



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:00 AM UTC

PDB ID : 9J34 / pdb_00009j34
EMDB ID : EMD-61105
Title : Cryo-EM structure of Arabidopsis CNGC1
Authors : Wang, J.P.; Zhang, P.; Zhang, X.
Deposited on : 2024-08-07
Resolution : 2.51 Å(reported)

This is a Full wwPDB EM Validation 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:

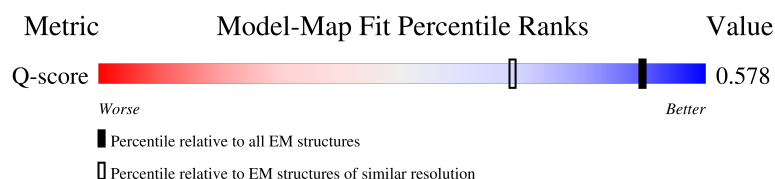
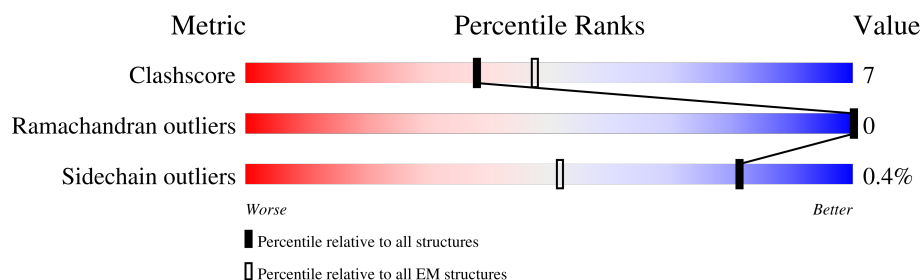
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.51 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	7159 (2.01 - 3.01)

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	716	 5% 57% 12% 30%
1	B	716	 5% 56% 13% 30%
1	C	716	 5% 57% 11% 30%
1	D	716	 5% 58% 11% 30%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16427 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 Cyclic nucleotide-gated ion channel 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	502	Total	C	N	O	S	0	0
			4104	2675	678	725	26		
1	A	502	Total	C	N	O	S	0	0
			4104	2675	678	725	26		
1	B	502	Total	C	N	O	S	0	0
			4104	2675	678	725	26		
1	C	502	Total	C	N	O	S	0	0
			4104	2675	678	725	26		

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	3	Total	Ca	0
			3	3	

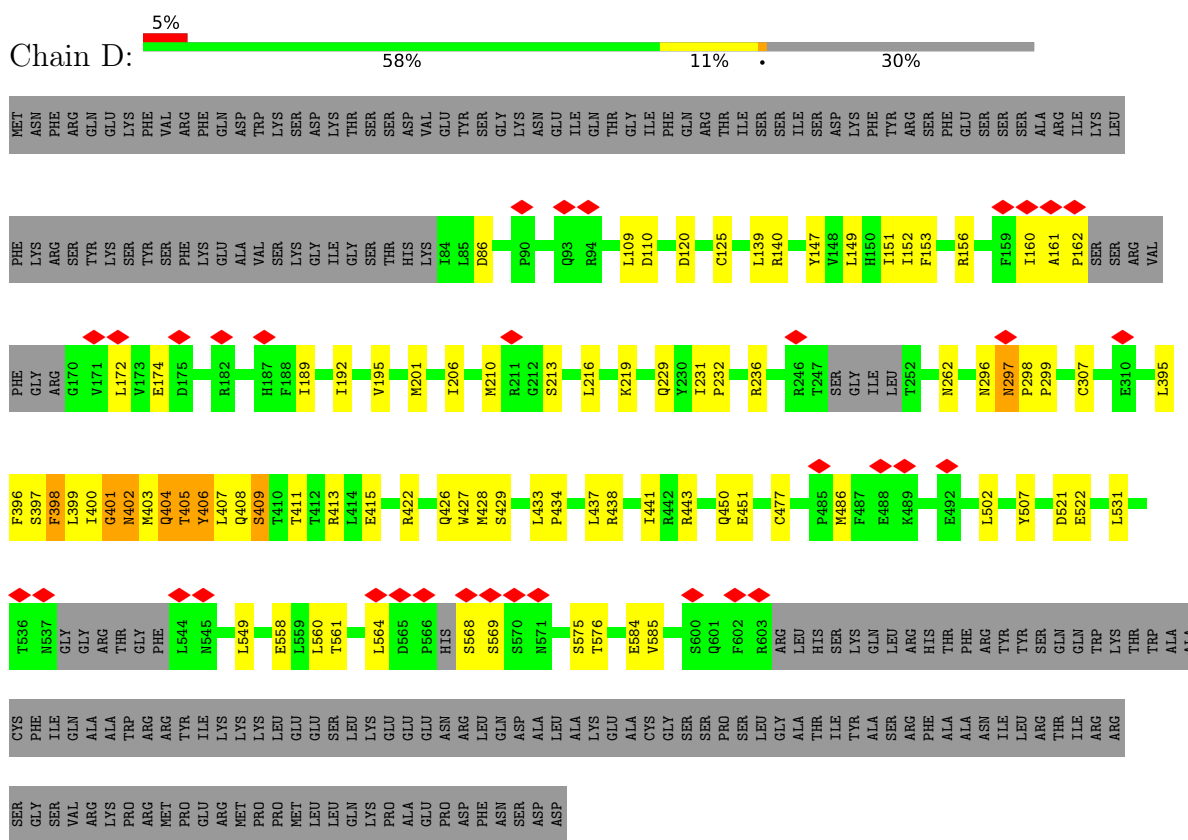
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	D	2	Total	O	0
			2	2	
3	A	2	Total	O	0
			2	2	
3	B	2	Total	O	0
			2	2	
3	C	2	Total	O	0
			2	2	

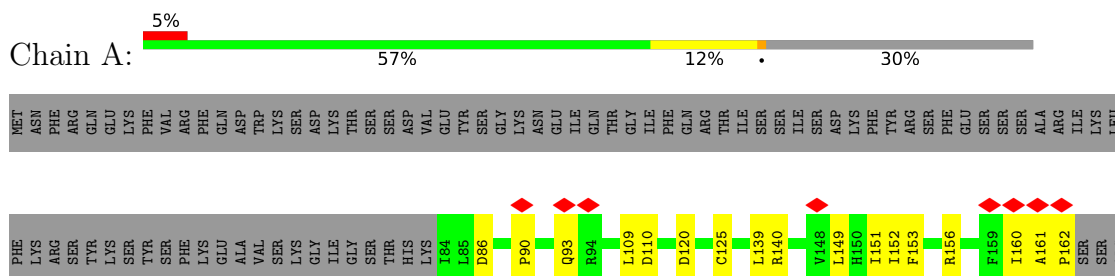
3 Residue-property plots

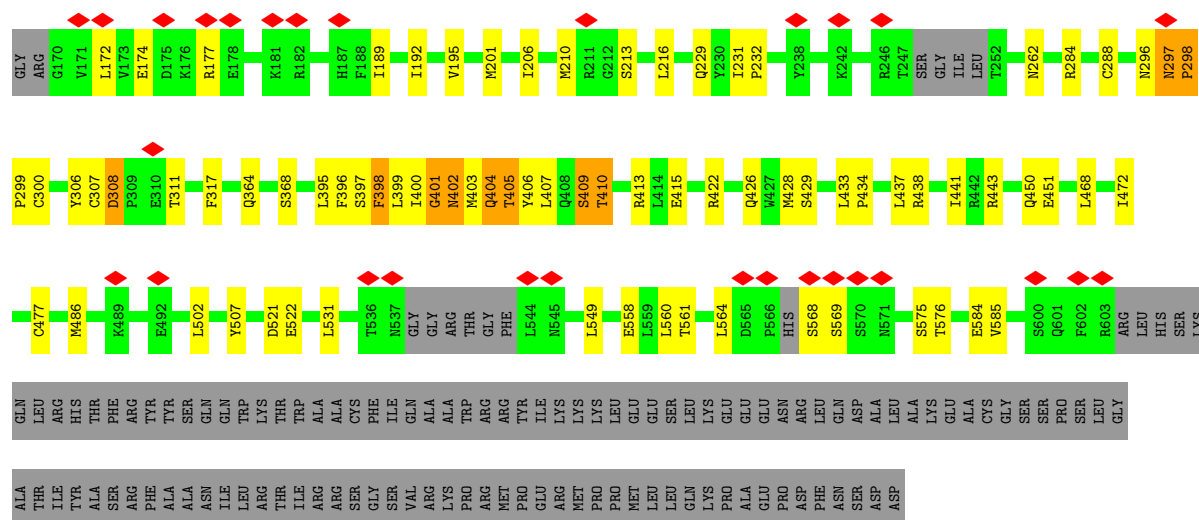
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Cyclic nucleotide-gated ion channel 1

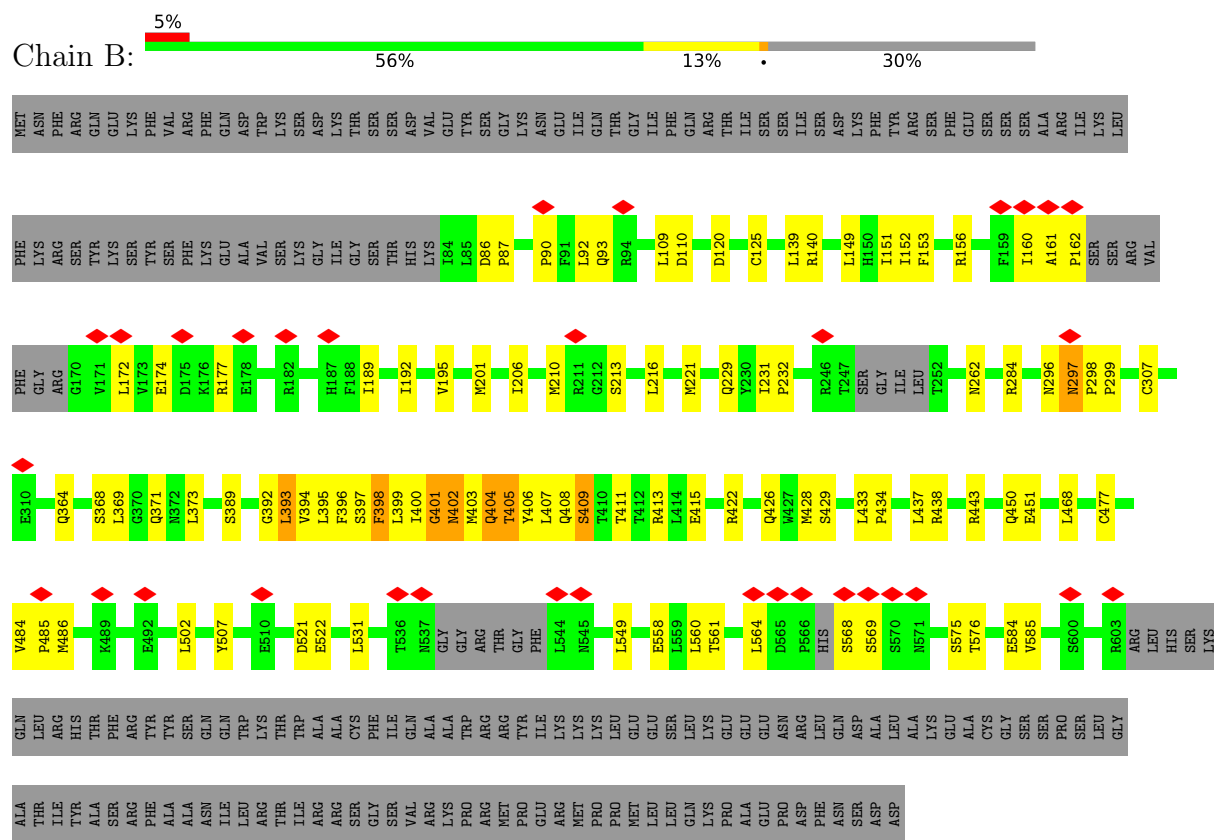


• Molecule 1: Cyclic nucleotide-gated ion channel 1

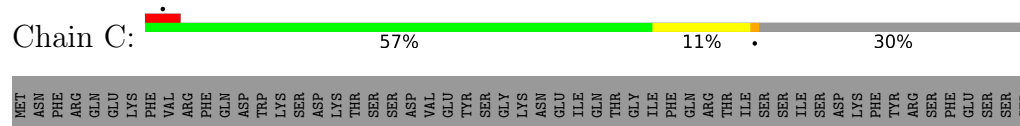




• Molecule 1: Cyclic nucleotide-gated ion channel 1



• Molecule 1: Cyclic nucleotide-gated ion channel 1



ILE	LEU	ARG	THR	ILE	ARG	ALA	ARG	CYS	PHE	GLY	SER	VAL	ARG	LYS	PRO	ARG	MET	PRO	GLU	MET	LEU	LEU	LEU	GLN	LYS	ALA	GLU	GLU	PRO	PRO	ASP	PHE	ASN	ASN	SER	ASP	ASP	ASP													
E522	L531	T536	N537	GLY	GLY	ARG	THR	GLY	PHE	L544	N545	L549	E558	L559	T561	L564	D565	P566	HIS	S568	S569	S570	N571	S575	T576	E584	V585	D593	K596	S600	R603	ARG	HIS	SER	LYS	GLN	LEU	ALA	THR	ILE	TYR	ALA	ALA	ASN							
L395	F396	F397	F398	L399	I400	G401	M402	M403	Q404	T405	Y406	L407	Q408	S409	T410	T411	T412	R413	L414	E415	E416	M417	R418	V419	A424	E425	Q426	W427	M428	S429	L433	P434	L437	R438	R443	Q450	E451	C477	P485	M486	K489	E492	L502	Y507	E510	D521					
PHE	LYS	ARG	SER	TYR	LYS	SER	TYR	SER	PHE	LYS	GLU	ALA	VAL	SER	LYS	GLY	ILE	GLY	SER	THR	HIS	LYS	LYS	I84	L85	D86	P87	P90	F91	L92	Q93	R94	L109	D110	D120	C125	L139	R140	L149	H150	I151	I152	F153	R156	F159	I160	A161	P162	SER	ARG	VAL
PHE	GLY	ARG	G170	V171	L172	V173	E174	D175	K176	R177	I189	I192	V195	M201	I206	M210	R211	Q229	Y230	I231	P232	R246	T247	SER	GLY	ILE	LEU	T252	N262	R284	W289	N296	N297	P298	P299	L304	L305	Y306	C307	E310	T311	Q371	V394								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	594717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	7.452	Depositor
Minimum map value	-5.423	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.43	Depositor
Map size (Å)	335.52, 335.52, 335.52	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.87	38/4202 (0.9%)	0.87	15/5689 (0.3%)
1	B	0.83	37/4202 (0.9%)	0.82	15/5689 (0.3%)
1	C	0.86	39/4202 (0.9%)	0.77	12/5689 (0.2%)
1	D	0.75	29/4202 (0.7%)	0.78	14/5689 (0.2%)
All	All	0.83	143/16808 (0.9%)	0.81	56/22756 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

All (143) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	ASP	C-N	21.52	1.59	1.33
1	C	304	LEU	C-N	14.60	1.54	1.33
1	B	404	GLN	N-CA	-10.71	1.31	1.46
1	C	424	ALA	C-N	9.75	1.46	1.33
1	B	404	GLN	CA-CB	-9.28	1.37	1.53
1	C	410	THR	C-N	9.24	1.49	1.34
1	B	396	PHE	N-CA	-9.21	1.34	1.46
1	C	396	PHE	N-CA	-9.21	1.34	1.46
1	A	404	GLN	N-CA	-8.95	1.34	1.46
1	B	393	LEU	C-O	-8.92	1.13	1.24
1	D	399	LEU	CA-C	-8.69	1.41	1.52
1	B	399	LEU	CA-C	-8.69	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	399	LEU	CA-C	-8.65	1.41	1.52
1	D	404	GLN	N-CA	-8.63	1.34	1.46
1	C	399	LEU	CA-C	-8.52	1.41	1.52
1	B	394	VAL	C-O	-8.32	1.14	1.24
1	D	401	GLY	C-O	-8.31	1.14	1.23
1	A	403	MET	CA-C	-8.29	1.41	1.52
1	B	401	GLY	C-O	-8.27	1.14	1.23
1	D	403	MET	CA-C	-8.25	1.42	1.52
1	B	395	LEU	CA-C	-8.22	1.41	1.52
1	C	401	GLY	C-O	-8.17	1.14	1.23
1	A	401	GLY	C-O	-8.15	1.14	1.23
1	A	405	THR	N-CA	-7.81	1.36	1.46
1	B	405	THR	C-O	-7.73	1.15	1.24
1	A	306	TYR	CA-C	-7.72	1.43	1.52
1	C	409	SER	CA-C	-7.71	1.42	1.52
1	C	404	GLN	N-CA	-7.64	1.36	1.46
1	C	306	TYR	CA-C	-7.58	1.43	1.52
1	B	409	SER	CA-C	-7.57	1.42	1.52
1	C	405	THR	C-O	-7.53	1.15	1.24
1	A	396	PHE	N-CA	-7.50	1.36	1.46
1	A	409	SER	CA-C	-7.44	1.42	1.52
1	C	395	LEU	CA-C	-7.35	1.42	1.52
1	C	407	LEU	CA-C	-7.22	1.43	1.52
1	C	399	LEU	CA-CB	-7.21	1.42	1.53
1	B	399	LEU	CA-CB	-7.18	1.42	1.53
1	C	405	THR	C-N	7.15	1.43	1.33
1	D	405	THR	C-O	-7.13	1.15	1.24
1	D	399	LEU	CA-CB	-7.12	1.42	1.53
1	D	405	THR	N-CA	-7.10	1.37	1.46
1	A	399	LEU	CA-CB	-7.09	1.42	1.53
1	D	396	PHE	N-CA	-7.08	1.37	1.46
1	A	401	GLY	CA-C	-7.08	1.44	1.52
1	B	403	MET	C-N	-6.96	1.23	1.33
1	B	407	LEU	CA-C	-6.95	1.43	1.52
1	D	395	LEU	C-N	-6.94	1.24	1.34
1	D	401	GLY	CA-C	-6.92	1.44	1.52
1	C	403	MET	CA-C	-6.92	1.44	1.52
1	C	401	GLY	CA-C	-6.91	1.44	1.52
1	D	407	LEU	CA-C	-6.91	1.43	1.52
1	B	399	LEU	C-N	-6.91	1.25	1.33
1	B	401	GLY	CA-C	-6.89	1.44	1.52
1	C	419	VAL	C-N	6.89	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	407	LEU	CA-C	-6.87	1.43	1.52
1	A	395	LEU	C-N	-6.85	1.23	1.33
1	D	399	LEU	C-N	-6.82	1.25	1.33
1	A	399	LEU	C-N	-6.75	1.25	1.33
1	C	395	LEU	C-N	-6.74	1.24	1.34
1	C	399	LEU	C-N	-6.74	1.25	1.33
1	C	311	THR	C-N	6.71	1.43	1.33
1	A	399	LEU	C-O	-6.71	1.16	1.24
1	A	410	THR	N-CA	-6.70	1.38	1.46
1	B	395	LEU	C-N	-6.70	1.24	1.34
1	B	405	THR	N-CA	-6.67	1.38	1.46
1	A	404	GLN	CA-CB	-6.67	1.41	1.53
1	B	399	LEU	C-O	-6.66	1.16	1.24
1	C	399	LEU	C-O	-6.65	1.16	1.24
1	D	399	LEU	C-O	-6.61	1.16	1.24
1	A	288	CYS	C-N	6.60	1.43	1.33
1	B	403	MET	C-O	-6.47	1.14	1.23
1	A	398	PHE	C-O	-6.45	1.16	1.24
1	D	402	ASN	C-N	-6.44	1.24	1.33
1	A	402	ASN	C-N	-6.44	1.25	1.33
1	B	396	PHE	CA-C	-6.42	1.44	1.52
1	B	402	ASN	C-N	-6.41	1.24	1.33
1	D	398	PHE	C-O	-6.37	1.16	1.24
1	B	398	PHE	C-O	-6.37	1.16	1.24
1	C	396	PHE	CA-C	-6.37	1.44	1.52
1	D	404	GLN	CA-CB	-6.35	1.42	1.53
1	C	398	PHE	C-O	-6.32	1.16	1.24
1	D	409	SER	CA-C	-6.24	1.44	1.52
1	A	405	THR	C-O	-6.22	1.16	1.24
1	C	402	ASN	C-N	-6.21	1.25	1.33
1	A	403	MET	C-O	-6.17	1.15	1.23
1	D	402	ASN	C-O	-6.16	1.16	1.24
1	B	402	ASN	C-O	-6.15	1.16	1.24
1	D	396	PHE	CA-C	-6.13	1.44	1.52
1	B	393	LEU	CA-C	-6.09	1.45	1.52
1	D	397	SER	C-O	-6.07	1.16	1.24
1	A	306	TYR	C-O	-6.06	1.17	1.24
1	B	404	GLN	C-N	-6.05	1.25	1.33
1	A	397	SER	C-O	-6.04	1.17	1.24
1	C	397	SER	C-O	-6.04	1.17	1.24
1	A	402	ASN	C-O	-6.02	1.16	1.24
1	B	397	SER	C-O	-5.99	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	410	THR	N-CA	-5.95	1.38	1.46
1	D	397	SER	N-CA	-5.94	1.39	1.46
1	B	403	MET	CA-C	-5.88	1.44	1.52
1	B	397	SER	N-CA	-5.86	1.39	1.46
1	C	397	SER	N-CA	-5.84	1.39	1.46
1	A	396	PHE	CA-C	-5.81	1.44	1.52
1	D	400	ILE	N-CA	-5.78	1.38	1.46
1	A	403	MET	C-N	-5.77	1.25	1.33
1	C	411	THR	C-O	-5.75	1.16	1.24
1	A	397	SER	N-CA	-5.73	1.39	1.46
1	A	400	ILE	N-CA	-5.68	1.39	1.46
1	B	400	ILE	N-CA	-5.68	1.39	1.46
1	D	403	MET	C-O	-5.67	1.15	1.23
1	C	403	MET	C-O	-5.62	1.15	1.23
1	B	399	LEU	N-CA	-5.61	1.39	1.46
1	C	400	ILE	N-CA	-5.61	1.39	1.46
1	C	409	SER	N-CA	-5.59	1.39	1.46
1	C	306	TYR	C-O	-5.59	1.17	1.24
1	D	399	LEU	N-CA	-5.59	1.39	1.46
1	A	399	LEU	N-CA	-5.56	1.39	1.46
1	A	413	ARG	C-O	-5.56	1.17	1.24
1	C	411	THR	N-CA	-5.54	1.39	1.46
1	C	405	THR	N-CA	-5.52	1.39	1.46
1	B	409	SER	N-CA	-5.48	1.38	1.46
1	C	402	ASN	C-O	-5.46	1.16	1.24
1	A	404	GLN	C-O	-5.46	1.16	1.24
1	C	399	LEU	N-CA	-5.45	1.39	1.46
1	D	404	GLN	C-O	-5.40	1.17	1.24
1	D	403	MET	C-N	-5.39	1.25	1.33
1	B	413	ARG	C-O	-5.31	1.17	1.24
1	B	404	GLN	C-O	-5.24	1.17	1.24
1	A	409	SER	N-CA	-5.23	1.39	1.46
1	D	407	LEU	C-O	-5.20	1.17	1.24
1	C	413	ARG	C-O	-5.19	1.17	1.24
1	A	407	LEU	C-O	-5.18	1.17	1.24
1	B	407	LEU	C-O	-5.18	1.17	1.24
1	C	407	LEU	C-O	-5.17	1.17	1.24
1	D	406	TYR	CA-CB	-5.12	1.45	1.53
1	A	398	PHE	CA-CB	-5.12	1.45	1.53
1	A	409	SER	C-N	-5.12	1.27	1.33
1	B	398	PHE	CA-CB	-5.12	1.45	1.53
1	A	406	TYR	CA-CB	-5.11	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	392	GLY	C-N	-5.11	1.27	1.33
1	D	413	ARG	C-O	-5.09	1.17	1.24
1	A	406	TYR	N-CA	-5.04	1.40	1.46
1	C	408	GLN	N-CA	-5.02	1.39	1.46
1	B	402	ASN	CA-C	-5.00	1.45	1.52

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	311	THR	O-C-N	20.73	146.85	123.22
1	A	311	THR	CA-C-N	-15.67	101.37	123.00
1	A	311	THR	C-N-CA	-15.67	101.37	123.00
1	D	307	CYS	CA-C-N	13.07	142.22	121.83
1	D	307	CYS	C-N-CA	13.07	142.22	121.83
1	B	307	CYS	CA-C-N	13.07	142.22	121.83
1	B	307	CYS	C-N-CA	13.07	142.22	121.83
1	B	404	GLN	CA-CB-CG	-10.02	94.07	114.10
1	C	297	ASN	CA-C-N	-9.15	110.96	120.38
1	C	297	ASN	C-N-CA	-9.15	110.96	120.38
1	D	297	ASN	CA-C-N	-8.85	111.27	120.38
1	D	297	ASN	C-N-CA	-8.85	111.27	120.38
1	B	297	ASN	CA-C-N	-8.28	111.85	120.38
1	B	297	ASN	C-N-CA	-8.28	111.85	120.38
1	B	392	GLY	O-C-N	-7.86	113.72	122.28
1	C	399	LEU	N-CA-C	7.79	119.77	111.28
1	A	174	GLU	CA-CB-CG	7.75	129.61	114.10
1	D	174	GLU	CA-CB-CG	7.73	129.56	114.10
1	B	174	GLU	CA-CB-CG	7.71	129.51	114.10
1	C	174	GLU	CA-CB-CG	7.70	129.50	114.10
1	A	399	LEU	N-CA-C	7.70	119.67	111.28
1	C	395	LEU	N-CA-C	7.68	121.90	112.23
1	B	399	LEU	N-CA-C	7.67	119.64	111.28
1	C	297	ASN	N-CA-C	-7.67	92.86	109.81
1	C	394	VAL	O-C-N	-7.64	113.16	121.80
1	D	297	ASN	N-CA-C	-7.59	93.03	109.81
1	D	399	LEU	N-CA-C	7.58	119.54	111.28
1	B	297	ASN	N-CA-C	-7.48	93.28	109.81
1	A	298	PRO	N-CA-C	-7.23	101.88	110.70
1	A	405	THR	N-CA-C	-7.07	102.78	111.40
1	C	307	CYS	CA-CB-SG	6.92	130.32	114.40
1	A	404	GLN	CA-CB-CG	-6.63	100.84	114.10
1	B	395	LEU	N-CA-C	6.39	119.23	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	ASN	CA-C-N	-6.33	113.86	120.38
1	A	297	ASN	C-N-CA	-6.33	113.86	120.38
1	D	405	THR	N-CA-C	-6.25	103.78	111.40
1	D	411	THR	N-CA-C	6.19	120.10	111.56
1	B	392	GLY	CA-C-N	6.14	128.42	120.44
1	B	392	GLY	C-N-CA	6.14	128.42	120.44
1	A	297	ASN	N-CA-C	-6.07	96.39	109.81
1	B	411	THR	N-CA-C	6.05	119.90	111.56
1	D	174	GLU	CB-CG-CD	5.91	122.65	112.60
1	B	174	GLU	CB-CG-CD	5.91	122.65	112.60
1	C	174	GLU	CB-CG-CD	5.91	122.64	112.60
1	A	174	GLU	CB-CG-CD	5.89	122.62	112.60
1	D	396	PHE	N-CA-C	5.86	118.62	111.82
1	A	307	CYS	CA-CB-SG	5.83	127.81	114.40
1	C	413	ARG	N-CA-C	-5.81	105.45	112.54
1	C	404	GLN	N-CA-C	-5.51	106.52	113.18
1	C	426	GLN	CA-CB-CG	5.29	124.69	114.10
1	B	426	GLN	CA-CB-CG	5.29	124.67	114.10
1	A	426	GLN	CA-CB-CG	5.28	124.66	114.10
1	D	413	ARG	N-CA-C	-5.28	105.99	112.90
1	D	426	GLN	CA-CB-CG	5.27	124.64	114.10
1	D	404	GLN	CA-CB-CG	-5.23	103.64	114.10
1	A	396	PHE	N-CA-C	5.18	118.76	112.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	308	ASP	Mainchain
1	C	424	ALA	Mainchain

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	4104	0	4127	66	0
1	B	4104	0	4127	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4104	0	4127	66	0
1	D	4104	0	4127	58	0
2	A	3	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
All	All	16427	0	16508	244	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 7.

All (244) 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:A:160:ILE:CG2	1:A:172:LEU:HD23	1.47	1.45
1:D:160:ILE:CG2	1:D:172:LEU:HD23	1.47	1.44
1:B:160:ILE:CG2	1:B:172:LEU:HD23	1.47	1.44
1:C:160:ILE:CG2	1:C:172:LEU:HD23	1.47	1.42
1:A:160:ILE:CG2	1:A:172:LEU:CD2	2.22	1.18
1:B:160:ILE:CG2	1:B:172:LEU:CD2	2.22	1.17
1:C:160:ILE:CG2	1:C:172:LEU:CD2	2.22	1.17
1:D:160:ILE:CG2	1:D:172:LEU:CD2	2.22	1.16
1:A:161:ALA:HB1	1:A:162:PRO:HD2	1.35	1.06
1:C:161:ALA:HB1	1:C:162:PRO:HD2	1.35	1.05
1:B:161:ALA:HB1	1:B:162:PRO:HD2	1.35	1.04
1:C:160:ILE:HG22	1:C:172:LEU:CD2	1.87	1.03
1:D:161:ALA:HB1	1:D:162:PRO:HD2	1.35	1.03
1:D:160:ILE:HG22	1:D:172:LEU:CD2	1.87	1.01
1:A:160:ILE:HG22	1:A:172:LEU:CD2	1.87	1.01
1:B:160:ILE:HG22	1:B:172:LEU:CD2	1.87	0.98
1:A:86:ASP:HB3	1:A:172:LEU:HD13	1.45	0.97
1:C:86:ASP:HB3	1:C:172:LEU:HD13	1.45	0.96
1:D:86:ASP:HB3	1:D:172:LEU:HD13	1.46	0.95
1:B:86:ASP:HB3	1:B:172:LEU:HD13	1.46	0.95
1:C:160:ILE:HG23	1:C:172:LEU:CD2	1.96	0.94
1:A:160:ILE:HG23	1:A:172:LEU:CD2	1.96	0.94
1:B:160:ILE:HG23	1:B:172:LEU:CD2	1.96	0.93
1:B:160:ILE:HG22	1:B:172:LEU:HD23	0.93	0.92
1:C:160:ILE:HG22	1:C:172:LEU:HD23	0.93	0.92
1:B:160:ILE:HG23	1:B:172:LEU:HD23	1.52	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ILE:HG22	1:A:172:LEU:HD23	0.93	0.91
1:D:160:ILE:HG22	1:D:172:LEU:HD23	0.93	0.91
1:D:160:ILE:HG23	1:D:172:LEU:HD23	1.52	0.90
1:D:160:ILE:HG23	1:D:172:LEU:CD2	1.96	0.90
1:A:160:ILE:HG23	1:A:172:LEU:HD23	1.52	0.90
1:C:160:ILE:HG23	1:C:172:LEU:HD23	1.52	0.88
1:B:369:LEU:HD13	1:B:393:LEU:HD23	1.60	0.82
1:C:262:ASN:HD22	1:C:402:ASN:HD22	1.27	0.82
1:B:86:ASP:CB	1:B:172:LEU:HD13	2.10	0.81
1:A:86:ASP:CB	1:A:172:LEU:HD13	2.10	0.81
1:C:86:ASP:CB	1:C:172:LEU:HD13	2.10	0.80
1:D:86:ASP:CB	1:D:172:LEU:HD13	2.10	0.80
1:D:262:ASN:HD22	1:D:402:ASN:HD22	1.27	0.80
1:D:558:GLU:OE2	1:D:576:THR:HG23	1.83	0.78
1:A:558:GLU:OE2	1:A:576:THR:HG23	1.83	0.78
1:C:558:GLU:OE2	1:C:576:THR:HG23	1.83	0.78
1:A:262:ASN:HD22	1:A:402:ASN:HD22	1.30	0.78
1:B:262:ASN:HD22	1:B:402:ASN:HD22	1.29	0.78
1:B:404:GLN:NE2	1:C:404:GLN:HG2	1.98	0.78
1:B:558:GLU:OE2	1:B:576:THR:HG23	1.83	0.77
1:D:560:LEU:HD12	1:D:561:THR:N	2.00	0.77
1:C:560:LEU:HD12	1:C:561:THR:N	2.00	0.77
1:B:161:ALA:HB1	1:B:162:PRO:CD	2.14	0.77
1:A:560:LEU:HD12	1:A:561:THR:N	2.00	0.77
1:B:560:LEU:HD12	1:B:561:THR:N	2.00	0.77
1:C:161:ALA:HB1	1:C:162:PRO:CD	2.14	0.77
1:A:161:ALA:HB1	1:A:162:PRO:CD	2.14	0.74
1:B:404:GLN:HE22	1:C:404:GLN:HG2	1.54	0.73
1:B:404:GLN:O	1:B:404:GLN:HG2	1.88	0.73
1:D:161:ALA:HB1	1:D:162:PRO:CD	2.14	0.72
1:A:297:ASN:HB2	1:A:298:PRO:HD3	1.73	0.70
1:A:422:ARG:NH2	1:B:409:SER:O	2.24	0.70
1:B:422:ARG:NH2	1:C:409:SER:O	2.25	0.69
1:D:86:ASP:HB3	1:D:172:LEU:CD1	2.24	0.68
1:A:86:ASP:HB3	1:A:172:LEU:CD1	2.23	0.67
1:D:262:ASN:HD22	1:D:402:ASN:ND2	1.93	0.66
1:C:401:GLY:O	1:C:405:THR:HG23	1.96	0.66
1:D:262:ASN:ND2	1:D:402:ASN:HD22	1.94	0.66
1:B:297:ASN:HB2	1:B:298:PRO:HD3	1.78	0.65
1:A:300:CYS:HB2	1:A:317:PHE:CZ	2.32	0.65
1:D:86:ASP:CB	1:D:172:LEU:CD1	2.76	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ASP:CB	1:A:172:LEU:CD1	2.76	0.64
1:B:86:ASP:CB	1:B:172:LEU:CD1	2.76	0.64
1:C:86:ASP:CB	1:C:172:LEU:CD1	2.76	0.64
1:B:401:GLY:O	1:B:405:THR:HG23	1.99	0.63
1:C:86:ASP:HB3	1:C:172:LEU:CD1	2.23	0.63
1:C:297:ASN:HB2	1:C:298:PRO:HD3	1.78	0.63
1:D:409:SER:HA	1:C:415:GLU:OE2	1.98	0.62
1:B:86:ASP:HB3	1:B:172:LEU:CD1	2.24	0.62
1:A:262:ASN:HD21	1:A:398:PHE:HB3	1.65	0.61
1:B:262:ASN:HD22	1:B:402:ASN:ND2	1.98	0.61
1:C:262:ASN:HD22	1:C:402:ASN:ND2	1.97	0.61
1:D:401:GLY:O	1:D:405:THR:HG23	2.00	0.61
1:A:262:ASN:HD22	1:A:402:ASN:ND2	1.99	0.61
1:A:401:GLY:O	1:A:405:THR:HG23	2.00	0.61
1:D:297:ASN:HB2	1:D:298:PRO:HD3	1.82	0.61
1:C:262:ASN:HD21	1:C:398:PHE:HB3	1.66	0.60
1:B:262:ASN:HD21	1:B:398:PHE:HB3	1.66	0.60
1:B:369:LEU:HD13	1:B:393:LEU:CD2	2.31	0.60
1:A:415:GLU:OE2	1:B:409:SER:HA	2.02	0.60
1:B:415:GLU:OE2	1:C:409:SER:HA	2.01	0.60
1:D:404:GLN:CD	1:C:404:GLN:HE22	2.11	0.59
1:D:404:GLN:O	1:D:404:GLN:HG2	2.03	0.58
1:A:262:ASN:ND2	1:A:402:ASN:HD22	2.02	0.58
1:B:389:SER:O	1:B:393:LEU:HG	2.04	0.57
1:B:262:ASN:ND2	1:B:402:ASN:HD22	2.00	0.56
1:C:262:ASN:ND2	1:C:402:ASN:HD22	1.98	0.56
1:D:477:CYS:HB3	1:D:502:LEU:HD12	1.88	0.56
1:A:568:SER:OG	1:A:569:SER:N	2.39	0.56
1:C:477:CYS:HB3	1:C:502:LEU:HD12	1.88	0.56
1:B:521:ASP:OD1	1:B:522:GLU:N	2.39	0.55
1:C:521:ASP:OD1	1:C:522:GLU:N	2.39	0.55
1:D:110:ASP:OD1	1:D:140:ARG:NH1	2.39	0.55
1:A:521:ASP:OD1	1:A:522:GLU:N	2.39	0.55
1:D:109:LEU:HD13	1:D:139:LEU:HB3	1.89	0.55
1:A:110:ASP:OD1	1:A:140:ARG:NH1	2.39	0.55
1:B:110:ASP:OD1	1:B:140:ARG:NH1	2.39	0.55
1:A:450:GLN:NE2	1:A:451:GLU:OE2	2.40	0.55
1:A:477:CYS:HB3	1:A:502:LEU:HD12	1.88	0.55
1:D:521:ASP:OD1	1:D:522:GLU:N	2.39	0.55
1:B:450:GLN:NE2	1:B:451:GLU:OE2	2.40	0.55
1:C:450:GLN:NE2	1:C:451:GLU:OE2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:LEU:HD13	1:C:139:LEU:HB3	1.89	0.55
1:D:450:GLN:NE2	1:D:451:GLU:OE2	2.40	0.54
1:D:568:SER:OG	1:D:569:SER:N	2.39	0.54
1:B:477:CYS:HB3	1:B:502:LEU:HD12	1.88	0.54
1:C:404:GLN:O	1:C:404:GLN:HG3	2.06	0.54
1:C:110:ASP:OD1	1:C:140:ARG:NH1	2.39	0.54
1:D:296:ASN:HB2	1:D:299:PRO:HA	1.90	0.54
1:B:443:ARG:NH2	1:B:584:GLU:OE1	2.41	0.54
1:B:568:SER:OG	1:B:569:SER:N	2.39	0.54
1:C:424:ALA:C	1:C:428:MET:HE2	2.33	0.54
1:A:443:ARG:NH2	1:A:584:GLU:OE1	2.41	0.54
1:B:109:LEU:HD13	1:B:139:LEU:HB3	1.89	0.54
1:B:161:ALA:CB	1:B:162:PRO:HD2	2.24	0.53
1:C:304:LEU:HD22	1:C:311:THR:HG21	1.90	0.53
1:A:109:LEU:HD13	1:A:139:LEU:HB3	1.89	0.53
1:C:296:ASN:HB2	1:C:299:PRO:HA	1.90	0.53
1:D:262:ASN:HD21	1:D:398:PHE:HB3	1.74	0.53
1:C:443:ARG:NH2	1:C:584:GLU:OE1	2.41	0.53
1:C:568:SER:OG	1:C:569:SER:N	2.39	0.53
1:D:443:ARG:NH2	1:D:584:GLU:OE1	2.41	0.52
1:B:296:ASN:HB2	1:B:299:PRO:HA	1.90	0.52
1:A:300:CYS:HB2	1:A:317:PHE:HZ	1.73	0.52
1:A:189:ILE:HA	1:A:192:ILE:HG22	1.93	0.51
1:D:422:ARG:NH2	1:A:409:SER:O	2.44	0.51
1:C:189:ILE:HA	1:C:192:ILE:HG22	1.93	0.51
1:A:404:GLN:O	1:A:404:GLN:HG2	2.10	0.51
1:B:404:GLN:HE21	1:B:408:GLN:NE2	2.09	0.51
1:D:189:ILE:HA	1:D:192:ILE:HG22	1.93	0.50
1:A:161:ALA:CB	1:A:162:PRO:CD	2.87	0.50
1:B:189:ILE:HA	1:B:192:ILE:HG22	1.93	0.50
1:A:296:ASN:HB2	1:A:299:PRO:HA	1.93	0.49
1:A:368:SER:HB3	1:B:371:GLN:HG2	1.95	0.49
1:B:558:GLU:OE1	1:B:575:SER:HA	2.13	0.49
1:C:558:GLU:OE1	1:C:575:SER:HA	2.13	0.49
1:A:507:TYR:HB2	1:A:585:VAL:HB	1.95	0.49
1:B:507:TYR:HB2	1:B:585:VAL:HB	1.95	0.49
1:B:560:LEU:HD12	1:B:560:LEU:C	2.38	0.49
1:C:424:ALA:O	1:C:428:MET:HE2	2.13	0.49
1:C:560:LEU:HD12	1:C:560:LEU:C	2.38	0.48
1:D:558:GLU:OE1	1:D:575:SER:HA	2.13	0.48
1:A:558:GLU:OE1	1:A:575:SER:HA	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:GLN:NE2	1:B:373:LEU:O	2.45	0.48
1:D:161:ALA:CB	1:D:162:PRO:HD2	2.25	0.48
1:C:160:ILE:CG2	1:C:172:LEU:HD21	2.36	0.48
1:D:507:TYR:HB2	1:D:585:VAL:HB	1.95	0.48
1:C:507:TYR:HB2	1:C:585:VAL:HB	1.95	0.48
1:D:560:LEU:HD12	1:D:560:LEU:C	2.38	0.47
1:A:560:LEU:HD12	1:A:560:LEU:C	2.38	0.47
1:B:531:LEU:HB2	1:B:549:LEU:HB2	1.97	0.47
1:A:231:ILE:HG13	1:A:232:PRO:HD3	1.96	0.47
1:A:429:SER:HB3	1:A:438:ARG:HH12	1.80	0.47
1:A:531:LEU:HB2	1:A:549:LEU:HB2	1.97	0.47
1:C:409:SER:OG	1:C:410:THR:HG23	2.15	0.47
1:B:231:ILE:HG13	1:B:232:PRO:HD3	1.96	0.47
1:D:160:ILE:CG2	1:D:172:LEU:HD21	2.36	0.46
1:D:427:TRP:HH2	1:A:472:ILE:HG21	1.79	0.46
1:D:531:LEU:HB2	1:D:549:LEU:HB2	1.97	0.46
1:D:231:ILE:HG13	1:D:232:PRO:HD3	1.96	0.46
1:D:429:SER:HB3	1:D:438:ARG:HH12	1.80	0.46
1:C:424:ALA:O	1:C:428:MET:HG3	2.16	0.46
1:C:231:ILE:HG13	1:C:232:PRO:HD3	1.96	0.46
1:C:531:LEU:HB2	1:C:549:LEU:HB2	1.97	0.46
1:A:300:CYS:HB2	1:A:317:PHE:CE1	2.51	0.45
1:B:404:GLN:HE22	1:C:404:GLN:CG	2.26	0.45
1:B:429:SER:HB3	1:B:438:ARG:HH12	1.80	0.45
1:B:160:ILE:CG2	1:B:172:LEU:HD21	2.36	0.45
1:B:434:PRO:HD2	1:B:437:LEU:HD12	1.98	0.45
1:C:429:SER:HB3	1:C:438:ARG:HH12	1.80	0.45
1:A:434:PRO:HD2	1:A:437:LEU:HD12	1.98	0.45
1:B:364:GLN:NE2	1:C:371:GLN:O	2.50	0.45
1:A:409:SER:OG	1:A:410:THR:HG23	2.16	0.45
1:D:206:ILE:HG22	1:D:210:MET:HE2	1.99	0.45
1:C:434:PRO:HD2	1:C:437:LEU:HD12	1.98	0.44
1:B:206:ILE:HG22	1:B:210:MET:HE2	1.99	0.44
1:B:153:PHE:HE1	1:B:156:ARG:HH21	1.65	0.44
1:C:206:ILE:HG22	1:C:210:MET:HE2	1.99	0.44
1:C:192:ILE:HA	1:C:195:VAL:HG12	2.00	0.44
1:D:434:PRO:HD2	1:D:437:LEU:HD12	1.98	0.44
1:D:153:PHE:HE1	1:D:156:ARG:HH21	1.65	0.44
1:A:206:ILE:HG22	1:A:210:MET:HE2	1.99	0.44
1:A:153:PHE:HE1	1:A:156:ARG:HH21	1.65	0.43
1:D:192:ILE:HA	1:D:195:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:SER:HB3	1:C:371:GLN:HG2	2.01	0.43
1:C:153:PHE:HE1	1:C:156:ARG:HH21	1.65	0.43
1:A:192:ILE:HA	1:A:195:VAL:HG12	2.00	0.43
1:B:192:ILE:HA	1:B:195:VAL:HG12	2.00	0.43
1:B:149:LEU:HD12	1:B:152:ILE:HD11	2.01	0.42
1:A:441:ILE:HG12	1:B:468:LEU:HD21	2.02	0.42
1:C:149:LEU:HD12	1:C:152:ILE:HD11	2.01	0.42
1:B:177:ARG:HA	1:B:177:ARG:HD3	1.92	0.42
1:D:428:MET:HG2	1:D:433:LEU:HD12	2.02	0.42
1:B:160:ILE:HG23	1:B:172:LEU:HD22	1.96	0.42
1:A:149:LEU:HD12	1:A:152:ILE:HD11	2.01	0.42
1:B:405:THR:O	1:B:406:TYR:C	2.61	0.42
1:C:486:MET:HE1	1:C:564:LEU:HD21	2.02	0.42
1:D:415:GLU:OE2	1:A:409:SER:HA	2.20	0.41
1:D:441:ILE:HG12	1:A:468:LEU:HD21	2.02	0.41
1:C:120:ASP:HB3	1:C:125:CYS:SG	2.61	0.41
1:A:428:MET:HG2	1:A:433:LEU:HD12	2.02	0.41
1:C:177:ARG:HD3	1:C:177:ARG:HA	1.92	0.41
1:D:149:LEU:HD12	1:D:152:ILE:HD11	2.01	0.41
1:A:160:ILE:CG2	1:A:172:LEU:HD21	2.36	0.41
1:B:120:ASP:HB3	1:B:125:CYS:SG	2.61	0.41
1:D:120:ASP:HB3	1:D:125:CYS:SG	2.61	0.41
1:A:120:ASP:HB3	1:A:125:CYS:SG	2.61	0.41
1:B:428:MET:HG2	1:B:433:LEU:HD12	2.02	0.41
1:A:213:SER:OG	1:A:216:LEU:HB3	2.21	0.41
1:A:284:ARG:HA	1:A:284:ARG:HD2	1.90	0.41
1:A:486:MET:HE1	1:A:564:LEU:HD21	2.02	0.41
1:B:484:VAL:HA	1:B:485:PRO:HD3	1.95	0.41
1:C:428:MET:HG2	1:C:433:LEU:HD12	2.01	0.41
1:C:284:ARG:HD2	1:C:284:ARG:HA	1.90	0.41
1:D:140:ARG:NH2	1:D:229:GLN:OE1	2.54	0.41
1:D:213:SER:OG	1:D:216:LEU:HB3	2.21	0.41
1:D:486:MET:HE1	1:D:564:LEU:HD21	2.02	0.41
1:A:422:ARG:CZ	1:B:409:SER:O	2.68	0.41
1:B:87:PRO:HA	1:B:92:LEU:HD22	2.03	0.41
1:A:140:ARG:NH2	1:A:229:GLN:OE1	2.54	0.41
1:A:160:ILE:HG23	1:A:172:LEU:HD22	1.95	0.41
1:A:177:ARG:HD3	1:A:177:ARG:HA	1.92	0.41
1:B:210:MET:HE1	1:B:221:MET:HG3	2.03	0.41
1:C:87:PRO:HA	1:C:92:LEU:HD22	2.03	0.41
1:B:213:SER:OG	1:B:216:LEU:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:596:LYS:HA	1:C:596:LYS:HD3	1.99	0.41
1:B:140:ARG:NH2	1:B:229:GLN:OE1	2.54	0.40
1:D:404:GLN:HE21	1:D:408:GLN:NE2	2.20	0.40
1:D:405:THR:O	1:D:406:TYR:C	2.62	0.40
1:A:90:PRO:HA	1:A:93:GLN:HG2	2.04	0.40
1:B:90:PRO:HA	1:B:93:GLN:HG2	2.04	0.40
1:C:289:TRP:HB3	1:C:305:LEU:HD22	2.03	0.40
1:C:417:MET:HE3	1:C:417:MET:HB3	1.91	0.40
1:D:219:LYS:HE2	1:D:219:LYS:HB3	1.96	0.40
1:B:284:ARG:HA	1:B:284:ARG:HD2	1.90	0.40
1:C:140:ARG:NH2	1:C:229:GLN:OE1	2.54	0.40
1:D:147:TYR:CZ	1:D:236:ARG:HD2	2.57	0.40
1:B:486:MET:HE1	1:B:564:LEU:HD21	2.02	0.40

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	492/716 (69%)	476 (97%)	16 (3%)	0	100	100
1	B	492/716 (69%)	476 (97%)	16 (3%)	0	100	100
1	C	492/716 (69%)	475 (96%)	17 (4%)	0	100	100
1	D	492/716 (69%)	476 (97%)	16 (3%)	0	100	100
All	All	1968/2864 (69%)	1903 (97%)	65 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	452/640 (71%)	450 (100%)	2 (0%)	84	93
1	B	452/640 (71%)	450 (100%)	2 (0%)	84	93
1	C	452/640 (71%)	450 (100%)	2 (0%)	84	93
1	D	452/640 (71%)	450 (100%)	2 (0%)	84	93
All	All	1808/2560 (71%)	1800 (100%)	8 (0%)	81	93

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	151	ILE
1	D	201	MET
1	A	151	ILE
1	A	201	MET
1	B	151	ILE
1	B	201	MET
1	C	151	ILE
1	C	201	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	262	ASN
1	D	353	GLN
1	D	371	GLN
1	D	408	GLN
1	D	446	GLN
1	D	503	GLN
1	D	537	ASN
1	A	262	ASN
1	A	353	GLN
1	A	408	GLN
1	A	446	GLN

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Mol	Chain	Res	Type
1	A	503	GLN
1	A	537	ASN
1	B	262	ASN
1	B	404	GLN
1	B	446	GLN
1	B	503	GLN
1	B	537	ASN
1	C	150	HIS
1	C	262	ASN
1	C	372	ASN
1	C	404	GLN
1	C	408	GLN
1	C	446	GLN
1	C	503	GLN
1	C	537	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 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.

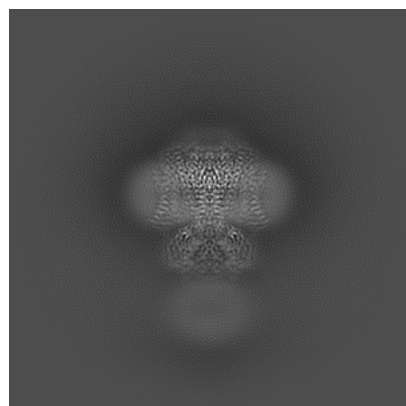
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61105. These allow visual inspection of the internal detail of the map and identification of artifacts.

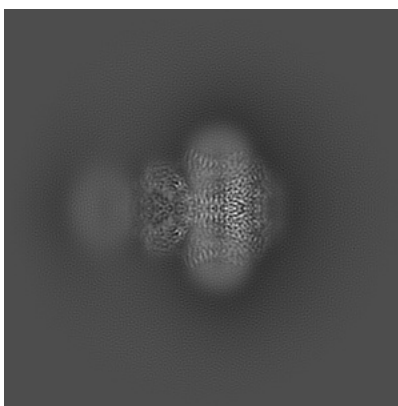
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

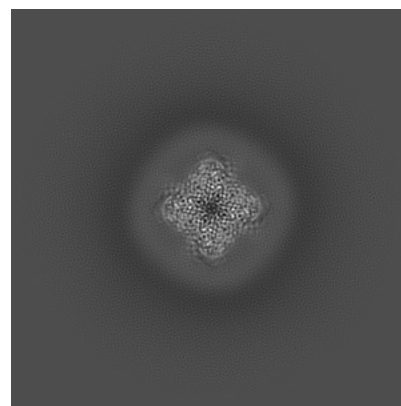
6.1.1 Primary map



X

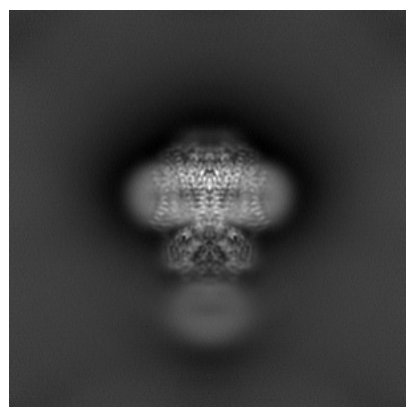


Y

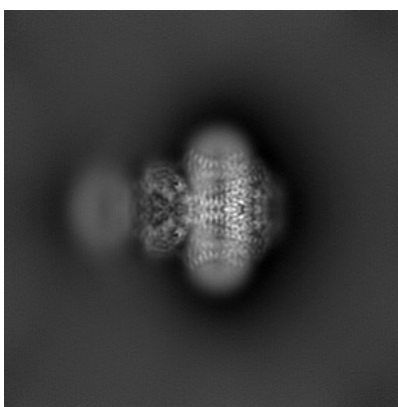


Z

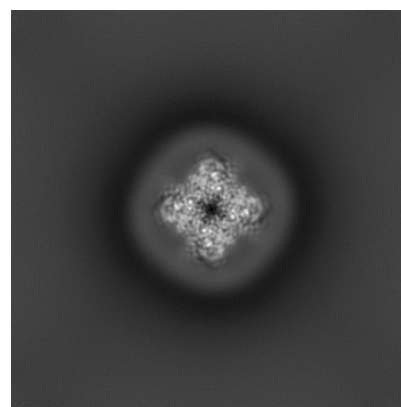
6.1.2 Raw map



X



Y

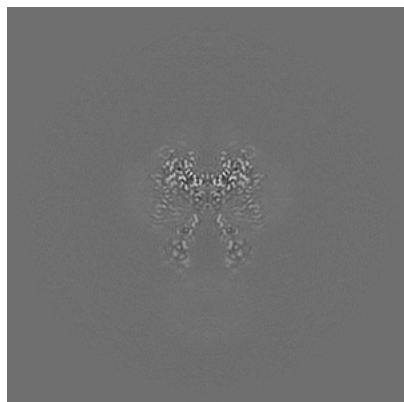


Z

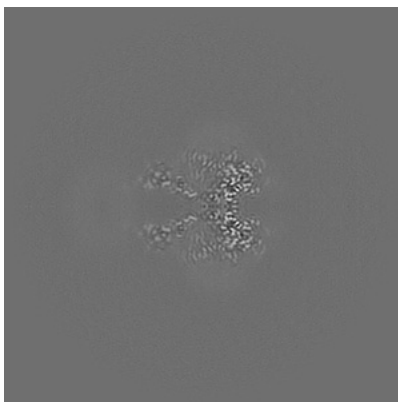
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

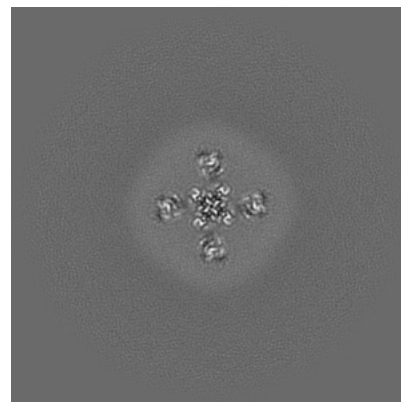
6.2.1 Primary map



X Index: 180

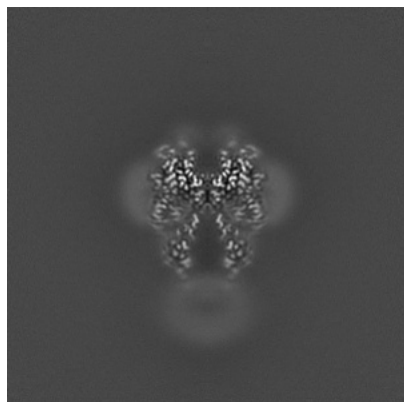


Y Index: 180

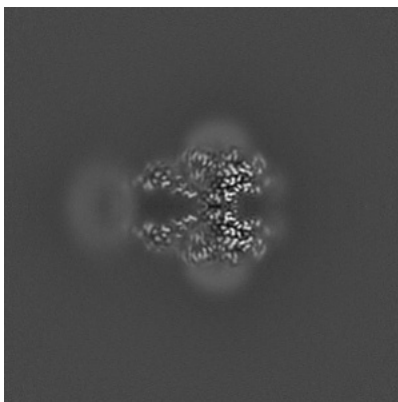


Z Index: 180

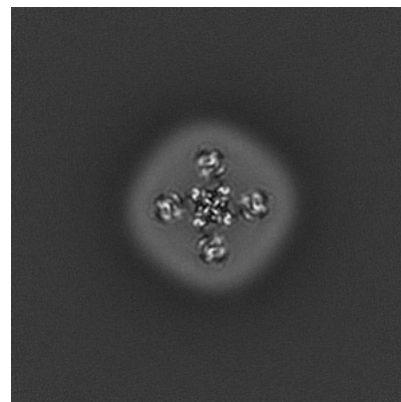
6.2.2 Raw map



X Index: 180



Y Index: 180

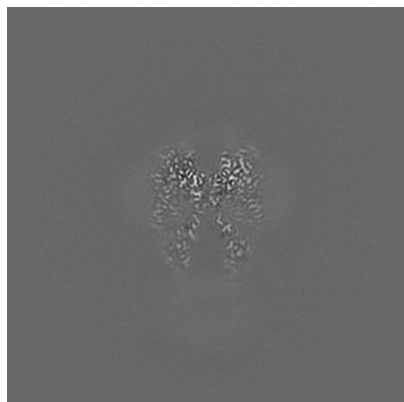


Z Index: 180

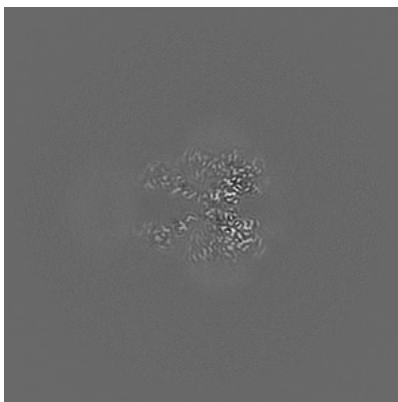
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

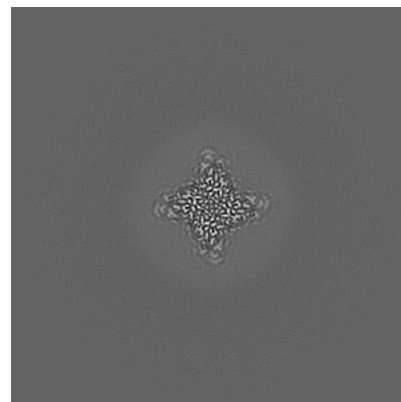
6.3.1 Primary map



X Index: 181

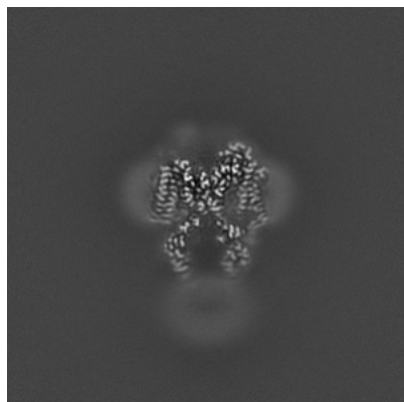


Y Index: 181

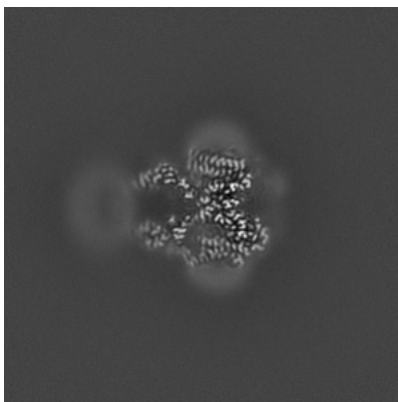


Z Index: 207

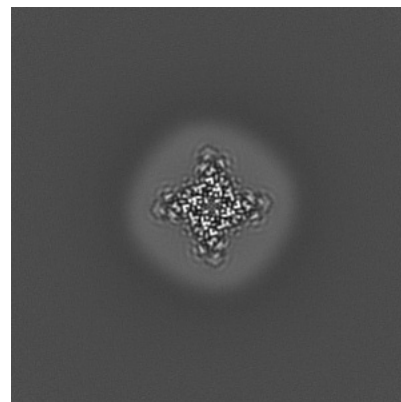
6.3.2 Raw map



X Index: 174



Y Index: 174

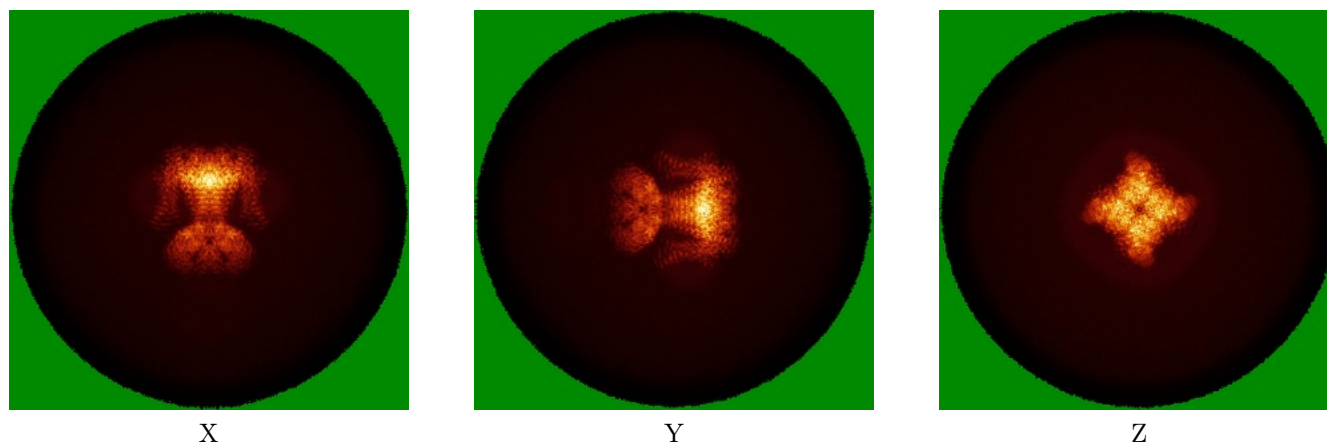


Z Index: 206

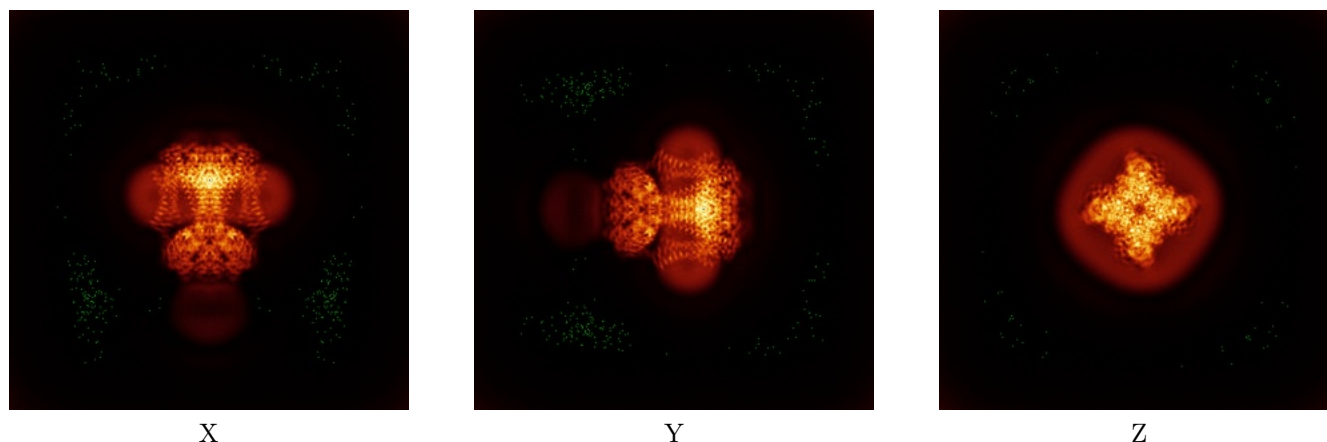
The images above show the largest variance slices of the map in three orthogonal directions.

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.

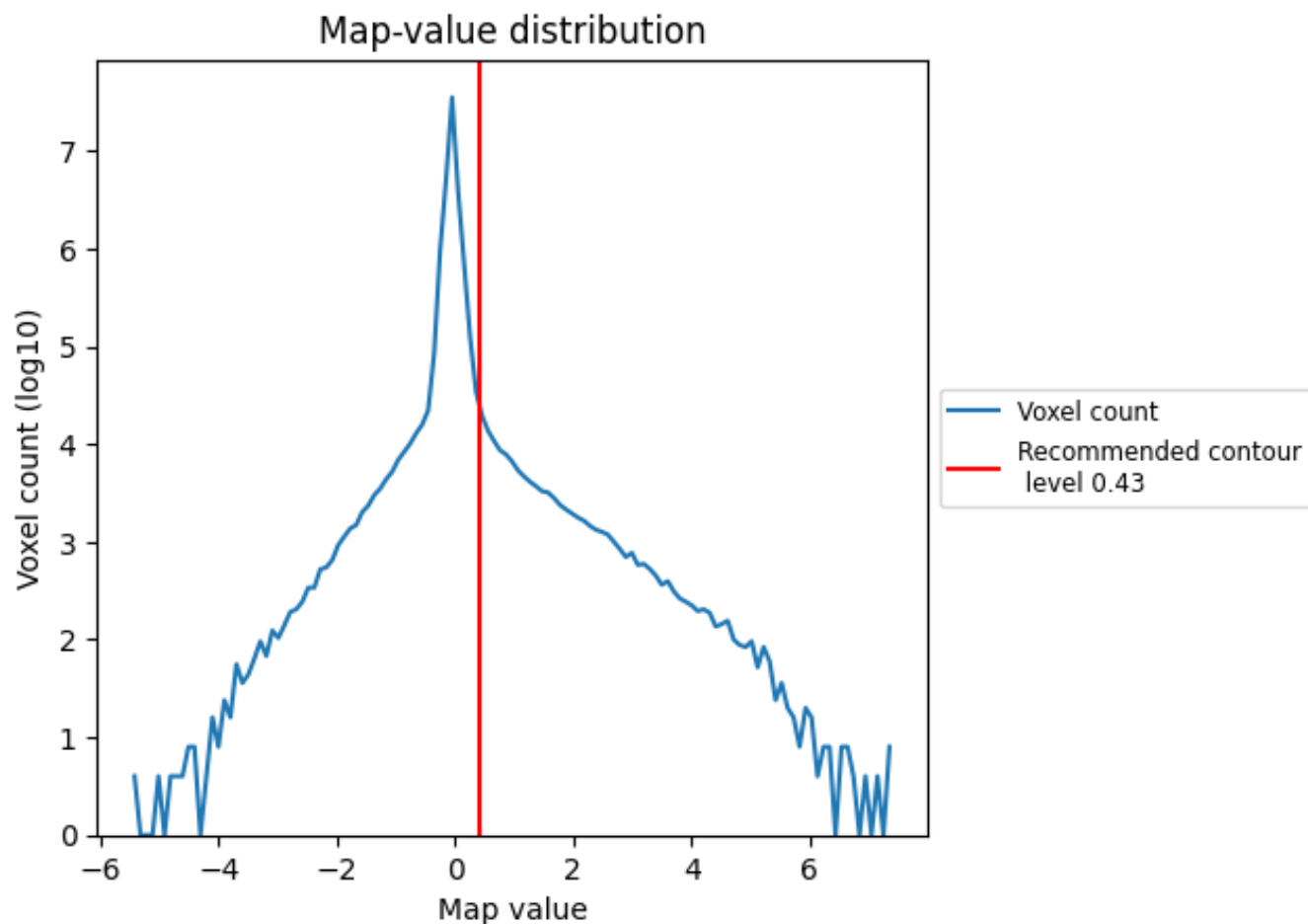
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

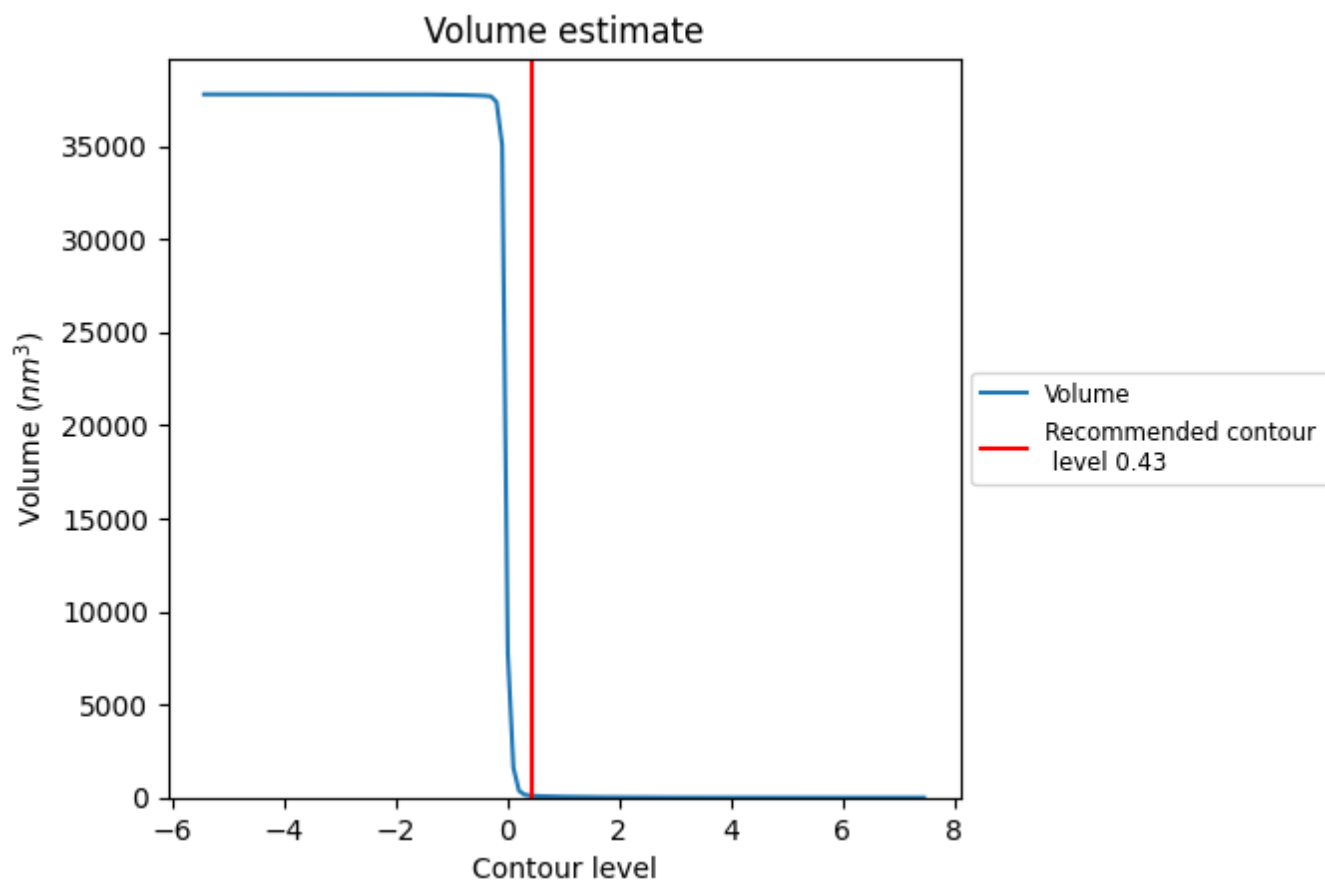
This section contains the results of statistical analysis of the map.

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.

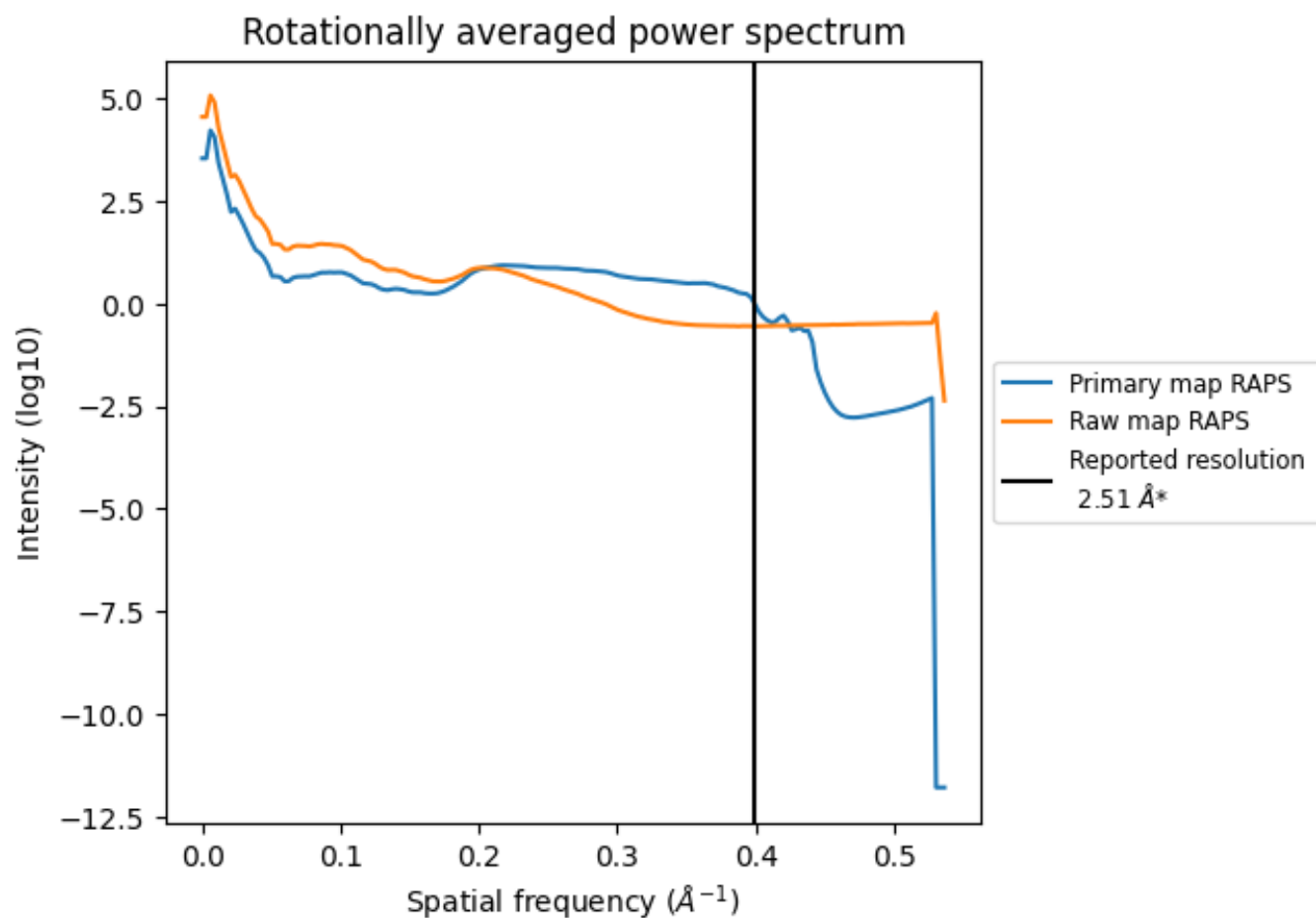
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 102 nm^3 ; this corresponds to an approximate mass of 92 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 ⓘ

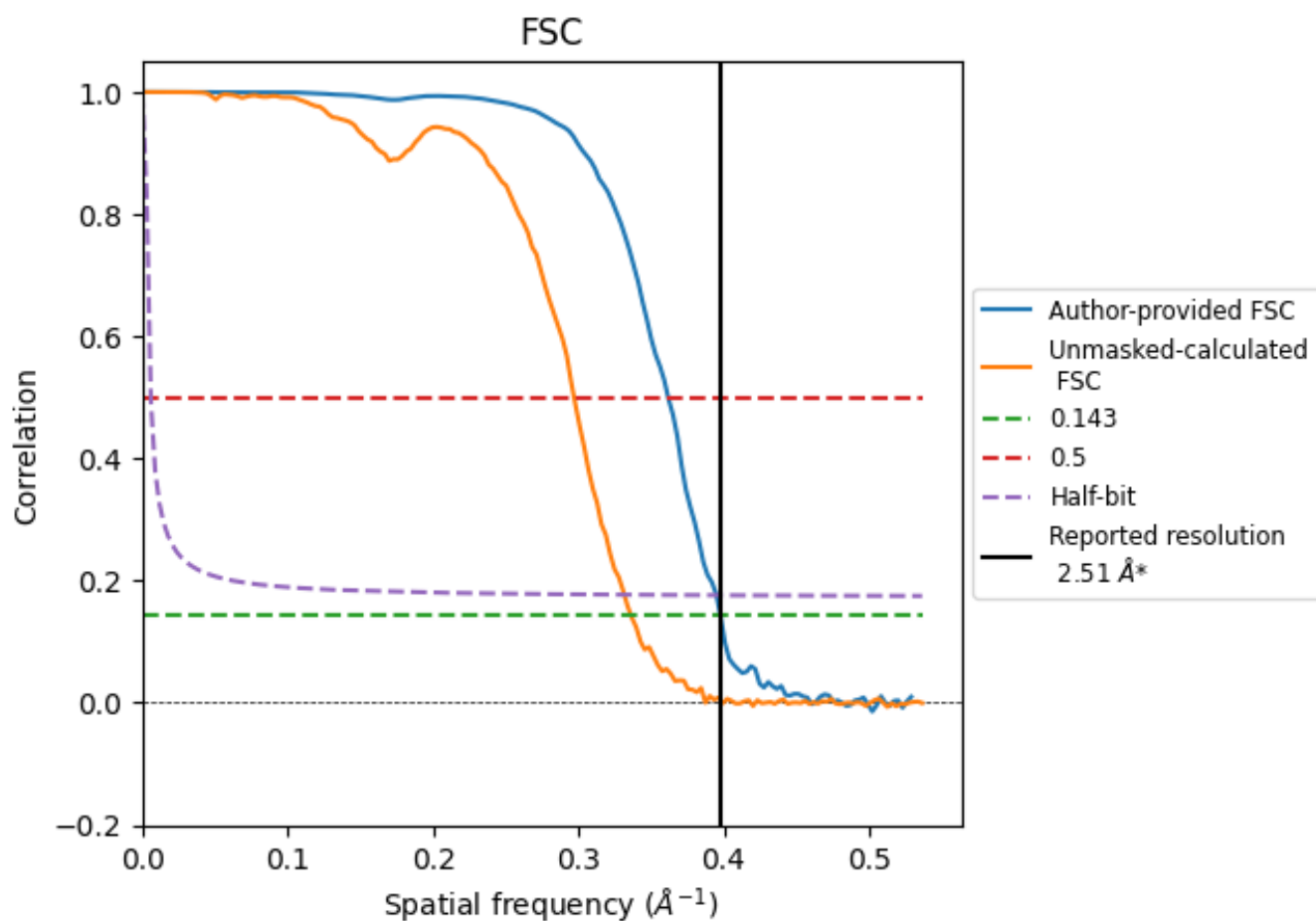


*Reported resolution corresponds to spatial frequency of 0.398 Å⁻¹

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 0.398 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.51	-	-
Author-provided FSC curve	2.51	2.76	2.53
Unmasked-calculated*	2.97	3.37	3.02

*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 2.97 differs from the reported value 2.51 by more than 10 %

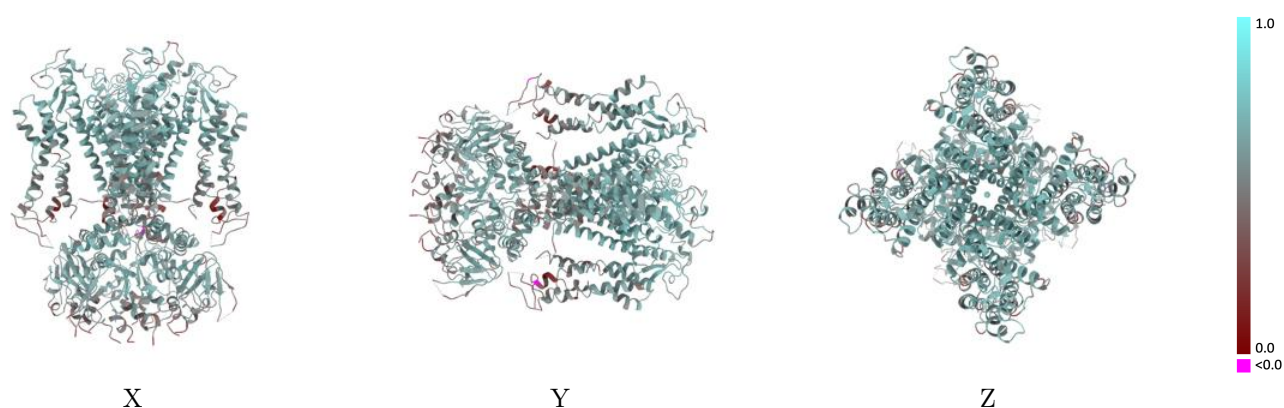
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-61105 and PDB model 9J34. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

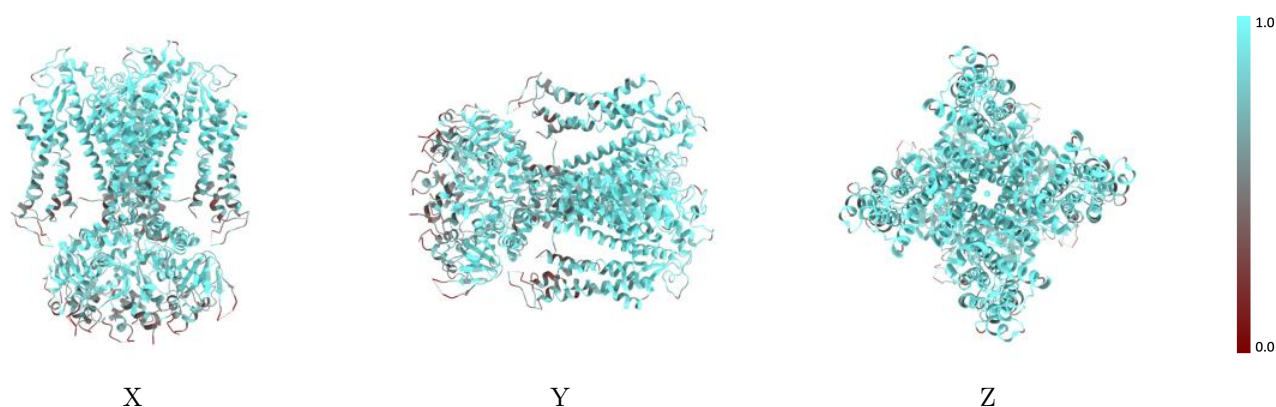
This section was not generated.

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



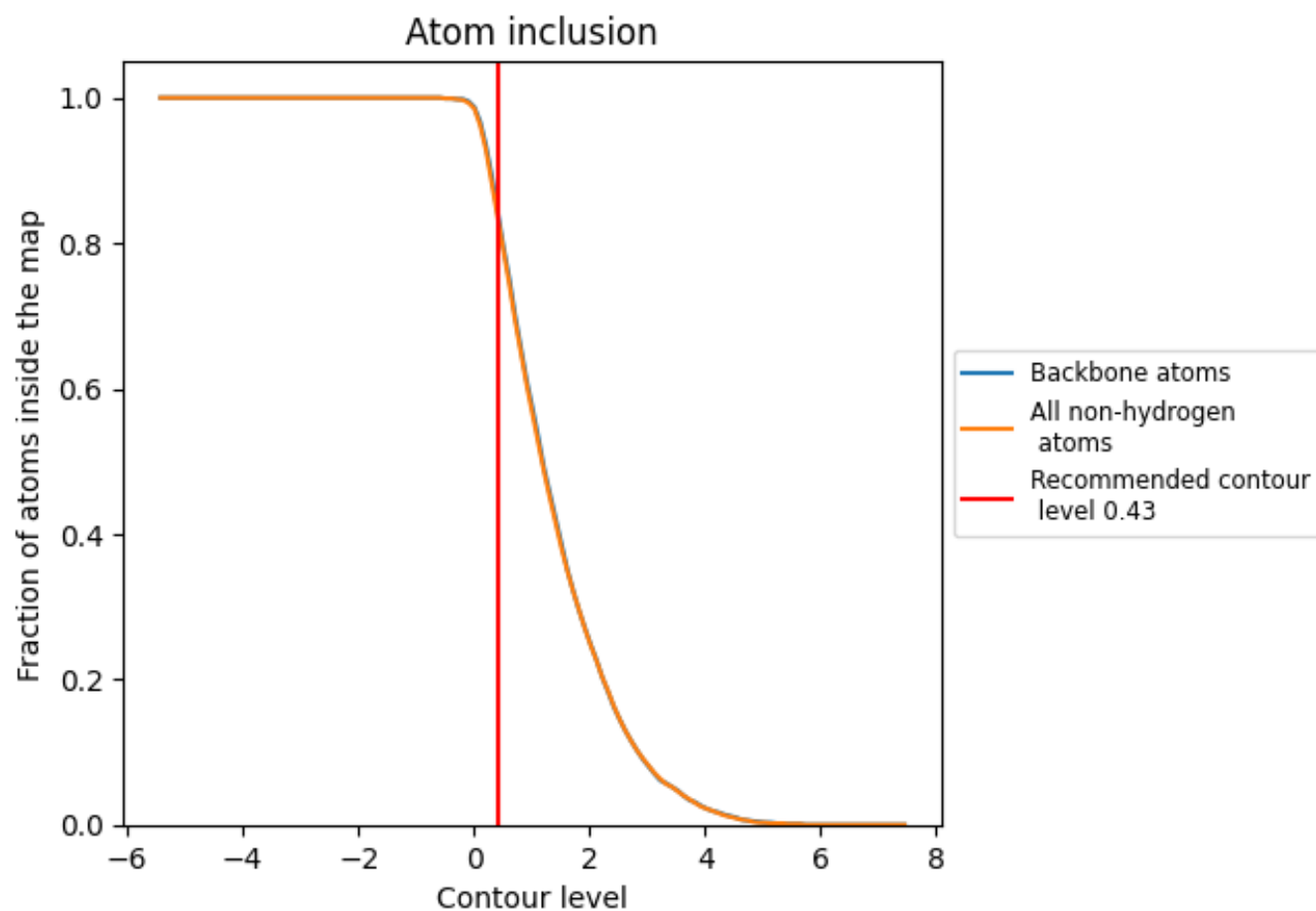
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.5780
A	0.8250	0.5690
B	0.8380	0.5870
C	0.8310	0.5720
D	0.8350	0.5840

