



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2025 – 11:17 AM EDT

PDB ID : 8VWQ / pdb_00008vwq
EMDB ID : EMD-43594
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) in the P/P conformation on a slippery CCC-C codon and Elongation Factor P bound (uL1 in the closed conformation)
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2024-02-02
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev126
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.45.1

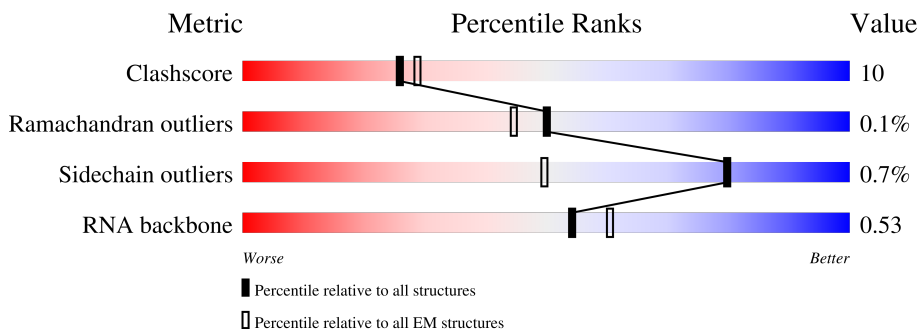
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Clashscore	210492	15764
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	1	2903	
2	2	1540	
3	3	120	
4	4	18	
5	5	77	
6	6	188	
7	A	224	



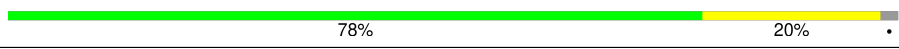




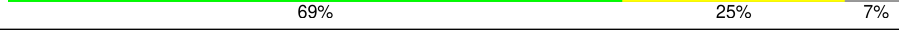
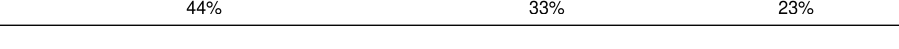
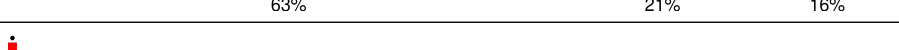

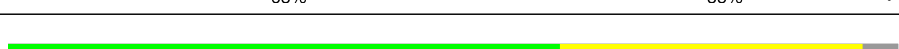


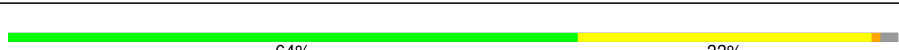




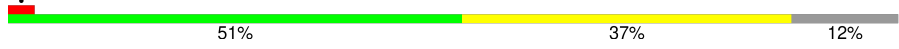
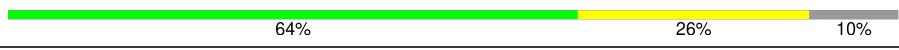



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Mol	Chain	Length	Quality of chain
8	B	273	
9	C	209	
10	D	201	
11	E	179	
12	F	177	
13	G	149	
14	J	142	
15	K	123	
16	L	144	
17	M	136	
18	N	127	
19	O	117	
20	P	115	
21	Q	118	
22	R	103	
23	S	110	
24	T	100	
25	U	104	
26	V	94	
27	W	84	
28	X	78	
29	Y	63	
30	Z	59	
31	a	70	
32	b	57	

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Mol	Chain	Length	Quality of chain
33	c	55	
34	d	46	
35	e	65	
36	f	38	
37	g	241	
38	h	233	
39	i	206	
40	j	167	
41	k	135	
42	l	179	
43	m	130	
44	n	130	
45	o	103	
46	p	129	
47	q	124	
48	r	118	
49	s	101	
50	t	89	
51	u	82	
52	v	84	
53	w	75	
54	x	92	
55	y	87	
56	z	71	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 147683 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2869	Total	C	N	O	P	0	0
			61599	27479	11343	19908	2869		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1914786293
1	1847	G	A	conflict	GB 1914786293
1	2069	A	G	conflict	GB 1914786293
1	2104	U	C	conflict	GB 1914786293

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1533	Total	C	N	O	P	0	0
			32907	14683	6036	10655	1533		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	8	Total	C	N	O	P	0	0
			167	75	29	55	8		

- Molecule 5 is a RNA chain called tRNA^{Pro}L (GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Elongation factor P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	188	Total	C	N	O	S	0	0
			1461	928	242	286	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	224	Total	C	N	O	S	0	0
			1663	1039	303	315	6		

- Molecule 8 is a protein called 50S ribosomal protein L2.

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

- Molecule 9 is a protein called 50S ribosomal protein L3.

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

- Molecule 10 is a protein called 50S ribosomal protein L4.

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

- Molecule 11 is a protein called 50S ribosomal protein L5.

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

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 13 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

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

- Molecule 16 is a protein called 50S ribosomal protein L15.

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

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

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

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called Ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 31 is a protein called 50S ribosomal protein L31.

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

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called 30S ribosomal protein S5.

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

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 56 is a protein called 30S ribosomal protein S21.

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

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	1	339	Total	Mg	0
			339	339	
57	2	183	Total	Mg	0
			183	183	
57	3	12	Total	Mg	0
			12	12	
57	B	4	Total	Mg	0
			4	4	
57	C	1	Total	Mg	0
			1	1	
57	D	4	Total	Mg	0
			4	4	
57	E	1	Total	Mg	0
			1	1	
57	J	1	Total	Mg	0
			1	1	
57	K	1	Total	Mg	0
			1	1	
57	L	2	Total	Mg	0
			2	2	
57	M	1	Total	Mg	0
			1	1	
57	P	2	Total	Mg	0
			2	2	

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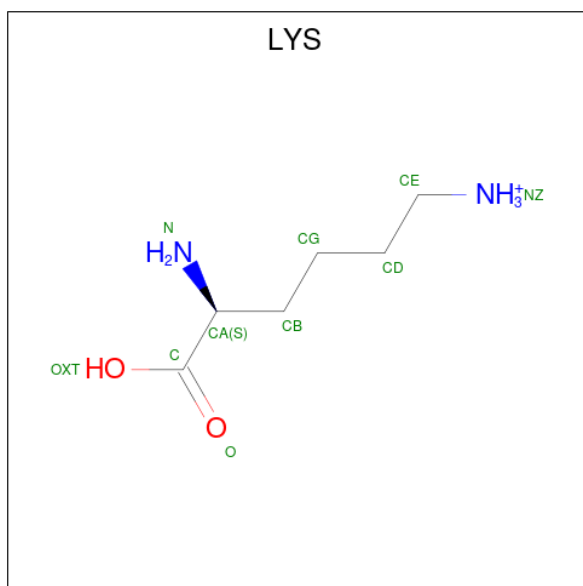
Mol	Chain	Residues	Atoms		AltConf
57	Q	2	Total 2	Mg 2	0
57	R	3	Total 3	Mg 3	0
57	S	1	Total 1	Mg 1	0
57	T	2	Total 2	Mg 2	0
57	V	1	Total 1	Mg 1	0
57	Z	2	Total 2	Mg 2	0
57	b	2	Total 2	Mg 2	0
57	d	1	Total 1	Mg 1	0
57	e	3	Total 3	Mg 3	0
57	f	1	Total 1	Mg 1	0
57	i	3	Total 3	Mg 3	0
57	j	2	Total 2	Mg 2	0
57	k	1	Total 1	Mg 1	0
57	l	2	Total 2	Mg 2	0
57	m	1	Total 1	Mg 1	0
57	o	1	Total 1	Mg 1	0
57	q	1	Total 1	Mg 1	0
57	t	1	Total 1	Mg 1	0
57	u	1	Total 1	Mg 1	0
57	w	1	Total 1	Mg 1	0
57	y	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
57	z	2	Total	Mg	0
			2	2	

- Molecule 58 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
58	5	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		AltConf
59	1	153	Total	O	0
			153	153	
59	2	78	Total	O	0
			78	78	
59	3	7	Total	O	0
			7	7	
59	4	1	Total	O	0
			1	1	
59	5	5	Total	O	0
			5	5	
59	6	5	Total	O	0
			5	5	
59	B	1	Total	O	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
59	C	2	Total 2	O 2	0
59	D	2	Total 2	O 2	0
59	E	9	Total 9	O 9	0
59	F	6	Total 6	O 6	0
59	G	6	Total 6	O 6	0
59	L	2	Total 2	O 2	0
59	M	2	Total 2	O 2	0
59	N	1	Total 1	O 1	0
59	O	3	Total 3	O 3	0
59	P	5	Total 5	O 5	0
59	S	3	Total 3	O 3	0
59	U	3	Total 3	O 3	0
59	V	5	Total 5	O 5	0
59	W	2	Total 2	O 2	0
59	Y	1	Total 1	O 1	0
59	a	15	Total 15	O 15	0
59	c	1	Total 1	O 1	0
59	f	1	Total 1	O 1	0
59	g	24	Total 24	O 24	0
59	h	5	Total 5	O 5	0
59	i	3	Total 3	O 3	0

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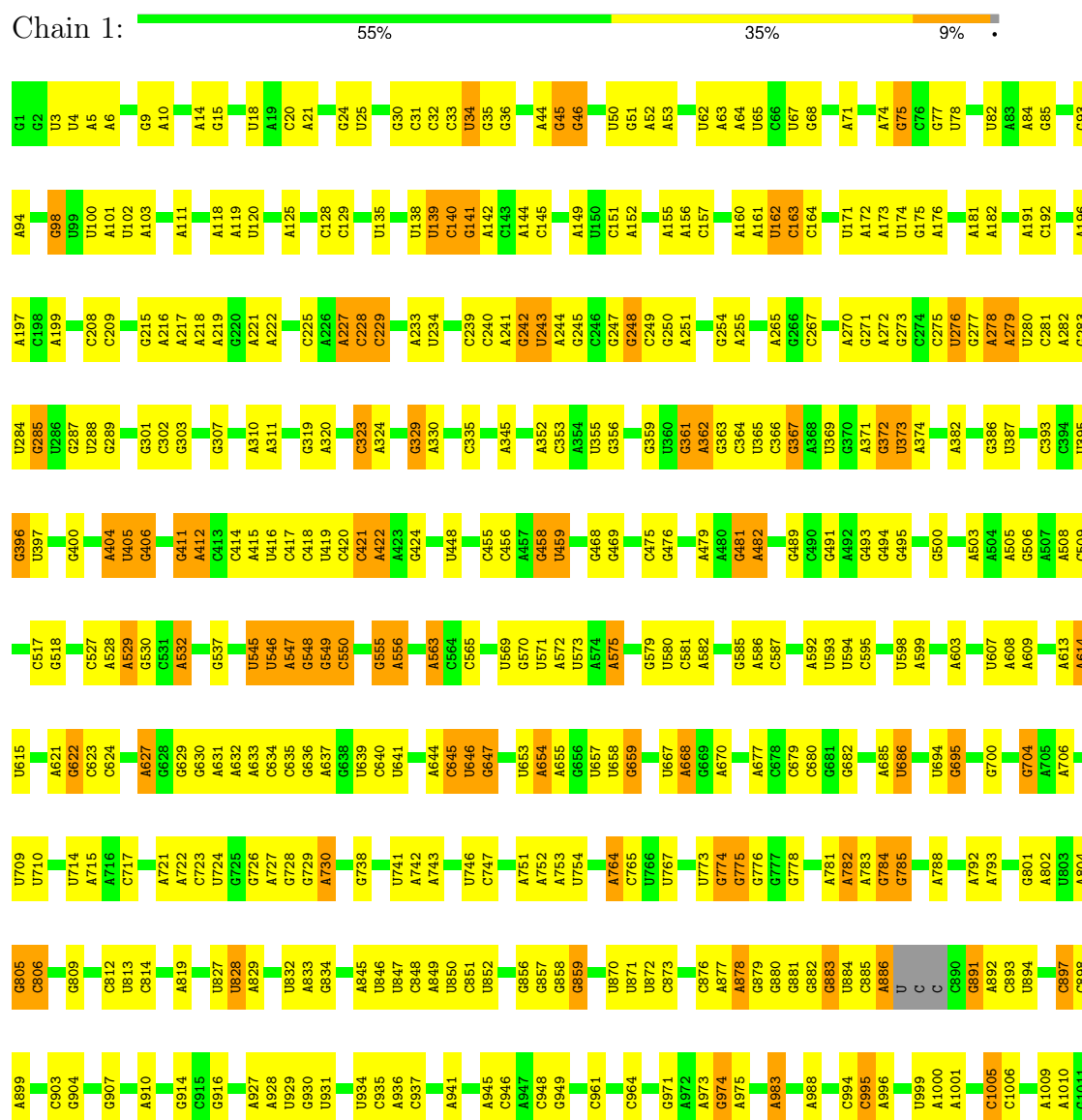
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Mol	Chain	Residues	Atoms		AltConf
59	j	3	Total 3	O 3	0
59	k	4	Total 4	O 4	0
59	l	9	Total 9	O 9	0
59	m	3	Total 3	O 3	0
59	n	6	Total 6	O 6	0
59	o	4	Total 4	O 4	0
59	p	2	Total 2	O 2	0
59	q	6	Total 6	O 6	0
59	r	4	Total 4	O 4	0
59	t	1	Total 1	O 1	0
59	u	2	Total 2	O 2	0
59	v	5	Total 5	O 5	0
59	w	11	Total 11	O 11	0
59	x	1	Total 1	O 1	0
59	z	10	Total 10	O 10	0

3 Residue-property plots

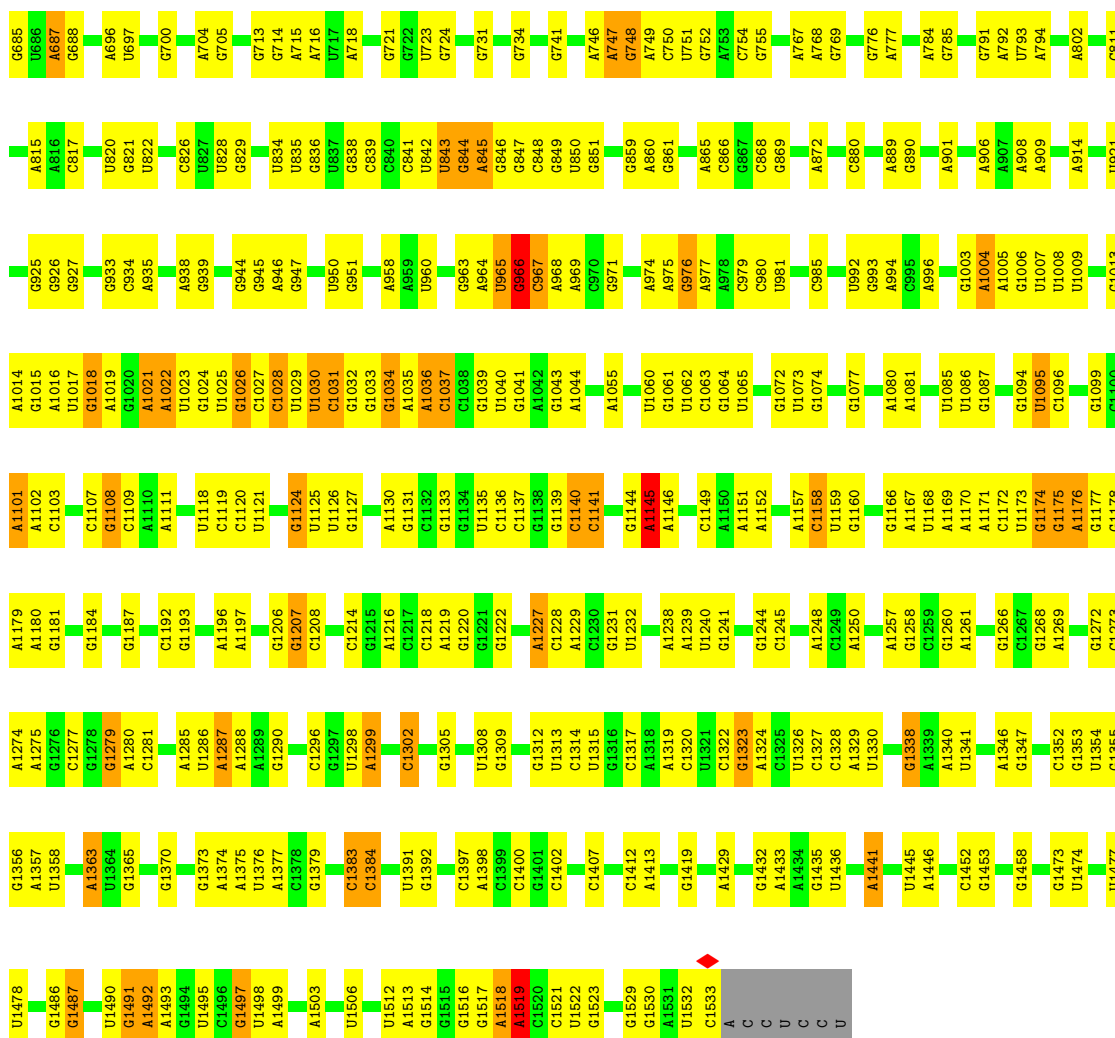
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S ribosomal RNA

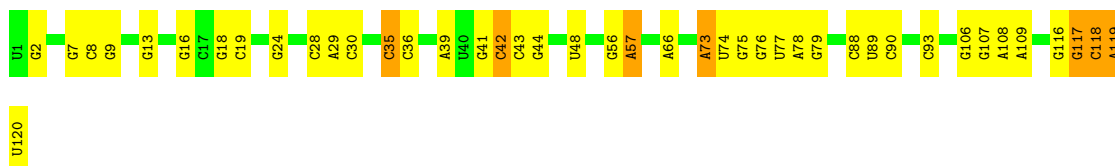


A2212	U2079	G1763	C1565	U1474	G1368	U1273	U181	G1093	U1012
U2213	A2080	C1764	A1566	G1475	G1368	A1274	G182	U1094	C1013
C2214	U2086	A1665	G1567	G1475	G1368	A1275	U183	A1095	A1014
C2215	G2087	C1771	G1568	G1478	U1379	C1278	U184	A1096	U1019
G2216	A2088	U1772	A1666	G1478	A1383	G1279	G185	U1097	U1019
U2220	U2092	A1672	A1570	G1482	A1383	G1280	G186	A1098	A1020
G2221	G2093	G1673	A1571	G1483	C1386	G1281	G190	A1099	A1021
C2222	A2094	G1674	A1572	U1484	A1387	U1282	C1196	U1099	G1022
C2225	C2095	C1675	G1573	U1485	G1388	G1283	G197	C1100	U1023
U2229	C2096	A1676	C1577	U1486	A1392	A1284	U198	C1102	G1026
G2230	A2097	G1681	U1578	U1486	A1393	A1285	U199	C1104	A1027
G2231	U2098	G1682	A1579	U1486	U1394	A1286	U199	U1105	A1028
C2232	U2099	U1683	C1582	U1491	A1395	G1292	A1204	G1106	U1033
U2233	G2100	G1684	A1583	G1492	A1395	C1293	A1205	G1110	G1034
G2234	A2101	C1685	U1584	U1494	U1397	G1295	G1206	A1111	U1035
U2238	G2102	A1789	C1585	A1495	G1401	G1296	C1211	G1112	A1039
G2239	C2103	C1790	A1586	A1496	U1405	G1296	G1212	C1114	A1040
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U2244	U2105	U1794	G1588	U1497	U1406	A1301	A1214	G1116	A1046
U2245	G2107	U1796	U1589	U1499	U1406	C1306	G1220	G1120	G1047
G2246	A2109	G1797	A1590	G1500	U1415	C1306	G1220	G1125	A1054
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U2250	U2111	U1799	A1593	A1504	G1416	U1309	U1224	A1126	G1056
G2251	C2112	C1800	U1594	A1505	G1417	G1310	U1225	G1130	U1057
C2252	U2113	G1801	C1595	A1508	G1418	G1311	A1226	G1131	U1058
U2258	A2114	A1802	A1596	A1509	A1419	C1315	G1227	G1132	G1059
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C2263	U2117	G1809	C1600	G1514	C1428	G1318	A1237	G1062	G1062
G2264	A2118	U1810	C1607	A1515	G1429	C1319	G1238	G1063	G1063
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G2279	C2124	U1827	G1618	U1534	U1442	A1330	A1247	A1069	A1069
U2282	A2051	G1736	G1619	A1535	U1443	C1330	G1248	A1070	A1070
C2283	A2052	G1737	G1620	U1536	G1444	G1333	U1249	C1071	C1071
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G2293	A1966	U1747	U1650	A1551	U1458	U1359	U1271	C1079	C1079
U2294	U1967	A1756	G1651	C1559	C1461	G1363	A1272	A1080	A1080
C2295	C1968	U1758	G1652	U1559	C1469	U1364	A1272	A1086	A1086
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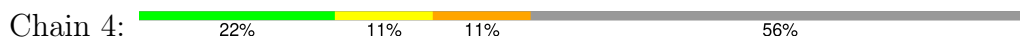




- Molecule 3: 5S ribosomal RNA

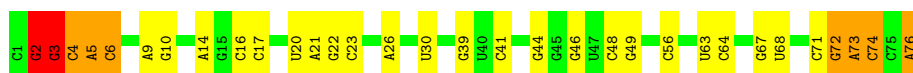


- Molecule 4: messenger RNA



- Molecule 5: tRNA^{ProL} (GGG)

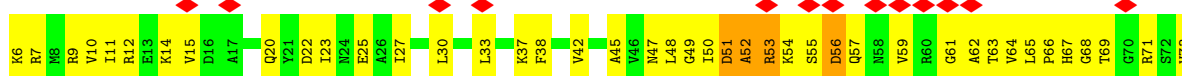
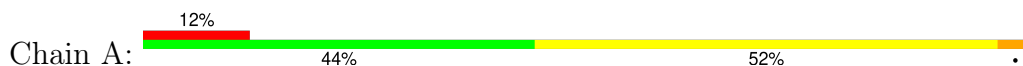




• Molecule 6: Elongation factor P



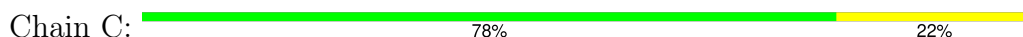
• Molecule 7: Large ribosomal subunit protein uL1

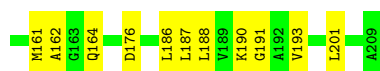


• Molecule 8: 50S ribosomal protein L2



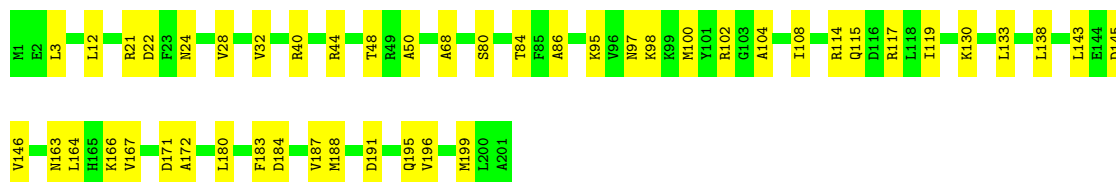
• Molecule 9: 50S ribosomal protein L3





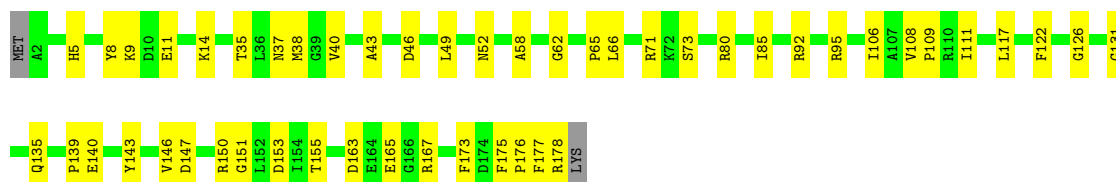
- Molecule 10: 50S ribosomal protein L4

Chain D: 77% 23%



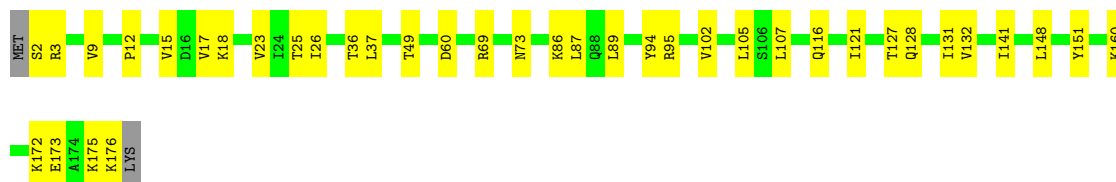
- Molecule 11: 50S ribosomal protein L5

Chain E: 72% 27%



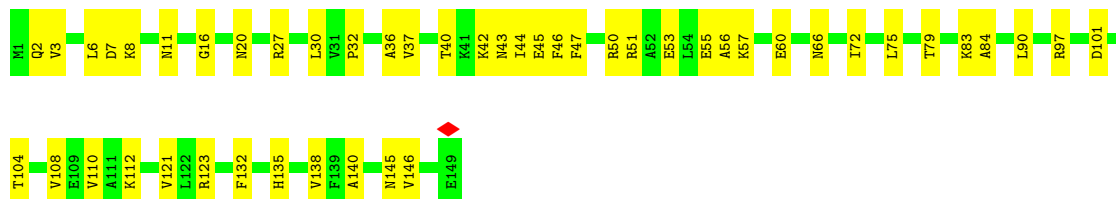
- Molecule 12: 50S ribosomal protein L6

Chain F: 77% 21%



- Molecule 13: Large ribosomal subunit protein bL9

Chain G: 68% 32%

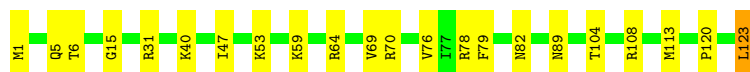
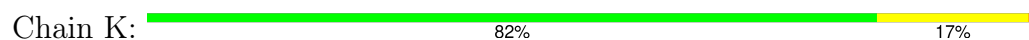


- Molecule 14: 50S ribosomal protein L13

Chain J: 80% 20%



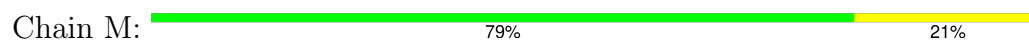
- Molecule 15: 50S ribosomal protein L14



- Molecule 16: 50S ribosomal protein L15



- Molecule 17: 50S ribosomal protein L16

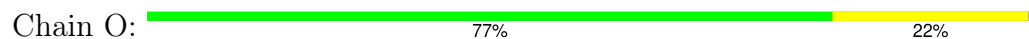


- Molecule 18: Large ribosomal subunit protein bL17

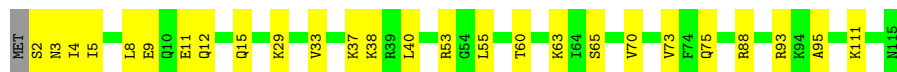


LYS
ALA
GLU
ALA
ALA
ALA
GLU


- Molecule 19: 50S ribosomal protein L18

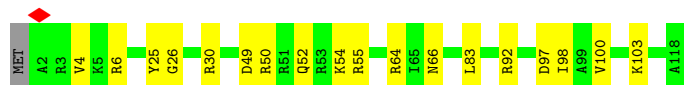


- Molecule 20: 50S ribosomal protein L19




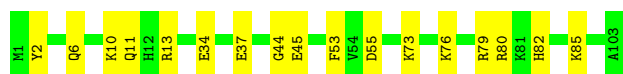
- Molecule 21: 50S ribosomal protein L20

Chain Q:  84% 15%




- Molecule 22: Ribosomal protein L21

Chain R:  83% 17%



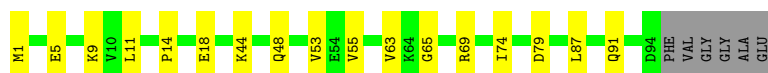
- Molecule 23: 50S ribosomal protein L22

Chain S:  77% 23%




- Molecule 24: 50S ribosomal protein L23

Chain T:  77% 17% 6%



- Molecule 25: 50S ribosomal protein L24

Chain U:  77% 22%




- Molecule 26: 50S ribosomal protein L25

Chain V:  71% 29%



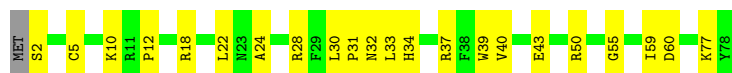
- Molecule 27: Large ribosomal subunit protein bL27

Chain W:  74% 14% 11%




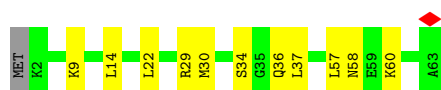
- Molecule 28: 50S ribosomal protein L28

Chain X:  71% 28%



- Molecule 29: 50S ribosomal protein L29

Chain Y:  81% 17%



- Molecule 30: Large ribosomal subunit protein uL30

Chain Z:  76% 22%



- Molecule 31: 50S ribosomal protein L31

Chain a:  11% 56% 39% 6%



- Molecule 32: 50S ribosomal protein L32

Chain b:  72% 26%




- Molecule 33: Large ribosomal subunit protein bL33

Chain c:  65% 29% 5%




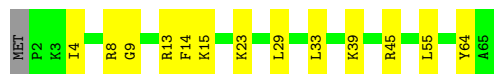
- Molecule 34: 50S ribosomal protein L34

Chain d:  78% 22%



- Molecule 35: 50S ribosomal protein L35

Chain e:  78% 20%



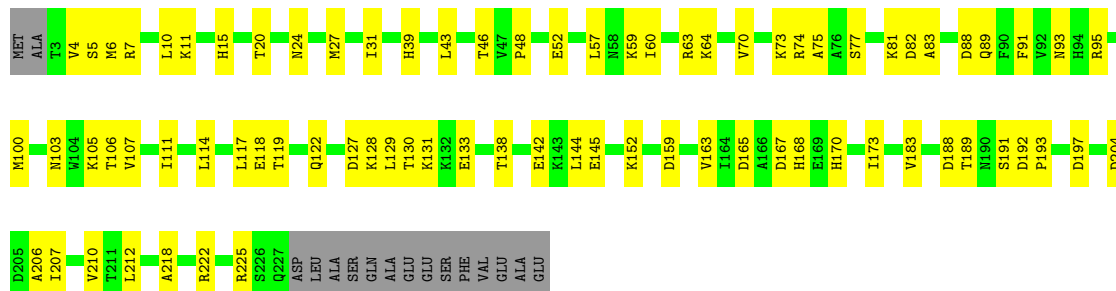
- Molecule 36: 50S ribosomal protein L36

Chain f:  76% 24%



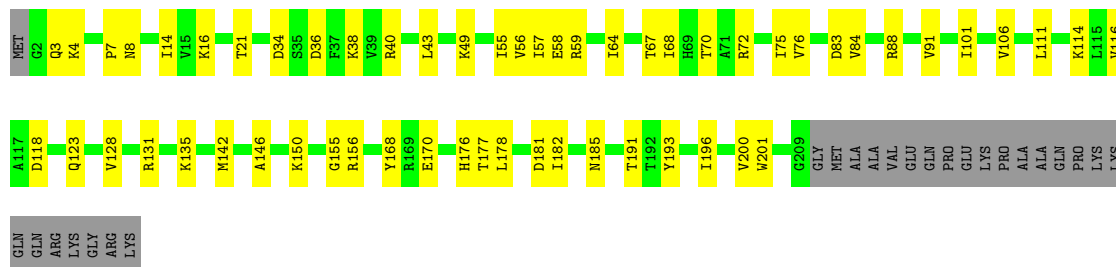
- Molecule 37: 30S ribosomal protein S2

Chain g:  61% 32% 7%



- Molecule 38: 30S ribosomal protein S3

Chain h:  65% 24% 11%



- Molecule 39: 30S ribosomal protein S4

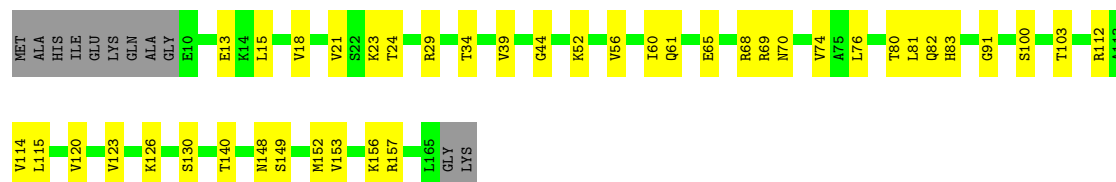
Chain i:  68% 31%





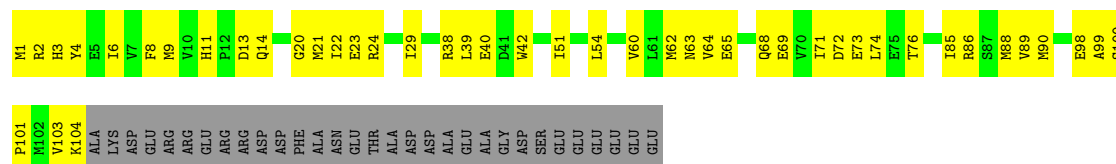
- Molecule 40: 30S ribosomal protein S5

Chain j: 69% 25% 7%



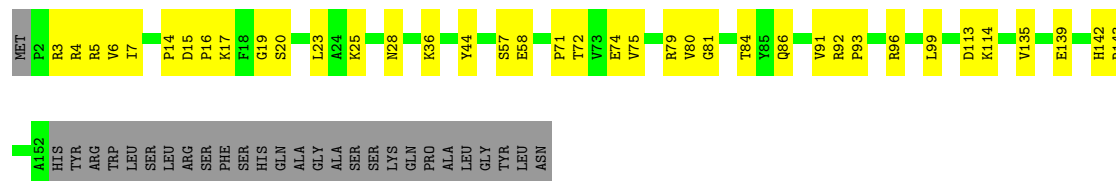
- Molecule 41: 30S ribosomal protein S6

Chain k: 44% 33% 23%



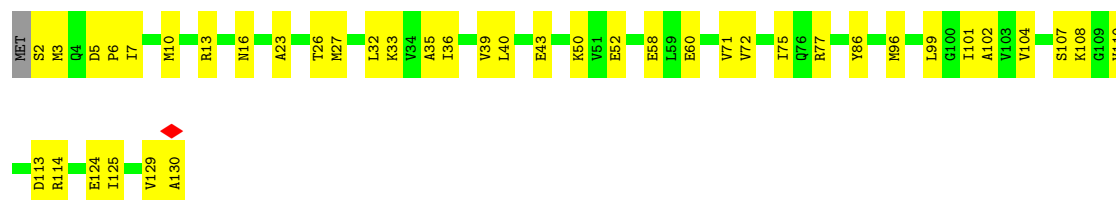
- Molecule 42: 30S ribosomal protein S7

Chain l: 63% 21% 16%



- Molecule 43: 30S ribosomal protein S8

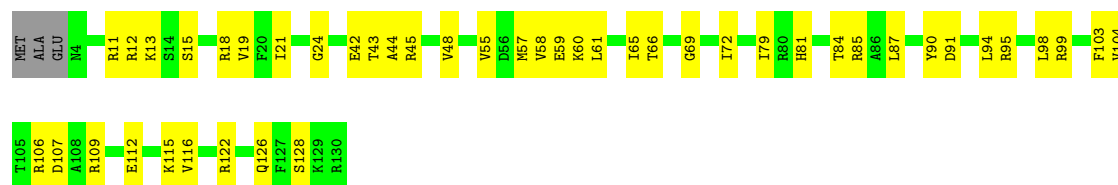
Chain m: 68% 32%



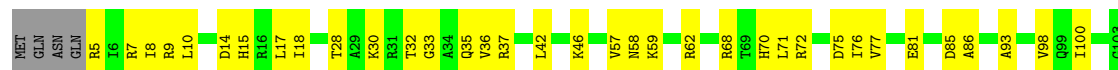
- Molecule 44: Small ribosomal subunit protein uS9

Chain n: 63% 35%

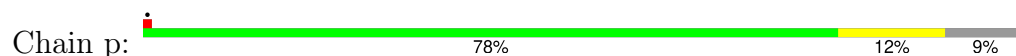




- Molecule 45: 30S ribosomal protein S10



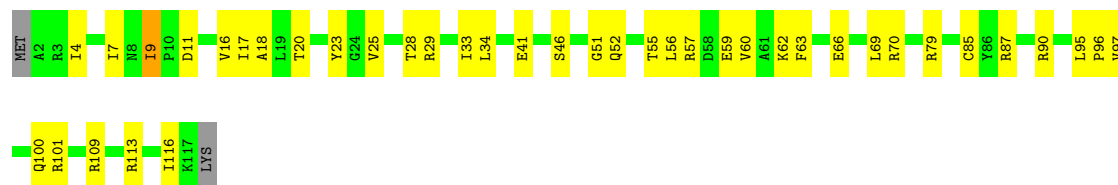
- Molecule 46: 30S ribosomal protein S11



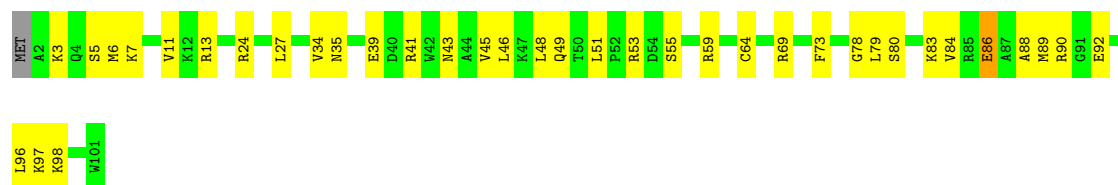
- Molecule 47: Small ribosomal subunit protein uS12



- Molecule 48: 30S ribosomal protein S13



- Molecule 49: Small ribosomal subunit protein uS14



- Molecule 50: Small ribosomal subunit protein uS15

Chain t:  71% 28%



- Molecule 51: 30S ribosomal protein S16

Chain u:  65% 35%



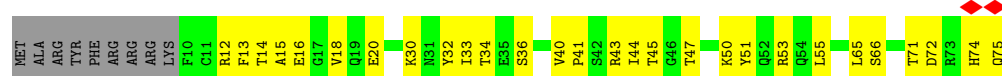
- Molecule 52: Small ribosomal subunit protein uS17

Chain v:  68% 27% 5%



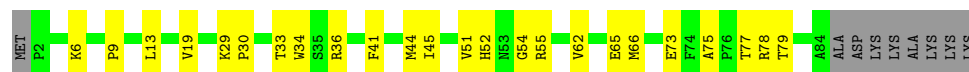
- Molecule 53: 30S ribosomal protein S18

Chain w:  51% 37% 12%




- Molecule 54: 30S ribosomal protein S19

Chain x:  64% 26% 10%



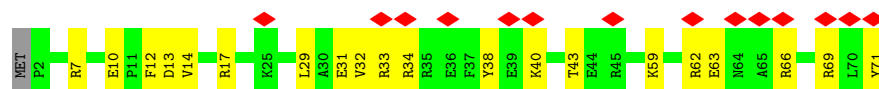
- Molecule 55: 30S ribosomal protein S20

Chain y:  79% 20%



- Molecule 56: 30S ribosomal protein S21

Chain z:  20% 70% 28%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	133607	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.07	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0023	Depositor
Map size (\AA)	547.3792, 547.3792, 547.3792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0691, 1.0691, 1.0691	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: KEO, MA6, 2MG, 5MC, 4OC, 0TD, UR3, G7M, PSU, 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	1	0.46	0/68991	0.37	0/107624
2	2	0.39	0/36565	0.32	1/57035 (0.0%)
3	3	0.36	0/2872	0.34	0/4478
4	4	0.42	0/185	0.40	0/285
5	5	0.37	0/1841	0.56	3/2870 (0.1%)
6	6	0.85	0/1470	1.00	9/1992 (0.5%)
7	A	0.37	0/1678	0.77	9/2262 (0.4%)
8	B	0.52	1/2121 (0.0%)	0.55	0/2852
9	C	0.45	0/1586	0.52	0/2134
10	D	0.42	0/1571	0.48	0/2113
11	E	0.32	0/1434	0.48	0/1926
12	F	0.30	0/1333	0.48	0/1805
13	G	0.29	0/1122	0.52	0/1515
14	J	0.44	0/1152	0.52	0/1551
15	K	0.51	0/955	0.58	0/1279
16	L	0.57	0/1062	0.74	3/1413 (0.2%)
17	M	0.43	0/1093	0.48	0/1460
18	N	0.64	0/964	0.67	1/1289 (0.1%)
19	O	0.33	0/902	0.51	0/1209
20	P	0.44	0/929	0.48	0/1242
21	Q	0.67	2/960 (0.2%)	0.52	0/1278
22	R	0.43	0/829	0.49	0/1107
23	S	0.52	0/864	0.53	0/1156
24	T	0.38	0/752	0.45	0/1005
25	U	0.36	0/796	0.47	0/1062
26	V	0.35	0/766	0.41	0/1025
27	W	0.44	0/582	0.53	0/769
28	X	0.57	0/635	0.49	0/848
29	Y	0.33	0/502	0.44	0/667
30	Z	0.42	0/452	0.50	0/605
31	a	0.19	0/531	0.44	0/709
32	b	0.46	0/450	0.62	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.55	0/433	0.50	0/576
34	d	0.48	0/380	0.52	0/498
35	e	0.72	0/513	0.73	1/676 (0.1%)
36	f	0.42	0/303	0.58	0/397
37	g	0.24	0/1791	0.47	0/2413
38	h	0.45	0/1663	0.55	0/2241
39	i	0.36	0/1665	0.52	1/2227 (0.0%)
40	j	0.41	0/1165	0.47	0/1568
41	k	0.31	0/867	0.47	0/1171
42	l	0.55	0/1195	0.58	0/1602
43	m	0.49	0/989	0.53	1/1326 (0.1%)
44	n	0.44	0/1034	0.54	0/1375
45	o	0.31	0/800	0.49	0/1082
46	p	0.37	0/893	0.50	0/1205
47	q	0.39	0/960	0.52	0/1286
48	r	0.31	0/909	0.47	0/1215
49	s	0.45	0/817	0.49	0/1088
50	t	0.34	0/722	0.45	0/964
51	u	0.34	0/659	0.48	0/884
52	v	0.45	0/657	0.52	0/881
53	w	0.32	0/553	0.48	0/743
54	x	0.40	0/680	0.55	0/915
55	y	0.32	0/675	0.40	0/895
56	z	0.20	0/597	0.45	0/792
All	All	0.44	3/158865 (0.0%)	0.42	29/237184 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Q	26	GLY	CA-C	-9.15	1.42	1.52
8	B	143	ASN	CA-C	-6.61	1.45	1.53
21	Q	25	TYR	CA-C	-6.23	1.44	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	L	36	LYS	N-CA-C	14.80	131.72	111.74
7	A	131	LEU	N-CA-C	9.73	121.48	111.07
39	i	23	SER	N-CA-C	9.06	120.76	111.07
5	5	2	G	C4'-C3'-O3'	8.93	122.79	109.40
35	e	33	LEU	N-CA-C	8.88	121.03	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1	61599	0	30981	884	0
2	2	32907	0	16572	443	0
3	3	2569	0	1300	29	0
4	4	167	0	88	4	0
5	5	1648	0	833	23	0
6	6	1461	0	1421	56	0
7	A	1663	0	1746	121	0
8	B	2082	0	2154	49	0
9	C	1565	0	1615	40	0
10	D	1552	0	1619	33	0
11	E	1410	0	1444	42	0
12	F	1313	0	1358	23	0
13	G	1111	0	1148	34	0
14	J	1129	0	1162	20	0
15	K	946	0	1023	19	0
16	L	1053	0	1129	35	0
17	M	1074	0	1157	22	0
18	N	951	0	994	20	0
19	O	892	0	923	18	0
20	P	917	0	962	24	0
21	Q	947	0	1019	11	0
22	R	816	0	839	14	0
23	S	857	0	922	19	0
24	T	746	0	811	13	0
25	U	788	0	844	17	0
26	V	753	0	780	22	0
27	W	575	0	592	10	0
28	X	625	0	652	17	0
29	Y	501	0	531	9	0
30	Z	448	0	488	10	0
31	a	522	0	524	21	0
32	b	444	0	458	15	0
33	c	426	0	464	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	d	377	0	418	8	0
35	e	504	0	572	14	0
36	f	302	0	343	6	0
37	g	1760	0	1787	60	0
38	h	1636	0	1710	39	0
39	i	1643	0	1706	48	0
40	j	1152	0	1196	27	0
41	k	848	0	846	31	0
42	l	1181	0	1238	30	0
43	m	979	0	1031	27	0
44	n	1022	0	1070	41	0
45	o	790	0	831	32	0
46	p	877	0	887	16	0
47	q	957	0	1017	28	0
48	r	900	0	965	35	0
49	s	805	0	844	27	0
50	t	714	0	734	19	0
51	u	649	0	666	20	0
52	v	648	0	691	17	0
53	w	544	0	560	25	0
54	x	663	0	688	20	0
55	y	669	0	719	13	0
56	z	589	0	629	19	0
57	1	339	0	0	0	0
57	2	183	0	0	0	0
57	3	12	0	0	0	0
57	B	4	0	0	0	0
57	C	1	0	0	0	0
57	D	4	0	0	0	0
57	E	1	0	0	0	0
57	J	1	0	0	0	0
57	K	1	0	0	0	0
57	L	2	0	0	0	0
57	M	1	0	0	0	0
57	P	2	0	0	0	0
57	Q	2	0	0	0	0
57	R	3	0	0	0	0
57	S	1	0	0	0	0
57	T	2	0	0	0	0
57	V	1	0	0	0	0
57	Z	2	0	0	0	0
57	b	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	d	1	0	0	0	0
57	e	3	0	0	0	0
57	f	1	0	0	0	0
57	i	3	0	0	0	0
57	j	2	0	0	0	0
57	k	1	0	0	0	0
57	l	2	0	0	0	0
57	m	1	0	0	0	0
57	o	1	0	0	0	0
57	q	1	0	0	0	0
57	t	1	0	0	0	0
57	u	1	0	0	0	0
57	w	1	0	0	0	0
57	y	1	0	0	0	0
57	z	2	0	0	0	0
58	5	9	0	12	0	0
59	1	153	0	0	36	0
59	2	78	0	0	17	0
59	3	7	0	0	1	0
59	4	1	0	0	0	0
59	5	5	0	0	0	0
59	6	5	0	0	1	0
59	B	1	0	0	0	0
59	C	2	0	0	0	0
59	D	2	0	0	0	0
59	E	9	0	0	1	0
59	F	6	0	0	0	0
59	G	6	0	0	1	0
59	L	2	0	0	0	0
59	M	2	0	0	0	0
59	N	1	0	0	0	0
59	O	3	0	0	0	0
59	P	5	0	0	2	0
59	S	3	0	0	0	0
59	U	3	0	0	0	0
59	V	5	0	0	4	0
59	W	2	0	0	1	0
59	Y	1	0	0	0	0
59	a	15	0	0	4	0
59	c	1	0	0	2	0
59	f	1	0	0	0	0
59	g	24	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	h	5	0	0	0	0
59	i	3	0	0	1	0
59	j	3	0	0	1	0
59	k	4	0	0	0	0
59	l	9	0	0	2	0
59	m	3	0	0	1	0
59	n	6	0	0	1	0
59	o	4	0	0	0	0
59	p	2	0	0	1	0
59	q	6	0	0	0	0
59	r	4	0	0	0	0
59	t	1	0	0	0	0
59	u	2	0	0	0	0
59	v	5	0	0	0	0
59	w	11	0	0	6	0
59	x	1	0	0	0	0
59	z	10	0	0	1	0
All	All	147683	0	99713	2424	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 10.

The worst 5 of 2424 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)
1:1:2190:G:H5''	59:1:3455:HOH:O	1.28	1.27
2:2:89:U:H3'	59:2:1801:HOH:O	1.40	1.22
1:1:1071:G:H5'	59:1:3494:HOH:O	1.34	1.22
1:1:894:U:H5''	59:1:3485:HOH:O	1.45	1.14
5:5:39:G:O2'	6:6:149:THR:HG22	1.50	1.11

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	
6	6	185/188 (98%)	174 (94%)	10 (5%)	1 (0%)	25	58
7	A	222/224 (99%)	194 (87%)	26 (12%)	2 (1%)	14	45
8	B	269/273 (98%)	253 (94%)	16 (6%)	0	100	100
9	C	207/209 (99%)	193 (93%)	14 (7%)	0	100	100
10	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
11	E	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
12	F	173/177 (98%)	163 (94%)	10 (6%)	0	100	100
13	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
14	J	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
15	K	121/123 (98%)	115 (95%)	5 (4%)	1 (1%)	16	48
16	L	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
17	M	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
18	N	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
19	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
20	P	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
21	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
22	R	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
23	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
24	T	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
25	U	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
26	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
27	W	73/84 (87%)	69 (94%)	4 (6%)	0	100	100
28	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
29	Y	60/63 (95%)	60 (100%)	0	0	100	100
30	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	a	64/70 (91%)	58 (91%)	6 (9%)	0	100	100
32	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
33	c	50/55 (91%)	48 (96%)	2 (4%)	0	100	100
34	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
35	e	62/65 (95%)	57 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	f	36/38 (95%)	36 (100%)	0	0	100	100
37	g	223/241 (92%)	204 (92%)	18 (8%)	1 (0%)	30	63
38	h	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
39	i	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
40	j	154/167 (92%)	146 (95%)	8 (5%)	0	100	100
41	k	102/135 (76%)	96 (94%)	6 (6%)	0	100	100
42	l	149/179 (83%)	135 (91%)	14 (9%)	0	100	100
43	m	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
44	n	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
45	o	97/103 (94%)	88 (91%)	9 (9%)	0	100	100
46	p	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
47	q	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
48	r	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
49	s	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
50	t	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
51	u	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
52	v	78/84 (93%)	72 (92%)	6 (8%)	0	100	100
53	w	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
54	x	81/92 (88%)	76 (94%)	5 (6%)	0	100	100
55	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
56	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	6014/6324 (95%)	5680 (94%)	329 (6%)	5 (0%)	50	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	56	ASP
37	g	128	LYS
6	6	165	PRO
7	A	135	GLY
15	K	120	PRO

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	
6	6	154/154 (100%)	142 (92%)	12 (8%)	10	35
7	A	173/173 (100%)	169 (98%)	4 (2%)	45	70
8	B	216/218 (99%)	214 (99%)	2 (1%)	75	88
9	C	164/164 (100%)	164 (100%)	0	100	100
10	D	165/165 (100%)	165 (100%)	0	100	100
11	E	148/150 (99%)	148 (100%)	0	100	100
12	F	136/138 (99%)	136 (100%)	0	100	100
13	G	114/114 (100%)	114 (100%)	0	100	100
14	J	116/116 (100%)	116 (100%)	0	100	100
15	K	104/104 (100%)	103 (99%)	1 (1%)	73	86
16	L	103/103 (100%)	103 (100%)	0	100	100
17	M	109/109 (100%)	109 (100%)	0	100	100
18	N	99/103 (96%)	97 (98%)	2 (2%)	50	74
19	O	86/87 (99%)	86 (100%)	0	100	100
20	P	99/100 (99%)	99 (100%)	0	100	100
21	Q	89/90 (99%)	88 (99%)	1 (1%)	70	84
22	R	84/84 (100%)	84 (100%)	0	100	100
23	S	93/93 (100%)	93 (100%)	0	100	100
24	T	81/84 (96%)	81 (100%)	0	100	100
25	U	84/85 (99%)	84 (100%)	0	100	100
26	V	78/78 (100%)	78 (100%)	0	100	100
27	W	57/62 (92%)	56 (98%)	1 (2%)	54	76
28	X	67/68 (98%)	66 (98%)	1 (2%)	60	80
29	Y	54/55 (98%)	54 (100%)	0	100	100
30	Z	48/49 (98%)	48 (100%)	0	100	100
31	a	59/62 (95%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	b	47/48 (98%)	47 (100%)	0	100	100
33	c	47/49 (96%)	47 (100%)	0	100	100
34	d	38/38 (100%)	38 (100%)	0	100	100
35	e	51/52 (98%)	50 (98%)	1 (2%)	50	74
36	f	34/34 (100%)	34 (100%)	0	100	100
37	g	187/199 (94%)	187 (100%)	0	100	100
38	h	171/190 (90%)	169 (99%)	2 (1%)	67	83
39	i	172/173 (99%)	172 (100%)	0	100	100
40	j	119/126 (94%)	118 (99%)	1 (1%)	79	89
41	k	91/116 (78%)	91 (100%)	0	100	100
42	l	124/147 (84%)	122 (98%)	2 (2%)	58	79
43	m	104/105 (99%)	104 (100%)	0	100	100
44	n	105/107 (98%)	104 (99%)	1 (1%)	73	86
45	o	86/90 (96%)	86 (100%)	0	100	100
46	p	90/99 (91%)	90 (100%)	0	100	100
47	q	102/103 (99%)	102 (100%)	0	100	100
48	r	94/96 (98%)	93 (99%)	1 (1%)	70	84
49	s	83/84 (99%)	82 (99%)	1 (1%)	67	83
50	t	76/77 (99%)	76 (100%)	0	100	100
51	u	65/65 (100%)	65 (100%)	0	100	100
52	v	74/78 (95%)	74 (100%)	0	100	100
53	w	57/65 (88%)	57 (100%)	0	100	100
54	x	72/79 (91%)	72 (100%)	0	100	100
55	y	65/66 (98%)	65 (100%)	0	100	100
56	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4994/5155 (97%)	4961 (99%)	33 (1%)	80	90

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	l	92	ARG
42	l	113	ASP
49	s	86	GLU

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Mol	Chain	Res	Type
7	A	53	ARG
6	6	187	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
39	i	74	ASN
46	p	101	ASN
40	j	89	HIS
43	m	38	ASN
49	s	35	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2865/2903 (98%)	516 (18%)	29 (1%)
2	2	1531/1540 (99%)	254 (16%)	6 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	8/18 (44%)	3 (37%)	1 (12%)
5	5	76/77 (98%)	18 (23%)	5 (6%)
All	All	4599/4658 (98%)	811 (17%)	41 (0%)

5 of 811 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	14	A
1	1	15	G
1	1	34	U
1	1	35	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2867	G
4	4	12	A
2	2	516	PSU
2	2	1383	C
5	5	3	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

13 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
2	5MC	2	967	2	19,22,23	3.57	8 (42%)	26,32,35	1.00	1 (3%)
2	2MG	2	1516	2	18,26,27	2.39	7 (38%)	16,38,41	2.15	6 (37%)
6	KEO	6	34	6	16,18,19	0.75	0	15,21,23	1.40	2 (13%)
2	G7M	2	527	2	20,26,27	3.98	9 (45%)	16,39,42	1.04	1 (6%)
2	5MC	2	1407	2	19,22,23	3.54	8 (42%)	26,32,35	1.02	1 (3%)
2	UR3	2	1498	2	19,22,23	2.71	7 (36%)	26,32,35	1.67	3 (11%)
2	MA6	2	1519	2	19,26,27	1.75	2 (10%)	18,38,41	2.96	3 (16%)
2	MA6	2	1518	2	19,26,27	1.75	3 (15%)	18,38,41	2.85	3 (16%)
47	0TD	q	89	47	8,9,10	1.96	1 (12%)	6,11,13	1.15	0
2	2MG	2	966	2	18,26,27	2.49	7 (38%)	16,38,41	1.65	5 (31%)
2	2MG	2	1207	2	18,26,27	2.47	7 (38%)	16,38,41	1.57	5 (31%)
2	4OC	2	1402	2	20,23,24	2.97	8 (40%)	25,32,35	0.96	2 (8%)
2	PSU	2	516	57,2	18,21,22	1.07	1 (5%)	21,30,33	1.93	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
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
6	KEO	6	34	6	-	7/19/20/22	-
2	G7M	2	527	2	-	3/3/25/26	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	1/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/7/29/30	0/3/3/3
2	MA6	2	1518	2	-	1/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	0TD	q	89	47	-	3/7/12/14	-
2	2MG	2	966	2	-	0/5/27/28	0/3/3/3
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	PSU	2	516	57,2	-	3/7/25/26	0/2/2/2

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	G7M	C8-N7	10.17	1.51	1.33
2	2	527	G7M	C8-N9	10.07	1.51	1.33
2	2	1407	5MC	C6-C5	8.76	1.48	1.34
2	2	967	5MC	C6-C5	8.63	1.48	1.34
2	2	1498	UR3	C2-N1	7.06	1.48	1.38

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-10.30	104.93	116.83
2	2	1518	MA6	N1-C6-N6	-9.83	105.48	116.83
2	2	1519	MA6	N3-C2-N1	-6.25	120.19	128.67
2	2	1518	MA6	N3-C2-N1	-6.08	120.42	128.67
2	2	1498	UR3	C4-N3-C2	-5.81	119.90	124.58

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	C2'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	6	34	KEO	2	0
2	2	1519	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1518	MA6	2	0
2	2	966	2MG	1	0
2	2	1207	2MG	1	0
2	2	516	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 587 ligands modelled in this entry, 586 are monoatomic - leaving 1 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	$\# Z > 2$
58	LYS	5	101	5	7,8,9	0.62	0	3,8,10	0.17	0

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
58	LYS	5	101	5	-	0/6/7/9	-

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.

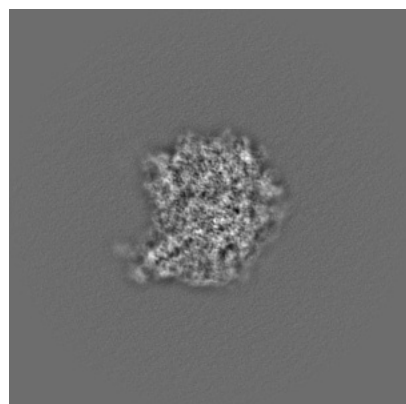
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43594. These allow visual inspection of the internal detail of the map and identification of artifacts.

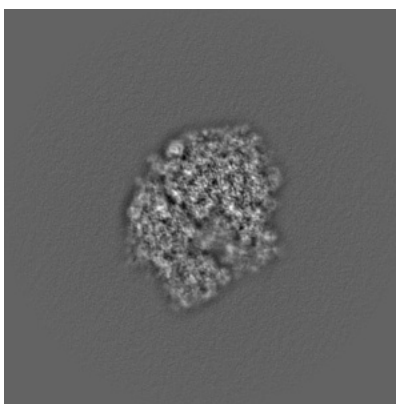
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

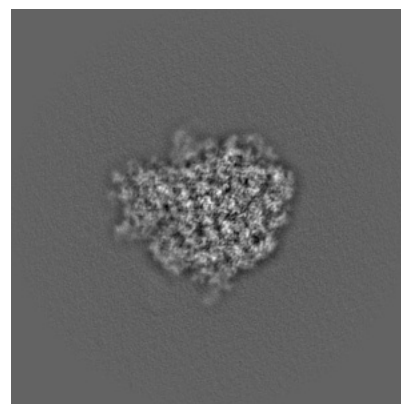
6.1.1 Primary map



X

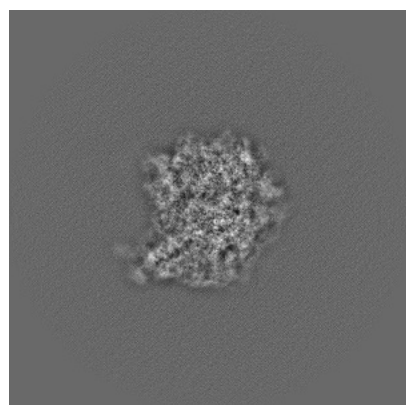


Y

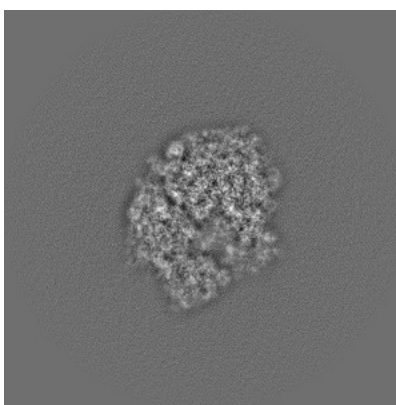


Z

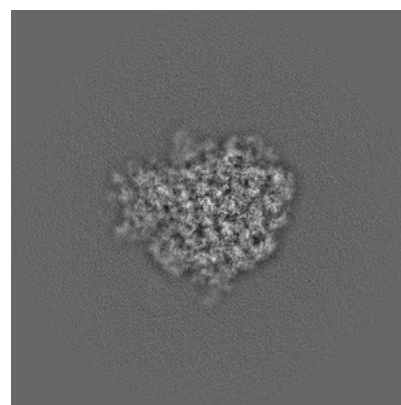
6.1.2 Raw map



X



Y

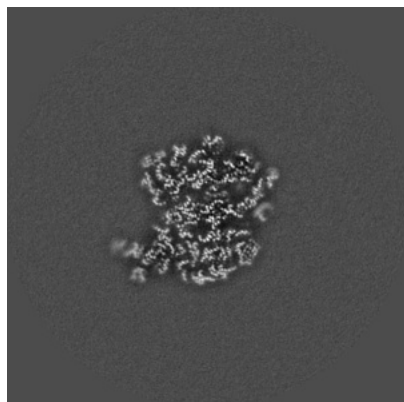


Z

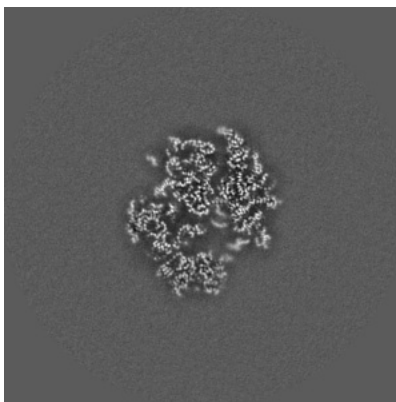
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

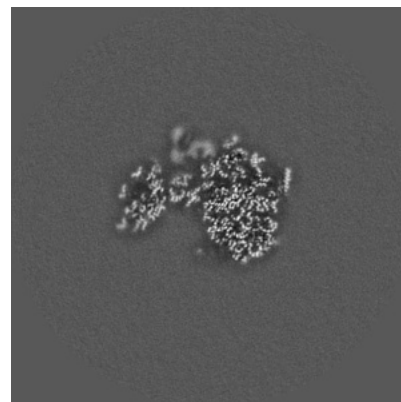
6.2.1 Primary map



X Index: 256

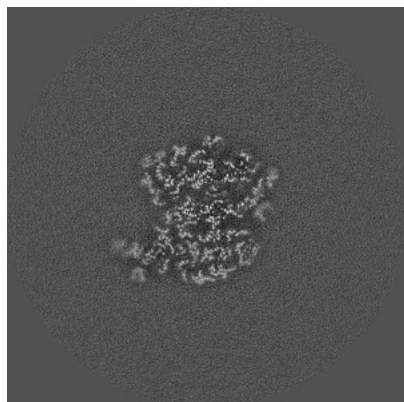


Y Index: 256

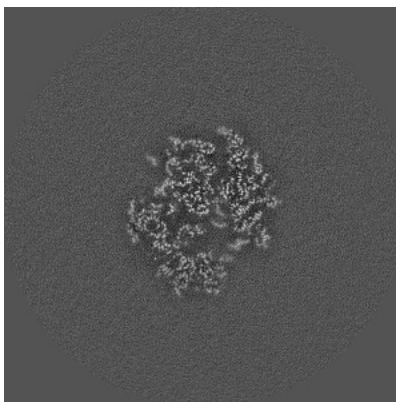


Z Index: 256

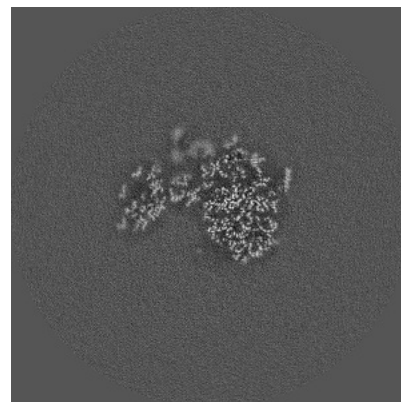
6.2.2 Raw map



X Index: 256



Y Index: 256

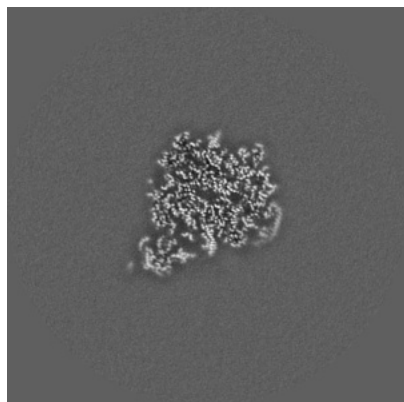


Z Index: 256

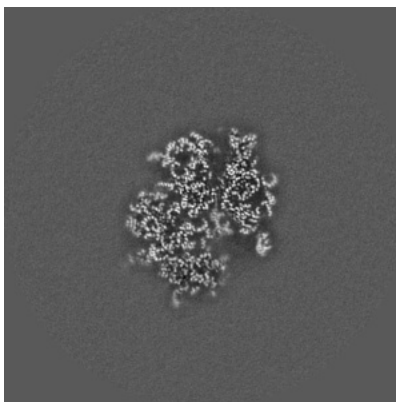
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

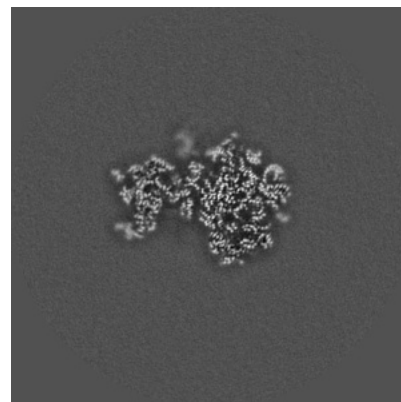
6.3.1 Primary map



X Index: 284

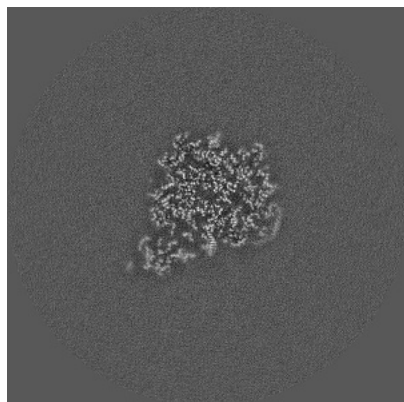


Y Index: 263

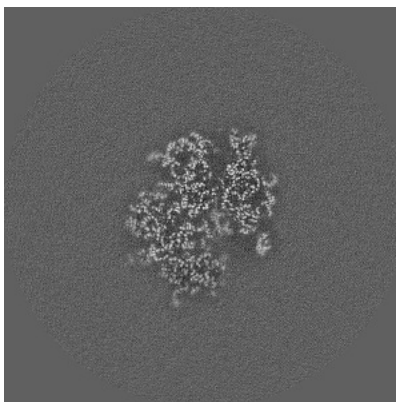


Z Index: 242

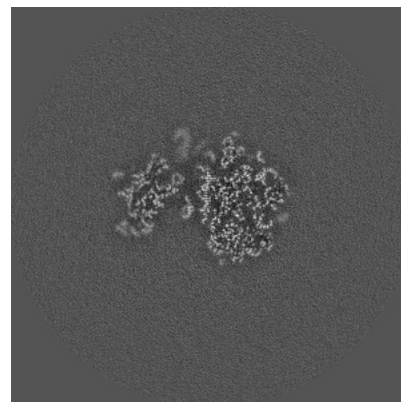
6.3.2 Raw map



X Index: 283



Y Index: 263

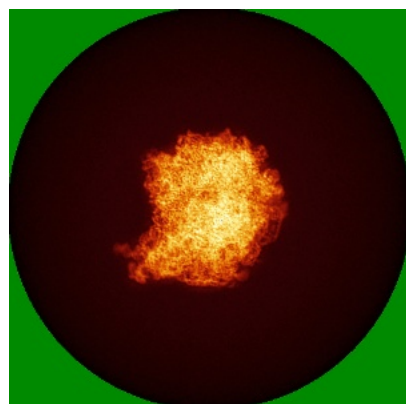


Z Index: 247

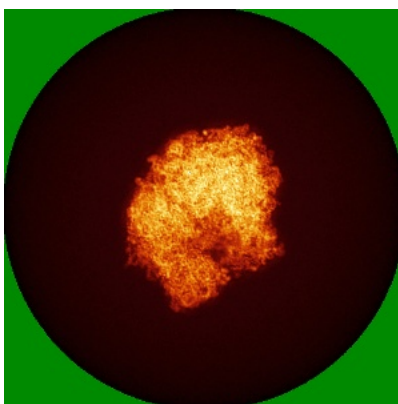
The images above show the largest variance slices of the map in three orthogonal directions.

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

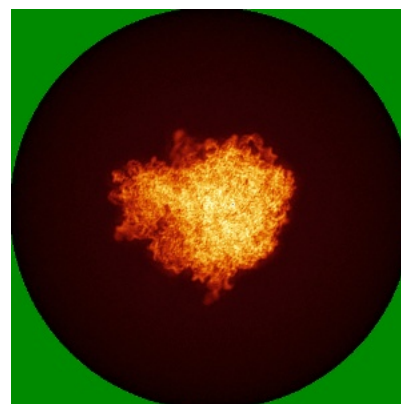
6.4.1 Primary map



X

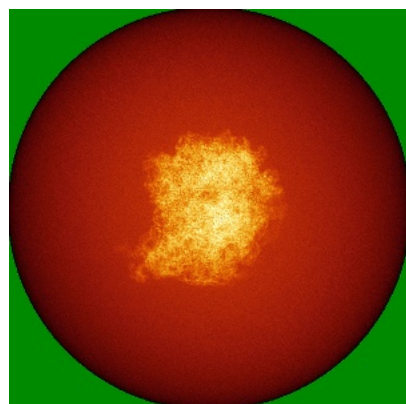


Y

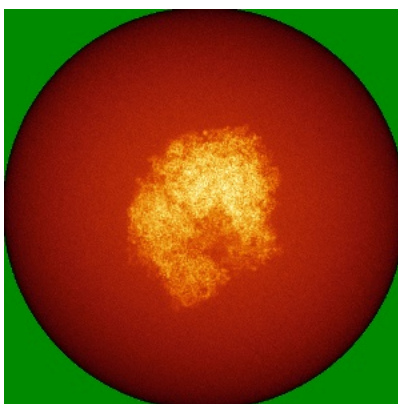


Z

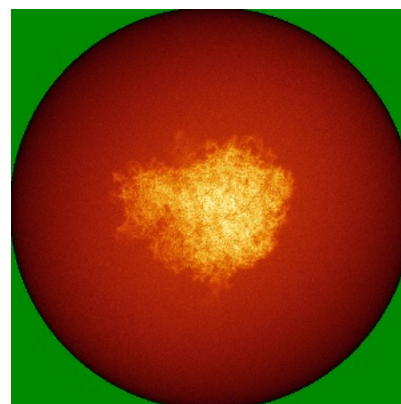
6.4.2 Raw map



X



Y

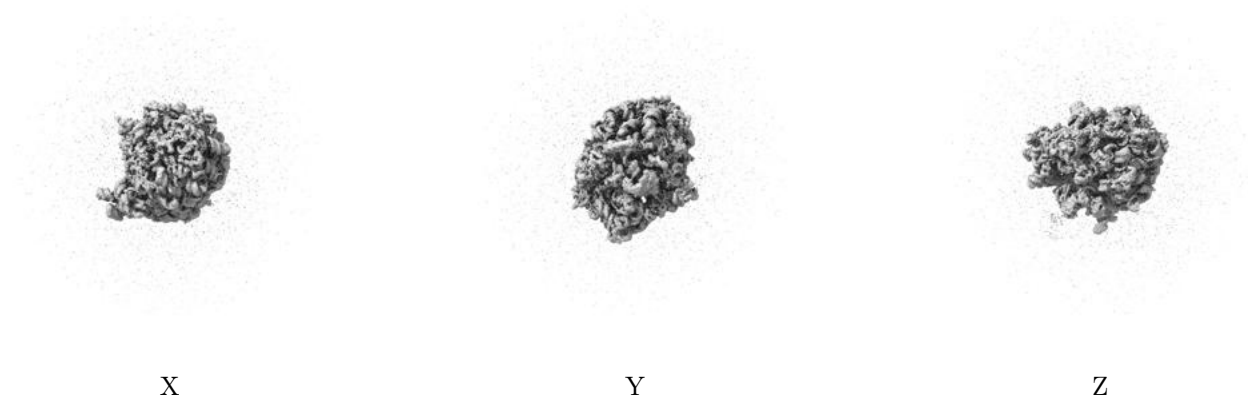


Z

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.

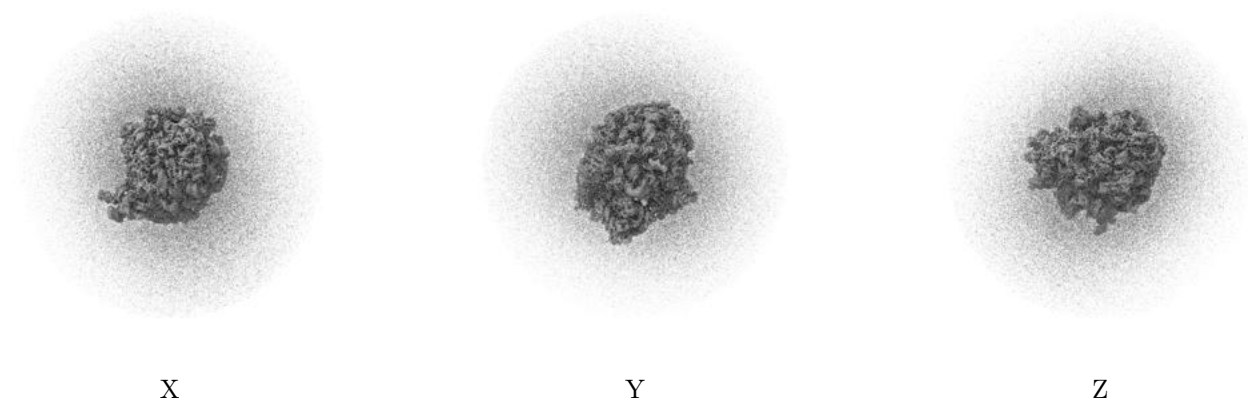
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0023. 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.

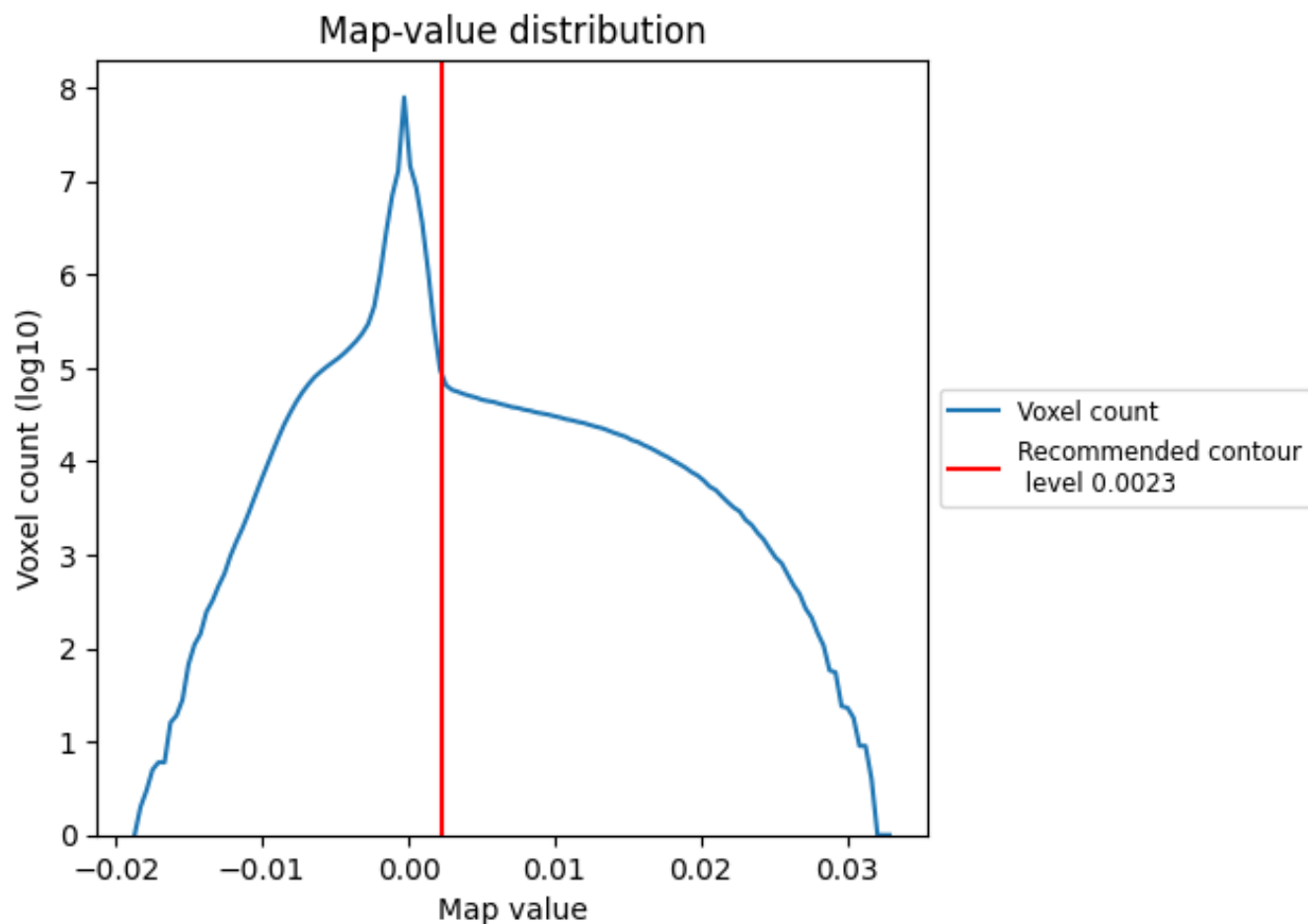
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

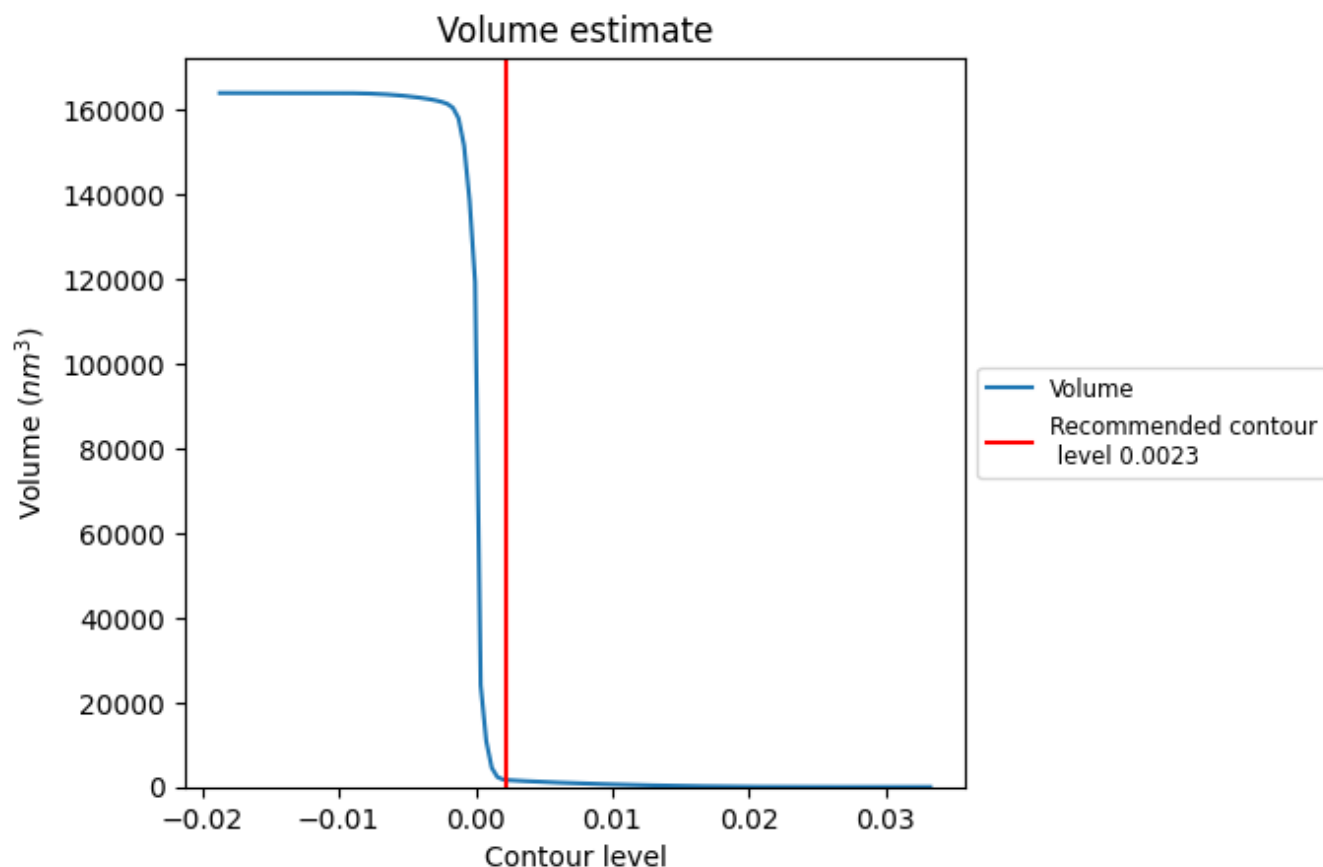
This section contains the results of statistical analysis of the map.

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.

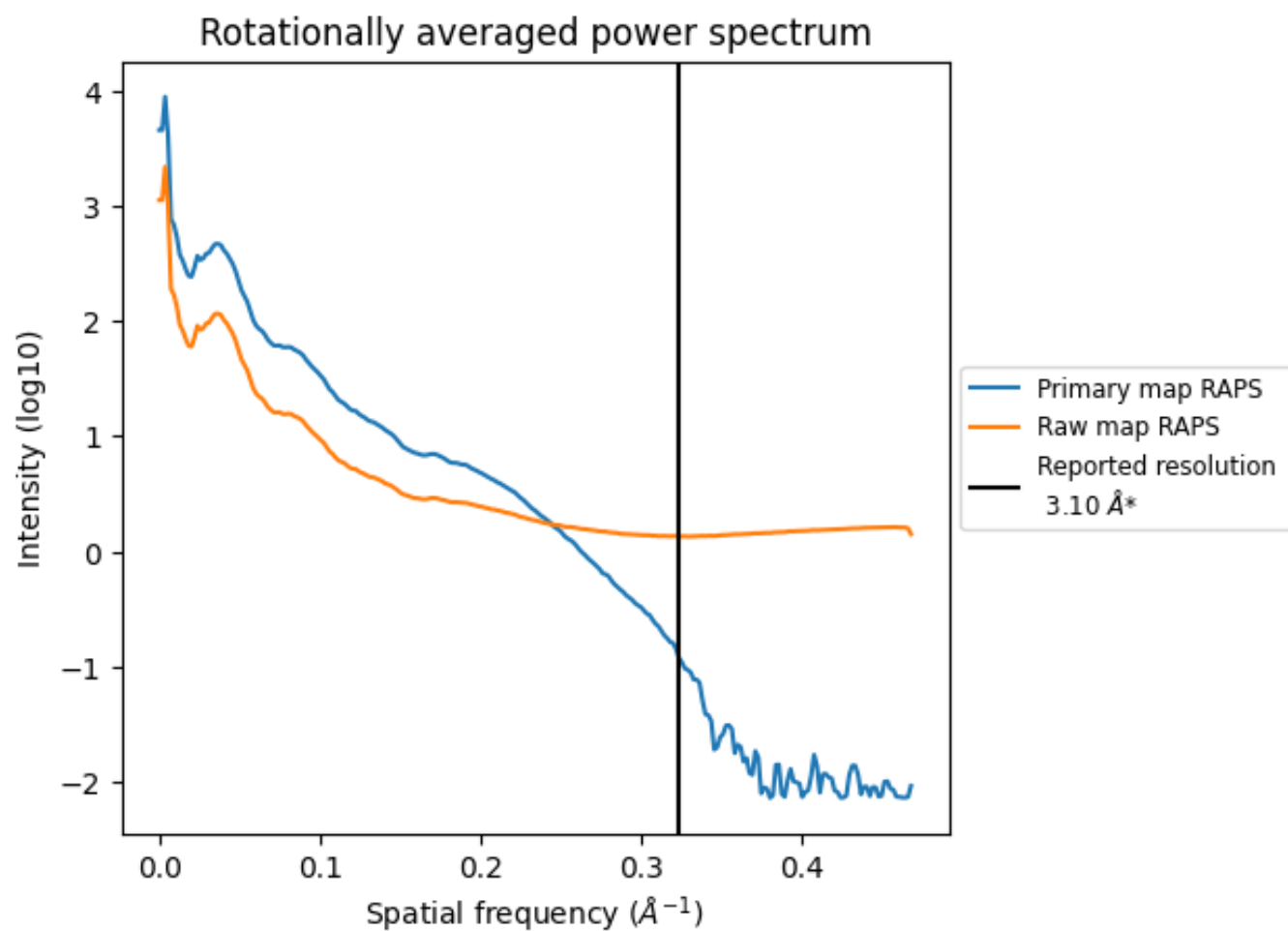
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1656 nm³; this corresponds to an approximate mass of 1496 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 ⓘ

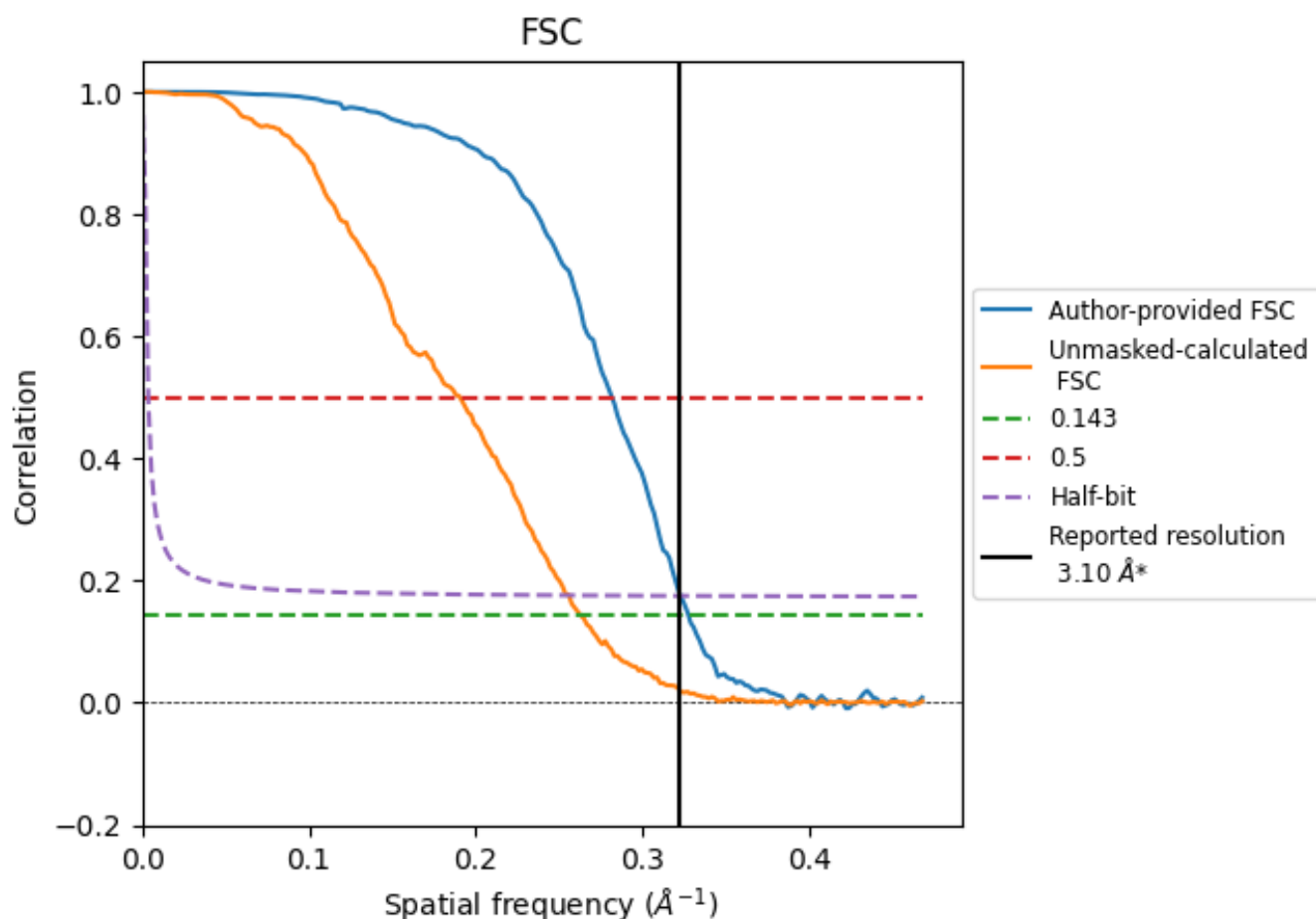


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

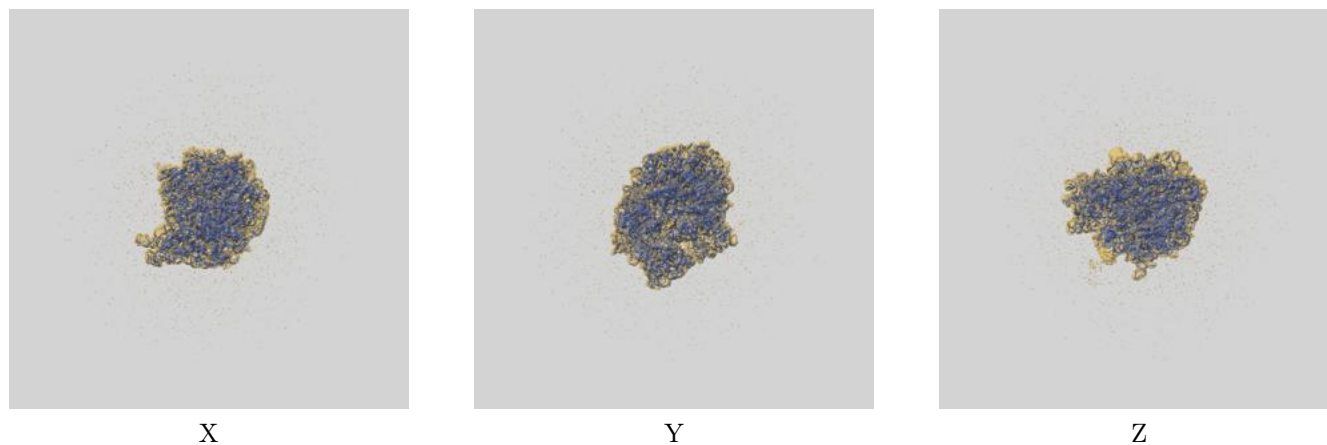
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.55	3.10
Unmasked-calculated*	3.80	5.25	3.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.80 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

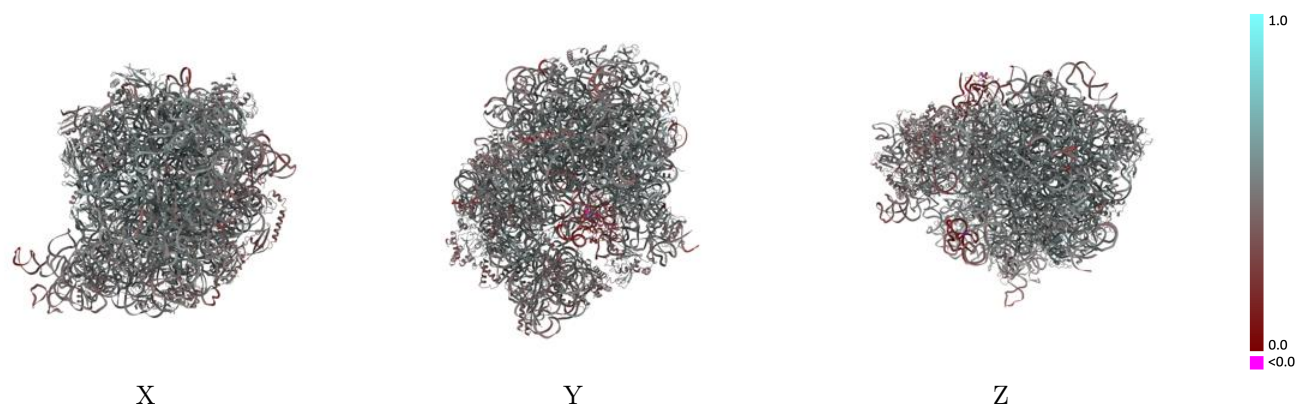
This section contains information regarding the fit between EMDB map EMD-43594 and PDB model 8VWQ. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



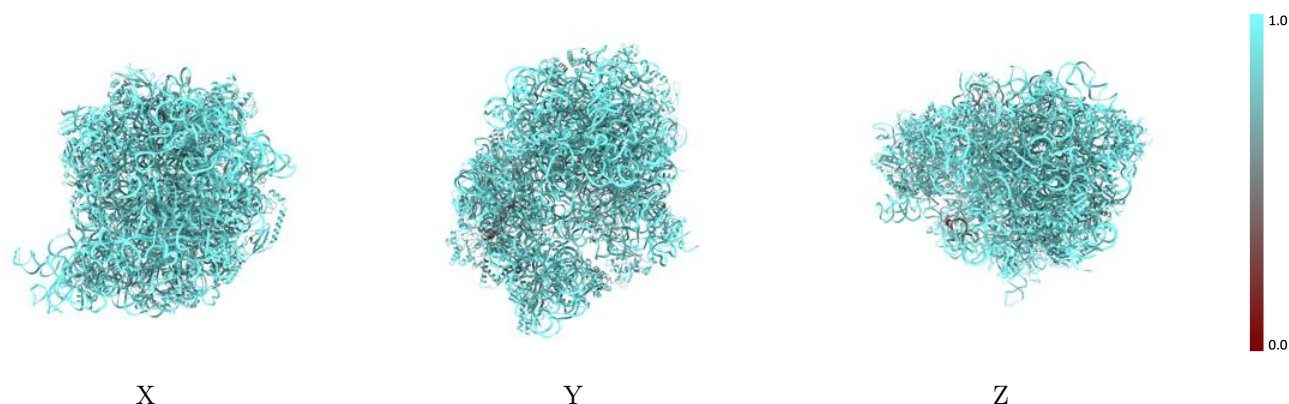
The images above show the 3D surface view of the map at the recommended contour level 0.0023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



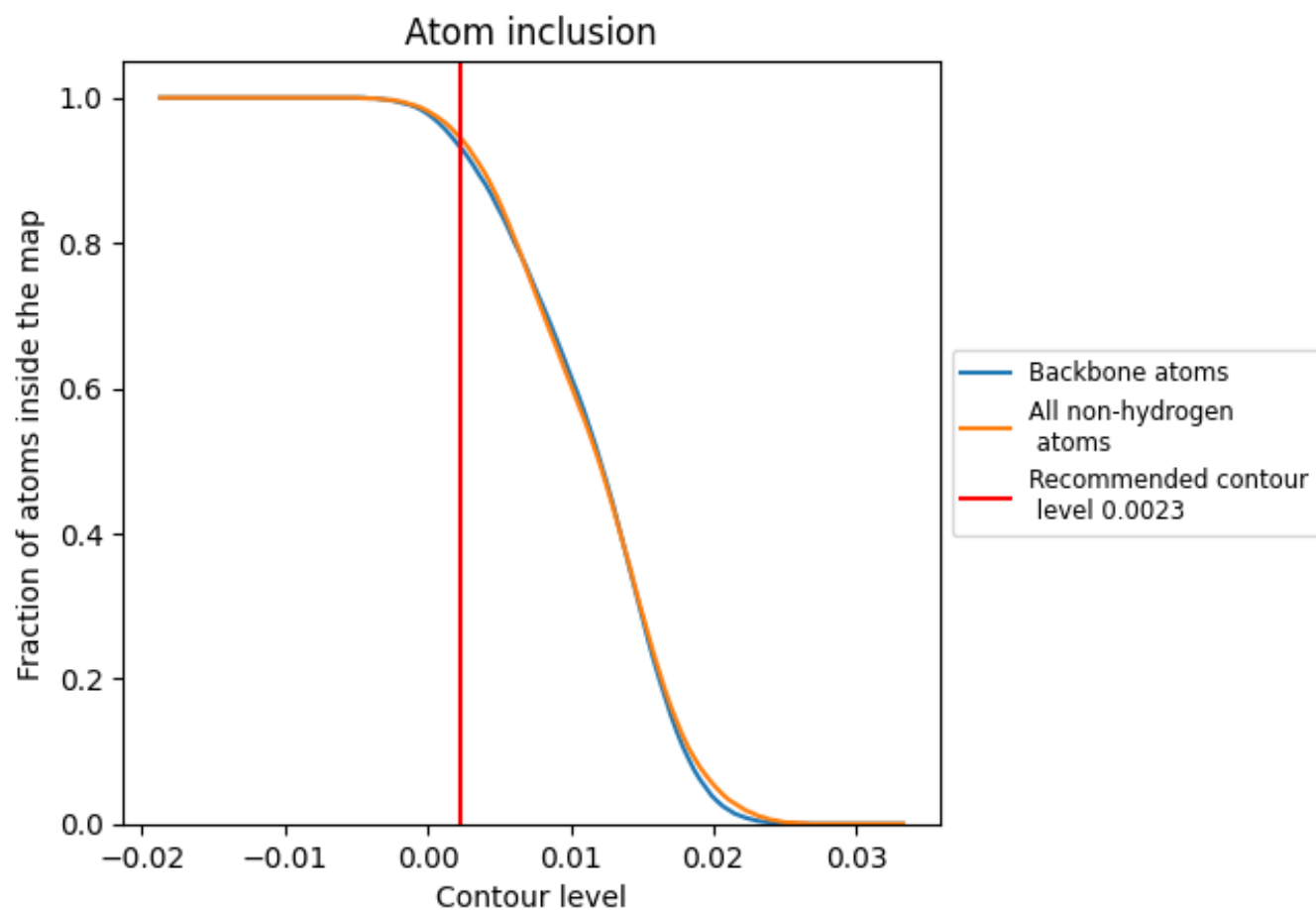
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0023).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.0023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4750
1	 0.9790	 0.4840
2	 0.9850	 0.4730
3	 0.9850	 0.4610
4	 0.9100	 0.4850
5	 0.9730	 0.4640
6	 0.8240	 0.4480
A	 0.7380	 0.2340
B	 0.8930	 0.5280
C	 0.9100	 0.5210
D	 0.9090	 0.4940
E	 0.8720	 0.4350
F	 0.9250	 0.4600
G	 0.9080	 0.3910
J	 0.9050	 0.5090
K	 0.8940	 0.5170
L	 0.9040	 0.5120
M	 0.9000	 0.5140
N	 0.8990	 0.5160
O	 0.9000	 0.4650
P	 0.8970	 0.5120
Q	 0.8830	 0.4990
R	 0.9150	 0.5120
S	 0.8780	 0.5100
T	 0.8610	 0.4930
U	 0.9120	 0.4860
V	 0.9270	 0.4810
W	 0.8770	 0.5150
X	 0.8970	 0.5050
Y	 0.9060	 0.4420
Z	 0.9130	 0.5070
a	 0.7500	 0.3880
b	 0.8880	 0.5120
c	 0.8990	 0.4940
d	 0.8620	 0.5250



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Chain	Atom inclusion	Q-score
e	 0.8600	 0.5320
f	 0.8430	 0.5120
g	 0.8460	 0.4180
h	 0.9000	 0.4680
i	 0.8520	 0.4550
j	 0.8900	 0.4890
k	 0.8990	 0.4500
l	 0.8870	 0.4360
m	 0.9020	 0.4870
n	 0.8610	 0.4590
o	 0.8680	 0.4450
p	 0.9110	 0.4710
q	 0.8830	 0.4950
r	 0.8910	 0.4470
s	 0.8710	 0.4530
t	 0.8960	 0.4550
u	 0.9000	 0.4900
v	 0.9000	 0.4660
w	 0.8110	 0.4290
x	 0.8860	 0.4480
y	 0.8400	 0.4320
z	 0.5870	 0.4060