



wwPDB EM Validation Summary Report ⓘ

Jul 14, 2024 – 06:41 pm BST

PDB ID : 7Z8J
EMDB ID : EMD-14553
Title : Cytoplasmic dynein (A2) bound to BICDR1
Authors : Chaaban, S.; Carter, A.P.
Deposited on : 2022-03-17
Resolution : 3.93 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

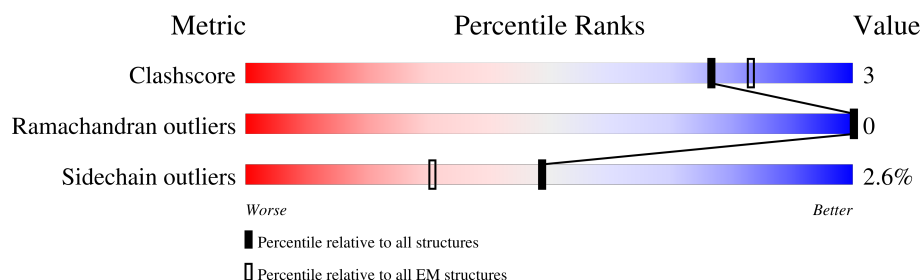
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.93 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.



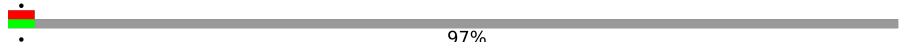
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	X	577	<div> <div>11%</div> <div>14%</div> <div>84%</div> </div>
1	x	577	<div> <div>14%</div> <div>16%</div> <div>84%</div> </div>
2	f	4646	<div> <div>6%</div> <div>14%</div> <div>85%</div> </div>
2	m	4646	<div> <div>11%</div> <div>89%</div> </div>
2	n	4646	<div> <div>97%</div> </div>
3	h	638	<div> <div>5%</div> <div>55%</div> <div>44%</div> </div>
3	o	638	<div> <div>55%</div> <div>44%</div> </div>
4	j	492	<div> <div>40%</div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
4	r	492	 97%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 20189 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 BICD family-like cargo adapter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	93	Total	C	N	O	S	0	0
			797	488	153	154	2		
1	x	93	Total	C	N	O	S	0	0
			797	488	153	154	2		

- Molecule 2 is a protein called Cytoplasmic dynein 1 heavy chain 1.

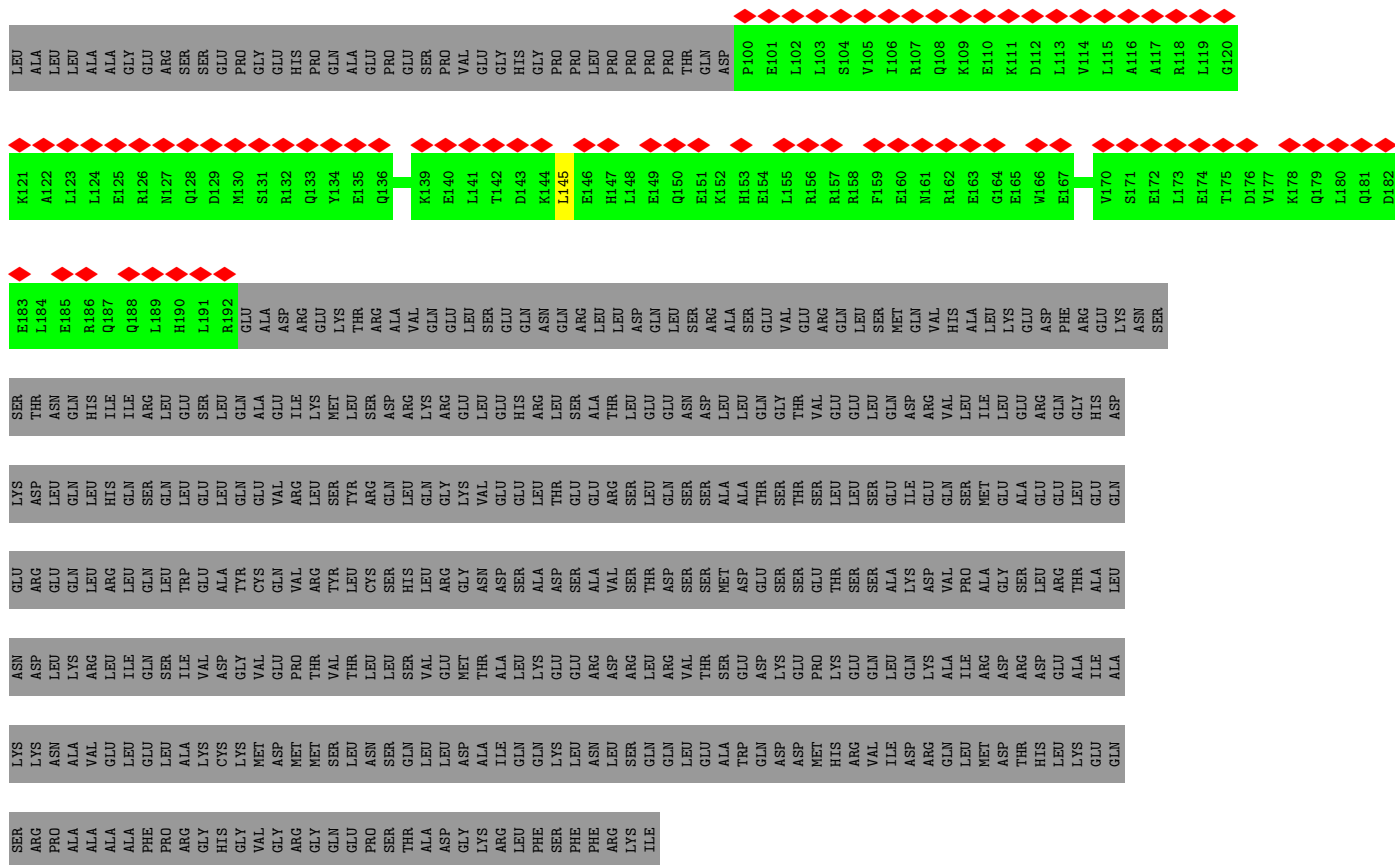
Mol	Chain	Residues	Atoms					AltConf	Trace
2	f	674	Total	C	N	O	S	0	0
			5545	3521	994	1009	21		
2	m	524	Total	C	N	O	S	0	0
			4333	2751	789	780	13		
2	n	126	Total	C	N	O	S	0	0
			1068	667	211	186	4		

- Molecule 3 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

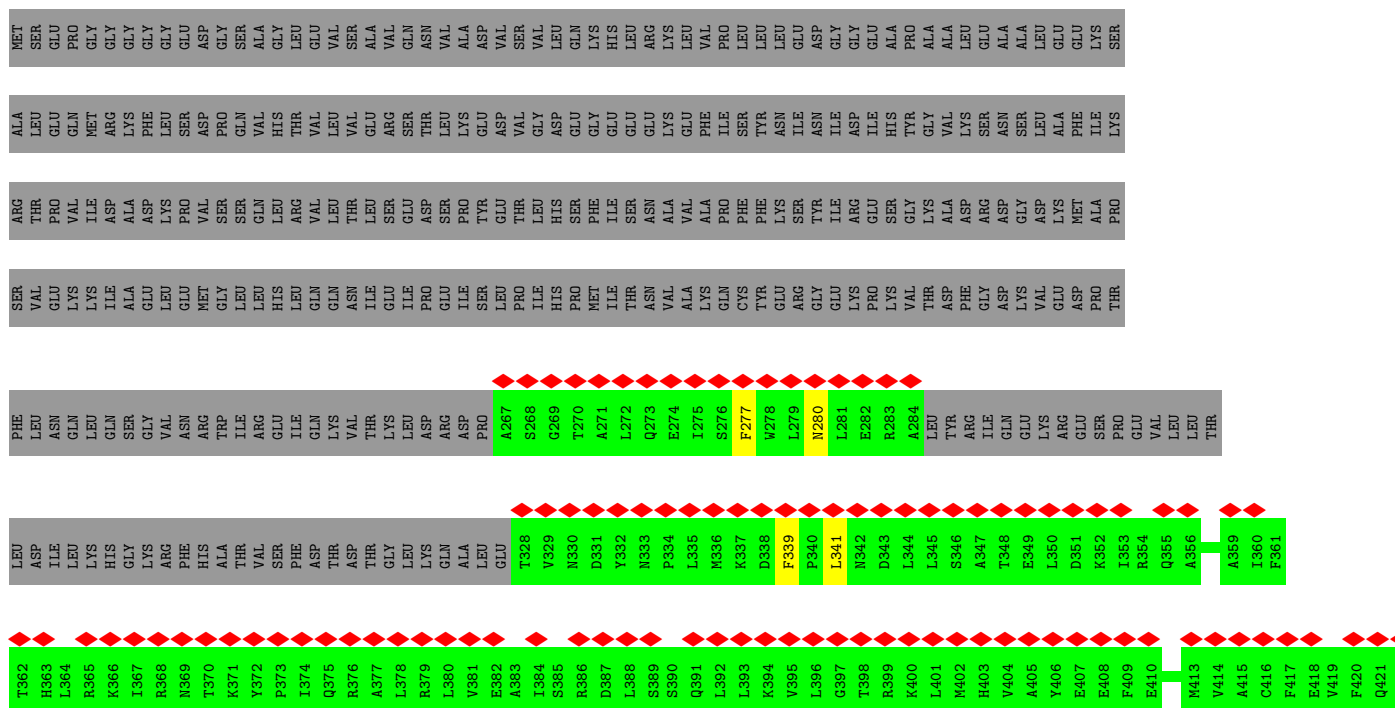
Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	358	Total	C	N	O	S	0	0
			2804	1769	490	530	15		
3	o	358	Total	C	N	O	S	0	0
			2808	1771	490	532	15		

- Molecule 4 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	247	Total	C	N	O	S	0	0
			1981	1278	331	362	10		
4	r	14	Total	C	N	O		0	0
			56	28	14	14			



- Molecule 2: Cytoplasmic dynein 1 heavy chain 1









[illegible]

- Molecule 2: Cytoplasmic dynein 1 heavy chain 1

Chain m:  11% 89%

PRO	GLN	ASP	MET	LYS	VAL	ALA	VAL	PHE	D513	D514	D515	D516	D517	N518	E521	E522	E528	N529	V530	D534	G535	L536	D537	V538	S539	K540	E541	G542	T543	E544	R552	Y553	D554	I557	D558	R559	V560	R563	L568	R569	D570	G573	T574	A575	K576	M581	F582								
H403	E407	E408	F409	E410	E418	D424	D425	E428	K429	L430	Q431	D436	I437	V438	K439	R440	K441	R442	E443	E444	M445	L446	K447	M448	R451	I452	R457	R467	Q475	R482	V483	L484	R485	PRO	GLN	VAL	THR	ALA	VAL	VAL	GLN	GLN	ASN	GLN	GLY	GLU	PRO	GLU							
HIS	ALA	THR	VAL	SER	PHE	THR	THR	GLY	L322	K323	Q324	N330	D331	Y332	N333	P334	L335	M336	K337	M342	D343	S346	A347	T348	E349	L350	D351	K352	Q355	R365	N369	R376	A377	L378	R379	R386	D387	K394	G397	T398	R399	K400	L401	M402											
PHE	LEU	ASN	LEU	GLN	SER	VAL	ASN	ARG	TRP	ILE	ARG	GLU	ILE	GLN	LYS	V259	T260	K261	L262	D263	R264	D265	P266	A267	S268	Q273	E274	I275	E282	R283	Y286	R287	I288	Q289	E290	K291	R292	GLU	SER	PRO	GLU	VAL	LEU	LEU	THR	LEU	ASP	ILE	LYS	HIS	GLY	LYS	ARG		
SER	VAL	PRO	LYS	ILE	ALA	GLU	GLU	MET	GLY	LEU	HIS	LEU	GLN	GLN	ASN	THR	LEU	VAL	GLN	THR	LEU	GLU	VAL	GLN	THR	LEU	GLY	GLU	ASN	VAL	ALA	VAL	GLN	PRO	PHE	SER	TYR	LEU	ASN	GLU	ILE	TYR	LYS	ALA	VAL	VAL	LEU	ASP	ALA	GLY	LYS	ALA	VAL	GLN	ARG
ALA	LEU	GLN	MET	ARG	LYS	PHE	SER	PRO	GLY	LEU	GLN	THR	VAL	GLU	ASN	THR	LEU	VAL	GLN	THR	LEU	GLU	VAL	GLN	THR	LEU	GLY	GLU	ASN	VAL	ALA	VAL	PHE	SER	TYR	LEU	ASN	GLU	ILE	ASP	ILE	TYR	GLY	VAL	VAL	LEU	ASP	ALA	GLY	LYS	ALA	VAL	GLN	ARG	
MET	SER	PRO	GLY	GLY	GLY	GLY	GLY	ASP	GLY	GLY	GLY	SER	PRO	GLY	GLY	GLN	VAL	GLN	THR	VAL	GLU	VAL	GLN	THR	VAL	GLN	LYS	HIS	ARG	LYS	ALA	VAL	PHE	SER	LEU	ASN	GLY	THR	LEU	ALA	VAL	VAL	LEU	ASP	ALA	GLY	LYS	ALA	VAL	GLN	ARG				







[illegible]

- Molecule 2: Cytoplasmic dynein 1 heavy chain 1

Chain n:  97%

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

- Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

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- Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78061	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00128	Depositor
Map size (Å)	955.776, 955.776, 955.776	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2445, 1.2445, 1.2445	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	X	0.42	0/805	0.74	0/1072
1	x	0.33	0/805	0.67	0/1072
2	f	0.36	0/5641	0.60	0/7605
2	m	0.33	0/4403	0.61	0/5927
2	n	0.36	0/1081	0.64	0/1442
3	h	0.38	0/2883	0.58	0/3932
3	o	0.41	0/2887	0.59	0/3938
4	j	0.28	0/2026	0.56	0/2731
4	r	0.23	0/55	0.34	0/67
All	All	0.36	0/20586	0.60	0/27786

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	X	797	0	797	5	0
1	x	797	0	797	0	0
2	f	5545	0	5644	0	0
2	m	4333	0	4444	0	0
2	n	1068	0	1079	0	0
3	h	2804	0	2670	0	0
3	o	2808	0	2673	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	j	1981	0	1950	0	0
4	r	56	0	15	0	0
All	All	20189	0	20069	5	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 3.

All (5) 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:X:173:LEU:HD13	1:X:173:LEU:HB3	2.60	0.56
1:X:180:LEU:HD23	1:X:180:LEU:HB3	2.45	0.51
1:X:115:LEU:O	1:X:119:LEU:HD23	2.15	0.47
1:X:155:LEU:HD23	1:X:155:LEU:O	2.15	0.46
1:X:110:GLU:HA	1:X:113:LEU:HD12	2.02	0.41

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	X	91/577 (16%)	91 (100%)	0	0	100	100
1	x	91/577 (16%)	91 (100%)	0	0	100	100
2	f	664/4646 (14%)	651 (98%)	13 (2%)	0	100	100
2	m	516/4646 (11%)	502 (97%)	14 (3%)	0	100	100
2	n	118/4646 (2%)	115 (98%)	3 (2%)	0	100	100
3	h	356/638 (56%)	343 (96%)	13 (4%)	0	100	100
3	o	356/638 (56%)	342 (96%)	14 (4%)	0	100	100
4	j	241/492 (49%)	236 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	r	12/492 (2%)	12 (100%)	0	0	100	100
All	All	2445/17352 (14%)	2383 (98%)	62 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	X	87/503 (17%)	82 (94%)	5 (6%)	20	49
1	x	87/503 (17%)	86 (99%)	1 (1%)	73	84
2	f	603/4125 (15%)	579 (96%)	24 (4%)	31	57
2	m	468/4125 (11%)	459 (98%)	9 (2%)	57	75
2	n	110/4125 (3%)	107 (97%)	3 (3%)	44	66
3	h	308/557 (55%)	304 (99%)	4 (1%)	69	81
3	o	309/557 (56%)	299 (97%)	10 (3%)	39	62
4	j	213/422 (50%)	212 (100%)	1 (0%)	88	93
All	All	2185/14917 (15%)	2128 (97%)	57 (3%)	49	67

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	f	987	PHE
3	o	548	ARG
2	m	352	LYS
3	o	520	PHE
3	o	342	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	f	889	ASN
3	o	419	GLN
1	x	133	GLN
2	f	342	ASN
2	f	280	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 monosaccharides 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.

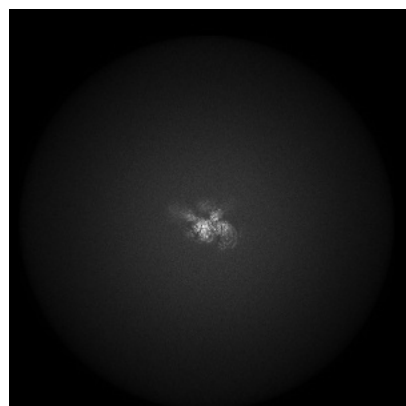
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14553. These allow visual inspection of the internal detail of the map and identification of artifacts.

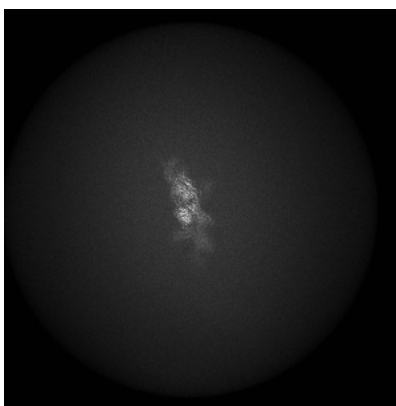
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

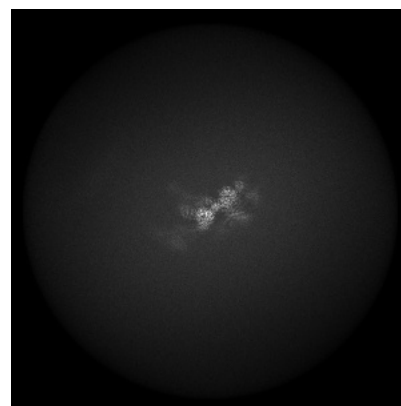
6.1.1 Primary map



X

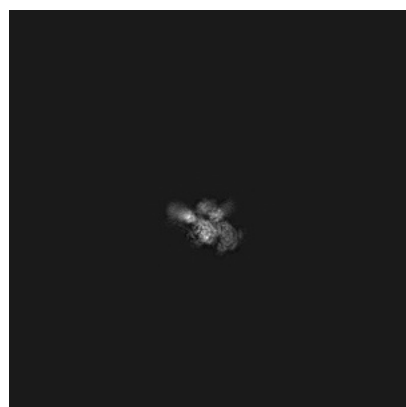


Y



Z

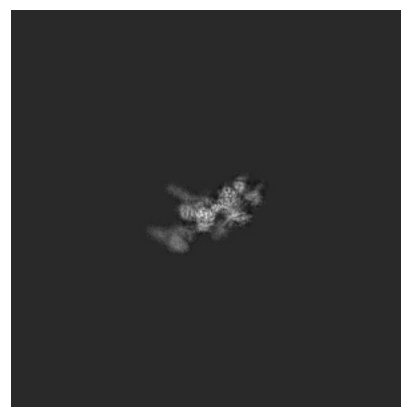
6.1.2 Raw map



X



Y

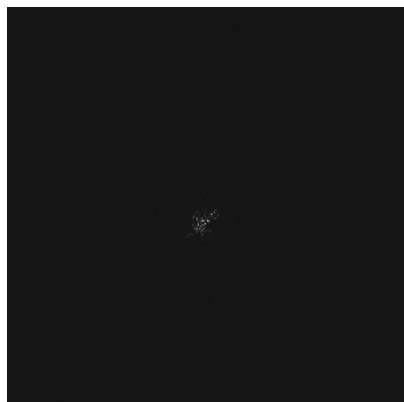


Z

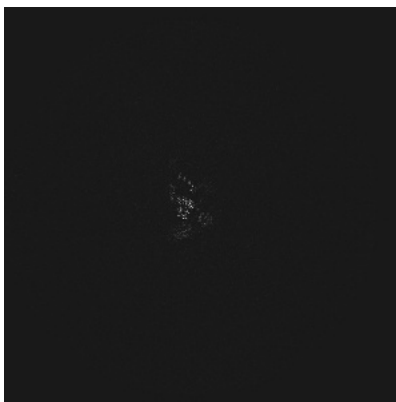
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

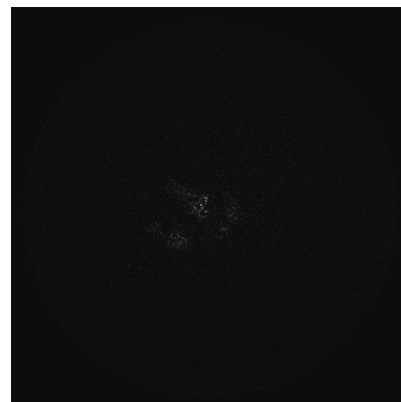
6.2.1 Primary map



X Index: 384

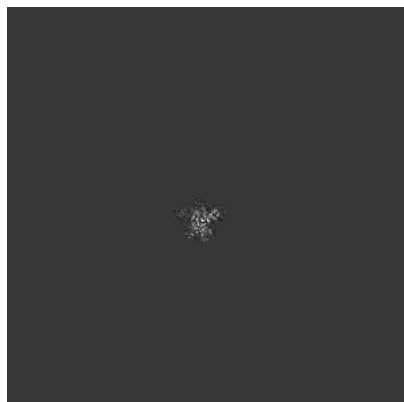


Y Index: 384



Z Index: 384

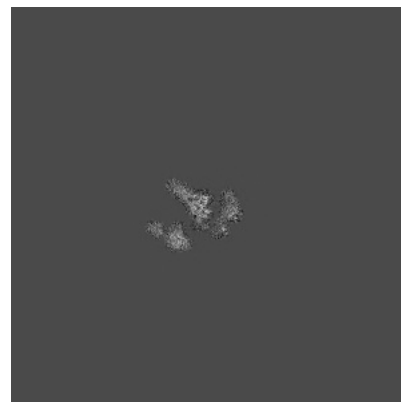
6.2.2 Raw map



X Index: 384



Y Index: 384

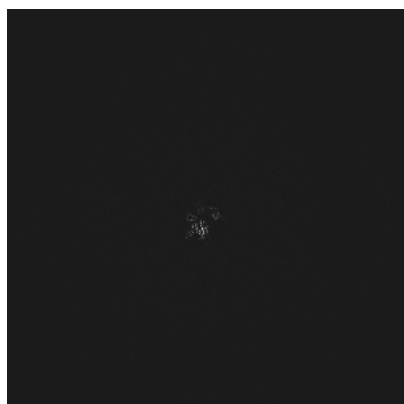


Z Index: 384

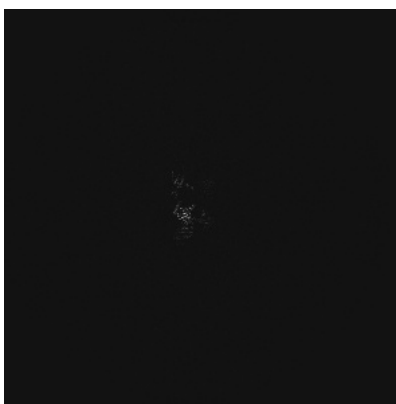
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

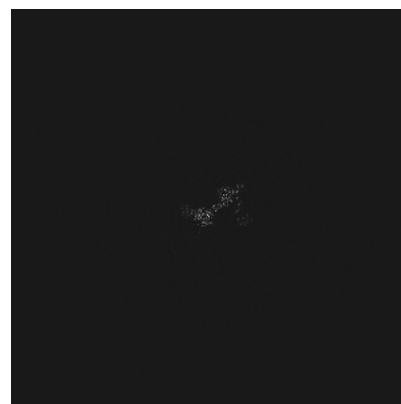
6.3.1 Primary map



X Index: 374

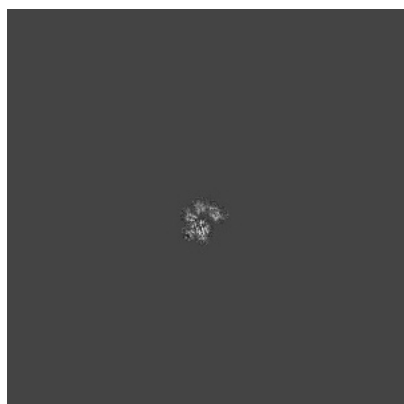


Y Index: 375



Z Index: 349

6.3.2 Raw map



X Index: 374



Y Index: 375

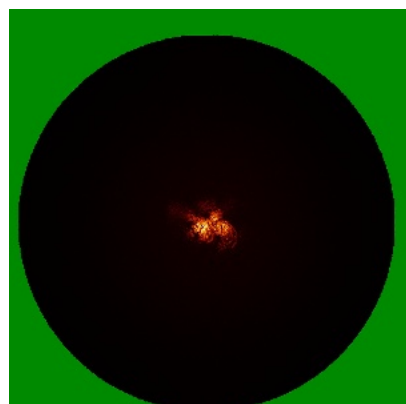


Z Index: 349

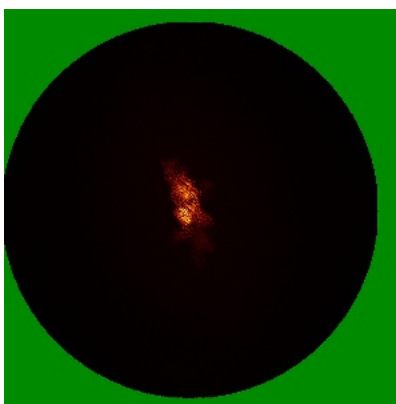
The images above show the largest variance slices of the map in three orthogonal directions.

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

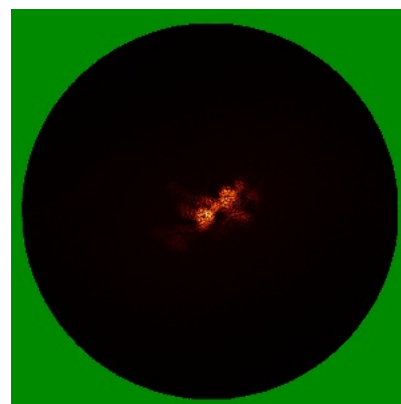
6.4.1 Primary map



X

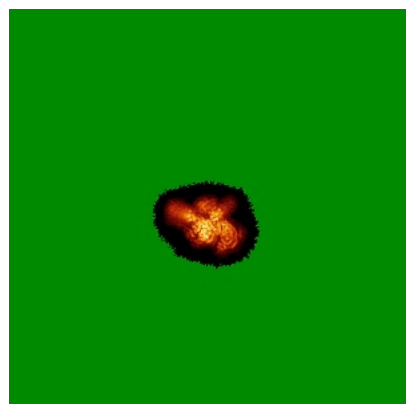


Y

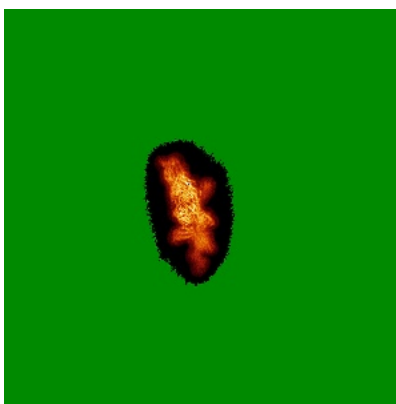


Z

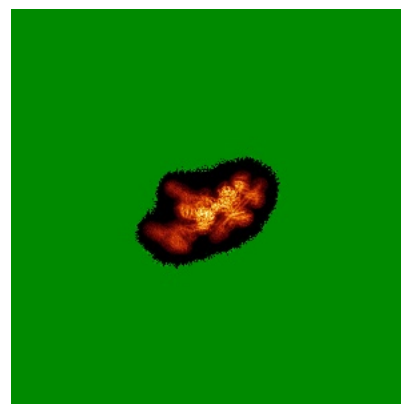
6.4.2 Raw map



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 0.00128. 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.

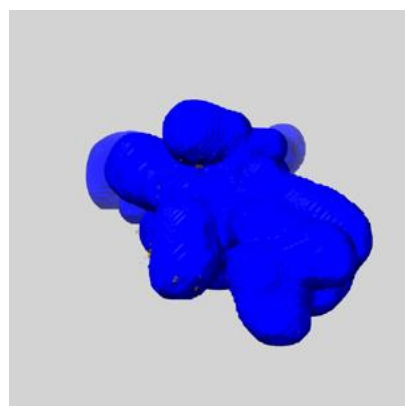
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

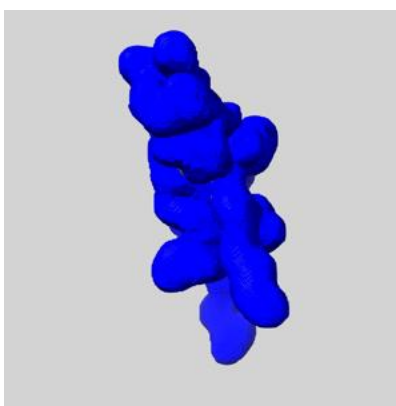
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

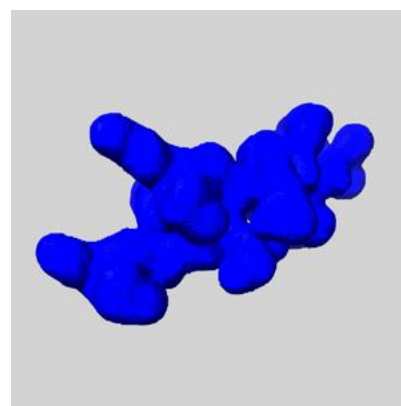
6.6.1 emd_14553_msk_1.map [i](#)



X



Y

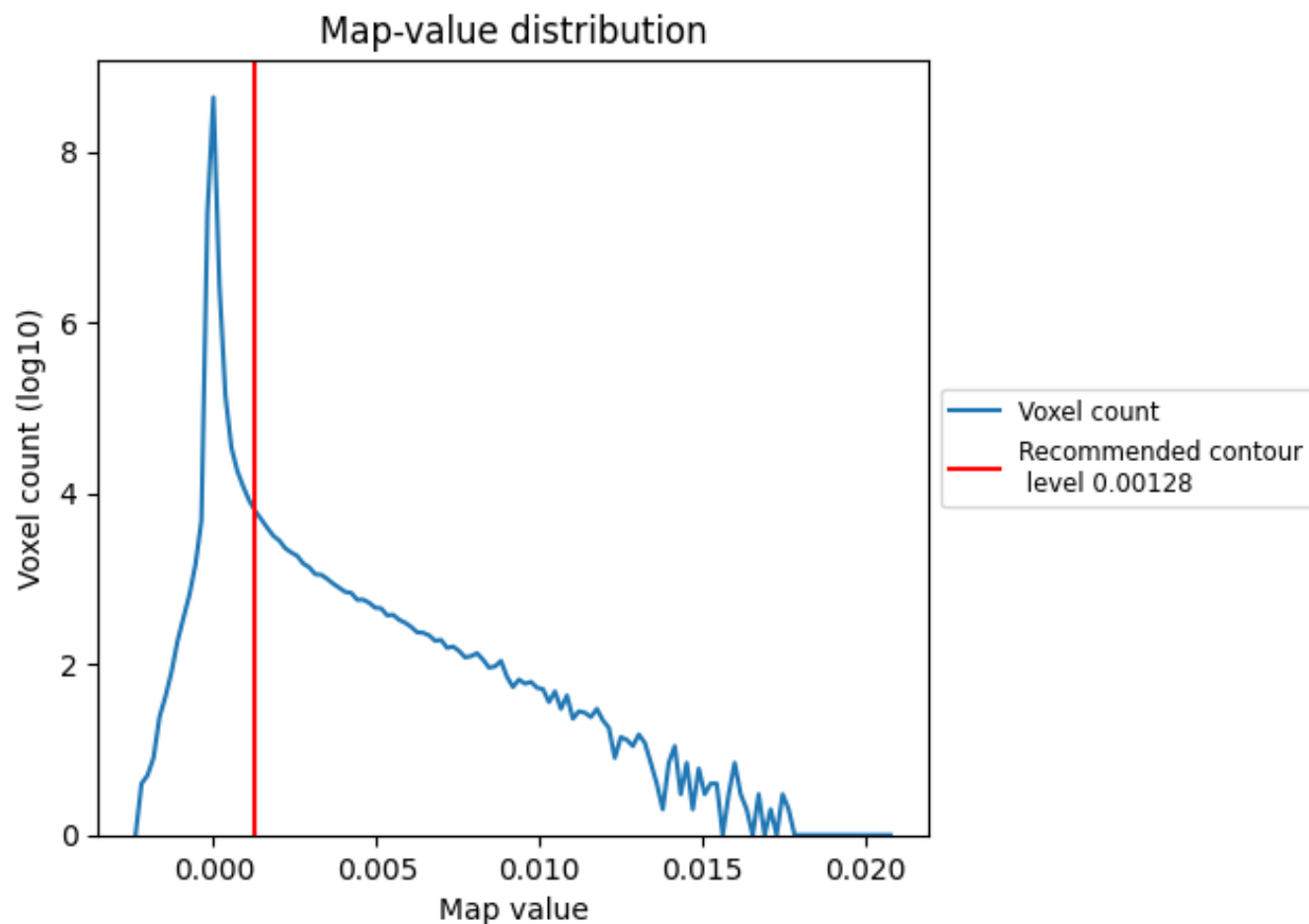


Z

7 Map analysis [i](#)

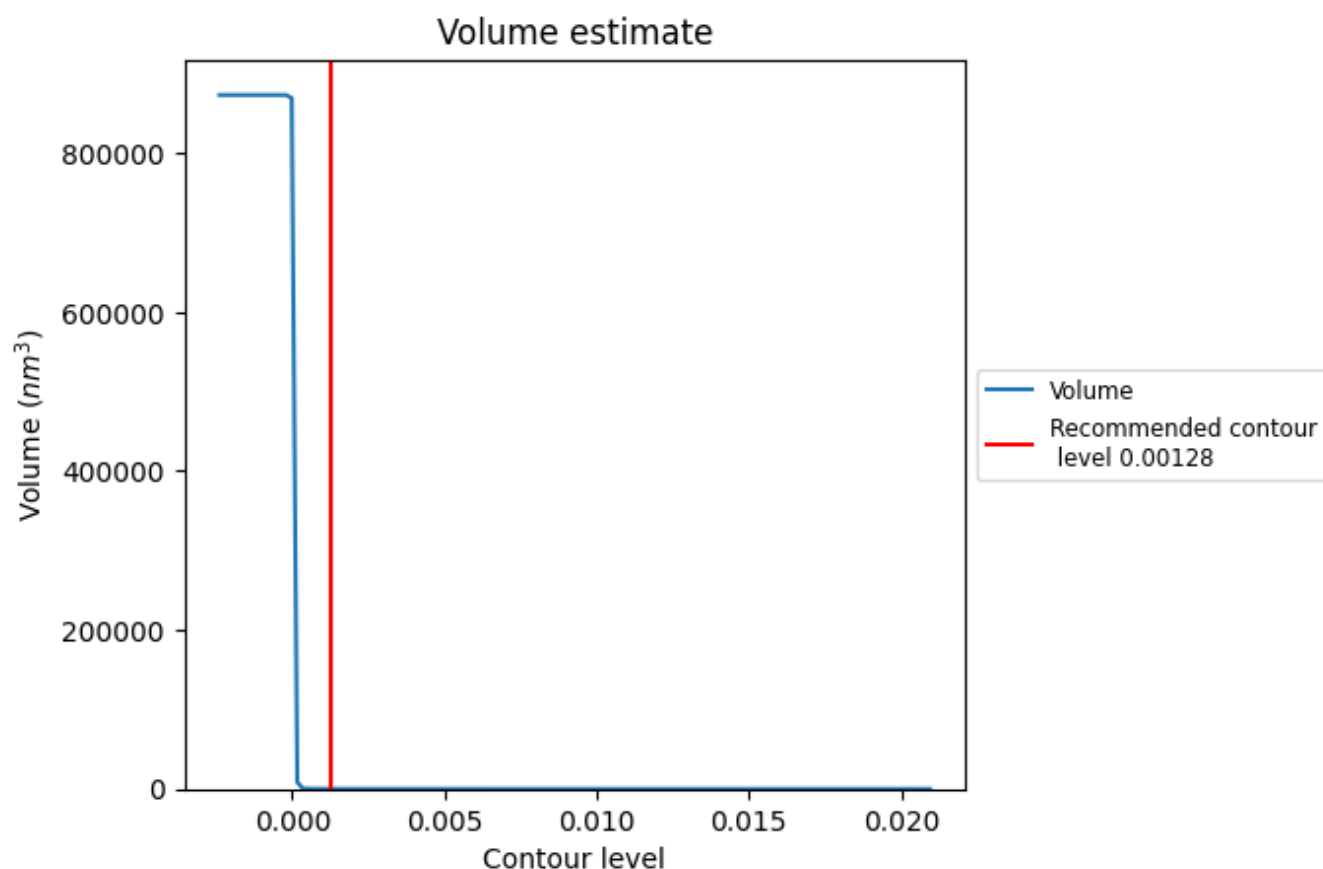
This section contains the results of statistical analysis of the map.

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.

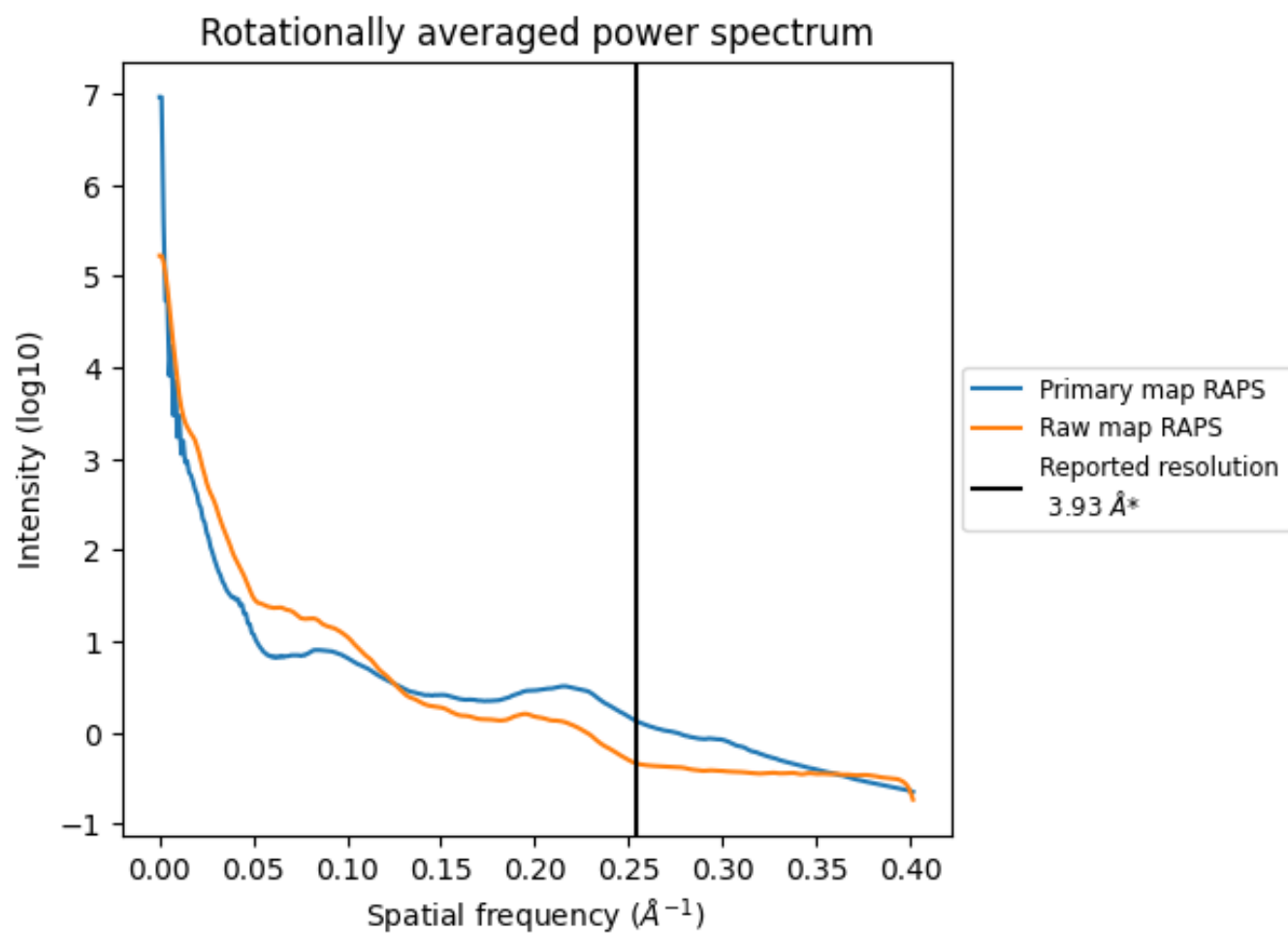
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 85 nm^3 ; this corresponds to an approximate mass of 77 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 ⓘ

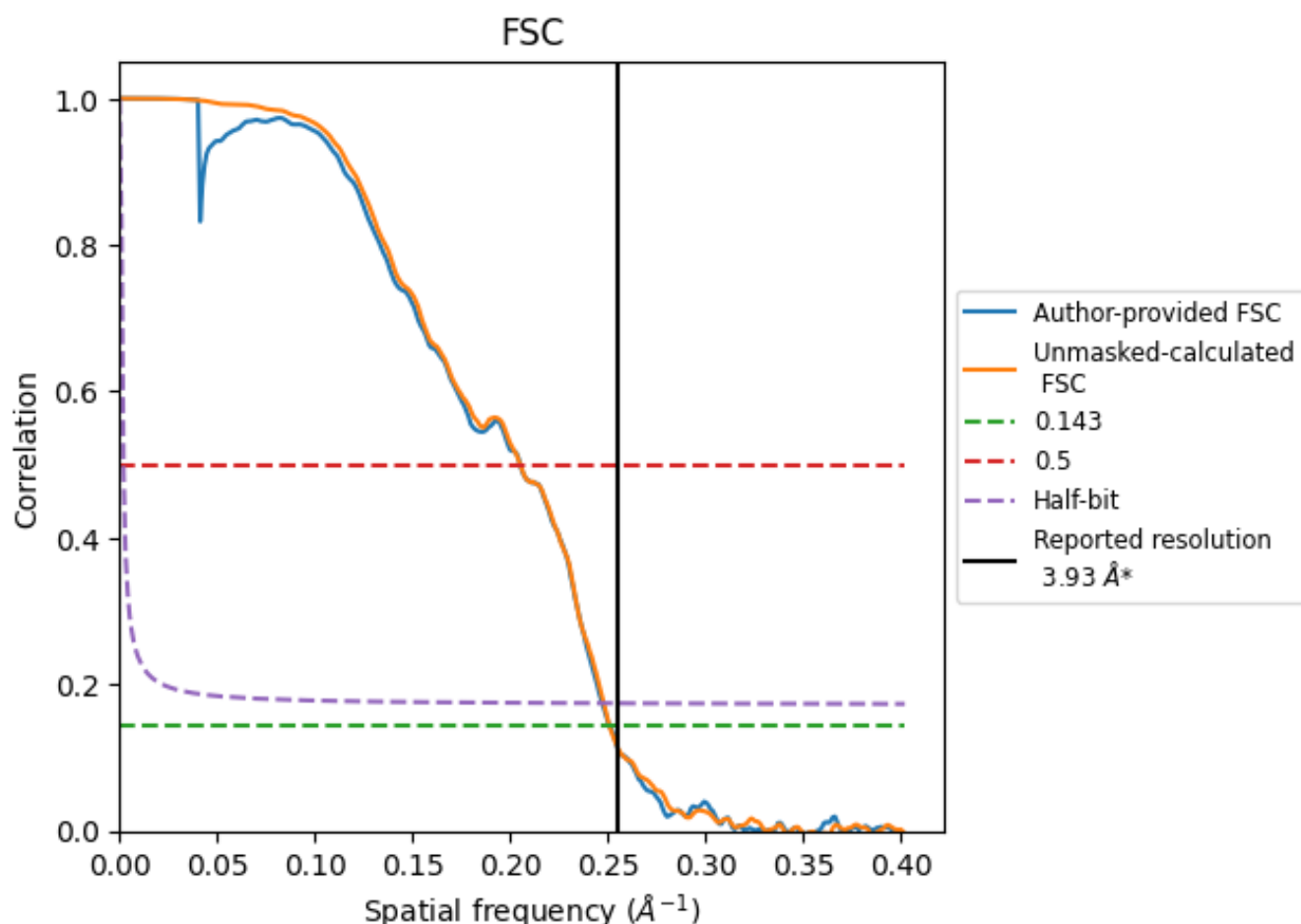


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 Å⁻¹

8.2 Resolution estimates [i](#)

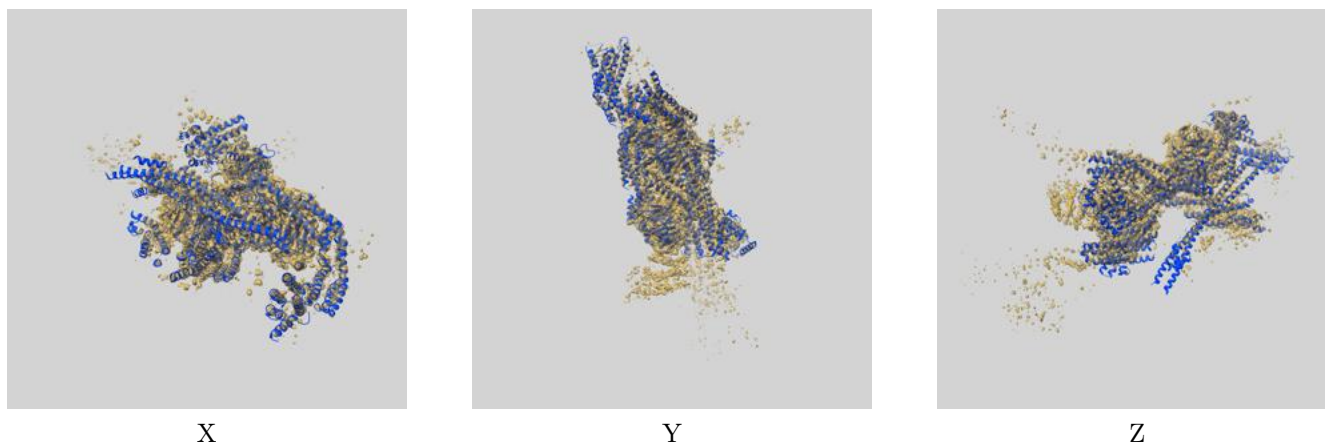
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	3.99	4.88	4.05
Unmasked-calculated*	3.99	4.88	4.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

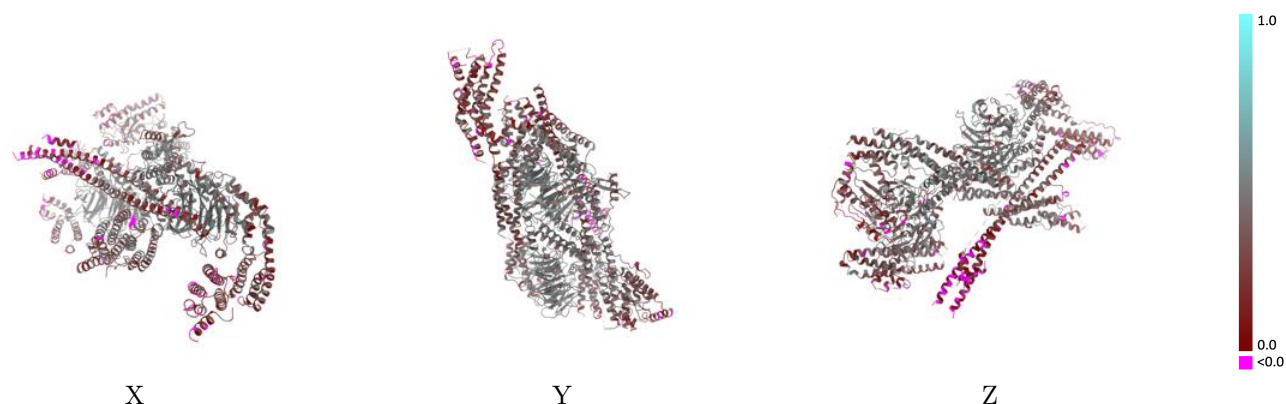
This section contains information regarding the fit between EMDB map EMD-14553 and PDB model 7Z8J. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



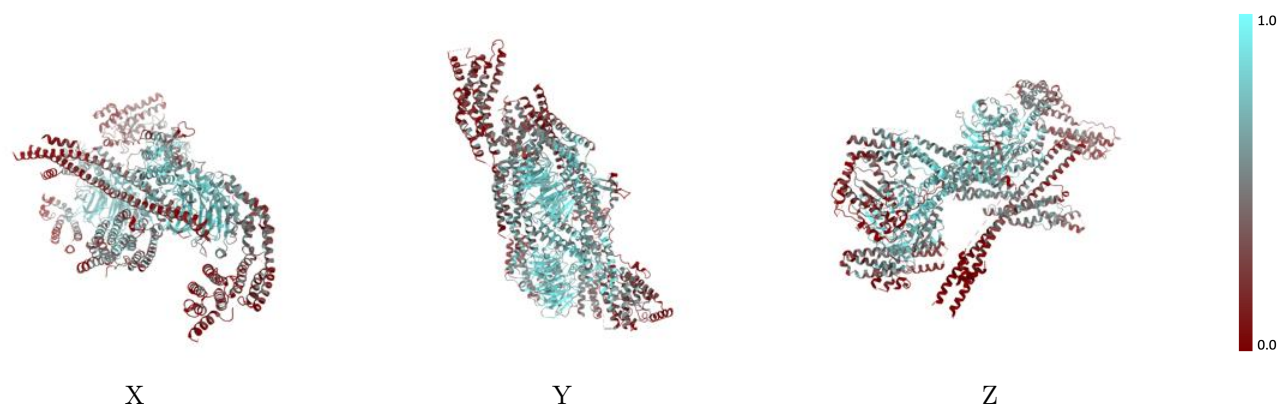
The images above show the 3D surface view of the map at the recommended contour level 0.00128 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



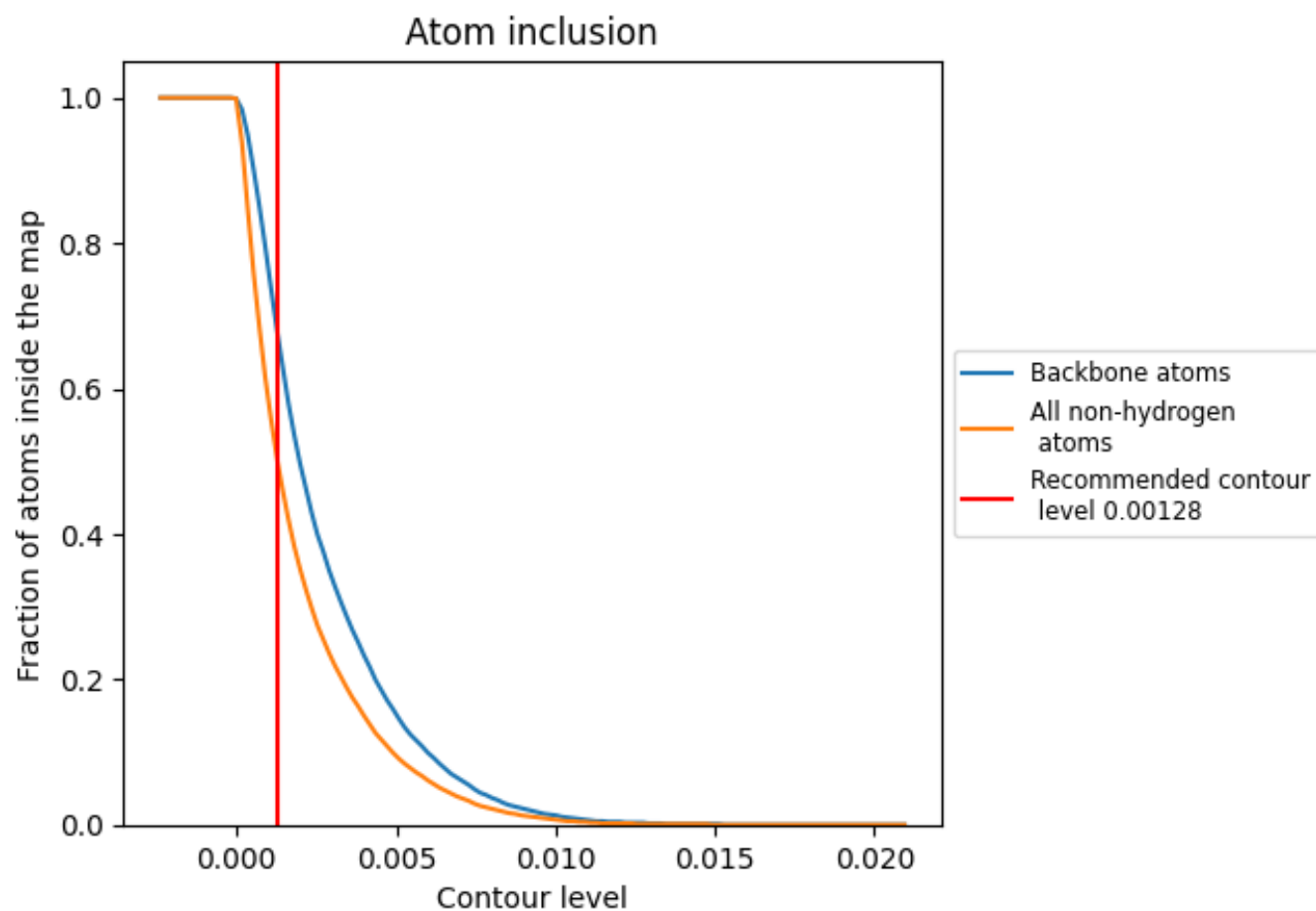
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00128).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 50% 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 (0.00128) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4990	<div></div> 0.3640
X	<div></div> 0.2690	<div></div> 0.2190
f	<div></div> 0.4550	<div></div> 0.3510
h	<div></div> 0.7210	<div></div> 0.4520
j	<div></div> 0.2100	<div></div> 0.2700
m	<div></div> 0.5350	<div></div> 0.3820
n	<div></div> 0.2230	<div></div> 0.2710
o	<div></div> 0.7800	<div></div> 0.4690
r	<div></div> 0.0000	<div></div> 0.1370
x	<div></div> 0.1900	<div></div> 0.2020

1.0

0.0

<0.0