



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:20 PM UTC

PDB ID : 4CG5 / pdb_00004cg5
EMDB ID : EMD-2511
Title : Cryo-EM of the Sec61-complex bound to the 80S ribosome translating a secretory substrate
Authors : Gogala, M.; Becker, T.; Beatrix, B.; Barrio-Garcia, C.; Berninghausen, O.; Beckmann, R.
Deposited on : 2013-11-21
Resolution : 7.40 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

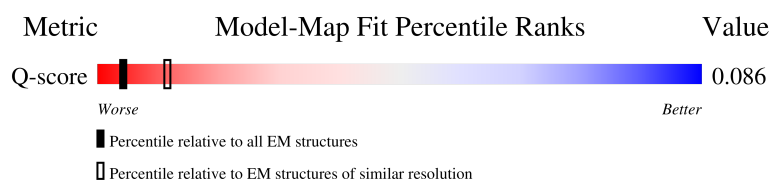
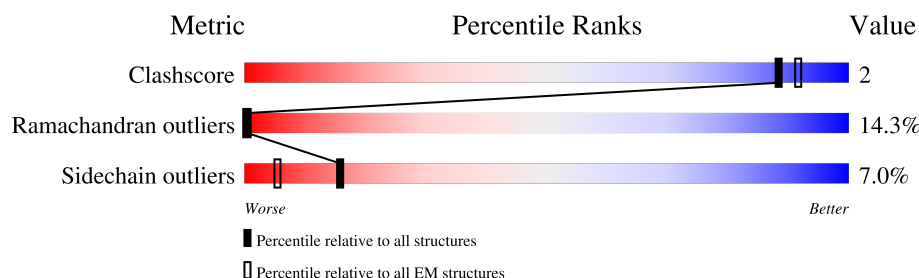
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	412 (6.90 - 7.90)

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		

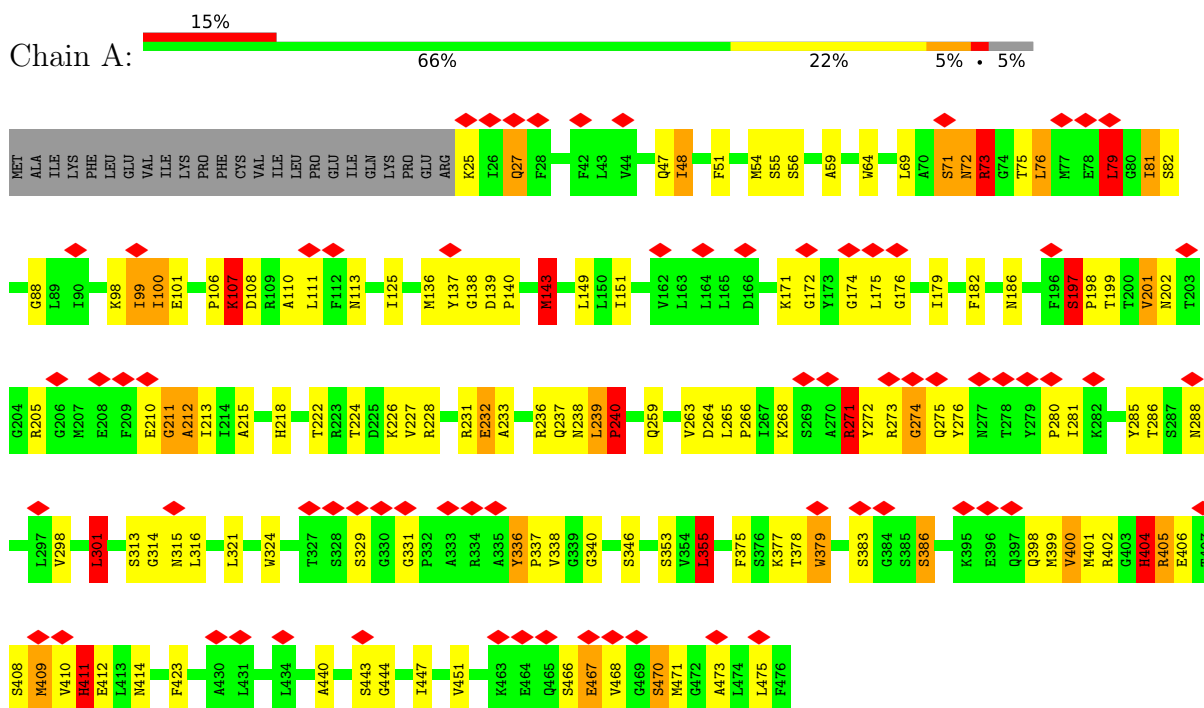
- Molecule 3 is a protein called PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT BETA.

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

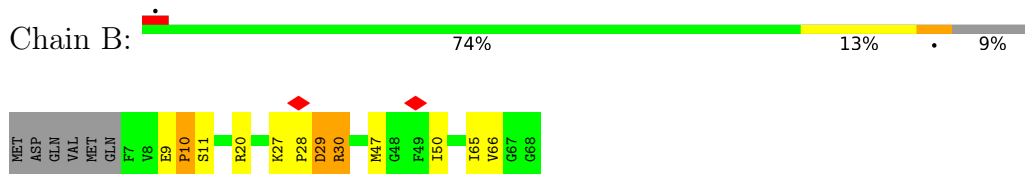
3 Residue-property plots

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.

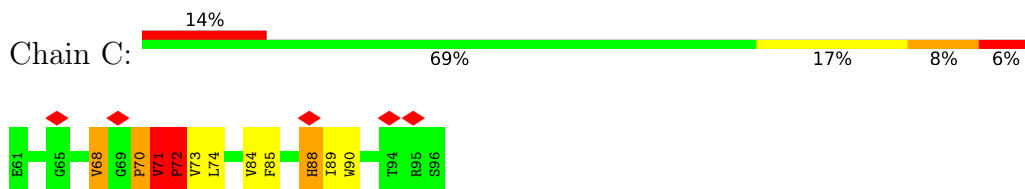
- Molecule 1: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT ALPHA ISOFORM 1



- Molecule 2: PROTEIN TRANSPORT PROTEIN SEC61 SUBUNIT GAMMA



- Molecule 3: PROTEIN 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	53248	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	1.033	Depositor
Minimum map value	-0.649	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.062	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	1.24	4/3552 (0.1%)	1.93	98/4815 (2.0%)
2	B	1.17	0/504	1.83	14/673 (2.1%)
3	C	1.16	0/289	2.10	10/391 (2.6%)
All	All	1.22	4/4345 (0.1%)	1.93	122/5879 (2.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	271	ARG	CD-NE	5.94	1.54	1.46
1	A	411	HIS	ND1-CE1	5.83	1.38	1.32
1	A	281	ILE	CA-C	-5.72	1.45	1.52
1	A	406	GLU	CA-CB	5.42	1.62	1.53

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	70	PRO	CB-CA-C	9.52	127.27	111.56
1	A	125	ILE	CA-C-N	8.91	129.87	119.98
1	A	125	ILE	C-N-CA	8.91	129.87	119.98
1	A	288	ASN	CA-C-N	8.82	125.80	120.24
1	A	288	ASN	C-N-CA	8.82	125.80	120.24
3	C	70	PRO	CA-N-CD	-7.79	101.10	112.00
3	C	88	HIS	CA-C-N	7.76	131.70	120.91
3	C	88	HIS	C-N-CA	7.76	131.70	120.91
1	A	408	SER	CA-C-N	7.60	136.05	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	SER	C-N-CA	7.60	136.05	121.54
1	A	466	SER	CA-C-N	7.57	135.99	121.54
1	A	466	SER	C-N-CA	7.57	135.99	121.54
1	A	211	GLY	CA-C-N	7.37	135.61	121.54
1	A	211	GLY	C-N-CA	7.37	135.61	121.54
1	A	79	LEU	N-CA-CB	7.30	122.83	110.49
1	A	48	ILE	N-CA-CB	7.19	116.06	110.45
1	A	409	MET	N-CA-C	7.19	126.11	110.80
1	A	151	ILE	CA-C-N	7.05	130.06	120.54
1	A	151	ILE	C-N-CA	7.05	130.06	120.54
1	A	264	ASP	CA-CB-CG	7.03	119.63	112.60
1	A	210	GLU	CA-C-N	6.93	134.99	121.41
1	A	210	GLU	C-N-CA	6.93	134.99	121.41
1	A	48	ILE	CA-C-N	6.80	126.40	119.19
1	A	48	ILE	C-N-CA	6.80	126.40	119.19
1	A	73	ARG	N-CA-CB	6.75	121.89	110.49
1	A	231	ARG	CA-C-N	6.67	134.27	121.54
1	A	231	ARG	C-N-CA	6.67	134.27	121.54
1	A	99	ILE	N-CA-C	-6.40	107.06	113.20
1	A	321	LEU	CA-C-N	6.40	127.04	119.94
1	A	321	LEU	C-N-CA	6.40	127.04	119.94
3	C	71	VAL	CA-C-N	6.36	127.79	119.84
3	C	71	VAL	C-N-CA	6.36	127.79	119.84
1	A	88	GLY	CA-C-N	6.30	130.26	120.82
1	A	88	GLY	C-N-CA	6.30	130.26	120.82
1	A	379	TRP	N-CA-CB	6.21	119.07	110.07
1	A	212	ALA	N-CA-C	6.20	124.00	110.80
1	A	259	GLN	CA-C-N	6.11	126.76	119.98
1	A	259	GLN	C-N-CA	6.11	126.76	119.98
1	A	411	HIS	N-CA-C	6.06	123.72	110.80
1	A	240	PRO	CA-C-N	6.03	128.97	120.28
1	A	240	PRO	C-N-CA	6.03	128.97	120.28
1	A	54	MET	N-CA-C	-6.01	102.38	111.34
1	A	274	GLY	CA-C-N	5.90	129.66	120.75
1	A	274	GLY	C-N-CA	5.90	129.66	120.75
1	A	401	MET	CA-C-N	5.87	130.47	122.07
1	A	401	MET	C-N-CA	5.87	130.47	122.07
2	B	11	SER	CA-C-N	5.85	128.92	120.79
2	B	11	SER	C-N-CA	5.85	128.92	120.79
1	A	402	ARG	N-CA-C	5.82	119.46	111.54
3	C	84	VAL	N-CA-C	5.75	116.49	110.62
1	A	386	SER	N-CA-CB	5.73	120.18	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	265	LEU	N-CA-C	5.67	122.35	109.81
2	B	10	PRO	CA-C-N	5.62	127.75	120.44
2	B	10	PRO	C-N-CA	5.62	127.75	120.44
1	A	440	ALA	N-CA-C	5.62	117.08	111.07
1	A	346	SER	CA-C-N	5.60	126.15	120.38
1	A	346	SER	C-N-CA	5.60	126.15	120.38
1	A	331	GLY	CA-C-O	-5.59	113.52	121.52
1	A	378	THR	N-CA-C	5.59	118.22	111.40
1	A	47	GLN	CA-C-N	5.58	124.80	120.33
1	A	47	GLN	C-N-CA	5.58	124.80	120.33
1	A	64	TRP	CA-C-N	5.57	127.75	120.28
1	A	64	TRP	C-N-CA	5.57	127.75	120.28
1	A	107	LYS	CA-C-N	5.57	132.18	121.54
1	A	107	LYS	C-N-CA	5.57	132.18	121.54
1	A	375	PHE	CA-CB-CG	-5.51	108.29	113.80
1	A	232	GLU	N-CA-C	5.50	122.53	110.80
1	A	451	VAL	N-CA-CB	5.50	118.02	110.54
2	B	30	ARG	CA-C-N	5.48	127.62	120.28
2	B	30	ARG	C-N-CA	5.48	127.62	120.28
3	C	72	PRO	N-CA-C	5.47	123.73	112.47
1	A	399	MET	CA-C-N	5.46	131.79	121.97
1	A	399	MET	C-N-CA	5.46	131.79	121.97
2	B	65	ILE	N-CA-C	-5.46	108.53	113.71
1	A	222	THR	CA-C-N	5.44	127.57	120.28
1	A	222	THR	C-N-CA	5.44	127.57	120.28
1	A	197	SER	CA-C-O	-5.43	112.72	120.16
1	A	404	HIS	CA-CB-CG	5.42	119.22	113.80
1	A	182	PHE	N-CA-CB	5.40	118.06	110.12
1	A	298	VAL	CA-C-N	5.40	127.51	120.28
1	A	298	VAL	C-N-CA	5.40	127.51	120.28
2	B	20	ARG	N-CA-C	5.39	117.16	111.28
1	A	27	GLN	N-CA-CB	5.38	119.58	110.49
2	B	50	ILE	CA-C-N	5.38	125.95	119.98
2	B	50	ILE	C-N-CA	5.38	125.95	119.98
2	B	29	ASP	CA-C-N	5.37	131.80	121.54
2	B	29	ASP	C-N-CA	5.37	131.80	121.54
1	A	338	VAL	N-CA-C	-5.34	107.27	112.29
1	A	263	VAL	N-CA-C	-5.33	100.64	108.11
1	A	71	SER	CA-C-N	5.33	131.72	121.54
1	A	71	SER	C-N-CA	5.33	131.72	121.54
1	A	467	GLU	N-CA-C	5.28	122.05	110.80
1	A	224	THR	CA-C-N	5.25	127.32	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	224	THR	C-N-CA	5.25	127.32	120.28
1	A	353	SER	CA-C-N	5.23	127.63	120.46
1	A	353	SER	C-N-CA	5.23	127.63	120.46
1	A	444	GLY	CA-C-N	5.22	127.28	120.28
1	A	444	GLY	C-N-CA	5.22	127.28	120.28
1	A	280	PRO	CA-C-O	-5.22	115.05	121.31
1	A	72	ASN	CA-C-N	5.21	131.50	121.54
1	A	72	ASN	C-N-CA	5.21	131.50	121.54
1	A	51	PHE	CB-CA-C	-5.21	102.00	110.85
1	A	423	PHE	CA-C-N	5.21	125.86	120.03
1	A	423	PHE	C-N-CA	5.21	125.86	120.03
2	B	47	MET	CA-C-N	5.19	125.74	119.98
2	B	47	MET	C-N-CA	5.19	125.74	119.98
1	A	301	LEU	N-CA-C	5.15	121.77	110.80
1	A	51	PHE	N-CA-C	5.11	116.93	111.36
1	A	331	GLY	O-C-N	-5.10	116.67	121.77
1	A	470	SER	N-CA-CB	5.05	119.03	110.49
1	A	475	LEU	N-CA-C	-5.05	104.86	112.99
1	A	106	PRO	CA-C-N	5.04	131.17	121.54
1	A	106	PRO	C-N-CA	5.04	131.17	121.54
1	A	179	ILE	CA-C-N	5.04	127.03	120.28
1	A	179	ILE	C-N-CA	5.04	127.03	120.28
1	A	99	ILE	CA-C-N	5.04	131.04	121.97
1	A	99	ILE	C-N-CA	5.04	131.04	121.97
1	A	286	THR	CA-C-N	5.04	127.03	120.28
1	A	286	THR	C-N-CA	5.04	127.03	120.28
3	C	85	PHE	CA-C-N	5.04	128.38	120.82
3	C	85	PHE	C-N-CA	5.04	128.38	120.82
1	A	355	LEU	N-CA-CB	5.02	118.98	110.49

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	MET	Peptide
1	A	266	PRO	Peptide
1	A	336	TYR	Peptide
1	A	377	LYS	Peptide
1	A	383	SER	Peptide
1	A	55	SER	Peptide
1	A	56	SER	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	12	0
2	B	494	0	527	1	0
3	C	281	0	294	3	0
All	All	4252	0	4396	16	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 (16) 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:404:HIS:CG	1:A:405:ARG:H	2.19	0.60
3:C:88:HIS:CG	3:C:89:ILE:H	2.20	0.60
1:A:197:SER:H	1:A:198:PRO:HD3	1.78	0.48
1:A:236:ARG:HB3	1:A:239:LEU:HD23	1.94	0.48
1:A:239:LEU:HB2	1:A:240:PRO:HD2	1.97	0.47
1:A:268:LYS:H	1:A:276:TYR:HB3	1.80	0.46
1:A:443:SER:H	1:A:447:ILE:HD12	1.81	0.46
1:A:411:HIS:HB2	1:A:414:ASN:HB3	1.98	0.46
1:A:76:LEU:H	1:A:76:LEU:HD13	1.82	0.45
1:A:404:HIS:CG	1:A:405:ARG:N	2.83	0.45
1:A:149:LEU:H	1:A:149:LEU:HD22	1.83	0.43
1:A:215:ALA:HB3	1:A:218:HIS:CD2	2.52	0.43
3:C:88:HIS:CG	3:C:89:ILE:N	2.85	0.43
2:B:9:GLU:HB2	2:B:10:PRO:HD3	2.01	0.43
3:C:71:VAL:HG22	3:C:72:PRO:HD2	2.00	0.43
1:A:239:LEU:HB2	1:A:240:PRO:CD	2.51	0.41

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%)	333 (74%)	50 (11%)	67 (15%)	0	3
2	B	60/68 (88%)	52 (87%)	3 (5%)	5 (8%)	0	9
3	C	34/36 (94%)	25 (74%)	3 (9%)	6 (18%)	0	2
All	All	544/580 (94%)	410 (75%)	56 (10%)	78 (14%)	0	3

All (78) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	59	ALA
1	A	72	ASN
1	A	73	ARG
1	A	79	LEU
1	A	81	ILE
1	A	82	SER
1	A	100	ILE
1	A	107	LYS
1	A	108	ASP
1	A	111	LEU
1	A	113	ASN
1	A	199	THR
1	A	201	VAL
1	A	202	ASN
1	A	211	GLY
1	A	212	ALA
1	A	228	ARG
1	A	232	GLU
1	A	233	ALA
1	A	238	ASN
1	A	239	LEU
1	A	271	ARG
1	A	272	TYR

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Mol	Chain	Res	Type
1	A	273	ARG
1	A	301	LEU
1	A	313	SER
1	A	315	ASN
1	A	336	TYR
1	A	337	PRO
1	A	400	VAL
1	A	409	MET
1	A	410	VAL
1	A	467	GLU
1	A	468	VAL
1	A	470	SER
1	A	473	ALA
2	B	30	ARG
3	C	68	VAL
3	C	70	PRO
3	C	71	VAL
3	C	72	PRO
1	A	75	THR
1	A	98	LYS
1	A	140	PRO
1	A	143	MET
1	A	176	GLY
1	A	213	ILE
1	A	274	GLY
1	A	314	GLY
1	A	386	SER
1	A	404	HIS
1	A	411	HIS
1	A	471	MET
2	B	66	VAL
1	A	71	SER
1	A	136	MET
1	A	139	ASP
1	A	171	LYS
1	A	174	GLY
1	A	324	TRP
1	A	340	GLY
1	A	355	LEU
1	A	398	GLN
1	A	412	GLU
2	B	29	ASP

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Mol	Chain	Res	Type
1	A	110	ALA
1	A	137	TYR
1	A	227	VAL
1	A	329	SER
2	B	27	LYS
3	C	90	TRP
1	A	237	GLN
1	A	138	GLY
1	A	172	GLY
2	B	28	PRO
3	C	73	VAL
1	A	197	SER

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%)	347 (92%)	28 (8%)	12	33
2	B	53/59 (90%)	53 (100%)	0	100	100
3	C	32/32 (100%)	28 (88%)	4 (12%)	4	16
All	All	460/489 (94%)	428 (93%)	32 (7%)	16	35

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	48	ILE
1	A	69	LEU
1	A	73	ARG
1	A	76	LEU
1	A	79	LEU
1	A	81	ILE
1	A	99	ILE
1	A	100	ILE
1	A	101	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	107	LYS
1	A	143	MET
1	A	175	LEU
1	A	186	ASN
1	A	201	VAL
1	A	205	ARG
1	A	226	LYS
1	A	240	PRO
1	A	271	ARG
1	A	275	GLN
1	A	285	TYR
1	A	301	LEU
1	A	316	LEU
1	A	355	LEU
1	A	379	TRP
1	A	400	VAL
1	A	404	HIS
1	A	405	ARG
3	C	68	VAL
3	C	71	VAL
3	C	72	PRO
3	C	74	LEU

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	116	GLN
1	A	186	ASN
1	A	218	HIS
1	A	300	ASN
1	A	306	GLN
1	A	343	HIS
1	A	360	HIS
1	A	411	HIS
2	B	13	GLN
2	B	58	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

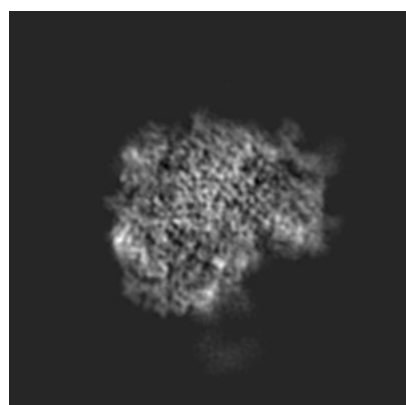
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2511. These allow visual inspection of the internal detail of the map and identification of artifacts.

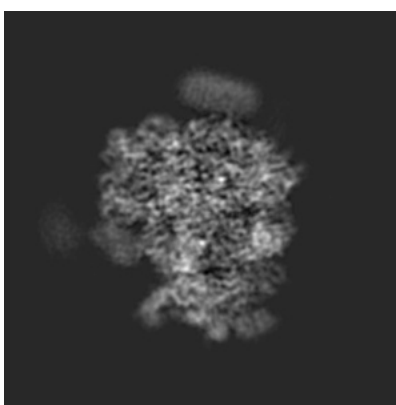
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

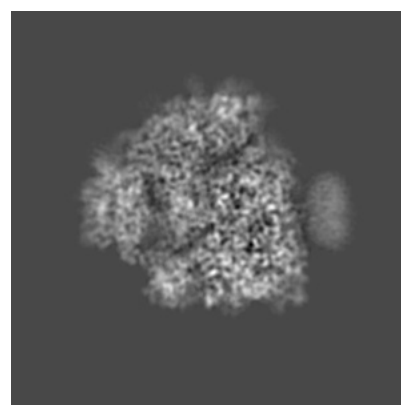
6.1.1 Primary map



X



Y

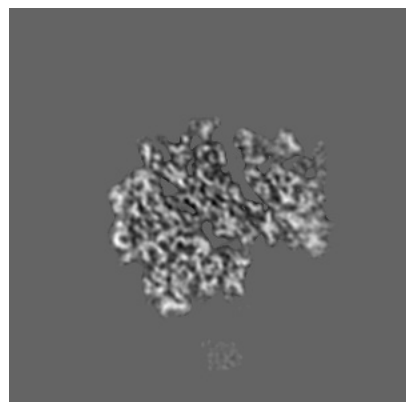


Z

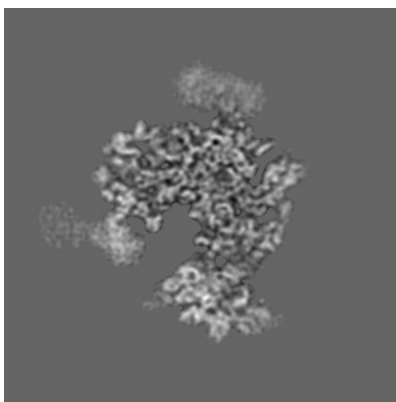
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

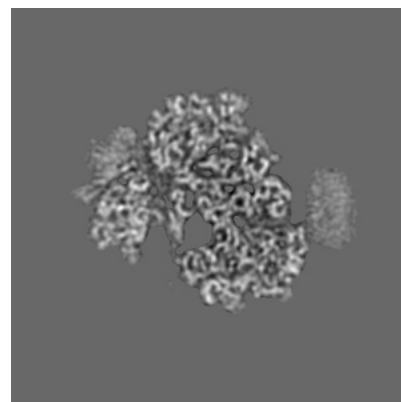
6.2.1 Primary map



X Index: 184



Y Index: 184

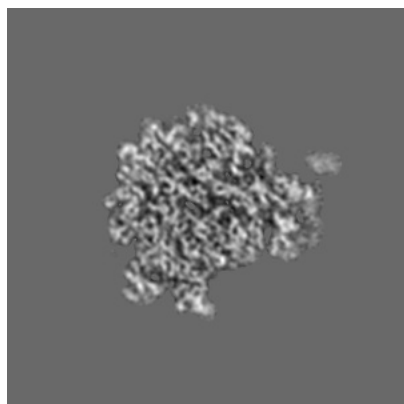


Z Index: 184

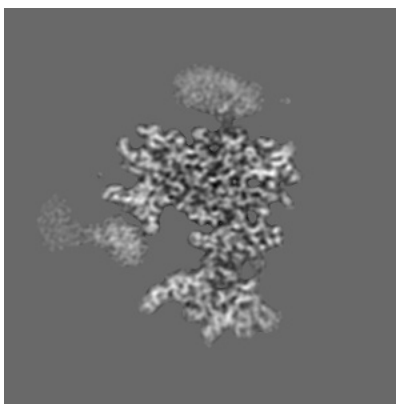
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

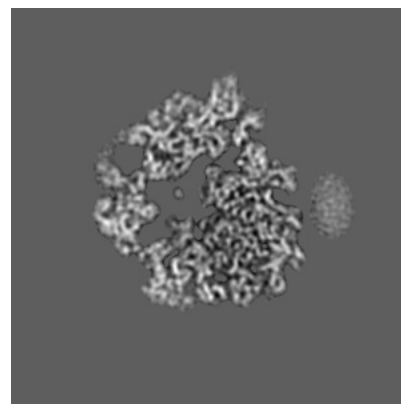
6.3.1 Primary map



X Index: 213



Y Index: 192

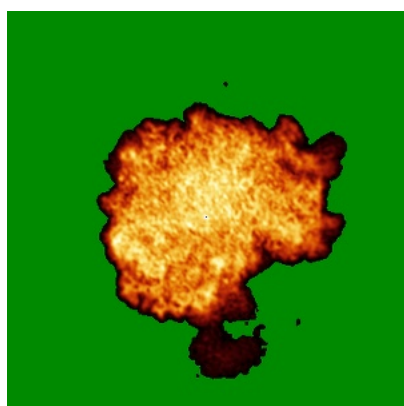


Z Index: 169

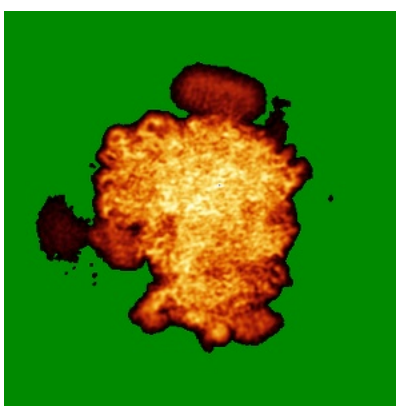
The images above show the largest variance slices of the map in three orthogonal directions.

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

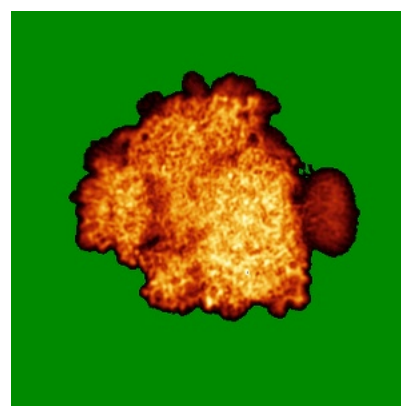
6.4.1 Primary map



X



Y

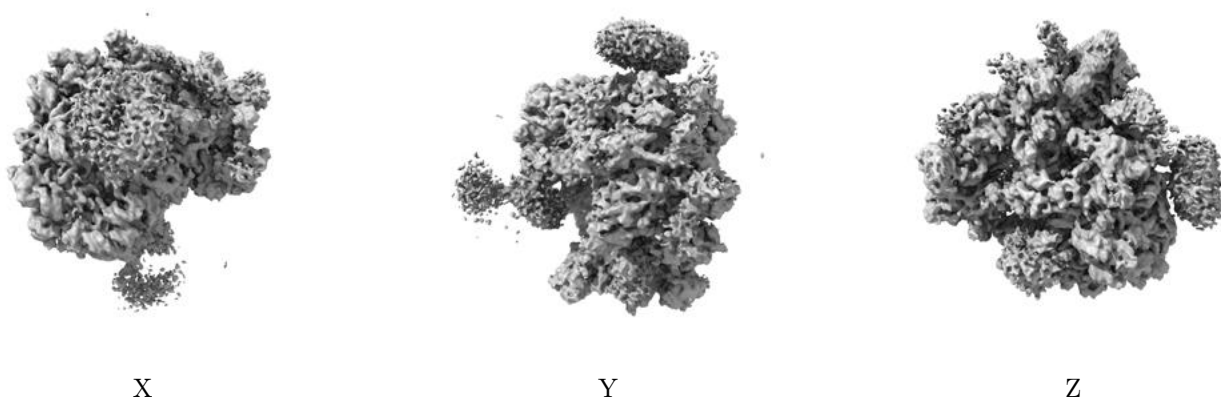


Z

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.

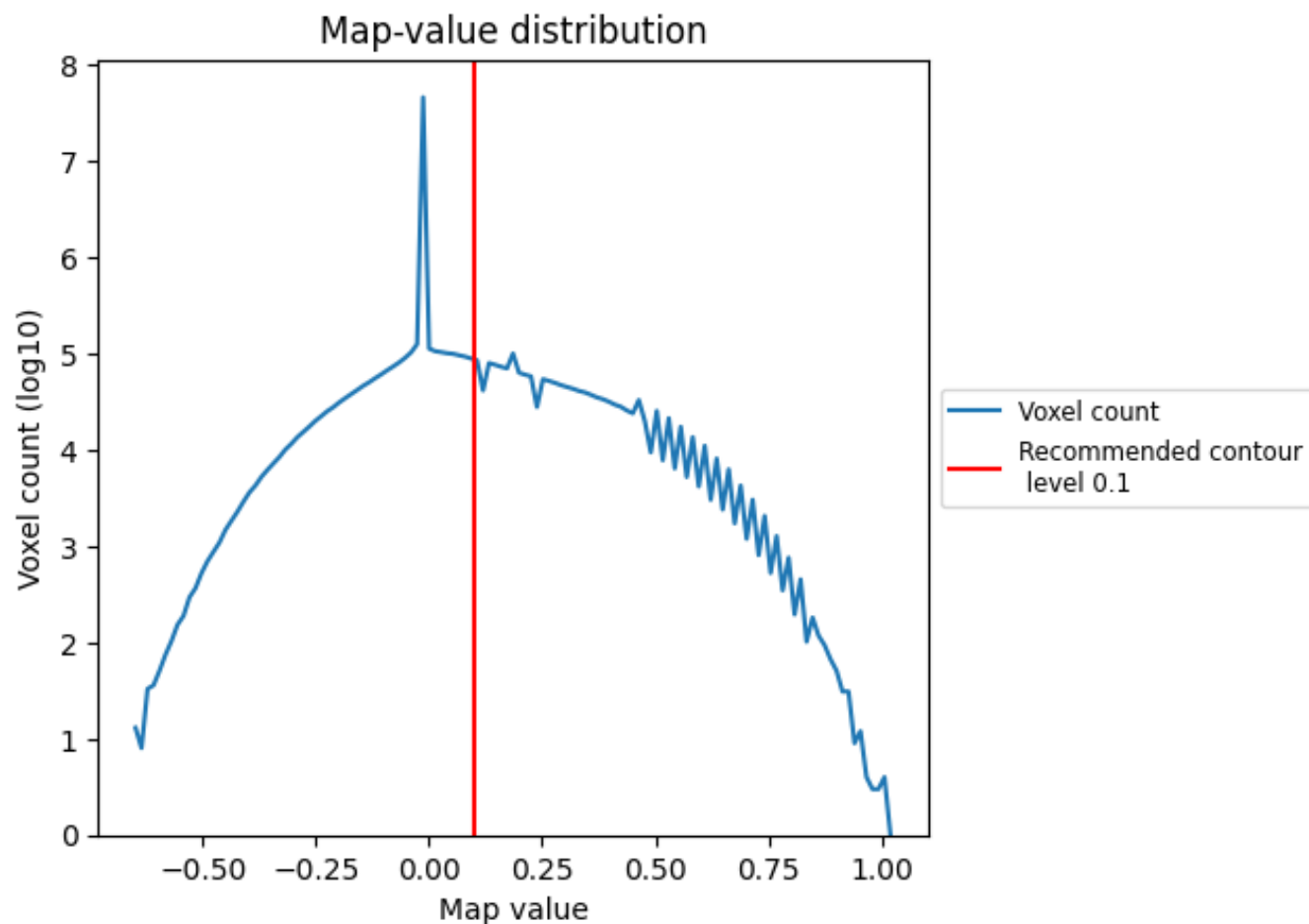
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

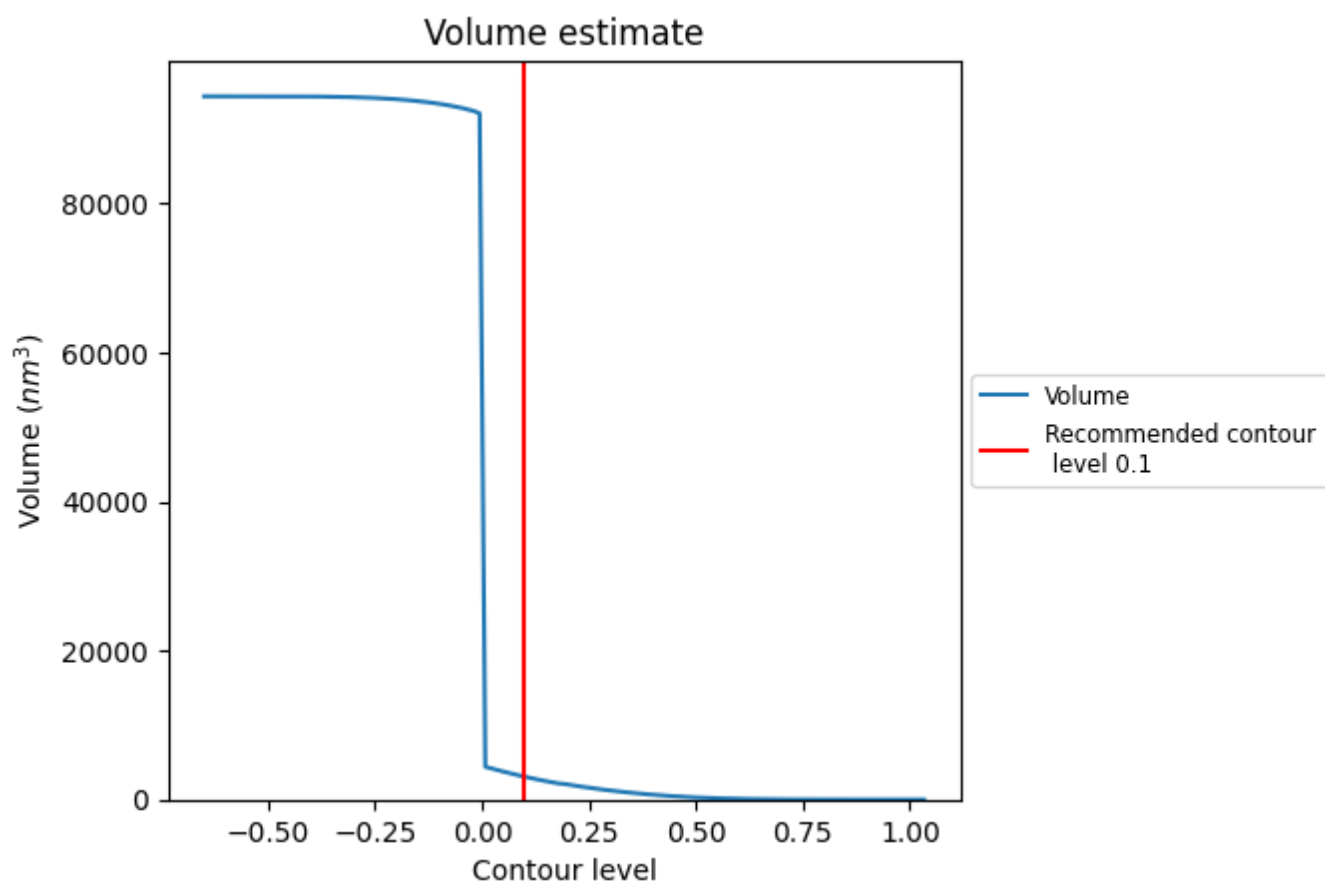
This section contains the results of statistical analysis of the map.

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.

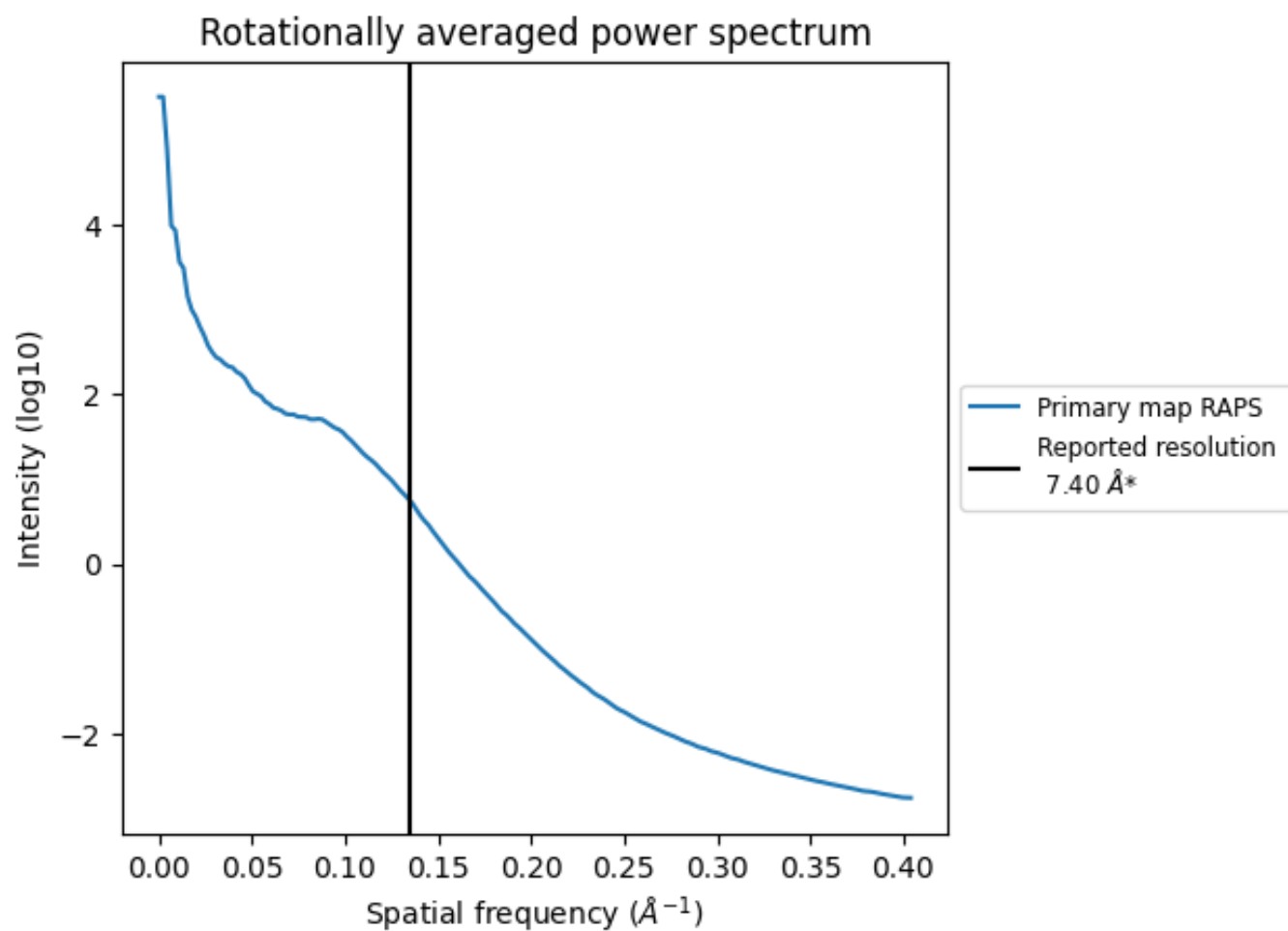
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3066 nm³; this corresponds to an approximate mass of 2769 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 0.135 Å⁻¹

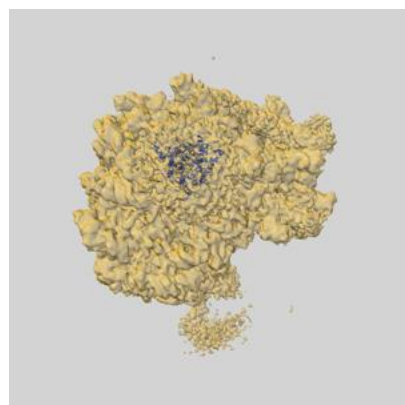
8 Fourier-Shell correlation

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

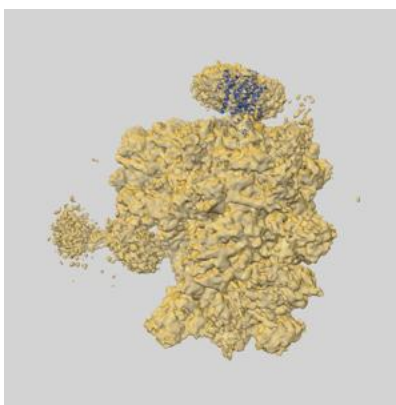
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2511 and PDB model 4CG5. Per-residue inclusion information can be found in section [3](#) on page [4](#).

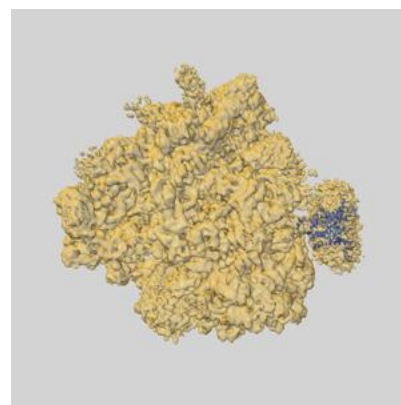
9.1 Map-model overlay [i](#)



X



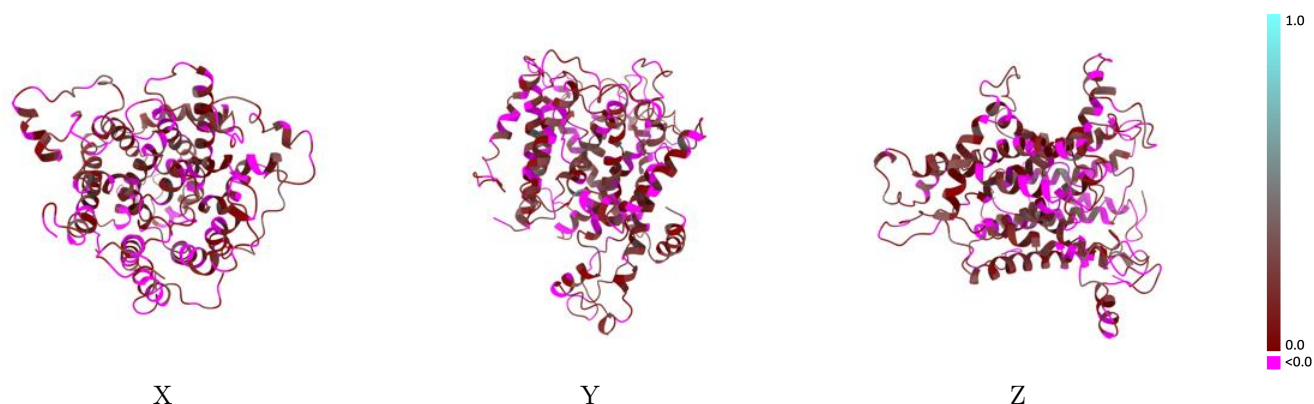
Y



Z

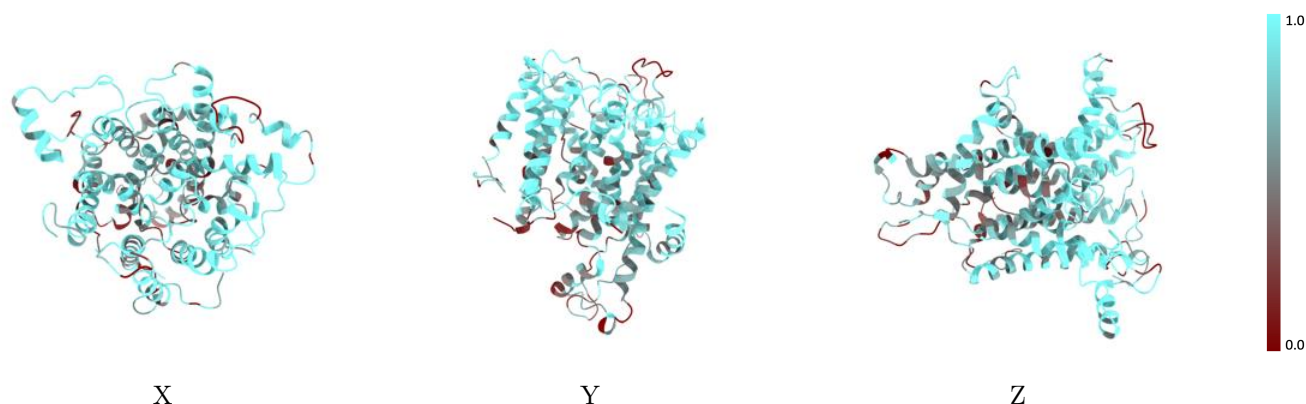
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



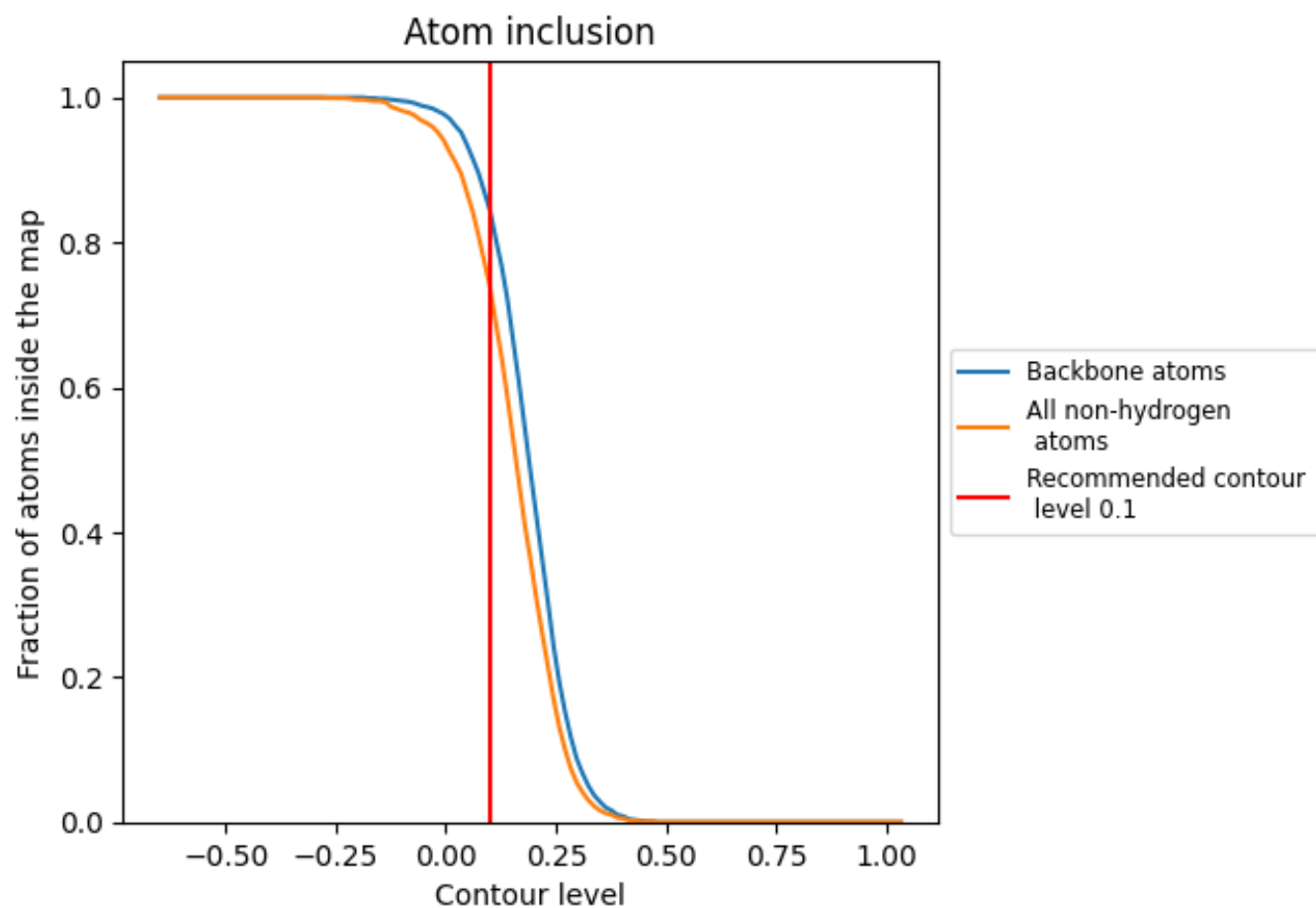
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 74% 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	0.7380	0.0860
A	0.7290	0.0850
B	0.8020	0.1320
C	0.7440	0.0180

