



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:42 PM UTC

PDB ID : 9K3M / pdb_00009k3m
EMDB ID : EMD-62019
Title : The structure of Microviridae PJNS001
Authors : Hu, W.L.; Chen, Y.B.; Wei, Y.M.; Gao, Y.
Deposited on : 2024-10-19
Resolution : 2.68 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:

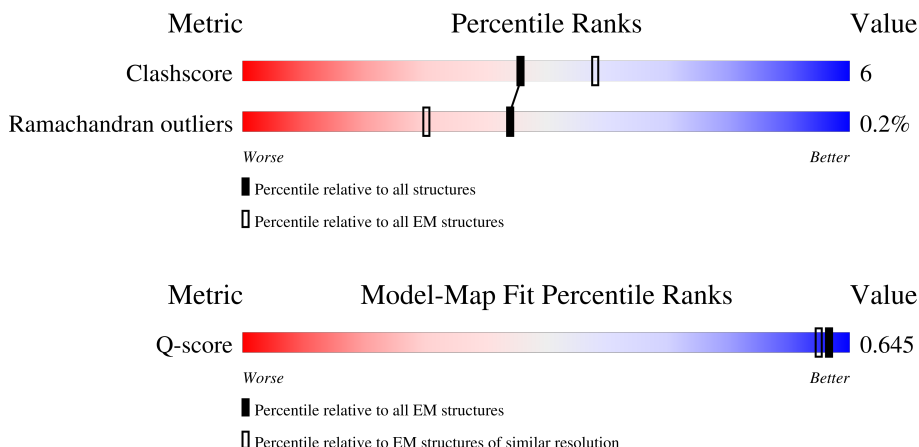
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.68 Å.

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



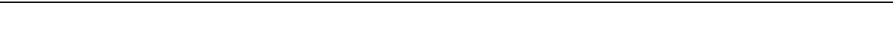
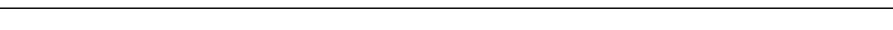
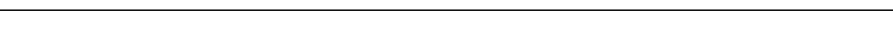
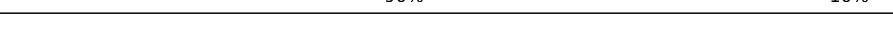
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	9255 (2.18 - 3.18)

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

Mol	Chain	Length	Quality of chain
1	A	427	91% 9%
1	AB	427	90% 10%
1	AE	427	91% 9%
1	BC	427	90% 9%
1	BF	427	90% 9%

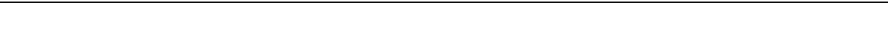
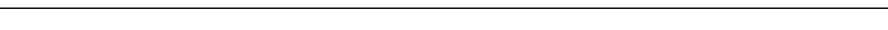
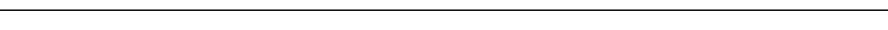
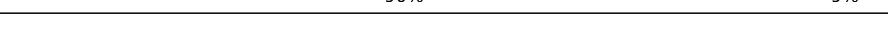
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Mol	Chain	Length	Quality of chain
1	CA	427	 90% 10%
1	CD	427	 91% 9%
1	D	427	 90% 10%
1	DB	427	 91% 9%
1	DE	427	 90% 10%
1	EC	427	 90% 9%
1	EF	427	 91% 9%
1	F	427	 91% 9%
1	FA	427	 91% 9%
1	FD	427	 91% 9%
1	GB	427	 90% 9%
1	GE	427	 91% 9%
1	HC	427	 90% 10%
1	HF	427	 90% 10%
1	I	427	 91% 9%
1	IA	427	 90% 9%
1	ID	427	 91% 9%
1	JB	427	 91% 9%
1	JE	427	 91% 9%
1	KC	427	 91% 9%
1	KF	427	 91% 9%
1	LA	427	 91% 9%
1	LD	427	 91% 9%
1	M	427	 90% 9%
1	MB	427	 90% 9%

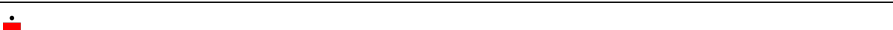
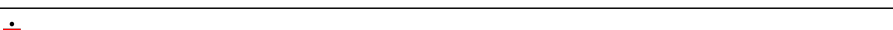
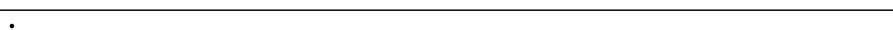
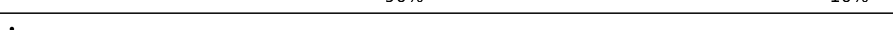
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Mol	Chain	Length	Quality of chain
1	ME	427	 90% 9%
1	NC	427	 91% 9%
1	NF	427	 91% 9%
1	OA	427	 90% 10%
1	OD	427	 91% 9%
1	P	427	 91% 9%
1	PB	427	 90% 9%
1	PE	427	 90% 10%
1	QC	427	 90% 9%
1	QF	427	 90% 9%
1	RA	427	 91% 9%
1	RD	427	 91% 9%
1	S	427	 90% 9%
1	SB	427	 90% 9%
1	SE	427	 90% 10%
1	TC	427	 91% 8%
1	TF	427	 90% 10%
1	UA	427	 91% 9%
1	UD	427	 91% 9%
1	VB	427	 91% 9%
1	VE	427	 91% 9%
1	W	427	 91% 9%
1	WC	427	 90% 10%
1	WF	427	 90% 10%
1	XA	427	 91% 9%

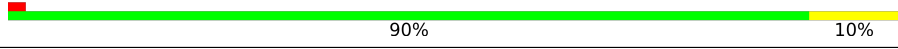
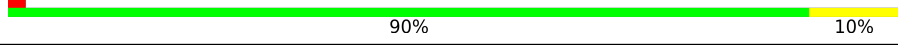
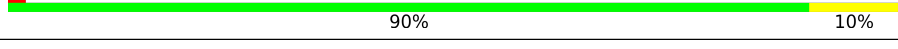
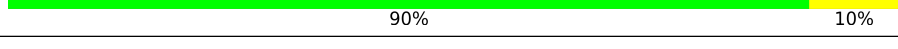
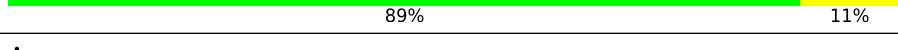
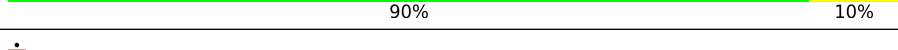
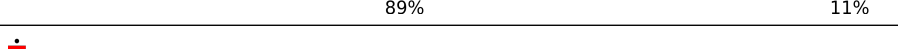
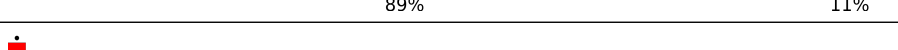
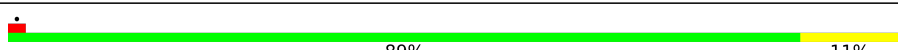
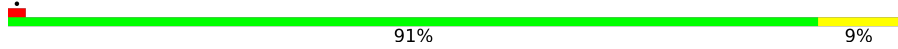
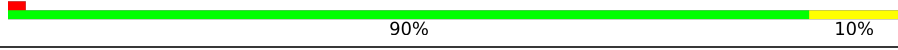
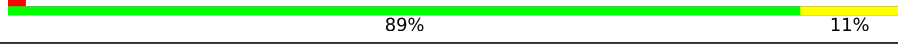
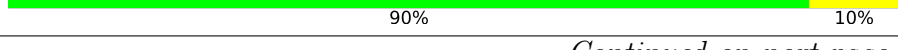
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Mol	Chain	Length	Quality of chain
1	XD	427	 90% 10%
1	YB	427	 90% 10%
1	YE	427	 91% 9%
1	Z	427	 91% 9%
1	ZC	427	 91% 9%
2	AA	175	 89% 11%
2	AD	175	 90% 10%
2	B	175	 90% 10%
2	BB	175	 90% 10%
2	BE	175	 89% 11%
2	CC	175	 90% 10%
2	CF	175	 90% 10%
2	DA	175	 90% 10%
2	DD	175	 90% 10%
2	E	175	 90% 10%
2	EB	175	 90% 10%
2	EE	175	 89% 11%
2	FC	175	 89% 11%
2	FF	175	 89% 11%
2	G	175	 90% 10%
2	GA	175	 89% 11%
2	GD	175	 90% 10%
2	HB	175	 89% 11%
2	HE	175	 90% 10%
2	IC	175	 90% 10%

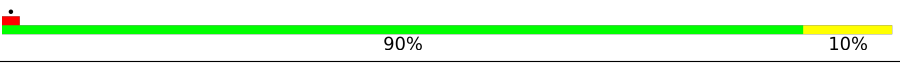
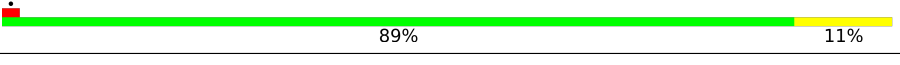
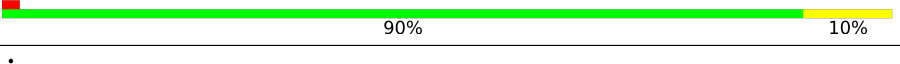
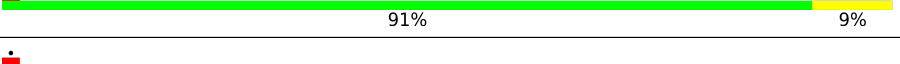
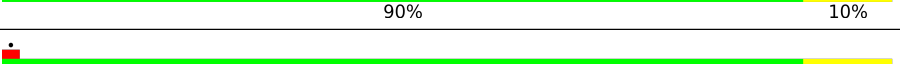
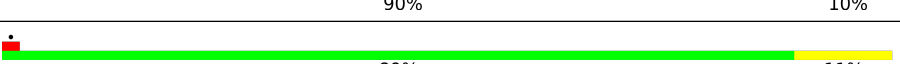
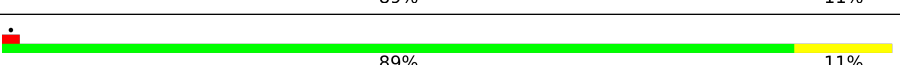
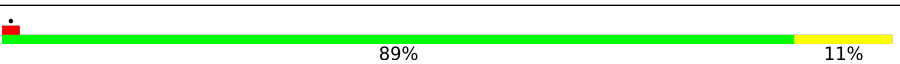
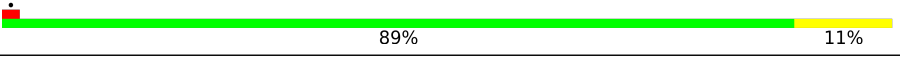
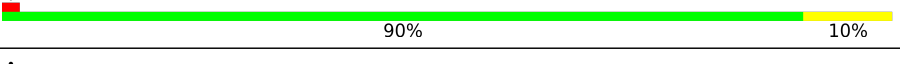
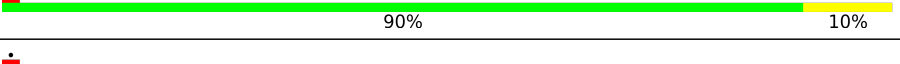
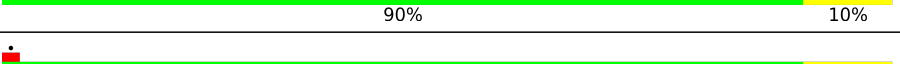
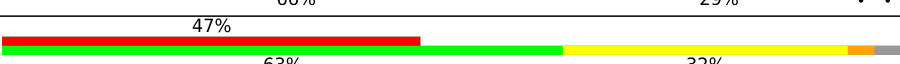
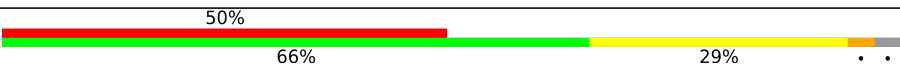
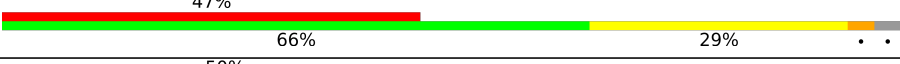
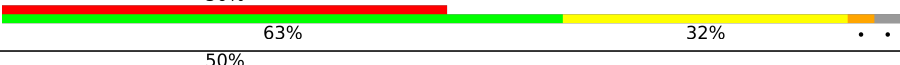
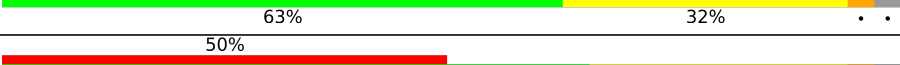
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Mol	Chain	Length	Quality of chain
2	IF	175	 88%12%
2	JA	175	 90%10%
2	JD	175	 90%10%
2	K	175	 90%10%
2	KB	175	 90%10%
2	KE	175	 90%10%
2	LC	175	 89%11%
2	LF	175	 90%10%
2	MA	175	 89%11%
2	MD	175	 89%11%
2	N	175	 89%11%
2	NB	175	 89%11%
2	NE	175	 90%10%
2	OC	175	 90%10%
2	OF	175	 90%10%
2	PA	175	 89%11%
2	PD	175	 90%10%
2	Q	175	 89%11%
2	QB	175	 89%11%
2	QE	175	 91%9%
2	RC	175	 90%10%
2	RF	175	 90%10%
2	SA	175	 89%11%
2	SD	175	 89%11%
2	T	175	 90%10%

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Mol	Chain	Length	Quality of chain
2	TB	175	
2	TE	175	
2	UC	175	
2	UF	175	
2	VA	175	
2	VD	175	
2	WB	175	
2	WE	175	
2	X	175	
2	XC	175	
2	XF	175	
2	YA	175	
2	YD	175	
2	ZB	175	
2	ZE	175	
3	AC	38	
3	AF	38	
3	BA	38	
3	BD	38	
3	C	38	
3	CB	38	
3	CE	38	
3	DC	38	
3	DF	38	
3	EA	38	

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Mol	Chain	Length	Quality of chain
3	ED	38	47% 66%29% ..
3	FB	38	50% 66%29% ..
3	FE	38	47% 66%29% ..
3	GC	38	50% 66%29% ..
3	GF	38	50% 66%29% ..
3	H	38	50% 63%32% ..
3	HA	38	47% 66%29% ..
3	HD	38	47% 66%29% ..
3	IB	38	50% 63%32% ..
3	IE	38	47% 66%29% ..
3	J	38	47% 63%32% ..
3	JC	38	50% 63%32% ..
3	JF	38	47% 66%29% ..
3	KA	38	47% 66%29% ..
3	KD	38	50% 66%29% ..
3	L	38	50% 66%29% ..
3	LB	38	47% 66%29% ..
3	LE	38	47% 66%29% ..
3	MC	38	47% 66%29% ..
3	MF	38	47% 66%29% ..
3	NA	38	50% 66%29% ..
3	ND	38	50% 63%32% ..
3	O	38	47% 66%29% ..
3	OB	38	47% 66%29% ..
3	OE	38	50% 66%29% ..

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Mol	Chain	Length	Quality of chain
3	PC	38	47% 66% 29% ..
3	PF	38	47% 66% 29% ..
3	QA	38	50% 66% 29% ..
3	QD	38	47% 63% 32% ..
3	R	38	47% 66% 29% ..
3	RB	38	50% 66% 29% ..
3	RE	38	50% 66% 29% ..
3	SC	38	47% 66% 29% ..
3	SF	38	50% 66% 29% ..
3	TA	38	47% 66% 29% ..
3	TD	38	47% 66% 29% ..
3	UB	38	50% 63% 32% ..
3	UE	38	47% 66% 29% ..
3	V	38	47% 66% 29% ..
3	VC	38	50% 66% 29% ..
3	VF	38	50% 66% 29% ..
3	WA	38	47% 63% 32% ..
3	WD	38	47% 63% 32% ..
3	XB	38	47% 66% 29% ..
3	XE	38	47% 66% 29% ..
3	Y	38	50% 66% 29% ..
3	YC	38	50% 63% 32% ..
3	YF	38	47% 66% 29% ..
3	ZA	38	47% 66% 29% ..
3	ZD	38	50% 66% 29% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 302160 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Capsid protein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	A	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	D	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	I	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	M	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	P	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	S	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	W	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	Z	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	CA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	FA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	IA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	LA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	OA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	RA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	UA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	XA	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	DB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	GB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	JB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	MB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	PB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	SB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	VB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	YB	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	BC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	EC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	HC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	KC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	NC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	QC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	TC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	WC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	ZC	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	CD	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	FD	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		
1	ID	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	LD	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	OD	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	RD	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	UD	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	XD	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	AE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	DE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	GE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	JE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	ME	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	PE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	SE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	VE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	YE	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	BF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	EF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	HF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	KF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	NF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	QF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0
1	TF	426	Total 3412	C 2172	N 590	O 636	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	WF	426	Total	C	N	O	S	0	0
			3412	2172	590	636	14		

- Molecule 2 is a protein called Major spike protein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	B	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	E	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	K	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	N	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	Q	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	T	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	X	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	AA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	DA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	GA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	JA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	MA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	PA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	SA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	VA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	YA	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	BB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	EB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	HB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	KB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	NB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	QB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	TB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	WB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	ZB	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	CC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	FC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	IC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	LC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	OC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	RC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	UC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	XC	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	AD	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	DD	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	GD	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	JD	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		
2	MD	175	Total	C	N	O	S	0	0
			1343	859	222	254	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	PD	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	SD	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	VD	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	YD	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	BE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	EE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	HE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	KE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	NE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	QE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	TE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	WE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	ZE	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	CF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	FF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	IF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	LF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	OF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	RF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	UF	175	Total 1343	C 859	N 222	O 254	S 8	0	0
2	XF	175	Total 1343	C 859	N 222	O 254	S 8	0	0

- Molecule 3 is a protein called DNA-binding protein J.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	37	Total	C	N	O	0	0
			281	174	63	44		
3	C	37	Total	C	N	O	0	0
			281	174	63	44		
3	H	37	Total	C	N	O	0	0
			281	174	63	44		
3	L	37	Total	C	N	O	0	0
			281	174	63	44		
3	O	37	Total	C	N	O	0	0
			281	174	63	44		
3	R	37	Total	C	N	O	0	0
			281	174	63	44		
3	V	37	Total	C	N	O	0	0
			281	174	63	44		
3	Y	37	Total	C	N	O	0	0
			281	174	63	44		
3	BA	37	Total	C	N	O	0	0
			281	174	63	44		
3	EA	37	Total	C	N	O	0	0
			281	174	63	44		
3	HA	37	Total	C	N	O	0	0
			281	174	63	44		
3	KA	37	Total	C	N	O	0	0
			281	174	63	44		
3	NA	37	Total	C	N	O	0	0
			281	174	63	44		
3	QA	37	Total	C	N	O	0	0
			281	174	63	44		
3	TA	37	Total	C	N	O	0	0
			281	174	63	44		
3	WA	37	Total	C	N	O	0	0
			281	174	63	44		
3	ZA	37	Total	C	N	O	0	0
			281	174	63	44		
3	CB	37	Total	C	N	O	0	0
			281	174	63	44		
3	FB	37	Total	C	N	O	0	0
			281	174	63	44		
3	IB	37	Total	C	N	O	0	0
			281	174	63	44		
3	LB	37	Total	C	N	O	0	0
			281	174	63	44		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	OB	37	Total	C	N	O	0	0
			281	174	63	44		
3	RB	37	Total	C	N	O	0	0
			281	174	63	44		
3	UB	37	Total	C	N	O	0	0
			281	174	63	44		
3	XB	37	Total	C	N	O	0	0
			281	174	63	44		
3	AC	37	Total	C	N	O	0	0
			281	174	63	44		
3	DC	37	Total	C	N	O	0	0
			281	174	63	44		
3	GC	37	Total	C	N	O	0	0
			281	174	63	44		
3	JC	37	Total	C	N	O	0	0
			281	174	63	44		
3	MC	37	Total	C	N	O	0	0
			281	174	63	44		
3	PC	37	Total	C	N	O	0	0
			281	174	63	44		
3	SC	37	Total	C	N	O	0	0
			281	174	63	44		
3	VC	37	Total	C	N	O	0	0
			281	174	63	44		
3	YC	37	Total	C	N	O	0	0
			281	174	63	44		
3	BD	37	Total	C	N	O	0	0
			281	174	63	44		
3	ED	37	Total	C	N	O	0	0
			281	174	63	44		
3	HD	37	Total	C	N	O	0	0
			281	174	63	44		
3	KD	37	Total	C	N	O	0	0
			281	174	63	44		
3	ND	37	Total	C	N	O	0	0
			281	174	63	44		
3	QD	37	Total	C	N	O	0	0
			281	174	63	44		
3	TD	37	Total	C	N	O	0	0
			281	174	63	44		
3	WD	37	Total	C	N	O	0	0
			281	174	63	44		

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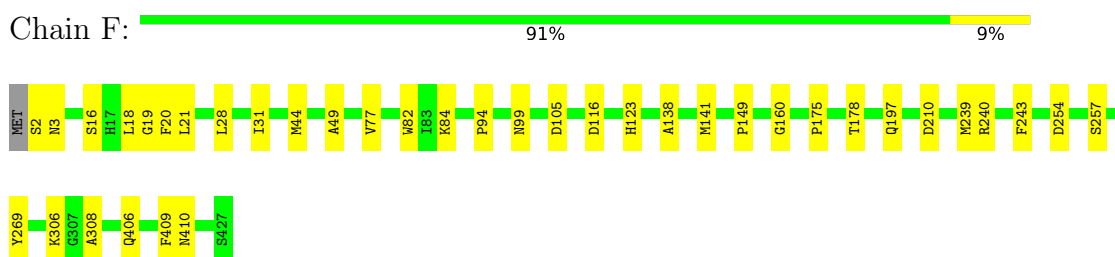
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Mol	Chain	Residues	Atoms				AltConf	Trace
3	ZD	37	Total	C	N	O	0	0
			281	174	63	44		
3	CE	37	Total	C	N	O	0	0
			281	174	63	44		
3	FE	37	Total	C	N	O	0	0
			281	174	63	44		
3	IE	37	Total	C	N	O	0	0
			281	174	63	44		
3	LE	37	Total	C	N	O	0	0
			281	174	63	44		
3	OE	37	Total	C	N	O	0	0
			281	174	63	44		
3	RE	37	Total	C	N	O	0	0
			281	174	63	44		
3	UE	37	Total	C	N	O	0	0
			281	174	63	44		
3	XE	37	Total	C	N	O	0	0
			281	174	63	44		
3	AF	37	Total	C	N	O	0	0
			281	174	63	44		
3	DF	37	Total	C	N	O	0	0
			281	174	63	44		
3	GF	37	Total	C	N	O	0	0
			281	174	63	44		
3	JF	37	Total	C	N	O	0	0
			281	174	63	44		
3	MF	37	Total	C	N	O	0	0
			281	174	63	44		
3	PF	37	Total	C	N	O	0	0
			281	174	63	44		
3	SF	37	Total	C	N	O	0	0
			281	174	63	44		
3	VF	37	Total	C	N	O	0	0
			281	174	63	44		
3	YF	37	Total	C	N	O	0	0
			281	174	63	44		

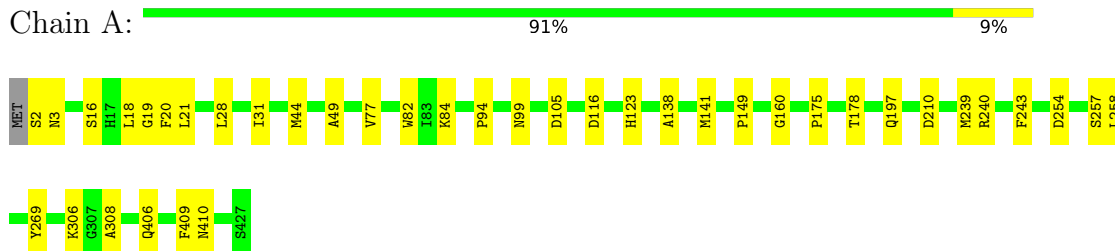
3 Residue-property plots [i](#)

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

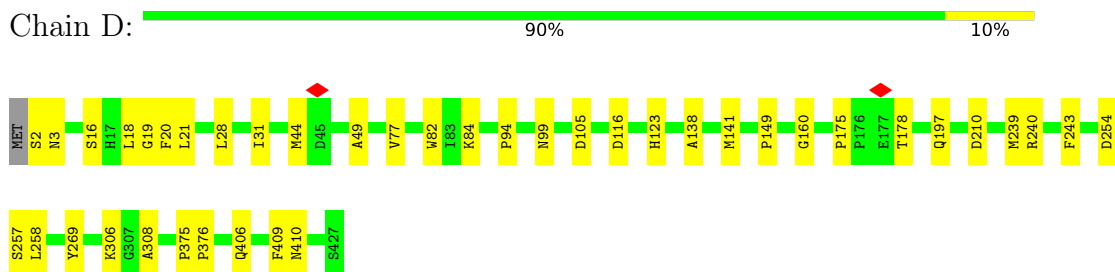
- Molecule 1: Capsid protein F



- Molecule 1: Capsid protein F

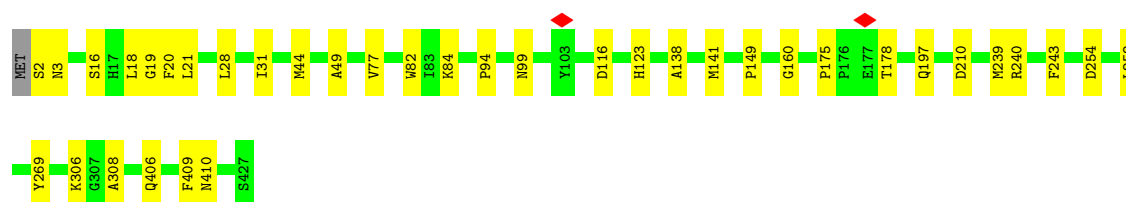


- Molecule 1: Capsid protein F



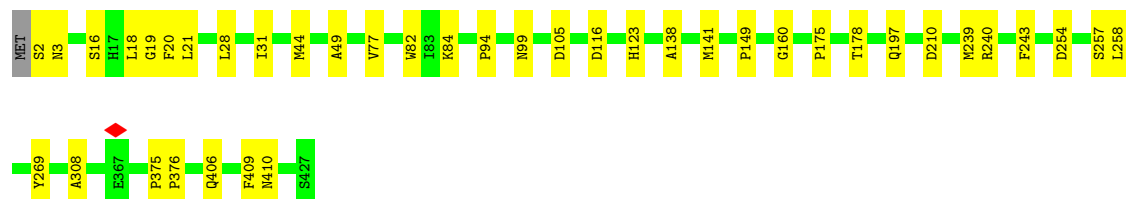
- Molecule 1: Capsid protein F





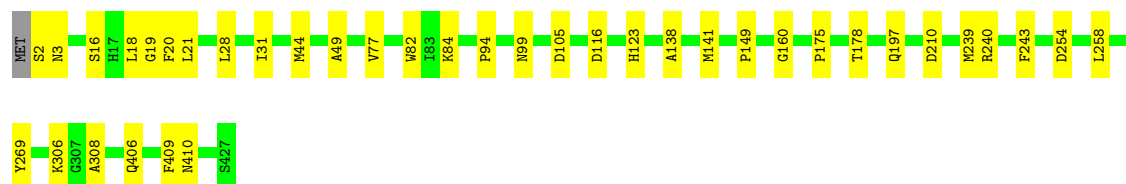
- Molecule 1: Capsid protein F

Chain M: 90% 9%



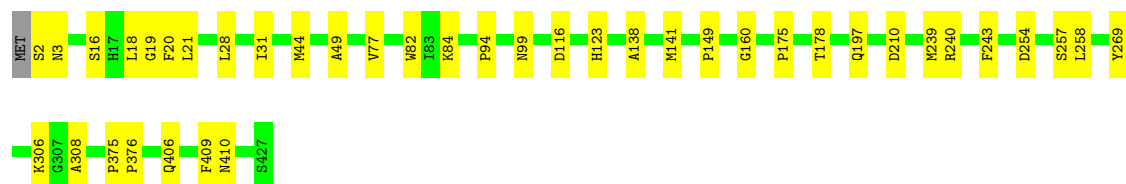
- Molecule 1: Capsid protein F

Chain P: 91% 9%



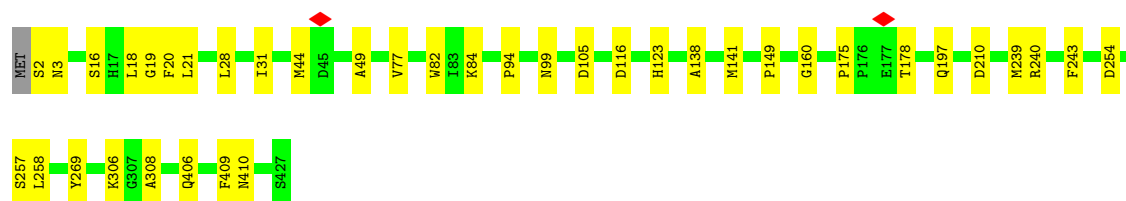
- Molecule 1: Capsid protein F

Chain S: 90% 9%



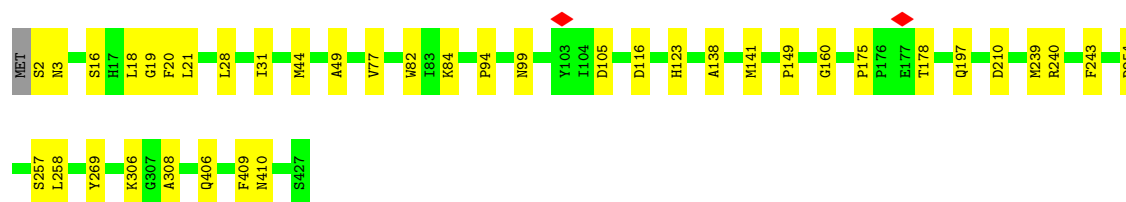
- Molecule 1: Capsid protein F

Chain W: 91% 9%



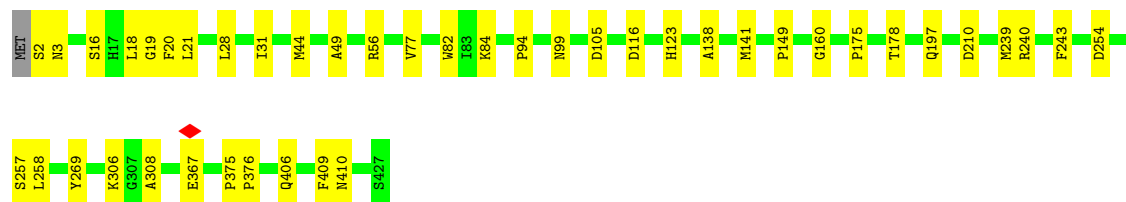
- Molecule 1: Capsid protein F

Chain Z:  91% 9%



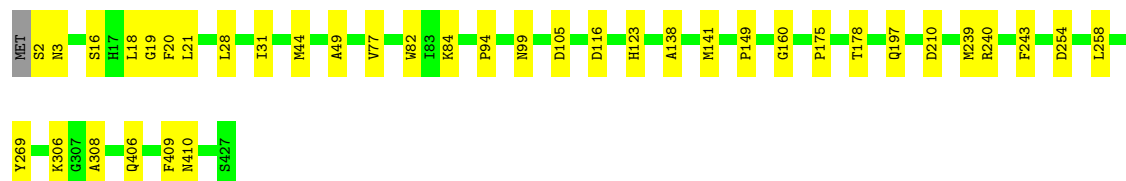
- Molecule 1: Capsid protein F

Chain CA:  90% 10%



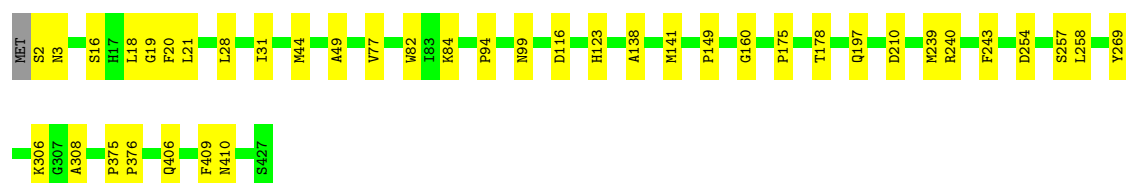
- Molecule 1: Capsid protein F

Chain FA:  91% 9%



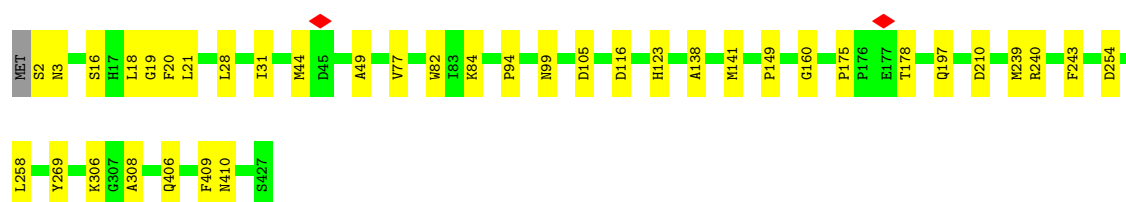
- Molecule 1: Capsid protein F

Chain IA:  90% 9%



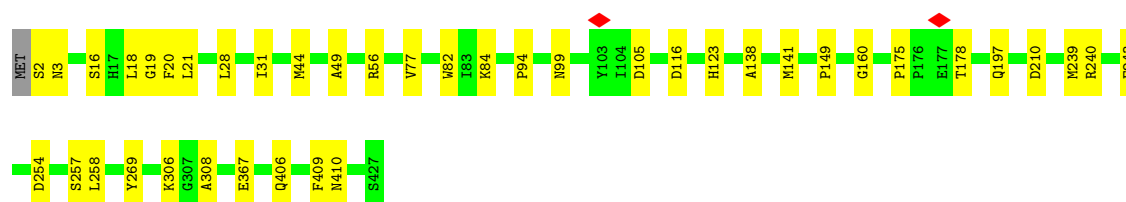
- Molecule 1: Capsid protein F

Chain LA:  91% 9%



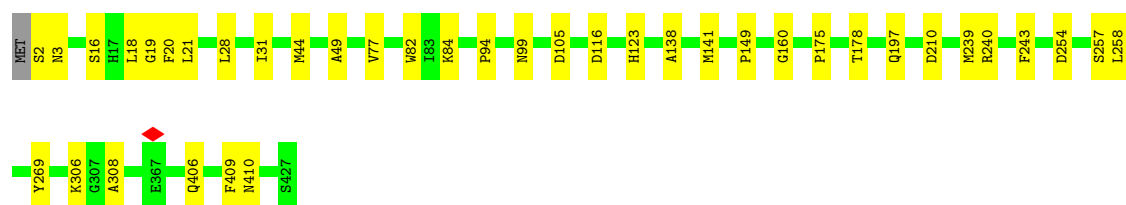
- Molecule 1: Capsid protein F

Chain OA:  90% 10%



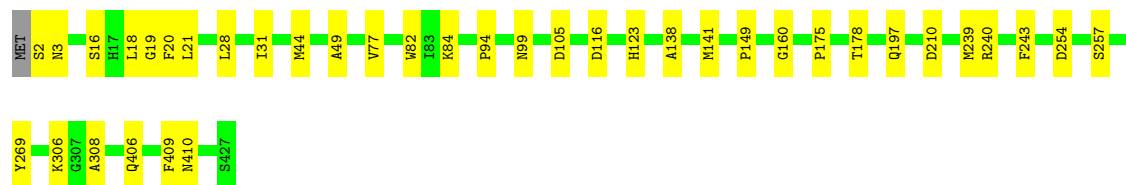
- Molecule 1: Capsid protein F

Chain RA:  91% 9%



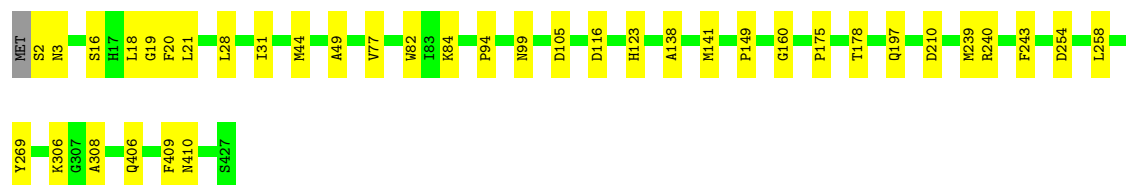
- Molecule 1: Capsid protein F

Chain UA:  91% 9%



- Molecule 1: Capsid protein F

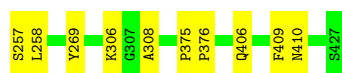
Chain XA:  91% 9%



- Molecule 1: Capsid protein F

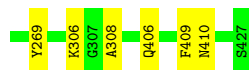
Chain AB:  90% 10%





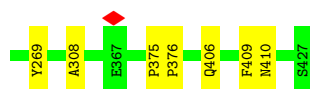
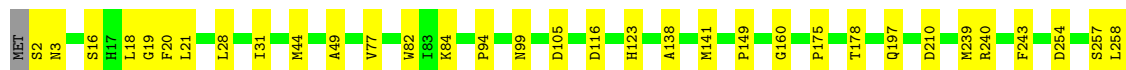
- Molecule 1: Capsid protein F

Chain DB: 91% 9%



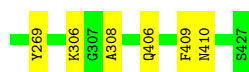
- Molecule 1: Capsid protein F

Chain GB: 90% 9%



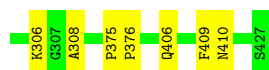
- Molecule 1: Capsid protein F

Chain JB: 91% 9%



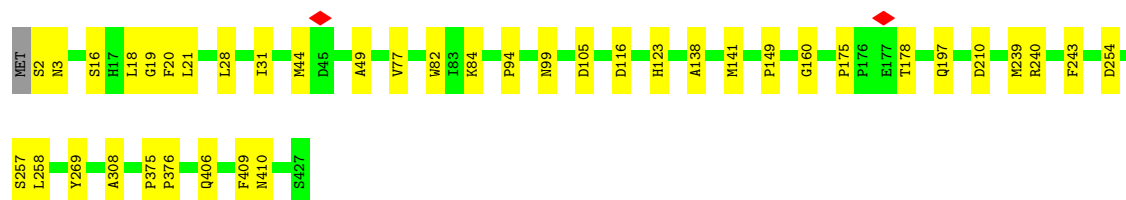
- Molecule 1: Capsid protein F

Chain MB: 90% 9%



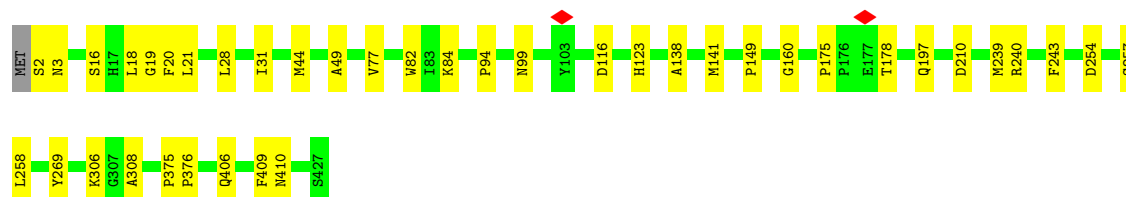
- Molecule 1: Capsid protein F

Chain PB: 90% 9%



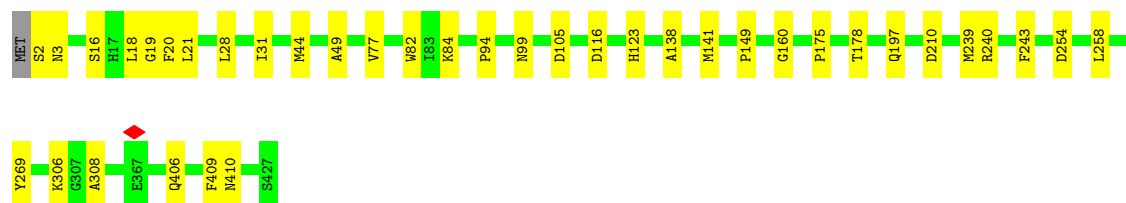
- Molecule 1: Capsid protein F

Chain SB: 90% 9%



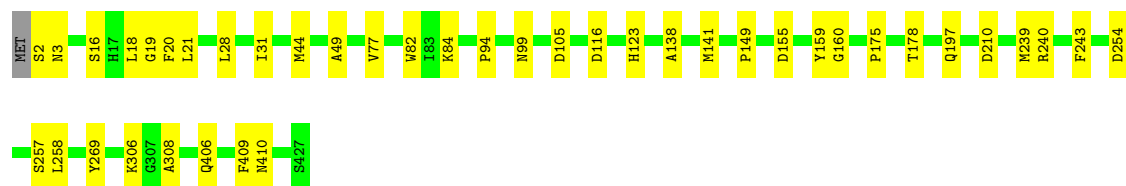
- Molecule 1: Capsid protein F

Chain VB: 91% 9%



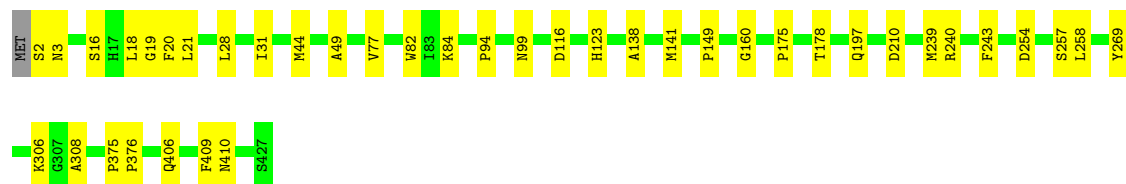
- Molecule 1: Capsid protein F

Chain YB: 90% 10%



- Molecule 1: Capsid protein F

Chain BC: 90% 9%



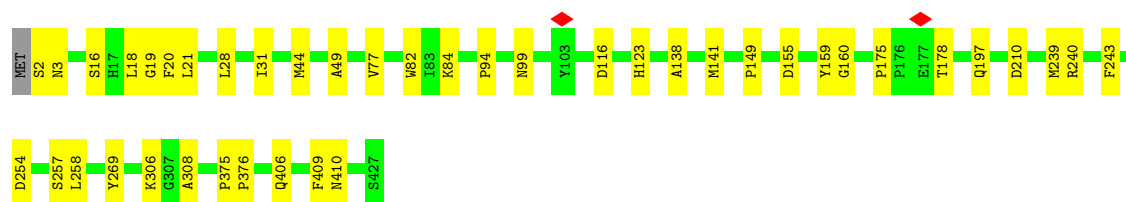
- Molecule 1: Capsid protein F

Chain EC:  90% 9%



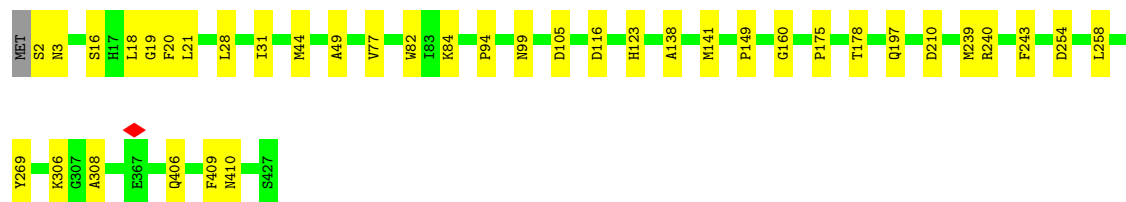
- Molecule 1: Capsid protein F

Chain HC:  90% 10%



- Molecule 1: Capsid protein F

Chain KC:  91% 9%



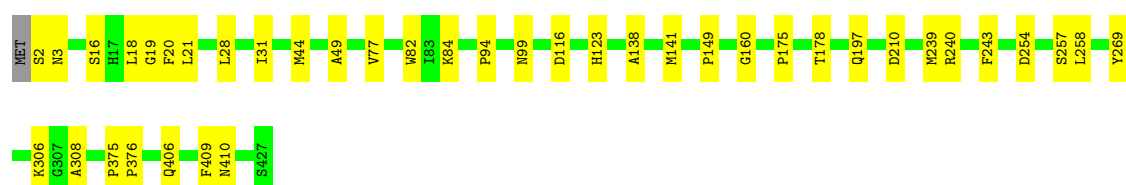
- Molecule 1: Capsid protein F

Chain NC:  91% 9%

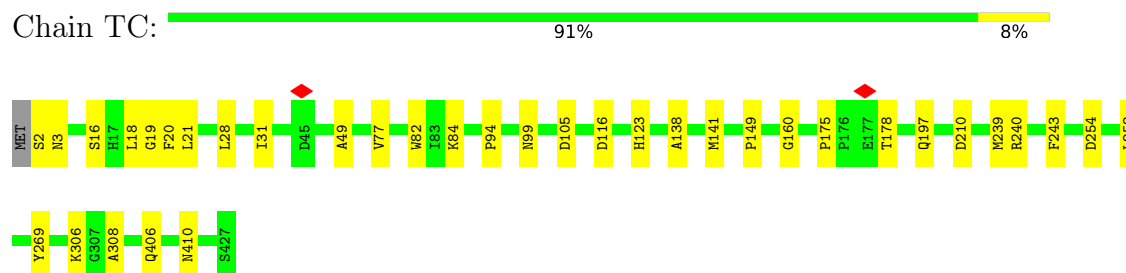


- Molecule 1: Capsid protein F

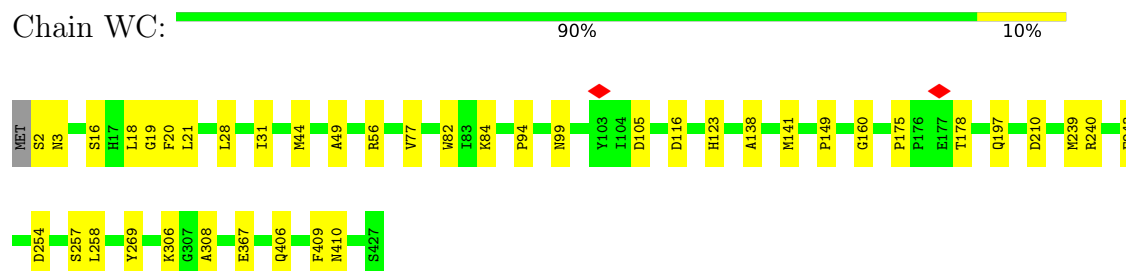
Chain QC:  90% 9%



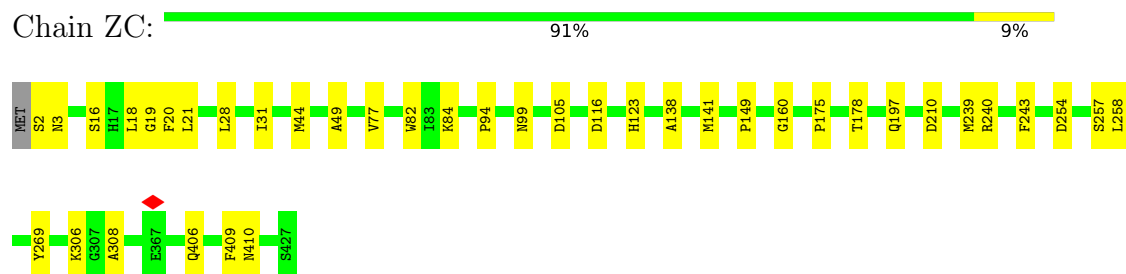
- Molecule 1: Capsid protein F



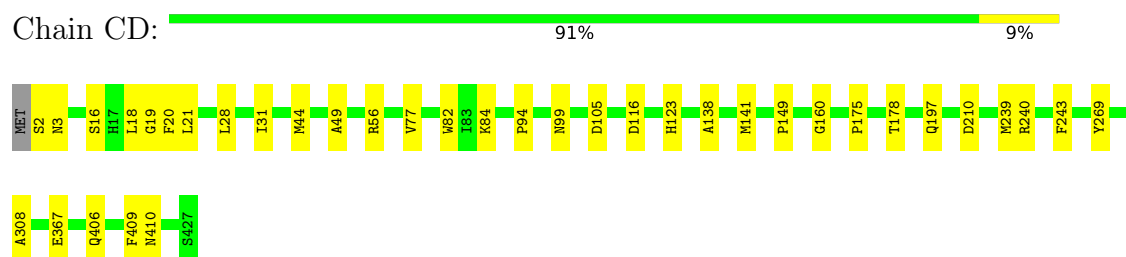
- Molecule 1: Capsid protein F



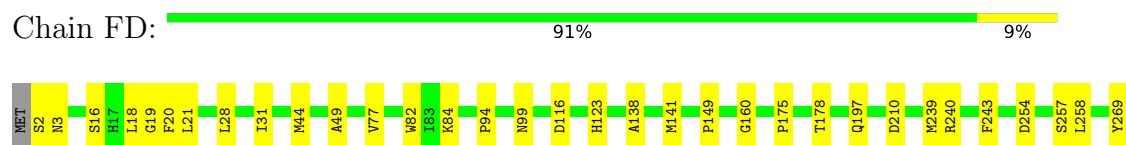
- Molecule 1: Capsid protein F



- Molecule 1: Capsid protein F

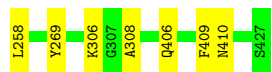


- Molecule 1: Capsid protein F

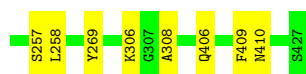
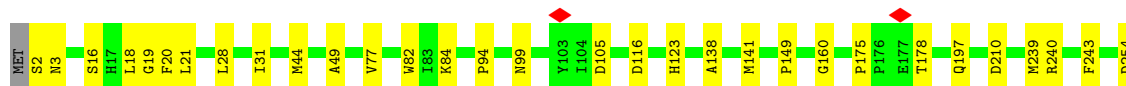




- Molecule 1: Capsid protein F



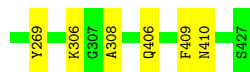
- Molecule 1: Capsid protein F



- Molecule 1: Capsid protein F

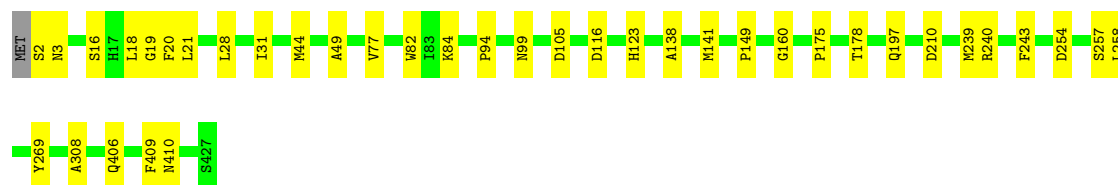


- Molecule 1: Capsid protein F



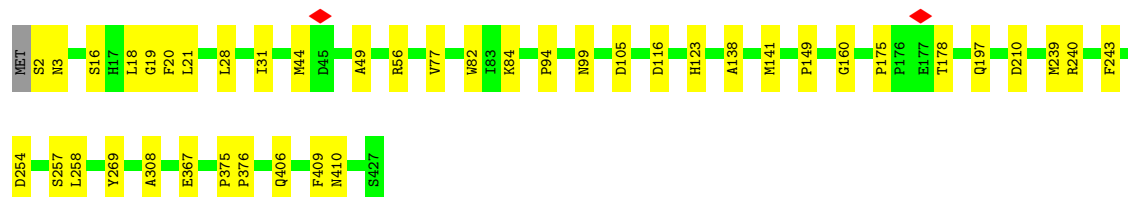
- Molecule 1: Capsid protein F





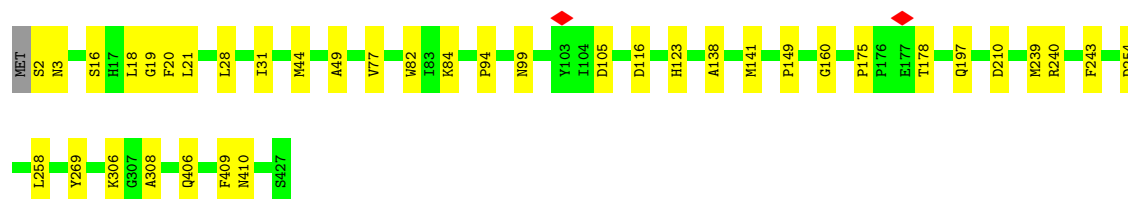
- Molecule 1: Capsid protein F

Chain XD: 90% 10%



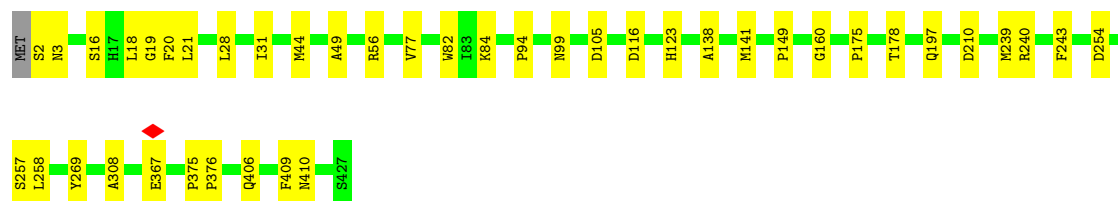
- Molecule 1: Capsid protein F

Chain AE: 91% 9%



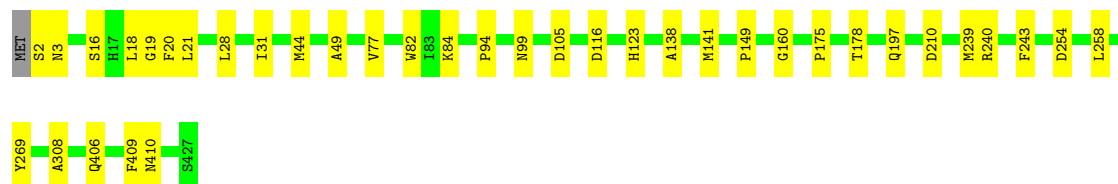
- Molecule 1: Capsid protein F

Chain DE: 90% 10%



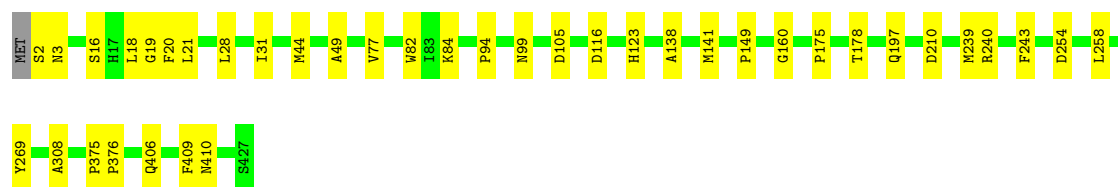
- Molecule 1: Capsid protein F

Chain GE: 91% 9%



- Molecule 1: Capsid protein F

Chain JE:  91% 9%



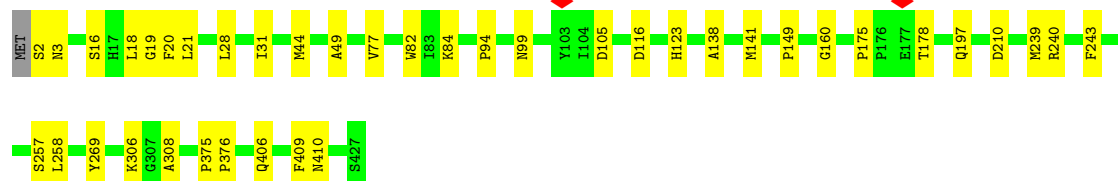
- Molecule 1: Capsid protein F

Chain ME:  90% 9%



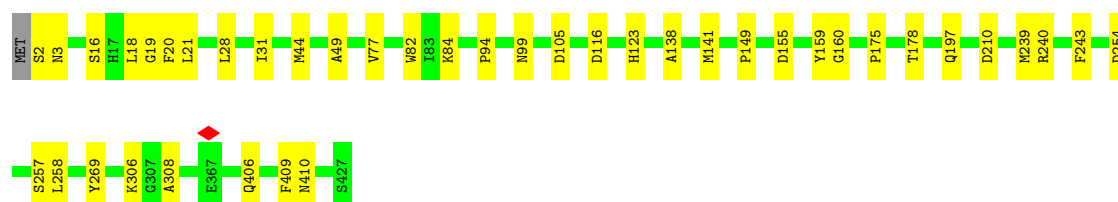
- Molecule 1: Capsid protein F

Chain PE:  90% 10%



- Molecule 1: Capsid protein F

Chain SE:  90% 10%



- Molecule 1: Capsid protein F

Chain VE:  91% 9%





- Molecule 1: Capsid protein F

Chain NF: 91% 9%



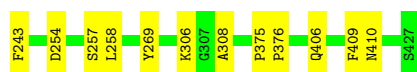
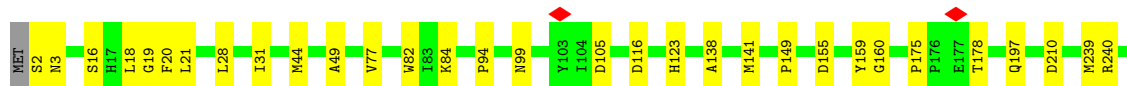
- Molecule 1: Capsid protein F

Chain QF: 90% 9%



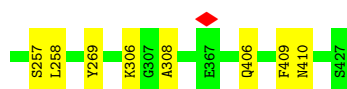
- Molecule 1: Capsid protein F

Chain TF: 90% 10%



- Molecule 1: Capsid protein F

Chain WF: 90% 10%

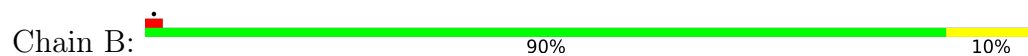


- Molecule 2: Major spike protein G

Chain G: 90% 10%



- Molecule 2: Major spike protein G



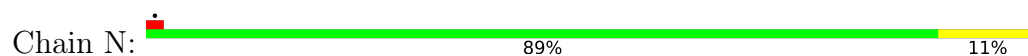
- Molecule 2: Major spike protein G



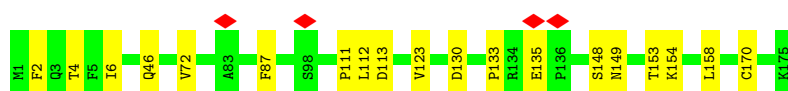
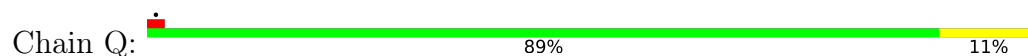
- Molecule 2: Major spike protein G



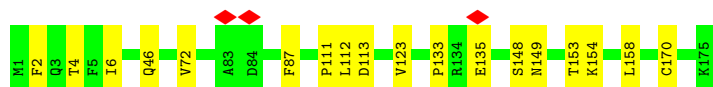
- Molecule 2: Major spike protein G



- Molecule 2: Major spike protein G

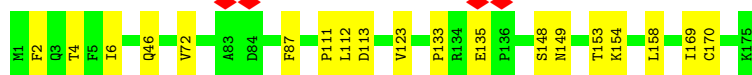


- Molecule 2: Major spike protein G



- Molecule 2: Major spike protein G

Chain X:  89% 11%



- Molecule 2: Major spike protein G

Chain AA:  89% 11%



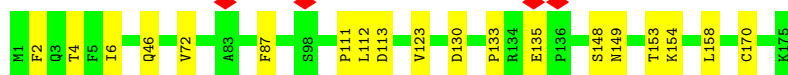
- Molecule 2: Major spike protein G

Chain DA:  90% 10%



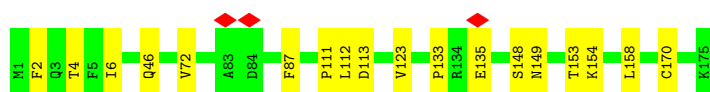
- Molecule 2: Major spike protein G

Chain GA:  89% 11%



- Molecule 2: Major spike protein G

Chain JA:  90% 10%



- Molecule 2: Major spike protein G

Chain MA:  89% 11%



- Molecule 2: Major spike protein G

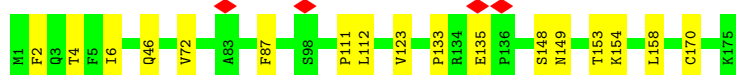
Chain PA:  89% 11%



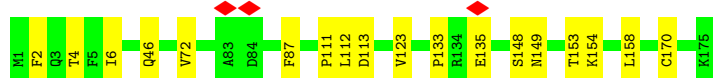
• Molecule 2: Major spike protein G

Chain SA:  89% 11%

• Molecule 2: Major spike protein G

Chain VA:  90% 10%

• Molecule 2: Major spike protein G

Chain YA:  90% 10%

• Molecule 2: Major spike protein G

Chain BB:  90% 10%

• Molecule 2: Major spike protein G

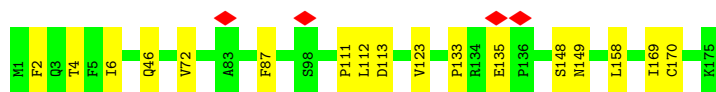
Chain EB:  90% 10%

• Molecule 2: Major spike protein G

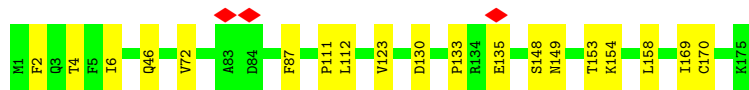
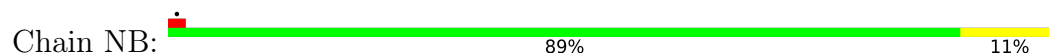
Chain HB:  89% 11%

• Molecule 2: Major spike protein G

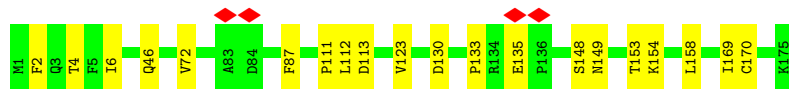
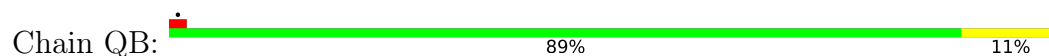
Chain KB:  90% 10%



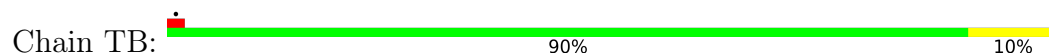
- Molecule 2: Major spike protein G



- Molecule 2: Major spike protein G



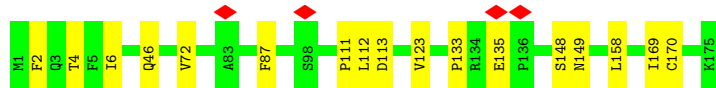
- Molecule 2: Major spike protein G



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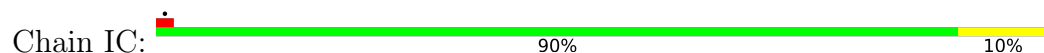
- Molecule 2: Major spike protein G



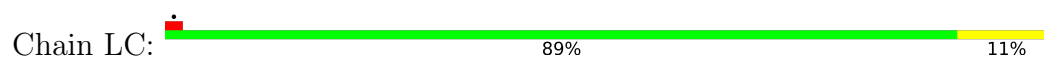
- Molecule 2: Major spike protein G



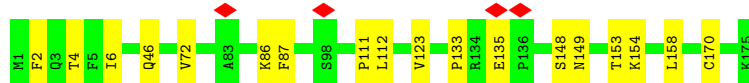
- Molecule 2: Major spike protein G



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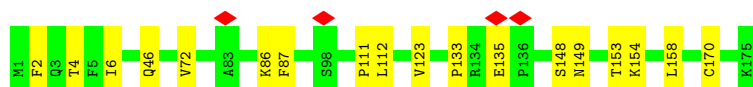
- Molecule 2: Major spike protein G

Chain AD:  90% 10%



- Molecule 2: Major spike protein G

Chain DD:  90% 10%



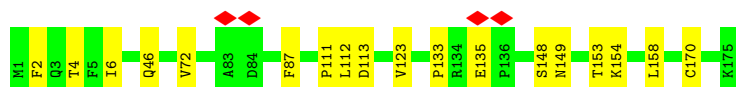
- Molecule 2: Major spike protein G

Chain GD:  90% 10%



- Molecule 2: Major spike protein G

Chain JD:  90% 10%



- Molecule 2: Major spike protein G

Chain MD:  89% 11%



- Molecule 2: Major spike protein G

Chain PD:  90% 10%



- Molecule 2: Major spike protein G

Chain SD:  89% 11%



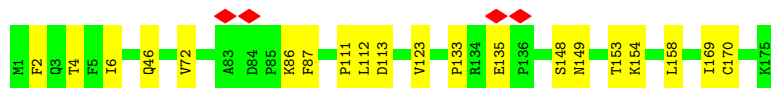
- Molecule 2: Major spike protein G



- Molecule 2: Major spike protein G



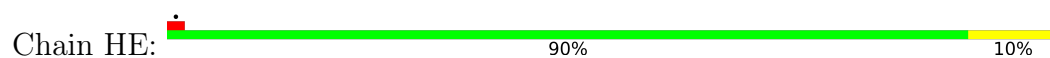
- Molecule 2: Major spike protein G



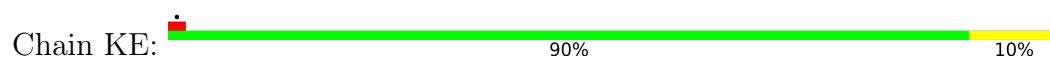
- Molecule 2: Major spike protein G



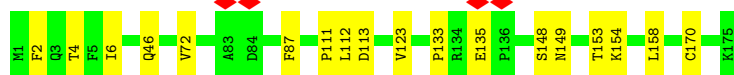
- Molecule 2: Major spike protein G



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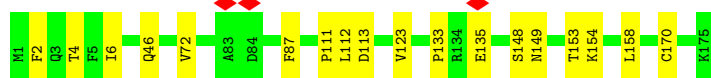
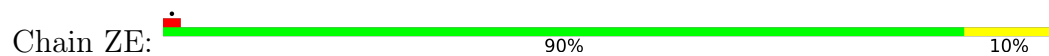
- Molecule 2: Major spike protein G



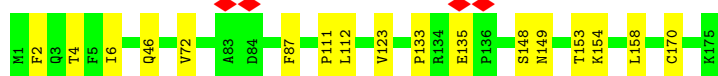
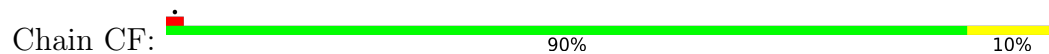
- Molecule 2: Major spike protein G



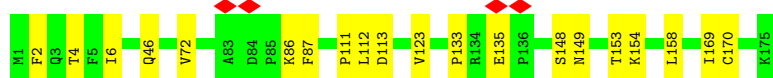
- Molecule 2: Major spike protein G



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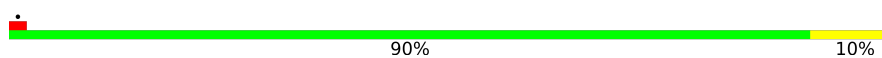


- Molecule 2: Major spike protein G

Chain IF:  88% 12%

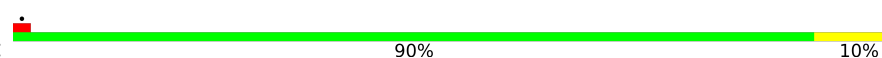


- Molecule 2: Major spike protein G

Chain LF:  90% 10%

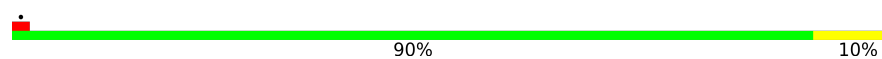


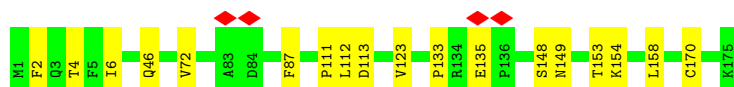
- Molecule 2: Major spike protein G

Chain OF:  90% 10%

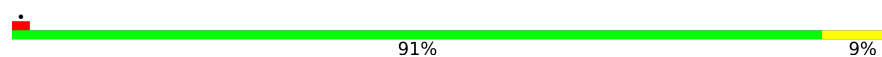


- Molecule 2: Major spike protein G

Chain RF:  90% 10%

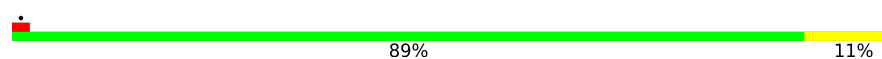


- Molecule 2: Major spike protein G

Chain UF:  91% 9%

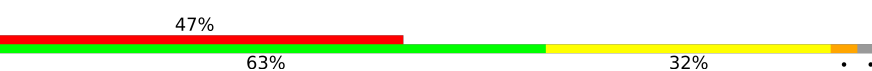


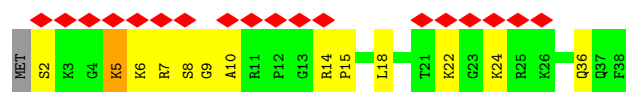
- Molecule 2: Major spike protein G

Chain XF:  89% 11%



- Molecule 3: DNA-binding protein J

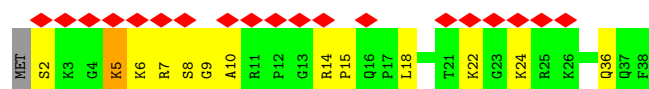
Chain J:  47% 63% 32%



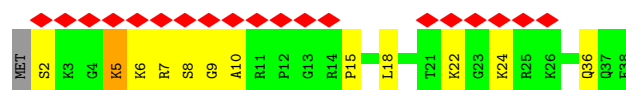
• Molecule 3: DNA-binding protein J



• Molecule 3: DNA-binding protein J



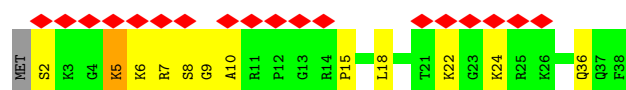
• Molecule 3: DNA-binding protein J



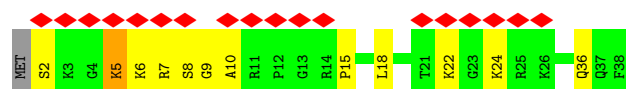
• Molecule 3: DNA-binding protein J



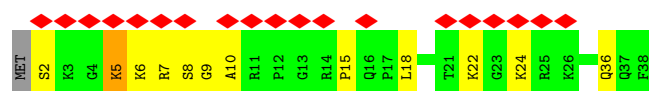
• Molecule 3: DNA-binding protein J



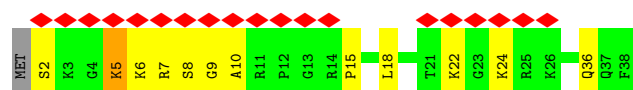
• Molecule 3: DNA-binding protein J



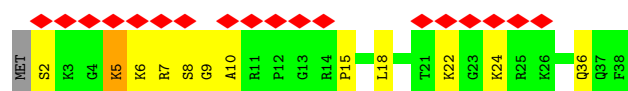
• Molecule 3: DNA-binding protein J



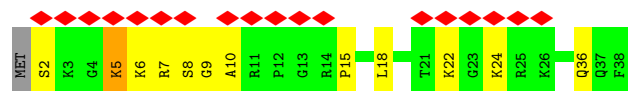
• Molecule 3: DNA-binding protein J



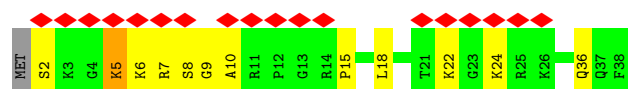
• Molecule 3: DNA-binding protein J



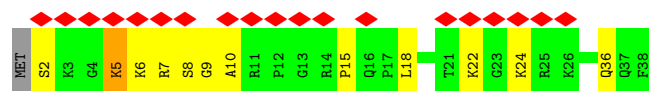
• Molecule 3: DNA-binding protein J



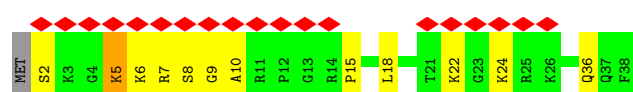
• Molecule 3: DNA-binding protein J



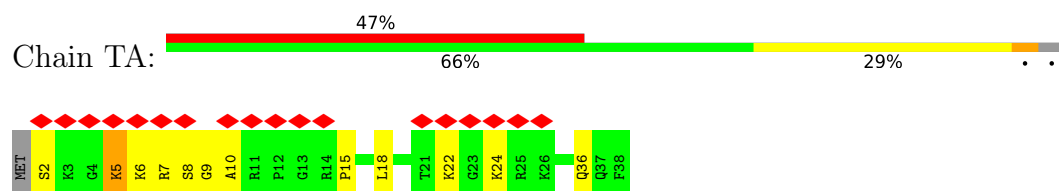
• Molecule 3: DNA-binding protein J



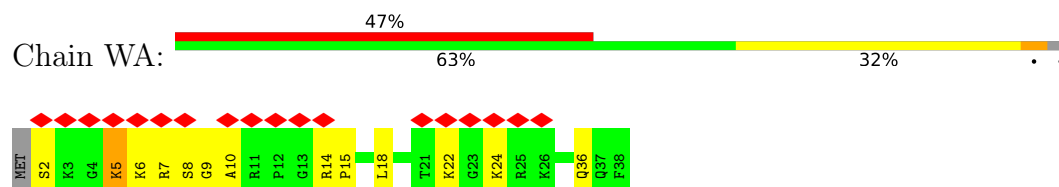
• Molecule 3: DNA-binding protein J



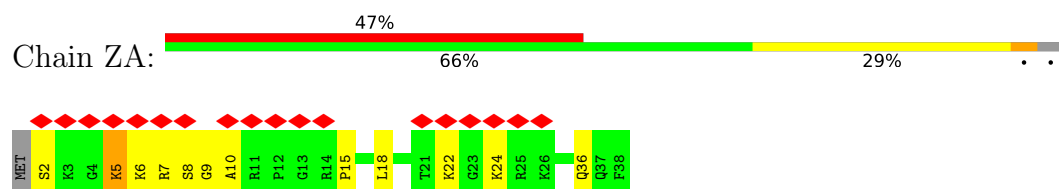
- Molecule 3: DNA-binding protein J



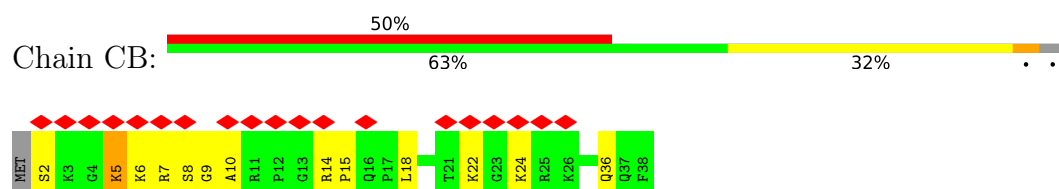
- Molecule 3: DNA-binding protein J



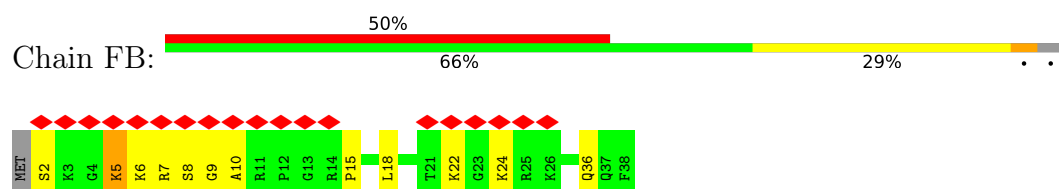
- Molecule 3: DNA-binding protein J



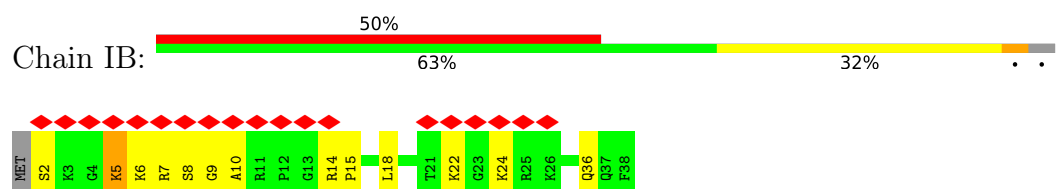
- Molecule 3: DNA-binding protein J



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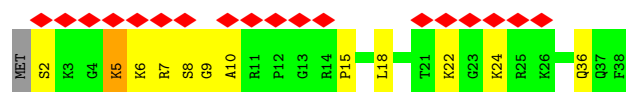


- Molecule 3: DNA-binding protein J



- Molecule 3: DNA-binding protein J

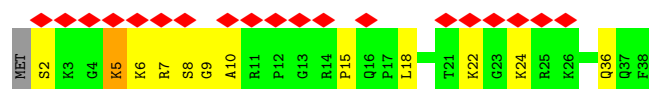




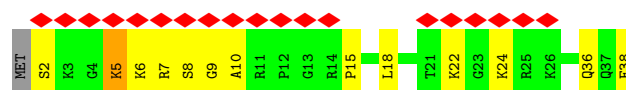
• Molecule 3: DNA-binding protein J



• Molecule 3: DNA-binding protein J



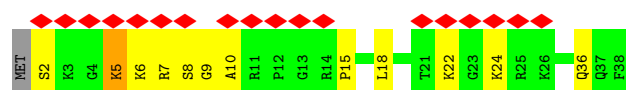
• Molecule 3: DNA-binding protein J



• Molecule 3: DNA-binding protein J



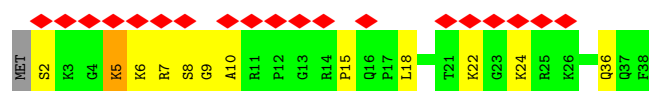
• Molecule 3: DNA-binding protein J



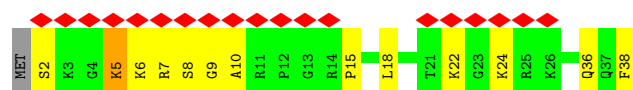
• Molecule 3: DNA-binding protein J



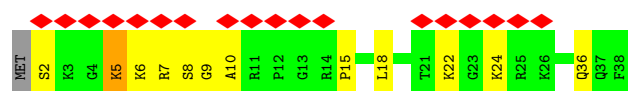
• Molecule 3: DNA-binding protein J



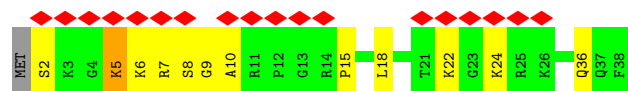
• Molecule 3: DNA-binding protein J



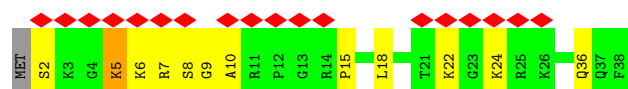
• Molecule 3: DNA-binding protein J



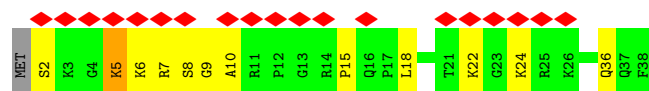
• Molecule 3: DNA-binding protein J



• Molecule 3: DNA-binding protein J



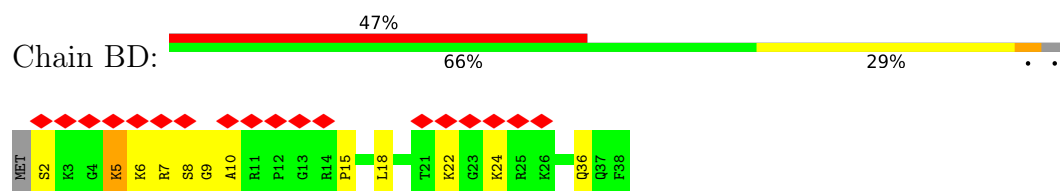
• Molecule 3: DNA-binding protein J



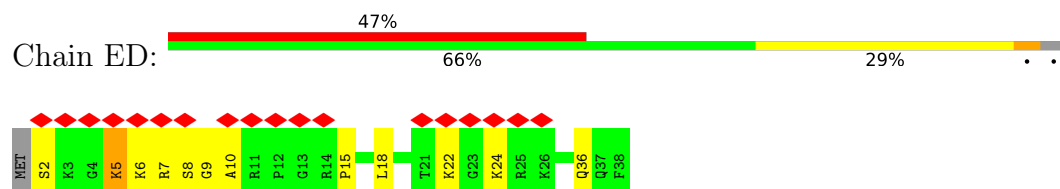
• Molecule 3: DNA-binding protein J



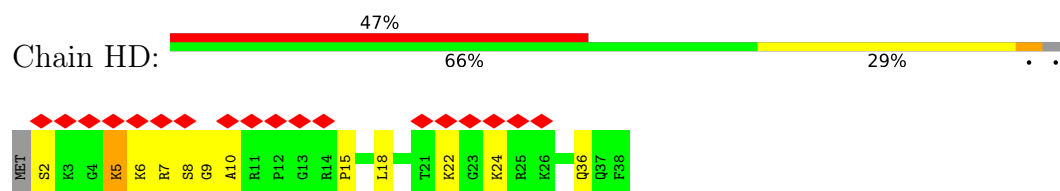
- Molecule 3: DNA-binding protein J



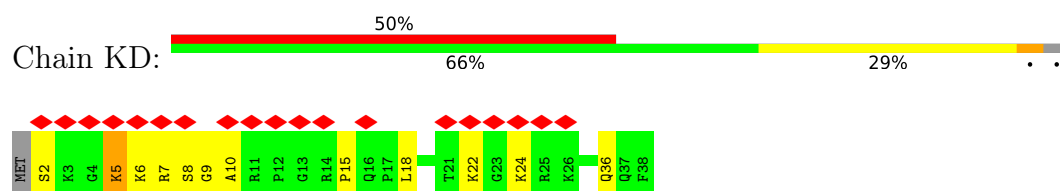
- Molecule 3: DNA-binding protein J



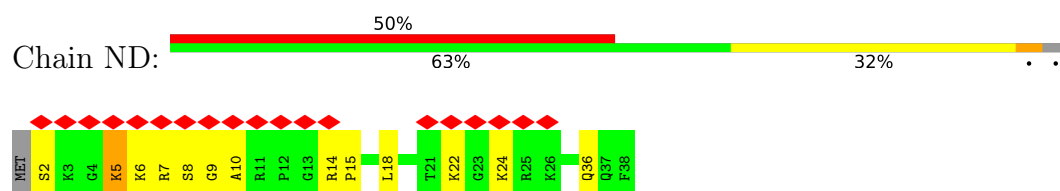
- Molecule 3: DNA-binding protein J



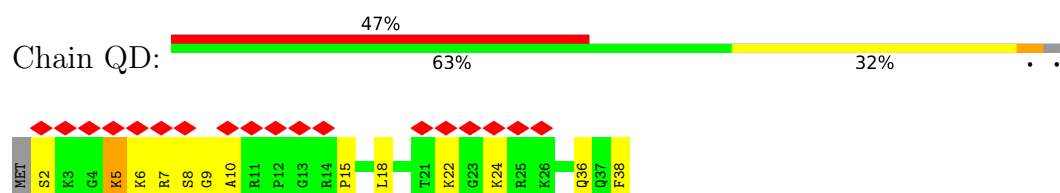
- Molecule 3: DNA-binding protein J



- Molecule 3: DNA-binding protein J

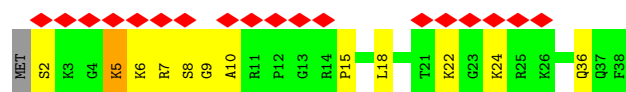


- Molecule 3: DNA-binding protein J



- Molecule 3: DNA-binding protein J

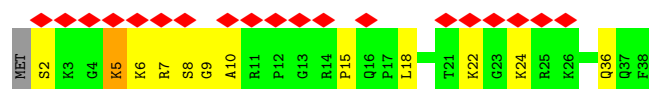




- Molecule 3: DNA-binding protein J



- Molecule 3: DNA-binding protein J



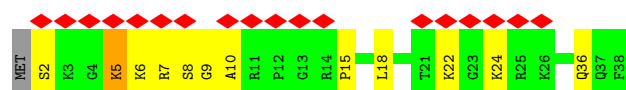
- Molecule 3: DNA-binding protein J



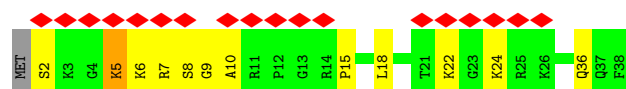
- Molecule 3: DNA-binding protein J



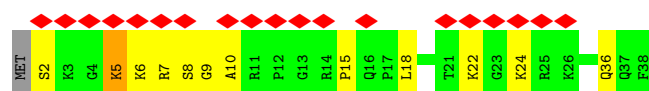
- Molecule 3: DNA-binding protein J



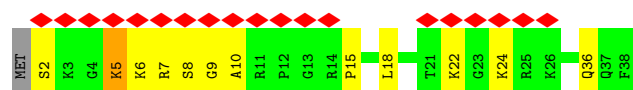
- Molecule 3: DNA-binding protein J



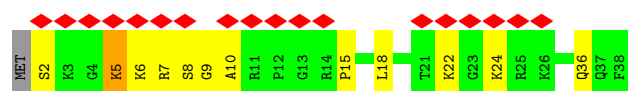
- Molecule 3: DNA-binding protein J



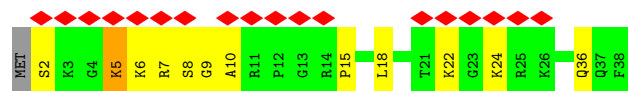
- Molecule 3: DNA-binding protein J



- Molecule 3: DNA-binding protein J



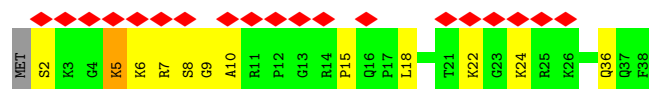
- Molecule 3: DNA-binding protein J



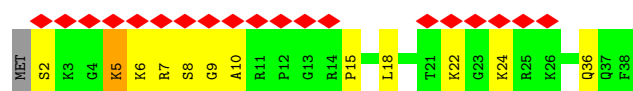
- Molecule 3: DNA-binding protein J



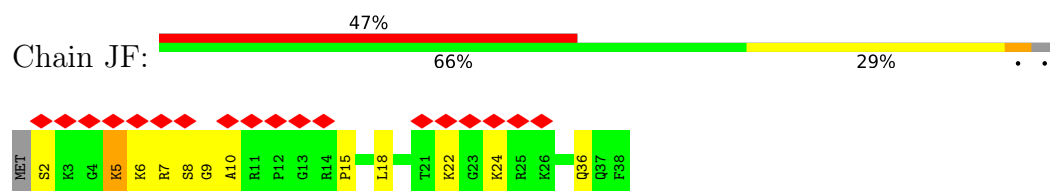
- Molecule 3: DNA-binding protein J



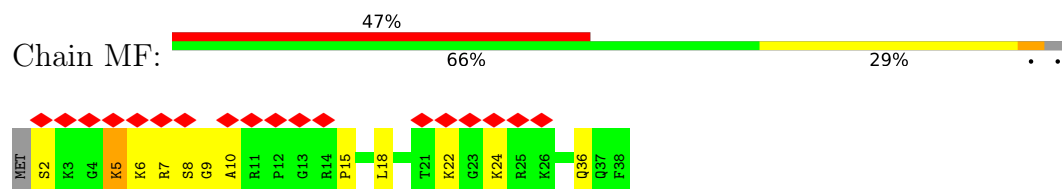
- Molecule 3: DNA-binding protein J



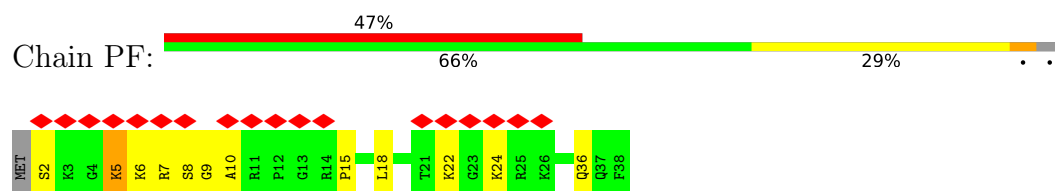
● Molecule 3: DNA-binding protein J



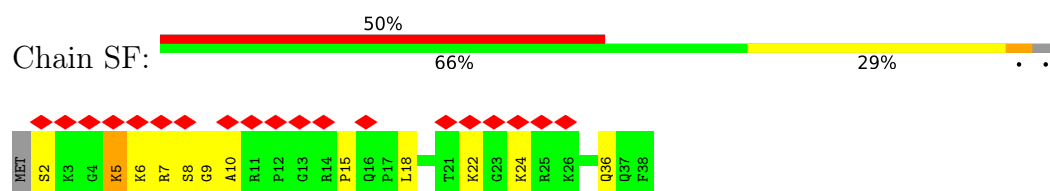
● Molecule 3: DNA-binding protein J



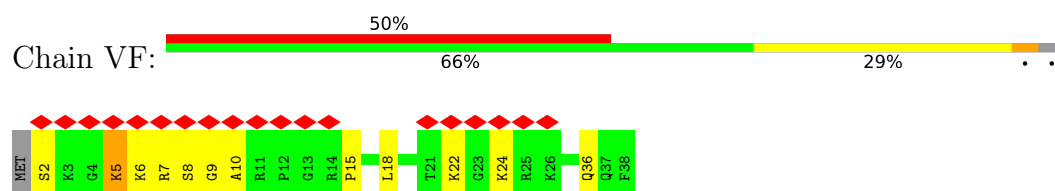
● Molecule 3: DNA-binding protein J



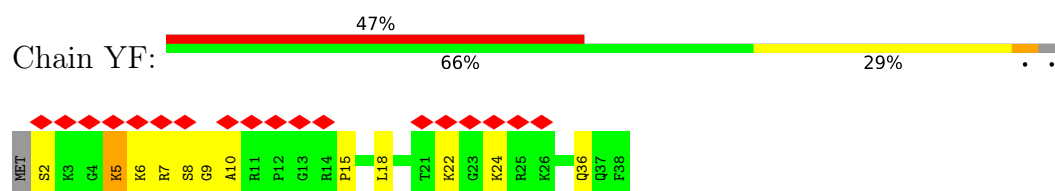
● Molecule 3: DNA-binding protein J



● Molecule 3: DNA-binding protein J



● Molecule 3: DNA-binding protein J



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	16905	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.088	Depositor
Minimum map value	-1.793	Depositor
Average map value	0.088	Depositor
Map value standard deviation	0.281	Depositor
Recommended contour level	1	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	1/3509 (0.0%)	0.37	0/4776
1	AB	0.29	1/3509 (0.0%)	0.37	0/4776
1	AE	0.29	1/3509 (0.0%)	0.37	0/4776
1	BC	0.29	1/3509 (0.0%)	0.37	0/4776
1	BF	0.29	1/3509 (0.0%)	0.37	0/4776
1	CA	0.29	1/3509 (0.0%)	0.37	0/4776
1	CD	0.29	1/3509 (0.0%)	0.37	0/4776
1	D	0.29	1/3509 (0.0%)	0.37	0/4776
1	DB	0.29	1/3509 (0.0%)	0.37	0/4776
1	DE	0.29	1/3509 (0.0%)	0.37	0/4776
1	EC	0.29	1/3509 (0.0%)	0.37	0/4776
1	EF	0.29	1/3509 (0.0%)	0.37	0/4776
1	F	0.29	1/3509 (0.0%)	0.37	0/4776
1	FA	0.29	1/3509 (0.0%)	0.37	0/4776
1	FD	0.29	1/3509 (0.0%)	0.37	0/4776
1	GB	0.29	1/3509 (0.0%)	0.37	0/4776
1	GE	0.29	1/3509 (0.0%)	0.37	0/4776
1	HC	0.29	1/3509 (0.0%)	0.37	0/4776
1	HF	0.29	1/3509 (0.0%)	0.37	0/4776
1	I	0.29	1/3509 (0.0%)	0.37	0/4776
1	IA	0.29	1/3509 (0.0%)	0.37	0/4776
1	ID	0.29	1/3509 (0.0%)	0.37	0/4776
1	JB	0.29	1/3509 (0.0%)	0.37	0/4776
1	JE	0.29	1/3509 (0.0%)	0.37	0/4776
1	KC	0.29	1/3509 (0.0%)	0.37	0/4776
1	KF	0.29	1/3509 (0.0%)	0.37	0/4776
1	LA	0.29	1/3509 (0.0%)	0.37	0/4776
1	LD	0.29	1/3509 (0.0%)	0.37	0/4776
1	M	0.29	1/3509 (0.0%)	0.37	0/4776
1	MB	0.29	1/3509 (0.0%)	0.37	0/4776
1	ME	0.29	1/3509 (0.0%)	0.37	0/4776
1	NC	0.29	1/3509 (0.0%)	0.37	0/4776
1	NF	0.29	1/3509 (0.0%)	0.37	0/4776
1	OA	0.29	1/3509 (0.0%)	0.37	0/4776

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	OD	0.29	1/3509 (0.0%)	0.37	0/4776
1	P	0.29	1/3509 (0.0%)	0.37	0/4776
1	PB	0.29	1/3509 (0.0%)	0.37	0/4776
1	PE	0.29	1/3509 (0.0%)	0.37	0/4776
1	QC	0.29	1/3509 (0.0%)	0.37	0/4776
1	QF	0.29	1/3509 (0.0%)	0.37	0/4776
1	RA	0.29	1/3509 (0.0%)	0.37	0/4776
1	RD	0.29	1/3509 (0.0%)	0.37	0/4776
1	S	0.29	1/3509 (0.0%)	0.37	0/4776
1	SB	0.29	1/3509 (0.0%)	0.37	0/4776
1	SE	0.29	1/3509 (0.0%)	0.37	0/4776
1	TC	0.29	1/3509 (0.0%)	0.37	0/4776
1	TF	0.29	1/3509 (0.0%)	0.37	0/4776
1	UA	0.29	1/3509 (0.0%)	0.37	0/4776
1	UD	0.29	1/3509 (0.0%)	0.37	0/4776
1	VB	0.29	1/3509 (0.0%)	0.37	0/4776
1	VE	0.29	1/3509 (0.0%)	0.37	0/4776
1	W	0.29	1/3509 (0.0%)	0.37	0/4776
1	WC	0.29	1/3509 (0.0%)	0.37	0/4776
1	WF	0.29	1/3509 (0.0%)	0.37	0/4776
1	XA	0.29	1/3509 (0.0%)	0.37	0/4776
1	XD	0.29	1/3509 (0.0%)	0.37	0/4776
1	YB	0.29	1/3509 (0.0%)	0.37	0/4776
1	YE	0.29	1/3509 (0.0%)	0.37	0/4776
1	Z	0.29	1/3509 (0.0%)	0.37	0/4776
1	ZC	0.29	1/3509 (0.0%)	0.37	0/4776
2	AA	0.23	0/1375	0.42	0/1877
2	AD	0.23	0/1375	0.41	0/1877
2	B	0.23	0/1375	0.41	0/1877
2	BB	0.23	0/1375	0.42	0/1877
2	BE	0.23	0/1375	0.41	0/1877
2	CC	0.23	0/1375	0.42	0/1877
2	CF	0.23	0/1375	0.41	0/1877
2	DA	0.23	0/1375	0.42	0/1877
2	DD	0.23	0/1375	0.41	0/1877
2	E	0.23	0/1375	0.42	0/1877
2	EB	0.23	0/1375	0.42	0/1877
2	EE	0.23	0/1375	0.42	0/1877
2	FC	0.23	0/1375	0.41	0/1877
2	FF	0.23	0/1375	0.42	0/1877
2	G	0.23	0/1375	0.41	0/1877
2	GA	0.23	0/1375	0.41	0/1877
2	GD	0.23	0/1375	0.41	0/1877

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	HB	0.23	0/1375	0.42	0/1877
2	HE	0.23	0/1375	0.41	0/1877
2	IC	0.23	0/1375	0.41	0/1877
2	IF	0.23	0/1375	0.42	0/1877
2	JA	0.23	0/1375	0.41	0/1877
2	JD	0.23	0/1375	0.42	0/1877
2	K	0.23	0/1375	0.41	0/1877
2	KB	0.23	0/1375	0.41	0/1877
2	KE	0.23	0/1375	0.42	0/1877
2	LC	0.23	0/1375	0.42	0/1877
2	LF	0.23	0/1375	0.41	0/1877
2	MA	0.23	0/1375	0.41	0/1877
2	MD	0.23	0/1375	0.42	0/1877
2	N	0.23	0/1375	0.41	0/1877
2	NB	0.23	0/1375	0.41	0/1877
2	NE	0.23	0/1375	0.41	0/1877
2	OC	0.23	0/1375	0.41	0/1877
2	OF	0.23	0/1375	0.42	0/1877
2	PA	0.23	0/1375	0.41	0/1877
2	PD	0.23	0/1375	0.42	0/1877
2	Q	0.23	0/1375	0.41	0/1877
2	QB	0.23	0/1375	0.42	0/1877
2	QE	0.23	0/1375	0.42	0/1877
2	RC	0.23	0/1375	0.42	0/1877
2	RF	0.23	0/1375	0.41	0/1877
2	SA	0.23	0/1375	0.41	0/1877
2	SD	0.23	0/1375	0.41	0/1877
2	T	0.23	0/1375	0.41	0/1877
2	TB	0.23	0/1375	0.41	0/1877
2	TE	0.23	0/1375	0.42	0/1877
2	UC	0.23	0/1375	0.42	0/1877
2	UF	0.23	0/1375	0.41	0/1877
2	VA	0.23	0/1375	0.42	0/1877
2	VD	0.23	0/1375	0.42	0/1877
2	WB	0.23	0/1375	0.41	0/1877
2	WE	0.23	0/1375	0.41	0/1877
2	X	0.23	0/1375	0.42	0/1877
2	XC	0.23	0/1375	0.41	0/1877
2	XF	0.23	0/1375	0.41	0/1877
2	YA	0.23	0/1375	0.41	0/1877
2	YD	0.23	0/1375	0.42	0/1877
2	ZB	0.23	0/1375	0.41	0/1877
2	ZE	0.23	0/1375	0.42	0/1877

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	AC	0.63	1/287 (0.3%)	0.69	0/380
3	AF	0.63	1/287 (0.3%)	0.69	0/380
3	BA	0.63	1/287 (0.3%)	0.69	0/380
3	BD	0.63	1/287 (0.3%)	0.69	0/380
3	C	0.63	1/287 (0.3%)	0.69	0/380
3	CB	0.63	1/287 (0.3%)	0.69	0/380
3	CE	0.63	1/287 (0.3%)	0.69	0/380
3	DC	0.63	1/287 (0.3%)	0.69	0/380
3	DF	0.63	1/287 (0.3%)	0.69	0/380
3	EA	0.63	1/287 (0.3%)	0.69	0/380
3	ED	0.63	1/287 (0.3%)	0.69	0/380
3	FB	0.63	1/287 (0.3%)	0.69	0/380
3	FE	0.63	1/287 (0.3%)	0.69	0/380
3	GC	0.63	1/287 (0.3%)	0.69	0/380
3	GF	0.63	1/287 (0.3%)	0.69	0/380
3	H	0.63	1/287 (0.3%)	0.69	0/380
3	HA	0.63	1/287 (0.3%)	0.69	0/380
3	HD	0.63	1/287 (0.3%)	0.69	0/380
3	IB	0.63	1/287 (0.3%)	0.69	0/380
3	IE	0.63	1/287 (0.3%)	0.69	0/380
3	J	0.63	1/287 (0.3%)	0.69	0/380
3	JC	0.63	1/287 (0.3%)	0.69	0/380
3	JF	0.63	1/287 (0.3%)	0.69	0/380
3	KA	0.63	1/287 (0.3%)	0.69	0/380
3	KD	0.63	1/287 (0.3%)	0.69	0/380
3	L	0.63	1/287 (0.3%)	0.69	0/380
3	LB	0.63	1/287 (0.3%)	0.69	0/380
3	LE	0.63	1/287 (0.3%)	0.69	0/380
3	MC	0.63	1/287 (0.3%)	0.69	0/380
3	MF	0.63	1/287 (0.3%)	0.69	0/380
3	NA	0.63	1/287 (0.3%)	0.69	0/380
3	ND	0.63	1/287 (0.3%)	0.69	0/380
3	O	0.63	1/287 (0.3%)	0.69	0/380
3	OB	0.63	1/287 (0.3%)	0.69	0/380
3	OE	0.63	1/287 (0.3%)	0.69	0/380
3	PC	0.63	1/287 (0.3%)	0.69	0/380
3	PF	0.63	1/287 (0.3%)	0.69	0/380
3	QA	0.63	1/287 (0.3%)	0.69	0/380
3	QD	0.63	1/287 (0.3%)	0.69	0/380
3	R	0.63	1/287 (0.3%)	0.69	0/380
3	RB	0.63	1/287 (0.3%)	0.69	0/380
3	RE	0.63	1/287 (0.3%)	0.69	0/380
3	SC	0.63	1/287 (0.3%)	0.69	0/380

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	SF	0.63	1/287 (0.3%)	0.69	0/380
3	TA	0.63	1/287 (0.3%)	0.69	0/380
3	TD	0.63	1/287 (0.3%)	0.69	0/380
3	UB	0.63	1/287 (0.3%)	0.69	0/380
3	UE	0.63	1/287 (0.3%)	0.69	0/380
3	V	0.63	1/287 (0.3%)	0.69	0/380
3	VC	0.63	1/287 (0.3%)	0.69	0/380
3	VF	0.63	1/287 (0.3%)	0.69	0/380
3	WA	0.63	1/287 (0.3%)	0.69	0/380
3	WD	0.63	1/287 (0.3%)	0.69	0/380
3	XB	0.63	1/287 (0.3%)	0.69	0/380
3	XE	0.63	1/287 (0.3%)	0.69	0/380
3	Y	0.63	1/287 (0.3%)	0.69	0/380
3	YC	0.63	1/287 (0.3%)	0.69	0/380
3	YF	0.63	1/287 (0.3%)	0.69	0/380
3	ZA	0.63	1/287 (0.3%)	0.69	0/380
3	ZD	0.63	1/287 (0.3%)	0.69	0/380
All	All	0.31	120/310260 (0.0%)	0.41	0/421980

The worst 5 of 120 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	GC	5	LYS	CA-C	-5.98	1.44	1.52
3	DC	5	LYS	CA-C	-5.97	1.44	1.52
3	SC	5	LYS	CA-C	-5.97	1.44	1.52
3	KD	5	LYS	CA-C	-5.97	1.44	1.52
3	WD	5	LYS	CA-C	-5.97	1.44	1.52

There are no bond angle outliers.

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	A	3412	0	3292	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AB	3412	0	3292	43	0
1	AE	3412	0	3292	43	0
1	BC	3412	0	3292	41	0
1	BF	3412	0	3292	44	0
1	CA	3412	0	3292	44	0
1	CD	3412	0	3292	42	0
1	D	3412	0	3292	44	0
1	DB	3412	0	3292	41	0
1	DE	3412	0	3292	45	0
1	EC	3412	0	3292	42	0
1	EF	3412	0	3292	43	0
1	F	3412	0	3292	40	0
1	FA	3412	0	3292	43	0
1	FD	3412	0	3292	41	0
1	GB	3412	0	3292	43	0
1	GE	3412	0	3292	41	0
1	HC	3412	0	3292	44	0
1	HF	3412	0	3292	45	0
1	I	3412	0	3292	41	0
1	IA	3412	0	3292	42	0
1	ID	3412	0	3292	42	0
1	JB	3412	0	3292	42	0
1	JE	3412	0	3292	42	0
1	KC	3412	0	3292	43	0
1	KF	3412	0	3292	41	0
1	LA	3412	0	3292	43	0
1	LD	3412	0	3292	43	0
1	M	3412	0	3292	43	0
1	MB	3412	0	3292	42	0
1	ME	3412	0	3292	42	0
1	NC	3412	0	3292	42	0
1	NF	3412	0	3292	42	0
1	OA	3412	0	3292	43	0
1	OD	3412	0	3292	42	0
1	P	3412	0	3292	43	0
1	PB	3412	0	3292	42	0
1	PE	3412	0	3292	44	0
1	QC	3412	0	3292	42	0
1	QF	3412	0	3292	42	0
1	RA	3412	0	3292	42	0
1	RD	3412	0	3292	44	0
1	S	3412	0	3292	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SB	3412	0	3292	43	0
1	SE	3412	0	3292	44	0
1	TC	3412	0	3292	41	0
1	TF	3412	0	3292	45	0
1	UA	3412	0	3292	40	0
1	UD	3412	0	3292	41	0
1	VB	3412	0	3292	43	0
1	VE	3412	0	3292	44	0
1	W	3412	0	3292	44	0
1	WC	3412	0	3292	44	0
1	WF	3412	0	3292	44	0
1	XA	3412	0	3292	42	0
1	XD	3412	0	3292	45	0
1	YB	3412	0	3292	43	0
1	YE	3412	0	3292	41	0
1	Z	3412	0	3292	42	0
1	ZC	3412	0	3292	43	0
2	AA	1343	0	1322	24	0
2	AD	1343	0	1322	23	0
2	B	1343	0	1322	23	0
2	BB	1343	0	1322	22	0
2	BE	1343	0	1322	25	0
2	CC	1343	0	1322	22	0
2	CF	1343	0	1322	20	0
2	DA	1343	0	1322	22	0
2	DD	1343	0	1322	22	0
2	E	1343	0	1322	21	0
2	EB	1343	0	1322	21	0
2	EE	1343	0	1322	26	0
2	FC	1343	0	1322	24	0
2	FF	1343	0	1322	25	0
2	G	1343	0	1322	23	0
2	GA	1343	0	1322	24	0
2	GD	1343	0	1322	22	0
2	HB	1343	0	1322	25	0
2	HE	1343	0	1322	22	0
2	IC	1343	0	1322	22	0
2	IF	1343	0	1322	27	0
2	JA	1343	0	1322	22	0
2	JD	1343	0	1322	22	0
2	K	1343	0	1322	21	0
2	KB	1343	0	1322	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	KE	1343	0	1322	23	0
2	LC	1343	0	1322	24	0
2	LF	1343	0	1322	21	0
2	MA	1343	0	1322	23	0
2	MD	1343	0	1322	23	0
2	N	1343	0	1322	25	0
2	NB	1343	0	1322	23	0
2	NE	1343	0	1322	23	0
2	OC	1343	0	1322	22	0
2	OF	1343	0	1322	23	0
2	PA	1343	0	1322	24	0
2	PD	1343	0	1322	23	0
2	Q	1343	0	1322	24	0
2	QB	1343	0	1322	24	0
2	QE	1343	0	1322	22	0
2	RC	1343	0	1322	22	0
2	RF	1343	0	1322	23	0
2	SA	1343	0	1322	23	0
2	SD	1343	0	1322	23	0
2	T	1343	0	1322	22	0
2	TB	1343	0	1322	22	0
2	TE	1343	0	1322	24	0
2	UC	1343	0	1322	22	0
2	UF	1343	0	1322	21	0
2	VA	1343	0	1322	22	0
2	VD	1343	0	1322	21	0
2	WB	1343	0	1322	24	0
2	WE	1343	0	1322	25	0
2	X	1343	0	1322	24	0
2	XC	1343	0	1322	23	0
2	XF	1343	0	1322	24	0
2	YA	1343	0	1322	21	0
2	YD	1343	0	1322	21	0
2	ZB	1343	0	1322	23	0
2	ZE	1343	0	1322	22	0
3	AC	281	0	288	28	0
3	AF	281	0	288	28	0
3	BA	281	0	288	26	0
3	BD	281	0	288	27	0
3	C	281	0	288	26	0
3	CB	281	0	288	26	0
3	CE	281	0	288	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	DC	281	0	288	29	0
3	DF	281	0	288	26	0
3	EA	281	0	288	27	0
3	ED	281	0	288	26	0
3	FB	281	0	288	28	0
3	FE	281	0	288	27	0
3	GC	281	0	288	26	0
3	GF	281	0	288	25	0
3	H	281	0	288	27	0
3	HA	281	0	288	26	0
3	HD	281	0	288	27	0
3	IB	281	0	288	27	0
3	IE	281	0	288	27	0
3	J	281	0	288	27	0
3	JC	281	0	288	25	0
3	JF	281	0	288	26	0
3	KA	281	0	288	26	0
3	KD	281	0	288	26	0
3	L	281	0	288	28	0
3	LB	281	0	288	28	0
3	LE	281	0	288	28	0
3	MC	281	0	288	26	0
3	MF	281	0	288	26	0
3	NA	281	0	288	26	0
3	ND	281	0	288	29	0
3	O	281	0	288	27	0
3	OB	281	0	288	28	0
3	OE	281	0	288	26	0
3	PC	281	0	288	26	0
3	PF	281	0	288	28	0
3	QA	281	0	288	26	0
3	QD	281	0	288	28	0
3	R	281	0	288	26	0
3	RB	281	0	288	26	0
3	RE	281	0	288	27	0
3	SC	281	0	288	26	0
3	SF	281	0	288	26	0
3	TA	281	0	288	27	0
3	TD	281	0	288	28	0
3	UB	281	0	288	25	0
3	UE	281	0	288	27	0
3	V	281	0	288	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	VC	281	0	288	26	0
3	VF	281	0	288	27	0
3	WA	281	0	288	27	0
3	WD	281	0	288	28	0
3	XB	281	0	288	26	0
3	XE	281	0	288	28	0
3	Y	281	0	288	26	0
3	YC	281	0	288	29	0
3	YF	281	0	288	27	0
3	ZA	281	0	288	26	0
3	ZD	281	0	288	26	0
All	All	302160	0	294120	3677	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 6.

The worst 5 of 3677 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:KB:112:LEU:HD13	2:KB:123:VAL:HG21	1.24	1.19
2:ZB:112:LEU:HD13	2:ZB:123:VAL:HG21	1.24	1.19
2:VA:112:LEU:HD13	2:VA:123:VAL:HG21	1.24	1.19
2:G:112:LEU:HD13	2:G:123:VAL:HG21	1.24	1.18
2:XC:112:LEU:HD13	2:XC:123:VAL:HG21	1.24	1.18

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	A	424/427 (99%)	405 (96%)	19 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	AE	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	BC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	BF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	CA	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	CD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	D	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	DB	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	DE	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	EC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	EF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	F	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	FA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	FD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	GB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	GE	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	HC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	HF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	I	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	IA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	ID	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	JB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	JE	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	KC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	KF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	LA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	LD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	M	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	MB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	ME	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	NC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	NF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	OA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	OD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	P	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	PB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	PE	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	QC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	QF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	RA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	RD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	S	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	SB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	SE	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	TC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	TF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	UA	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	UD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	VB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	VE	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	W	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	WC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	WF	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	XA	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	XD	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	YB	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	YE	424/427 (99%)	406 (96%)	18 (4%)	0	100	100
1	Z	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
1	ZC	424/427 (99%)	405 (96%)	19 (4%)	0	100	100
2	AA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	AD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	B	173/175 (99%)	157 (91%)	16 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	BB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	BE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	CC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	CF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	DA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	DD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	E	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	EB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	EE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	FC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	FF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	G	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	GA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	GD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	HB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	HE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	IC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	IF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	JA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	JD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	K	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	KB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	KE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	LC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	LF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	MA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	MD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	N	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	NB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	NE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	OC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	OF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	PA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	PD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	Q	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	QB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	QE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	RC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	RF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	SA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	SD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	T	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	TB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	TE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	UC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	UF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	VA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	VD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	WB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	WE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	X	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	XC	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	XF	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	YA	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	YD	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	ZB	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
2	ZE	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
3	AC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	AF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	BA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	BD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	C	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	CE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	DC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	DF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	EA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	ED	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	FB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	FE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	GC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	GF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	H	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	HA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	HD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	IB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	IE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	J	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	JC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	JF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	KA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	KD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	L	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	LB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	LE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	MC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	MF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	NA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	ND	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	O	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	OB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	OE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	PC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	PF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	QA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	QD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	R	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	RB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	RE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	SC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	SF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	TA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	TD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	UB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	UE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	V	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	VC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	VF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	WA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	WD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	XB	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	XE	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	Y	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	YC	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	YF	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	ZA	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
3	ZD	35/38 (92%)	29 (83%)	5 (14%)	1 (3%)	3	8
All	All	37920/38400 (99%)	35467 (94%)	2393 (6%)	60 (0%)	44	65

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	J	6	LYS
3	C	6	LYS
3	H	6	LYS
3	L	6	LYS
3	O	6	LYS

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 [i](#)

There are no chain breaks in this entry.

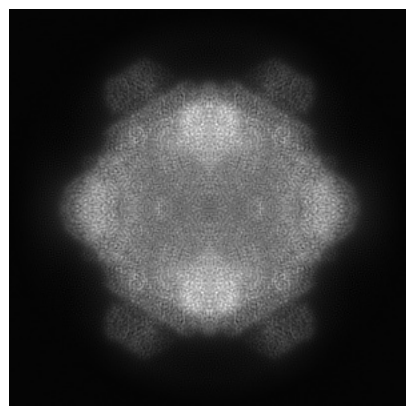
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62019. These allow visual inspection of the internal detail of the map and identification of artifacts.

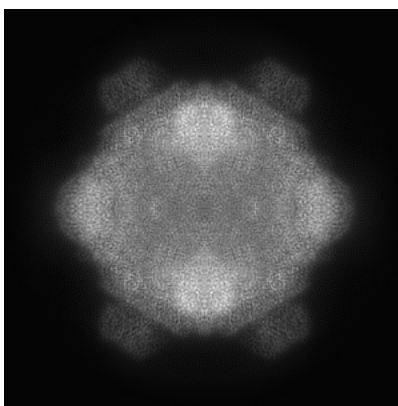
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

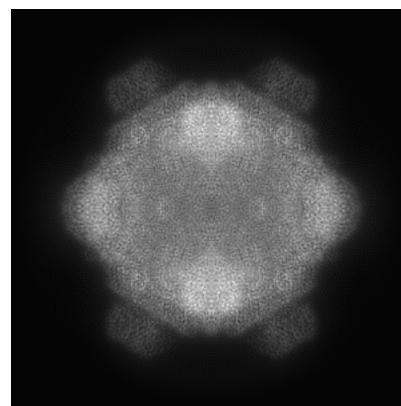
6.1.1 Primary map



X

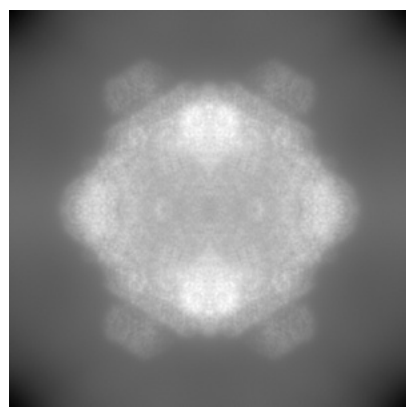


Y

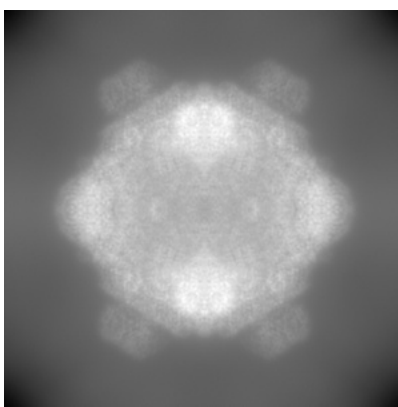


Z

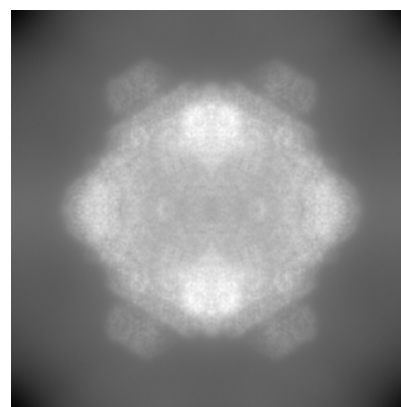
6.1.2 Raw map



X



Y

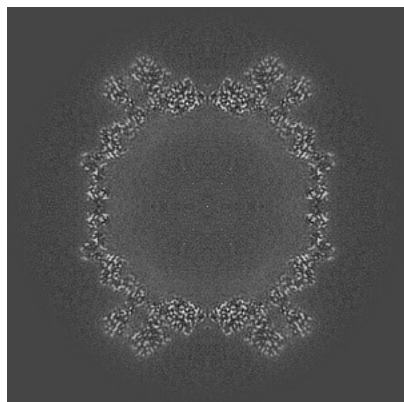


Z

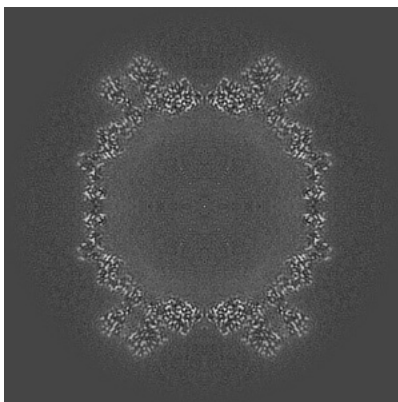
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

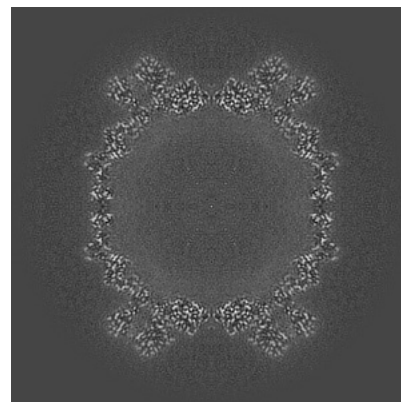
6.2.1 Primary map



X Index: 200

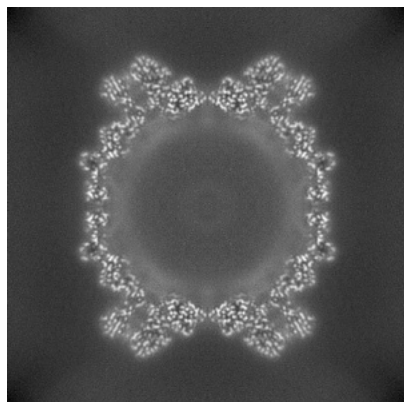


Y Index: 200

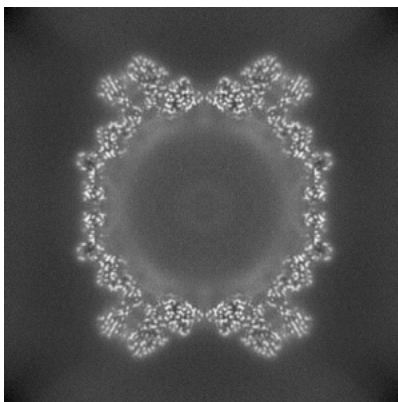


Z Index: 200

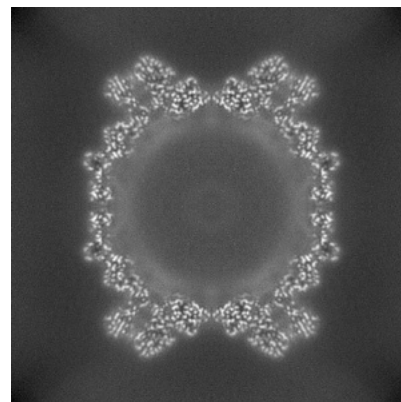
6.2.2 Raw map



X Index: 200



Y Index: 200

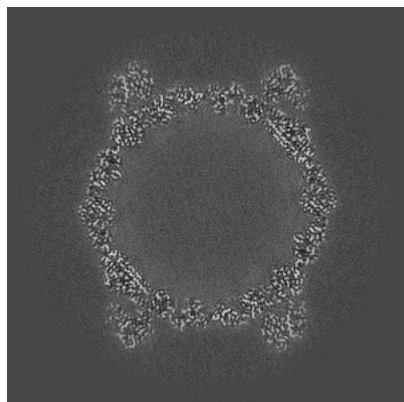


Z Index: 200

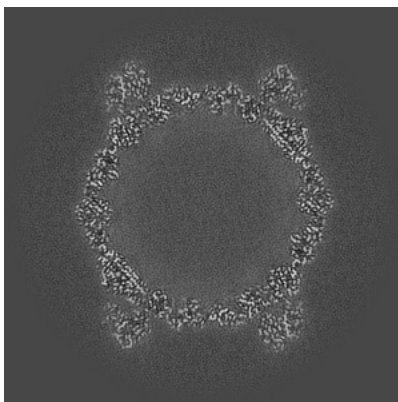
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

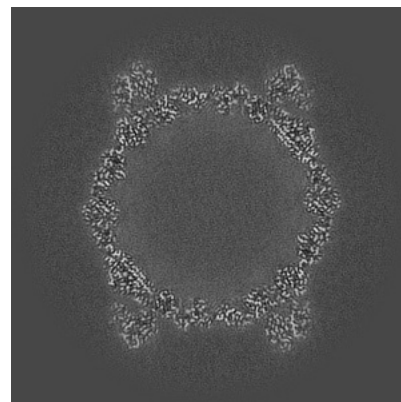
6.3.1 Primary map



X Index: 178

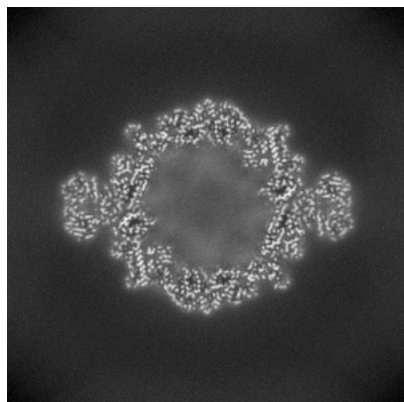


Y Index: 178

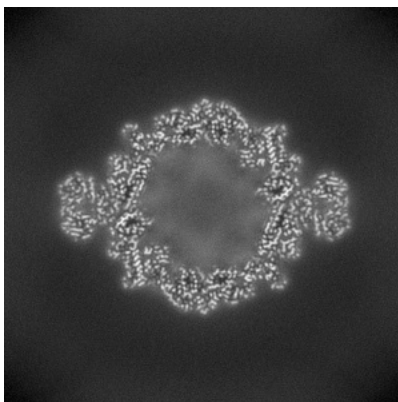


Z Index: 178

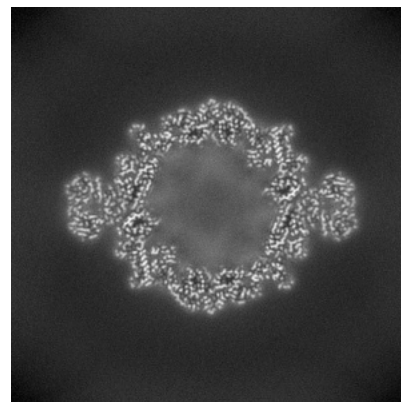
6.3.2 Raw map



X Index: 125



Y Index: 125

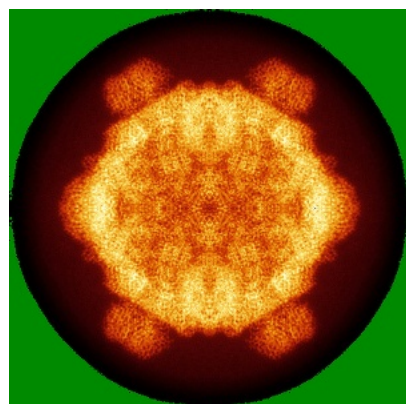


Z Index: 125

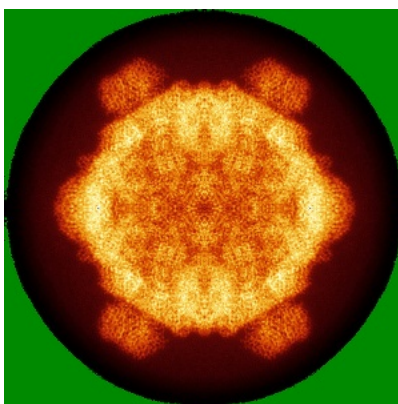
The images above show the largest variance slices of the map in three orthogonal directions.

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

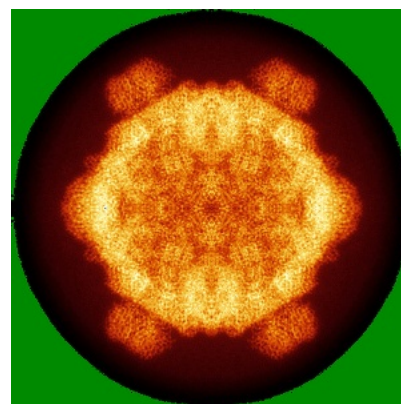
6.4.1 Primary map



X

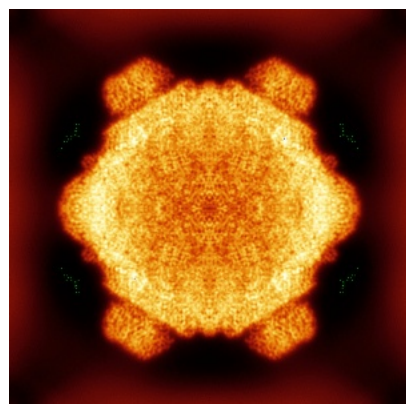


Y

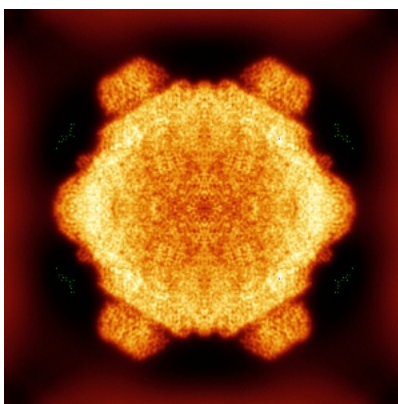


Z

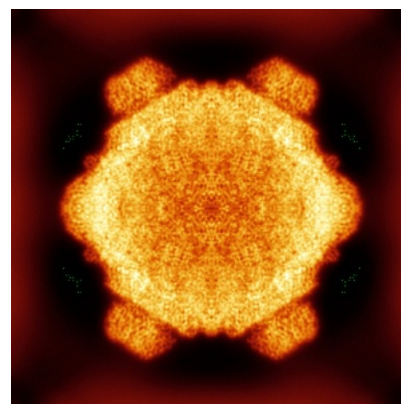
6.4.2 Raw map



X



Y

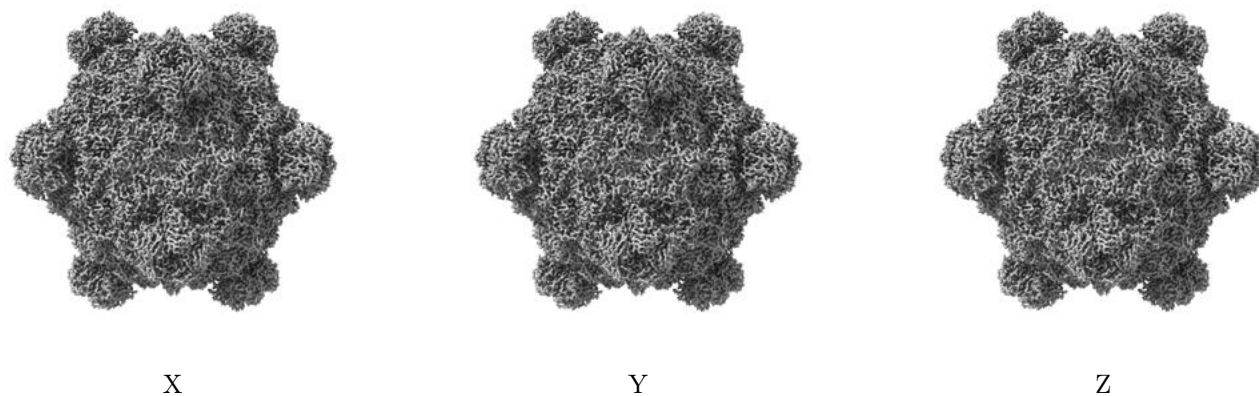


Z

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.

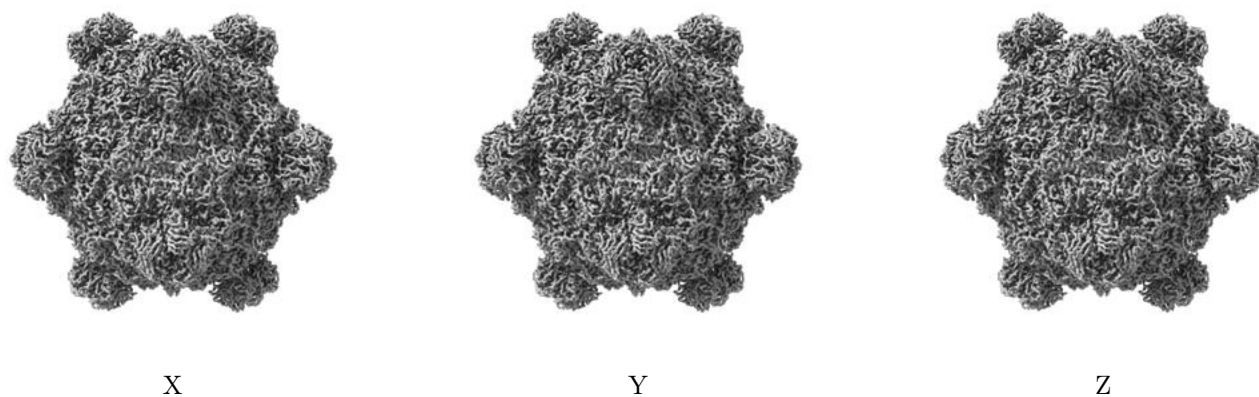
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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.

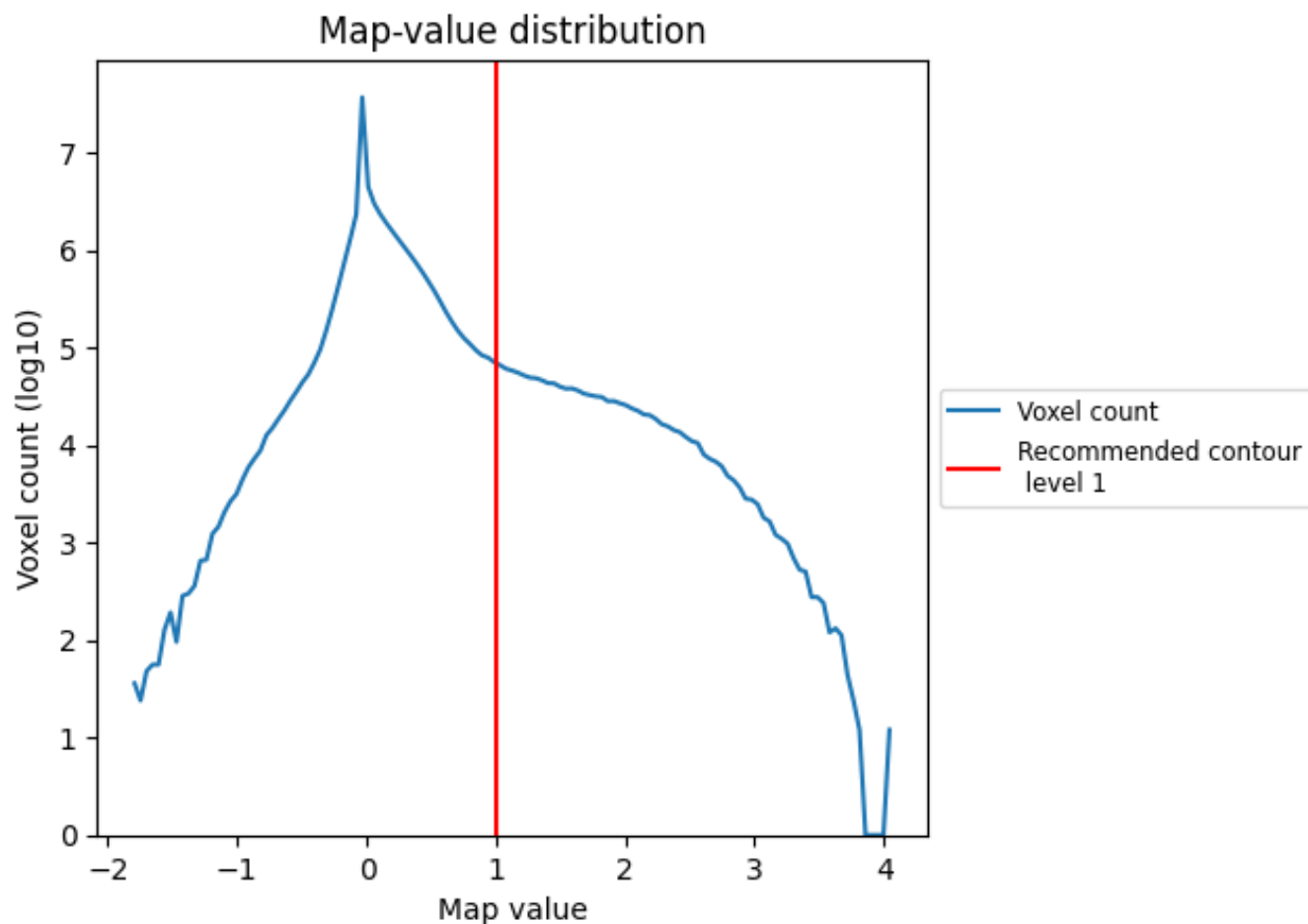
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

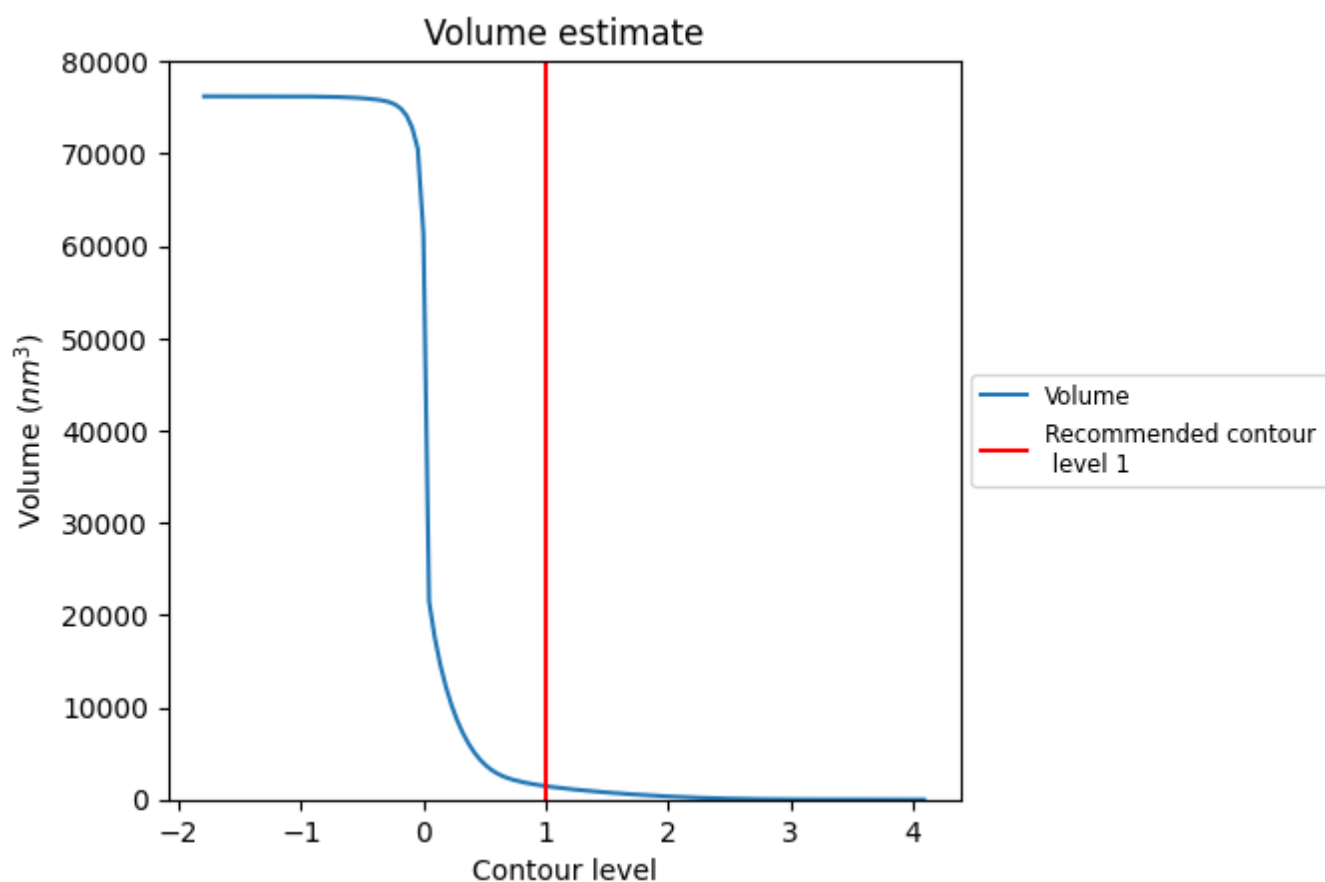
This section contains the results of statistical analysis of the map.

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.

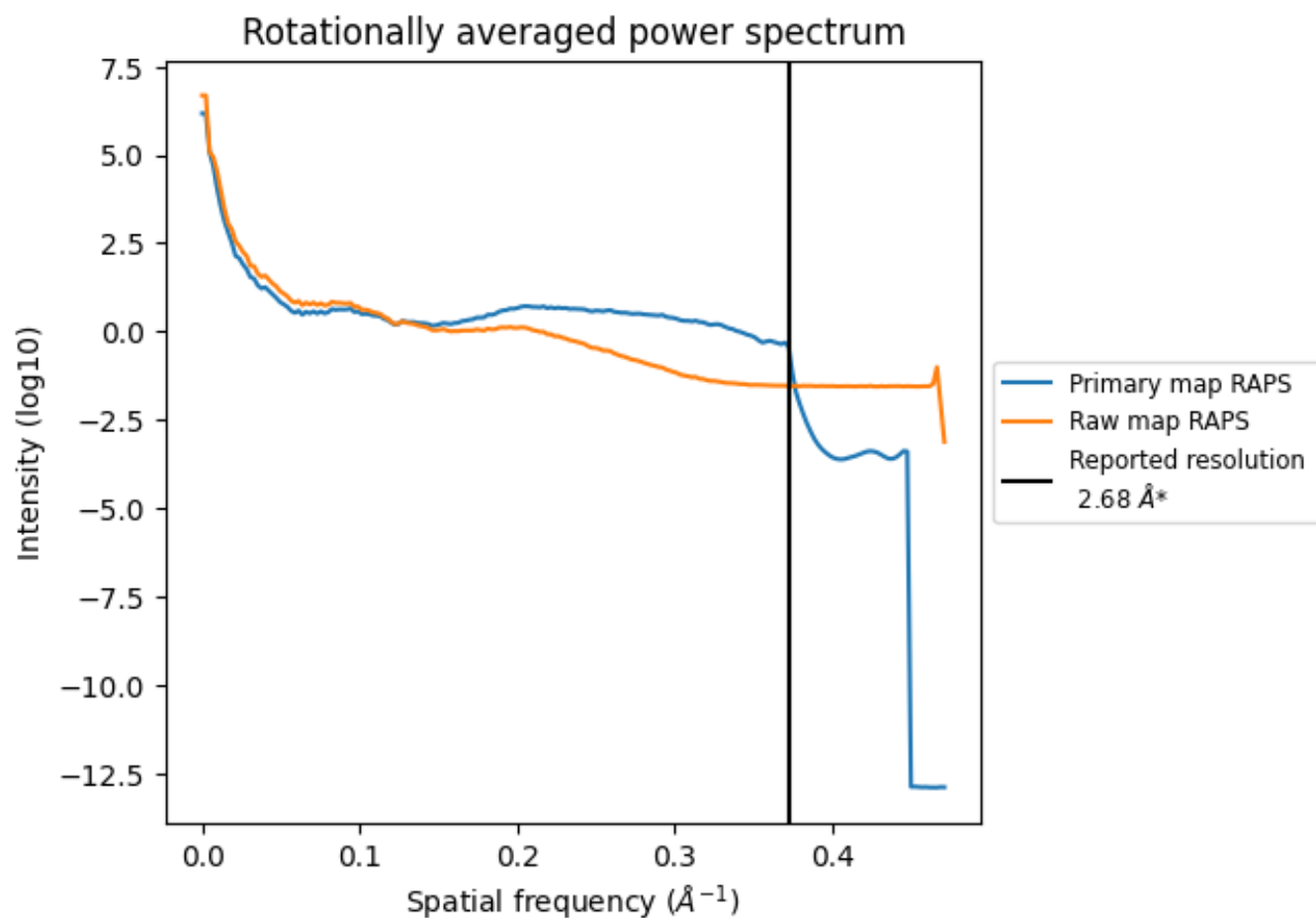
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1454 nm³; this corresponds to an approximate mass of 1314 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

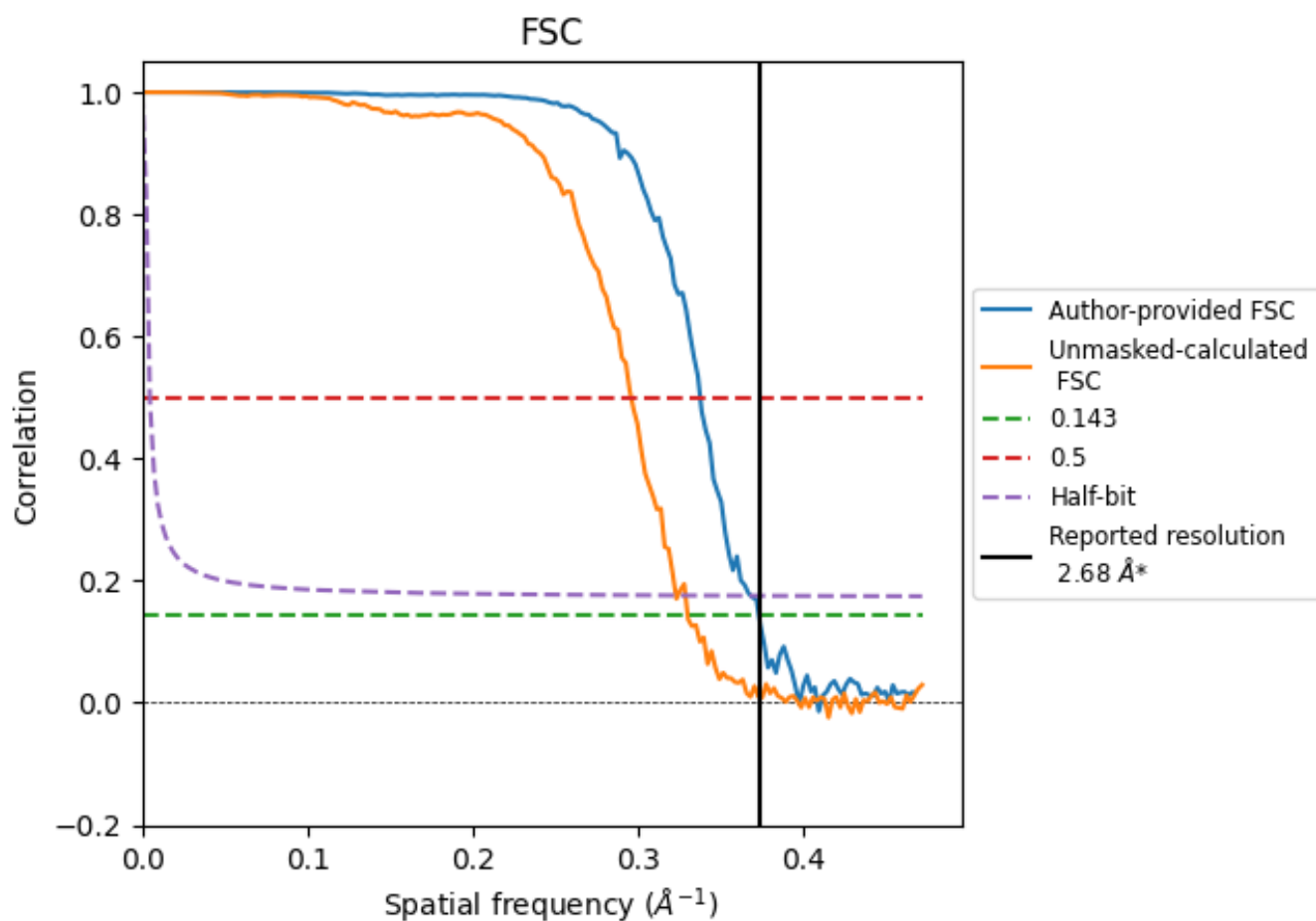


*Reported resolution corresponds to spatial frequency of 0.373 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

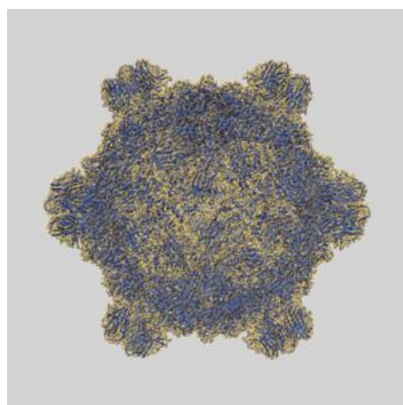
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.68	-	-
Author-provided FSC curve	2.68	2.96	2.72
Unmasked-calculated*	3.03	3.38	3.10

*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 3.03 differs from the reported value 2.68 by more than 10 %

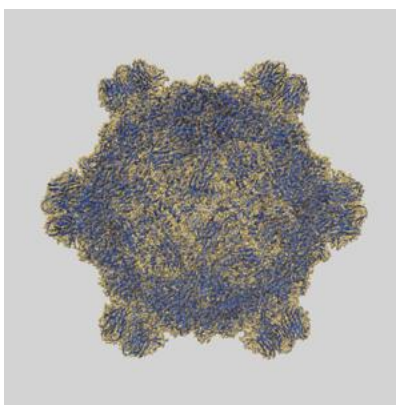
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62019 and PDB model 9K3M. Per-residue inclusion information can be found in section [3](#) on page [19](#).

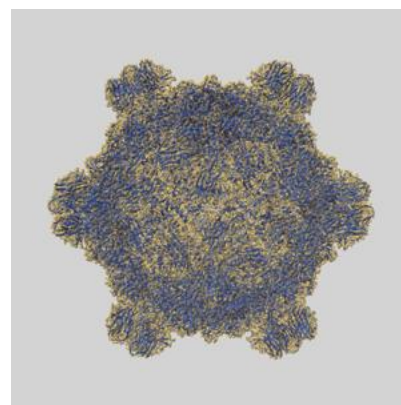
9.1 Map-model overlay [i](#)



X



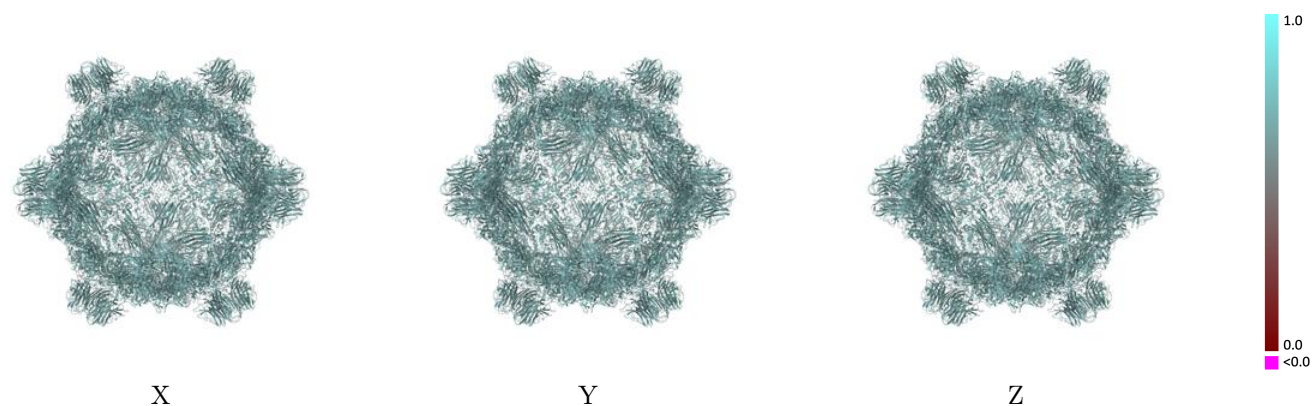
Y



Z

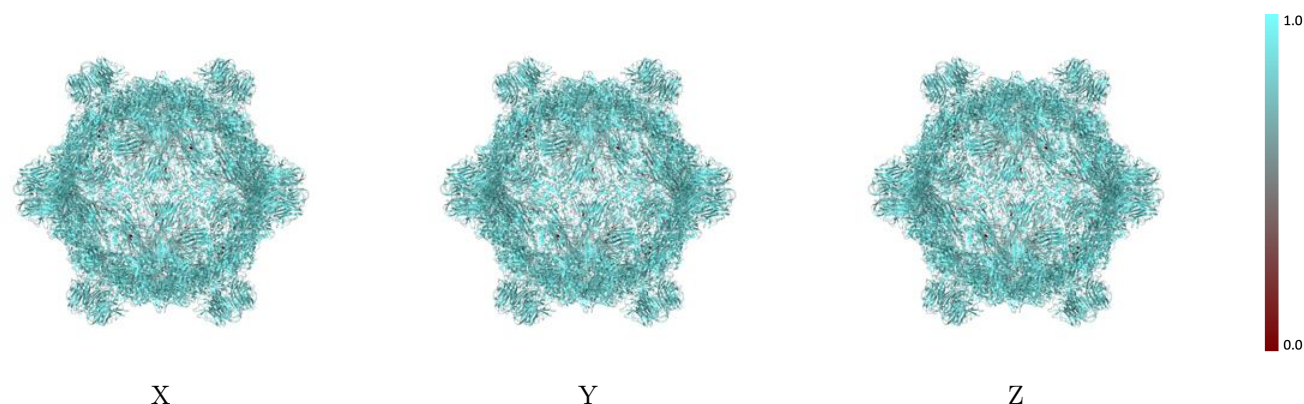
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



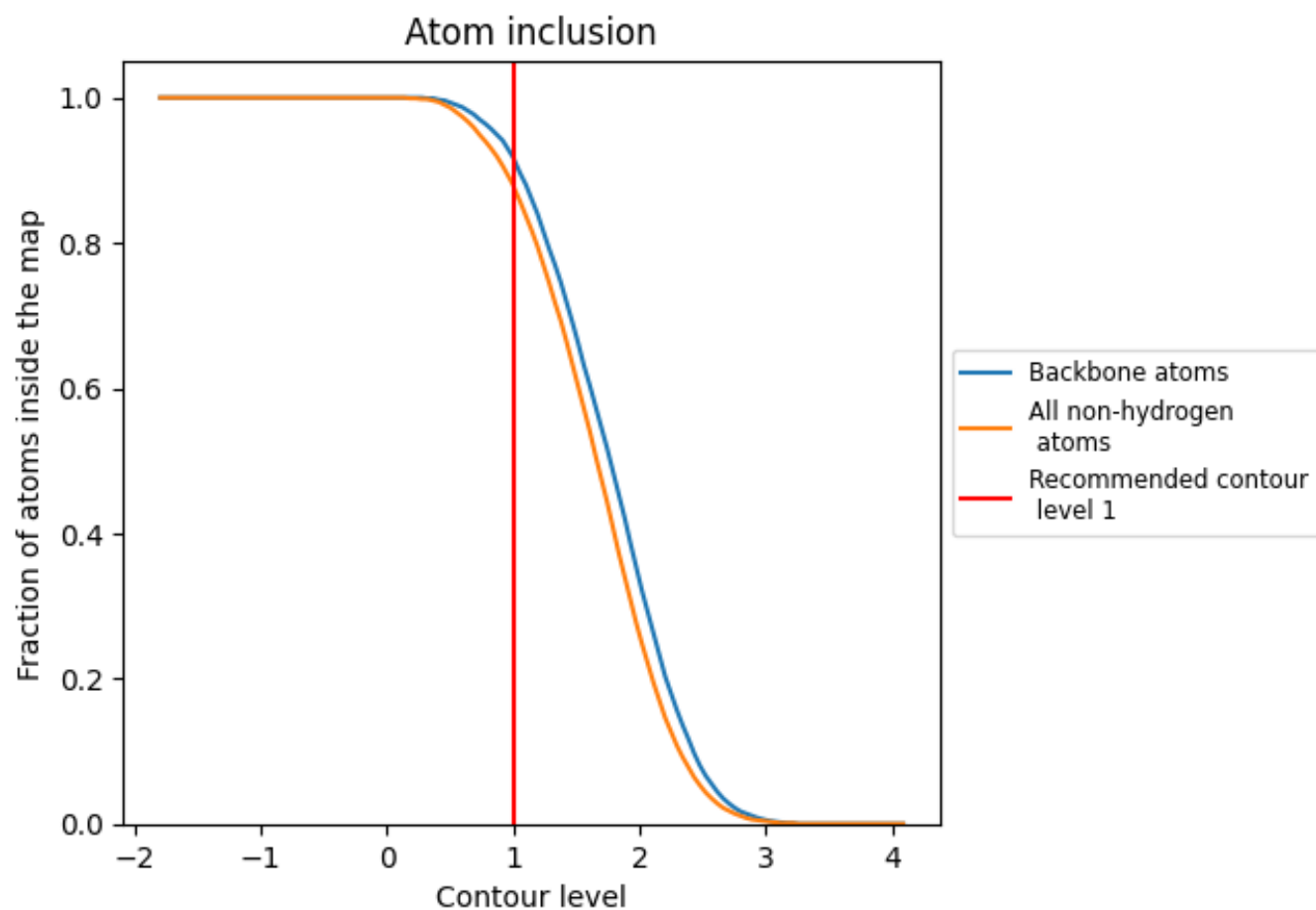
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.6450
A	 0.9240	 0.6540
AA	 0.8400	 0.6380
AB	 0.9230	 0.6540
AC	 0.5090	 0.5700
AD	 0.8440	 0.6370
AE	 0.9210	 0.6540
AF	 0.5240	 0.5630
B	 0.8420	 0.6380
BA	 0.5090	 0.5610
BB	 0.8420	 0.6360
BC	 0.9240	 0.6540
BD	 0.5090	 0.5630
BE	 0.8390	 0.6370
BF	 0.9230	 0.6530
C	 0.5240	 0.5630
CA	 0.9220	 0.6530
CB	 0.5020	 0.5610
CC	 0.8430	 0.6370
CD	 0.9250	 0.6580
CE	 0.5090	 0.5640
CF	 0.8390	 0.6370
D	 0.9230	 0.6540
DA	 0.8430	 0.6390
DB	 0.9210	 0.6530
DC	 0.5240	 0.5650
DD	 0.8530	 0.6390
DE	 0.9230	 0.6540
DF	 0.5020	 0.5620
E	 0.8420	 0.6380
EA	 0.5090	 0.5600
EB	 0.8390	 0.6380
EC	 0.9230	 0.6520
ED	 0.5090	 0.5740
EE	 0.8450	 0.6360



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Chain	Atom inclusion	Q-score
EF	 0.9210	 0.6550
F	 0.9260	 0.6590
FA	 0.9260	 0.6580
FB	 0.5090	 0.5650
FC	 0.8420	 0.6370
FD	 0.9240	 0.6530
FE	 0.5090	 0.5630
FF	 0.8390	 0.6370
G	 0.8540	 0.6390
GA	 0.8550	 0.6410
GB	 0.9220	 0.6530
GC	 0.5020	 0.5600
GD	 0.8430	 0.6370
GE	 0.9260	 0.6580
GF	 0.5090	 0.5620
H	 0.5020	 0.5610
HA	 0.5090	 0.5700
HB	 0.8440	 0.6370
HC	 0.9220	 0.6520
HD	 0.5240	 0.5670
HE	 0.8540	 0.6410
HF	 0.9230	 0.6540
I	 0.9210	 0.6540
IA	 0.9240	 0.6530
IB	 0.5060	 0.5620
IC	 0.8400	 0.6360
ID	 0.9230	 0.6520
IE	 0.5090	 0.5720
IF	 0.8450	 0.6360
J	 0.5090	 0.5720
JA	 0.8420	 0.6350
JB	 0.9250	 0.6600
JC	 0.5130	 0.5600
JD	 0.8420	 0.6340
JE	 0.9240	 0.6540
JF	 0.5090	 0.5630
K	 0.8390	 0.6400
KA	 0.5240	 0.5640
KB	 0.8530	 0.6410
KC	 0.9220	 0.6540
KD	 0.5020	 0.5580
KE	 0.8440	 0.6370

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Chain	Atom inclusion	Q-score
KF	 0.9260	 0.6580
L	 0.5090	 0.5600
LA	 0.9230	 0.6530
LB	 0.5090	 0.5700
LC	 0.8440	 0.6370
LD	 0.9220	 0.6520
LE	 0.5240	 0.5630
LF	 0.8540	 0.6410
M	 0.9220	 0.6530
MA	 0.8420	 0.6350
MB	 0.9240	 0.6540
MC	 0.5090	 0.5590
MD	 0.8400	 0.6370
ME	 0.9230	 0.6520
MF	 0.5090	 0.5690
N	 0.8420	 0.6370
NA	 0.5020	 0.5580
NB	 0.8430	 0.6360
NC	 0.9250	 0.6600
ND	 0.5130	 0.5620
NE	 0.8390	 0.6380
NF	 0.9240	 0.6540
O	 0.5090	 0.5600
OA	 0.9210	 0.6530
OB	 0.5240	 0.5620
OC	 0.8530	 0.6410
OD	 0.9220	 0.6530
OE	 0.5020	 0.5580
OF	 0.8440	 0.6340
P	 0.9260	 0.6590
PA	 0.8400	 0.6390
PB	 0.9230	 0.6530
PC	 0.5090	 0.5730
PD	 0.8430	 0.6360
PE	 0.9210	 0.6520
PF	 0.5240	 0.5620
Q	 0.8540	 0.6420
QA	 0.5090	 0.5630
QB	 0.8420	 0.6340
QC	 0.9240	 0.6530
QD	 0.5090	 0.5640
QE	 0.8390	 0.6360

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Chain	Atom inclusion	Q-score
QF	 0.9220	 0.6530
R	 0.5090	 0.5670
RA	 0.9220	 0.6520
RB	 0.5020	 0.5610
RC	 0.8430	 0.6370
RD	 0.9260	 0.6590
RE	 0.5090	 0.5590
RF	 0.8390	 0.6380
S	 0.9240	 0.6530
SA	 0.8430	 0.6370
SB	 0.9210	 0.6530
SC	 0.5240	 0.5630
SD	 0.8540	 0.6410
SE	 0.9230	 0.6520
SF	 0.5020	 0.5630
T	 0.8420	 0.6360
TA	 0.5090	 0.5640
TB	 0.8400	 0.6390
TC	 0.9230	 0.6520
TD	 0.5090	 0.5690
TE	 0.8450	 0.6330
TF	 0.9210	 0.6520
UA	 0.9260	 0.6580
UB	 0.5130	 0.5630
UC	 0.8420	 0.6340
UD	 0.9240	 0.6540
UE	 0.5090	 0.5640
UF	 0.8390	 0.6370
V	 0.5240	 0.5640
VA	 0.8540	 0.6410
VB	 0.9220	 0.6540
VC	 0.5020	 0.5550
VD	 0.8440	 0.6340
VE	 0.9260	 0.6580
VF	 0.5090	 0.5620
W	 0.9230	 0.6530
WA	 0.5090	 0.5710
WB	 0.8440	 0.6370
WC	 0.9210	 0.6520
WD	 0.5240	 0.5650
WE	 0.8540	 0.6430
WF	 0.9230	 0.6530

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Chain	Atom inclusion	Q-score
X	 0.8420	 0.6370
XA	 0.9230	 0.6530
XB	 0.5090	 0.5620
XC	 0.8400	 0.6350
XD	 0.9220	 0.6540
XE	 0.5090	 0.5720
XF	 0.8450	 0.6340
Y	 0.5020	 0.5610
YA	 0.8420	 0.6360
YB	 0.9250	 0.6610
YC	 0.5130	 0.5600
YD	 0.8390	 0.6370
YE	 0.9240	 0.6530
YF	 0.5090	 0.5650
Z	 0.9210	 0.6540
ZA	 0.5240	 0.5640
ZB	 0.8530	 0.6420
ZC	 0.9220	 0.6540
ZD	 0.5020	 0.5630
ZE	 0.8440	 0.6340