



wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 08:11 AM EST

PDB ID : 6OIG
EMDB ID : EMD-20077
Title : Subunit joining exposes nascent pre-40S rRNA for processing and quality control
Authors : Rai, J.; Parker, M.D.; Ghalei, H.; Johnson, M.C.; Karbstein, K.; Stroupe, M.E.
Deposited on : 2019-04-09
Resolution : 3.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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

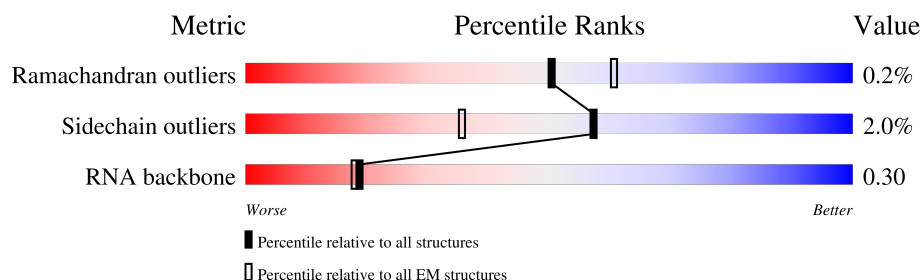
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



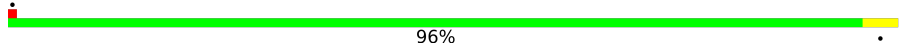
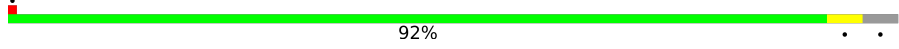
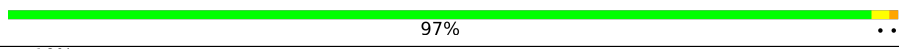
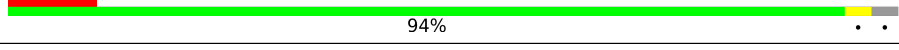
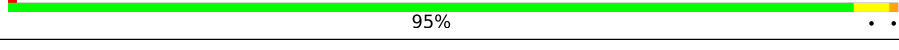
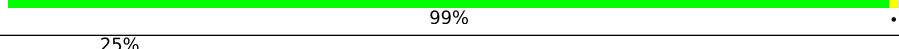
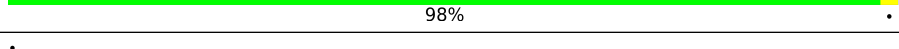
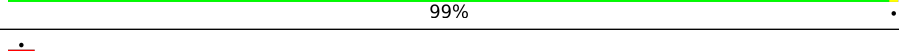
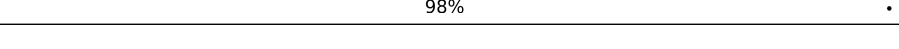
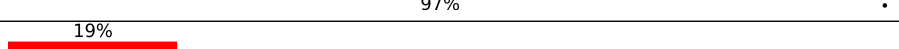
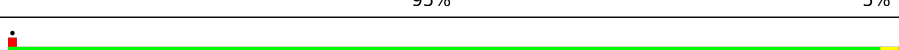
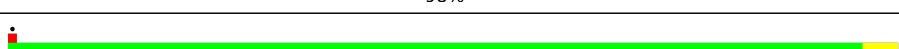
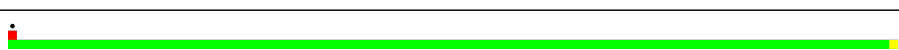
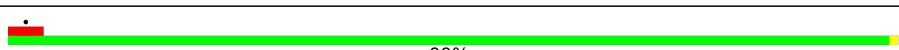
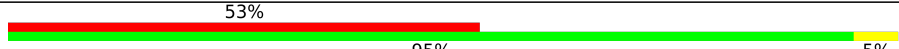


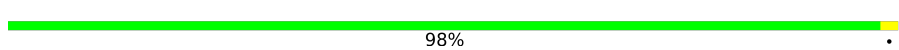
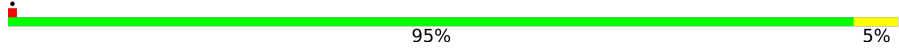

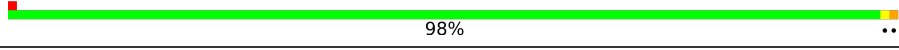
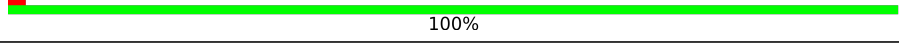
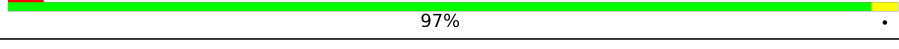
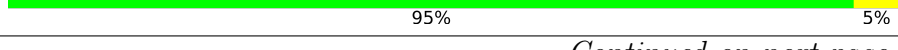

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	Z	204	
2	A	252	
3	B	386	
4	C	361	
5	D	296	
6	E	175	
7	F	222	
8	G	233	

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Mol	Chain	Length	Quality of chain
9	H	191	
10	I	220	
11	J	169	
12	s	155	
13	L	193	
14	M	136	
15	N	203	
16	O	197	
17	P	183	
18	Q	185	
19	R	188	
20	S	172	
21	T	159	
22	U	100	
23	V	136	
24	W	135	
25	X	121	
26	Y	126	
27	Z	135	
28	a	148	
29	b	58	
30	c	97	
31	d	109	
32	e	127	
33	f	106	

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Mol	Chain	Length	Quality of chain
34	g	112	 98% ..
35	h	119	 98% .
36	i	99	 97% .
37	j	87	 93% 7%
38	k	77	 97% .
39	l	50	 94% 6%
40	m	52	 98% .
41	o	105	 99% .
42	p	91	 98% ..
43	q	219	 19% 63% 35%
44	5	3394	 36% 45% 15% .
45	8	158	 28% 55% 16%
46	7	121	 41% 49% 10%
47	x	47	 51% 100%
48	y	46	 74% 100%

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 129140 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 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	z	204	Total	C	N	O	S	0	0
			1602	1026	277	290	9		

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 6 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 7 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 11 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 12 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	s	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	183	Total	C	N	O		0	0
			1443	896	287	260			

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	188	Total	C	N	O		0	0
			1522	935	326	261			

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1446	930	267	245	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1277	805	246	222	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	135	Total	C	N	O	S	0	0
			1089	682	219	187	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			969	623	170	174	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	126	Total	C	N	O		0	0
			994	625	192	177			

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	135	Total	C	N	O		0	0
			1093	710	202	181			

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1174	749	231	191	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	58	Total	C	N	O		0	0
			463	289	100	74			

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	77	Total	C	N	O		0	0
			613	391	115	107			

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 41 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0,60S acidic ribosomal protein P0,AO, L1OE.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	143	Total	C	N	O	S	0	0
			1077	687	192	195	3		

- Molecule 44 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5	3243	Total	C	N	O	P	0	0
			69359	30981	12493	22643	3242		

- Molecule 45 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 47 is a protein called P1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	x	47	Total	C	N	O	0	0
			235	141	47	47		

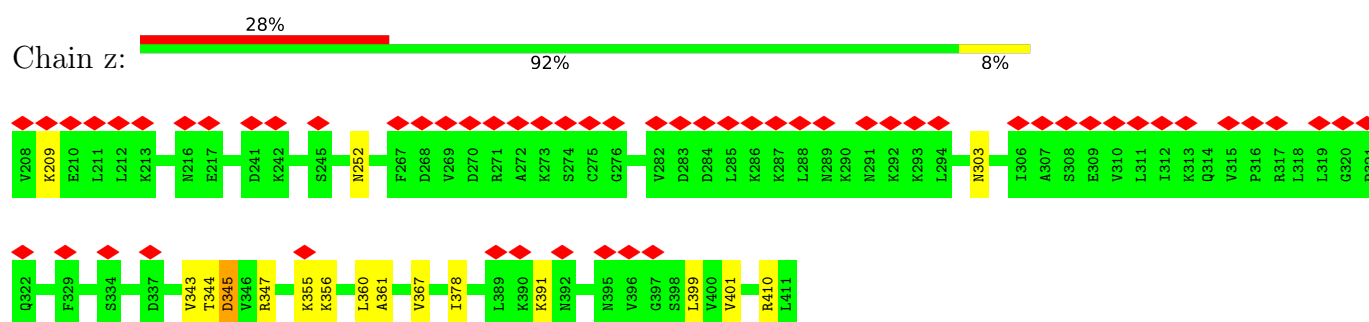
- Molecule 48 is a protein called P2.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	y	46	Total	C	N	O	0	0
			230	138	46	46		

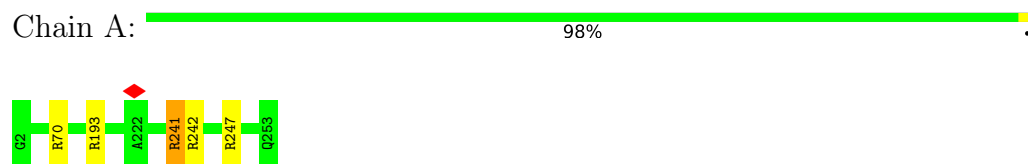
3 Residue-property plots [i](#)

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.

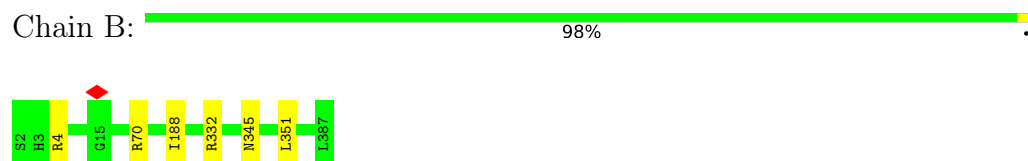
- Molecule 1: 60S ribosomal protein L1-A



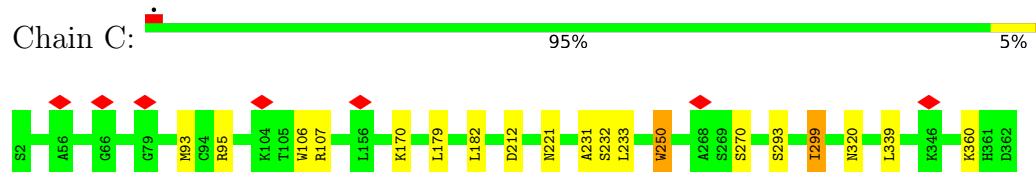
- Molecule 2: 60S ribosomal protein L2-A



- Molecule 3: 60S ribosomal protein L3

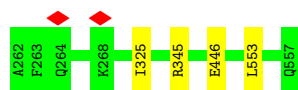


- Molecule 4: 60S ribosomal protein L4-A

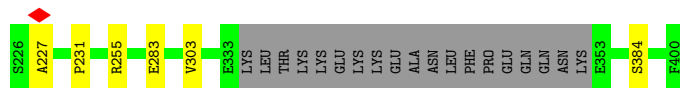
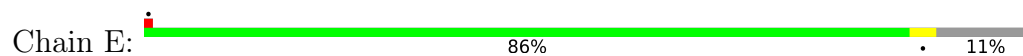


- Molecule 5: 60S ribosomal protein L5





- Molecule 6: 60S ribosomal protein L6-A



- Molecule 7: 60S ribosomal protein L7-A



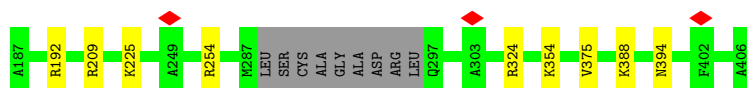
- Molecule 8: 60S ribosomal protein L8-A



- Molecule 9: 60S ribosomal protein L9-A



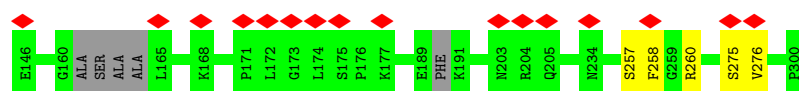
- Molecule 10: 60S ribosomal protein L10



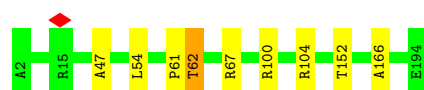
- Molecule 11: 60S ribosomal protein L11-B



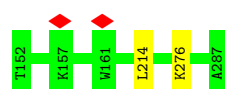
- Molecule 12: 60S ribosomal protein L12-A



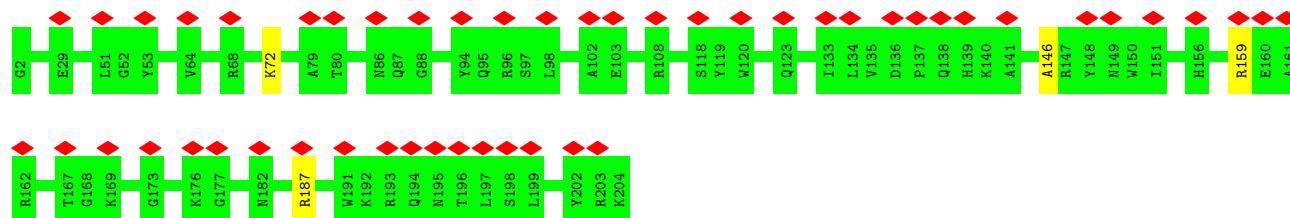
- Molecule 13: 60S ribosomal protein L13-A



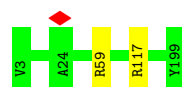
- Molecule 14: 60S ribosomal protein L14-A



- Molecule 15: 60S ribosomal protein L15-A



- Molecule 16: 60S ribosomal protein L16-A



- Molecule 17: 60S ribosomal protein L17-A



- Molecule 18: 60S ribosomal protein L18-A

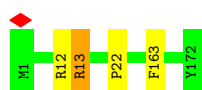




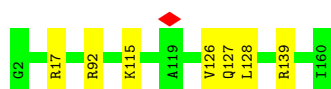
- Molecule 19: 60S ribosomal protein L19-A



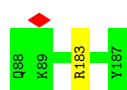
- Molecule 20: 60S ribosomal protein L20-A



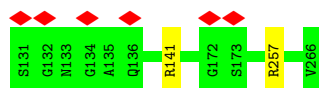
- Molecule 21: 60S ribosomal protein L21-A



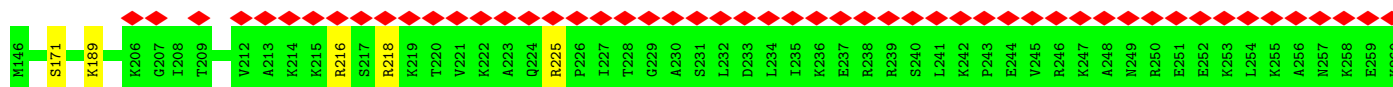
- Molecule 22: 60S ribosomal protein L22-A

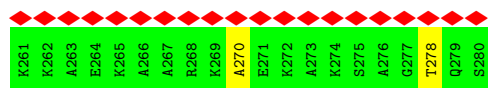


- Molecule 23: 60S ribosomal protein L23-A



- Molecule 24: 60S ribosomal protein L24-A





- Molecule 25: 60S ribosomal protein L25



- Molecule 26: 60S ribosomal protein L26-A



- Molecule 27: 60S ribosomal protein L27-A



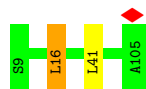
- Molecule 28: 60S ribosomal protein L28



- Molecule 29: 60S ribosomal protein L29

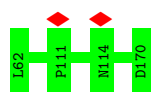


- Molecule 30: 60S ribosomal protein L30



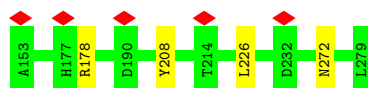
- Molecule 31: 60S ribosomal protein L31-A

Chain d:  100%



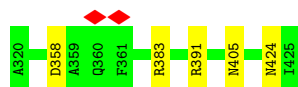
- Molecule 32: 60S ribosomal protein L32

Chain e:  97%



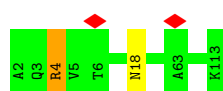
- Molecule 33: 60S ribosomal protein L33-A

Chain f:  95%



- Molecule 34: 60S ribosomal protein L34-A

Chain g:  98%



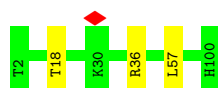
- Molecule 35: 60S ribosomal protein L35-A

Chain h:  98%




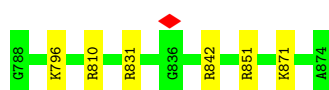
- Molecule 36: 60S ribosomal protein L36-A

Chain i:  97%

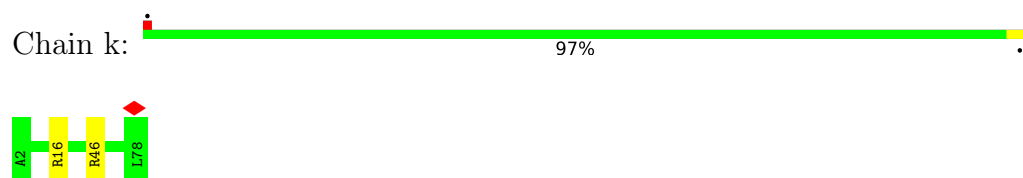


- Molecule 37: 60S ribosomal protein L37-A

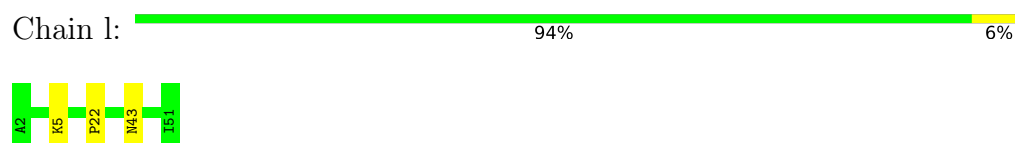
Chain j:  93%



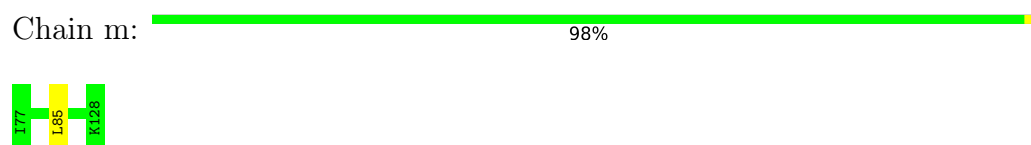
- Molecule 38: 60S ribosomal protein L38



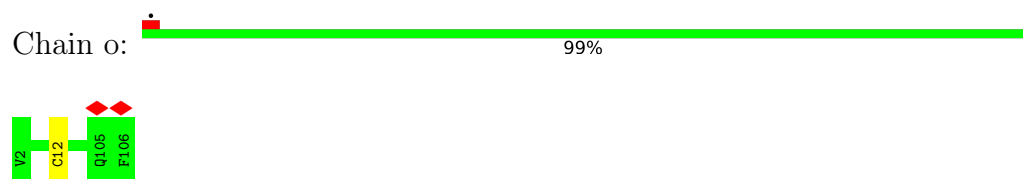
- Molecule 39: 60S ribosomal protein L39



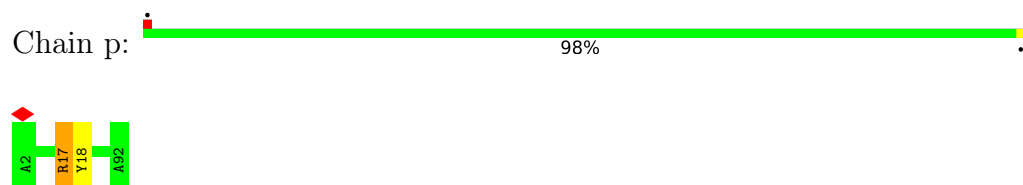
- Molecule 40: Ubiquitin-60S ribosomal protein L40



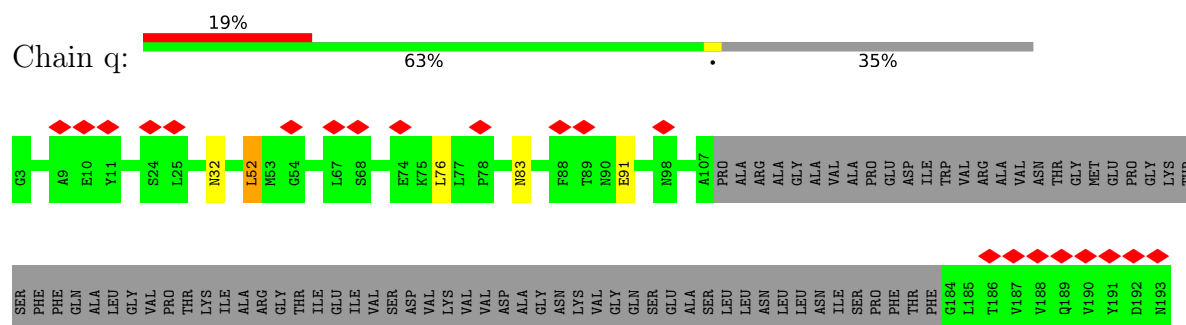
- Molecule 41: 60S ribosomal protein L42-A

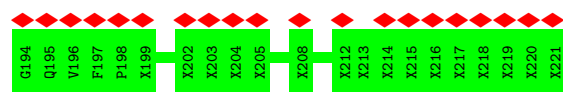


- Molecule 42: 60S ribosomal protein L43-A



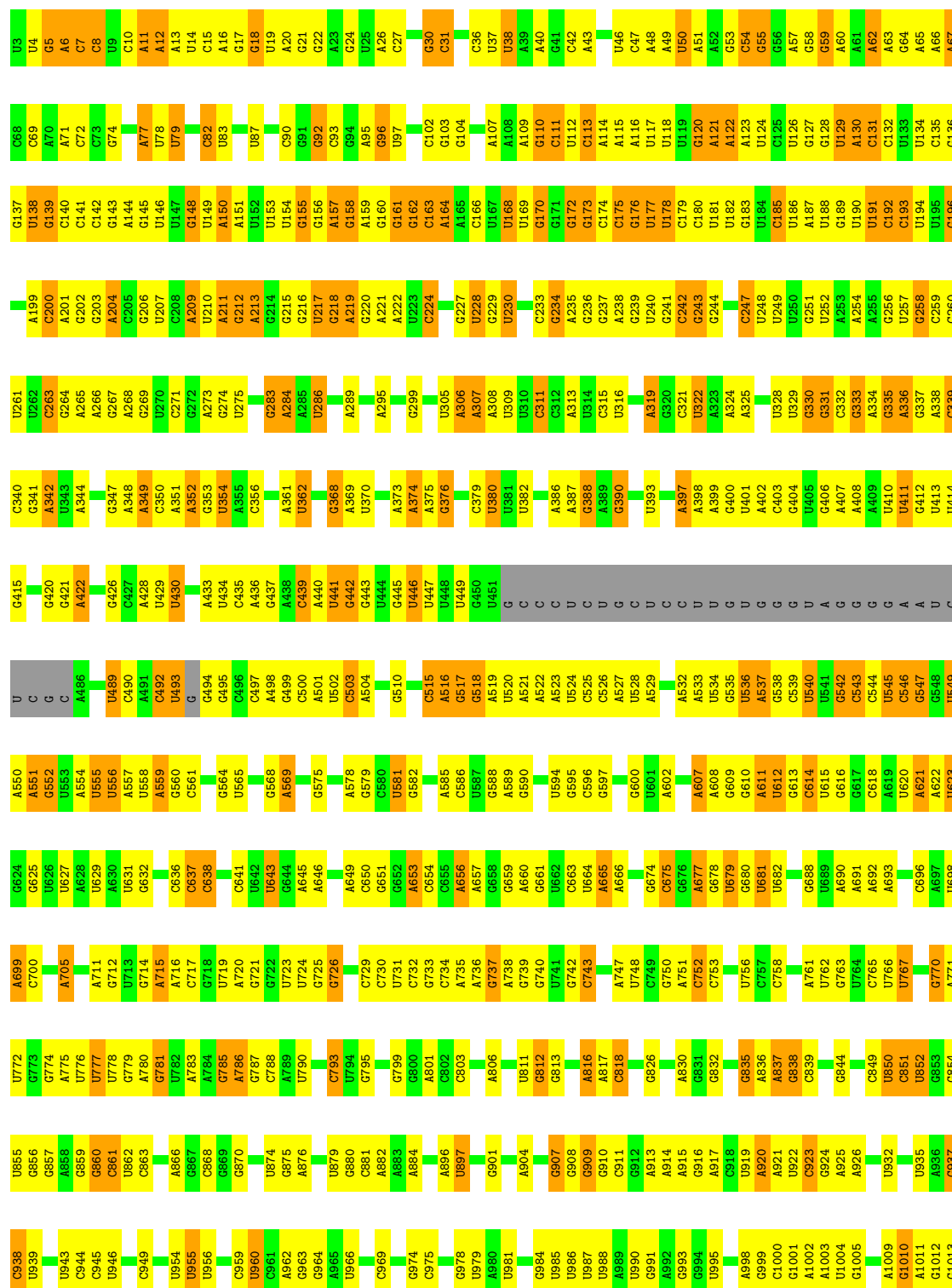
- Molecule 43: 60S acidic ribosomal protein P0,60S acidic ribosomal protein P0,AO, L10E





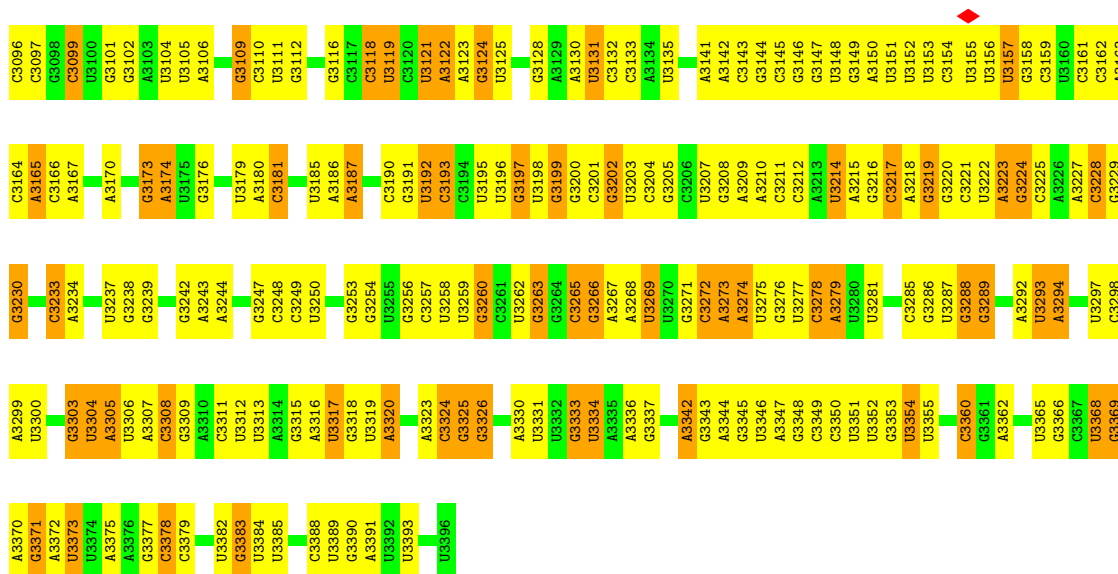
• Molecule 44: 25S ribosomal RNA

Chain 5: 36% 45% 15%

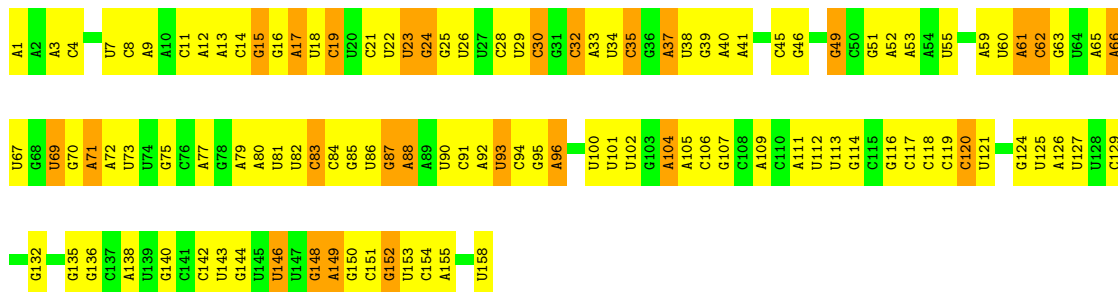




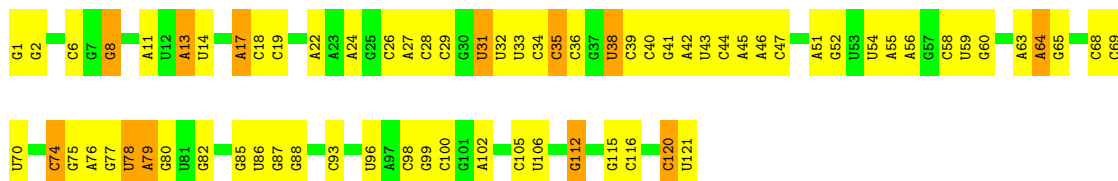




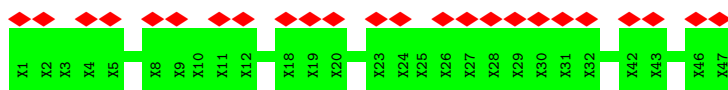
• Molecule 45: 5.8S ribosomal RNA



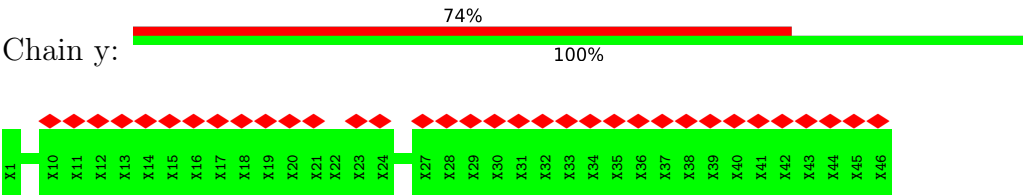
• Molecule 46: 5S ribosomal RNA



• Molecule 47: P1



• Molecule 48: P2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	0.232	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	476.16, 476.16, 476.16	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.24, 1.24, 1.24	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	z	0.46	0/1620	0.88	2/2164 (0.1%)
2	A	0.44	0/1952	0.69	0/2622
3	B	0.43	0/3153	0.71	1/4239 (0.0%)
4	C	0.44	1/2802 (0.0%)	0.73	1/3792 (0.0%)
5	D	0.50	0/2426	0.67	1/3271 (0.0%)
6	E	0.47	0/1261	0.74	0/1694
7	F	0.52	0/1822	0.71	0/2451
8	G	0.46	0/1850	0.69	0/2495
9	H	0.54	0/1540	0.78	2/2073 (0.1%)
10	I	0.51	0/1754	0.72	0/2350
11	J	0.48	0/1375	0.78	0/1842
12	s	0.34	0/734	0.71	1/1015 (0.1%)
13	L	0.45	0/1568	0.73	0/2106
14	M	0.47	0/1069	0.70	0/1438
15	N	0.41	0/1758	0.68	0/2354
16	O	0.46	0/1586	0.67	0/2128
17	P	0.46	0/1466	0.70	0/1968
18	Q	0.44	0/1466	0.74	1/1965 (0.1%)
19	R	0.95	2/1539 (0.1%)	0.91	5/2050 (0.2%)
20	S	0.47	0/1482	0.69	0/1990
21	T	0.47	0/1301	0.69	0/1743
22	U	0.46	0/812	0.71	0/1099
23	V	0.43	0/1019	0.68	0/1369
24	W	0.48	0/1099	0.74	0/1446
25	X	0.45	0/984	0.74	0/1325
26	Y	0.46	0/1005	0.82	1/1341 (0.1%)
27	Z	0.49	0/1119	0.71	0/1497
28	a	0.41	0/1205	0.74	3/1612 (0.2%)
29	b	0.46	0/474	0.83	1/629 (0.2%)
30	c	0.49	0/751	0.75	2/1008 (0.2%)
31	d	0.46	0/904	0.66	0/1213
32	e	0.46	0/1041	0.79	1/1394 (0.1%)
33	f	0.42	0/869	0.68	0/1168
34	g	0.43	0/891	0.69	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.49	0/979	0.70	0/1301
36	i	0.50	0/779	0.73	0/1034
37	j	0.47	0/697	0.76	0/923
38	k	0.42	0/619	0.78	2/826 (0.2%)
39	l	0.44	0/444	0.73	0/588
40	m	0.47	0/424	0.76	1/562 (0.2%)
41	o	0.53	1/861 (0.1%)	0.75	0/1136
42	p	0.50	0/702	0.73	0/934
43	q	0.51	0/977	0.88	1/1313 (0.1%)
44	5	1.16	111/77625 (0.1%)	1.70	2290/121004 (1.9%)
45	8	1.20	12/3747 (0.3%)	1.69	115/5832 (2.0%)
46	7	1.22	5/2884 (0.2%)	1.74	93/4491 (2.1%)
All	All	0.96	132/138435 (0.1%)	1.43	2524/203986 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	z	0	8
2	A	0	2
4	C	0	11
5	D	0	2
6	E	0	4
7	F	0	4
8	G	0	1
9	H	0	2
10	I	0	1
11	J	0	2
12	s	0	4
13	L	0	3
14	M	0	1
15	N	0	1
17	P	0	2
18	Q	0	2
19	R	0	3
20	S	0	3
21	T	0	4
24	W	0	3
25	X	0	2
26	Y	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	Z	0	1
28	a	0	1
29	b	0	2
32	e	0	2
33	f	0	1
34	g	0	1
37	j	0	2
42	p	0	1
43	q	0	3
All	All	0	85

The worst 5 of 132 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	5	2263	C	O3'-P	-83.01	0.61	1.61
19	R	312	VAL	CA-C	31.59	2.35	1.52
44	5	2279	A	O3'-P	29.63	1.96	1.61
44	5	1749	A	N9-C4	-10.94	1.31	1.37
46	7	1	G	OP3-P	-10.82	1.48	1.61

The worst 5 of 2524 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	5	2279	A	P-O3'-C3'	35.94	162.82	119.70
44	5	2263	C	P-O3'-C3'	32.49	158.69	119.70
44	5	2279	A	O3'-P-O5'	-30.93	45.23	104.00
44	5	2263	C	OP1-P-O3'	24.51	159.12	105.20
44	5	2263	C	OP2-P-O3'	-22.12	56.55	105.20

There are no chirality outliers.

5 of 85 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	z	345	ASP	Peptide
1	z	347	ARG	Peptide
1	z	355	LYS	Peptide
1	z	361	ALA	Peptide
1	z	367	VAL	Peptide

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	z	199/204 (98%)	138 (69%)	61 (31%)	0	100	100
2	A	250/252 (99%)	204 (82%)	46 (18%)	0	100	100
3	B	384/386 (100%)	315 (82%)	67 (17%)	2 (0%)	29	66
4	C	359/361 (99%)	292 (81%)	65 (18%)	2 (1%)	25	62
5	D	294/296 (99%)	263 (90%)	31 (10%)	0	100	100
6	E	152/175 (87%)	133 (88%)	19 (12%)	0	100	100
7	F	220/222 (99%)	188 (86%)	31 (14%)	1 (0%)	29	66
8	G	231/233 (99%)	199 (86%)	32 (14%)	0	100	100
9	H	189/191 (99%)	159 (84%)	30 (16%)	0	100	100
10	I	207/220 (94%)	173 (84%)	34 (16%)	0	100	100
11	J	167/169 (99%)	140 (84%)	27 (16%)	0	100	100
12	s	144/155 (93%)	93 (65%)	51 (35%)	0	100	100
13	L	191/193 (99%)	161 (84%)	27 (14%)	3 (2%)	9	44
14	M	134/136 (98%)	117 (87%)	17 (13%)	0	100	100
15	N	201/203 (99%)	171 (85%)	29 (14%)	1 (0%)	29	66
16	O	195/197 (99%)	171 (88%)	24 (12%)	0	100	100
17	P	181/183 (99%)	156 (86%)	25 (14%)	0	100	100
18	Q	183/185 (99%)	157 (86%)	26 (14%)	0	100	100
19	R	186/188 (99%)	159 (86%)	26 (14%)	1 (0%)	29	66
20	S	170/172 (99%)	143 (84%)	27 (16%)	0	100	100
21	T	157/159 (99%)	136 (87%)	21 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	U	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
23	V	134/136 (98%)	113 (84%)	21 (16%)	0	100	100
24	W	126/135 (93%)	101 (80%)	24 (19%)	1 (1%)	19	57
25	X	119/121 (98%)	102 (86%)	17 (14%)	0	100	100
26	Y	124/126 (98%)	105 (85%)	19 (15%)	0	100	100
27	Z	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	19	57
28	a	146/148 (99%)	124 (85%)	21 (14%)	1 (1%)	22	60
29	b	56/58 (97%)	47 (84%)	8 (14%)	1 (2%)	8	42
30	c	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
31	d	107/109 (98%)	88 (82%)	19 (18%)	0	100	100
32	e	125/127 (98%)	105 (84%)	20 (16%)	0	100	100
33	f	104/106 (98%)	86 (83%)	18 (17%)	0	100	100
34	g	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
35	h	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
36	i	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
37	j	85/87 (98%)	70 (82%)	15 (18%)	0	100	100
38	k	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
39	l	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	7	40
40	m	50/52 (96%)	37 (74%)	13 (26%)	0	100	100
41	o	103/105 (98%)	83 (81%)	20 (19%)	0	100	100
42	p	89/91 (98%)	75 (84%)	13 (15%)	1 (1%)	14	51
43	q	117/219 (53%)	91 (78%)	26 (22%)	0	100	100
All	All	6652/6889 (97%)	5580 (84%)	1056 (16%)	16 (0%)	50	79

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	F	369	GLN
13	L	62	THR
27	Z	33	LYS
13	L	61	PRO
15	N	146	ALA

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	z	179/185 (97%)	171 (96%)	8 (4%)	27	57
2	A	194/194 (100%)	190 (98%)	4 (2%)	53	74
3	B	322/322 (100%)	319 (99%)	3 (1%)	78	88
4	C	288/288 (100%)	282 (98%)	6 (2%)	53	74
5	D	244/244 (100%)	243 (100%)	1 (0%)	91	95
6	E	134/152 (88%)	132 (98%)	2 (2%)	65	81
7	F	186/186 (100%)	184 (99%)	2 (1%)	73	85
8	G	191/191 (100%)	187 (98%)	4 (2%)	53	74
9	H	171/171 (100%)	167 (98%)	4 (2%)	50	72
10	I	180/186 (97%)	172 (96%)	8 (4%)	28	57
11	J	147/147 (100%)	143 (97%)	4 (3%)	44	69
13	L	154/154 (100%)	150 (97%)	4 (3%)	46	69
14	M	107/107 (100%)	106 (99%)	1 (1%)	78	88
15	N	175/175 (100%)	173 (99%)	2 (1%)	73	85
16	O	160/160 (100%)	158 (99%)	2 (1%)	69	82
17	P	145/145 (100%)	142 (98%)	3 (2%)	53	74
18	Q	150/150 (100%)	148 (99%)	2 (1%)	69	82
19	R	153/153 (100%)	148 (97%)	5 (3%)	38	65
20	S	156/156 (100%)	154 (99%)	2 (1%)	69	82
21	T	136/136 (100%)	133 (98%)	3 (2%)	52	72
22	U	87/87 (100%)	86 (99%)	1 (1%)	73	85
23	V	104/104 (100%)	102 (98%)	2 (2%)	57	76
24	W	114/114 (100%)	111 (97%)	3 (3%)	46	69
25	X	105/105 (100%)	103 (98%)	2 (2%)	57	76
26	Y	109/109 (100%)	106 (97%)	3 (3%)	43	68
27	Z	115/115 (100%)	114 (99%)	1 (1%)	78	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	a	118/118 (100%)	115 (98%)	3 (2%)	47	70
29	b	46/46 (100%)	44 (96%)	2 (4%)	29	58
30	c	81/81 (100%)	80 (99%)	1 (1%)	71	84
31	d	96/96 (100%)	96 (100%)	0	100	100
32	e	109/109 (100%)	108 (99%)	1 (1%)	78	88
33	f	90/90 (100%)	86 (96%)	4 (4%)	28	57
34	g	95/95 (100%)	93 (98%)	2 (2%)	53	74
35	h	104/104 (100%)	102 (98%)	2 (2%)	57	76
36	i	81/81 (100%)	78 (96%)	3 (4%)	34	62
37	j	70/70 (100%)	66 (94%)	4 (6%)	20	52
38	k	68/68 (100%)	67 (98%)	1 (2%)	65	81
39	l	45/45 (100%)	43 (96%)	2 (4%)	28	57
40	m	47/47 (100%)	47 (100%)	0	100	100
41	o	90/90 (100%)	90 (100%)	0	100	100
42	p	71/71 (100%)	70 (99%)	1 (1%)	67	81
43	q	105/165 (64%)	103 (98%)	2 (2%)	57	76
All	All	5522/5612 (98%)	5412 (98%)	110 (2%)	57	75

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	P	171	ARG
23	V	141	ARG
43	q	76	LEU
36	i	57	LEU
18	Q	276	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
21	T	146	ASN
31	d	115	GLN
42	p	34	HIS
24	W	249	ASN
28	a	125	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	5	3231/3394 (95%)	1469 (45%)	32 (0%)
45	8	157/158 (99%)	85 (54%)	0
46	7	120/121 (99%)	41 (34%)	0
All	All	3508/3673 (95%)	1595 (45%)	32 (0%)

5 of 1595 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	5	4	U
44	5	5	G
44	5	6	A
44	5	7	C
44	5	8	C

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	5	2541	U
44	5	3121	U
44	5	705	A
44	5	637	C
44	5	3228	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 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	5	9
24	W	4

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2083:G	O3'	2084:C	P	19.95
1	W	217:SER	C	218:ARG	N	12.39
1	W	219:LYS	C	220:THR	N	9.79
1	W	229:GLY	C	230:ALA	N	9.10
1	5	2513:U	O3'	2514:U	P	8.49

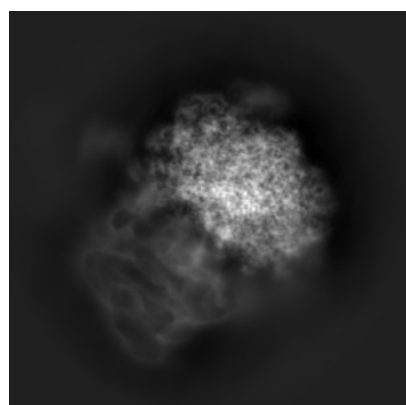
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20077. These allow visual inspection of the internal detail of the map and identification of artifacts.

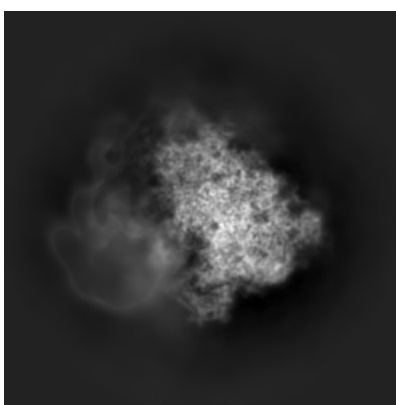
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

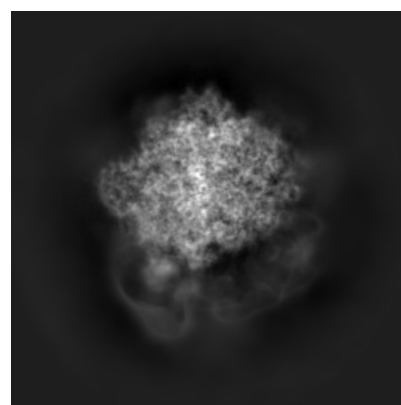
6.1.1 Primary map



X



Y

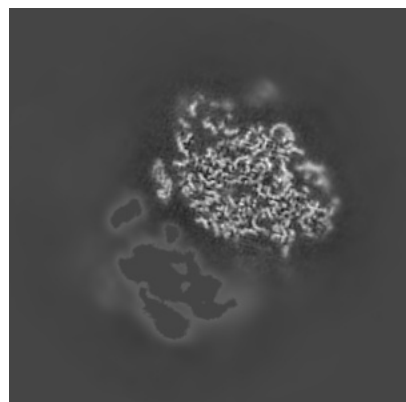


Z

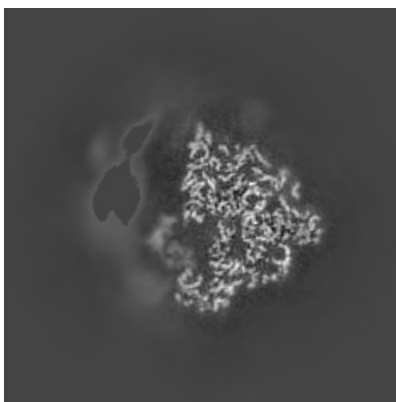
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

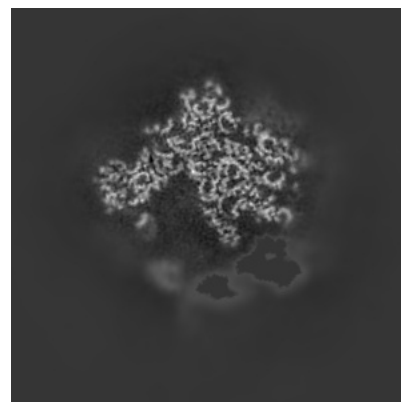
6.2.1 Primary map



X Index: 192



Y Index: 192

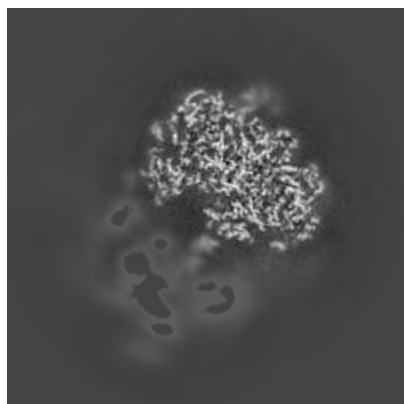


Z Index: 192

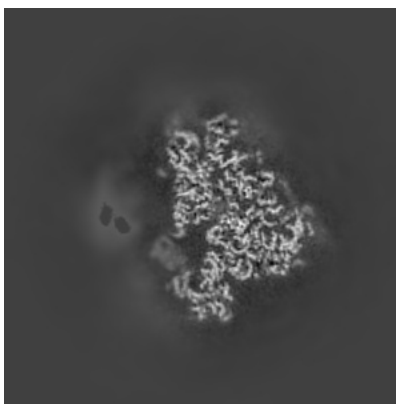
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

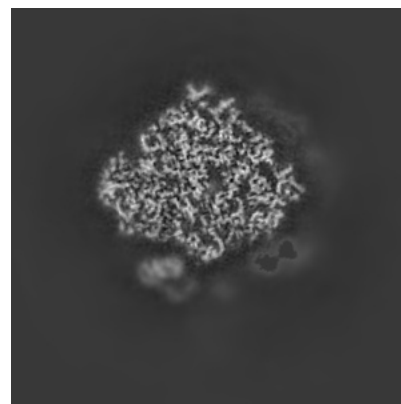
6.3.1 Primary map



X Index: 179



Y Index: 209



Z Index: 209

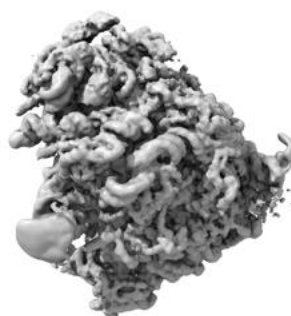
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

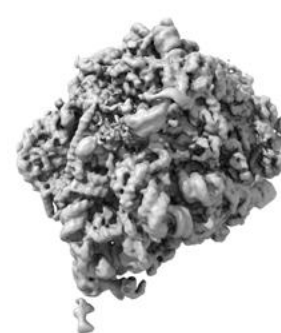
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

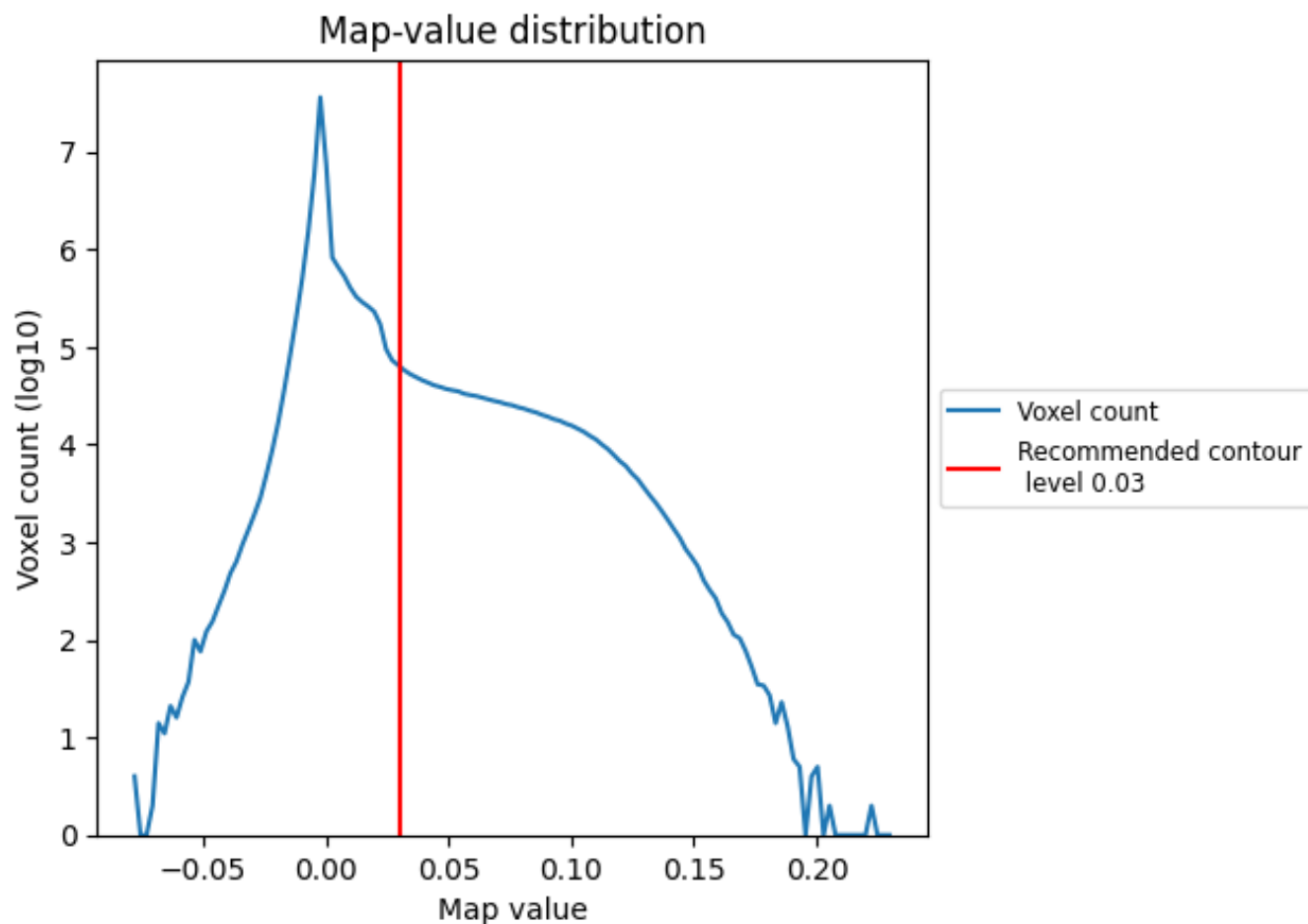
6.5 Mask visualisation

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

7 Map analysis [i](#)

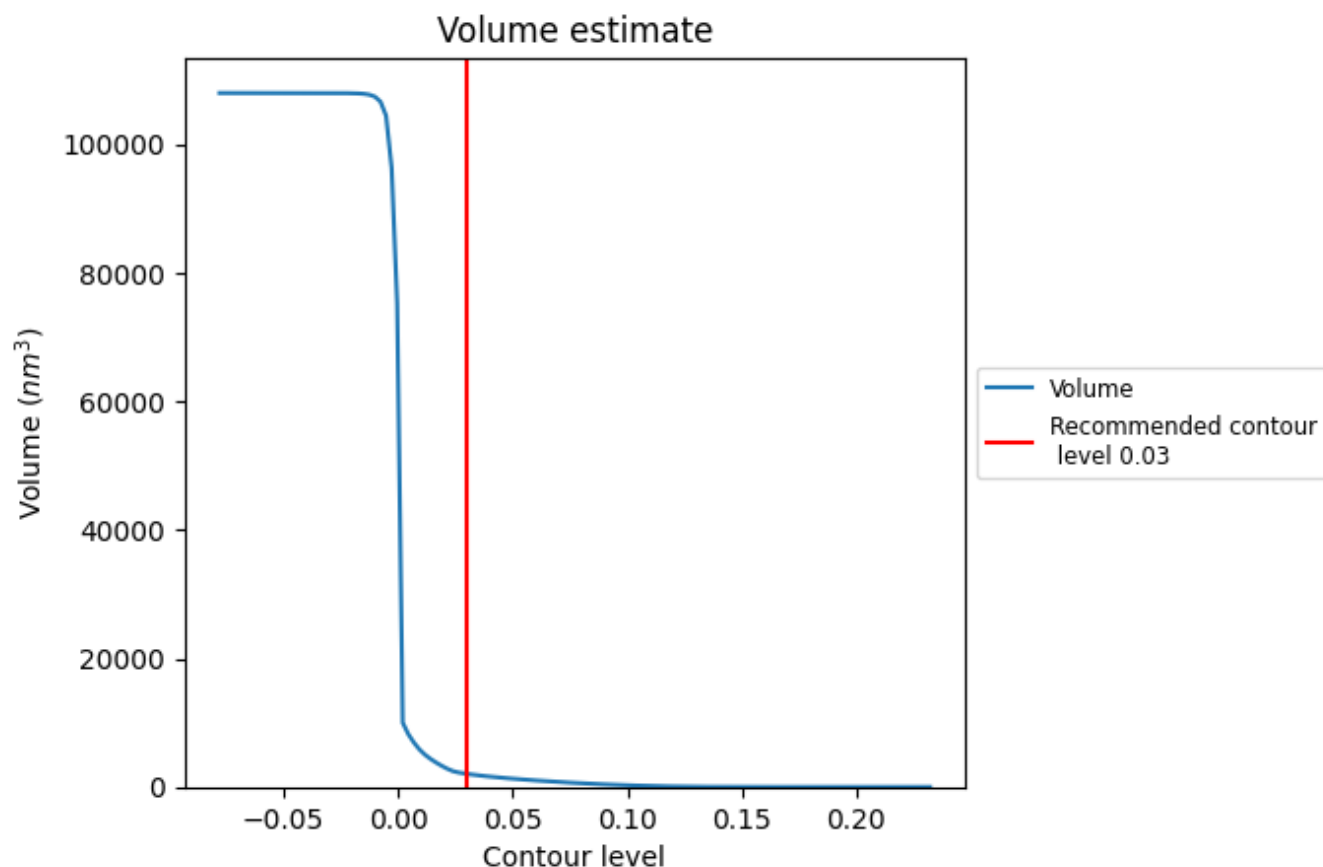
This section contains the results of statistical analysis of the map.

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.

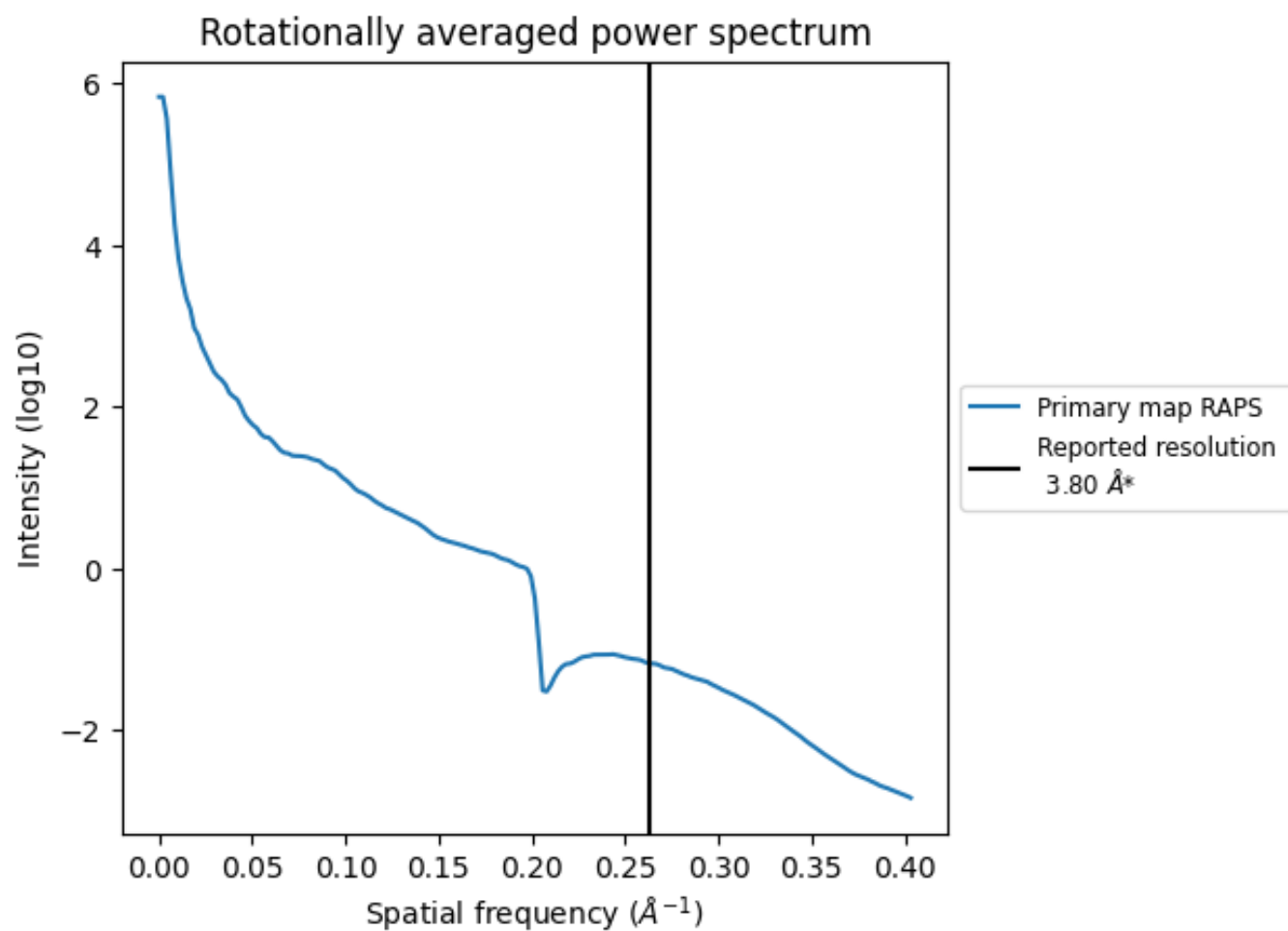
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2037 nm^3 ; this corresponds to an approximate mass of 1840 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 0.263 Å⁻¹

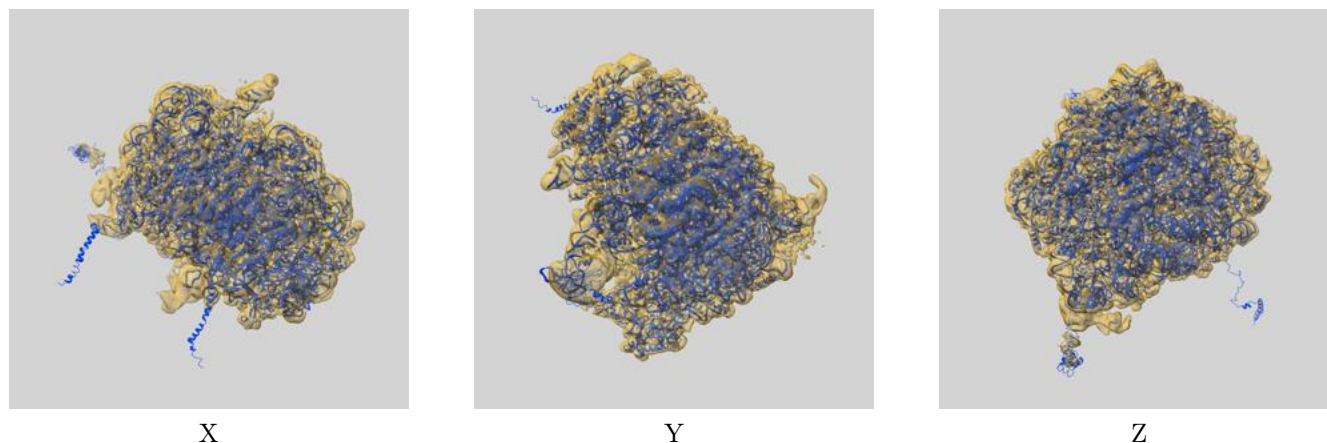
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

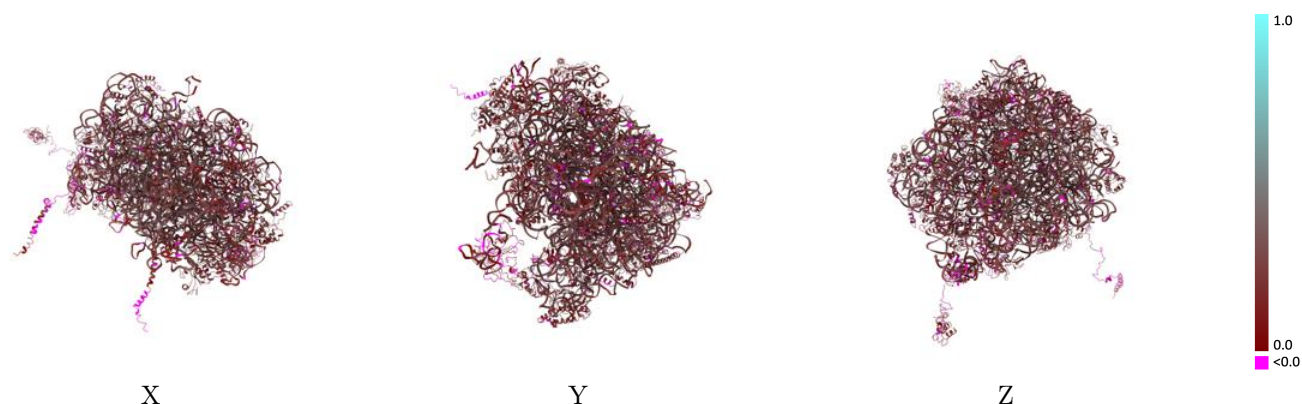
This section contains information regarding the fit between EMDB map EMD-20077 and PDB model 6OIG. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



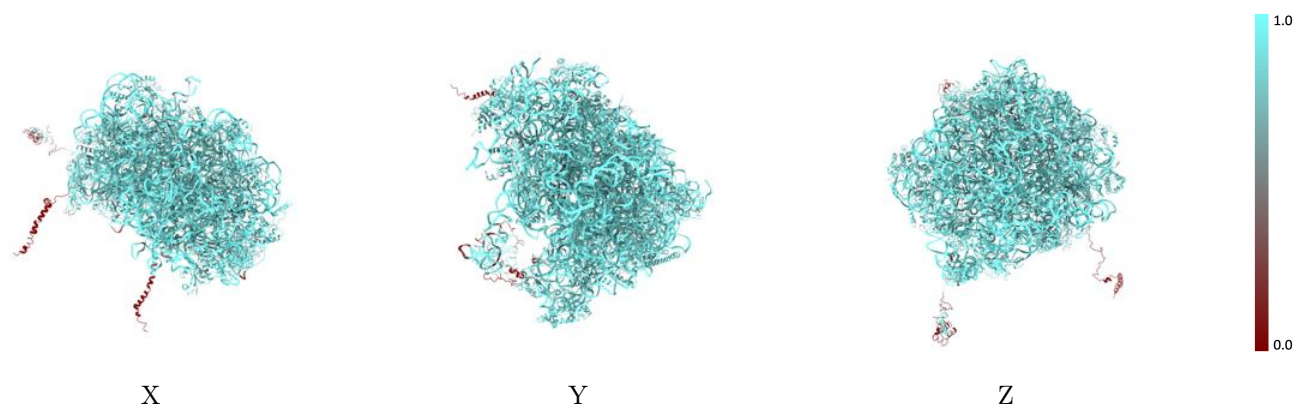
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



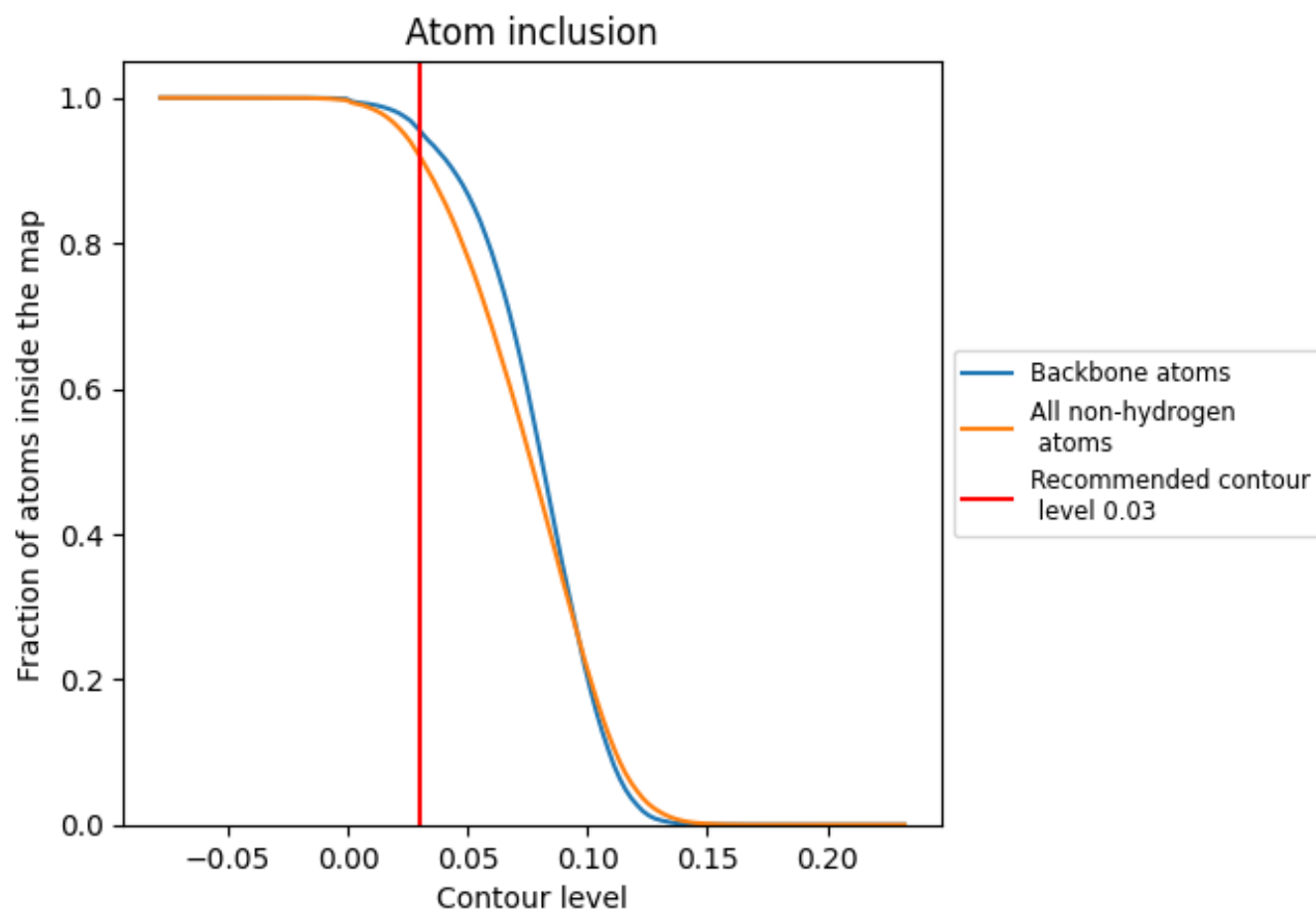
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9202	 0.2310
5	 0.9799	 0.2690
7	 0.9961	 0.2860
8	 0.9812	 0.2620
A	 0.8423	 0.2020
B	 0.8839	 0.2050
C	 0.8761	 0.1820
D	 0.8794	 0.1900
E	 0.8748	 0.1800
F	 0.8721	 0.2000
G	 0.8763	 0.2030
H	 0.8719	 0.1790
I	 0.8264	 0.1350
J	 0.8602	 0.1810
L	 0.8951	 0.1870
M	 0.8802	 0.1810
N	 0.6716	 0.0710
O	 0.8792	 0.2020
P	 0.8676	 0.1890
Q	 0.8711	 0.2090
R	 0.7116	 0.1660
S	 0.8795	 0.2100
T	 0.9009	 0.2100
U	 0.8747	 0.2240
V	 0.7969	 0.2140
W	 0.3945	 0.0920
X	 0.8300	 0.1850
Y	 0.8831	 0.1610
Z	 0.8778	 0.2180
a	 0.8793	 0.2060
b	 0.8212	 0.1460
c	 0.8659	 0.2460
d	 0.8484	 0.1830
e	 0.8290	 0.1620
f	 0.8674	 0.1840



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Chain	Atom inclusion	Q-score
g	 0.8580	 0.1910
h	 0.8750	 0.1740
i	 0.8740	 0.2150
j	 0.8811	 0.1430
k	 0.8567	 0.2030
l	 0.8365	 0.1750
m	 0.8738	 0.2340
o	 0.8347	 0.1790
p	 0.8597	 0.2020
q	 0.7014	 0.0560
s	 0.9009	 0.0890
x	 0.4723	 0.1690
y	 0.2522	 0.1190
z	 0.6650	 0.0620