



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 04:17 AM UTC

PDB ID : 9JPM / pdb_00009jpm
EMDB ID : EMD-61706
Title : Structure of the Bacterial Ribosome with human tRNA Lys(mcm5s2U34) and mRNA(AAA)
Authors : Ishiguro, K.; Mo, Y.; Shirouzu, M.; Suzuki, T.
Deposited on : 2024-09-26
Resolution : 2.43 Å(reported)
Based on initial model : 7y7e

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

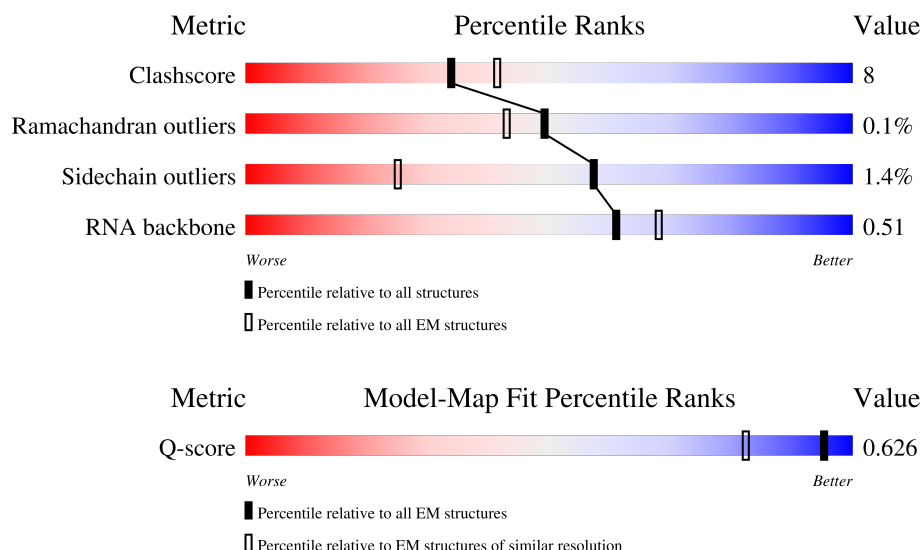
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.43 Å.

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



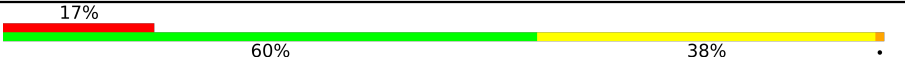







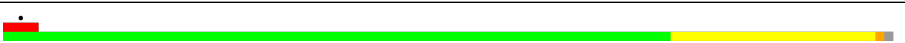

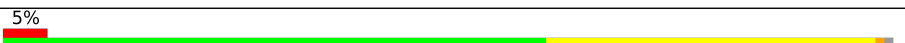


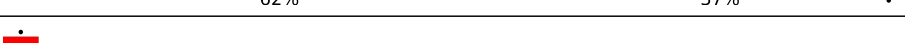
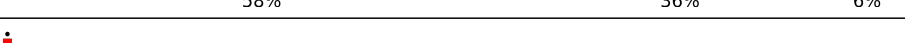
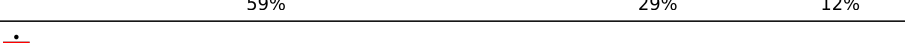
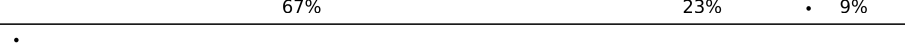
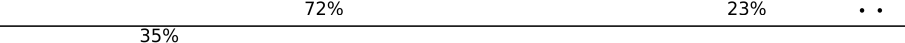
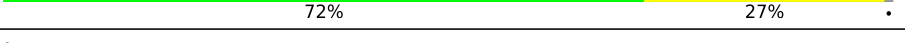






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5787 (1.94 - 2.93)

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	A	1542	
2	B	241	
3	C	233	




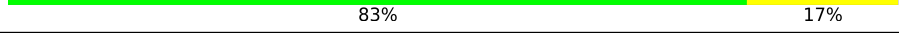
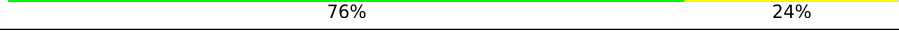
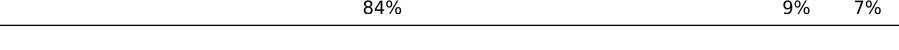
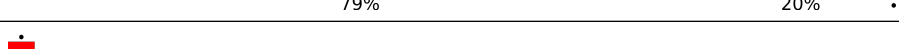




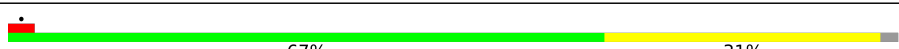

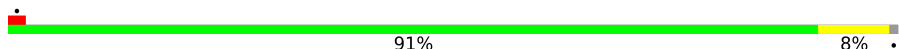





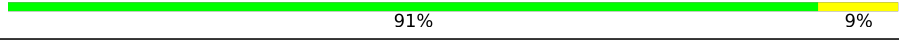





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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	a	2904	
23	b	120	
24	c	273	
25	d	209	
26	e	201	
27	f	179	
28	g	177	

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Mol	Chain	Length	Quality of chain
29	h	149	
30	i	142	
31	j	123	
32	k	144	
33	l	136	
34	m	127	
35	n	117	
36	o	115	
37	p	118	
38	q	103	
39	r	110	
40	s	100	
41	t	104	
42	u	94	
43	v	85	
44	w	78	
45	x	63	
46	y	59	
47	z	57	
48	0	55	
49	1	46	
50	2	65	
51	3	38	
52	4	70	
53	X	35	

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Mol	Chain	Length	Quality of chain
54	Z	77	<div><div></div><div>5%</div><div>62%</div><div>23%</div><div>14%</div></div>
55	V	76	<div><div></div><div>47%</div><div>33%</div><div>14%</div><div>• •</div></div>

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 141982 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0
			32466	14487	5964	10503	1512		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2761	Total	C	N	O	P	0	0
			59301	26460	10925	19155	2761		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	X	11	Total	C	N	O	P	0	0
			233	105	41	76	11		

- Molecule 54 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Z	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

- Molecule 55 is a RNA chain called A-site tRNA-Lys.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	V	73	Total	C	N	O	P	S	0	0
			1579	712	279	514	72	2		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	83	Total	Mg	0
			83	83	
56	M	1	Total	Mg	0
			1	1	
56	a	292	Total	Mg	0
			292	292	
56	b	6	Total	Mg	0
			6	6	
56	d	1	Total	Mg	0
			1	1	
56	p	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	
56	X	1	Total	Mg	0
			1	1	
56	Z	4	Total	Mg	0
			4	4	
56	V	1	Total	Mg	0
			1	1	

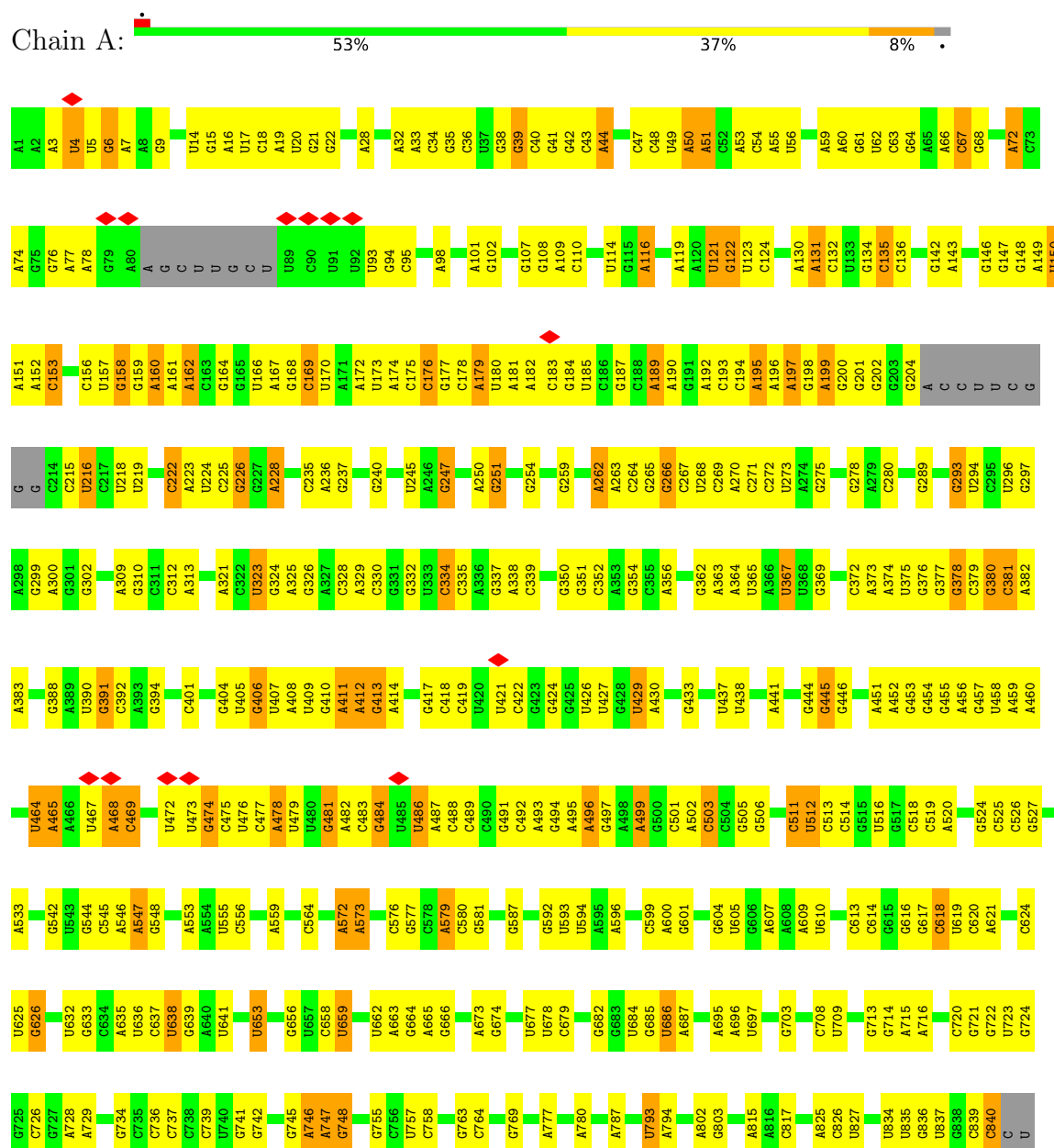
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	3	1	Total	Zn	0
			1	1	
57	4	1	Total	Zn	0
			1	1	

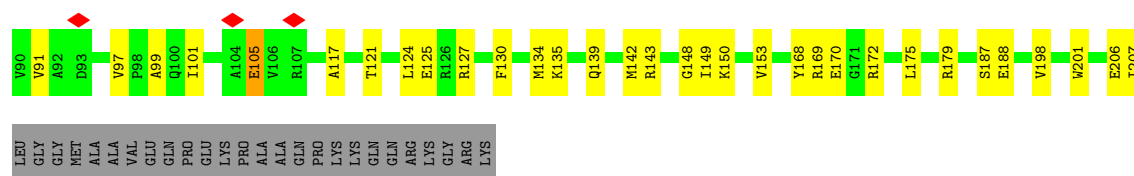
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

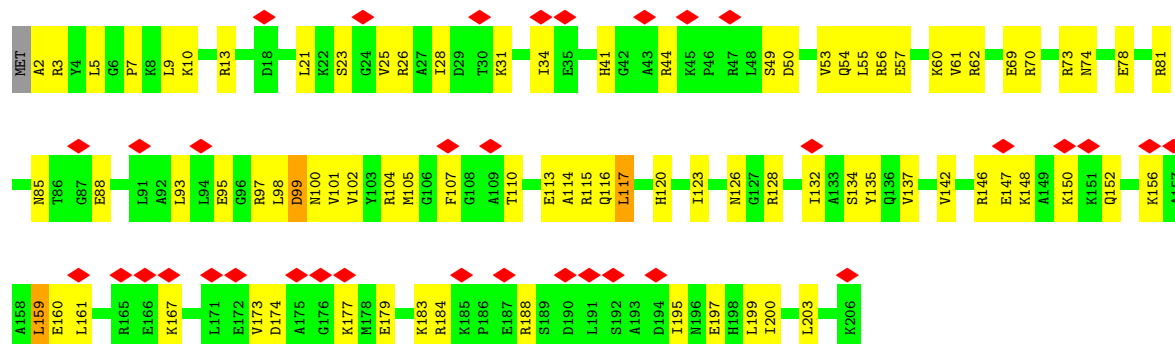
• Molecule 1: 16S rRNA







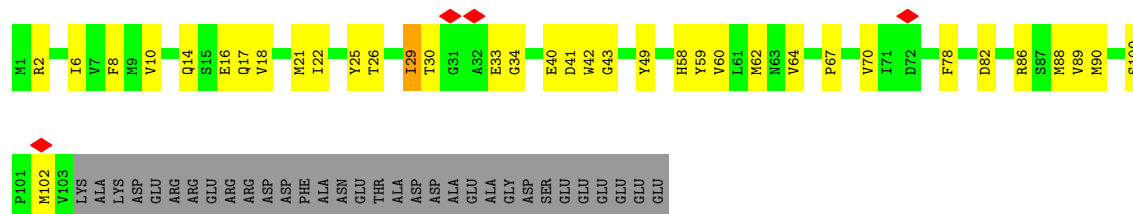
• Molecule 4: 30S ribosomal protein S4



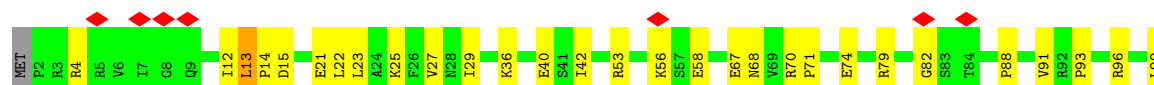
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6, fully modified isoform



• Molecule 7: 30S ribosomal protein S7





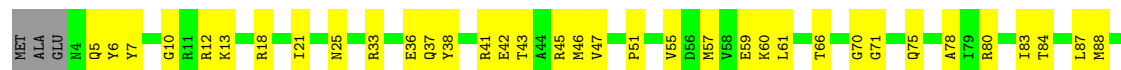
- Molecule 8: 30S ribosomal protein S8

Chain H: 67% 32%



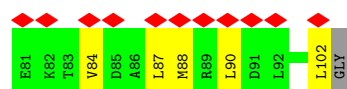
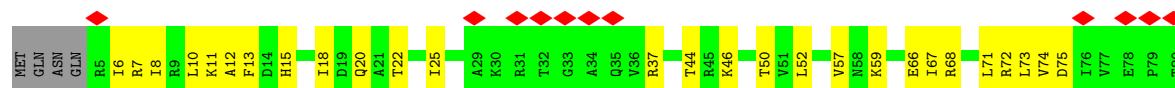
- Molecule 9: 30S ribosomal protein S9

Chain I: 60% 38%



- Molecule 10: 30S ribosomal protein S10

Chain J: 21% 64% 31% 5%



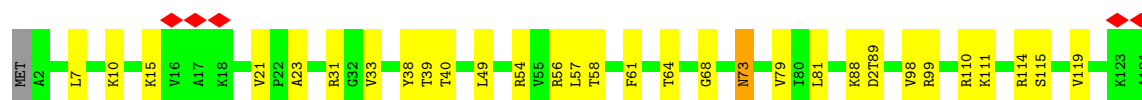
- Molecule 11: 30S ribosomal protein S11

Chain K: 66% 23% 9%

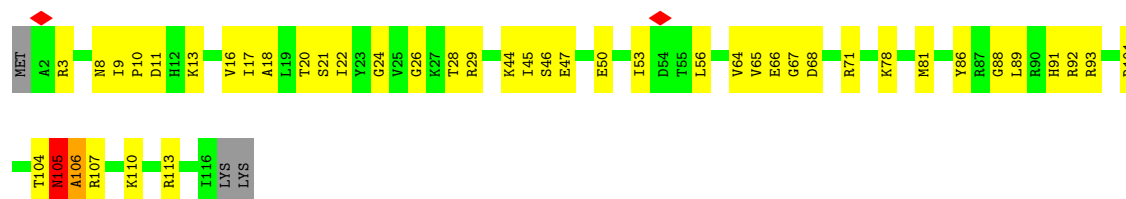


- Molecule 12: 30S ribosomal protein S12

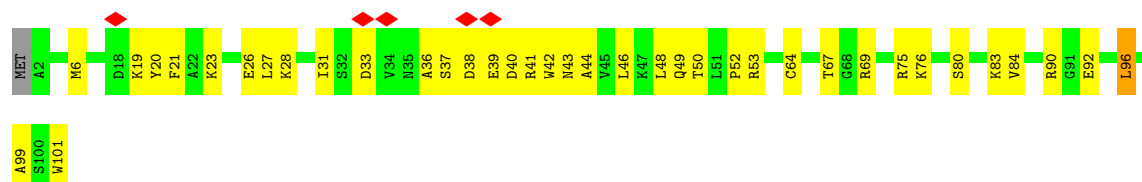
Chain L: 75% 23%



- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14



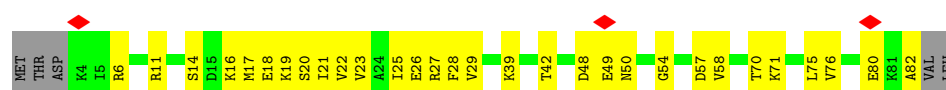
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16



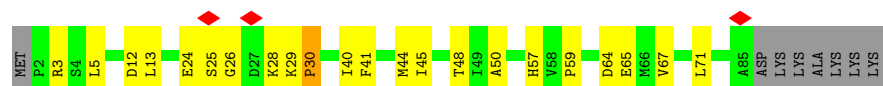
- Molecule 17: 30S ribosomal protein S17



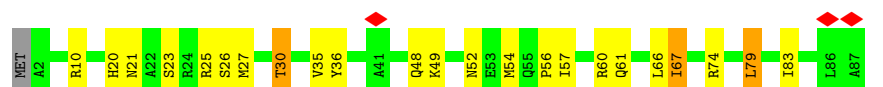
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



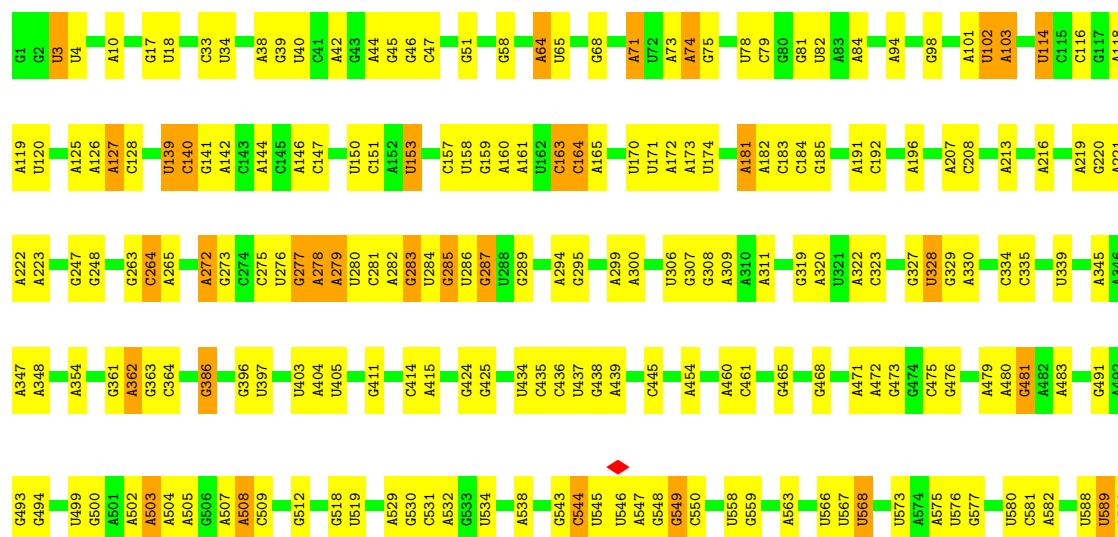
- Molecule 20: 30S ribosomal protein S20



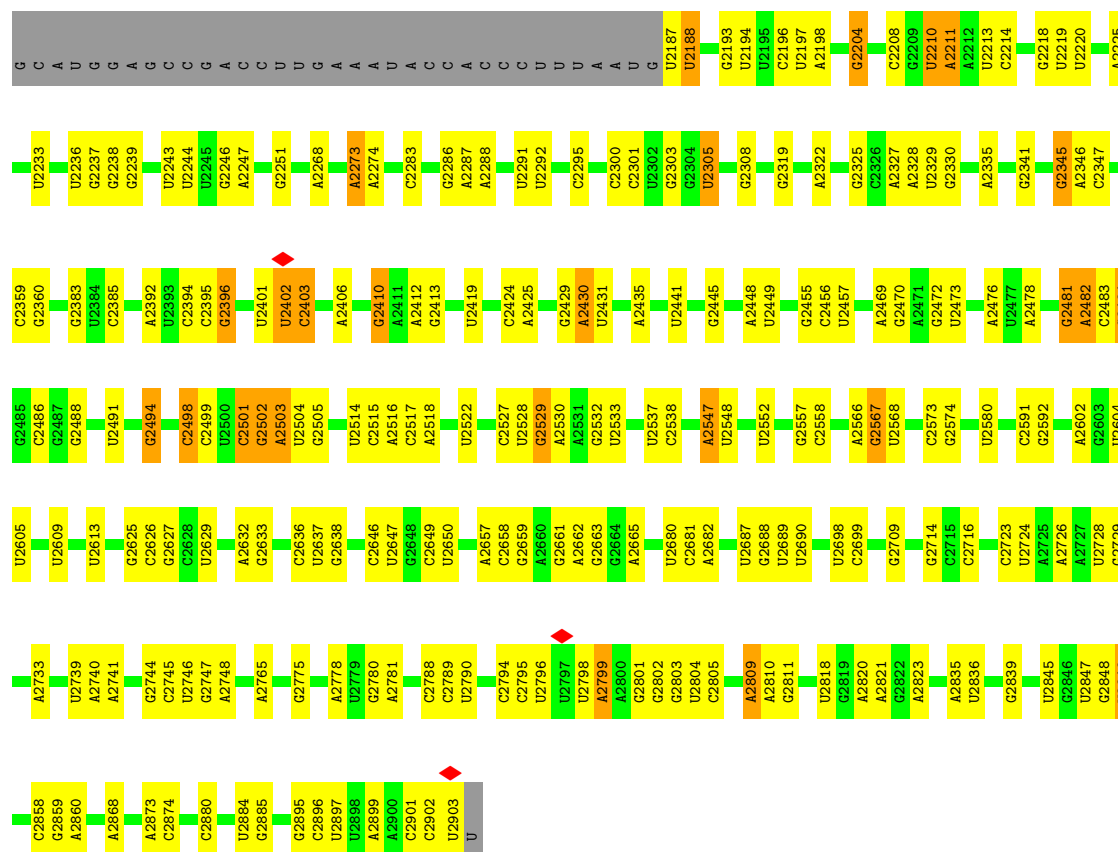
- Molecule 21: 30S ribosomal protein S21



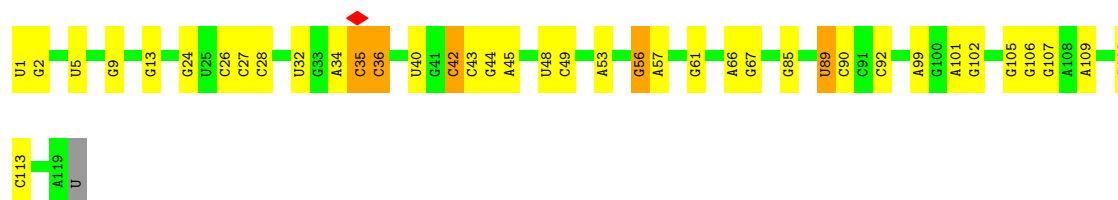
- Molecule 22: 23S rRNA



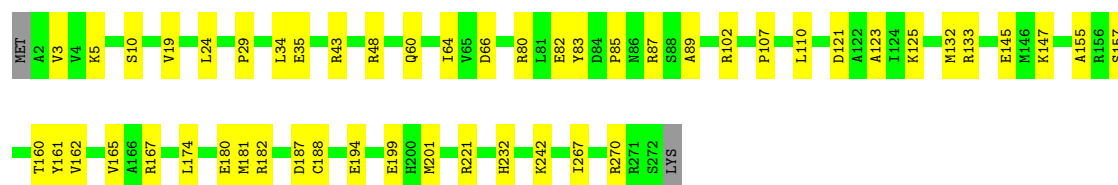
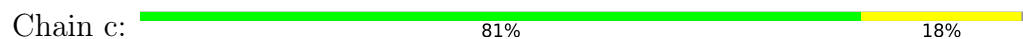
G2083	C1967	G103	U1563	G1232	G1110	A1048	C914	G834	A716	U591
G2086	G1968	C1704	C1564	G1236	A1111	C1052	C915	U839	C717	A592
G2087	A1969	G1710	A1469	A1237	G1112	C	G916	C840	A721	U593
C2091	C1943	G1714	G1356	U1242	G1115	A	A917	A845	C723	U594
C2091	G1972	G1715	G1357	C1243	G1116	G	A927	U846	C723	U596
A2097	A1947	G1720	G1361	G1250	G1122	A	A928	U847	G729	G600
U2098	A1948	G1721	C1362	G1253	G1125	U	U931	U848	A730	C801
G2102	A1953	A1722	A1365	A1254	U1132	G	U931	U849	G738	A602
C	U1856	G1723	U1485	U1255	U1133	U	C946	U850	A739	A603
C	G1857	G1724	U1486	G1256	A1134	G	U947	C851	C740	C811
C	A1858	C1728	A1378	A1265	C1135	U	C948	G856	U741	G612
U	U1864	U1729	U1379	A1265	U1141	U	U955	G857	A742	A613
U	G1867	C1730	A1495	A1272	A1142	U	U958	G858	A743	A614
U	C1870	G1731	A1496	A1275	A1143	C	A959	G859	U744	U615
G	A1871	C1732	U1497	A1286	A1144	A	A960	U860	U746	G620
G	A1872	C1732	C1386	A1286	U1150	A	C961	A861	U747	A621
G	G1873	C1732	A1387	A1286	C1150	G	G974	G864	U754	A627
G	C1874	U1736	U1392	A1286	A1156	C	U983	G865	U755	A632
A	G1875	A1744	U1397	A1286	C1170	C	A984	G866	A760	A633
U	A1876	A1745	C1398	A1286	G1171	C	G989	U870	C834	C834
A	A1877	A1746	G1401	A1286	U1179	A	U012	U871	C835	C835
A	A1878	A1747	U1402	A1286	C1172	G	C1013	U872	A637	A637
G	C1879	U1747	U1405	A1286	U	U	C995	A764	A764	C838
G	U1880	C1764	U1406	A1286	A	U	A996	C765	C765	U639
U	U1881	U1773	G1407	A1286	U	U	C997	U766	U766	U639
G	U1882	A1773	G1408	A1286	G1177	U	C996	A644	C840	C840
G	C1902	U1782	U1416	A1286	C1178	U	A1009	U875	A644	A644
G	G1906	A1794	C1417	A1286	U1179	A	U012	G776	C645	C645
C	U1911	C1795	C1418	A1286	U1180	A	C1013	A782	U646	U646
U	U1911	U1796	A1419	A1286	U1181	G	U019	G783	G647	G647
U	G2055	G1797	U1420	A1286	G1182	A	U1019	G784	U653	U653
U	G2056	U1798	G1421	A1286	U1183	A	A1020	G785	A654	A654
U	A1916	G1799	A1525	A1286	U1184	G	A1021	A788	U657	U657
A	U1917	C1800	C1526	A1286	G1187	C	G1022	U789	U658	U658
A	G1929	A1801	G1527	A1286	U1199	U	G1025	G659	G659	G659
G	U1930	A1802	A1428	A1286	C1200	A	A1027	A668	A668	A668
U	U1931	A1803	G1430	A1286	U1203	A	A1028	U810	G882	G882
G	G1933	A1808	A1431	A1286	A1204	U	U1033	C812	A885	A885
A	A1937	G1814	U1647	A1286	A1205	C	U1034	U811	U885	U885
C	A1938	A1815	A1435	A1286	G1210	C	U1035	C812	U886	U886
C	U1939	C1816	G1436	A1286	C1211	U	A1040	C814	C887	C887
C	A2071	G1817	U1537	A1286	G1212	C	G1041	C817	U888	U888
C	C2072	U1818	G1445	A1286	U1223	A	C1044	U827	A693	A693
C	C2073	A1819	A1446	A1286	A1226	U	A1045	U828	U703	U703
A	U2074	U1820	C1447	A1286	U1231	G	A1046	G704	G704	G704
G	C1962	G1674	A1548	A1286	U1231	U	C1047	A833	A715	A715
U	C1965	A1677	A1549	A1286	U1231	U	C1047	A833	A715	A715
U	A1966	A1678	G1560	A1286	U1231	U	C1047	A833	A715	A715



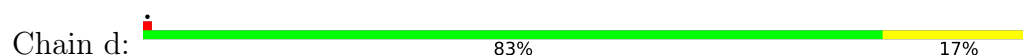
• Molecule 23: 5S rRNA

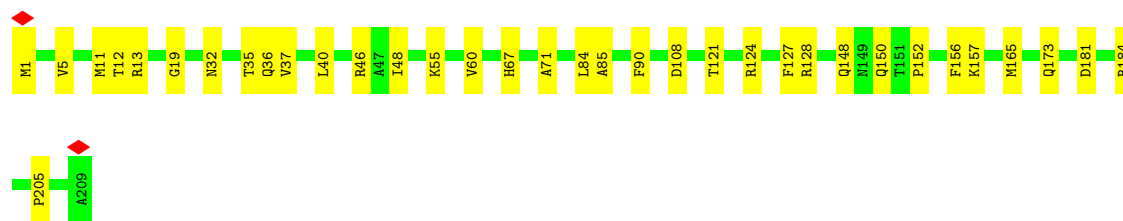


• Molecule 24: 50S ribosomal protein L2

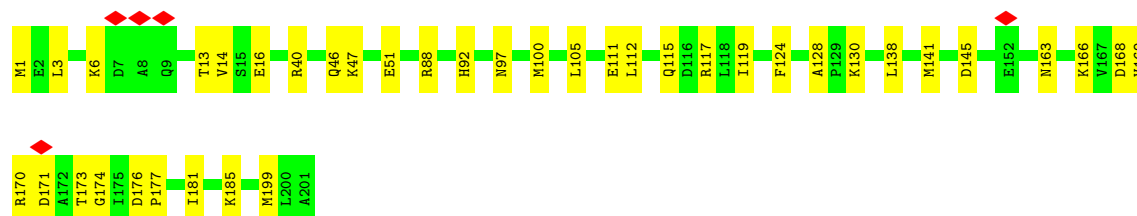
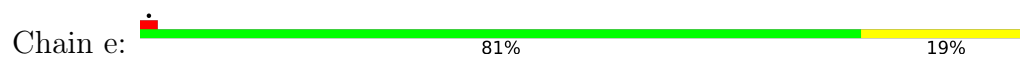


• Molecule 25: 50S ribosomal protein L3

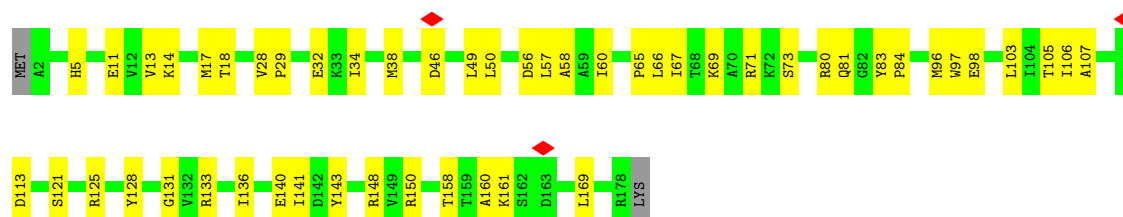




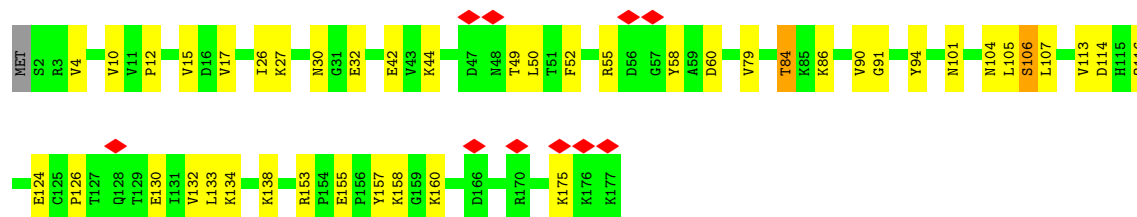
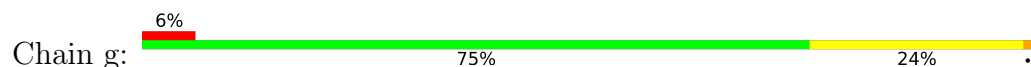
- Molecule 26: 50S ribosomal protein L4



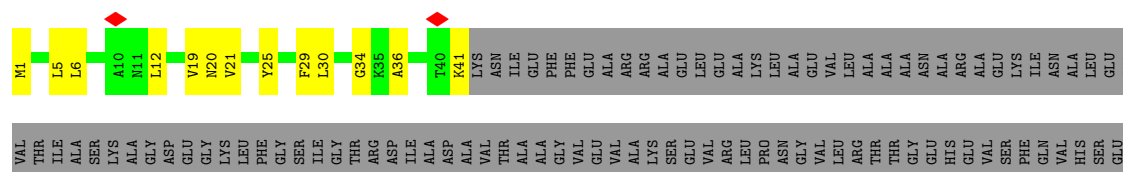
- Molecule 27: 50S ribosomal protein L5



- Molecule 28: 50S ribosomal protein L6



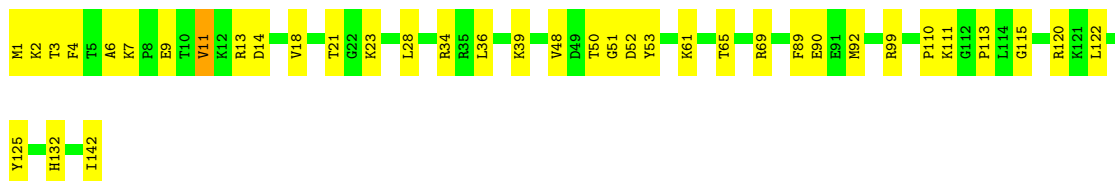
- Molecule 29: 50S ribosomal protein L9




VAL
PHE
ALA
LYS
VAL
ILE
VAL
ASN
VAL
ALA
GLU

- Molecule 30: 50S ribosomal protein L13

Chain i:  73% 26%




- Molecule 31: 50S ribosomal protein L14

Chain j:  83% 17%



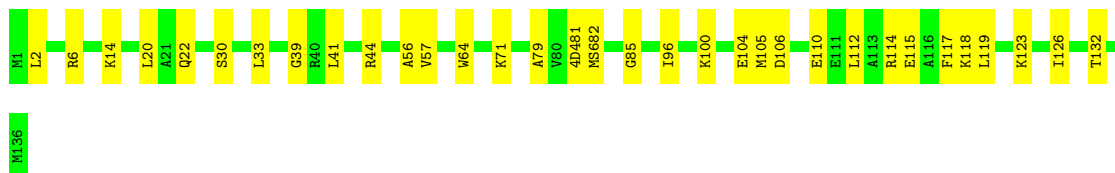
- Molecule 32: 50S ribosomal protein L15

Chain k:  83% 17%




- Molecule 33: 50S ribosomal protein L16

Chain l:  76% 24%




- Molecule 34: 50S ribosomal protein L17

Chain m:  84% 9% 7%

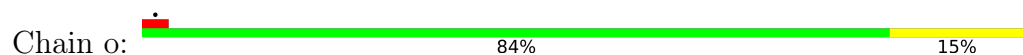


- Molecule 35: 50S ribosomal protein L18

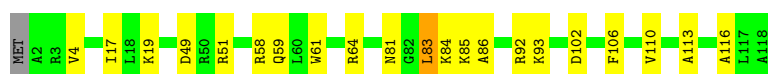
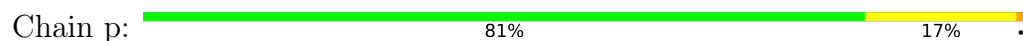
Chain n:  79% 20%



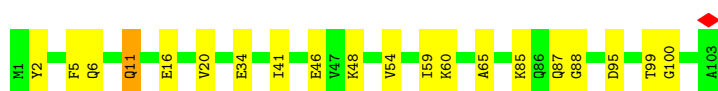
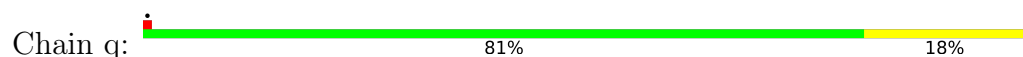
- Molecule 36: 50S ribosomal protein L19



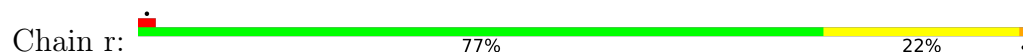
- Molecule 37: 50S ribosomal protein L20



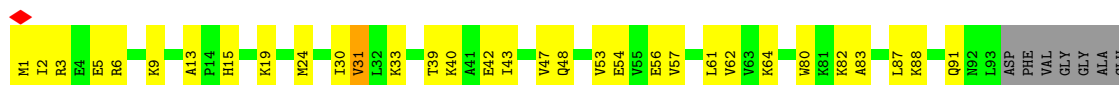
- Molecule 38: 50S ribosomal protein L21



- Molecule 39: 50S ribosomal protein L22



- Molecule 40: 50S ribosomal protein L23

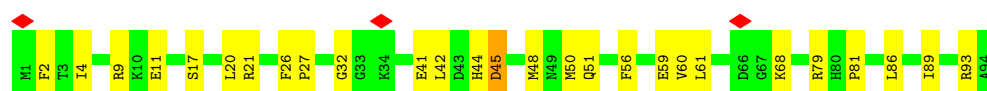


- Molecule 41: 50S ribosomal protein L24




- Molecule 42: 50S ribosomal protein L25

Chain u:  71% 28%




- Molecule 43: 50S ribosomal protein L27

Chain v:  91% 8%



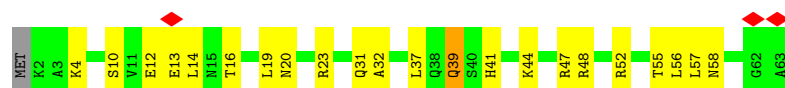
- Molecule 44: 50S ribosomal protein L28

Chain w:  78% 21%




- Molecule 45: 50S ribosomal protein L29

Chain x:  5% 63% 33%



- Molecule 46: 50S ribosomal protein L30

Chain y:  83% 15%




- Molecule 47: 50S ribosomal protein L32

Chain z:  75% 23%



- Molecule 48: 50S ribosomal protein L33

Chain 0:  84% 9% 7%




- Molecule 49: 50S ribosomal protein L34

Chain 1:  91% 9%



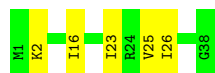
- Molecule 50: 50S ribosomal protein L35

Chain 2:  86% 11% ..



- Molecule 51: 50S ribosomal protein L36

Chain 3:  87% 13%



- Molecule 52: 50S ribosomal protein L31

Chain 4:  10% 51% 34% 14%



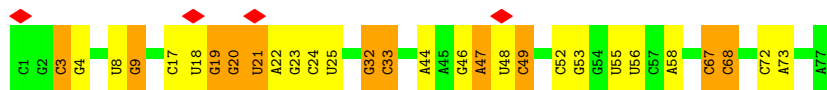
- Molecule 53: mRNA

Chain X:  31% 69%



- Molecule 54: P-site tRNA-fMet

Chain Z:  5% 62% 23% 14%



- Molecule 55: A-site tRNA-Lys

Chain V:  47% 33% 14% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	423074	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.138	Depositor
Minimum map value	-0.059	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0107	Depositor
Map size (Å)	439.10498, 439.10498, 439.10498	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8285, 0.8285, 0.8285	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, 6MZ, 1MA, G7M, UR3, MG, 2MU, 3TD, 4SU, MEQ, OMC, 2MG, 2MA, PSU, H2U, 1MG, IAS, MS6, D2T, OMG, 70U, 12A, 4OC, OMU, 4D4, ZN, 5MC, 5MU

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	A	0.50	0/36073	0.46	0/56264
2	B	0.28	0/1784	0.51	0/2403
3	C	0.41	0/1651	0.53	0/2225
4	D	0.31	0/1665	0.50	0/2227
5	E	0.45	0/1165	0.55	0/1568
6	F	0.38	0/858	0.57	0/1160
7	G	0.35	0/1219	0.48	0/1635
8	H	0.42	0/989	0.49	0/1326
9	I	0.41	0/1034	0.57	0/1375
10	J	0.42	0/796	0.65	0/1077
11	K	0.44	0/884	0.58	0/1191
12	L	0.41	0/960	0.52	0/1286
13	M	0.39	0/900	0.56	0/1204
14	N	0.44	0/817	0.56	0/1088
15	O	0.42	0/722	0.54	0/964
16	P	0.32	0/653	0.56	0/877
17	Q	0.34	0/650	0.49	0/871
18	R	0.41	0/553	0.54	0/742
19	S	0.42	0/685	0.68	3/922 (0.3%)
20	T	0.36	0/676	0.48	0/895
21	U	0.30	0/597	0.50	0/792
22	a	0.65	0/65842	0.48	2/102711 (0.0%)
23	b	0.49	0/2850	0.41	0/4444
24	c	0.53	0/2121	0.55	0/2852
25	d	0.51	0/1576	0.53	0/2119
26	e	0.45	0/1571	0.48	0/2113
27	f	0.36	0/1434	0.49	0/1926
28	g	0.34	0/1343	0.51	0/1816
29	h	0.39	0/306	0.59	0/413
30	i	0.51	0/1152	0.51	0/1551
31	j	0.51	0/955	0.52	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	k	0.49	0/1062	0.57	0/1413
33	l	0.52	0/1073	0.60	1/1433 (0.1%)
34	m	0.53	0/958	0.55	0/1281
35	n	0.38	0/902	0.53	0/1209
36	o	0.48	0/929	0.51	0/1242
37	p	0.56	0/960	0.54	0/1278
38	q	0.49	0/829	0.53	0/1107
39	r	0.54	0/864	0.54	0/1156
40	s	0.42	0/744	0.56	0/994
41	t	0.40	0/787	0.58	0/1051
42	u	0.42	0/766	0.52	0/1025
43	v	0.49	0/642	0.51	0/848
44	w	0.48	0/635	0.56	0/848
45	x	0.39	0/502	0.53	0/667
46	y	0.47	0/453	0.54	0/605
47	z	0.51	0/450	0.53	0/599
48	0	0.45	0/424	0.52	0/565
49	1	0.51	0/380	0.56	0/498
50	2	0.54	0/513	0.51	0/676
51	3	0.51	0/303	0.56	0/397
52	4	0.31	0/488	0.54	1/649 (0.2%)
53	X	0.52	0/260	0.37	0/402
54	Z	0.44	0/1725	0.42	0/2687
55	V	0.37	0/1429	0.41	0/2217
All	All	0.55	0/152559	0.49	7/228163 (0.0%)

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
13	M	0	2
50	2	0	1
All	All	0	3

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	59	PRO	CA-N-CD	-8.28	100.41	112.00
19	S	59	PRO	N-CD-CG	-7.45	92.02	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	512	G	O4'-C1'-N9	6.18	117.47	108.20
22	a	2501	C	C4'-C3'-O3'	6.13	118.60	109.40
52	4	5	ILE	N-CA-C	-5.69	108.30	113.71

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	2	31	HIS	Peptide
13	M	105	ASN	Peptide
13	M	65	VAL	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32466	0	16359	483	0
2	B	1753	0	1780	75	0
3	C	1624	0	1696	42	0
4	D	1643	0	1707	74	0
5	E	1152	0	1196	30	0
6	F	839	0	833	34	0
7	G	1203	0	1254	31	0
8	H	979	0	1031	29	0
9	I	1022	0	1070	39	0
10	J	786	0	828	24	0
11	K	877	0	884	24	0
12	L	957	0	1017	24	0
13	M	891	0	952	36	0
14	N	805	0	844	33	0
15	O	714	0	734	18	0
16	P	643	0	661	24	0
17	Q	641	0	682	23	0
18	R	544	0	565	18	0
19	S	668	0	693	20	0
20	T	670	0	719	20	0
21	U	589	0	629	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	a	59301	0	29849	481	0
23	b	2549	0	1291	18	0
24	c	2082	0	2154	36	0
25	d	1566	0	1618	23	0
26	e	1552	0	1619	23	0
27	f	1410	0	1444	33	0
28	g	1323	0	1371	31	0
29	h	303	0	327	10	0
30	i	1129	0	1162	26	0
31	j	946	0	1023	13	0
32	k	1053	0	1129	20	0
33	l	1075	0	1144	19	0
34	m	945	0	989	8	0
35	n	892	0	923	16	0
36	o	917	0	962	13	0
37	p	947	0	1019	16	0
38	q	816	0	839	11	0
39	r	857	0	922	15	0
40	s	738	0	807	26	0
41	t	779	0	831	24	0
42	u	753	0	780	22	0
43	v	634	0	653	6	0
44	w	625	0	652	11	0
45	x	501	0	531	22	0
46	y	449	0	488	6	0
47	z	444	0	458	9	0
48	0	417	0	451	2	0
49	1	377	0	418	3	0
50	2	504	0	572	6	0
51	3	302	0	340	4	0
52	4	480	0	478	20	0
53	X	233	0	118	0	0
54	Z	1645	0	842	12	0
55	V	1579	0	820	20	0
56	A	83	0	0	0	0
56	M	1	0	0	0	0
56	V	1	0	0	0	0
56	X	1	0	0	0	0
56	Z	4	0	0	0	0
56	a	292	0	0	0	0
56	b	6	0	0	0	0
56	d	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	p	1	0	0	0	0
56	z	1	0	0	0	0
57	3	1	0	0	0	0
57	4	1	0	0	0	0
All	All	141982	0	95158	1922	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1922 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:G:H1	1:A:426:U:H3	1.11	0.99
41:t:47:LYS:HD2	41:t:48:PRO:HD2	1.47	0.96
25:d:5:VAL:H	25:d:32:ASN:HD21	1.14	0.94
1:A:409:U:H3	1:A:433:G:H1	1.10	0.93
28:g:104:ASN:ND2	28:g:114:ASP:OD1	2.03	0.92

There are no symmetry-related clashes.

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	
2	B	222/241 (92%)	203 (91%)	19 (9%)	0	100	100
3	C	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
4	D	203/206 (98%)	186 (92%)	17 (8%)	0	100	100
5	E	154/167 (92%)	146 (95%)	8 (5%)	0	100	100
6	F	101/135 (75%)	96 (95%)	5 (5%)	0	100	100
7	G	151/179 (84%)	139 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
9	I	125/130 (96%)	117 (94%)	8 (6%)	0	100	100
10	J	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	12	13
11	K	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
12	L	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
13	M	113/118 (96%)	102 (90%)	9 (8%)	2 (2%)	6	5
14	N	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
17	Q	77/84 (92%)	69 (90%)	8 (10%)	0	100	100
18	R	64/75 (85%)	58 (91%)	6 (9%)	0	100	100
19	S	82/92 (89%)	76 (93%)	6 (7%)	0	100	100
20	T	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
21	U	68/71 (96%)	68 (100%)	0	0	100	100
24	c	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
25	d	206/209 (99%)	198 (96%)	8 (4%)	0	100	100
26	e	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
27	f	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
28	g	174/177 (98%)	153 (88%)	21 (12%)	0	100	100
29	h	39/149 (26%)	32 (82%)	7 (18%)	0	100	100
30	i	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
31	j	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
32	k	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
33	l	132/136 (97%)	123 (93%)	9 (7%)	0	100	100
34	m	116/127 (91%)	108 (93%)	8 (7%)	0	100	100
35	n	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
36	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
37	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
38	q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
39	r	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
40	s	91/100 (91%)	80 (88%)	11 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	t	100/104 (96%)	89 (89%)	11 (11%)	0	100	100
42	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
43	v	82/85 (96%)	78 (95%)	4 (5%)	0	100	100
44	w	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
45	x	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	y	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	z	54/57 (95%)	54 (100%)	0	0	100	100
48	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	7	6
51	3	36/38 (95%)	36 (100%)	0	0	100	100
52	4	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
All	All	5487/5913 (93%)	5161 (94%)	322 (6%)	4 (0%)	49	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	57	VAL
13	M	105	ASN
13	M	106	ALA
50	2	32	ILE

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	
2	B	186/199 (94%)	184 (99%)	2 (1%)	65	75
3	C	170/190 (90%)	167 (98%)	3 (2%)	51	64
4	D	172/173 (99%)	167 (97%)	5 (3%)	37	49
5	E	119/126 (94%)	117 (98%)	2 (2%)	53	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	90/116 (78%)	88 (98%)	2 (2%)	45	59
7	G	126/147 (86%)	124 (98%)	2 (2%)	55	68
8	H	104/105 (99%)	103 (99%)	1 (1%)	68	77
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	85 (99%)	1 (1%)	63	74
11	K	89/98 (91%)	87 (98%)	2 (2%)	45	59
12	L	102/103 (99%)	100 (98%)	2 (2%)	48	62
13	M	93/96 (97%)	90 (97%)	3 (3%)	34	46
14	N	83/84 (99%)	82 (99%)	1 (1%)	63	74
15	O	76/77 (99%)	75 (99%)	1 (1%)	61	72
16	P	65/65 (100%)	65 (100%)	0	100	100
17	Q	73/78 (94%)	71 (97%)	2 (3%)	39	52
18	R	57/65 (88%)	57 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	61 (94%)	4 (6%)	16	22
21	U	60/61 (98%)	60 (100%)	0	100	100
24	c	216/218 (99%)	215 (100%)	1 (0%)	81	87
25	d	163/163 (100%)	163 (100%)	0	100	100
26	e	165/165 (100%)	163 (99%)	2 (1%)	63	74
27	f	148/150 (99%)	147 (99%)	1 (1%)	76	83
28	g	137/138 (99%)	132 (96%)	5 (4%)	31	42
29	h	32/114 (28%)	32 (100%)	0	100	100
30	i	116/116 (100%)	114 (98%)	2 (2%)	53	66
31	j	104/104 (100%)	101 (97%)	3 (3%)	37	49
32	k	103/103 (100%)	102 (99%)	1 (1%)	68	77
33	l	107/107 (100%)	106 (99%)	1 (1%)	70	80
34	m	98/103 (95%)	98 (100%)	0	100	100
35	n	86/87 (99%)	85 (99%)	1 (1%)	63	74
36	o	99/100 (99%)	99 (100%)	0	100	100
37	p	89/90 (99%)	86 (97%)	3 (3%)	32	45
38	q	84/84 (100%)	81 (96%)	3 (4%)	31	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	r	93/93 (100%)	92 (99%)	1 (1%)	65	75
40	s	80/84 (95%)	79 (99%)	1 (1%)	61	72
41	t	83/85 (98%)	83 (100%)	0	100	100
42	u	78/78 (100%)	77 (99%)	1 (1%)	61	72
43	v	62/63 (98%)	62 (100%)	0	100	100
44	w	67/68 (98%)	67 (100%)	0	100	100
45	x	54/55 (98%)	52 (96%)	2 (4%)	30	41
46	y	48/49 (98%)	48 (100%)	0	100	100
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	44 (96%)	2 (4%)	26	36
49	1	38/38 (100%)	37 (97%)	1 (3%)	40	53
50	2	51/52 (98%)	51 (100%)	0	100	100
51	3	34/34 (100%)	34 (100%)	0	100	100
52	4	55/62 (89%)	55 (100%)	0	100	100
All	All	4576/4825 (95%)	4512 (99%)	64 (1%)	57	70

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	s	31	VAL
45	x	39	GLN
13	M	105	ASN
13	M	16	VAL
45	x	56	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
28	g	104	ASN
37	p	81	ASN
28	g	128	GLN
34	m	107	ASN
45	x	36	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1542 (97%)	262 (17%)	7 (0%)
22	a	2757/2904 (94%)	361 (13%)	0
23	b	118/120 (98%)	19 (16%)	0
53	X	10/35 (28%)	0	0
54	Z	76/77 (98%)	13 (17%)	1 (1%)
55	V	70/76 (92%)	12 (17%)	2 (2%)
All	All	4539/4754 (95%)	667 (14%)	10 (0%)

5 of 667 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	7	A
1	A	9	G

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	Z	67	C
55	V	10	2MG
55	V	48	5MC
1	A	723	U
1	A	1026	G

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

58 non-standard protein/DNA/RNA residues are modelled in this entry.

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
55	2MG	V	10	55	23,26,27	2.69	7 (30%)	33,38,41	2.25	10 (30%)
55	2MG	V	6	55	23,26,27	2.67	7 (30%)	33,38,41	2.09	8 (24%)
1	2MG	A	1516	1	23,26,27	2.50	7 (30%)	33,38,41	2.21	13 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	OMG	a	2251	22,54	23,26,27	2.52	8 (34%)	32,38,41	1.91	8 (25%)
1	5MC	A	967	1	19,22,23	3.86	9 (47%)	26,32,35	1.02	2 (7%)
1	PSU	A	516	1,56	18,21,22	1.08	2 (11%)	21,30,33	1.88	5 (23%)
22	PSU	a	2457	22	18,21,22	1.21	1 (5%)	21,30,33	2.08	4 (19%)
55	PSU	V	39	55	18,21,22	1.03	1 (5%)	21,30,33	1.88	4 (19%)
55	2MU	V	54	55	20,23,24	1.42	5 (25%)	27,33,36	2.00	7 (25%)
55	H2U	V	47	55	18,21,22	1.07	2 (11%)	19,30,33	1.19	2 (10%)
22	G7M	a	2069	22	23,26,27	2.64	7 (30%)	34,39,42	1.80	10 (29%)
22	PSU	a	955	22	18,21,22	1.19	1 (5%)	21,30,33	2.01	5 (23%)
22	1MG	a	745	22	23,26,27	2.67	8 (34%)	33,39,42	1.68	8 (24%)
22	PSU	a	2580	22	18,21,22	1.31	3 (16%)	21,30,33	2.18	6 (28%)
1	G7M	A	527	1	23,26,27	2.73	8 (34%)	34,39,42	1.76	9 (26%)
1	4OC	A	1402	1,56	20,23,24	2.78	8 (40%)	25,32,35	1.08	2 (8%)
54	OMC	Z	33	54	19,22,23	2.68	7 (36%)	25,31,34	0.74	0
55	70U	V	34	55,53	22,26,27	1.17	1 (4%)	27,37,40	0.85	1 (3%)
22	PSU	a	746	22,56	18,21,22	1.28	3 (16%)	21,30,33	2.18	5 (23%)
33	4D4	l	81	33	9,11,12	1.53	1 (11%)	7,13,15	2.22	4 (57%)
33	MS6	l	82	33	5,7,8	1.10	1 (20%)	2,7,9	1.33	0
55	G7M	V	46	55	23,26,27	2.81	8 (34%)	34,39,42	1.77	10 (29%)
55	5MC	V	49	55	19,22,23	3.86	9 (47%)	26,32,35	1.13	3 (11%)
22	2MG	a	2445	22	23,26,27	2.47	6 (26%)	33,38,41	2.17	10 (30%)
54	H2U	Z	21	54	18,21,22	1.00	2 (11%)	19,30,33	0.98	1 (5%)
22	2MG	a	1835	22	23,26,27	2.44	7 (30%)	33,38,41	2.35	10 (30%)
22	2MA	a	2503	22,56	22,25,26	3.71	10 (45%)	32,37,40	3.05	10 (31%)
55	5MC	V	48	55	19,22,23	3.79	9 (47%)	26,32,35	1.10	2 (7%)
22	H2U	a	2449	22	18,21,22	1.49	2 (11%)	19,30,33	0.79	0
22	OMC	a	2498	22,56	19,22,23	2.59	7 (36%)	25,31,34	1.02	1 (4%)
11	IAS	K	119	11	6,7,8	1.01	0	3,8,10	1.31	1 (33%)
55	PSU	V	27	55	18,21,22	0.97	1 (5%)	21,30,33	1.76	4 (19%)
1	MA6	A	1518	1	23,26,27	1.59	5 (21%)	33,38,41	2.32	12 (36%)
22	6MZ	a	2030	22	22,25,26	2.65	6 (27%)	29,36,39	2.41	11 (37%)
1	MA6	A	1519	1	23,26,27	1.64	5 (21%)	33,38,41	2.33	12 (36%)
1	2MG	A	1207	1	23,26,27	2.57	7 (30%)	33,38,41	2.16	8 (24%)
22	PSU	a	2604	22	18,21,22	1.15	1 (5%)	21,30,33	2.20	5 (23%)
54	5MU	Z	55	54	19,22,23	4.58	6 (31%)	27,32,35	3.75	9 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	5MU	a	1939	22	19,22,23	4.51	7 (36%)	27,32,35	3.78	10 (37%)
22	3TD	a	1915	22	19,22,23	4.05	8 (42%)	23,32,35	1.89	2 (8%)
55	PSU	V	55	55	18,21,22	1.03	2 (11%)	21,30,33	2.09	5 (23%)
54	4SU	Z	8	54	18,21,22	4.19	8 (44%)	25,30,33	2.46	5 (20%)
54	PSU	Z	56	54	18,21,22	1.11	1 (5%)	21,30,33	1.82	3 (14%)
22	OMU	a	2552	22	19,22,23	2.61	6 (31%)	25,31,34	2.17	5 (20%)
1	2MG	A	966	1	23,26,27	2.54	6 (26%)	33,38,41	2.42	10 (30%)
1	5MC	A	1407	1	19,22,23	3.42	8 (42%)	26,32,35	1.10	3 (11%)
12	D2T	L	89	12	8,9,10	2.32	2 (25%)	6,11,13	1.18	1 (16%)
25	MEQ	d	150	25	8,9,10	1.41	2 (25%)	5,10,12	1.20	1 (20%)
22	5MU	a	747	22	19,22,23	4.60	7 (36%)	27,32,35	3.69	10 (37%)
22	6MZ	a	1618	22	22,25,26	2.60	6 (27%)	29,36,39	2.32	10 (34%)
22	PSU	a	2504	22	18,21,22	1.05	1 (5%)	21,30,33	1.82	3 (14%)
1	UR3	A	1498	1	19,22,23	2.74	6 (31%)	26,32,35	1.67	4 (15%)
55	1MA	V	58	55	21,25,26	0.56	0	30,37,40	0.74	1 (3%)
55	12A	V	37	55,56	33,36,37	0.87	0	46,52,55	1.36	7 (15%)
22	PSU	a	1917	22	18,21,22	1.15	2 (11%)	21,30,33	2.04	5 (23%)
22	PSU	a	2605	22	18,21,22	1.18	1 (5%)	21,30,33	2.14	4 (19%)
22	5MC	a	1962	22	19,22,23	3.60	8 (42%)	26,32,35	1.23	3 (11%)
22	PSU	a	1911	22	18,21,22	0.99	2 (11%)	21,30,33	1.97	3 (14%)

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
55	2MG	V	10	55	-	0/9/27/28	0/3/3/3
55	2MG	V	6	55	-	1/9/27/28	0/3/3/3
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
22	OMG	a	2251	22,54	-	1/9/27/28	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1,56	-	0/7/25/26	0/2/2/2
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
55	PSU	V	39	55	-	0/7/25/26	0/2/2/2
55	2MU	V	54	55	-	0/9/27/28	0/2/2/2
55	H2U	V	47	55	-	6/7/38/39	0/2/2/2
22	G7M	a	2069	22	-	1/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
1	4OC	A	1402	1,56	-	0/9/29/30	0/2/2/2
54	OMC	Z	33	54	-	1/9/27/28	0/2/2/2
55	70U	V	34	55,53	-	1/13/31/32	0/2/2/2
22	PSU	a	746	22,56	-	2/7/25/26	0/2/2/2
33	4D4	l	81	33	-	1/11/12/14	-
33	MS6	l	82	33	-	1/4/6/8	-
55	G7M	V	46	55	-	1/7/25/26	0/3/3/3
55	5MC	V	49	55	-	2/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	0/9/27/28	0/3/3/3
54	H2U	Z	21	54	-	2/7/38/39	0/2/2/2
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
22	2MA	a	2503	22,56	-	2/7/25/26	0/3/3/3
55	5MC	V	48	55	-	2/7/25/26	0/2/2/2
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2
22	OMC	a	2498	22,56	-	0/9/27/28	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
55	PSU	V	27	55	-	2/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
22	6MZ	a	2030	22	-	2/9/27/28	0/3/3/3
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
54	5MU	Z	55	54	-	0/7/25/26	0/2/2/2
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	3TD	a	1915	22	-	0/7/25/26	0/2/2/2
55	PSU	V	55	55	-	0/7/25/26	0/2/2/2
54	4SU	Z	8	54	-	0/7/25/26	0/2/2/2
54	PSU	Z	56	54	-	0/7/25/26	0/2/2/2
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
1	2MG	A	966	1	-	2/9/27/28	0/3/3/3
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
12	D2T	L	89	12	-	1/7/12/14	-
25	MEQ	d	150	25	-	1/8/9/11	-
22	5MU	a	747	22	-	1/7/25/26	0/2/2/2
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
22	PSU	a	2504	22	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
55	1MA	V	58	55	-	2/7/25/26	0/3/3/3
55	12A	V	37	55,56	-	4/25/43/44	0/3/3/3
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2

The worst 5 of 271 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	12.56	1.49	1.35
22	a	2503	2MA	C4-N3	11.02	1.48	1.34
54	Z	55	5MU	C6-N1	10.45	1.55	1.38
54	Z	55	5MU	C2-N1	10.25	1.54	1.38
22	a	747	5MU	C6-N1	10.22	1.55	1.38

The worst 5 of 317 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	Z	55	5MU	C5-C4-N3	12.46	126.16	115.32
22	a	1939	5MU	C5-C4-N3	12.33	126.04	115.32
22	a	747	5MU	C5-C4-N3	11.50	125.32	115.32
54	Z	55	5MU	C5-C6-N1	-9.99	112.46	123.31
22	a	1939	5MU	C5-C6-N1	-9.99	112.47	123.31

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	Z	21	H2U	O4'-C1'-N1-C2
54	Z	21	H2U	O4'-C1'-N1-C6
22	a	2251	OMG	C1'-C2'-O2'-CM2
55	V	47	H2U	O4'-C1'-N1-C6
55	V	47	H2U	C2'-C1'-N1-C2

There are no ring outliers.

14 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	V	10	2MG	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1516	2MG	1	0
1	A	967	5MC	1	0
54	Z	33	OMC	1	0
54	Z	21	H2U	1	0
22	a	2503	2MA	1	0
22	a	2498	OMC	1	0
11	K	119	IAS	1	0
22	a	2030	6MZ	2	0
1	A	1519	MA6	1	0
1	A	1207	2MG	1	0
22	a	1939	5MU	1	0
55	V	58	1MA	1	0
55	V	37	12A	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 393 ligands modelled in this entry, 393 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

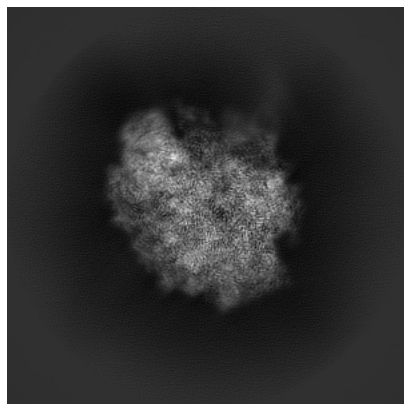
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61706. These allow visual inspection of the internal detail of the map and identification of artifacts.

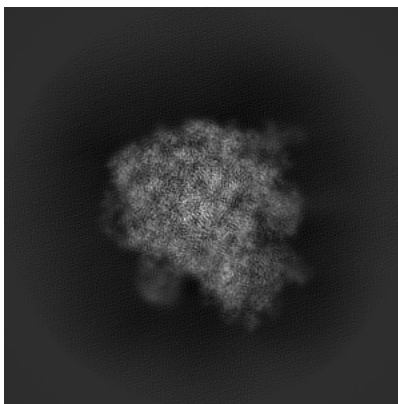
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

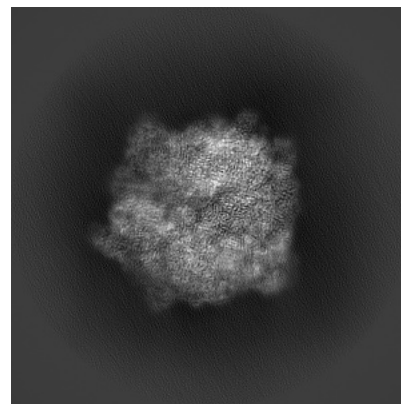
6.1.1 Primary map



X

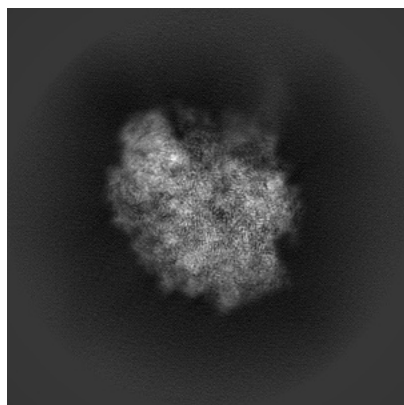


Y

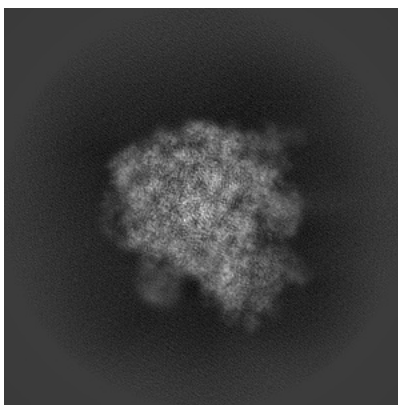


Z

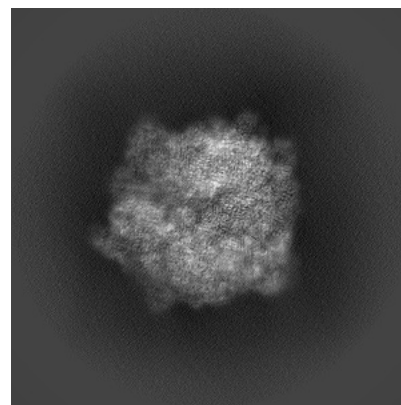
6.1.2 Raw map



X



Y

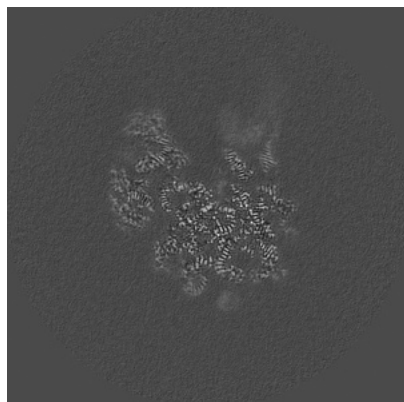


Z

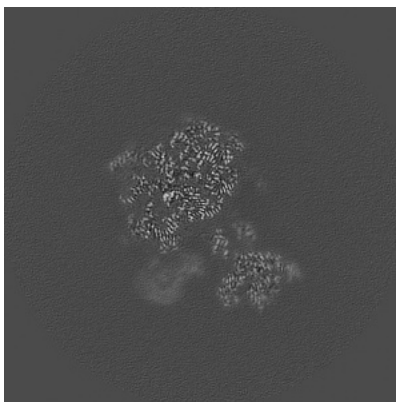
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

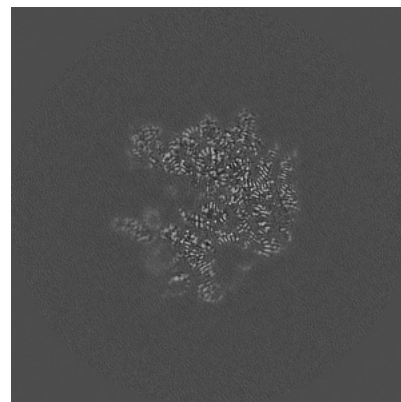
6.2.1 Primary map



X Index: 265

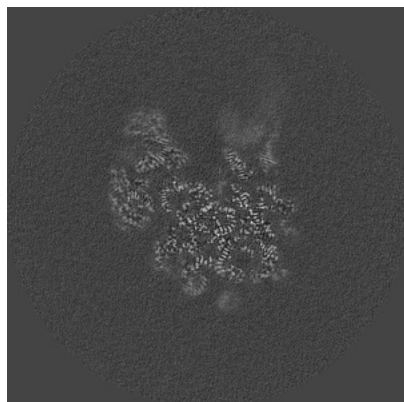


Y Index: 265

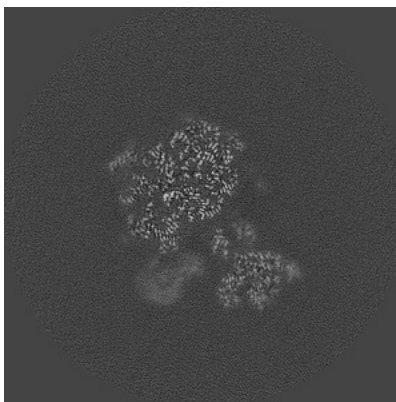


Z Index: 265

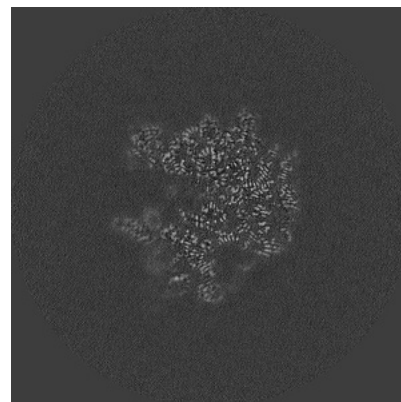
6.2.2 Raw map



X Index: 265



Y Index: 265

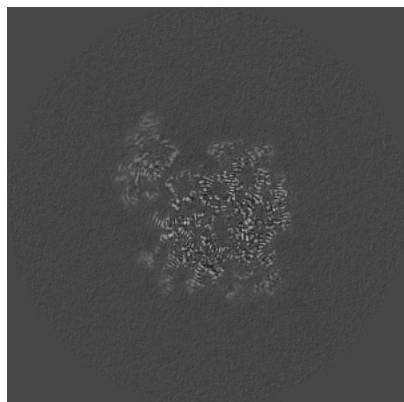


Z Index: 265

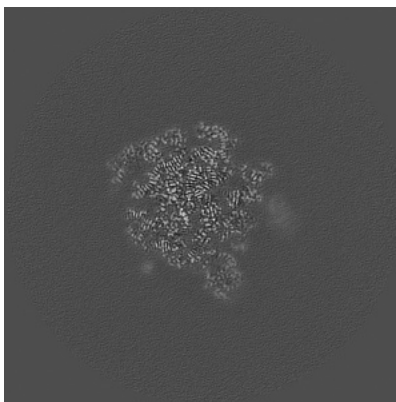
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

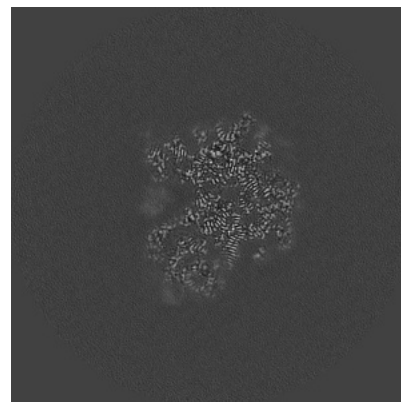
6.3.1 Primary map



X Index: 294

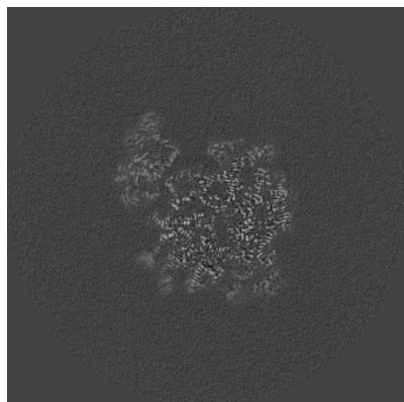


Y Index: 318

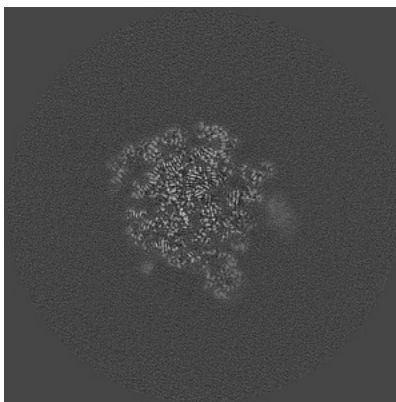


Z Index: 244

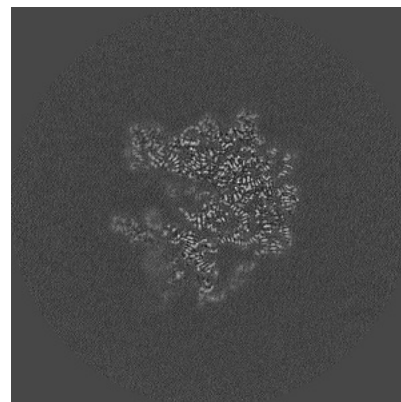
6.3.2 Raw map



X Index: 294



Y Index: 318

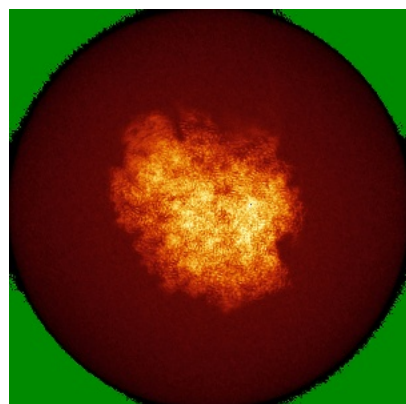


Z Index: 268

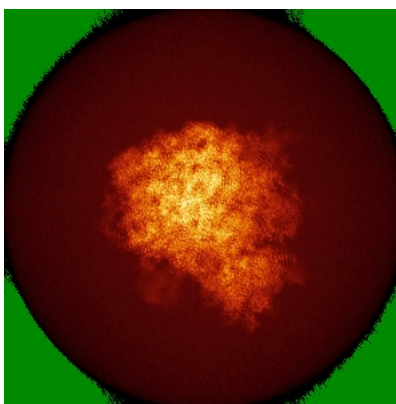
The images above show the largest variance slices of the map in three orthogonal directions.

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

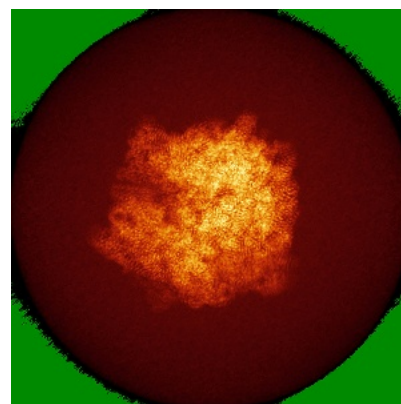
6.4.1 Primary map



X

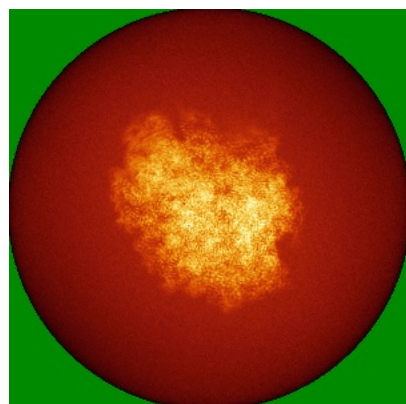


Y

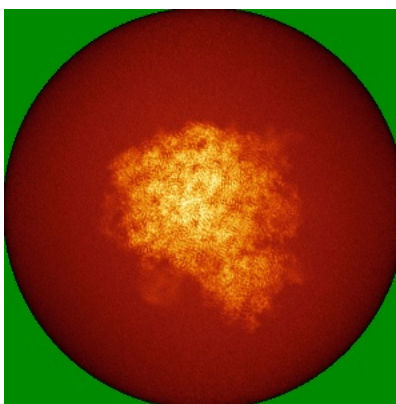


Z

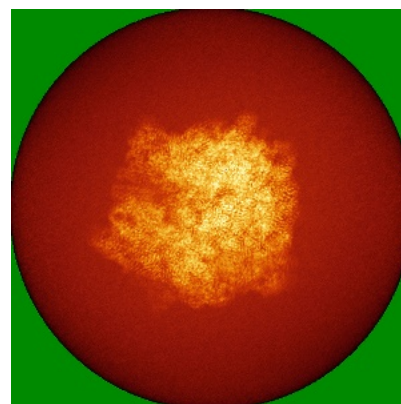
6.4.2 Raw map



X



Y

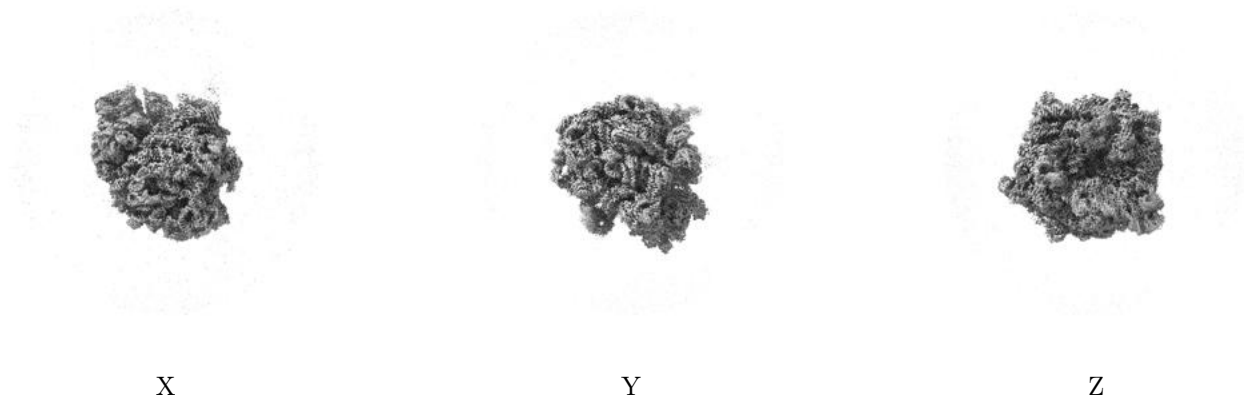


Z

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

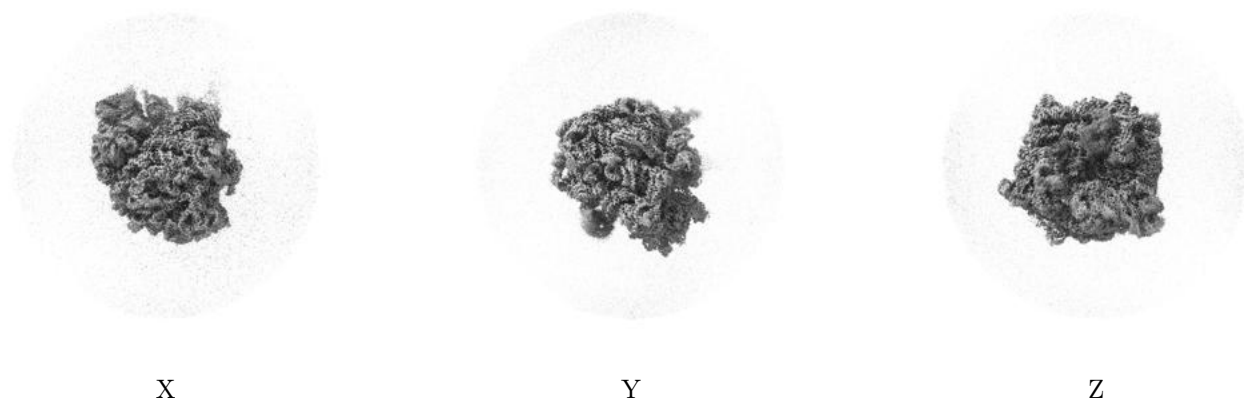
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0107. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

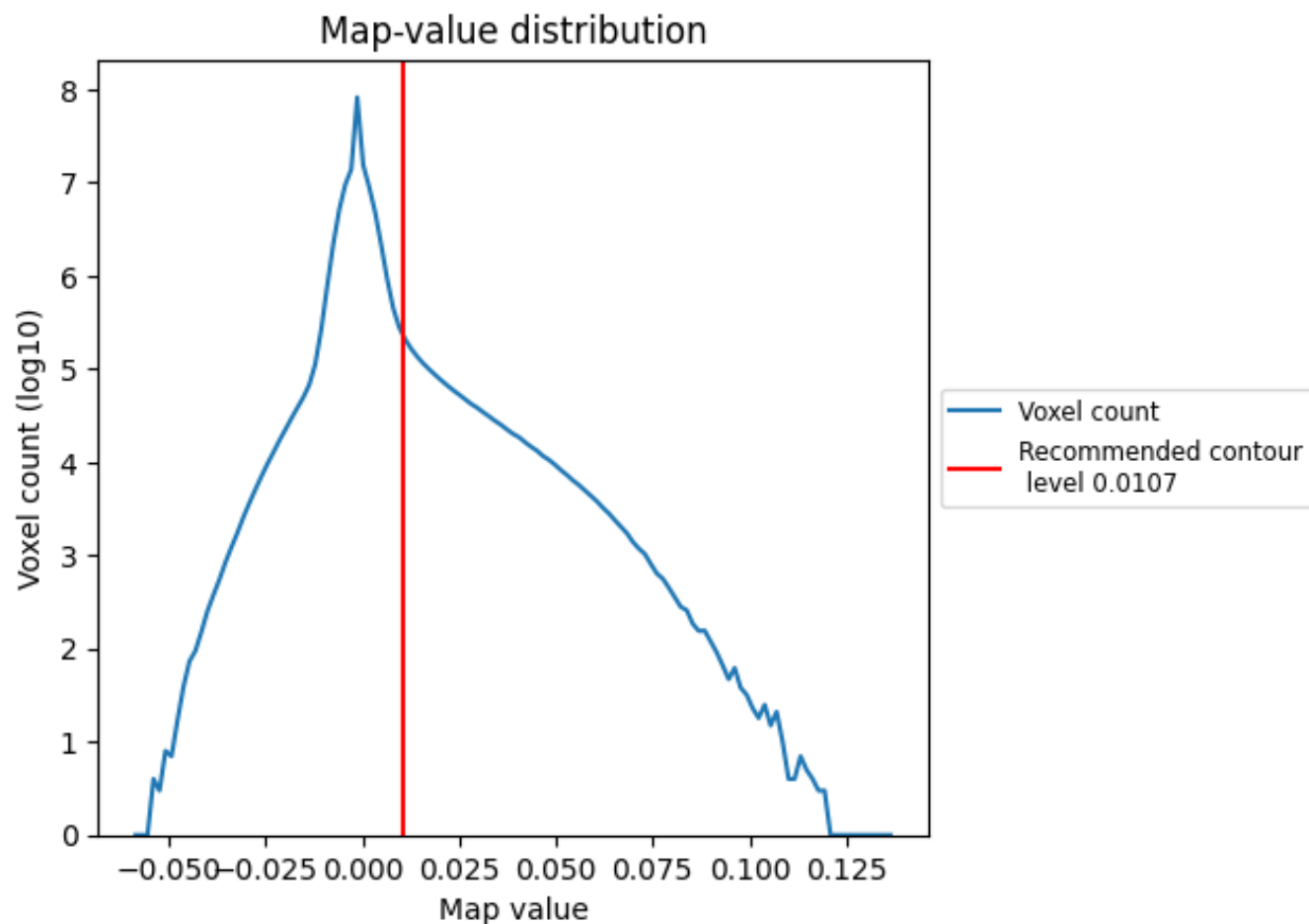
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

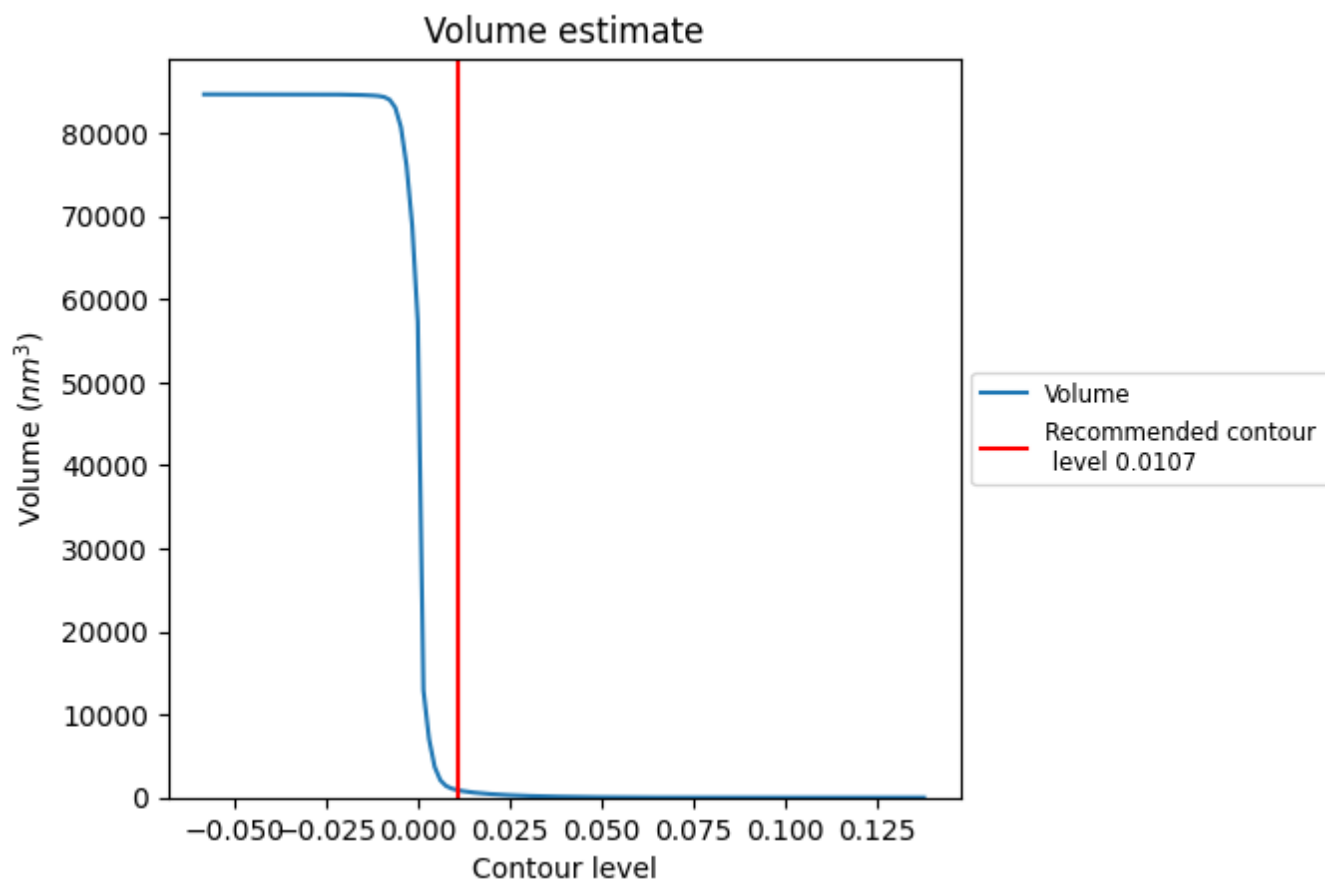
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

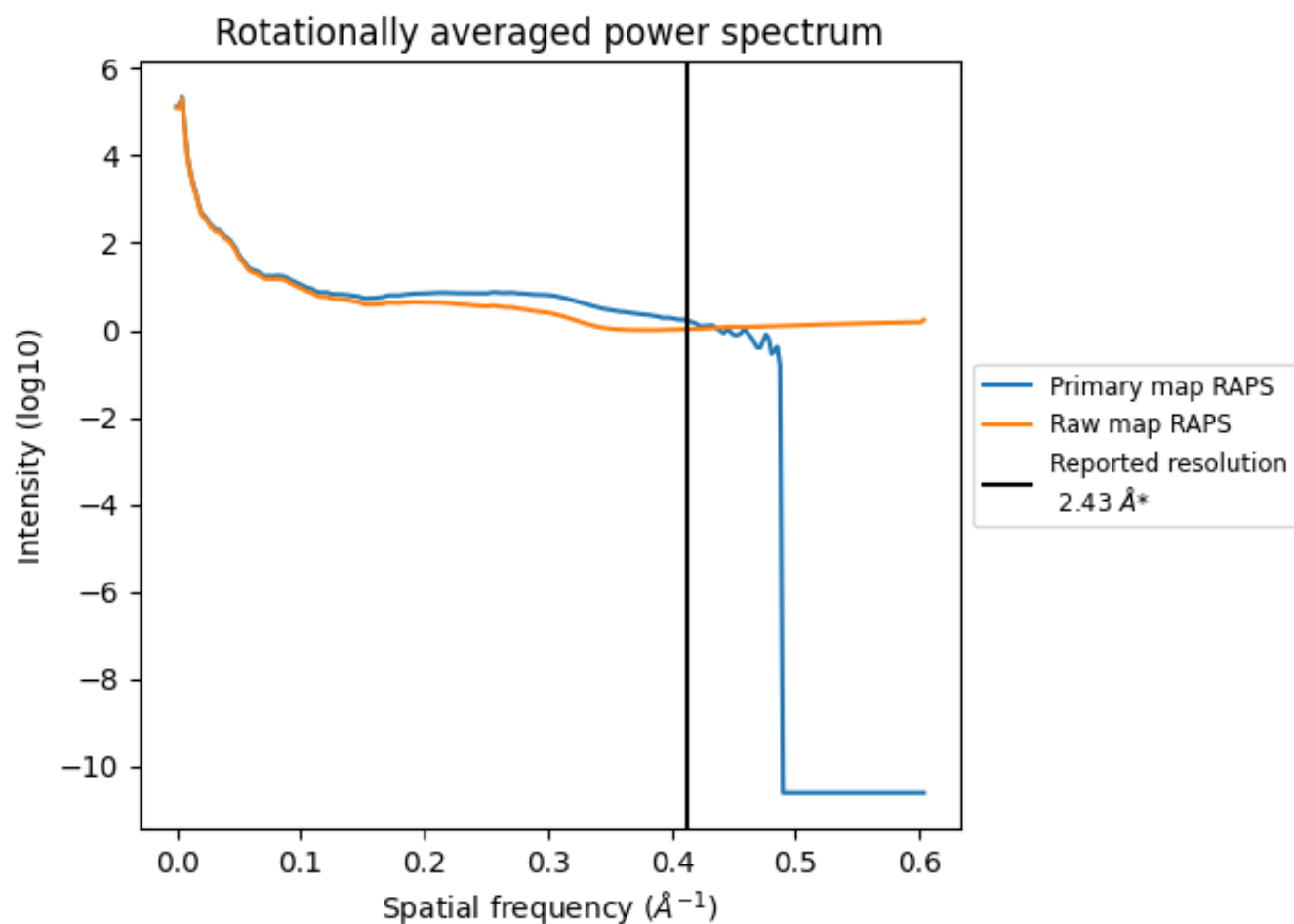
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 896 nm^3 ; this corresponds to an approximate mass of 809 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 ⓘ

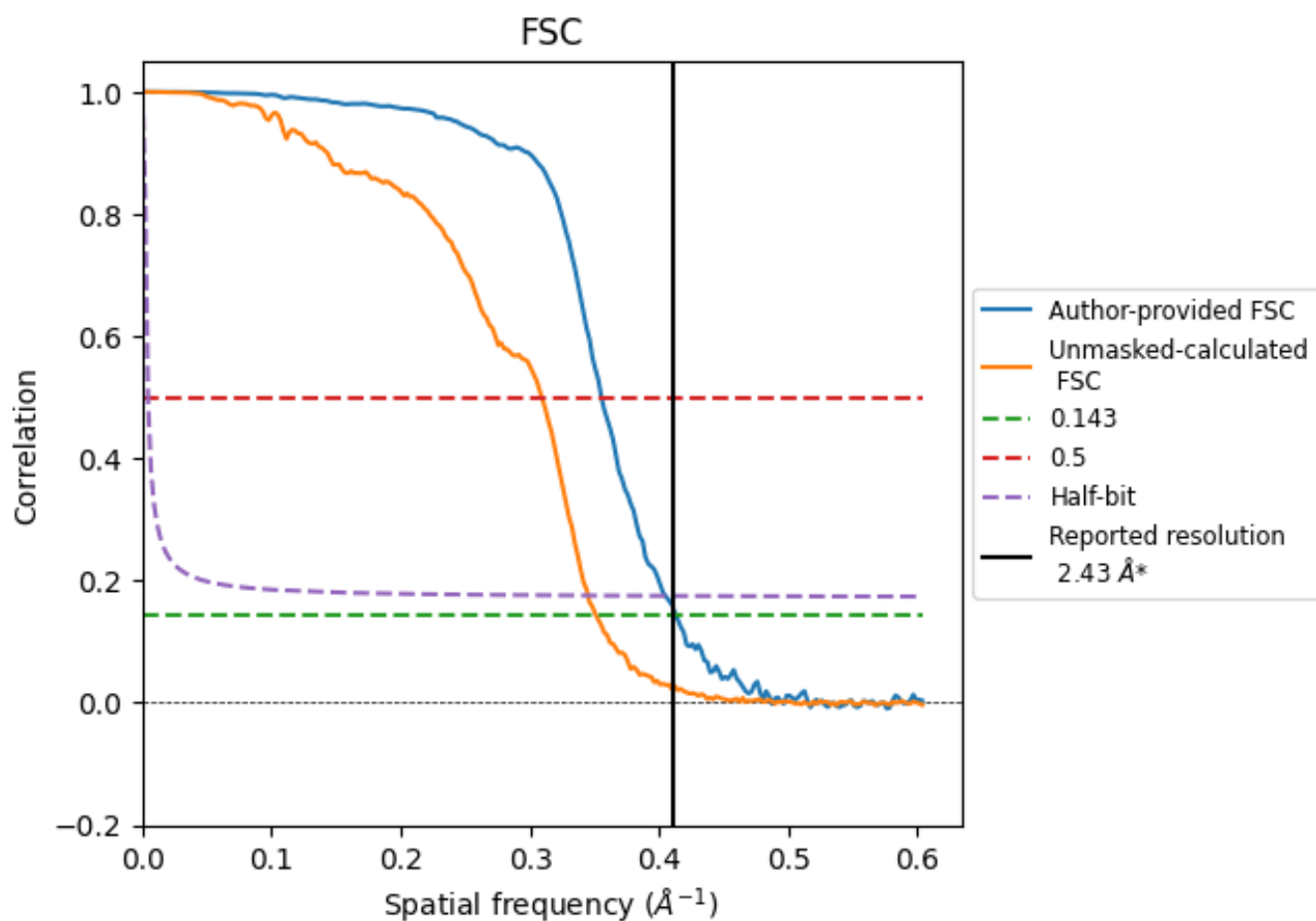


*Reported resolution corresponds to spatial frequency of 0.412 Å⁻¹

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 0.412 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.43	-	-
Author-provided FSC curve	2.42	2.81	2.47
Unmasked-calculated*	2.85	3.23	2.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.85 differs from the reported value 2.43 by more than 10 %

9 Map-model fit [i](#)

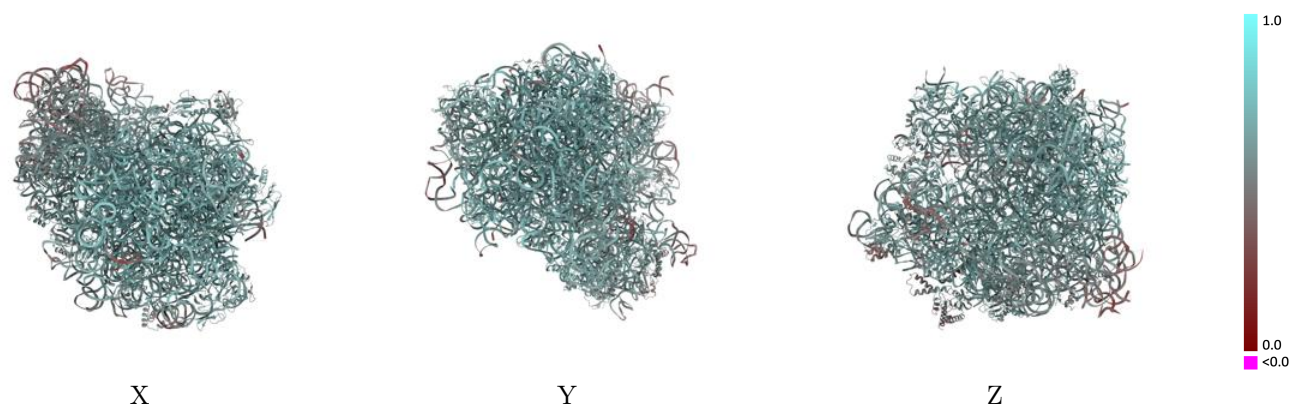
This section contains information regarding the fit between EMDB map EMD-61706 and PDB model 9JPM. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



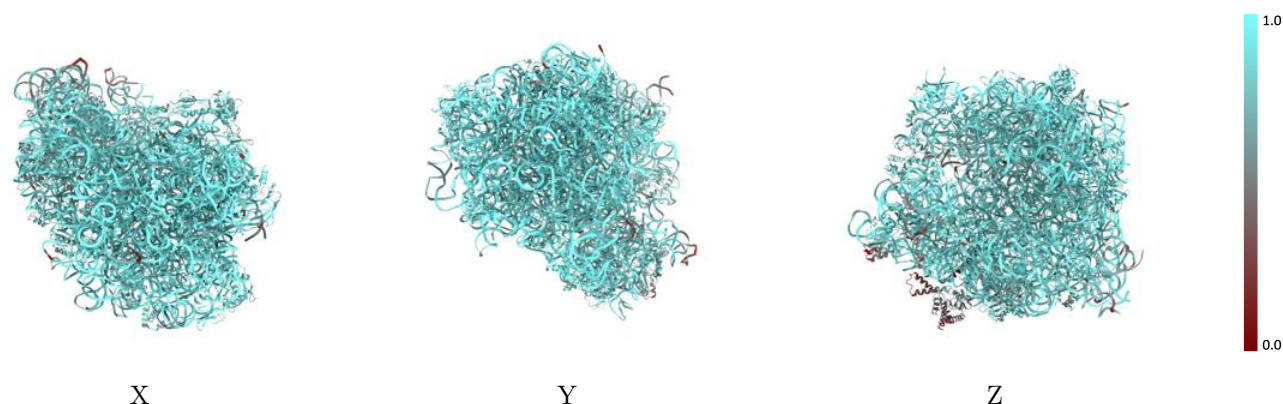
The images above show the 3D surface view of the map at the recommended contour level 0.0107 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



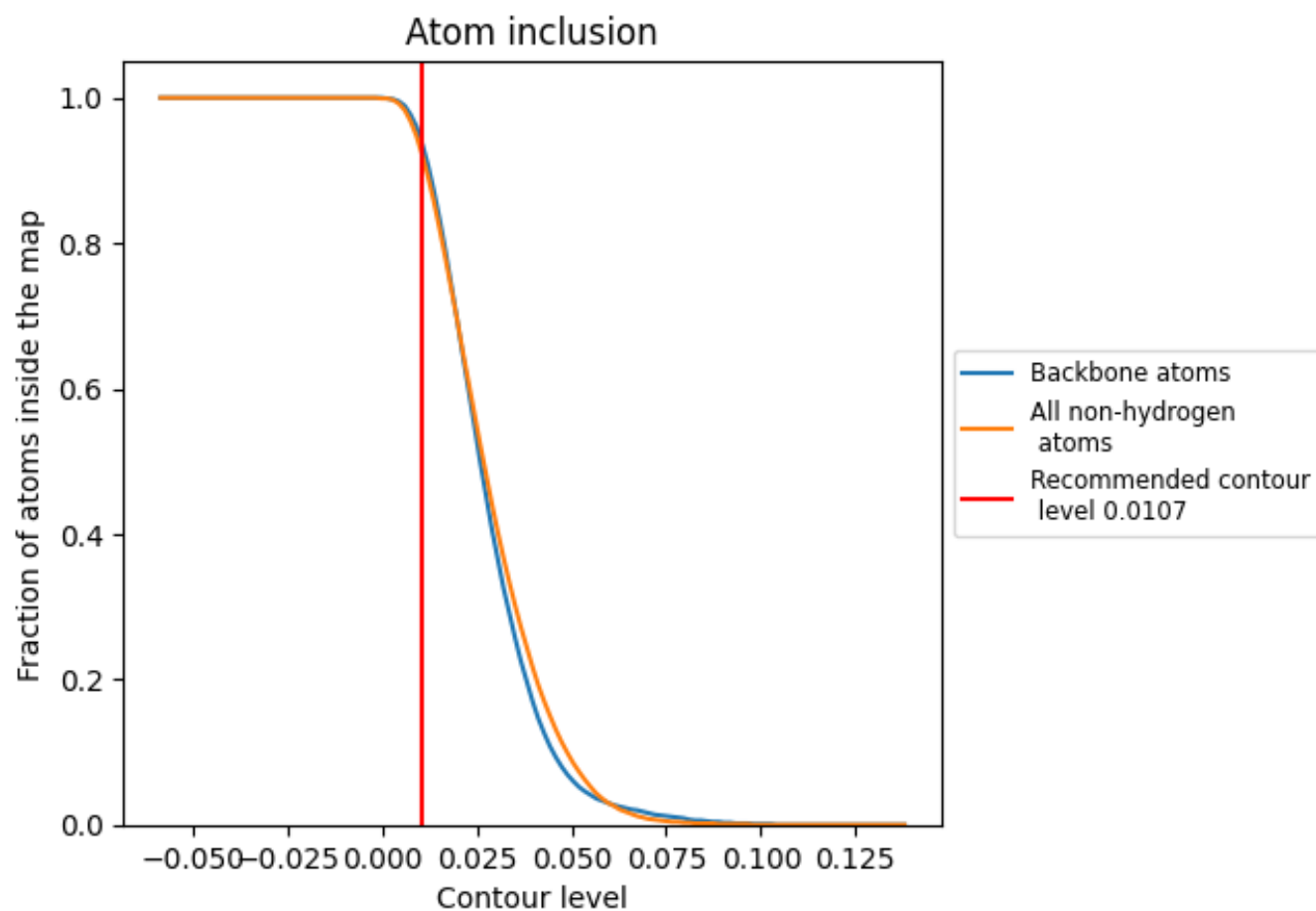
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0107).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% 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 (0.0107) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.6260
0	 0.9270	 0.6660
1	 0.9750	 0.6960
2	 0.9800	 0.7020
3	 0.9390	 0.6460
4	 0.7160	 0.5280
A	 0.9260	 0.5990
B	 0.4300	 0.5060
C	 0.8330	 0.5890
D	 0.6670	 0.5190
E	 0.8790	 0.6190
F	 0.8020	 0.5550
G	 0.8080	 0.5970
H	 0.8880	 0.6110
I	 0.8520	 0.5980
J	 0.6570	 0.5320
K	 0.8750	 0.6180
L	 0.8940	 0.6380
M	 0.8620	 0.5980
N	 0.8510	 0.5910
O	 0.8750	 0.6050
P	 0.7330	 0.5140
Q	 0.8100	 0.5980
R	 0.8260	 0.5880
S	 0.8620	 0.5890
T	 0.7590	 0.5410
U	 0.5080	 0.5250
V	 0.8770	 0.5850
X	 0.9190	 0.6290
Z	 0.8730	 0.5970
a	 0.9680	 0.6520
b	 0.9600	 0.6210
c	 0.9660	 0.6790
d	 0.9360	 0.6770
e	 0.8750	 0.6240



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Chain	Atom inclusion	Q-score
f	 0.8180	 0.5910
g	 0.7810	 0.5690
h	 0.7800	 0.5690
i	 0.9410	 0.6660
j	 0.9450	 0.6810
k	 0.9310	 0.6600
l	 0.9340	 0.6610
m	 0.9810	 0.6920
n	 0.9110	 0.6250
o	 0.9090	 0.6670
p	 0.9680	 0.6740
q	 0.9070	 0.6310
r	 0.9320	 0.6670
s	 0.8520	 0.5920
t	 0.8540	 0.5710
u	 0.8560	 0.6080
v	 0.9320	 0.6830
w	 0.9320	 0.6430
x	 0.7610	 0.5350
y	 0.9290	 0.6460
z	 0.9320	 0.6680