



wwPDB EM Validation Summary Report ⓘ

Dec 28, 2024 – 01:30 PM EST

PDB ID : 7B70
EMDB ID : EMD-12063
Title : TRAPPCore plus C8 (355-596) and C11 (1-718) from MiniTRAPPIII
Authors : Galindo, A.; Munro, S.; Planelles-Herrero, V.J.
Deposited on : 2020-12-09
Resolution : 4.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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<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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

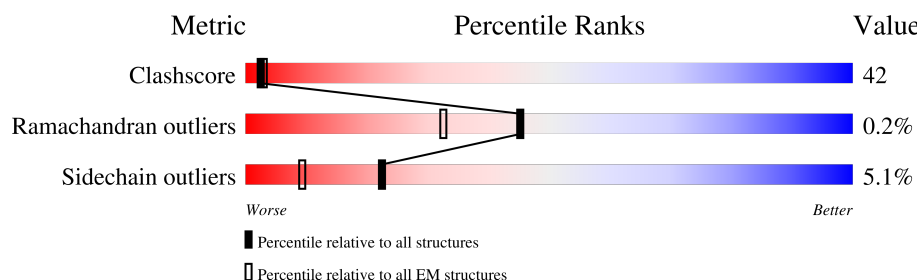
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	178	
1	G	178	
2	B	152	
3	C	145	
4	D	219	
5	E	139	
6	F	194	
7	H	138	

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Mol	Chain	Length	Quality of chain
8	I	246	<div><div></div><div>11%</div><div>36%</div><div>32%</div><div>16%</div><div>•</div><div>15%</div></div>
9	J	718	<div><div></div><div>38%</div><div>47%</div><div>•</div><div>14%</div></div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 17084 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 Trafficking protein particle complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	165	Total	C	N	O	S	0	0
			1337	847	229	253	8		
1	G	169	Total	C	N	O	S	0	0
			1363	861	233	261	8		

- Molecule 2 is a protein called GEO08327p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	151	Total	C	N	O	S	0	0
			1226	780	211	227	8		

- Molecule 3 is a protein called Trafficking protein particle complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	145	Total	C	N	O	S	0	0
			1204	792	194	216	2		

- Molecule 4 is a protein called Trafficking protein particle complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	219	Total	C	N	O	S	0	0
			1741	1125	279	330	7		

- Molecule 5 is a protein called Probable trafficking protein particle complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	139	Total	C	N	O	S	0	0
			1177	759	199	214	5		

- Molecule 6 is a protein called Trafficking protein particle complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	164	Total	C	N	O	S	0	0
			1333	852	225	250	6		

- Molecule 7 is a protein called TRAPPC2L.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	138	Total	C	N	O	S	0	0
			1089	697	179	207	6		

- Molecule 8 is a protein called FI18195p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	208	Total	C	N	O	S	0	0
			1710	1096	301	301	12		

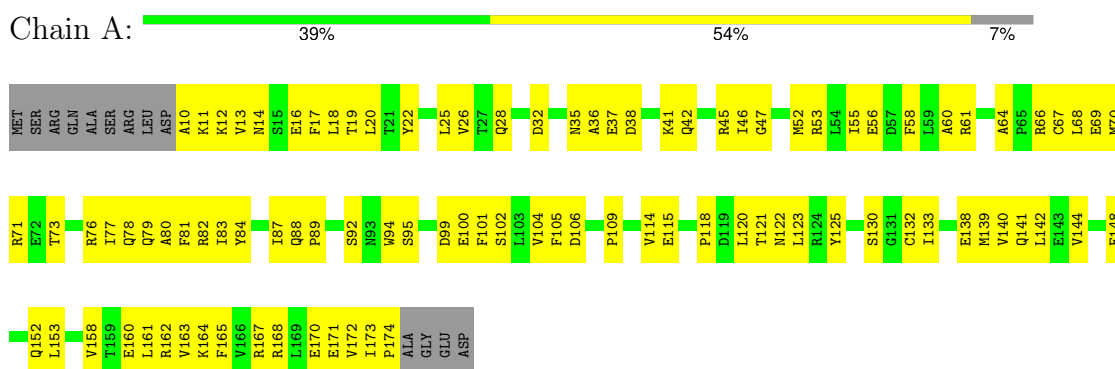
- Molecule 9 is a protein called Trafficking protein particle complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	614	Total	C	N	O	S	0	0
			4904	3125	864	882	33		

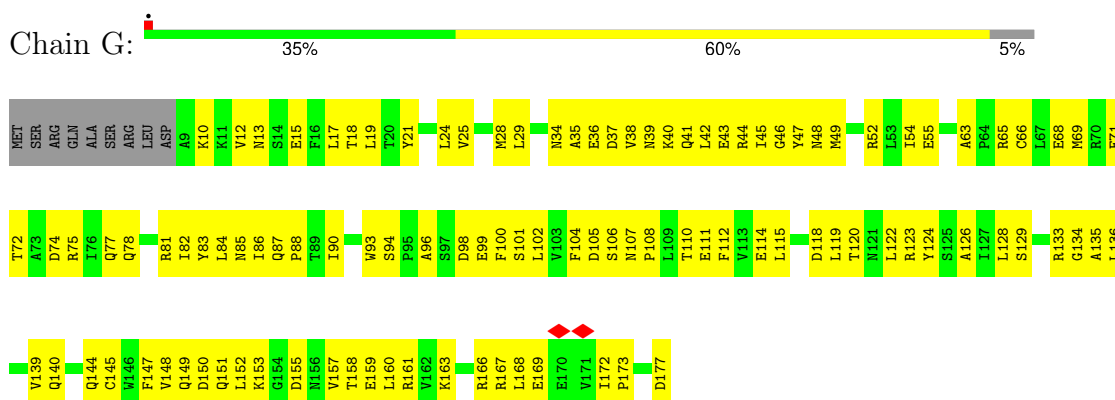
3 Residue-property plots

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.

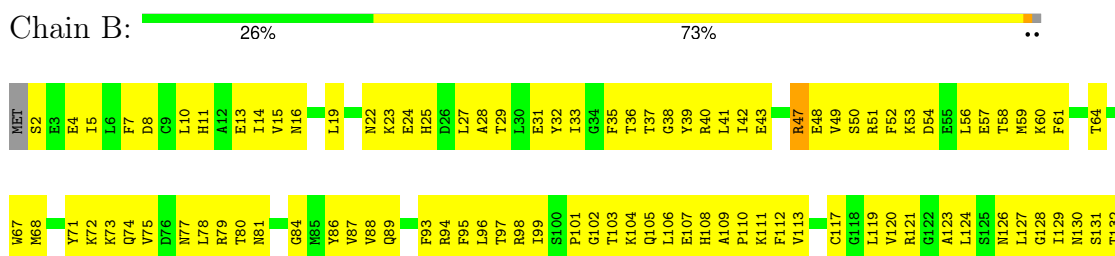
- Molecule 1: Trafficking protein particle complex subunit



- Molecule 1: Trafficking protein particle complex subunit



- Molecule 2: GEO08327p1



V133
T134
A135
E136
V137
Q138
S139
I140
P141
A142
C143
K144
F145
H146
I147
E148
V149
M150
R151
M152


- Molecule 3: Trafficking protein particle complex subunit

Chain C:  42% 58%

K1
T2
F3
F4
N5
L6
Y7
D10
K11
F12
F12
L16
H17
Y18
A19
E20
V21
T24
K25
K26
S27
T30
R31
E32
E33
M41
L42
F43
S44
L45
K46
S47
F48
K51
I52
S53
P54
H55
D56
F57
K58
E59
L62
Y63
Y64
K65
T66
N67
R68
L71
H72
Y73
L74

F77
S78
G79
L80
K81
F82
F83
L84
N85
T86
D87
T88
T89
F91
Y91
N92
V93
K94
E95
L96
Q98
Q99
I100
Y101
A102
K103
V104
V105
V106
E107
F108
V109
V110
R111
D112
P117
S123
E124
L125
F126
K129
R135
Q136
S137
F138
I139
F140
G141
I142
R143
N144
I145

- Molecule 4: Trafficking protein particle complex subunit

Chain D:  38% 61%

M1
I2
I3
Y4
G5
V6
Y7
I8
V9
S10
K11
L15
I16
F17
N18
N21
N22
V23
P24
R25
H28
E29
K30
F31
F32
L36
D37
L40
D41
Y42
V47
S50
F51
N52
R53
K54
D55
G56
L57
N58
V59
G60
H61
V62
L63
V64
A65
V66
V71
T75
L76

D77
D78
G79
R80
D81
V82
R83
T84
T85
L86
D87
A88
N91
Y92
P93
I94
N95
L96
K97
S99
R100
K102
M103
T104
T105
M106
E107
K108
I109
F110
L111
F115
Y116
P117
L118
F119
A120
I121
A122
S123
Q124
L125
S126
P127
E128
P129
K130
S131
S132
G133
I134
E135
I136
L137
E138
A139

D140
T143
C146
Q148
T149
L150
G152
I153
K154
F155
I156
I157
T161
N162
L163
D167
L168
L169
R171
K172
V173
Y174
E175
L176
Y177
S178
D179
V180
V181
L182
K183
N184
P185
F186
Y187
S188
L189
E190
M191
P192
I193
R194
L197
F198
D199
N200
Q203
V209
T212

G213
I214
S215
N216
I217
D218
K219

- Molecule 5: Probable trafficking protein particle complex subunit 2

Chain E:  36% 63%

H1
S2
Y3
Y4
Y5
F6
V7
I8
V9
G10
Q11
M12
D13
M14
P15
I16
Y17
E18
K19
E20
F21
V24
N25
K26
E27
L28
R29
K30
E31
D32
H33
R34
H35
L36
T37
Q38
F39
I40
A41
H42
L45
D46
L47
V48
D49
E50
H51
K52
W53
K54
T55
A56
N57
M58
Q59
K61
S62

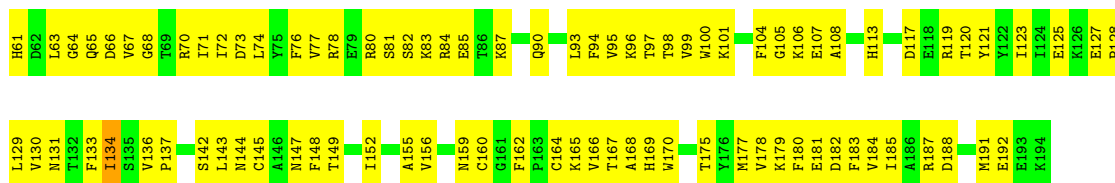
I63
D64
R65
F70
V71
S72
A73
F74
T75
T76
A77
S78
Q79
R81
F82
I83
I84
V85
H86
D87
N88
K89
N90
D91
E92
G93
I94
K95
N96
F97
F98
N99
H100
M101
Y102
M110
M111
A112
F113
Y114
T118
P119
I120
K121
E126
K127
K128
S129
E130
I131
F132
G133
M134
L135
Y136

L137
L138
S139

- Molecule 6: Trafficking protein particle complex subunit 5

Chain F:  28% 56% 15%

MET
GLU
LYS
LEU
GLU
ALA
LYS
ILE
SER
SER
MET
ARG
PRO
ARG
SER
ASN
ILE
LEU
ASP
ARG
PRO
LEU
SER
LYS
GLY
LYS
THR
GLU
VAL
S31
Q32
S33
I34
V35
A36
L37
L38
F39
S40
E41
I42
I43
Q44
Y45
S46
Q47
S48
R49
V50
F51
T52
V53
P54
E55
I56
Q57
T58
R59
K61
L60



• Molecule 7: TRAPPC2L



• Molecule 8: FI18195p1



PRO	LYS	ASN	PHE	GLU	LYS	LYS	MET	ARG	LEU	GLU	PRO	GLY	S676	L680	F681	C682	S683	T684	E685	A686	Q687	Q688	N692	T693	Q694	L695	V698	R699	L700	E701	A702	H703	M704	G705	T706	D707	Q708	V709	T714	N716																		
Q599	L600	I601	V602	L605	T606	D607	I608	P609	L610	R611	I612	R613	S614	F615	H616	L619	A620	D621	P625	Q626	ASN	SER	TYR	LYS	LEU	GLU	ALA	LEU	LYS	TYR	PHE	CYS	PHE	PRO	THR	LEU	THR	THR	GLN	LEU	ARG	GLY	GLN	LYS	GLN	PRO	ASP	ASP	GLU	GLN	LEU	ASN	PRO	SER	GLN	GLU		
D523	Q524	R527	I528	L529	I530	W535	Q536	V541	P542	F543	M544	P545	K546	P551	Q554	A555	L556	W557	T558	S559	A560	L561	A562	N563	V564	K565	S566	PRO	ILE	GLN	ILE	ASP	R497	C498	A499	L500	VAL	L501	V505	A506	D507	Y508	I509	S512	V513	S514	A515	L516	S517	D518	L518	R519	H520	Q521	L598			
K443	C444	L445	R446	F447	R448	K449	I453	D454	M455	A456	E457	E458	Y459	L460	K461	S462	L471	Y472	L475	M476	Y479	K483	W484	T485	T486	I487	F488	T489	L492	R497	C498	A499	L500	VAL	L501	V505	A506	D507	Y508	I509	S512	V513	S514	A515	L516	S517	D518	L518	R519	H520	Q521	L598						
M367	E368	A369	Y370	M373	S377	GLU	ALA	THR	PRO	THR	PRO	PRO	ILE	GLN	ASN	ASN	LEU	SER	LEU	TYR	THR	GLU	PHE	PHE	GLY	ILE	ARG	ALA	VAL	LYS	THR	GLY	ASP	LEU	L343	Q344	T345	Q346	H347	P348	G349	I350	Y351	H352	K353	K354	A355	A356	E357	F358	V359	M360	K361	R362	R363	D364	A365	Q366
F297	I298	I299	H300	K303	H304	K305	R307	F310	K311	D312	L313	A314	F315	E316	H317	H318	A319	W320	L321	Q324	H325	L331	F332	C333	E334	A335	I336	G339	L343	Q344	T345	Q346	H347	P348	G349	I350	Y351	H352	K353	K354	A355	A356	E357	F358	V359	M360	K361	R362	R363	D364	A365	Q366						
I226	Q229	F230	K231	L232	G233	F234	V235	M238	R239	Q240	S243	T244	Q245	Q246	K247	H248	Y249	A252	N255	L256	D257	E258	I259	R260	I261	C266	I269	K270	A273	G274	F275	L276	N277	Y278	K279	I280	L283	M284	F285	K286	L287	K288	T289	P290	R291	D292	A293	I294	N295	Q296								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	486758	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 ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	502.56, 502.56, 502.56	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2564, 1.2564, 1.2564	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.43	0/1360	0.63	0/1841
1	G	0.39	0/1386	0.56	0/1876
2	B	0.43	0/1250	0.61	0/1686
3	C	0.40	0/1237	0.58	0/1675
4	D	0.42	0/1776	0.64	1/2406 (0.0%)
5	E	0.42	0/1207	0.57	1/1623 (0.1%)
6	F	0.40	0/1359	0.60	0/1833
7	H	0.46	0/1108	0.73	1/1498 (0.1%)
8	I	0.60	0/1749	0.66	0/2360
9	J	0.34	0/5004	0.55	0/6769
All	All	0.42	0/17436	0.60	3/23567 (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
4	D	0	1
6	F	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	197	LEU	CB-CG-CD1	8.39	125.27	111.00
5	E	36	LEU	CA-CB-CG	5.46	127.86	115.30
7	H	38	VAL	CB-CA-C	5.08	121.06	111.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	214	ILE	Peptide
6	F	134	ILE	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	1337	0	1334	103	0
1	G	1363	0	1352	110	0
2	B	1226	0	1217	161	0
3	C	1204	0	1213	104	0
4	D	1741	0	1768	164	0
5	E	1177	0	1151	101	0
6	F	1333	0	1338	142	0
7	H	1089	0	1099	175	0
8	I	1710	0	1682	193	0
9	J	4904	0	4942	340	0
All	All	17084	0	17096	1438	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 42.

The worst 5 of 1438 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)
8:I:510:THR:HG21	8:I:533:MET:CE	1.41	1.49
8:I:575:TYR:CA	8:I:579:GLY:HA3	1.38	1.47
8:I:575:TYR:HA	8:I:579:GLY:CA	1.42	1.45
8:I:514:MET:CG	8:I:526:VAL:HG11	1.53	1.38
8:I:537:GLU:OE1	8:I:545:LEU:HD11	1.24	1.35

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	163/178 (92%)	145 (89%)	18 (11%)	0	100	100
1	G	167/178 (94%)	150 (90%)	17 (10%)	0	100	100
2	B	149/152 (98%)	124 (83%)	25 (17%)	0	100	100
3	C	143/145 (99%)	125 (87%)	18 (13%)	0	100	100
4	D	217/219 (99%)	177 (82%)	40 (18%)	0	100	100
5	E	137/139 (99%)	122 (89%)	15 (11%)	0	100	100
6	F	162/194 (84%)	145 (90%)	17 (10%)	0	100	100
7	H	136/138 (99%)	114 (84%)	21 (15%)	1 (1%)	19	55
8	I	204/246 (83%)	183 (90%)	17 (8%)	4 (2%)	6	34
9	J	604/718 (84%)	544 (90%)	60 (10%)	0	100	100
All	All	2082/2307 (90%)	1829 (88%)	248 (12%)	5 (0%)	45	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	435	TYR
8	I	520	ALA
8	I	559	PRO
7	H	43	CYS
8	I	536	GLU

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	149/159 (94%)	149 (100%)	0	100	100
1	G	151/159 (95%)	151 (100%)	0	100	100
2	B	136/137 (99%)	135 (99%)	1 (1%)	81	86
3	C	133/133 (100%)	133 (100%)	0	100	100
4	D	199/199 (100%)	198 (100%)	1 (0%)	86	89
5	E	129/129 (100%)	128 (99%)	1 (1%)	79	84
6	F	149/177 (84%)	148 (99%)	1 (1%)	81	86
7	H	120/120 (100%)	118 (98%)	2 (2%)	56	72
8	I	173/204 (85%)	89 (51%)	84 (49%)	0	0
9	J	526/621 (85%)	520 (99%)	6 (1%)	70	80
All	All	1865/2038 (92%)	1769 (95%)	96 (5%)	22	43

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	I	525	GLU
8	I	556	THR
8	I	528	LYS
8	I	540	LEU
8	I	562	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	33	HIS
9	J	129	ASN
9	J	119	GLN
9	J	318	HIS
5	E	38	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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](#)

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.

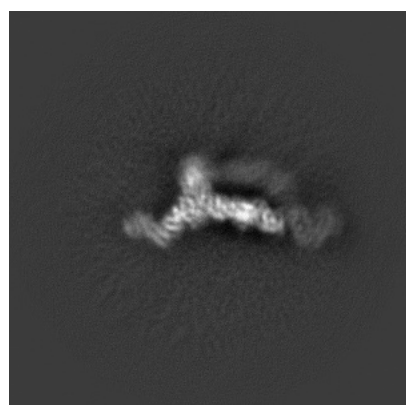
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12063. These allow visual inspection of the internal detail of the map and identification of artifacts.

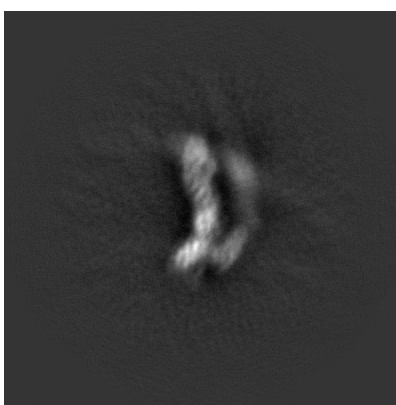
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

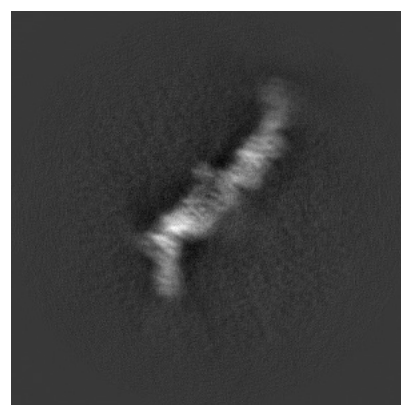
6.1.1 Primary map



X



Y

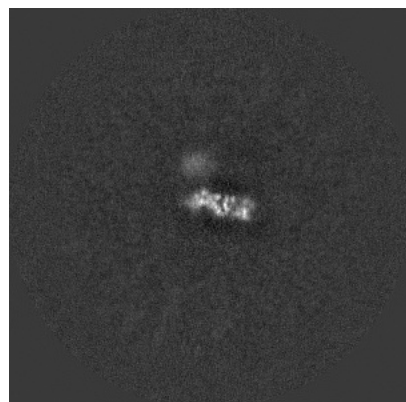


Z

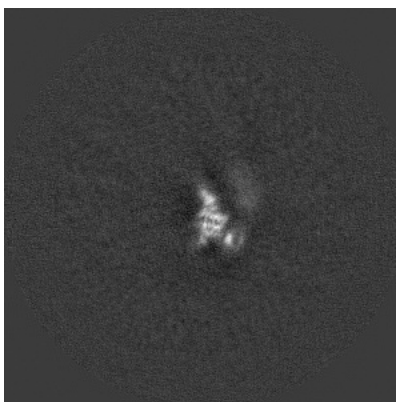
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

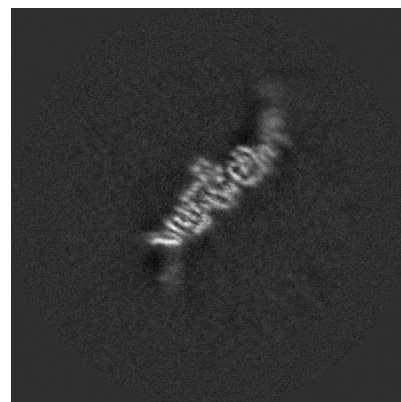
6.2.1 Primary map



X Index: 200



Y Index: 200

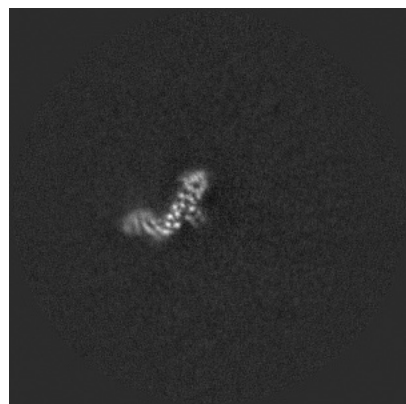


Z Index: 200

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

6.3 Largest variance slices [i](#)

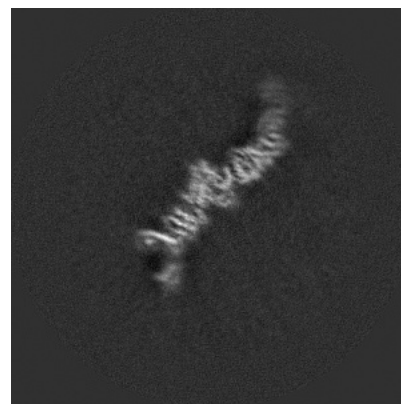
6.3.1 Primary map



X Index: 158



Y Index: 182

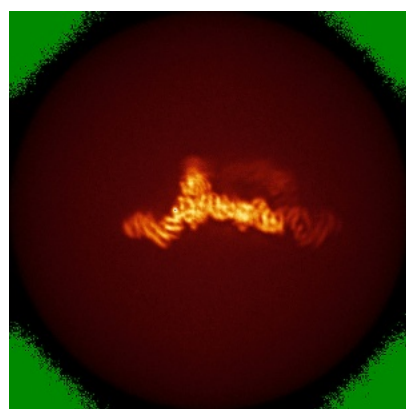


Z Index: 195

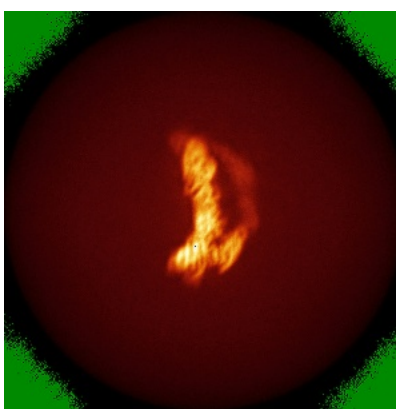
The images above show the largest variance slices of the map in three orthogonal directions.

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

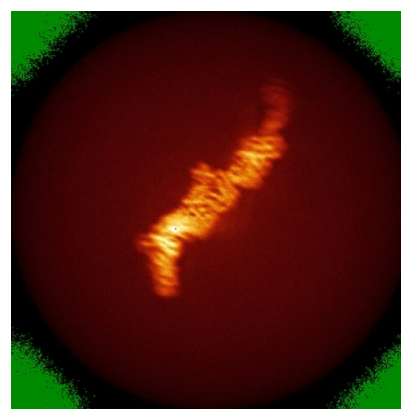
6.4.1 Primary map



X



Y

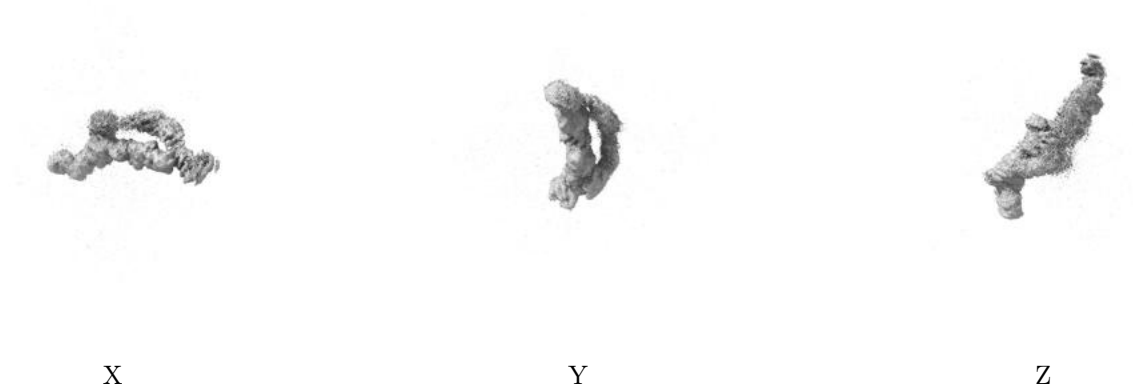


Z

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 0.006. 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 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_12063_msk_1.map [i](#)



X



Y

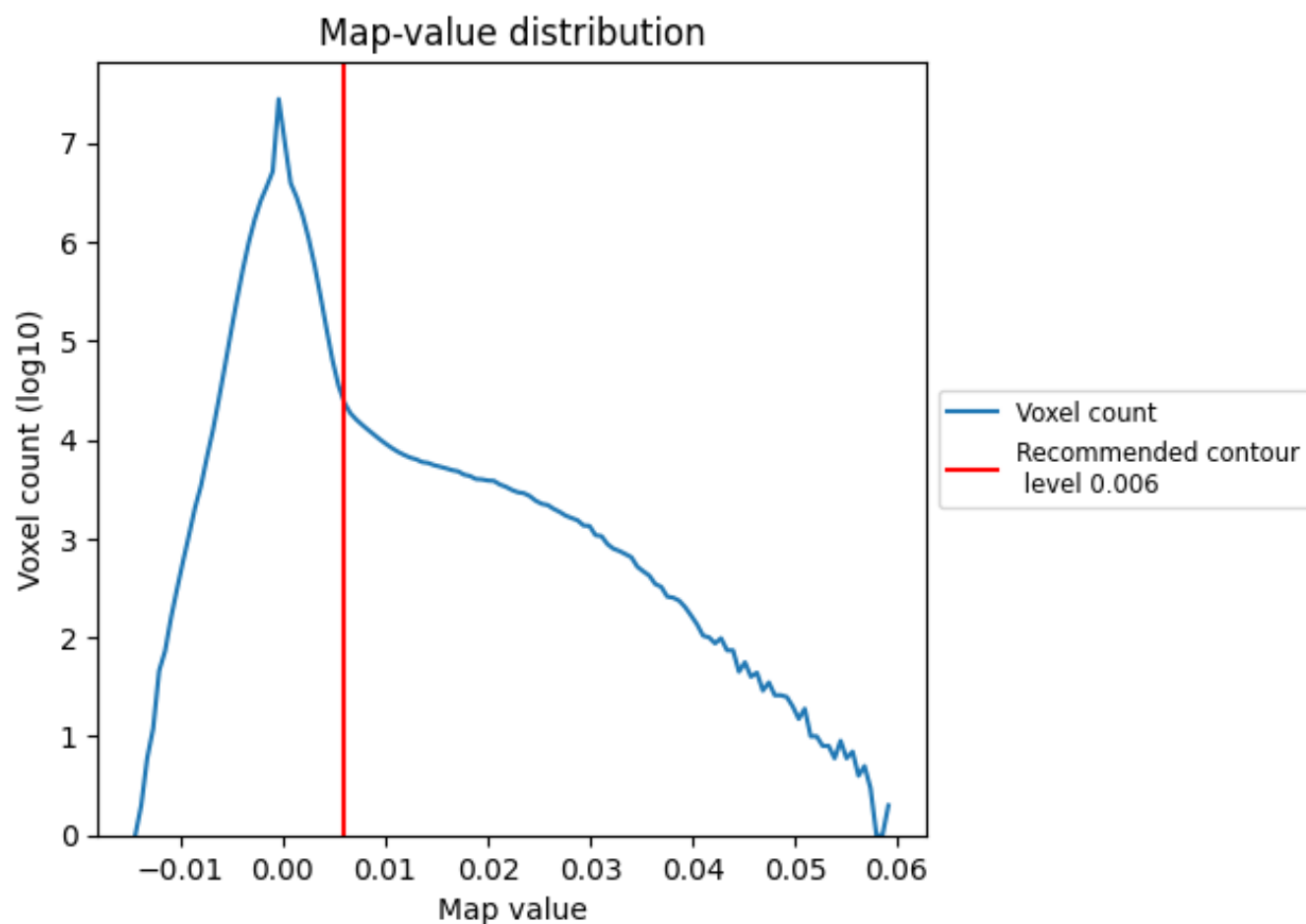


Z

7 Map analysis [i](#)

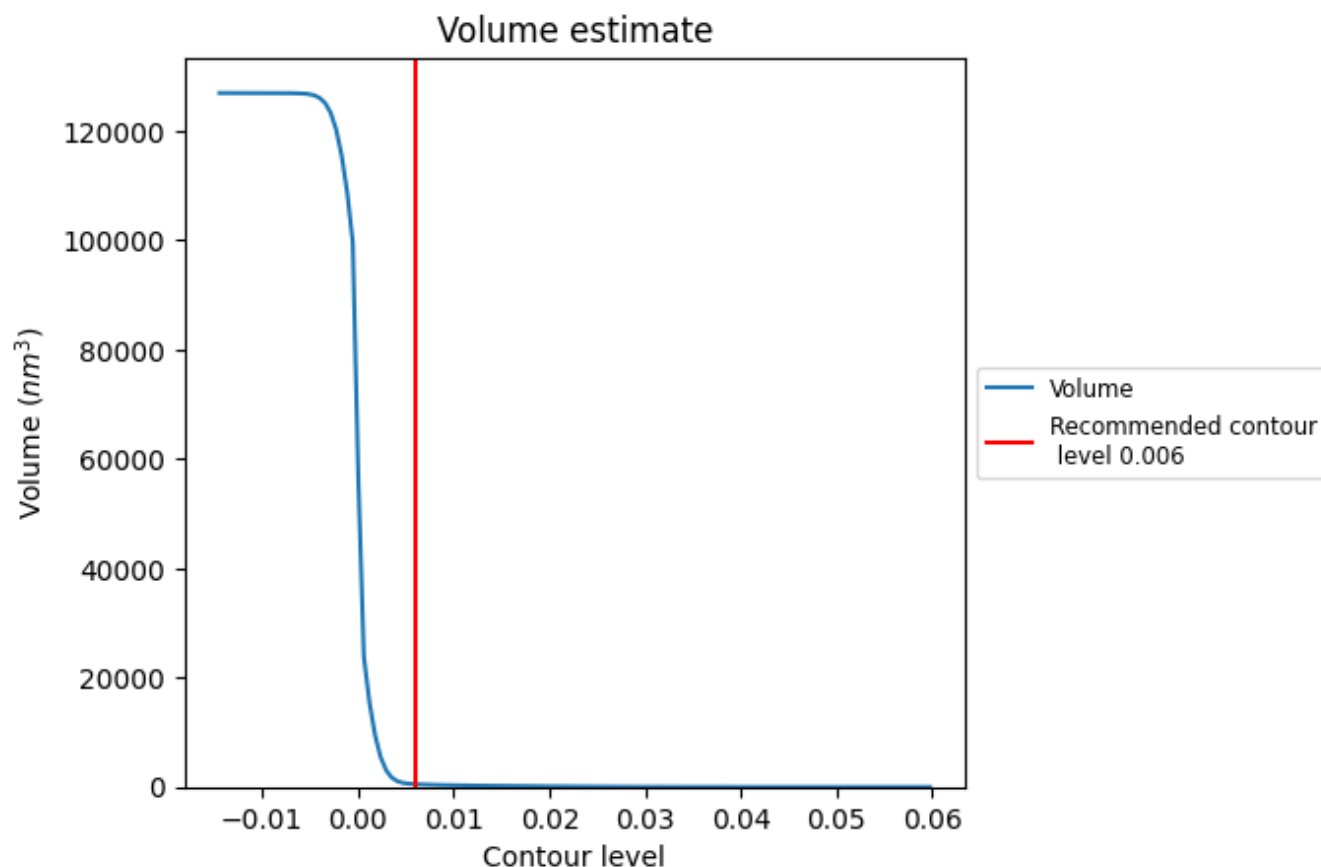
This section contains the results of statistical analysis of the map.

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.

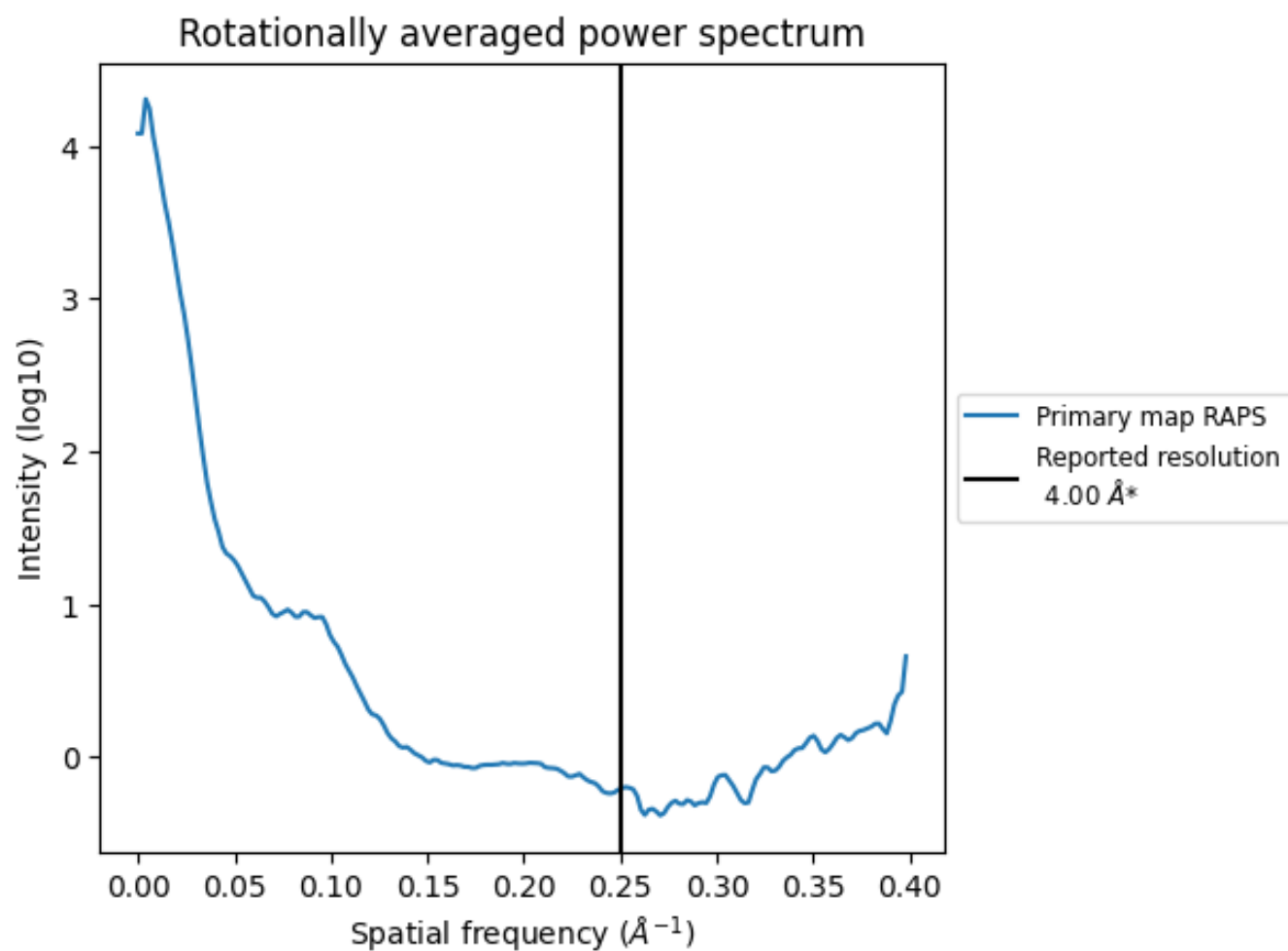
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 515 nm³; this corresponds to an approximate mass of 465 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 ⓘ

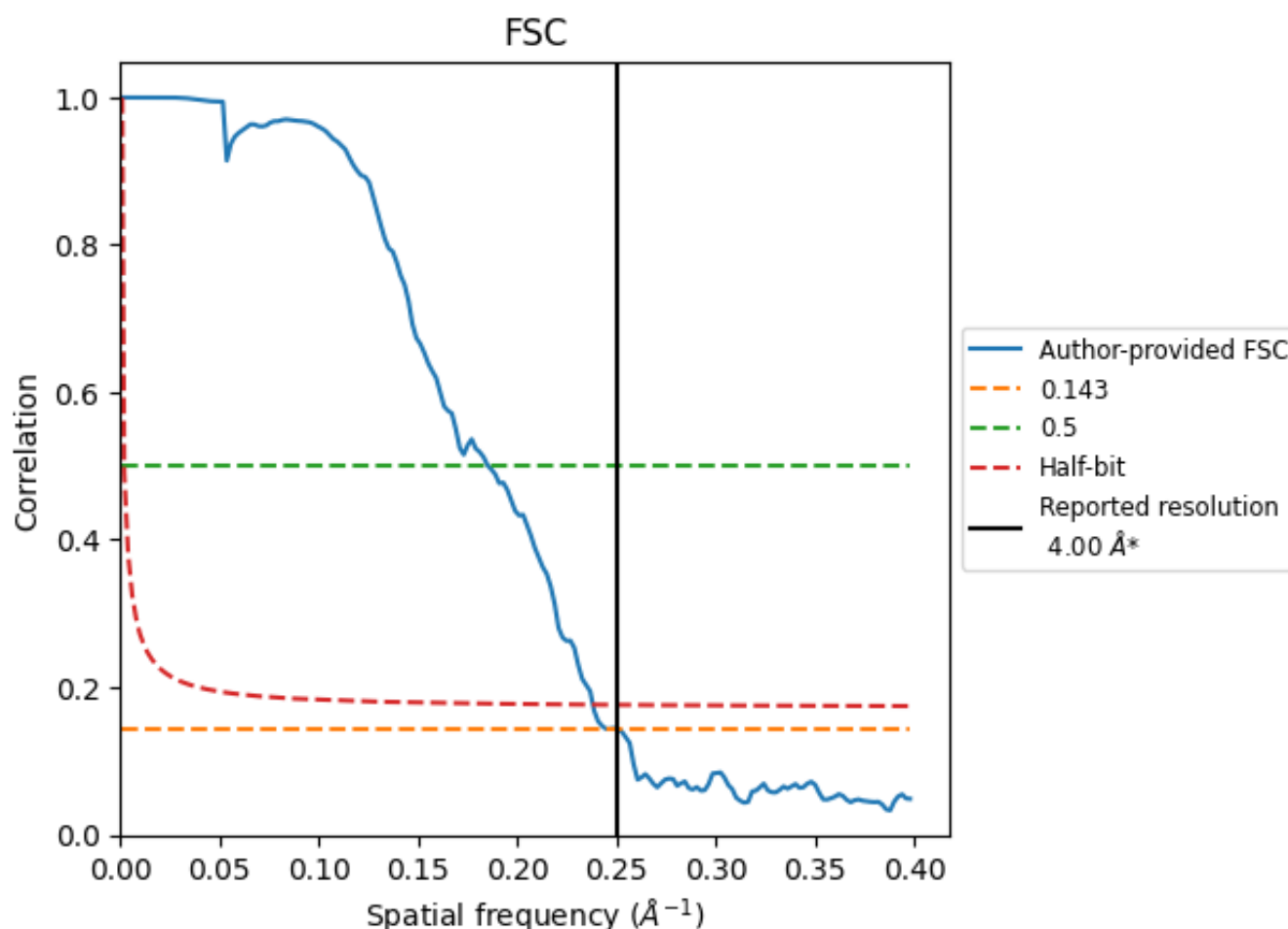


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

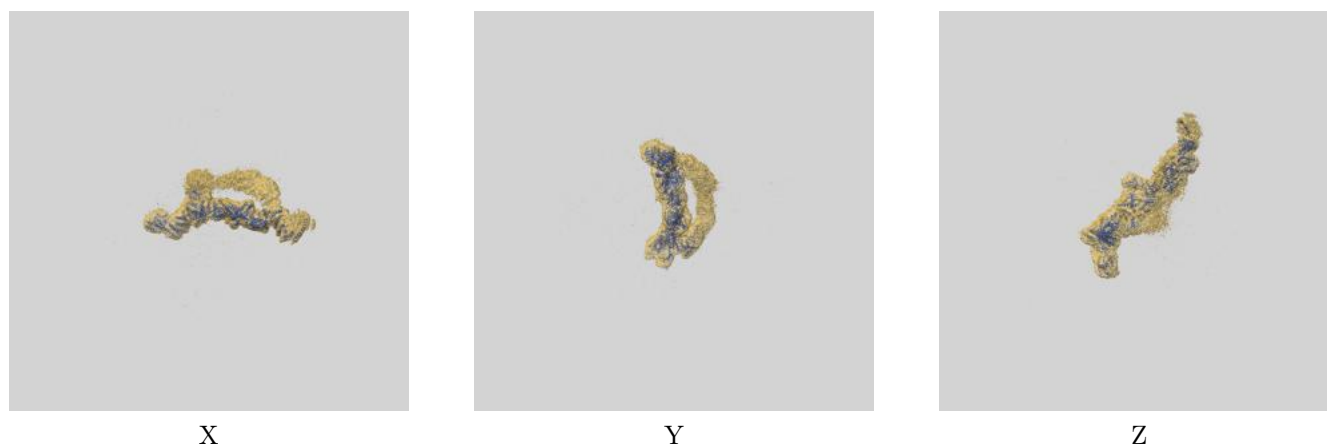
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.99	5.39	4.20
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

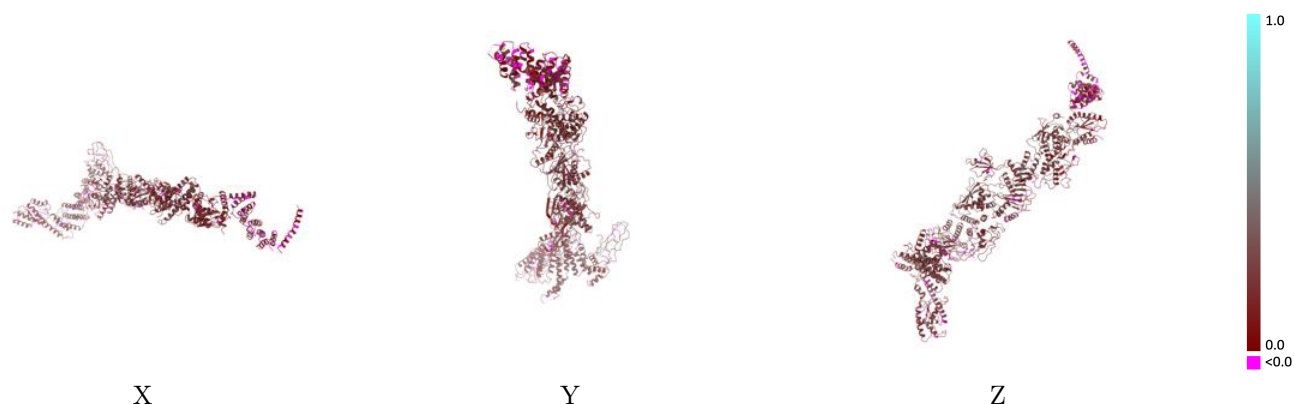
This section contains information regarding the fit between EMDB map EMD-12063 and PDB model 7B70. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



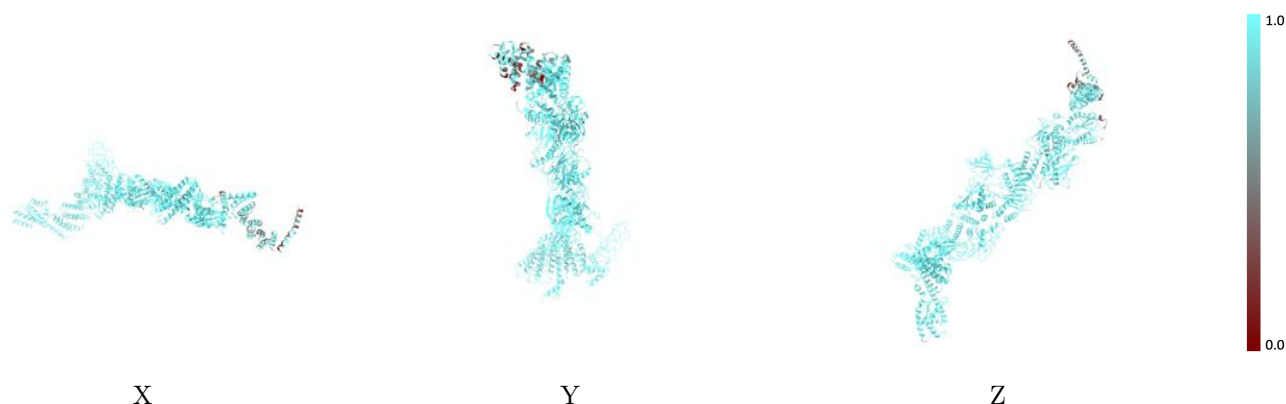
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



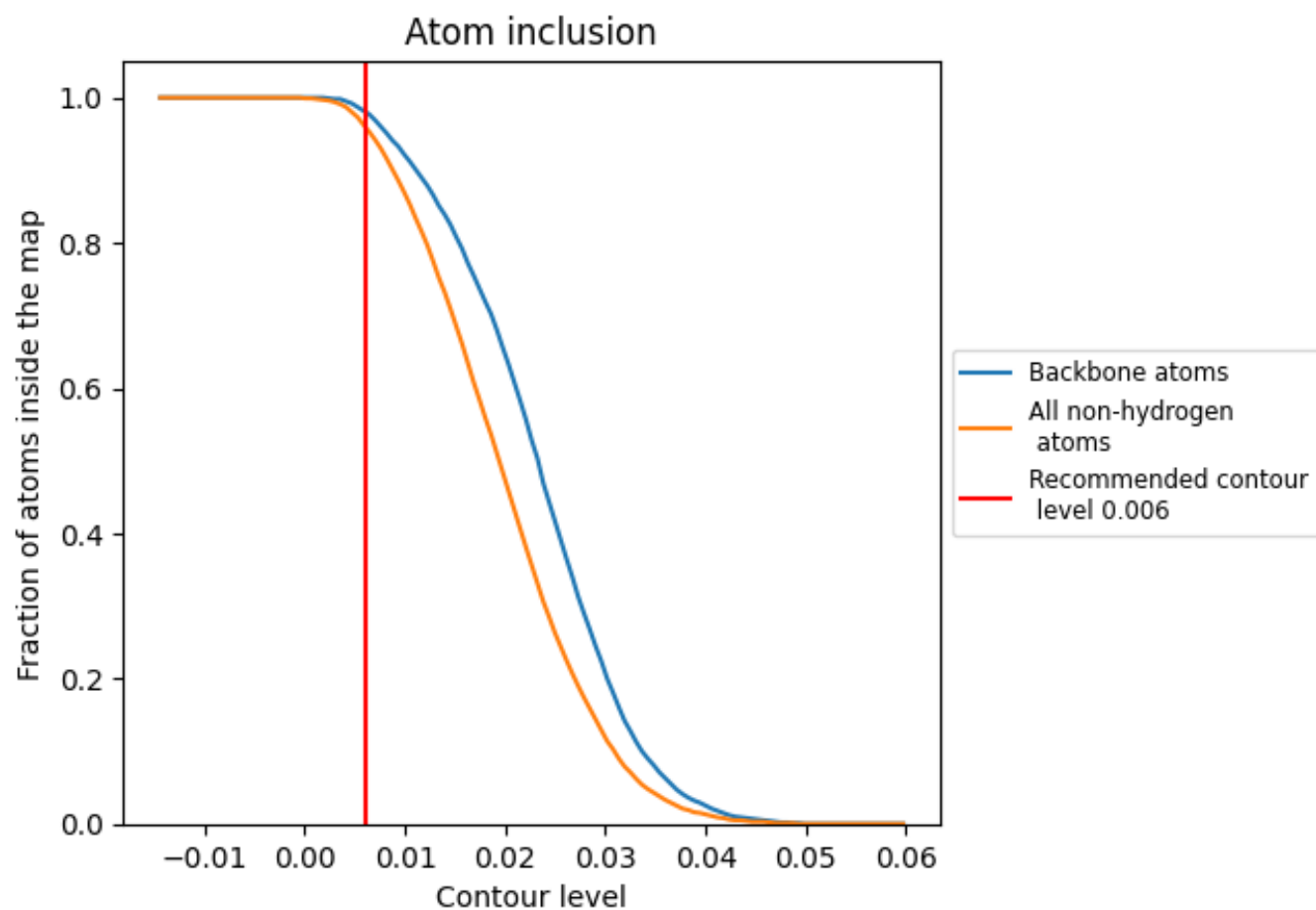
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9600	<div></div> 0.1920
A	<div></div> 0.9940	<div></div> 0.2610
B	<div></div> 0.9910	<div></div> 0.1860
C	<div></div> 0.9720	<div></div> 0.2220
D	<div></div> 0.9830	<div></div> 0.2260
E	<div></div> 0.9540	<div></div> 0.1620
F	<div></div> 0.9770	<div></div> 0.2210
G	<div></div> 0.9720	<div></div> 0.1840
H	<div></div> 0.9700	<div></div> 0.2110
I	<div></div> 0.7760	<div></div> 0.0990
J	<div></div> 0.9880	<div></div> 0.1850

1.0

0.0

<0.0