



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 01:15 PM UTC

PDB ID : 4CG6 / pdb_00004cg6
EMDB ID : EMD-2512
Title : Cryo-em of the Sec61-complex bound to the 80s ribosome translating a membrane-inserting substrate
Authors : Gogala, M.; Becker, T.; Beatrix, B.; Barrio-Garcia, C.; Berninghausen, O.; Beckmann, R.
Deposited on : 2013-11-21
Resolution : 7.80 Å(reported)
Based on initial model : 2WWB

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

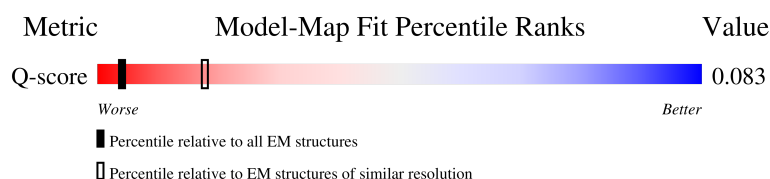
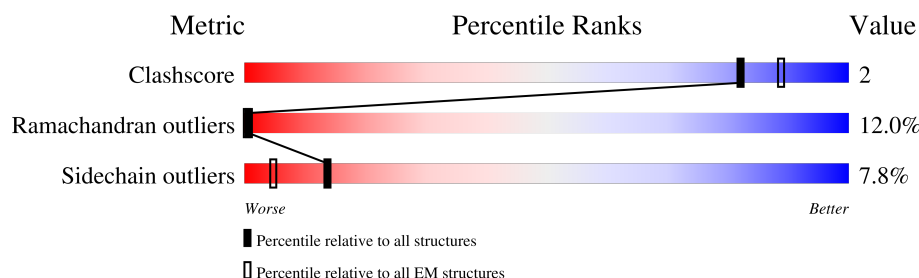
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 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	370 (7.30 - 8.30)

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	45% 68% 17% 8% • 5%
2	B	68	51% 76% 15% 9%
3	C	96	19% 31% 5% • 63%
4	D	17	35% 76% 18% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4383 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.

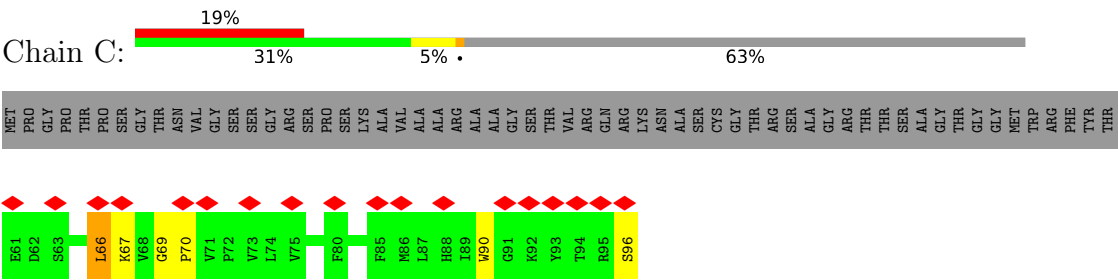
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

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

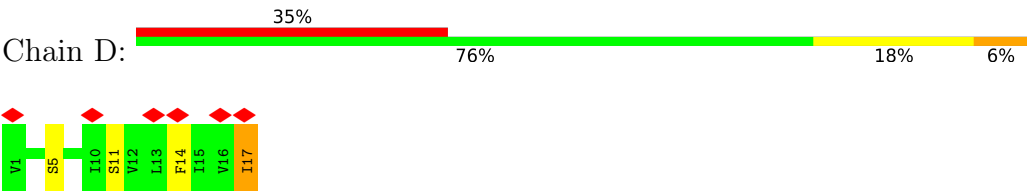
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	36	Total	C	N	O	S	0	0
			281	188	44	47	2		

- Molecule 4 is a protein called PEPTIDE.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	17	Total	C	N	O	0	0
			131	93	17	21		



• Molecule 4: PEPTIDE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30455	Depositor
Resolution determination method	Not provided	
CTF correction method	ON 3D-VOLUME (SPIDER)	Depositor
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	0.793	Depositor
Minimum map value	-0.351	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.1	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.16	1/3552 (0.0%)	1.89	105/4815 (2.2%)
2	B	1.29	1/504 (0.2%)	1.68	6/673 (0.9%)
3	C	1.29	1/289 (0.3%)	1.76	4/391 (1.0%)
4	D	1.75	2/133 (1.5%)	2.00	5/179 (2.8%)
All	All	1.20	5/4478 (0.1%)	1.86	120/6058 (2.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	96	SER	C-O	-11.57	1.00	1.23
4	D	17	ILE	C-OXT	-11.56	1.00	1.23
4	D	17	ILE	C-O	-11.56	1.00	1.23
2	B	68	GLY	C-O	-11.55	1.00	1.23
1	A	476	PHE	C-O	-11.53	1.00	1.23

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	288	ASN	CA-C-N	9.49	126.22	120.24
1	A	288	ASN	C-N-CA	9.49	126.22	120.24
1	A	405	ARG	CA-C-N	9.14	139.00	121.54
1	A	405	ARG	C-N-CA	9.14	139.00	121.54
3	C	70	PRO	CA-C-N	8.52	125.61	120.24
3	C	70	PRO	C-N-CA	8.52	125.61	120.24
1	A	47	GLN	CA-C-N	7.77	125.13	120.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	GLN	C-N-CA	7.77	125.13	120.24
1	A	441	ILE	CA-C-N	7.70	128.47	120.00
1	A	441	ILE	C-N-CA	7.70	128.47	120.00
1	A	113	ASN	CA-C-N	7.31	128.09	119.98
1	A	113	ASN	C-N-CA	7.31	128.09	119.98
1	A	347	PRO	N-CA-C	-7.29	101.81	110.70
1	A	227	VAL	CB-CA-C	7.28	123.22	111.29
1	A	139	ASP	CA-C-O	-7.16	111.39	118.34
1	A	45	CYS	CA-C-N	7.09	129.78	120.28
1	A	45	CYS	C-N-CA	7.09	129.78	120.28
1	A	239	LEU	N-CA-C	6.92	122.98	113.16
1	A	140	PRO	CA-N-CD	-6.88	102.37	112.00
1	A	60	ASP	N-CA-CB	6.81	122.49	110.37
1	A	179	ILE	N-CA-CB	6.81	122.47	111.23
1	A	239	LEU	CA-C-O	-6.81	111.74	118.34
1	A	204	GLY	CA-C-N	6.66	129.21	120.28
1	A	204	GLY	C-N-CA	6.66	129.21	120.28
1	A	283	LEU	CB-CA-C	6.54	116.30	109.83
1	A	111	LEU	N-CA-CB	6.33	121.19	110.49
1	A	408	SER	N-CA-C	-6.32	97.34	110.80
1	A	218	HIS	CA-CB-CG	6.31	120.11	113.80
1	A	240	PRO	CA-N-CD	-6.27	103.22	112.00
1	A	475	LEU	N-CA-CB	6.21	120.99	110.49
4	D	14	PHE	N-CA-CB	6.17	119.19	110.12
1	A	240	PRO	N-CA-C	6.17	125.17	112.47
1	A	85	VAL	CA-C-N	6.16	128.53	120.28
1	A	85	VAL	C-N-CA	6.16	128.53	120.28
1	A	135	GLY	CA-C-N	6.10	128.46	120.28
1	A	135	GLY	C-N-CA	6.10	128.46	120.28
1	A	347	PRO	CB-CA-C	6.04	118.29	110.92
1	A	193	TRP	CA-C-N	5.97	128.28	120.28
1	A	193	TRP	C-N-CA	5.97	128.28	120.28
1	A	244	ASN	CA-CB-CG	5.93	118.53	112.60
2	B	43	GLY	CA-C-N	5.90	128.19	120.28
2	B	43	GLY	C-N-CA	5.90	128.19	120.28
1	A	160	LEU	N-CA-C	-5.85	104.49	111.69
1	A	235	TYR	CB-CA-C	5.82	122.01	110.42
1	A	224	THR	CA-C-N	5.74	127.97	120.28
1	A	224	THR	C-N-CA	5.74	127.97	120.28
1	A	119	PHE	CA-C-N	5.74	126.35	119.98
1	A	119	PHE	C-N-CA	5.74	126.35	119.98
1	A	271	ARG	N-CA-CB	5.74	120.18	110.49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	GLU	N-CA-CB	5.70	118.38	110.17
3	C	66	LEU	CA-C-N	5.66	132.34	121.54
3	C	66	LEU	C-N-CA	5.66	132.34	121.54
1	A	61	PRO	CA-N-CD	-5.64	104.10	112.00
1	A	68	ILE	CA-C-N	5.64	127.78	120.44
1	A	68	ILE	C-N-CA	5.64	127.78	120.44
1	A	134	THR	CA-C-N	5.64	125.46	120.10
1	A	134	THR	C-N-CA	5.64	125.46	120.10
2	B	33	PHE	N-CA-CB	5.60	118.36	110.12
1	A	325	SER	N-CA-CB	5.58	119.92	110.49
4	D	11	SER	CA-C-N	5.58	128.11	120.46
4	D	11	SER	C-N-CA	5.58	128.11	120.46
1	A	61	PRO	N-CA-C	5.56	123.93	112.47
1	A	60	ASP	CA-C-N	5.50	126.72	119.84
1	A	60	ASP	C-N-CA	5.50	126.72	119.84
1	A	75	THR	CA-C-N	5.49	127.64	120.28
1	A	75	THR	C-N-CA	5.49	127.64	120.28
1	A	287	SER	CA-C-N	5.45	127.58	120.28
1	A	287	SER	C-N-CA	5.45	127.58	120.28
2	B	42	ILE	CA-C-N	5.45	126.03	119.98
2	B	42	ILE	C-N-CA	5.45	126.03	119.98
1	A	304	ILE	CA-C-N	5.43	127.83	120.38
1	A	304	ILE	C-N-CA	5.43	127.83	120.38
1	A	407	THR	N-CA-CB	5.43	119.67	110.49
1	A	447	ILE	N-CA-C	5.43	115.63	110.42
1	A	348	PRO	CA-C-N	5.42	131.90	121.54
1	A	348	PRO	C-N-CA	5.42	131.90	121.54
1	A	227	VAL	N-CA-CB	5.42	120.17	111.23
1	A	27	GLN	N-CA-CB	5.40	119.62	110.49
1	A	244	ASN	N-CA-CB	5.37	117.86	110.07
1	A	336	TYR	CB-CA-C	5.37	120.75	110.17
1	A	296	ALA	N-CA-C	5.36	117.12	111.28
1	A	48	ILE	CA-C-N	5.33	124.97	119.05
1	A	48	ILE	C-N-CA	5.33	124.97	119.05
1	A	209	PHE	N-CA-C	5.31	122.10	110.80
1	A	331	GLY	CA-C-N	5.29	125.05	119.76
1	A	331	GLY	C-N-CA	5.29	125.05	119.76
1	A	442	GLY	CA-C-N	5.29	127.80	120.29
1	A	442	GLY	C-N-CA	5.29	127.80	120.29
1	A	104	ASP	CA-C-N	5.28	134.68	121.80
1	A	104	ASP	C-N-CA	5.28	134.68	121.80
1	A	38	THR	CA-C-N	5.23	127.29	120.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	38	THR	C-N-CA	5.23	127.29	120.28
1	A	347	PRO	CA-C-O	-5.21	113.00	120.56
1	A	234	PHE	CA-CB-CG	5.17	118.97	113.80
1	A	69	LEU	CA-C-N	5.16	131.40	121.54
1	A	69	LEU	C-N-CA	5.16	131.40	121.54
1	A	41	ILE	CA-C-N	5.14	127.17	120.28
1	A	41	ILE	C-N-CA	5.14	127.17	120.28
1	A	112	PHE	CA-C-N	5.13	131.33	121.54
1	A	112	PHE	C-N-CA	5.13	131.33	121.54
1	A	446	GLY	N-CA-C	5.12	120.24	113.37
2	B	65	ILE	N-CA-C	-5.11	108.85	113.71
1	A	99	ILE	CA-C-N	5.11	131.17	121.97
1	A	99	ILE	C-N-CA	5.11	131.17	121.97
1	A	184	ALA	CA-C-N	5.10	127.12	120.28
1	A	184	ALA	C-N-CA	5.10	127.12	120.28
1	A	284	PHE	N-CA-C	-5.10	107.11	113.38
1	A	58	SER	CA-C-N	5.08	131.24	121.54
1	A	58	SER	C-N-CA	5.08	131.24	121.54
1	A	404	HIS	CA-C-N	5.07	131.97	121.32
1	A	404	HIS	C-N-CA	5.07	131.97	121.32
1	A	100	ILE	CA-C-N	5.07	131.22	121.54
1	A	100	ILE	C-N-CA	5.07	131.22	121.54
4	D	5	SER	CA-C-N	5.06	126.94	120.56
4	D	5	SER	C-N-CA	5.06	126.94	120.56
1	A	238	ASN	N-CA-CB	5.06	119.04	110.49
1	A	404	HIS	CA-CB-CG	5.04	118.84	113.80
1	A	157	VAL	CA-C-N	5.03	127.43	120.29
1	A	157	VAL	C-N-CA	5.03	127.43	120.29
1	A	349	GLU	N-CA-CB	5.01	118.96	110.49

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	203	THR	Peptide
1	A	272	TYR	Peptide
1	A	276	TYR	Sidechain
1	A	313	SER	Peptide
1	A	403	GLY	Peptide
1	A	406	GLU	Peptide
1	A	414	ASN	Peptide
1	A	440	ALA	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	3477	0	3575	19	0
2	B	494	0	527	0	0
3	C	281	0	294	1	0
4	D	131	0	147	2	0
All	All	4383	0	4543	22	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 2.

All (22) 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:358:PRO:O	1:A:359:VAL:HG23	1.52	1.10
1:A:356:GLU:O	1:A:358:PRO:HD3	1.64	0.96
1:A:358:PRO:O	1:A:359:VAL:CG2	2.30	0.77
1:A:356:GLU:O	1:A:358:PRO:CD	2.33	0.76
4:D:17:ILE:OXT	4:D:17:ILE:HG22	1.92	0.68
1:A:357:ASP:O	1:A:359:VAL:N	2.30	0.65
1:A:99:ILE:HG23	1:A:100:ILE:H	1.64	0.63
1:A:343:HIS:CE1	1:A:360:HIS:HE1	2.17	0.62
4:D:17:ILE:OXT	4:D:17:ILE:CG2	2.49	0.60
1:A:448:LEU:HD22	1:A:448:LEU:H	1.67	0.59
1:A:357:ASP:O	1:A:358:PRO:C	2.48	0.54
1:A:358:PRO:O	1:A:359:VAL:CB	2.57	0.52
1:A:355:LEU:C	1:A:357:ASP:H	2.18	0.52
1:A:231:ARG:HG2	1:A:233:ALA:H	1.75	0.51
1:A:227:VAL:HG12	1:A:228:ARG:H	1.79	0.48
1:A:343:HIS:CE1	1:A:360:HIS:CE1	2.99	0.47
3:C:66:LEU:H	3:C:66:LEU:HD23	1.82	0.45
1:A:347:PRO:HG3	1:A:355:LEU:HD23	1.98	0.45
1:A:440:ALA:HB3	1:A:444:GLY:C	2.42	0.44
1:A:214:ILE:HD13	1:A:214:ILE:H	1.83	0.44
1:A:347:PRO:HB2	1:A:348:PRO:HD2	2.01	0.43
1:A:352:GLY:O	1:A:355:LEU:HD11	2.18	0.43

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%)	344 (76%)	47 (10%)	59 (13%)	0	4
2	B	60/68 (88%)	54 (90%)	1 (2%)	5 (8%)	0	9
3	C	34/96 (35%)	29 (85%)	2 (6%)	3 (9%)	0	8
4	D	15/17 (88%)	15 (100%)	0	0	100	100
All	All	559/657 (85%)	442 (79%)	50 (9%)	67 (12%)	1	4

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	50	LEU
1	A	59	ALA
1	A	60	ASP
1	A	61	PRO
1	A	70	ALA
1	A	75	THR
1	A	98	LYS
1	A	99	ILE
1	A	100	ILE
1	A	102	VAL
1	A	105	THR
1	A	110	ALA
1	A	113	ASN
1	A	140	PRO
1	A	179	ILE
1	A	207	MET
1	A	209	PHE
1	A	227	VAL
1	A	233	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	238	ASN
1	A	240	PRO
1	A	275	GLN
1	A	325	SER
1	A	327	THR
1	A	336	TYR
1	A	347	PRO
1	A	349	GLU
1	A	350	SER
1	A	357	ASP
1	A	358	PRO
1	A	359	VAL
1	A	398	GLN
1	A	400	VAL
1	A	406	GLU
1	A	408	SER
1	A	412	GLU
1	A	441	ILE
1	A	470	SER
1	A	475	LEU
2	B	30	ARG
1	A	101	GLU
1	A	107	LYS
1	A	111	LEU
1	A	271	ARG
2	B	27	LYS
2	B	66	VAL
3	C	67	LYS
3	C	69	GLY
1	A	108	ASP
1	A	109	ARG
1	A	147	ILE
1	A	231	ARG
1	A	280	PRO
1	A	467	GLU
2	B	29	ASP
1	A	53	ILE
1	A	266	PRO
3	C	90	TRP
1	A	62	PHE
1	A	224	THR
1	A	356	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	407	THR
1	A	382	VAL
1	A	468	VAL
1	A	198	PRO
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%)	338 (90%)	37 (10%)	7	24
2	B	53/59 (90%)	53 (100%)	0	100	100
3	C	32/74 (43%)	32 (100%)	0	100	100
4	D	16/16 (100%)	16 (100%)	0	100	100
All	All	476/547 (87%)	439 (92%)	37 (8%)	14	32

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	48	ILE
1	A	50	LEU
1	A	53	ILE
1	A	54	MET
1	A	61	PRO
1	A	89	LEU
1	A	140	PRO
1	A	165	LEU
1	A	205	ARG
1	A	208	GLU
1	A	209	PHE
1	A	210	GLU
1	A	213	ILE
1	A	214	ILE
1	A	218	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	226	LYS
1	A	230	LEU
1	A	231	ARG
1	A	234	PHE
1	A	235	TYR
1	A	240	PRO
1	A	264	ASP
1	A	265	LEU
1	A	275	GLN
1	A	276	TYR
1	A	282	LYS
1	A	283	LEU
1	A	297	LEU
1	A	298	VAL
1	A	336	TYR
1	A	337	PRO
1	A	357	ASP
1	A	404	HIS
1	A	414	ASN
1	A	448	LEU
1	A	458	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	315	ASN
1	A	343	HIS
1	A	360	HIS
1	A	456	GLN
3	C	88	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

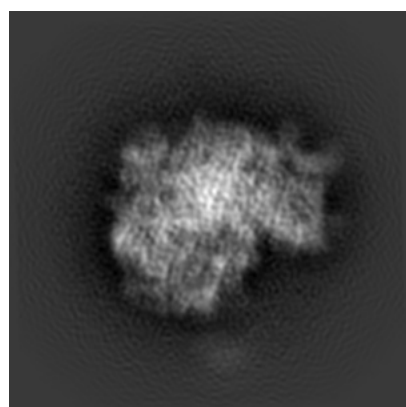
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2512. These allow visual inspection of the internal detail of the map and identification of artifacts.

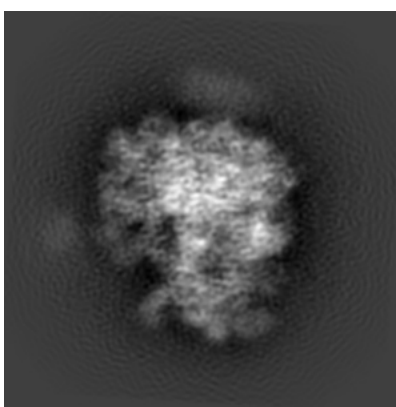
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

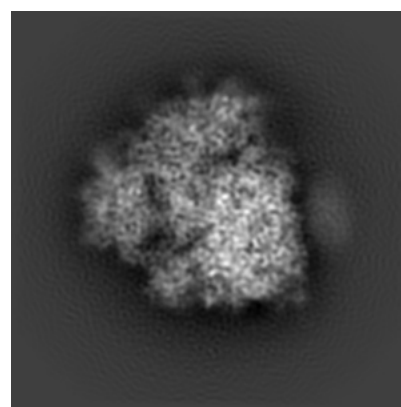
6.1.1 Primary map



X



Y

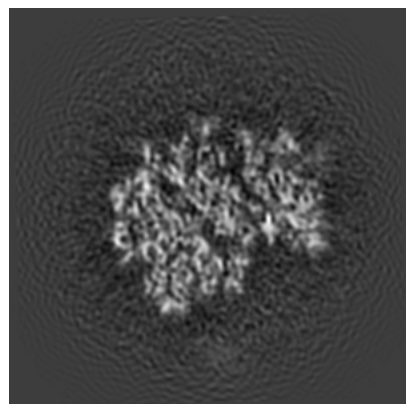


Z

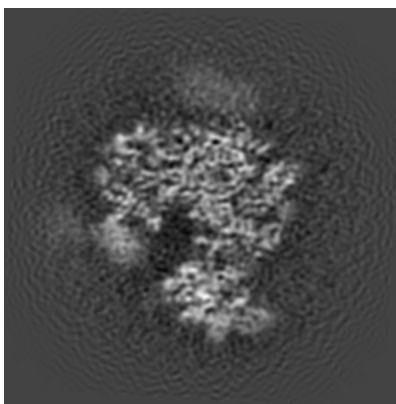
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

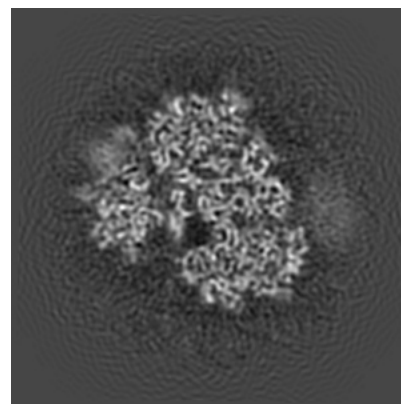
6.2.1 Primary map



X Index: 184



Y Index: 184

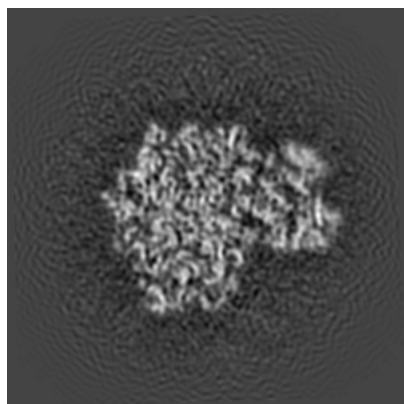


Z Index: 184

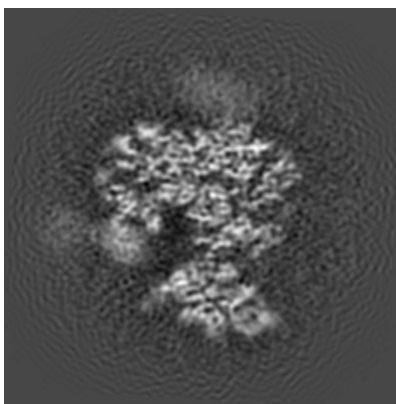
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

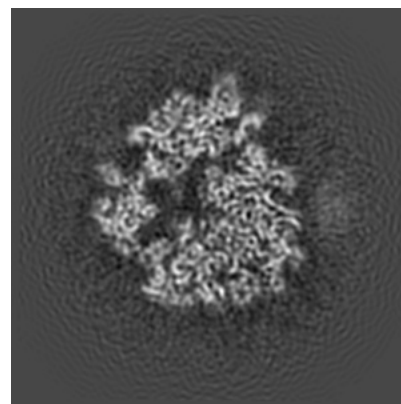
6.3.1 Primary map



X Index: 197



Y Index: 187

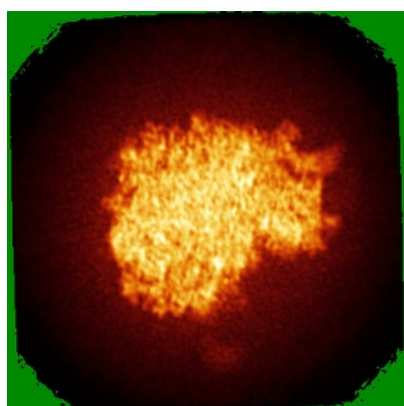


Z Index: 168

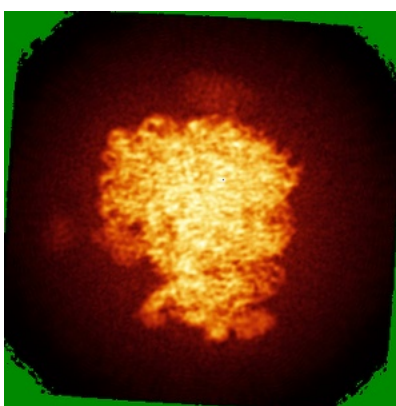
The images above show the largest variance slices of the map in three orthogonal directions.

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

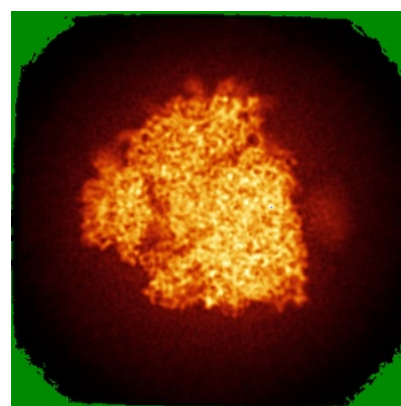
6.4.1 Primary map



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

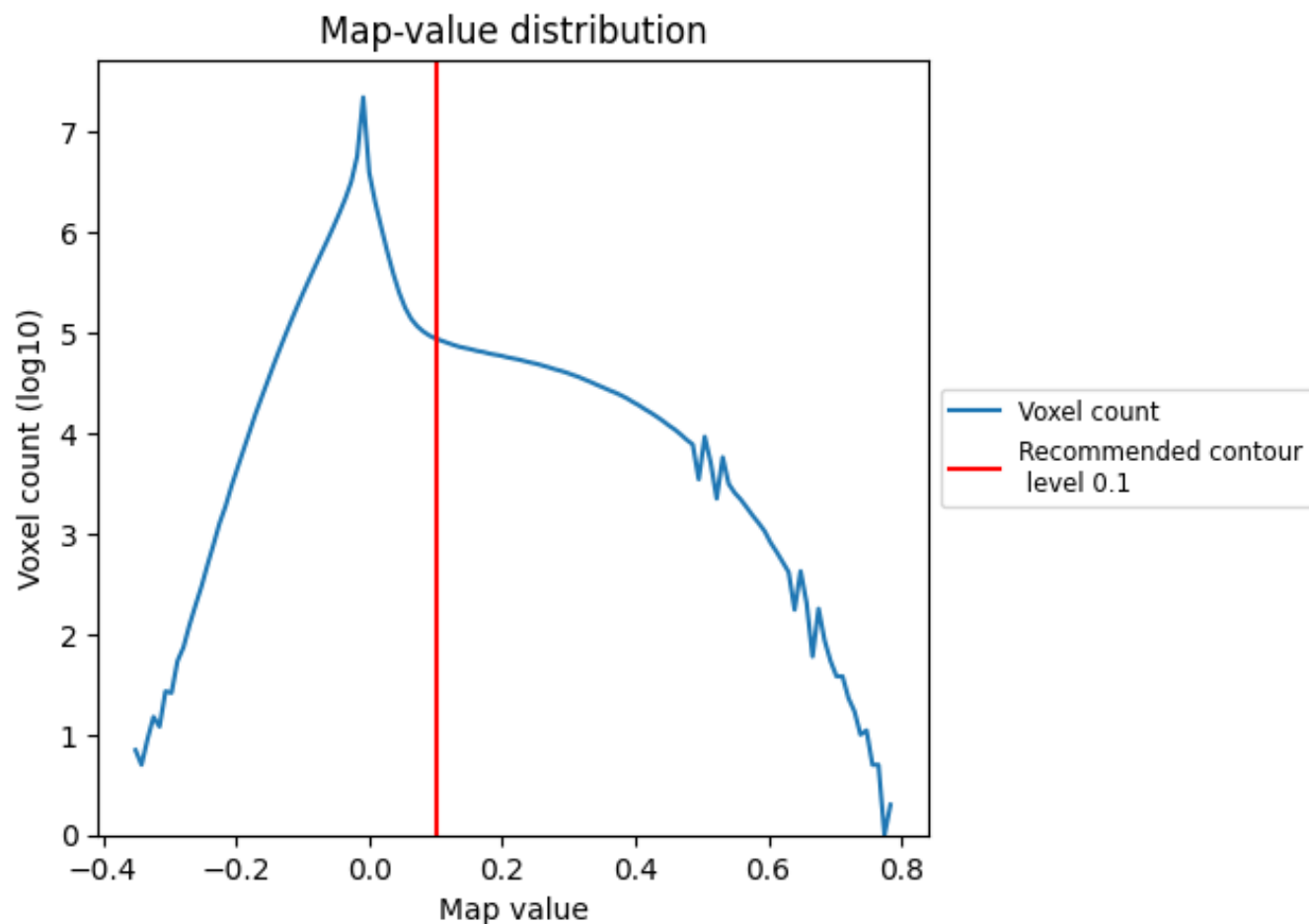
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

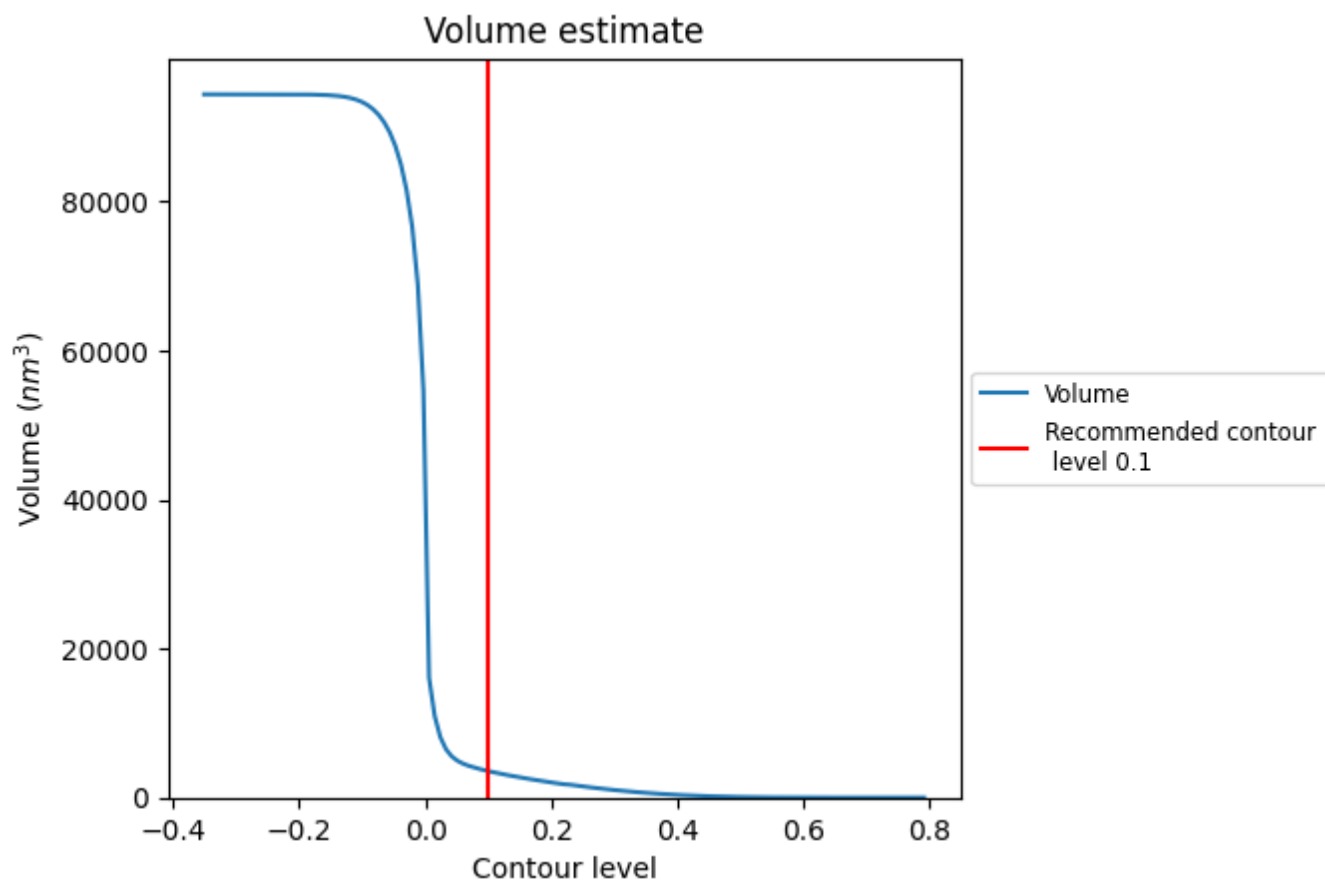
This section contains the results of statistical analysis of the map.

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.

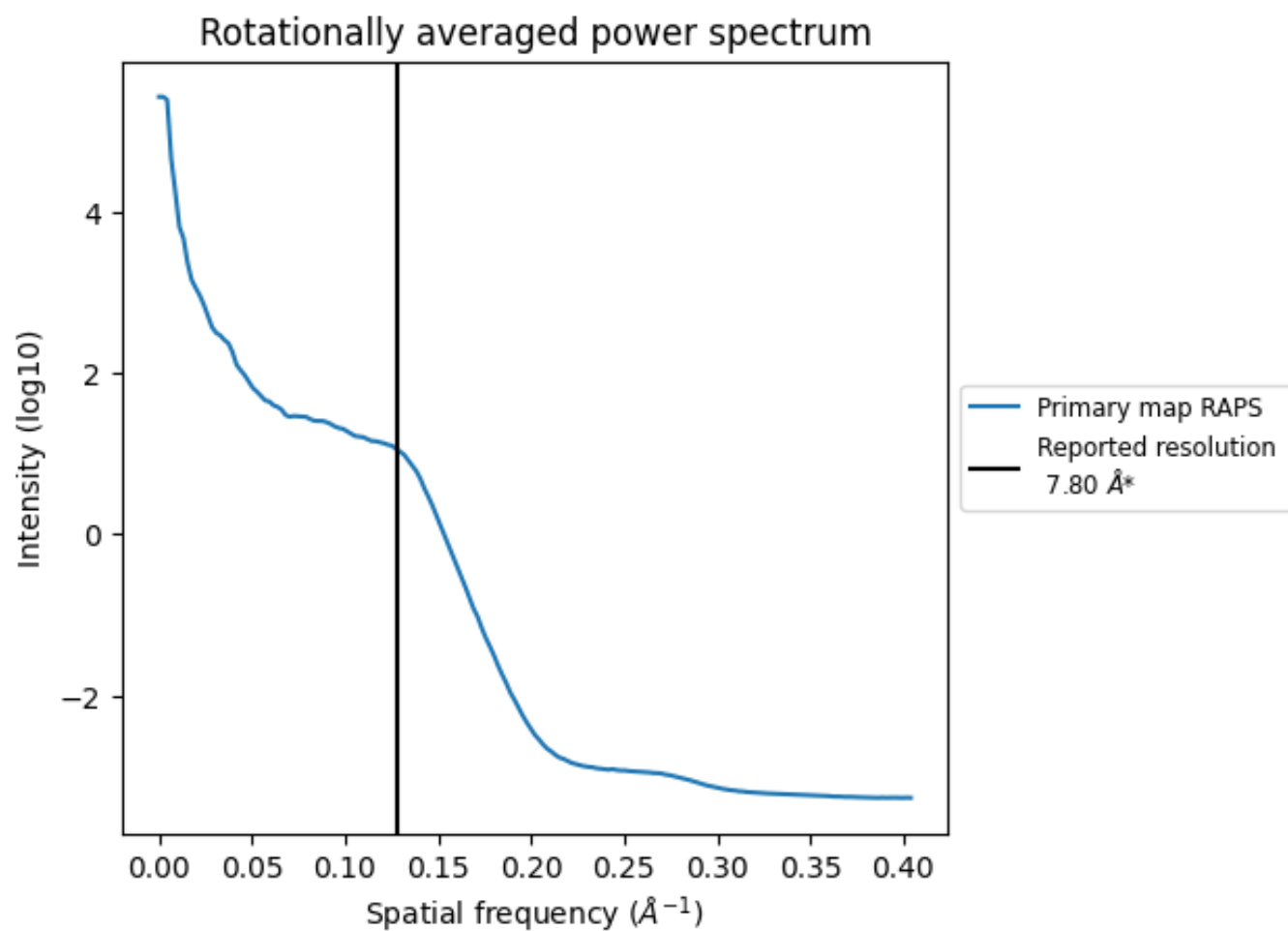
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3560 nm³; this corresponds to an approximate mass of 3215 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 0.128 Å⁻¹

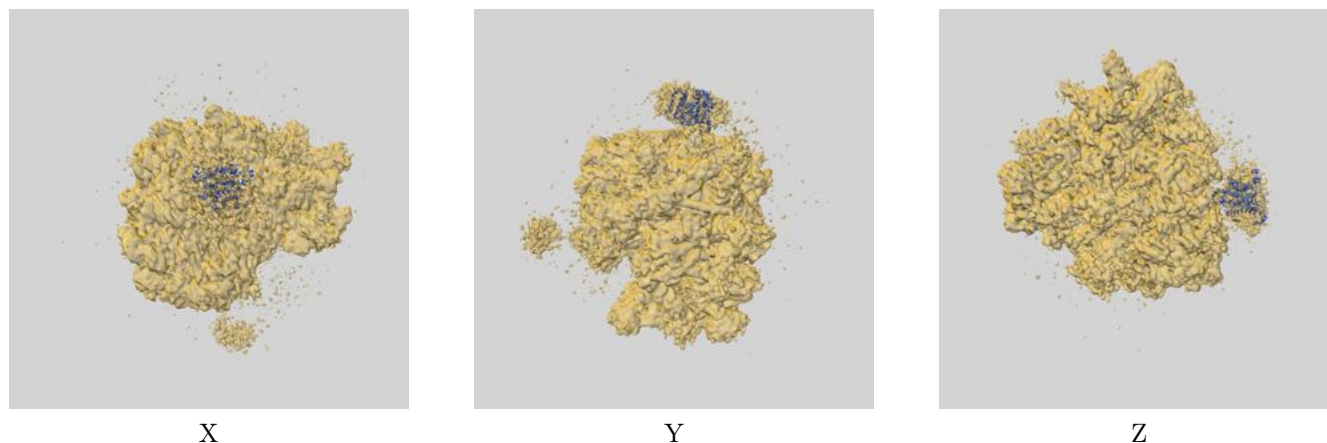
8 Fourier-Shell correlation ⓘ

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-2512 and PDB model 4CG6. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.1 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](#)

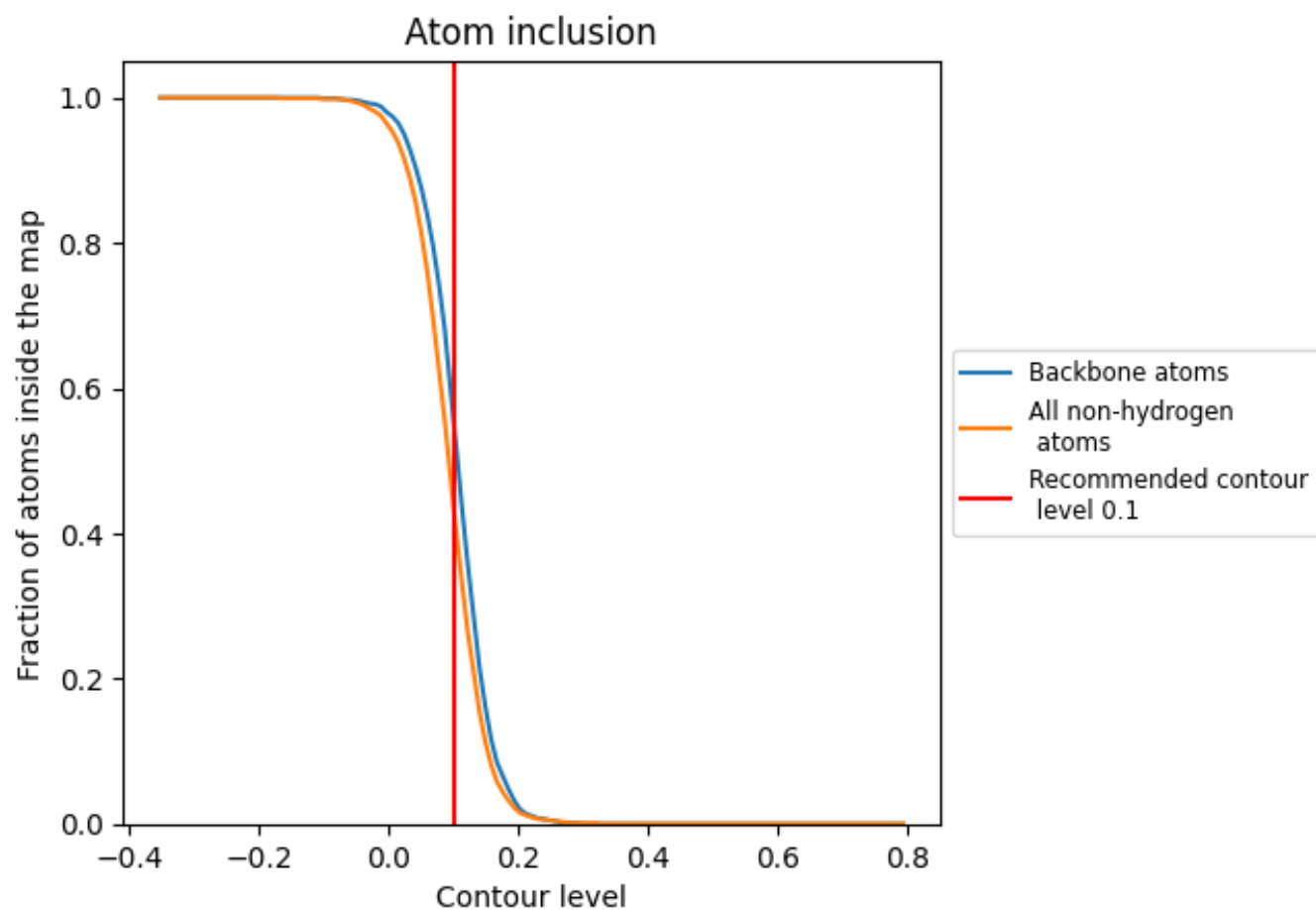


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 44% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4370	0.0830
A	0.4510	0.0910
B	0.3770	0.0400
C	0.3760	0.0630
D	0.4350	0.0950

