



## wwPDB EM Validation Summary Report ⓘ

Jan 1, 2025 – 12:54 AM EST

PDB ID : 8RJC  
EMDB ID : EMD-19197  
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD rhodopsin intermediate in complex with Sec61-TRAP, open conformation 1  
Authors : Lewis, A.J.O.; Hegde, R.S.  
Deposited on : 2023-12-20  
Resolution : 2.90 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](mailto: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>.

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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

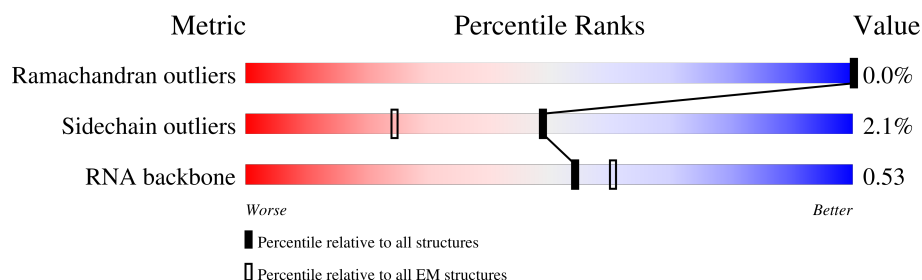
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 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.



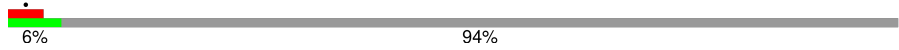
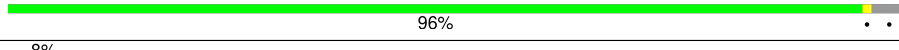
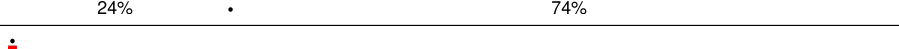
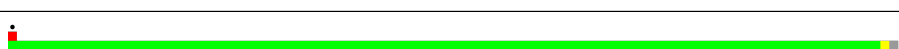

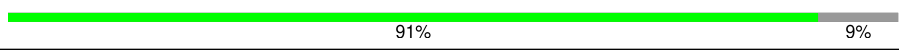

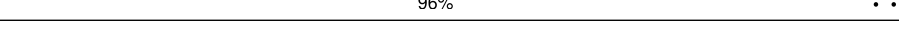
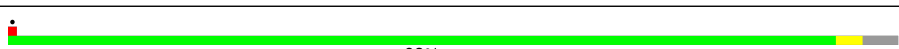

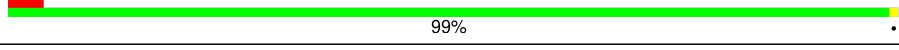
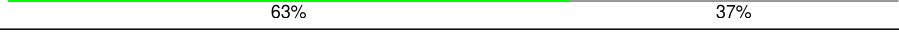
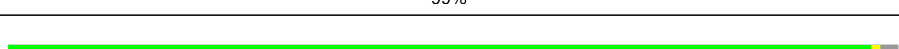
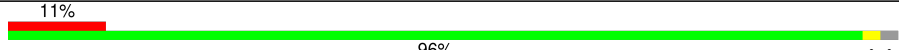
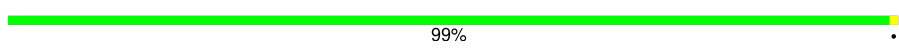

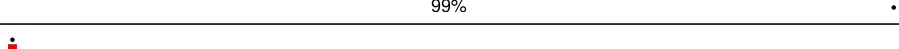

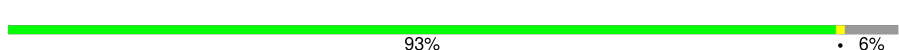





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	1	476	<div> <div>17%</div> <div>95%</div> </div>
2	2	96	<div> <div>31%</div> <div>67%</div> </div>
3	3	68	<div> <div>87%</div> <div>10%</div> </div>
4	4	66	<div> <div>14%</div> <div>47%</div> <div>53%</div> </div>
5	5	286	<div> <div>49%</div> <div>61%</div> <div>38%</div> </div>
6	6	183	<div> <div>75%</div> <div>87%</div> <div>11%</div> </div>
7	7	185	<div> <div>42%</div> <div>94%</div> </div>
8	8	173	<div> <div>75%</div> <div>87%</div> <div>13%</div> </div>


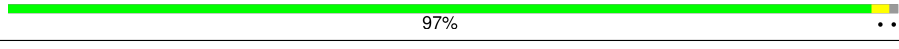
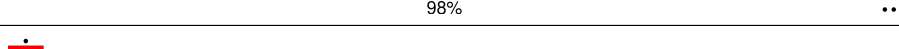
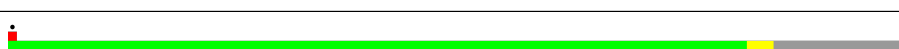

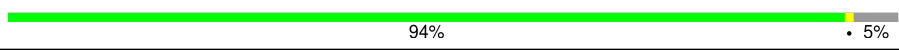
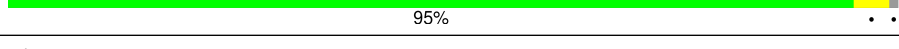
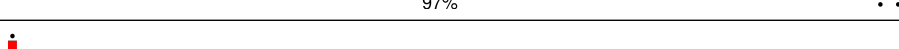
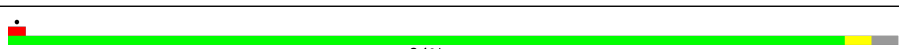

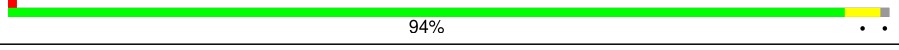
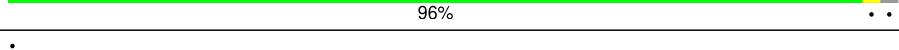
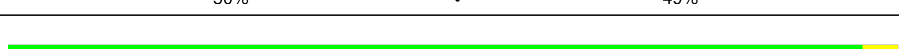
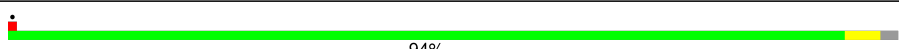
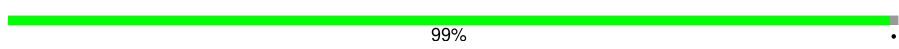

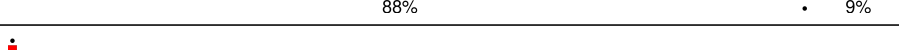

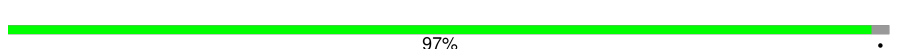




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Mol	Chain	Length	Quality of chain
9	9	593	
10	A	257	
11	B	229	
12	C	425	
13	D	297	
14	E	291	
15	F	247	
16	G	319	
17	H	192	
18	I	214	
19	J	178	
20	K	3543	
21	L	211	
22	M	218	
23	N	204	
24	O	203	
25	P	184	
26	Q	187	
27	R	196	
28	S	176	
29	T	160	
30	U	128	
31	V	140	
32	W	157	
33	X	156	

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Mol	Chain	Length	Quality of chain
34	Y	145	
35	Z	136	
36	a	148	
37	b	226	
38	c	115	
39	d	125	
40	e	135	
41	f	110	
42	g	116	
43	h	123	
44	i	105	
45	j	97	
46	k	70	
47	l	51	
48	m	102	
49	n	25	
50	o	106	
51	p	92	
52	q	76	
53	r	137	
54	u	120	
55	v	156	
56	w	403	

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 255550 atoms, of which 108756 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 Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
1	1	461	Total	C	H	N	O	S	0	0
			7275	2347	3700	576	629	23		

- Molecule 2 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	2	32	Total	C	H	N	O	S	0	0
			524	171	273	40	38	2		

- Molecule 3 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace	
3	3	66	Total	C	H	N	O	S	0	0
			1105	351	571	92	86	5		

- Molecule 4 is a protein called Stress-associated endoplasmic reticulum protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
4	4	31	Total	C	H	N	O	S	0	0
			504	145	260	55	43	1		

- Molecule 5 is a protein called Translocon-associated protein subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace	
5	5	178	Total	C	H	N	O	S	0	0
			2813	919	1390	231	269	4		

- Molecule 6 is a protein called Translocon-associated protein subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace	
6	6	162	Total	C	H	N	O	S	0	0
			2507	813	1244	212	236	2		

- Molecule 7 is a protein called Translocon-associated protein subunit gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	7	179	Total	C	H	N	O	S	0	0
			2942	947	1490	239	263	3		

- Molecule 8 is a protein called Translocon-associated protein subunit delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	8	150	Total	C	H	N	O	S	0	0
			2335	755	1149	199	229	3		

- Molecule 9 is a protein called Calnexin.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	9	38	Total	C	H	N	O	S	0	0
			610	206	309	43	50	2		

- Molecule 10 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	248	Total	C	H	N	O	S	0	0
			3892	1189	1994	389	314	6		

- Molecule 11 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	B	59	Total	C	H	N	O	S	0	0
			856	283	424	67	80	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	C	362	Total	C	H	N	O	S	0	0
			5937	1812	3054	577	480	14		

- Molecule 13 is a protein called Ribosomal\_L18\_c domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	D	293	Total	C	H	N	O	S	0	0
			4816	1512	2425	438	427	14		

- Molecule 14 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	E	223	Total	C	H	N	O	S	0	0
			3754	1154	1963	341	293	3		

- Molecule 15 is a protein called Ribosomal Protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	F	225	Total	C	H	N	O	S	0	0
			3872	1205	1997	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	G	233	Total	C	H	N	O	S	0	0
			3908	1199	2029	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 17 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	H	190	Total	C	H	N	O	S	0	0
			3114	954	1598	284	272	6		

- Molecule 18 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	I	205	Total	C	H	N	O	S	0	0
			3380	1056	1716	321	274	13		

- Molecule 19 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	J	170	Total	C	H	N	O	S	0	0
			2763	861	1401	254	241	6		

- Molecule 20 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	K	3543	Total	C	H	N	O	P	0	0
			114335	33833	38363	13910	24686	3543		

- Molecule 21 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	L	210	Total	C	H	N	O	S	0	0
			3525	1065	1823	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 22 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	M	138	Total	C	H	N	O	S	0	0
			2349	727	1212	221	182	7		

- Molecule 23 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	N	203	Total	C	H	N	O	S	0	0
			3454	1072	1753	359	266	4		

- Molecule 24 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	O	199	Total	C	H	N	O	S	0	0
			3410	1051	1780	319	255	5		

- Molecule 25 is a protein called uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	P	181	Total	C	H	N	O	S	0	0
			3012	924	1542	282	254	10		

- Molecule 26 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Q	187	Total	C	H	N	O	S	0	0
			3153	946	1638	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 27 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	R	155	Total	C	H	N	O	S	0	0
			2730	808	1436	278	199	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 28 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	S	176	Total	C	H	N	O	S	0	0
			2972	930	1510	285	236	11		

- Molecule 29 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	T	159	Total	C	H	N	O	S	0	0
			2667	823	1369	252	217	6		

- Molecule 30 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	U	102	Total	C	H	N	O	S	0	0
			1693	534	859	146	152	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 31 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	V	131	Total	C	H	N	O	S	0	0
			2019	618	1040	184	172	5		

- Molecule 32 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	W	63	Total	C	H	N	O	S	0	0
			1070	337	542	103	85	3		

- Molecule 33 is a protein called Ribosomal\_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	X	118	Total	C	H	N	O	S	0	0
			2008	618	1041	181	167	1		

- Molecule 34 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	Y	134	Total	C	H	N	O	S	0	0
			2320	700	1205	226	186	3		

- Molecule 35 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	Z	135	Total	C	H	N	O	S	0	0
			2292	714	1185	208	182	3		

- Molecule 36 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	a	147	Total	C	H	N	O	S	0	0
			2372	734	1210	239	185	4		

- Molecule 37 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	b	104	Total	C	H	N	O	S	0	0
			1771	527	923	189	129	3		

- Molecule 38 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	c	98	Total	C	H	N	O	S	0	0
			1557	481	796	134	140	6		

- Molecule 39 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	d	107	Total	C	H	N	O	S	0	0
			1820	560	932	171	155	2		

- Molecule 40 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	e	128	Total	C	H	N	O	S	0	0
			2203	667	1150	216	165	5		

- Molecule 41 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	f	109	Total	C	H	N	O	S	0	0
			1789	555	913	174	143	4		

- Molecule 42 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	g	114	Total	C	H	N	O	S	0	0
			1910	566	1004	187	147	6		

- Molecule 43 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	h	122	Total	C	H	N	O	S	0	0
			2161	640	1148	204	168	1		

- Molecule 44 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	i	102	Total	C	H	N	O	S	0	0
			1747	520	917	176	129	5		

- Molecule 45 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	j	86	Total	C	H	N	O	S	0	0
			1448	434	743	155	111	5		

- Molecule 46 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 47 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	l	50	Total	C	H	N	O	S	0	0
			928	286	481	96	64	1		

- Molecule 48 is a protein called eL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	m	52	Total	C	H	N	O	S	0	0
			899	266	470	90	67	6		

- Molecule 49 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	n	25	Total	C	H	N	O	S	0	0
			529	145	289	64	28	3		

- Molecule 50 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	o	104	Total	C	H	N	O	S	0	0
			1778	533	927	174	138	6		

- Molecule 51 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	p	91	Total	C	H	N	O	S	0	0
			1470	445	762	136	120	7		

- Molecule 52 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	q	76	Total	C	H	N	O	P	0	0
			2439	723	823	291	527	75		

- Molecule 53 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	r	124	Total	C	H	N	O	S	0	0
			2046	616	1052	205	167	6		

- Molecule 54 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	120	Total	C	H	N	O	P	0	0
			3854	1141	1296	456	842	119		

- Molecule 55 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	156	Total	C	H	N	O	P	0	0
			4997	1480	1683	585	1094	155		

- Molecule 56 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	394	Total	C	H	N	O	S	0	0
			6487	2020	3315	597	542	13		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	I	1	Total	Mg	0
			1	1	
57	K	201	Total	Mg	0
			201	201	
57	V	1	Total	Mg	0
			1	1	
57	a	1	Total	Mg	0
			1	1	
57	g	1	Total	Mg	0
			1	1	
57	j	1	Total	Mg	0
			1	1	
57	u	7	Total	Mg	0
			7	7	
57	v	4	Total	Mg	0
			4	4	
57	w	1	Total	Mg	0
			1	1	

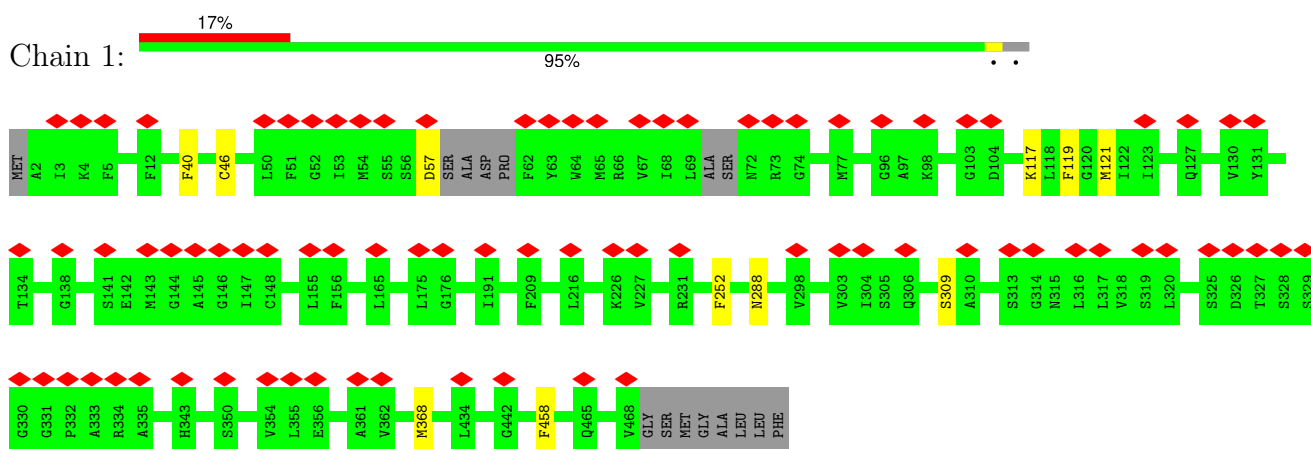
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	g	1	Total 1	Zn 1	0
58	j	1	Total 1	Zn 1	0
58	m	1	Total 1	Zn 1	0
58	o	1	Total 1	Zn 1	0
58	p	1	Total 1	Zn 1	0

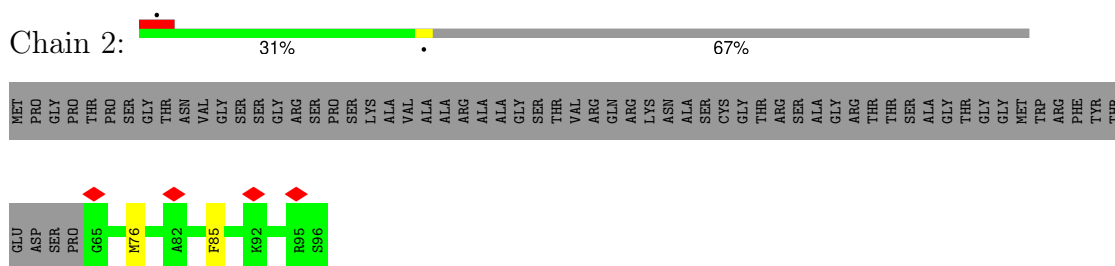
### 3 Residue-property plots

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.

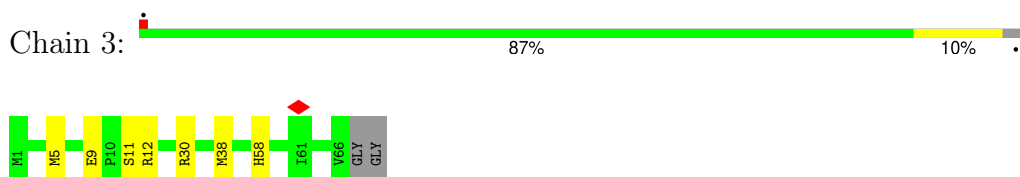
- Molecule 1: Protein transport protein Sec61 subunit alpha isoform 1



- Molecule 2: Protein transport protein Sec61 subunit beta

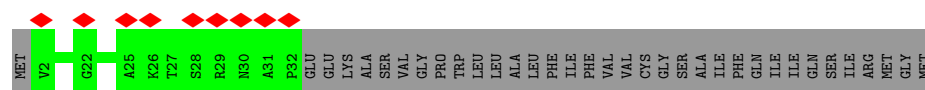


- Molecule 3: Protein transport protein Sec61 subunit gamma

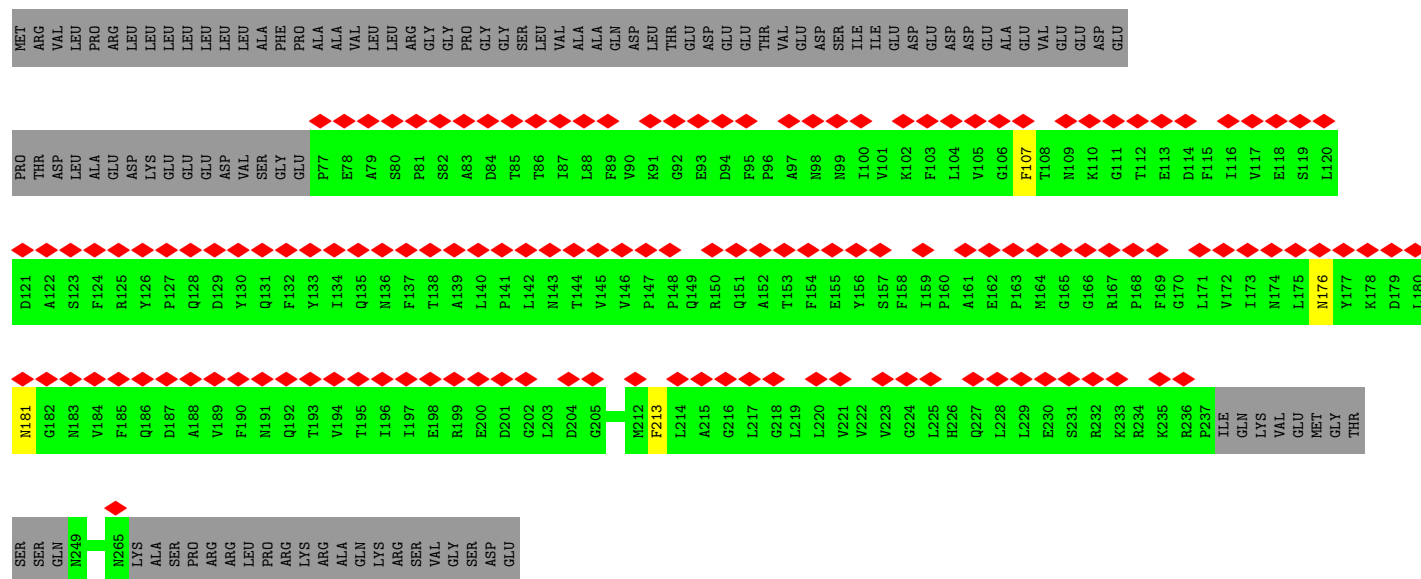


- Molecule 4: Stress-associated endoplasmic reticulum protein

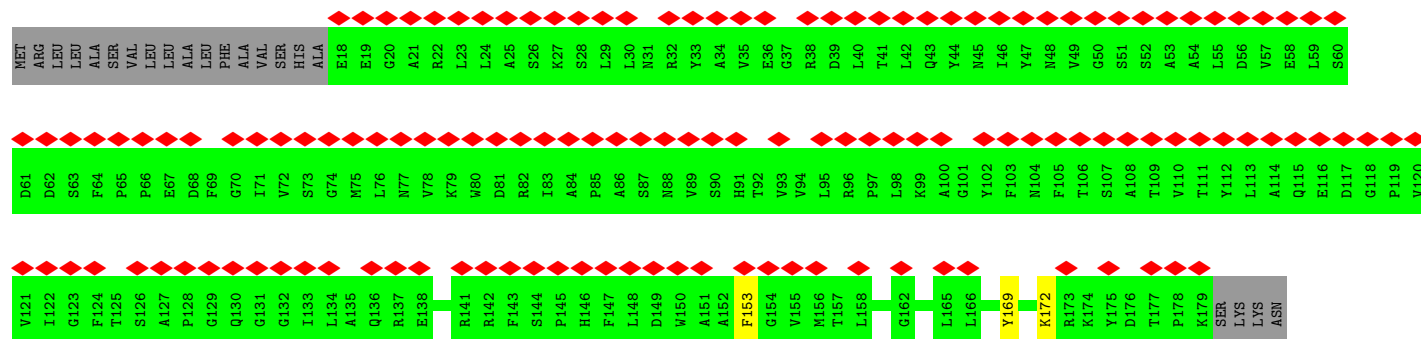
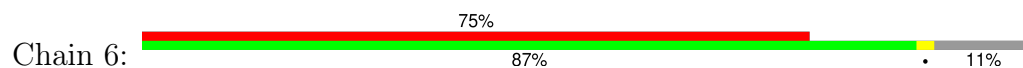




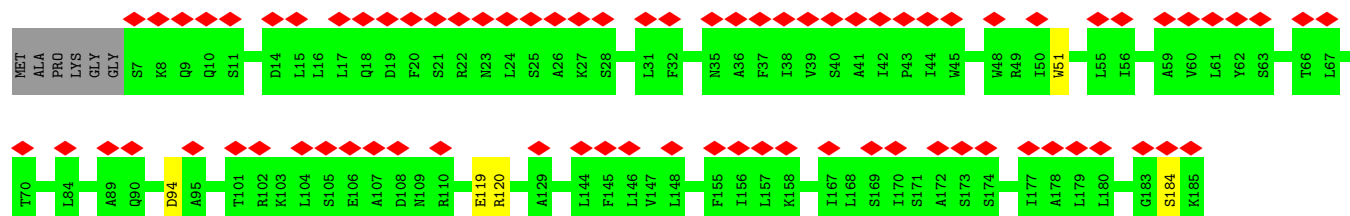
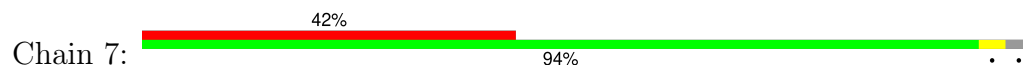
• Molecule 5: Translocon-associated protein subunit alpha



• Molecule 6: Translocon-associated protein subunit beta

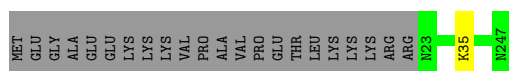


• Molecule 7: Translocon-associated protein subunit gamma









- Molecule 16: 60S ribosomal protein L7a

Chain G: 71% 27%



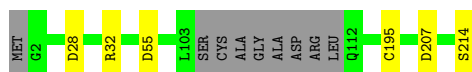
- Molecule 17: 60S ribosomal protein L9

Chain H: 96%



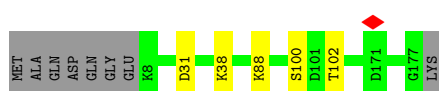
- Molecule 18: 60S ribosomal protein L10

Chain I: 93%



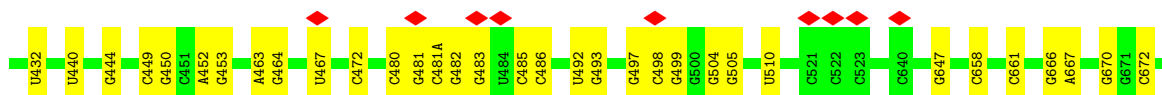
- Molecule 19: 60S ribosomal protein L11

Chain J: 93%

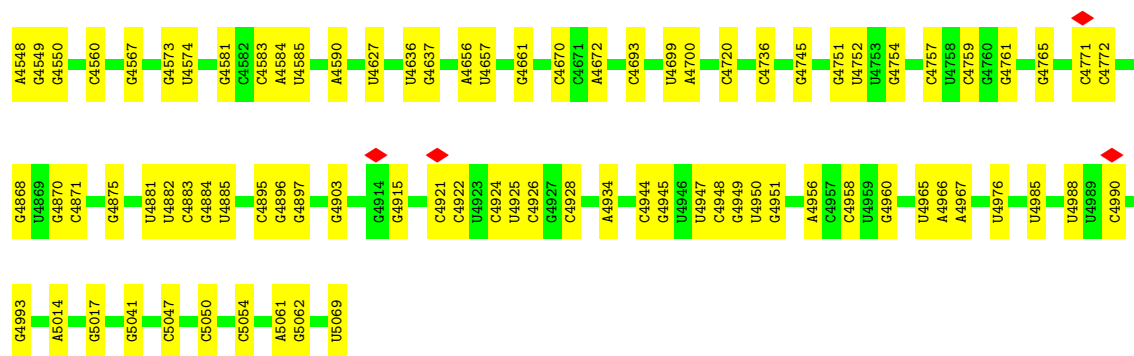


- Molecule 20: 28S rRNA

Chain K: 82% 18%

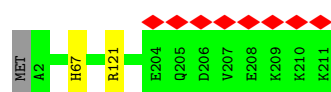






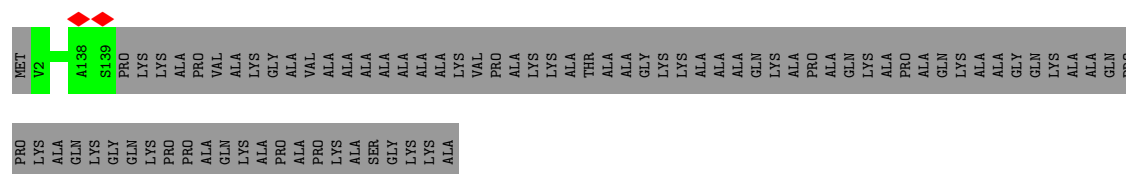
- Molecule 21: 60S ribosomal protein L13

Chain L: 99%



- Molecule 22: 60S ribosomal protein L14

Chain M: 63% 37%



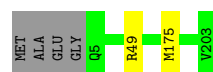
- Molecule 23: Ribosomal protein L15

Chain N: 99%



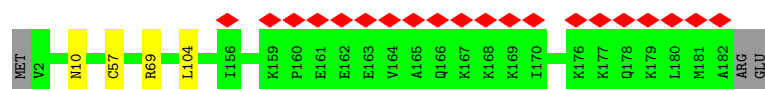
- Molecule 24: 60S ribosomal protein L13

Chain O: 97%



- Molecule 25: uL22


Chain P: 11% 96%

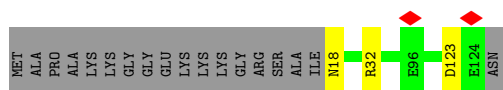


- [illegible]



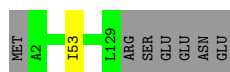
- Molecule 39: 60S ribosomal protein L31

Chain d:  83% 14%



- Molecule 40: Ribosomal protein L32

Chain e:  94% 5%



- Molecule 41: 60S ribosomal protein L35a

Chain f:  95% 2%



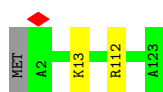
- Molecule 42: 60S ribosomal protein L34

Chain g:  97% 2%



- Molecule 43: 60S ribosomal protein L35

Chain h:  98% 2%




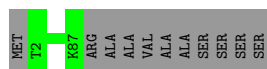
- Molecule 44: 60S ribosomal protein L36

Chain i:  94% 2%



- Molecule 45: Ribosomal protein L37

Chain j:  89% 11%



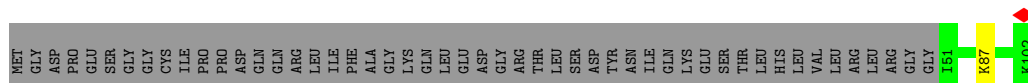
- Molecule 46: 60S ribosomal protein L38



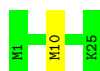
- Molecule 47: 60S ribosomal protein L39-like



- Molecule 48: eL40



- Molecule 49: 60S ribosomal protein L41



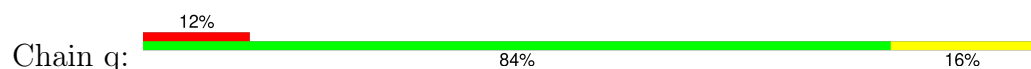
- Molecule 50: 60S ribosomal protein L36a-like

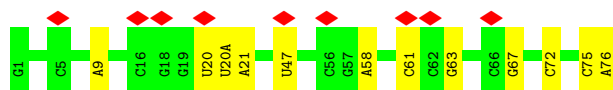


- Molecule 51: 60S ribosomal protein L37a

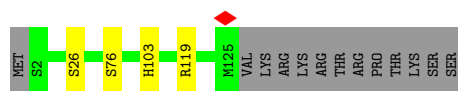
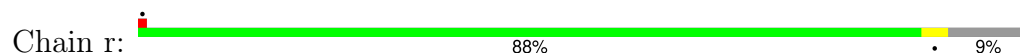


- Molecule 52: P-site tRNA





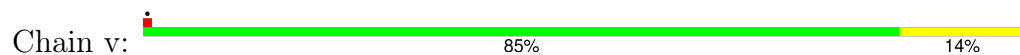
- Molecule 53: 60S ribosomal protein L28



- Molecule 54: 5S rRNA



- Molecule 55: 5.8S rRNA



- Molecule 56: Ribosomal protein L3



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	54	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.200	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0231	Depositor
Map size ( $\text{\AA}$ )	562.7185, 562.7185, 562.7185	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.339806, 1.339806, 1.339806	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	1	0.27	0/3651	0.46	0/4947
2	2	0.30	0/258	0.45	0/348
3	3	0.28	0/544	0.51	0/728
4	4	0.26	0/245	0.53	0/325
5	5	0.27	0/1457	0.50	0/1980
6	6	0.26	0/1296	0.48	0/1764
7	7	0.26	0/1482	0.43	0/2001
8	8	0.25	0/1215	0.47	0/1656
9	9	0.25	0/311	0.43	0/427
10	A	0.36	0/1936	0.61	0/2596
11	B	0.27	0/446	0.55	0/610
12	C	0.34	0/2937	0.55	0/3946
13	D	0.34	0/2437	0.52	0/3264
14	E	0.32	0/1825	0.54	0/2445
15	F	0.35	0/1911	0.54	0/2549
16	G	0.31	0/1910	0.52	0/2569
17	H	0.32	0/1535	0.54	0/2063
18	I	0.34	0/1702	0.55	0/2272
19	J	0.30	0/1385	0.55	0/1852
20	K	0.65	0/84980	0.81	11/132536 (0.0%)
21	L	0.32	0/1733	0.60	0/2316
22	M	0.33	0/1158	0.56	0/1547
23	N	0.38	0/1746	0.62	0/2338
24	O	0.35	0/1662	0.53	0/2222
25	P	0.33	0/1498	0.52	0/2003
26	Q	0.36	0/1539	0.61	0/2054
27	R	0.31	0/1310	0.57	0/1734
28	S	0.37	0/1501	0.55	0/2012
29	T	0.35	0/1326	0.56	0/1770
30	U	0.31	0/848	0.52	0/1138
31	V	0.34	0/993	0.54	0/1332
32	W	0.38	0/541	0.54	0/720

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	X	0.34	0/984	0.51	0/1323
34	Y	0.33	0/1132	0.56	0/1504
35	Z	0.36	0/1130	0.54	0/1507
36	a	0.35	0/1191	0.55	0/1590
37	b	0.30	0/861	0.57	0/1138
38	c	0.34	0/771	0.51	0/1034
39	d	0.34	0/903	0.58	0/1216
40	e	0.35	0/1071	0.57	0/1429
41	f	0.37	0/895	0.59	0/1198
42	g	0.36	0/916	0.59	0/1220
43	h	0.31	0/1021	0.57	0/1348
44	i	0.30	0/841	0.58	0/1112
45	j	0.39	0/720	0.62	0/952
46	k	0.32	0/575	0.51	0/761
47	l	0.33	0/459	0.57	0/608
48	m	0.34	0/435	0.56	0/575
49	n	0.27	0/241	0.77	0/305
50	o	0.34	0/864	0.56	0/1140
51	p	0.34	0/718	0.60	0/953
52	q	0.28	0/1805	0.78	0/2809
53	r	0.32	0/1010	0.57	0/1354
54	u	0.66	0/2858	0.77	0/4455
55	v	0.64	0/3701	0.78	1/5766 (0.0%)
56	w	0.36	0/3240	0.55	0/4339
All	All	0.54	0/157660	0.72	12/231700 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	K	3741	C	N3-C2-O2	-6.80	117.14	121.90
20	K	2806	A	O4'-C1'-N9	5.85	112.88	108.20
20	K	417	G	O4'-C1'-N9	5.63	112.70	108.20
55	v	81	C	C2-N1-C1'	5.53	124.89	118.80
20	K	3741	C	N1-C2-O2	5.31	122.09	118.90

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	1	455/476 (96%)	442 (97%)	13 (3%)	0	100	100
2	2	30/96 (31%)	30 (100%)	0	0	100	100
3	3	64/68 (94%)	64 (100%)	0	0	100	100
4	4	29/66 (44%)	28 (97%)	1 (3%)	0	100	100
5	5	174/286 (61%)	170 (98%)	4 (2%)	0	100	100
6	6	160/183 (87%)	156 (98%)	4 (2%)	0	100	100
7	7	177/185 (96%)	172 (97%)	5 (3%)	0	100	100
8	8	148/173 (86%)	146 (99%)	2 (1%)	0	100	100
9	9	34/593 (6%)	34 (100%)	0	0	100	100
10	A	246/257 (96%)	238 (97%)	8 (3%)	0	100	100
11	B	57/229 (25%)	45 (79%)	11 (19%)	1 (2%)	7	25
12	C	360/425 (85%)	350 (97%)	10 (3%)	0	100	100
13	D	291/297 (98%)	288 (99%)	3 (1%)	0	100	100
14	E	215/291 (74%)	207 (96%)	8 (4%)	0	100	100
15	F	223/247 (90%)	217 (97%)	6 (3%)	0	100	100
16	G	229/319 (72%)	225 (98%)	4 (2%)	0	100	100
17	H	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
18	I	201/214 (94%)	198 (98%)	3 (2%)	0	100	100
19	J	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
21	L	208/211 (99%)	203 (98%)	5 (2%)	0	100	100
22	M	136/218 (62%)	130 (96%)	6 (4%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	N	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
24	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100
25	P	179/184 (97%)	176 (98%)	3 (2%)	0	100	100
26	Q	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
27	R	153/196 (78%)	151 (99%)	2 (1%)	0	100	100
28	S	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
29	T	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
30	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
31	V	129/140 (92%)	129 (100%)	0	0	100	100
32	W	61/157 (39%)	60 (98%)	1 (2%)	0	100	100
33	X	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
34	Y	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
35	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
36	a	145/148 (98%)	137 (94%)	7 (5%)	1 (1%)	19	49
37	b	100/226 (44%)	94 (94%)	6 (6%)	0	100	100
38	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
39	d	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
40	e	126/135 (93%)	122 (97%)	4 (3%)	0	100	100
41	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
42	g	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
43	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
44	i	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
45	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
46	k	67/70 (96%)	67 (100%)	0	0	100	100
47	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
48	m	50/102 (49%)	50 (100%)	0	0	100	100
49	n	23/25 (92%)	23 (100%)	0	0	100	100
50	o	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
51	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
53	r	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
56	w	392/403 (97%)	385 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7698/9662 (80%)	7512 (98%)	184 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	a	40	HIS
11	B	120	VAL

### 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	1	388/398 (98%)	377 (97%)	11 (3%)	38	73
2	2	28/74 (38%)	26 (93%)	2 (7%)	12	36
3	3	59/59 (100%)	52 (88%)	7 (12%)	4	13
4	4	26/55 (47%)	26 (100%)	0	100	100
5	5	157/249 (63%)	153 (98%)	4 (2%)	42	75
6	6	135/152 (89%)	132 (98%)	3 (2%)	47	78
7	7	161/164 (98%)	156 (97%)	5 (3%)	35	70
8	8	130/146 (89%)	130 (100%)	0	100	100
9	9	35/526 (7%)	34 (97%)	1 (3%)	37	72
10	A	190/199 (96%)	188 (99%)	2 (1%)	70	90
11	B	48/172 (28%)	45 (94%)	3 (6%)	15	42
12	C	302/347 (87%)	296 (98%)	6 (2%)	50	79
13	D	247/250 (99%)	245 (99%)	2 (1%)	79	93
14	E	197/251 (78%)	191 (97%)	6 (3%)	36	71
15	F	196/215 (91%)	195 (100%)	1 (0%)	86	96
16	G	200/272 (74%)	195 (98%)	5 (2%)	42	75
17	H	169/171 (99%)	164 (97%)	5 (3%)	36	71
18	I	175/181 (97%)	169 (97%)	6 (3%)	32	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	J	143/149 (96%)	138 (96%)	5 (4%)	31	66
21	L	175/176 (99%)	173 (99%)	2 (1%)	70	90
22	M	117/161 (73%)	117 (100%)	0	100	100
23	N	171/172 (99%)	170 (99%)	1 (1%)	84	95
24	O	171/173 (99%)	169 (99%)	2 (1%)	67	89
25	P	160/163 (98%)	156 (98%)	4 (2%)	42	75
26	Q	164/164 (100%)	163 (99%)	1 (1%)	84	95
27	R	138/175 (79%)	133 (96%)	5 (4%)	30	65
28	S	157/157 (100%)	156 (99%)	1 (1%)	84	95
29	T	139/140 (99%)	135 (97%)	4 (3%)	37	72
30	U	92/114 (81%)	86 (94%)	6 (6%)	14	40
31	V	101/107 (94%)	100 (99%)	1 (1%)	73	91
32	W	55/126 (44%)	55 (100%)	0	100	100
33	X	106/134 (79%)	104 (98%)	2 (2%)	52	81
34	Y	124/135 (92%)	122 (98%)	2 (2%)	58	84
35	Z	117/118 (99%)	114 (97%)	3 (3%)	41	74
36	a	119/120 (99%)	118 (99%)	1 (1%)	79	93
37	b	84/172 (49%)	83 (99%)	1 (1%)	67	89
38	c	84/98 (86%)	81 (96%)	3 (4%)	30	65
39	d	98/110 (89%)	95 (97%)	3 (3%)	35	70
40	e	114/121 (94%)	113 (99%)	1 (1%)	75	92
41	f	88/89 (99%)	84 (96%)	4 (4%)	23	56
42	g	98/99 (99%)	96 (98%)	2 (2%)	50	79
43	h	109/110 (99%)	107 (98%)	2 (2%)	54	82
44	i	86/89 (97%)	83 (96%)	3 (4%)	31	66
45	j	73/80 (91%)	73 (100%)	0	100	100
46	k	64/65 (98%)	61 (95%)	3 (5%)	22	55
47	l	47/48 (98%)	46 (98%)	1 (2%)	48	78
48	m	48/90 (53%)	47 (98%)	1 (2%)	48	78
49	n	24/24 (100%)	23 (96%)	1 (4%)	25	59
50	o	92/94 (98%)	88 (96%)	4 (4%)	25	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	p	74/75 (99%)	74 (100%)	0	100	100
53	r	108/121 (89%)	104 (96%)	4 (4%)	29	64
56	w	342/348 (98%)	340 (99%)	2 (1%)	84	95
All	All	6725/8198 (82%)	6581 (98%)	144 (2%)	49	78

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	d	123	ASP
56	w	297	LYS
41	f	37	ASP
46	k	64	LEU
14	E	213	LYS

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

Mol	Chain	Res	Type
36	a	28	HIS
51	p	56	HIS
16	G	212	HIS
18	I	143	GLN
27	R	75	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	K	3521/3543 (99%)	606 (17%)	51 (1%)
52	q	74/76 (97%)	12 (16%)	0
54	u	119/120 (99%)	8 (6%)	0
55	v	155/156 (99%)	23 (14%)	0
All	All	3869/3895 (99%)	649 (16%)	51 (1%)

5 of 649 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	K	5	A
20	K	13	U
20	K	25	A
20	K	39	A

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Mol	Chain	Res	Type
20	K	42	A

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	K	2089	G
20	K	2695	A
20	K	4884	G
20	K	2104	A
20	K	2489	C

## 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 223 ligands modelled in this entry, 223 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	K	23
52	q	1

The worst 5 of 24 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	2113:G	O3'	2258:C	P	41.87
1	K	1252:C	O3'	1271:G	P	35.95
1	K	1219:G	O3'	1233:G	P	24.34
1	K	990:C	O3'	1064:G	P	17.41
1	K	4138:C	O3'	4146:G	P	17.32

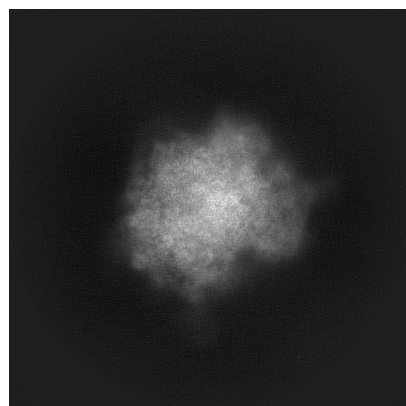
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19197. These allow visual inspection of the internal detail of the map and identification of artifacts.

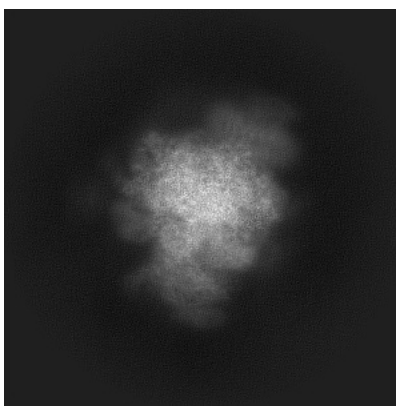
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

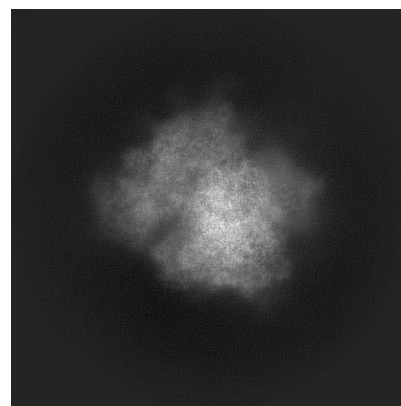
#### 6.1.1 Primary map



X

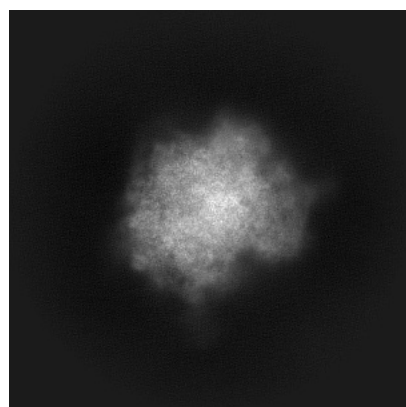


Y

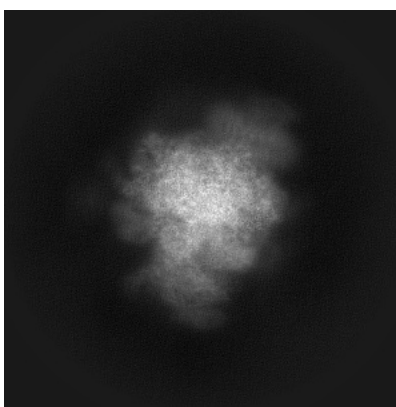


Z

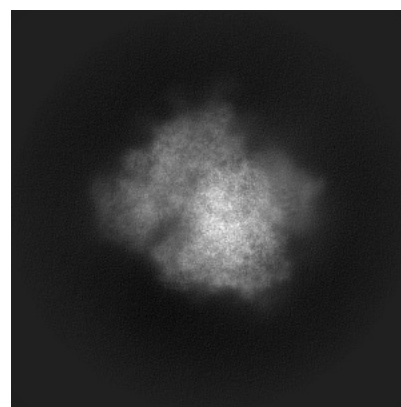
#### 6.1.2 Raw map



X



Y

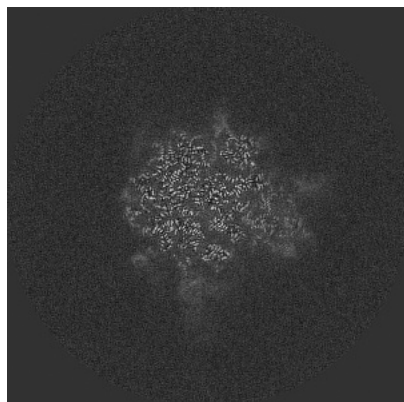


Z

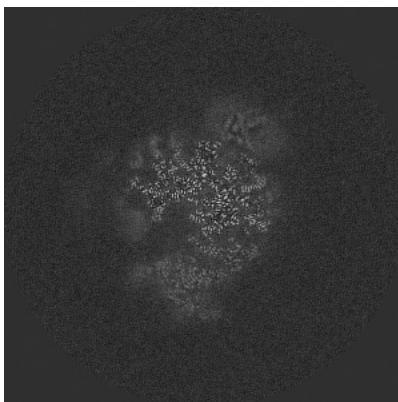
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

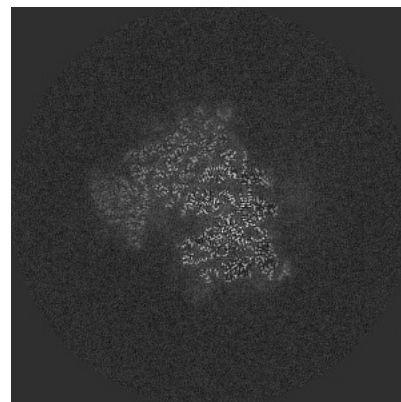
### 6.2.1 Primary map



X Index: 210

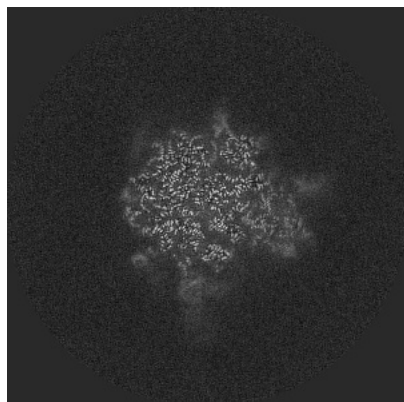


Y Index: 210

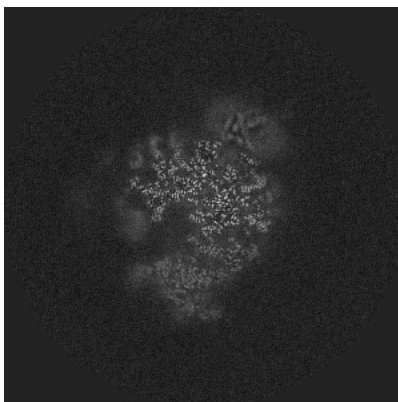


Z Index: 210

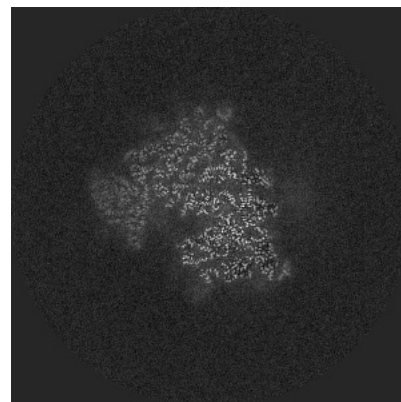
### 6.2.2 Raw map



X Index: 210



Y Index: 210

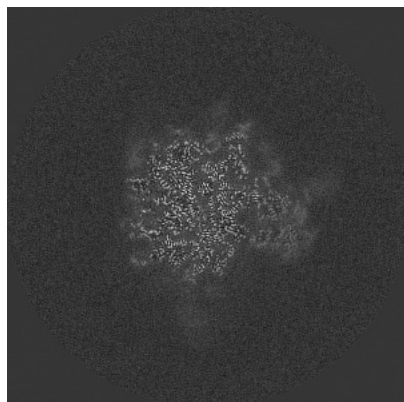


Z Index: 210

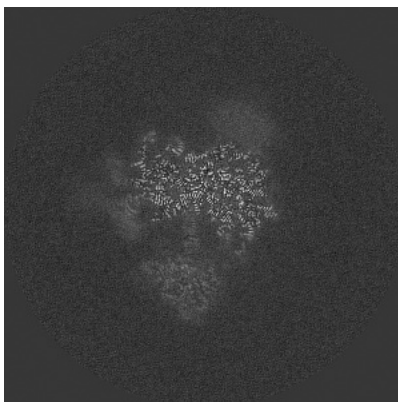
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

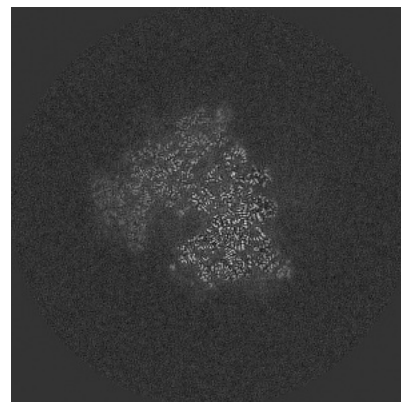
### 6.3.1 Primary map



X Index: 220

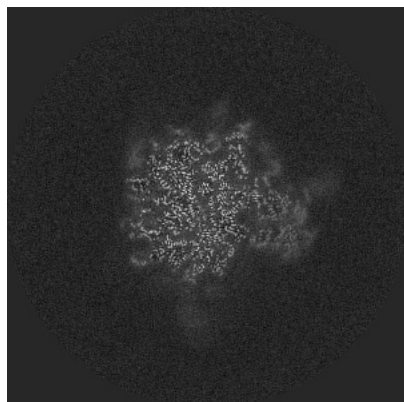


Y Index: 195

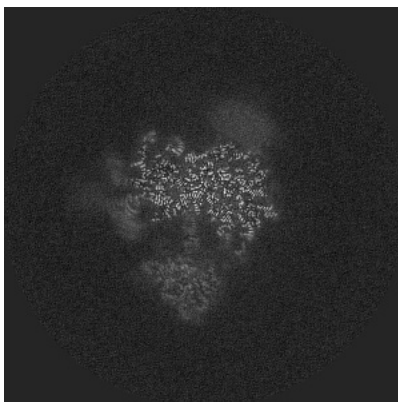


Z Index: 207

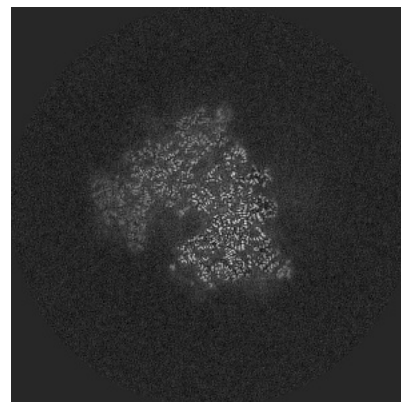
### 6.3.2 Raw map



X Index: 220



Y Index: 195

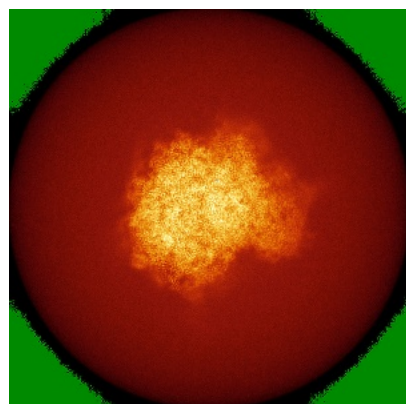


Z Index: 207

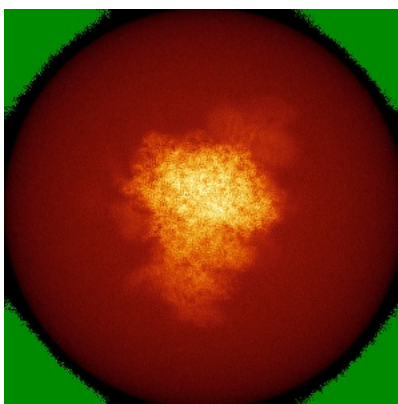
The images above show the largest variance slices of the map in three orthogonal directions.

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

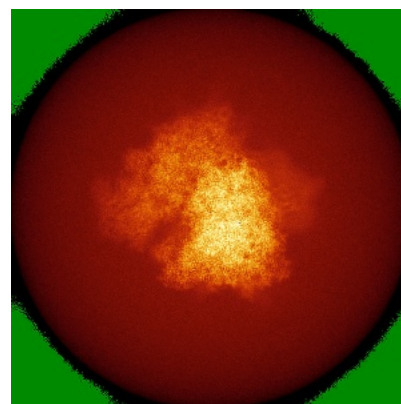
### 6.4.1 Primary map



X

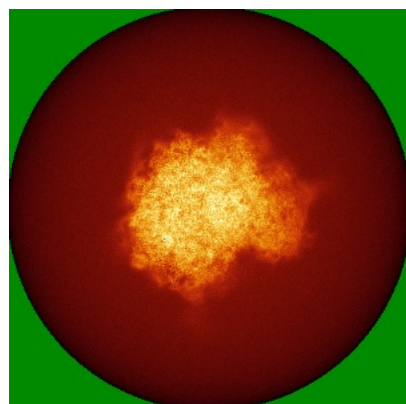


Y

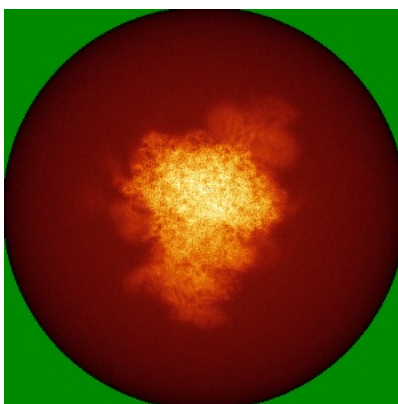


Z

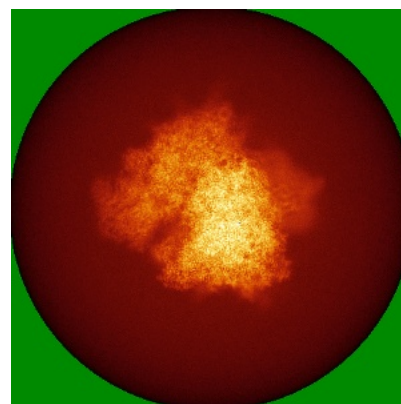
### 6.4.2 Raw map



X



Y

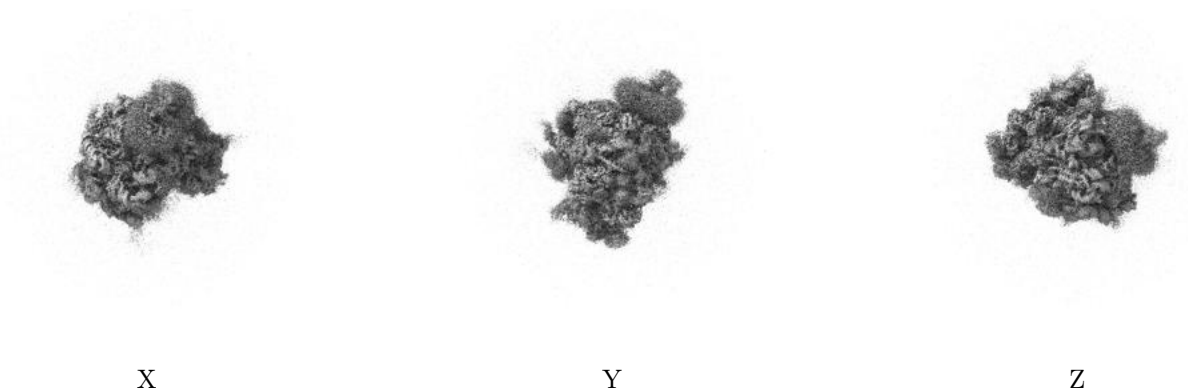


Z

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.

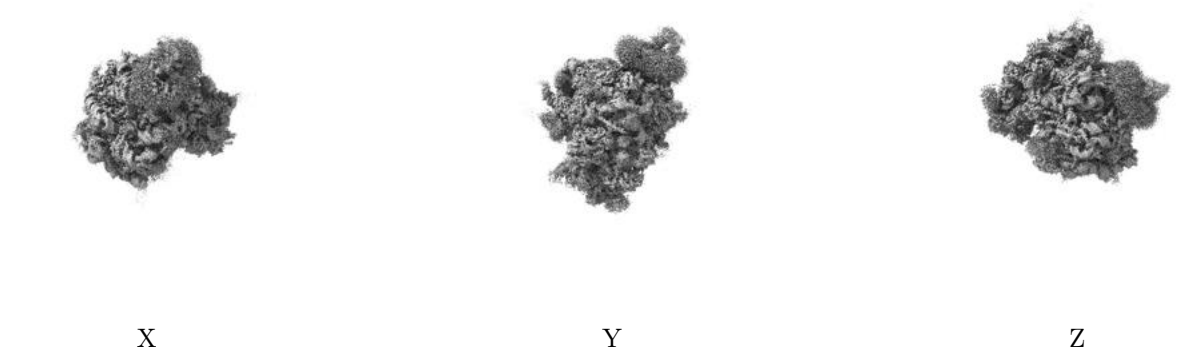
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0231. 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.

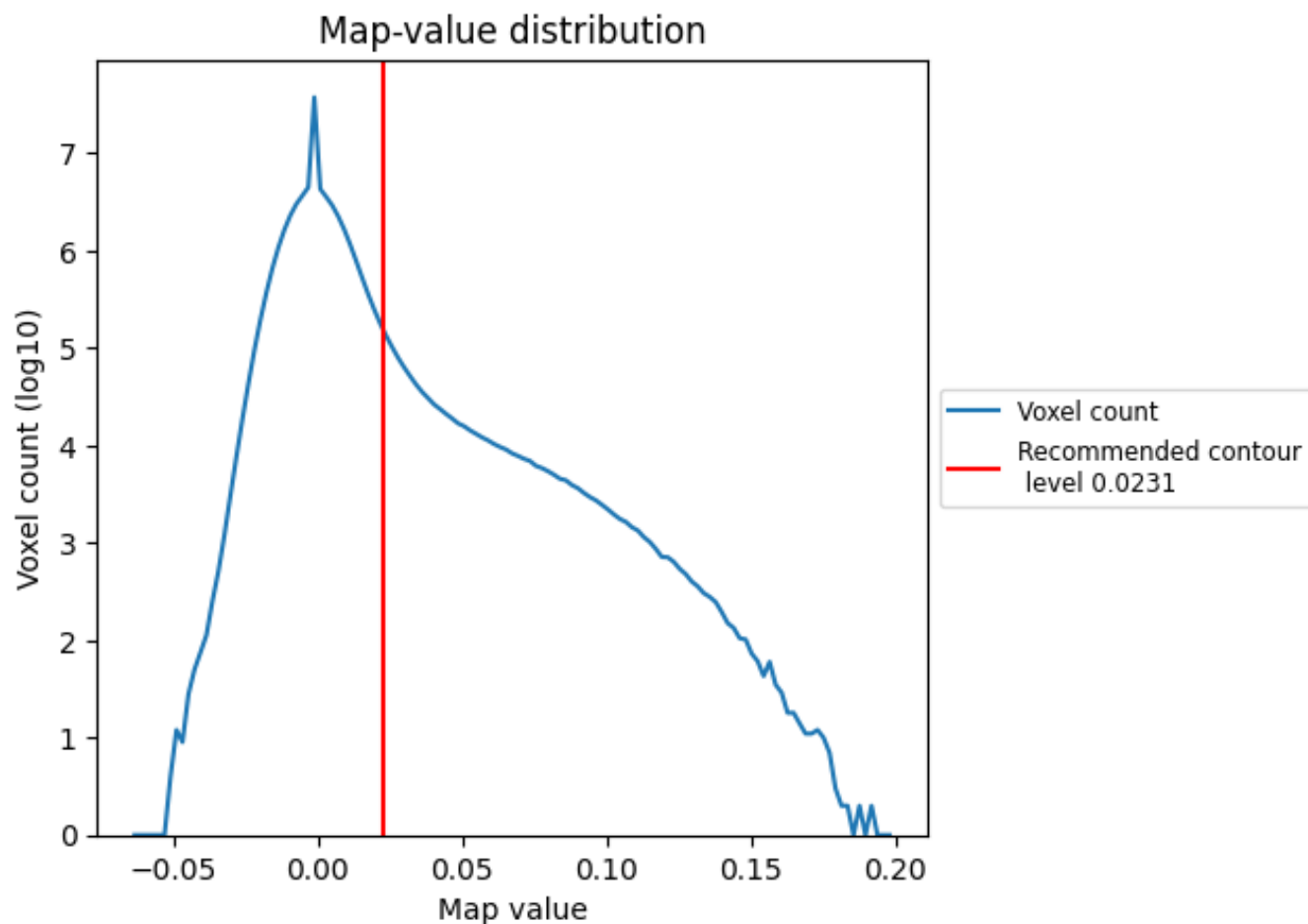
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

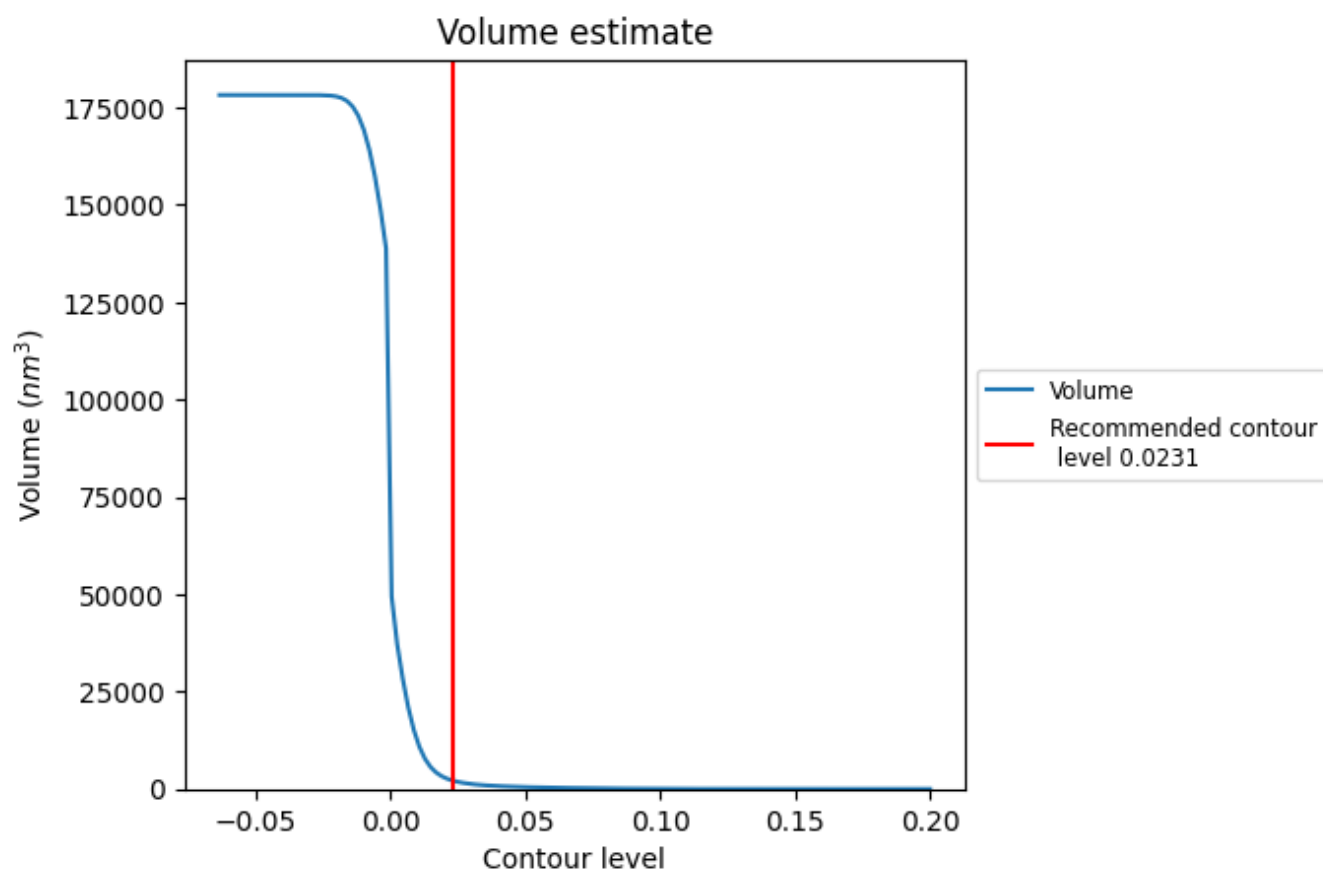
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

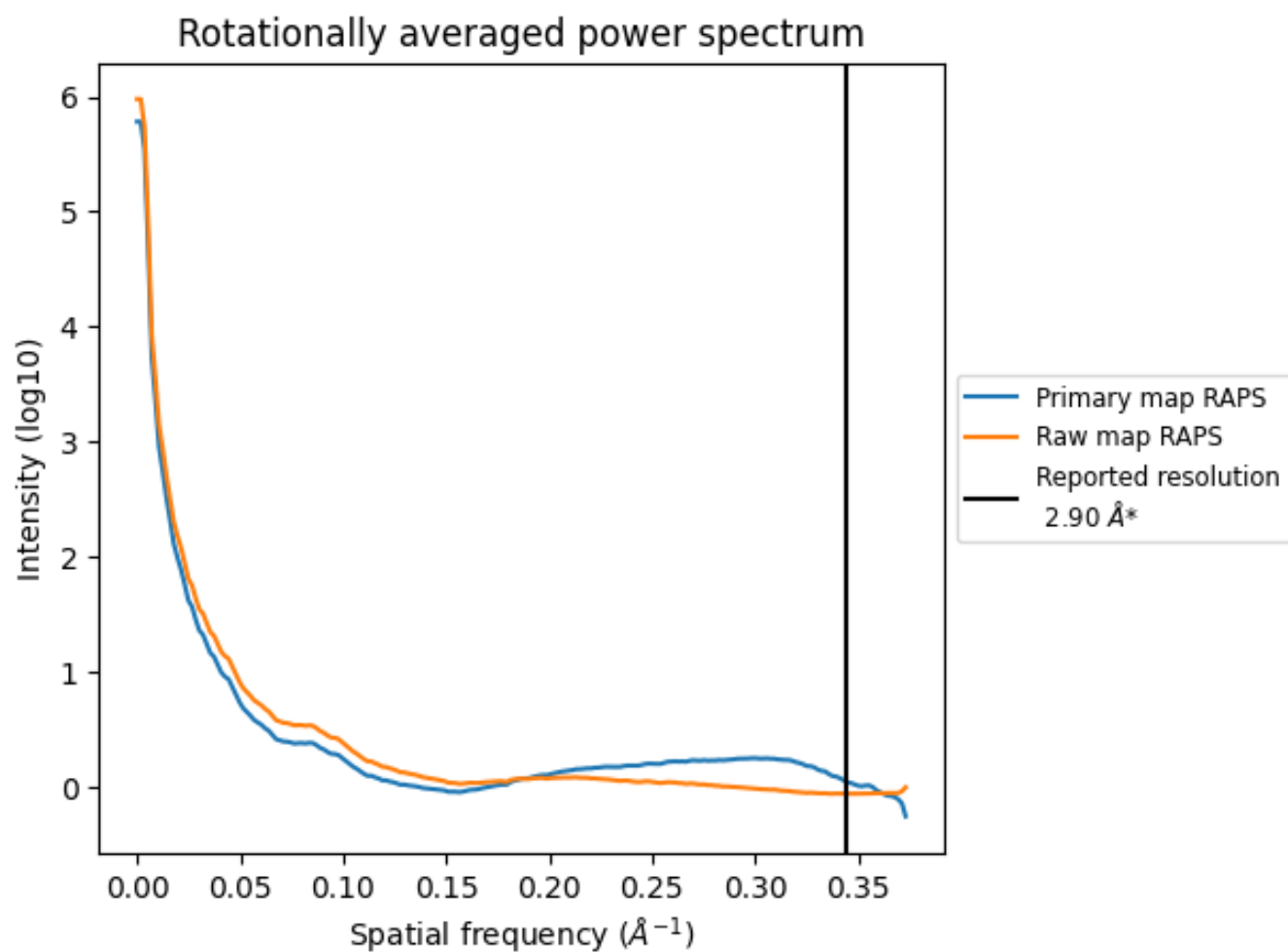
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2152  $\text{nm}^3$ ; this corresponds to an approximate mass of 1944 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 ⓘ

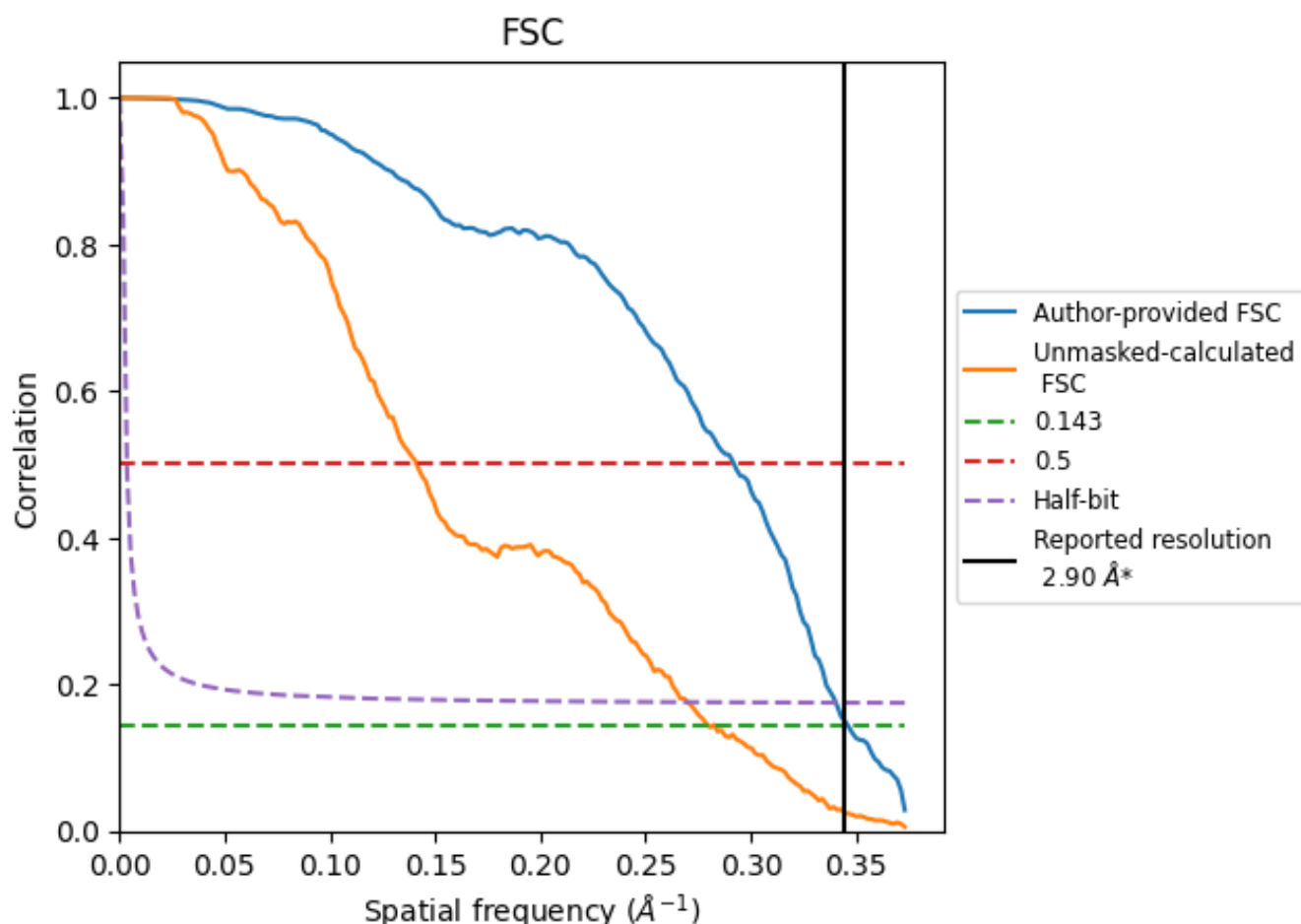


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 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 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

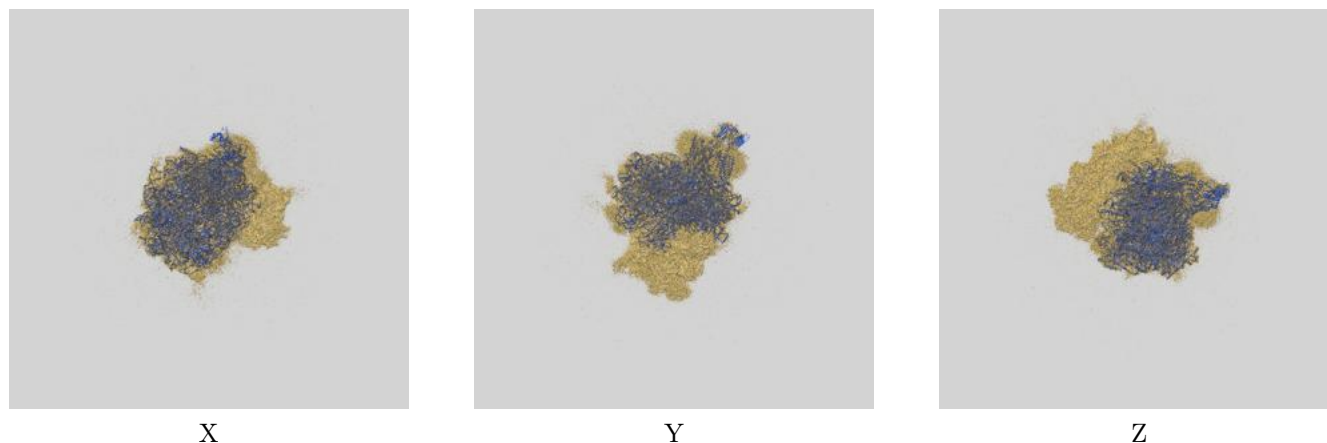
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.42	2.94
Unmasked-calculated*	3.57	7.08	3.70

\*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 3.57 differs from the reported value 2.90061 by more than 10 %

## 9 Map-model fit [i](#)

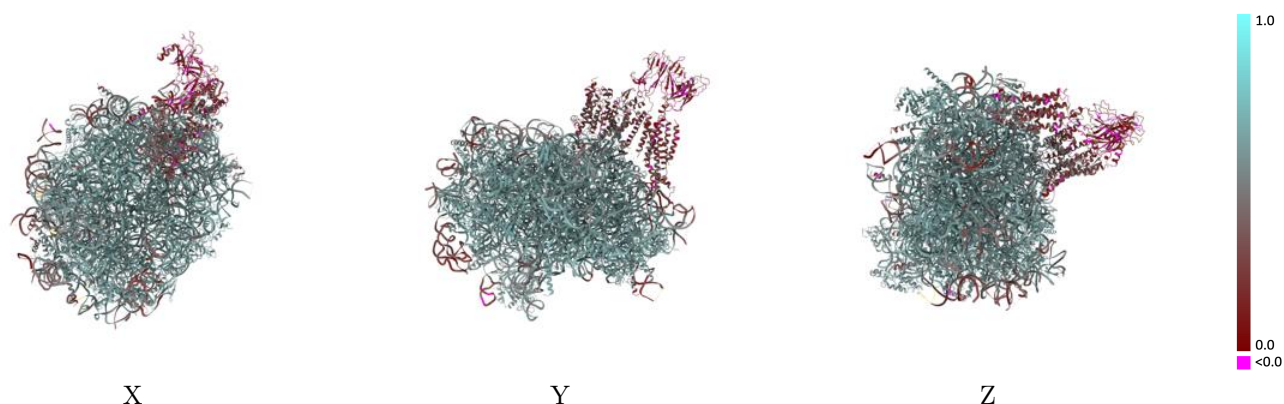
This section contains information regarding the fit between EMDB map EMD-19197 and PDB model 8RJC. Per-residue inclusion information can be found in section [3](#) on page [16](#).

### 9.1 Map-model overlay [i](#)



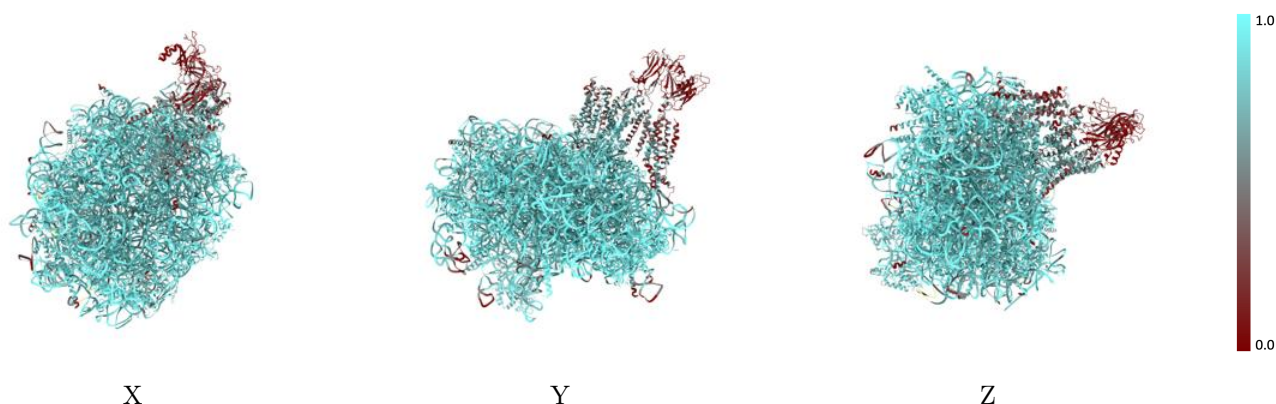
The images above show the 3D surface view of the map at the recommended contour level 0.0231 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



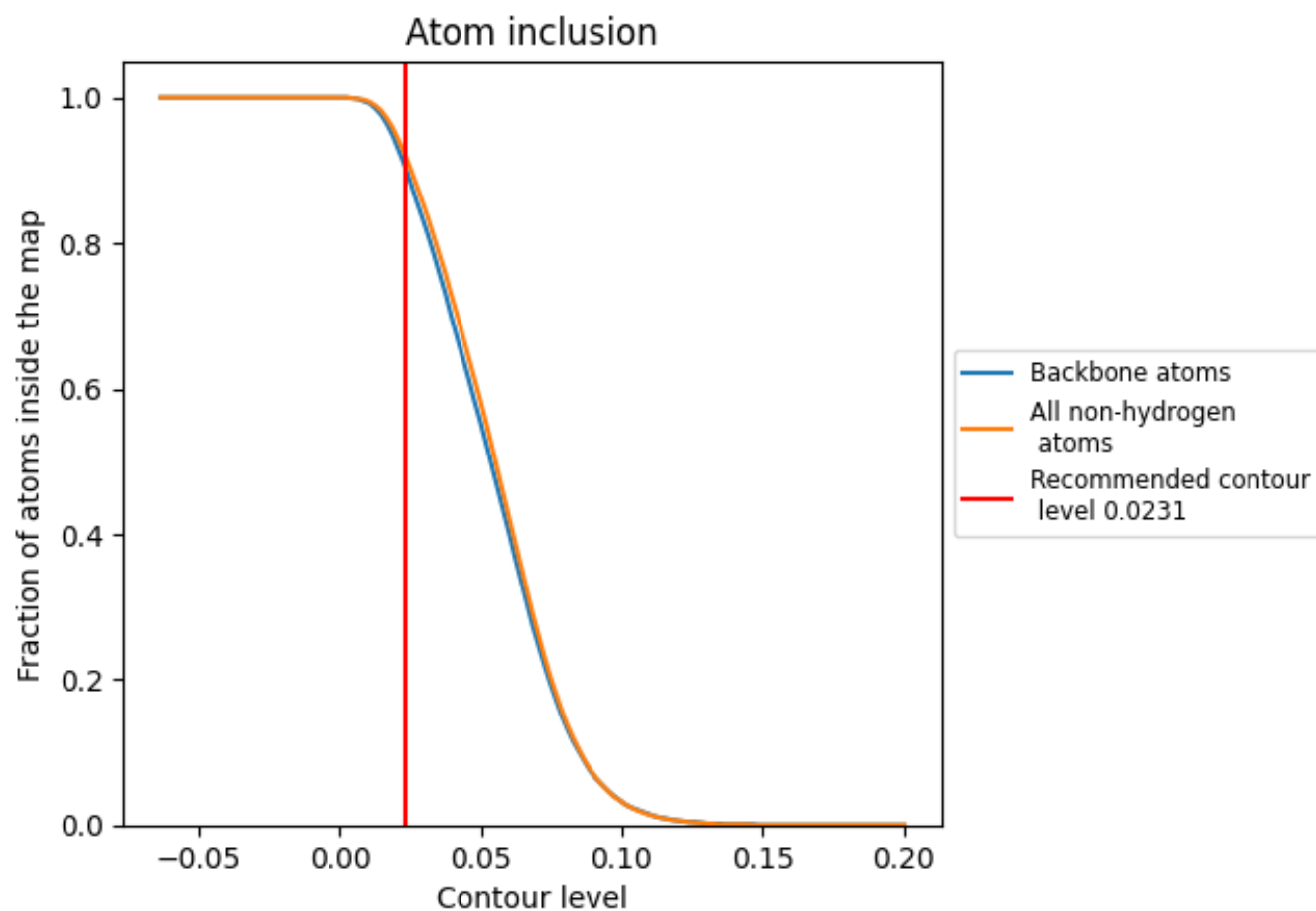
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0231).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.0231) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.5680
1	 0.6560	 0.3620
2	 0.5830	 0.3360
3	 0.7660	 0.4230
4	 0.6230	 0.4960
5	 0.2650	 0.2140
6	 0.2000	 0.1640
7	 0.4590	 0.2590
8	 0.1590	 0.1770
9	 0.3030	 0.2120
A	 0.9920	 0.6440
B	 0.5900	 0.2820
C	 0.9690	 0.6260
D	 0.9290	 0.6020
E	 0.9160	 0.5890
F	 0.9800	 0.6310
G	 0.8900	 0.5820
H	 0.9520	 0.6200
I	 0.9640	 0.6220
J	 0.8910	 0.5780
K	 0.9550	 0.5740
L	 0.9140	 0.6060
M	 0.9490	 0.6170
N	 0.9990	 0.6520
O	 0.9740	 0.6350
P	 0.8550	 0.5860
Q	 0.9850	 0.6380
R	 0.9780	 0.6270
S	 0.9800	 0.6330
T	 0.9620	 0.6180
U	 0.8250	 0.5070
V	 0.9770	 0.6300
W	 0.9800	 0.6240
X	 0.9660	 0.6160
Y	 0.9520	 0.6210



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Chain	Atom inclusion	Q-score
Z	 0.9530	 0.6060
a	 0.9800	 0.6400
b	 0.8830	 0.5630
c	 0.9450	 0.6110
d	 0.9520	 0.6080
e	 0.9860	 0.6380
f	 0.9860	 0.6490
g	 0.9350	 0.6110
h	 0.9410	 0.6070
i	 0.9420	 0.6000
j	 0.9990	 0.6420
k	 0.8760	 0.5900
l	 0.9860	 0.6270
m	 0.9520	 0.6220
n	 0.9860	 0.6000
o	 0.9660	 0.6250
p	 0.9680	 0.6190
q	 0.6760	 0.4560
r	 0.9760	 0.6230
u	 0.9910	 0.6150
v	 0.9750	 0.5980
w	 0.9730	 0.6320