



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:29 PM UTC

PDB ID : 4CG7 / pdb_00004cg7
EMDB ID : EMD-2510
Title : Cryo-EM of the Sec61-complex bound to the idle 80S ribosome
Authors : Gogala, M.; Becker, T.; Beatrix, B.; Barrio-Garcia, C.; Berninghausen, O.; Beckmann, R.
Deposited on : 2013-11-21
Resolution : 6.90 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 EMD 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

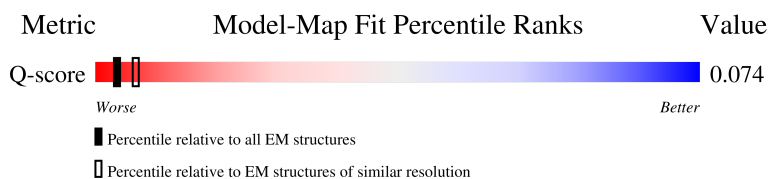
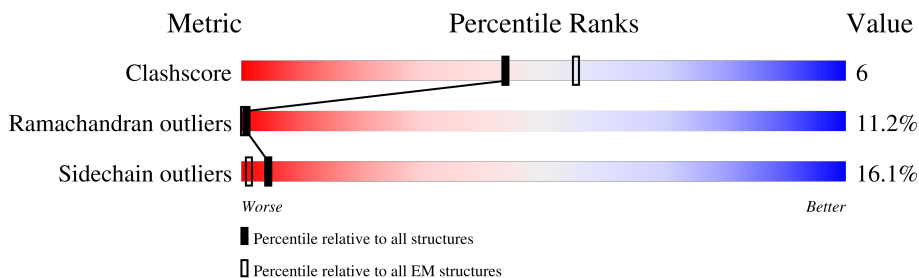
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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	479 (6.40 - 7.40)

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	476	
2	B	68	
3	C	36	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4252 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 PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT ALPHA ISOFORM 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	452	Total	C	N	O	S	0	0
			3477	2275	560	619	23		

- Molecule 2 is a protein called PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT GAMMA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 3 is a protein called TRANSPORT PROTEIN SEC61 SUBUNIT BETA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	36	Total	C	N	O	S	0	0
			281	188	44	47	2		

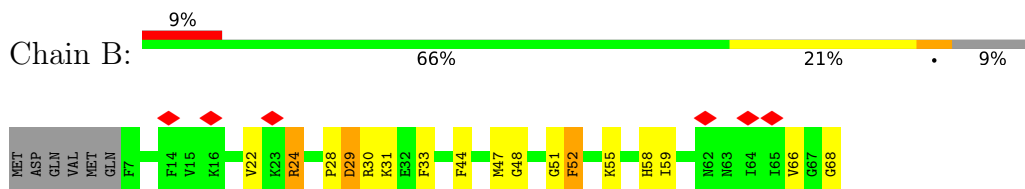
3 Residue-property plots

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: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT ALPHA ISOFORM 1



- Molecule 2: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT GAMMA



- Molecule 3: TRANSPORT PROTEIN SEC61 SUBUNIT BETA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	162655	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	148721	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	1.356	Depositor
Minimum map value	-0.635	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	455.36322, 455.36322, 455.36322	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2374, 1.2374, 1.2374	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.19	1/3552 (0.0%)	1.99	127/4815 (2.6%)
2	B	1.30	1/504 (0.2%)	1.89	16/673 (2.4%)
3	C	1.48	2/289 (0.7%)	2.20	18/391 (4.6%)
All	All	1.23	4/4345 (0.1%)	1.99	161/5879 (2.7%)

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	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	476	PHE	C-O	-11.58	1.00	1.23
3	C	96	SER	C-OXT	-11.57	1.00	1.23
3	C	96	SER	C-O	-11.56	1.00	1.23
2	B	68	GLY	C-O	-11.55	1.00	1.23

All (161) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	PRO	CA-N-CD	-12.77	94.12	112.00
1	A	48	ILE	CB-CA-C	12.28	121.36	109.33
1	A	48	ILE	N-CA-C	11.71	118.80	109.19
3	C	80	PHE	CA-CB-CG	11.58	125.38	113.80
1	A	119	PHE	CA-C-N	10.46	131.59	119.98
1	A	119	PHE	C-N-CA	10.46	131.59	119.98
1	A	196	PHE	CA-CB-CG	10.07	123.87	113.80
1	A	414	ASN	CA-CB-CG	9.52	122.12	112.60
3	C	70	PRO	CA-C-N	9.45	126.19	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	70	PRO	C-N-CA	9.45	126.19	120.24
1	A	300	ASN	CA-CB-CG	9.24	121.84	112.60
1	A	132	VAL	N-CA-CB	8.42	120.40	110.55
1	A	44	VAL	CA-C-N	8.21	131.28	120.28
1	A	44	VAL	C-N-CA	8.21	131.28	120.28
1	A	67	VAL	CB-CA-C	-7.79	101.63	112.14
3	C	81	ILE	N-CA-CB	7.74	122.19	110.58
1	A	115	ALA	CA-C-N	7.66	130.54	120.28
1	A	115	ALA	C-N-CA	7.66	130.54	120.28
1	A	414	ASN	N-CA-CB	7.63	121.42	110.13
2	B	52	PHE	CA-CB-CG	7.51	121.31	113.80
1	A	43	LEU	CA-C-N	7.49	130.72	120.46
1	A	43	LEU	C-N-CA	7.49	130.72	120.46
1	A	48	ILE	CA-C-N	7.49	129.20	119.84
1	A	48	ILE	C-N-CA	7.49	129.20	119.84
1	A	423	PHE	CA-C-N	7.38	128.32	119.99
1	A	423	PHE	C-N-CA	7.38	128.32	119.99
1	A	304	ILE	N-CA-CB	7.37	120.57	110.54
1	A	61	PRO	CA-C-N	7.31	135.50	121.54
1	A	61	PRO	C-N-CA	7.31	135.50	121.54
1	A	50	LEU	N-CA-C	7.30	120.67	111.69
1	A	213	ILE	CA-C-N	7.16	134.86	121.97
1	A	213	ILE	C-N-CA	7.16	134.86	121.97
1	A	186	ASN	CA-CB-CG	7.11	119.71	112.60
1	A	272	TYR	N-CA-C	-7.01	95.86	110.80
1	A	116	GLN	N-CA-CB	6.98	120.38	110.12
3	C	71	VAL	CA-C-O	-6.97	112.93	118.85
1	A	65	MET	CA-C-N	6.94	129.57	120.28
1	A	65	MET	C-N-CA	6.94	129.57	120.28
1	A	49	PRO	N-CA-C	6.72	126.32	112.47
1	A	79	LEU	N-CA-C	6.68	120.53	110.64
1	A	128	SER	N-CA-CB	6.67	120.50	110.22
1	A	27	GLN	N-CA-CB	6.61	121.66	110.49
3	C	72	PRO	N-CA-C	6.58	126.02	112.47
3	C	80	PHE	CB-CA-C	6.53	121.63	110.79
1	A	272	TYR	N-CA-CB	6.46	121.41	110.49
3	C	73	VAL	CA-C-N	6.43	128.89	120.28
3	C	73	VAL	C-N-CA	6.43	128.89	120.28
1	A	145	ALA	CA-C-N	6.38	127.06	119.98
1	A	145	ALA	C-N-CA	6.38	127.06	119.98
1	A	292	ILE	CA-C-N	6.37	128.81	120.28
1	A	292	ILE	C-N-CA	6.37	128.81	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	VAL	CA-C-N	6.36	129.18	120.46
1	A	67	VAL	C-N-CA	6.36	129.18	120.46
1	A	149	LEU	CA-C-N	6.29	128.70	120.28
1	A	149	LEU	C-N-CA	6.29	128.70	120.28
1	A	449	LEU	CA-C-N	6.24	128.64	120.28
1	A	449	LEU	C-N-CA	6.24	128.64	120.28
1	A	81	ILE	N-CA-C	6.22	122.28	109.34
1	A	359	VAL	CA-C-N	6.22	128.53	120.44
1	A	359	VAL	C-N-CA	6.22	128.53	120.44
1	A	266	PRO	N-CA-C	-6.20	107.54	114.92
3	C	81	ILE	CA-C-N	6.20	128.58	120.28
3	C	81	ILE	C-N-CA	6.20	128.58	120.28
1	A	178	GLY	CA-C-N	6.13	128.86	120.46
1	A	178	GLY	C-N-CA	6.13	128.86	120.46
1	A	62	PHE	CA-C-N	6.06	128.68	120.44
1	A	62	PHE	C-N-CA	6.06	128.68	120.44
1	A	139	ASP	N-CA-C	-6.04	102.78	108.22
1	A	423	PHE	CA-CB-CG	-6.02	107.78	113.80
1	A	47	GLN	N-CA-C	6.00	117.48	111.07
1	A	71	SER	N-CA-CB	5.94	120.53	110.49
3	C	71	VAL	CA-C-N	5.93	127.26	119.84
3	C	71	VAL	C-N-CA	5.93	127.26	119.84
1	A	173	TYR	N-CA-CB	5.92	120.50	110.49
1	A	49	PRO	N-CA-CB	5.87	109.41	103.25
1	A	105	THR	CA-C-N	5.86	125.56	119.05
1	A	105	THR	C-N-CA	5.86	125.56	119.05
1	A	79	LEU	N-CA-CB	5.86	118.21	109.19
1	A	137	TYR	CA-C-N	5.86	132.89	121.41
1	A	137	TYR	C-N-CA	5.86	132.89	121.41
1	A	56	SER	N-CA-CB	5.85	120.37	110.49
2	B	58	HIS	CA-C-N	5.80	123.89	120.24
2	B	58	HIS	C-N-CA	5.80	123.89	120.24
1	A	72	ASN	CA-CB-CG	5.78	118.38	112.60
3	C	79	LEU	CA-C-N	5.77	128.01	120.28
3	C	79	LEU	C-N-CA	5.77	128.01	120.28
1	A	48	ILE	C-N-CD	-5.77	101.35	125.00
1	A	175	LEU	N-CA-C	-5.77	98.52	110.80
1	A	358	PRO	CA-C-N	5.73	132.28	121.97
1	A	358	PRO	C-N-CA	5.73	132.28	121.97
2	B	59	ILE	N-CA-CB	5.72	114.11	110.50
3	C	81	ILE	CA-CB-CG1	5.70	120.09	110.40
2	B	47	MET	CA-C-N	5.67	126.24	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	47	MET	C-N-CA	5.67	126.24	120.00
1	A	287	SER	CA-C-N	5.62	127.81	120.28
1	A	287	SER	C-N-CA	5.62	127.81	120.28
1	A	134	THR	N-CA-C	5.59	117.37	111.28
1	A	93	LEU	CA-C-N	5.54	128.16	120.29
1	A	93	LEU	C-N-CA	5.54	128.16	120.29
1	A	55	SER	N-CA-CB	5.54	119.86	110.49
1	A	148	CYS	CA-C-N	5.54	132.13	121.54
1	A	148	CYS	C-N-CA	5.54	132.13	121.54
2	B	29	ASP	CA-C-N	5.49	132.03	121.54
2	B	29	ASP	C-N-CA	5.49	132.03	121.54
1	A	359	VAL	N-CA-C	-5.49	97.93	109.34
1	A	325	SER	N-CA-C	-5.47	106.38	113.16
1	A	180	SER	CA-C-N	5.45	127.58	120.28
1	A	180	SER	C-N-CA	5.45	127.58	120.28
1	A	136	MET	N-CA-CB	5.40	120.84	110.90
1	A	148	CYS	CA-C-O	-5.40	115.14	120.70
1	A	268	LYS	N-CA-CB	5.38	119.58	110.49
1	A	407	THR	N-CA-C	-5.38	106.41	112.87
1	A	373	ALA	CA-C-N	5.36	127.46	120.28
1	A	373	ALA	C-N-CA	5.36	127.46	120.28
1	A	125	ILE	CA-C-N	5.35	125.89	120.00
1	A	125	ILE	C-N-CA	5.35	125.89	120.00
1	A	333	ALA	CA-C-N	5.34	127.44	120.28
1	A	333	ALA	C-N-CA	5.34	127.44	120.28
1	A	330	GLY	CA-C-N	5.31	130.20	121.87
1	A	330	GLY	C-N-CA	5.31	130.20	121.87
1	A	111	LEU	CA-C-N	5.30	131.67	121.54
1	A	111	LEU	C-N-CA	5.30	131.67	121.54
2	B	22	VAL	CA-C-N	5.27	127.35	120.28
2	B	22	VAL	C-N-CA	5.27	127.35	120.28
1	A	98	LYS	CA-C-N	5.27	127.56	120.50
1	A	98	LYS	C-N-CA	5.27	127.56	120.50
3	C	76	MET	CA-C-N	5.26	127.33	120.28
3	C	76	MET	C-N-CA	5.26	127.33	120.28
1	A	199	THR	N-CA-C	-5.25	99.61	110.80
1	A	441	ILE	CA-C-N	5.21	125.76	119.98
1	A	441	ILE	C-N-CA	5.21	125.76	119.98
1	A	85	VAL	CA-C-N	5.20	127.25	120.28
1	A	85	VAL	C-N-CA	5.20	127.25	120.28
1	A	142	GLU	N-CA-CB	5.20	119.28	110.49
1	A	137	TYR	N-CA-C	-5.18	106.64	113.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	PHE	CA-C-N	5.18	127.22	120.28
1	A	42	PHE	C-N-CA	5.18	127.22	120.28
1	A	49	PRO	CB-CA-C	5.18	120.11	111.56
1	A	169	LEU	N-CA-C	-5.18	107.13	113.50
1	A	38	THR	CA-C-N	5.15	127.18	120.28
1	A	38	THR	C-N-CA	5.15	127.18	120.28
1	A	303	VAL	N-CA-C	5.14	115.86	110.62
1	A	346	SER	CA-C-N	5.12	125.65	120.38
1	A	346	SER	C-N-CA	5.12	125.65	120.38
1	A	146	GLY	CA-C-N	5.09	131.13	121.97
1	A	146	GLY	C-N-CA	5.09	131.13	121.97
2	B	31	LYS	CA-C-N	5.08	127.09	120.28
2	B	31	LYS	C-N-CA	5.08	127.09	120.28
1	A	234	PHE	CA-CB-CG	-5.06	108.74	113.80
2	B	48	GLY	CA-C-N	5.05	127.05	120.28
2	B	48	GLY	C-N-CA	5.05	127.05	120.28
2	B	51	GLY	CA-C-N	5.04	127.03	120.28
2	B	51	GLY	C-N-CA	5.04	127.03	120.28
1	A	62	PHE	N-CA-C	5.03	121.52	110.80
1	A	27	GLN	CA-C-N	5.03	127.02	120.28
1	A	27	GLN	C-N-CA	5.03	127.02	120.28
1	A	304	ILE	CA-CB-CG1	5.03	118.95	110.40
1	A	217	PHE	CA-CB-CG	-5.03	108.77	113.80
1	A	462	VAL	CB-CA-C	-5.02	106.48	111.30
1	A	404	HIS	CA-C-N	5.01	131.11	121.54
1	A	404	HIS	C-N-CA	5.01	131.11	121.54

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	MET	Peptide
1	A	176	GLY	Peptide
1	A	266	PRO	Peptide
1	A	273	ARG	Peptide
1	A	285	TYR	Sidechain
1	A	357	ASP	Peptide
1	A	358	PRO	Peptide
1	A	47	GLN	Peptide
1	A	48	ILE	Peptide
1	A	59	ALA	Peptide
1	A	64	TRP	Peptide

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Mol	Chain	Res	Type	Group
1	A	70	ALA	Peptide
1	A	73	ARG	Sidechain

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	3477	0	3575	56	0
2	B	494	0	527	1	0
3	C	281	0	294	2	0
All	All	4252	0	4396	56	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (56) 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:405:ARG:HB3	1:A:408:SER:CB	1.28	1.56
1:A:405:ARG:HB3	1:A:408:SER:OG	1.28	1.32
1:A:405:ARG:CB	1:A:408:SER:CB	2.20	1.19
1:A:405:ARG:HB3	1:A:408:SER:HB2	1.21	1.08
1:A:408:SER:O	1:A:409:MET:HG2	1.53	1.06
1:A:402:ARG:NE	1:A:409:MET:O	1.88	1.06
1:A:402:ARG:CZ	1:A:409:MET:O	2.05	1.05
1:A:405:ARG:CB	1:A:408:SER:OG	2.08	1.01
1:A:405:ARG:CB	1:A:408:SER:HB2	1.87	1.00
1:A:402:ARG:NH2	1:A:409:MET:O	1.93	0.99
1:A:405:ARG:HD3	1:A:408:SER:OG	1.68	0.91
1:A:405:ARG:CA	1:A:408:SER:HB2	2.06	0.85
1:A:408:SER:C	1:A:410:VAL:H	1.80	0.85
1:A:405:ARG:CD	1:A:408:SER:OG	2.30	0.78
1:A:405:ARG:C	1:A:408:SER:HB2	2.10	0.76
1:A:405:ARG:O	1:A:406:GLU:HB2	1.87	0.74
1:A:408:SER:C	1:A:410:VAL:N	2.46	0.73
1:A:291:ILE:HD13	1:A:425:GLY:O	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:SER:O	1:A:409:MET:CG	2.38	0.68
1:A:69:LEU:HD21	1:A:80:GLY:H	1.59	0.67
1:A:408:SER:O	1:A:410:VAL:N	2.30	0.65
1:A:410:VAL:O	1:A:414:ASN:OD1	2.16	0.63
1:A:400:VAL:HG13	1:A:403:GLY:H	1.64	0.62
1:A:406:GLU:O	1:A:409:MET:SD	2.60	0.60
1:A:405:ARG:CG	1:A:408:SER:OG	2.52	0.58
1:A:291:ILE:HD11	1:A:429:GLY:H	1.69	0.57
1:A:405:ARG:HB3	1:A:408:SER:HB3	1.66	0.56
1:A:404:HIS:O	1:A:408:SER:HB3	2.07	0.53
1:A:291:ILE:HD12	1:A:372:CYS:HB3	1.92	0.52
1:A:268:LYS:HB2	1:A:400:VAL:HG11	1.91	0.51
1:A:406:GLU:C	1:A:408:SER:H	2.17	0.51
1:A:406:GLU:C	1:A:408:SER:N	2.65	0.51
1:A:399:MET:O	1:A:400:VAL:HG12	2.11	0.50
1:A:441:ILE:HG12	1:A:444:GLY:H	1.75	0.50
1:A:410:VAL:O	1:A:414:ASN:HB3	2.13	0.49
1:A:64:TRP:CZ2	1:A:300:ASN:HB2	2.49	0.48
1:A:291:ILE:HD11	1:A:429:GLY:N	2.29	0.47
1:A:68:ILE:HG23	1:A:85:VAL:CG1	2.44	0.47
1:A:405:ARG:HD3	1:A:408:SER:HG	1.75	0.47
1:A:187:ILE:HB	1:A:450:ALA:HB1	1.98	0.46
1:A:214:ILE:HD13	1:A:214:ILE:H	1.82	0.45
1:A:410:VAL:O	1:A:414:ASN:CG	2.59	0.45
1:A:64:TRP:CH2	1:A:300:ASN:HB2	2.52	0.45
1:A:408:SER:HB3	1:A:409:MET:H	1.60	0.44
1:A:48:ILE:HG22	3:C:80:PHE:CE1	2.53	0.44
1:A:38:THR:HG22	1:A:42:PHE:CZ	2.54	0.43
1:A:89:LEU:HD13	1:A:297:LEU:HD23	2.01	0.43
1:A:270:ALA:HB3	1:A:276:TYR:HB3	2.01	0.43
1:A:210:GLU:HB2	2:B:52:PHE:CE1	2.55	0.42
1:A:199:THR:HB	1:A:200:THR:H	1.76	0.41
1:A:68:ILE:HG23	1:A:85:VAL:HG13	2.03	0.41
1:A:91:MET:HA	1:A:116:GLN:HE22	1.86	0.41
1:A:53:ILE:HD13	3:C:96:SER:H	1.86	0.41
1:A:407:THR:O	1:A:410:VAL:HG12	2.20	0.40
1:A:410:VAL:O	1:A:414:ASN:CB	2.70	0.40
1:A:405:ARG:CB	1:A:408:SER:HB3	2.38	0.40

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	450/476 (94%)	356 (79%)	41 (9%)	53 (12%)	0	4
2	B	60/68 (88%)	51 (85%)	4 (7%)	5 (8%)	0	9
3	C	34/36 (94%)	27 (79%)	4 (12%)	3 (9%)	0	8
All	All	544/580 (94%)	434 (80%)	49 (9%)	61 (11%)	1	5

All (61) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	49	PRO
1	A	54	MET
1	A	55	SER
1	A	56	SER
1	A	62	PHE
1	A	71	SER
1	A	81	ILE
1	A	102	VAL
1	A	138	GLY
1	A	147	ILE
1	A	149	LEU
1	A	173	TYR
1	A	175	LEU
1	A	199	THR
1	A	214	ILE
1	A	222	THR
1	A	227	VAL
1	A	272	TYR
1	A	316	LEU
1	A	335	ALA
1	A	400	VAL
1	A	412	GLU
1	A	468	VAL

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Mol	Chain	Res	Type
1	A	470	SER
1	A	473	ALA
2	B	24	ARG
2	B	30	ARG
3	C	70	PRO
3	C	72	PRO
1	A	59	ALA
1	A	237	GLN
1	A	273	ARG
1	A	359	VAL
1	A	408	SER
1	A	409	MET
1	A	471	MET
2	B	66	VAL
1	A	70	ALA
1	A	145	ALA
1	A	231	ARG
1	A	270	ALA
1	A	317	LEU
1	A	349	GLU
1	A	398	GLN
1	A	405	ARG
1	A	406	GLU
1	A	466	SER
2	B	29	ASP
3	C	94	THR
1	A	271	ARG
1	A	315	ASN
1	A	226	LYS
1	A	236	ARG
1	A	337	PRO
1	A	382	VAL
1	A	439	GLY
1	A	51	PHE
1	A	103	GLY
1	A	52	GLY
2	B	28	PRO

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	375/398 (94%)	311 (83%)	64 (17%)	2	10
2	B	53/59 (90%)	49 (92%)	4 (8%)	12	33
3	C	32/32 (100%)	26 (81%)	6 (19%)	1	8
All	All	460/489 (94%)	386 (84%)	74 (16%)	4	11

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	29	LYS
1	A	47	GLN
1	A	48	ILE
1	A	49	PRO
1	A	60	ASP
1	A	65	MET
1	A	69	LEU
1	A	76	LEU
1	A	79	LEU
1	A	81	ILE
1	A	82	SER
1	A	89	LEU
1	A	92	GLN
1	A	111	LEU
1	A	112	PHE
1	A	116	GLN
1	A	128	SER
1	A	129	ILE
1	A	155	LEU
1	A	175	LEU
1	A	179	ILE
1	A	180	SER
1	A	186	ASN
1	A	187	ILE
1	A	189	GLU
1	A	192	VAL
1	A	196	PHE
1	A	199	THR
1	A	214	ILE

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Mol	Chain	Res	Type
1	A	220	LEU
1	A	223	ARG
1	A	227	VAL
1	A	230	LEU
1	A	236	ARG
1	A	261	PHE
1	A	265	LEU
1	A	267	ILE
1	A	275	GLN
1	A	276	TYR
1	A	281	ILE
1	A	282	LYS
1	A	284	PHE
1	A	285	TYR
1	A	288	ASN
1	A	295	SER
1	A	297	LEU
1	A	298	VAL
1	A	300	ASN
1	A	301	LEU
1	A	304	ILE
1	A	311	ARG
1	A	400	VAL
1	A	402	ARG
1	A	405	ARG
1	A	407	THR
1	A	408	SER
1	A	409	MET
1	A	410	VAL
1	A	414	ASN
1	A	417	ILE
1	A	441	ILE
1	A	445	THR
1	A	454	ILE
2	B	24	ARG
2	B	33	PHE
2	B	44	PHE
2	B	55	LYS
3	C	72	PRO
3	C	74	LEU
3	C	78	LEU
3	C	80	PHE

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Mol	Chain	Res	Type
3	C	81	ILE
3	C	84	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	116	GLN
1	A	237	GLN
1	A	244	ASN
1	A	306	GLN
1	A	315	ASN
1	A	343	HIS
1	A	360	HIS
2	B	58	HIS
3	C	88	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

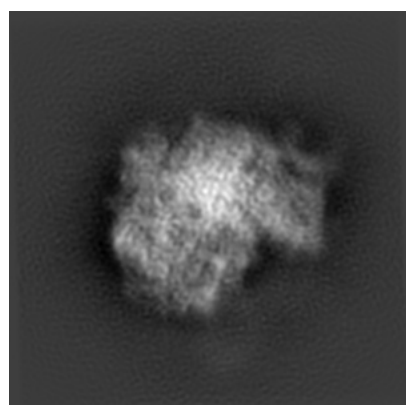
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2510. These allow visual inspection of the internal detail of the map and identification of artifacts.

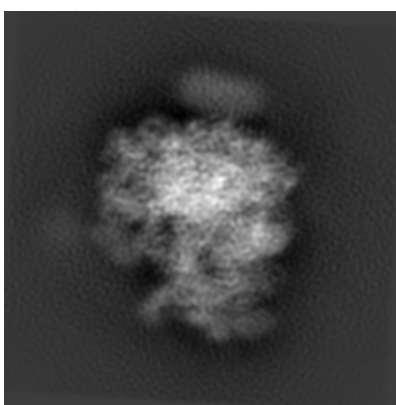
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

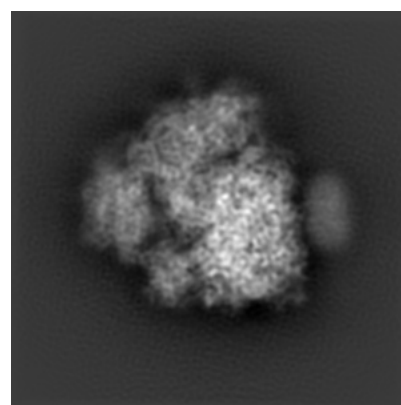
6.1.1 Primary map



X



Y

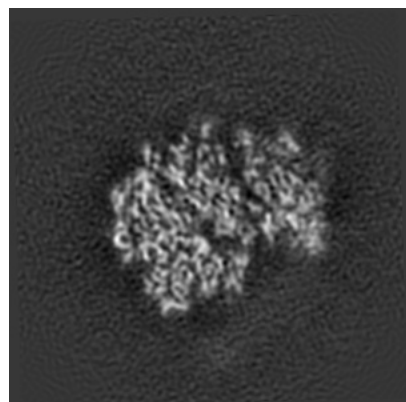


Z

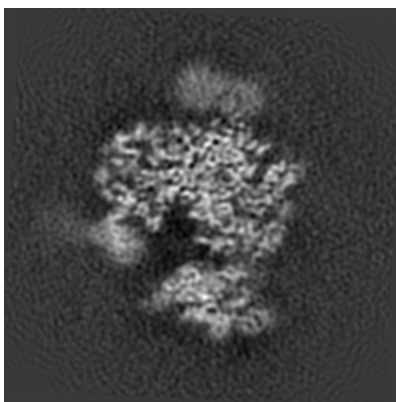
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

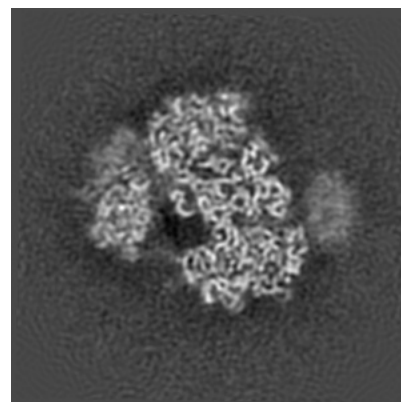
6.2.1 Primary map



X Index: 184



Y Index: 184

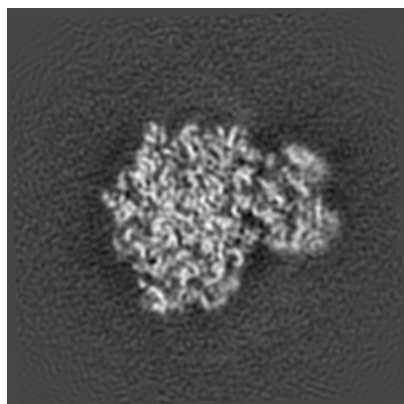


Z Index: 184

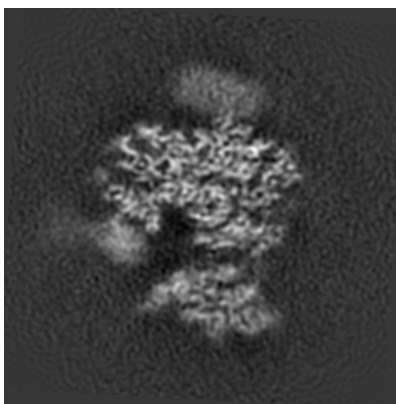
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

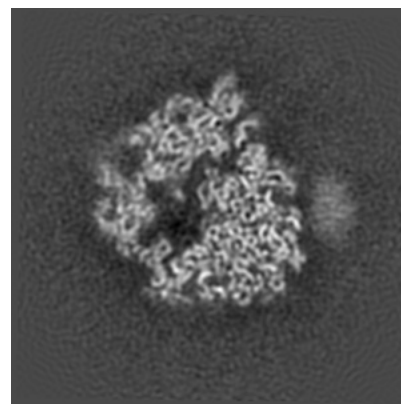
6.3.1 Primary map



X Index: 197



Y Index: 188

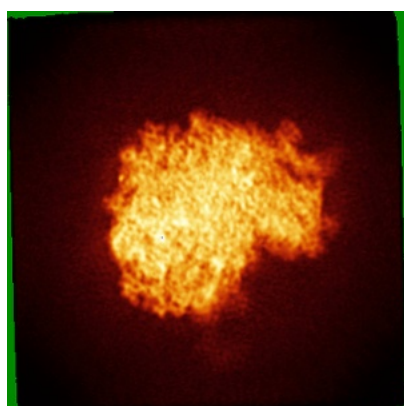


Z Index: 171

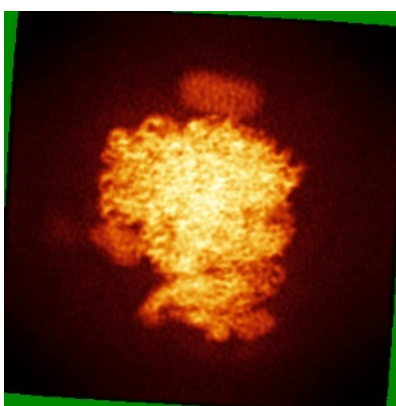
The images above show the largest variance slices of the map in three orthogonal directions.

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

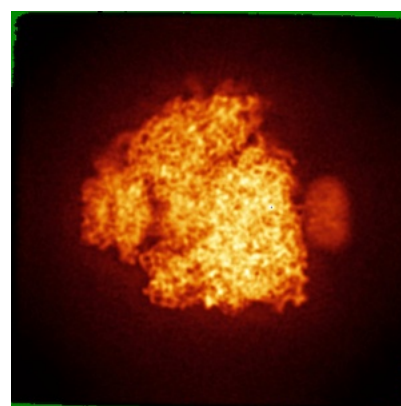
6.4.1 Primary map



X



Y

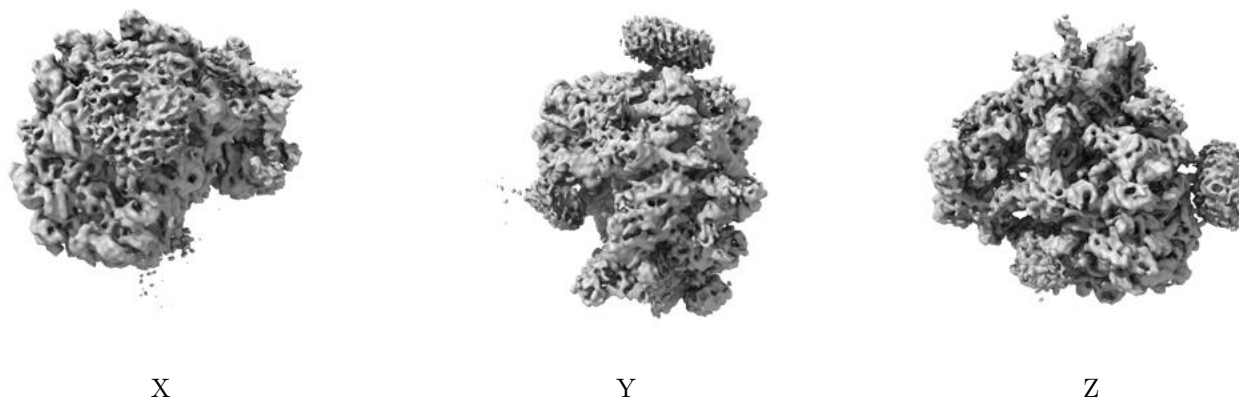


Z

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 0.23. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

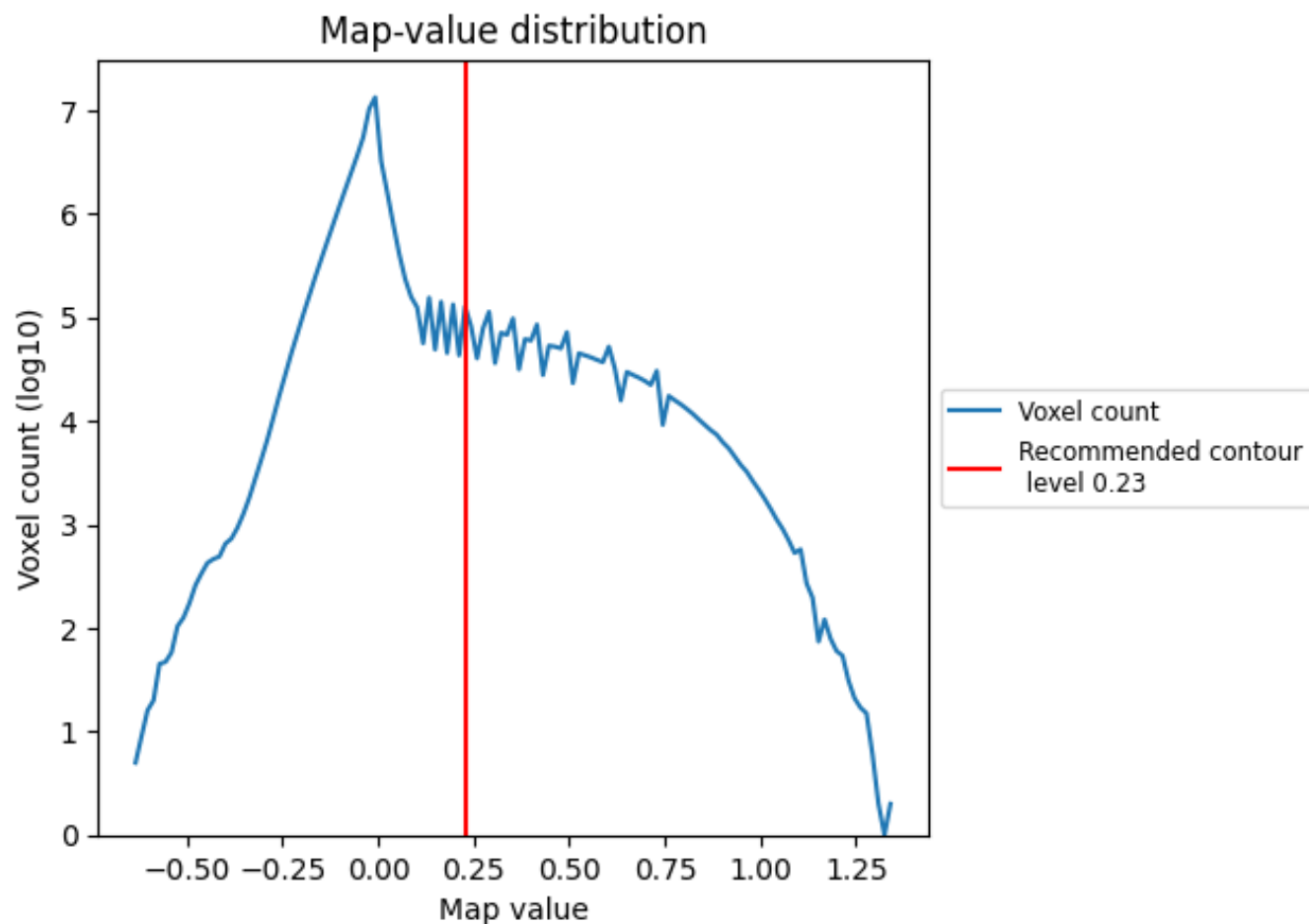
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

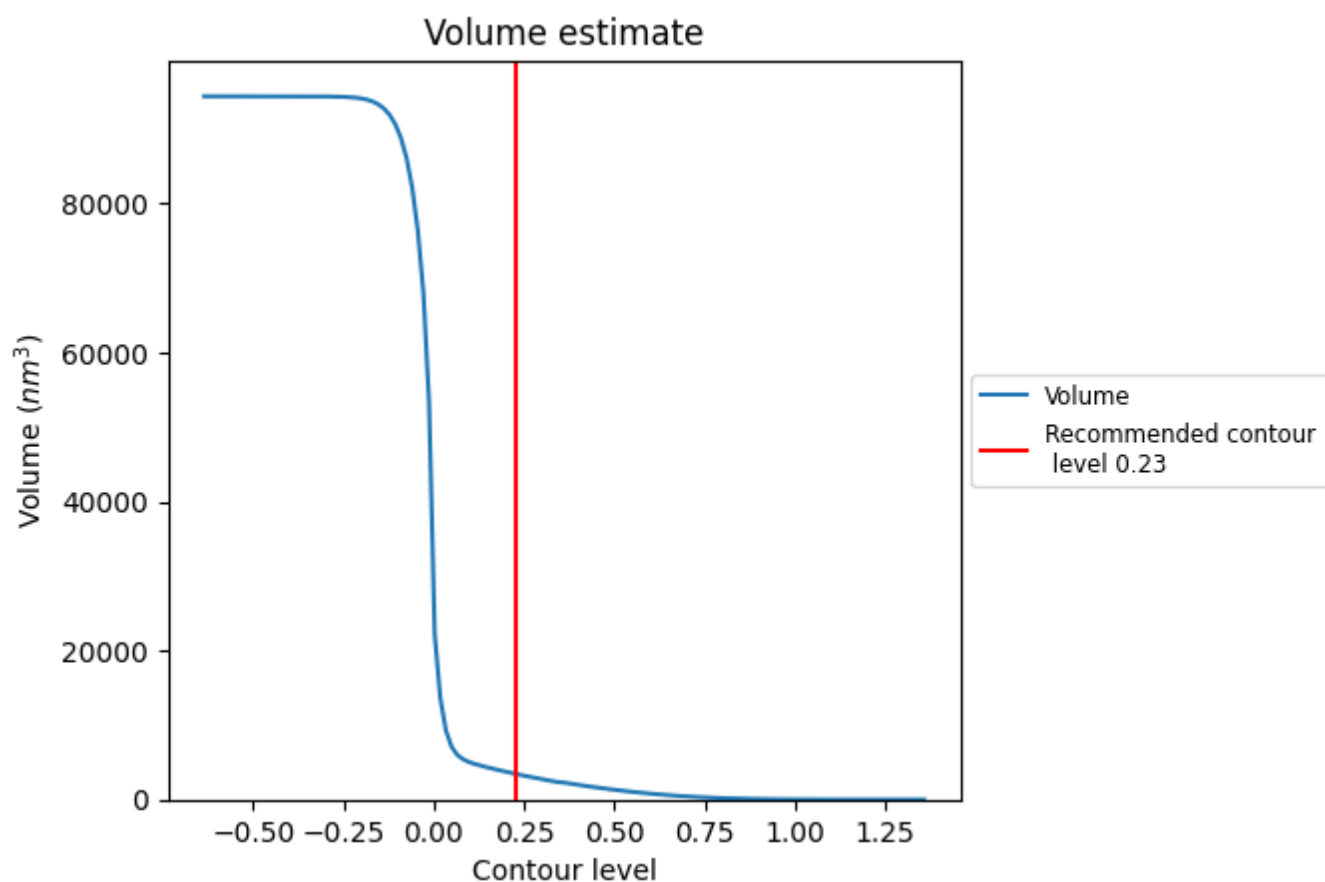
This section contains the results of statistical analysis of the map.

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.

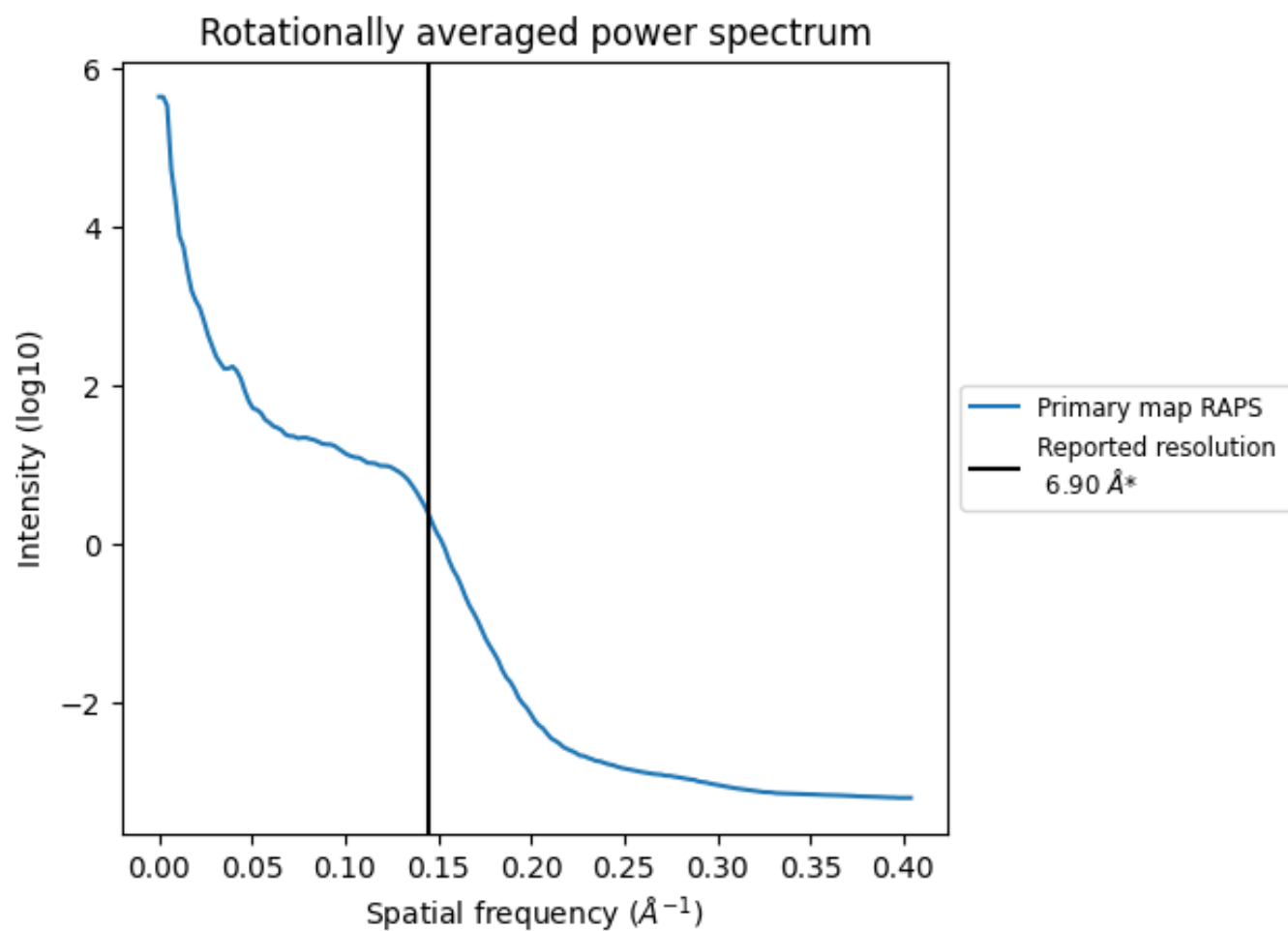
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3414 nm³; this corresponds to an approximate mass of 3084 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 0.145 Å⁻¹

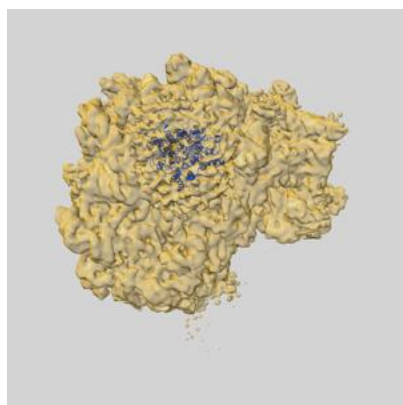
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

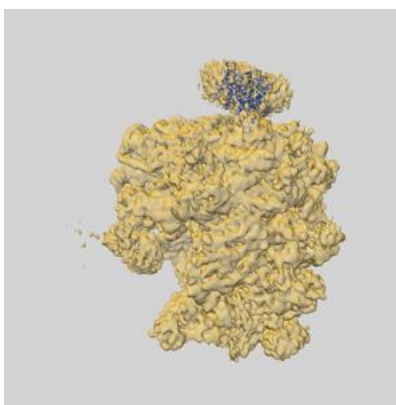
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2510 and PDB model 4CG7. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

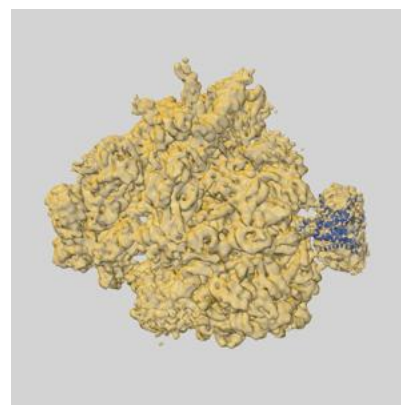
9.1 Map-model overlay [i](#)



X



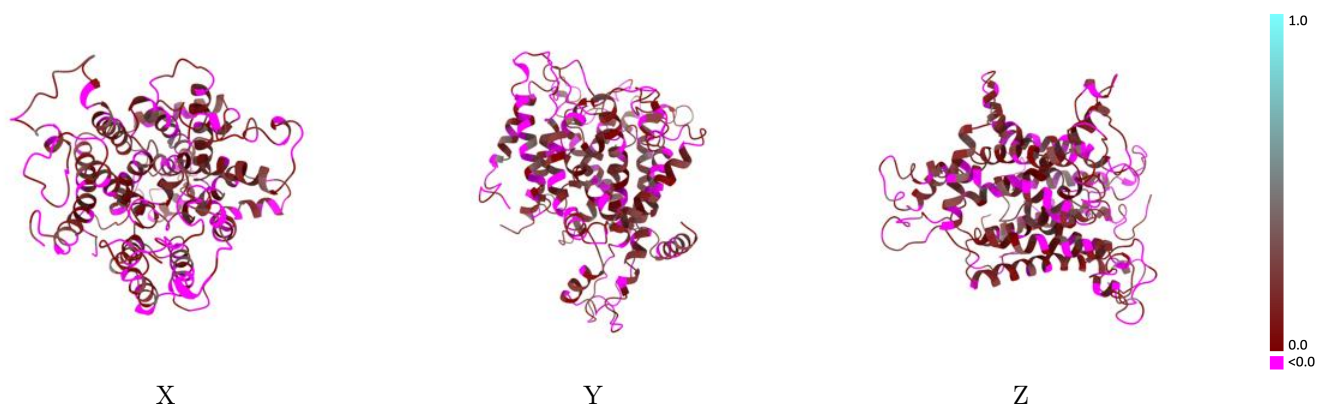
Y



Z

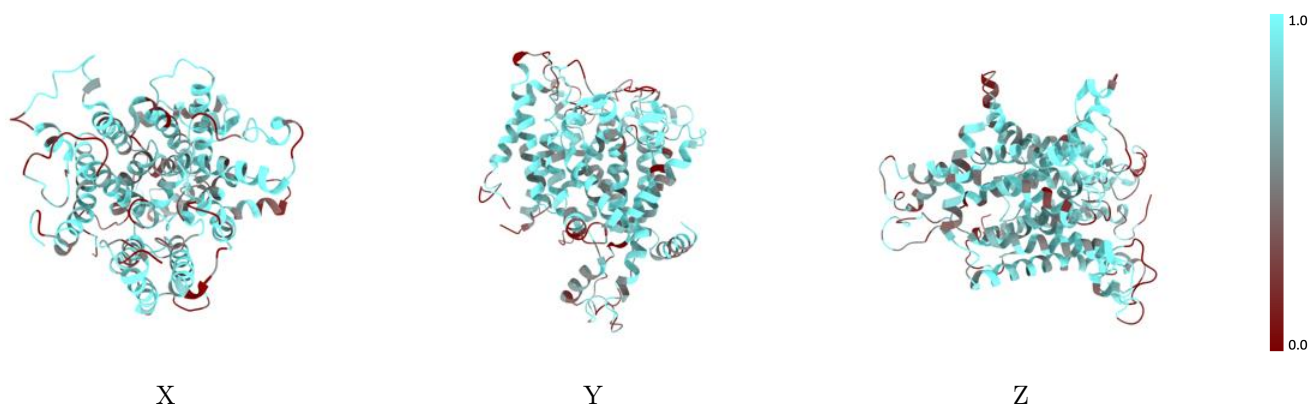
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



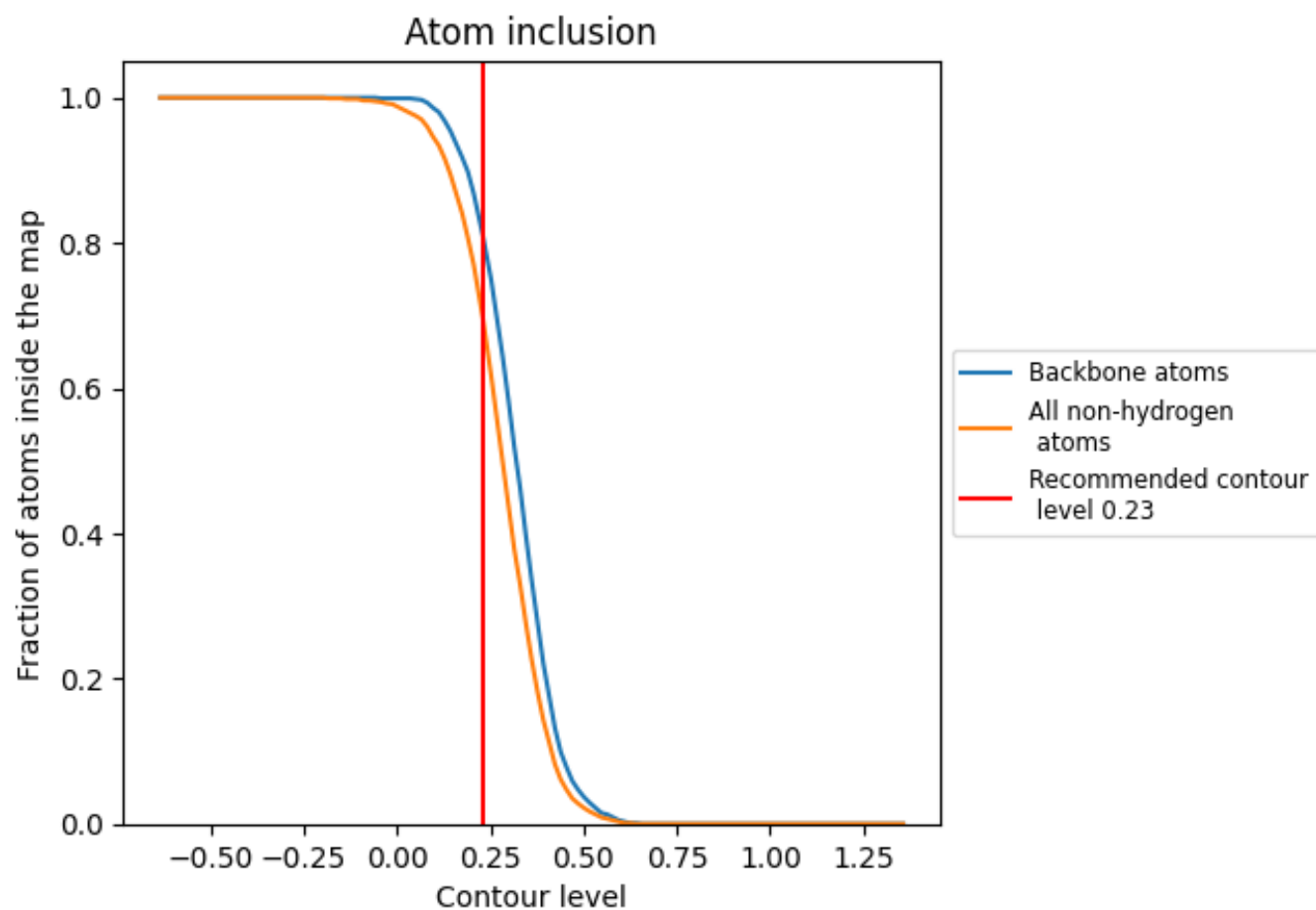
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 70% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6950	0.0740
A	0.6950	0.0750
B	0.7280	0.1060
C	0.6280	0.0030

