



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:40 AM UTC

PDB ID : 8HPQ / pdb_00008hpq
EMDB ID : EMD-34940
Title : Cryo-EM structure of SARS-CoV-2 Omicron BA.4 S-trimer in complex with
fab L4.65 and L5.34
Authors : Gao, G.F.; Liu, S.
Deposited on : 2022-12-12
Resolution : 2.85 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:

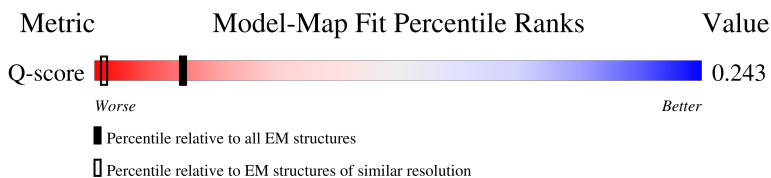
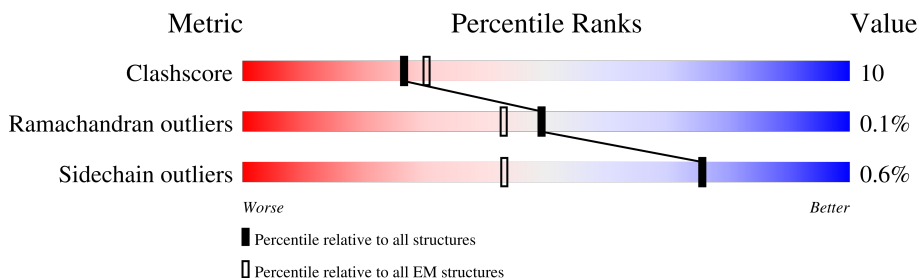
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.85 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11965 (2.35 - 3.35)

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	1129	
1	B	1129	
1	C	1129	
2	H	231	

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Mol	Chain	Length	Quality of chain
2	I	231	55% 77% 23%
2	P	231	63% 77% 23%
3	J	215	71% 73% 27%
3	L	215	52% 72% 28%
3	Q	215	73% 73% 27%
4	E	224	58% 81% 19%
4	M	224	28% 82% 18%
4	R	224	54% 80% 20%
5	F	216	60% 71% 29%
5	N	216	40% 71% 29%
5	S	216	59% 72% 28%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 44355 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 Spike protein S2'.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1029	Total	C	N	O	S	1	0
			8059	5158	1342	1522	37		
1	B	1029	Total	C	N	O	S	1	0
			8059	5158	1342	1522	37		
1	C	1029	Total	C	N	O	S	1	0
			8059	5158	1342	1522	37		

There are 111 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	ILE	THR	conflict	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	43	SER	ALA	variant	UNP P0DTC2
A	?	-	HIS	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	156	ASP	GLY	variant	UNP P0DTC2
A	353	ASP	GLY	variant	UNP P0DTC2
A	385	PHE	SER	variant	UNP P0DTC2
A	387	PRO	SER	variant	UNP P0DTC2
A	389	PHE	SER	variant	UNP P0DTC2
A	390	ALA	THR	variant	UNP P0DTC2
A	419	ASN	ASP	variant	UNP P0DTC2
A	422	SER	ARG	variant	UNP P0DTC2
A	431	ASN	LYS	variant	UNP P0DTC2
A	454	LYS	ASN	variant	UNP P0DTC2
A	466	ARG	LEU	variant	UNP P0DTC2
A	491	ASN	SER	variant	UNP P0DTC2
A	492	LYS	THR	variant	UNP P0DTC2
A	498	ALA	GLU	variant	UNP P0DTC2
A	500	VAL	PHE	variant	UNP P0DTC2
A	512	ARG	GLN	variant	UNP P0DTC2
A	515	TYR	ASN	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	519	HIS	TYR	variant	UNP P0DTC2
A	628	GLY	ASP	variant	UNP P0DTC2
A	669	TYR	HIS	variant	UNP P0DTC2
A	778	LYS	ASN	variant	UNP P0DTC2
A	810	TYR	ASP	variant	UNP P0DTC2
A	831	PRO	PHE	conflict	UNP P0DTC2
A	906	PRO	ALA	conflict	UNP P0DTC2
A	913	PRO	ALA	conflict	UNP P0DTC2
A	956	PRO	ALA	conflict	UNP P0DTC2
A	968	HIS	GLN	variant	UNP P0DTC2
A	983	LYS	ASN	variant	UNP P0DTC2
A	1000	PRO	LYS	conflict	UNP P0DTC2
A	1001	PRO	VAL	conflict	UNP P0DTC2
B	38	ILE	THR	conflict	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	43	SER	ALA	variant	UNP P0DTC2
B	?	-	HIS	deletion	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	156	ASP	GLY	variant	UNP P0DTC2
B	353	ASP	GLY	variant	UNP P0DTC2
B	385	PHE	SER	variant	UNP P0DTC2
B	387	PRO	SER	variant	UNP P0DTC2
B	389	PHE	SER	variant	UNP P0DTC2
B	390	ALA	THR	variant	UNP P0DTC2
B	419	ASN	ASP	variant	UNP P0DTC2
B	422	SER	ARG	variant	UNP P0DTC2
B	431	ASN	LYS	variant	UNP P0DTC2
B	454	LYS	ASN	variant	UNP P0DTC2
B	466	ARG	LEU	variant	UNP P0DTC2
B	491	ASN	SER	variant	UNP P0DTC2
B	492	LYS	THR	variant	UNP P0DTC2
B	498	ALA	GLU	variant	UNP P0DTC2
B	500	VAL	PHE	variant	UNP P0DTC2
B	512	ARG	GLN	variant	UNP P0DTC2
B	515	TYR	ASN	variant	UNP P0DTC2
B	519	HIS	TYR	variant	UNP P0DTC2
B	628	GLY	ASP	variant	UNP P0DTC2
B	669	TYR	HIS	variant	UNP P0DTC2
B	778	LYS	ASN	variant	UNP P0DTC2
B	810	TYR	ASP	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	831	PRO	PHE	conflict	UNP P0DTC2
B	906	PRO	ALA	conflict	UNP P0DTC2
B	913	PRO	ALA	conflict	UNP P0DTC2
B	956	PRO	ALA	conflict	UNP P0DTC2
B	968	HIS	GLN	variant	UNP P0DTC2
B	983	LYS	ASN	variant	UNP P0DTC2
B	1000	PRO	LYS	conflict	UNP P0DTC2
B	1001	PRO	VAL	conflict	UNP P0DTC2
C	38	ILE	THR	conflict	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	43	SER	ALA	variant	UNP P0DTC2
C	?	-	HIS	deletion	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	156	ASP	GLY	variant	UNP P0DTC2
C	353	ASP	GLY	variant	UNP P0DTC2
C	385	PHE	SER	variant	UNP P0DTC2
C	387	PRO	SER	variant	UNP P0DTC2
C	389	PHE	SER	variant	UNP P0DTC2
C	390	ALA	THR	variant	UNP P0DTC2
C	419	ASN	ASP	variant	UNP P0DTC2
C	422	SER	ARG	variant	UNP P0DTC2
C	431	ASN	LYS	variant	UNP P0DTC2
C	454	LYS	ASN	variant	UNP P0DTC2
C	466	ARG	LEU	variant	UNP P0DTC2
C	491	ASN	SER	variant	UNP P0DTC2
C	492	LYS	THR	variant	UNP P0DTC2
C	498	ALA	GLU	variant	UNP P0DTC2
C	500	VAL	PHE	variant	UNP P0DTC2
C	512	ARG	GLN	variant	UNP P0DTC2
C	515	TYR	ASN	variant	UNP P0DTC2
C	519	HIS	TYR	variant	UNP P0DTC2
C	628	GLY	ASP	variant	UNP P0DTC2
C	669	TYR	HIS	variant	UNP P0DTC2
C	778	LYS	ASN	variant	UNP P0DTC2
C	810	TYR	ASP	variant	UNP P0DTC2
C	831	PRO	PHE	conflict	UNP P0DTC2
C	906	PRO	ALA	conflict	UNP P0DTC2
C	913	PRO	ALA	conflict	UNP P0DTC2
C	956	PRO	ALA	conflict	UNP P0DTC2
C	968	HIS	GLN	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	983	LYS	ASN	variant	UNP P0DTC2
C	1000	PRO	LYS	conflict	UNP P0DTC2
C	1001	PRO	VAL	conflict	UNP P0DTC2

- Molecule 2 is a protein called fab L4.65.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	231	Total	C	N	O	S	0	0
			1756	1115	287	347	7		
2	P	231	Total	C	N	O	S	0	0
			1756	1115	287	347	7		
2	I	231	Total	C	N	O	S	0	0
			1756	1115	287	347	7		

- Molecule 3 is a protein called fab L4.65.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	215	Total	C	N	O	S	0	0
			1658	1036	281	336	5		
3	Q	215	Total	C	N	O	S	0	0
			1658	1036	281	336	5		
3	J	215	Total	C	N	O	S	0	0
			1658	1036	281	336	5		

- Molecule 4 is a protein called fab L5.34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	224	Total	C	N	O	S	0	0
			1656	1040	279	329	8		
4	E	224	Total	C	N	O	S	0	0
			1656	1040	279	329	8		
4	R	224	Total	C	N	O	S	0	0
			1656	1040	279	329	8		

- Molecule 5 is a protein called fab L5.34.

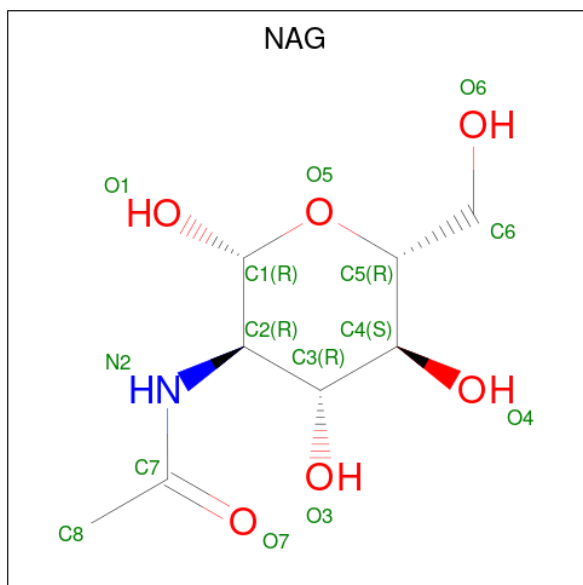
Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	216	Total	C	N	O	S	0	0
			1642	1020	280	336	6		
5	F	216	Total	C	N	O	S	0	0
			1642	1020	280	336	6		

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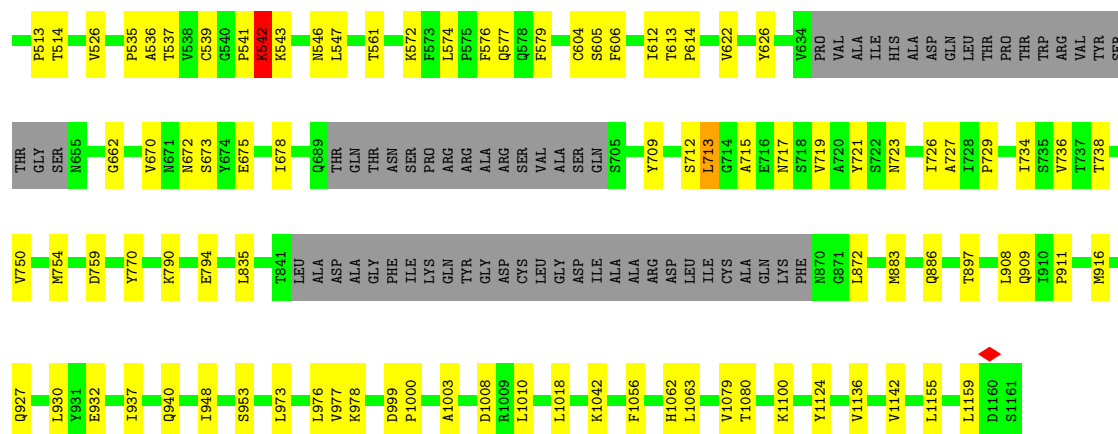
Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	216	Total	C	N	O	S	0	0
			1642	1020	280	336	6		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

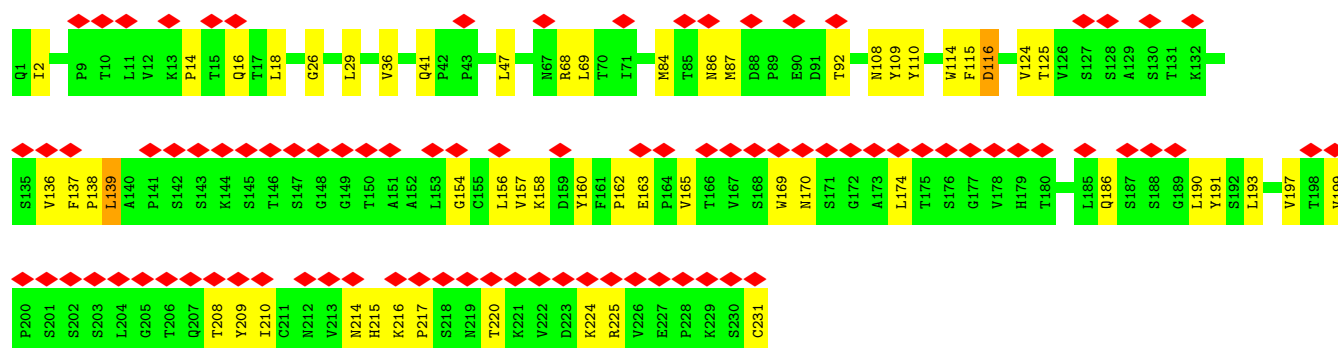
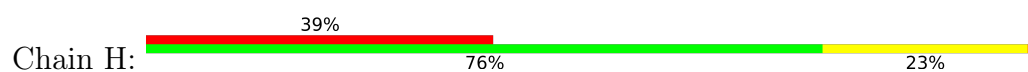


Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	

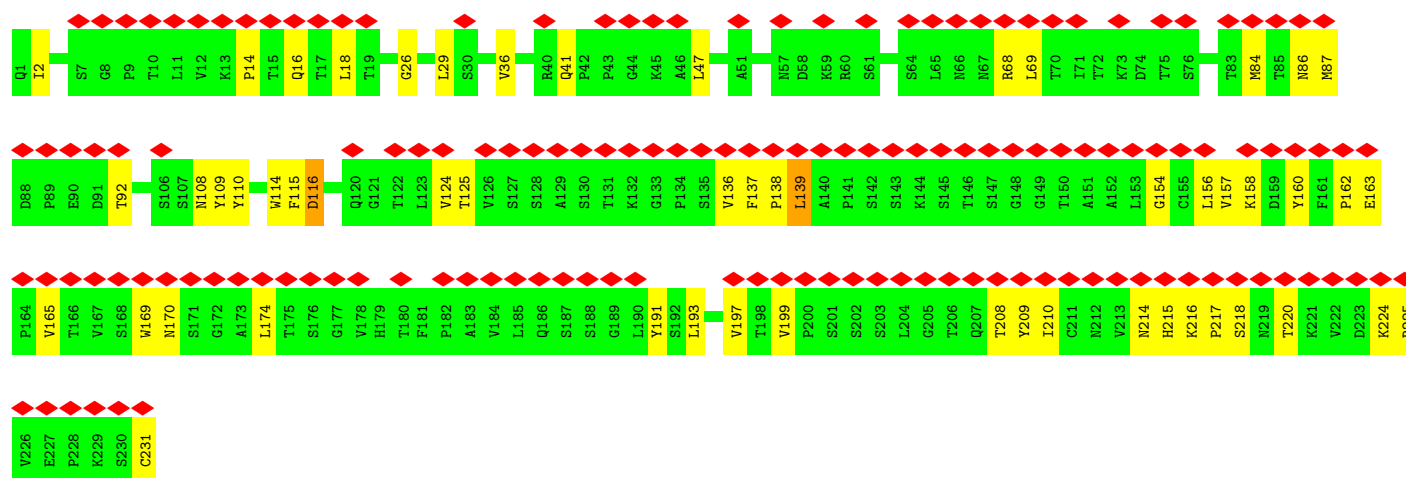
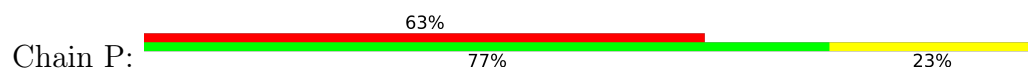
[illegible]



• Molecule 2: fab L4.65

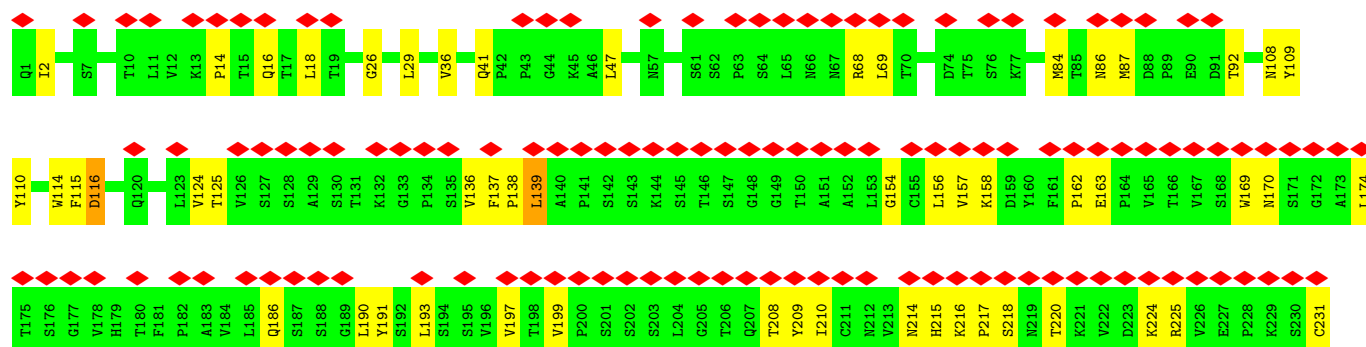


• Molecule 2: fab L4.65

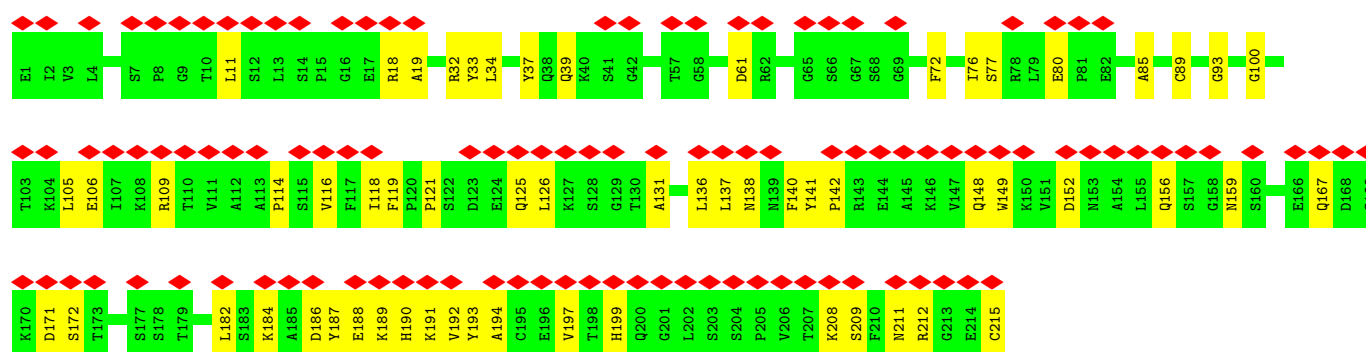


• Molecule 2: fab L4.65

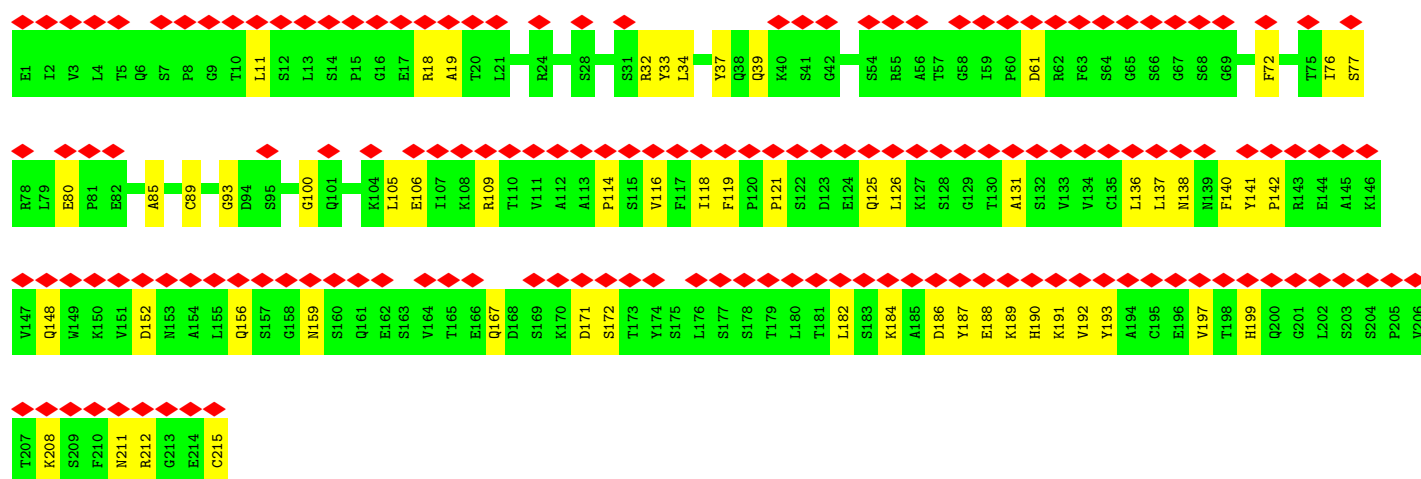
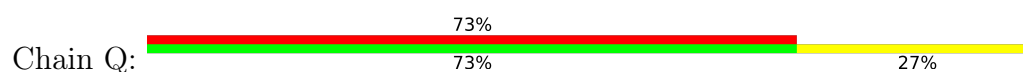




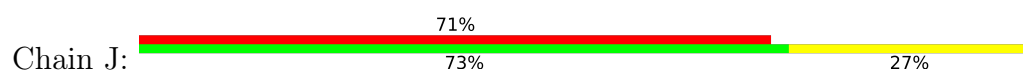
• Molecule 3: fab L4.65

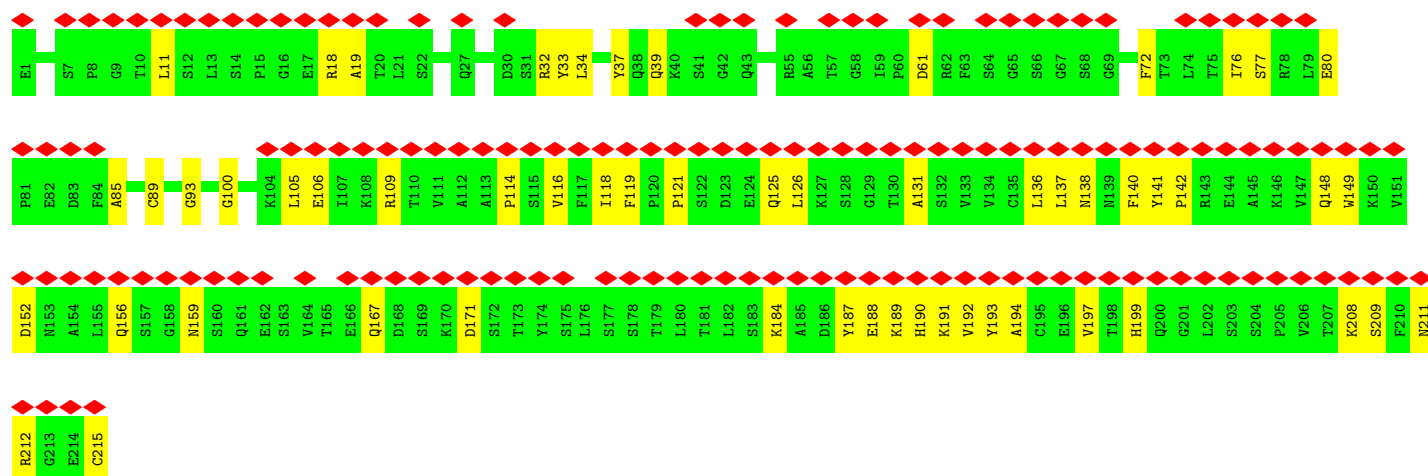


• Molecule 3: fab L4.65

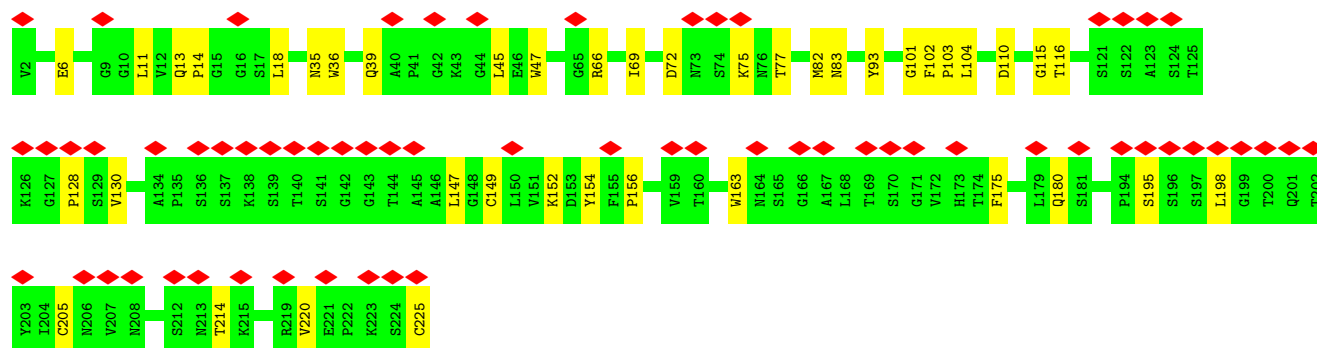
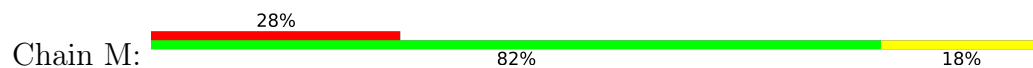


• Molecule 3: fab L4.65

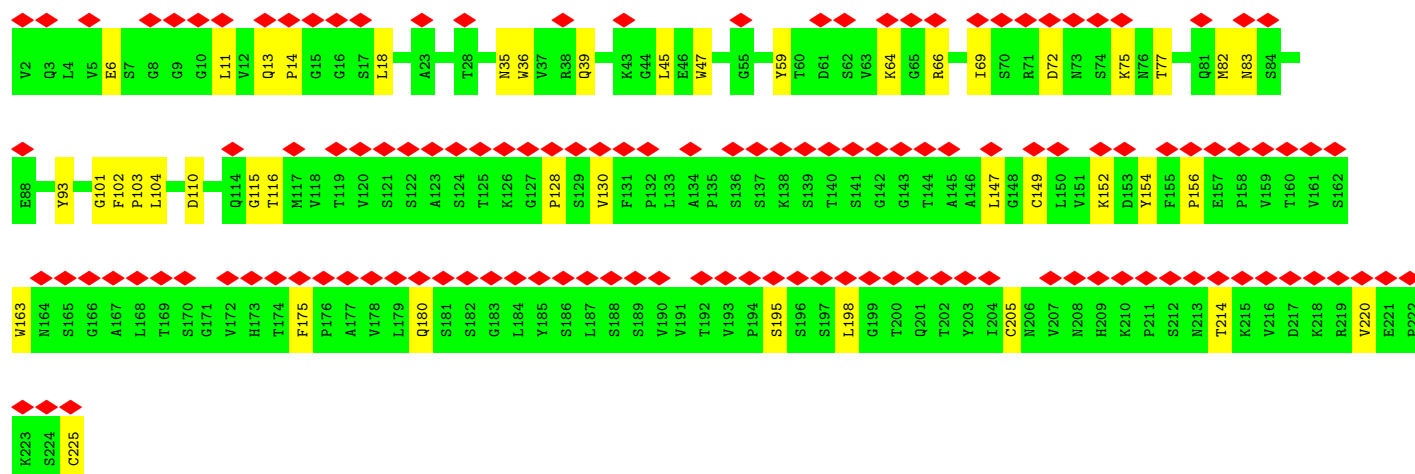
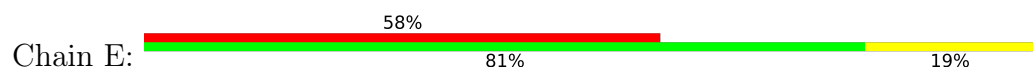




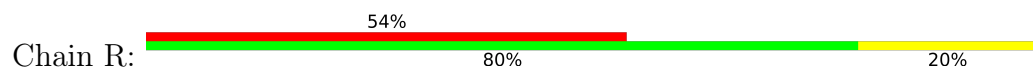
• Molecule 4: fab L5.34

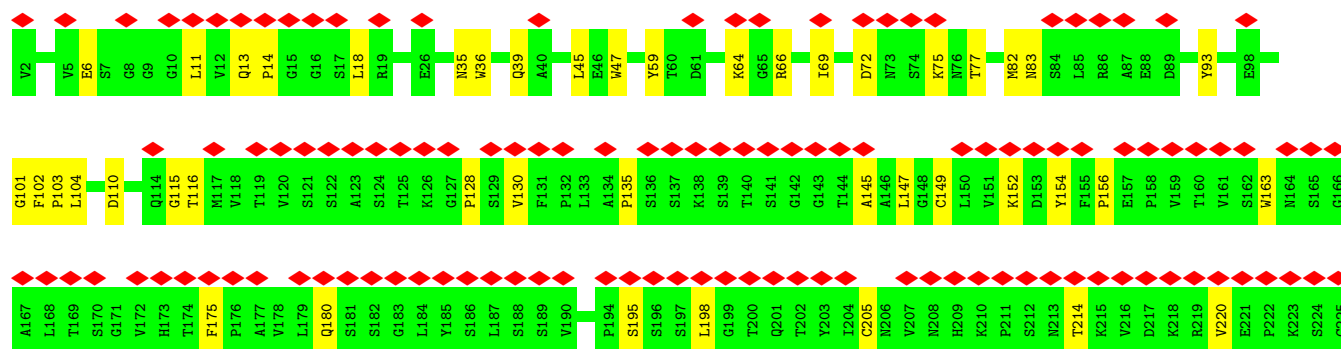


• Molecule 4: fab L5.34

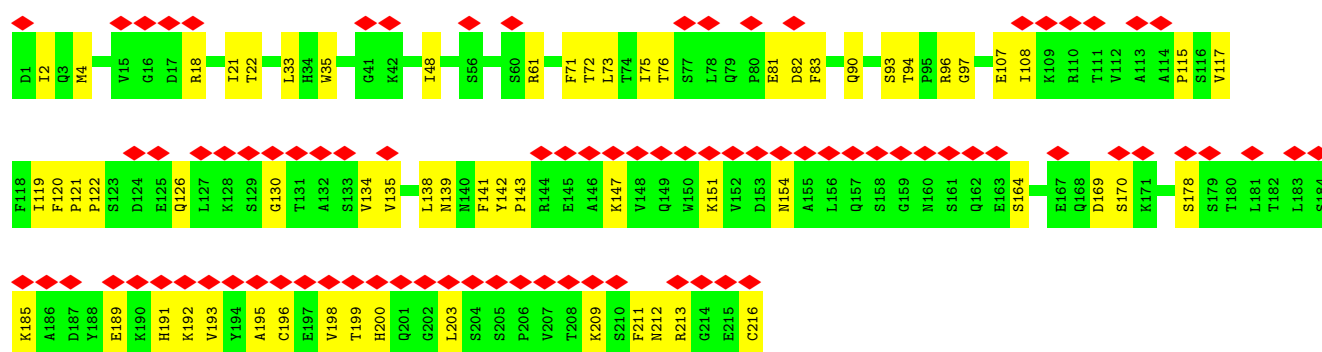


• Molecule 4: fab L5.34

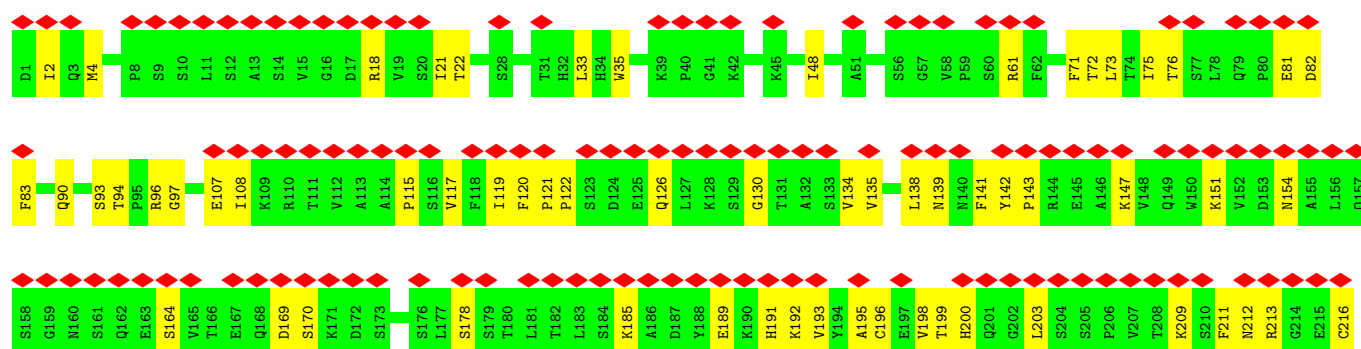




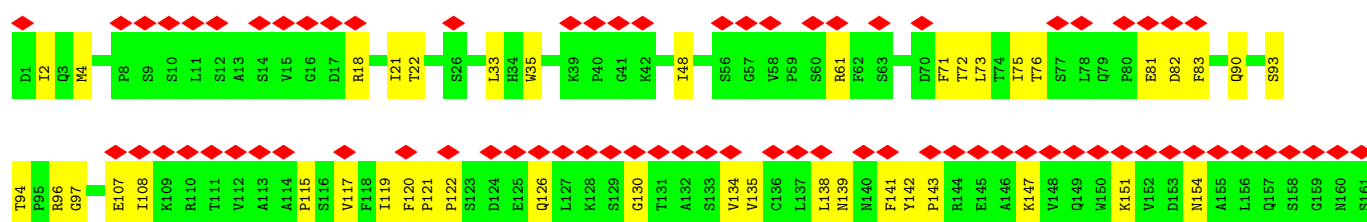
• Molecule 5: fab L5.34



• Molecule 5: fab L5.34



• Molecule 5: fab L5.34



Q162	E163	S164	V165	T166	E167	Q168	D169	S170	K171	D172	Y175	S176	L177	S178	S179	T180	L181	T182	L183	S184	K185	A186	D187	Y188	E189	K190	H191	K192	V193	Y194	A195	C196	E197	V198	T199	H200	Q201	G202	L203	S204	S205	P206	V207	T208	K209	S210	F211	N212	R213	G214	E215	C216
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	593563	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.39	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	8.550	Depositor
Minimum map value	-5.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	430.08, 430.08, 430.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.84, 0.84, 0.84	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.43	8/8248 (0.1%)	0.66	21/11214 (0.2%)
1	B	0.41	6/8249 (0.1%)	0.61	12/11217 (0.1%)
1	C	0.33	6/8249 (0.1%)	0.65	13/11217 (0.1%)
2	H	0.15	0/1805	0.45	2/2471 (0.1%)
2	I	0.15	0/1805	0.45	2/2471 (0.1%)
2	P	0.15	0/1805	0.45	2/2471 (0.1%)
3	J	0.14	0/1694	0.35	0/2294
3	L	0.14	0/1694	0.35	0/2294
3	Q	0.14	0/1694	0.35	0/2294
4	E	0.16	0/1694	0.37	0/2308
4	M	0.16	0/1694	0.37	0/2308
4	R	0.16	0/1694	0.38	0/2308
5	F	0.14	0/1676	0.35	0/2272
5	N	0.14	0/1676	0.34	0/2272
5	S	0.14	0/1676	0.35	0/2272
All	All	0.31	20/45353 (0.0%)	0.54	52/61683 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
1	C	0	3
2	H	0	1
2	I	0	1
2	P	0	1
All	All	0	11

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	343	PHE	C-N	23.08	1.87	1.33
1	A	343	PHE	C-N	22.57	1.86	1.33
1	C	321	THR	C-N	8.59	1.44	1.33
1	A	719	VAL	C-N	-6.76	1.25	1.33
1	B	330	SER	CA-CB	-6.34	1.42	1.53

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	THR	O-C-N	-20.05	97.13	123.19
1	A	321	THR	O-C-N	-17.71	100.16	123.19
1	C	321	THR	CA-C-N	16.73	146.24	122.99
1	C	321	THR	C-N-CA	16.73	146.24	122.99
1	A	321	THR	CA-C-N	14.73	143.47	122.99

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	321	THR	Mainchain
1	A	393	CYS	Peptide
1	B	321	THR	Mainchain
1	B	393	CYS	Peptide
2	H	116	ASP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8059	0	7855	190	0
1	B	8059	0	7856	213	0
1	C	8059	0	7857	213	0
2	H	1756	0	1713	38	0
2	I	1756	0	1713	38	0
2	P	1756	0	1713	38	0
3	J	1658	0	1599	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	1658	0	1599	42	0
3	Q	1658	0	1599	39	0
4	E	1656	0	1620	33	0
4	M	1656	0	1620	32	0
4	R	1656	0	1620	32	0
5	F	1642	0	1599	41	0
5	N	1642	0	1599	42	0
5	S	1642	0	1599	40	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
6	C	14	0	13	0	0
All	All	44355	0	43200	875	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 10.

The worst 5 of 875 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:PHE:CE1	1:C:374:ASN:ND2	1.73	1.54
1:B:181:THR:CA	1:C:371:ARG:NH1	1.67	1.50
1:B:181:THR:CB	1:C:371:ARG:HH22	1.22	1.48
1:B:182:PHE:HE1	1:C:374:ASN:ND2	0.95	1.43
1:B:181:THR:HB	1:C:371:ARG:NH2	1.27	1.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1006/1129 (89%)	974 (97%)	31 (3%)	1 (0%)	48 68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	1008/1129 (89%)	977 (97%)	29 (3%)	2 (0%)	43	62
1	C	1008/1129 (89%)	982 (97%)	26 (3%)	0	100	100
2	H	229/231 (99%)	213 (93%)	16 (7%)	0	100	100
2	I	229/231 (99%)	213 (93%)	16 (7%)	0	100	100
2	P	229/231 (99%)	213 (93%)	16 (7%)	0	100	100
3	J	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
3	L	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
3	Q	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
4	E	222/224 (99%)	210 (95%)	12 (5%)	0	100	100
4	M	222/224 (99%)	210 (95%)	12 (5%)	0	100	100
4	R	222/224 (99%)	210 (95%)	12 (5%)	0	100	100
5	F	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
5	N	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
5	S	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
All	All	5656/6045 (94%)	5441 (96%)	212 (4%)	3 (0%)	49	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	THR
1	B	344	PRO
1	B	716	GLU

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	A	898/983 (91%)	889 (99%)	9 (1%)	68	83
1	B	898/983 (91%)	887 (99%)	11 (1%)	63	80
1	C	898/983 (91%)	889 (99%)	9 (1%)	68	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	204/204 (100%)	204 (100%)	0	100	100
2	I	204/204 (100%)	204 (100%)	0	100	100
2	P	204/204 (100%)	204 (100%)	0	100	100
3	J	186/186 (100%)	186 (100%)	0	100	100
3	L	186/186 (100%)	186 (100%)	0	100	100
3	Q	186/186 (100%)	186 (100%)	0	100	100
4	E	187/187 (100%)	187 (100%)	0	100	100
4	M	187/187 (100%)	187 (100%)	0	100	100
4	R	187/187 (100%)	187 (100%)	0	100	100
5	F	189/189 (100%)	189 (100%)	0	100	100
5	N	189/189 (100%)	189 (100%)	0	100	100
5	S	189/189 (100%)	189 (100%)	0	100	100
All	All	4992/5247 (95%)	4963 (99%)	29 (1%)	76	89

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	543	LYS
1	C	713	LEU
1	B	546	ASN
1	C	347	THR
1	B	545	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	135	ASN
1	C	921	ASN
1	C	253	GLN
1	C	431	ASN
1	C	1006	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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	B	1201	1	14,14,15	0.23	0	17,19,21	0.45	0
6	NAG	C	1201	1	14,14,15	0.23	0	17,19,21	0.45	0
6	NAG	A	1201	1	14,14,15	0.23	0	17,19,21	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1201	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1201	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1201	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1201	NAG	C4-C5-C6-O6
6	C	1201	NAG	C4-C5-C6-O6
6	A	1201	NAG	O5-C5-C6-O6
6	B	1201	NAG	O5-C5-C6-O6
6	C	1201	NAG	O5-C5-C6-O6

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	4
1	B	3
1	C	2

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	43:SER	C	44:TYR	N	10.12
1	B	43:SER	C	44:TYR	N	10.12
1	C	43:SER	C	44:TYR	N	10.12
1	A	330:SER	C	331:ASN	N	2.69
1	A	605:SER	C	606:PHE	N	2.52

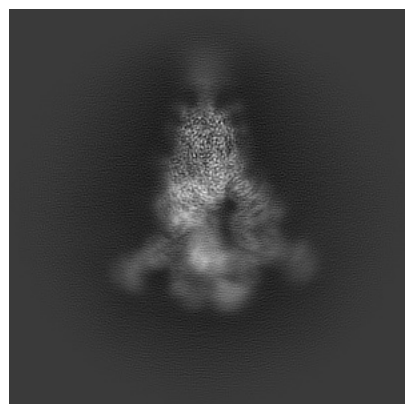
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34940. These allow visual inspection of the internal detail of the map and identification of artifacts.

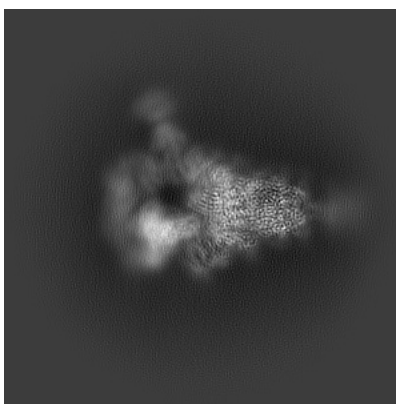
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

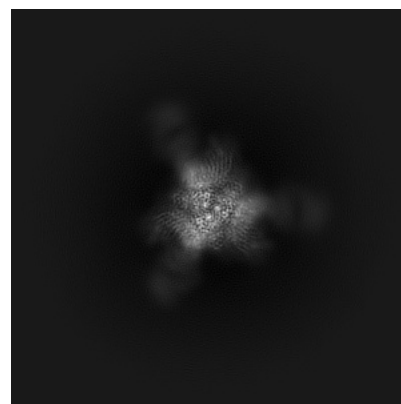
6.1.1 Primary map



X

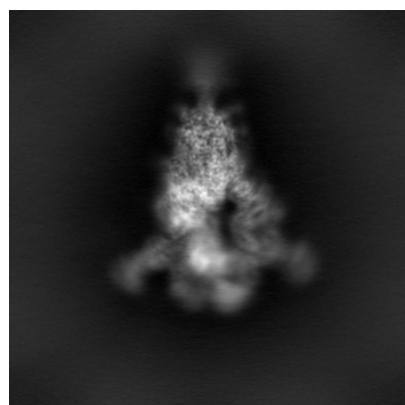


Y

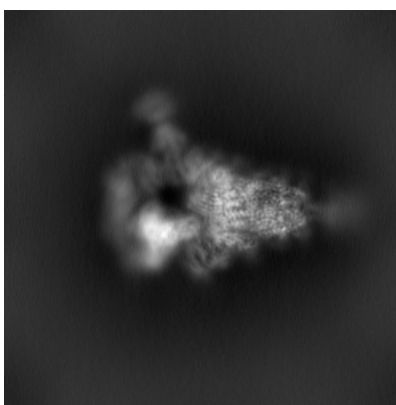


Z

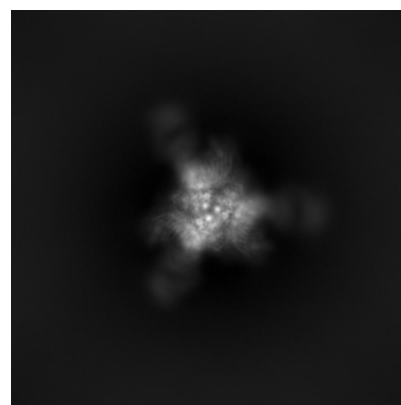
6.1.2 Raw map



X



Y

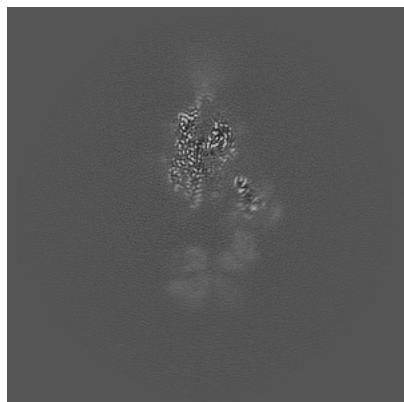


Z

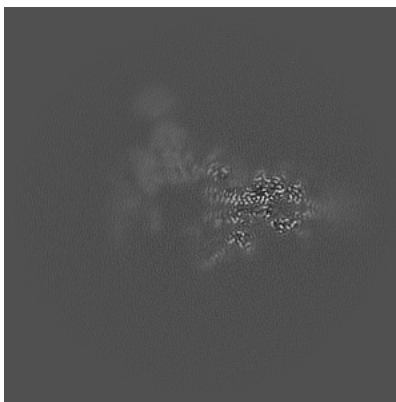
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

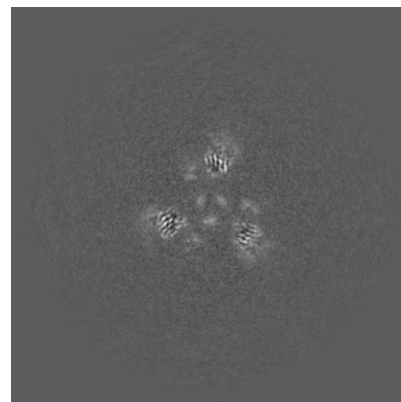
6.2.1 Primary map



X Index: 256

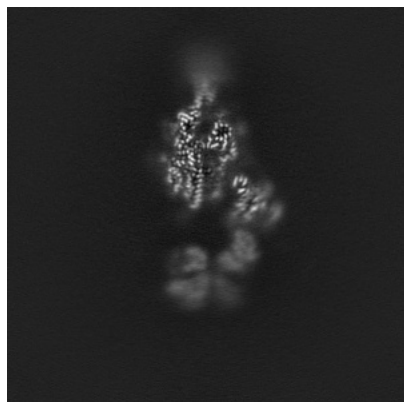


Y Index: 256

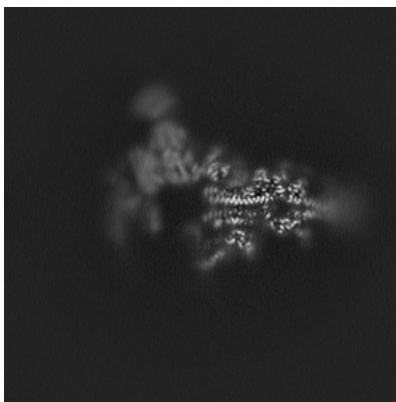


Z Index: 256

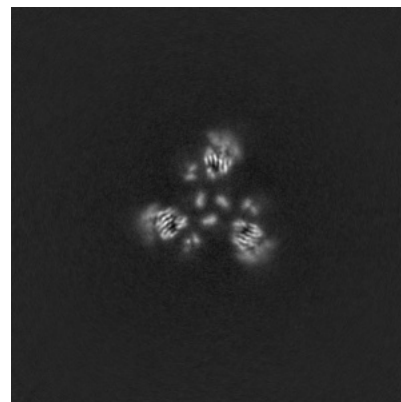
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

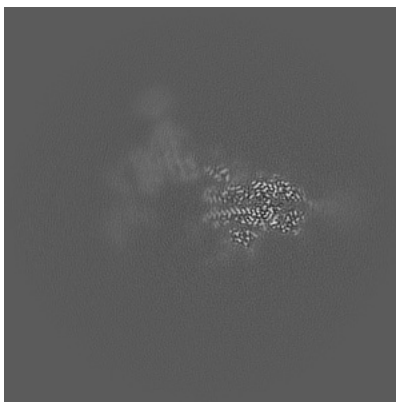
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

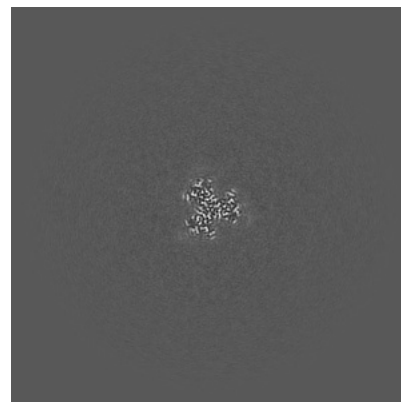
6.3.1 Primary map



X Index: 248

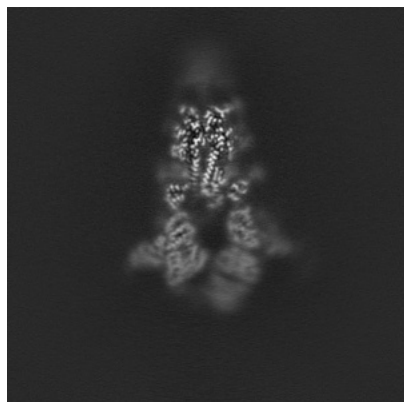


Y Index: 262

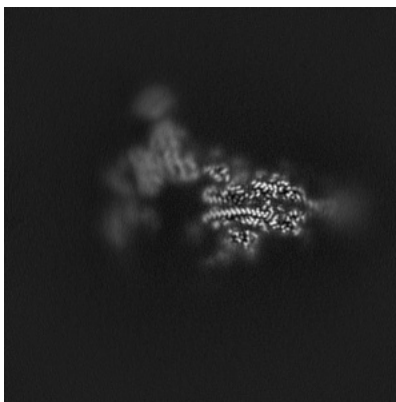


Z Index: 335

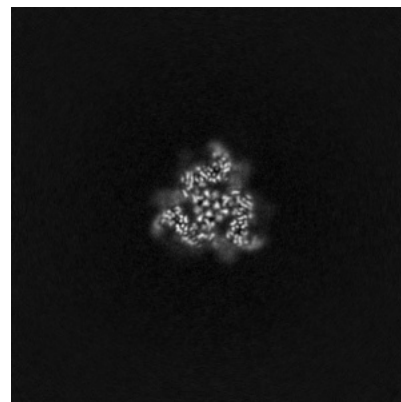
6.3.2 Raw map



X Index: 237



Y Index: 262

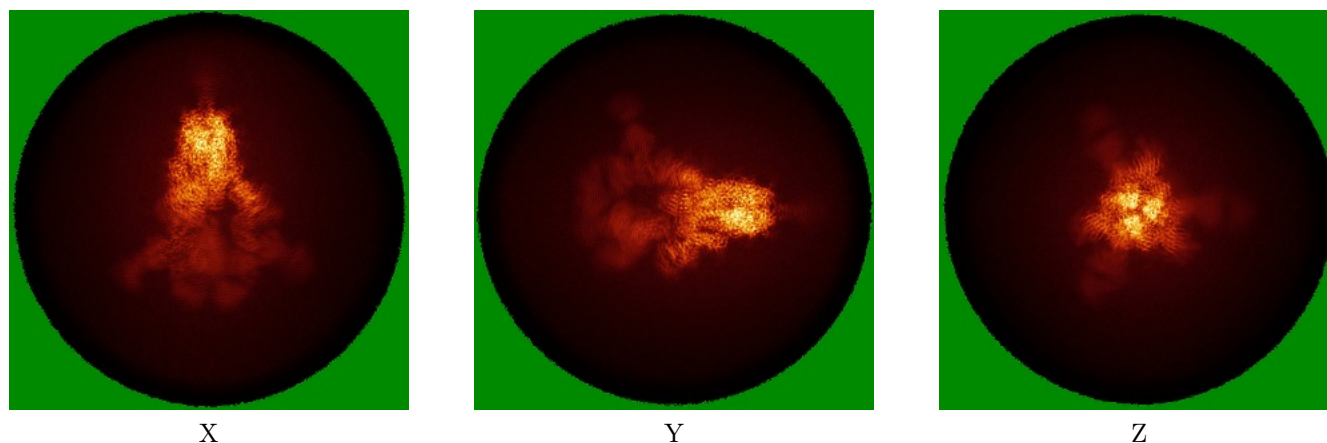


Z Index: 284

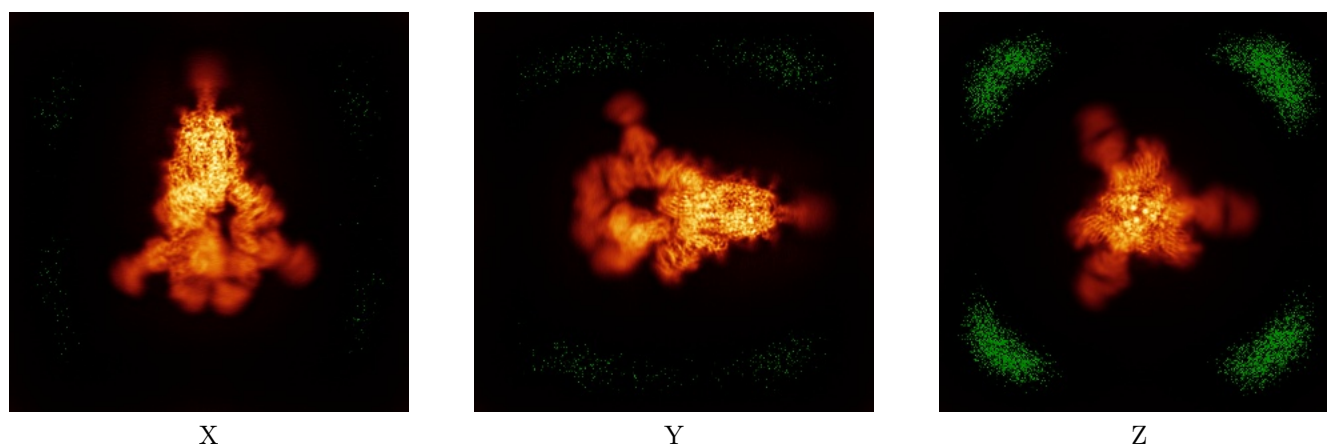
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

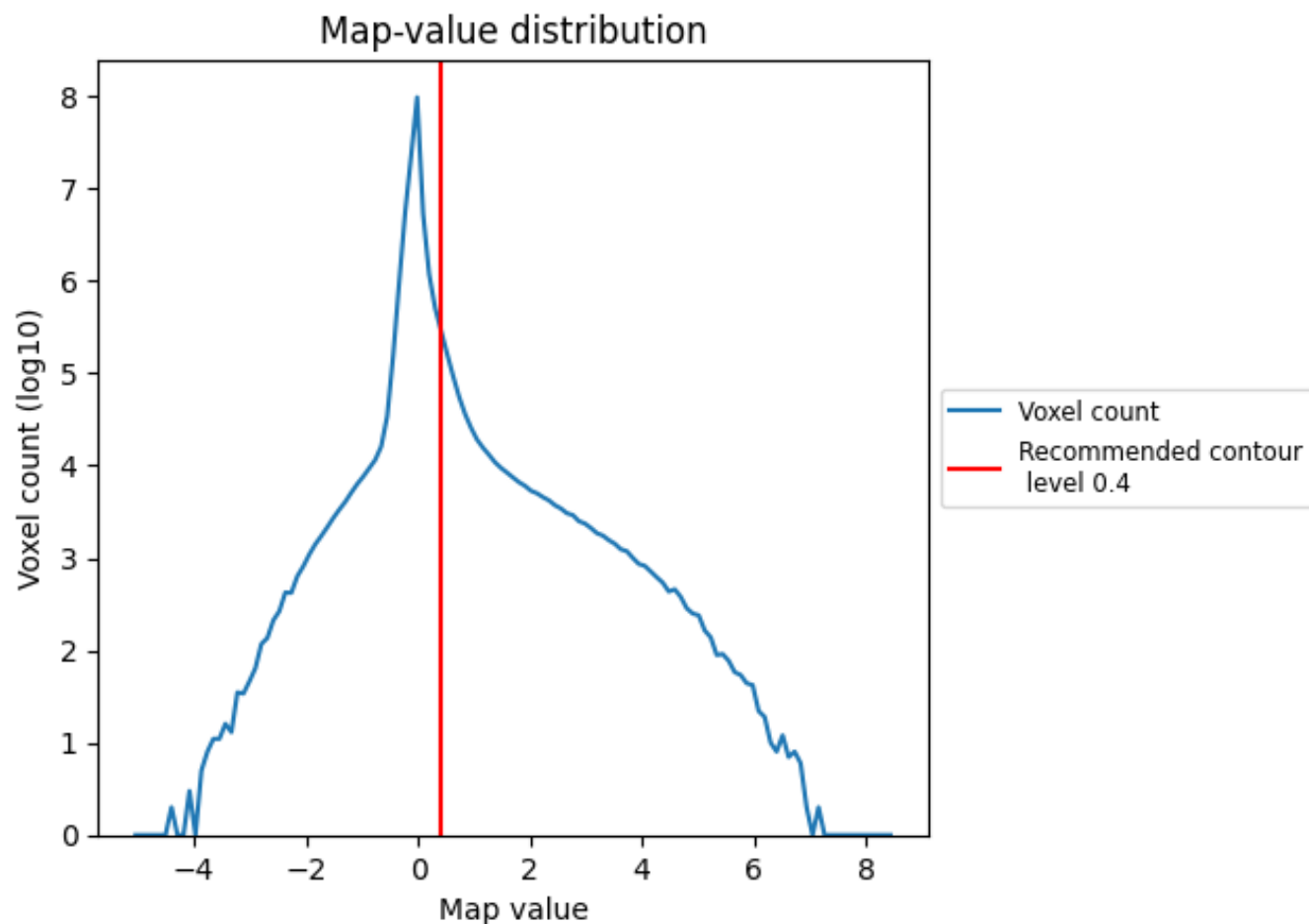
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

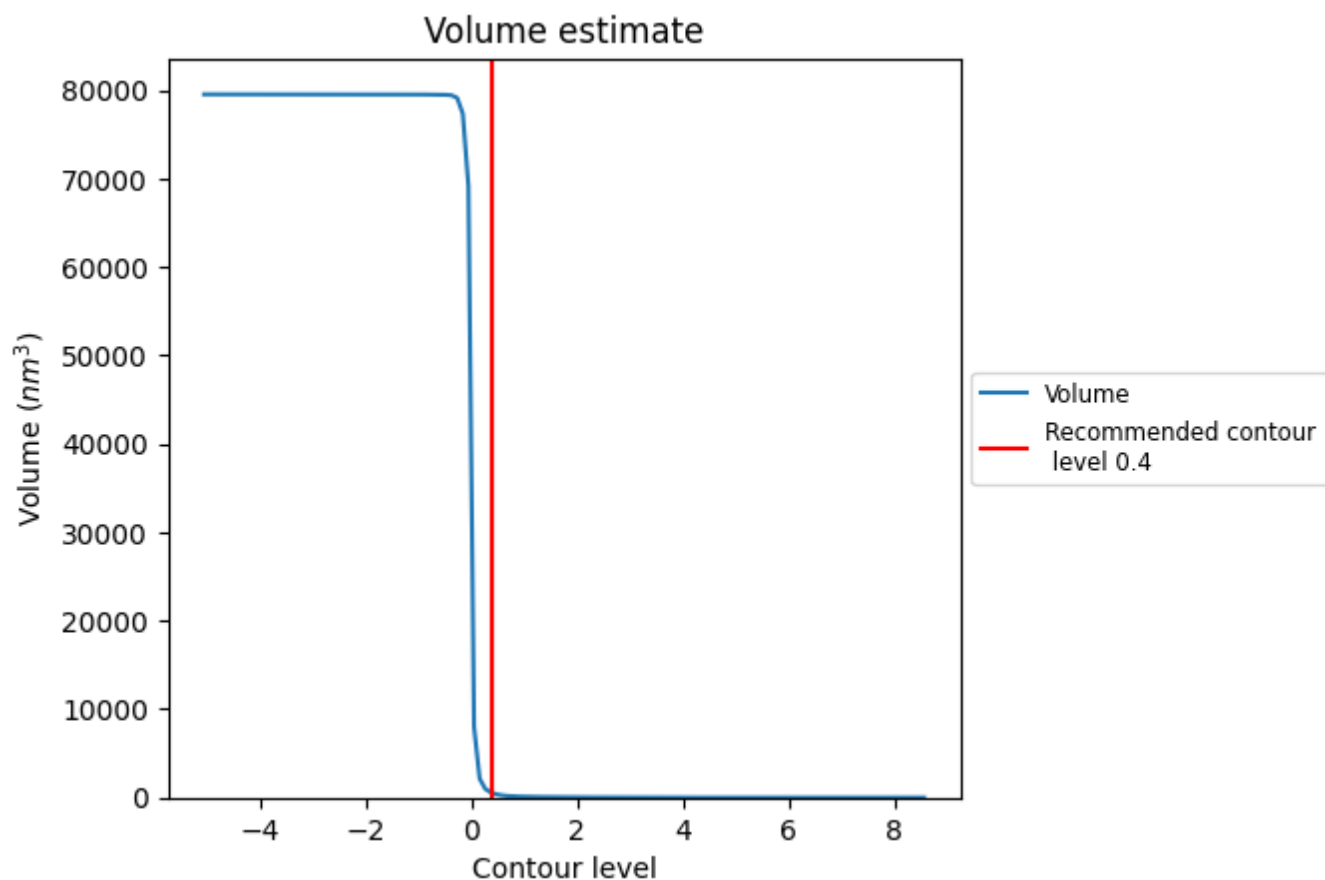
This section contains the results of statistical analysis of the map.

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.

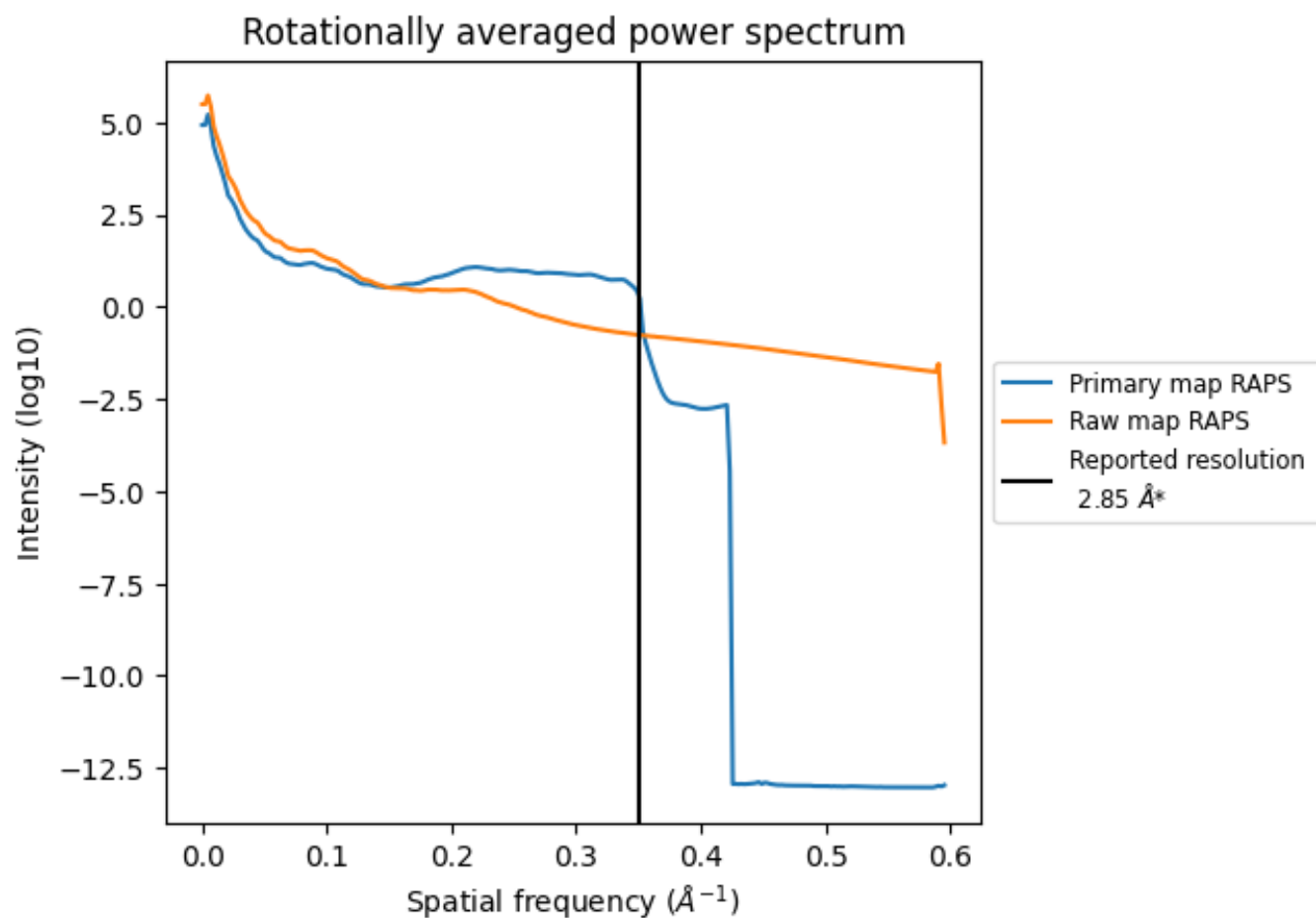
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 523 nm^3 ; this corresponds to an approximate mass of 473 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 ⓘ

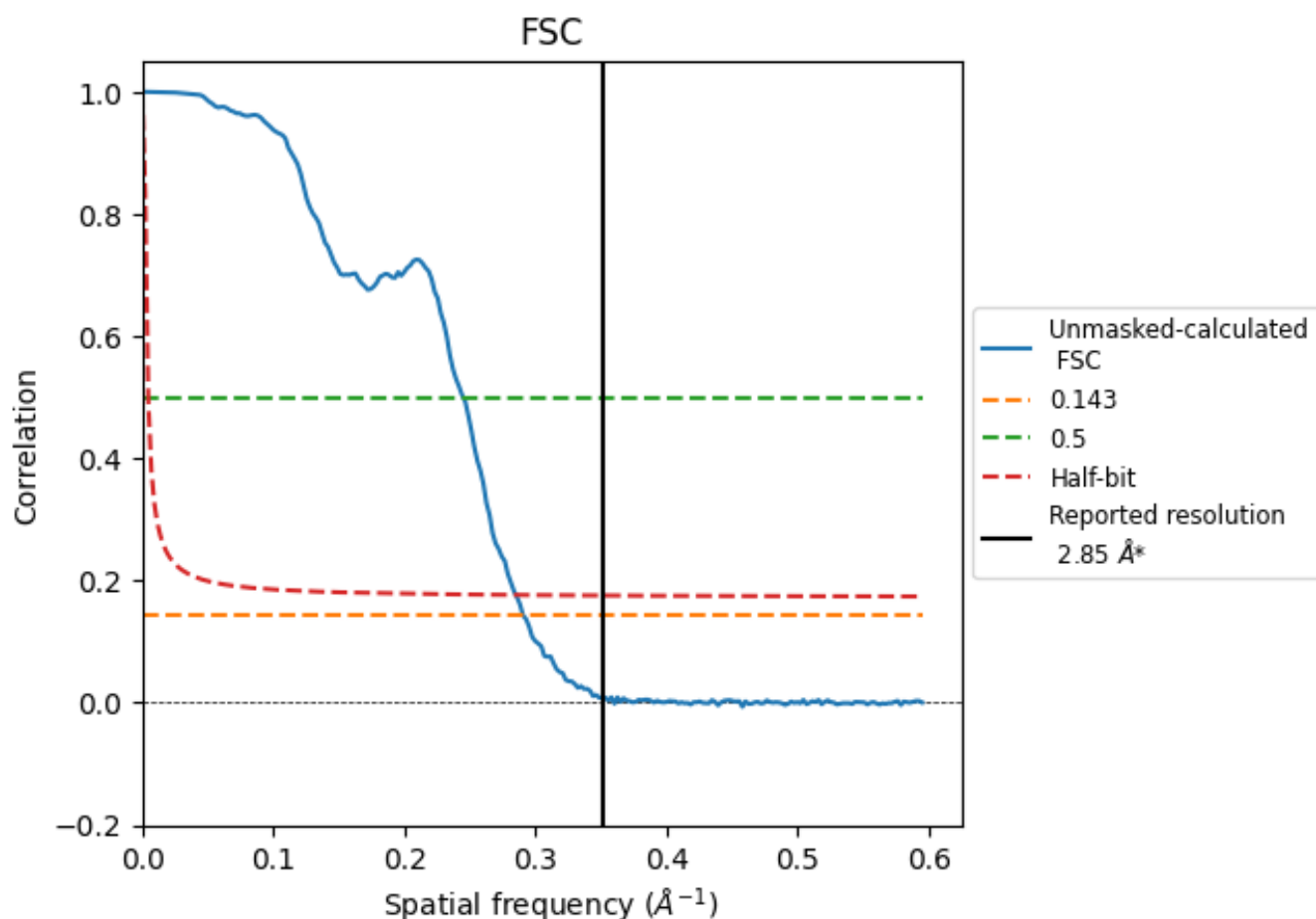


*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

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 0.351 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.44	4.08	3.51

*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 3.44 differs from the reported value 2.85 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34940 and PDB model 8HPQ. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

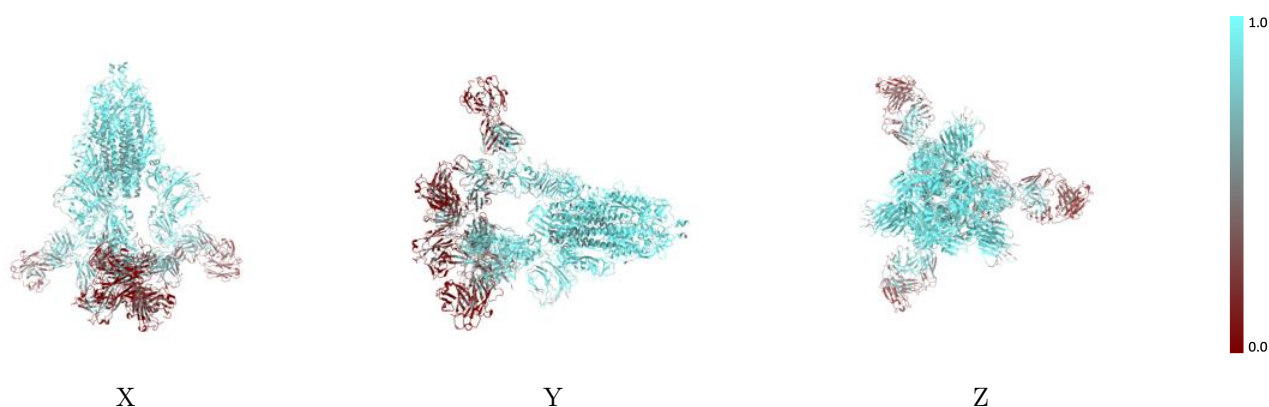
This section was not generated.

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



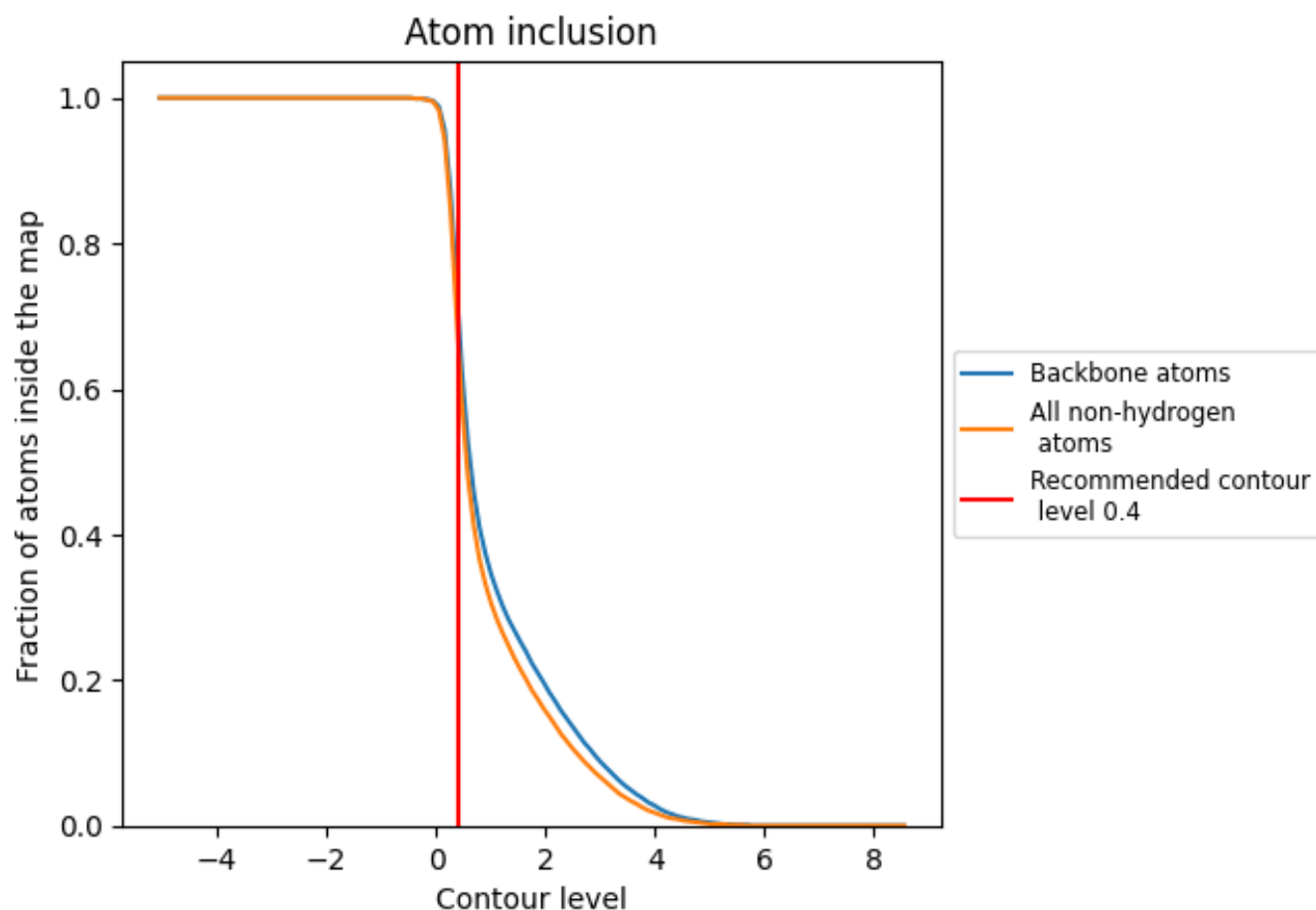
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 67% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6690	 0.2430
A	 0.8980	 0.4180
B	 0.8760	 0.3850
C	 0.8930	 0.4050
E	 0.3620	 0.0280
F	 0.3610	 0.0290
H	 0.5200	 0.0790
I	 0.4060	 0.0520
J	 0.2960	 0.0350
L	 0.4460	 0.0710
M	 0.5920	 0.0990
N	 0.5160	 0.0910
P	 0.3370	 0.0300
Q	 0.2590	 0.0240
R	 0.4060	 0.0400
S	 0.3580	 0.0360

