



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:39 PM UTC

PDB ID : 6YW5 / pdb_00006yw5
EMDB ID : EMD-10958
Title : The structure of the small subunit of the mitoribosome from *Neurospora crassa*
Authors : Amunts, A.; Itoh, Y.; Naschberger, A.
Deposited on : 2020-04-29
Resolution : 2.85 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:

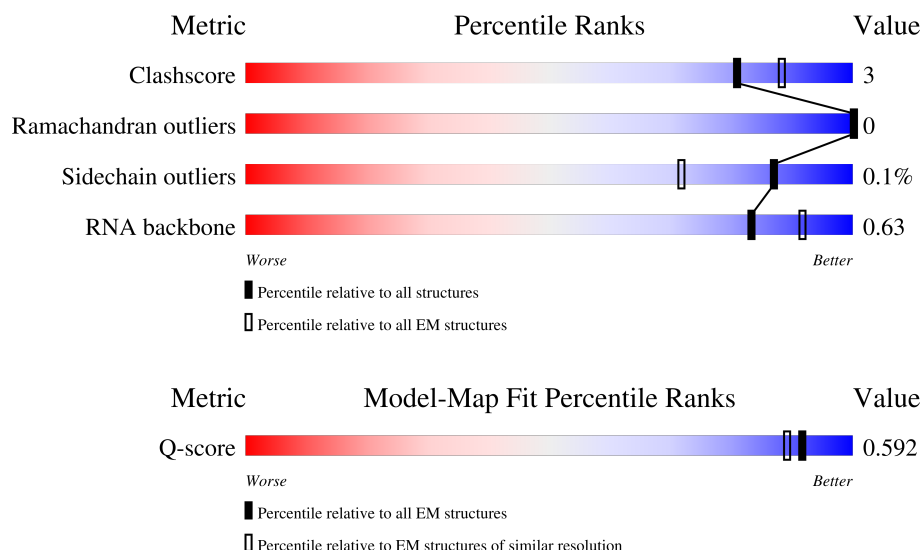
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11965 (2.35 - 3.35)

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	AA	470	 14% (red), 70% (green), 9% (yellow), 21% (grey)
2	BB	428	 64% (green), 32% (grey), 4% (red), 2% (yellow)
3	CC	508	 81% (green), 6% (red), 6% (yellow), 14% (grey)

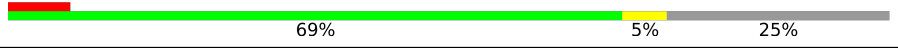
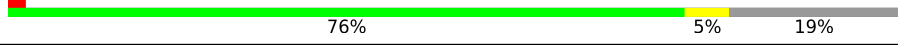
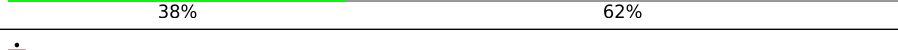
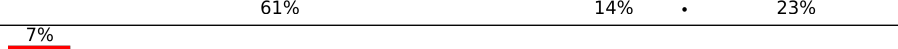
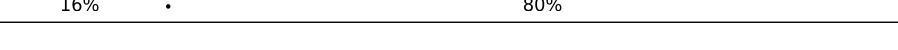
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Mol	Chain	Length	Quality of chain
4	DD	453	
5	EE	477	
6	FF	117	
7	GG	309	
8	HH	161	
9	II	315	
10	JJ	268	
11	KK	376	
12	LL	174	
13	MM	119	
14	NN	113	
15	OO	320	
16	PP	107	
17	QQ	165	
18	RR	256	
19	SS	91	
20	TT	236	
21	UU	253	
22	VV	316	
23	WW	396	
24	XX	469	
25	YY	108	
26	ZZ	382	
27	11	90	
28	22	344	

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Mol	Chain	Length	Quality of chain
29	33	236	
30	44	310	
30	55	310	
31	66	348	
32	77	414	
33	88	508	
34	00	95	
34	99	95	
35	aa	1864	
36	V	219	

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 167560 atoms, of which 76668 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 uS2m.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AA	372	Total	C	H	N	O	S	0	0
			5790	1827	2907	507	543	6		

- Molecule 2 is a protein called Mito ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	BB	290	Total	C	H	N	O	S	0	0
			4570	1426	2301	423	414	6		

- Molecule 3 is a protein called Ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	CC	438	Total	C	H	N	O	S	0	0
			7539	2388	3897	636	613	5		

- Molecule 4 is a protein called Mito ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	DD	290	Total	C	H	N	O	S	0	0
			4716	1501	2373	430	401	11		

- Molecule 5 is a protein called 37S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	EE	367	Total	C	H	N	O	S	0	0
			5799	1799	2918	526	544	12		

- Molecule 6 is a protein called Mito ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	FF	117	Total	C	H	N	O	S	0	0
			1902	591	966	176	166	3		

- Molecule 7 is a protein called Ribosomal_S7 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	GG	223	Total	C	H	N	O	S	0	0
			3524	1098	1799	318	303	6		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	HH	160	Total	C	H	N	O	S	0	0
			2522	783	1286	226	221	6		

- Molecule 9 is a protein called uS9m.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	II	247	Total	C	H	N	O	S	0	0
			3995	1253	2026	366	345	5		

- Molecule 10 is a protein called 37S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	JJ	188	Total	C	H	N	O	S	0	0
			3105	998	1554	273	272	8		

- Molecule 11 is a protein called Mitochondrial ribosomal protein subunit S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	KK	124	Total	C	H	N	O	S	0	0
			2020	625	1025	195	170	5		

- Molecule 12 is a protein called Mitochondrial 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	LL	128	Total	C	H	N	O	S	0	0
			1991	591	1032	198	165	5		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	MM	118	Total	C	H	N	O	S	0	0
			1925	586	987	186	162	4		

- Molecule 14 is a protein called Mitochondrial 40S ribosomal protein MRP2.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	NN	112	Total	C	H	N	O	S	0	0
			1876	573	961	184	151	7		

- Molecule 15 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	OO	276	Total	C	H	N	O	S	0	0
			4429	1361	2230	431	402	5		

- Molecule 16 is a protein called Ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	PP	98	Total	C	H	N	O	S	0	0
			1612	510	826	141	135			

- Molecule 17 is a protein called Mitochondrial 37S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	QQ	158	Total	C	H	N	O	S	0	0
			2561	789	1314	234	219	5		

- Molecule 18 is a protein called Mito ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	RR	134	Total	C	H	N	O	S	0	0
			2169	679	1089	206	190	5		

- Molecule 19 is a protein called Mitochondrial ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	SS	81	Total	C	H	N	O	S	0	0
			1325	422	677	118	107	1		

- Molecule 20 is a protein called Mito ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	TT	88	Total	C	H	N	O	S	0	0
			1519	470	772	157	120			

- Molecule 21 is a protein called 37S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	UU	224	Total	C	H	N	O	S	0	0
			3686	1165	1842	342	330	7		

- Molecule 22 is a protein called mS26.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	VV	261	Total	C	H	N	O	S	0	0
			4193	1300	2112	390	388	3		

- Molecule 23 is a protein called mS27.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	WW	353	Total	C	H	N	O	S	0	0
			5745	1804	2901	514	516	10		

- Molecule 24 is a protein called Mitochondrial ribosomal protein DAP3.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	XX	408	Total	C	H	N	O	S	0	0
			6447	2010	3271	562	588	16		

- Molecule 25 is a protein called mS33.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	YY	99	Total	C	H	N	O	S	0	0
			1609	491	823	152	142	1		

- Molecule 26 is a protein called 37S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	ZZ	312	Total	C	H	N	O	S	0	0
			5114	1631	2528	450	495	10		

- Molecule 27 is a protein called 37S ribosomal protein mrp10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	11	88	Total	C	H	N	O	S	0	0
			1358	417	686	128	121	6		

- Molecule 28 is a protein called DUF1713 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	22	33	Total	C	H	N	O	S	0	0
			661	187	359	70	44	1		

- Molecule 29 is a protein called IGR domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	33	193	Total	C	H	N	O	S	0	0
			3161	989	1607	295	268	2		

- Molecule 30 is a protein called Fe superoxide dismutase.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	44	260	Total	C	H	N	O	S	0	0
			4045	1318	1983	355	378	11		
30	55	232	Total	C	H	N	O	S	0	0
			3651	1195	1793	316	337	10		

- Molecule 31 is a protein called mS42.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	66	283	Total	C	H	N	O	S	0	0
			4629	1455	2330	425	415	4		

- Molecule 32 is a protein called mS46.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	77	179	Total	C	H	N	O	S	0	0
			2796	893	1396	227	277	3		

- Molecule 33 is a protein called 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	88	467	Total	C	H	N	O	S	0	0
			7327	2340	3650	634	691	12		

- Molecule 34 is a protein called mS47.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	00	48	Total	C	H	N	O		0	0
			823	252	417	77	77			
34	99	36	Total	C	H	N	O		0	0
			639	191	333	59	56			

- Molecule 35 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	aa	1435	Total	C	H	N	O	P	0	0
			45984	13712	15376	5486	9975	1435		

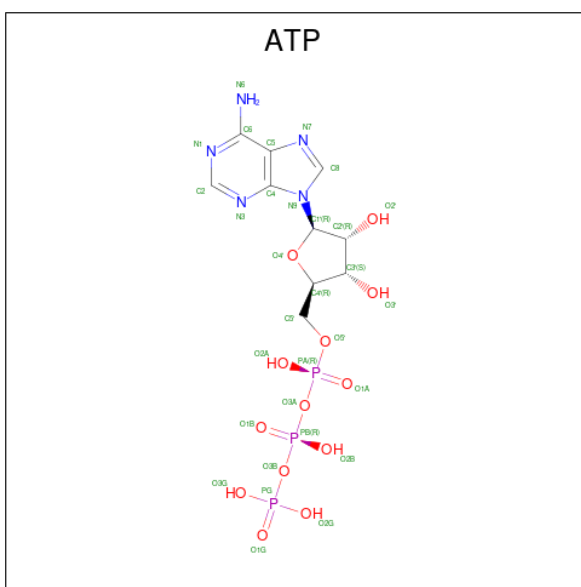
- Molecule 36 is a protein called IF1.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	43	Total	C	H	N	O	S	0	0
			641	206	309	56	69	1		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	BB	1	Total	Mg	0
			1	1	
37	KK	1	Total	Mg	0
			1	1	
37	QQ	1	Total	Mg	0
			1	1	
37	XX	1	Total	Mg	0
			1	1	
37	YY	1	Total	Mg	0
			1	1	
37	00	1	Total	Mg	0
			1	1	
37	aa	91	Total	Mg	0
			91	91	

- Molecule 38 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
38	XX	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

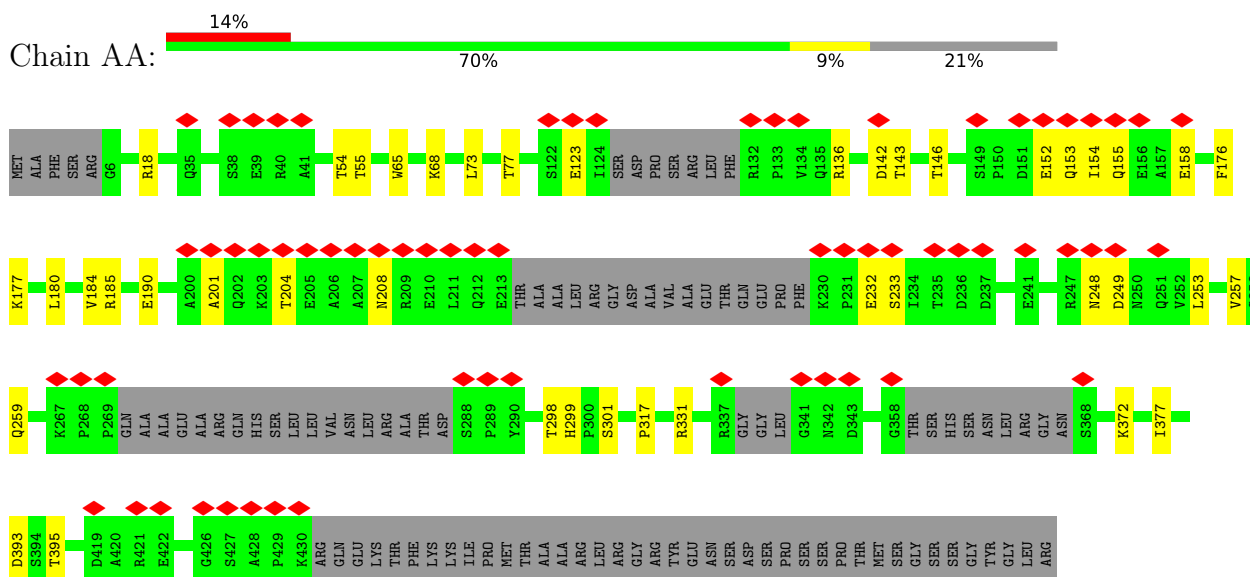
- Molecule 39 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
39	77	1	Total K 1 1	0
39	88	1	Total K 1 1	0
39	aa	20	Total K 20 20	0

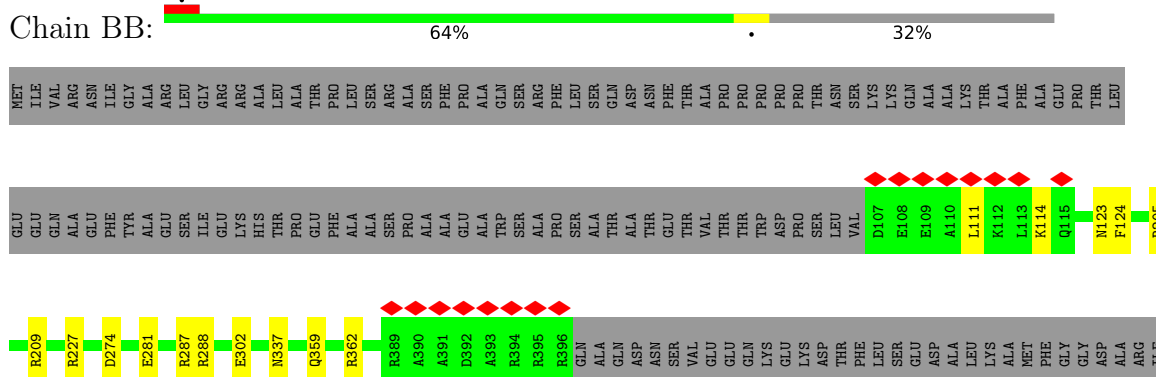
3 Residue-property plots

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.

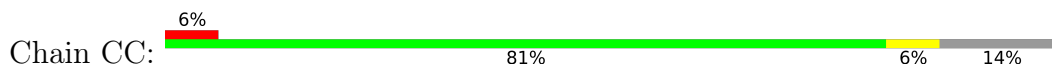
- Molecule 1: uS2m



- Molecule 2: Mito ribosomal protein S2



- Molecule 3: Ribosomal protein S5, mitochondrial



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

LYS
LEU
ALA
THR
ASN
PHE
ILE
GLY
LEU
ARG
ASP
THR
GLU
D263
N266
T267
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G343
N344
E345
G346
R347
R350
V356
L362
G376

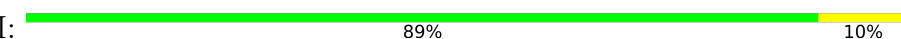
- Molecule 12: Mitochondrial 30S ribosomal protein S12

Chain LL:  68% 6% 26%

MET
ALA
THR
PHE
LEU
ARG
ASN
LEU
PHE
SER
GLN
ALA
GLN
PRO
SER
LEU
LEU
ARG
ARG
PRO
MET
PRO
SER
SER
SER
ILE
LEU
PRO
ALA
ALA
ALA
ARG
LEU
PHE
SER
SER
THR
PRO
ALA
GLN
ASN
A45
R59
A60
R61
V81
K90
R100
I109
I113

Q134
L143
L148
R160
K169
K170
A171
S172
VAL
GLY

- Molecule 13: 40S ribosomal protein S13

Chain MM:  89% 10%

MET
V2
N10
E11
Y23
G26
S30
I65
D68
R71
L95
R98
N113
G119

- Molecule 14: Mitochondrial 40S ribosomal protein MRP2

Chain NN:  87% 12%

MET
S2
L9
T15
D22
R26
A32
Q57
M63
T67
N74
R75
G80
R87
M91
I105
V113

- Molecule 15: Ribosomal protein S15

Chain OO:  6% 84% 14%

MET
PRO
PRO
ARG
LEU
PRO
GLY
PRO
GLN
GLY
ARG
LEU
SER
THR
CYS
LEU
ARG
PRO
ALA
VAL
ALA
SER
PRO
ALA
ALA
GLN
GLN
LEU
PRO
LEU
ILE
GLN
THR
ALA
ASN
I38
V62
T87
F90
S93
K106
VAL
GLY
PRO
ASP
GLY
GLN
LEU
V114
E115
E116
A152

E153
D154
R155
L156
T157
A158
D159
P160
E161
K162
E163
D164
R163
E188
R218
R235
R295
L320

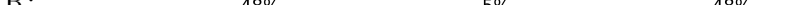
- Molecule 16: Ribosomal protein S16, mitochondrial

Chain PP:  84% 7% 8%

MET
V2
L5
V22
T48
K57
I70
L84
Q98
P99
ALA
GLN
GLU
GLN
LYS
THR
LYS
LYS
ALA

- Molecule 17: Mitochondrial 37S ribosomal protein S17

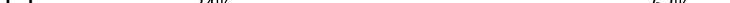
MET	A6	T9	L29	K44	Q47	L65	D69	V70	S80	K81	R84	V87	P93	A94	E100	R101	K121	K157	S160	L163	Q162	K163	VAL	ASP
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- Chain RR: 

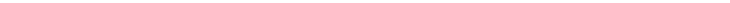
[illegible]

- Chain SS: 

Sequence logo for the 1000bp upstream region of the P26 promoter. The y-axis represents information content in bits, ranging from 0.00 to 0.25. The x-axis shows amino acid positions from MET to LYS. Red diamonds indicate positions with high information content (above 0.15 bits). These positions are P26, E27, P28, G29, K30, K31, R40, D63, L64, and K89. The background is color-coded: grey for positions MET to PHE, yellow for K9, P16, R40, D63, and L64, and green for P26 to K31 and K89.

- Chain TT: 

GLY	GLY	GLY	TYR	SER	SER	LYS	PRO	SER	PRO	MET	GLN	THR	TRP	ASN	GLU	THR	ASP	PHE	GLU	THR	ARG	HIS	PRO	Q149	Q150	E151	L152	M153	I154	R155	T160	H169	D171	L176	L179	W236																		
GLY	GLY	LEU	TYR	SER	SER	LYS	PRO	SER	PRO	MET	GLN	THR	TRP	ASN	GLU	THR	ASP	PHE	GLU	THR	ARG	HIS	PRO	PRO	Q149	Q150	E151	L152	M153	I154	R155	T160	H169	D171	L176	L179	W236																	
LEU	ASN	ASN	LYS	PRO	ALA	GLY	ALA	ALA	GLY	GLY	SER	SER	PRO	GLY	ALA	THR	ASP	ALA	SER	SER	ARG	ALA	PRO	ARG	PRO	THR	ASN	ASP	SER	TRP	SER	ILE	VAL	ASP	ALA	ILE	LYS	ASP	SER	ASN	SER	THR	THR	SER	SER	SER	SER	SER	SER	SER	ALA			
MET	GLU	LEU	ARG	SER	ALA	GLN	VAL	CYS	ARG	THR	THR	ALA	ALA	ALA	ALA	ALA	SER	SER	ALA	ALA	ARG	SER	SER	GLY	ALA	ALA	ALA	PHE	SER	THR	SER	ALA	ARG	PHE	GLN	LEU	GLN	PRO	PRO	ASN	PRO	PRO	TYR	VAL	SER	GLY	SER	ARG	ILE	GLU	THR	LEU	ARG	ALA

- Chain UU:  83% 7% 6% 11%

ALA	LEU	GLU	GLU	SER	GLU	ASP	LEU	LEU	ALA	GLN	ASN	MET	G2	K3	N23	I24	R89	I102	V114	E128	ARG	HIS	GLY	ASN	ASN	TRP	MET	LEU	THR	ARG	ILE	ALA	ASN	ASP	S129	R133	D150	M190	E193	M194	K195	T196	K201	E207	R210	Q211	E212	R215	A216	S217	M218	Y219	T220	N221	V222	V223	D224	N225
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	-----	-----	-----	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

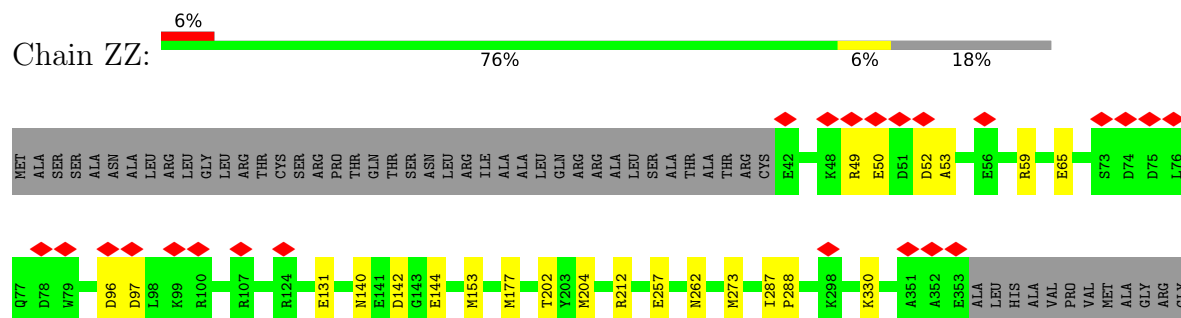
- 

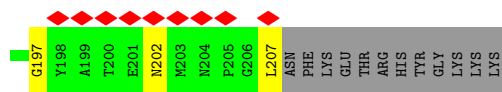
- Molecule 23: mS27

- Molecule 24: Mitochondrial ribosomal protein DAP3

- Molecule 25: mS33

- Molecule 26: 37S ribosomal protein S24, mitochondrial





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	131806	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	49.868	Depositor
Minimum map value	-22.282	Depositor
Average map value	0.002	Depositor
Map value standard deviation	1.102	Depositor
Recommended contour level	3.74	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, K, 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	AA	0.09	0/2948	0.23	0/3995
2	BB	0.10	0/2314	0.26	0/3142
3	CC	0.10	0/3713	0.22	0/4978
4	DD	0.10	0/2409	0.25	0/3255
5	EE	0.10	0/2929	0.24	0/3947
6	FF	0.11	0/953	0.26	0/1285
7	GG	0.09	0/1766	0.25	0/2392
8	HH	0.11	0/1260	0.27	0/1707
9	II	0.10	0/2013	0.24	0/2720
10	JJ	0.11	0/1590	0.27	0/2140
11	KK	0.10	0/1015	0.27	0/1357
12	LL	0.11	0/973	0.29	0/1305
13	MM	0.10	0/951	0.28	0/1274
14	NN	0.12	0/930	0.26	0/1243
15	OO	0.10	0/2243	0.25	0/3016
16	PP	0.11	0/806	0.25	0/1096
17	QQ	0.09	0/1268	0.24	0/1701
18	RR	0.11	0/1105	0.25	0/1491
19	SS	0.10	0/667	0.23	0/902
20	TT	0.12	0/762	0.27	0/1015
21	UU	0.10	0/1890	0.26	0/2554
22	VV	0.09	0/2121	0.24	0/2851
23	WW	0.09	0/2898	0.24	0/3911
24	XX	0.09	0/3235	0.24	0/4374
25	YY	0.10	0/797	0.30	0/1070
26	ZZ	0.09	0/2645	0.22	0/3566
27	11	0.10	0/686	0.25	0/929
28	22	0.13	0/302	0.29	0/388
29	33	0.11	0/1589	0.26	0/2140
30	44	0.08	0/2121	0.22	0/2879
30	55	0.08	0/1912	0.21	0/2600
31	66	0.09	0/2349	0.24	0/3163

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	77	0.09	0/1431	0.19	0/1934
33	88	0.09	0/3760	0.23	0/5085
34	00	0.08	0/409	0.18	0/540
34	99	0.08	0/307	0.17	0/405
35	aa	0.10	0/34270	0.17	0/53383
36	V	0.08	0/336	0.22	0/452
All	All	0.10	0/95673	0.22	0/136185

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	AA	2883	2907	2907	36	0
2	BB	2269	2301	2301	11	0
3	CC	3642	3897	3897	22	0
4	DD	2343	2373	2373	24	0
5	EE	2881	2918	2918	10	0
6	FF	936	966	966	4	0
7	GG	1725	1799	1799	12	0
8	HH	1236	1286	1286	9	0
9	II	1969	2026	2026	15	0
10	JJ	1551	1554	1554	13	0
11	KK	995	1025	1025	9	0
12	LL	959	1032	1032	8	0
13	MM	938	987	986	6	0
14	NN	915	961	961	10	0
15	OO	2199	2230	2230	7	0
16	PP	786	826	826	6	0
17	QQ	1247	1314	1314	12	0
18	RR	1080	1089	1089	9	0
19	SS	648	677	677	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	TT	747	772	772	8	0
21	UU	1844	1842	1842	13	0
22	VV	2081	2112	2112	18	0
23	WW	2844	2901	2900	12	0
24	XX	3176	3271	3271	13	0
25	YY	786	823	823	7	0
26	ZZ	2586	2528	2528	18	0
27	11	672	686	686	4	0
28	22	302	359	359	4	0
29	33	1554	1607	1607	7	0
30	44	2062	1983	1982	15	0
30	55	1858	1793	1793	13	0
31	66	2299	2330	2330	13	0
32	77	1400	1396	1396	2	0
33	88	3677	3650	3650	24	0
34	00	406	417	417	1	0
34	99	306	333	333	0	0
35	aa	30608	15376	15374	116	0
36	V	332	309	309	7	0
37	00	1	0	0	0	0
37	BB	1	0	0	0	0
37	KK	1	0	0	0	0
37	QQ	1	0	0	0	0
37	XX	1	0	0	0	0
37	YY	1	0	0	0	0
37	aa	91	0	0	0	0
38	XX	31	12	12	1	0
39	77	1	0	0	0	0
39	88	1	0	0	0	0
39	aa	20	0	0	0	0
All	All	90892	76668	76663	416	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.

The worst 5 of 416 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:BB:359:GLN:OE1	2:BB:362:ARG:NH2	2.11	0.84
24:XX:152:ARG:NH1	24:XX:415:LYS:O	2.12	0.82
26:ZZ:212:ARG:NH1	26:ZZ:257:GLU:OE1	2.12	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:88:409:GLU:N	33:88:409:GLU:OE1	2.13	0.82
35:aa:1039:U:O2'	35:aa:1040:A:O4'	1.95	0.82

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	AA	360/470 (77%)	355 (99%)	5 (1%)	0	100	100
2	BB	288/428 (67%)	285 (99%)	3 (1%)	0	100	100
3	CC	432/508 (85%)	425 (98%)	7 (2%)	0	100	100
4	DD	286/453 (63%)	282 (99%)	4 (1%)	0	100	100
5	EE	363/477 (76%)	358 (99%)	5 (1%)	0	100	100
6	FF	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
7	GG	221/309 (72%)	218 (99%)	3 (1%)	0	100	100
8	HH	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
9	II	245/315 (78%)	242 (99%)	3 (1%)	0	100	100
10	JJ	186/268 (69%)	181 (97%)	5 (3%)	0	100	100
11	KK	122/376 (32%)	118 (97%)	4 (3%)	0	100	100
12	LL	126/174 (72%)	119 (94%)	7 (6%)	0	100	100
13	MM	116/119 (98%)	112 (97%)	4 (3%)	0	100	100
14	NN	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
15	OO	272/320 (85%)	266 (98%)	6 (2%)	0	100	100
16	PP	96/107 (90%)	94 (98%)	2 (2%)	0	100	100
17	QQ	156/165 (94%)	155 (99%)	1 (1%)	0	100	100
18	RR	132/256 (52%)	130 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	SS	79/91 (87%)	78 (99%)	1 (1%)	0	100	100
20	TT	86/236 (36%)	85 (99%)	1 (1%)	0	100	100
21	UU	222/253 (88%)	219 (99%)	3 (1%)	0	100	100
22	VV	255/316 (81%)	253 (99%)	2 (1%)	0	100	100
23	WW	349/396 (88%)	345 (99%)	4 (1%)	0	100	100
24	XX	404/469 (86%)	399 (99%)	5 (1%)	0	100	100
25	YY	97/108 (90%)	95 (98%)	2 (2%)	0	100	100
26	ZZ	310/382 (81%)	309 (100%)	1 (0%)	0	100	100
27	11	86/90 (96%)	85 (99%)	1 (1%)	0	100	100
28	22	31/344 (9%)	31 (100%)	0	0	100	100
29	33	191/236 (81%)	189 (99%)	2 (1%)	0	100	100
30	44	258/310 (83%)	253 (98%)	5 (2%)	0	100	100
30	55	228/310 (74%)	222 (97%)	6 (3%)	0	100	100
31	66	281/348 (81%)	279 (99%)	2 (1%)	0	100	100
32	77	177/414 (43%)	176 (99%)	1 (1%)	0	100	100
33	88	465/508 (92%)	452 (97%)	13 (3%)	0	100	100
34	00	46/95 (48%)	46 (100%)	0	0	100	100
34	99	34/95 (36%)	34 (100%)	0	0	100	100
36	V	39/219 (18%)	36 (92%)	3 (8%)	0	100	100
All	All	7422/10356 (72%)	7303 (98%)	119 (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	AA	314/393 (80%)	314 (100%)	0	100	100
2	BB	237/347 (68%)	236 (100%)	1 (0%)	84	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CC	405/461 (88%)	404 (100%)	1 (0%)	87	95
4	DD	242/377 (64%)	242 (100%)	0	100	100
5	EE	308/392 (79%)	308 (100%)	0	100	100
6	FF	99/99 (100%)	99 (100%)	0	100	100
7	GG	186/260 (72%)	186 (100%)	0	100	100
8	HH	134/135 (99%)	134 (100%)	0	100	100
9	II	206/263 (78%)	205 (100%)	1 (0%)	81	90
10	JJ	166/227 (73%)	166 (100%)	0	100	100
11	KK	108/324 (33%)	108 (100%)	0	100	100
12	LL	103/142 (72%)	103 (100%)	0	100	100
13	MM	98/99 (99%)	97 (99%)	1 (1%)	68	83
14	NN	96/97 (99%)	96 (100%)	0	100	100
15	OO	230/265 (87%)	230 (100%)	0	100	100
16	PP	85/92 (92%)	85 (100%)	0	100	100
17	QQ	132/138 (96%)	131 (99%)	1 (1%)	73	86
18	RR	118/218 (54%)	117 (99%)	1 (1%)	73	86
19	SS	70/80 (88%)	70 (100%)	0	100	100
20	TT	75/191 (39%)	75 (100%)	0	100	100
21	UU	193/218 (88%)	193 (100%)	0	100	100
22	VV	224/268 (84%)	224 (100%)	0	100	100
23	WW	300/333 (90%)	300 (100%)	0	100	100
24	XX	345/391 (88%)	345 (100%)	0	100	100
25	YY	83/89 (93%)	83 (100%)	0	100	100
26	ZZ	278/328 (85%)	277 (100%)	1 (0%)	84	92
27	11	73/75 (97%)	73 (100%)	0	100	100
28	22	33/293 (11%)	33 (100%)	0	100	100
29	33	163/195 (84%)	163 (100%)	0	100	100
30	44	215/250 (86%)	215 (100%)	0	100	100
30	55	195/250 (78%)	193 (99%)	2 (1%)	68	83
31	66	245/303 (81%)	245 (100%)	0	100	100
32	77	153/304 (50%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	88	388/419 (93%)	388 (100%)	0	100	100
34	00	43/78 (55%)	43 (100%)	0	100	100
34	99	34/78 (44%)	34 (100%)	0	100	100
36	V	33/170 (19%)	33 (100%)	0	100	100
All	All	6410/8642 (74%)	6401 (100%)	9 (0%)	87	95

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	55	93	GLN
30	55	237	ASN
13	MM	65	ILE
17	QQ	29	ILE
18	RR	175	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
24	XX	194	HIS
33	88	365	HIS
25	YY	10	GLN
30	55	181	GLN
9	II	160	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	aa	1430/1864 (76%)	174 (12%)	0

5 of 174 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	aa	49	U
35	aa	51	G
35	aa	54	G
35	aa	67	G
35	aa	77	A

There are no RNA pucker outliers to report.

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 120 ligands modelled in this entry, 119 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
38	ATP	XX	501	37	32,33,33	2.41	6 (18%)	48,52,52	1.79	9 (18%)

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
38	ATP	XX	501	37	-	2/22/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	XX	501	ATP	C2'-C1'	-8.02	1.28	1.53
38	XX	501	ATP	PB-O3A	5.55	1.65	1.59
38	XX	501	ATP	PA-O3A	5.53	1.65	1.59
38	XX	501	ATP	PB-O3B	5.04	1.64	1.59
38	XX	501	ATP	C8-N9	-2.33	1.33	1.37

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	XX	501	ATP	C4-N9-C8	5.81	111.84	105.74
38	XX	501	ATP	N9-C8-N7	-5.00	106.84	113.94
38	XX	501	ATP	C5-C4-N3	-4.39	120.67	126.72
38	XX	501	ATP	N3-C4-N9	4.31	134.49	127.17
38	XX	501	ATP	C5-N7-C8	3.36	108.73	103.45

There are no chirality outliers.

All (2) torsion outliers are listed below:

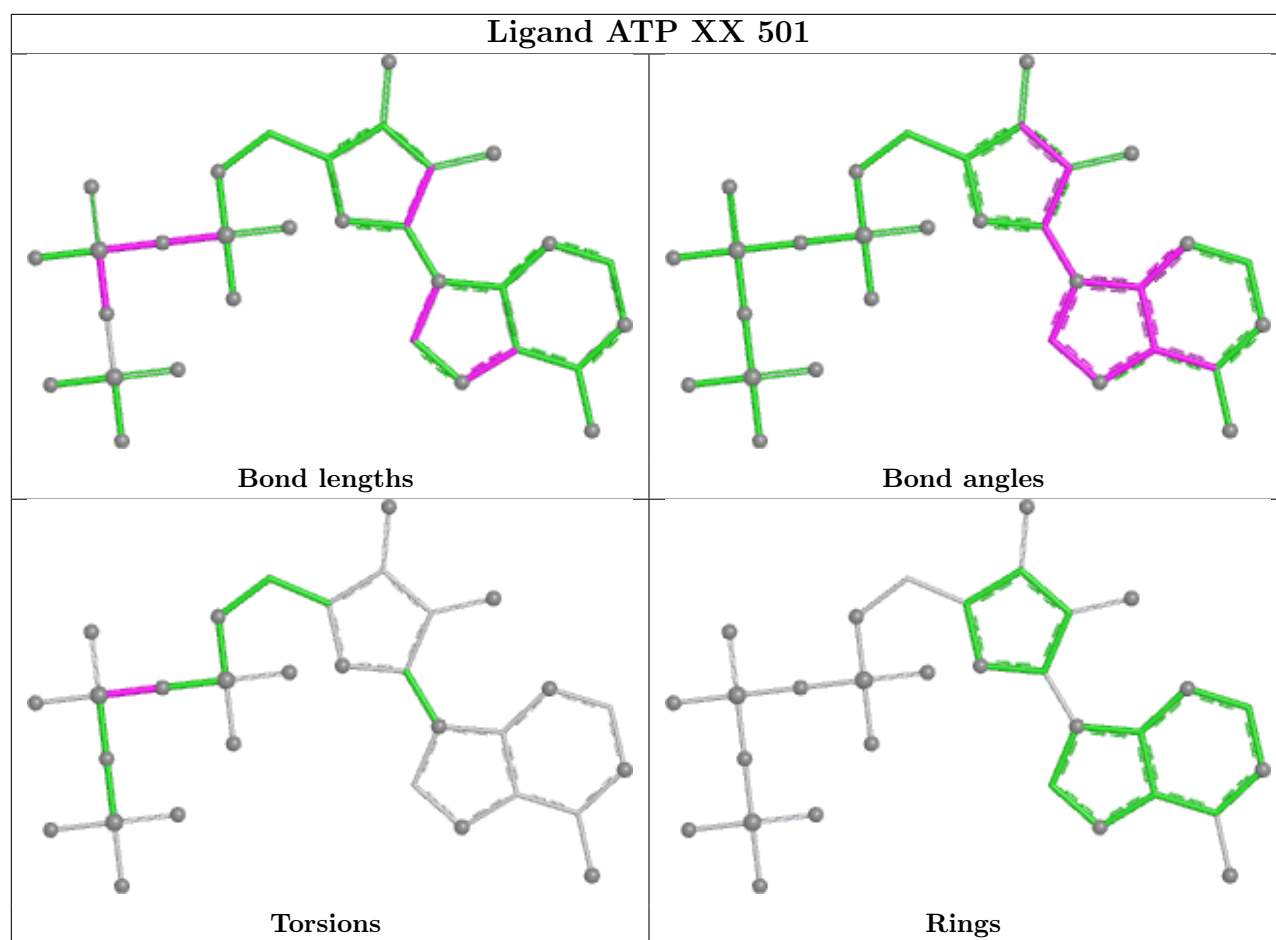
Mol	Chain	Res	Type	Atoms
38	XX	501	ATP	PA-O3A-PB-O2B
38	XX	501	ATP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	XX	501	ATP	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

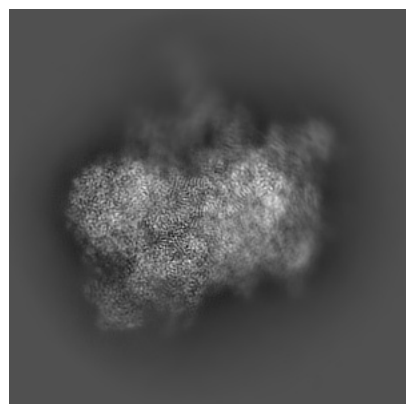
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10958. These allow visual inspection of the internal detail of the map and identification of artifacts.

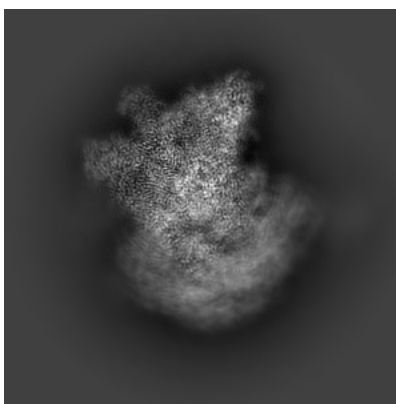
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

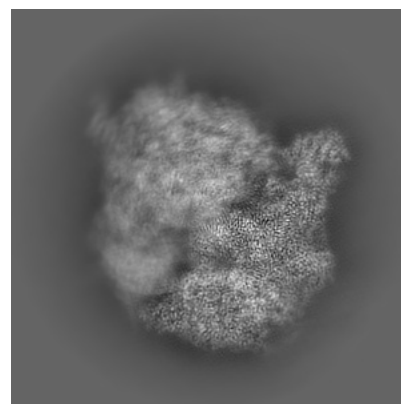
6.1.1 Primary map



X

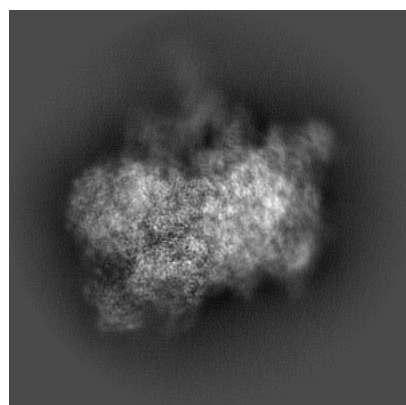


Y

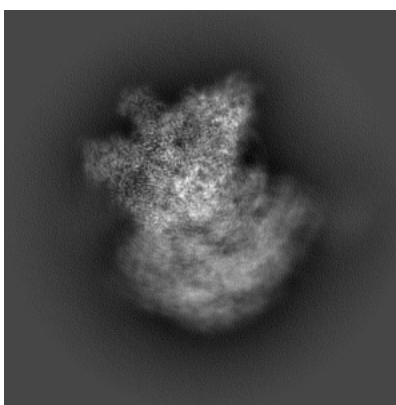


Z

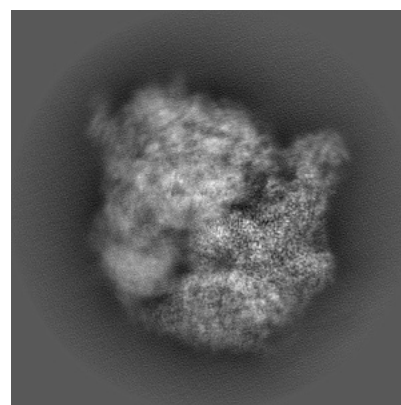
6.1.2 Raw map



X



Y

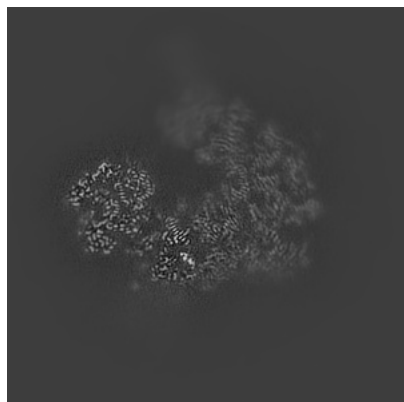


Z

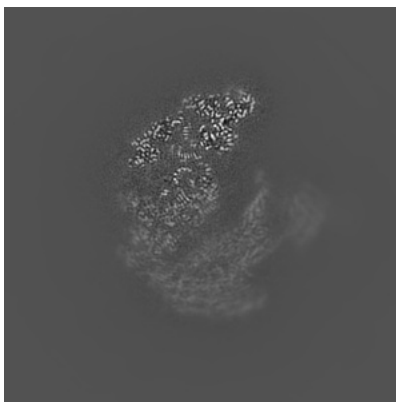
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

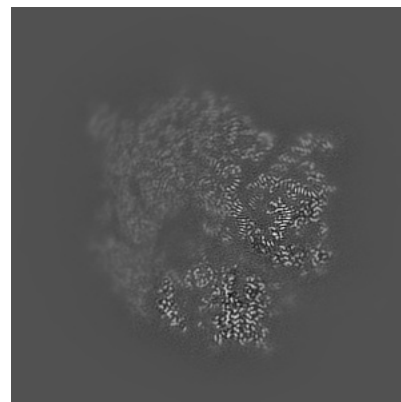
6.2.1 Primary map



X Index: 200

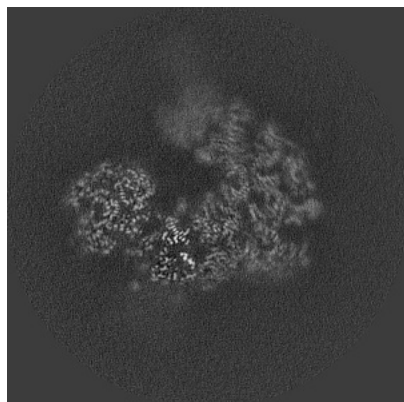


Y Index: 200

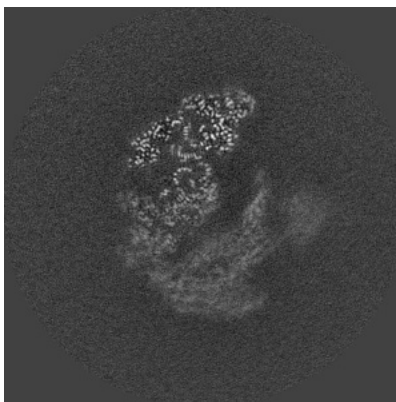


Z Index: 200

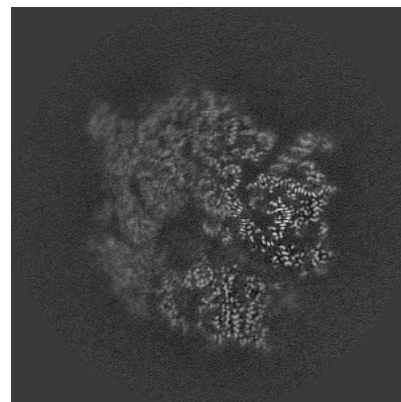
6.2.2 Raw map



X Index: 200



Y Index: 200

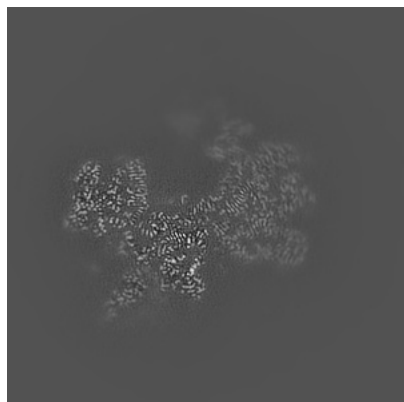


Z Index: 200

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

6.3 Largest variance slices [i](#)

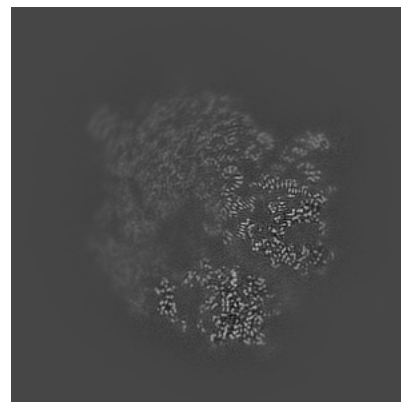
6.3.1 Primary map



X Index: 225

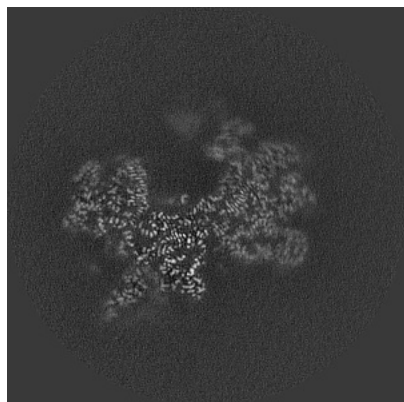


Y Index: 181

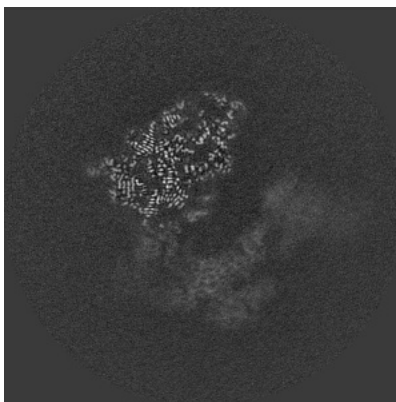


Z Index: 202

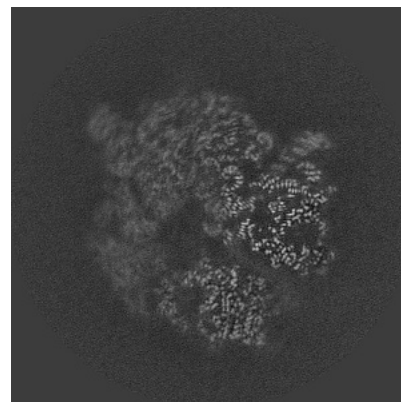
6.3.2 Raw map



X Index: 225



Y Index: 181

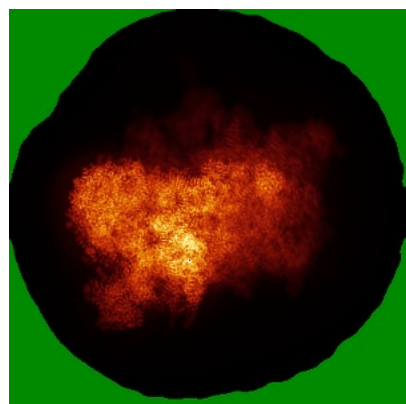


Z Index: 202

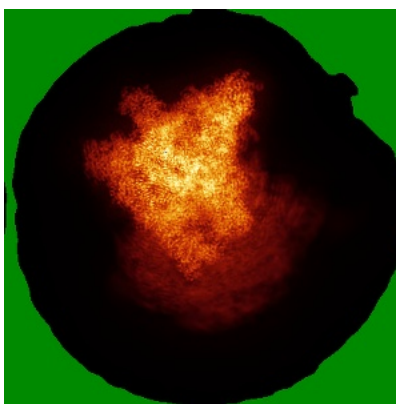
The images above show the largest variance slices of the map in three orthogonal directions.

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

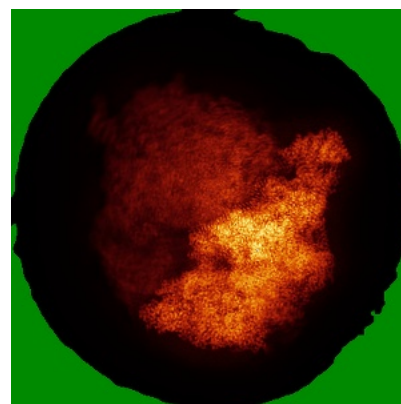
6.4.1 Primary map



X

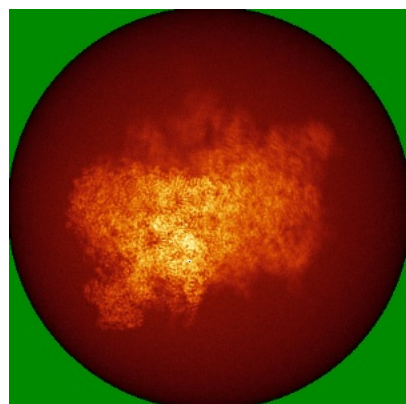


Y

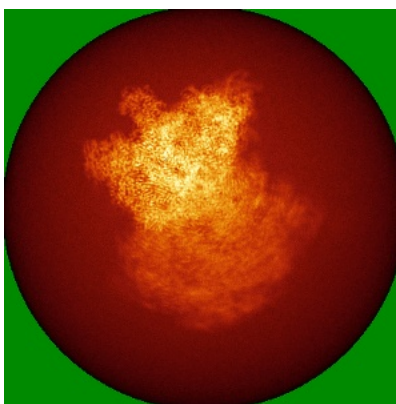


Z

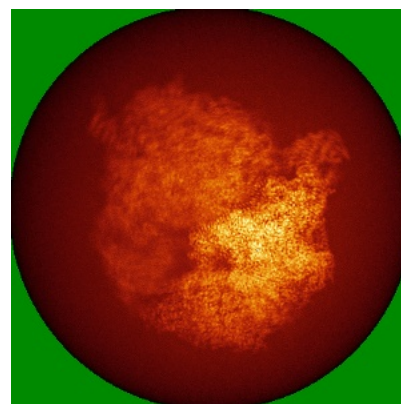
6.4.2 Raw map



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](#)

This section was not generated.

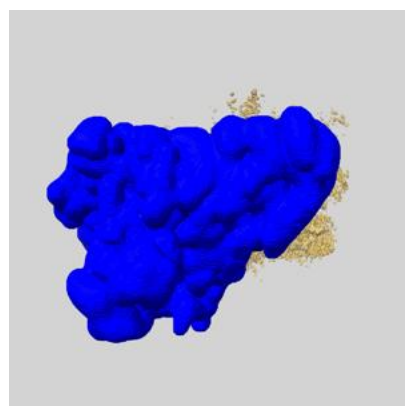
6.6 Mask visualisation [i](#)

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

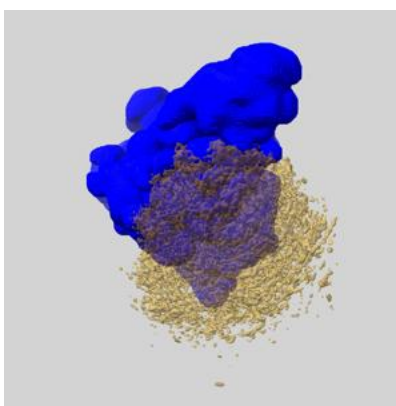
A mask typically either:

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

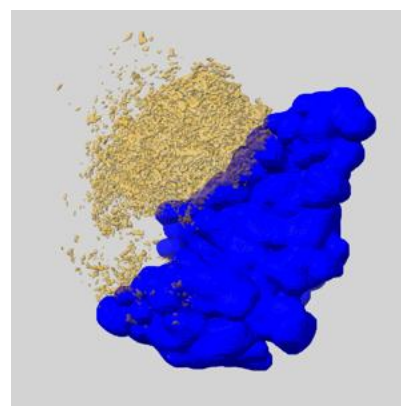
6.6.1 emd_10958_msk_1.map [i](#)



X



Y

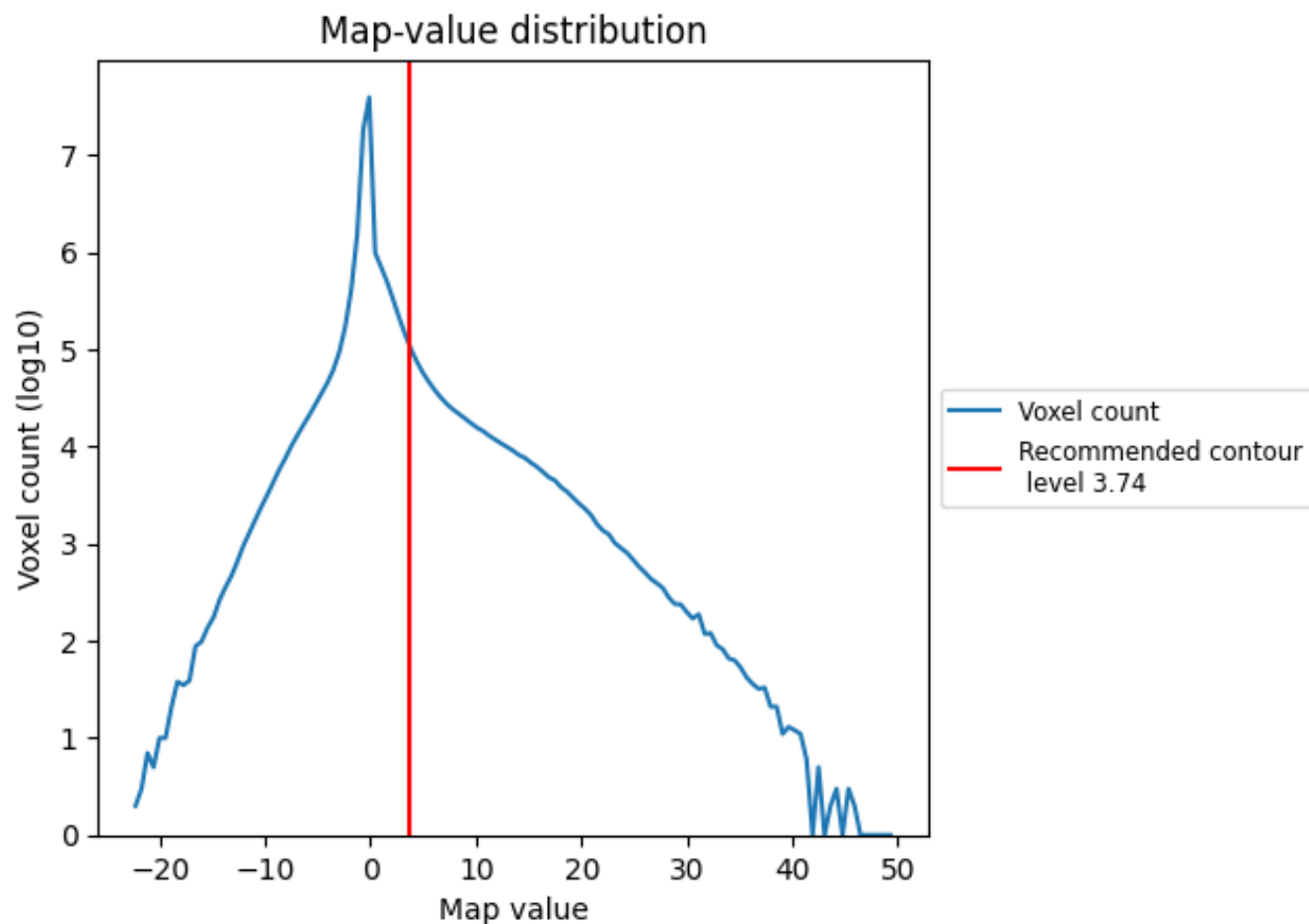


Z

7 Map analysis [i](#)

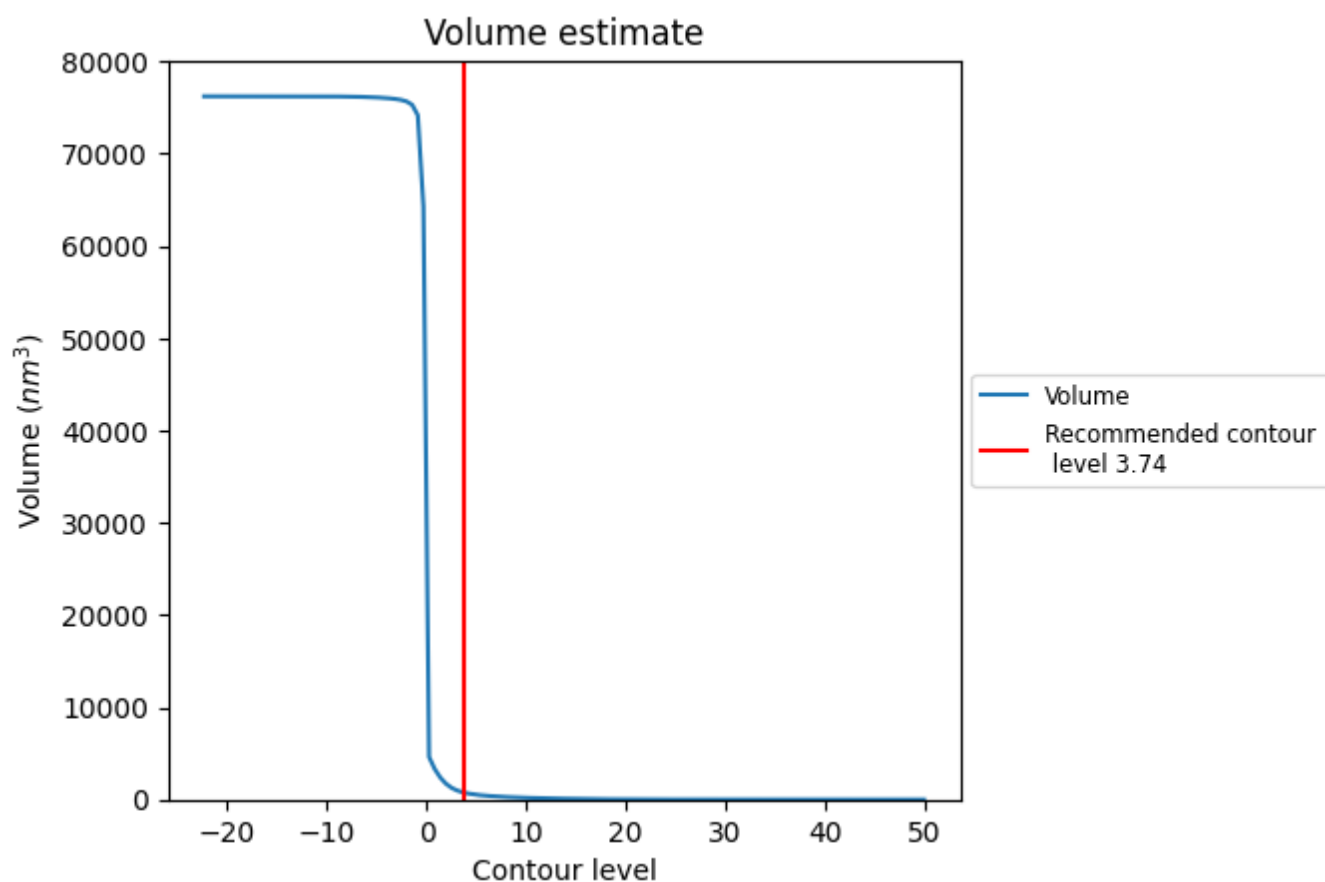
This section contains the results of statistical analysis of the map.

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.

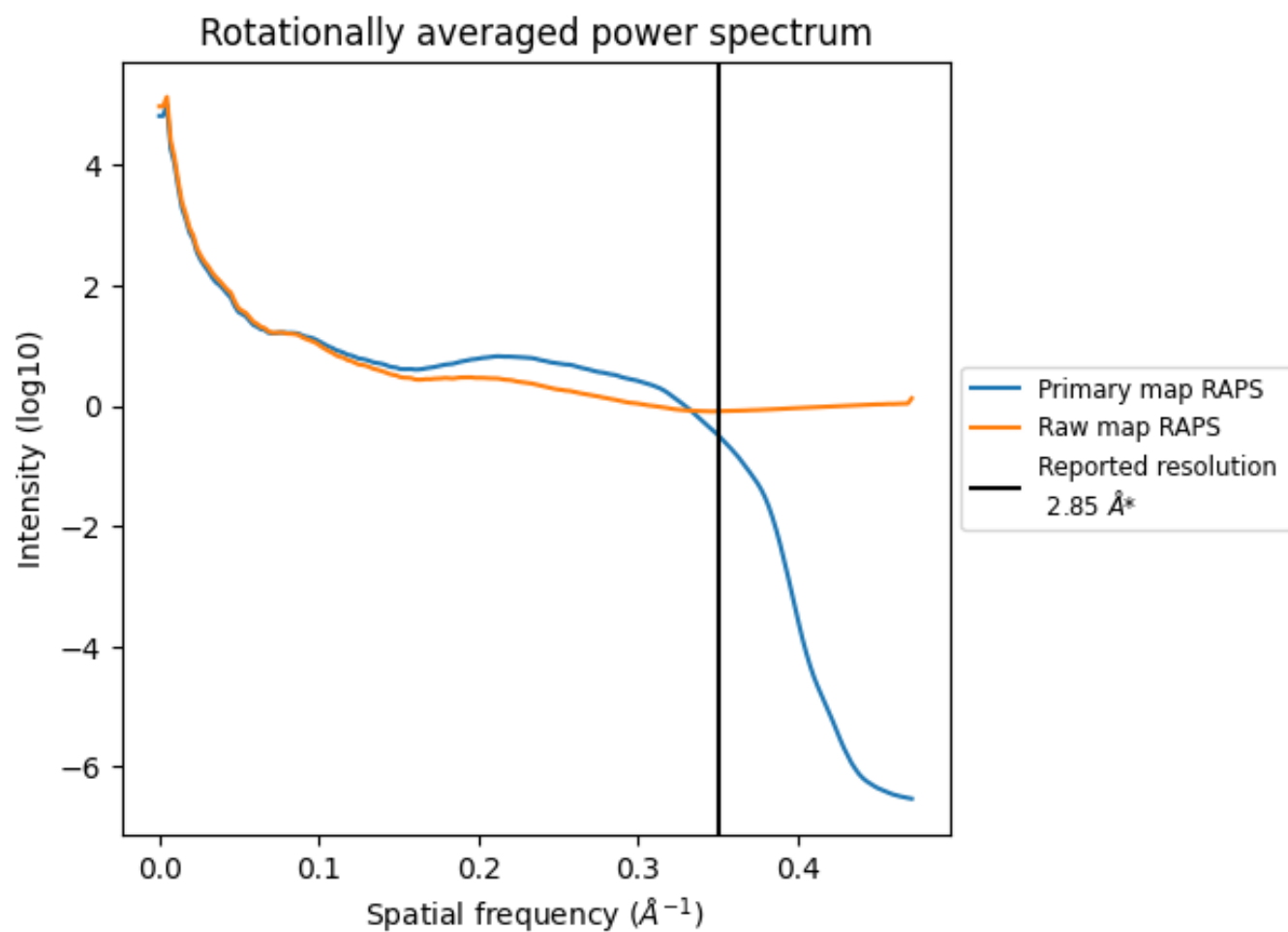
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 765 nm³; this corresponds to an approximate mass of 691 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 ⓘ

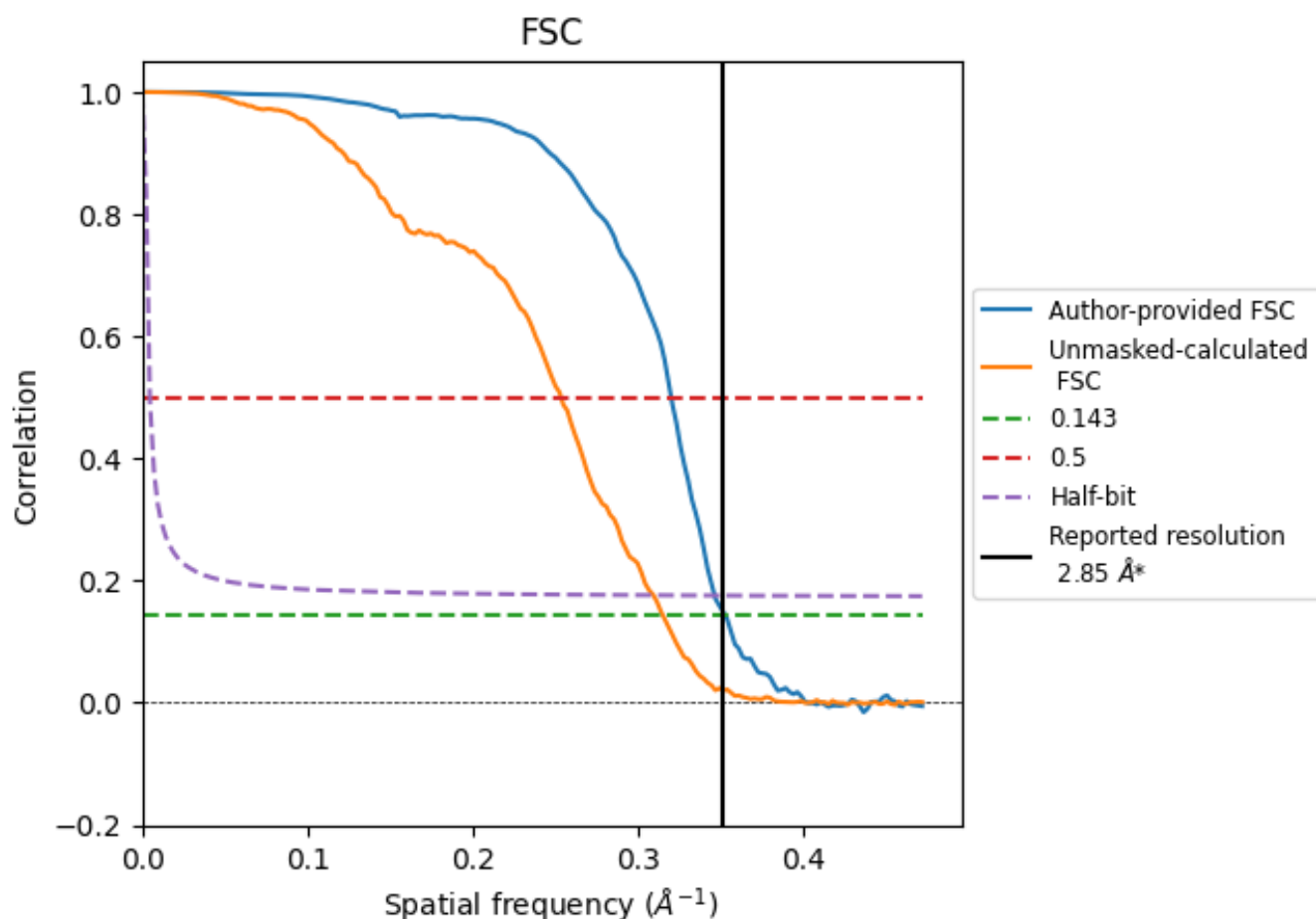


*Reported resolution corresponds to spatial frequency of $0.351 \text{ \AA}^{-1}$

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 0.351 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.84	3.13	2.89
Unmasked-calculated*	3.18	3.95	3.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.18 differs from the reported value 2.85 by more than 10 %

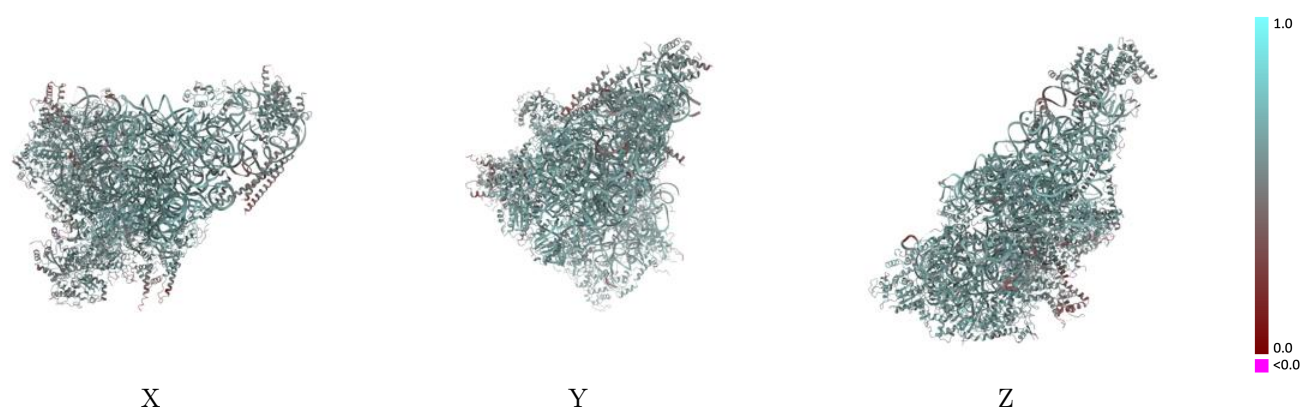
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10958 and PDB model 6YW5. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)

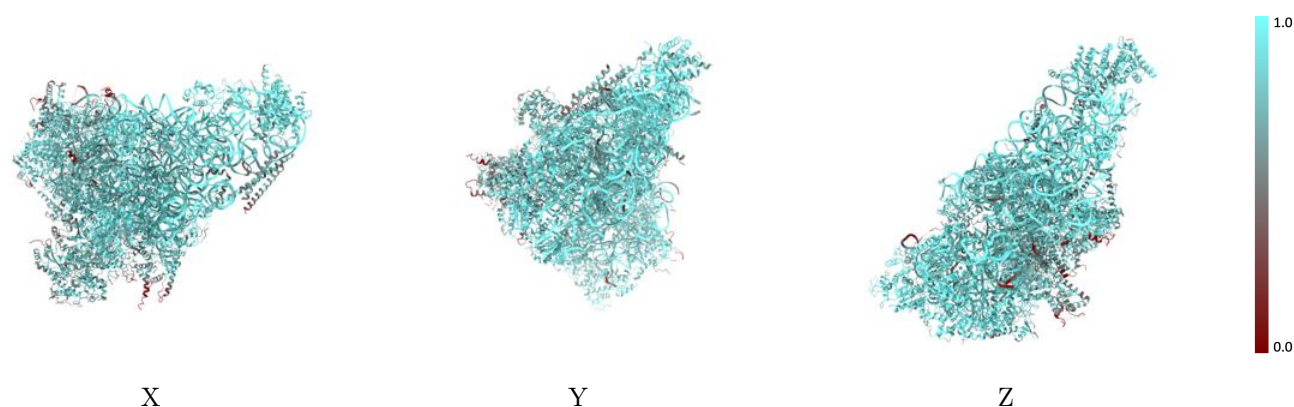
This section was not generated.

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



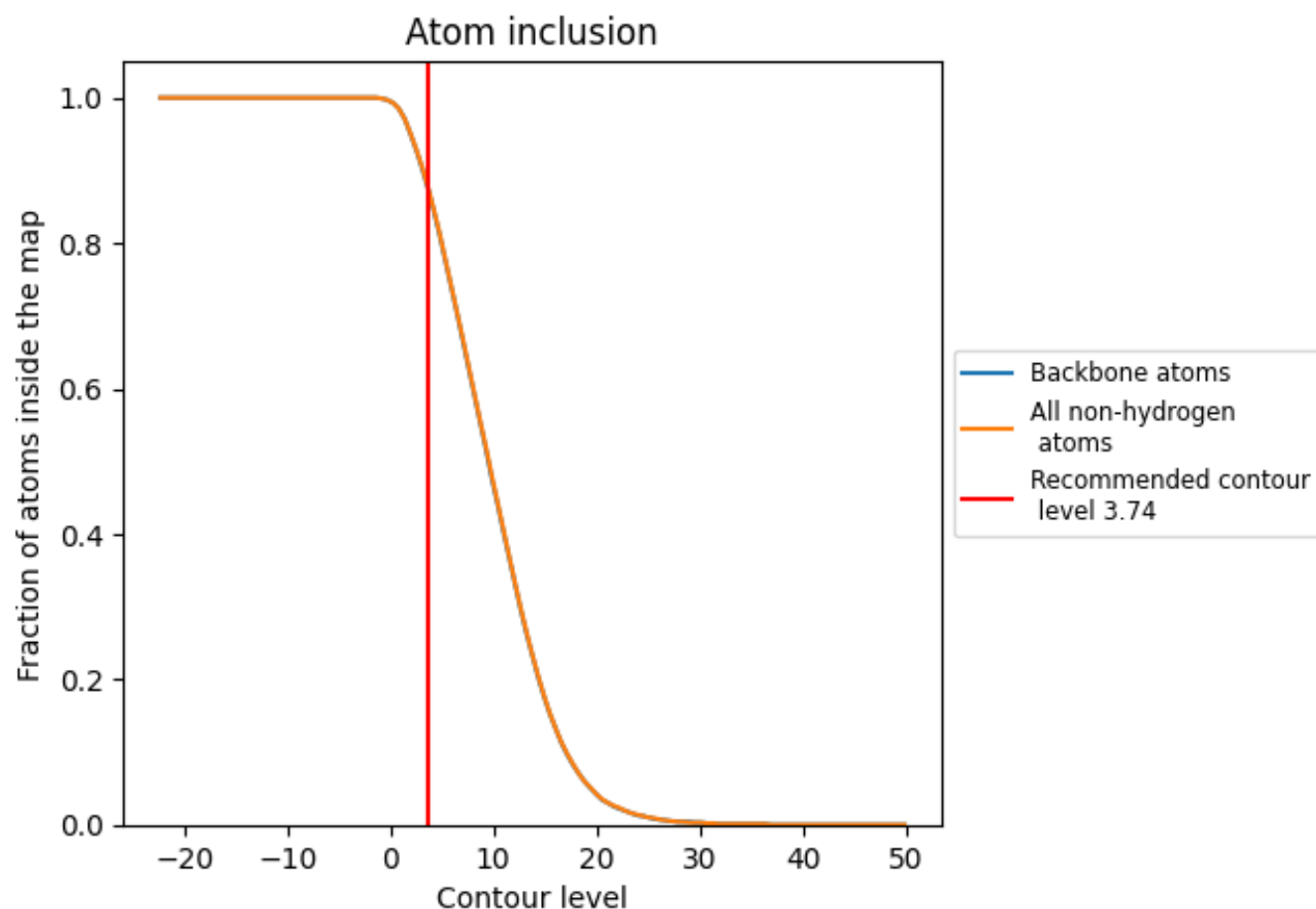
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.74).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (3.74) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.5920
00	 0.6670	 0.4860
11	 0.8020	 0.5780
22	 0.8950	 0.6220
33	 0.8840	 0.5730
44	 0.7460	 0.5390
55	 0.7080	 0.5290
66	 0.8400	 0.5910
77	 0.8650	 0.5860
88	 0.8100	 0.5720
99	 0.5300	 0.4110
AA	 0.7000	 0.5410
BB	 0.8560	 0.6010
CC	 0.8360	 0.5770
DD	 0.8610	 0.6040
EE	 0.8610	 0.5970
FF	 0.9100	 0.6270
GG	 0.8410	 0.5760
HH	 0.9260	 0.6370
II	 0.8610	 0.5820
JJ	 0.9300	 0.6160
KK	 0.9090	 0.6190
LL	 0.9010	 0.6170
MM	 0.9140	 0.6030
NN	 0.9610	 0.6370
OO	 0.8320	 0.5920
PP	 0.9160	 0.6250
QQ	 0.8340	 0.5910
RR	 0.7730	 0.5670
SS	 0.8630	 0.5930
TT	 0.8870	 0.6300
UU	 0.8320	 0.5920
V	 0.5760	 0.5110
VV	 0.7700	 0.5670
WW	 0.8880	 0.5500



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Chain	Atom inclusion	Q-score
XX	 0.9000	 0.5870
YY	 0.8760	 0.5980
ZZ	 0.7970	 0.5470
aa	 0.9500	 0.6150