



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 06:53 PM UTC

PDB ID : 9HAR / pdb_00009har
EMDB ID : EMD-52004
Title : pT=3 virus-like particle of ssRNA phage ESE017 coat protein
Authors : Kalnins, G.
Deposited on : 2024-11-05
Resolution : 2.80 Å(reported)
Based on initial model : .

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.dev132
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) : 2.49

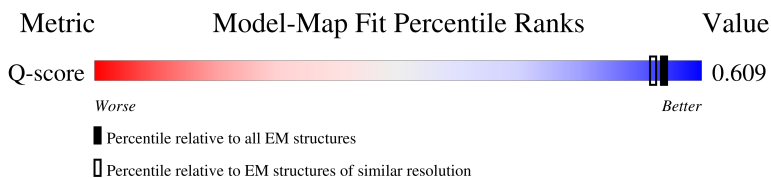
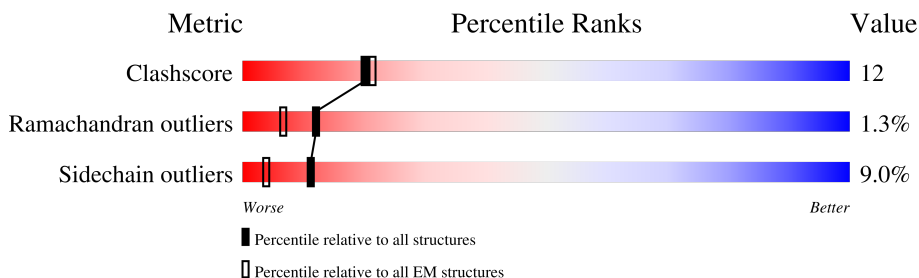
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



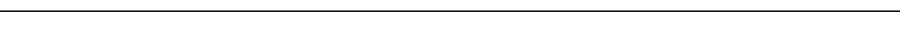
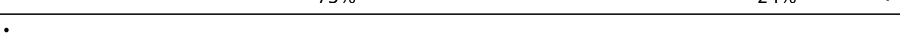
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	AA	132	 67% 31% .
1	AB	132	 67% 31% .
1	AC	132	 60% 38% .
1	AD	132	 73% 24% .

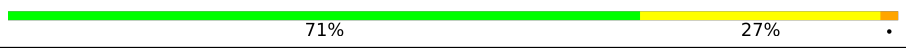
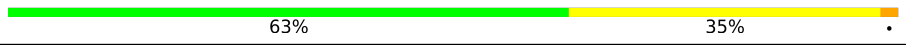
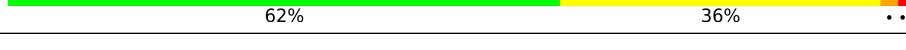
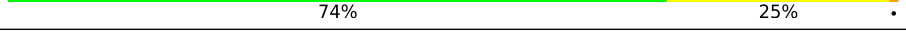
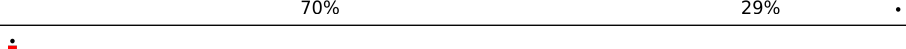
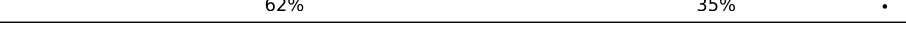
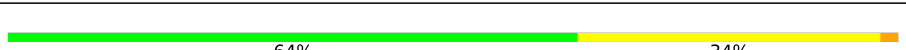
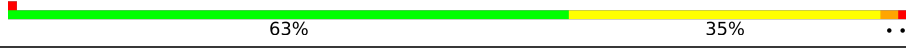
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Mol	Chain	Length	Quality of chain
1	AE	132	 69%30%.
1	AF	132	 66%32%..
1	AG	132	 74%25%.
1	AH	132	 67%31%.
1	AI	132	 59%40%.
1	AJ	132	 69%30%.
1	AK	132	 67%30%..
1	AL	132	 59%38%.
1	AM	132	 73%27%.
1	AN	132	 72%27%.
1	AO	132	 61%36%.
1	AP	132	 73%26%.
1	AQ	132	 70%28%.
1	AR	132	 63%34%.
1	AS	132	 75%24%.
1	AT	132	 65%33%.
1	AU	132	 61%38%.
1	AV	132	 65%33%.
1	AW	132	 67%29%.
1	AX	132	 58%39%.
1	AY	132	 74%25%.
1	AZ	132	 70%28%.
1	BA	132	 60%37%.
1	BB	132	 72%27%.
1	BC	132	 66%33%..

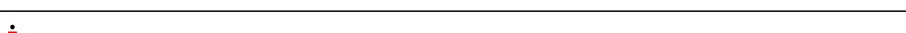
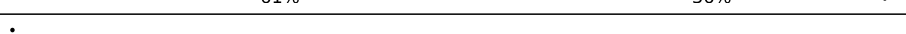
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Mol	Chain	Length	Quality of chain
1	BD	132	
1	BE	132	
1	BF	132	
1	BG	132	
1	BH	132	
1	BI	132	
1	BJ	132	
1	BK	132	
1	BL	132	
1	BM	132	
1	BN	132	
1	BO	132	
1	BP	132	
1	BQ	132	
1	BR	132	
1	BS	132	
1	BT	132	
1	BU	132	
1	BV	132	
1	BW	132	
1	BX	132	
1	BY	132	
1	BZ	132	
1	CA	132	
1	CB	132	

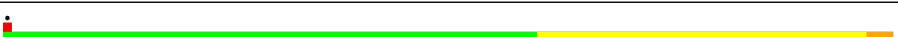
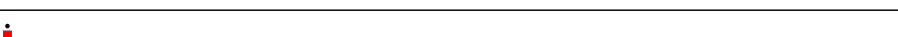
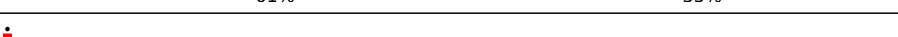
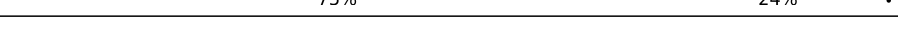
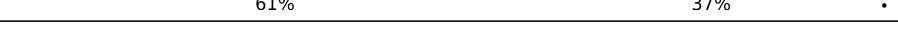
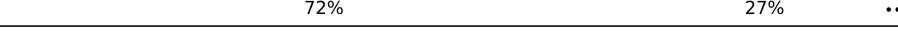
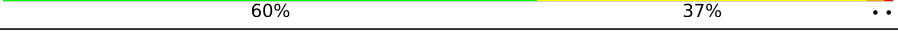
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Mol	Chain	Length	Quality of chain
1	CC	132	
1	CD	132	
1	CE	132	
1	CF	132	
1	CG	132	
1	CH	132	
1	CI	132	
1	CJ	132	
1	CK	132	
1	CL	132	
1	CM	132	
1	CN	132	
1	CO	132	
1	CP	132	
1	CQ	132	
1	CR	132	
1	CS	132	
1	CT	132	
1	CU	132	
1	CV	132	
1	CW	132	
1	CX	132	
1	CY	132	
1	CZ	132	
1	DA	132	

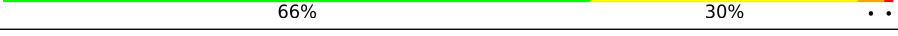
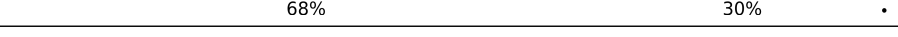
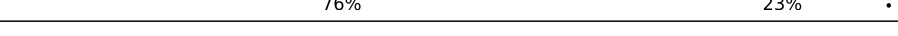
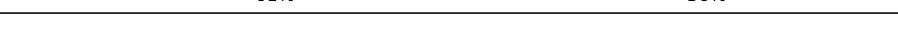
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Mol	Chain	Length	Quality of chain
1	DB	132	
1	DC	132	
1	DD	132	
1	DE	132	
1	DF	132	
1	DG	132	
1	DH	132	
1	DI	132	
1	DJ	132	
1	DK	132	
1	DL	132	
1	DM	132	
1	DN	132	
1	DO	132	
1	DP	132	
1	DQ	132	
1	DR	132	
1	DS	132	
1	DT	132	
1	DU	132	
1	DV	132	
1	DW	132	
1	DX	132	
1	DY	132	
1	DZ	132	

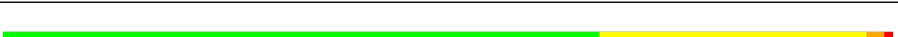
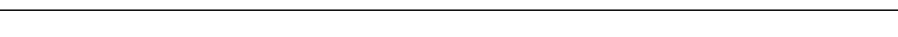
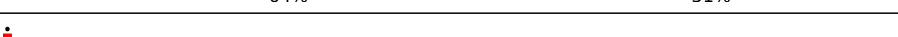
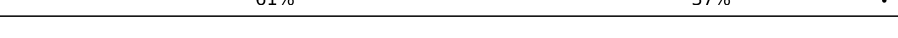
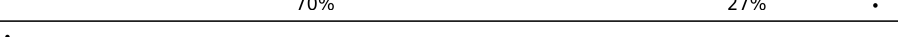
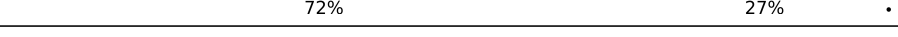
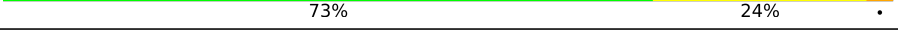
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Mol	Chain	Length	Quality of chain
1	EA	132	
1	EB	132	
1	EC	132	
1	ED	132	
1	EE	132	
1	EF	132	
1	EG	132	
1	EH	132	
1	EI	132	
1	EJ	132	
1	EK	132	
1	EL	132	
1	EM	132	
1	EN	132	
1	EO	132	
1	EP	132	
1	EQ	132	
1	ER	132	
1	ES	132	
1	ET	132	
1	EU	132	
1	EV	132	
1	EW	132	
1	EX	132	
1	EY	132	

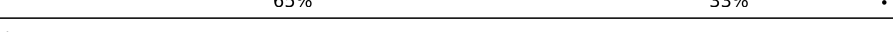
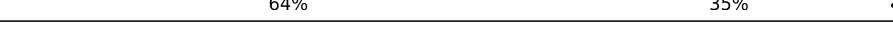
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Mol	Chain	Length	Quality of chain
1	EZ	132	 77% 21% .
1	FA	132	 71% 28% .
1	FB	132	 62% 36% ..
1	FC	132	 78% 21% .
1	FD	132	 70% 28% .
1	FE	132	 59% 38% .
1	FF	132	 70% 28% .
1	FG	132	 69% 28% .
1	FH	132	 61% 36% .
1	FI	132	 76% 23% .
1	FJ	132	 67% 30% ..
1	FK	132	 66% 32% .
1	FL	132	 66% 31% .
1	FM	132	 64% 31% ..
1	FN	132	 61% 37% .
1	FO	132	 78% 21% .
1	FP	132	 70% 27% .
1	FQ	132	 60% 37% .
1	FR	132	 72% 27% .
1	FS	132	 73% 24% .
1	FT	132	 64% 33% .
1	FU	132	 74% 25% .
1	FV	132	 67% 31% ..
1	FW	132	 66% 32% .
1	FX	132	 76% 23% .

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Mol	Chain	Length	Quality of chain
1	FY	132	 71%26%.
1	FZ	132	 58%39%.
1	GA	132	 67%30%.
1	GB	132	 64%31%..
1	GC	132	 61%38%.
1	GD	132	 75%24%.
1	GE	132	 71%27%..
1	GF	132	 64%33%..
1	GG	132	 74%25%.
1	GH	132	 66%32%.
1	GI	132	 64%36%.
1	GJ	132	 77%23%.
1	GK	132	 70%28%.
1	GL	132	 64%33%.
1	GM	132	 65%32%.
1	GN	132	 65%33%.
1	GO	132	 64%35%.
1	GP	132	 75%24%.
1	GQ	132	 67%31%..
1	GR	132	 67%30%.
1	GS	132	 73%27%.
1	GT	132	 70%27%..
1	GU	132	 63%33%..
1	GV	132	 71%27%.
1	GW	132	 69%28%.

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Mol	Chain	Length	Quality of chain
1	GX	132	63% 33% 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 176040 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 Coat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AB	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AC	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AD	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AE	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AF	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AG	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AH	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AI	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AJ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AK	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AL	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AM	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AN	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AO	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AP	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	AQ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AS	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AT	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AV	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AW	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AX	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AY	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	AZ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BA	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BB	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BC	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BD	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BE	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BF	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BG	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BH	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BI	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BJ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BK	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	BL	132	Total 978	C 609	N 168	O 200	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BN	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BO	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BP	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BQ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BR	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BS	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BT	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BU	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BV	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BW	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BX	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BY	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	BZ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CA	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CB	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CC	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CD	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CE	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CF	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	CG	132	Total	C	N	O	S	0	0
			978	609	168	200	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CI	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CJ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CK	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CL	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CM	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CN	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CO	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CP	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CQ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CR	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CS	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CT	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CV	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CW	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CX	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CY	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	CZ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DA	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DB	132	Total 978	C 609	N 168	O 200	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DD	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DE	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DF	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DG	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DH	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DI	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DJ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DK	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DL	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DM	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DN	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DO	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DP	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DQ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DR	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DS	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DT	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DV	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	DW	132	Total 978	C 609	N 168	O 200	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
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			978	609	168	200	1		
1	DY	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	DZ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EA	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EB	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EC	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	ED	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EE	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EF	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EG	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EH	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EI	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EJ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EK	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	EL	132	Total	C	N	O	S	0	0
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1	EN	132	Total	C	N	O	S	0	0
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1	EO	132	Total	C	N	O	S	0	0
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1	EQ	132	Total	C	N	O	S	0	0
			978	609	168	200	1		
1	ER	132	Total	C	N	O	S	0	0
			978	609	168	200	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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1	ET	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EV	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EW	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EX	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EY	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	EZ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FA	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FB	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FC	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FD	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FE	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FF	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FG	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FH	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FI	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FJ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FK	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FL	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FM	132	Total 978	C 609	N 168	O 200	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
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1	FO	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FP	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FQ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FR	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FS	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FT	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FV	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FW	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FX	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FY	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	FZ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GA	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GB	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GC	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GD	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GE	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GF	132	Total 978	C 609	N 168	O 200	S 1	0	0
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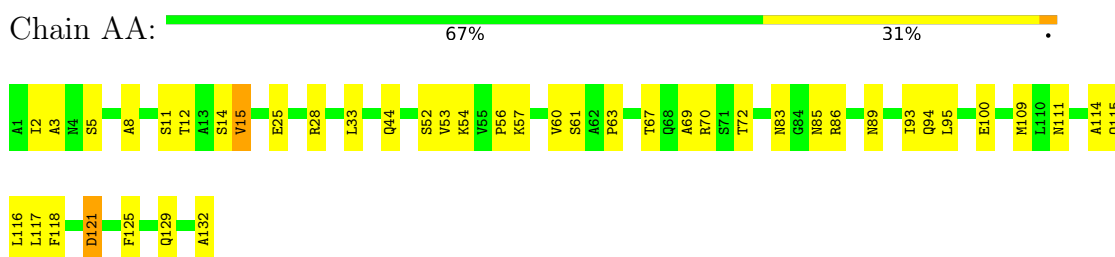
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Mol	Chain	Residues	Atoms					AltConf	Trace
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1	GK	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GL	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GM	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GN	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GO	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GP	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GQ	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GR	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GS	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GT	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GU	132	Total 978	C 609	N 168	O 200	S 1	0	0
1	GV	132	Total 978	C 609	N 168	O 200	S 1	0	0
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1	GX	132	Total 978	C 609	N 168	O 200	S 1	0	0

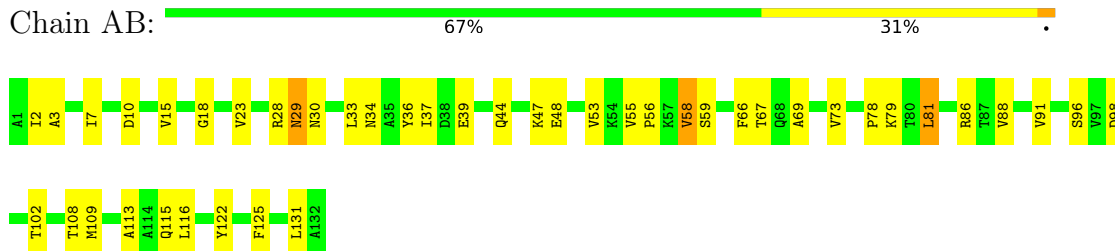
3 Residue-property plots

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.

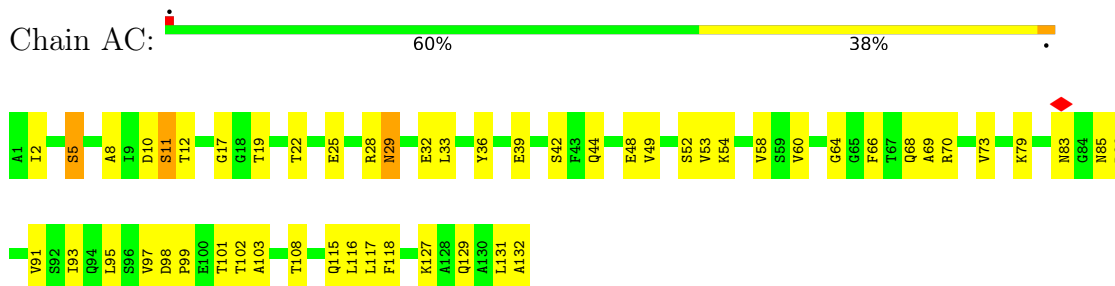
• Molecule 1: Coat protein



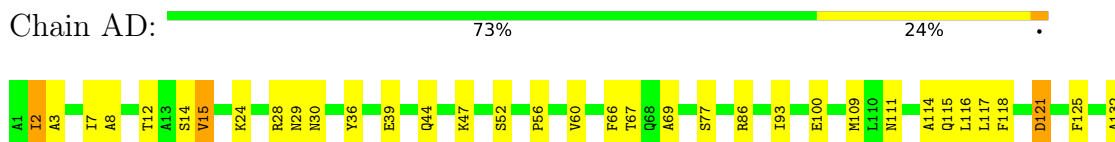
• Molecule 1: Coat protein



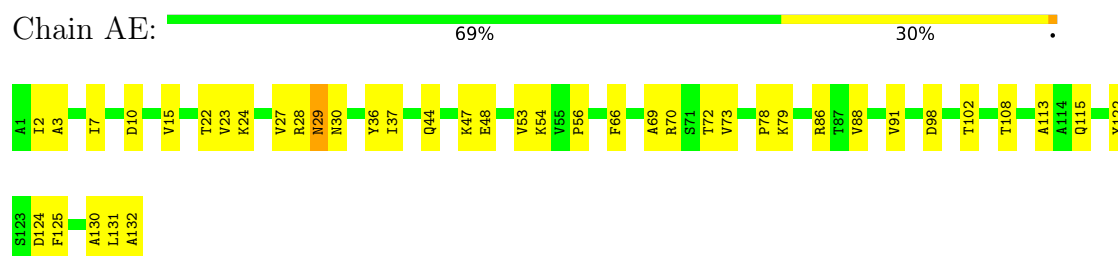
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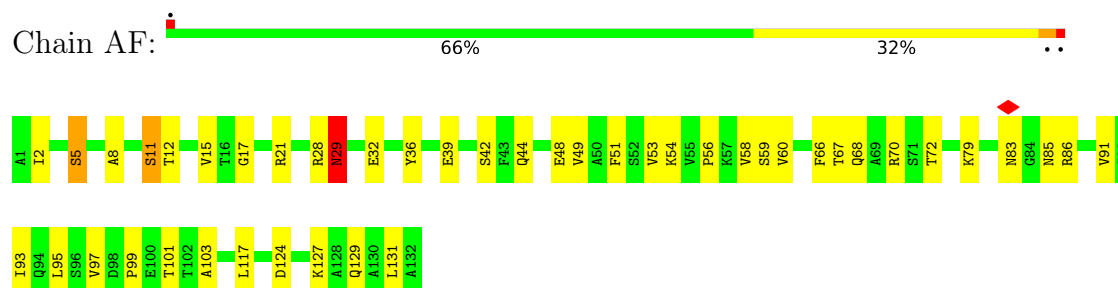
• Molecule 1: Coat protein



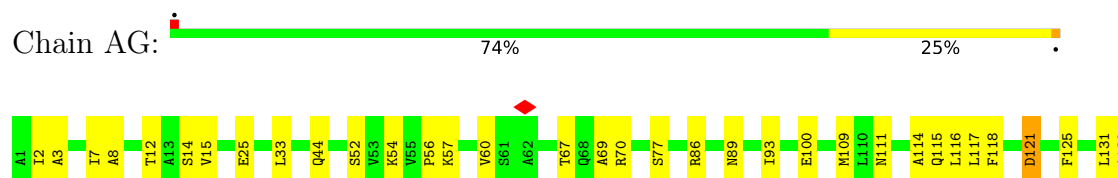
- Molecule 1: Coat protein



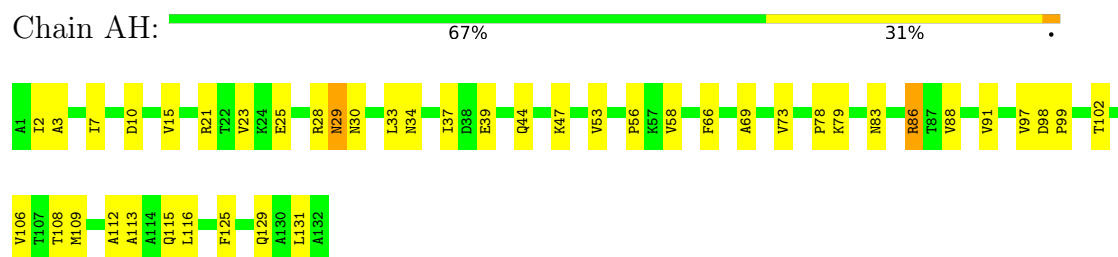
- Molecule 1: Coat protein



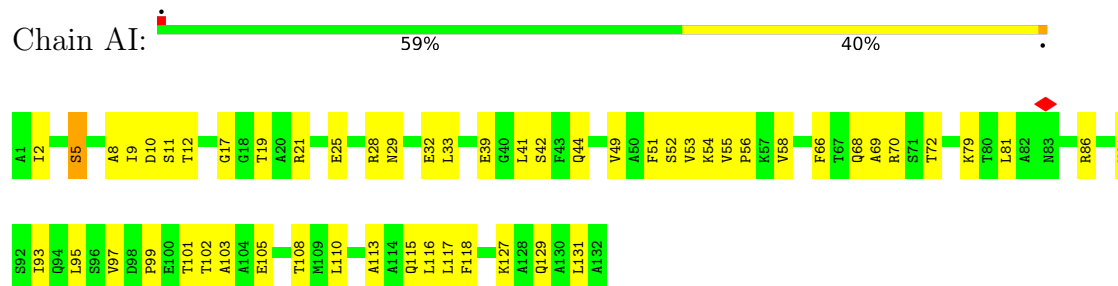
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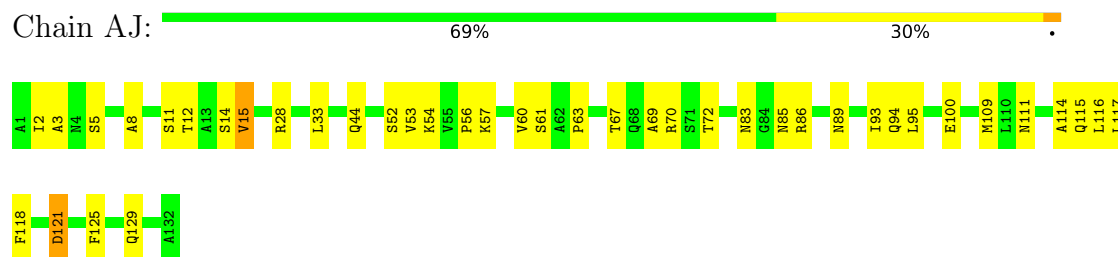
- Molecule 1: Coat protein



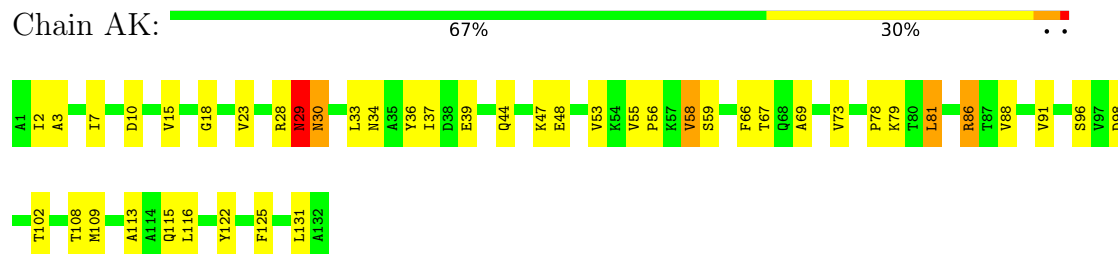
- Molecule 1: Coat protein



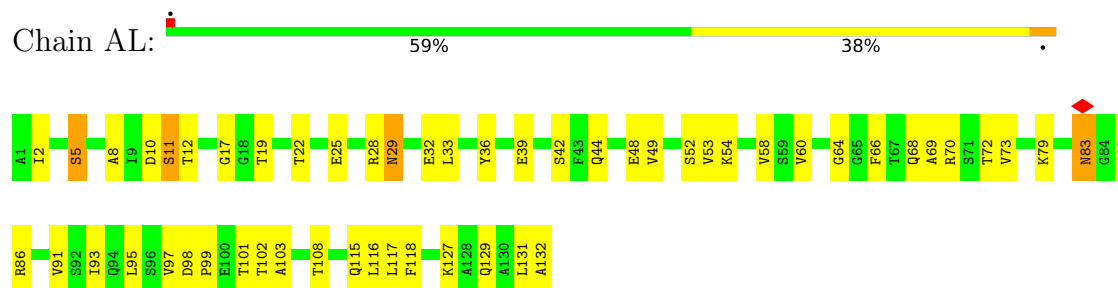
- Molecule 1: Coat protein



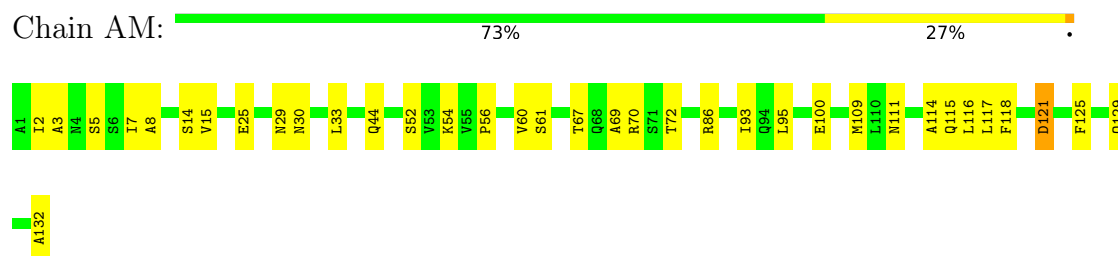
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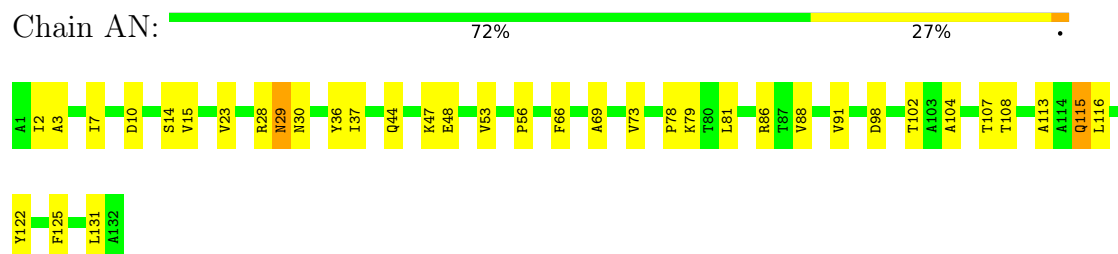
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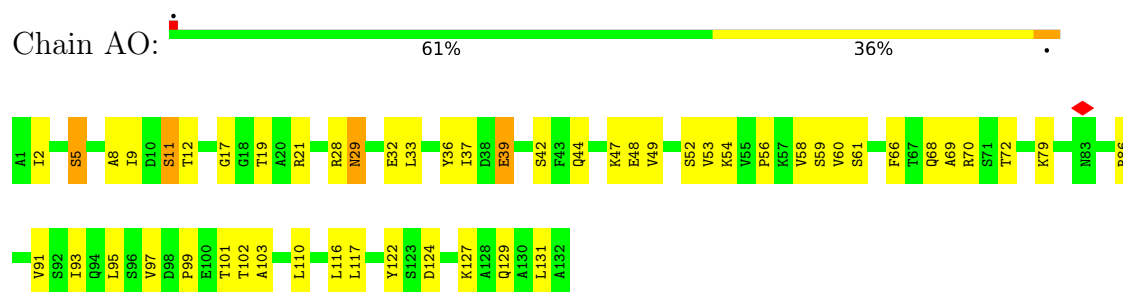
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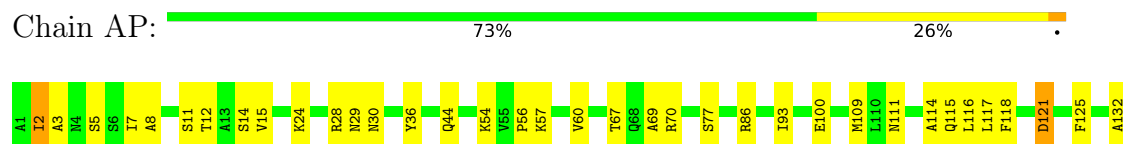
- Molecule 1: Coat protein



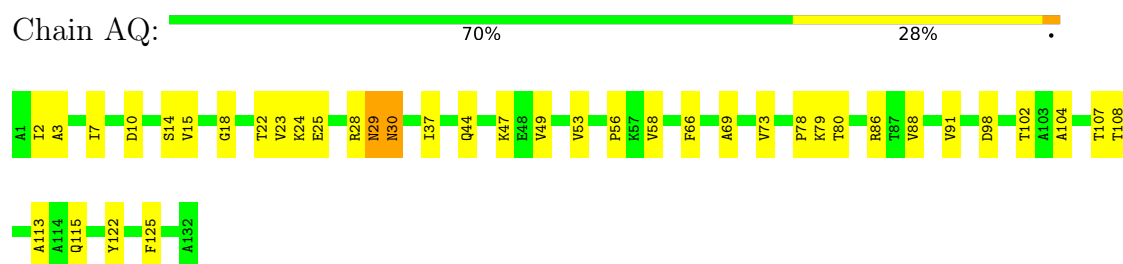
- Molecule 1: Coat protein



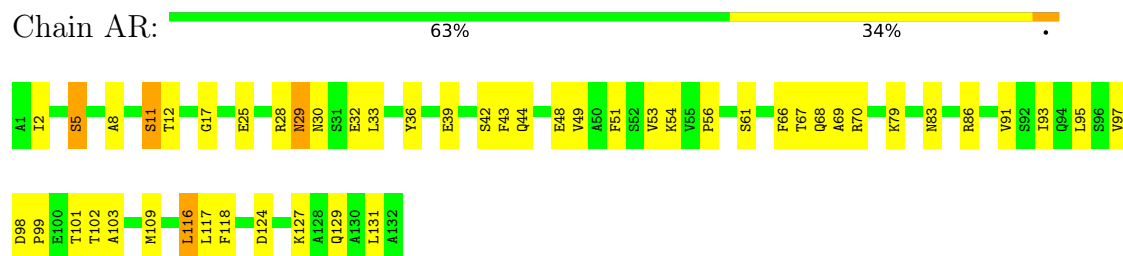
- Molecule 1: Coat protein



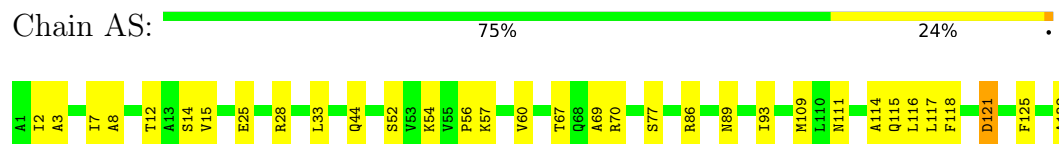
- Molecule 1: Coat protein



- Molecule 1: Coat protein

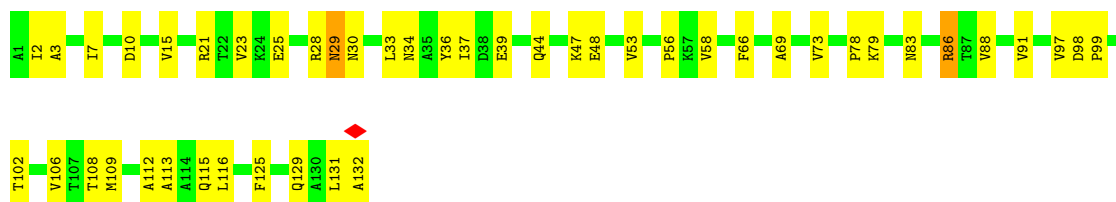


- Molecule 1: Coat protein

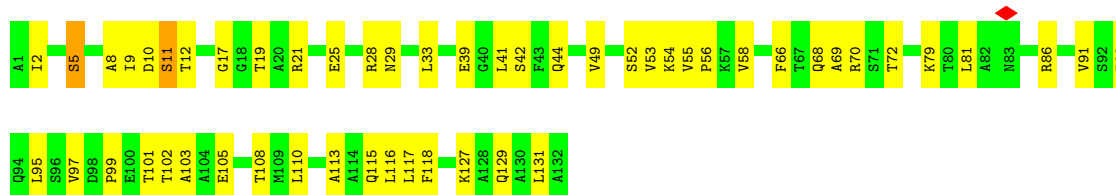


- Molecule 1: Coat protein

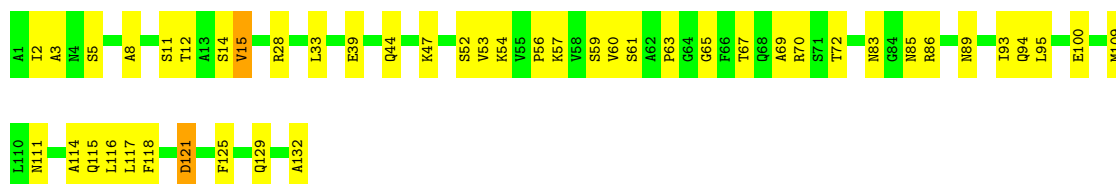




- Molecule 1: Coat protein



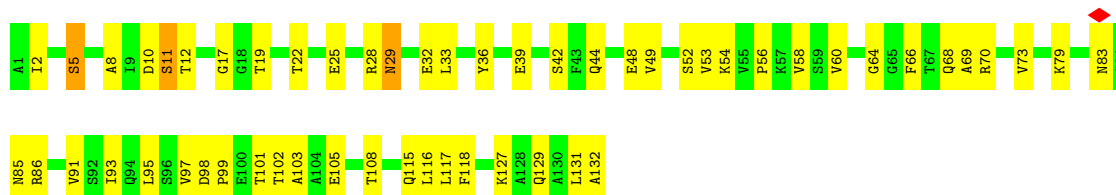
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



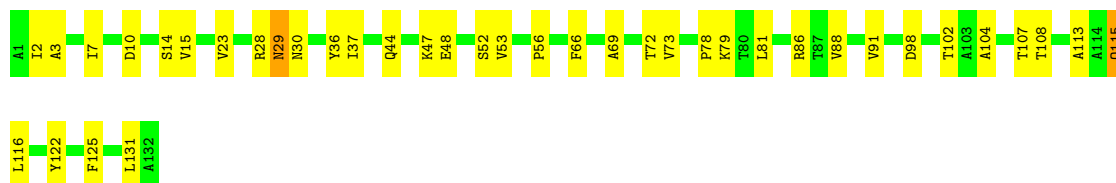
- Molecule 1: Coat protein

Chain AY:  74% 25% .



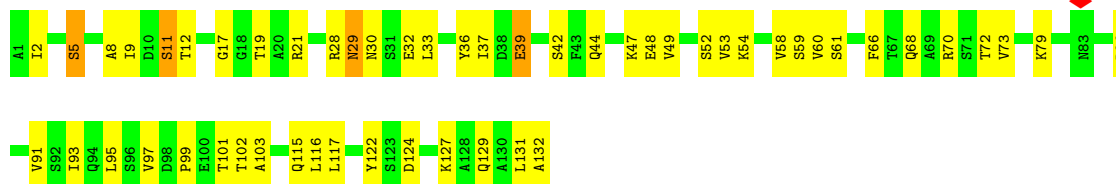
• Molecule 1: Coat protein

Chain AZ:  70% 28% .



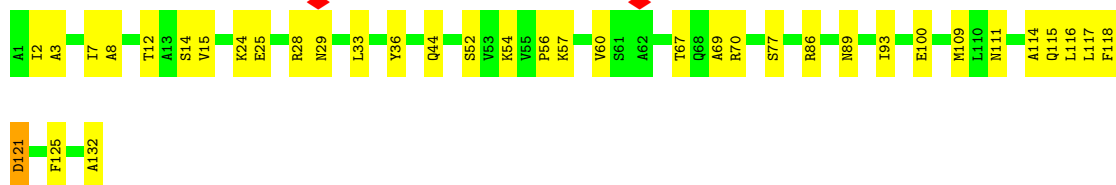
• Molecule 1: Coat protein

Chain BA:  60% 37% .



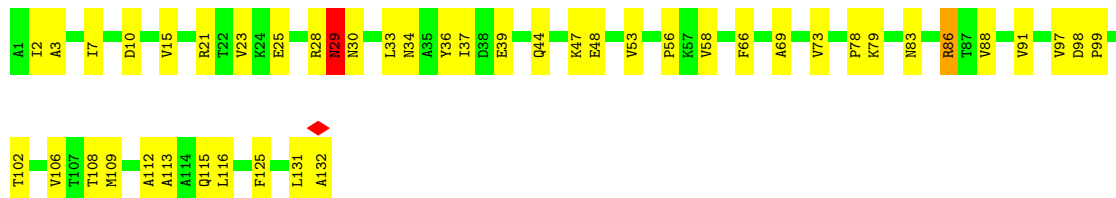
• Molecule 1: Coat protein

Chain BB:  72% 27% .

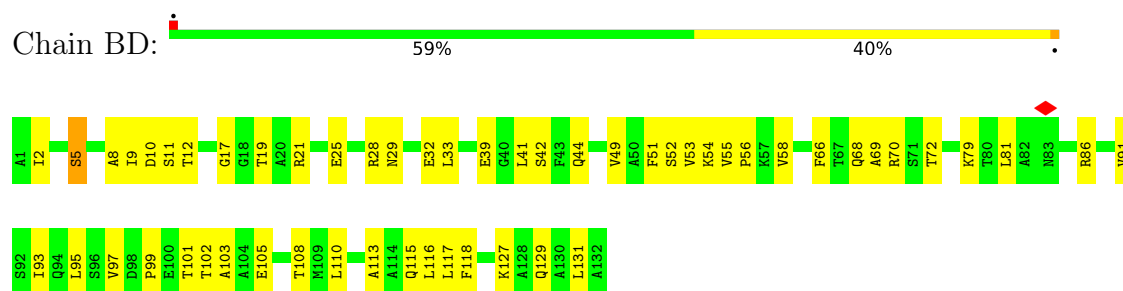


• Molecule 1: Coat protein

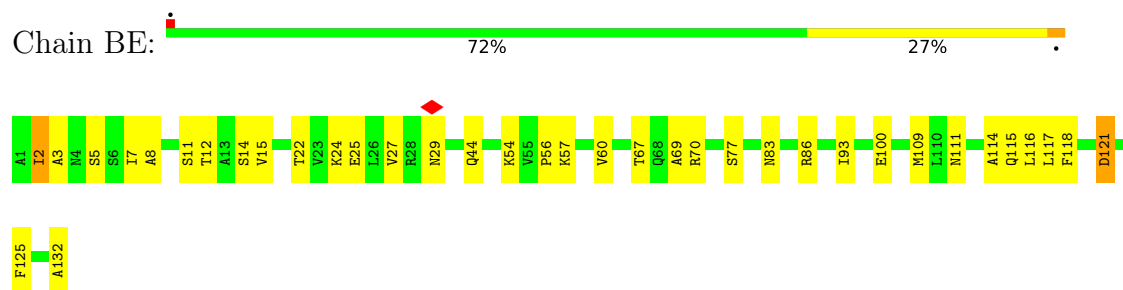
Chain BC:  66% 33% ..



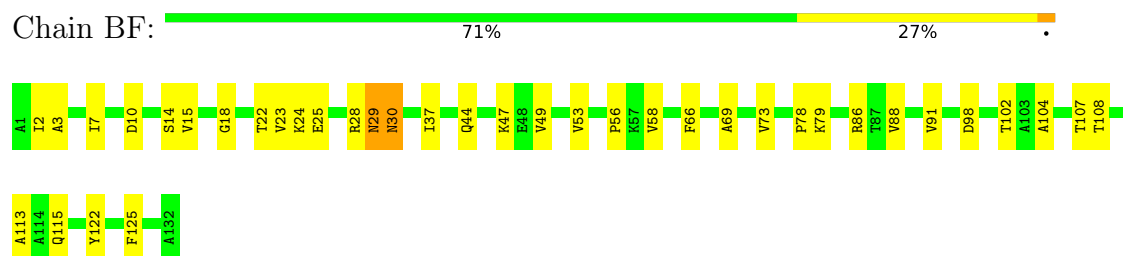
• Molecule 1: Coat protein



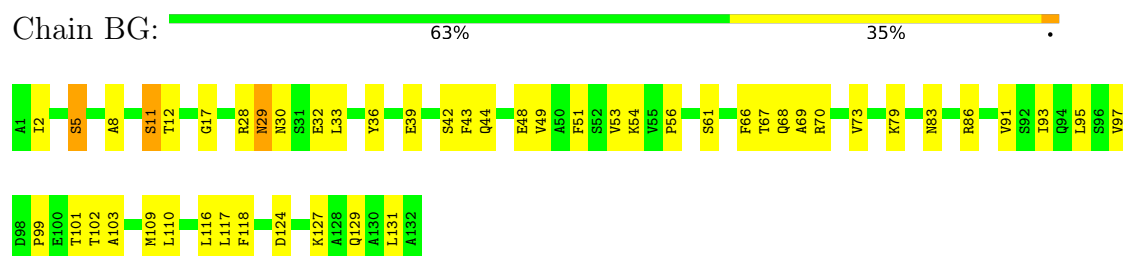
- Molecule 1: Coat protein



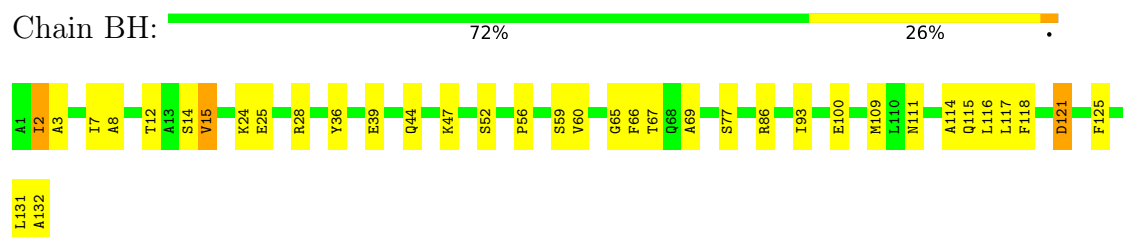
- Molecule 1: Coat protein



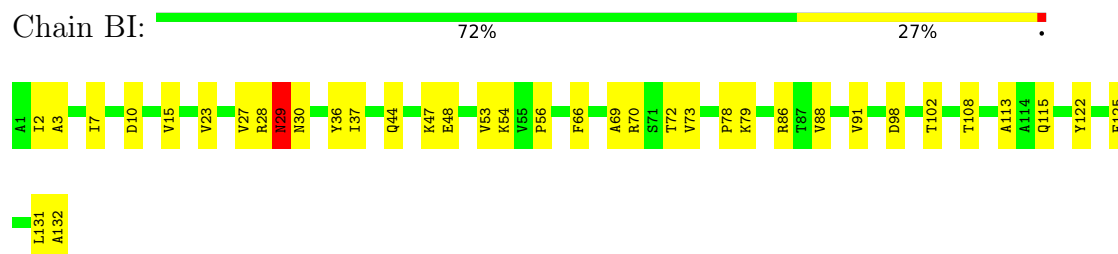
- Molecule 1: Coat protein



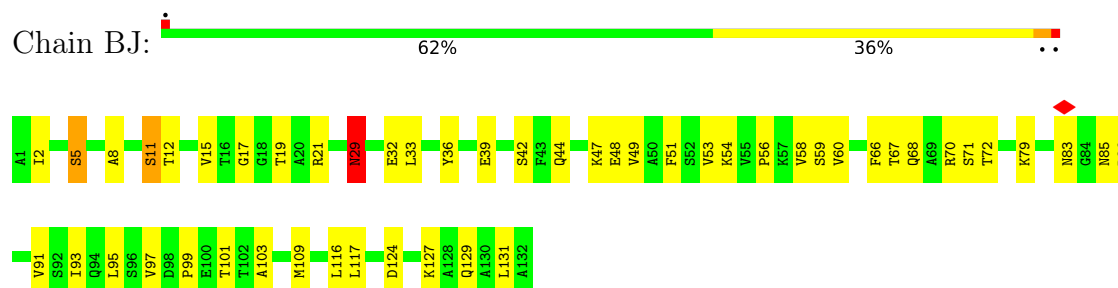
- Molecule 1: Coat protein



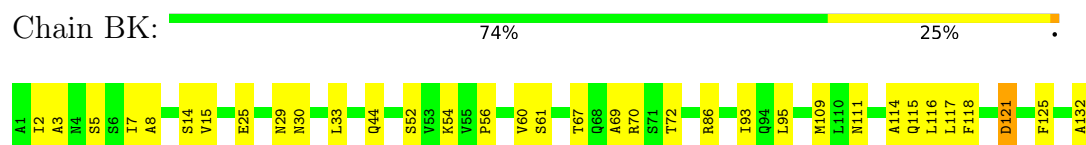
- Molecule 1: Coat protein



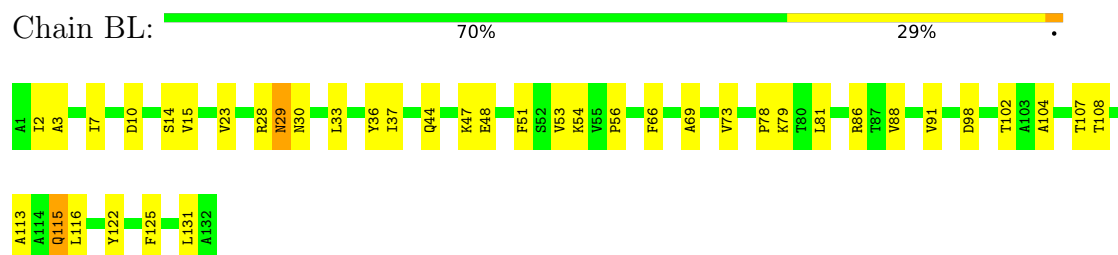
- Molecule 1: Coat protein



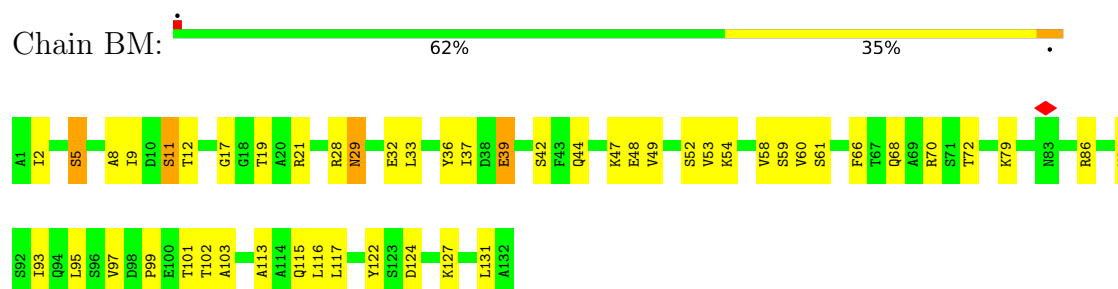
- Molecule 1: Coat protein



- Molecule 1: Coat protein

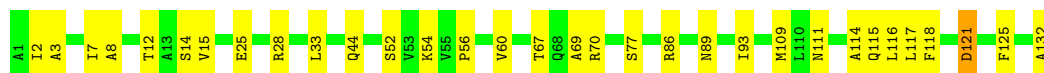


- Molecule 1: Coat protein



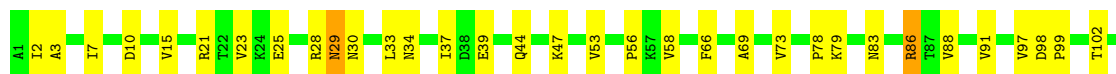
- Molecule 1: Coat protein

Chain BN:  76% 23%



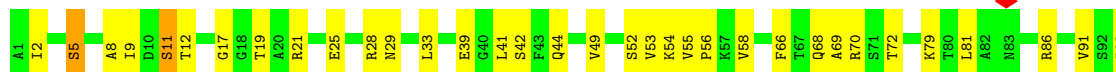
• Molecule 1: Coat protein

Chain BO:  67% 32%



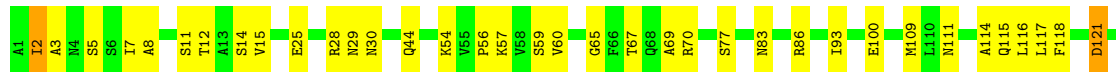
• Molecule 1: Coat protein

Chain BP:  63% 36%



• Molecule 1: Coat protein

Chain BQ:  71% 27%



• Molecule 1: Coat protein

Chain BR:  70% 28%



• Molecule 1: Coat protein

Chain BS:  64% 34%



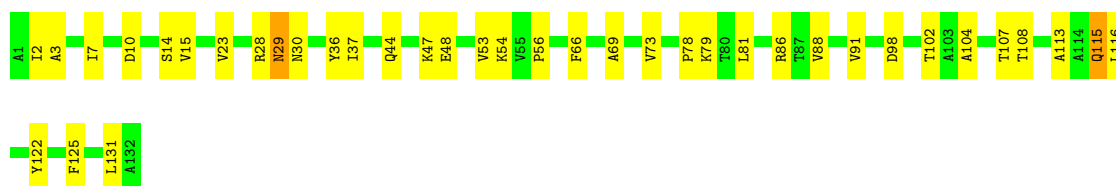
- Molecule 1: Coat protein

Chain BT: 73% 27% .



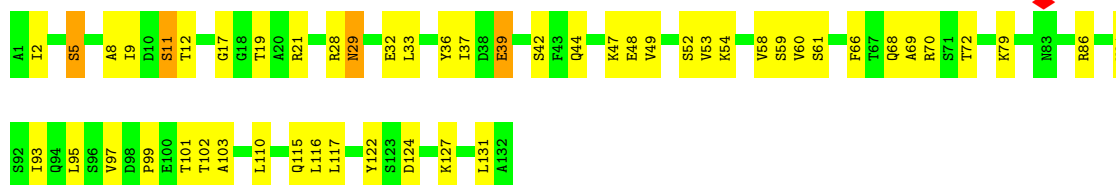
- Molecule 1: Coat protein

Chain BU: 71% 27% .



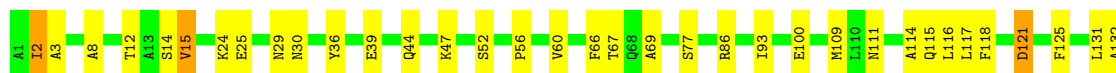
- Molecule 1: Coat protein

Chain BV: 61% 36% .



- Molecule 1: Coat protein

Chain BW: 73% 24% .



- Molecule 1: Coat protein

Chain BX: 69% 30% .





- Molecule 1: Coat protein

Chain BY: 63% 35% ..



- Molecule 1: Coat protein

Chain BZ: 70% 29% .



- Molecule 1: Coat protein

Chain CA: 66% 31% .



- Molecule 1: Coat protein

Chain CB: 63% 34% .



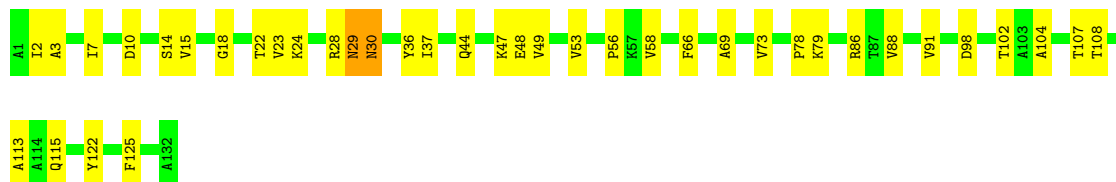
- Molecule 1: Coat protein

Chain CC: 72% 27% .



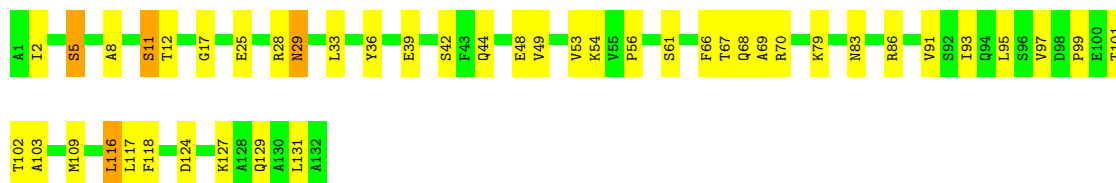
- Molecule 1: Coat protein

Chain CD: 70% 28% .



- Molecule 1: Coat protein

Chain CE: 67% 30% .



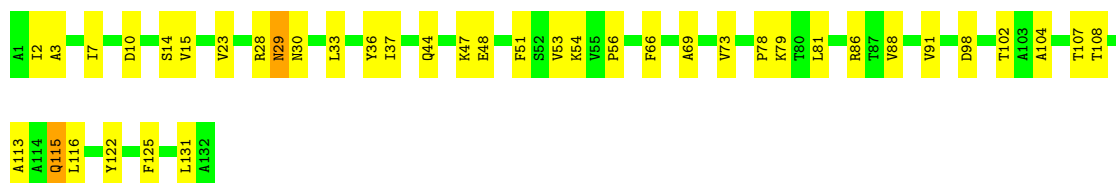
- Molecule 1: Coat protein

Chain CF: 73% 26% .



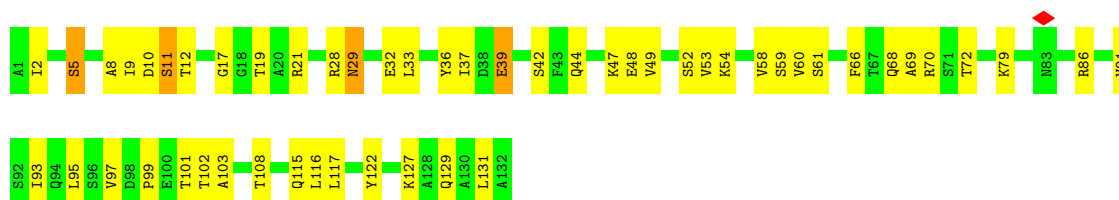
- Molecule 1: Coat protein

Chain CG: 70% 29% .



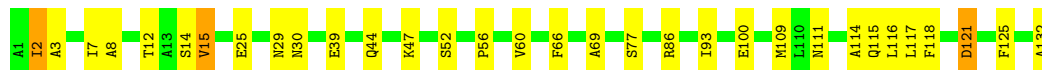
- Molecule 1: Coat protein

Chain CH: 61% 36% .



- Molecule 1: Coat protein

Chain CI: 76% 22% .



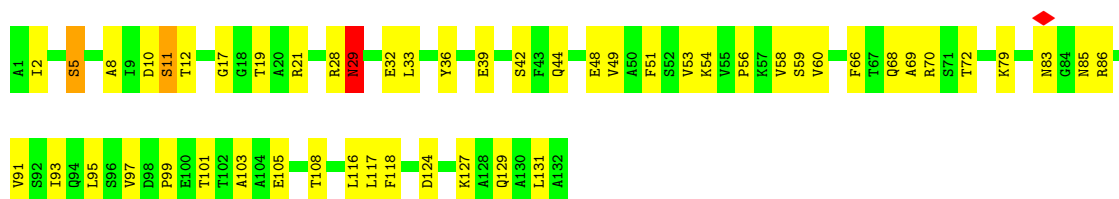
- Molecule 1: Coat protein

Chain CJ: 70% 30% .



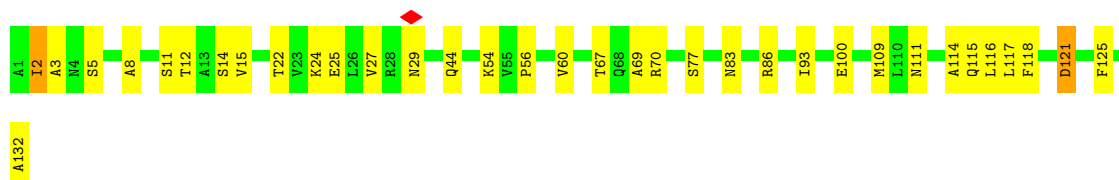
- Molecule 1: Coat protein

Chain CK: 61% 36% ..



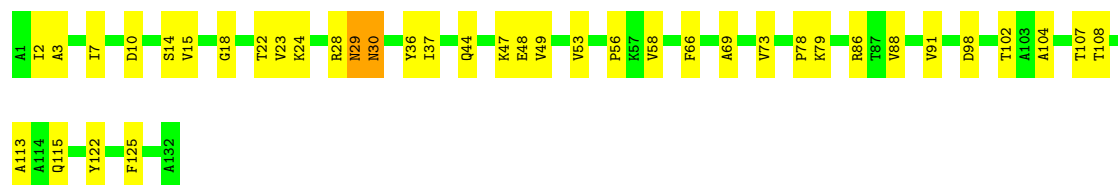
- Molecule 1: Coat protein

Chain CL: 73% 25% .



- Molecule 1: Coat protein

Chain CM: 70% 28% .



- Molecule 1: Coat protein



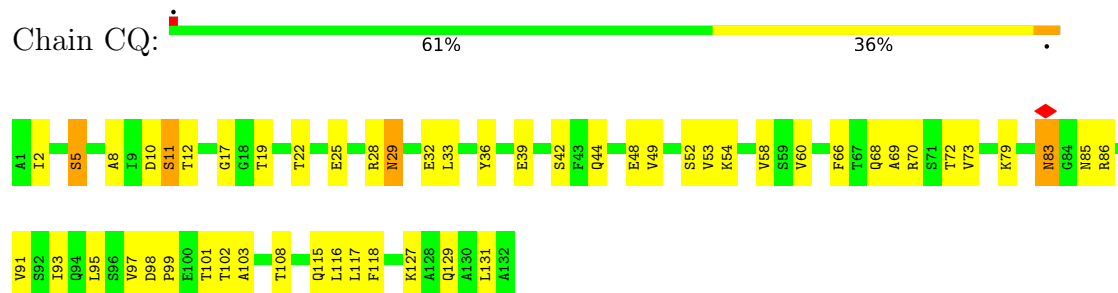
- Molecule 1: Coat protein



- Molecule 1: Coat protein

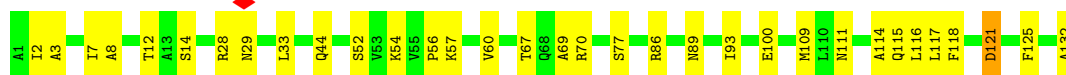


- Molecule 1: Coat protein



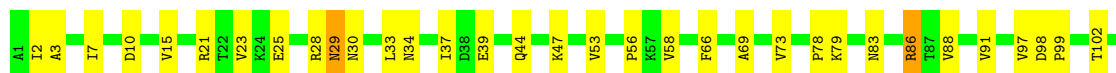
- Molecule 1: Coat protein

Chain CR:  75% 24%



• Molecule 1: Coat protein

Chain CS:  67% 31%



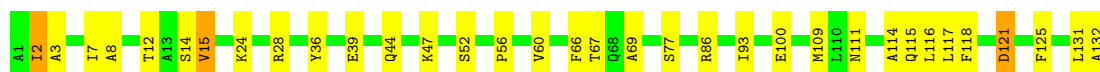
• Molecule 1: Coat protein

Chain CT:  61% 38%



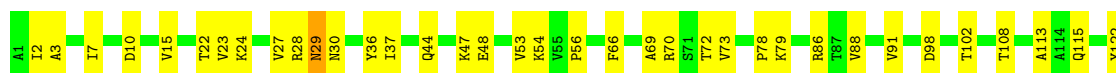
• Molecule 1: Coat protein

Chain CU:  74% 23%



• Molecule 1: Coat protein

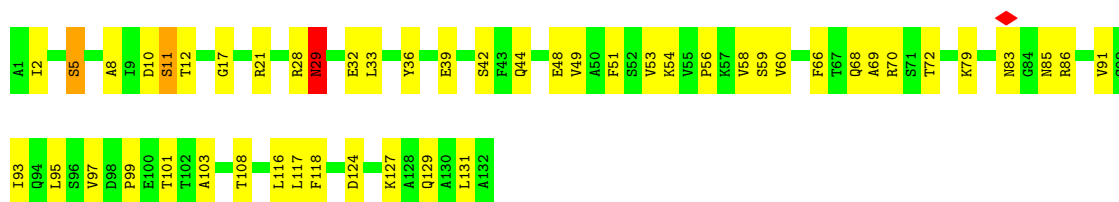
Chain CV:  70% 29%



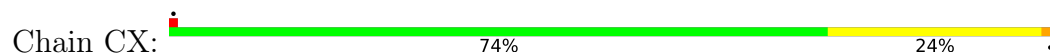
• Molecule 1: Coat protein

Chain CW:  63% 35%

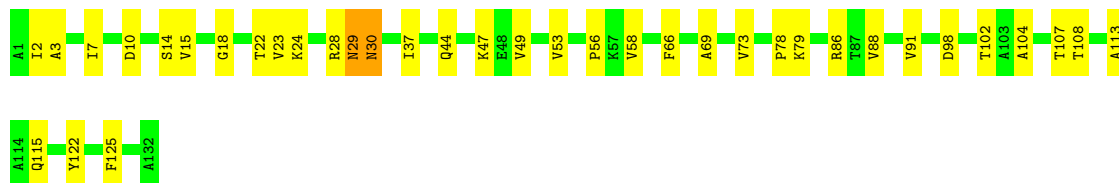




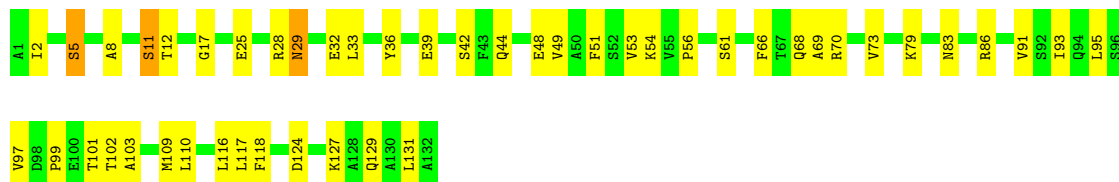
- Molecule 1: Coat protein



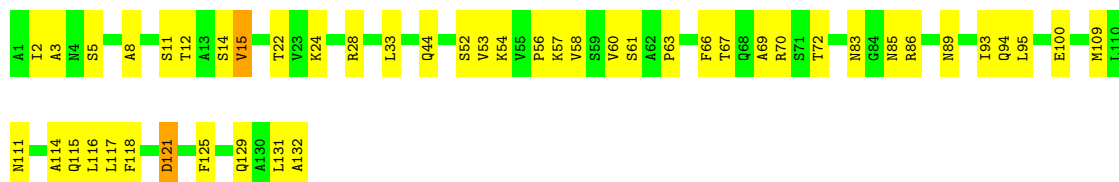
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

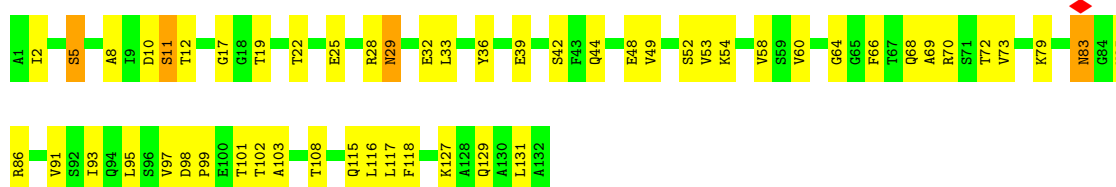


- Molecule 1: Coat protein

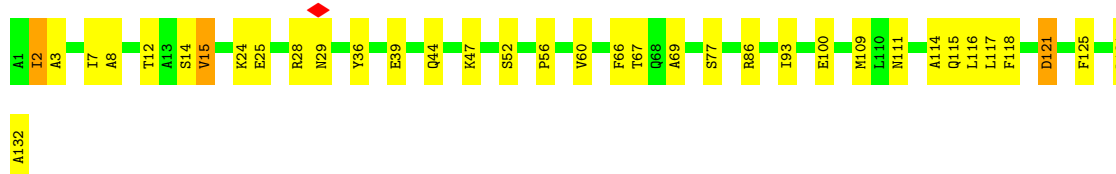
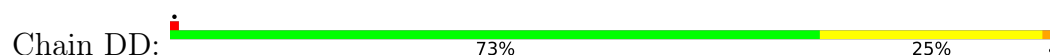




- Molecule 1: Coat protein



- Molecule 1: Coat protein



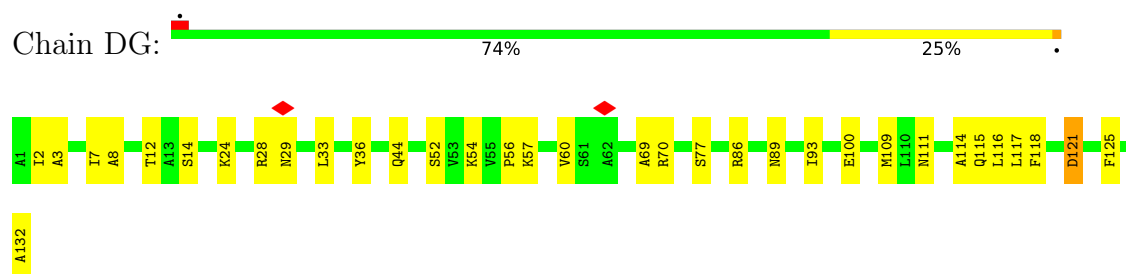
- Molecule 1: Coat protein



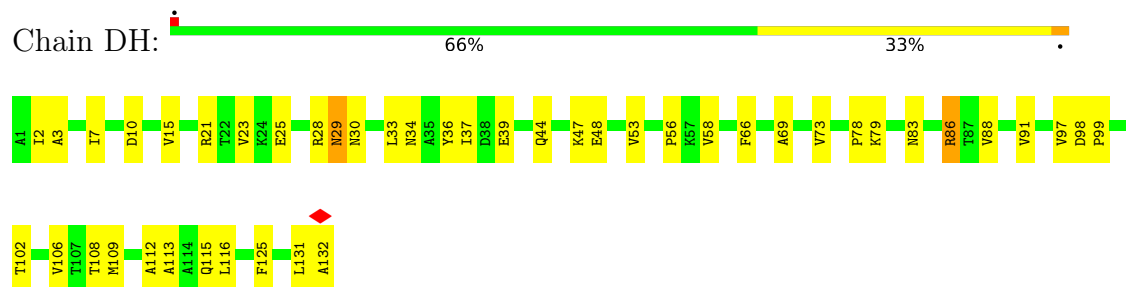
- Molecule 1: Coat protein



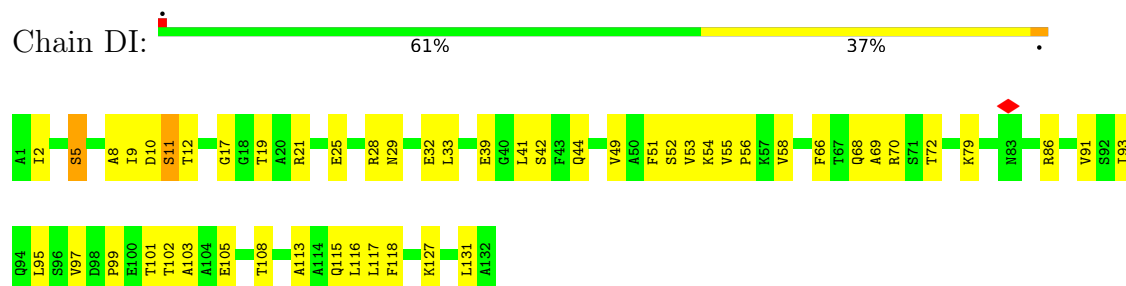
- Molecule 1: Coat protein



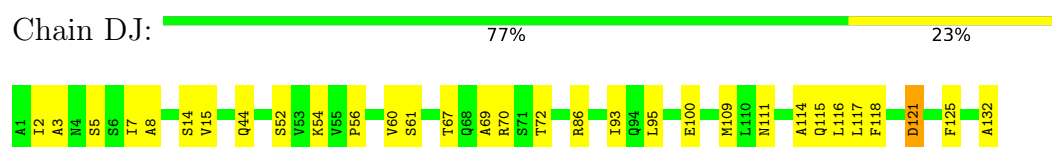
- Molecule 1: Coat protein



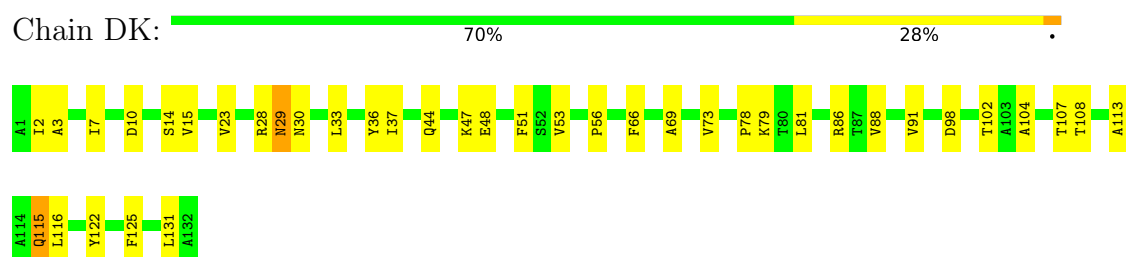
- Molecule 1: Coat protein



- Molecule 1: Coat protein

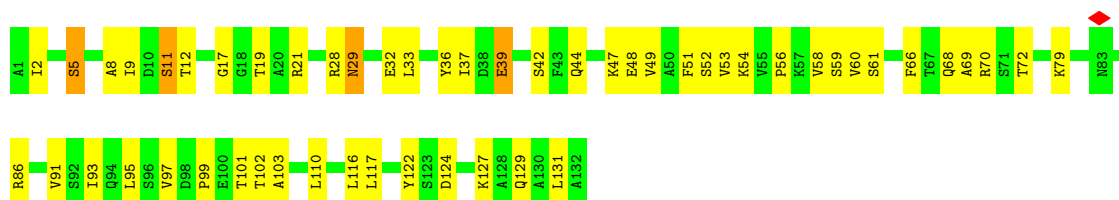


- Molecule 1: Coat protein



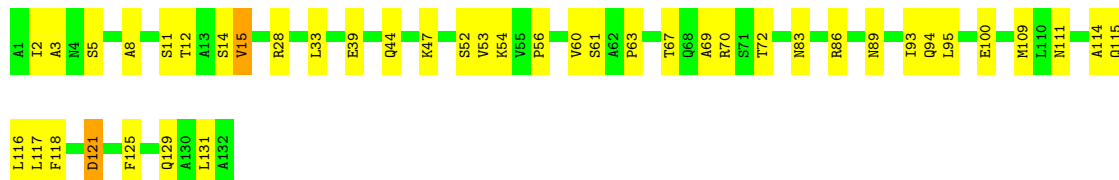
- Molecule 1: Coat protein





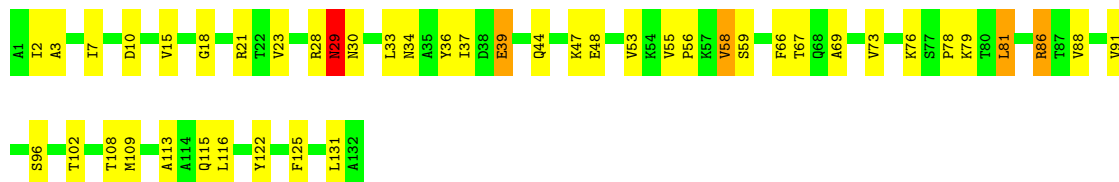
- Molecule 1: Coat protein

Chain DM: 68% 30% .



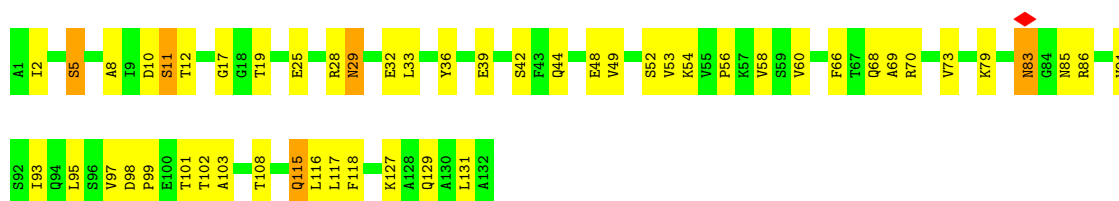
- Molecule 1: Coat protein

Chain DN: 66% 30% . .



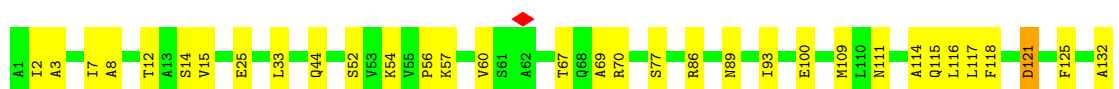
- Molecule 1: Coat protein

Chain DO: 61% 35% .



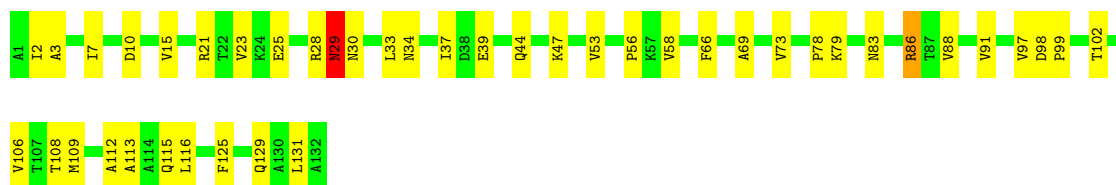
- Molecule 1: Coat protein

Chain DP: 75% 24% .



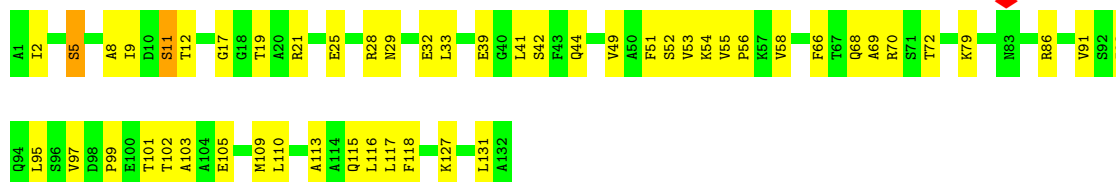
- Molecule 1: Coat protein

Chain DQ: 67% 31% . .



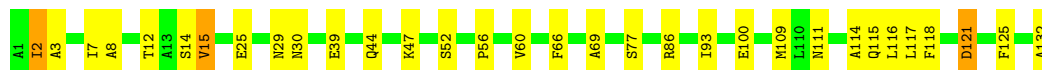
- Molecule 1: Coat protein

Chain DR: 61% 37% .



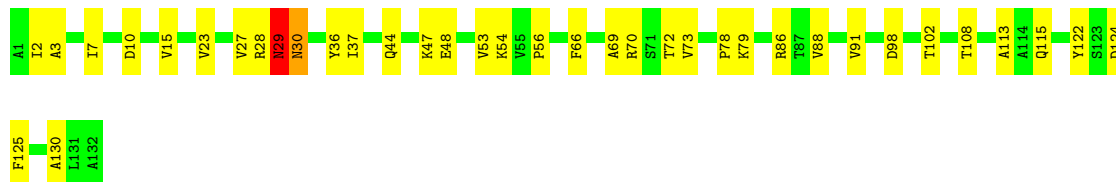
- Molecule 1: Coat protein

Chain DS: 76% 22% .



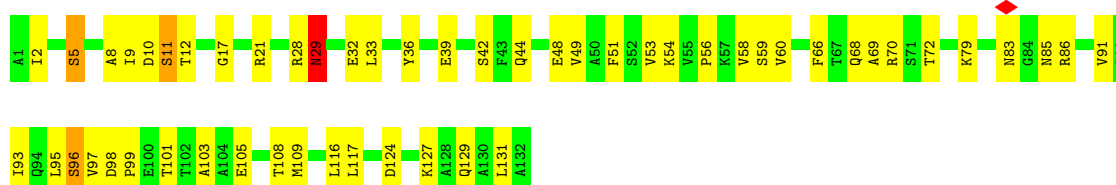
- Molecule 1: Coat protein

Chain DT: 72% 27% ..



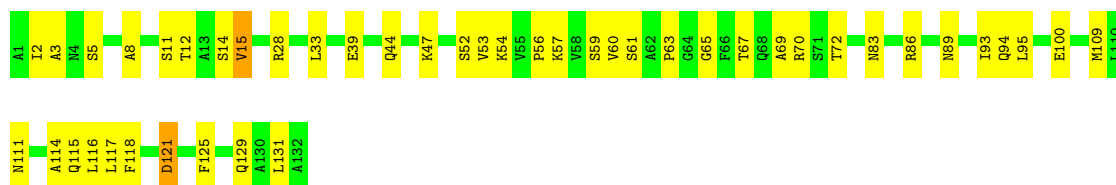
- Molecule 1: Coat protein

Chain DU: 60% 37% ..



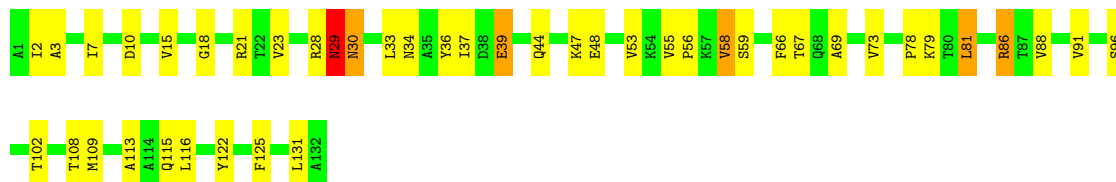
- Molecule 1: Coat protein

Chain DV: 66% 33% .



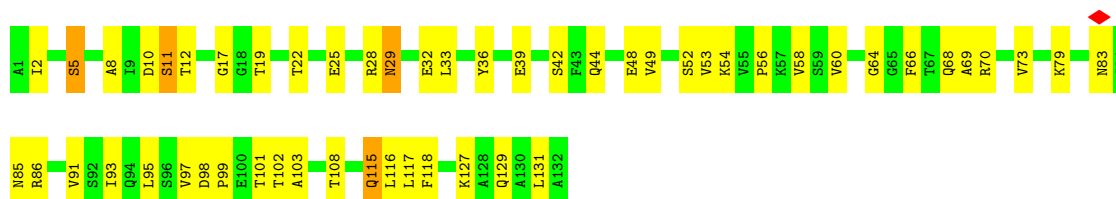
- Molecule 1: Coat protein

Chain DW: 67% 29%



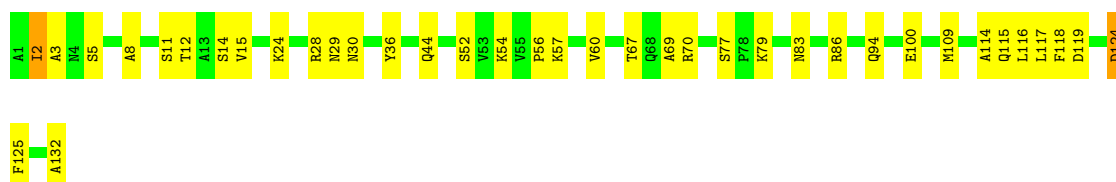
- Molecule 1: Coat protein

Chain DX: 60% 37%



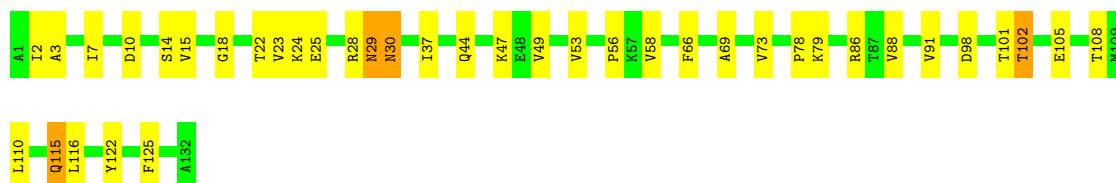
- Molecule 1: Coat protein

Chain DY: 71% 27%



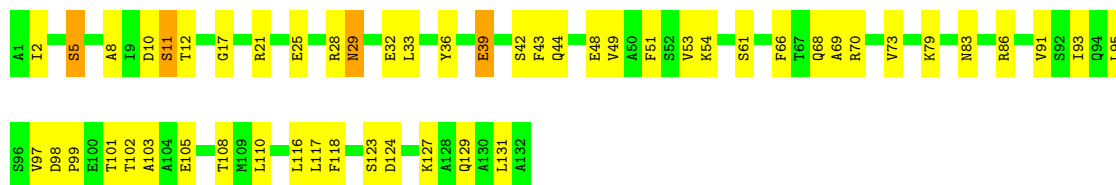
- Molecule 1: Coat protein

Chain DZ: 70% 27%



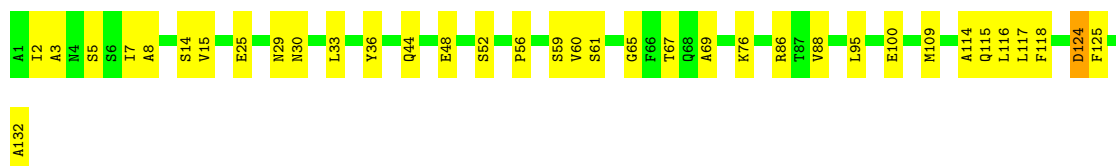
- Molecule 1: Coat protein

Chain EA:  61% 36%



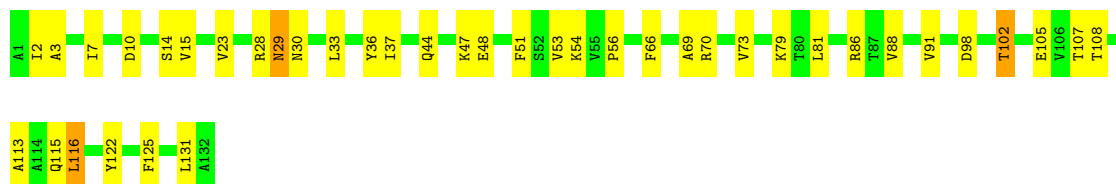
• Molecule 1: Coat protein

Chain EB:  73% 27%



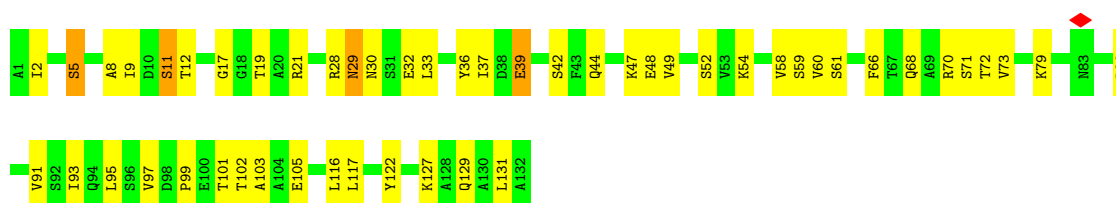
• Molecule 1: Coat protein

Chain EC:  70% 28%



• Molecule 1: Coat protein

Chain ED:  61% 36%



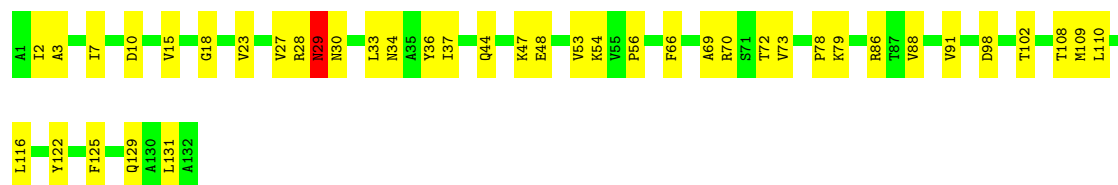
• Molecule 1: Coat protein

Chain EE:  75% 23%

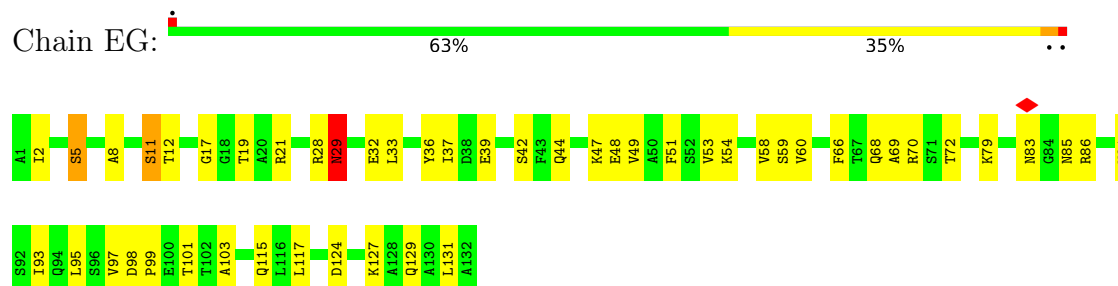


• Molecule 1: Coat protein

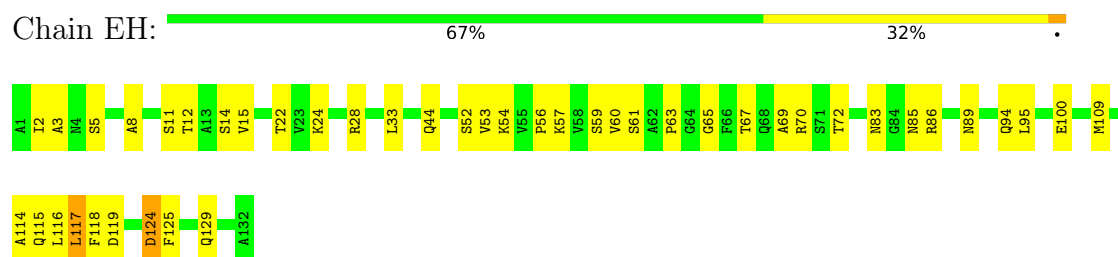
Chain EF:  69% 30%



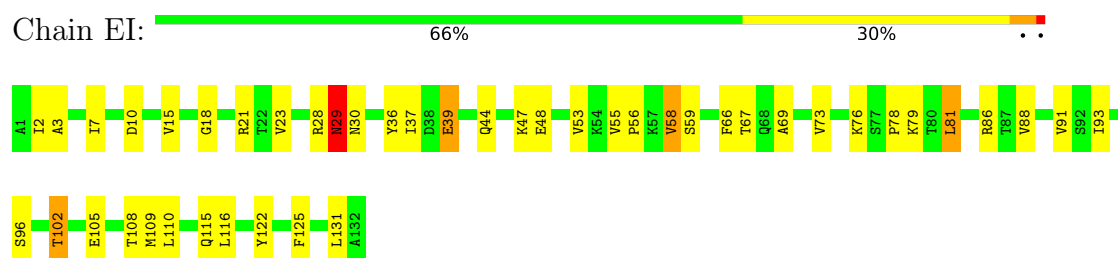
- Molecule 1: Coat protein



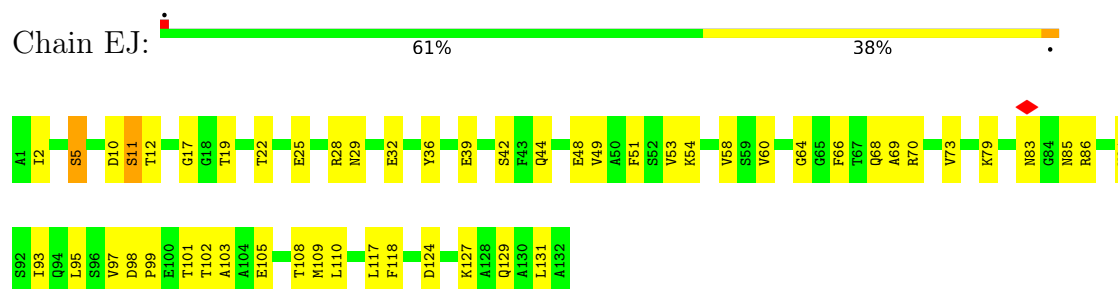
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

Chain EK:  68% 30% .



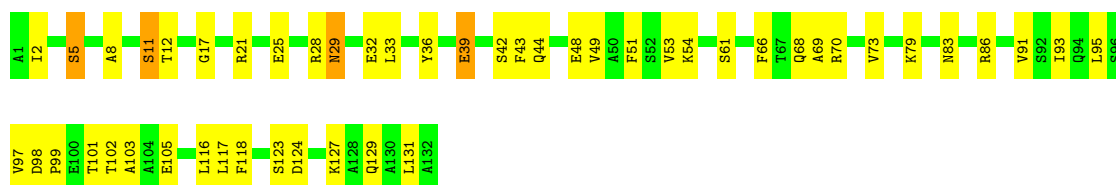
• Molecule 1: Coat protein

Chain EL:  69% 28% .



• Molecule 1: Coat protein

Chain EM:  63% 34% .



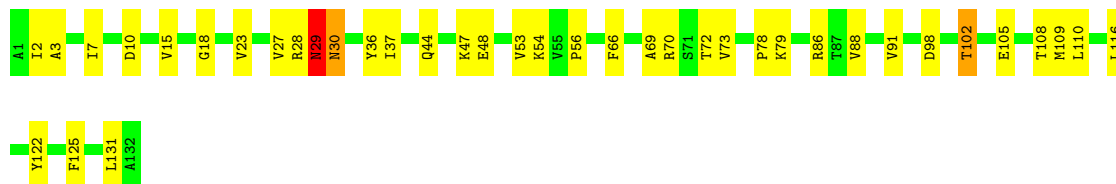
• Molecule 1: Coat protein

Chain EN:  76% 23% .



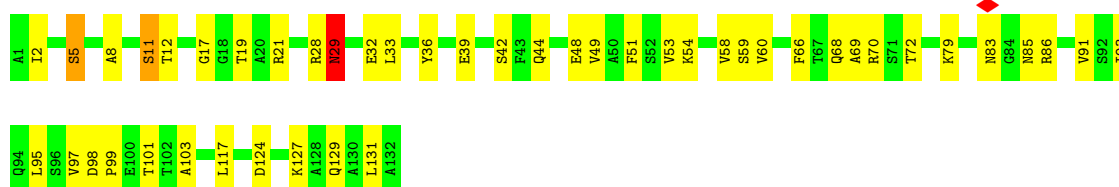
• Molecule 1: Coat protein

Chain EO:  70% 27% ..



• Molecule 1: Coat protein

Chain EP:  65% 33% ..



- Molecule 1: Coat protein

Chain EQ: 74% 25% .



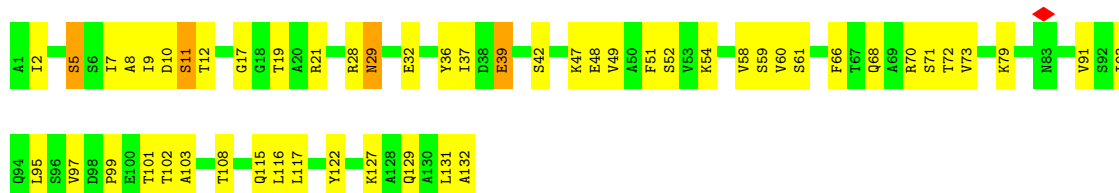
- Molecule 1: Coat protein

Chain ER: 70% 27% .



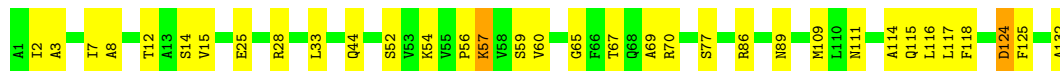
- Molecule 1: Coat protein

Chain ES: 61% 36% .



- Molecule 1: Coat protein

Chain ET: 74% 24% .



- Molecule 1: Coat protein

Chain EU: 68% 30% .

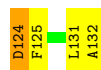
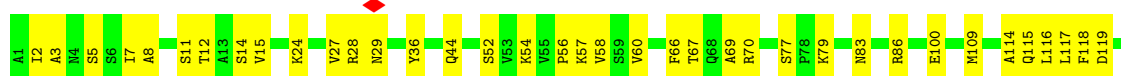




- Molecule 1: Coat protein



- Molecule 1: Coat protein



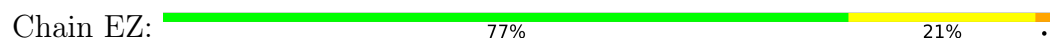
- Molecule 1: Coat protein

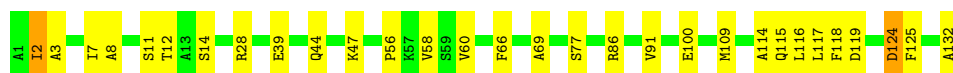


- Molecule 1: Coat protein



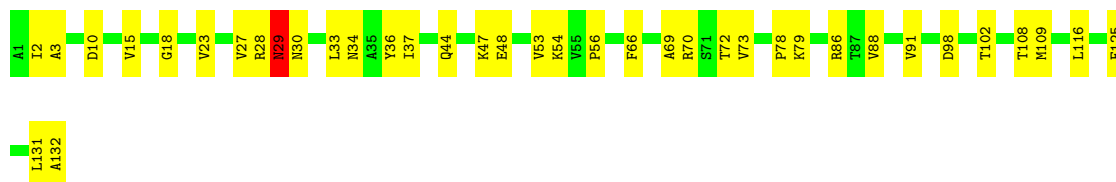
- Molecule 1: Coat protein





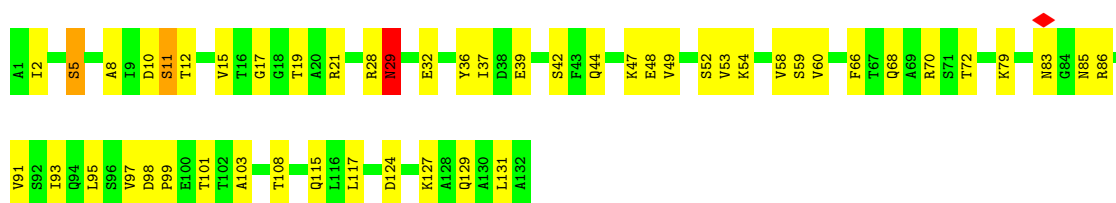
- Molecule 1: Coat protein

Chain FA: 71% 28%



- Molecule 1: Coat protein

Chain FB: 62% 36%



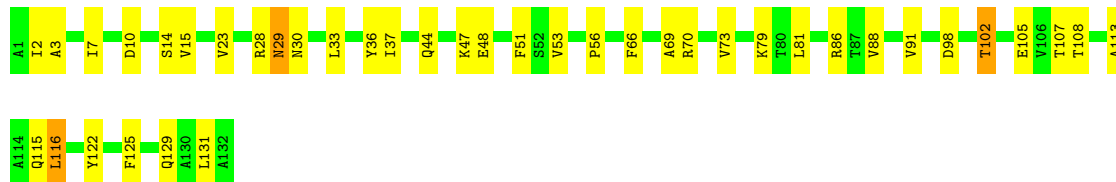
- Molecule 1: Coat protein

Chain FC: 78% 21%



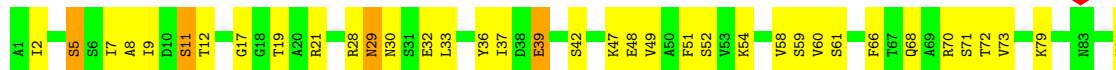
- Molecule 1: Coat protein

Chain FD: 70% 28%



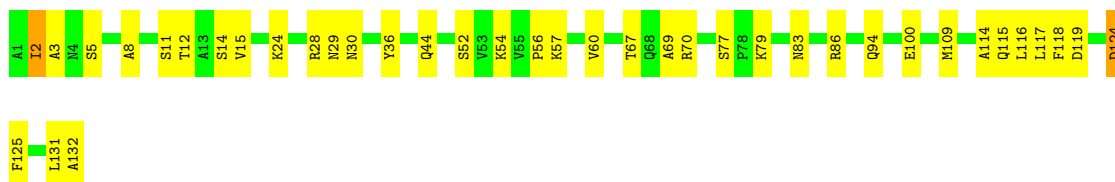
- Molecule 1: Coat protein

Chain FE: 59% 38%

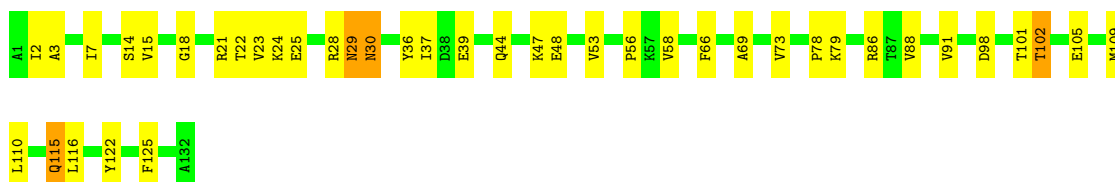




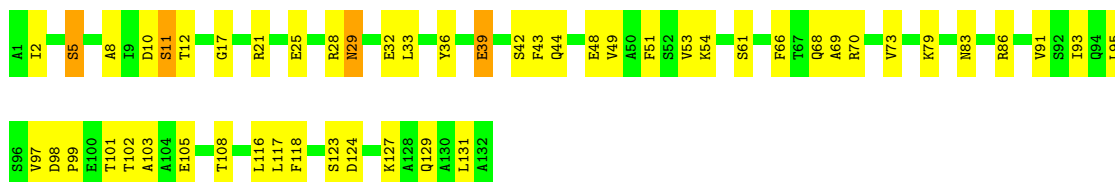
- Molecule 1: Coat protein



- Molecule 1: Coat protein



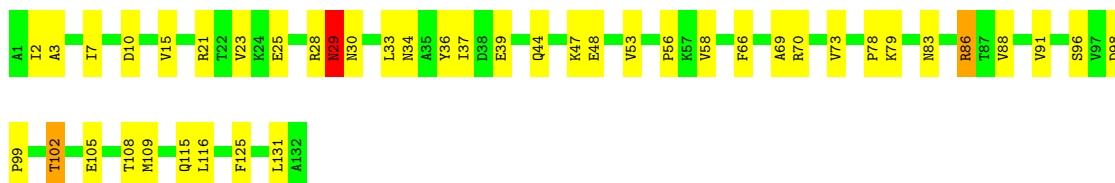
- Molecule 1: Coat protein



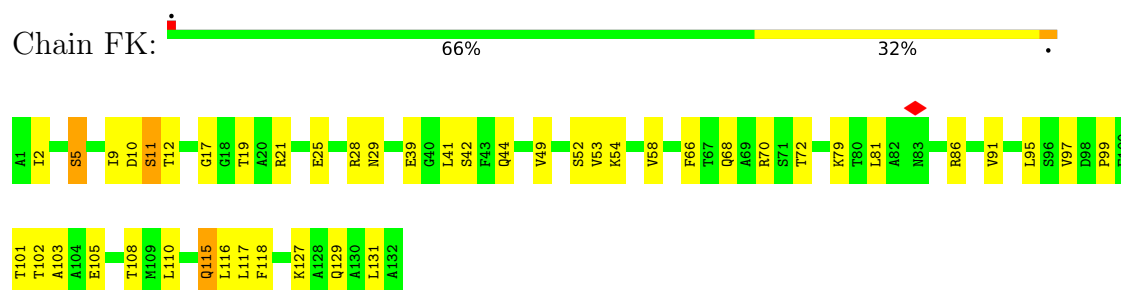
- Molecule 1: Coat protein



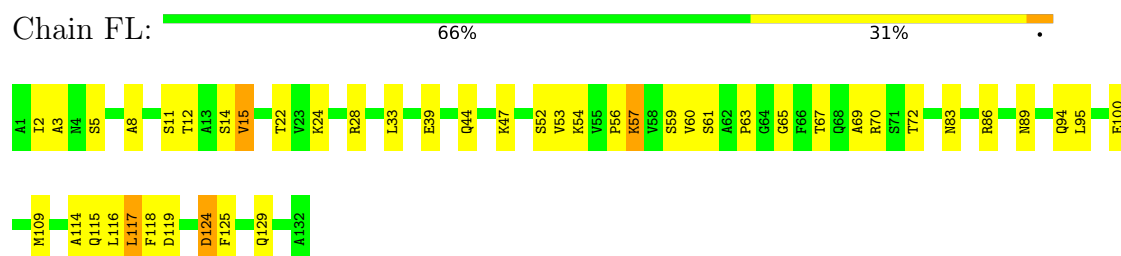
- Molecule 1: Coat protein



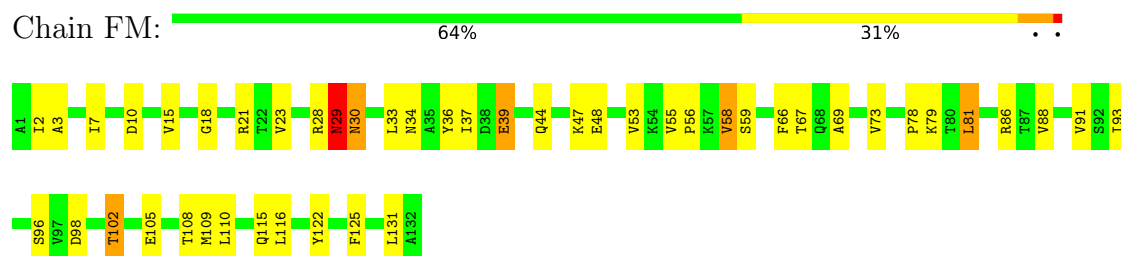
- Molecule 1: Coat protein



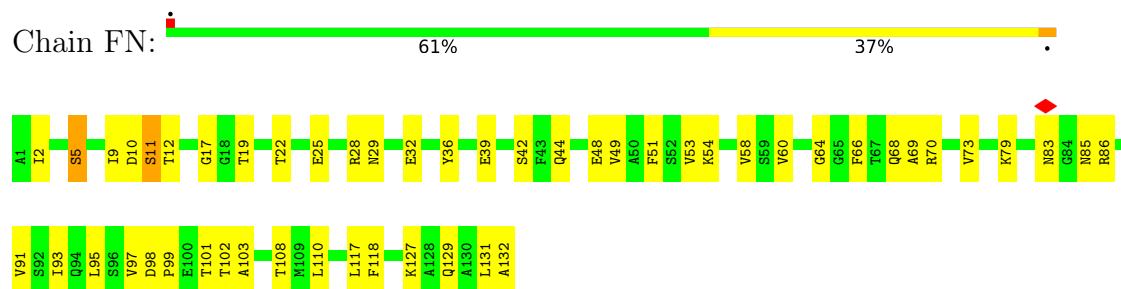
- Molecule 1: Coat protein



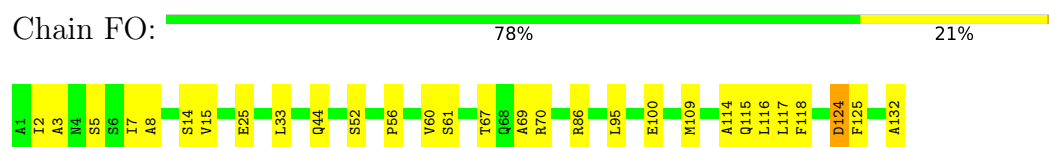
- Molecule 1: Coat protein



- Molecule 1: Coat protein

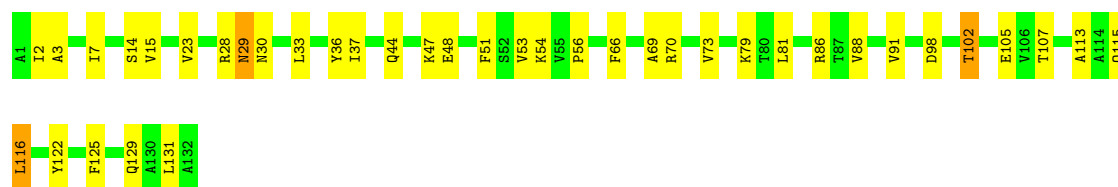


- Molecule 1: Coat protein



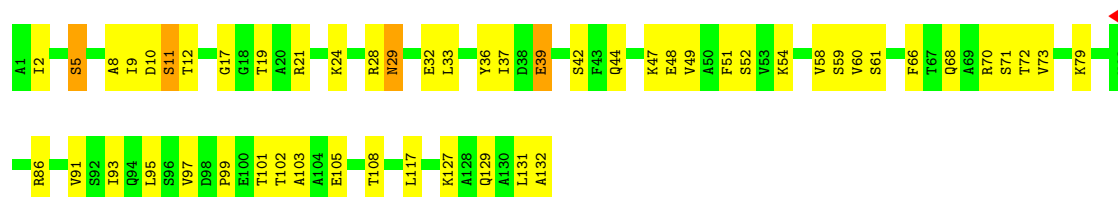
- Molecule 1: Coat protein

Chain FP:  70% 27% .



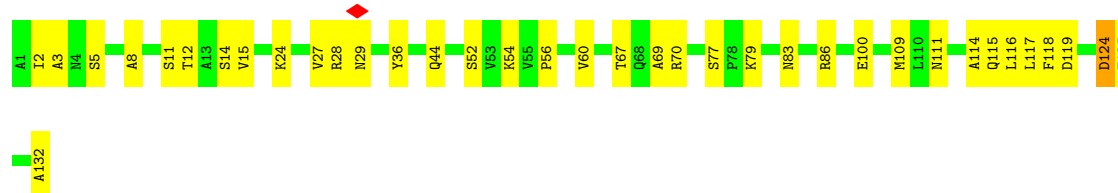
• Molecule 1: Coat protein

Chain FQ:  60% 37% .



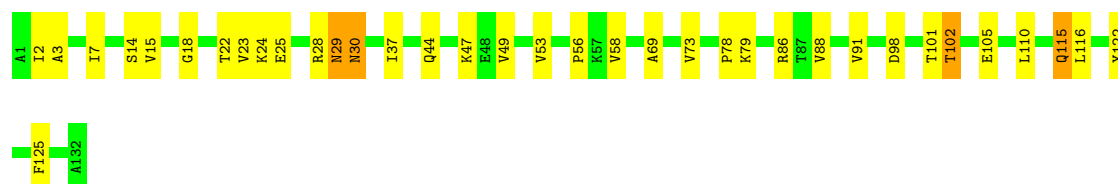
• Molecule 1: Coat protein

Chain FR:  72% 27% .



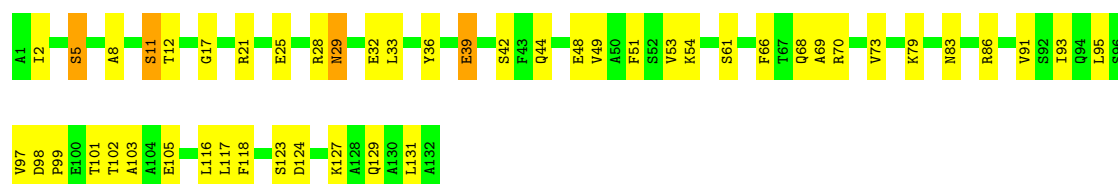
• Molecule 1: Coat protein

Chain FS:  73% 24% .

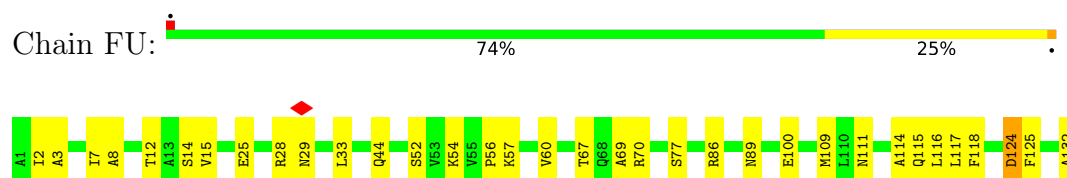


• Molecule 1: Coat protein

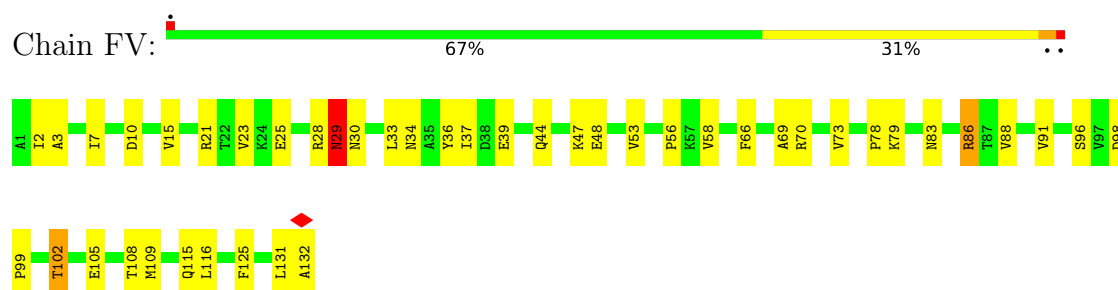
Chain FT:  64% 33% .



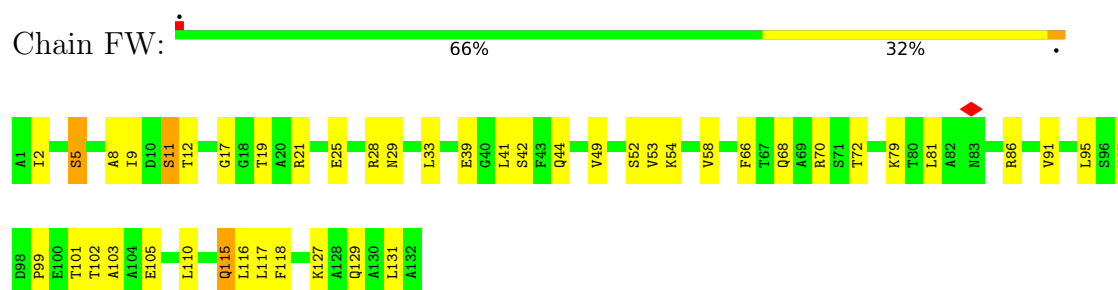
● Molecule 1: Coat protein



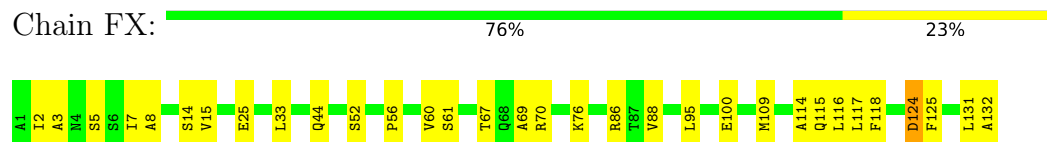
● Molecule 1: Coat protein



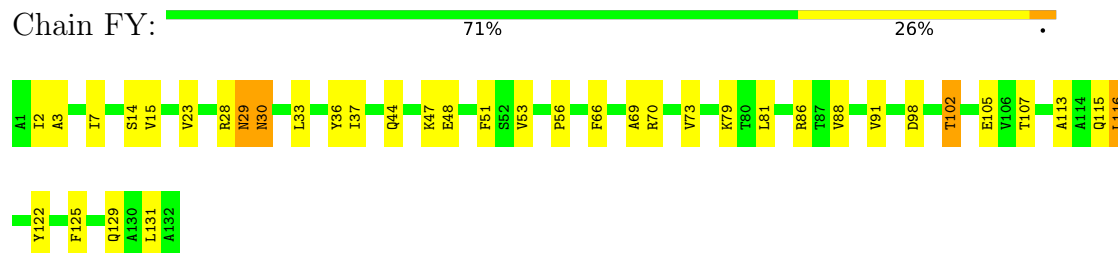
● Molecule 1: Coat protein



● Molecule 1: Coat protein



● Molecule 1: Coat protein

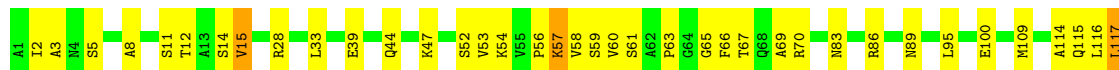


● Molecule 1: Coat protein

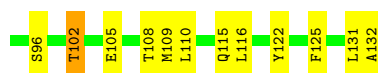




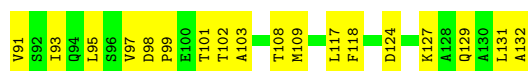
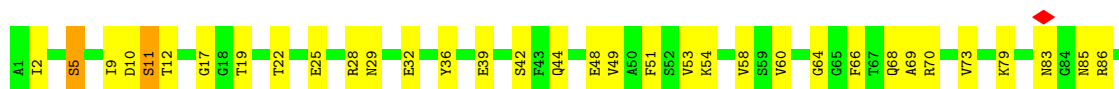
• Molecule 1: Coat protein



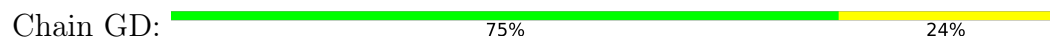
• Molecule 1: Coat protein



• Molecule 1: Coat protein



• Molecule 1: Coat protein

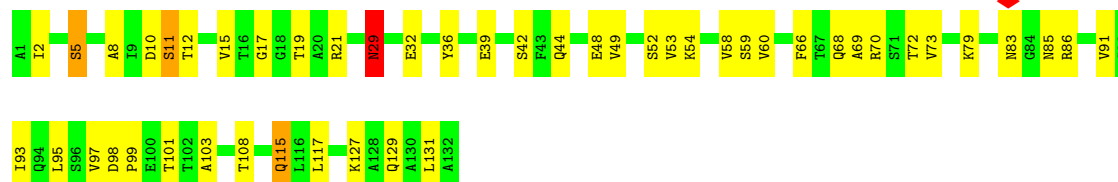


• Molecule 1: Coat protein

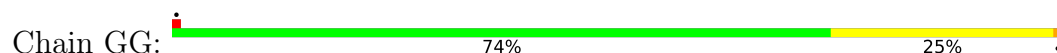




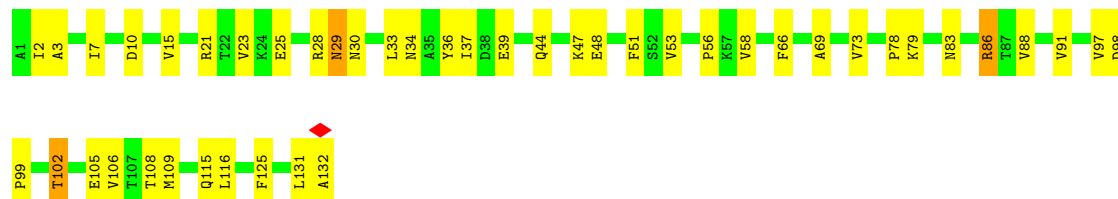
- Molecule 1: Coat protein



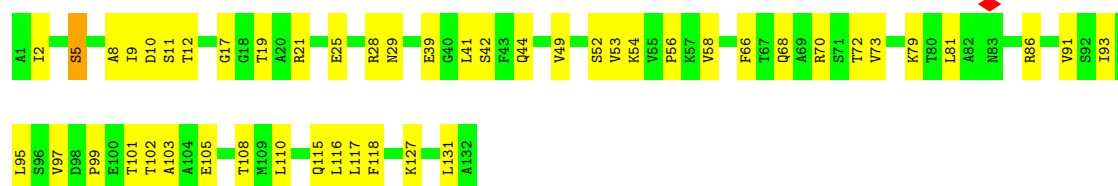
- Molecule 1: Coat protein



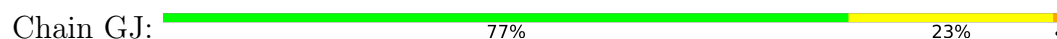
- Molecule 1: Coat protein



- Molecule 1: Coat protein



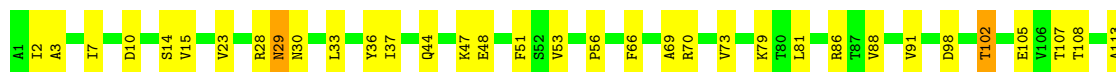
- Molecule 1: Coat protein





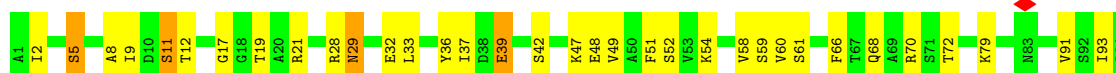
- Molecule 1: Coat protein

Chain GK: 70% 28% .



- Molecule 1: Coat protein

Chain GL: 64% 33% .



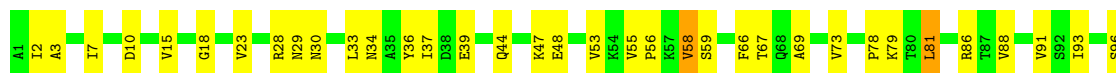
- Molecule 1: Coat protein

Chain GM: 65% 32% .



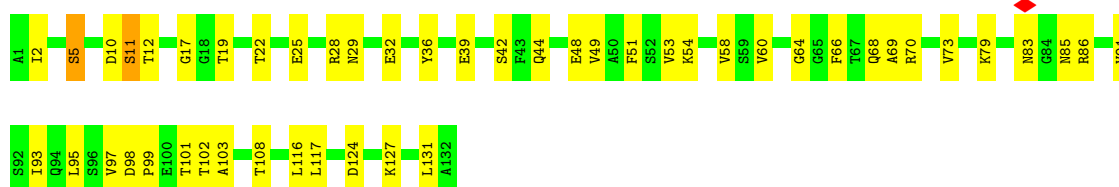
- Molecule 1: Coat protein

Chain GN: 65% 33% .

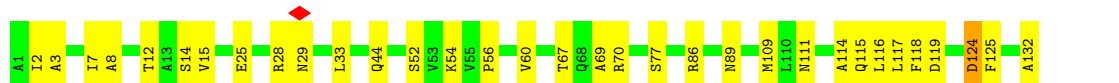
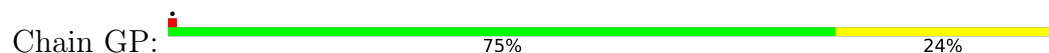


- Molecule 1: Coat protein

Chain GO: 64% 35% .



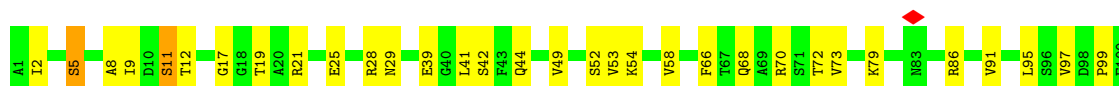
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein





- Molecule 1: Coat protein

Chain GU: 63% 33%



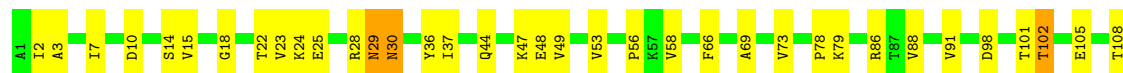
- Molecule 1: Coat protein

Chain GV: 71% 27%



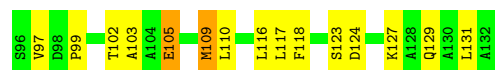
- Molecule 1: Coat protein

Chain GW: 69% 28%



- Molecule 1: Coat protein

Chain GX: 63% 33% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	15154	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.4	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0107	Depositor
Map size (Å)	400.896, 400.896, 400.896	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.783, 0.783, 0.783	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	AA	0.25	0/990	0.53	2/1346 (0.1%)
1	AB	0.21	0/990	0.49	0/1346
1	AC	0.21	0/990	0.51	0/1346
1	AD	0.21	0/990	0.45	0/1346
1	AE	0.20	0/990	0.48	0/1346
1	AF	0.21	0/990	0.53	0/1346
1	AG	0.21	0/990	0.47	0/1346
1	AH	0.20	0/990	0.48	0/1346
1	AI	0.21	0/990	0.54	0/1346
1	AJ	0.25	0/990	0.53	2/1346 (0.1%)
1	AK	0.21	0/990	0.49	0/1346
1	AL	0.21	0/990	0.52	0/1346
1	AM	0.21	0/990	0.46	0/1346
1	AN	0.20	0/990	0.49	0/1346
1	AO	0.21	0/990	0.52	0/1346
1	AP	0.21	0/990	0.47	0/1346
1	AQ	0.20	0/990	0.49	0/1346
1	AR	0.21	0/990	0.53	0/1346
1	AS	0.21	0/990	0.46	0/1346
1	AT	0.20	0/990	0.48	0/1346
1	AU	0.22	0/990	0.54	0/1346
1	AV	0.25	0/990	0.53	2/1346 (0.1%)
1	AW	0.21	0/990	0.49	0/1346
1	AX	0.21	0/990	0.51	0/1346
1	AY	0.21	0/990	0.46	0/1346
1	AZ	0.20	0/990	0.49	0/1346
1	BA	0.21	0/990	0.52	0/1346
1	BB	0.21	0/990	0.47	0/1346
1	BC	0.20	0/990	0.49	0/1346
1	BD	0.21	0/990	0.54	0/1346
1	BE	0.21	0/990	0.46	0/1346
1	BF	0.20	0/990	0.49	0/1346
1	BG	0.21	0/990	0.53	0/1346
1	BH	0.21	0/990	0.46	0/1346

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.21	0/990	0.49	0/1346
1	BJ	0.21	0/990	0.53	0/1346
1	BK	0.21	0/990	0.47	0/1346
1	BL	0.21	0/990	0.50	0/1346
1	BM	0.21	0/990	0.51	0/1346
1	BN	0.21	0/990	0.46	0/1346
1	BO	0.20	0/990	0.48	0/1346
1	BP	0.21	0/990	0.54	0/1346
1	BQ	0.21	0/990	0.47	0/1346
1	BR	0.20	0/990	0.49	0/1346
1	BS	0.21	0/990	0.53	0/1346
1	BT	0.21	0/990	0.46	0/1346
1	BU	0.21	0/990	0.50	0/1346
1	BV	0.21	0/990	0.52	0/1346
1	BW	0.21	0/990	0.45	0/1346
1	BX	0.19	0/990	0.47	0/1346
1	BY	0.21	0/990	0.53	0/1346
1	BZ	0.25	0/990	0.52	2/1346 (0.1%)
1	CA	0.21	0/990	0.49	0/1346
1	CB	0.21	0/990	0.51	0/1346
1	CC	0.21	0/990	0.47	0/1346
1	CD	0.20	0/990	0.49	0/1346
1	CE	0.21	0/990	0.53	0/1346
1	CF	0.21	0/990	0.47	0/1346
1	CG	0.21	0/990	0.50	0/1346
1	CH	0.21	0/990	0.52	0/1346
1	CI	0.21	0/990	0.45	0/1346
1	CJ	0.19	0/990	0.47	0/1346
1	CK	0.21	0/990	0.53	0/1346
1	CL	0.21	0/990	0.46	0/1346
1	CM	0.20	0/990	0.49	0/1346
1	CN	0.21	0/990	0.53	0/1346
1	CO	0.25	0/990	0.53	2/1346 (0.1%)
1	CP	0.21	0/990	0.49	0/1346
1	CQ	0.21	0/990	0.51	0/1346
1	CR	0.21	0/990	0.46	0/1346
1	CS	0.20	0/990	0.48	0/1346
1	CT	0.21	0/990	0.55	0/1346
1	CU	0.21	0/990	0.46	0/1346
1	CV	0.20	0/990	0.48	0/1346
1	CW	0.21	0/990	0.53	0/1346
1	CX	0.21	0/990	0.46	0/1346
1	CY	0.20	0/990	0.49	0/1346

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CZ	0.21	0/990	0.53	0/1346
1	DA	0.25	0/990	0.53	2/1346 (0.1%)
1	DB	0.21	0/990	0.49	0/1346
1	DC	0.21	0/990	0.51	0/1346
1	DD	0.21	0/990	0.45	0/1346
1	DE	0.19	0/990	0.48	0/1346
1	DF	0.21	0/990	0.53	0/1346
1	DG	0.21	0/990	0.46	0/1346
1	DH	0.20	0/990	0.48	0/1346
1	DI	0.21	0/990	0.54	0/1346
1	DJ	0.21	0/990	0.47	0/1346
1	DK	0.21	0/990	0.49	0/1346
1	DL	0.21	0/990	0.52	0/1346
1	DM	0.25	0/990	0.53	2/1346 (0.1%)
1	DN	0.21	0/990	0.49	0/1346
1	DO	0.21	0/990	0.51	0/1346
1	DP	0.21	0/990	0.47	0/1346
1	DQ	0.20	0/990	0.49	0/1346
1	DR	0.22	0/990	0.55	0/1346
1	DS	0.21	0/990	0.46	0/1346
1	DT	0.20	0/990	0.49	0/1346
1	DU	0.21	0/990	0.53	0/1346
1	DV	0.25	0/990	0.53	2/1346 (0.1%)
1	DW	0.21	0/990	0.49	0/1346
1	DX	0.21	0/990	0.51	0/1346
1	DY	0.21	0/990	0.45	0/1346
1	DZ	0.20	0/990	0.49	0/1346
1	EA	0.21	0/990	0.50	0/1346
1	EB	0.20	0/990	0.44	0/1346
1	EC	0.20	0/990	0.49	0/1346
1	ED	0.21	0/990	0.50	0/1346
1	EE	0.21	0/990	0.44	0/1346
1	EF	0.20	0/990	0.49	0/1346
1	EG	0.21	0/990	0.51	0/1346
1	EH	0.25	0/990	0.52	2/1346 (0.1%)
1	EI	0.21	0/990	0.49	0/1346
1	EJ	0.21	0/990	0.50	0/1346
1	EK	0.21	0/990	0.45	0/1346
1	EL	0.20	0/990	0.49	0/1346
1	EM	0.21	0/990	0.50	0/1346
1	EN	0.21	0/990	0.44	0/1346
1	EO	0.20	0/990	0.49	0/1346
1	EP	0.21	0/990	0.50	0/1346

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	EQ	0.20	0/990	0.45	0/1346
1	ER	0.20	0/990	0.49	0/1346
1	ES	0.21	0/990	0.50	0/1346
1	ET	0.20	0/990	0.44	0/1346
1	EU	0.20	0/990	0.47	0/1346
1	EV	0.21	0/990	0.51	0/1346
1	EW	0.21	0/990	0.45	0/1346
1	EX	0.20	0/990	0.49	0/1346
1	EY	0.21	0/990	0.50	0/1346
1	EZ	0.21	0/990	0.44	0/1346
1	FA	0.20	0/990	0.49	0/1346
1	FB	0.21	0/990	0.50	0/1346
1	FC	0.20	0/990	0.45	0/1346
1	FD	0.20	0/990	0.49	0/1346
1	FE	0.21	0/990	0.50	0/1346
1	FF	0.21	0/990	0.45	0/1346
1	FG	0.20	0/990	0.49	0/1346
1	FH	0.21	0/990	0.50	0/1346
1	FI	0.20	0/990	0.45	0/1346
1	FJ	0.20	0/990	0.47	0/1346
1	FK	0.21	0/990	0.51	0/1346
1	FL	0.25	0/990	0.52	2/1346 (0.1%)
1	FM	0.21	0/990	0.49	0/1346
1	FN	0.21	0/990	0.50	0/1346
1	FO	0.20	0/990	0.45	0/1346
1	FP	0.20	0/990	0.49	0/1346
1	FQ	0.21	0/990	0.50	0/1346
1	FR	0.21	0/990	0.45	0/1346
1	FS	0.20	0/990	0.49	0/1346
1	FT	0.21	0/990	0.50	0/1346
1	FU	0.21	0/990	0.44	0/1346
1	FV	0.20	0/990	0.48	0/1346
1	FW	0.21	0/990	0.51	0/1346
1	FX	0.20	0/990	0.45	0/1346
1	FY	0.20	0/990	0.49	0/1346
1	FZ	0.21	0/990	0.50	0/1346
1	GA	0.25	0/990	0.52	2/1346 (0.1%)
1	GB	0.21	0/990	0.49	0/1346
1	GC	0.21	0/990	0.50	0/1346
1	GD	0.21	0/990	0.44	0/1346
1	GE	0.20	0/990	0.49	0/1346
1	GF	0.21	0/990	0.50	0/1346
1	GG	0.20	0/990	0.44	0/1346

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GH	0.21	0/990	0.48	0/1346
1	GI	0.21	0/990	0.51	0/1346
1	GJ	0.21	0/990	0.45	0/1346
1	GK	0.20	0/990	0.49	0/1346
1	GL	0.21	0/990	0.50	0/1346
1	GM	0.25	0/990	0.52	2/1346 (0.1%)
1	GN	0.21	0/990	0.48	0/1346
1	GO	0.21	0/990	0.50	0/1346
1	GP	0.20	0/990	0.44	0/1346
1	GQ	0.20	0/990	0.48	0/1346
1	GR	0.21	0/990	0.51	0/1346
1	GS	0.21	0/990	0.44	0/1346
1	GT	0.20	0/990	0.49	0/1346
1	GU	0.21	0/990	0.50	0/1346
1	GV	0.21	0/990	0.45	0/1346
1	GW	0.20	0/990	0.48	0/1346
1	GX	0.21	0/990	0.50	0/1346
All	All	0.21	0/178200	0.49	24/242280 (0.0%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AV	63	PRO	CA-N-CD	-6.65	102.69	112.00
1	BZ	63	PRO	CA-N-CD	-6.60	102.75	112.00
1	GA	63	PRO	CA-N-CD	-6.60	102.76	112.00
1	CO	63	PRO	N-CD-CG	-6.60	93.30	103.20
1	DA	63	PRO	N-CD-CG	-6.60	93.30	103.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	978	0	988	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AB	978	0	988	32	0
1	AC	978	0	988	45	0
1	AD	978	0	988	27	0
1	AE	978	0	988	30	0
1	AF	978	0	988	38	0
1	AG	978	0	988	24	0
1	AH	978	0	988	31	0
1	AI	978	0	988	46	0
1	AJ	978	0	988	29	0
1	AK	978	0	988	35	0
1	AL	978	0	988	42	0
1	AM	978	0	988	23	0
1	AN	978	0	988	26	0
1	AO	978	0	988	44	0
1	AP	978	0	988	25	0
1	AQ	978	0	988	28	0
1	AR	978	0	988	43	0
1	AS	978	0	988	21	0
1	AT	978	0	988	30	0
1	AU	978	0	988	45	0
1	AV	978	0	988	32	0
1	AW	978	0	988	30	0
1	AX	978	0	988	47	0
1	AY	978	0	988	24	0
1	AZ	978	0	988	26	0
1	BA	978	0	988	43	0
1	BB	978	0	988	26	0
1	BC	978	0	988	33	0
1	BD	978	0	988	45	0
1	BE	978	0	988	25	0
1	BF	978	0	988	27	0
1	BG	978	0	988	42	0
1	BH	978	0	988	27	0
1	BI	978	0	988	28	0
1	BJ	978	0	988	40	0
1	BK	978	0	988	22	0
1	BL	978	0	988	25	0
1	BM	978	0	988	39	0
1	BN	978	0	988	20	0
1	BO	978	0	988	29	0
1	BP	978	0	988	44	0
1	BQ	978	0	988	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BR	978	0	988	28	0
1	BS	978	0	988	42	0
1	BT	978	0	988	24	0
1	BU	978	0	988	26	0
1	BV	978	0	988	41	0
1	BW	978	0	988	30	0
1	BX	978	0	988	28	0
1	BY	978	0	988	43	0
1	BZ	978	0	988	31	0
1	CA	978	0	988	36	0
1	CB	978	0	988	40	0
1	CC	978	0	988	27	0
1	CD	978	0	988	26	0
1	CE	978	0	988	38	0
1	CF	978	0	988	23	0
1	CG	978	0	988	25	0
1	CH	978	0	988	42	0
1	CI	978	0	988	26	0
1	CJ	978	0	988	26	0
1	CK	978	0	988	44	0
1	CL	978	0	988	24	0
1	CM	978	0	988	26	0
1	CN	978	0	988	38	0
1	CO	978	0	988	32	0
1	CP	978	0	988	36	0
1	CQ	978	0	988	41	0
1	CR	978	0	988	24	0
1	CS	978	0	988	29	0
1	CT	978	0	988	40	0
1	CU	978	0	988	26	0
1	CV	978	0	988	27	0
1	CW	978	0	988	44	0
1	CX	978	0	988	24	0
1	CY	978	0	988	25	0
1	CZ	978	0	988	41	0
1	DA	978	0	988	32	0
1	DB	978	0	988	32	0
1	DC	978	0	988	42	0
1	DD	978	0	988	28	0
1	DE	978	0	988	29	0
1	DF	978	0	988	44	0
1	DG	978	0	988	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DH	978	0	988	31	0
1	DI	978	0	988	40	0
1	DJ	978	0	988	20	0
1	DK	978	0	988	27	0
1	DL	978	0	988	45	0
1	DM	978	0	988	30	0
1	DN	978	0	988	37	0
1	DO	978	0	988	42	0
1	DP	978	0	988	22	0
1	DQ	978	0	988	30	0
1	DR	978	0	988	41	0
1	DS	978	0	988	24	0
1	DT	978	0	988	28	0
1	DU	978	0	988	44	0
1	DV	978	0	988	32	0
1	DW	978	0	988	36	0
1	DX	978	0	988	44	0
1	DY	978	0	988	30	0
1	DZ	978	0	988	29	0
1	EA	978	0	988	44	0
1	EB	978	0	988	22	0
1	EC	978	0	988	26	0
1	ED	978	0	988	41	0
1	EE	978	0	988	27	0
1	EF	978	0	988	30	0
1	EG	978	0	988	44	0
1	EH	978	0	988	32	0
1	EI	978	0	988	40	0
1	EJ	978	0	988	40	0
1	EK	978	0	988	33	0
1	EL	978	0	988	31	0
1	EM	978	0	988	42	0
1	EN	978	0	988	27	0
1	EO	978	0	988	29	0
1	EP	978	0	988	42	0
1	EQ	978	0	988	23	0
1	ER	978	0	988	26	0
1	ES	978	0	988	40	0
1	ET	978	0	988	21	0
1	EU	978	0	988	29	0
1	EV	978	0	988	40	0
1	EW	978	0	988	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EX	978	0	988	29	0
1	EY	978	0	988	40	0
1	EZ	978	0	988	20	0
1	FA	978	0	988	29	0
1	FB	978	0	988	40	0
1	FC	978	0	988	18	0
1	FD	978	0	988	25	0
1	FE	978	0	988	47	0
1	FF	978	0	988	30	0
1	FG	978	0	988	31	0
1	FH	978	0	988	40	0
1	FI	978	0	988	21	0
1	FJ	978	0	988	29	0
1	FK	978	0	988	37	0
1	FL	978	0	988	33	0
1	FM	978	0	988	39	0
1	FN	978	0	988	37	0
1	FO	978	0	988	18	0
1	FP	978	0	988	25	0
1	FQ	978	0	988	45	0
1	FR	978	0	988	28	0
1	FS	978	0	988	26	0
1	FT	978	0	988	41	0
1	FU	978	0	988	24	0
1	FV	978	0	988	33	0
1	FW	978	0	988	38	0
1	FX	978	0	988	20	0
1	FY	978	0	988	24	0
1	FZ	978	0	988	46	0
1	GA	978	0	988	31	0
1	GB	978	0	988	41	0
1	GC	978	0	988	39	0
1	GD	978	0	988	25	0
1	GE	978	0	988	30	0
1	GF	978	0	988	40	0
1	GG	978	0	988	25	0
1	GH	978	0	988	34	0
1	GI	978	0	988	37	0
1	GJ	978	0	988	19	0
1	GK	978	0	988	23	0
1	GL	978	0	988	41	0
1	GM	978	0	988	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GN	978	0	988	34	0
1	GO	978	0	988	35	0
1	GP	978	0	988	23	0
1	GQ	978	0	988	32	0
1	GR	978	0	988	33	0
1	GS	978	0	988	25	0
1	GT	978	0	988	29	0
1	GU	978	0	988	38	0
1	GV	978	0	988	28	0
1	GW	978	0	988	30	0
1	GX	978	0	988	42	0
All	All	176040	0	177840	4352	0

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

The worst 5 of 4352 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)
1:DU:54:LYS:HB3	1:DU:70:ARG:HG3	1.47	0.97
1:BJ:54:LYS:HB3	1:BJ:70:ARG:HG3	1.47	0.94
1:CE:54:LYS:HB3	1:CE:70:ARG:HG3	1.49	0.93
1:CN:54:LYS:HB3	1:CN:70:ARG:HG3	1.49	0.93
1:AB:78:PRO:HB3	1:AB:86:ARG:HH12	1.33	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	AA	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AB	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	AC	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	AD	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	AE	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	AF	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	AG	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AH	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	AI	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	AJ	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AK	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	AL	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	AM	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AN	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	AO	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	AP	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	AQ	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	AR	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	AS	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AT	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	AU	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	AV	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AW	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	AX	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	AY	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	AZ	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	BA	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	BB	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	BC	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	BD	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	BE	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	BF	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BG	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	BH	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	BI	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	BJ	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	BK	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	BL	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	BM	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	BN	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	BO	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	BP	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	BQ	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	BR	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	BS	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	BT	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	BU	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	BV	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	BW	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	BX	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	BY	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	BZ	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	CA	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CB	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	CC	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	CD	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CE	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	CF	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	CG	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CH	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	CI	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	CJ	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	CK	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CL	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	CM	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CN	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	CO	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	CP	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CQ	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	CR	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	CS	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	CT	130/132 (98%)	114 (88%)	15 (12%)	1 (1%)	16	44
1	CU	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	CV	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	CW	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	CX	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	CY	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	CZ	130/132 (98%)	110 (85%)	19 (15%)	1 (1%)	16	44
1	DA	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	DB	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	DC	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	DD	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	DE	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	DF	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	DG	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	DH	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	DI	130/132 (98%)	114 (88%)	15 (12%)	1 (1%)	16	44
1	DJ	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	DK	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	DL	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	DM	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	DN	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	DO	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	DP	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DQ	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	DR	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	DS	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	DT	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	DU	130/132 (98%)	114 (88%)	15 (12%)	1 (1%)	16	44
1	DV	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	DW	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	DX	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	DY	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	DZ	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	EA	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	EB	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	EC	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	ED	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	EE	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	EF	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	EG	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	EH	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	EI	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	EJ	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	EK	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	EL	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	EM	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	EN	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	EO	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	EP	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	EQ	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	ER	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	ES	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	ET	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	EU	130/132 (98%)	116 (89%)	11 (8%)	3 (2%)	5	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EV	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	EW	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	EX	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	EY	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	EZ	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	FA	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	FB	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	FC	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	FD	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	FE	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	FF	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	FG	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	FH	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	FI	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	FJ	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	FK	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	FL	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	FM	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	FN	130/132 (98%)	115 (88%)	14 (11%)	1 (1%)	16	44
1	FO	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	16	44
1	FP	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	FQ	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	FR	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	FS	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	FT	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44
1	FU	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	FV	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	FW	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	FX	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	16	44
1	FY	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	FZ	130/132 (98%)	111 (85%)	18 (14%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GA	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	GB	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	GC	130/132 (98%)	114 (88%)	15 (12%)	1 (1%)	16	44
1	GD	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	GE	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	GF	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	GG	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	GH	130/132 (98%)	118 (91%)	9 (7%)	3 (2%)	5	18
1	GI	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	GJ	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	16	44
1	GK	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	GL	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	GM	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	GN	130/132 (98%)	119 (92%)	8 (6%)	3 (2%)	5	18
1	GO	130/132 (98%)	115 (88%)	14 (11%)	1 (1%)	16	44
1	GP	130/132 (98%)	119 (92%)	10 (8%)	1 (1%)	16	44
1	GQ	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	GR	130/132 (98%)	113 (87%)	16 (12%)	1 (1%)	16	44
1	GS	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	GT	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	GU	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
1	GV	130/132 (98%)	117 (90%)	12 (9%)	1 (1%)	16	44
1	GW	130/132 (98%)	117 (90%)	10 (8%)	3 (2%)	5	18
1	GX	130/132 (98%)	112 (86%)	17 (13%)	1 (1%)	16	44
All	All	23400/23760 (98%)	20904 (89%)	2196 (9%)	300 (1%)	12	31

5 of 300 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AC	29	ASN
1	AF	29	ASN
1	AI	29	ASN
1	AL	29	ASN
1	AO	29	ASN

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	AA	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AB	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	AC	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	AD	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	AE	107/107 (100%)	101 (94%)	6 (6%)	19	50
1	AF	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AG	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	AH	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AI	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	AJ	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AK	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	AL	107/107 (100%)	94 (88%)	13 (12%)	5	16
1	AM	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AN	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	AO	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	AP	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	AQ	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AR	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	AS	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	AT	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AU	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AV	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AW	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AX	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	AY	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	AZ	107/107 (100%)	99 (92%)	8 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	BB	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	BC	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BD	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	BE	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BF	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	BG	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BH	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	BI	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	BJ	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	BK	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BL	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BM	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	BN	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	BO	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BP	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BQ	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BR	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	BS	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BT	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BU	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BV	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	BW	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	BX	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	BY	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	BZ	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CA	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CB	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	CC	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	CD	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CE	107/107 (100%)	97 (91%)	10 (9%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CF	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CG	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	CH	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	CI	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CJ	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	CK	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CL	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	CM	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CN	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CO	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CP	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	CQ	107/107 (100%)	94 (88%)	13 (12%)	5	16
1	CR	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	CS	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CT	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	CU	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CV	107/107 (100%)	101 (94%)	6 (6%)	19	50
1	CW	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CX	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	CY	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	CZ	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	DA	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DB	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	DC	107/107 (100%)	93 (87%)	14 (13%)	4	14
1	DD	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	DE	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	DF	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	DG	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	DH	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	DI	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DJ	107/107 (100%)	97 (91%)	10 (9%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DK	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	DL	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	DM	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DN	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DO	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	DP	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	DQ	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	DR	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DS	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	DT	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	DU	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	DV	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	DW	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	DX	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	DY	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	DZ	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EA	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	EB	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	EC	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	ED	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	EE	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	EF	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	EG	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EH	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EI	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	EJ	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	EK	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	EL	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EM	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	EN	107/107 (100%)	101 (94%)	6 (6%)	19	50
1	EO	107/107 (100%)	98 (92%)	9 (8%)	10	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EP	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	EQ	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	ER	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	ES	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	ET	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	EU	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EV	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	EW	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	EX	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EY	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	EZ	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	FA	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	FB	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FC	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	FD	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	FE	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FF	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	FG	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	FH	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FI	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	FJ	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FK	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FL	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FM	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FN	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FO	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	FP	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	FQ	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FR	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	FS	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FT	107/107 (100%)	96 (90%)	11 (10%)	7	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FU	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	FV	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FW	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	FX	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	FY	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	FZ	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	GA	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	GB	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	GC	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	GD	107/107 (100%)	101 (94%)	6 (6%)	19	50
1	GE	107/107 (100%)	99 (92%)	8 (8%)	12	37
1	GF	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	GG	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	GH	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	GI	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	GJ	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	GK	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	GL	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	GM	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	GN	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	GO	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	GP	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	GQ	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	GR	107/107 (100%)	95 (89%)	12 (11%)	6	19
1	GS	107/107 (100%)	100 (94%)	7 (6%)	15	43
1	GT	107/107 (100%)	97 (91%)	10 (9%)	8	27
1	GU	107/107 (100%)	93 (87%)	14 (13%)	4	14
1	GV	107/107 (100%)	98 (92%)	9 (8%)	10	32
1	GW	107/107 (100%)	96 (90%)	11 (10%)	7	23
1	GX	107/107 (100%)	96 (90%)	11 (10%)	7	23
All	All	19260/19260 (100%)	17525 (91%)	1735 (9%)	11	28

5 of 1735 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DU	96	SER
1	ER	98	ASP
1	GK	129	GLN
1	DX	39	GLU
1	DU	72	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 345 such sidechains are listed below:

Mol	Chain	Res	Type
1	EC	94	GLN
1	FH	34	ASN
1	EE	68	GLN
1	EQ	29	ASN
1	FS	94	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

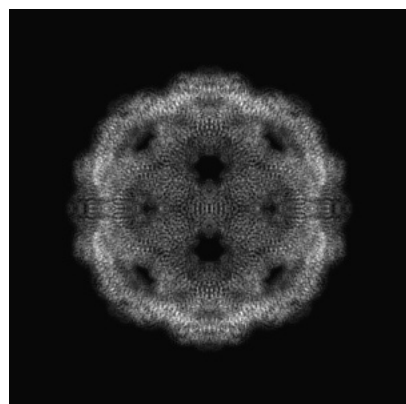
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52004. These allow visual inspection of the internal detail of the map and identification of artifacts.

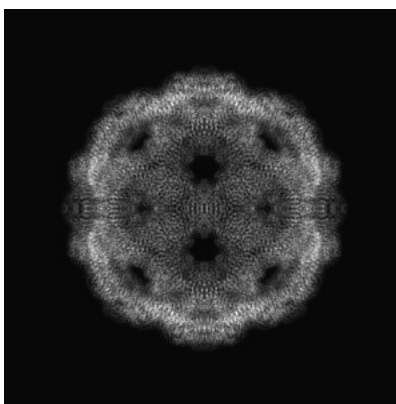
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

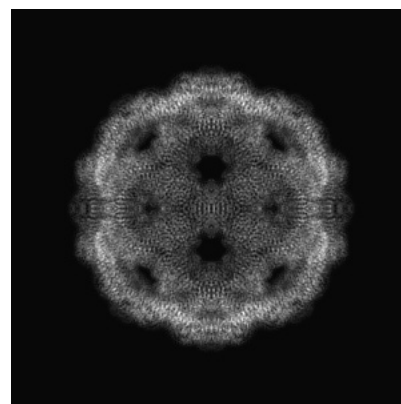
6.1.1 Primary map



X

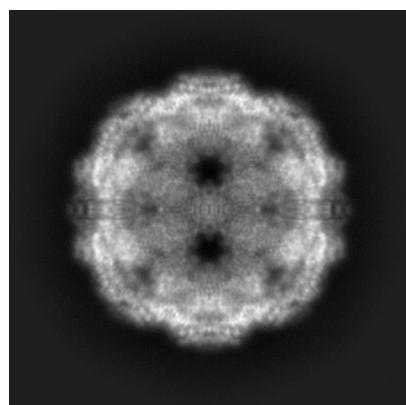


Y

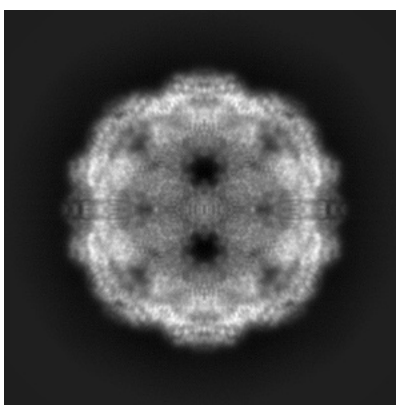


Z

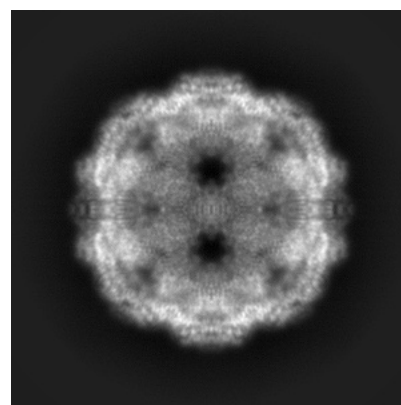
6.1.2 Raw map



X



Y

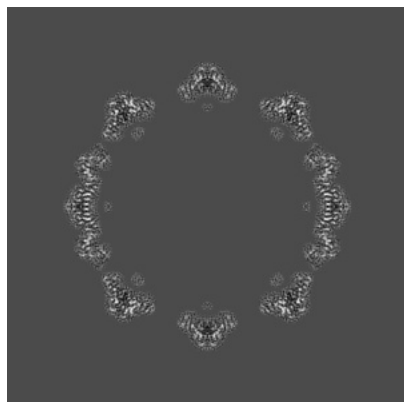


Z

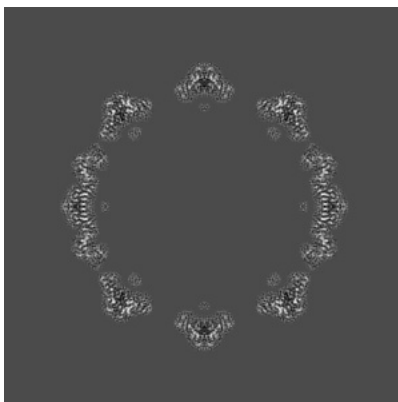
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

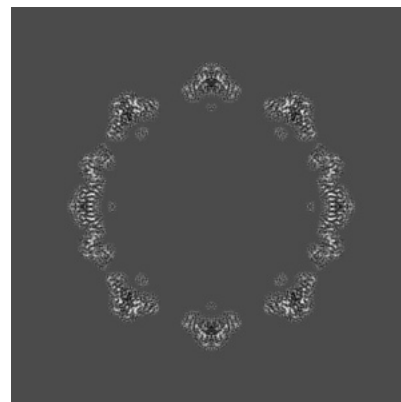
6.2.1 Primary map



X Index: 256

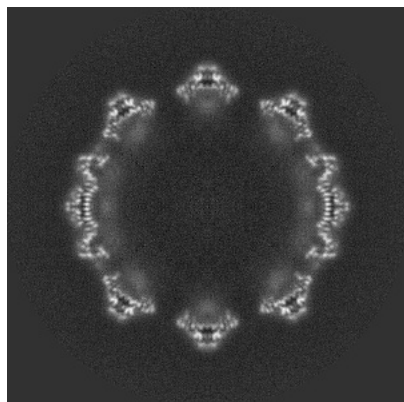


Y Index: 256

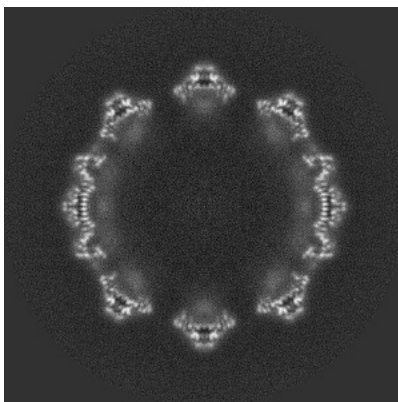


Z Index: 256

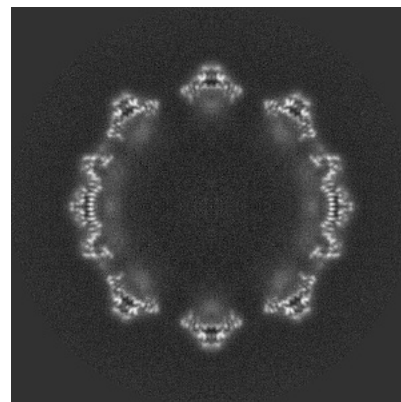
6.2.2 Raw map



X Index: 256



Y Index: 256

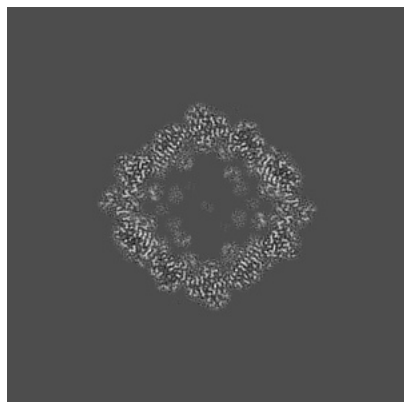


Z Index: 256

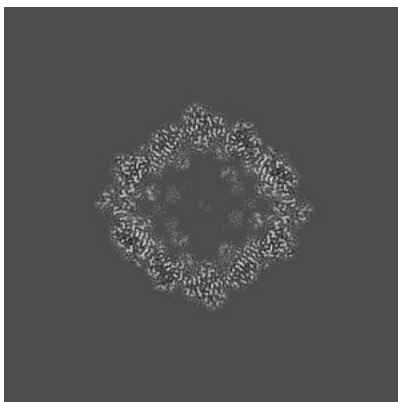
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

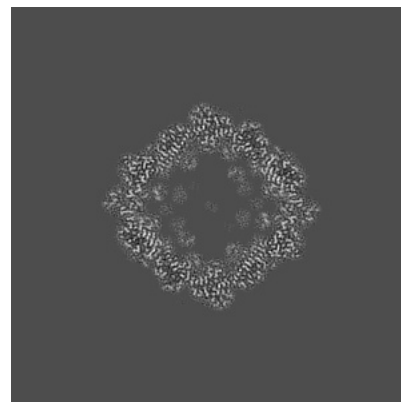
6.3.1 Primary map



X Index: 381

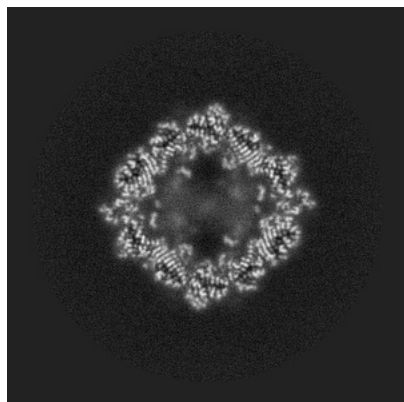


Y Index: 381

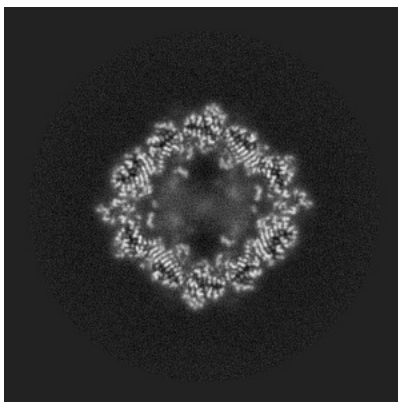


Z Index: 381

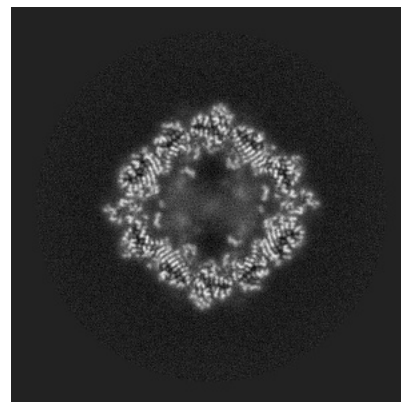
6.3.2 Raw map



X Index: 130



Y Index: 130

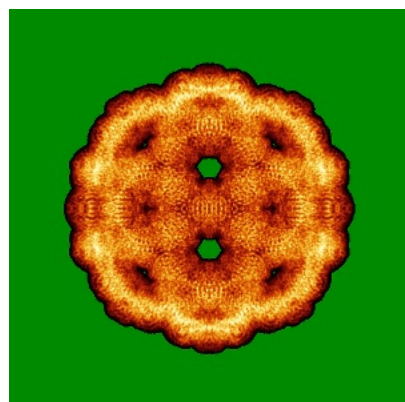


Z Index: 130

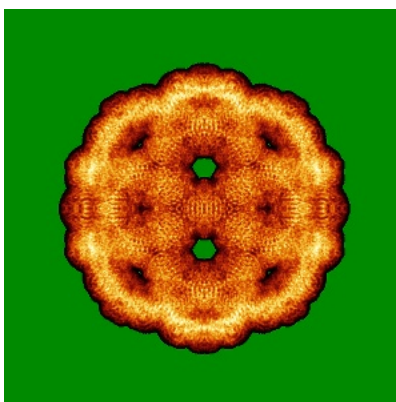
The images above show the largest variance slices of the map in three orthogonal directions.

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

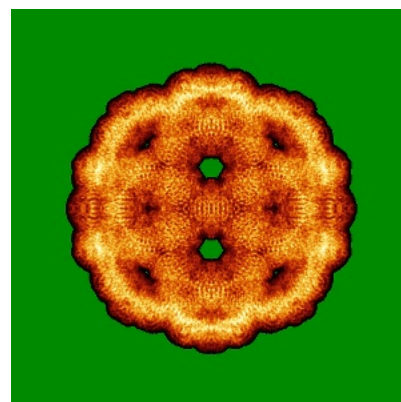
6.4.1 Primary map



X

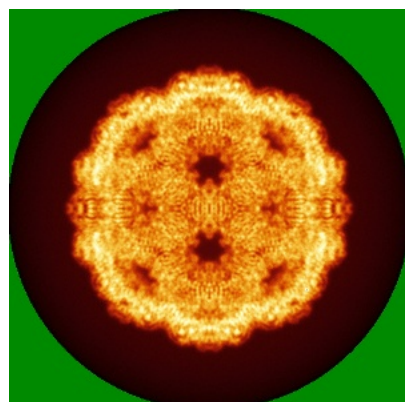


Y

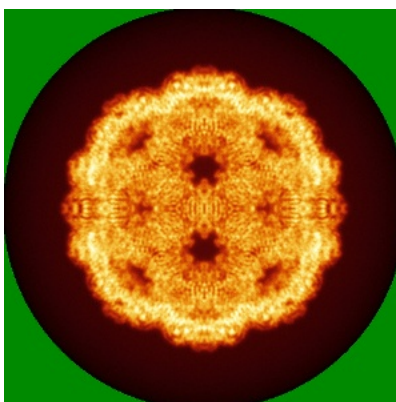


Z

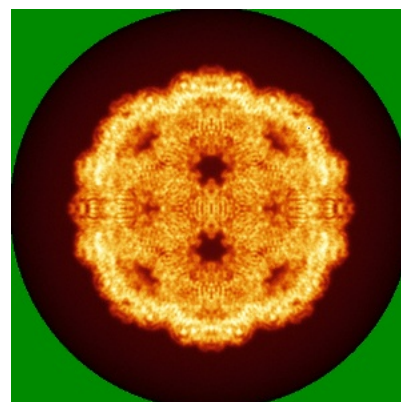
6.4.2 Raw map



X



Y

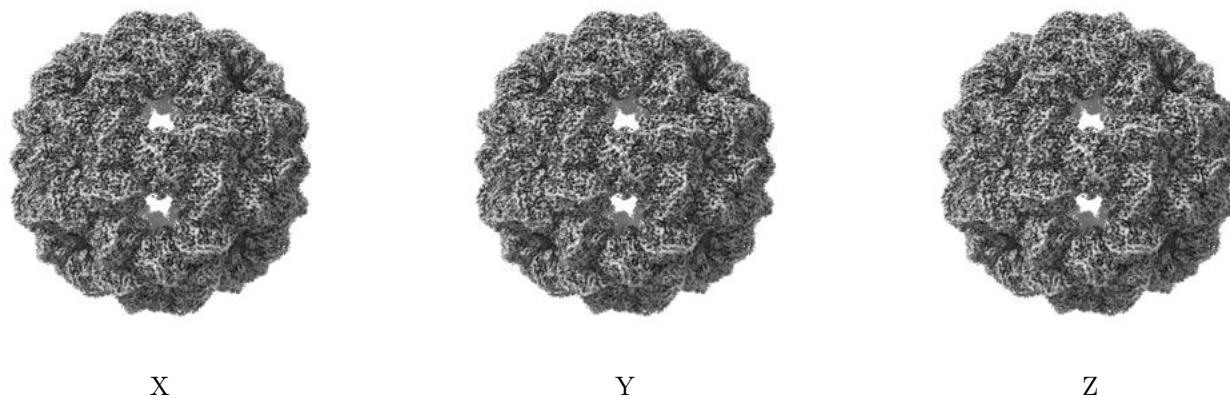


Z

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.

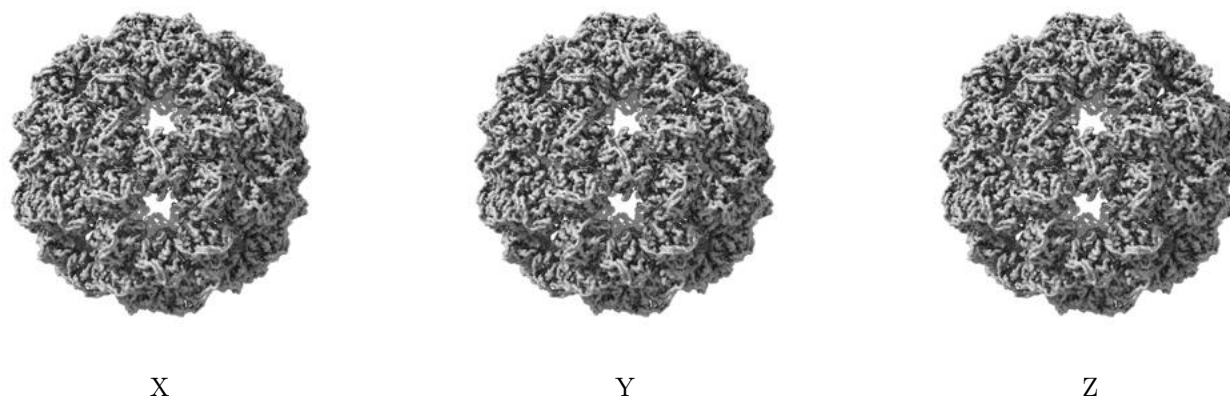
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0107. 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



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.

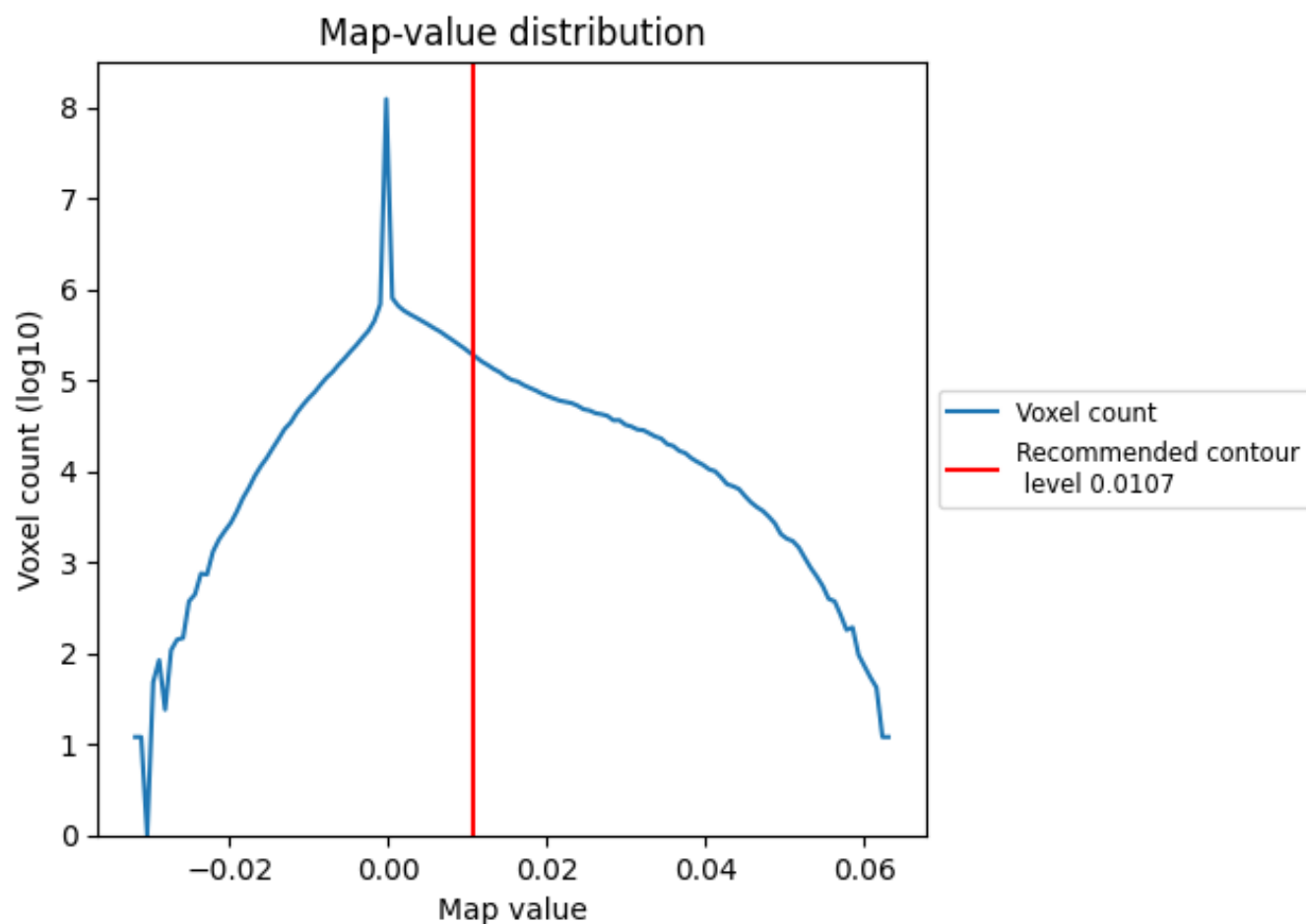
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

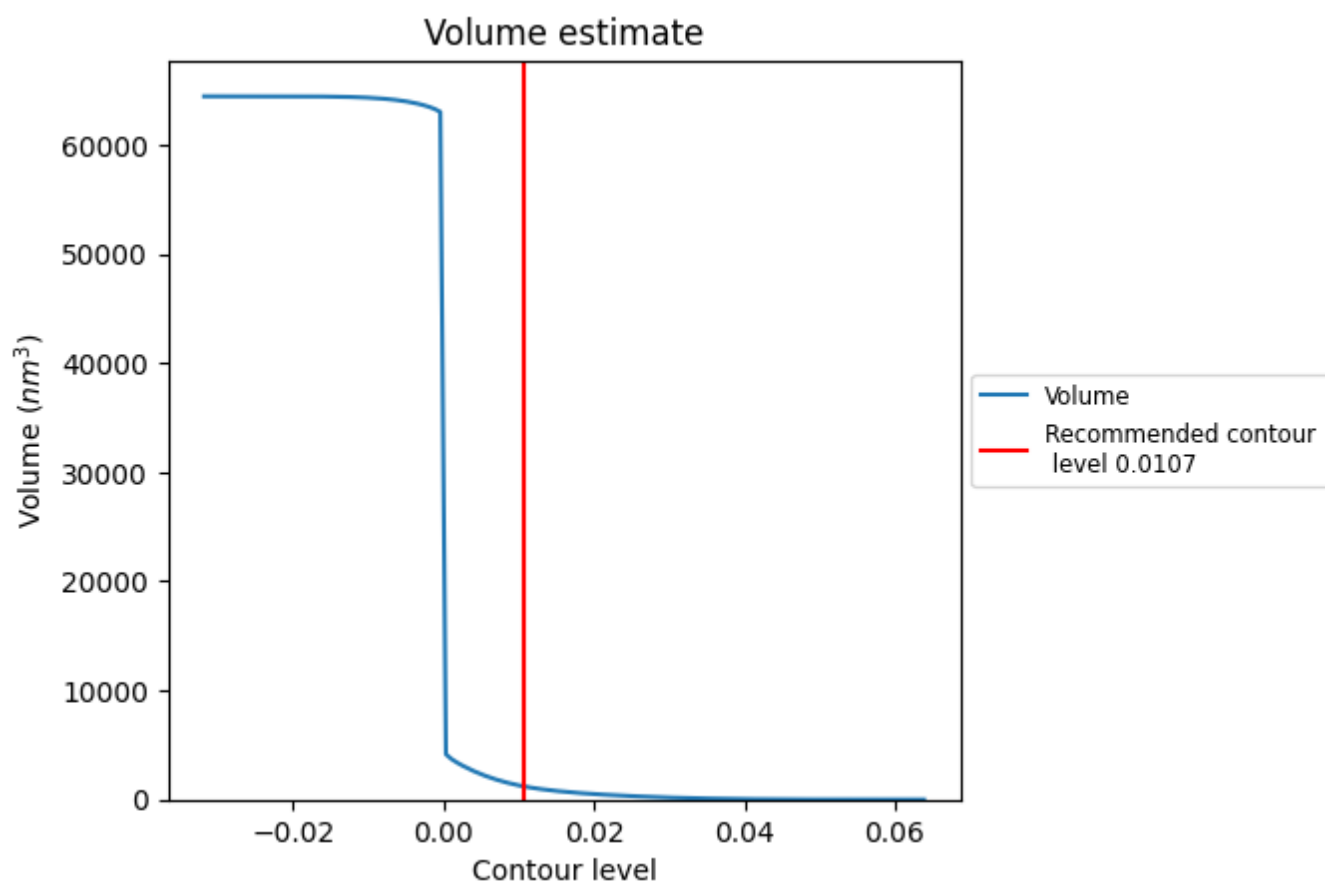
This section contains the results of statistical analysis of the map.

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.

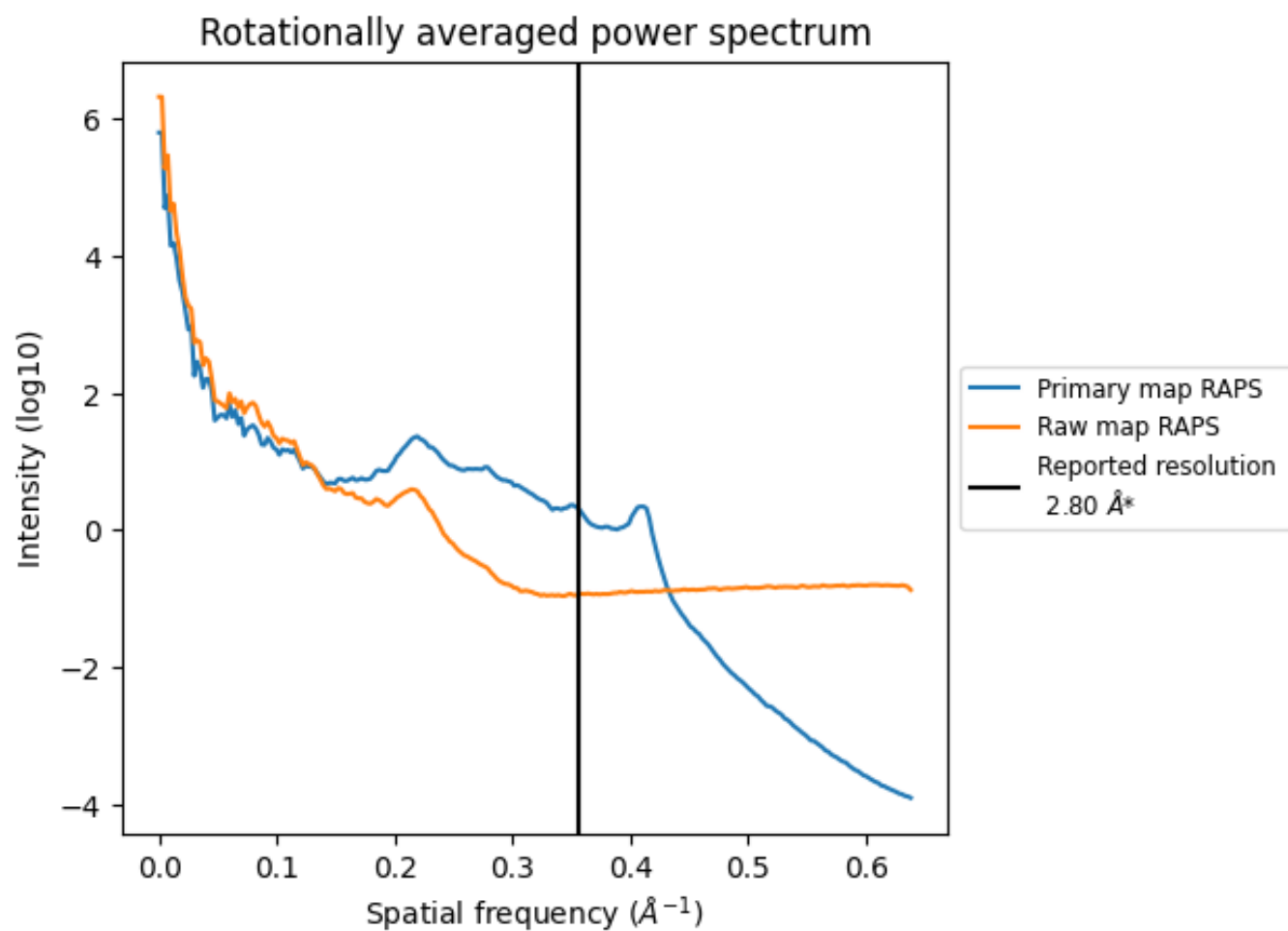
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1204 nm³; this corresponds to an approximate mass of 1088 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 ⓘ

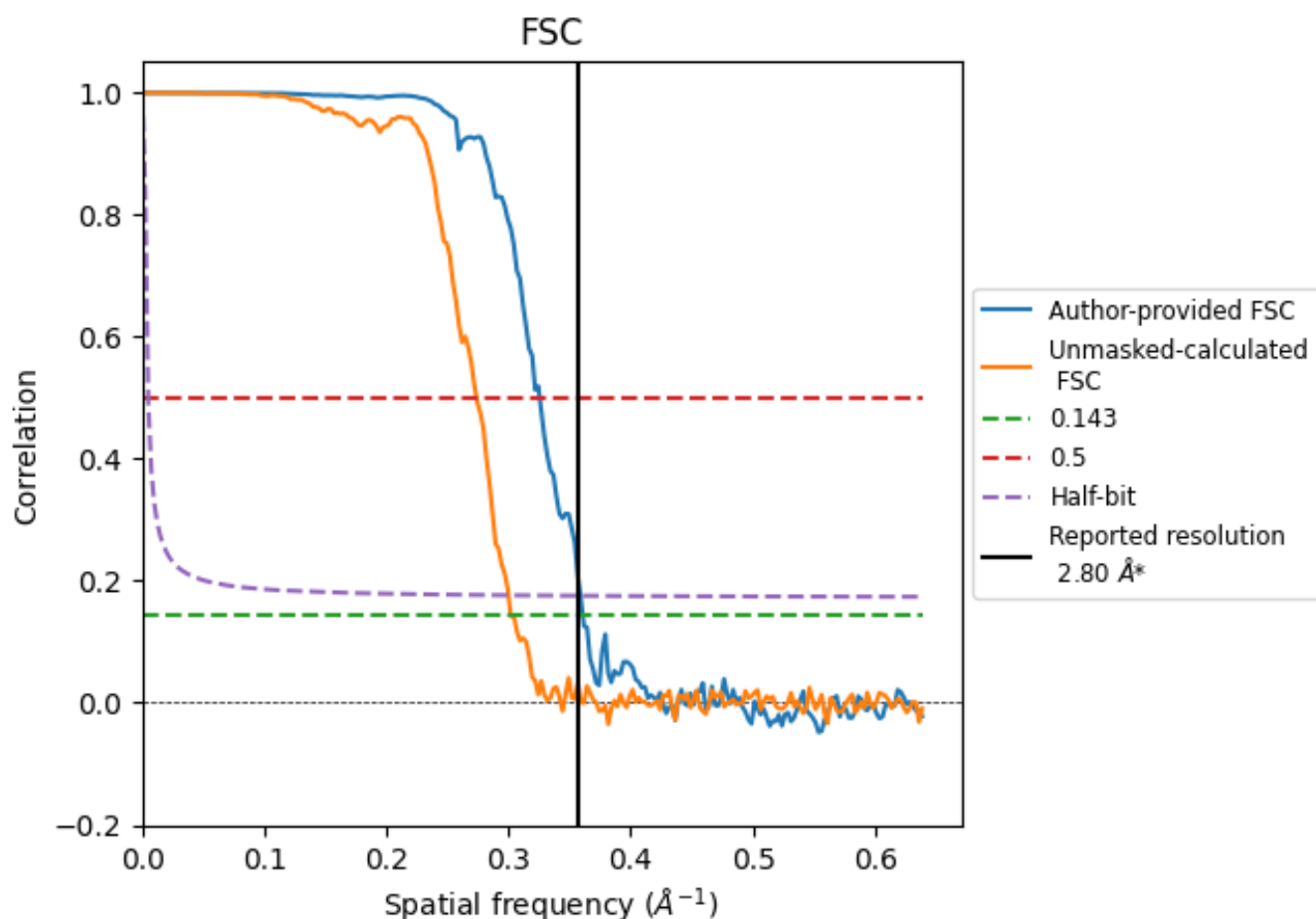


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.357 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

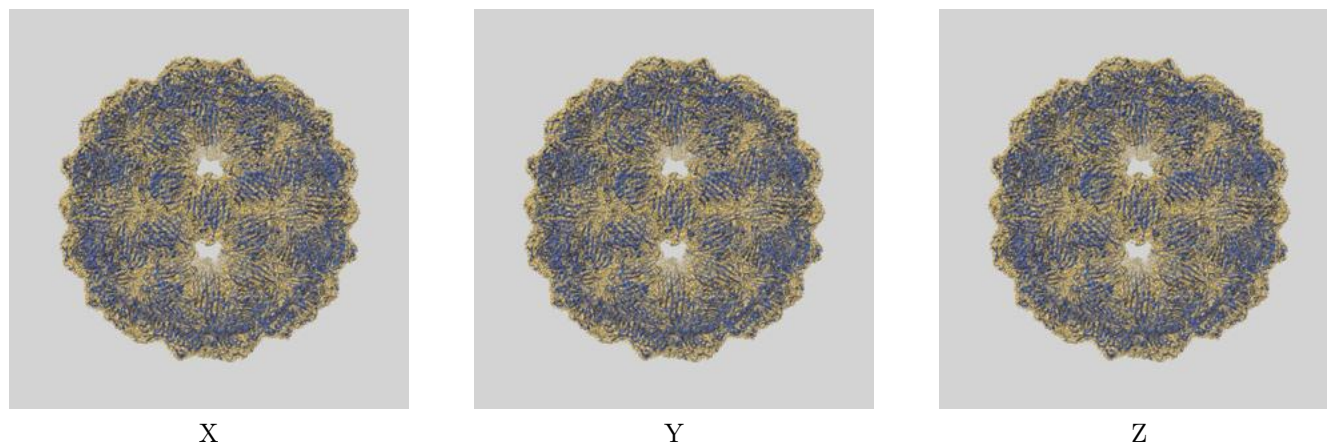
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.77	3.07	2.79
Unmasked-calculated*	3.31	3.65	3.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.31 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

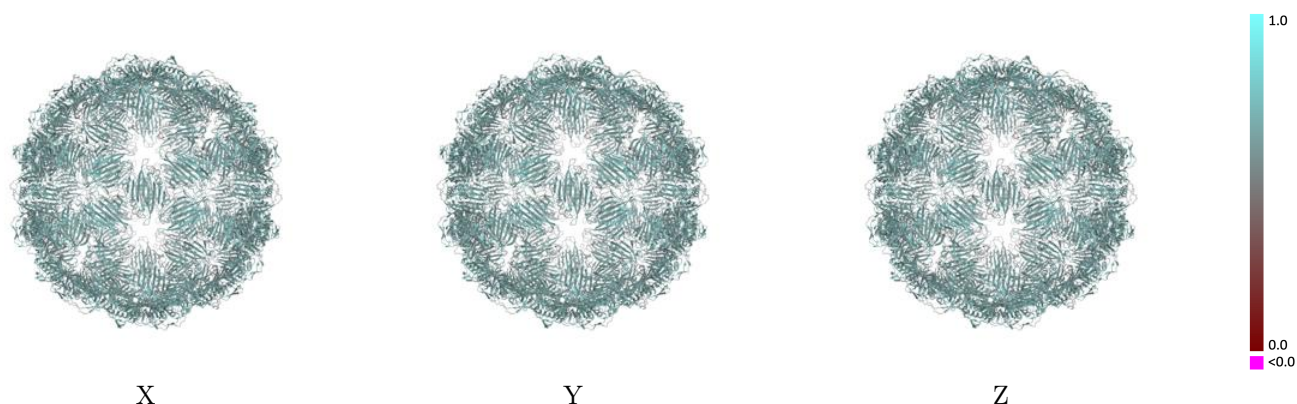
This section contains information regarding the fit between EMDB map EMD-52004 and PDB model 9HAR. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



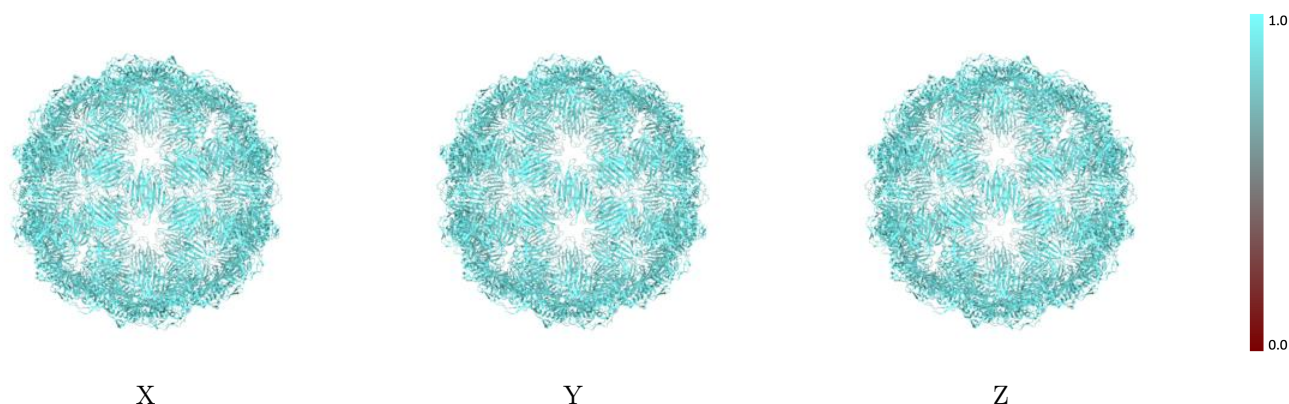
The images above show the 3D surface view of the map at the recommended contour level 0.0107 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



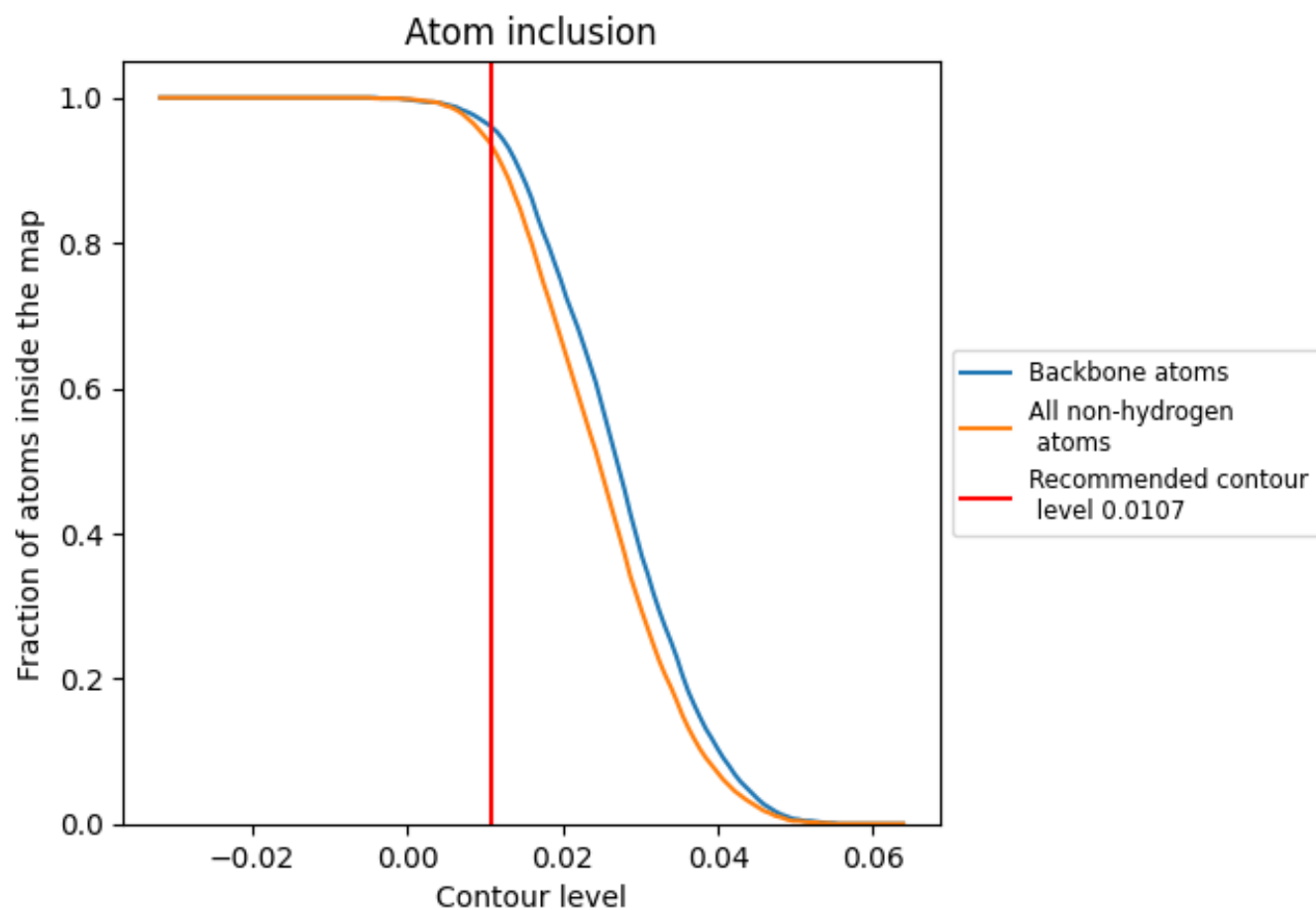
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0107).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.0107) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9370	 0.6090
AA	 0.9360	 0.6200
AB	 0.9520	 0.6200
AC	 0.9200	 0.5850
AD	 0.9380	 0.6210
AE	 0.9480	 0.6200
AF	 0.9170	 0.5860
AG	 0.9370	 0.6170
AH	 0.9550	 0.6170
AI	 0.9170	 0.5810
AJ	 0.9370	 0.6200
AK	 0.9500	 0.6180
AL	 0.9210	 0.5840
AM	 0.9420	 0.6180
AN	 0.9510	 0.6160
AO	 0.9230	 0.5830
AP	 0.9340	 0.6220
AQ	 0.9540	 0.6220
AR	 0.9180	 0.5870
AS	 0.9350	 0.6170
AT	 0.9520	 0.6190
AU	 0.9160	 0.5890
AV	 0.9360	 0.6200
AW	 0.9520	 0.6180
AX	 0.9200	 0.5870
AY	 0.9420	 0.6210
AZ	 0.9480	 0.6200
BA	 0.9210	 0.5850
BB	 0.9360	 0.6200
BC	 0.9500	 0.6200
BD	 0.9170	 0.5870
BE	 0.9320	 0.6190
BF	 0.9530	 0.6210
BG	 0.9200	 0.5840
BH	 0.9360	 0.6180



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Chain	Atom inclusion	Q-score
BI	 0.9470	 0.6170
BJ	 0.9200	 0.5840
BK	 0.9420	 0.6190
BL	 0.9490	 0.6170
BM	 0.9230	 0.5870
BN	 0.9350	 0.6180
BO	 0.9520	 0.6210
BP	 0.9160	 0.5830
BQ	 0.9340	 0.6220
BR	 0.9540	 0.6200
BS	 0.9200	 0.5850
BT	 0.9420	 0.6210
BU	 0.9480	 0.6180
BV	 0.9220	 0.5850
BW	 0.9380	 0.6220
BX	 0.9480	 0.6200
BY	 0.9190	 0.5840
BZ	 0.9360	 0.6180
CA	 0.9500	 0.6180
CB	 0.9200	 0.5840
CC	 0.9340	 0.6210
CD	 0.9550	 0.6190
CE	 0.9200	 0.5820
CF	 0.9400	 0.6230
CG	 0.9490	 0.6210
CH	 0.9210	 0.5870
CI	 0.9380	 0.6220
CJ	 0.9480	 0.6190
CK	 0.9190	 0.5840
CL	 0.9320	 0.6200
CM	 0.9540	 0.6210
CN	 0.9200	 0.5850
CO	 0.9350	 0.6190
CP	 0.9520	 0.6190
CQ	 0.9200	 0.5840
CR	 0.9350	 0.6200
CS	 0.9520	 0.6210
CT	 0.9170	 0.5880
CU	 0.9360	 0.6190
CV	 0.9480	 0.6220
CW	 0.9210	 0.5800
CX	 0.9320	 0.6220

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Chain	Atom inclusion	Q-score
CY	 0.9550	 0.6210
CZ	 0.9200	 0.5860
DA	 0.9350	 0.6220
DB	 0.9520	 0.6210
DC	 0.9200	 0.5900
DD	 0.9340	 0.6190
DE	 0.9490	 0.6220
DF	 0.9200	 0.5820
DG	 0.9350	 0.6200
DH	 0.9530	 0.6190
DI	 0.9180	 0.5900
DJ	 0.9390	 0.6170
DK	 0.9500	 0.6170
DL	 0.9230	 0.5830
DM	 0.9360	 0.6210
DN	 0.9500	 0.6190
DO	 0.9200	 0.5850
DP	 0.9370	 0.6170
DQ	 0.9510	 0.6180
DR	 0.9170	 0.5830
DS	 0.9380	 0.6210
DT	 0.9470	 0.6220
DU	 0.9190	 0.5870
DV	 0.9360	 0.6210
DW	 0.9510	 0.6200
DX	 0.9200	 0.5860
DY	 0.9430	 0.6270
DZ	 0.9570	 0.6230
EA	 0.9190	 0.5860
EB	 0.9450	 0.6220
EC	 0.9540	 0.6180
ED	 0.9190	 0.5820
EE	 0.9400	 0.6260
EF	 0.9520	 0.6210
EG	 0.9190	 0.5820
EH	 0.9420	 0.6230
EI	 0.9520	 0.6180
EJ	 0.9210	 0.5910
EK	 0.9430	 0.6240
EL	 0.9570	 0.6190
EM	 0.9190	 0.5850
EN	 0.9400	 0.6250

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Chain	Atom inclusion	Q-score
EO	 0.9500	 0.6200
EP	 0.9190	 0.5810
EQ	 0.9450	 0.6220
ER	 0.9550	 0.6180
ES	 0.9210	 0.5850
ET	 0.9390	 0.6220
EU	 0.9520	 0.6190
EV	 0.9170	 0.5890
EW	 0.9390	 0.6220
EX	 0.9570	 0.6220
EY	 0.9200	 0.5840
EZ	 0.9370	 0.6210
FA	 0.9520	 0.6180
FB	 0.9170	 0.5870
FC	 0.9420	 0.6240
FD	 0.9550	 0.6210
FE	 0.9190	 0.5870
FF	 0.9430	 0.6260
FG	 0.9570	 0.6210
FH	 0.9190	 0.5850
FI	 0.9400	 0.6230
FJ	 0.9540	 0.6200
FK	 0.9180	 0.5890
FL	 0.9410	 0.6200
FM	 0.9520	 0.6190
FN	 0.9210	 0.5880
FO	 0.9420	 0.6230
FP	 0.9570	 0.6190
FQ	 0.9210	 0.5910
FR	 0.9390	 0.6260
FS	 0.9570	 0.6240
FT	 0.9210	 0.5860
FU	 0.9380	 0.6220
FV	 0.9520	 0.6190
FW	 0.9180	 0.5840
FX	 0.9410	 0.6230
FY	 0.9570	 0.6190
FZ	 0.9190	 0.5880
GA	 0.9390	 0.6220
GB	 0.9520	 0.6210
GC	 0.9220	 0.5870
GD	 0.9380	 0.6230

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Chain	Atom inclusion	Q-score
GE	 0.9510	 0.6210
GF	 0.9170	 0.5870
GG	 0.9380	 0.6230
GH	 0.9550	 0.6200
GI	 0.9170	 0.5910
GJ	 0.9420	 0.6240
GK	 0.9520	 0.6220
GL	 0.9200	 0.5860
GM	 0.9400	 0.6230
GN	 0.9550	 0.6200
GO	 0.9210	 0.5880
GP	 0.9380	 0.6230
GQ	 0.9520	 0.6210
GR	 0.9180	 0.5900
GS	 0.9380	 0.6210
GT	 0.9510	 0.6180
GU	 0.9200	 0.5830
GV	 0.9390	 0.6240
GW	 0.9590	 0.6240
GX	 0.9200	 0.5850