



Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 07:44 PM EST

PDB ID : 6WNW
EMDB ID : EMD-21858
Title : Active 70S ribosome without free 5S rRNA and bound with A- and P- tRNA
Authors : Loveland, A.B.; Korostelev, A.A.; Mankin, A.S.; Huang, S.; Aleksashin, N.A.; Klepacki, D.; Reier, K.; Kefi, A.; Szal, A.; Remme, J.; Jaeger, L.; Vazquez-Laslop, N.
Deposited on : 2020-04-23
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM Validation 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

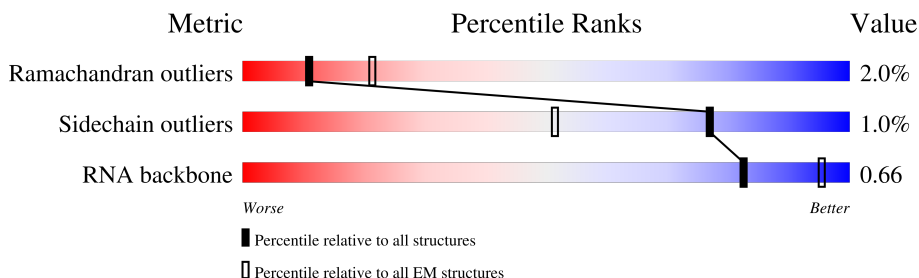
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



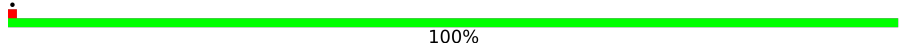
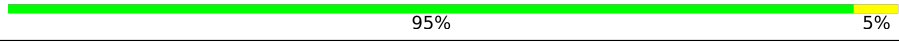
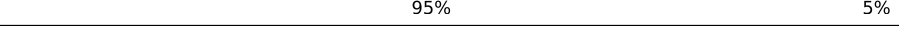
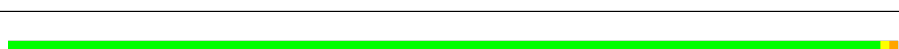
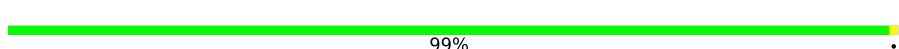
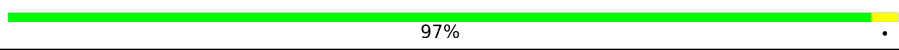
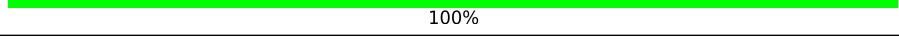
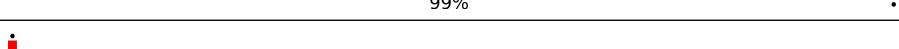

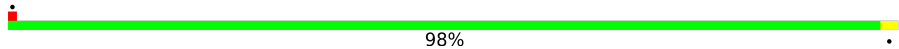
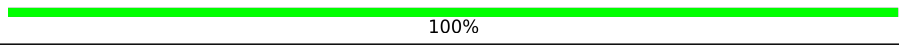
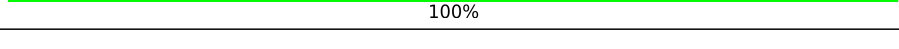
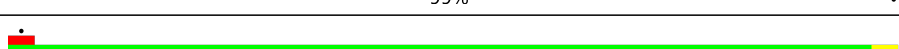
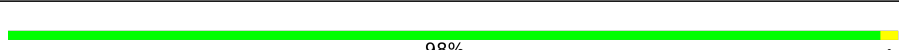
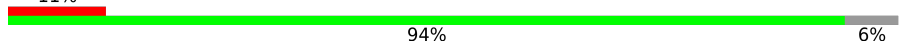
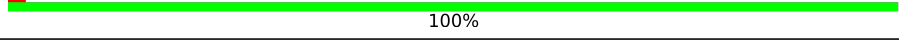
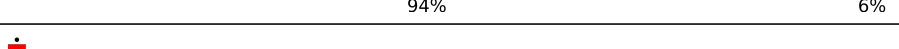

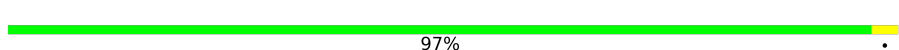
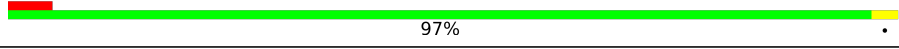
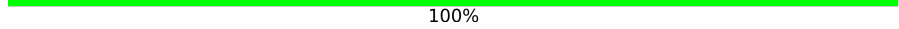



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	b	271	
2	c	209	
3	d	201	
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	

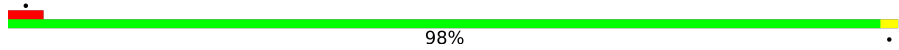
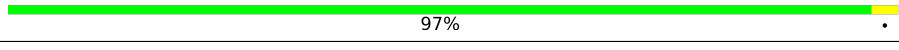
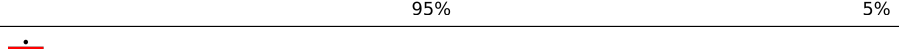
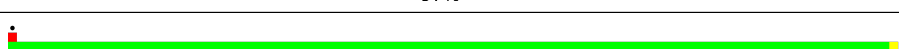
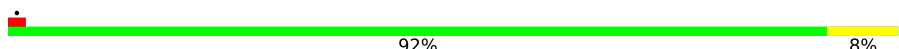
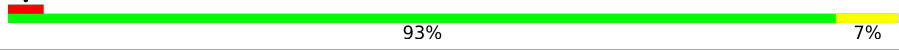
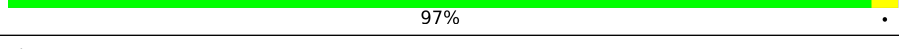
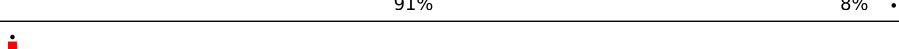
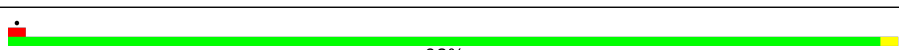
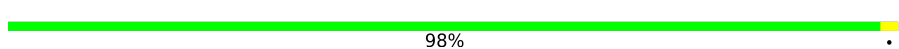
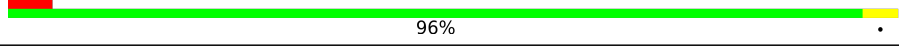
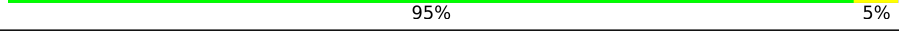
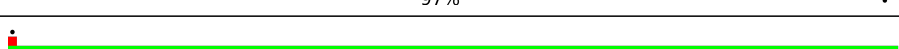
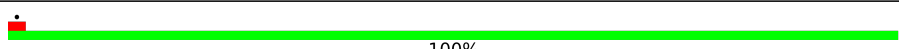


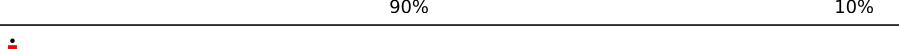

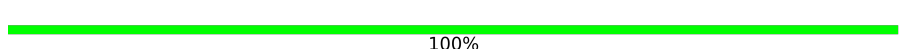





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Mol	Chain	Length	Quality of chain
9	j	142	 100%
10	k	122	 95% 5%
11	l	143	 95% 5%
12	m	136	 97% .
13	n	120	 98% ..
14	o	116	 99% .
15	p	114	 97% .
16	q	117	 100%
17	r	103	 99% .
18	s	110	 98% .
19	t	93	 100%
20	u	102	 98% .
21	v	94	 100%
22	w	75	 100%
23	x	77	 99% .
24	y	63	 97% .
25	z	58	 98% .
26	A	70	 11% 94% 6%
27	B	56	 100%
28	C	50	 94% 6%
29	D	46	 98% .
30	E	64	 98% .
31	F	38	 97% .
32	G	225	 5% 97% .
33	H	206	100%

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Mol	Chain	Length	Quality of chain
34	I	205	 98%
35	J	157	 97%
36	K	100	 95%5%
37	L	151	 97%
38	M	129	 99%
39	N	127	 92%8%
40	O	98	 93%7%
41	P	116	 97%
42	Q	123	 91%8%
43	R	114	 96%
44	S	100	 98%
45	T	88	 98%
46	U	82	 5%96%
47	V	80	 95%5%
48	W	65	 97%
49	X	79	 100%
50	Y	85	 100%
51	Z	65	 8%88%12%
52	a	223	 40%57%40%
53	3	1539	 90%10%
54	4	3031	 88%12%
55	5	77	 91%9%
56	1	10	 100%
57	7	76	 5%88%12%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 149080 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23s-5s joint ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	3031	Total	C	N	O	P	0	0
			65057	29021	11966	21040	3030		

- Molecule 55 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	1	10	Total	C	N	O	P	0	0
			213	96	39	68	10		

- Molecule 57 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

3 Residue-property plots [i](#)

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.

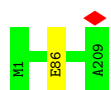
- Molecule 1: 50S ribosomal protein L2

Chain b:  98%



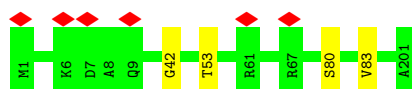
- Molecule 2: 50S ribosomal protein L3

Chain c:  100%



- Molecule 3: 50S ribosomal protein L4

Chain d:  98%



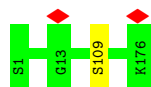
- Molecule 4: 50S ribosomal protein L5

Chain e:  98%

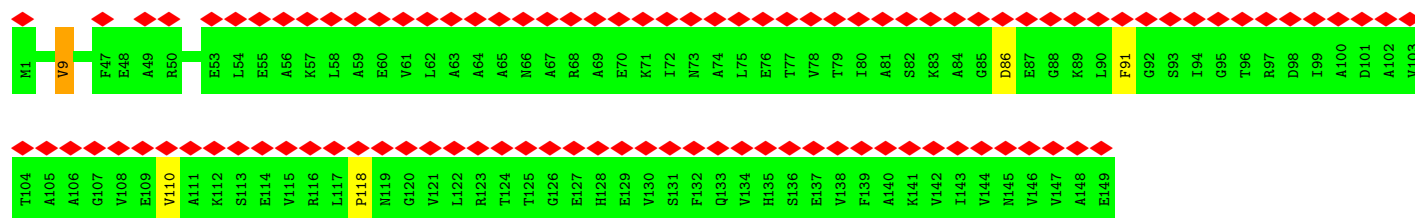
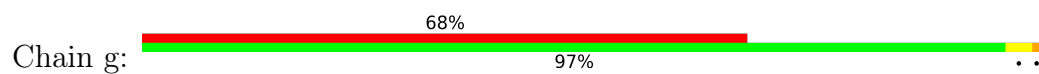


- Molecule 5: 50S ribosomal protein L6

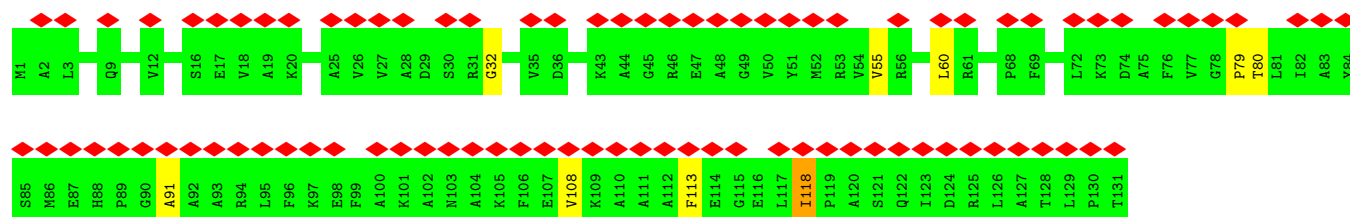
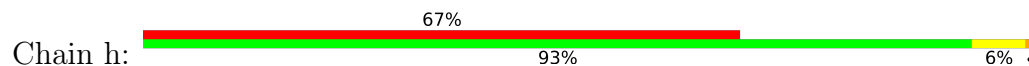
Chain f:  99%



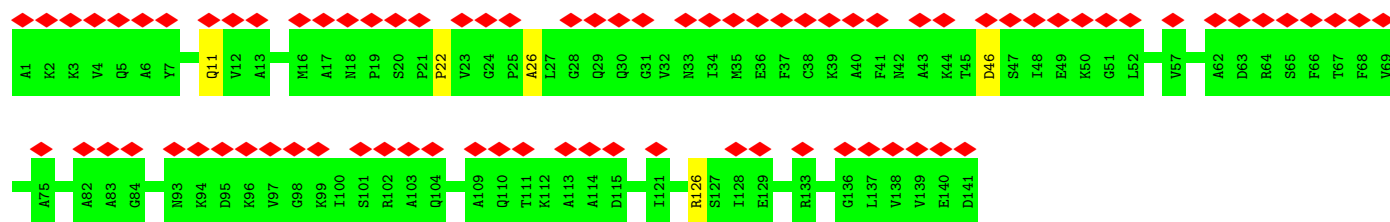
- Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15





- Molecule 12: 50S ribosomal protein L16

Chain m:  97%



- Molecule 13: 50S ribosomal protein L17

Chain n:  98%



- Molecule 14: 50S ribosomal protein L18

Chain o:  99%



- Molecule 15: 50S ribosomal protein L19

Chain p:  97%



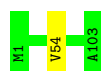
- Molecule 16: 50S ribosomal protein L20

Chain q:  100%

There are no outlier residues recorded for this chain.

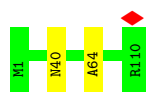
- Molecule 17: 50S ribosomal protein L21

Chain r:  99%



- Molecule 18: 50S ribosomal protein L22

Chain s:  98%



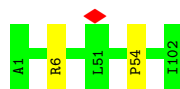
- Molecule 19: 50S ribosomal protein L23

Chain t:  100%



- Molecule 20: 50S ribosomal protein L24

Chain u:  98%



- Molecule 21: 50S ribosomal protein L25

Chain v:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L27

Chain w:  100%



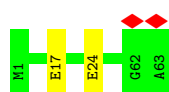
- Molecule 23: 50S ribosomal protein L28

Chain x:  99%



- Molecule 24: 50S ribosomal protein L29

Chain y:  97%



- Molecule 25: 50S ribosomal protein L30

Chain z:  98%



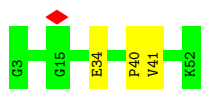
- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



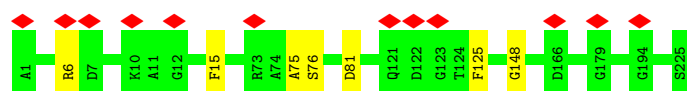
- Molecule 30: 50S ribosomal protein L35



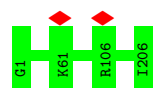
- Molecule 31: 50S ribosomal protein L36



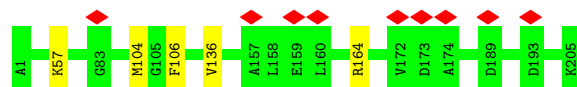
- Molecule 32: 30S ribosomal protein S2



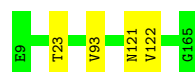
- Molecule 33: 30S ribosomal protein S3



- Molecule 34: 30S ribosomal protein S4



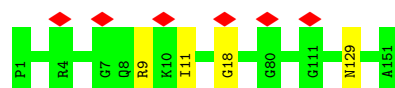
- Molecule 35: 30S ribosomal protein S5



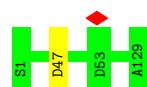
- Molecule 36: 30S ribosomal protein S6




- Molecule 37: 30S ribosomal protein S7

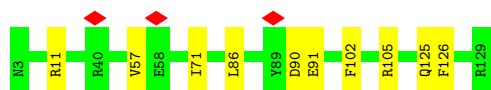


- Molecule 38: 30S ribosomal protein S8



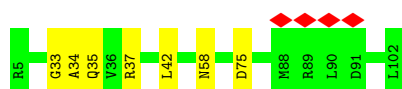
- Molecule 39: 30S ribosomal protein S9

Chain N:  92% 8%



- Molecule 40: 30S ribosomal protein S10

Chain O:  93% 7%



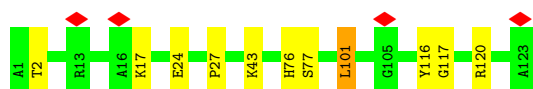
- Molecule 41: 30S ribosomal protein S11

Chain P:  97% .



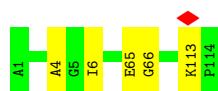
- Molecule 42: 30S ribosomal protein S12

Chain Q:  91% 8% .



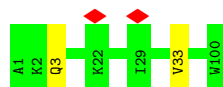
- Molecule 43: 30S ribosomal protein S13

Chain R:  96% .



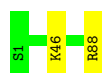
- Molecule 44: 30S ribosomal protein S14

Chain S:  98% .

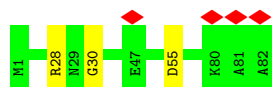


- Molecule 45: 30S ribosomal protein S15

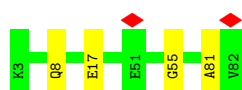
Chain T:  98% .



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18



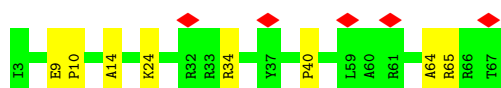
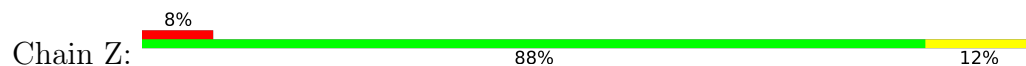
- Molecule 49: 30S ribosomal protein S19



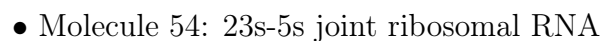
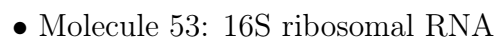
- Molecule 50: 30S ribosomal protein S20

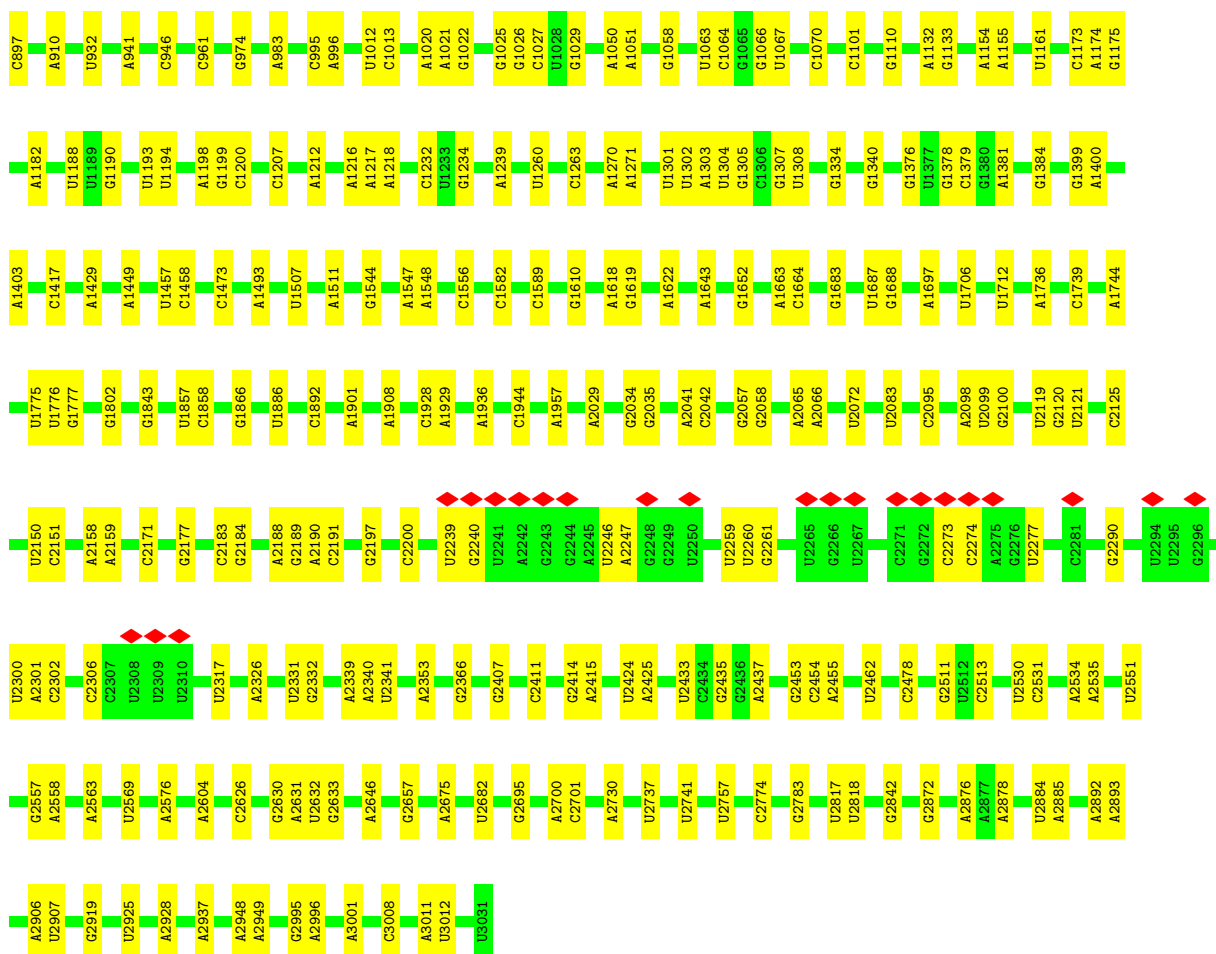


- Molecule 51: 30S ribosomal protein S21

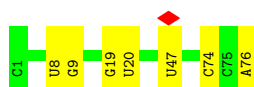
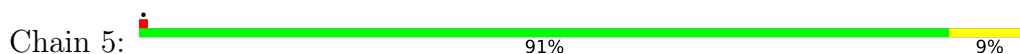


- Molecule 52: 50S ribosomal protein L1





- Molecule 55: tRNA^fMet

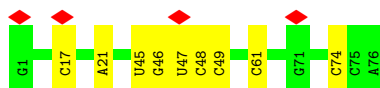
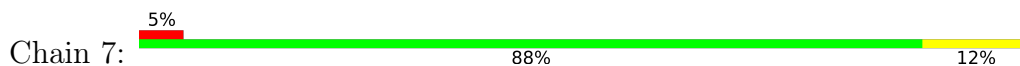


- Molecule 56: mRNA



There are no outlier residues recorded for this chain.

- Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	17.526	Depositor
Minimum map value	-5.137	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.802	Depositor
Recommended contour level	2.5	Depositor
Map size (\AA)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.30	0/2122	0.60	0/2852
2	c	0.32	0/1586	0.56	0/2134
3	d	0.34	0/1571	0.55	0/2113
4	e	0.38	0/1435	0.54	0/1926
5	f	0.33	0/1343	0.55	0/1816
6	g	0.45	0/1122	0.62	0/1515
7	h	0.47	0/1002	0.67	0/1350
8	i	0.45	0/1046	0.61	0/1410
9	j	0.31	0/1152	0.53	0/1551
10	k	0.31	0/948	0.59	0/1268
11	l	0.33	0/1054	0.56	0/1403
12	m	0.33	0/1093	0.54	0/1460
13	n	0.31	0/974	0.55	0/1301
14	o	0.32	0/902	0.57	0/1209
15	p	0.32	0/929	0.56	0/1242
16	q	0.31	0/960	0.48	0/1278
17	r	0.35	0/829	0.62	0/1107
18	s	0.29	0/864	0.58	0/1156
19	t	0.32	0/745	0.55	0/994
20	u	0.35	0/788	0.57	0/1051
21	v	0.35	0/766	0.55	0/1025
22	w	0.34	0/582	0.53	0/769
23	x	0.32	0/635	0.53	0/848
24	y	0.33	0/510	0.51	0/677
25	z	0.30	0/453	0.53	0/605
26	A	0.40	0/531	0.65	0/709
27	B	0.30	0/450	0.55	0/599
28	C	0.36	0/417	0.58	0/554
29	D	0.34	0/380	0.55	0/498
30	E	0.30	0/513	0.53	0/676
31	F	0.27	0/303	0.57	0/397
32	G	0.38	0/1788	0.57	0/2408
33	H	0.35	0/1652	0.52	0/2225
34	I	0.39	0/1665	0.57	0/2227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	J	0.34	0/1170	0.58	0/1573
36	K	0.37	0/836	0.63	0/1128
37	L	0.36	0/1196	0.55	0/1602
38	M	0.33	0/989	0.57	0/1326
39	N	0.37	0/1034	0.60	0/1375
40	O	0.35	0/797	0.66	0/1077
41	P	0.34	0/886	0.61	0/1195
42	Q	0.34	0/969	0.63	0/1300
43	R	0.34	0/893	0.55	0/1193
44	S	0.36	0/817	0.53	0/1088
45	T	0.32	0/722	0.56	0/964
46	U	0.40	0/659	0.58	0/884
47	V	0.35	0/658	0.57	0/881
48	W	0.38	0/545	0.55	0/731
49	X	0.38	0/653	0.57	0/877
50	Y	0.35	0/671	0.48	0/888
51	Z	0.45	0/551	0.67	0/728
52	a	0.45	0/1034	0.60	0/1387
53	3	0.39	0/36963	0.67	0/57662
54	4	0.35	0/72860	0.67	0/113668
55	5	0.43	0/1832	0.65	0/2855
56	1	0.53	0/238	0.68	0/368
57	7	0.50	0/1809	0.67	0/2819
All	All	0.36	0/161892	0.64	0/241922

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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	232 (86%)	35 (13%)	2 (1%)	22	61
2	c	207/209 (99%)	192 (93%)	14 (7%)	1 (0%)	29	67
3	d	199/201 (99%)	183 (92%)	12 (6%)	4 (2%)	7	38
4	e	175/177 (99%)	149 (85%)	24 (14%)	2 (1%)	14	51
5	f	174/176 (99%)	156 (90%)	17 (10%)	1 (1%)	25	64
6	g	147/149 (99%)	118 (80%)	26 (18%)	3 (2%)	7	38
7	h	129/131 (98%)	88 (68%)	32 (25%)	9 (7%)	1	8
8	i	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	4	28
9	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
10	k	120/122 (98%)	110 (92%)	7 (6%)	3 (2%)	5	32
11	l	141/143 (99%)	123 (87%)	13 (9%)	5 (4%)	3	24
12	m	134/136 (98%)	126 (94%)	5 (4%)	3 (2%)	6	35
13	n	118/120 (98%)	103 (87%)	13 (11%)	2 (2%)	9	42
14	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	17	56
15	p	112/114 (98%)	101 (90%)	10 (9%)	1 (1%)	17	56
16	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	r	101/103 (98%)	87 (86%)	13 (13%)	1 (1%)	15	54
18	s	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	8	39
19	t	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
20	u	100/102 (98%)	87 (87%)	11 (11%)	2 (2%)	7	38
21	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	w	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	x	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
24	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	9	43
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	A	64/70 (91%)	55 (86%)	9 (14%)	0	100	100
27	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
28	C	48/50 (96%)	42 (88%)	4 (8%)	2 (4%)	3	20
29	D	44/46 (96%)	40 (91%)	4 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	E	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	9	43
31	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	5	29
32	G	223/225 (99%)	201 (90%)	17 (8%)	5 (2%)	6	35
33	H	204/206 (99%)	180 (88%)	24 (12%)	0	100	100
34	I	203/205 (99%)	169 (83%)	33 (16%)	1 (0%)	29	67
35	J	155/157 (99%)	133 (86%)	18 (12%)	4 (3%)	5	31
36	K	98/100 (98%)	78 (80%)	15 (15%)	5 (5%)	2	15
37	L	149/151 (99%)	127 (85%)	19 (13%)	3 (2%)	7	38
38	M	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	19	58
39	N	125/127 (98%)	102 (82%)	17 (14%)	6 (5%)	2	17
40	O	96/98 (98%)	74 (77%)	15 (16%)	7 (7%)	1	7
41	P	114/116 (98%)	95 (83%)	17 (15%)	2 (2%)	8	41
42	Q	121/123 (98%)	91 (75%)	21 (17%)	9 (7%)	1	7
43	R	112/114 (98%)	96 (86%)	12 (11%)	4 (4%)	3	23
44	S	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	7	38
45	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	13	49
46	U	80/82 (98%)	60 (75%)	18 (22%)	2 (2%)	5	32
47	V	78/80 (98%)	61 (78%)	14 (18%)	3 (4%)	3	22
48	W	63/65 (97%)	59 (94%)	2 (3%)	2 (3%)	4	26
49	X	77/79 (98%)	67 (87%)	10 (13%)	0	100	100
50	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
51	Z	63/65 (97%)	45 (71%)	13 (21%)	5 (8%)	1	6
52	a	130/223 (58%)	106 (82%)	20 (15%)	4 (3%)	4	26
All	All	5983/6182 (97%)	5179 (87%)	687 (12%)	117 (2%)	11	38

All (117) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
3	d	83	VAL
6	g	9	VAL
7	h	55	VAL
7	h	80	THR
10	k	92	GLU

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Mol	Chain	Res	Type
11	l	31	GLY
12	m	59	ARG
13	n	117	ASP
14	o	34	HIS
17	r	54	VAL
24	y	24	GLU
30	E	31	ILE
31	F	37	GLN
32	G	15	PHE
32	G	76	SER
35	J	93	VAL
35	J	122	VAL
39	N	57	VAL
39	N	71	ILE
39	N	91	GLU
40	O	34	ALA
40	O	58	ASN
41	P	92	ARG
43	R	4	ALA
45	T	46	LYS
47	V	17	GLU
47	V	81	ALA
51	Z	24	LYS
51	Z	34	ARG
5	f	109	SER
7	h	60	LEU
7	h	91	ALA
7	h	113	PHE
13	n	118	ARG
32	G	6	ARG
34	I	106	PHE
36	K	86	ARG
36	K	99	ALA
37	L	11	ILE
37	L	18	GLY
39	N	90	ASP
39	N	125	GLN
40	O	35	GLN
41	P	126	ARG
42	Q	2	THR
42	Q	24	GLU
42	Q	43	LYS

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Mol	Chain	Res	Type
42	Q	77	SER
43	R	6	ILE
43	R	65	GLU
43	R	66	GLY
44	S	3	GLN
48	W	17	VAL
2	c	86	GLU
6	g	91	PHE
7	h	118	ILE
8	i	46	ASP
11	l	29	LYS
12	m	69	PRO
15	p	64	SER
32	G	75	ALA
36	K	56	LYS
37	L	129	ASN
40	O	33	GLY
40	O	37	ARG
40	O	42	LEU
42	Q	76	HIS
42	Q	101	LEU
42	Q	117	GLY
44	S	33	VAL
51	Z	9	GLU
52	a	52	ALA
52	a	202	THR
1	b	147	PRO
3	d	53	THR
4	e	40	GLY
7	h	32	GLY
7	h	79	PRO
8	i	11	GLN
8	i	26	ALA
10	k	93	GLN
11	l	10	GLU
11	l	115	GLU
12	m	6	ARG
18	s	40	ASN
35	J	23	THR
36	K	92	THR
39	N	102	PHE
40	O	75	ASP

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Mol	Chain	Res	Type
42	Q	116	TYR
46	U	28	ARG
52	a	6	LYS
6	g	118	PRO
8	i	22	PRO
10	k	106	GLU
18	s	64	ALA
20	u	6	ARG
28	C	41	VAL
35	J	121	ASN
38	M	47	ASP
51	Z	64	ALA
3	d	80	SER
32	G	148	GLY
36	K	54	LEU
47	V	55	GLY
48	W	13	THR
51	Z	14	ALA
52	a	178	VAL
42	Q	27	PRO
7	h	108	VAL
20	u	54	PRO
4	e	138	PRO
11	l	88	GLY
3	d	42	GLY
28	C	40	PRO
46	U	30	GLY

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	b	216/216 (100%)	212 (98%)	4 (2%)	57	81
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	e	148/148 (100%)	146 (99%)	2 (1%)	67	86
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	111 (97%)	3 (3%)	46	76
7	h	100/100 (100%)	99 (99%)	1 (1%)	76	90
8	i	109/109 (100%)	108 (99%)	1 (1%)	78	91
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	100 (97%)	3 (3%)	42	74
11	l	102/102 (100%)	100 (98%)	2 (2%)	55	80
12	m	109/109 (100%)	108 (99%)	1 (1%)	78	91
13	n	100/100 (100%)	99 (99%)	1 (1%)	76	90
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	97 (98%)	2 (2%)	55	80
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	66 (98%)	1 (2%)	65	85
24	y	55/55 (100%)	54 (98%)	1 (2%)	59	82
25	z	48/48 (100%)	47 (98%)	1 (2%)	53	79
26	A	59/62 (95%)	59 (100%)	0	100	100
27	B	47/47 (100%)	47 (100%)	0	100	100
28	C	45/45 (100%)	44 (98%)	1 (2%)	52	79
29	D	38/38 (100%)	37 (97%)	1 (3%)	46	76
30	E	51/51 (100%)	51 (100%)	0	100	100
31	F	34/34 (100%)	34 (100%)	0	100	100
32	G	186/186 (100%)	184 (99%)	2 (1%)	73	88
33	H	170/170 (100%)	170 (100%)	0	100	100
34	I	172/172 (100%)	168 (98%)	4 (2%)	50	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	J	119/119 (100%)	119 (100%)	0	100	100
36	K	87/87 (100%)	87 (100%)	0	100	100
37	L	124/124 (100%)	123 (99%)	1 (1%)	81	93
38	M	104/104 (100%)	104 (100%)	0	100	100
39	N	105/105 (100%)	101 (96%)	4 (4%)	33	67
40	O	86/86 (100%)	86 (100%)	0	100	100
41	P	89/89 (100%)	88 (99%)	1 (1%)	73	88
42	Q	103/103 (100%)	100 (97%)	3 (3%)	42	74
43	R	92/92 (100%)	91 (99%)	1 (1%)	73	88
44	S	83/83 (100%)	83 (100%)	0	100	100
45	T	76/76 (100%)	75 (99%)	1 (1%)	69	87
46	U	65/65 (100%)	64 (98%)	1 (2%)	65	85
47	V	74/74 (100%)	73 (99%)	1 (1%)	67	86
48	W	56/56 (100%)	56 (100%)	0	100	100
49	X	70/70 (100%)	70 (100%)	0	100	100
50	Y	65/65 (100%)	65 (100%)	0	100	100
51	Z	55/55 (100%)	52 (94%)	3 (6%)	21	57
52	a	110/174 (63%)	108 (98%)	2 (2%)	59	82
All	All	4967/5034 (99%)	4918 (99%)	49 (1%)	77	90

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	42	ARG
1	b	129	LEU
1	b	203	VAL
1	b	222	THR
4	e	29	ARG
4	e	168	LEU
6	g	9	VAL
6	g	86	ASP
6	g	110	VAL
7	h	118	ILE
8	i	126	ARG
10	k	53	LYS
10	k	58	LEU

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Mol	Chain	Res	Type
10	k	80	ASP
11	l	64	PHE
11	l	94	THR
12	m	97	GLN
13	n	117	ASP
15	p	19	PHE
15	p	88	ARG
23	x	77	TYR
24	y	17	GLU
25	z	30	ARG
28	C	34	GLU
29	D	1	MET
32	G	81	ASP
32	G	125	PHE
34	I	57	LYS
34	I	104	MET
34	I	136	VAL
34	I	164	ARG
37	L	9	ARG
39	N	11	ARG
39	N	86	LEU
39	N	105	ARG
39	N	126	PHE
41	P	73	VAL
42	Q	17	LYS
42	Q	101	LEU
42	Q	120	ARG
43	R	113	LYS
45	T	88	ARG
46	U	55	ASP
47	V	8	GLN
51	Z	10	PRO
51	Z	40	PRO
51	Z	65	ARG
52	a	208	TYR
52	a	225	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	20	ASN
1	b	36	ASN

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Mol	Chain	Res	Type
1	b	52	HIS
1	b	59	GLN
1	b	85	ASN
1	b	89	ASN
1	b	127	ASN
1	b	133	ASN
1	b	162	GLN
2	c	32	ASN
2	c	49	GLN
2	c	136	ASN
2	c	164	GLN
3	d	41	GLN
3	d	97	ASN
3	d	165	HIS
4	e	4	HIS
4	e	20	ASN
4	e	51	ASN
5	f	37	ASN
5	f	115	GLN
6	g	18	GLN
7	h	4	ASN
8	i	33	ASN
8	i	104	GLN
9	j	58	ASN
9	j	135	GLN
9	j	138	GLN
10	k	5	GLN
10	k	29	HIS
11	l	54	GLN
11	l	93	ASN
12	m	60	GLN
12	m	97	GLN
13	n	3	HIS
13	n	18	GLN
13	n	81	ASN
14	o	100	HIS
16	q	36	GLN
17	r	86	GLN
17	r	89	HIS
17	r	91	GLN
19	t	48	GLN
20	u	39	ASN

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Mol	Chain	Res	Type
20	u	52	ASN
20	u	68	ASN
22	w	8	ASN
23	x	22	ASN
24	y	20	ASN
24	y	27	ASN
25	z	8	GLN
26	A	20	ASN
27	B	5	ASN
32	G	17	HIS
32	G	167	HIS
33	H	7	ASN
33	H	175	HIS
33	H	184	ASN
34	I	39	GLN
34	I	58	GLN
34	I	73	ASN
34	I	115	GLN
34	I	130	ASN
34	I	151	GLN
34	I	163	GLN
36	K	14	GLN
36	K	63	ASN
38	M	17	GLN
38	M	66	GLN
38	M	75	GLN
39	N	3	ASN
39	N	4	GLN
39	N	24	ASN
39	N	31	GLN
39	N	74	GLN
39	N	125	GLN
40	O	56	HIS
41	P	27	ASN
41	P	39	ASN
41	P	63	GLN
42	Q	4	ASN
42	Q	72	ASN
42	Q	111	GLN
44	S	34	ASN
46	U	29	ASN
46	U	63	GLN

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Mol	Chain	Res	Type
47	V	30	HIS
48	W	18	GLN
49	X	13	HIS
49	X	51	HIS
50	Y	20	ASN
52	a	57	GLN
52	a	67	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	150 (9%)	1 (0%)
54	4	3030/3031 (99%)	345 (11%)	13 (0%)
55	5	76/77 (98%)	7 (9%)	0
56	1	9/10 (90%)	0	0
57	7	75/76 (98%)	9 (12%)	0
All	All	4728/4733 (99%)	511 (10%)	14 (0%)

All (511) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	6	G
53	3	7	A
53	3	9	G
53	3	22	G
53	3	32	A
53	3	39	G
53	3	48	C
53	3	51	A
53	3	70	U
53	3	71	A
53	3	82	G
53	3	87	C
53	3	94	G
53	3	100	G
53	3	144	G
53	3	164	G
53	3	173	U
53	3	183	C
53	3	210	C
53	3	247	G

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Mol	Chain	Res	Type
53	3	251	G
53	3	266	G
53	3	267	C
53	3	280	C
53	3	281	G
53	3	289	G
53	3	328	C
53	3	345	C
53	3	351	G
53	3	352	C
53	3	367	U
53	3	372	C
53	3	411	A
53	3	412	A
53	3	413	G
53	3	421	U
53	3	422	C
53	3	423	G
53	3	429	U
53	3	441	A
53	3	467	U
53	3	481	G
53	3	485	U
53	3	486	U
53	3	497	G
53	3	499	A
53	3	500	G
53	3	511	C
53	3	518	C
53	3	547	A
53	3	561	U
53	3	572	A
53	3	573	A
53	3	575	G
53	3	576	C
53	3	577	G
53	3	618	C
53	3	642	A
53	3	665	A
53	3	702	A
53	3	703	G
53	3	724	G

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Mol	Chain	Res	Type
53	3	755	G
53	3	777	A
53	3	794	A
53	3	815	A
53	3	817	C
53	3	818	G
53	3	819	A
53	3	821	G
53	3	843	U
53	3	844	G
53	3	846	G
53	3	871	U
53	3	890	G
53	3	902	G
53	3	926	G
53	3	934	C
53	3	935	A
53	3	960	U
53	3	961	U
53	3	966	G
53	3	969	A
53	3	975	A
53	3	976	G
53	3	977	A
53	3	992	U
53	3	993	G
53	3	1004	A
53	3	1028	C
53	3	1030	U
53	3	1031	C
53	3	1032	G
53	3	1034	G
53	3	1053	G
53	3	1054	C
53	3	1064	G
53	3	1094	G
53	3	1101	A
53	3	1130	A
53	3	1136	C
53	3	1137	C
53	3	1138	G
53	3	1139	G

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Mol	Chain	Res	Type
53	3	1140	C
53	3	1159	U
53	3	1168	U
53	3	1182	G
53	3	1184	G
53	3	1191	A
53	3	1196	A
53	3	1198	G
53	3	1201	A
53	3	1202	U
53	3	1212	U
53	3	1213	A
53	3	1225	A
53	3	1238	A
53	3	1241	G
53	3	1257	A
53	3	1258	G
53	3	1261	A
53	3	1275	A
53	3	1278	G
53	3	1280	A
53	3	1282	C
53	3	1286	U
53	3	1287	A
53	3	1300	G
53	3	1302	C
53	3	1317	C
53	3	1320	C
53	3	1346	A
53	3	1347	G
53	3	1363	A
53	3	1364	U
53	3	1378	C
53	3	1379	G
53	3	1395	C
53	3	1419	G
53	3	1441	A
53	3	1446	A
53	3	1452	C
53	3	1492	A
53	3	1503	A
53	3	1506	U

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Mol	Chain	Res	Type
53	3	1517	G
53	3	1529	G
53	3	1530	G
53	3	1533	C
54	4	10	A
54	4	12	U
54	4	34	U
54	4	35	G
54	4	46	G
54	4	51	G
54	4	71	A
54	4	74	A
54	4	75	G
54	4	119	A
54	4	120	U
54	4	139	U
54	4	140	C
54	4	141	G
54	4	162	U
54	4	163	C
54	4	181	A
54	4	196	A
54	4	216	A
54	4	221	A
54	4	222	A
54	4	228	C
54	4	229	C
54	4	233	A
54	4	248	G
54	4	249	C
54	4	255	A
54	4	265	A
54	4	266	G
54	4	276	U
54	4	294	A
54	4	301	G
54	4	311	A
54	4	323	C
54	4	324	A
54	4	329	G
54	4	330	A
54	4	361	G

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Mol	Chain	Res	Type
54	4	371	A
54	4	372	G
54	4	386	G
54	4	387	U
54	4	404	A
54	4	406	G
54	4	411	G
54	4	412	A
54	4	424	G
54	4	457	A
54	4	481	G
54	4	491	G
54	4	504	A
54	4	505	A
54	4	508	A
54	4	529	A
54	4	530	G
54	4	532	A
54	4	533	G
54	4	543	G
54	4	545	U
54	4	548	G
54	4	563	A
54	4	573	U
54	4	574	A
54	4	575	A
54	4	588	U
54	4	603	A
54	4	613	A
54	4	614	A
54	4	627	A
54	4	637	A
54	4	646	U
54	4	654	A
54	4	655	A
54	4	669	G
54	4	686	U
54	4	695	G
54	4	714	U
54	4	717	C
54	4	730	A
54	4	747	C

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Mol	Chain	Res	Type
54	4	752	A
54	4	764	A
54	4	775	G
54	4	776	G
54	4	782	A
54	4	784	G
54	4	785	G
54	4	805	G
54	4	812	C
54	4	819	A
54	4	827	U
54	4	828	U
54	4	830	G
54	4	845	A
54	4	846	U
54	4	847	U
54	4	858	G
54	4	860	U
54	4	878	A
54	4	887	U
54	4	888	C
54	4	896	A
54	4	897	C
54	4	910	A
54	4	932	U
54	4	941	A
54	4	946	C
54	4	961	C
54	4	974	G
54	4	983	A
54	4	995	C
54	4	996	A
54	4	1012	U
54	4	1013	C
54	4	1021	A
54	4	1022	G
54	4	1025	G
54	4	1026	G
54	4	1027	C
54	4	1029	G
54	4	1050	A
54	4	1051	A

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Mol	Chain	Res	Type
54	4	1058	G
54	4	1063	U
54	4	1064	C
54	4	1066	G
54	4	1067	U
54	4	1070	C
54	4	1101	C
54	4	1110	G
54	4	1133	G
54	4	1154	A
54	4	1155	A
54	4	1161	U
54	4	1173	C
54	4	1174	A
54	4	1175	G
54	4	1182	A
54	4	1188	U
54	4	1190	G
54	4	1193	U
54	4	1194	U
54	4	1198	A
54	4	1199	G
54	4	1200	C
54	4	1207	C
54	4	1212	A
54	4	1216	A
54	4	1217	A
54	4	1218	A
54	4	1232	C
54	4	1234	G
54	4	1239	A
54	4	1260	U
54	4	1263	C
54	4	1270	A
54	4	1271	A
54	4	1301	U
54	4	1302	U
54	4	1303	A
54	4	1304	U
54	4	1305	G
54	4	1307	G
54	4	1308	U

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Mol	Chain	Res	Type
54	4	1334	G
54	4	1340	G
54	4	1376	G
54	4	1378	G
54	4	1379	C
54	4	1381	A
54	4	1384	G
54	4	1399	G
54	4	1400	A
54	4	1403	A
54	4	1417	C
54	4	1429	A
54	4	1449	A
54	4	1457	U
54	4	1458	C
54	4	1473	C
54	4	1493	A
54	4	1507	U
54	4	1511	A
54	4	1544	G
54	4	1547	A
54	4	1548	A
54	4	1556	C
54	4	1582	C
54	4	1589	C
54	4	1610	G
54	4	1618	A
54	4	1619	G
54	4	1622	A
54	4	1643	A
54	4	1652	G
54	4	1663	A
54	4	1664	C
54	4	1683	G
54	4	1687	U
54	4	1688	G
54	4	1697	A
54	4	1706	U
54	4	1712	U
54	4	1736	A
54	4	1739	C
54	4	1744	A

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Mol	Chain	Res	Type
54	4	1775	U
54	4	1776	U
54	4	1777	G
54	4	1802	G
54	4	1843	G
54	4	1857	U
54	4	1858	C
54	4	1866	G
54	4	1886	U
54	4	1892	C
54	4	1901	A
54	4	1908	A
54	4	1928	C
54	4	1929	A
54	4	1936	A
54	4	1944	C
54	4	1957	A
54	4	2029	A
54	4	2034	G
54	4	2035	G
54	4	2041	A
54	4	2042	C
54	4	2057	G
54	4	2058	G
54	4	2065	A
54	4	2066	A
54	4	2072	U
54	4	2083	U
54	4	2095	C
54	4	2098	A
54	4	2099	U
54	4	2100	G
54	4	2119	U
54	4	2120	G
54	4	2121	U
54	4	2125	C
54	4	2150	U
54	4	2151	C
54	4	2158	A
54	4	2159	A
54	4	2171	C
54	4	2177	G

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Mol	Chain	Res	Type
54	4	2183	C
54	4	2184	G
54	4	2188	A
54	4	2189	G
54	4	2190	A
54	4	2191	C
54	4	2197	G
54	4	2200	C
54	4	2239	U
54	4	2240	G
54	4	2246	U
54	4	2247	A
54	4	2259	U
54	4	2260	U
54	4	2261	G
54	4	2273	C
54	4	2274	C
54	4	2277	U
54	4	2290	G
54	4	2300	U
54	4	2301	A
54	4	2302	C
54	4	2306	C
54	4	2317	U
54	4	2326	A
54	4	2331	U
54	4	2332	G
54	4	2339	A
54	4	2340	A
54	4	2341	U
54	4	2353	A
54	4	2366	G
54	4	2407	G
54	4	2411	C
54	4	2414	G
54	4	2415	A
54	4	2425	A
54	4	2433	U
54	4	2435	G
54	4	2437	A
54	4	2453	G
54	4	2455	A

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Mol	Chain	Res	Type
54	4	2462	U
54	4	2478	C
54	4	2511	G
54	4	2513	C
54	4	2530	U
54	4	2531	C
54	4	2534	A
54	4	2535	A
54	4	2551	U
54	4	2557	G
54	4	2558	A
54	4	2563	A
54	4	2569	U
54	4	2576	A
54	4	2604	A
54	4	2626	C
54	4	2630	G
54	4	2631	A
54	4	2632	U
54	4	2633	G
54	4	2646	A
54	4	2657	G
54	4	2675	A
54	4	2682	U
54	4	2695	G
54	4	2700	A
54	4	2701	C
54	4	2730	A
54	4	2737	U
54	4	2741	U
54	4	2757	U
54	4	2774	C
54	4	2783	G
54	4	2817	U
54	4	2818	U
54	4	2842	G
54	4	2872	G
54	4	2876	A
54	4	2878	A
54	4	2885	A
54	4	2892	A
54	4	2893	A

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Mol	Chain	Res	Type
54	4	2906	A
54	4	2907	U
54	4	2919	G
54	4	2925	U
54	4	2928	A
54	4	2937	A
54	4	2948	A
54	4	2949	A
54	4	2995	G
54	4	2996	A
54	4	3008	C
54	4	3011	A
54	4	3012	U
55	5	8	U
55	5	9	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	74	C
55	5	76	A
57	7	17	C
57	7	21	A
57	7	45	U
57	7	46	G
57	7	47	U
57	7	48	C
57	7	49	C
57	7	61	C
57	7	74	C

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	3	1190	G
54	4	227	A
54	4	490	C
54	4	774	G
54	4	859	G
54	4	1020	A
54	4	1025	G
54	4	1132	A
54	4	1154	A

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Mol	Chain	Res	Type
54	4	1618	A
54	4	2424	U
54	4	2454	C
54	4	2884	U
54	4	3001	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

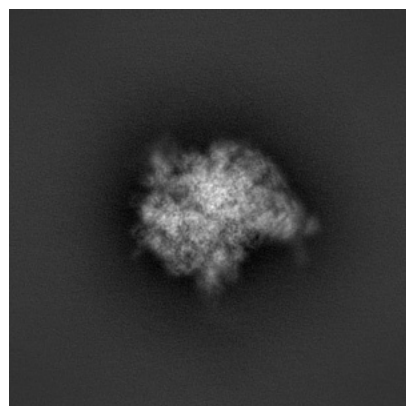
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21858. These allow visual inspection of the internal detail of the map and identification of artifacts.

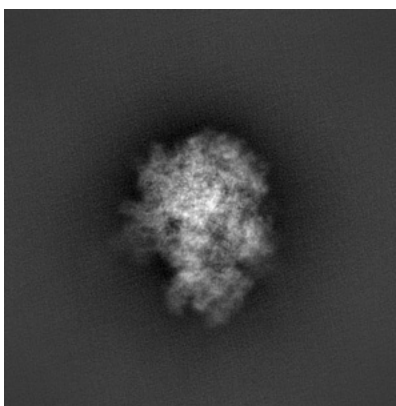
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

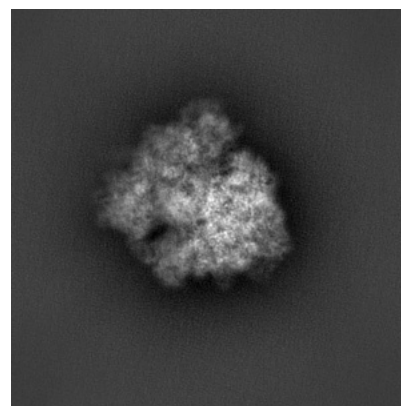
6.1.1 Primary map



X

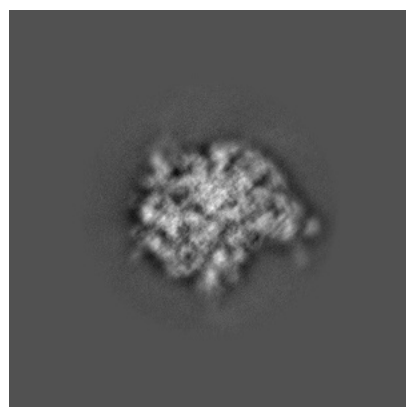


Y

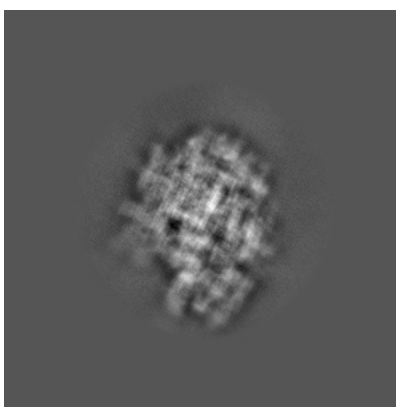


Z

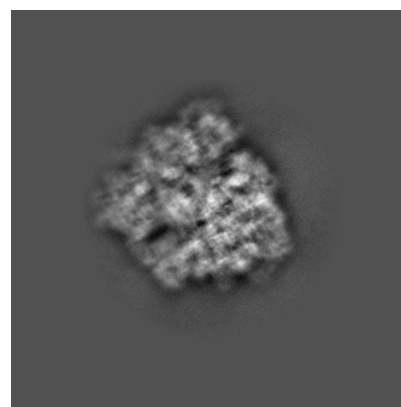
6.1.2 Raw map



X



Y

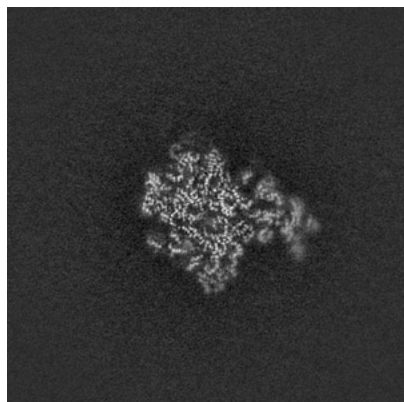


Z

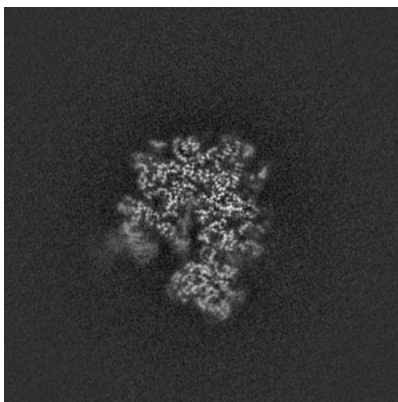
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

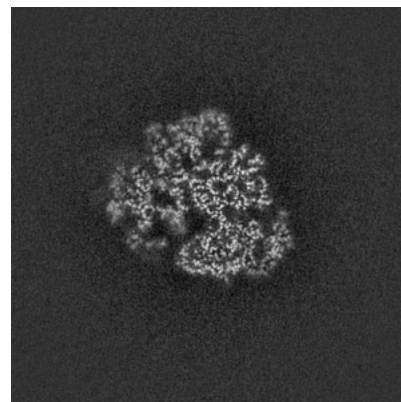
6.2.1 Primary map



X Index: 304

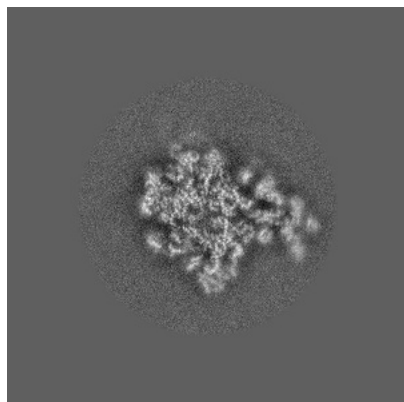


Y Index: 304

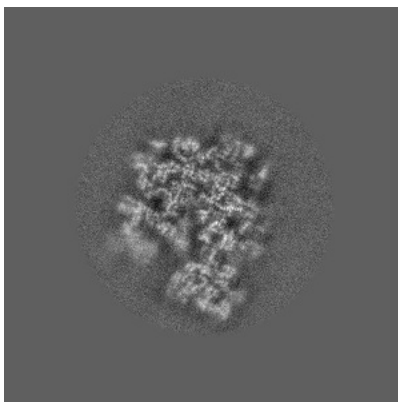


Z Index: 304

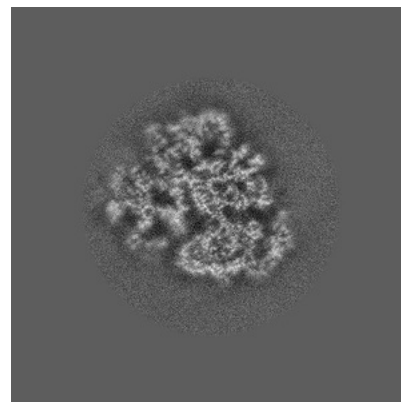
6.2.2 Raw map



X Index: 304



Y Index: 304

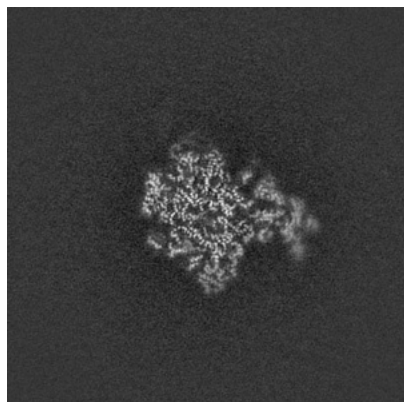


Z Index: 304

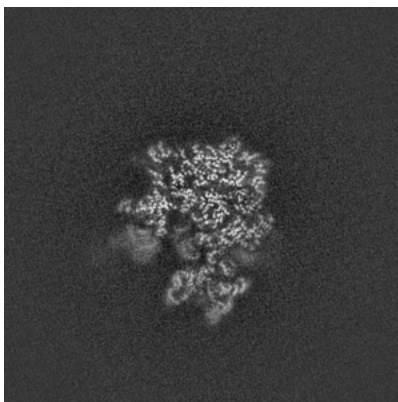
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

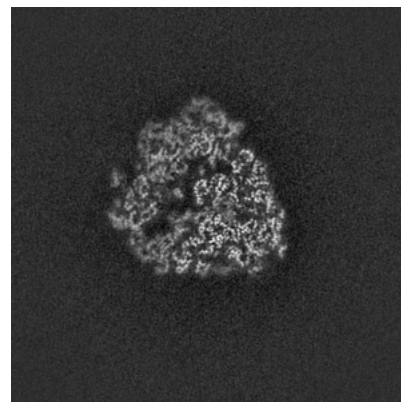
6.3.1 Primary map



X Index: 303

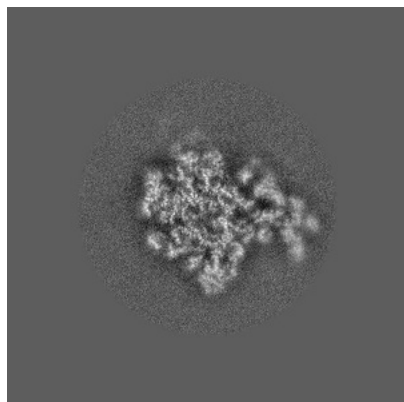


Y Index: 317

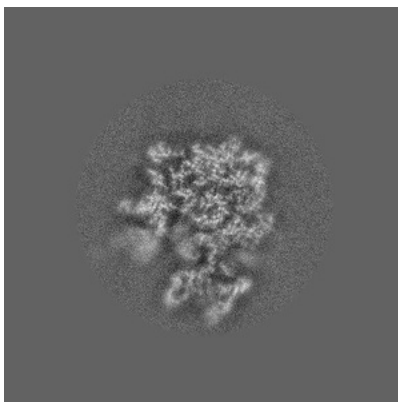


Z Index: 290

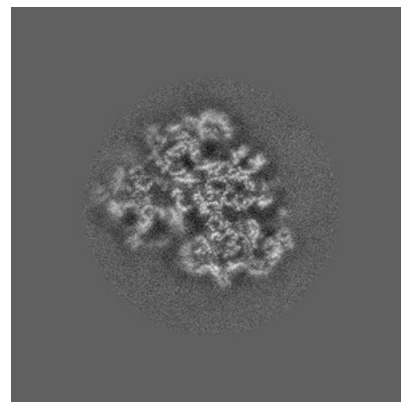
6.3.2 Raw map



X Index: 302



Y Index: 318



Z Index: 307

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

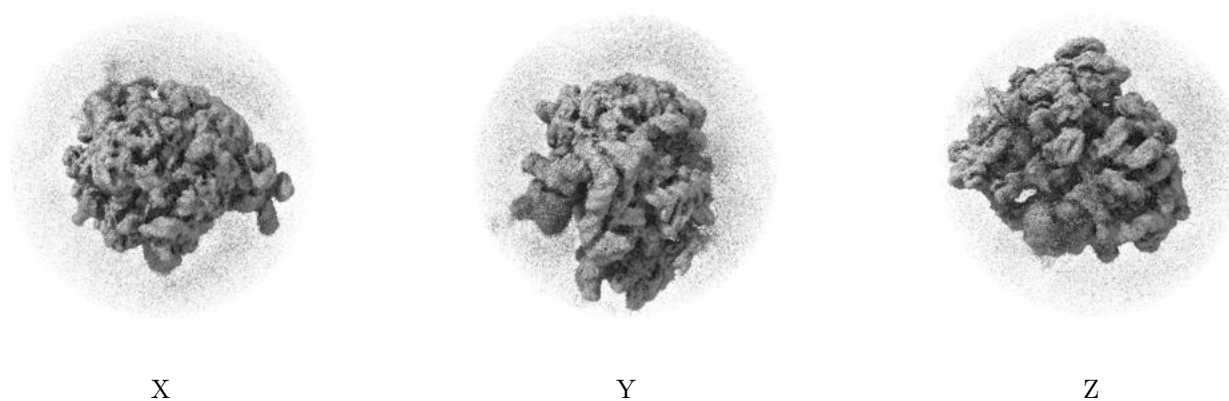
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

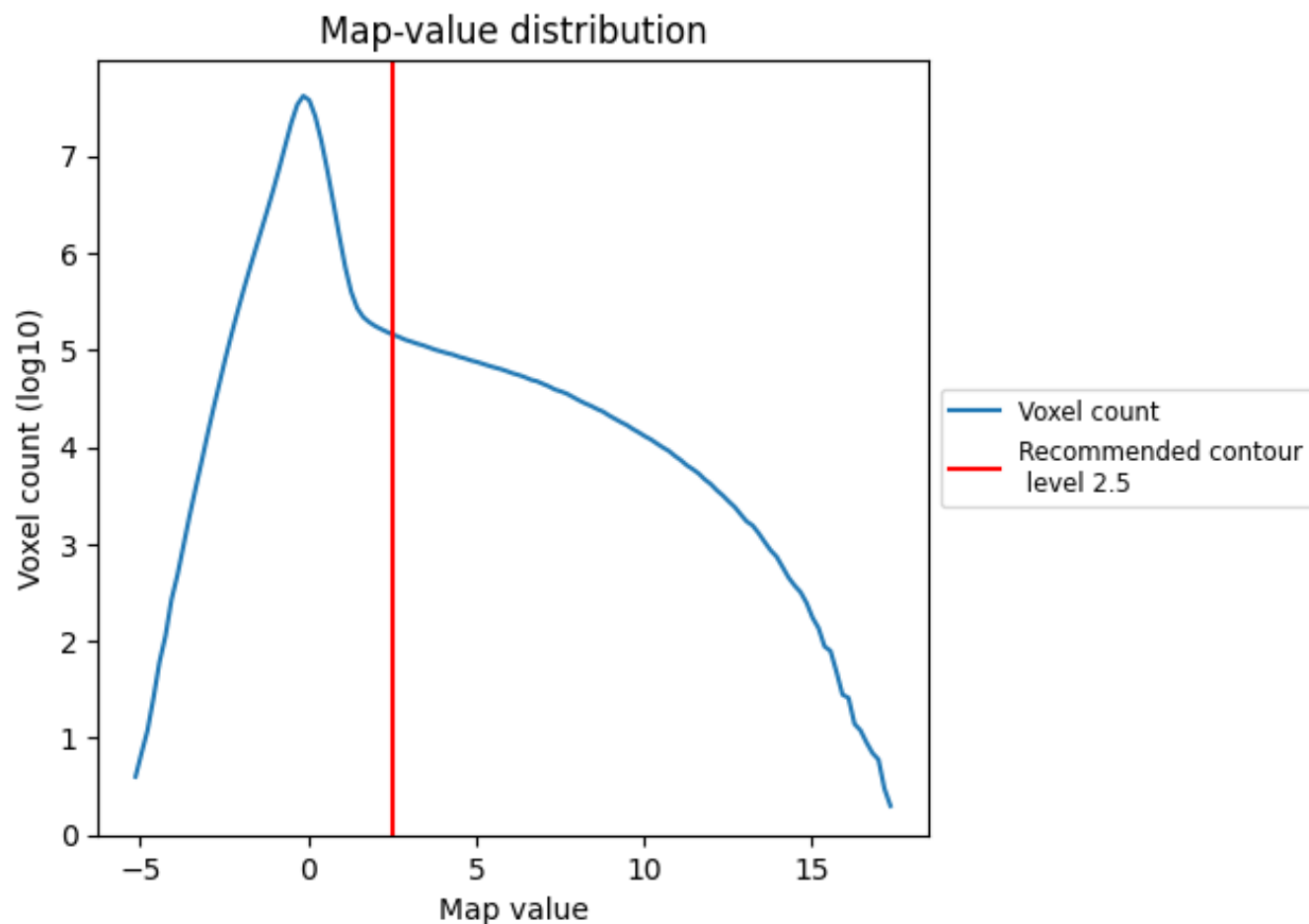
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

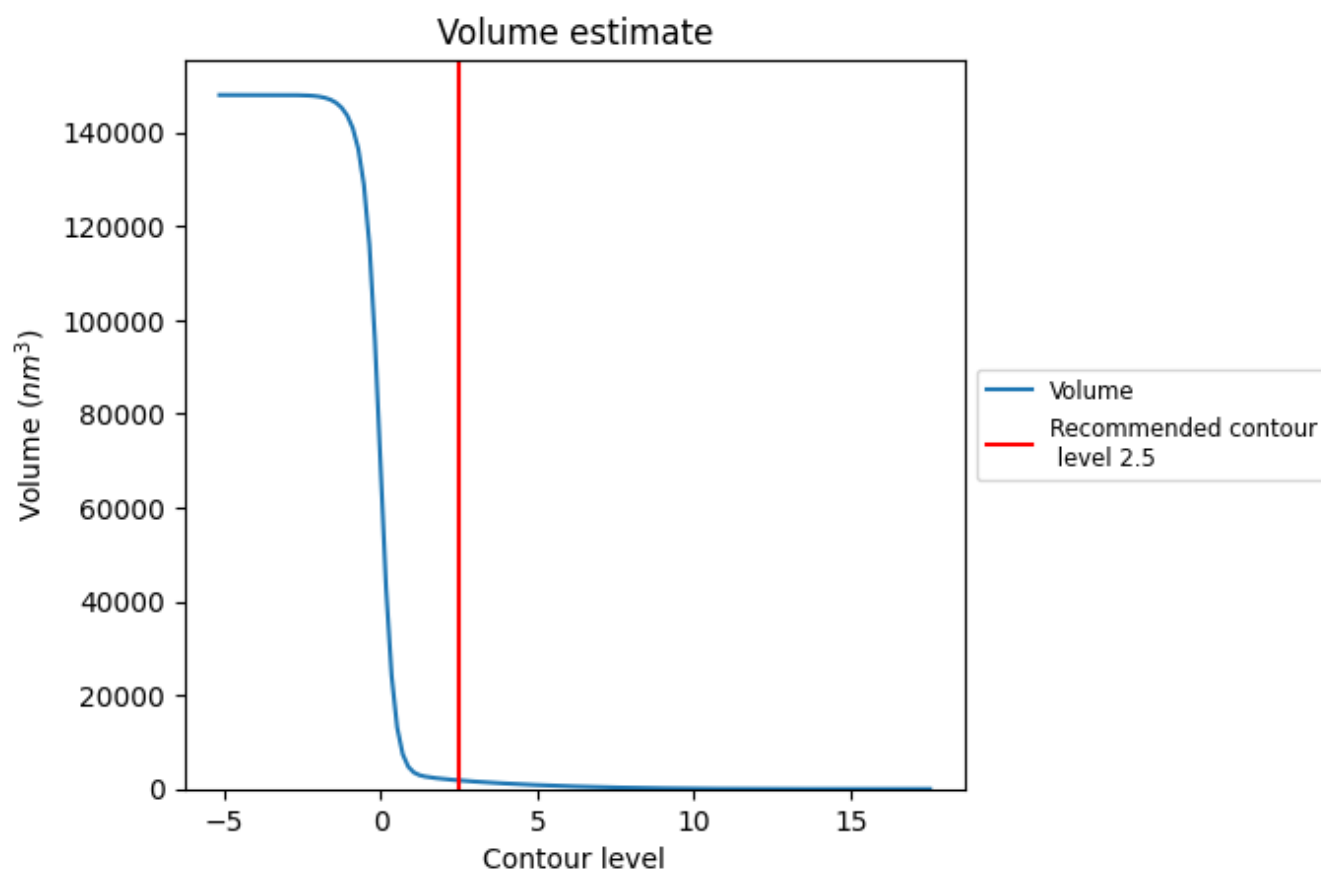
This section contains the results of statistical analysis of the map.

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.

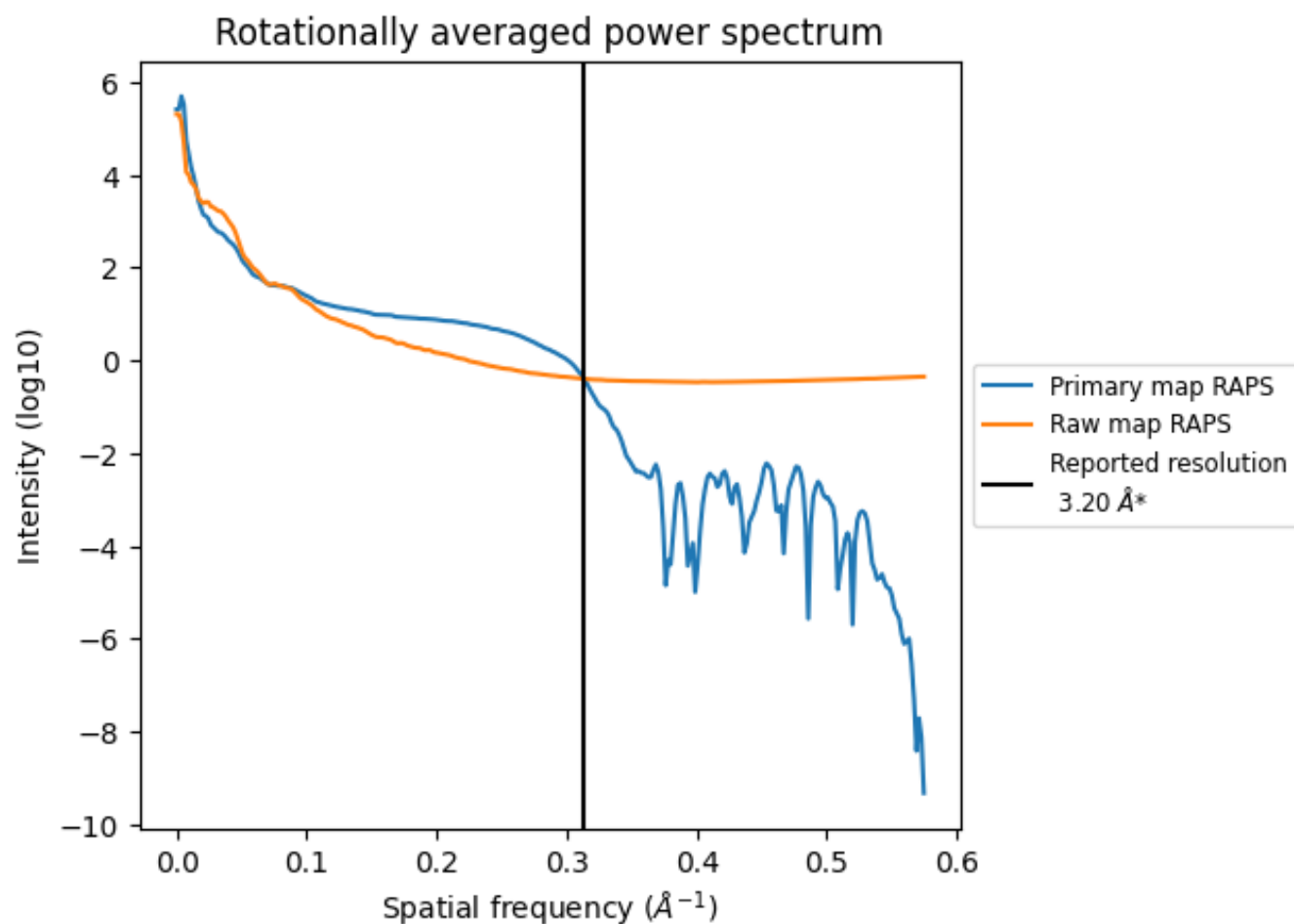
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1831 nm^3 ; this corresponds to an approximate mass of 1654 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 ⓘ

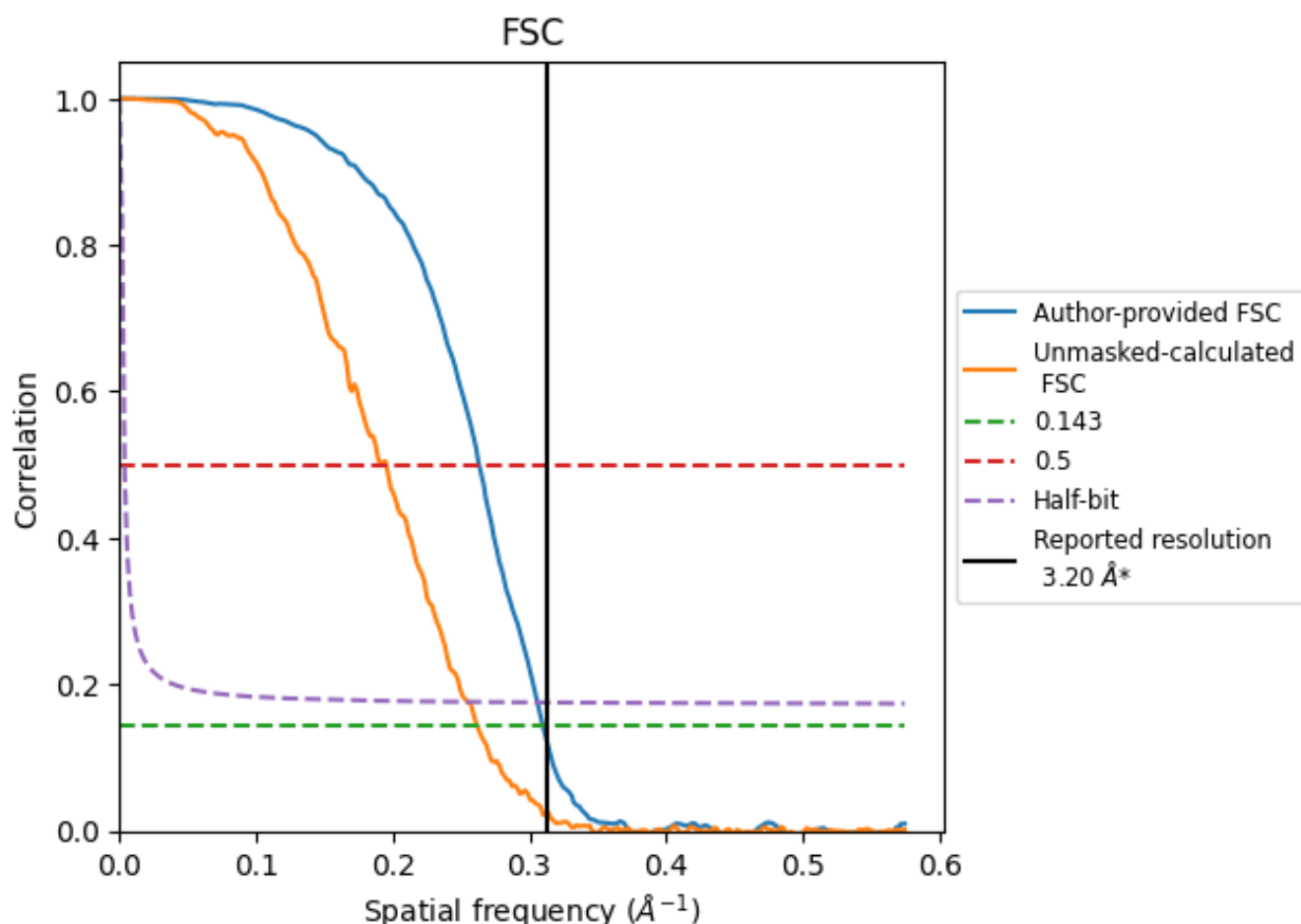


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}

8.2 Resolution estimates [i](#)

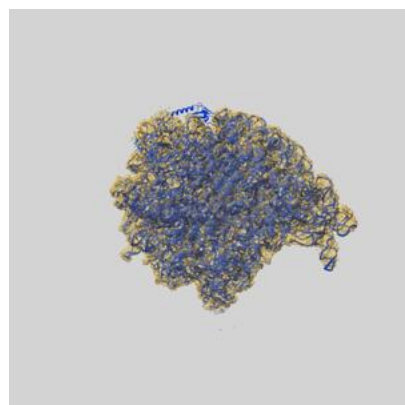
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.80	3.27
Unmasked-calculated*	3.82	5.24	3.92

*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 3.82 differs from the reported value 3.2 by more than 10 %

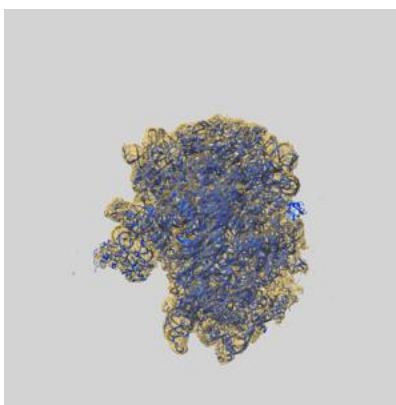
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21858 and PDB model 6WNW. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

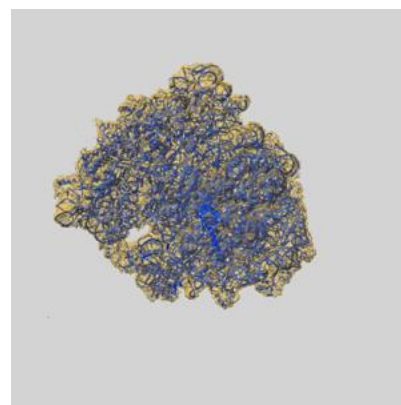
9.1 Map-model overlay [i](#)



X



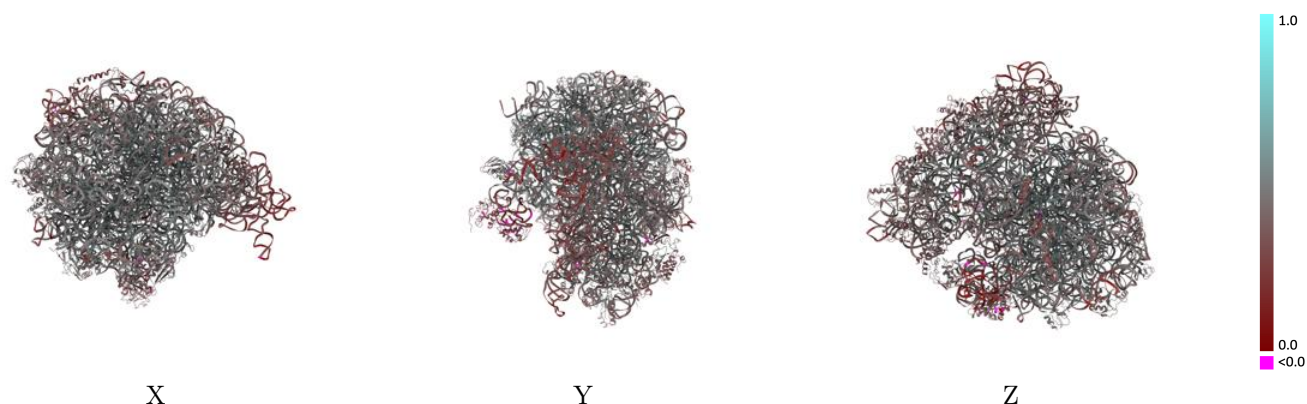
Y



Z

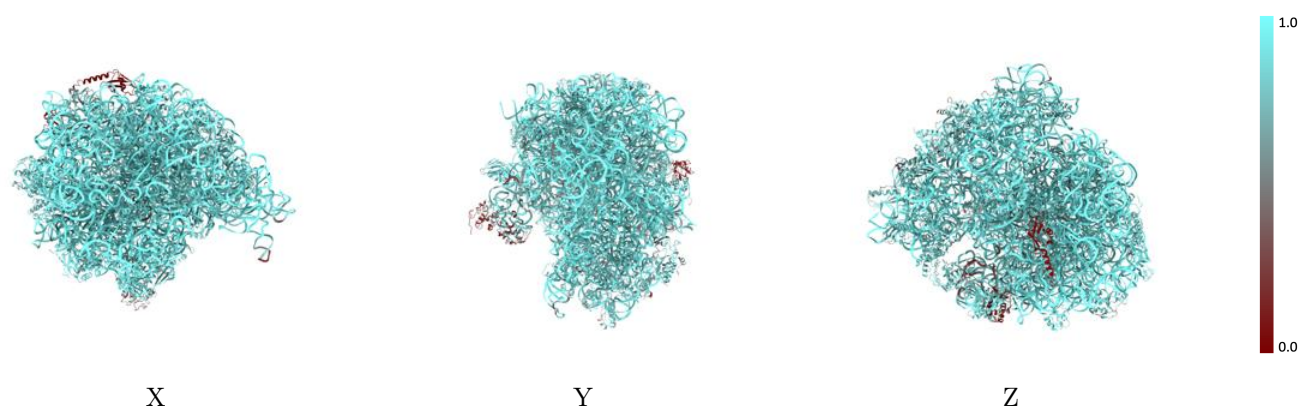
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



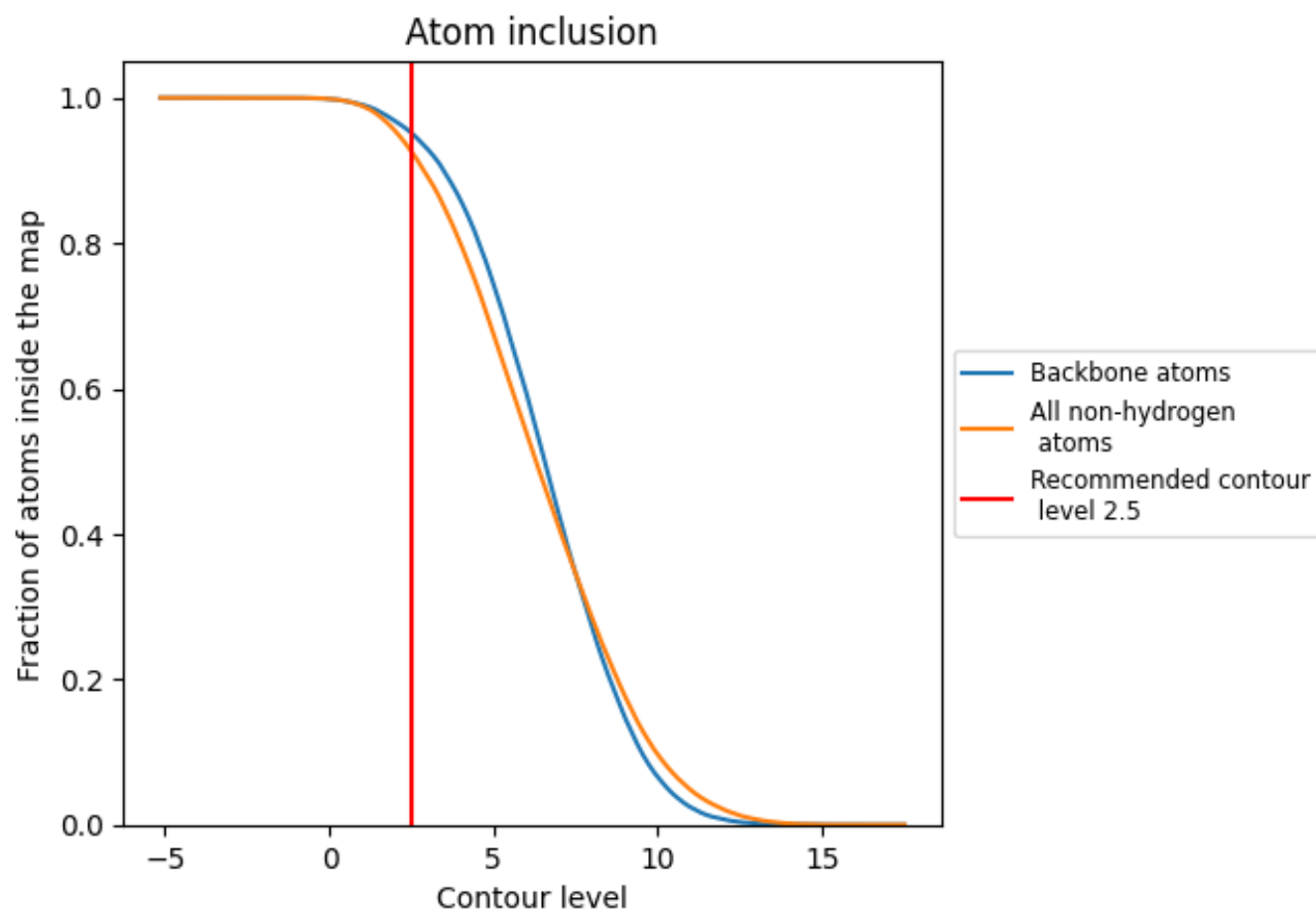
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9264	 0.4300
1	 0.9437	 0.4570
3	 0.9753	 0.4050
4	 0.9789	 0.4510
5	 0.9451	 0.4090
7	 0.7838	 0.3290
A	 0.7867	 0.3940
B	 0.9159	 0.4750
C	 0.8234	 0.4620
D	 0.9268	 0.5000
E	 0.9450	 0.5130
F	 0.9041	 0.4920
G	 0.7740	 0.3920
H	 0.8322	 0.4340
I	 0.8119	 0.3380
J	 0.8670	 0.4460
K	 0.8720	 0.3990
L	 0.7712	 0.3840
M	 0.8719	 0.4490
N	 0.8693	 0.3890
O	 0.7835	 0.3970
P	 0.9066	 0.4350
Q	 0.8426	 0.4200
R	 0.8779	 0.3930
S	 0.8695	 0.4080
T	 0.9087	 0.4380
U	 0.8485	 0.3730
V	 0.8847	 0.3980
W	 0.8951	 0.4330
X	 0.8907	 0.4100
Y	 0.8646	 0.3600
Z	 0.7162	 0.3550
a	 0.2891	 0.2280
b	 0.9127	 0.5010
c	 0.9168	 0.4930



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Chain	Atom inclusion	Q-score
d	 0.8401	 0.4480
e	 0.8755	 0.4100
f	 0.8951	 0.4240
g	 0.2609	 0.3500
h	 0.3158	 0.2410
i	 0.3943	 0.2430
j	 0.9009	 0.4710
k	 0.8796	 0.4960
l	 0.9154	 0.4780
m	 0.8954	 0.4910
n	 0.9328	 0.4860
o	 0.9154	 0.4420
p	 0.8739	 0.4710
q	 0.9251	 0.4800
r	 0.9034	 0.4750
s	 0.8672	 0.4810
t	 0.8838	 0.4530
u	 0.8893	 0.4360
v	 0.9051	 0.4600
w	 0.9159	 0.5050
x	 0.9151	 0.4850
y	 0.8531	 0.3960
z	 0.8947	 0.4760