



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 11:41 AM EST

PDB ID : 6N8J
EMDB ID : EMD-0369
Title : Cryo-EM structure of late nuclear (LN) pre-60S ribosomal subunit
Authors : Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.
Deposited on : 2018-11-29
Resolution : 3.50 Å(reported)
Based on initial model : 3JCT

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:

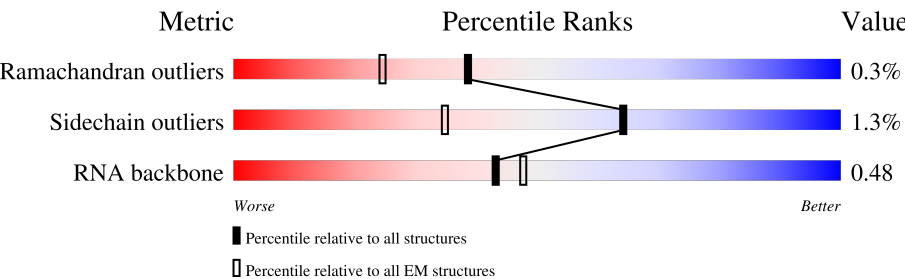
EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.50 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	D	297	
2	J	174	
3	A	254	
4	a	149	
5	B	387	
6	b	647	
7	C	362	
8	c	105	

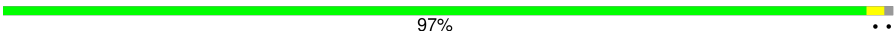


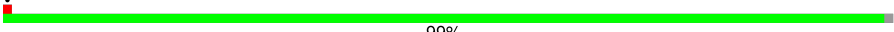









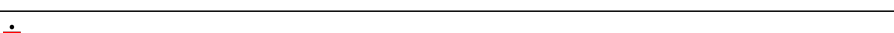


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Mol	Chain	Length	Quality of chain
9	d	113	
10	E	176	
11	e	130	
12	F	244	
13	f	107	
14	G	256	
15	g	121	
16	I	166	
17	H	191	
18	h	120	
19	i	100	
20	j	88	
21	k	78	
22	m	486	
23	L	199	
24	l	51	
25	M	138	
26	p	92	
27	N	204	
28	u	199	
29	O	199	
30	P	184	
31	Q	186	
32	R	189	
33	r	261	

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Mol	Chain	Length	Quality of chain
34	S	172	
35	T	160	
36	U	121	
37	V	137	
38	W	236	
39	X	142	
40	Y	127	
41	y	245	
42	Z	136	
43	z	106	
44	K	165	
45	q	106	
46	o	59	
47	1	3396	
48	2	121	
49	3	158	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 132554 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 L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	255	Total	C	N	O	S	0	0
			2047	1303	354	388	2		

- Molecule 2 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	161	Total	C	N	O	S	0	0
			1283	808	240	231	4		

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 4 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	94	Total	C	N	O	S	0	0
			742	484	131	126	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 6 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	647	Total	C	N	O	S	0	0
			5215	3267	940	982	26		

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 8 is a protein called 60S ribosomal protein L30.

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

- Molecule 9 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	160	Total	C	N	O	S	0	0
			1274	820	230	223	1		

- Molecule 11 is a protein called 60S ribosomal protein L32.

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

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 13 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 15 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 16 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	131	Total	C	N	O	S	0	0
			1056	660	195	198	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 18 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 19 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 20 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 21 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 22 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	m	378	Total	C	N	O	S	0	0
			3006	1913	535	550	8		

- Molecule 23 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L	187	Total	C	N	O	0	0
			1491	929	306	256		

- Molecule 24 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 25 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 26 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 27 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 28 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	149	Total	C	N	O	S	0	0
			1256	788	252	207	9		

- Molecule 29 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 30 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	P	183	Total	C	N	O	S	0	0
			1438	893	286	259			

- Molecule 31 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Q	154	Total	C	N	O	S	0	0
			1191	753	231	205	2		

- Molecule 32 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	154	Total	C	N	O	S	0	0
			1241	772	262	207			

- Molecule 33 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	r	204	Total	C	N	O	S	0	0
			1647	1039	317	284	7		

- Molecule 34 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	S	170	Total	C	N	O	S	0	0
			1425	916	265	241	3		

- Molecule 35 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	T	61	Total	C	N	O	S	0	0
			476	295	95	85	1		

- Molecule 36 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	U	104	Total	C	N	O	S	0	0
			826	535	136	155			

- Molecule 37 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 38 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	W	227	Total	C	N	O	S	0	0
			1814	1149	310	350	5		

- Molecule 39 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 40 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Y	126	Total	C	N	O	S	0	0
			993	625	192	176			

- Molecule 41 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	y	242	Total	C	N	O	S	0	0
			1826	1131	317	372	6		

- Molecule 42 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 43 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 44 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	K	147	Total	C	N	O	0	0
			821	501	159	161		

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	97	Total	C	N	O	S	0	0
			783	493	158	127	5		

- Molecule 46 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	o	54	Total	C	N	O	0	0
			433	271	94	68		

- Molecule 47 is a RNA chain called *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	3047	Total	C	N	O	P	0	0
			65181	29115	11755	21264	3047		

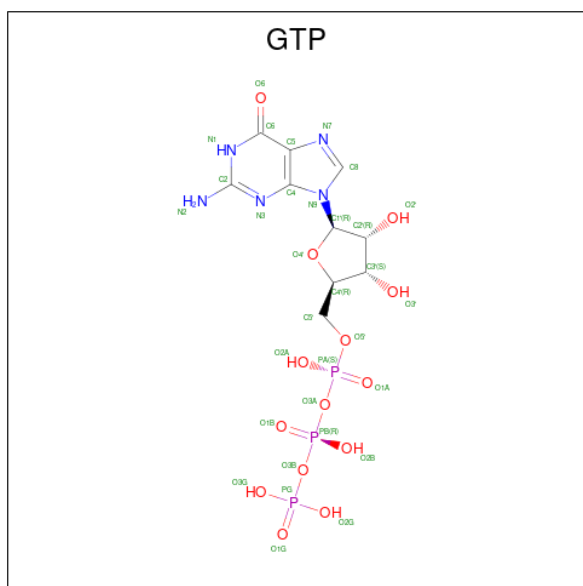
- Molecule 48 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 49 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

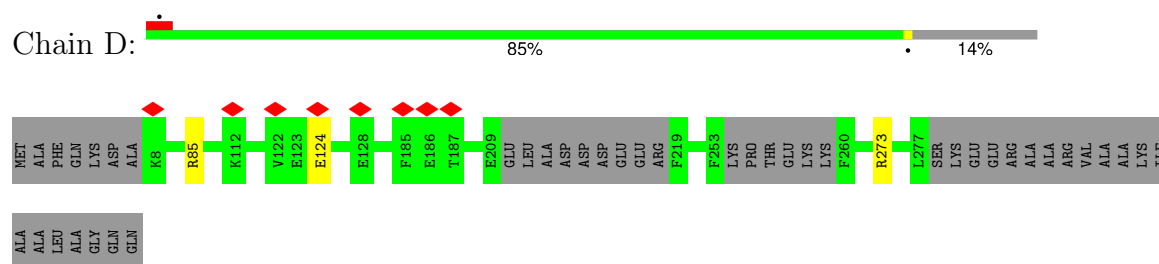
- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



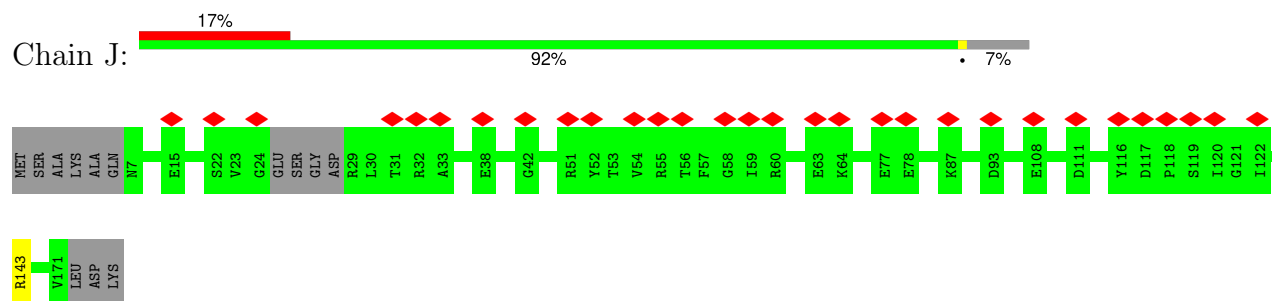
3 Residue-property plots [i](#)

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.

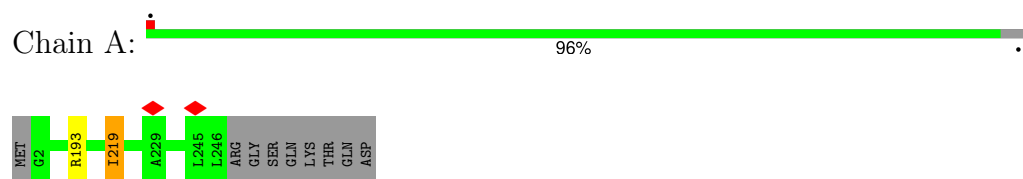
- Molecule 1: 60S ribosomal protein L5



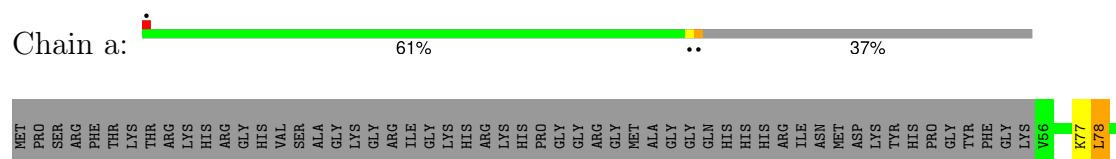
- Molecule 2: 60S ribosomal protein L11-A



- Molecule 3: 60S ribosomal protein L2-A



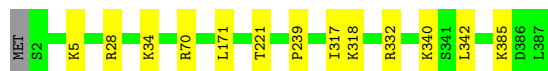
- Molecule 4: 60S ribosomal protein L28





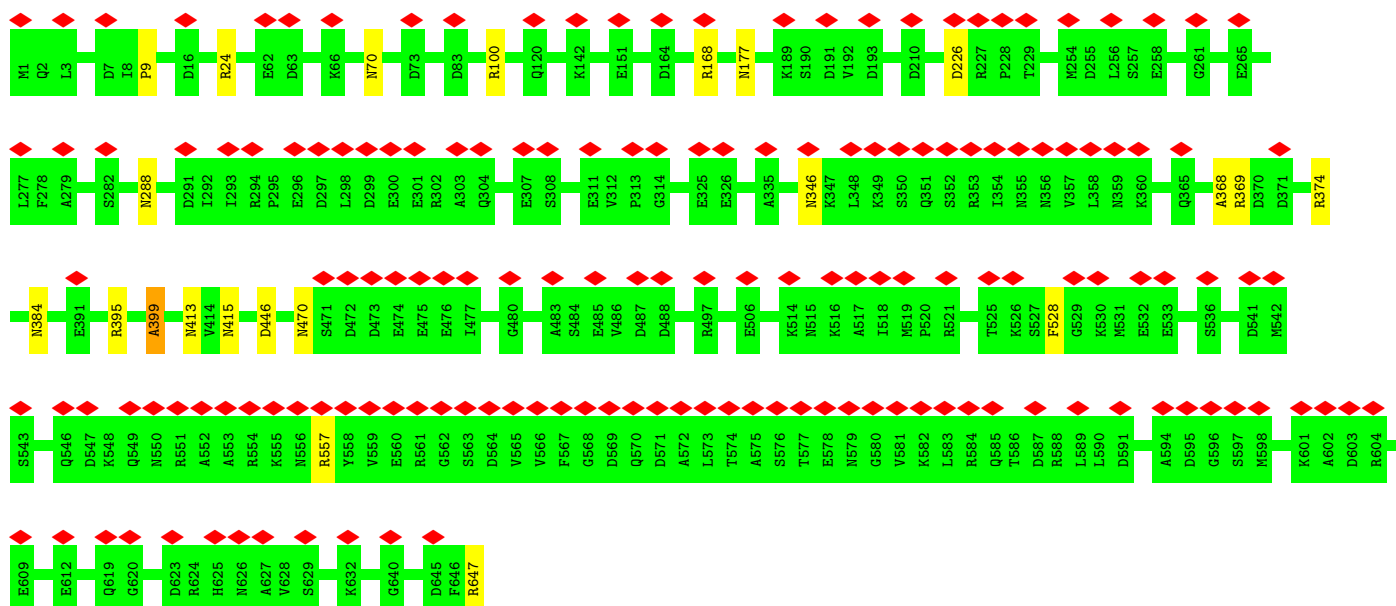
- Molecule 5: 60S ribosomal protein L3

Chain B: 96%



- Molecule 6: Nucleolar GTP-binding protein 1

Chain b: 25% 97%



- Molecule 7: 60S ribosomal protein L4-A

Chain C: 98%

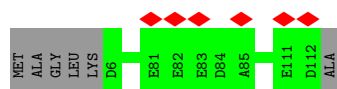


- Molecule 8: 60S ribosomal protein L30

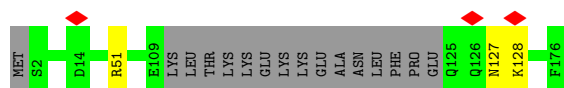
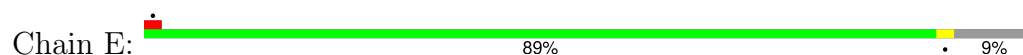
Chain c: 90% 8%



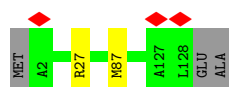
- Molecule 9: 60S ribosomal protein L31-A



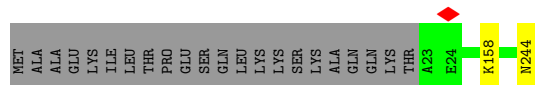
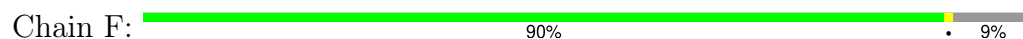
- Molecule 10: 60S ribosomal protein L6-A



- Molecule 11: 60S ribosomal protein L32



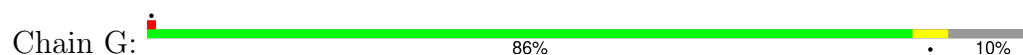
- Molecule 12: 60S ribosomal protein L7-A



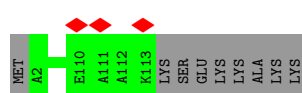
- Molecule 13: 60S ribosomal protein L33-A



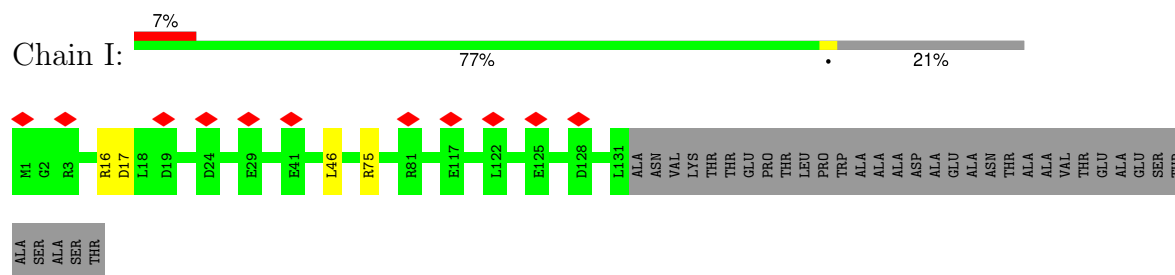
- Molecule 14: 60S ribosomal protein L8-A



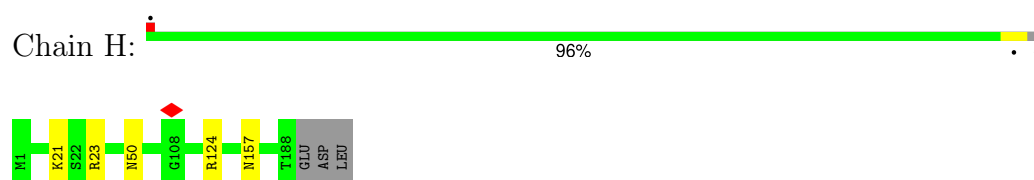
- Molecule 15: 60S ribosomal protein L34-A



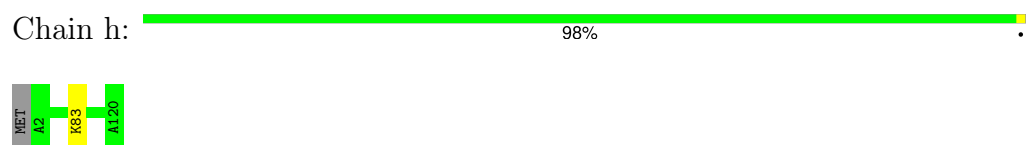
- Molecule 16: Bud site selection protein 20



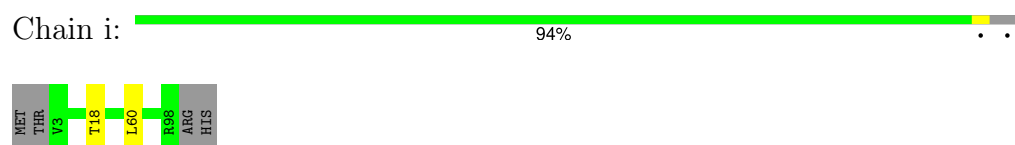
- Molecule 17: 60S ribosomal protein L9-A



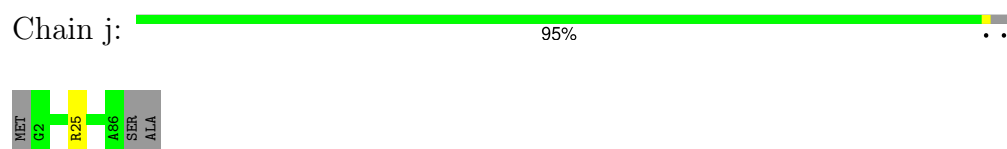
- Molecule 18: 60S ribosomal protein L35-A



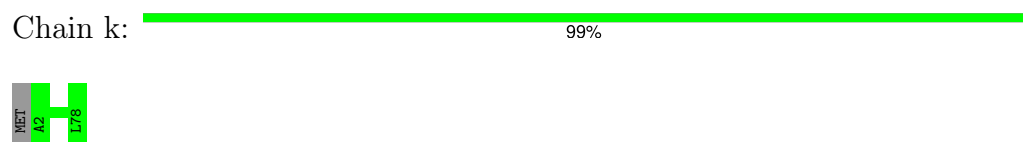
- Molecule 19: 60S ribosomal protein L36-A



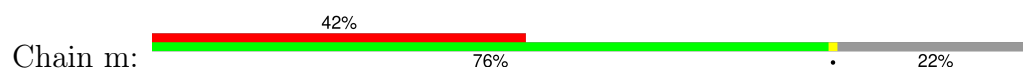
- Molecule 20: 60S ribosomal protein L37-A

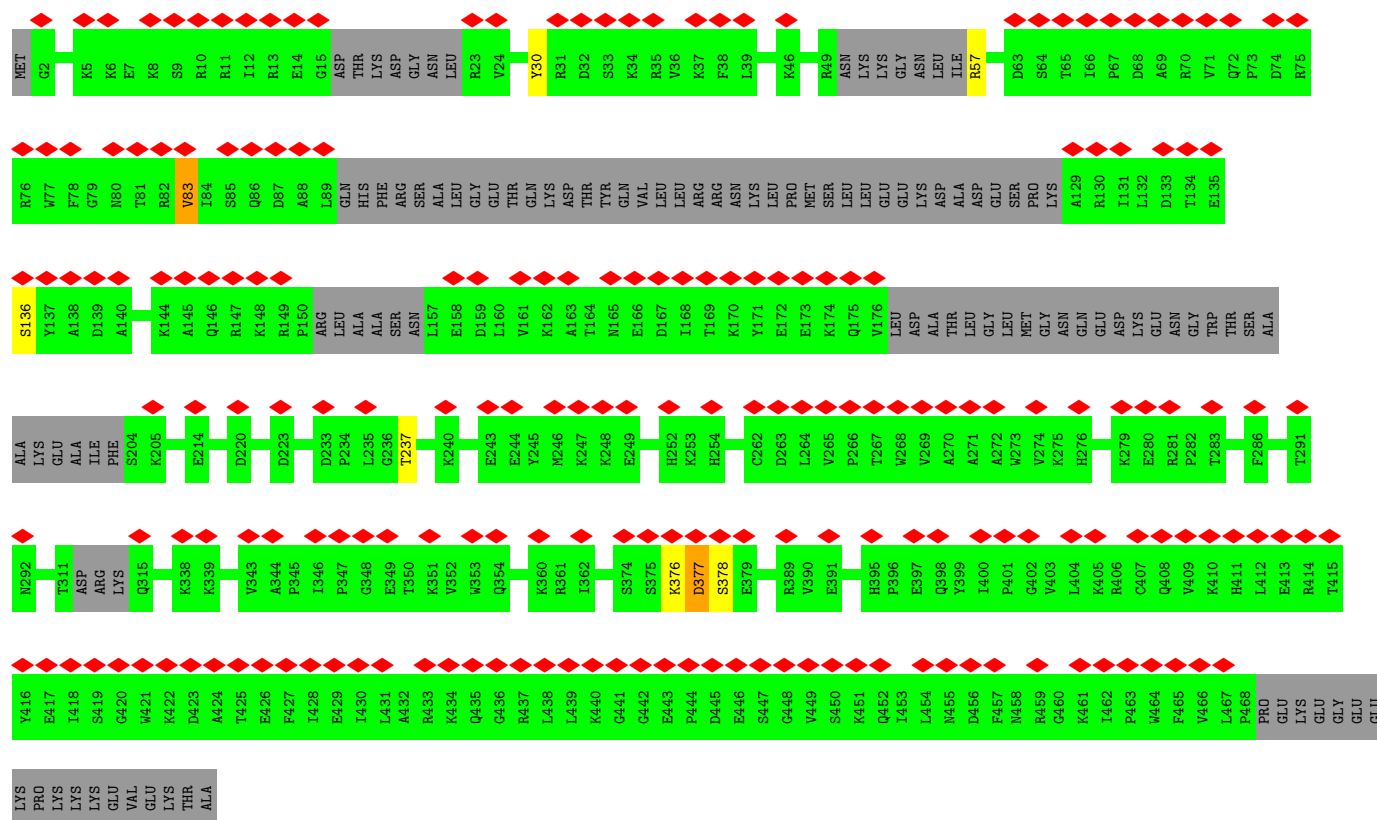


- Molecule 21: 60S ribosomal protein L38



- Molecule 22: Nucleolar GTP-binding protein 2





- Molecule 23: 60S ribosomal protein L13-A

Chain L: 91% (Good), 6% (Medium)



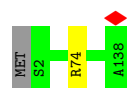
- Molecule 24: 60S ribosomal protein L39

Chain l: 94% (Good), 2% (Medium), 2% (Poor)



- Molecule 25: 60S ribosomal protein L14-A

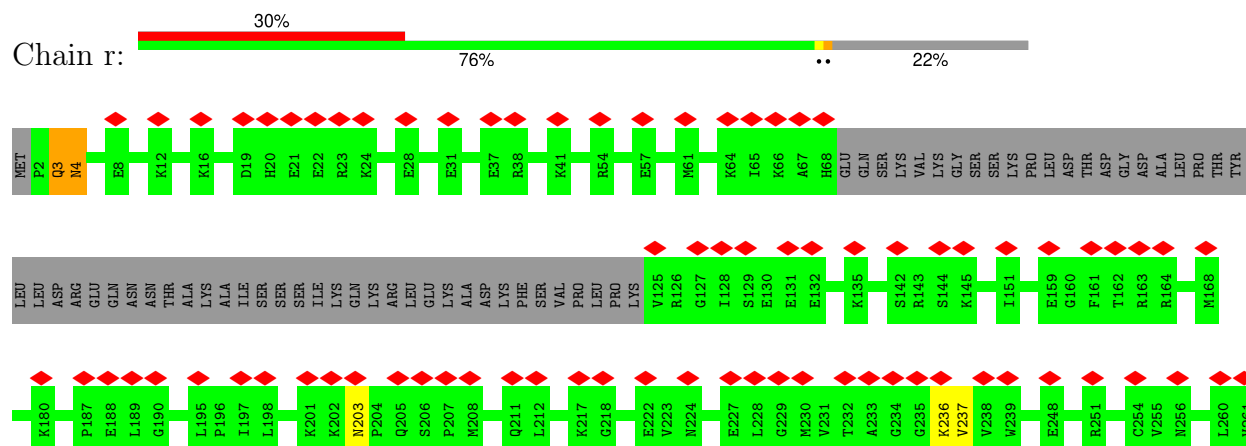
Chain M: 99% (Good), 1% (Medium), 1% (Poor)



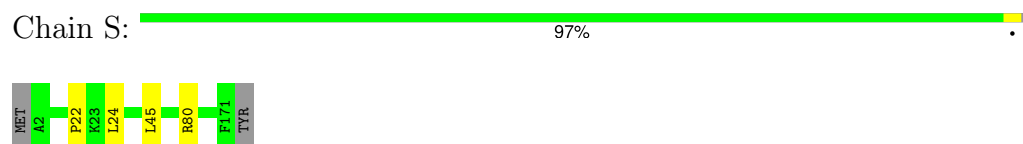
- Molecule 26: 60S ribosomal protein L43-A

Chain p: 98% (Good), 1% (Medium), 1% (Poor)

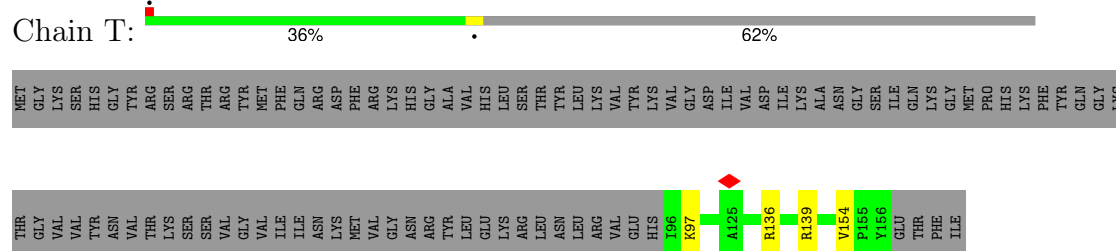
Chain r:



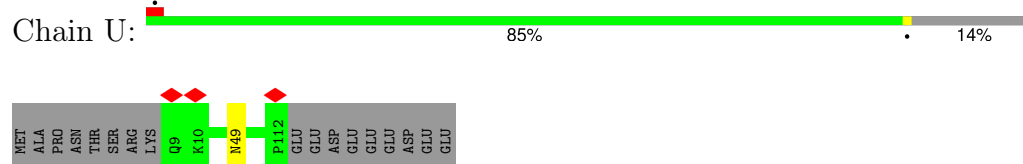
Chain S:



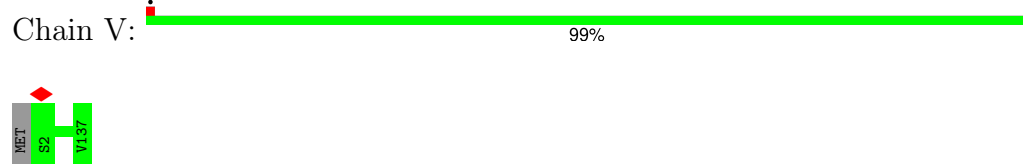
Chain T:



Chain U:

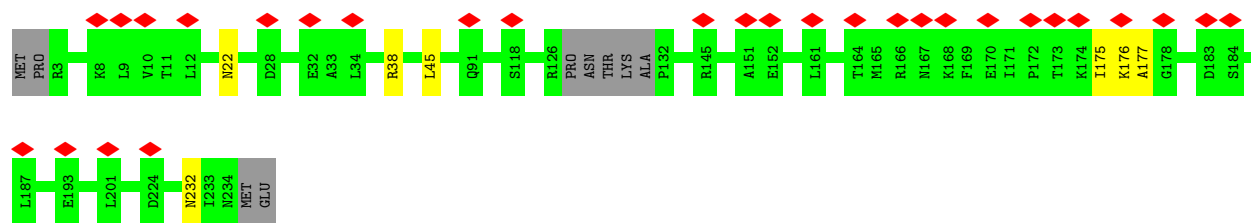


Chain V:

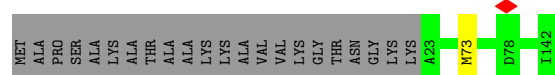
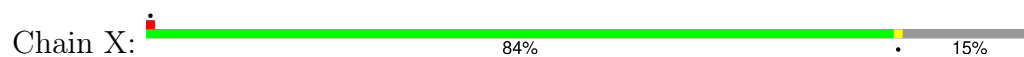


Chain W:

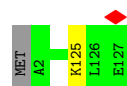




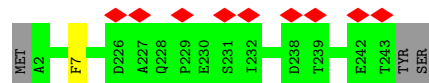
- Molecule 39: 60S ribosomal protein L25



- Molecule 40: 60S ribosomal protein L26-A



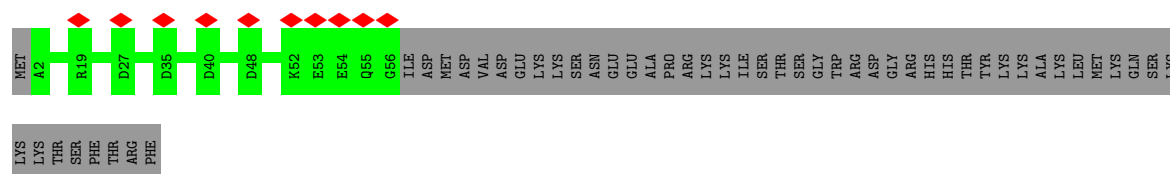
- Molecule 41: Eukaryotic translation initiation factor 6



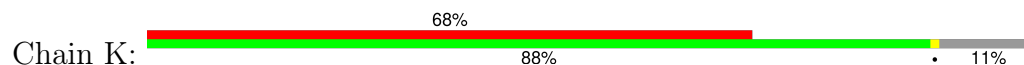
- Molecule 42: 60S ribosomal protein L27-A



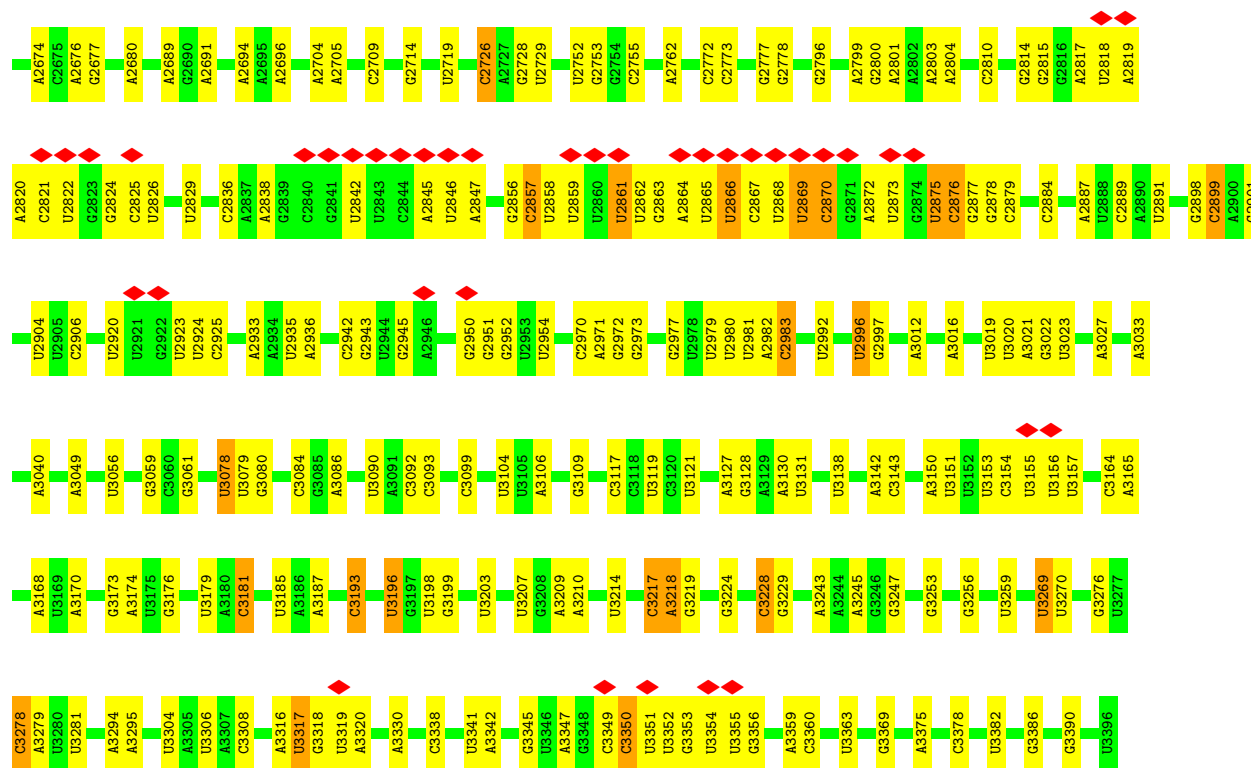
- Molecule 43: UPF0642 protein YBL028C



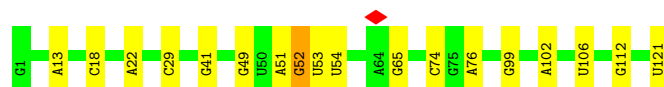
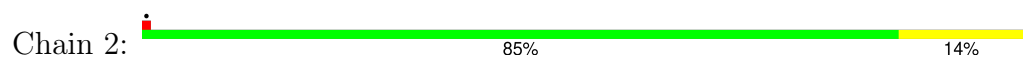
- Molecule 44: 60S ribosomal protein L12



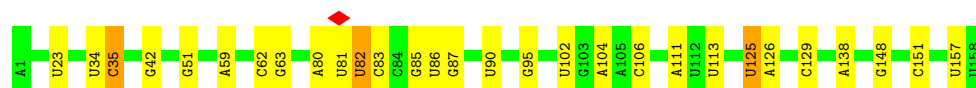
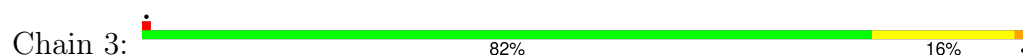




• Molecule 48: 5S rRNA



• Molecule 49: 5.8S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	88117	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.018	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	D	0.31	0/2093	0.53	0/2827
2	J	0.28	0/1303	0.55	0/1747
3	A	0.45	0/1897	0.63	0/2550
4	a	0.42	0/758	0.51	0/1023
5	B	0.48	0/3152	0.65	1/4239 (0.0%)
6	b	0.32	0/5301	0.58	0/7125
7	C	0.42	0/2801	0.59	1/3792 (0.0%)
8	c	0.39	0/751	0.54	0/1008
9	d	0.46	0/887	0.57	0/1191
10	E	0.36	0/1295	0.58	0/1740
11	e	0.41	0/1041	0.55	0/1394
12	F	0.41	0/1821	0.59	0/2451
13	f	0.49	0/868	0.55	0/1168
14	G	0.41	0/1830	0.65	0/2469
15	g	0.46	0/891	0.62	0/1191
16	I	0.33	0/1072	0.58	1/1440 (0.1%)
17	H	0.40	0/1514	0.58	0/2039
18	h	0.40	0/978	0.55	0/1301
19	i	0.35	0/749	0.58	0/995
20	j	0.46	0/685	0.60	0/908
21	k	0.38	0/618	0.57	0/826
22	m	0.31	0/3066	0.60	1/4135 (0.0%)
23	L	0.41	0/1516	0.61	0/2037
24	l	0.40	0/443	0.62	0/588
25	M	0.38	0/1074	0.53	0/1446
26	p	0.42	0/701	0.58	0/934
27	N	0.52	0/1757	0.62	2/2354 (0.1%)
28	u	0.38	0/1278	0.60	1/1699 (0.1%)
29	O	0.44	0/1585	0.55	0/2128
30	P	0.45	0/1461	0.57	0/1964
31	Q	0.41	0/1211	0.63	1/1633 (0.1%)
32	R	0.43	0/1258	0.60	0/1679

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	r	0.33	0/1675	0.62	0/2236
34	S	0.42	0/1460	0.58	0/1962
35	T	0.31	0/483	0.54	0/650
36	U	0.38	0/843	0.57	0/1143
37	V	0.42	0/1018	0.59	0/1369
38	W	0.30	0/1843	0.56	1/2483 (0.0%)
39	X	0.44	0/974	0.58	0/1314
40	Y	0.38	0/1004	0.56	0/1341
41	y	0.36	0/1848	0.57	0/2516
42	Z	0.41	0/1118	0.59	0/1497
43	z	0.29	0/445	0.42	0/585
44	K	0.30	0/363	0.67	1/494 (0.2%)
45	q	0.34	0/795	0.56	0/1050
46	o	0.34	0/444	0.55	0/592
47	1	0.78	0/72960	0.98	181/113744 (0.2%)
48	2	0.48	0/2883	0.87	1/4491 (0.0%)
49	3	0.86	0/3746	0.95	7/5832 (0.1%)
All	All	0.64	0/141557	0.84	199/207320 (0.1%)

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	D	0	1
3	A	0	1
5	B	0	3
6	b	0	5
7	C	0	1
12	F	0	1
14	G	0	3
16	I	0	1
17	H	0	1
18	h	0	1
22	m	0	5
23	L	0	1
33	r	0	3
34	S	0	1
35	T	0	1
38	W	0	2
40	Y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	y	0	1
All	All	0	33

There are no bond length outliers.

The worst 5 of 199 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	1	2861	U	C2-N1-C1'	12.05	132.16	117.70
47	1	2861	U	N1-C2-O2	11.44	130.81	122.80
47	1	3217	C	N1-C2-O2	11.23	125.64	118.90
47	1	765	C	N1-C2-O2	10.71	125.33	118.90
47	1	922	U	C2-N1-C1'	10.28	130.03	117.70

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	219	ILE	Peptide
5	B	221	THR	Peptide
5	B	317	ILE	Peptide
5	B	340	LYS	Peptide
1	D	124	GLU	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	D	249/297 (84%)	237 (95%)	12 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	157/174 (90%)	143 (91%)	14 (9%)	0	100	100
3	A	243/254 (96%)	218 (90%)	24 (10%)	1 (0%)	30	64
4	a	92/149 (62%)	85 (92%)	5 (5%)	2 (2%)	5	31
5	B	384/387 (99%)	340 (88%)	39 (10%)	5 (1%)	10	41
6	b	645/647 (100%)	584 (90%)	58 (9%)	3 (0%)	25	59
7	C	359/362 (99%)	326 (91%)	30 (8%)	3 (1%)	16	51
8	c	95/105 (90%)	95 (100%)	0	0	100	100
9	d	105/113 (93%)	98 (93%)	7 (7%)	0	100	100
10	E	156/176 (89%)	147 (94%)	9 (6%)	0	100	100
11	e	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
12	F	220/244 (90%)	202 (92%)	18 (8%)	0	100	100
13	f	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
14	G	228/256 (89%)	206 (90%)	21 (9%)	1 (0%)	30	64
15	g	110/121 (91%)	104 (94%)	6 (6%)	0	100	100
16	I	129/166 (78%)	118 (92%)	10 (8%)	1 (1%)	16	51
17	H	186/191 (97%)	169 (91%)	16 (9%)	1 (0%)	25	59
18	h	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
19	i	94/100 (94%)	88 (94%)	6 (6%)	0	100	100
20	j	83/88 (94%)	77 (93%)	6 (7%)	0	100	100
21	k	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
22	m	364/486 (75%)	332 (91%)	29 (8%)	3 (1%)	16	51
23	L	185/199 (93%)	163 (88%)	21 (11%)	1 (0%)	25	59
24	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
25	M	135/138 (98%)	128 (95%)	7 (5%)	0	100	100
26	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
27	N	201/204 (98%)	184 (92%)	17 (8%)	0	100	100
28	u	147/199 (74%)	137 (93%)	9 (6%)	1 (1%)	19	53
29	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
30	P	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
31	Q	152/186 (82%)	143 (94%)	9 (6%)	0	100	100
32	R	152/189 (80%)	147 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	r	200/261 (77%)	173 (86%)	26 (13%)	1 (0%)	25	59
34	S	168/172 (98%)	151 (90%)	16 (10%)	1 (1%)	22	56
35	T	59/160 (37%)	52 (88%)	7 (12%)	0	100	100
36	U	102/121 (84%)	93 (91%)	9 (9%)	0	100	100
37	V	134/137 (98%)	128 (96%)	6 (4%)	0	100	100
38	W	223/236 (94%)	211 (95%)	11 (5%)	1 (0%)	30	64
39	X	118/142 (83%)	113 (96%)	5 (4%)	0	100	100
40	Y	124/127 (98%)	117 (94%)	7 (6%)	0	100	100
41	y	240/245 (98%)	221 (92%)	19 (8%)	0	100	100
42	Z	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
43	z	53/106 (50%)	52 (98%)	1 (2%)	0	100	100
44	K	53/165 (32%)	48 (91%)	5 (9%)	0	100	100
45	q	95/106 (90%)	90 (95%)	5 (5%)	0	100	100
46	o	52/59 (88%)	48 (92%)	4 (8%)	0	100	100
All	All	7559/8565 (88%)	6981 (92%)	553 (7%)	25 (0%)	38	68

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	339	LEU
33	r	4	ASN
38	W	177	ALA
3	A	219	ILE
4	a	78	LEU

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	D	211/245 (86%)	209 (99%)	2 (1%)	75	86
2	J	138/150 (92%)	137 (99%)	1 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	188/196 (96%)	187 (100%)	1 (0%)	86	93
4	a	77/119 (65%)	75 (97%)	2 (3%)	41	66
5	B	322/323 (100%)	318 (99%)	4 (1%)	67	82
6	b	571/573 (100%)	556 (97%)	15 (3%)	41	66
7	C	288/289 (100%)	286 (99%)	2 (1%)	81	89
8	c	81/88 (92%)	79 (98%)	2 (2%)	42	67
9	d	94/97 (97%)	94 (100%)	0	100	100
10	E	138/153 (90%)	135 (98%)	3 (2%)	47	70
11	e	109/111 (98%)	107 (98%)	2 (2%)	54	74
12	F	186/205 (91%)	185 (100%)	1 (0%)	86	93
13	f	90/91 (99%)	90 (100%)	0	100	100
14	G	189/208 (91%)	184 (97%)	5 (3%)	41	66
15	g	95/103 (92%)	95 (100%)	0	100	100
16	I	116/141 (82%)	115 (99%)	1 (1%)	75	86
17	H	168/171 (98%)	165 (98%)	3 (2%)	54	74
18	h	104/105 (99%)	104 (100%)	0	100	100
19	i	78/82 (95%)	76 (97%)	2 (3%)	41	66
20	j	69/71 (97%)	68 (99%)	1 (1%)	62	79
21	k	68/69 (99%)	68 (100%)	0	100	100
22	m	326/428 (76%)	325 (100%)	1 (0%)	91	96
23	L	147/159 (92%)	143 (97%)	4 (3%)	40	65
24	l	45/46 (98%)	43 (96%)	2 (4%)	24	53
25	M	108/109 (99%)	107 (99%)	1 (1%)	75	86
26	p	71/72 (99%)	70 (99%)	1 (1%)	62	79
27	N	175/176 (99%)	174 (99%)	1 (1%)	84	91
28	u	132/180 (73%)	128 (97%)	4 (3%)	36	63
29	O	160/162 (99%)	158 (99%)	2 (1%)	65	81
30	P	144/146 (99%)	142 (99%)	2 (1%)	62	79
31	Q	126/151 (83%)	125 (99%)	1 (1%)	79	88
32	R	127/154 (82%)	126 (99%)	1 (1%)	79	88
33	r	178/229 (78%)	175 (98%)	3 (2%)	56	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	S	154/156 (99%)	152 (99%)	2 (1%)	65	81
35	T	50/137 (36%)	47 (94%)	3 (6%)	16	43
36	U	91/107 (85%)	90 (99%)	1 (1%)	70	83
37	V	104/105 (99%)	104 (100%)	0	100	100
38	W	201/213 (94%)	198 (98%)	3 (2%)	60	77
39	X	104/118 (88%)	103 (99%)	1 (1%)	73	84
40	Y	109/110 (99%)	109 (100%)	0	100	100
41	y	207/211 (98%)	207 (100%)	0	100	100
42	Z	115/116 (99%)	115 (100%)	0	100	100
43	z	48/95 (50%)	48 (100%)	0	100	100
44	K	31/65 (48%)	31 (100%)	0	100	100
45	q	84/91 (92%)	84 (100%)	0	100	100
46	o	43/47 (92%)	42 (98%)	1 (2%)	45	69
All	All	6460/7173 (90%)	6379 (99%)	81 (1%)	64	81

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	u	27	LYS
34	S	80	ARG
28	u	100	ARG
31	Q	147	ARG
36	U	49	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
37	V	7	GLN
38	W	22	ASN
9	d	17	HIS
7	C	221	ASN
38	W	91	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	1	3040/3396 (89%)	704 (23%)	43 (1%)
48	2	120/121 (99%)	17 (14%)	1 (0%)
49	3	157/158 (99%)	28 (17%)	2 (1%)
All	All	3317/3675 (90%)	749 (22%)	46 (1%)

5 of 749 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
47	1	13	A
47	1	14	U
47	1	39	A
47	1	40	A
47	1	43	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	1	2537	U
47	1	3020	U
47	1	2541	U
47	1	2857	C
47	1	3153	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	b	701	51	29,34,34	1.17	2 (6%)	35,54,54	1.30	3 (8%)
50	GTP	m	501	51	29,34,34	1.26	2 (6%)	35,54,54	1.24	4 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	b	701	51	-	4/18/38/38	0/3/3/3
50	GTP	m	501	51	-	0/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	m	501	GTP	C5-C6	-4.30	1.39	1.47
50	b	701	GTP	C5-C6	-4.15	1.39	1.47
50	b	701	GTP	C2-N3	2.14	1.38	1.33
50	m	501	GTP	C2-N3	2.07	1.38	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	b	701	GTP	C8-N7-C5	3.75	108.93	102.55
50	m	501	GTP	C8-N7-C5	3.66	108.78	102.55
50	m	501	GTP	C5-C6-N1	3.05	119.90	114.07
50	b	701	GTP	C2-N1-C6	-3.02	119.59	125.11
50	b	701	GTP	C5-C6-N1	3.01	119.81	114.07

There are no chirality outliers.

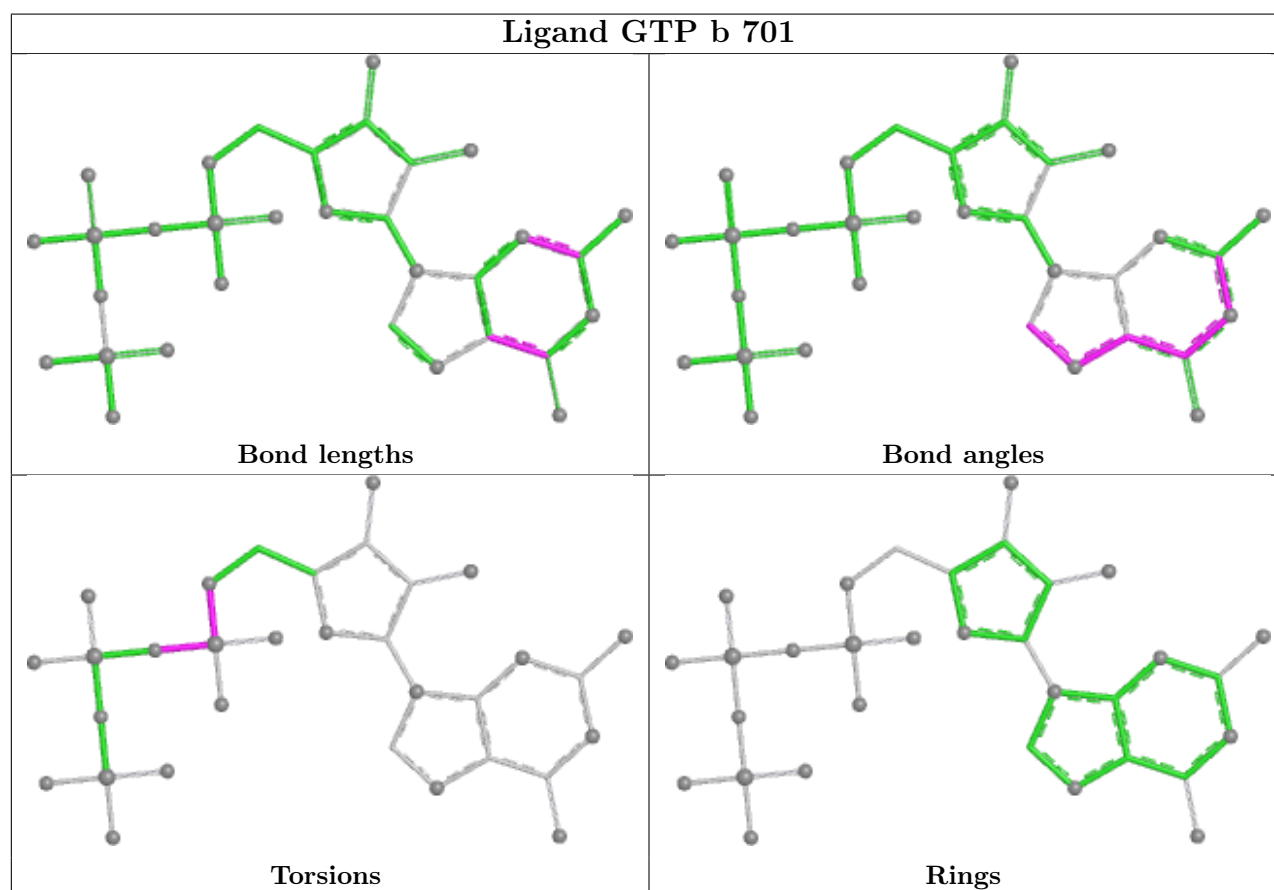
All (4) torsion outliers are listed below:

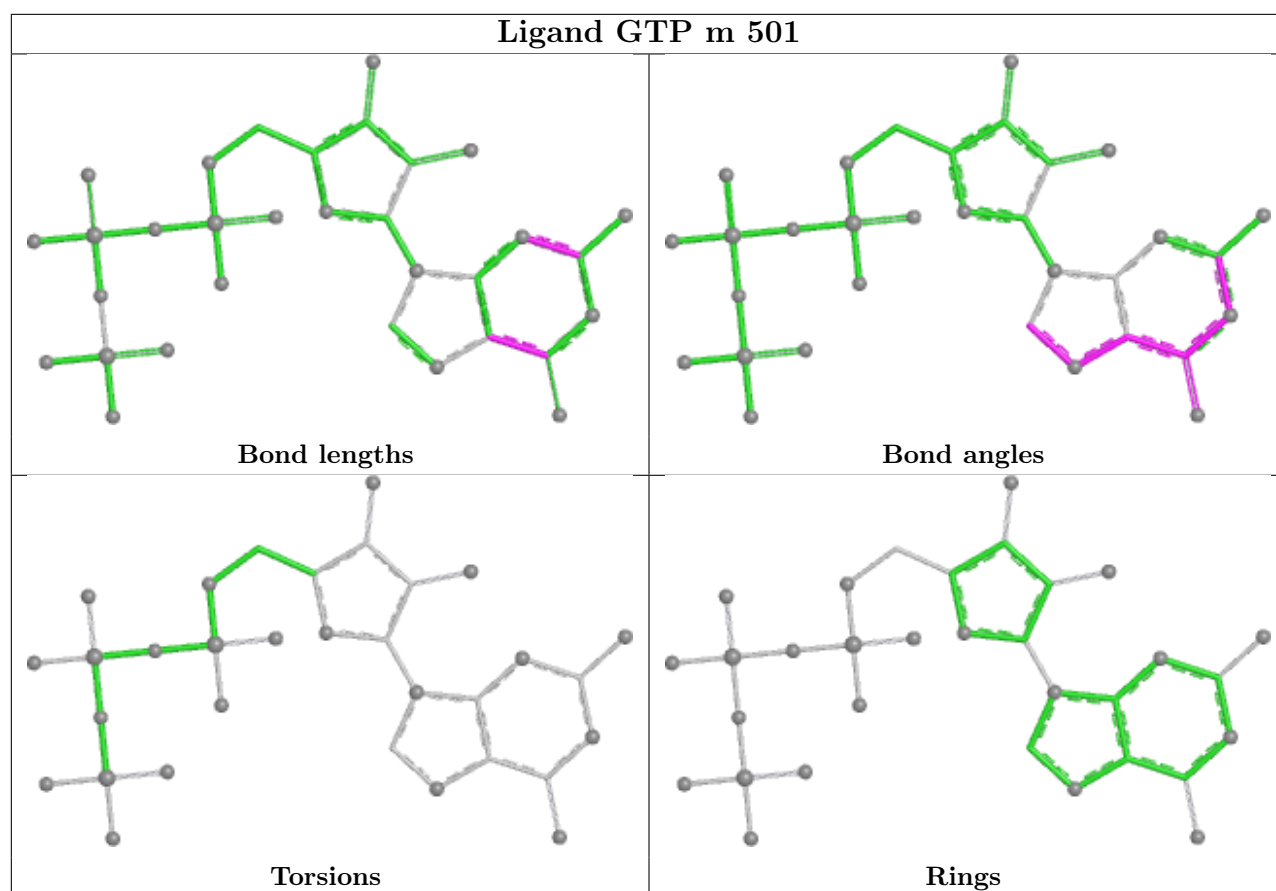
Mol	Chain	Res	Type	Atoms
50	b	701	GTP	C5'-O5'-PA-O3A
50	b	701	GTP	C5'-O5'-PA-O2A
50	b	701	GTP	PB-O3A-PA-O2A
50	b	701	GTP	PB-O3A-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

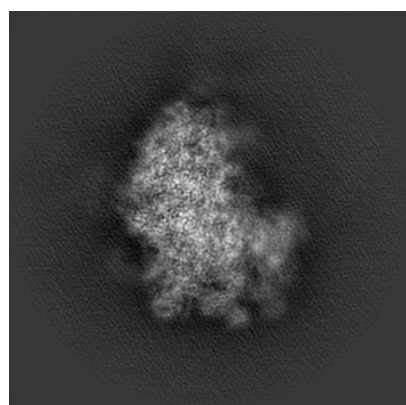
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0369. These allow visual inspection of the internal detail of the map and identification of artifacts.

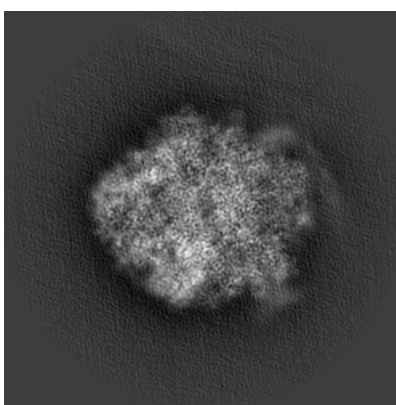
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

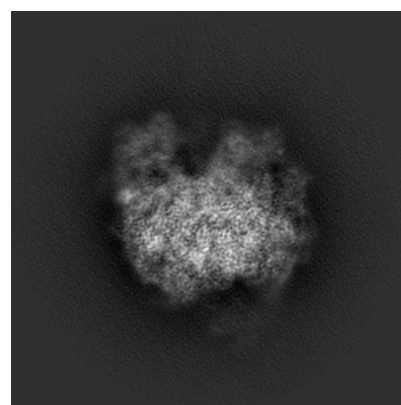
6.1.1 Primary map



X



Y

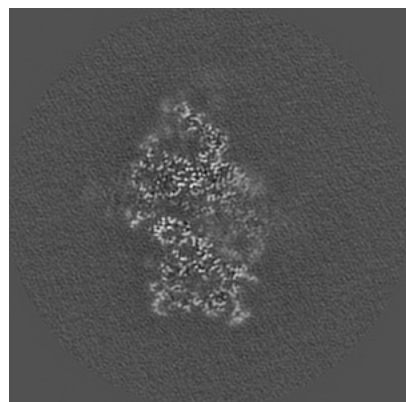


Z

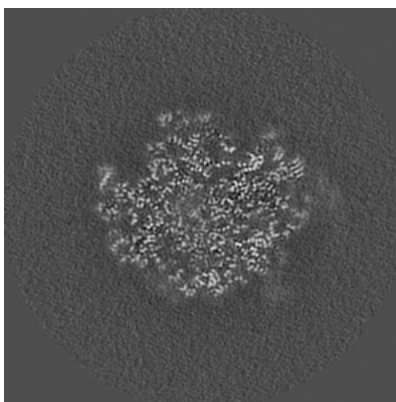
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

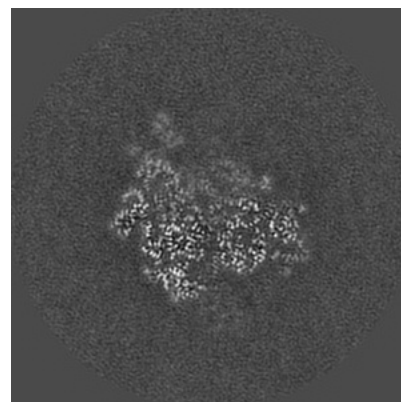
6.2.1 Primary map



X Index: 192



Y Index: 192

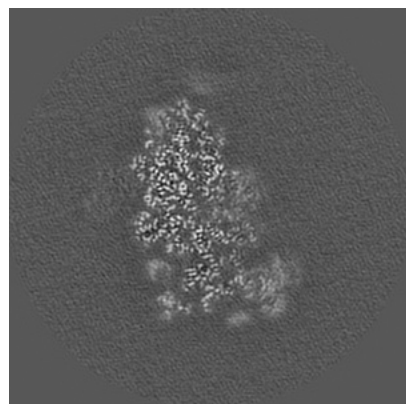


Z Index: 192

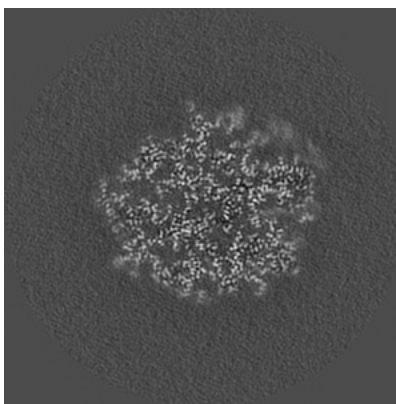
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

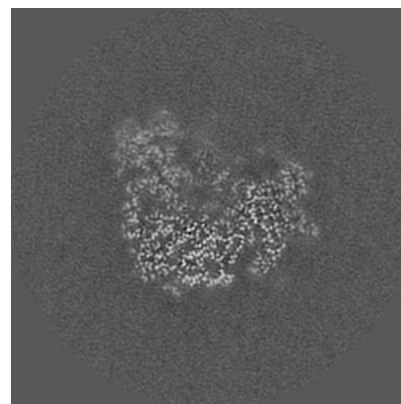
6.3.1 Primary map



X Index: 209



Y Index: 165

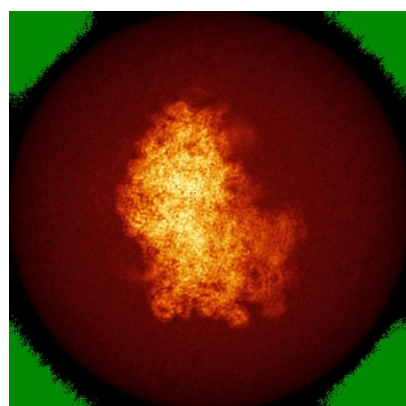


Z Index: 177

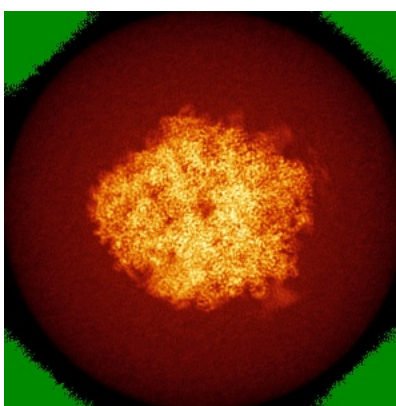
The images above show the largest variance slices of the map in three orthogonal directions.

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

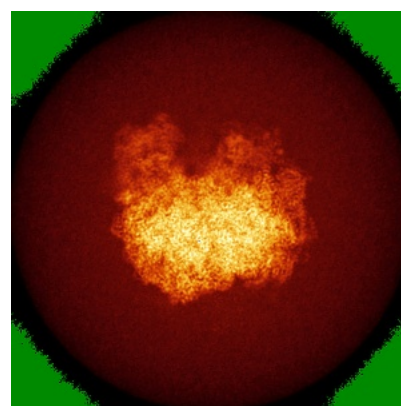
6.4.1 Primary map



X



Y

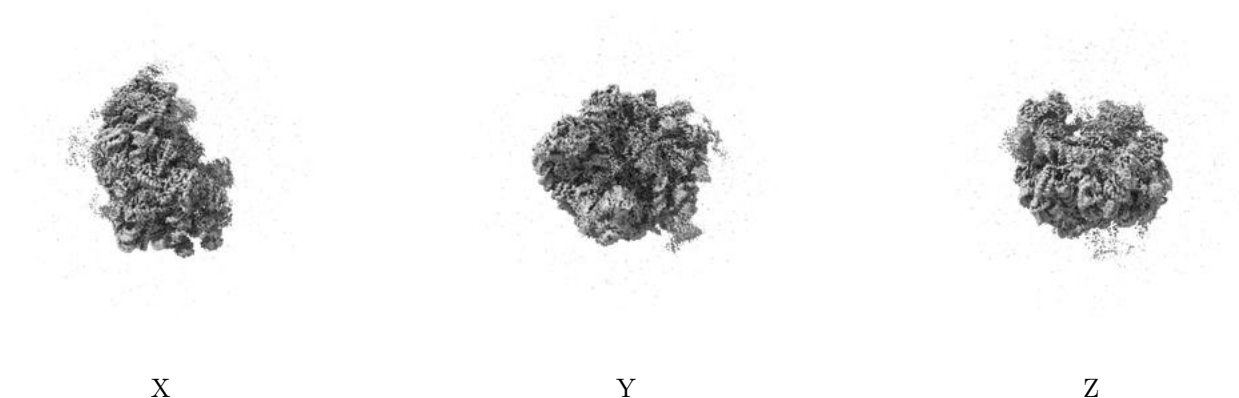


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

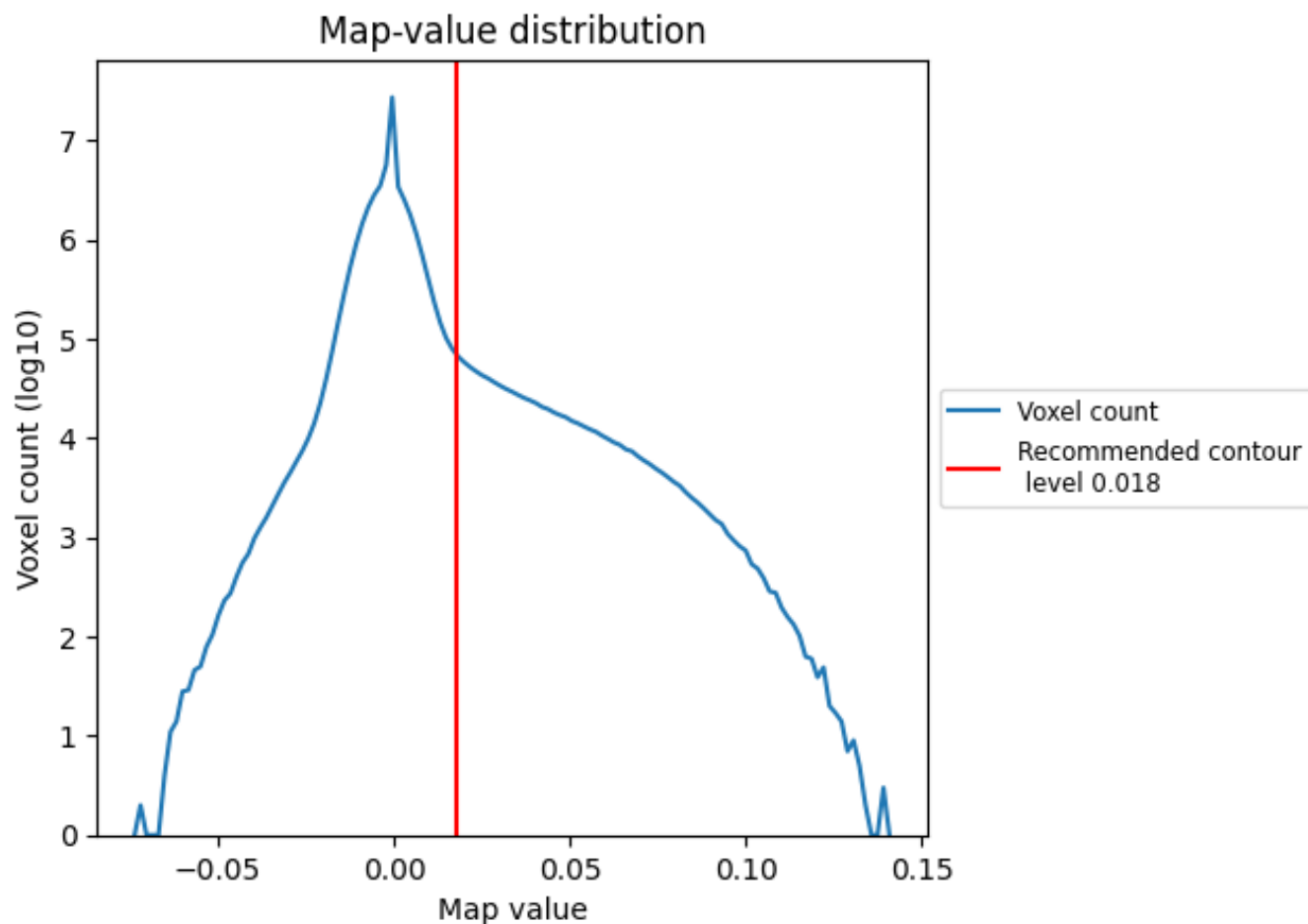
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

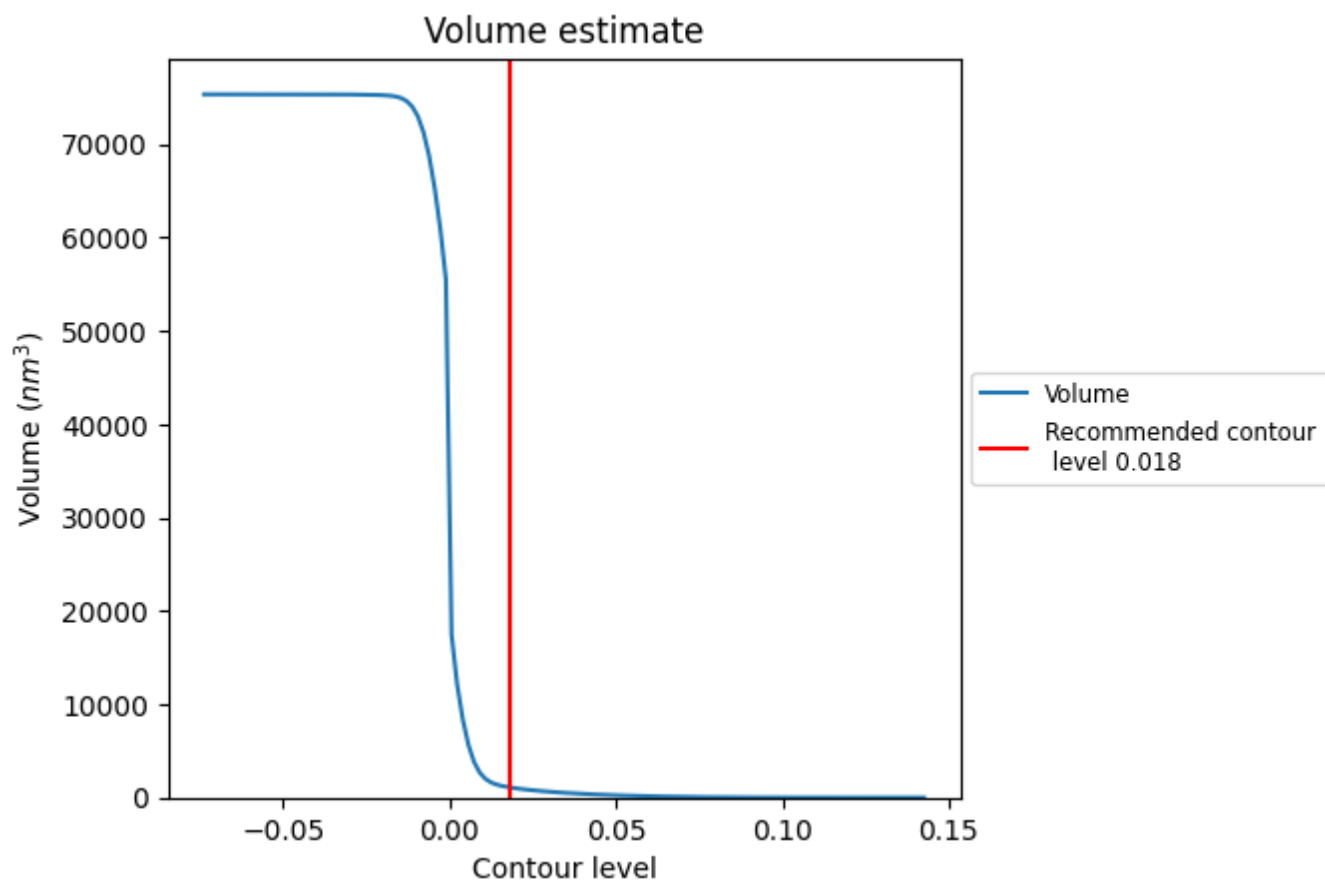
This section contains the results of statistical analysis of the map.

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.

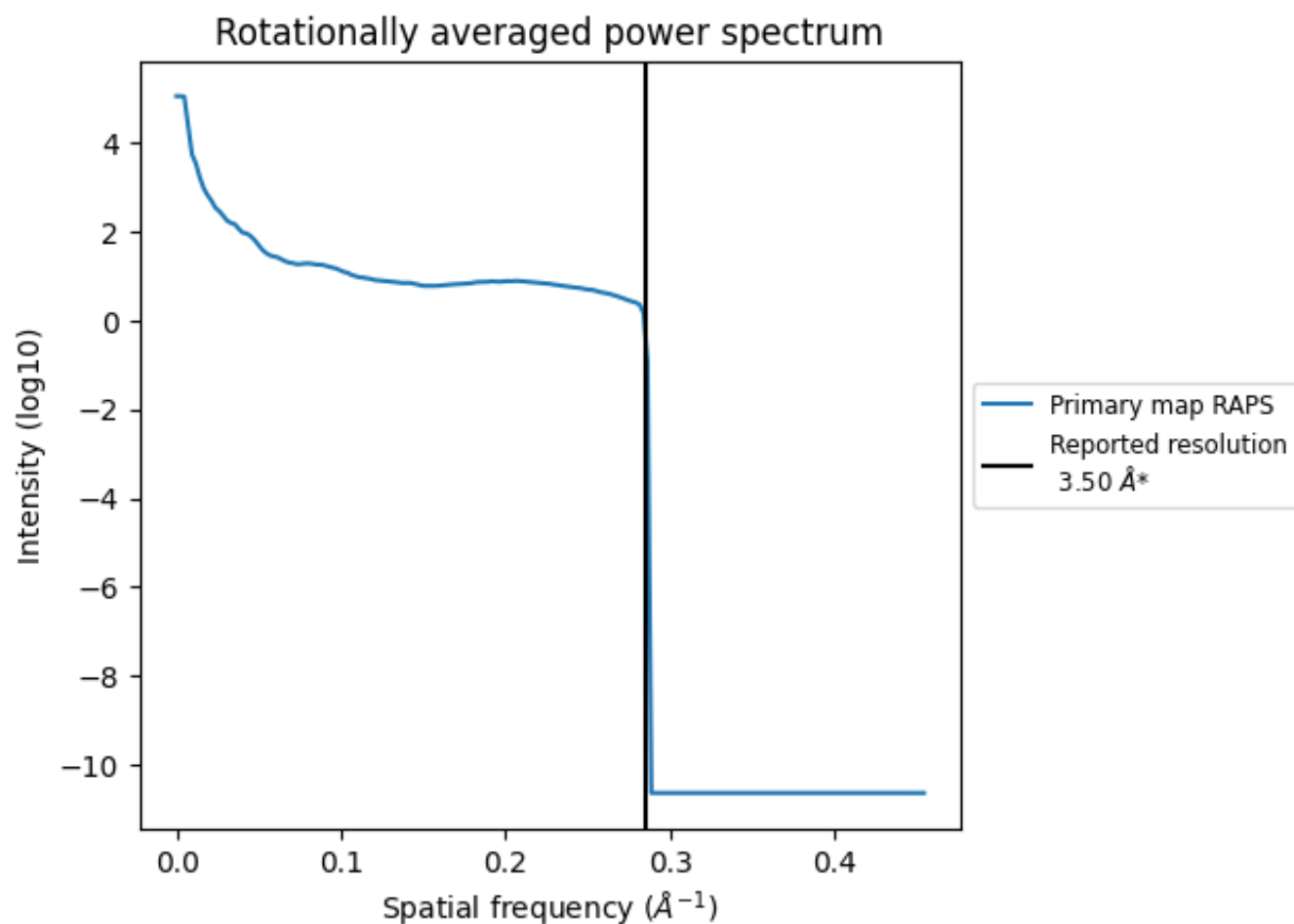
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1094 nm³; this corresponds to an approximate mass of 988 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 ⓘ

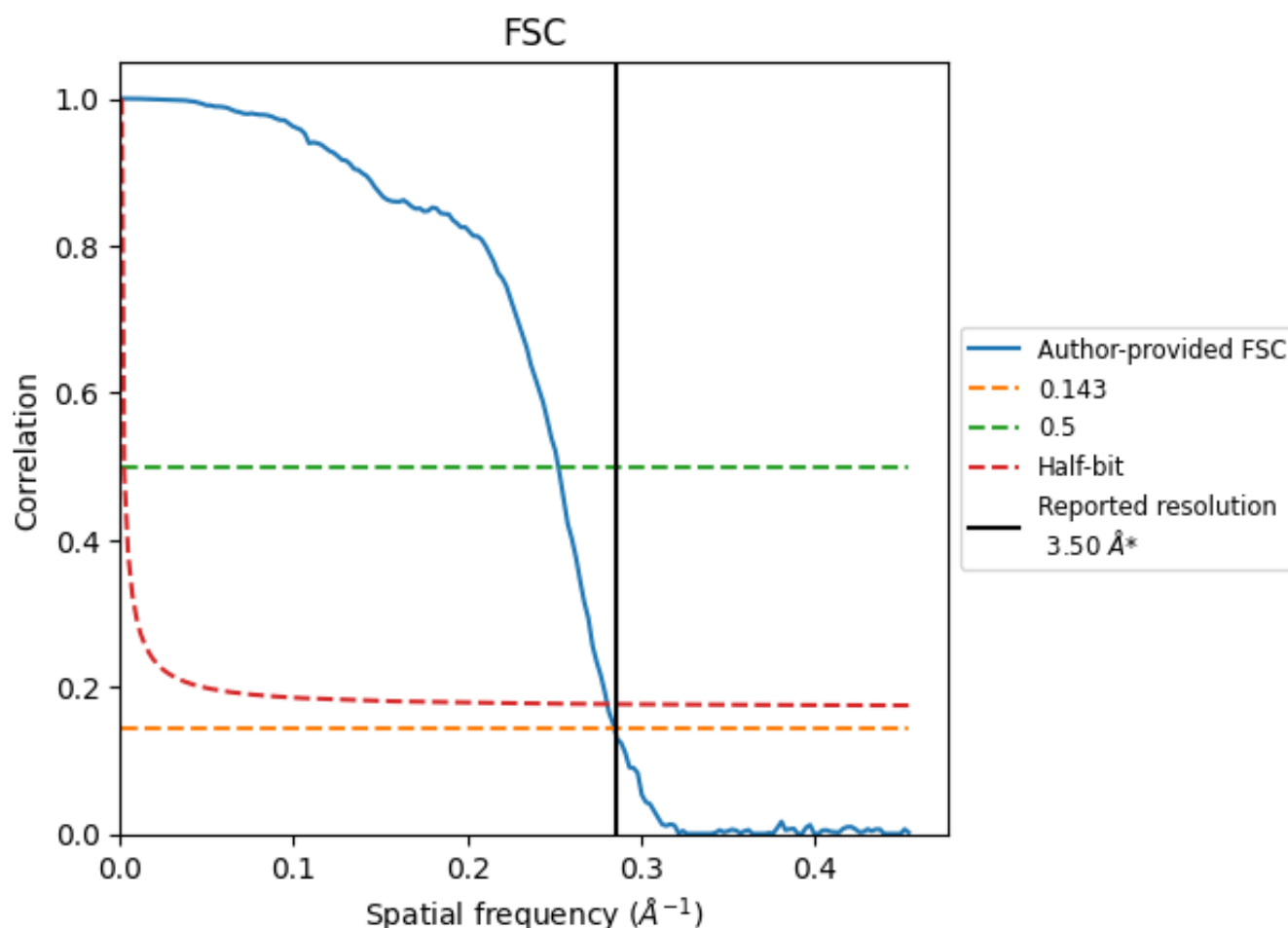


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

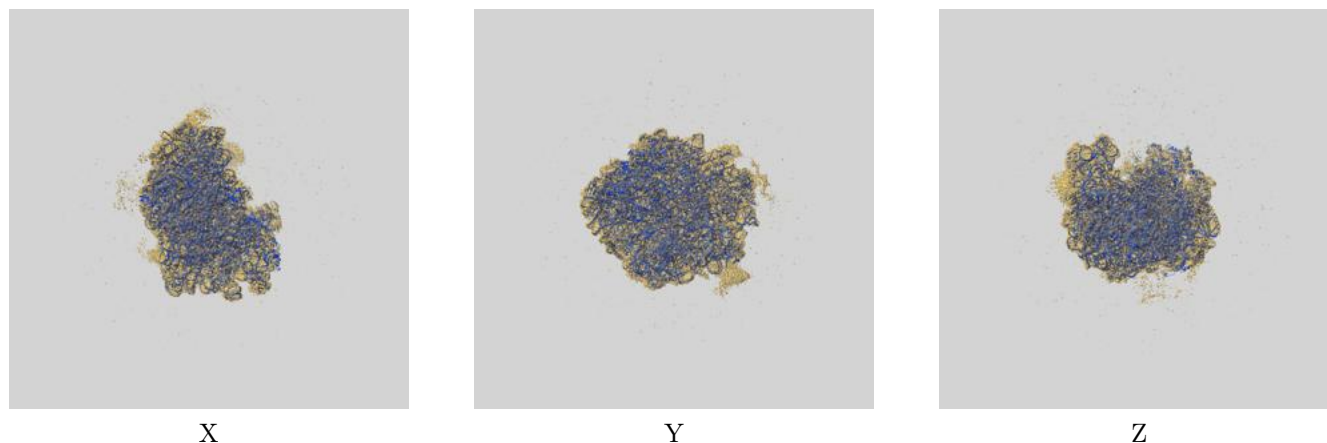
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.51	3.96	3.56
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

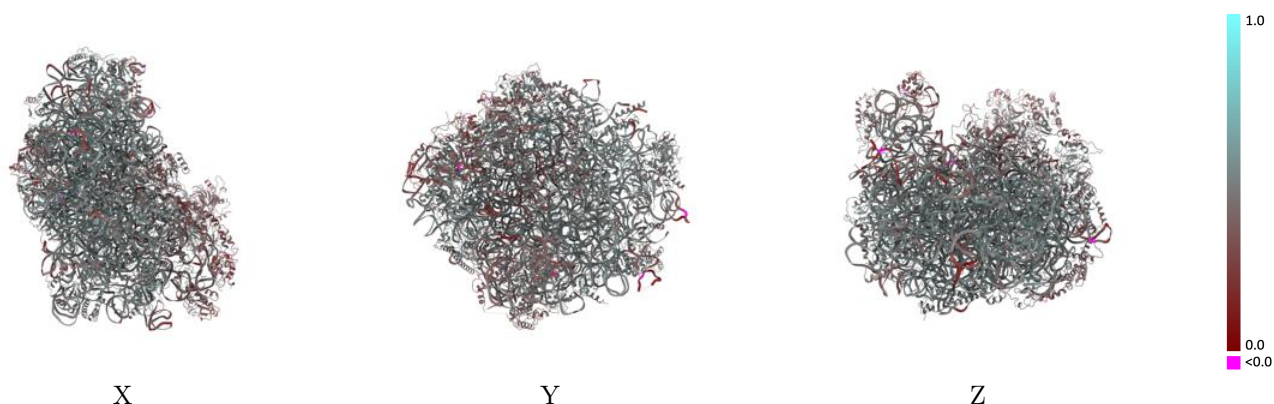
This section contains information regarding the fit between EMDB map EMD-0369 and PDB model 6N8J. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



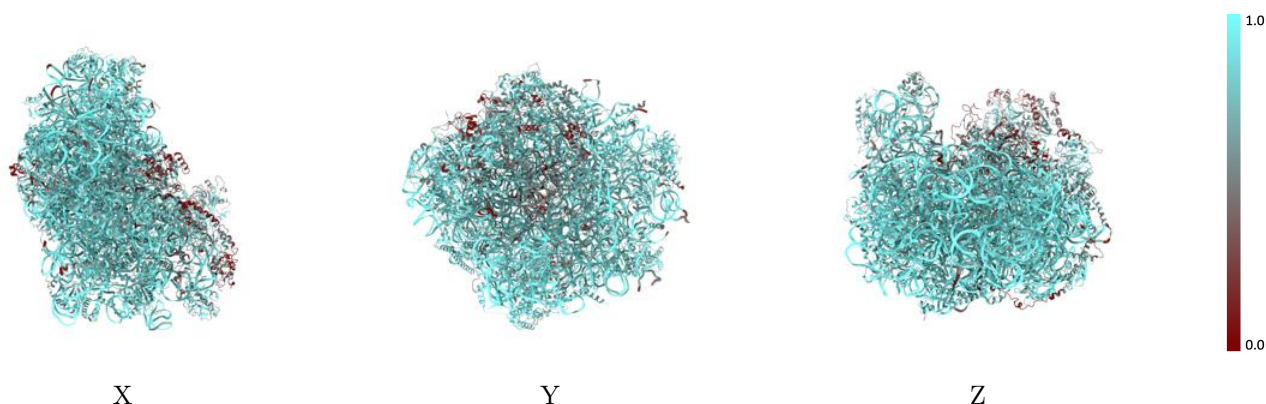
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



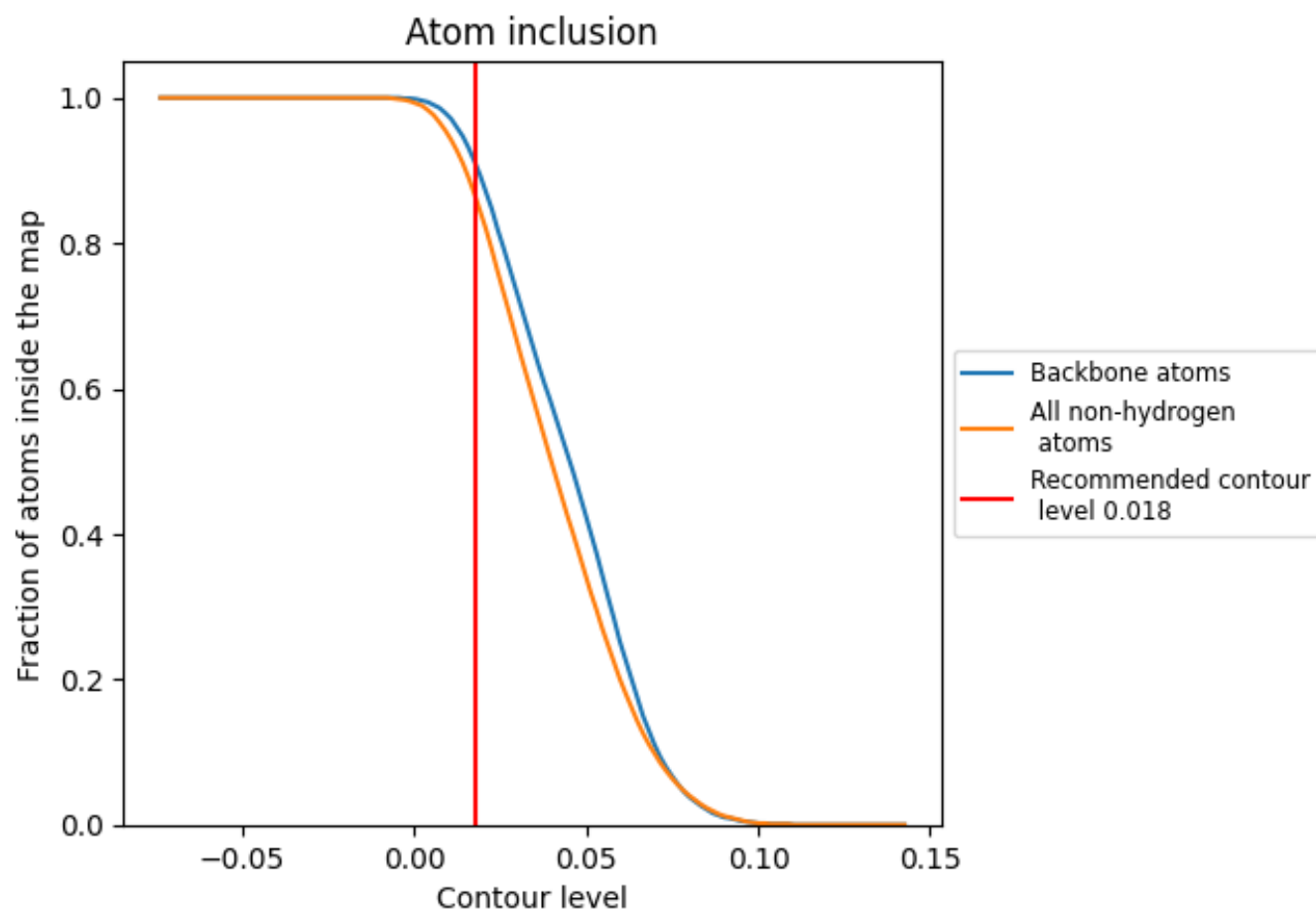
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 86% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.4780
1	 0.9330	 0.4830
2	 0.9450	 0.4320
3	 0.9630	 0.5070
A	 0.8600	 0.5270
B	 0.8800	 0.5120
C	 0.8710	 0.5110
D	 0.7940	 0.4160
E	 0.8250	 0.4850
F	 0.8650	 0.4940
G	 0.8600	 0.4840
H	 0.8610	 0.4960
I	 0.6780	 0.4640
J	 0.6580	 0.3470
K	 0.3020	 0.3010
L	 0.8890	 0.5060
M	 0.8690	 0.4940
N	 0.8830	 0.5340
O	 0.8750	 0.5220
P	 0.8510	 0.5090
Q	 0.8830	 0.5060
R	 0.8700	 0.5090
S	 0.8640	 0.5040
T	 0.7820	 0.4030
U	 0.8290	 0.4380
V	 0.8410	 0.5120
W	 0.6750	 0.3830
X	 0.8720	 0.5170
Y	 0.8840	 0.5080
Z	 0.8390	 0.4960
a	 0.8740	 0.5080
b	 0.5750	 0.4120
c	 0.8510	 0.4860
d	 0.8490	 0.5110
e	 0.8460	 0.5280



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Chain	Atom inclusion	Q-score
f	 0.8840	 0.5370
g	 0.8160	 0.5070
h	 0.8720	 0.5100
i	 0.8850	 0.4980
j	 0.9080	 0.5480
k	 0.7850	 0.4780
l	 0.8990	 0.5410
m	 0.4040	 0.3880
o	 0.7070	 0.4640
p	 0.8510	 0.5000
q	 0.6640	 0.4760
r	 0.4790	 0.4260
u	 0.7870	 0.4690
y	 0.8160	 0.4830
z	 0.6200	 0.4520