



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 01:30 AM UTC

PDB ID : 7KFT / pdb_00007kft
EMDB ID : EMD-22855
Title : Partial Cas6-RT-Cas1–Cas2 complex
Authors : Hoel, C.M.; Wang, J.Y.; Doudna, J.A.; Brohawn, S.G.
Deposited on : 2020-10-14
Resolution : 3.40 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

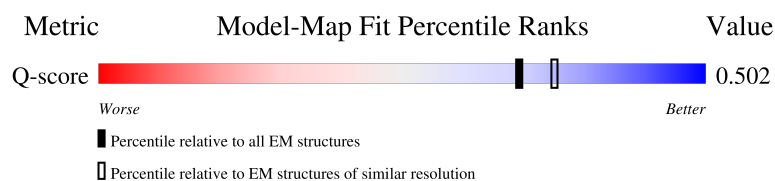
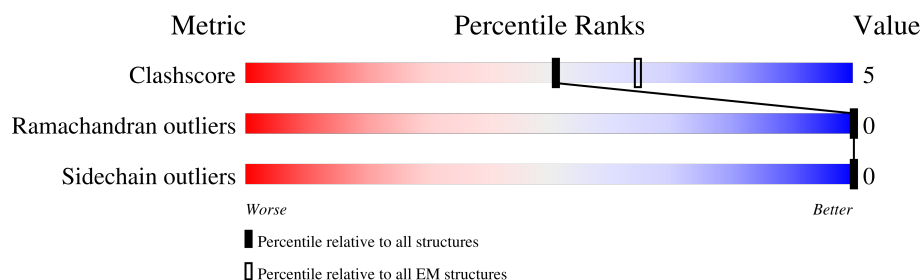
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	99	52% 62% 29% 9%
1	B	99	13% 80% 17% .
2	C	984	. 48% 10% 42%
2	D	984	. 30% . 66%

Continued on next page...

Mol	Chain	Length	Quality of chain
2	E	984	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11680 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 Cas2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	96	Total	C	N	O	S	0	0
			796	505	147	142	2		
1	A	90	Total	C	N	O	S	0	0
			756	477	141	136	2		

- Molecule 2 is a protein called Cas6-RT-Cas1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	332	Total	C	N	O	S	0	0
			2727	1728	513	481	5		
2	C	568	Total	C	N	O	S	0	0
			4601	2949	809	832	11		
2	E	341	Total	C	N	O	S	0	0
			2800	1774	525	496	5		

Protein	Residue	Score	Significance
H918	H918	0.89	Significant
	L919	0.69	Not Significant
	G920	0.70	Significant
	Q921	0.71	Significant
	K963	0.77	Significant
	Q969	0.72	Significant
	E979	0.45	Not Significant
	L980	0.64	Significant
	K981	0.65	Significant
	K986	0.67	Significant
H653	H653	0.65	Significant
	L654	0.64	Significant
	H765	0.66	Significant
	Q767	0.67	Significant
	R768	0.68	Significant
	Q769	0.69	Significant
	T770	0.70	Significant
	L771	0.71	Significant
	K772	0.73	Significant
	R774	0.74	Significant
H801	H801	0.80	Significant
	N820	0.82	Significant
	H828	0.83	Significant
	K831	0.83	Significant
	R834	0.84	Significant
	P840	0.84	Significant
	A863	0.86	Significant
	K869	0.86	Significant
	Q874	0.87	Significant
	A881	0.88	Significant
H885	H885	0.88	Significant
	I886	0.86	Significant
	M887	0.87	Significant
	F912	0.91	Significant
	K916	0.91	Significant
	D917	0.91	Significant
	L918	0.91	Significant
	K919	0.91	Significant
	L920	0.91	Significant
	K921	0.91	Significant

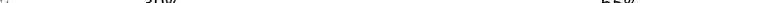
Chain C:



WORLDWIDE
PDB
PROTEIN DATA BANK

ARG	TYR	VAL	GLY	LEU	ILE	ASN	ARG	PHE	GLN	LYS	PHE	SER	LYS	ASP	LYS	THR	LEU	HIS	GLN	HIS	TYR	GLN	GLN	GLN	LEU	LYS	ASN	ALA	ALA	MET	HIS	ASN	GLN	GLN	SER	SER	GLN	PHE	GLN	VAL	TRP	LYS	GLU	LEU	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 2: Cas6-RT-Cas1

Chain E:  30% 65%

ASN	ASP	LEU	PHE	ASP	GLY	ILE	PRO	VAL	SER	SER	LYS	GLU	SER	LEU	ALA	TYR	THR	LEU	GLN	ARG	ALA	MET	GLU	GLY	GLN	LEU	ALA	TRP	HIS	LYS	ALA	ALA	ASN	THR	GLN	GLU	PRO	LEU	ASP	ILE	GLN	TRP	GLN	TRP	TYR	GLN	THR	SER	THR	VAL	ARG	ILE	LEU	HIS	ALA	ASP	HIS	LYS	TYR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

HIS	PRO	ASP	LEU	TYR	TRP	ILE	ASP	THR	PRO	TYR	PHE	GLY	LYS	ASP	ALA	GLU	LYS	ASN	THR	LEU	GLY	GLY	MET	ALA	GLY	ASN	PHE	THR	LEU	SER	LYS	PRO	GLY	ILE	GLU	PRO	GLY	LEU	LEU	ALA	MET	MET	ILE	LEU	LEU	THR	GLN	MET	VAL	GLY	VAL	GLY	GLN	ARG	ARG	THR	SER	GLY	LEU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER	GLN	VAL	GLN	SER	ALA	ILE	GLY	GLN	LEU	ARG	LYS	HIS	GLN	TYR	THR	ALA	PRO	LYS	LEU	GLN	GLY	PHE	THR	ILE	PRO	LYS	LYS	ASP	GLY	THR	GLU	ARG	LEU	LEU	ALA	VAL	SER	PRO	PRO	TYR	LEU	ASP	ASP	ARG	ILE	LEU	LEU	GLN	LYS	ALA	ALA	ALA	ALA	ILE	VAL	THR	PRO	GLY	LEU	ASP	THR	ILE	TYR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

PHE ASP ASP PHE PHE ILE ILE LEU CYS LYS SER GLN HIS HIS ALA ALA GLN GLN ALA ALA VAL VAL GLU GLN SER SER LYS LYS VAL VAL LYS LYS LEU LEU SER SER ILE ILE VAL VAL GLU GLY LYS THR LYS HIS HIS ILE ILE ILE GLN LEU LEU ASN ASN GLN GLN PHE ARG PHE PHE LEU LEU TYR TYR PHE ARG ARG ARG ASP ASP HIS HIS ALA ALA

GLU	ILE	ALA	GLY	GLU	LYS	SER	ASP	GLY	ARG	THR	THR	PHE	ALA	ALA	GLU	GLN	THR	PRO	THR	ASN	LEU	PRO	PRO	TRP	LEU	ALA	ASN	LEU	GLY	THR	LYS	SER	PRO	GLN	PRO	LEU	ASP	ASP	ASP	LEU	PRO	H641	H650	H653	D666	N669	E685	Q686	A689	V690	T695
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------

The chart displays the distribution of 1000 samples across 100 categories. The categories are labeled with codes (e.g., L700, P701, R705, etc.) and are color-coded: green for categories 1-10, yellow for 11-90, and orange for 91-100. Red diamonds indicate categories with a value of 10 or more. The chart shows a high concentration of samples in the first few categories, with a sharp decline thereafter.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	129175	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	62.598	Depositor
Minimum map value	-41.692	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	9	Depositor
Map size ($\text{\AA}$)	474.80002, 474.80002, 474.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.187, 1.187, 1.187	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	0.22	0/771	0.51	0/1034
1	B	0.24	0/812	0.54	0/1092
2	C	0.22	0/4706	0.48	0/6379
2	D	0.24	0/2787	0.47	0/3759
2	E	0.26	0/2861	0.52	0/3857
All	All	0.24	0/11937	0.49	0/16121

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	756	0	765	21	0
1	B	796	0	813	13	0
2	C	4601	0	4613	57	0
2	D	2727	0	2751	22	0
2	E	2800	0	2826	26	0
All	All	11680	0	11768	128	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 5.

All (128) 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)
2:D:699:THR:HG22	2:D:701:PRO:HD2	1.67	0.75
2:E:860:LEU:HD11	2:E:886:ILE:HD12	1.74	0.69
2:E:714:HIS:NE2	2:E:857:ASP:OD2	2.25	0.68
2:C:200:ILE:HG12	2:C:284:THR:HG21	1.76	0.67
2:E:906:GLN:O	2:E:933:ARG:NH2	2.28	0.67
2:E:699:THR:HG22	2:E:701:PRO:HD2	1.78	0.65
1:B:31:GLN:HB3	1:B:34:VAL:HB	1.78	0.65
2:C:14:VAL:HG12	2:C:117:LEU:HG	1.77	0.65
2:C:427:LYS:HA	2:C:539:ALA:HA	1.78	0.64
2:E:766:ASN:HB3	2:E:892:HIS:HD2	1.63	0.63
1:B:44:ARG:NE	2:E:685:GLU:OE1	2.29	0.63
1:B:5:LEU:HD23	1:B:71:LEU:HD11	1.81	0.62
1:A:10:VAL:HB	1:A:16:ARG:HB3	1.81	0.62
2:C:120:LEU:O	2:C:319:ARG:NH1	2.34	0.60
2:E:916:LYS:HB3	2:E:920:GLY:HA2	1.82	0.60
2:C:33:ASP:OD2	2:C:37:ARG:NH1	2.35	0.60
1:B:75:THR:HG23	1:A:70:ASN:HB3	1.82	0.60
2:C:153:LEU:HD23	2:C:156:GLN:HE21	1.66	0.60
2:C:620:PRO:HD2	2:C:623:LEU:HD12	1.83	0.60
2:D:863:ALA:O	2:D:963:LYS:NZ	2.33	0.59
2:C:17:LYS:HB3	2:C:113:LYS:HB2	1.85	0.59
2:C:233:TYR:HB3	2:C:270:LYS:HB2	1.83	0.59
2:C:445:GLY:O	2:C:447:HIS:ND1	2.37	0.58
2:C:449:VAL:HG12	2:C:545:LEU:HD23	1.86	0.57
2:C:16:LEU:HD13	2:C:112:ILE:HG23	1.85	0.57
2:D:667:ASN:HB3	2:E:918:HIS:HE1	1.70	0.57
2:D:801:ARG:NH2	2:D:874:GLN:OE1	2.38	0.57
1:A:31:GLN:HG2	1:A:32:GLY:H	1.70	0.57
1:B:64:ASN:ND2	1:A:83:ASN:OD1	2.38	0.56
2:C:333:PRO:HA	2:C:336:ILE:HD12	1.88	0.56
2:E:801:ARG:NH2	2:E:871:ILE:O	2.38	0.56
1:B:46:ARG:NH2	2:C:554:GLN:OE1	2.31	0.56
2:C:465:GLN:HG3	2:C:520:ILE:HD11	1.87	0.56
2:D:707:LEU:HD21	2:D:726:VAL:HG12	1.87	0.56
1:A:10:VAL:HG13	1:A:63:GLU:HG3	1.88	0.56
2:C:35:PHE:HD1	2:C:36:LEU:HD12	1.71	0.55
1:A:70:ASN:OD1	1:A:71:LEU:N	2.39	0.55
2:C:258:LEU:HD22	2:C:292:ARG:HH12	1.72	0.55
2:D:831:LYS:HE2	2:C:577:ILE:HD11	1.88	0.55
1:B:10:VAL:HG13	1:B:63:GLU:HG3	1.89	0.55
2:C:582:GLN:HG2	2:C:621:PRO:HB3	1.88	0.55
2:E:832:ARG:NH2	2:E:846:SER:OG	2.32	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:PHE:HB2	1:B:66:ILE:HG12	1.90	0.54
2:C:193:PRO:HB3	2:C:234:ILE:HG13	1.90	0.54
2:E:666:ASP:HB3	2:E:669:ASN:H	1.73	0.53
2:D:834:ARG:HG2	2:C:577:ILE:HB	1.91	0.53
2:E:835:ARG:HB2	2:E:836:PRO:HD3	1.91	0.52
2:C:525:ASP:OD1	2:C:526:SER:N	2.43	0.52
2:E:690:VAL:HG13	2:E:713:VAL:HG23	1.91	0.52
1:A:81:ASP:OD1	1:A:82:ILE:N	2.41	0.51
2:C:168:VAL:HG23	2:C:298:GLY:HA2	1.92	0.51
2:E:836:PRO:O	2:E:838:LYS:HG3	2.09	0.51
1:B:31:GLN:NE2	1:A:65:ASN:OD1	2.44	0.50
2:C:561:GLN:O	2:C:565:GLU:HG3	2.12	0.50
2:C:344:GLU:HA	2:C:347:THR:HB	1.94	0.50
2:C:430:SER:HB2	2:C:433:GLN:HB3	1.94	0.49
2:C:121:PHE:CE2	2:C:135:TYR:HB2	2.47	0.49
2:C:498:ILE:HD13	2:C:587:LEU:HD11	1.94	0.49
1:A:26:TYR:OH	1:A:47:GLN:NE2	2.38	0.49
2:D:726:VAL:HG22	2:E:726:VAL:HG22	1.95	0.49
2:C:233:TYR:HB3	2:C:270:LYS:HE2	1.94	0.48
1:B:20:SER:O	1:B:24:GLU:HG3	2.13	0.48
1:A:53:HIS:HA	1:A:56:ILE:HG12	1.95	0.48
1:A:13:ASP:OD1	1:A:14:LYS:N	2.47	0.48
2:C:429:LEU:HD12	2:C:434:VAL:HG21	1.94	0.48
2:E:961:GLN:HG2	2:E:974:PHE:HA	1.94	0.48
2:C:415:ASP:OD1	2:C:425:TYR:OH	2.24	0.48
2:C:619:LEU:HD23	2:C:623:LEU:HD13	1.95	0.48
2:D:773:LYS:NZ	2:D:979:GLU:OE2	2.48	0.47
2:C:71:VAL:HG21	2:C:320:VAL:HG12	1.97	0.47
1:A:16:ARG:HA	1:A:19:LEU:HD23	1.95	0.47
1:A:20:SER:O	1:A:24:GLU:HG2	2.15	0.47
1:A:48:LEU:O	1:A:52:ILE:HG12	2.14	0.47
2:D:771:LEU:HD12	2:D:781:LEU:HD13	1.96	0.47
2:C:201:TYR:OH	2:C:224:GLN:OE1	2.32	0.47
2:C:50:LEU:HD11	2:C:81:THR:HG21	1.98	0.46
2:E:650:GLN:OE1	2:E:952:HIS:NE2	2.46	0.46
2:C:431:ARG:HB3	2:C:435:ARG:HH21	1.81	0.46
2:E:881:ALA:O	2:E:885:ASP:HB2	2.15	0.46
1:A:48:LEU:HA	1:A:51:LYS:HE2	1.98	0.46
2:D:653:HIS:CD2	2:D:689:ALA:HB3	2.50	0.46
2:D:775:LYS:HG2	2:D:778:ARG:HH21	1.81	0.46
2:C:326:LEU:O	2:C:330:ILE:HG12	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:473:LEU:HG	2:C:474:LEU:HD12	1.98	0.45
2:C:36:LEU:HD22	2:C:52:ILE:HD11	1.99	0.45
2:D:820:ASN:O	2:D:828:HIS:NE2	2.49	0.45
1:B:31:GLN:HG3	1:B:32:GLY:H	1.82	0.45
1:A:47:GLN:O	1:A:51:LYS:HG3	2.17	0.45
2:C:191:LEU:HD21	2:C:261:MET:HE1	1.99	0.45
1:B:1:MET:HE1	2:E:686:GLN:HA	1.98	0.44
1:A:8:PHE:HB3	1:A:66:ILE:HD12	1.98	0.44
2:C:143:GLN:HB3	2:C:313:LEU:HB2	1.99	0.44
2:E:849:TYR:OH	2:E:895:GLU:OE2	2.35	0.44
2:D:881:ALA:O	2:D:885:ASP:HB2	2.18	0.43
1:A:77:LYS:HB3	1:A:77:LYS:HE2	1.75	0.43
2:C:245:ASP:OD1	2:C:245:ASP:N	2.44	0.43
2:E:884:SER:HA	2:E:887:MET:HE2	2.00	0.43
2:C:200:ILE:HG22	2:C:280:MET:HE2	2.00	0.43
2:C:584:PHE:O	2:C:587:LEU:HB2	2.18	0.43
2:E:705:ARG:HA	2:E:705:ARG:HD3	1.85	0.43
2:D:840:PRO:HB3	2:D:912:PHE:CZ	2.54	0.43
2:C:278:LEU:O	2:C:282:ILE:HG12	2.19	0.43
2:D:778:ARG:O	2:D:782:GLN:HG2	2.19	0.43
2:D:745:MET:HE1	2:D:969:GLN:OE1	2.19	0.43
2:C:360:VAL:HG12	2:C:398:TYR:HB2	2.00	0.43
2:C:228:LYS:HA	2:C:228:LYS:HD3	1.86	0.42
2:E:951:LEU:HG	2:E:955:LEU:HD23	2.01	0.42
2:D:884:SER:HA	2:D:887:MET:HG2	2.01	0.42
2:E:790:LYS:HE3	2:E:790:LYS:HB2	1.86	0.42
2:C:286:MET:HE2	2:C:315:LEU:HB2	2.00	0.42
2:C:160:ILE:HG22	2:C:304:HIS:HA	2.02	0.42
2:C:347:THR:HG23	2:C:349:ILE:H	1.84	0.42
2:D:764:ILE:HA	2:D:767:GLN:HG2	2.02	0.41
2:E:653:HIS:ND1	2:E:689:ALA:HB3	2.34	0.41
2:C:17:LYS:HE2	2:C:65:GLY:HA2	2.02	0.41
1:A:6:ILE:HB	1:A:35:PHE:HB2	2.03	0.41
2:C:162:TRP:O	2:C:264:ASN:HA	2.20	0.41
2:D:765:HIS:O	2:D:769:GLN:HG2	2.21	0.41
2:D:869:LYS:HA	2:D:869:LYS:HD2	1.92	0.41
2:C:69:ARG:HB2	2:C:323:SER:HB2	2.03	0.41
2:C:330:ILE:HD13	2:C:409:VAL:HG21	2.03	0.41
2:C:171:LEU:HD22	2:C:183:ARG:HG2	2.02	0.41
1:B:87:ILE:HA	1:B:87:ILE:HD12	1.81	0.40
1:A:8:PHE:HB3	1:A:66:ILE:CD1	2.52	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:LYS:O	1:A:55:ILE:HD12	2.21	0.40
2:C:192:THR:HB	2:C:195:LEU:HB3	2.03	0.40
2:D:667:ASN:HB3	2:E:918:HIS:CE1	2.53	0.40
2:C:357:LEU:HA	2:C:360:VAL:HG22	2.04	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	88/99 (89%)	86 (98%)	2 (2%)	0	100	100
1	B	94/99 (95%)	89 (95%)	5 (5%)	0	100	100
2	C	556/984 (56%)	531 (96%)	25 (4%)	0	100	100
2	D	330/984 (34%)	318 (96%)	12 (4%)	0	100	100
2	E	339/984 (34%)	316 (93%)	23 (7%)	0	100	100
All	All	1407/3150 (45%)	1340 (95%)	67 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	85/91 (93%)	85 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	89/91 (98%)	89 (100%)	0	100	100
2	C	499/859 (58%)	499 (100%)	0	100	100
2	D	291/859 (34%)	291 (100%)	0	100	100
2	E	299/859 (35%)	299 (100%)	0	100	100
All	All	1263/2759 (46%)	1263 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	64	ASN
1	B	80	HIS
1	A	78	HIS
1	A	83	ASN
2	D	653	HIS
2	D	667	ASN
2	D	714	HIS
2	D	738	ASN
2	D	782	GLN
2	D	820	ASN
2	D	875	GLN
2	D	879	HIS
2	D	918	HIS
2	D	967	HIS
2	C	57	ASN
2	C	156	GLN
2	C	310	HIS
2	C	433	GLN
2	C	518	ASN
2	C	579	GLN
2	C	582	GLN
2	E	646	GLN
2	E	758	GLN
2	E	769	GLN
2	E	918	HIS
2	E	968	ASN

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 [i](#)

There are no chain breaks in this entry.

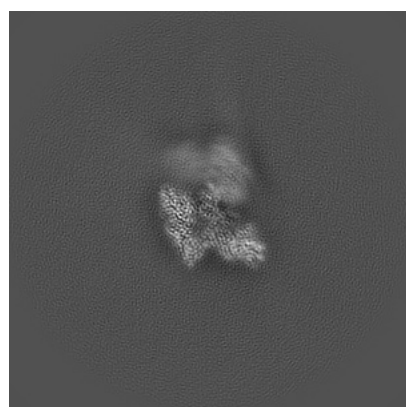
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22855. These allow visual inspection of the internal detail of the map and identification of artifacts.

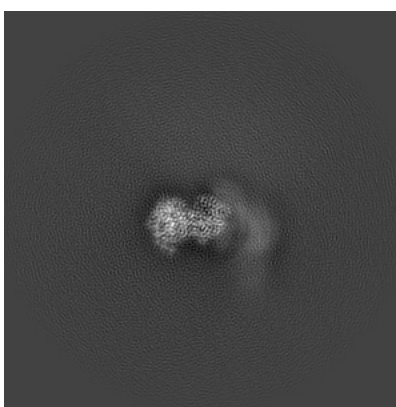
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

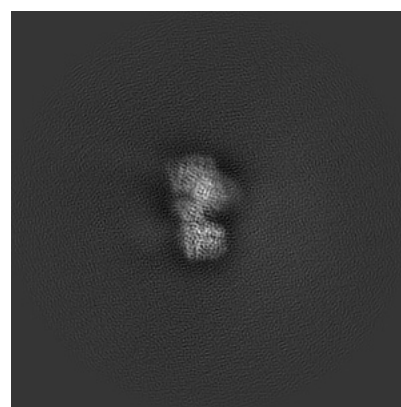
6.1.1 Primary map



X



Y

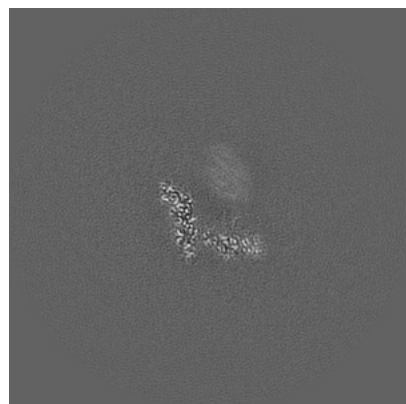


Z

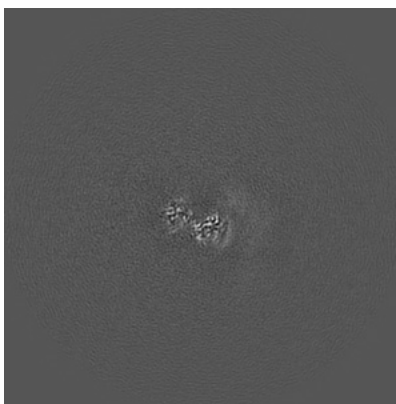
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

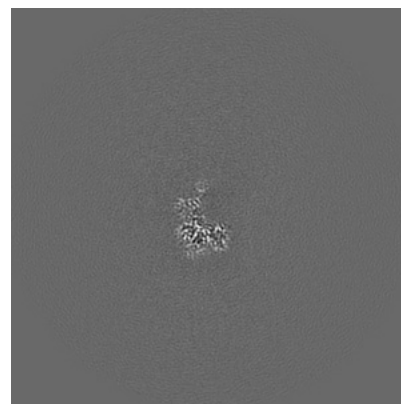
6.2.1 Primary map



X Index: 200



Y Index: 200

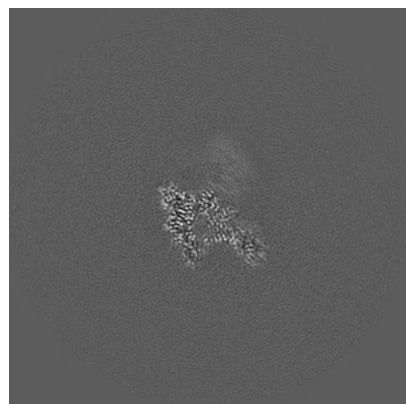


Z Index: 200

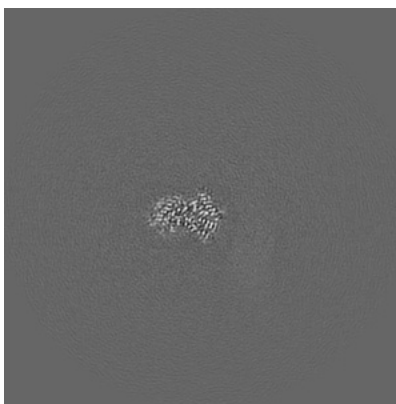
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

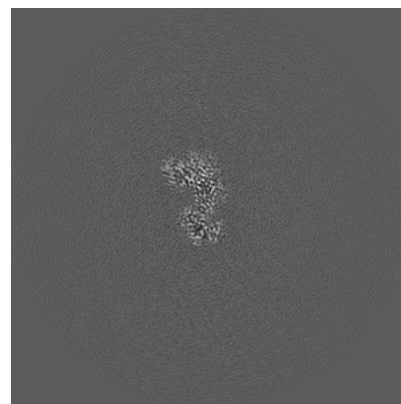
6.3.1 Primary map



X Index: 186



Y Index: 178

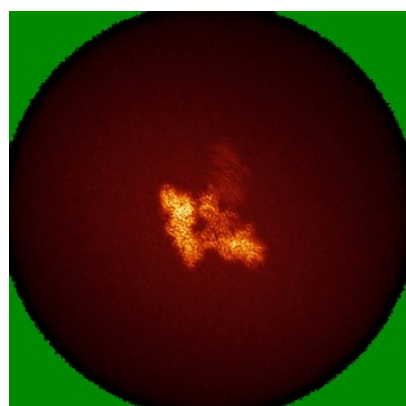


Z Index: 166

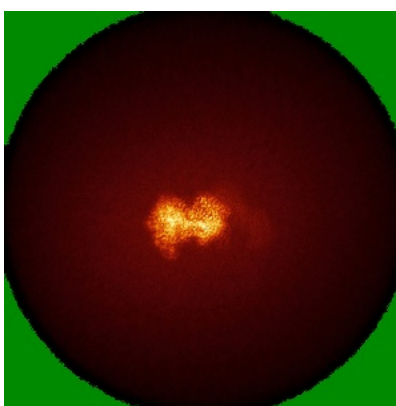
The images above show the largest variance slices of the map in three orthogonal directions.

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

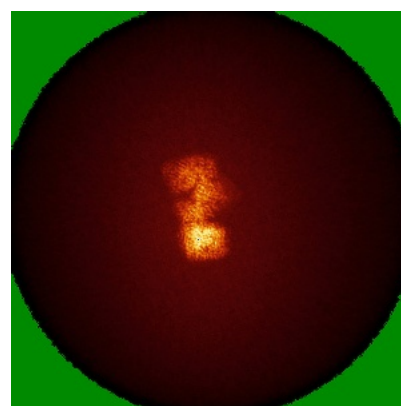
6.4.1 Primary map



X



Y

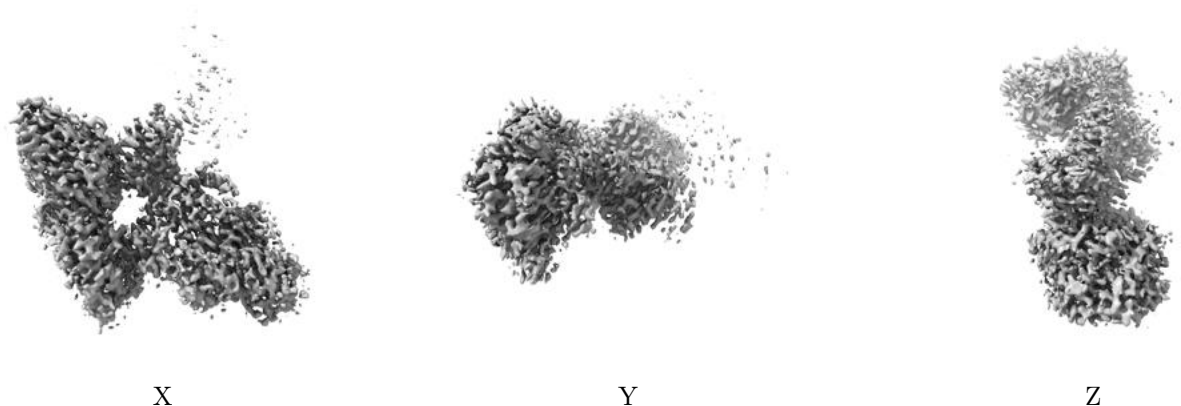


Z

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

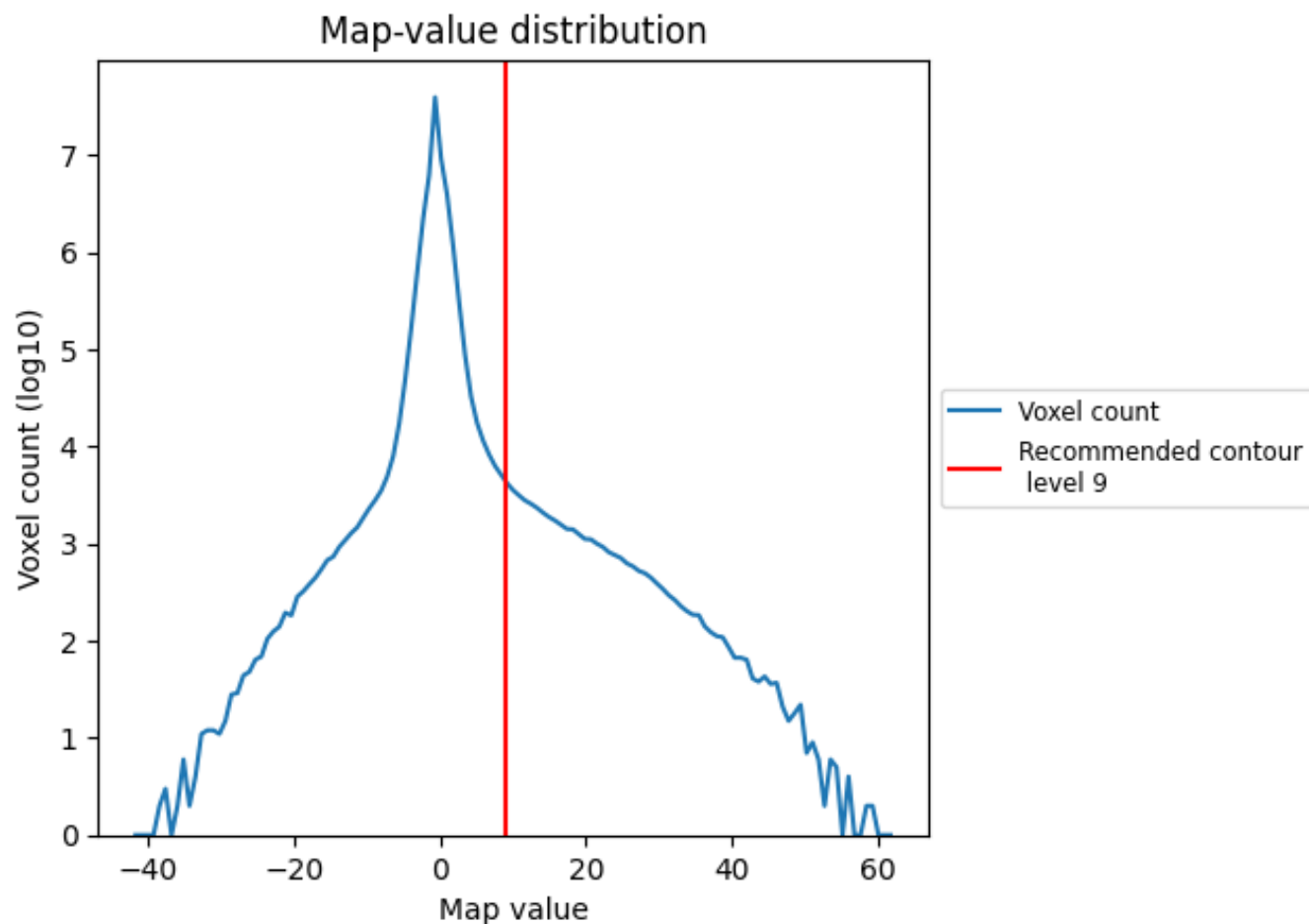
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

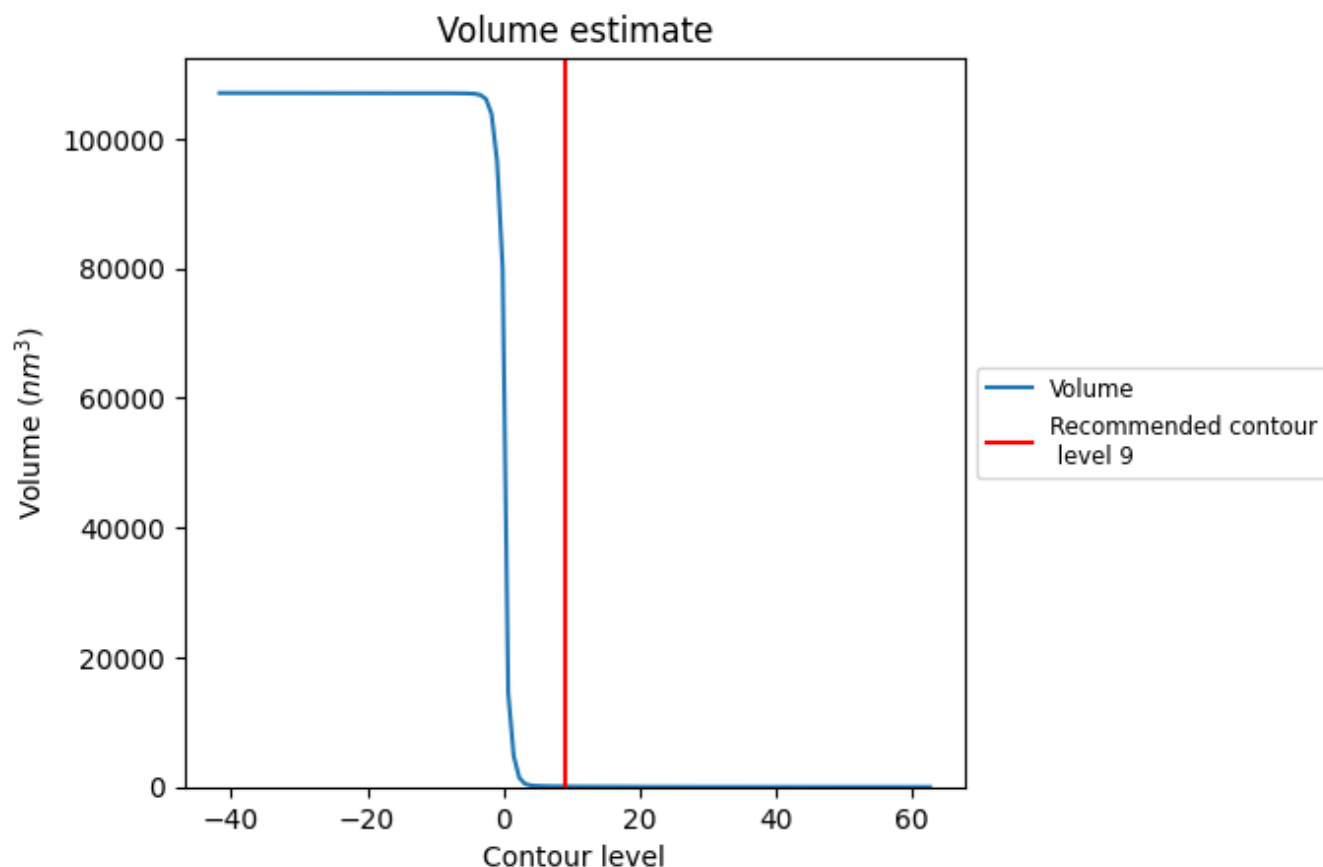
This section contains the results of statistical analysis of the map.

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.

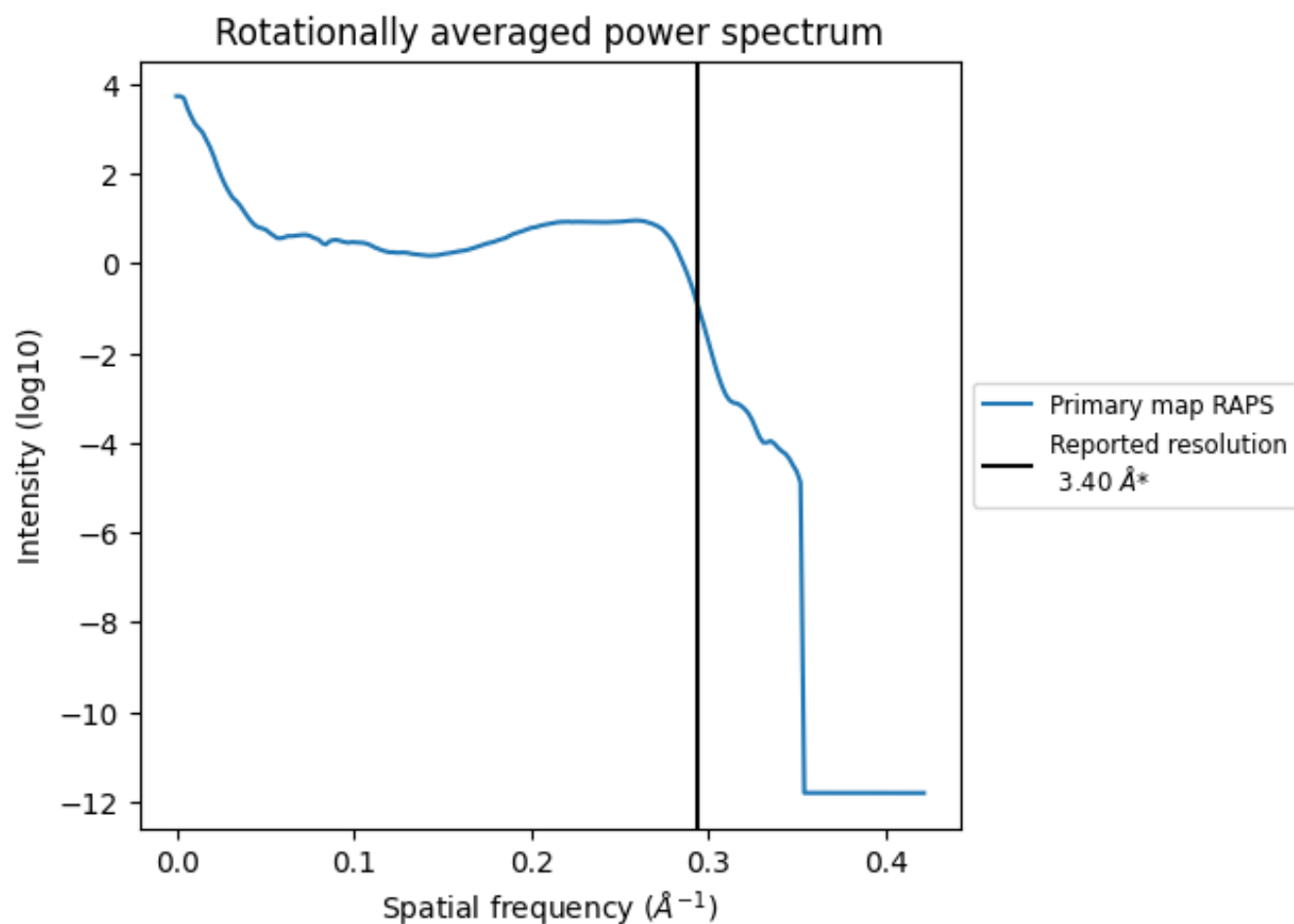
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 73 nm^3 ; this corresponds to an approximate mass of 66 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 0.294 Å⁻¹

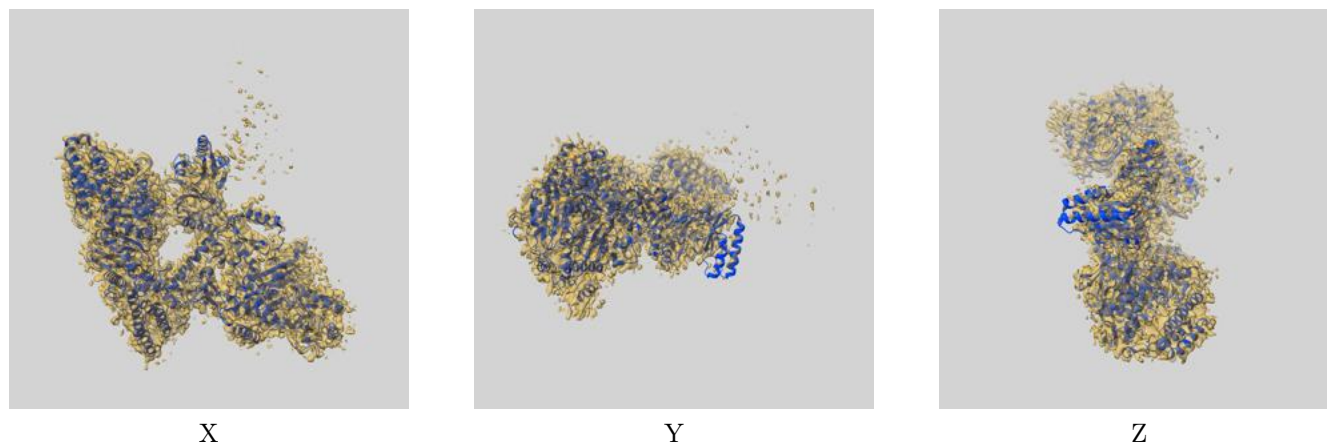
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

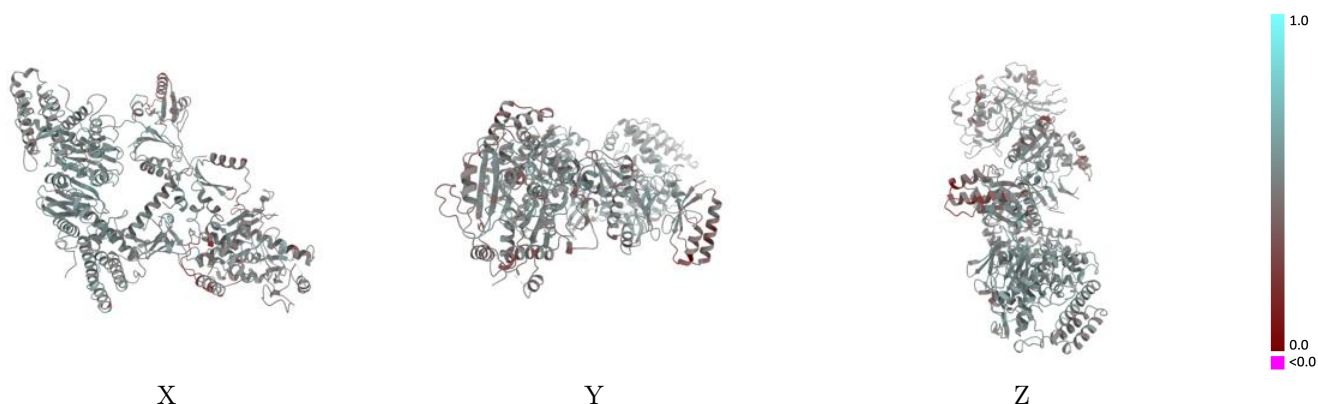
This section contains information regarding the fit between EMDB map EMD-22855 and PDB model 7KFT. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



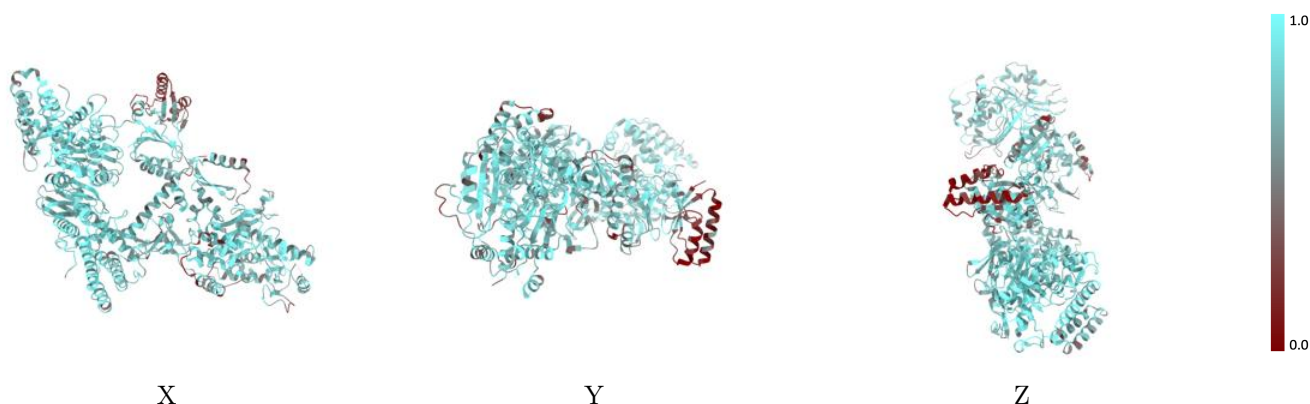
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



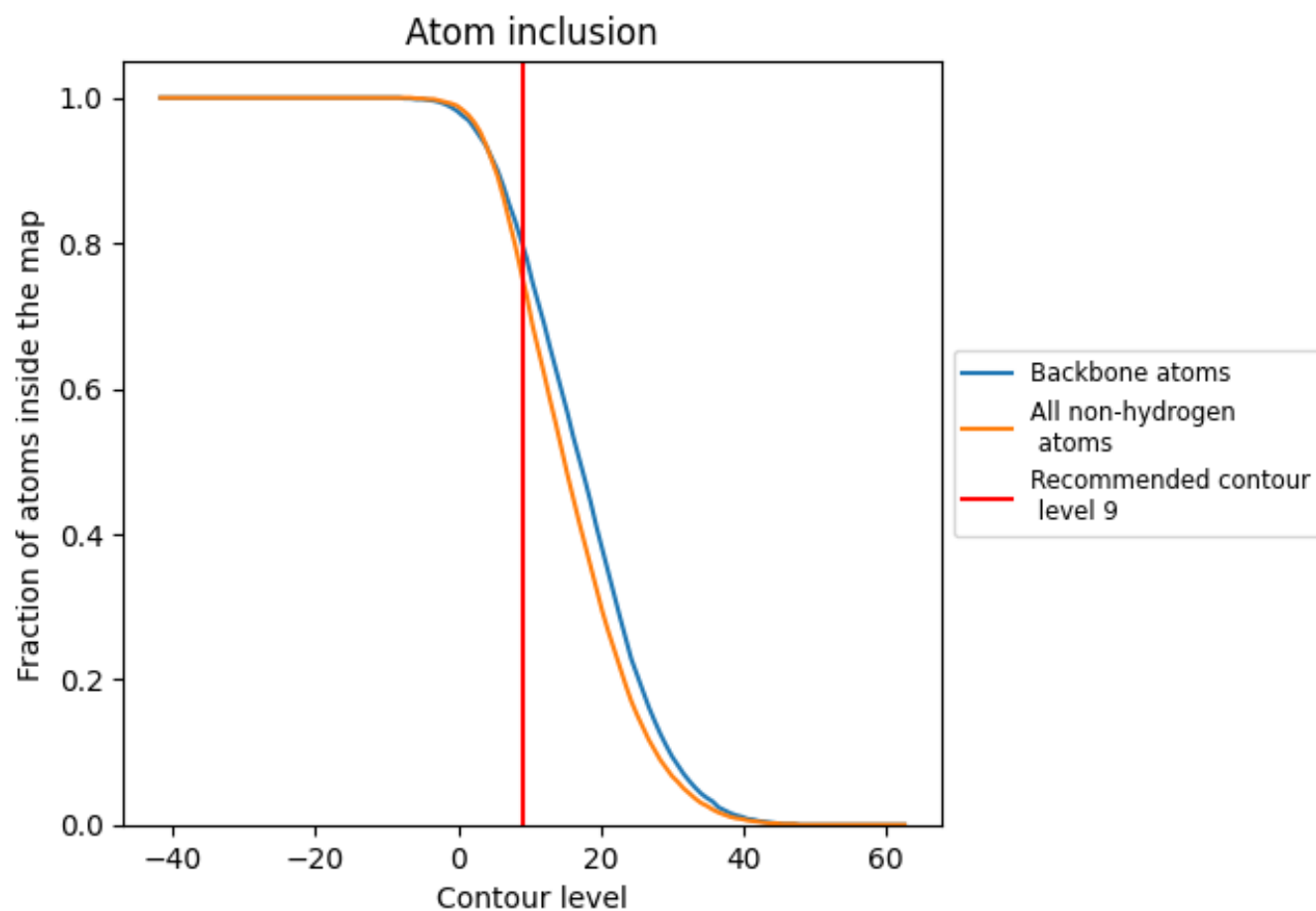
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 75% 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 (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7540	0.5020
A	0.4000	0.4240
B	0.7030	0.5060
C	0.7370	0.4820
D	0.8220	0.5280
E	0.8280	0.5300

