



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 02:27 PM JST

PDB ID : 9K2V / pdb_00009k2v
EMDB ID : EMD-61998
Title : Cyanophage A4 pre-ejectosome
Authors : Hou, P.; Li, Q.; Zhou, C.Z.
Deposited on : 2024-10-18
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

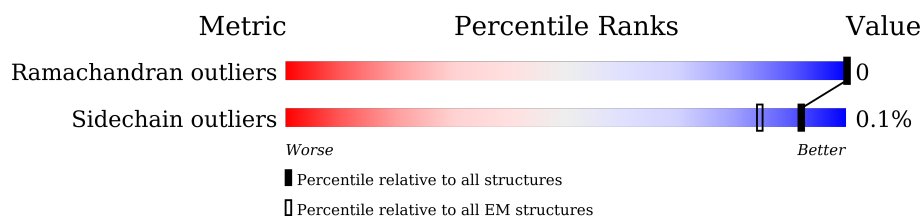
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


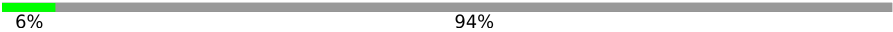
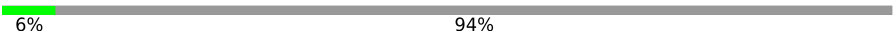
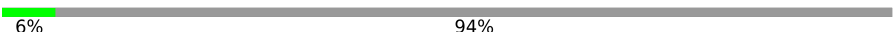
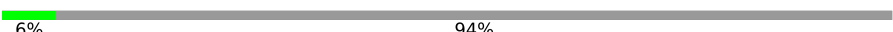
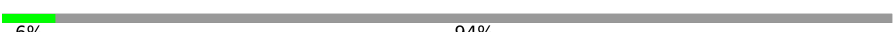



The reported resolution of this entry is 3.40 Å.

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.



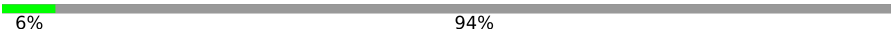













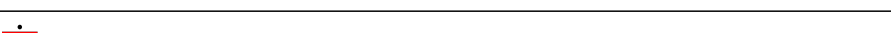
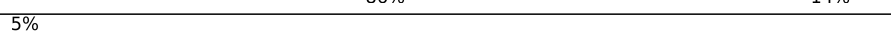





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	F	653	 6% 94%
1	G	653	 6% 94%
1	H	653	 6% 94%
1	I	653	 6% 94%
1	J	653	 6% 94%
1	K	653	 6% 94%
1	L	653	 6% 94%
1	M	653	 6% 94%
1	N	653	 6% 94%

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Mol	Chain	Length	Quality of chain
1	O	653	 6% 94%
2	V	380	 24% 76%
2	W	380	 24% 76%
2	X	380	 24% 76%
2	Y	380	 24% 76%
2	Z	380	 24% 76%
2	v	380	 24% 76%
2	w	380	 24% 76%
2	x	380	 24% 76%
2	y	380	 24% 76%
2	z	380	 24% 76%
3	A	1058	 5% 86% 14%
3	B	1058	 5% 85% 14%
3	C	1058	 5% 86% 14%
3	D	1058	 5% 86% 14%
3	E	1058	 5% 86% 14%
3	a	1058	 44% 56%
3	b	1058	 43% 56%
3	c	1058	 43% 56%
3	d	1058	 43% 56%
3	e	1058	 44% 56%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 63405 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 Portal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	K	40	Total	C	N	O	0	0
			290	178	50	62		
1	M	40	Total	C	N	O	0	0
			290	178	50	62		
1	O	40	Total	C	N	O	0	0
			290	178	50	62		
1	G	40	Total	C	N	O	0	0
			290	178	50	62		
1	I	40	Total	C	N	O	0	0
			290	178	50	62		
1	F	40	Total	C	N	O	0	0
			290	178	50	62		
1	H	40	Total	C	N	O	0	0
			290	178	50	62		
1	J	40	Total	C	N	O	0	0
			290	178	50	62		
1	L	40	Total	C	N	O	0	0
			290	178	50	62		
1	N	40	Total	C	N	O	0	0
			290	178	50	62		

- Molecule 2 is a protein called Internal virion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	W	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	X	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	Y	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	Z	92	Total	C	N	O	S	0	0
			706	422	138	142	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	v	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	w	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	x	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	y	92	Total	C	N	O	S	0	0
			706	422	138	142	4		
2	z	92	Total	C	N	O	S	0	0
			706	422	138	142	4		

- Molecule 3 is a protein called Internal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	907	Total	C	N	O	S	0	0
			7028	4342	1304	1361	21		
3	d	462	Total	C	N	O	S	0	0
			3660	2236	682	732	10		
3	A	907	Total	C	N	O	S	0	0
			7028	4342	1304	1361	21		
3	e	462	Total	C	N	O	S	0	0
			3660	2236	682	732	10		
3	B	907	Total	C	N	O	S	0	0
			7028	4342	1304	1361	21		
3	a	462	Total	C	N	O	S	0	0
			3660	2236	682	732	10		
3	C	907	Total	C	N	O	S	0	0
			7028	4342	1304	1361	21		
3	b	462	Total	C	N	O	S	0	0
			3660	2236	682	732	10		
3	D	907	Total	C	N	O	S	0	0
			7028	4342	1304	1361	21		
3	c	462	Total	C	N	O	S	0	0
			3660	2236	682	732	10		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	E	1	Total	Zn	0
			1	1	
4	A	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Zn 1	0
4	C	1	Total 1	Zn 1	0
4	D	1	Total 1	Zn 1	0







GLU	PRO	GLN	THR	GLY	GLN	ALA	PRO	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN
TYR	VAL	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO

● Molecule 1: Portal protein

Chain H: 6%															94%																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
GLU	PRO	GLN	THR	GLY	ALA	ASP	PRO	GLN	GLU	ASP	THR	GLY	GLN	ASP	GLU	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN	THR	VAL	HIS	ASN

● Molecule 1: Portal protein

Chain J: <div><div></div></div> 6%																94%															
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	TYR	LYS	THR	ILE	THR	ALA	SER	GLN	ILE	PRO																
TYR	VAL	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
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GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
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GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
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GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
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ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GLN	ARG	MET	ASP	PHE	ILE	THR	ALA	SER	GLN	ILE	PRO																
ASP	HIS	ARG	GLN	THR	GLY	GLN	ALA	PRO	ASP	GLU	Q612	T613	Q614	ASP	GLN																
GLU	ALA	ARG	ILE	GL																											

PHE ALA GLY LEU LEU SER SER GLY VAL ASN ALN ASN PHE ASN THR THR GLN GLN VAL LEU LEU GLN GLN GLN LYS GLN GLN THR THR TYR TYR ASN ASN SER GLY ILE LEU LEU ASN SER SER ASN ASN PHE LYS GLY THR THR ASN ASN THR THR PHE LYS GLY TYR TYR ASN

- Molecule 2: Internal virion protein



SER	GLN	GLN	LEU	THR	GLY	ALA	GLU	ASP	ALA	THR	LYS	GLU	LEU	GLN	ARG	ARG	LEU	ASP	THR	ARG	ASP	VAL	VAL	GLY	GLY	GLY	GLY	SER	SER	SER	SER	SER	GLN	GLN	ASN	ALA	ASP	LEU	LEU	GLY	THR	ILE	ASP	LYS	VAL	VAL	ALA	ALA	LYS	VAL	LEU	GLN	GLY	THR
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[illegible]

ALA	ALA	ALA	ALA	ARG	GLU	THR	ALA	VAL	ASN	ALA	ALA	ASP	MET	MET	ASN	ARG	GLN	THR	THR	VAL	ASN	ASN	ASP	ASP	LEU	ALA	ALA	GLU	MET	GLY	Tyr	GLN	GLN	GLN	THR	SER	ALA	VAL	ASN	SER	SER	GLN	GLN	ASN	ASN	MET	SER	GLY	ILE	ALA	GLN	Tyr	GLY	SER	ILE	GLY	Tyr
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ASN	THR	PHE	ALA	GLY	LEU	SER	SER	GLY	VAL	ASN	ALA	PHE	THR	TYR	GLN	GLY	VAL	LEU	GLY	GLN	ASN	ALA	LEU	ASN	ASN	GLN	GLN	LYS	GLN	THR	TYR	ASN	GLY	ALA	THR	ASN	ASN	ASN	THR	PHE	LYS	GLY	GLY	TYR	ASN
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- Molecule 2: Internal virion protein



MI E87 Q88 M89 D90 A91 A92 THR THR LYS LYS GLN GLN GLN GLN GLN ARG LEU LEU GLN GLN THR THR MET MET SER SER GLY ILE ILE GLU GLU GLN GLN LYS LYS ASP ASP ARG ASP GLN THR THR GLU GLU GLN GLN GLN MET MET MET VAL VAL GLY GLY ALA ALA GLU GLU VAL VAL PHE PHE GLN GLN THR THR LEU LEU GLN GLN GLN LEU LEU ALA ALA GLN GLN GLN LEU LEU GLY GLY VAL VAL VAL ASN ASN ALA ALA

SER	SER	GLN	GLN	THR	GLY	ALA	ALA	ASP	ALA	THR	LYS	LEU	GLU	GLN	GLY	ARG	LEU	ASP	THR	ARG	ASP	VAL	LEU	ALA	ALA	GLY	VAL	SER	THR	SER	SER	GLN	GLN	ASN	ALA	ASP	LEU	GLY	SER	LEU	GLY	SER	THR	THR	ILE	ASP	LYS	VAL	VAL	ALA	LYS	VAL	LEU	GLN	GLY	THR
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[illegible]




ASN	ALA	ALA	ALA	ALA	ARG	GLU	THR	VAL	ASN	ASP	MET	ASN	ARG	GLN	THR	ASP	THR	VAL	ASN	ASN	ASP	LEU	ALA	GLU	MET	GLY	TYR	GLN	VAL	GLN	THR	SER	SER	ALA	ALA	ASN	ASN	ALA	ALA	MET	SER	GLY	ILE	ILE	ASN	ALA	GLN	TYR	SER	GLY	ILE	TYR
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GLY	ASN	THR	PHE	ALA	ALA	GLY	LEU	SER	SER	GLY	VAL	GLN	ASN	ASN	PHE	ASN	THR	TYR	GLN	GLY	VAL	LEU	GLY	GLN	GLN	GLN	LYS	GLN	MET	THR	TYR	LEU	ASN	GLY	GLY	ILE	LEU	SER	ASN	GLY	ALA	THR	ASN	ASN	ASN	PHE	LYS	GLY	TYR	GLN
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- Molecule 2: Internal virion protein










































SER	GLN	GLN	LEU	THR	GLY	ALA	GLU	ASP	ALA	THR	LYS	GLU	LEU	GLN	ARG	ARG	LEU	ASP	THR	ARG	ASP	VAL	VAL	GLY	GLY	LEU	GLY	SER	SER	SER	THR	SER	SER	GLN	GLN	GLN	ASN	ALA	ASP	LEU	LEU	GLY	THR	ILE	ASP	LYS	VAL	VAL	ALA	LYS	VAL	LEU	GLN	GLY	THR	TRP
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ASN	THR	PHE	GLY	LEU	LEU	SER	SER	GLY	VAL	ASN	ASN	ALA	ALA	ASN	ASN	THR	THR	GLN	GLY	VAL	LEU	LEU	GLY	GLN	GLN	ASN	ALA	LEU	ASN	ASN	GLN	GLN	LYS	GLN	LYS	THR	THR	THR	PHE	GLY	GLY	TYR	GLN
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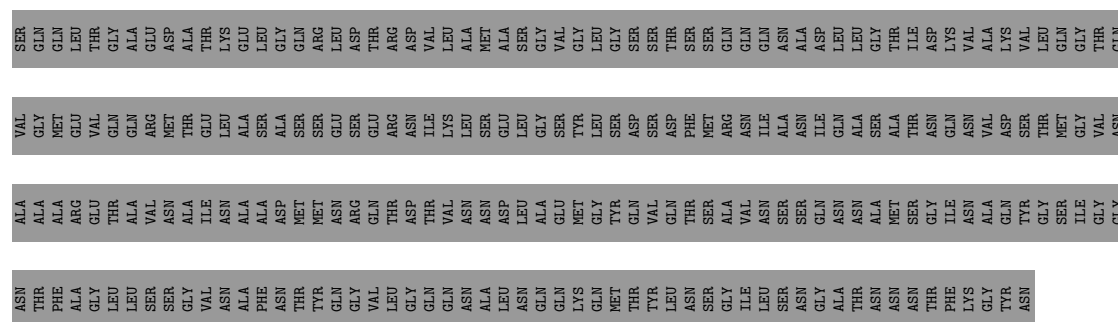
Chain x: 24% 76%

ASN	THR	PHE	ALA	GLY	LEU	LEU	SER	SER	GLY	VAL	ASN	ALA	ALA	PHE	ASN	ASN	THR	TYR	GLN	GLY	VAL	LEU	GLY	GLN	GLN	GLN	ASN	ASN	LEU	ALA	LEU	ASN	ASN	GLN	GLN	LYS	THR	THR	TYR	LEU	ASN	ASN	GLY	ILE	SER	ASN	GLY	ALA	THR	PHE	LYS	GLY	TYR	ASN
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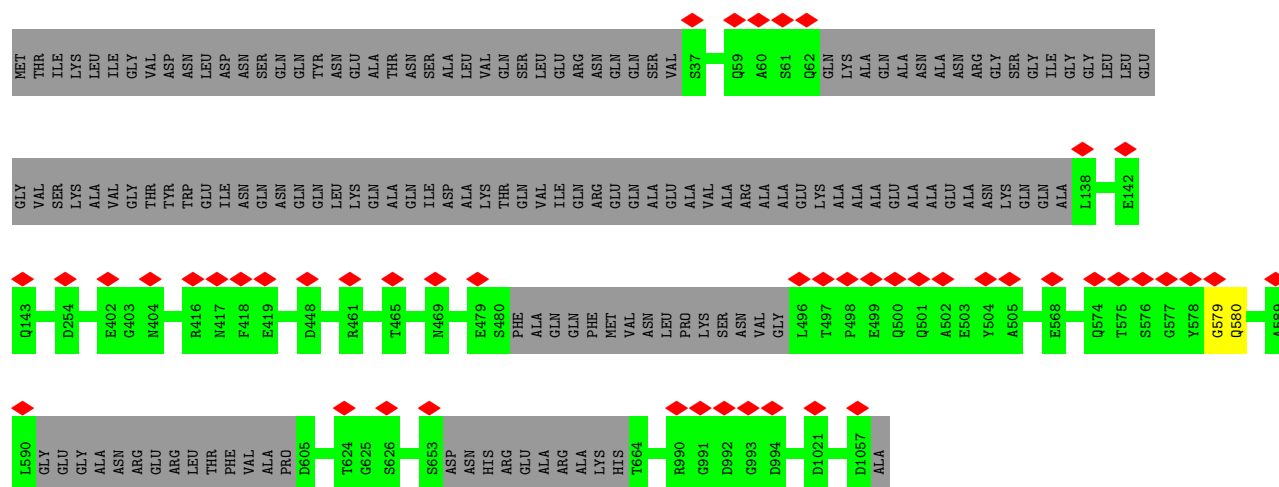
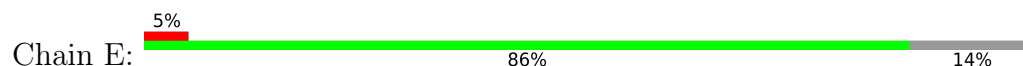
Chain γ :  24% 76%

	GLY	ASN	THR	THR	PHE	ALA	GLY	LEU	LEU	SER	SER	VAL	ASN	ALA	ASN	THR	TYR	GLN	GLY	VAL	LEU	GLY	GLN	GLN	GLN	GLN	ASN	ALA	ALA	LEU	ASN	ASN	GLN	GLN	GLN	GLN	MET	THR	THR	TYR	LEU	ASN	ASN	SER	SER	ILE	LEU	GLY	GLY	GLY	ALA	ALA	THR	THR	THR	PHE	LYS	LYS	GLY	TYR
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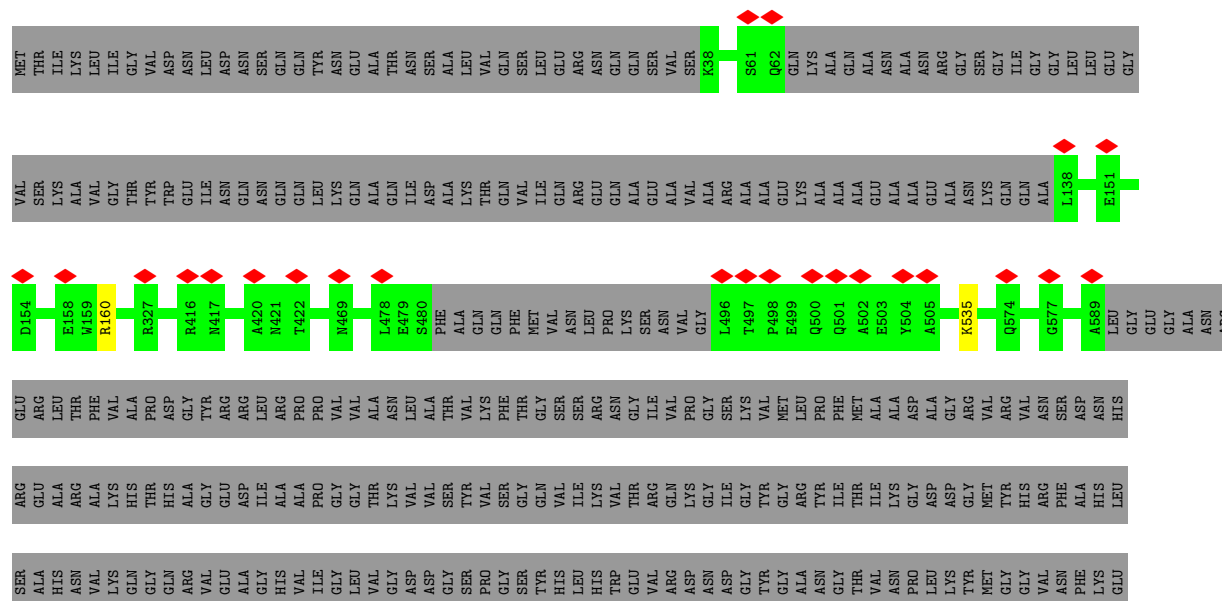
Chain z:  24% 76%

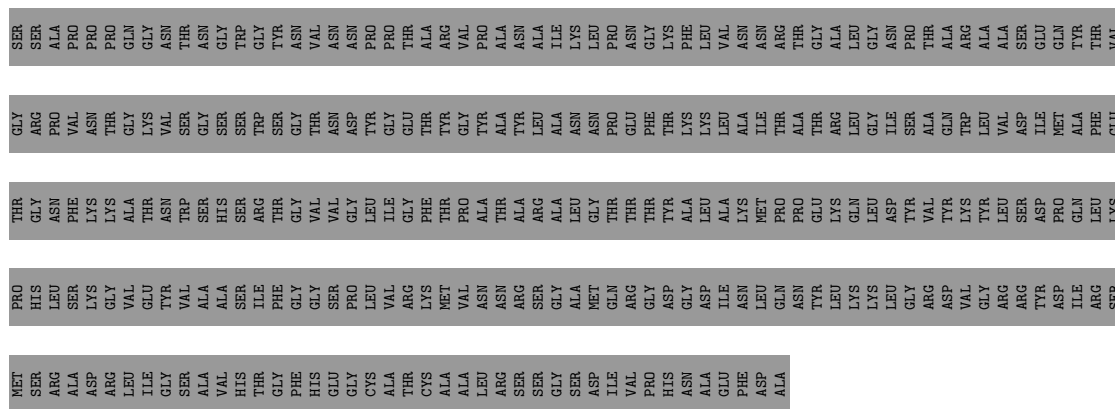


- Molecule 3: Internal protein

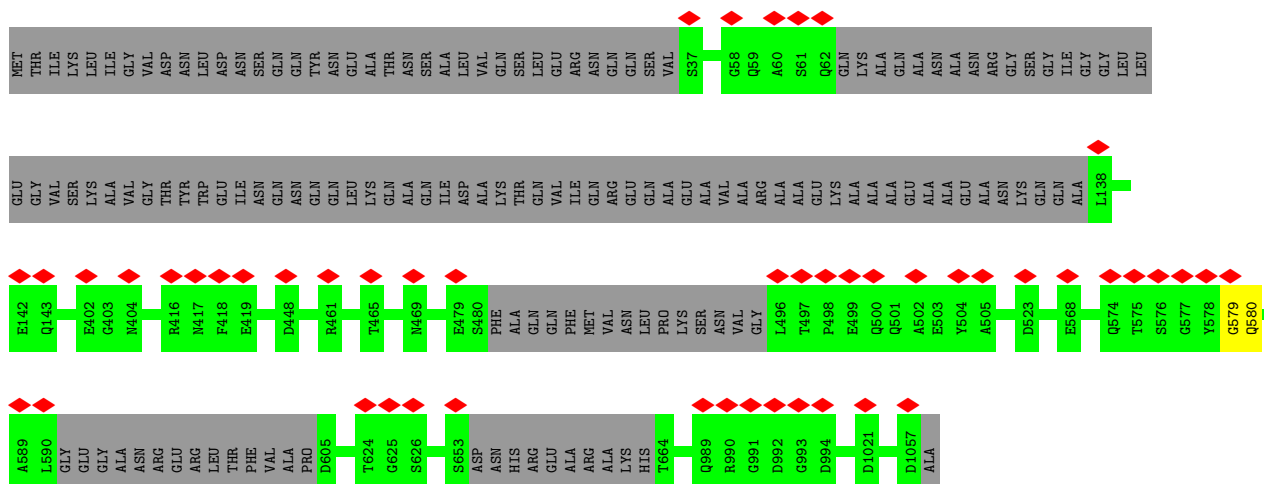
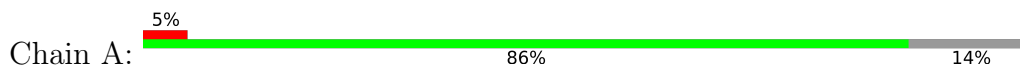


- Molecule 3: Internal protein

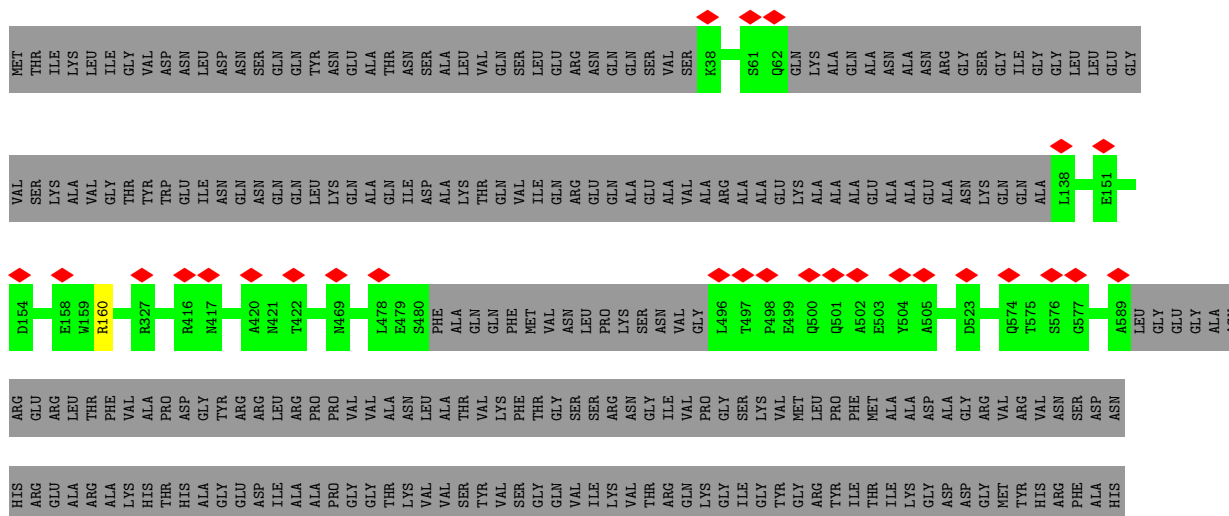
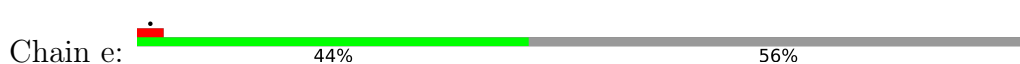




- Molecule 3: Internal protein




- Molecule 3: Internal protein



ARG	ARG	LEU	VAL	ALA	GLY	TYR	ARG	VAL	LEU
TYR	ASP	SER	ILE	SER	VAL	HIS	ARG	VAL	GLY
ASP	PRO	GLN	MET	GLN	ASN	PHE	ASN	SER	GLY
ILE	GLN	ALA	ALA	TYR	PHE	ALA	ASN	ASP	ASN
ARG	LEU	PHE	THR	THR	LYS	HIS	LEU	HIS	ASN
SER	LYS	GLU	VAL	VAL	GLU	LEU	SER	ARG	ARG
MET	PRO	THR	GLY	ARG	SER	ALA	GLU	ARG	ARG
SER	HIS	GLY	GLY	PRO	ASN	HIS	ASN	ALA	LEU
ARG	LEU	ASN	PHE	VAL	PRO	ASN	ARG	THR	THR
ALA	SER	LYS	LYS	ASN	PRO	VAL	ALA	ALA	PHE
ASP	LYS	LYS	LYS	THR	PRO	LYS	VAL	LYS	VAL
ARG	VAL	ALA	ALA	GLY	GLN	GLN	HIS	ALA	ALA
LEU	VAL	ALA	THR	LYS	GLY	THR	GLN	THR	PRO
ILE	GLU	THR	THR	LYS	GLY	ASN	GLN	HIS	ASP
GLY	TYR	ASN	VAL	VAL	THR	ASN	GLN	ALA	GLY
SER	VAL	TRP	THR	SER	THR	VAL	VAL	PRO	PRO
ALA	ALA	SER	GLY	GLY	ASN	VAL	ILE	ASP	ASN
VAL	ALA	HIS	SER	SER	TRP	GLY	GLU	VAL	VAL
VAL	SER	SER	SER	SER	TRP	GLY	GLU	VAL	ASN
HIS	ILE	ILE	ARG	TRP	GLY	TYR	HIS	ALA	LEU
GLY	PHE	PHE	THR	SER	TYR	THR	ASP	VAL	PRO
PHE	GLY	GLY	GLY	GLY	THR	VAL	ASP	PRO	PRO
HIS	GLY	GLY	VAL	THR	VAL	ILE	ASP	GLY	GLY
GLU	SER	SER	GLY	ASN	ASN	GLY	GLY	GLN	VAL
GLY	PRO	GLY	GLY	ASP	ASN	ARG	GLY	GLN	VAL
CYS	LEU	VAL	ILE	GLY	PRO	THR	ASP	VAL	LEU
ALA	ALA	VAL	ILE	GLY	GLY	THR	ASP	VAL	LEU
THR	THR	ARG	GLY	THR	THR	ALA	ASP	VAL	ASN
CYS	LYS	LYS	PHE	THR	ALA	TYR	ASN	GLY	GLY
ALA	MET	THR	THR	TYR	ARG	GLY	GLY	THR	THR
ALA	VAL	VAL	PRO	GLY	VAL	VAL	SER	TYR	VAL
LEU	ASN	ASN	ALA	TYR	PRO	GLY	PRO	VAL	LYS
ARG	ASN	ASN	THR	ALA	ALA	GLY	SER	SER	PHE
SER	SER	SER	ALA	TYR	ALA	ASN	GLY	THR	THR
SER	SER	SER	ARG	LEU	LEU	ASN	GLN	VAL	GLY
GLY	GLY	GLY	LEU	ALA	ILE	HIS	ASN	GLY	ASN
ASP	ASP	ASP	GLY	ASN	LYS	LEU	LYS	TRP	GLY
ILE	ILE	ILE	THR	PRO	PRO	THR	ASN	GLY	ASN
VAL	VAL	VAL	THR	GLU	GLY	VAL	ARG	GLY	ILE
PRO	PRO	GLY	THR	PHE	GLY	VAL	THR	ARG	ILE
HIS	ASN	ASP	TYR	THR	PHE	THR	ARG	GLN	VAL
ASN	GLY	GLY	ALA	LYS	LYS	LYS	ASN	LYS	PRO
ALA	ALA	ALA	LYS	LYS	THR	THR	ASN	THR	THR
ASP	ASP	ASP	LEU	ILE	ASN	ASN	ASN	TYR	VAL
ALA	ALA	ALA	MET	THR	THR	THR	ASN	GLY	GLY
ASP	ASP	ASP	THR	ALA	VAL	VAL	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL
ASP	ASP	ASP	THR	THR	THR	THR	ASN	GLY	VAL
ALA	ALA	ALA	THR	THR	THR	THR	ASN	GLY	VAL

- Molecule 3: Internal protein

Chain D:  86% 14%

The diagram illustrates the mapping of amino acid abbreviations to their corresponding chemical structures. It is organized into two main horizontal tracks. The top track lists amino acids from MET to LEU, with their structures shown as small 3D models. The bottom track lists amino acids from A589 to LEU, with their structures shown as small 2D chemical structures. Red diamond markers indicate specific points of interest or mapping between the two tracks.

Top Track (Amino Acid Abbreviations):

- MET, THR, ILE, LYS, LEU, ILE, GLY, VAL, ASP, ASN, LEU, THR, ASP, ASN, SER, GLN, GLN, TYR, ASN, GLU, ALA, THR, ASN, SER, ALA, VAL, LEU, VAL, GLN, SER, LEU, GLU, ARG, ASN, GLN, GLN, SER, VAL

Bottom Track (Amino Acid Abbreviations):

- A589, L590, GLY, GLU, GLY, ALA, ASN, ARG, GLU, ARG, LEU, THR, PHE, VAL, ALA, PRO, D605, T624, G625, S626, S653, ASP, ASN, HIS, ARG, GLU, ALA, ARG, ALA, LYS, HIS, T664, R990, G991, D992, G993, D994, D1021, D1057, ALA

Chemical Structures:

- Top track structures are shown as small 3D models, often with a red diamond marker above them.
- Bottom track structures are shown as small 2D chemical structures, often with a red diamond marker above them.

Mapping and Markers:

- Red diamond markers indicate specific points of interest or mapping between the two tracks.
- For example, the structure of MET (top) is mapped to A589 (bottom).
- Similarly, the structure of LEU (top) is mapped to L590 (bottom).

- Molecule 3: Internal protein

Chain c: 43% 56%

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107142	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (\AA)	321.00003, 321.00003, 321.00003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	F	0.25	0/293	0.43	0/400
1	G	0.25	0/293	0.44	0/400
1	H	0.24	0/293	0.43	0/400
1	I	0.25	0/293	0.44	0/400
1	J	0.24	0/293	0.44	0/400
1	K	0.24	0/293	0.44	0/400
1	L	0.24	0/293	0.43	0/400
1	M	0.25	0/293	0.43	0/400
1	N	0.24	0/293	0.43	0/400
1	O	0.25	0/293	0.42	0/400
2	V	0.24	0/708	0.48	0/949
2	W	0.24	0/708	0.48	0/949
2	X	0.25	0/708	0.47	0/949
2	Y	0.24	0/708	0.48	0/949
2	Z	0.24	0/708	0.49	0/949
2	v	0.26	0/708	0.47	0/949
2	w	0.27	0/708	0.50	0/949
2	x	0.26	0/708	0.48	0/949
2	y	0.26	0/708	0.46	0/949
2	z	0.26	0/708	0.50	0/949
3	A	0.25	0/7146	0.50	3/9662 (0.0%)
3	B	0.25	0/7146	0.51	4/9662 (0.0%)
3	C	0.25	0/7146	0.49	0/9662
3	D	0.25	0/7146	0.49	0/9662
3	E	0.25	0/7146	0.51	3/9662 (0.0%)
3	a	0.26	0/3701	0.49	0/4993
3	b	0.26	0/3701	0.51	1/4993 (0.0%)
3	c	0.26	0/3701	0.59	4/4993 (0.1%)
3	d	0.26	0/3701	0.48	0/4993
3	e	0.26	0/3701	0.50	0/4993
All	All	0.25	0/64245	0.50	15/86765 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	a	0	1
3	b	0	1
3	c	0	1
3	d	0	1
3	e	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	c	162	GLY	N-CA-C	-15.49	74.37	113.10
3	c	161	SER	CB-CA-C	12.46	133.76	110.10
3	A	579	GLY	N-CA-C	-9.90	88.35	113.10
3	B	579	GLY	N-CA-C	-9.38	89.64	113.10
3	E	579	GLY	N-CA-C	-9.35	89.73	113.10

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	a	160	ARG	Sidechain
3	b	160	ARG	Sidechain
3	c	160	ARG	Sidechain
3	d	160	ARG	Sidechain
3	e	160	ARG	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	G	38/653 (6%)	37 (97%)	1 (3%)	0	100	100
1	H	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	I	38/653 (6%)	37 (97%)	1 (3%)	0	100	100
1	J	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	K	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	L	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	M	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	N	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
1	O	38/653 (6%)	36 (95%)	2 (5%)	0	100	100
2	V	90/380 (24%)	90 (100%)	0	0	100	100
2	W	90/380 (24%)	90 (100%)	0	0	100	100
2	X	90/380 (24%)	90 (100%)	0	0	100	100
2	Y	90/380 (24%)	90 (100%)	0	0	100	100
2	Z	90/380 (24%)	90 (100%)	0	0	100	100
2	v	90/380 (24%)	90 (100%)	0	0	100	100
2	w	90/380 (24%)	90 (100%)	0	0	100	100
2	x	90/380 (24%)	90 (100%)	0	0	100	100
2	y	90/380 (24%)	90 (100%)	0	0	100	100
2	z	90/380 (24%)	90 (100%)	0	0	100	100
3	A	897/1058 (85%)	873 (97%)	24 (3%)	0	100	100
3	B	897/1058 (85%)	870 (97%)	27 (3%)	0	100	100
3	C	897/1058 (85%)	869 (97%)	28 (3%)	0	100	100
3	D	897/1058 (85%)	869 (97%)	28 (3%)	0	100	100
3	E	897/1058 (85%)	868 (97%)	29 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	a	456/1058 (43%)	451 (99%)	5 (1%)	0	100	100
3	b	456/1058 (43%)	452 (99%)	4 (1%)	0	100	100
3	c	456/1058 (43%)	451 (99%)	5 (1%)	0	100	100
3	d	456/1058 (43%)	449 (98%)	7 (2%)	0	100	100
3	e	456/1058 (43%)	451 (99%)	5 (1%)	0	100	100
All	All	8045/20910 (38%)	7865 (98%)	180 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	30/572 (5%)	30 (100%)	0	100	100
1	G	30/572 (5%)	30 (100%)	0	100	100
1	H	30/572 (5%)	30 (100%)	0	100	100
1	I	30/572 (5%)	30 (100%)	0	100	100
1	J	30/572 (5%)	30 (100%)	0	100	100
1	K	30/572 (5%)	30 (100%)	0	100	100
1	L	30/572 (5%)	30 (100%)	0	100	100
1	M	30/572 (5%)	30 (100%)	0	100	100
1	N	30/572 (5%)	30 (100%)	0	100	100
1	O	30/572 (5%)	30 (100%)	0	100	100
2	V	73/306 (24%)	73 (100%)	0	100	100
2	W	73/306 (24%)	73 (100%)	0	100	100
2	X	73/306 (24%)	73 (100%)	0	100	100
2	Y	73/306 (24%)	73 (100%)	0	100	100
2	Z	73/306 (24%)	73 (100%)	0	100	100
2	v	73/306 (24%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	w	73/306 (24%)	73 (100%)	0	100	100
2	x	73/306 (24%)	73 (100%)	0	100	100
2	y	73/306 (24%)	73 (100%)	0	100	100
2	z	73/306 (24%)	73 (100%)	0	100	100
3	A	735/850 (86%)	735 (100%)	0	100	100
3	B	735/850 (86%)	735 (100%)	0	100	100
3	C	735/850 (86%)	735 (100%)	0	100	100
3	D	735/850 (86%)	734 (100%)	1 (0%)	92	97
3	E	735/850 (86%)	735 (100%)	0	100	100
3	a	386/850 (45%)	386 (100%)	0	100	100
3	b	386/850 (45%)	385 (100%)	1 (0%)	91	95
3	c	386/850 (45%)	385 (100%)	1 (0%)	91	95
3	d	386/850 (45%)	385 (100%)	1 (0%)	91	95
3	e	386/850 (45%)	386 (100%)	0	100	100
All	All	6635/17280 (38%)	6631 (100%)	4 (0%)	92	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	d	535	LYS
3	b	535	LYS
3	D	527	GLN
3	c	140	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
3	a	363	GLN
3	b	225	GLN
3	C	335	GLN
3	C	982	ASN
3	D	41	GLN

5.3.3 RNA ⓘ

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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

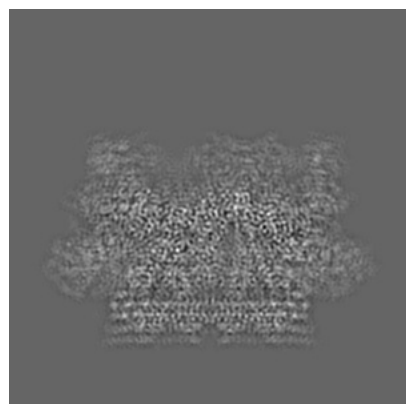
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61998. These allow visual inspection of the internal detail of the map and identification of artifacts.

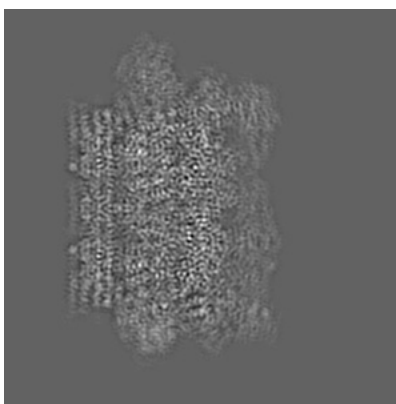
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

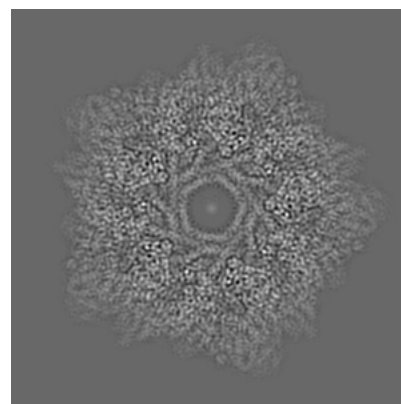
6.1.1 Primary map



X

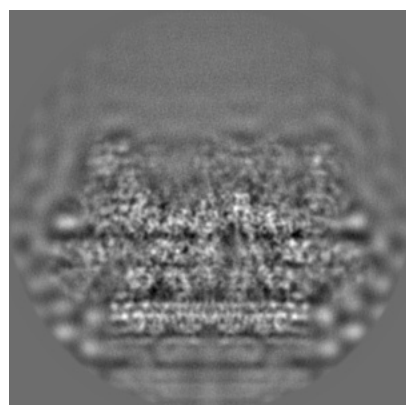


Y

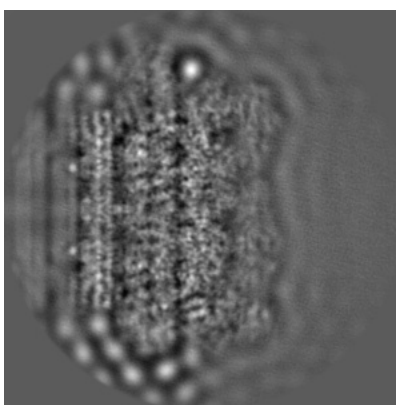


Z

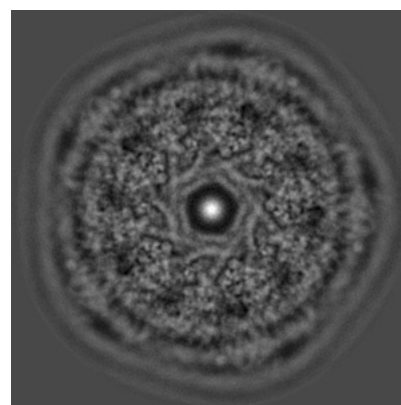
6.1.2 Raw map



X



Y

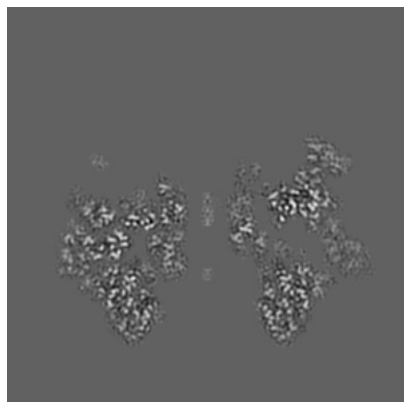


Z

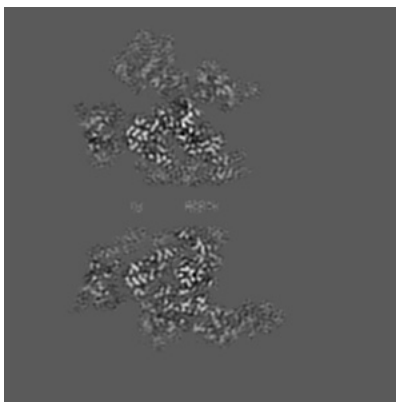
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

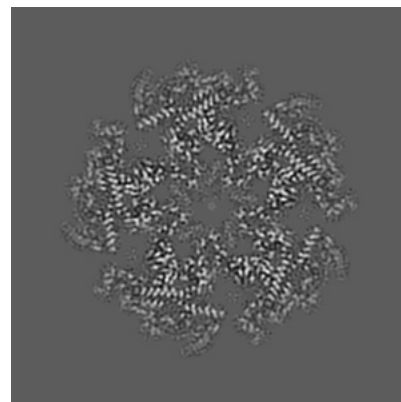
6.2.1 Primary map



X Index: 150

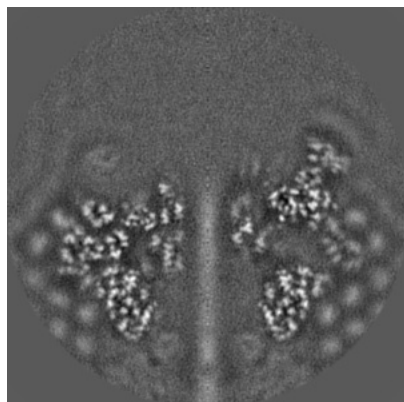


Y Index: 150

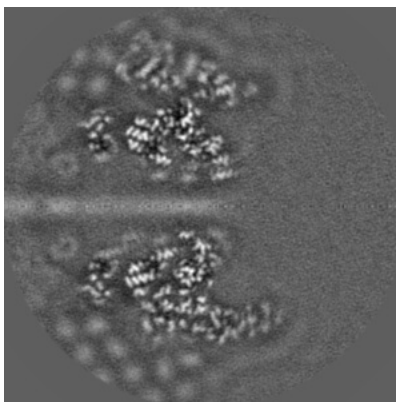


Z Index: 150

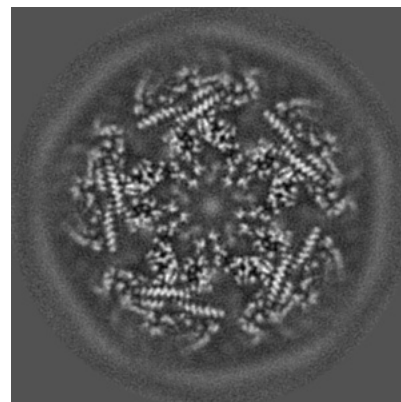
6.2.2 Raw map



X Index: 150



Y Index: 150

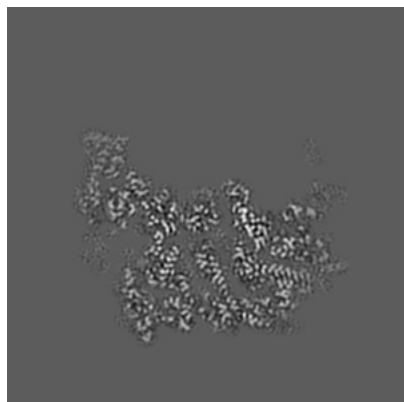


Z Index: 150

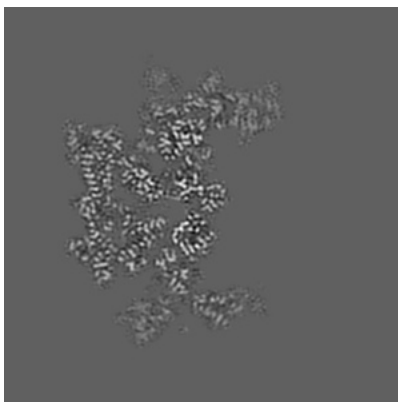
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

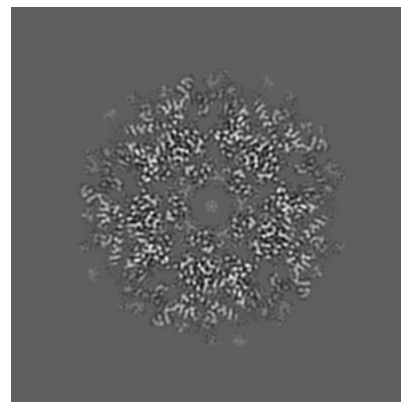
6.3.1 Primary map



X Index: 108

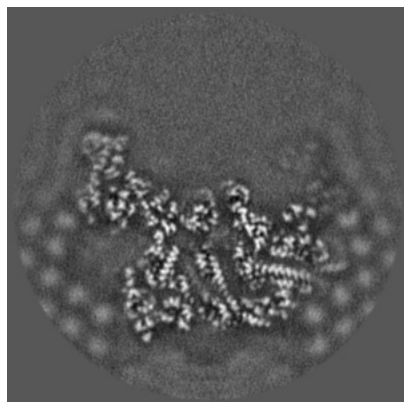


Y Index: 199

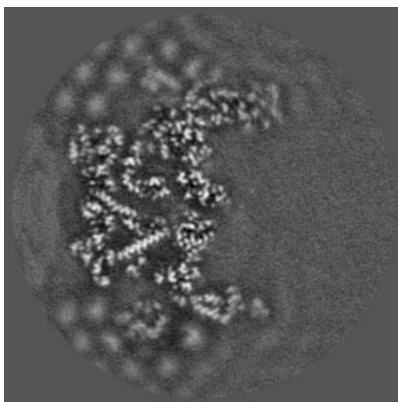


Z Index: 139

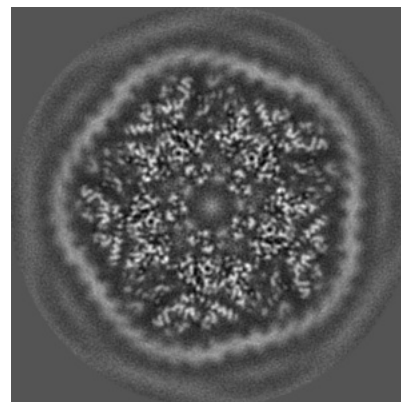
6.3.2 Raw map



X Index: 108



Y Index: 196

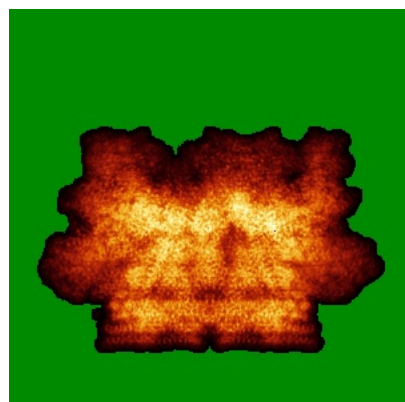


Z Index: 139

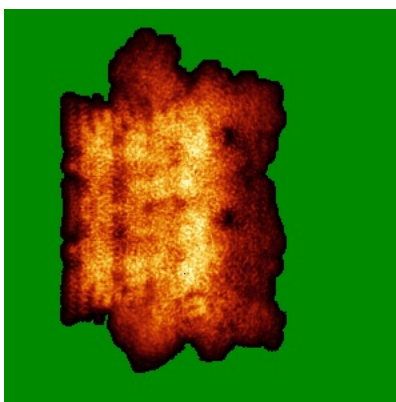
The images above show the largest variance slices of the map in three orthogonal directions.

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

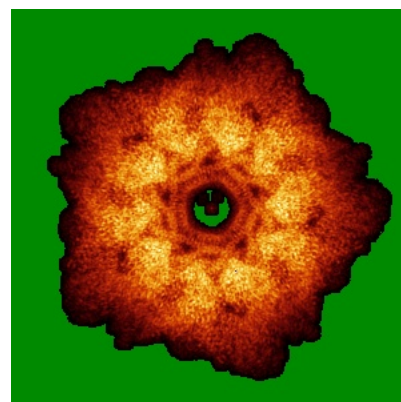
6.4.1 Primary map



X

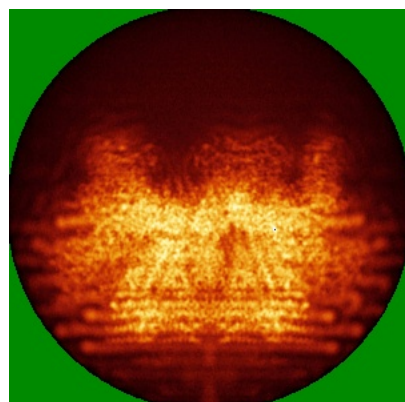


Y

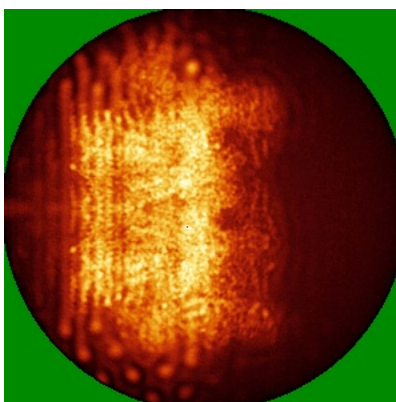


Z

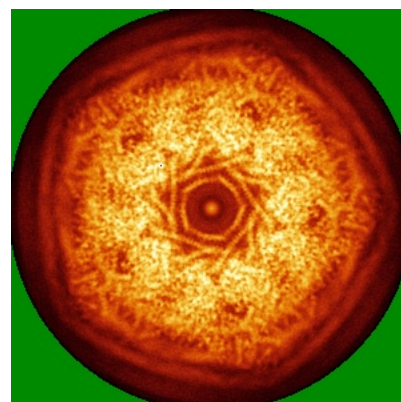
6.4.2 Raw map



X



Y

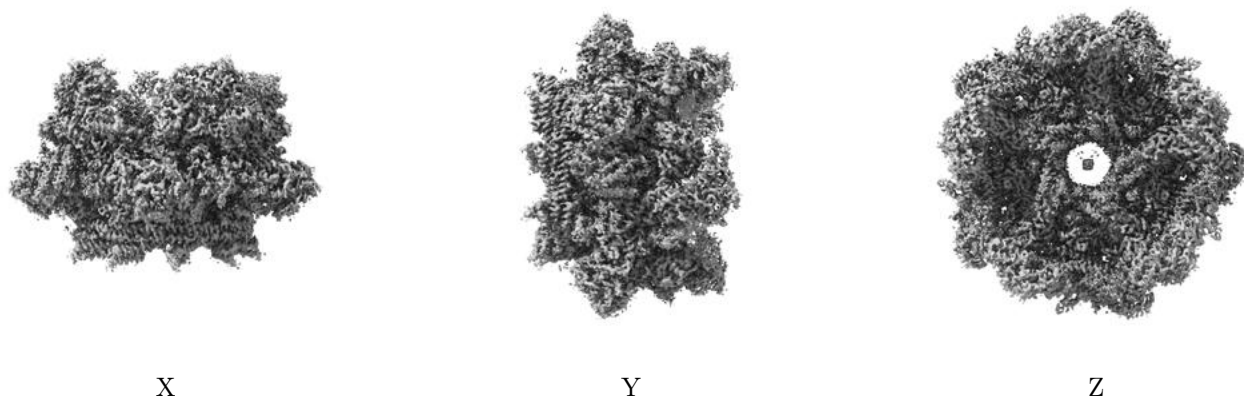


Z

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

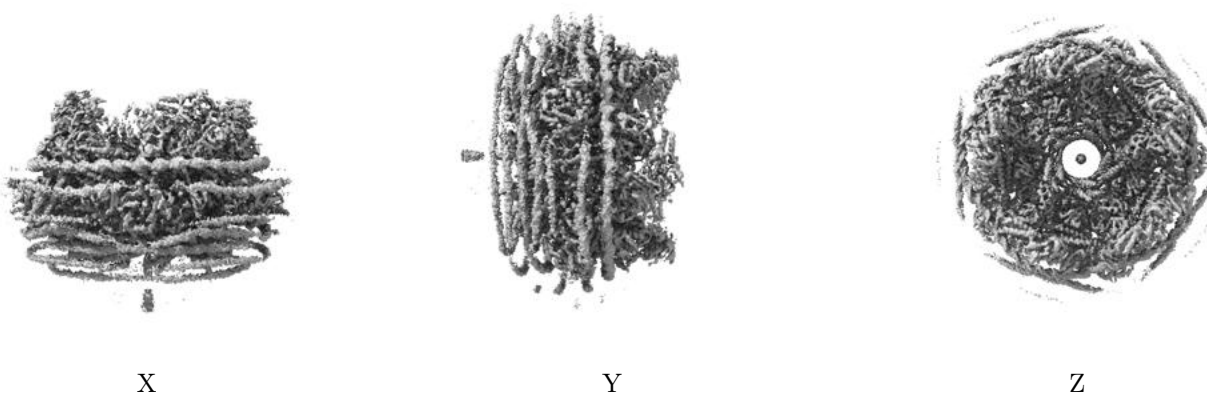
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. 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.

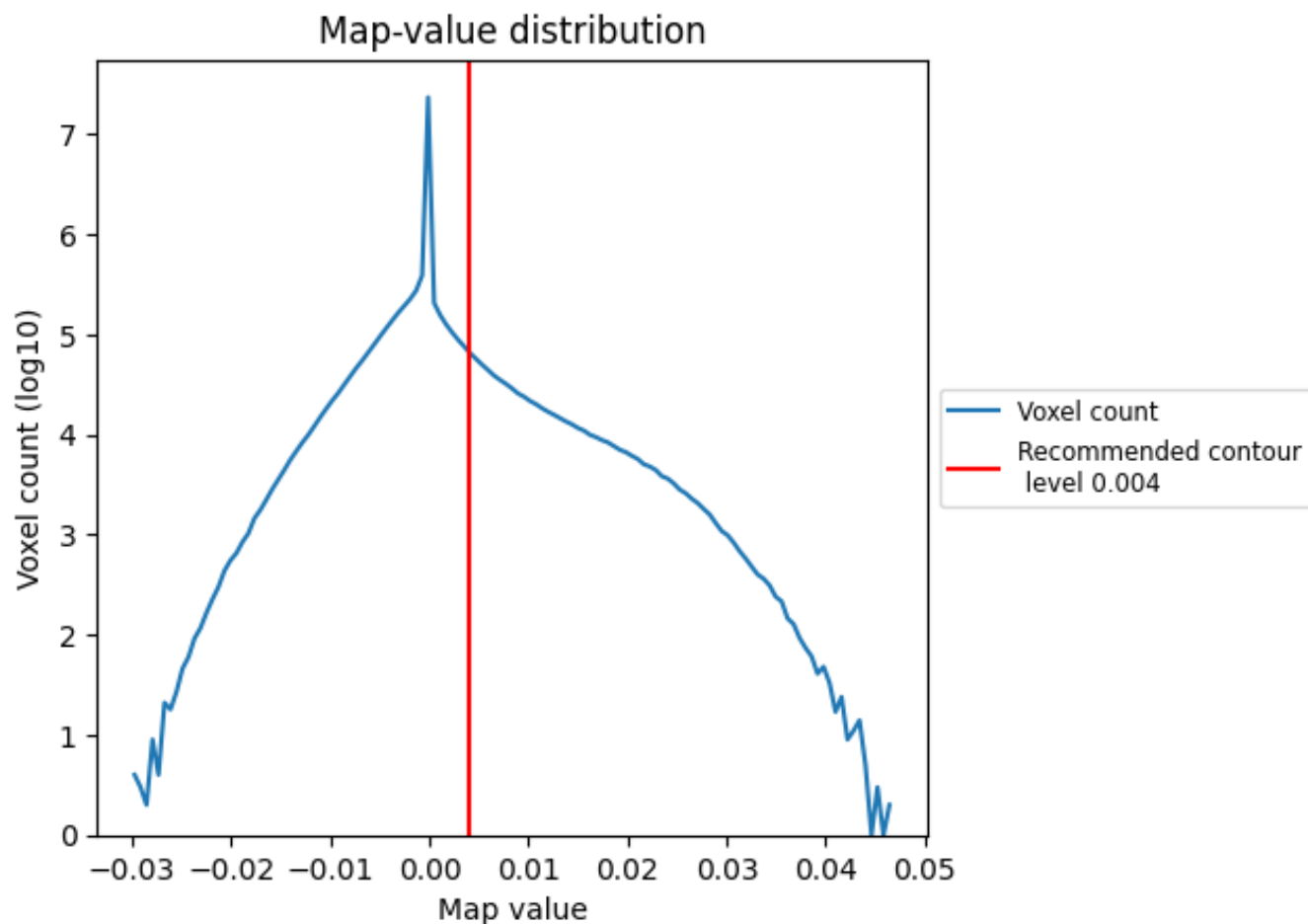
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

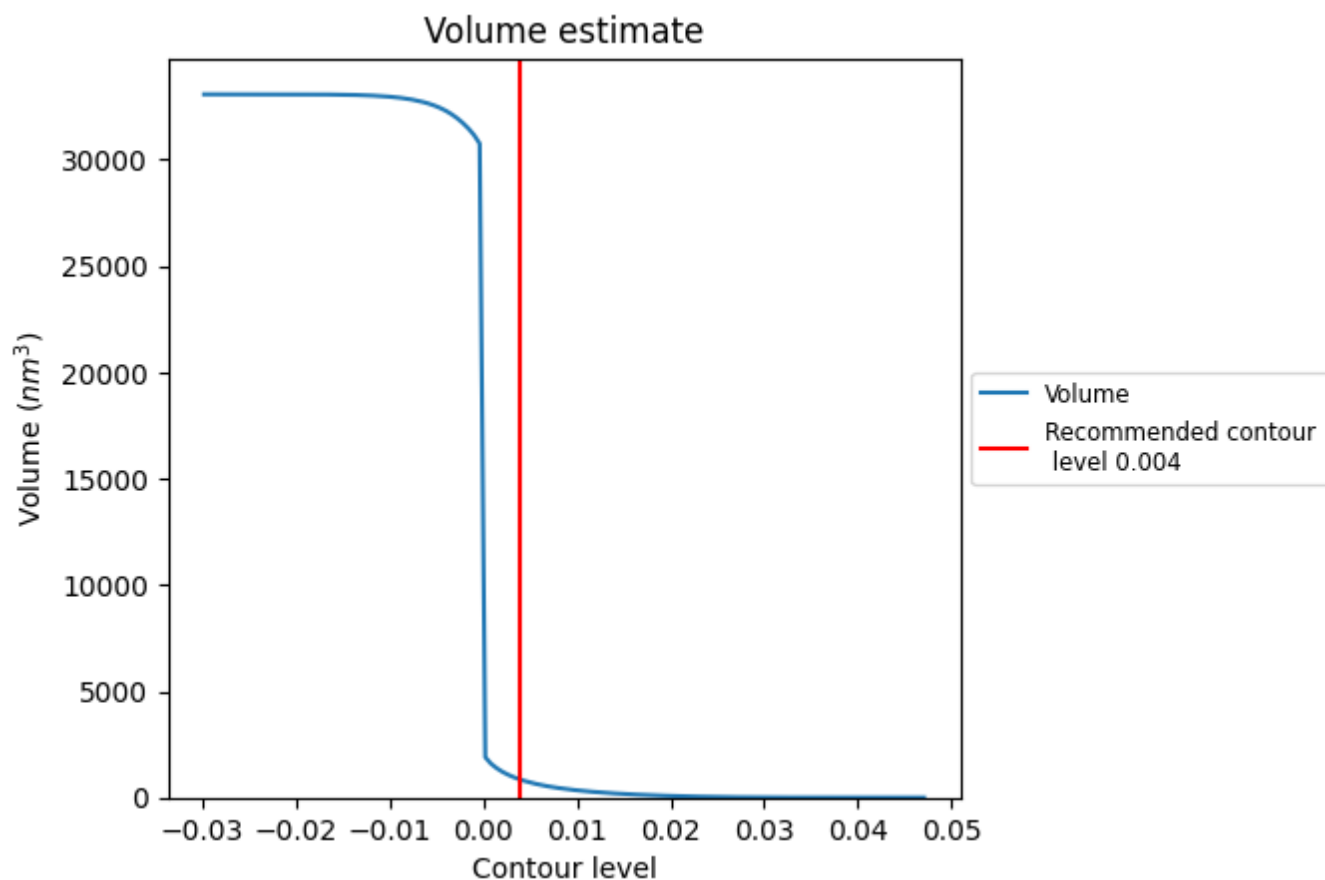
This section contains the results of statistical analysis of the map.

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.

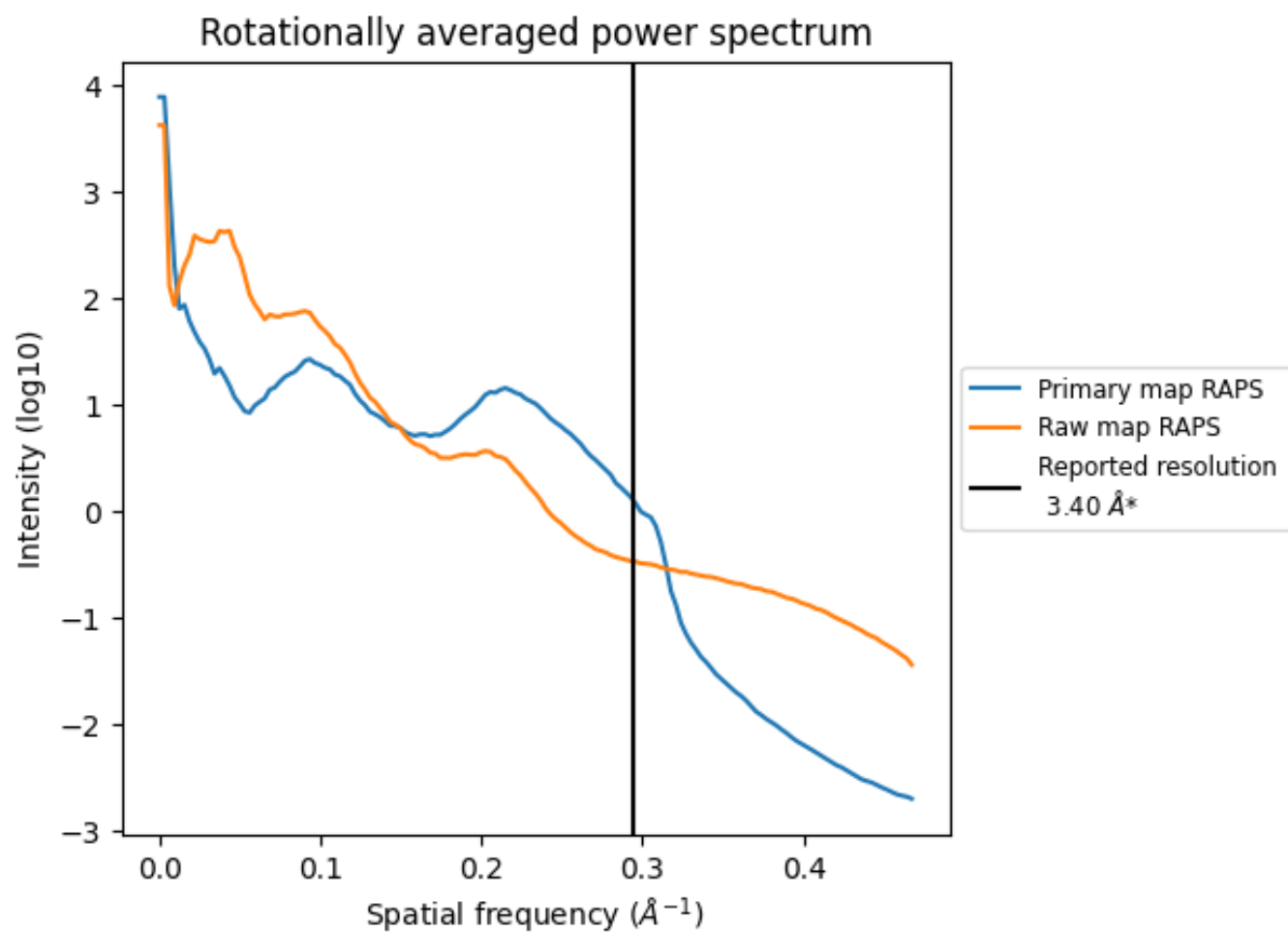
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 843 nm^3 ; this corresponds to an approximate mass of 761 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 ⓘ

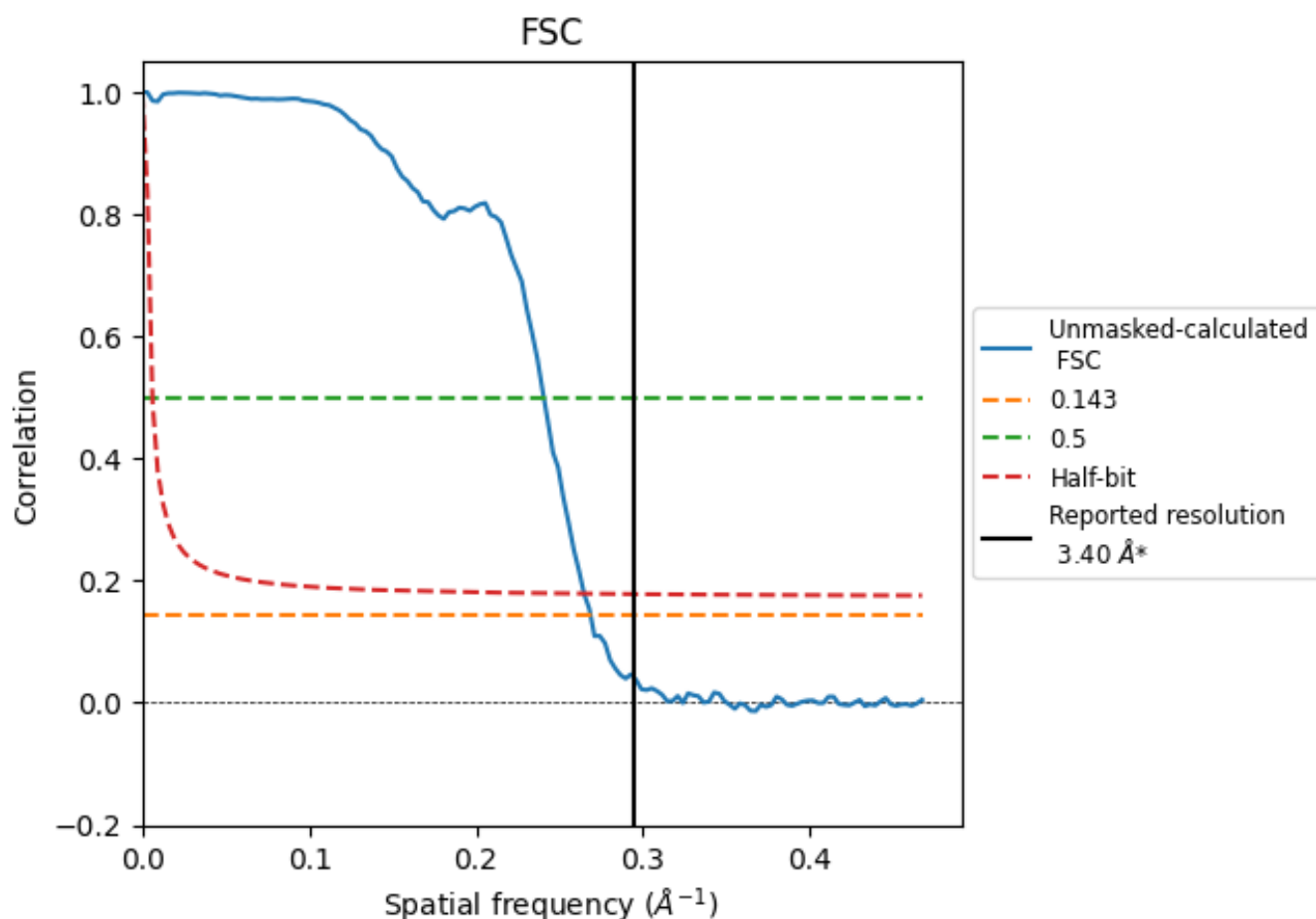


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

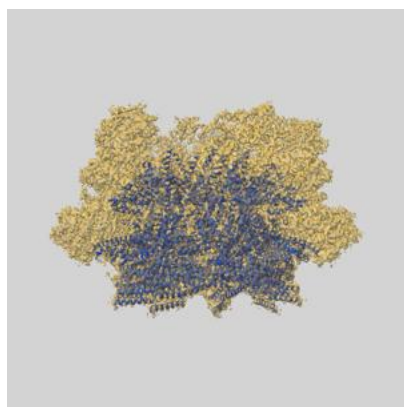
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.72	4.16	3.78

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

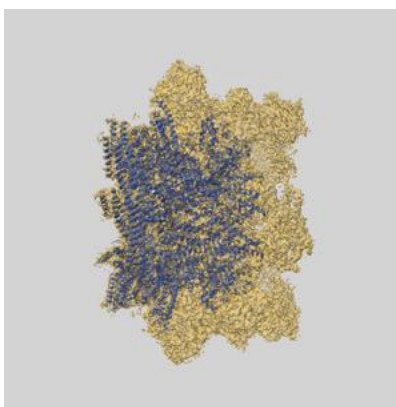
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61998 and PDB model 9K2V. Per-residue inclusion information can be found in section [3](#) on page [7](#).

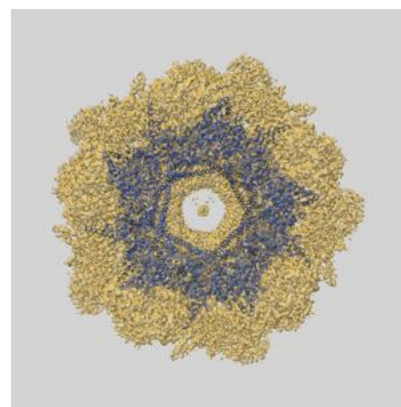
9.1 Map-model overlay [i](#)



X



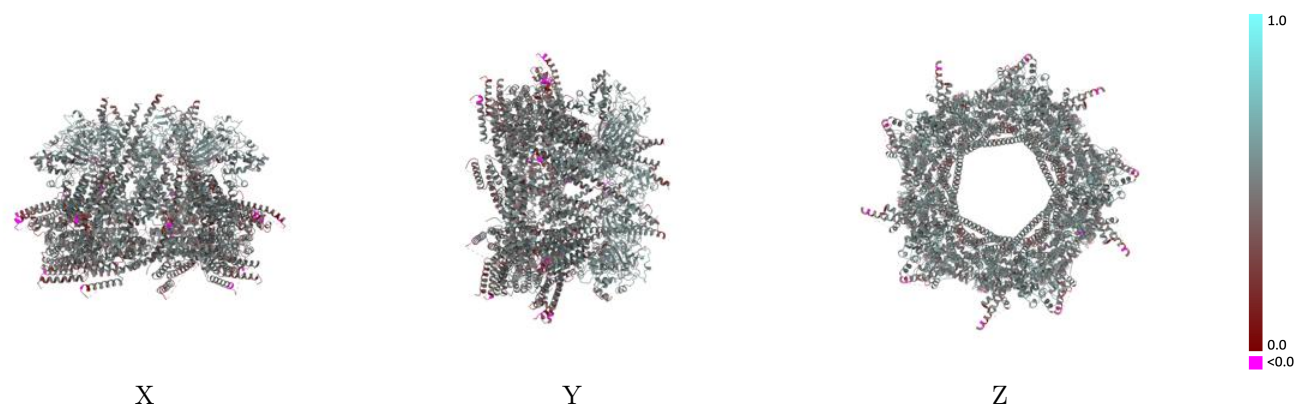
Y



Z

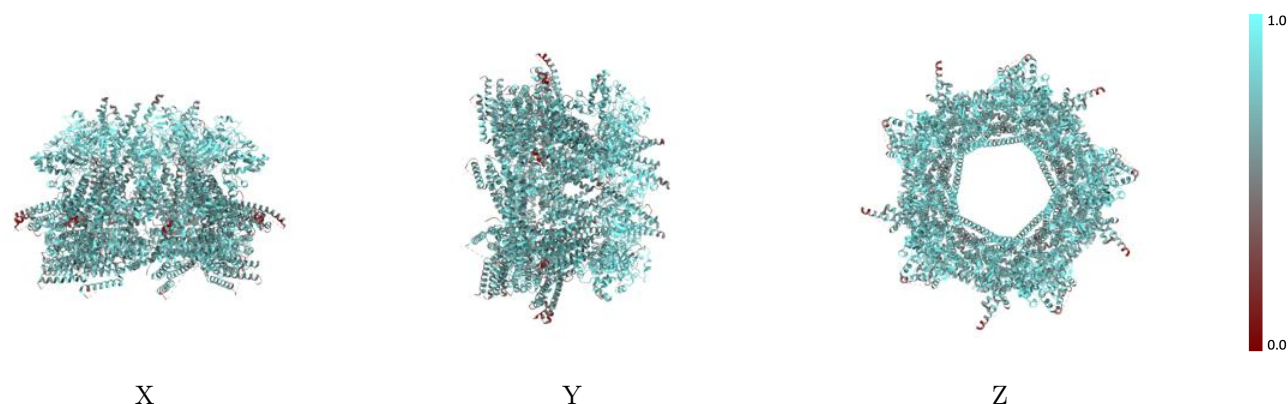
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



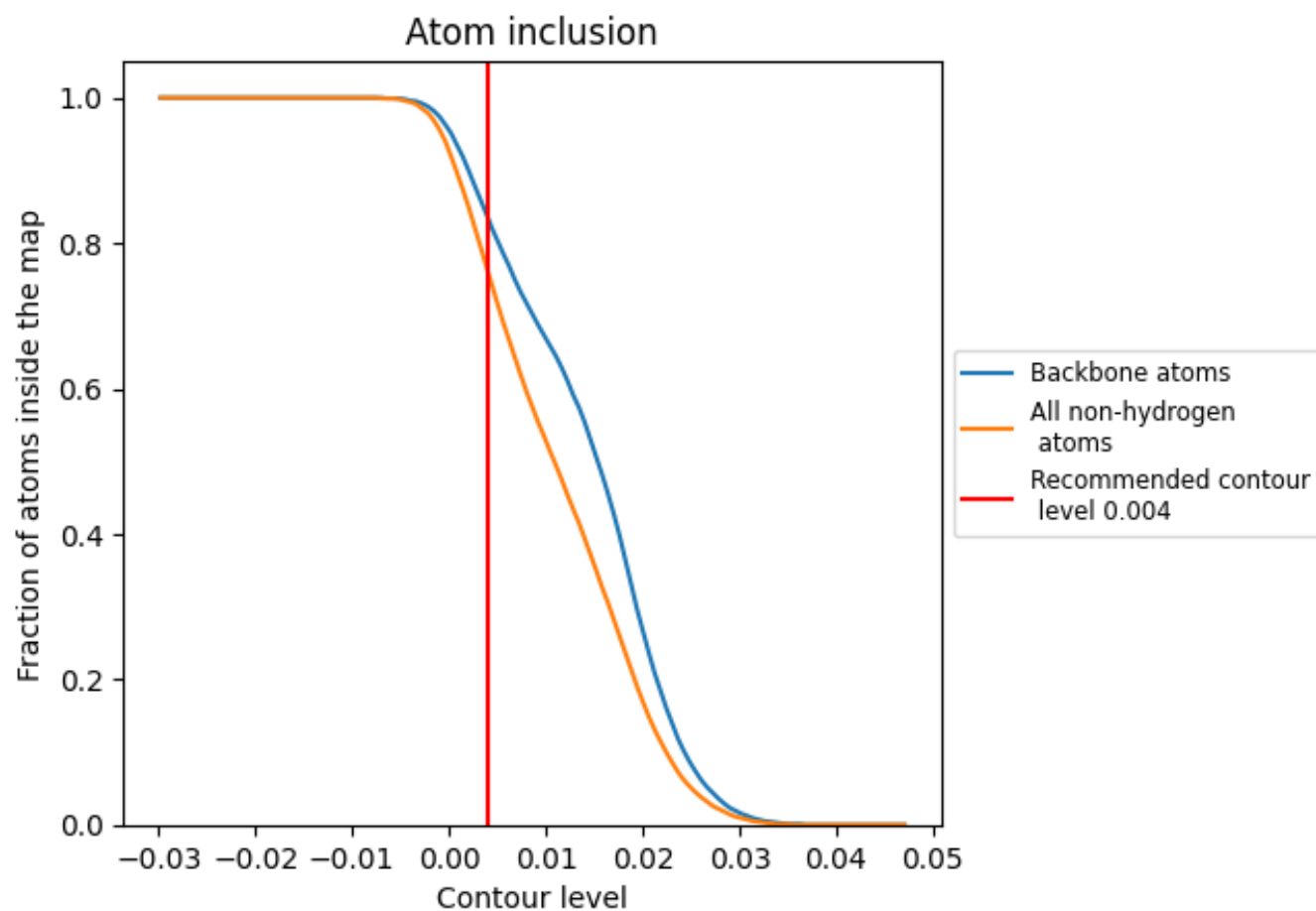
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.004).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7620	 0.4800
A	 0.7770	 0.4950
B	 0.7800	 0.4950
C	 0.7780	 0.4940
D	 0.7810	 0.4940
E	 0.7770	 0.4960
F	 0.7680	 0.4950
G	 0.7610	 0.4510
H	 0.7820	 0.4910
I	 0.7580	 0.4570
J	 0.7850	 0.4990
K	 0.7510	 0.4640
L	 0.7850	 0.4980
M	 0.7650	 0.4680
N	 0.7960	 0.4990
O	 0.7470	 0.4550
V	 0.7580	 0.4870
W	 0.7630	 0.4760
X	 0.7510	 0.4750
Y	 0.7700	 0.4780
Z	 0.7630	 0.4830
a	 0.7260	 0.4560
b	 0.7300	 0.4580
c	 0.7350	 0.4610
d	 0.7290	 0.4560
e	 0.7310	 0.4590
v	 0.7510	 0.4550
w	 0.7440	 0.4510
x	 0.7570	 0.4620
y	 0.7440	 0.4520
z	 0.7470	 0.4560

