



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:04 PM UTC

PDB ID : 8Z9C / pdb_00008z9c
EMDB ID : EMD-39859
Title : Cryo-EM structure of NTR-bound type VII CRISPR-Cas complex at substrate-engaged state I
Authors : Zhang, H.; Deng, Z.; Li, X.
Deposited on : 2024-04-23
Resolution : 3.01 Å(reported)

This is a wwPDB EM Validation Summary 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

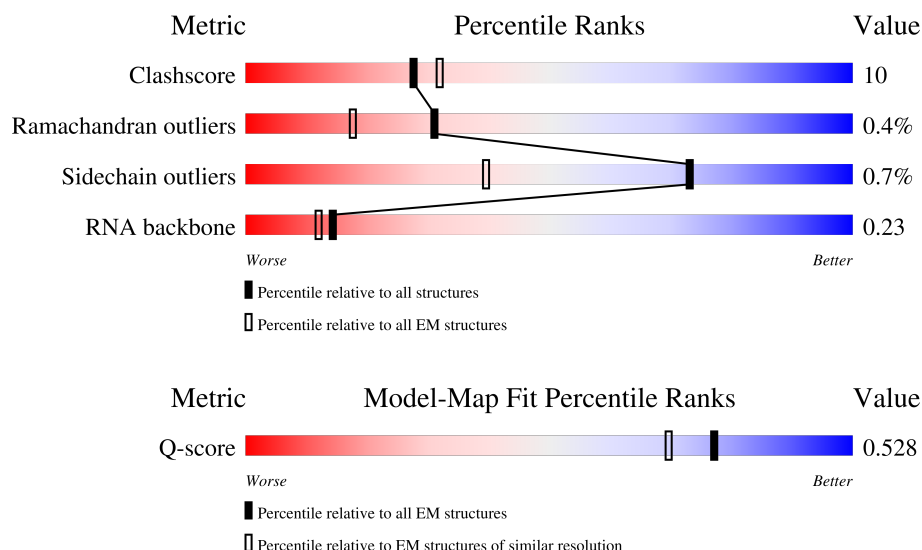
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13882 (2.51 - 3.51)

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	200	
1	B	200	
1	C	200	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	D	200	 76% 23% .
1	E	200	 82% 17%
1	F	200	 76% 20% .
1	J	200	 79% 19% ..
2	G	240	 70% 20% . 7%
3	H	609	 72% 19% . 7%
3	I	609	 21% 5% 74%
3	K	609	 35% 9% 55%
3	L	609	 21% 5% 74%
4	M	60	 8% 42% 30% 20%
5	N	54	 19% 35% 22% 24%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23182 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 structure.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	158	Total	C	N	O	S	0	0
			1154	730	197	219	8		
1	B	199	Total	C	N	O	S	0	0
			1535	957	274	296	8		
1	C	199	Total	C	N	O	S	0	0
			1547	965	278	296	8		
1	D	199	Total	C	N	O	S	0	0
			1543	962	277	296	8		
1	E	199	Total	C	N	O	S	0	0
			1541	960	277	296	8		
1	F	194	Total	C	N	O	S	0	0
			1465	915	256	286	8		
1	J	198	Total	C	N	O	S	0	0
			1532	956	273	295	8		

- Molecule 2 is a protein called Protein structure.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	223	Total	C	N	O	S	0	0
			1658	1059	277	318	4		

- Molecule 3 is a protein called Protein structure.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	565	Total	C	N	O	S	0	0
			4486	2857	750	866	13		
3	I	159	Total	C	N	O	S	0	0
			1330	852	222	249	7		
3	K	274	Total	C	N	O	S	0	0
			2182	1404	364	406	8		
3	L	160	Total	C	N	O	S	0	0
			1320	843	220	250	7		

- Molecule 4 is a RNA chain called RNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	48	Total	C	N	O	P	0	0
			1003	448	165	342	48		

- Molecule 5 is a RNA chain called RNA (41-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	41	Total	C	N	O	P	0	0
			877	393	165	278	41		

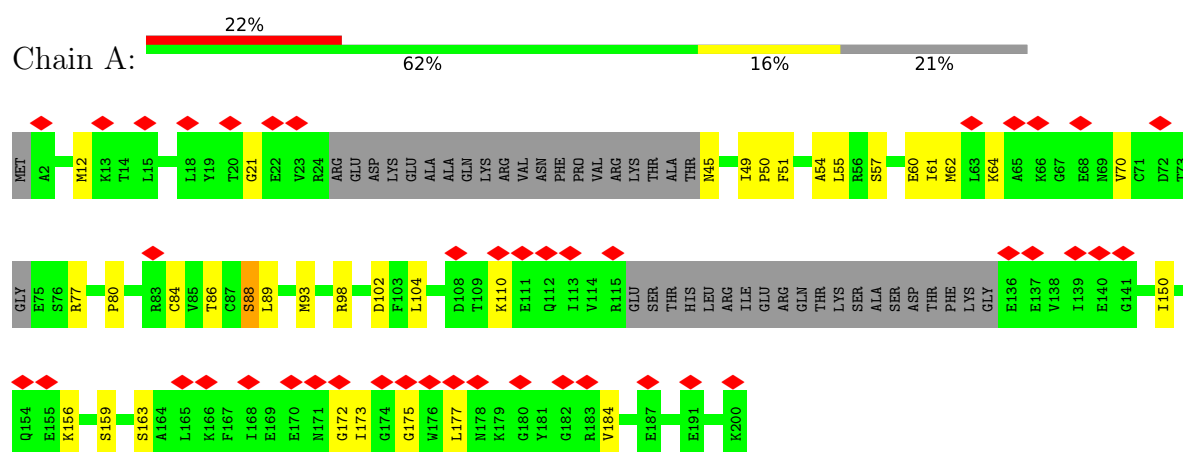
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Zn	0
			1	1	
6	B	1	Total	Zn	0
			1	1	
6	C	1	Total	Zn	0
			1	1	
6	D	1	Total	Zn	0
			1	1	
6	E	1	Total	Zn	0
			1	1	
6	F	1	Total	Zn	0
			1	1	
6	G	1	Total	Zn	0
			1	1	
6	H	1	Total	Zn	0
			1	1	
6	J	1	Total	Zn	0
			1	1	

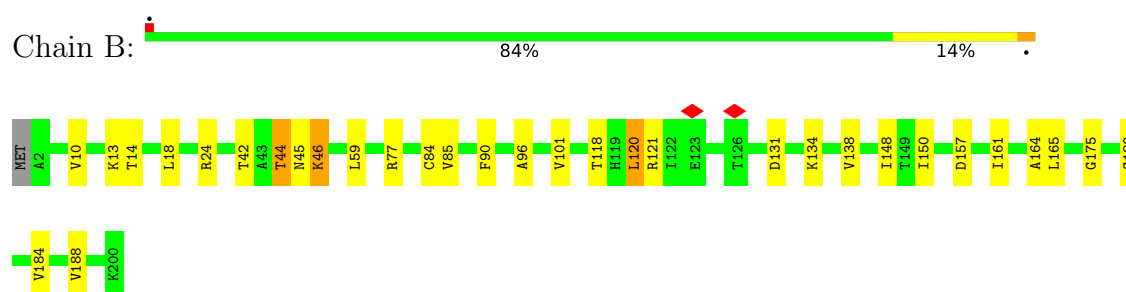
3 Residue-property plots

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.

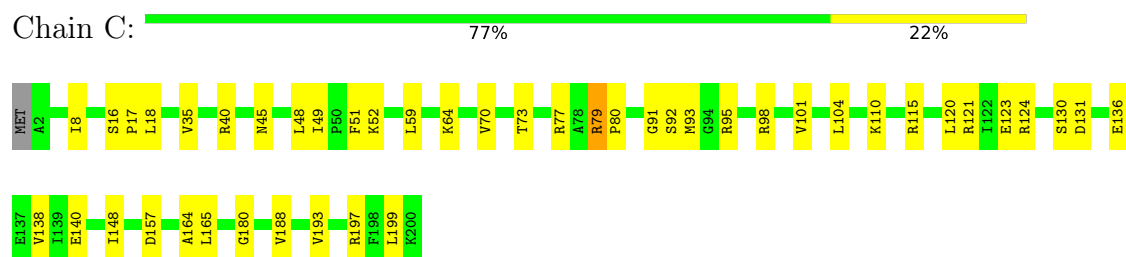
- Molecule 1: Protein structure



- Molecule 1: Protein structure

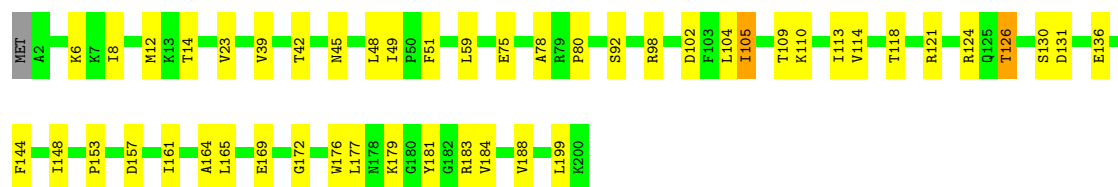


- Molecule 1: Protein structure



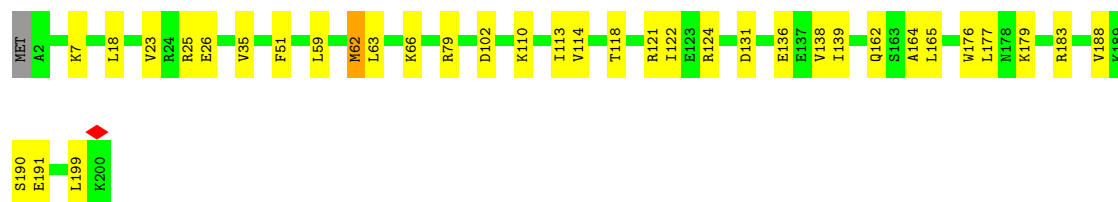
- Molecule 1: Protein structure

Chain D:  76% 23% .



• Molecule 1: Protein structure

Chain E:  82% 17%



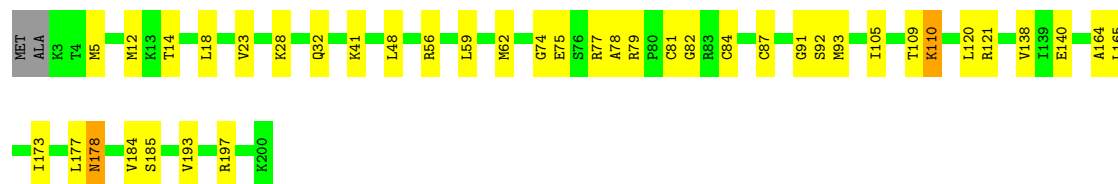
• Molecule 1: Protein structure

Chain F:  76% 20% .



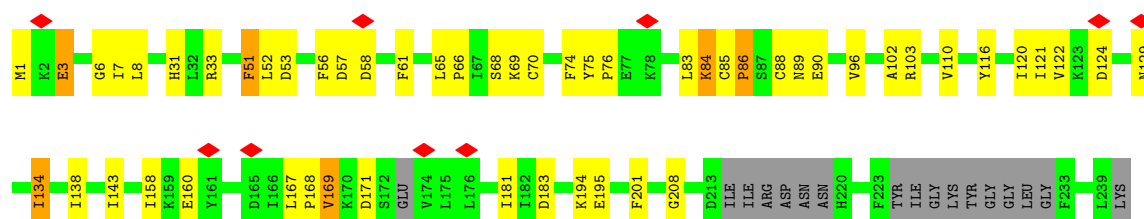
• Molecule 1: Protein structure

Chain J:  79% 19% ..



• Molecule 2: Protein structure

Chain G:  70% 20% 7%

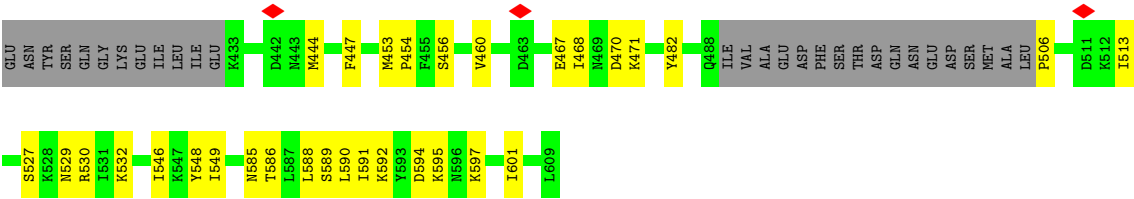


Chain H:

Lys	Lys	V238	I103	M1
Met	L239	L239	N108	L2
Arg	N246	N246	D116	K3
Ser	F247	F247	I124	F4
Gln	N248	N248	E127	L5
Ile	F249	F249	P250	V11
Val	I380	I380	I253	T12
Ala	I383	I383	Y144	G13
Asp	Y388	Y388	N145	S14
Glu	K392	K392	P256	A15
Phe	V393	V393	L264	F16
Ser	F394	F394	I265	L17
Thr	A407	A407	L271	I25
Asp	K408	K408	L272	L26
Asn	R409	R409	K273	L27
Gln	R416	R416	K275	D28
Ser	V417	V417	L276	C29
Met	L419	L419	R277	E34
Asp	M422	M422	R278	Lys
Arg	Thr	Thr	L283	Gly
Glu	Ser	Ser	D284	Ile
Asn	Gln	Gln	L285	Ile
Ser	Gly	Gly	V310	Leu
Met	Lys	Lys	S313	Lys
Asp	E428	E428	M317	Asp
Arg	L437	L437	L318	N41
Asp	T441	T441	I323	L49
Gln	M444	M444	L327	I52
Ser	F447	F447	E328	L57
Met	M453	M453	F340	C58
Asp	F454	F454	Q344	L59
Glu	F455	F455	N347	L60
Ser	S456	S456	G350	T61
Met	V460	V460	R351	H62
Asp	E461	E461	E357	A63
Gln	K462	K462	Thr	S68
Ser	R465	R465	Asn	G69
Met	I466	I466	Val	L70
Asp	E467	E467	M472	V71
Arg	D475	D475	D475	L74
Gln	E481	E481	E481	V75
Asn	Thr	Thr	Thr	K79
Ser	Asn	Asn	Asn	K82
Met	L609	L609	L609	I83

[illegible]





● Molecule 4: RNA (48-MER)



● Molecule 5: RNA (41-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	223443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.154	Depositor
Minimum map value	-1.025	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	285.0, 285.0, 285.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.43	1/1166 (0.1%)	0.81	1/1571 (0.1%)
1	B	0.38	0/1554	0.77	1/2085 (0.0%)
1	C	0.43	1/1566 (0.1%)	0.67	1/2099 (0.0%)
1	D	0.36	0/1562	0.68	1/2095 (0.0%)
1	E	0.38	0/1560	0.71	0/2092
1	F	0.49	2/1483 (0.1%)	0.83	4/1995 (0.2%)
1	J	0.58	3/1551 (0.2%)	0.72	1/2081 (0.0%)
2	G	0.52	1/1685 (0.1%)	0.93	0/2269
3	H	0.54	7/4564 (0.2%)	0.81	5/6168 (0.1%)
3	I	0.39	1/1361 (0.1%)	0.67	0/1840
3	K	0.52	3/2219 (0.1%)	0.83	4/2994 (0.1%)
3	L	0.34	0/1351	0.69	0/1830
4	M	0.43	0/1117	0.59	0/1736
5	N	0.44	0/981	0.63	0/1524
All	All	0.47	19/23720 (0.1%)	0.76	18/32379 (0.1%)

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	109	THR	C-N	11.92	1.49	1.33
1	J	177	LEU	C-N	10.13	1.48	1.33
3	H	522	ASN	C-N	-9.00	1.23	1.33
3	H	246	ASN	C-N	-8.92	1.21	1.33
2	G	51	PHE	C-N	8.15	1.44	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	523	ILE	N-CA-C	-8.25	104.98	112.90
1	J	109	THR	O-C-N	6.68	130.49	122.68

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	508	MET	CA-C-N	6.26	131.46	120.87
3	K	508	MET	C-N-CA	6.26	131.46	120.87
3	H	349	ARG	CA-C-N	5.74	126.45	120.03

There are no chirality outliers.

There are no planarity outliers.

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	1154	0	1126	22	0
1	B	1535	0	1558	25	0
1	C	1547	0	1586	33	0
1	D	1543	0	1575	38	0
1	E	1541	0	1568	30	0
1	F	1465	0	1468	33	0
1	J	1532	0	1559	30	0
2	G	1658	0	1556	40	0
3	H	4486	0	4365	85	0
3	I	1330	0	1276	22	0
3	K	2182	0	2093	49	0
3	L	1320	0	1234	27	0
4	M	1003	0	508	64	0
5	N	877	0	447	42	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
6	J	1	0	0	0	0
All	All	23182	0	21919	437	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 10.

The worst 5 of 437 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)
3:K:444:MET:HE2	3:K:451:ARG:HG2	1.49	0.94
2:G:1:MET:HA	2:G:122:VAL:O	1.76	0.85
3:L:506:PRO:N	3:L:592:LYS:HZ2	1.75	0.84
1:A:80:PRO:HD2	1:A:93:MET:HG2	1.59	0.84
4:M:-6:A:H3'	4:M:-5:A:H8	1.46	0.81

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	150/200 (75%)	137 (91%)	12 (8%)	1 (1%)	18	51
1	B	197/200 (98%)	187 (95%)	8 (4%)	2 (1%)	12	43
1	C	197/200 (98%)	191 (97%)	6 (3%)	0	100	100
1	D	197/200 (98%)	187 (95%)	10 (5%)	0	100	100
1	E	197/200 (98%)	186 (94%)	11 (6%)	0	100	100
1	F	192/200 (96%)	173 (90%)	19 (10%)	0	100	100
1	J	196/200 (98%)	188 (96%)	8 (4%)	0	100	100
2	G	215/240 (90%)	195 (91%)	14 (6%)	6 (3%)	4	19
3	H	553/609 (91%)	522 (94%)	31 (6%)	0	100	100
3	I	155/609 (26%)	150 (97%)	4 (3%)	1 (1%)	21	54
3	K	256/609 (42%)	239 (93%)	17 (7%)	0	100	100
3	L	156/609 (26%)	153 (98%)	3 (2%)	0	100	100
All	All	2661/4076 (65%)	2508 (94%)	143 (5%)	10 (0%)	31	63

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	70	VAL
1	B	157	ASP
2	G	57	ASP
1	B	46	LYS
2	G	86	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	117/170 (69%)	116 (99%)	1 (1%)	70	84
1	B	166/170 (98%)	164 (99%)	2 (1%)	63	81
1	C	169/170 (99%)	169 (100%)	0	100	100
1	D	168/170 (99%)	167 (99%)	1 (1%)	78	87
1	E	167/170 (98%)	166 (99%)	1 (1%)	78	87
1	F	157/170 (92%)	156 (99%)	1 (1%)	78	87
1	J	167/170 (98%)	166 (99%)	1 (1%)	78	87
2	G	163/209 (78%)	160 (98%)	3 (2%)	51	76
3	H	484/556 (87%)	482 (100%)	2 (0%)	84	89
3	I	146/556 (26%)	144 (99%)	2 (1%)	59	79
3	K	228/556 (41%)	226 (99%)	2 (1%)	70	84
3	L	142/556 (26%)	142 (100%)	0	100	100
All	All	2274/3623 (63%)	2258 (99%)	16 (1%)	73	85

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	463	ASP
1	J	178	ASN
2	G	195	GLU
3	I	562	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	134	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	516	ASN
3	L	558	ASN
3	I	604	ASN
3	L	479	ASN
3	I	558	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	M	48/60 (80%)	21 (43%)	5 (10%)
5	N	39/54 (72%)	14 (35%)	2 (5%)
All	All	87/114 (76%)	35 (40%)	7 (8%)

5 of 35 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	M	-8	U
4	M	-7	U
4	M	-6	A
4	M	-5	A
4	M	-3	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	M	34	C
4	M	36	C
5	N	32	A
5	N	26	A
4	M	4	C

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](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

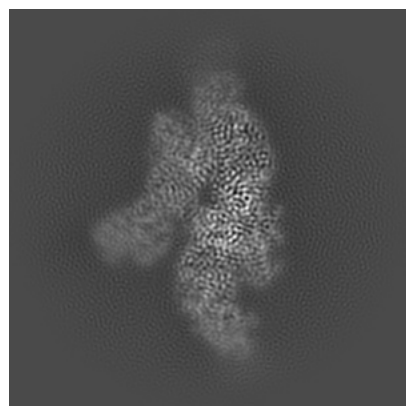
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39859. These allow visual inspection of the internal detail of the map and identification of artifacts.

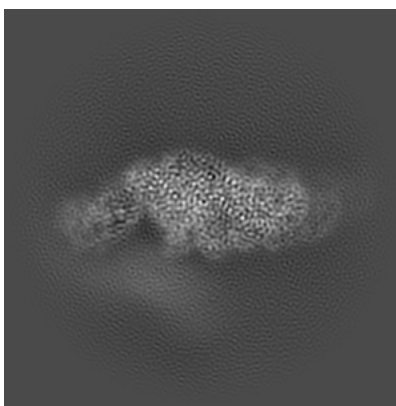
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

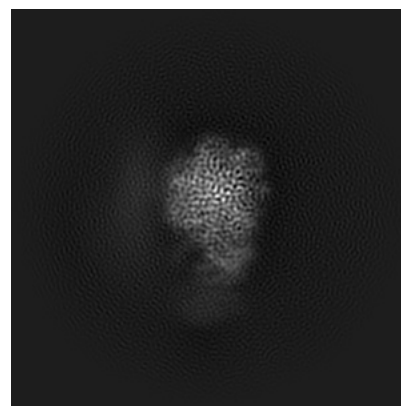
6.1.1 Primary map



X

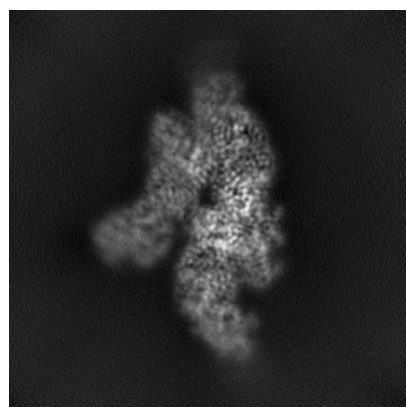


Y

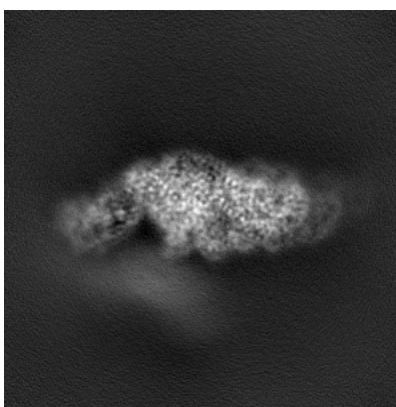


Z

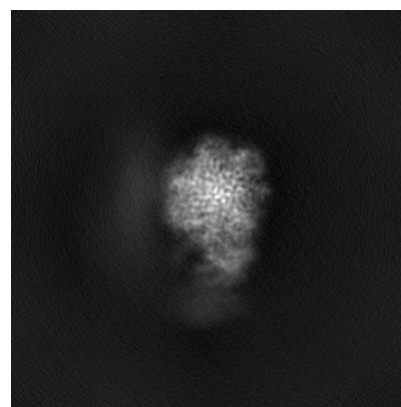
6.1.2 Raw map



X



Y

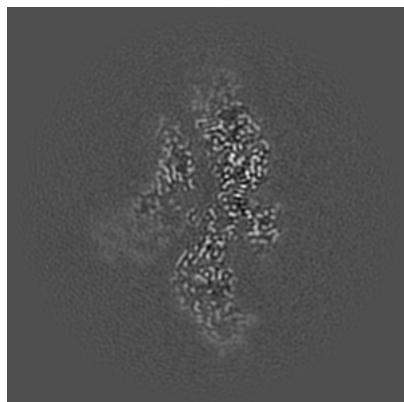


Z

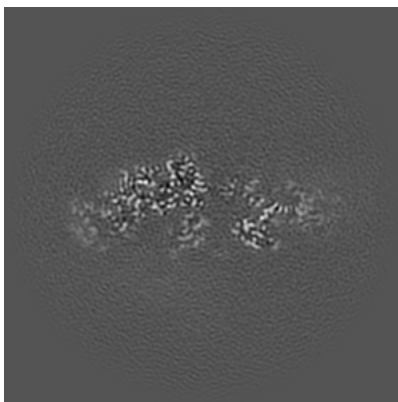
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

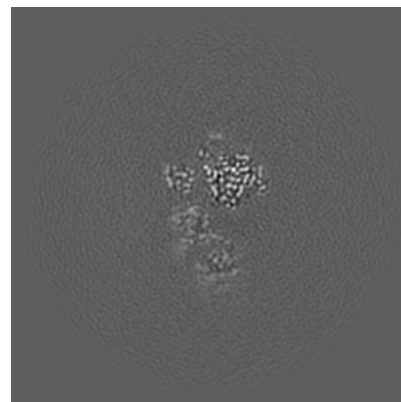
6.2.1 Primary map



X Index: 150

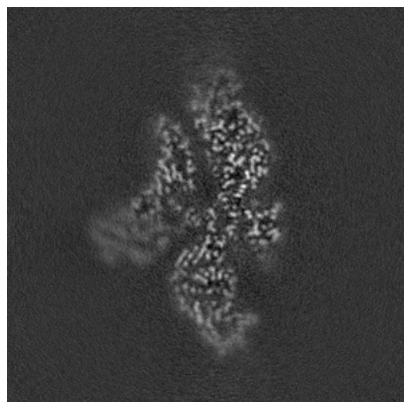


Y Index: 150

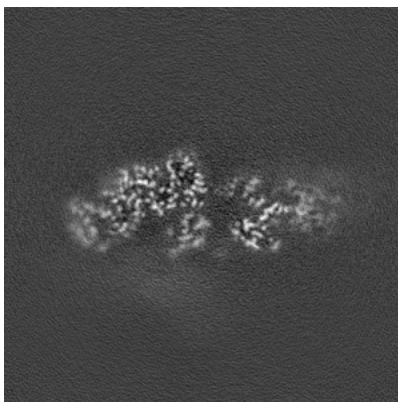


Z Index: 150

6.2.2 Raw map



X Index: 150



Y Index: 150

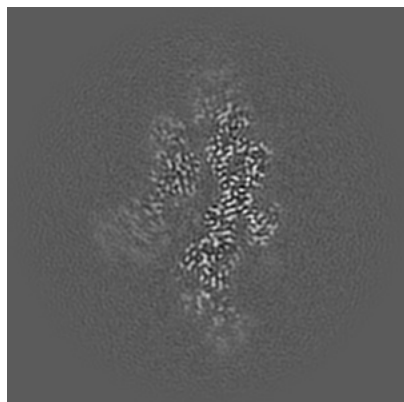


Z Index: 150

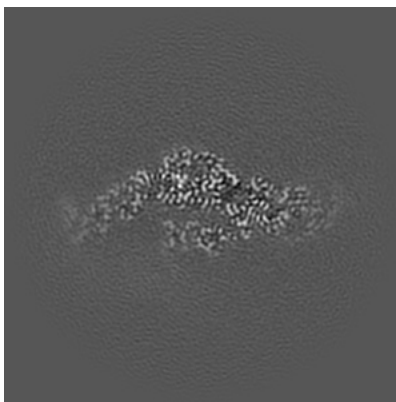
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

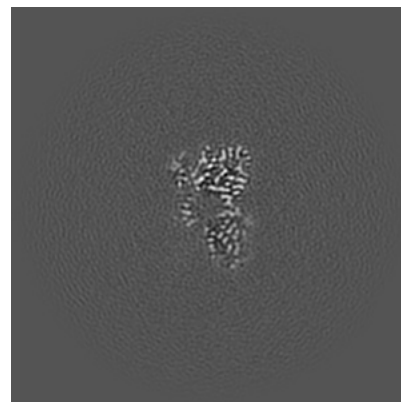
6.3.1 Primary map



X Index: 154

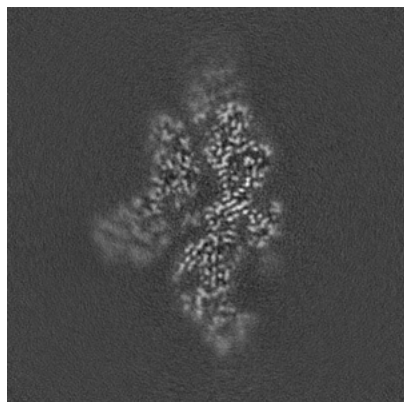


Y Index: 165

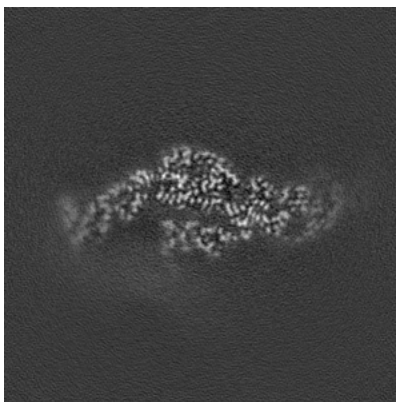


Z Index: 172

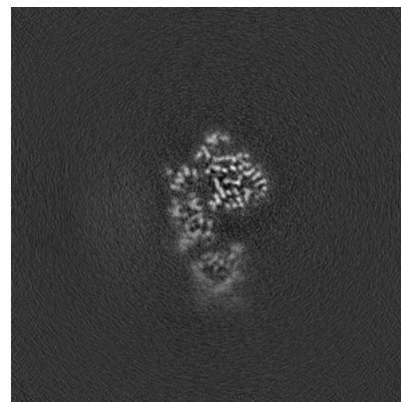
6.3.2 Raw map



X Index: 153



Y Index: 165

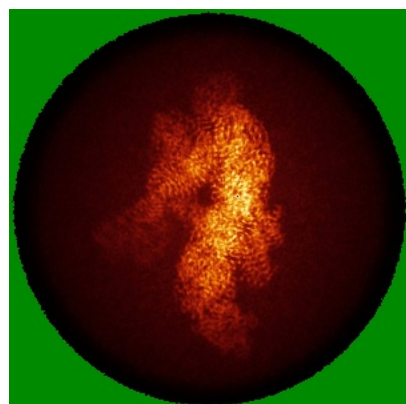


Z Index: 147

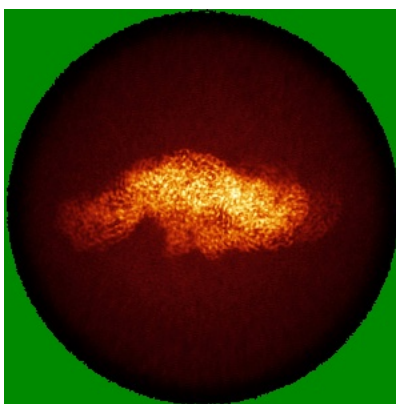
The images above show the largest variance slices of the map in three orthogonal directions.

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

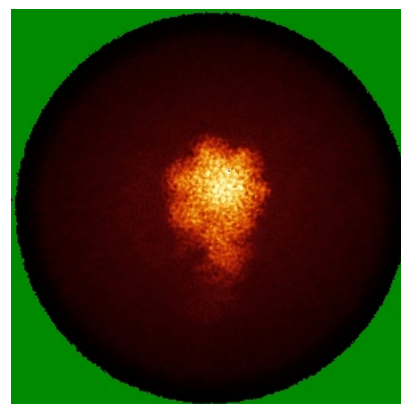
6.4.1 Primary map



X

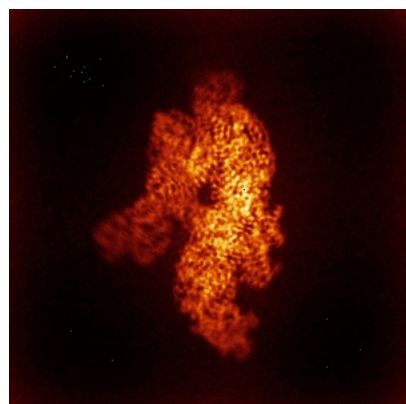


Y

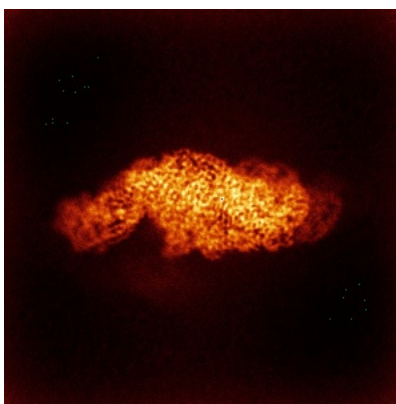


Z

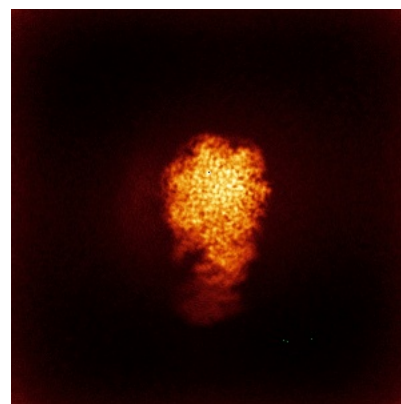
6.4.2 Raw map



X



Y

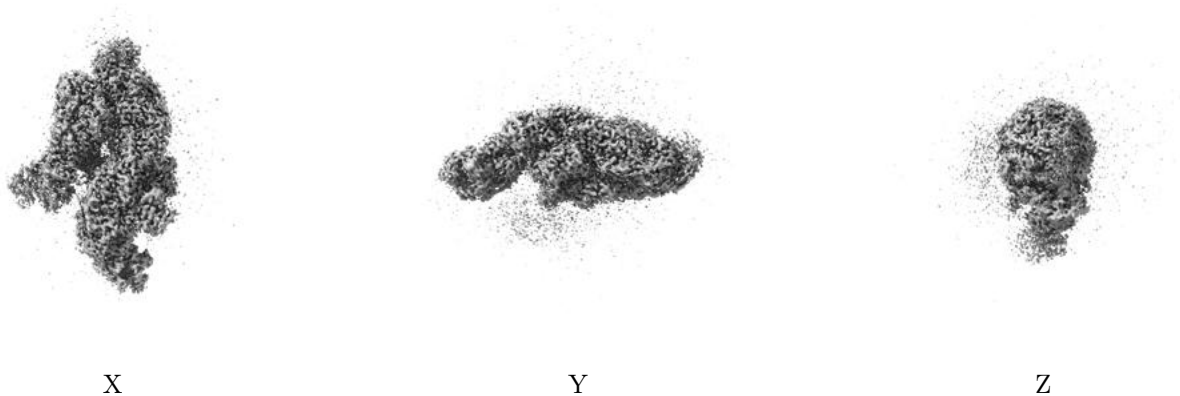


Z

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.

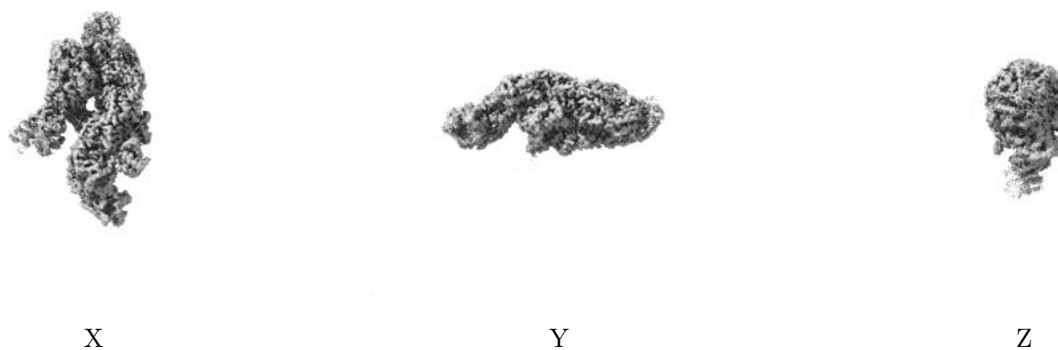
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

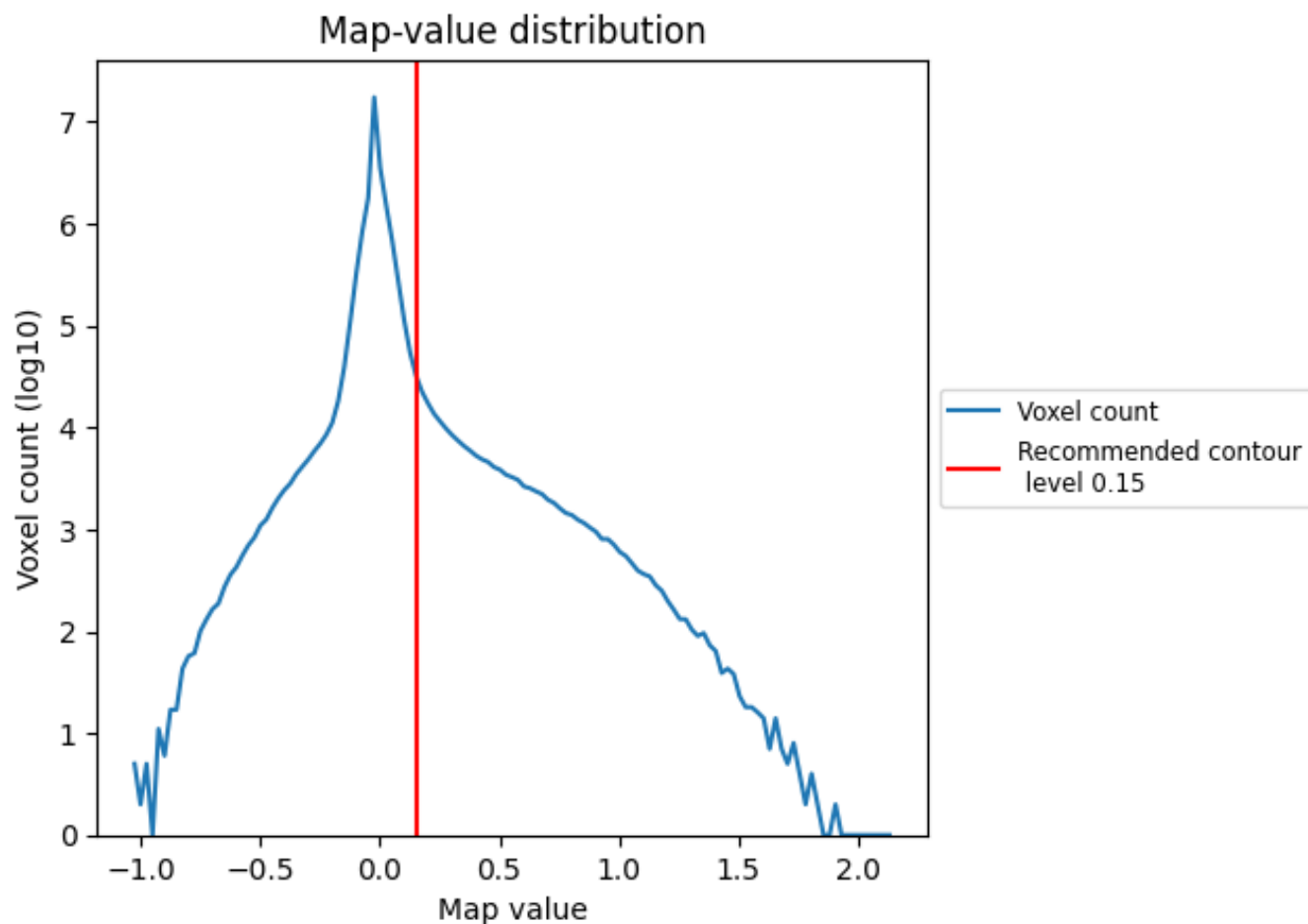
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

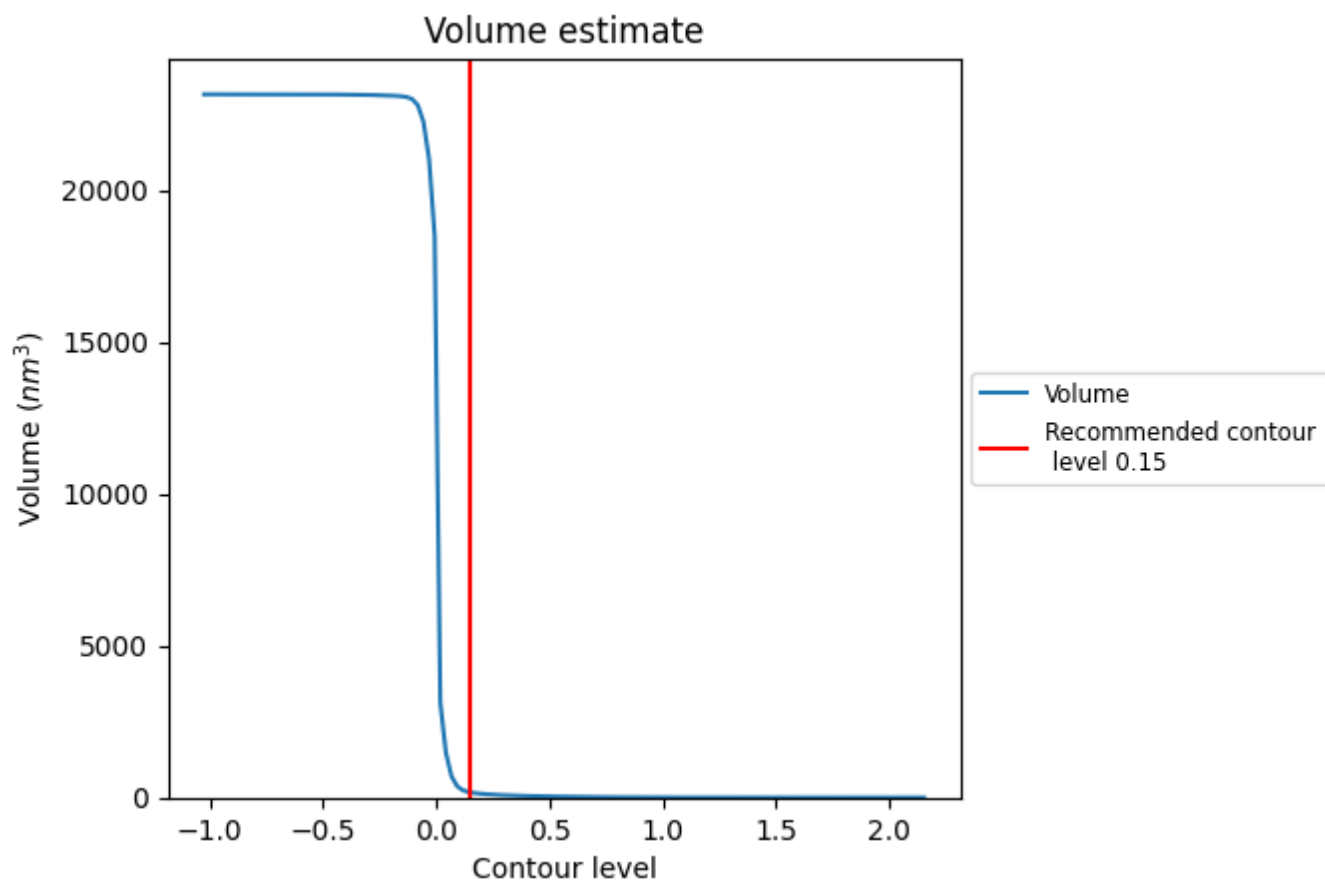
This section contains the results of statistical analysis of the map.

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.

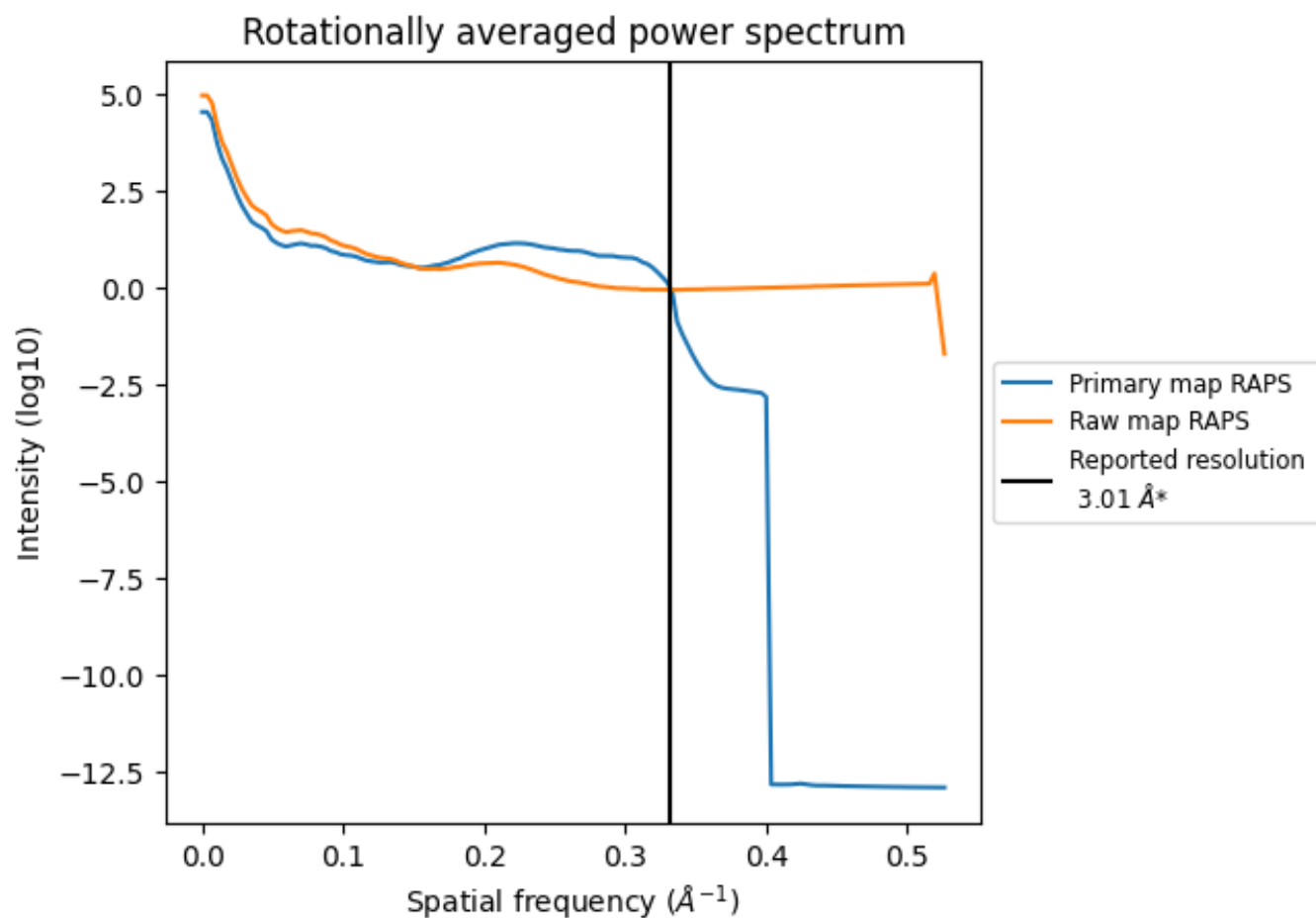
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 173 nm^3 ; this corresponds to an approximate mass of 156 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 ⓘ

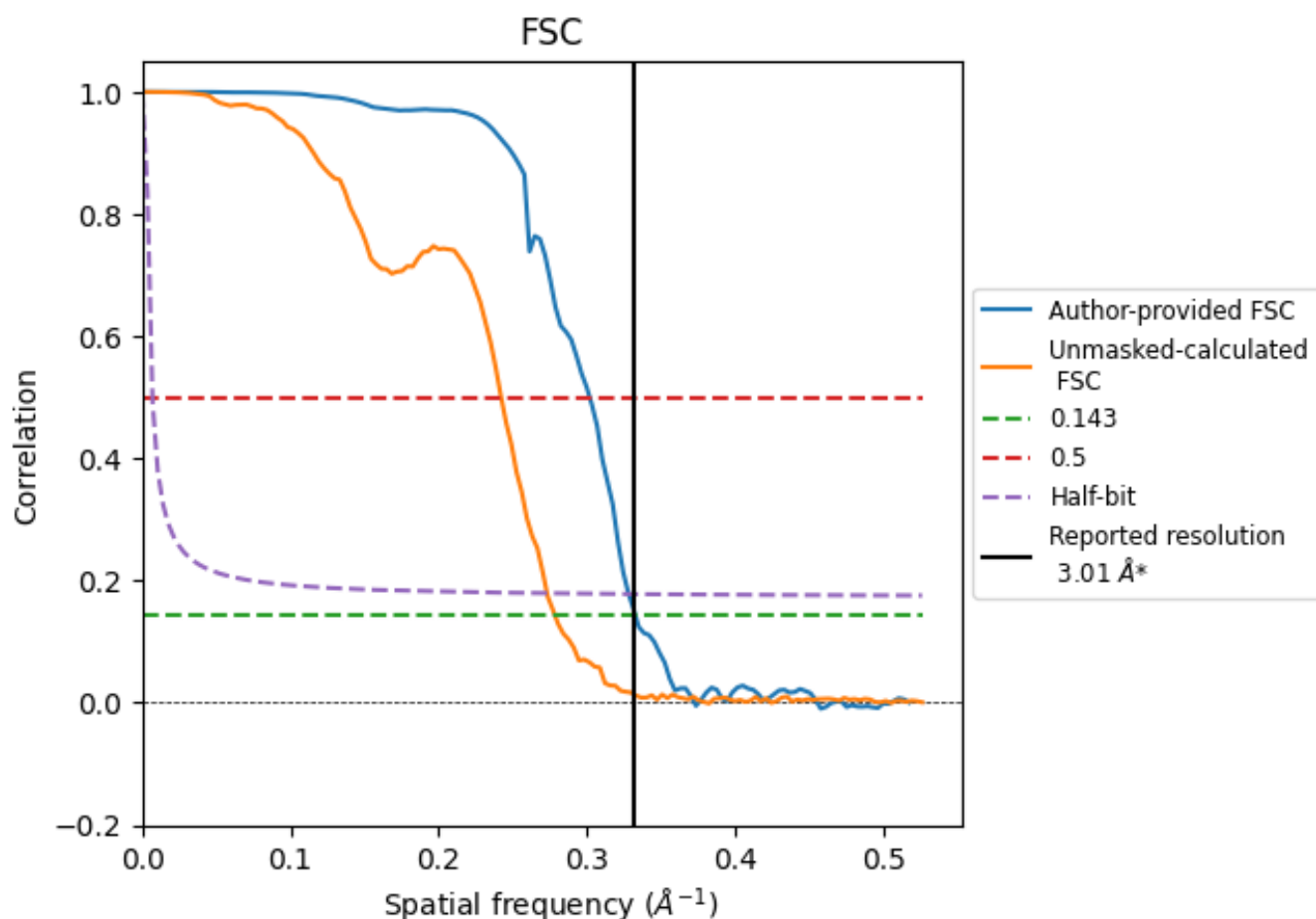


*Reported resolution corresponds to spatial frequency of 0.332 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.332 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.01	-	-
Author-provided FSC curve	3.00	3.31	3.05
Unmasked-calculated*	3.59	4.13	3.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.59 differs from the reported value 3.01 by more than 10 %

9 Map-model fit [i](#)

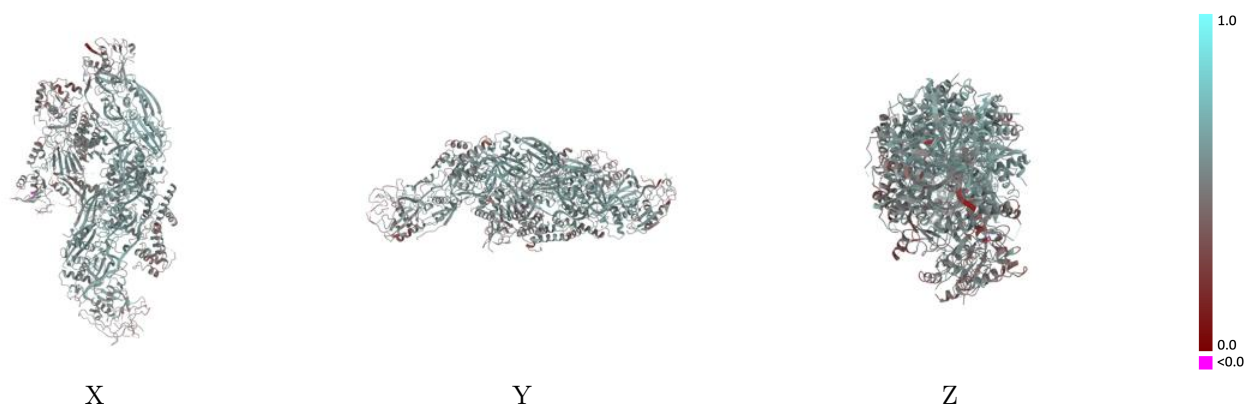
This section contains information regarding the fit between EMDB map EMD-39859 and PDB model 8Z9C. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



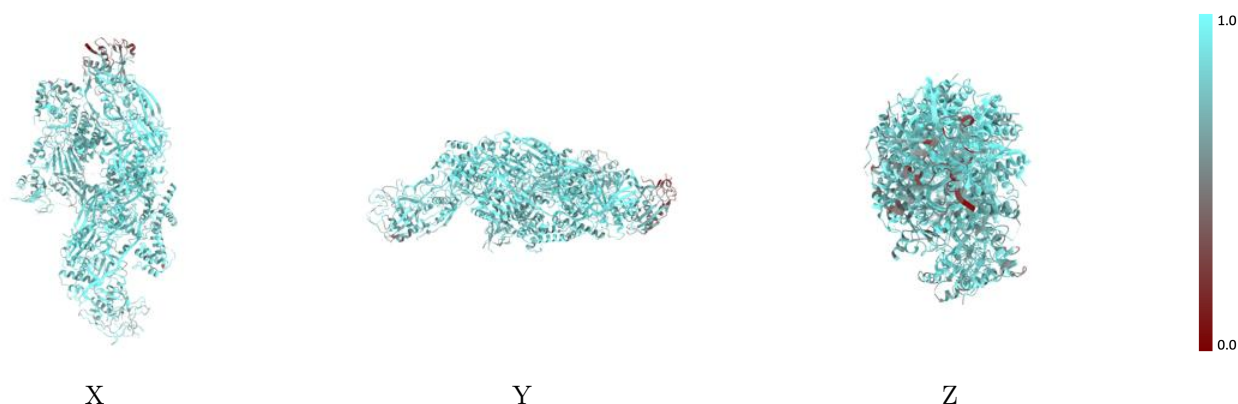
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



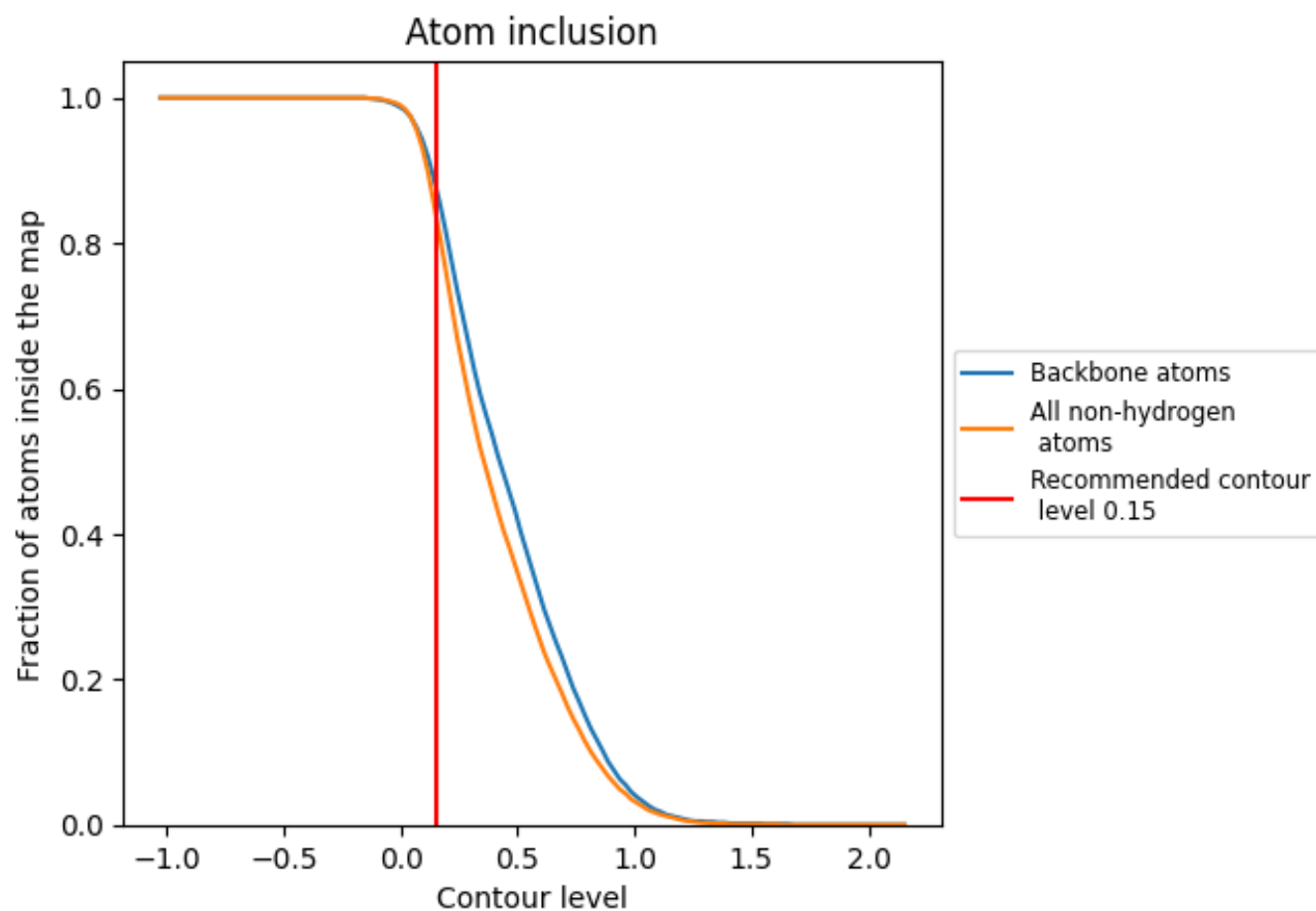
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8430	0.5280
A	0.5760	0.4920
B	0.8780	0.5620
C	0.9290	0.5940
D	0.9260	0.5910
E	0.9060	0.5800
F	0.8750	0.5500
G	0.7530	0.4710
H	0.8160	0.4910
I	0.8290	0.4950
J	0.9210	0.5750
K	0.8030	0.4860
L	0.7980	0.4710
M	0.9290	0.5650
N	0.9430	0.5720

1.0

0.0

<0.0