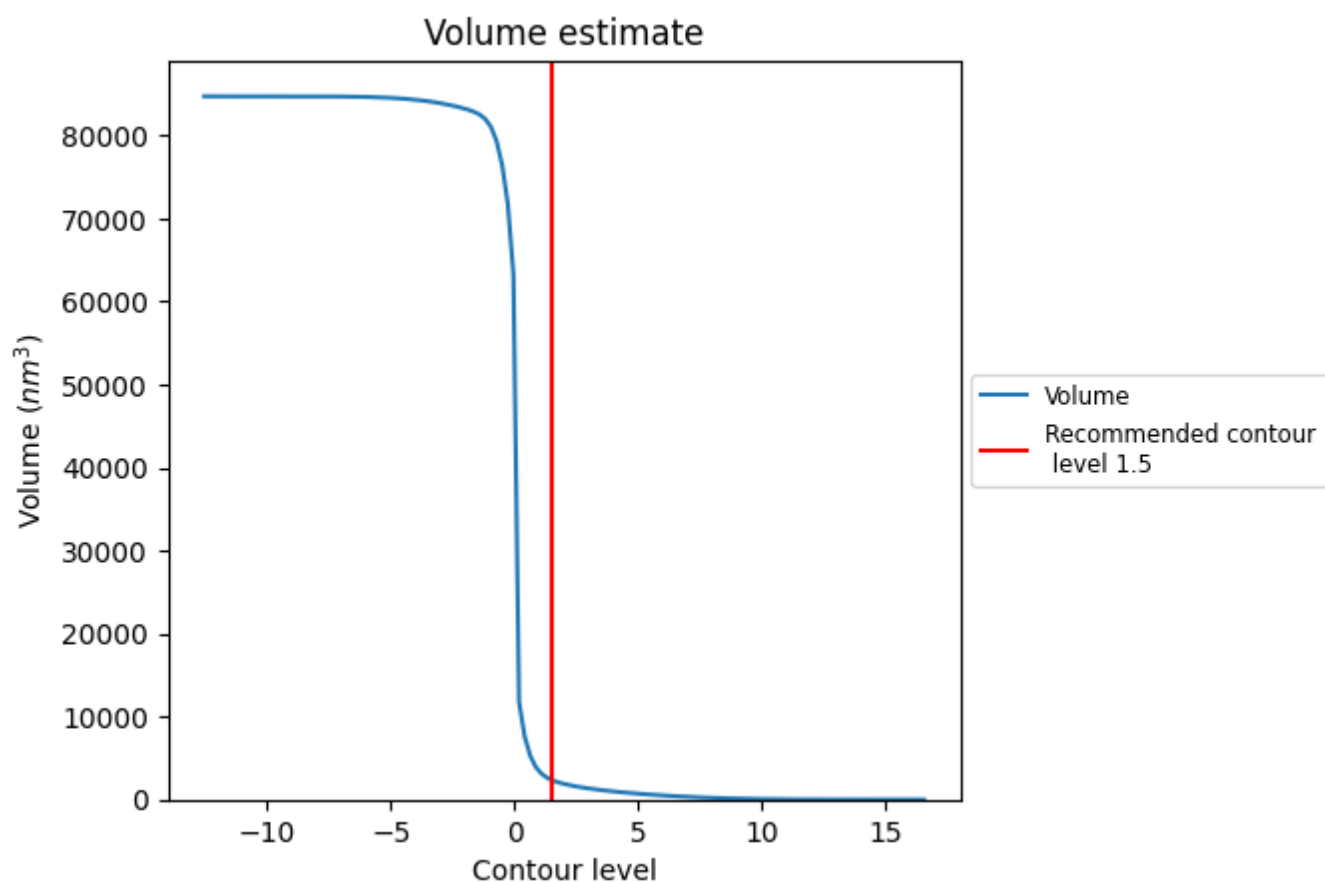
This section contains the results of statistical analysis of the map.

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.

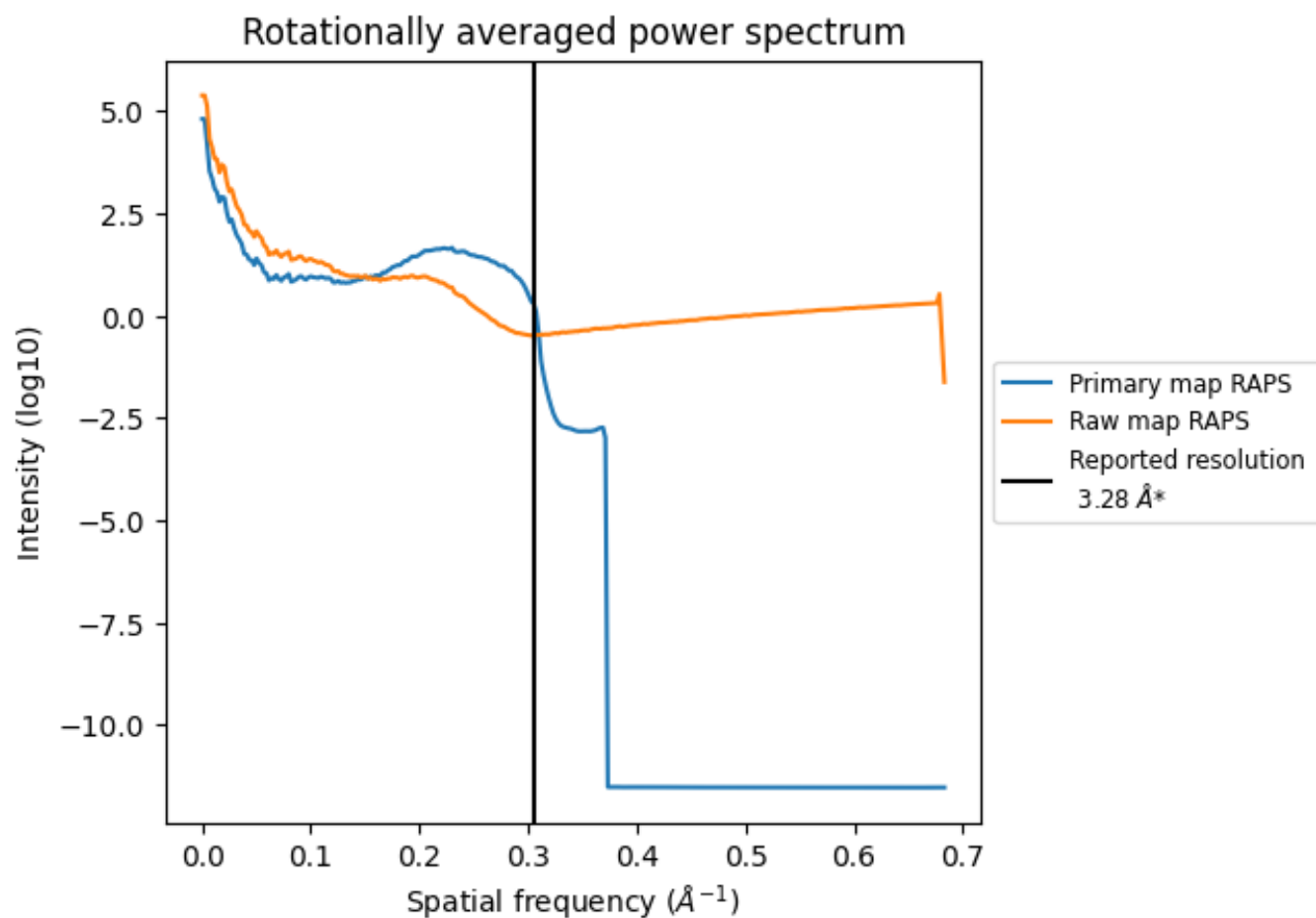
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2361 nm^3 ; this corresponds to an approximate mass of 2132 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 ⓘ

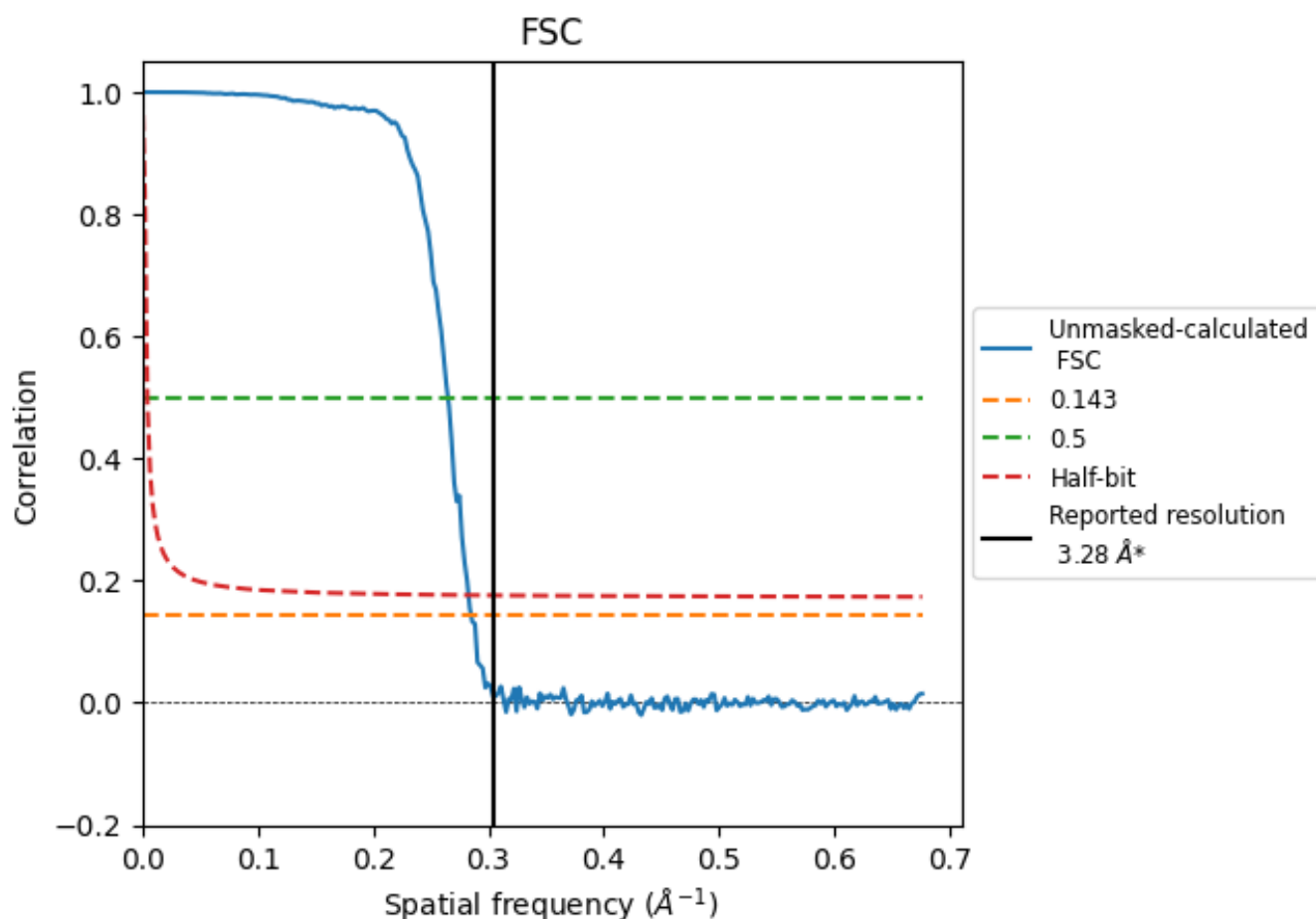


*Reported resolution corresponds to spatial frequency of $0.305 \text{ \AA}^{-1}$

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 0.305 Å⁻¹

8.2 Resolution estimates [i](#)

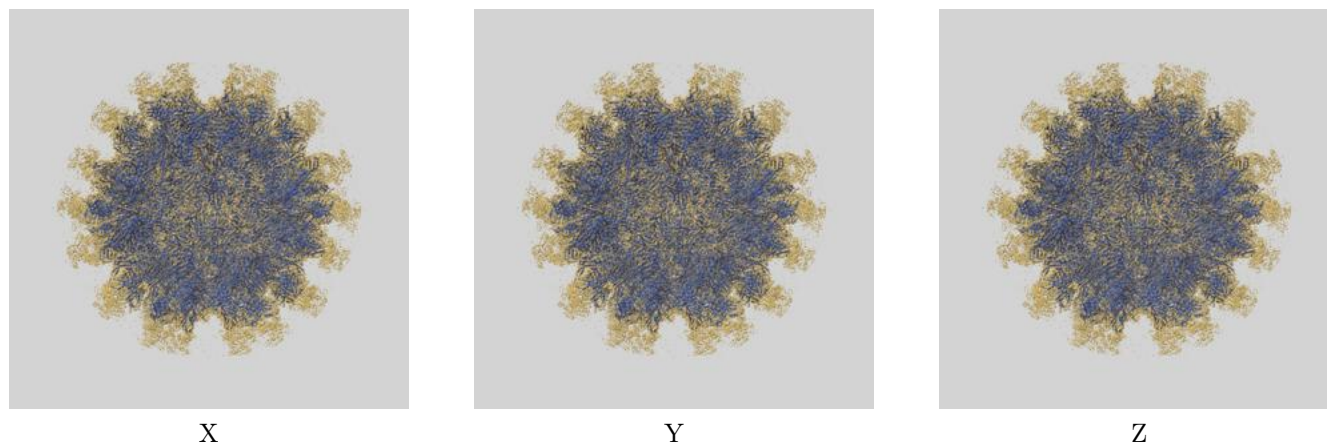
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.51	3.78	3.54

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

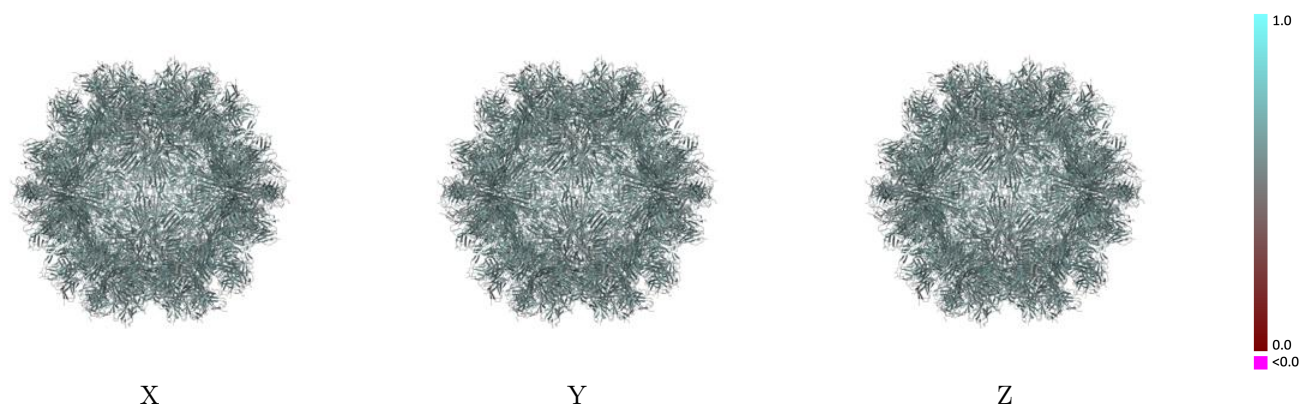
This section contains information regarding the fit between EMDB map EMD-76770 and PDB model 12US. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



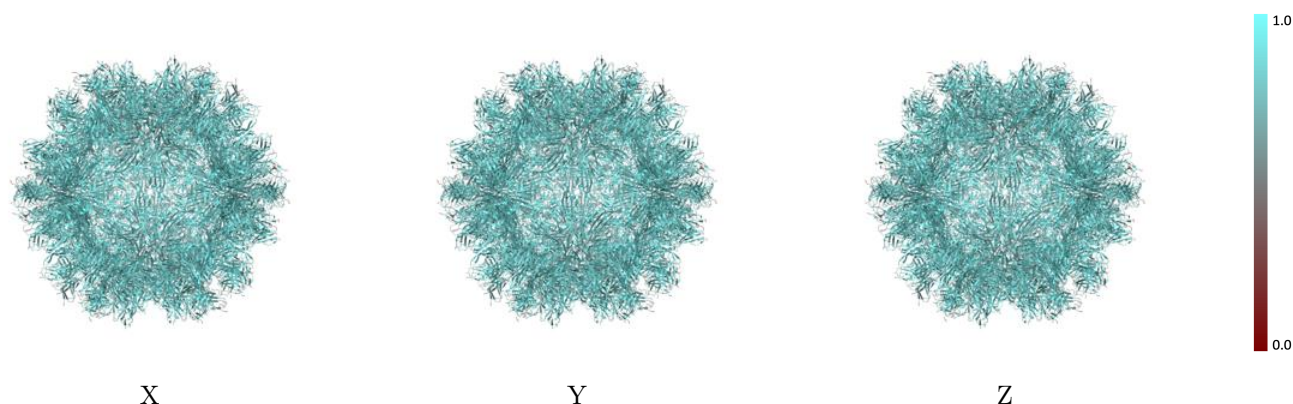
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



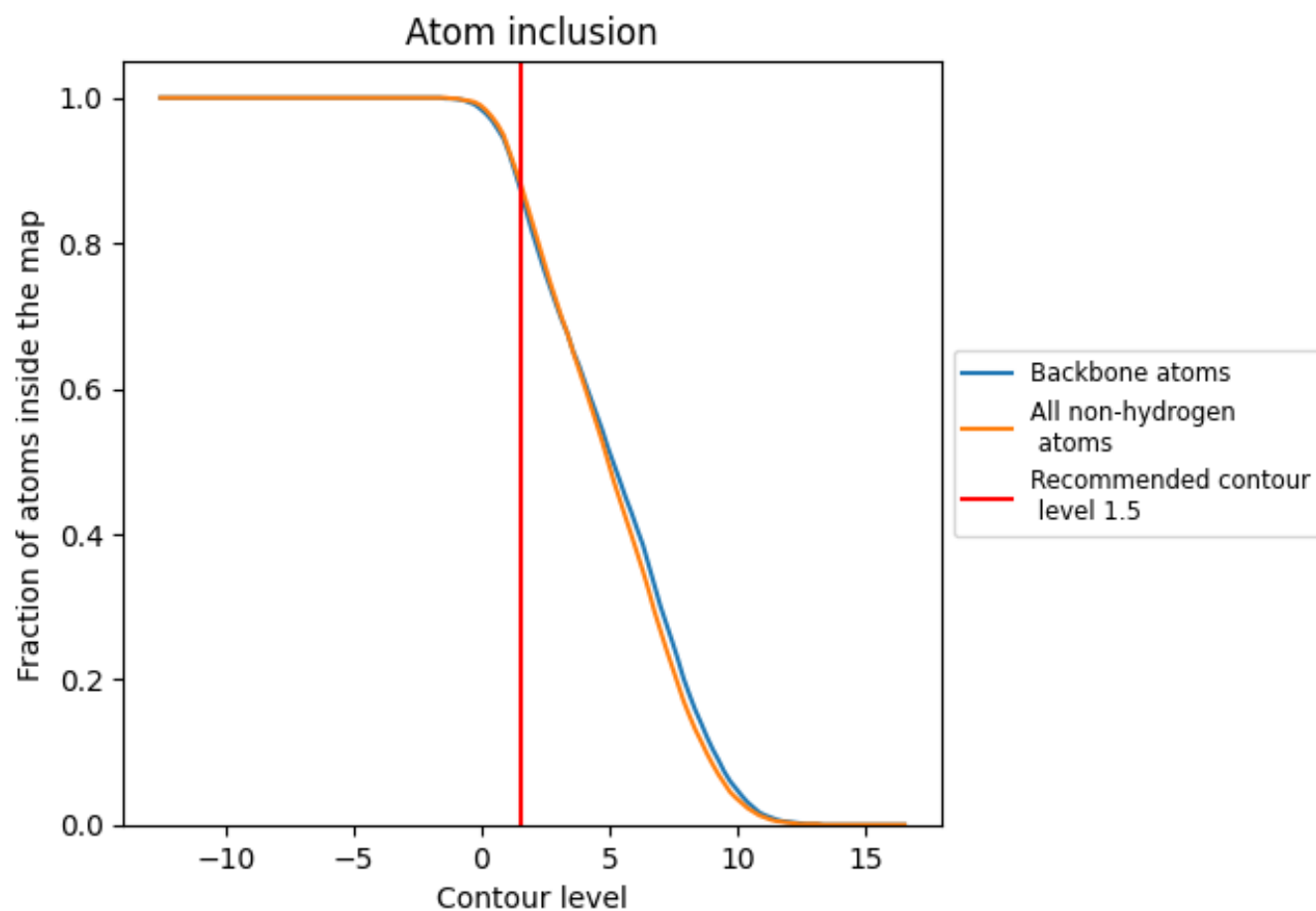
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8850	 0.5800
1	 0.9210	 0.5950
1h	 0.8330	 0.5580
1l	 0.7680	 0.5380
2	 0.9210	 0.5940
2h	 0.8330	 0.5600
2l	 0.7670	 0.5370
3	 0.9210	 0.5950
3h	 0.8330	 0.5590
3l	 0.7670	 0.5380
4	 0.9210	 0.5950
4h	 0.8330	 0.5580
4l	 0.7680	 0.5390
5	 0.9210	 0.5940
5h	 0.8330	 0.5560
5l	 0.7670	 0.5370
6	 0.9210	 0.5950
6h	 0.8330	 0.5580
6l	 0.7670	 0.5370
7	 0.9220	 0.5950
7h	 0.8290	 0.5550
7l	 0.7650	 0.5380
8	 0.9220	 0.5940
8h	 0.8240	 0.5540
8l	 0.7610	 0.5320
A	 0.9210	 0.5950
Ah	 0.8320	 0.5590
Al	 0.7670	 0.5410
B	 0.9230	 0.5940
Bh	 0.8320	 0.5550
Bl	 0.7560	 0.5360
C	 0.9220	 0.5940
Ch	 0.8310	 0.5570
Cl	 0.7630	 0.5350
D	 0.9220	 0.5950



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Chain	Atom inclusion	Q-score
Dh	 0.8290	 0.5550
DI	 0.7650	 0.5370
E	 0.9220	 0.5950
Eh	 0.8240	 0.5570
El	 0.7610	 0.5360
F	 0.9210	 0.5940
Fh	 0.8330	 0.5570
Fl	 0.7670	 0.5380
G	 0.9220	 0.5940
Gh	 0.8240	 0.5570
Gl	 0.7610	 0.5390
H	 0.9220	 0.5940
Hh	 0.8290	 0.5560
HI	 0.7650	 0.5360
I	 0.9220	 0.5940
Ih	 0.8310	 0.5600
Il	 0.7630	 0.5370
J	 0.9240	 0.5950
Jh	 0.8320	 0.5590
JI	 0.7560	 0.5360
K	 0.9220	 0.5940
Kh	 0.8320	 0.5590
KI	 0.7630	 0.5370
L	 0.9240	 0.5940
Lh	 0.8320	 0.5570
LI	 0.7560	 0.5360
M	 0.9220	 0.5950
Mh	 0.8250	 0.5550
MI	 0.7610	 0.5380
N	 0.9220	 0.5950
Nh	 0.8290	 0.5560
NI	 0.7650	 0.5380
O	 0.9220	 0.5950
Oh	 0.8240	 0.5570
OI	 0.7610	 0.5350
P	 0.9220	 0.5940
Ph	 0.8290	 0.5560
PI	 0.7650	 0.5370
Q	 0.9220	 0.5940
Qh	 0.8310	 0.5570
QI	 0.7630	 0.5380
R	 0.9230	 0.5940

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Chain	Atom inclusion	Q-score
Rh	 0.8320	 0.5560
Rl	 0.7560	 0.5380
S	 0.9240	 0.5940
Sh	 0.8320	 0.5590
Sl	 0.7560	 0.5350
T	 0.9220	 0.5940
Th	 0.8320	 0.5570
Tl	 0.7630	 0.5380
U	 0.9240	 0.5950
Uh	 0.8320	 0.5580
Ul	 0.7560	 0.5380
V	 0.9220	 0.5950
Vh	 0.8310	 0.5590
VI	 0.7630	 0.5370
W	 0.9220	 0.5950
Wh	 0.8290	 0.5600
Wl	 0.7650	 0.5400
X	 0.9220	 0.5930
Xh	 0.8250	 0.5570
Xl	 0.7610	 0.5330
Y	 0.9220	 0.5940
Yh	 0.8300	 0.5550
Yl	 0.7660	 0.5390
Z	 0.9220	 0.5930
Zh	 0.8240	 0.5550
Zl	 0.7610	 0.5330
a	 0.9220	 0.5950
ah	 0.8310	 0.5580
al	 0.7630	 0.5360
b	 0.9220	 0.5940
bh	 0.8230	 0.5560
bl	 0.7620	 0.5350
c	 0.9220	 0.5950
ch	 0.8290	 0.5560
cl	 0.7650	 0.5400
d	 0.9220	 0.5940
dh	 0.8290	 0.5570
dl	 0.7650	 0.5370
e	 0.9220	 0.5950
eh	 0.8290	 0.5570
el	 0.7650	 0.5380
f	 0.9220	 0.5950

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Chain	Atom inclusion	Q-score
fh	 0.8240	 0.5560
fl	 0.7610	 0.5340
g	 0.9220	 0.5940
gh	 0.8320	 0.5580
gl	 0.7630	 0.5360
h	 0.9220	 0.5950
hh	 0.8330	 0.5590
hl	 0.7680	 0.5380
i	 0.9220	 0.5940
ih	 0.8250	 0.5580
il	 0.7610	 0.5350
j	 0.9220	 0.5950
jh	 0.8310	 0.5570
jl	 0.7630	 0.5360
k	 0.9230	 0.5950
kh	 0.8320	 0.5550
kl	 0.7560	 0.5350
l	 0.9240	 0.5950
lh	 0.8320	 0.5590
ll	 0.7560	 0.5360
m	 0.9240	 0.5940
mh	 0.8320	 0.5570
ml	 0.7560	 0.5380
n	 0.9220	 0.5950
nh	 0.8240	 0.5580
nl	 0.7610	 0.5380
o	 0.9220	 0.5940
oh	 0.8310	 0.5580
ol	 0.7630	 0.5390
p	 0.9210	 0.5940
ph	 0.8330	 0.5580
pl	 0.7670	 0.5380
q	 0.9220	 0.5950
qh	 0.8240	 0.5570
ql	 0.7610	 0.5370
r	 0.9220	 0.5950
rh	 0.8310	 0.5580
rl	 0.7630	 0.5370
s	 0.9210	 0.5960
sh	 0.8330	 0.5560
sl	 0.7670	 0.5390
t	 0.9240	 0.5950

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Chain	Atom inclusion	Q-score
th	 0.8320	 0.5590
tl	 0.7560	 0.5370
u	 0.9240	 0.5950
uh	 0.8320	 0.5540
ul	 0.7530	 0.5340
v	 0.9240	 0.5940
vh	 0.8320	 0.5590
vl	 0.7560	 0.5360
w	 0.9220	 0.5940
wh	 0.8330	 0.5570
wl	 0.7670	 0.5390
x	 0.9220	 0.5940
xh	 0.8320	 0.5600
xl	 0.7630	 0.5350
y	 0.9220	 0.5940
yh	 0.8290	 0.5580
yl	 0.7650	 0.5370
z	 0.9220	 0.5960
zh	 0.8290	 0.5580
zl	 0.7650	 0.5390