



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:04 PM UTC

PDB ID : 7MO9 / pdb_00007mo9
EMDB ID : EMD-23921
Title : Cryo-EM map of the c-MET II/HGF I/HGF II (K4 and SPH) sub-complex
Authors : Uchikawa, E.; Chen, Z.M.; Xiao, G.Y.; Zhang, X.W.; Bai, X.C.
Deposited on : 2021-05-01
Resolution : 4.00 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:

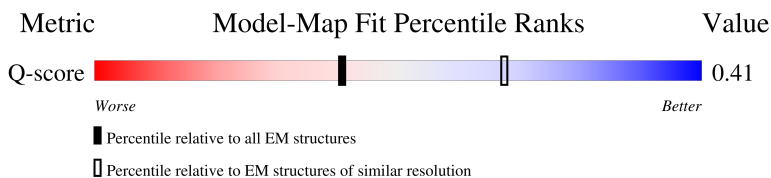
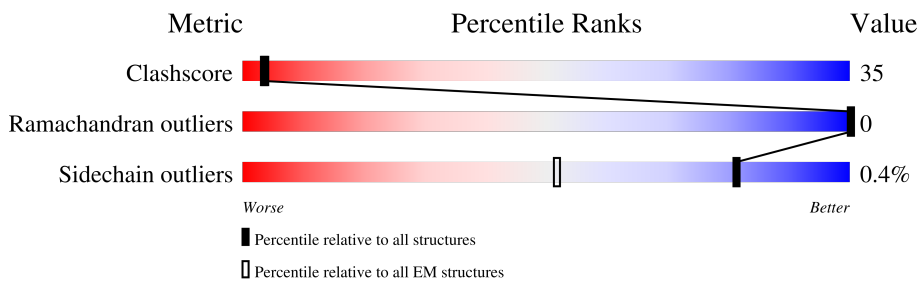
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 4.00 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	7587 (3.50 - 4.50)

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	728	
1	D	728	
2	E	1390	
3	B	6	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9755 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.

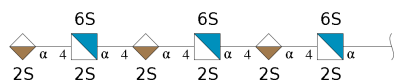
- Molecule 1 is a protein called Hepatocyte growth factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	254	2047	1283	370	373	21	0	0
1	D	305	2287	1443	404	418	22	0	0

- Molecule 2 is a protein called Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	688	5324	3373	905	1006	40	0	0

- Molecule 3 is an oligosaccharide called 2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	6	97	35	3	51	8	0	0

PRO	THR	THR	SER	VAL	ALA	VAL	LYS	GLY	GLY	T691	H542	V370	P295	G225	G139	Y71
THR	ASP	ILE	ALA	VAL	GLY	VAL	THR	GLY	D643	L622	I452	F370	L296	F226	T140	V72
VAL	GLY	ASN	GLY	ASN	THR	ASN	LYS	SER	K544	K623	L455	F374	I299	M227	R143	N74
GLY	ASP	PRO	PRO	VAL	THR	ILE	PHE	ILE	C545	C624	G460	L300	T301	L229	M149	E75
ILE	VAL	VAL	ASP	THR	THR	CYS	THR	GLY	V546	T625	R461	T301	L301	T230	H150	E76
THR	THR	THR	THR	THR	GLY	GLY	MET	PRO	R547	V626	R461	L301	L301	D231	D77	D76
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	E548	V626	F462	L301	L301	Q232	T151	Q79
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	E549	V626	M463	L301	L301	S233	H151	K80
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	C551	C551	V466	L301	L301	S233	K80	V81
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L552	L552	R469	L301	L301	S233	A82	A82
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	W556	W556	V477	L301	L301	S233	E83	E83
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	Q559	Q559	N478	L301	L301	S233	Y84	Y84
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	I560	I560	N478	L301	L301	S233	K85	K85
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	C561	C561	N478	L301	L301	S233	T86	T86
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L562	L562	N478	L301	L301	S233	E91	E91
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	P563	P563	N478	L301	L301	S233	P93	P93
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	Y566	Y566	N478	L301	L301	S233	C95	C95
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	F569	F569	N478	L301	L301	S233	F96	F96
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	P570	P570	N478	L301	L301	S233	Q99	Q99
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	N571	N571	N478	L301	L301	S233	D100	D100
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L575	L575	N478	L301	L301	S233	C101	C101
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	E576	E576	N478	L301	L301	S233	K104	K104
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	R580	R580	N478	L301	L301	S233	A105	A105
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L581	L581	N478	L301	L301	S233	N106	N106
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	T582	T582	N478	L301	L301	S233	LEU	LEU
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	I583	I583	N478	L301	L301	S233	SER	SER
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	C584	C584	N478	L301	L301	S233	GLY	GLY
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	D587	D587	N478	L301	L301	S233	G110	G110
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	F588	F588	N478	L301	L301	S233	K113	K113
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	G589	G589	N478	L301	L301	S233	D114	D114
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	F590	F590	N478	L301	L301	S233	M115	M115
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	R591	R591	N478	L301	L301	S233	I116	I116
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	R592	R592	N478	L301	L301	S233	I201	I201
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L593	L593	N478	L301	L301	S233	M117	M117
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	M594	M594	N478	L301	L301	S233	M118	M118
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	K595	K595	N478	L301	L301	S233	A119	A119
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	F596	F596	N478	L301	L301	S233	L120	L120
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	D597	D597	N478	L301	L301	S233	D123	D123
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L598	L598	N478	L301	L301	S233	T124	T124
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	K599	K599	N478	L301	L301	S233	Y125	Y125
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	K600	K600	N478	L301	L301	S233	Y126	Y126
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	T601	T601	N478	L301	L301	S233	D127	D127
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	R602	R602	N478	L301	L301	S233	D128	D128
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	L603	L603	N478	L301	L301	S233	Q129	Q129
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	M604	M604	N478	L301	L301	S233	L130	L130
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	T611	T611	N478	L301	L301	S233	C133	C133
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	S617	S617	N478	L301	L301	S233	V136	V136
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	T618	T618	N478	L301	L301	S233	N137	N137
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	M619	M619	N478	L301	L301	S233	K223	K223
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP	N620	N620	N478	L301	L301	S233	M294	M294
THR	THR	THR	THR	THR	GLY	VAL	LEU	ASP			N478	L301	L301	S233	D224	D224

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45471	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.077	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	291.6, 291.6, 291.6	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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: IDS, SGN

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	0.36	0/2105	0.73	0/2840
1	D	0.37	0/2344	0.64	0/3196
2	E	0.45	1/5444 (0.0%)	0.69	3/7397 (0.0%)
All	All	0.41	1/9893 (0.0%)	0.69	3/13433 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	86	THR	CA-CB	-6.31	1.43	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	561	CYS	CA-C-N	7.47	131.10	120.49
2	E	561	CYS	C-N-CA	7.47	131.10	120.49
2	E	413	ARG	CB-CG-CD	-5.75	98.06	111.30

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	2047	0	1933	179	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2287	0	2128	165	0
2	E	5324	0	5126	326	0
3	B	97	0	34	3	0
All	All	9755	0	9221	659	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 35.

The worst 5 of 659 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:E:189:LYS:O	2:E:192:PHE:HB2	1.55	1.04
1:A:36:ARG:O	1:A:72:ASN:ND2	2.01	0.93
1:D:415:TRP:HB2	1:D:438:ASN:H	1.35	0.90
2:E:176:VAL:HA	2:E:217:ARG:HH21	1.35	0.90
2:E:232:GLN:NE2	2:E:415:GLU:OE2	2.08	0.86

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	250/728 (34%)	224 (90%)	26 (10%)	0	100	100
1	D	299/728 (41%)	275 (92%)	24 (8%)	0	100	100
2	E	678/1390 (49%)	615 (91%)	63 (9%)	0	100	100
All	All	1227/2846 (43%)	1114 (91%)	113 (9%)	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	224/646 (35%)	222 (99%)	2 (1%)	70	76
1	D	235/646 (36%)	235 (100%)	0	100	100
2	E	598/1246 (48%)	596 (100%)	2 (0%)	86	85
All	All	1057/2538 (42%)	1053 (100%)	4 (0%)	81	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	ASN
1	A	258	ASN
2	E	38	ASN
2	E	594	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	396	HIS
2	E	607	ASN
1	D	644	GLN
1	D	646	HIS
2	E	275	HIS

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

6 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SGN	B	1	3	15,18,20	1.33	1 (6%)	20,26,31	1.53	3 (15%)
3	IDS	B	2	3	16,16,17	1.12	0	16,24,26	1.00	1 (6%)
3	SGN	B	3	3	19,19,20	3.78	4 (21%)	23,29,31	1.54	3 (13%)
3	IDS	B	4	3	16,16,17	1.28	2 (12%)	16,24,26	1.11	1 (6%)
3	SGN	B	5	3	13,13,20	4.17	4 (30%)	12,19,31	2.23	3 (25%)
3	IDS	B	6	3	15,15,17	1.08	0	14,22,26	2.50	6 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SGN	B	1	3	-	3/8/27/31	0/1/1/1
3	IDS	B	2	3	-	1/9/26/29	0/1/1/1
3	SGN	B	3	3	-	3/11/28/31	0/1/1/1
3	IDS	B	4	3	-	0/9/26/29	1/1/1/1
3	SGN	B	5	3	-	5/5/19/31	0/1/1/1
3	IDS	B	6	3	-	6/9/22/29	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	5	SGN	O2S-S1	9.95	1.53	1.42
3	B	5	SGN	O1S-S1	9.72	1.53	1.42
3	B	3	SGN	O2S-S1	9.72	1.53	1.42
3	B	3	SGN	O1S-S1	9.35	1.52	1.42
3	B	3	SGN	S1-N2	8.33	1.70	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	6	IDS	C1-O5-C5	-5.91	104.22	113.81
3	B	5	SGN	O1S-S1-O2S	-5.13	108.94	120.36
3	B	6	IDS	C1-C2-C3	-5.08	102.68	109.84
3	B	3	SGN	O1S-S1-O2S	-4.89	109.48	120.36
3	B	5	SGN	C3-C2-N2	3.80	115.31	110.32

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1	SGN	C4-C5-C6-O6
3	B	1	SGN	O5-C5-C6-O6
3	B	2	IDS	C3-C2-O2-S
3	B	3	SGN	C2-N2-S1-O1S
3	B	3	SGN	C2-N2-S1-O3S

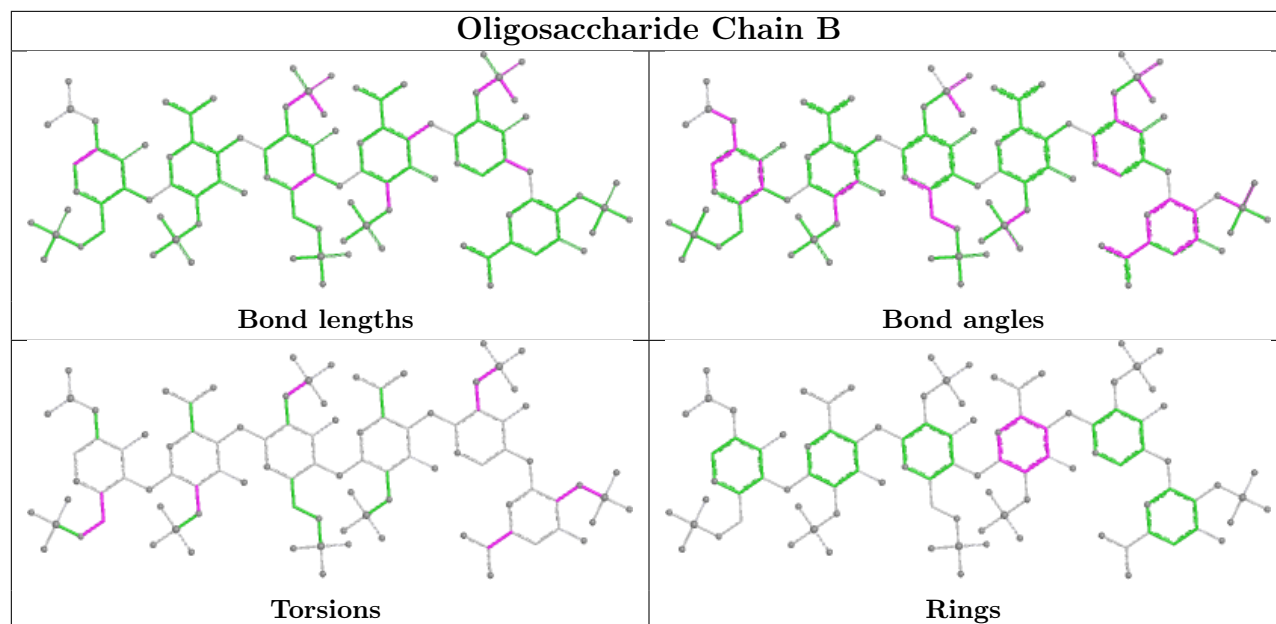
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	4	IDS	C1-C2-C3-C4-C5-O5

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	4	IDS	2	0
3	B	2	IDS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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.

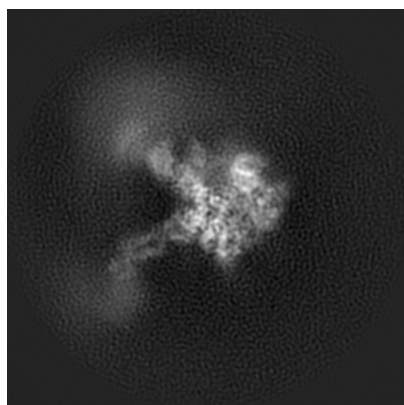
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23921. These allow visual inspection of the internal detail of the map and identification of artifacts.

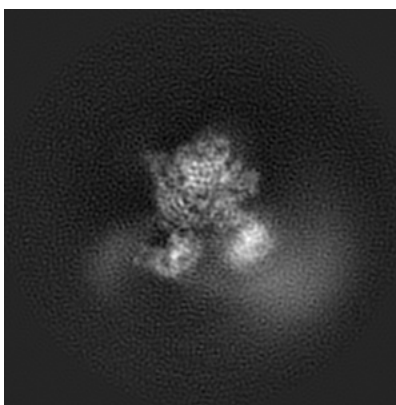
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

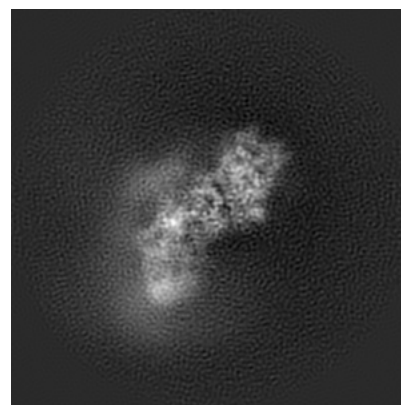
6.1.1 Primary map



X



Y

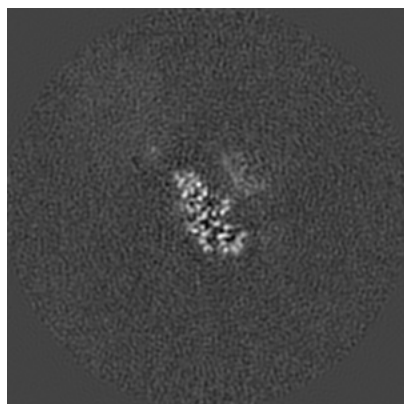


Z

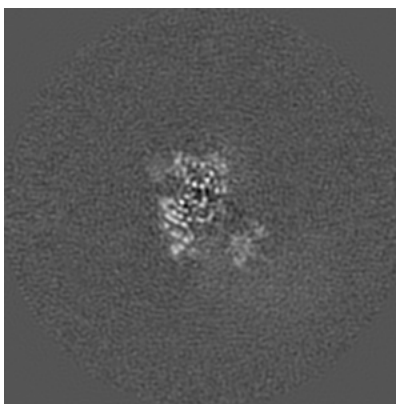
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

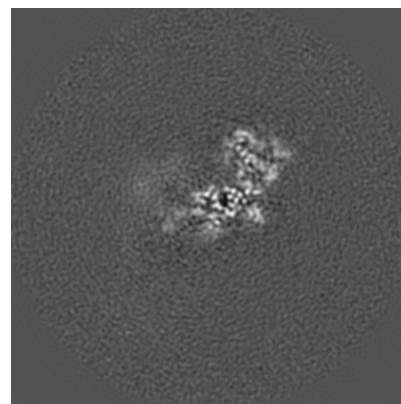
6.2.1 Primary map



X Index: 135



Y Index: 135

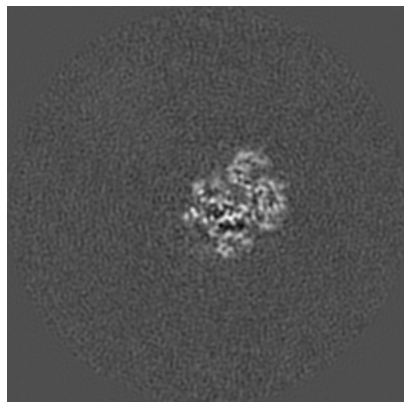


Z Index: 135

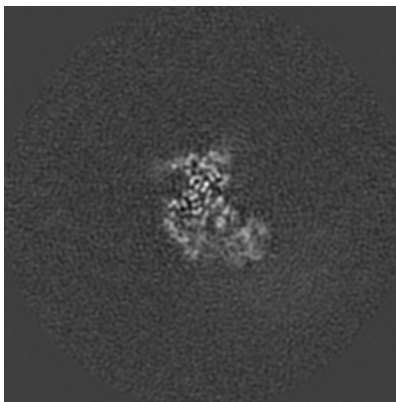
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

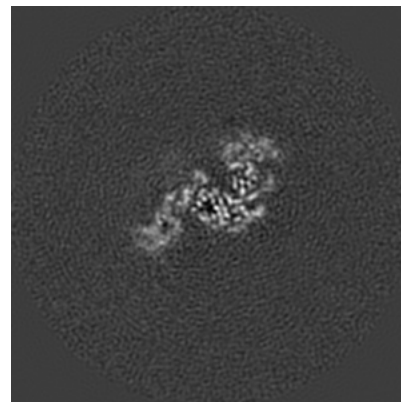
6.3.1 Primary map



X Index: 155



Y Index: 131

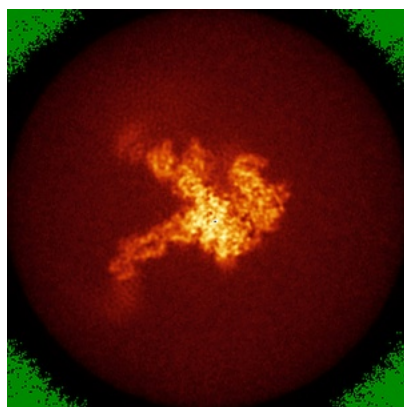


Z Index: 125

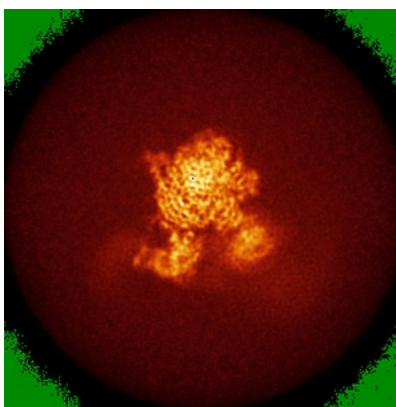
The images above show the largest variance slices of the map in three orthogonal directions.

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

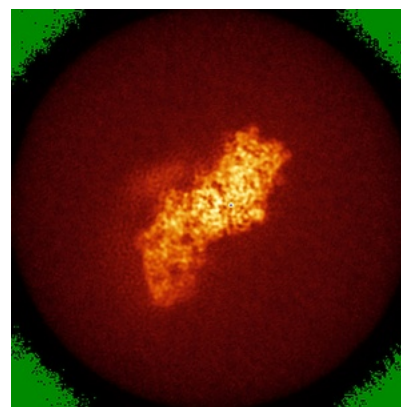
6.4.1 Primary map



X



Y

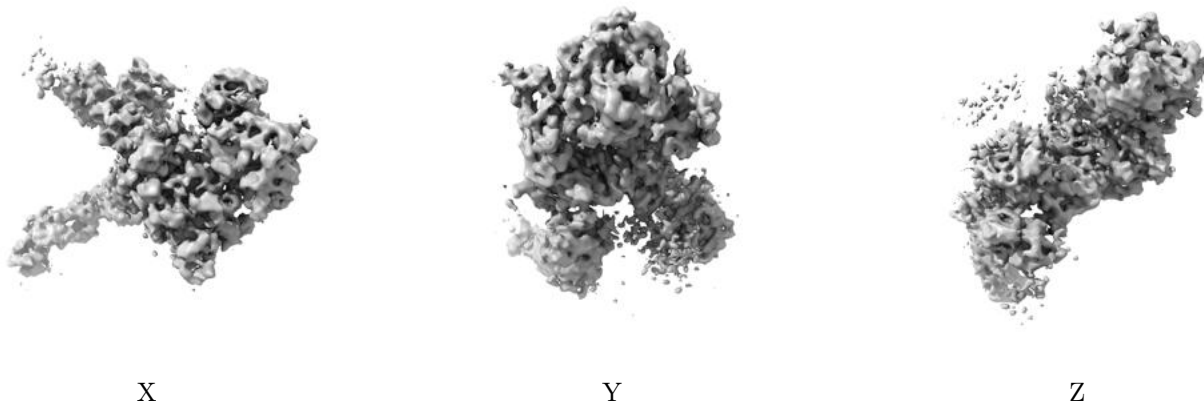


Z

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

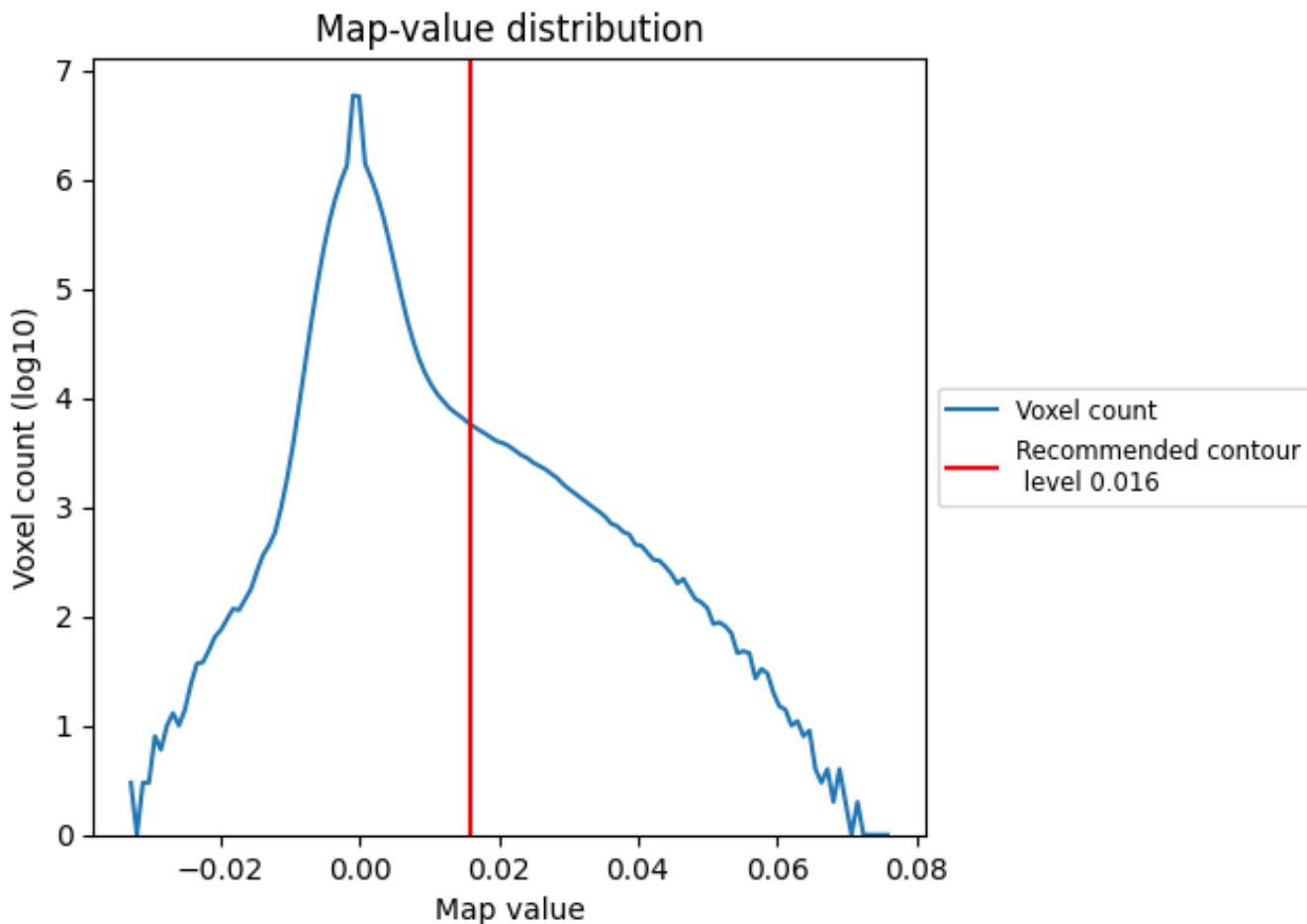
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

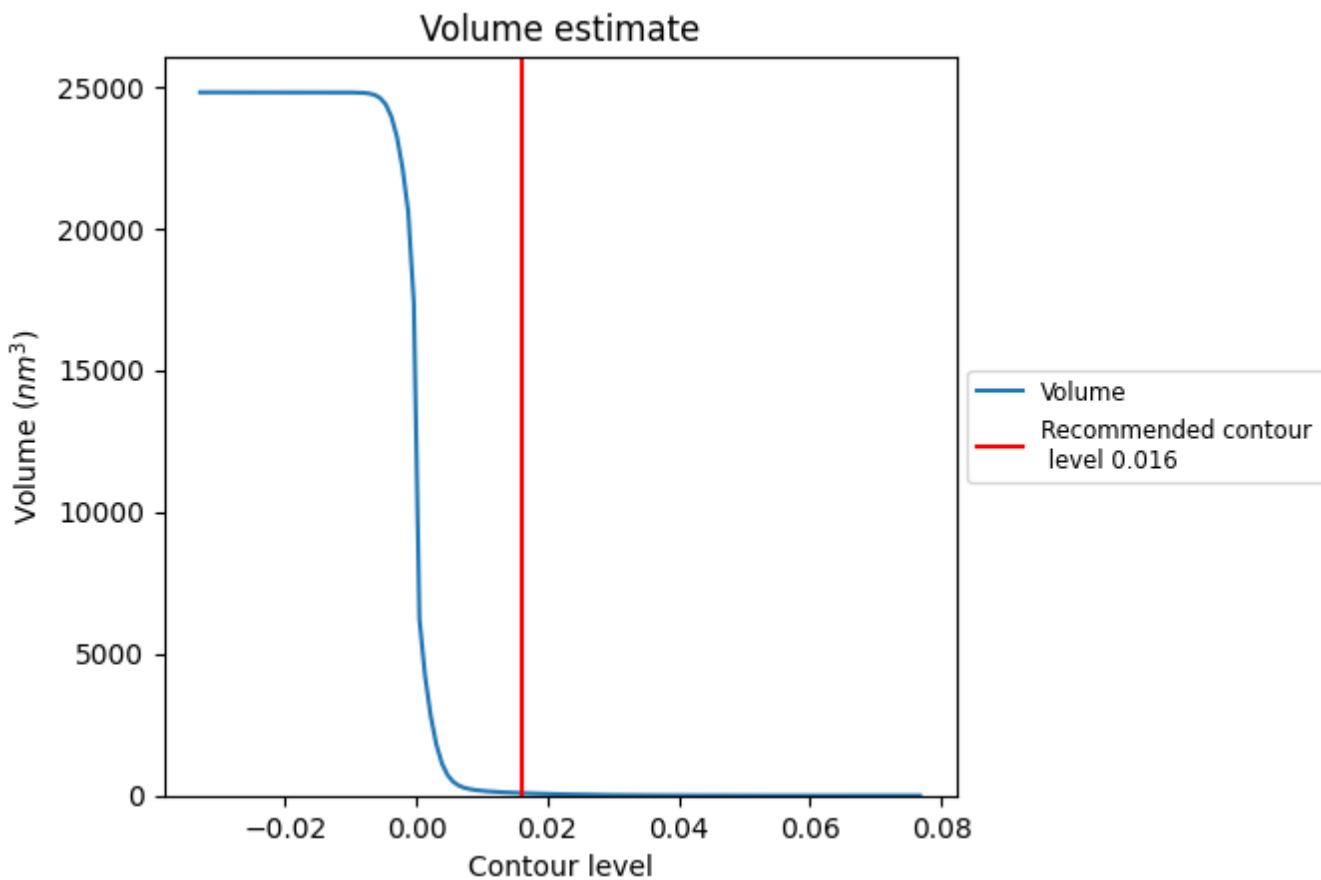
This section contains the results of statistical analysis of the map.

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.

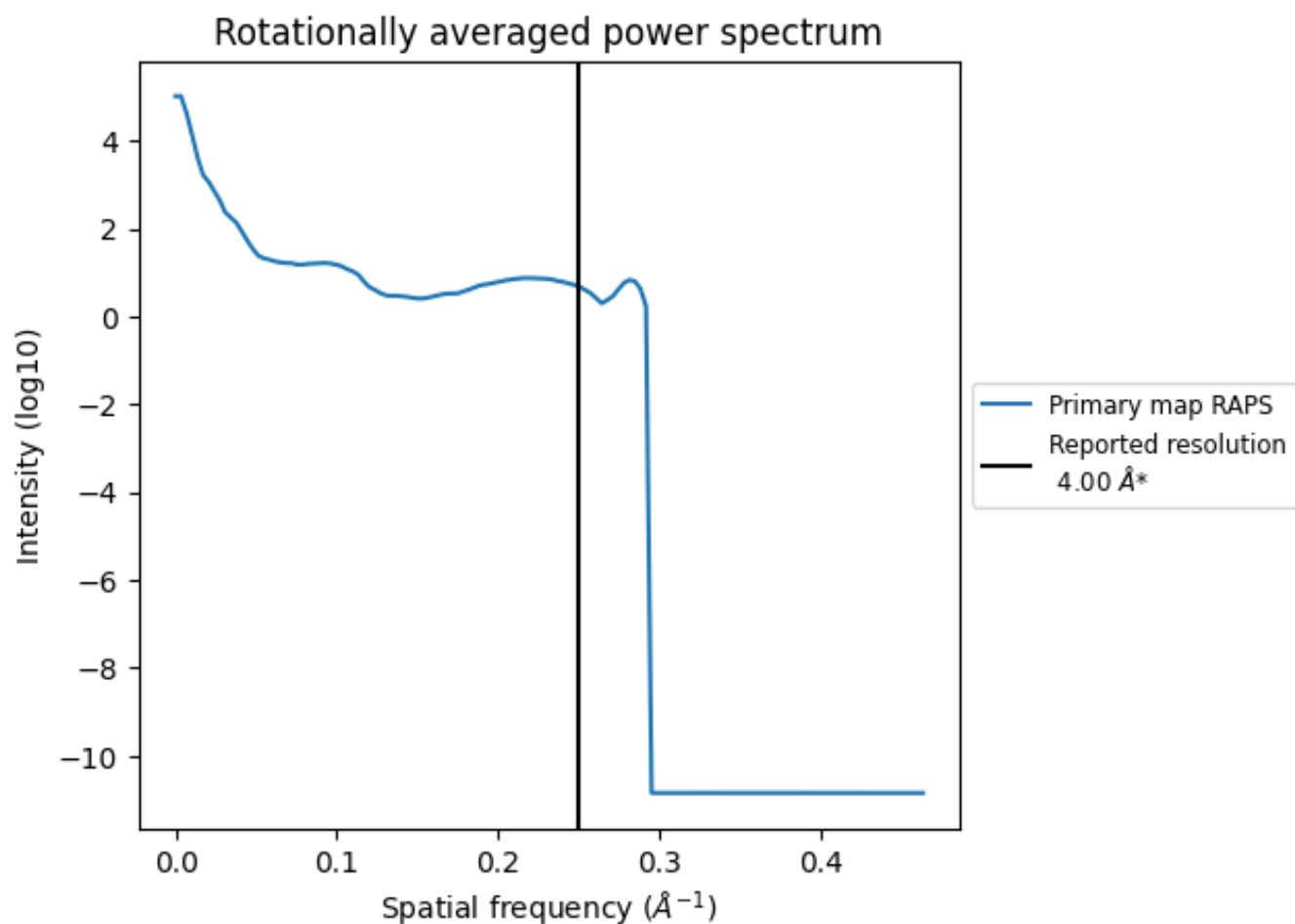
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 87 nm³; this corresponds to an approximate mass of 79 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

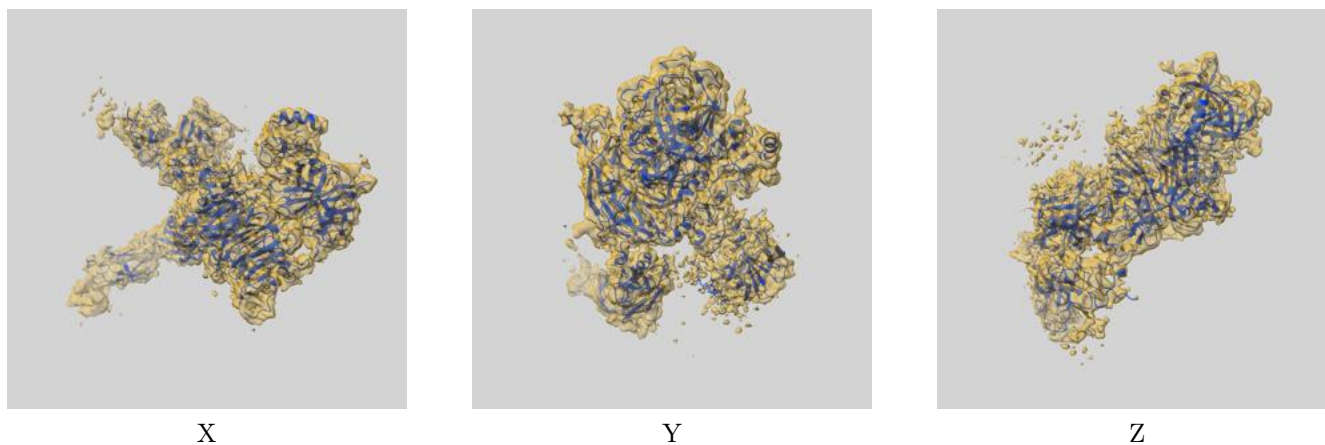
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

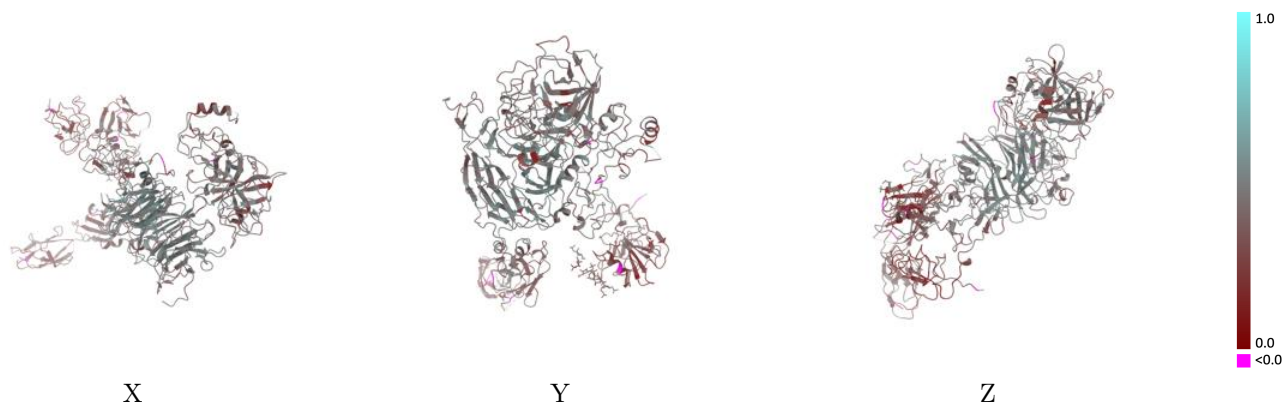
This section contains information regarding the fit between EMDB map EMD-23921 and PDB model 7MO9. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



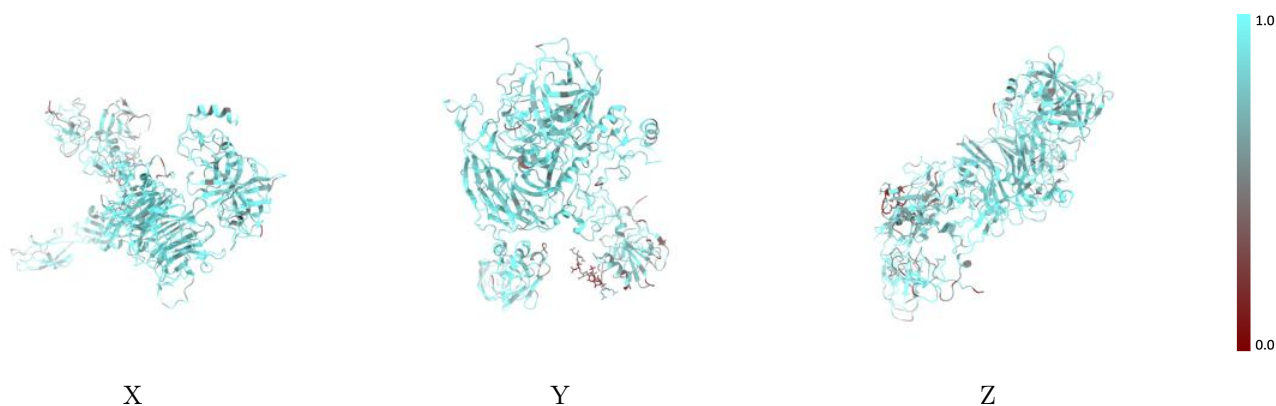
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



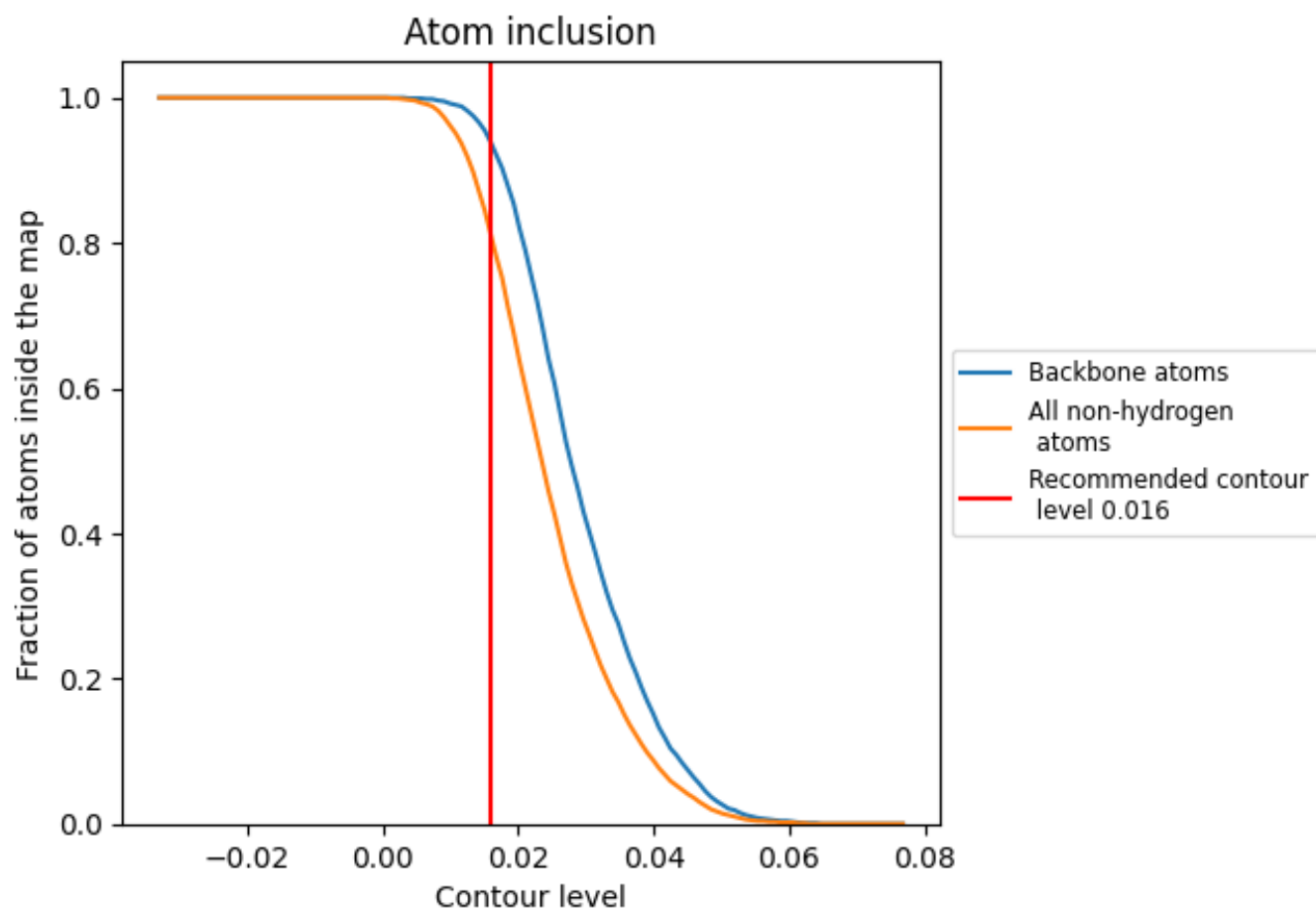
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).











9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 81% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8100	 0.4100
A	 0.7350	 0.3300
B	 0.3400	 0.3710
D	 0.8210	 0.4140
E	 0.8430	 0.4400

