



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 03:10 AM UTC

PDB ID : 6OMF / pdb_00006omf
EMDB ID : EMD-20090
Title : CryoEM structure of SigmaS-transcription initiation complex with activator CrI
Authors : Jaramillo Cartagena, A.; Darst, S.A.; Campbell, E.A.
Deposited on : 2019-04-18
Resolution : 3.26 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:

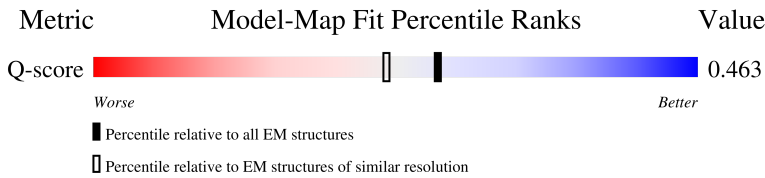
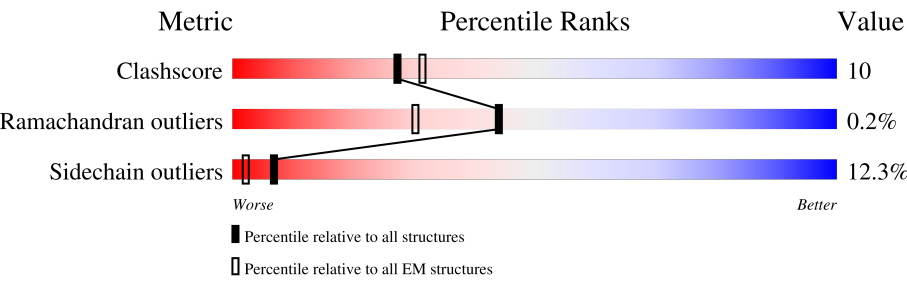
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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.



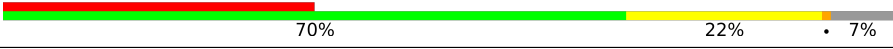
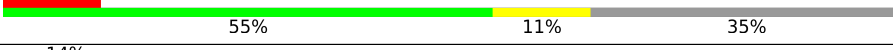
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14557 (2.76 - 3.76)

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	239	7% 63% 29% 5% .
1	B	239	. 61% 29% 7%
2	C	1342	6% 69% 26% .
3	D	1407	10% 66% 25% 5% .

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Mol	Chain	Length	Quality of chain
4	E	91	
5	F	331	
6	J	136	
7	T	66	
8	N	66	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 30251 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	233	Total	C	N	O	S	0	0
			1806	1127	317	356	6		
1	B	223	Total	C	N	O	S	0	0
			1714	1070	302	336	6		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	expression tag	UNP P0A7Z6
A	236	VAL	-	expression tag	UNP P0A7Z6
A	237	LEU	-	expression tag	UNP P0A7Z6
A	238	PHE	-	expression tag	UNP P0A7Z6
A	239	GLN	-	expression tag	UNP P0A7Z6
B	235	GLU	-	expression tag	UNP P0A7Z6
B	236	VAL	-	expression tag	UNP P0A7Z6
B	237	LEU	-	expression tag	UNP P0A7Z6
B	238	PHE	-	expression tag	UNP P0A7Z6
B	239	GLN	-	expression tag	UNP P0A7Z6

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1336	Total	C	N	O	S	0	0
			10382	6522	1851	1960	49		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoS.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	278	Total	C	N	O	S	0	0
			2244	1406	415	419	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	SER	-	expression tag	UNP S5ZIY8

- Molecule 6 is a protein called Sigma factor-binding protein Crl.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	127	Total	C	N	O	S	0	0
			1024	667	166	187	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-2	GLY	-	expression tag	UNP A0A0F7J6B7
J	-1	PRO	-	expression tag	UNP A0A0F7J6B7
J	0	HIS	-	expression tag	UNP A0A0F7J6B7

- Molecule 7 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	43	Total	C	N	O	P	0	0
			876	418	155	260	43		

- Molecule 8 is a DNA chain called Non-template DNA strand.

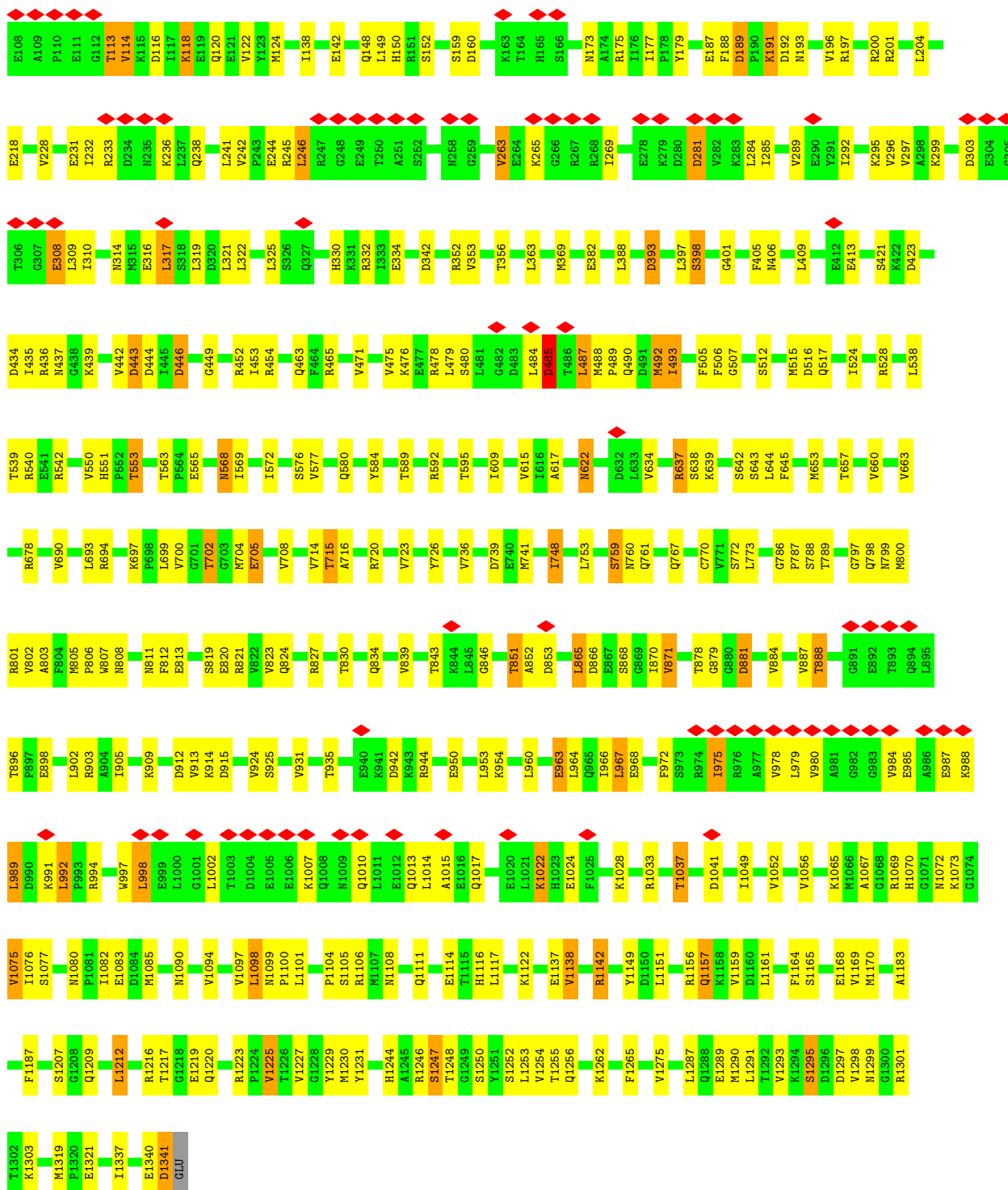
Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	49	Total	C	N	O	P	0	0
			1008	481	191	288	48		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	D	1	Total 1	Mg 1	0

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

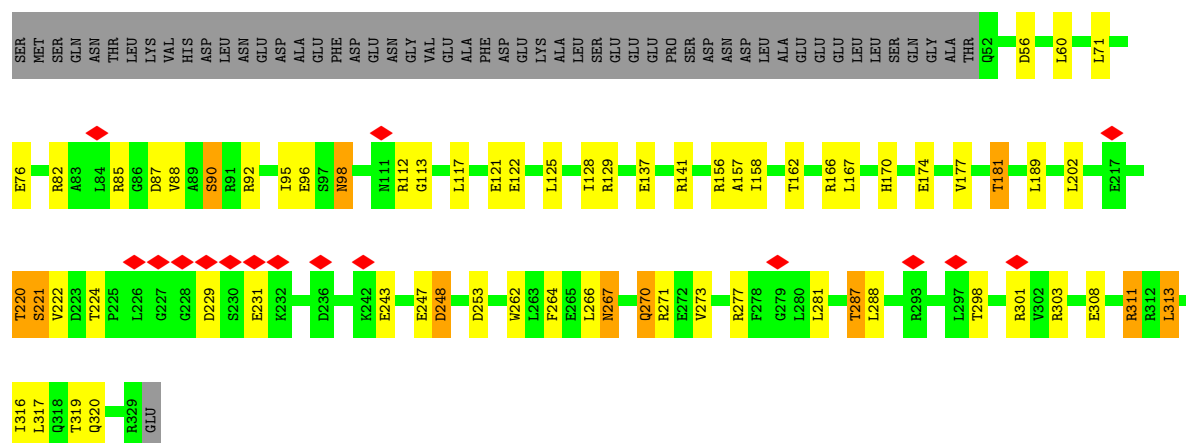
Mol	Chain	Residues	Atoms		AltConf
10	D	2	Total 2	Zn 2	0



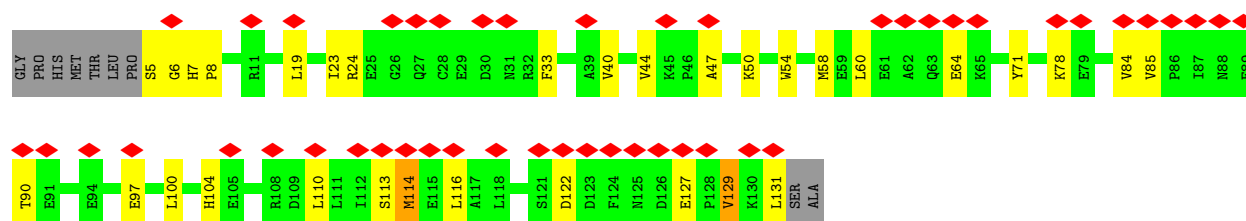




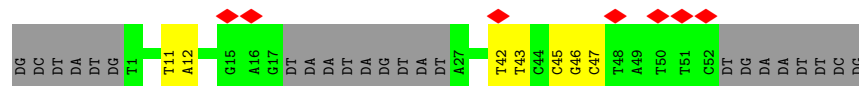
• Molecule 5: RNA polymerase sigma factor RpoS



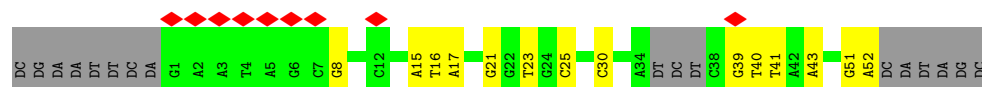
• Molecule 6: Sigma factor-binding protein Crl



• Molecule 7: Template DNA strand



• Molecule 8: Non-template DNA strand



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	292000	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 ($e^-/\text{\AA}^2$)	1.42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.935	Depositor
Minimum map value	-2.803	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.097	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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, MG

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	0.55	0/1828	0.67	2/2479 (0.1%)
1	B	0.46	0/1734	0.64	2/2349 (0.1%)
2	C	0.55	0/10736	0.61	6/14487 (0.0%)
3	D	0.63	17/10539 (0.2%)	0.65	7/14232 (0.0%)
4	E	0.48	0/629	0.64	0/847
5	F	0.40	0/2273	0.56	0/3065
6	J	0.25	0/1054	0.52	0/1433
7	T	0.42	0/979	0.56	0/1505
8	N	0.42	0/1132	0.60	0/1744
All	All	0.55	17/30904 (0.1%)	0.62	17/42141 (0.0%)

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	1
1	B	0	1
2	C	0	2
3	D	0	3
All	All	0	7

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	300	GLN	CA-C	-11.35	1.37	1.52
3	D	305	ALA	CA-C	-8.93	1.43	1.52
3	D	302	ALA	C-O	-8.64	1.13	1.24
3	D	302	ALA	CA-CB	-8.25	1.40	1.53
3	D	304	ASP	C-O	-8.15	1.13	1.24

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	305	ALA	N-CA-C	-7.60	102.82	112.93
3	D	301	GLU	N-CA-C	-6.98	105.30	113.88
3	D	903	LEU	CA-C-N	6.71	134.35	121.54
3	D	903	LEU	C-N-CA	6.71	134.35	121.54
3	D	300	GLN	CB-CA-C	-6.39	97.69	110.42

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	7	GLU	Peptide
1	B	19	VAL	Peptide
2	C	398	SER	Peptide
2	C	485	ASP	Peptide
3	D	119	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	1806	0	1835	48	0
1	B	1714	0	1748	44	0
2	C	10567	0	10585	214	0
3	D	10382	0	10594	238	0
4	E	627	0	634	11	0
5	F	2244	0	2279	46	0
6	J	1024	0	949	16	0
7	T	876	0	487	7	0
8	N	1008	0	554	11	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
All	All	30251	0	29665	588	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 588 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:236:VAL:HG13	1:B:16:ILE:CG2	1.79	1.13
3:D:300:GLN:NE2	3:D:304:ASP:OD2	1.85	1.08
3:D:299:LEU:O	3:D:302:ALA:N	1.85	1.06
3:D:300:GLN:NE2	3:D:300:GLN:O	1.90	1.05
1:A:233:ASP:O	1:A:235:GLU:OE1	1.80	1.00

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	231/239 (97%)	208 (90%)	22 (10%)	1 (0%)	30	59
1	B	219/239 (92%)	203 (93%)	16 (7%)	0	100	100
2	C	1338/1342 (100%)	1234 (92%)	104 (8%)	0	100	100
3	D	1330/1407 (94%)	1233 (93%)	92 (7%)	5 (0%)	30	59
4	E	77/91 (85%)	69 (90%)	8 (10%)	0	100	100
5	F	276/331 (83%)	266 (96%)	10 (4%)	0	100	100
6	J	125/136 (92%)	118 (94%)	7 (6%)	0	100	100
All	All	3596/3785 (95%)	3331 (93%)	259 (7%)	6 (0%)	44	70

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	300	GLN
3	D	304	ASP
3	D	904	ALA
1	A	8	PHE
3	D	299	LEU

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	201/206 (98%)	162 (81%)	39 (19%)	1	6
1	B	190/206 (92%)	165 (87%)	25 (13%)	4	17
2	C	1155/1157 (100%)	1012 (88%)	143 (12%)	4	19
3	D	1118/1168 (96%)	983 (88%)	135 (12%)	5	20
4	E	67/75 (89%)	64 (96%)	3 (4%)	24	52
5	F	236/287 (82%)	215 (91%)	21 (9%)	9	30
6	J	104/123 (85%)	91 (88%)	13 (12%)	4	19
All	All	3071/3222 (95%)	2692 (88%)	379 (12%)	7	19

5 of 379 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	354	VAL
3	D	798	ARG
3	D	407	VAL
3	D	564	VAL
3	D	877	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	667	GLN
3	D	1227	HIS
3	D	669	GLN
3	D	910	ASN
3	D	1238	GLN

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](#)

Of 3 ligands modelled in this entry, 3 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.

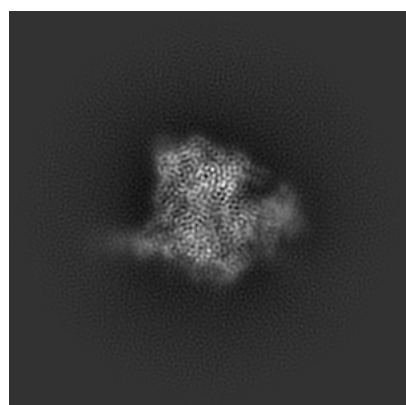
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20090. These allow visual inspection of the internal detail of the map and identification of artifacts.

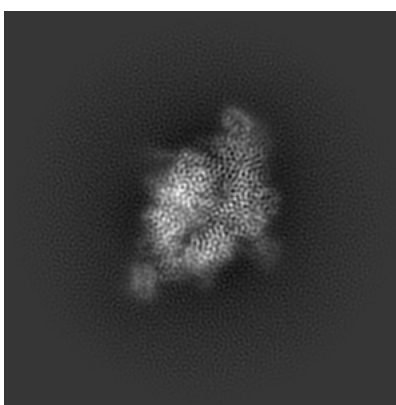
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

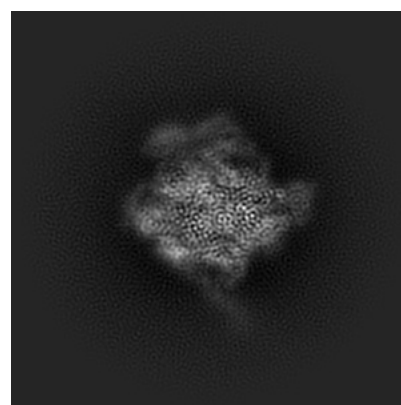
6.1.1 Primary map



X



Y

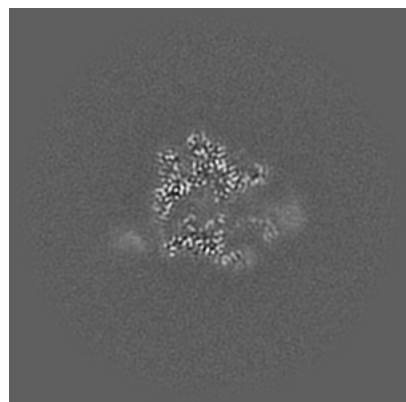


Z

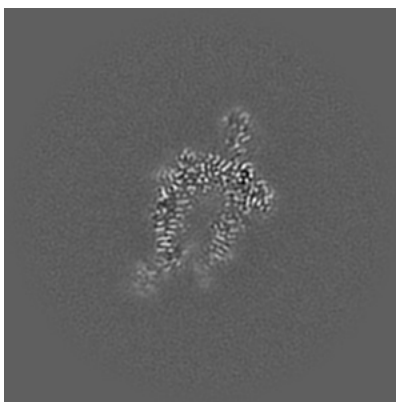
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

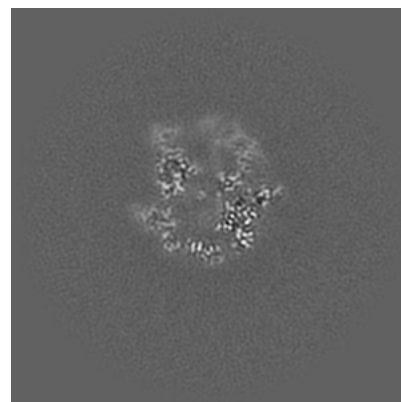
6.2.1 Primary map



X Index: 128



Y Index: 128

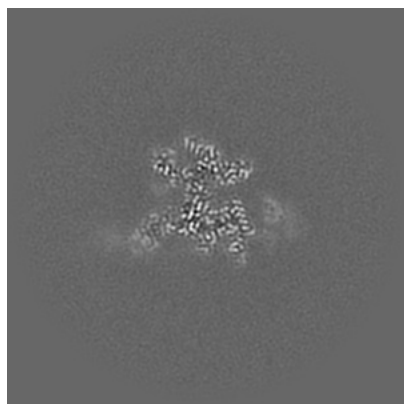


Z Index: 128

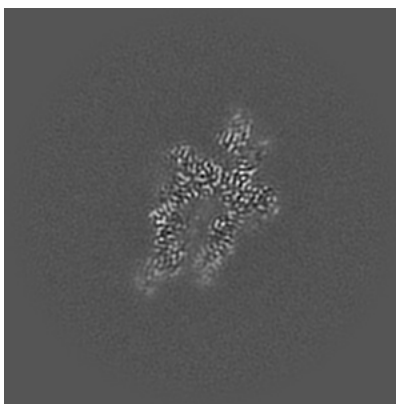
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

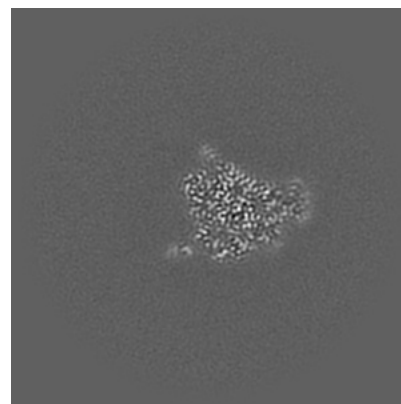
6.3.1 Primary map



X Index: 141



Y Index: 123

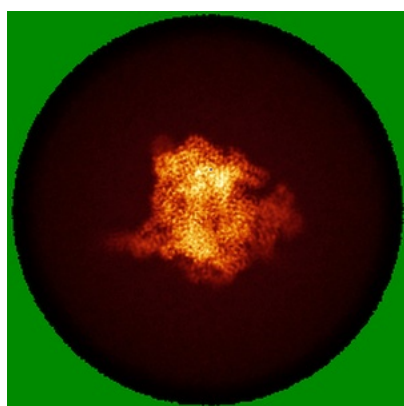


Z Index: 151

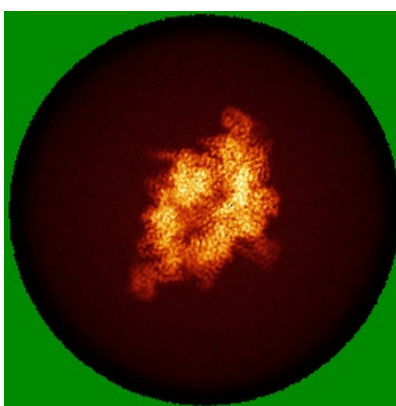
The images above show the largest variance slices of the map in three orthogonal directions.

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

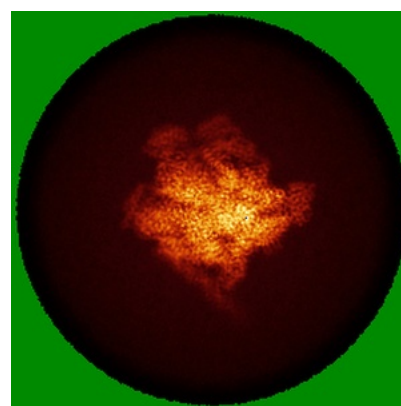
6.4.1 Primary map



X



Y

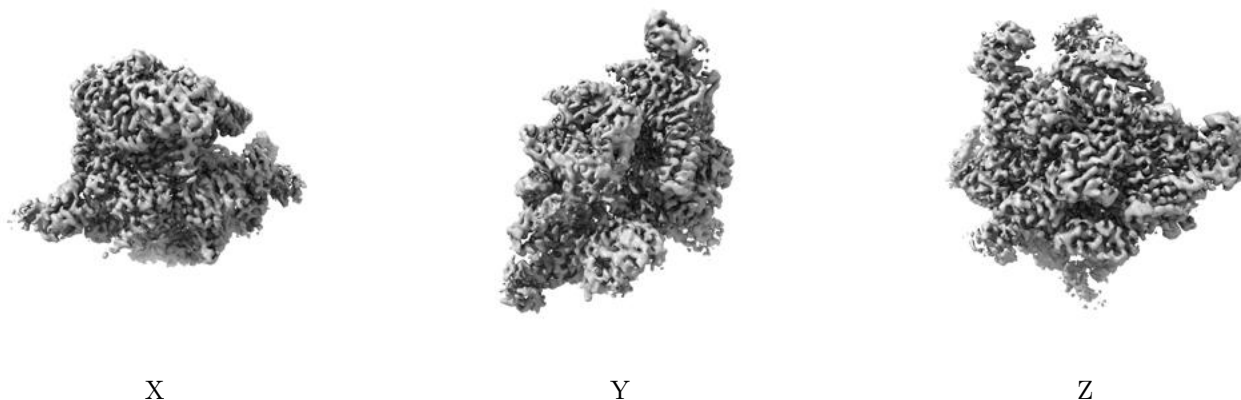


Z

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

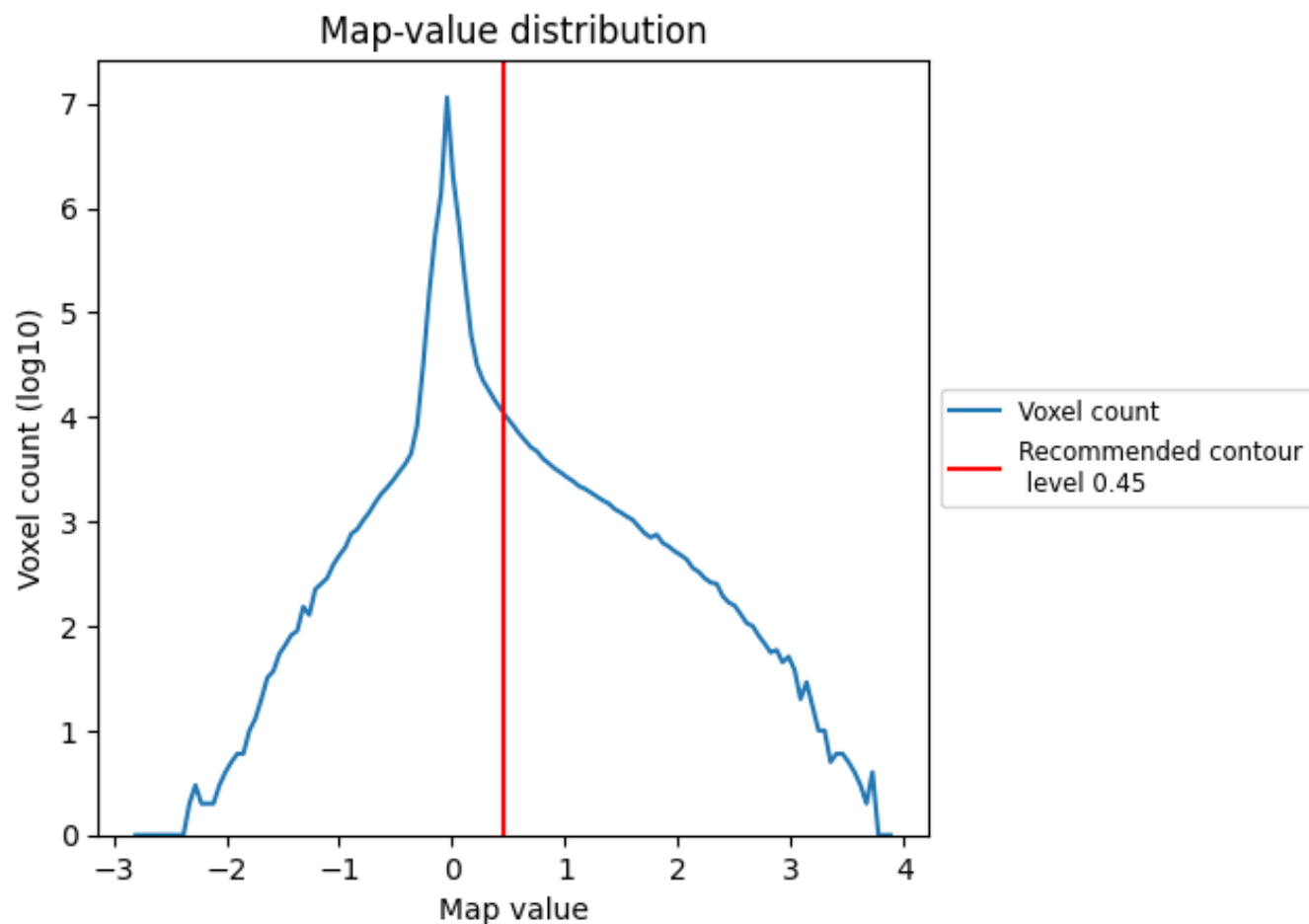
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

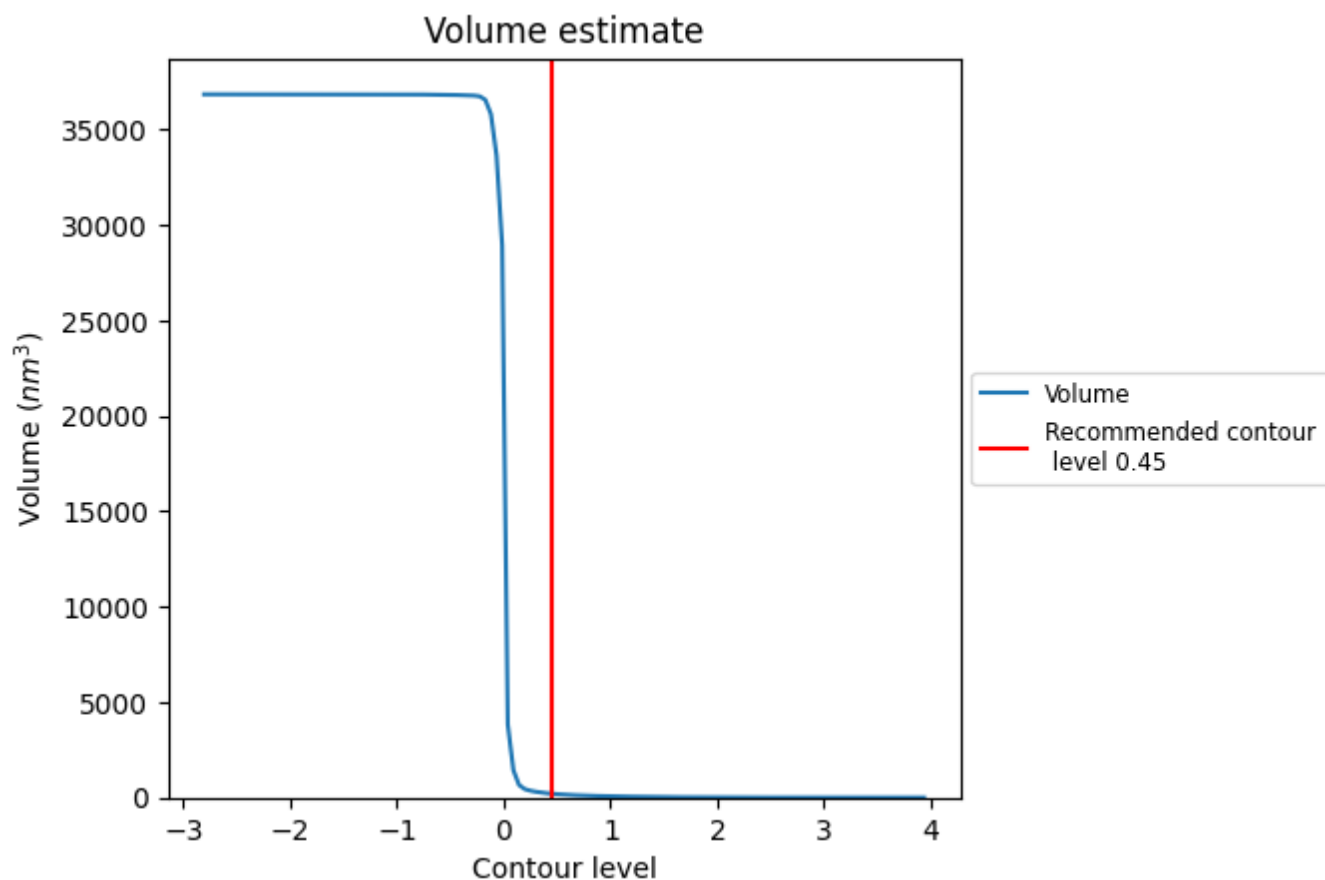
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

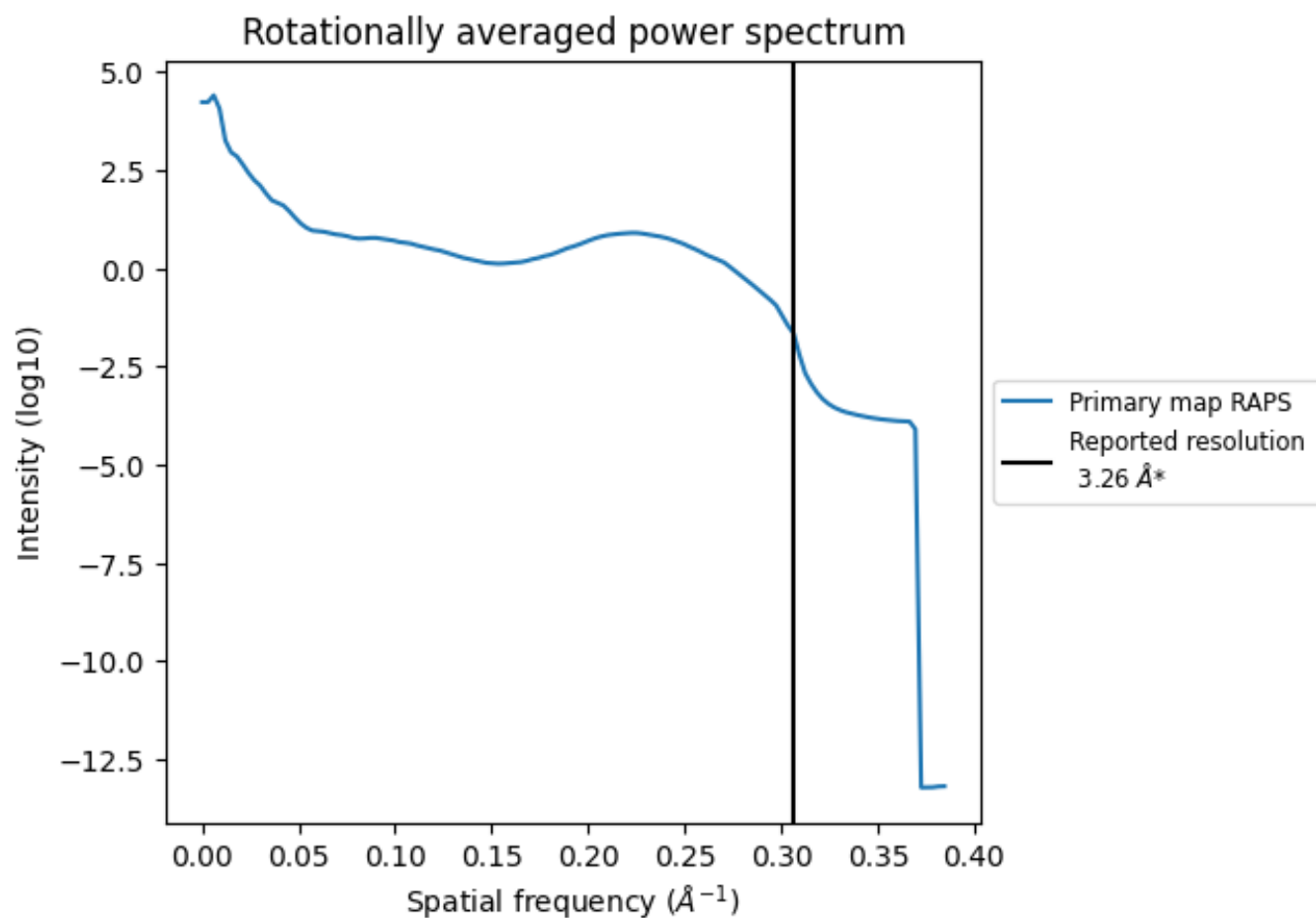
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 203 nm³; this corresponds to an approximate mass of 183 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 0.307 Å⁻¹

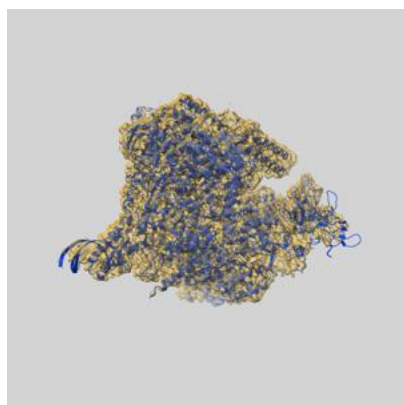
8 Fourier-Shell correlation

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

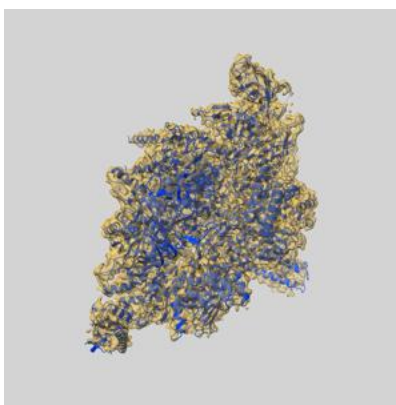
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20090 and PDB model 6OMF. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

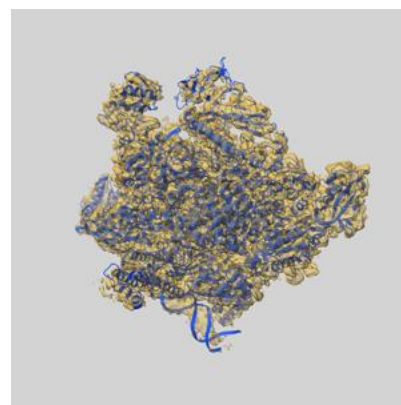
9.1 Map-model overlay [i](#)



X



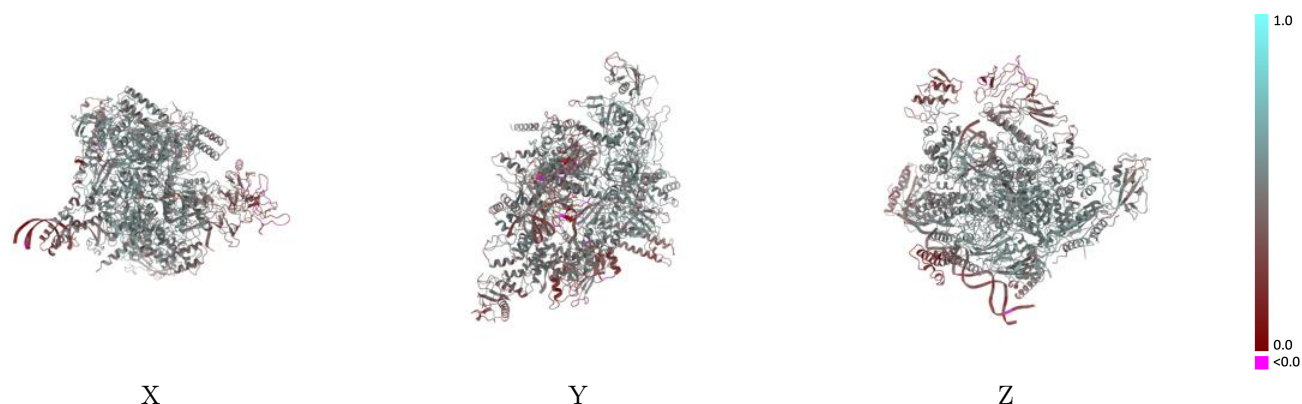
Y



Z

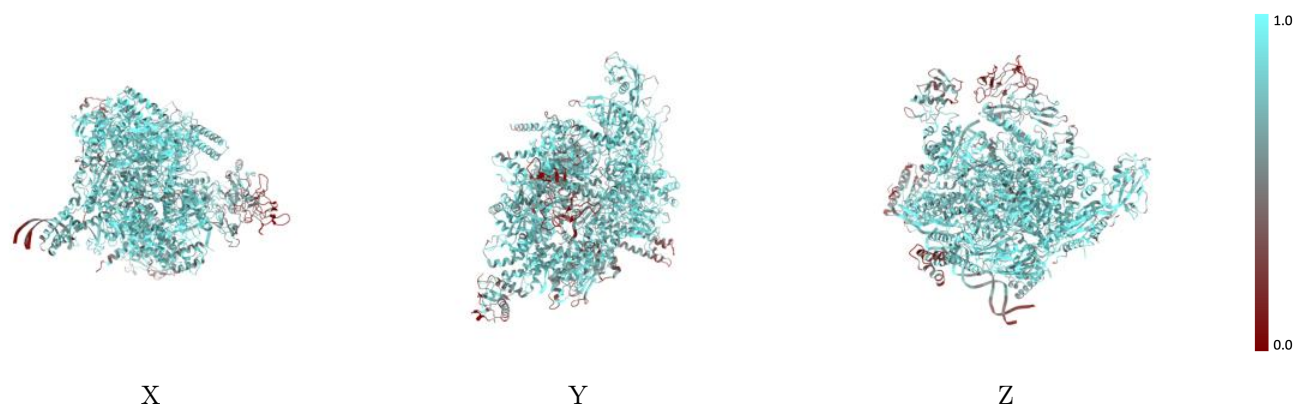
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



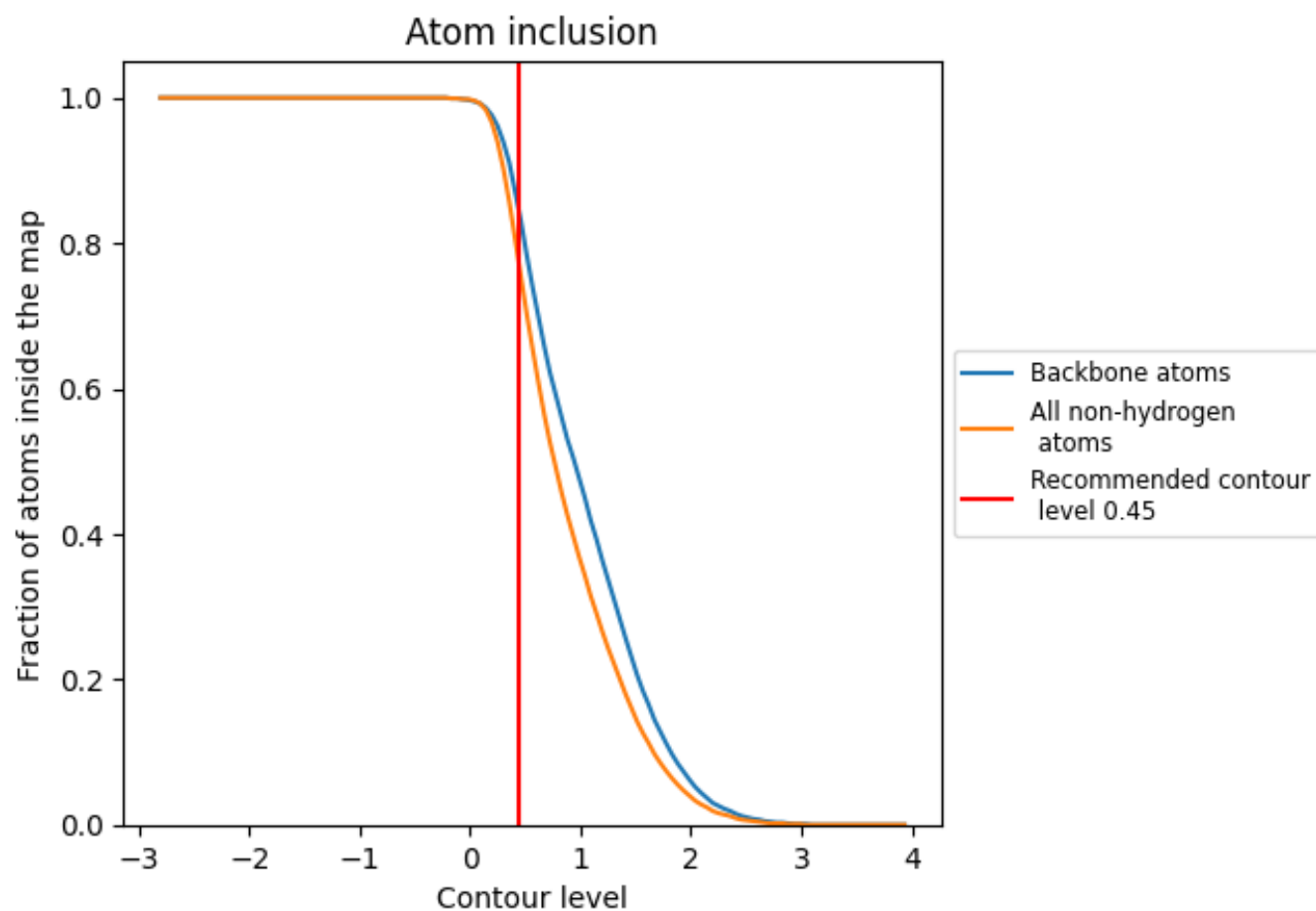
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 76% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7650	0.4630
A	0.8210	0.5020
B	0.7810	0.4680
C	0.7880	0.4830
D	0.7680	0.4740
E	0.7640	0.4840
F	0.7680	0.4560
J	0.5190	0.3690
N	0.6740	0.3060
T	0.7020	0.3110

1.0

0.0

<0.0