



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 12:33 PM UTC

PDB ID : 6WDC / pdb_00006wdc
EMDB ID : EMD-21631
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure IV-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 4.20 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.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

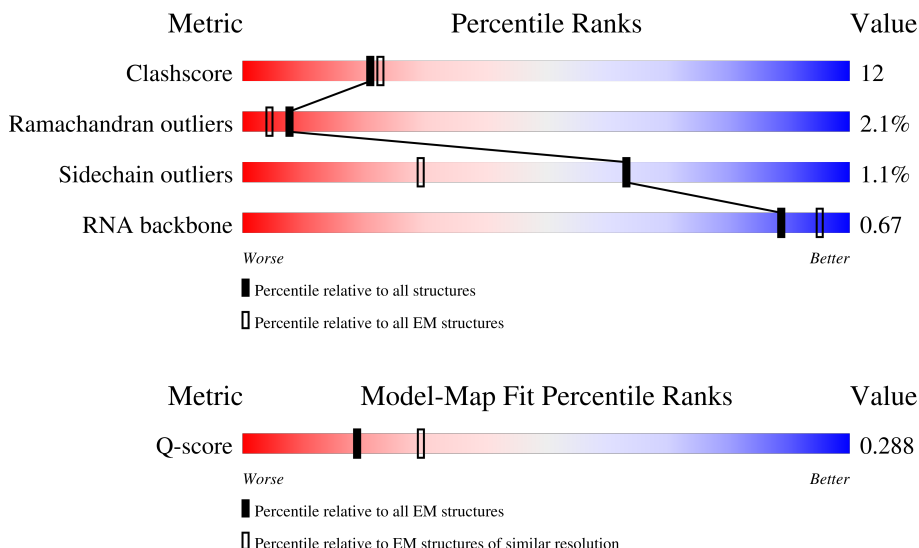
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



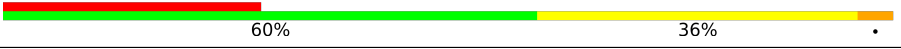
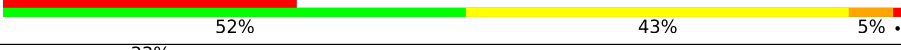
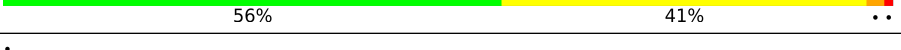
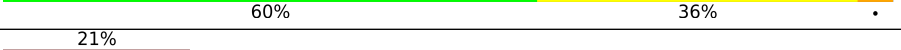
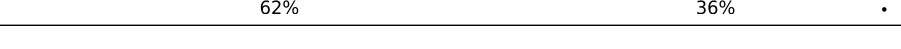
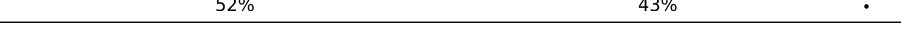
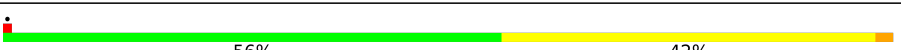
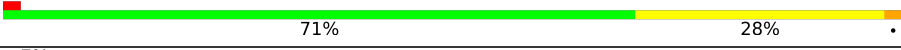
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

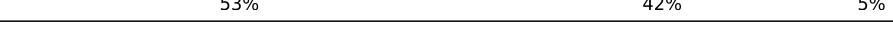
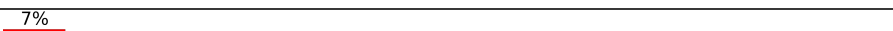
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	52% 41% 8%
55	5	77	61% 32% 6%
55	6	77	5% 66% 32% .
56	4	18	56% 39% 6%
57	7	76	72% 14% 9% .

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 150149 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

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

- Molecule 32 is a protein called 30S ribosomal protein S3.

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

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

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

- Molecule 35 is a protein called 30S ribosomal protein S6.

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

- Molecule 36 is a protein called 30S ribosomal protein S7.

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

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

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

- Molecule 40 is a protein called 30S ribosomal protein S11.

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

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

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

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18.

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

- Molecule 48 is a protein called 30S ribosomal protein S19.

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

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

- Molecule 51 is a protein called 50S ribosomal protein L1.

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

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

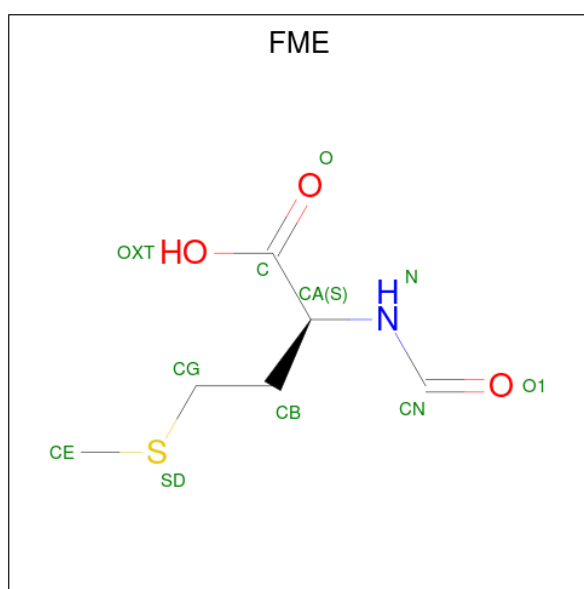
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	73	Total	C	N	O	P	0	0
			1557	695	279	511	72		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

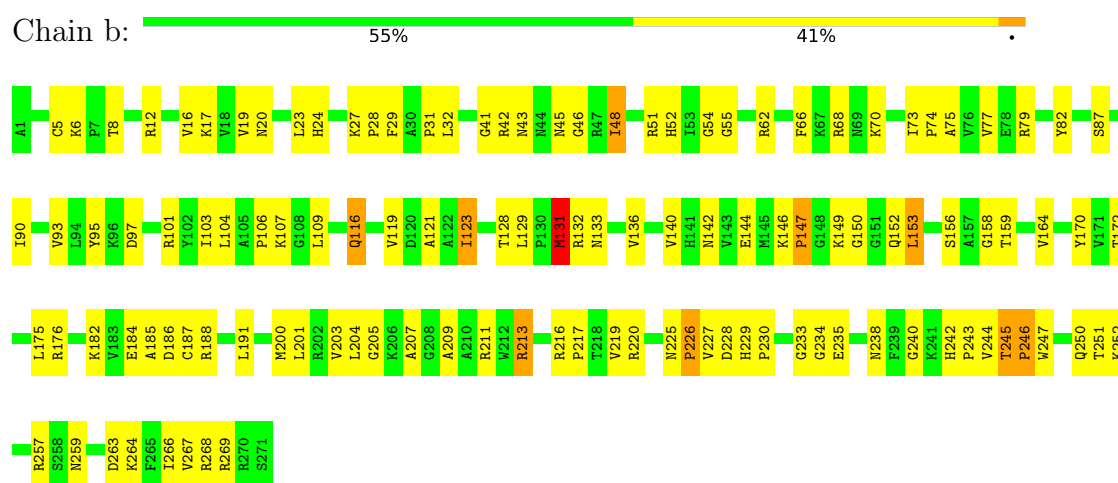


Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

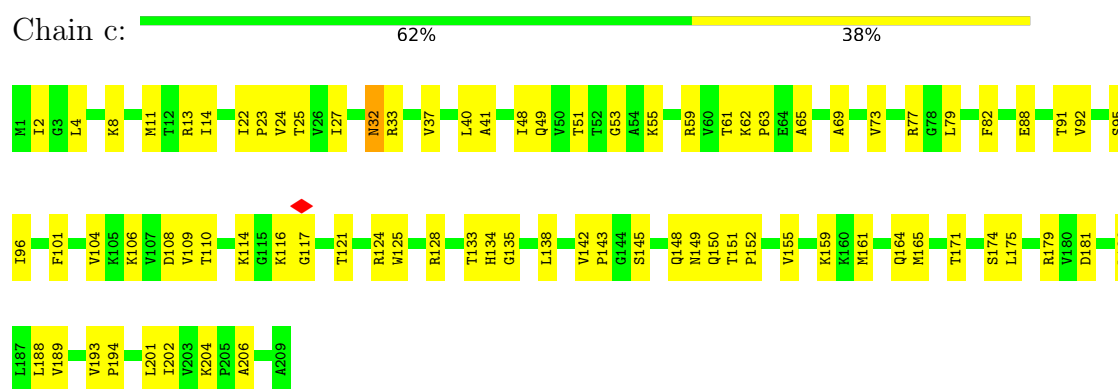
3 Residue-property plots

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.

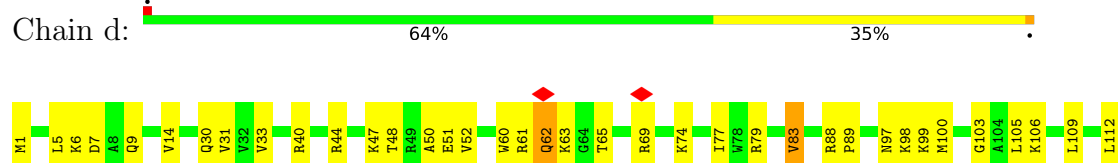
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

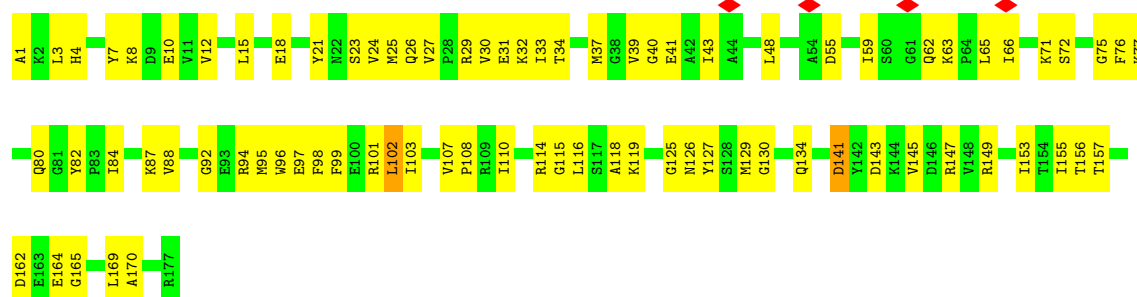


• Molecule 3: 50S ribosomal protein L4

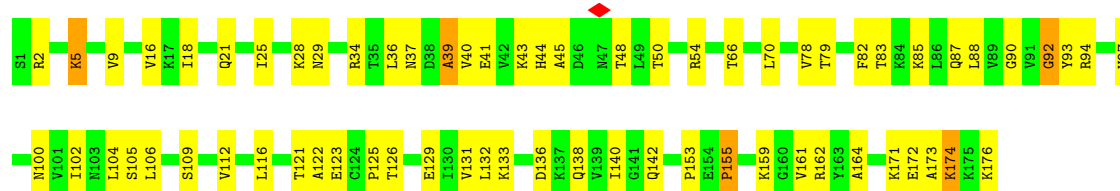




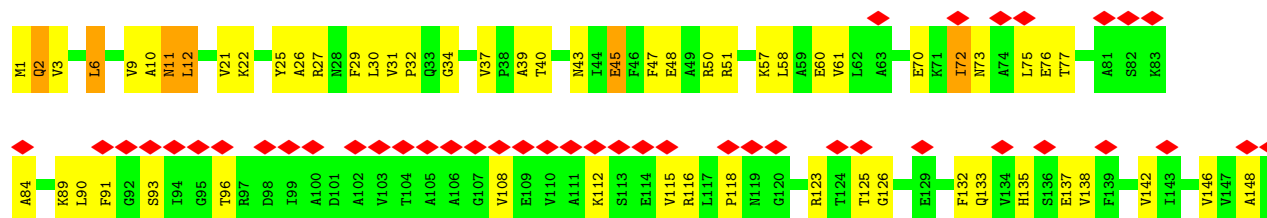
• Molecule 4: 50S ribosomal protein L5



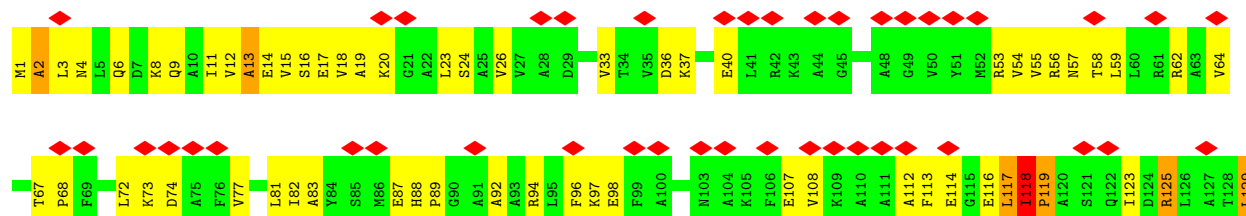
• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9

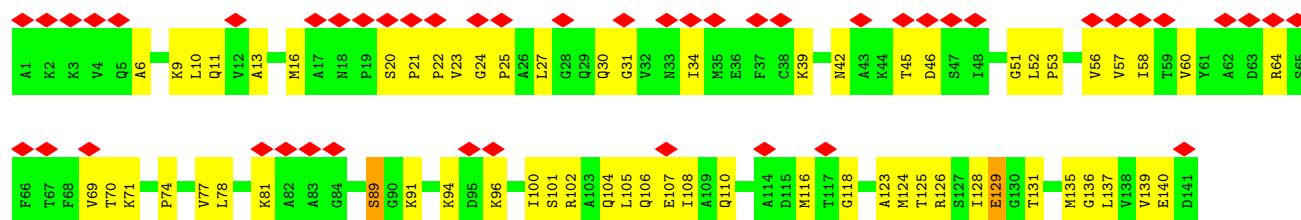


• Molecule 7: 50S ribosomal protein L10

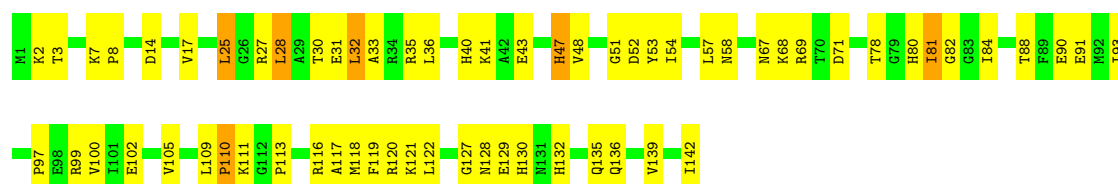




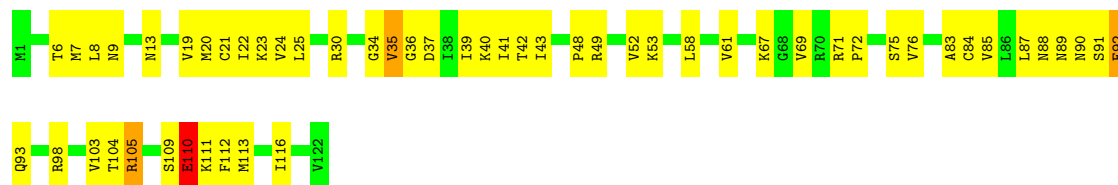
- Molecule 8: 50S ribosomal protein L11



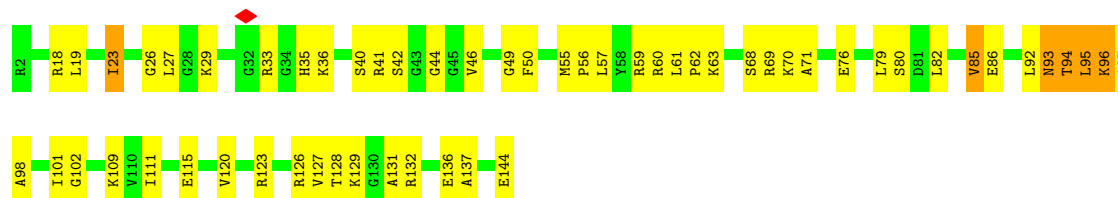
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

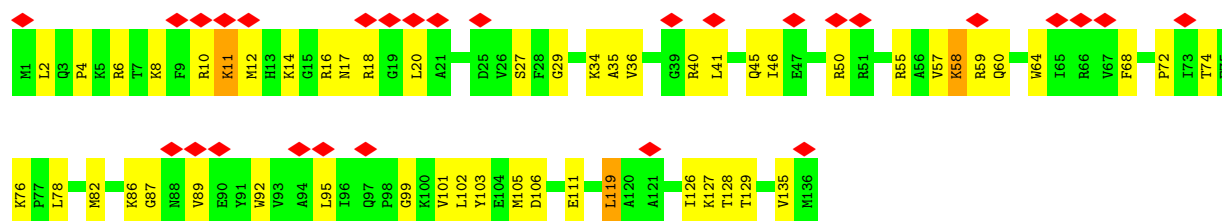


- Molecule 11: 50S ribosomal protein L15



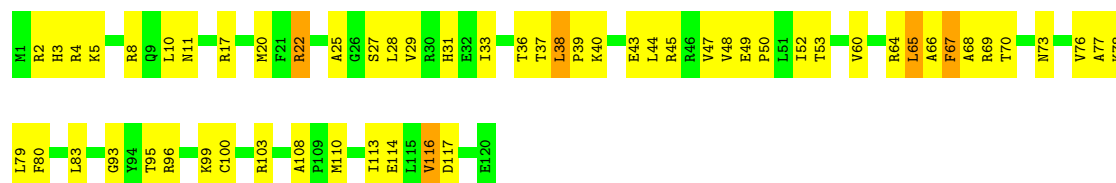
- Molecule 12: 50S ribosomal protein L16





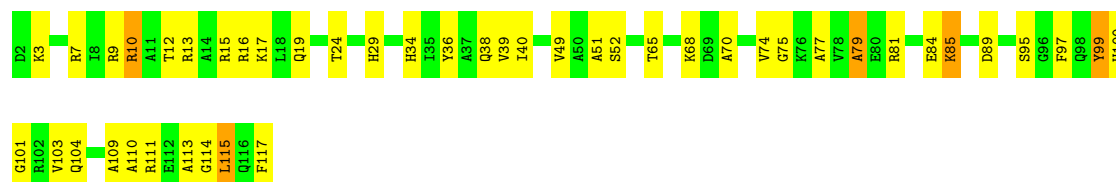
• Molecule 13: 50S ribosomal protein L17

Chain n: 52% 43% .



• Molecule 14: 50S ribosomal protein L18

Chain o: 61% 34% .



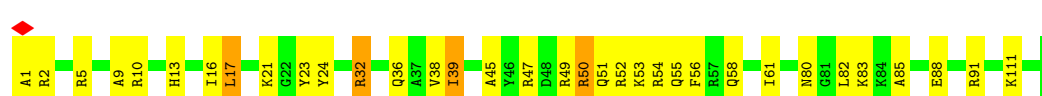
• Molecule 15: 50S ribosomal protein L19

Chain p: 69% 27% .



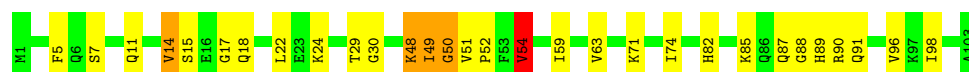
• Molecule 16: 50S ribosomal protein L20

Chain q: 71% 26% .

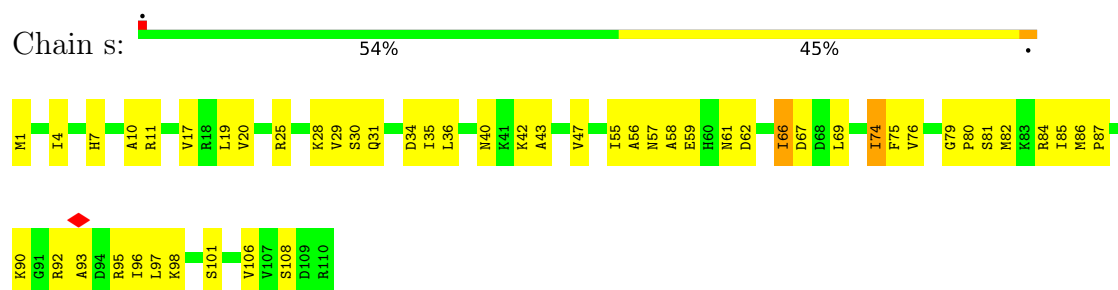


• Molecule 17: 50S ribosomal protein L21

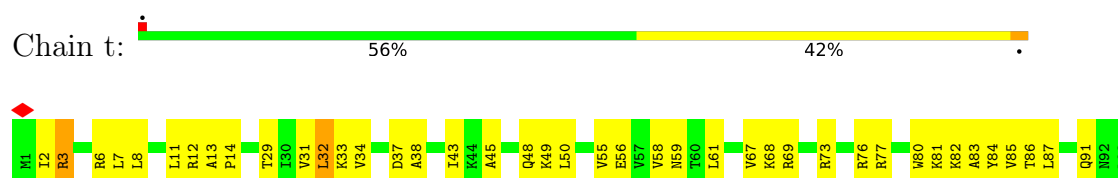
Chain r: 71% 24% . .



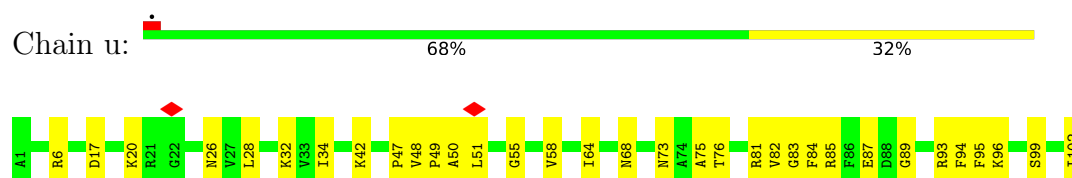
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



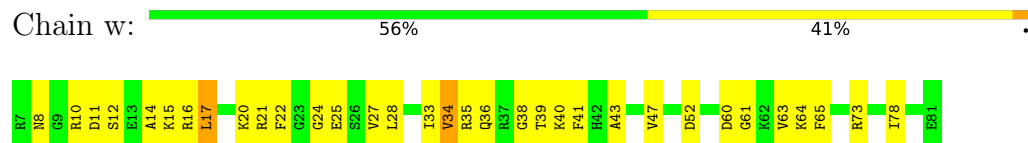
- Molecule 20: 50S ribosomal protein L24



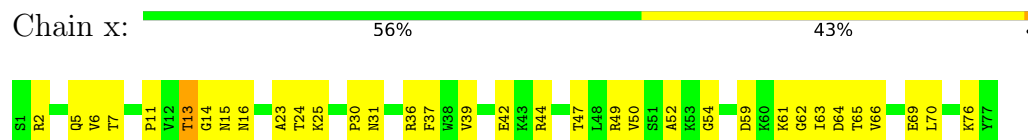
- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



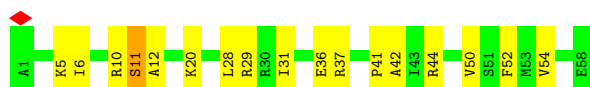
- Molecule 24: 50S ribosomal protein L29

Chain y:  71% 25% . .



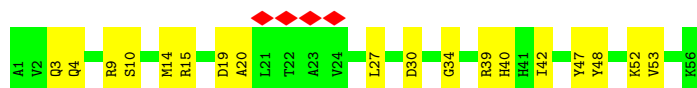
- Molecule 25: 50S ribosomal protein L30

Chain z:  71% 28% .



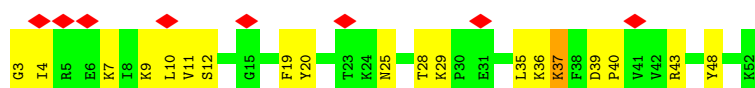
- Molecule 26: 50S ribosomal protein L32

Chain B:  7% 68% 32%



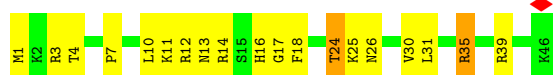
- Molecule 27: 50S ribosomal protein L33

Chain C:  16% 62% 36% .



- Molecule 28: 50S ribosomal protein L34

Chain D:  59% 37% .

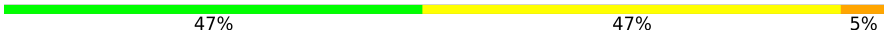


- Molecule 29: 50S ribosomal protein L35

Chain E:  64% 30% 6%

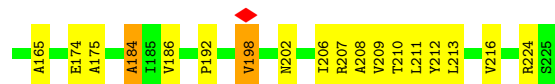


- Molecule 30: 50S ribosomal protein L36

Chain F:  47% 47% 5%



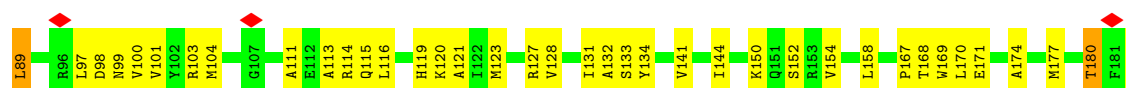
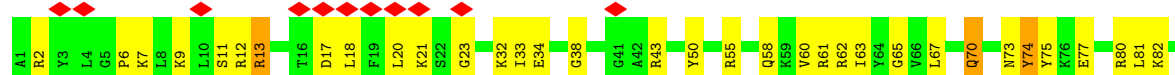
• Molecule 31: 30S ribosomal protein S2



• Molecule 32: 30S ribosomal protein S3

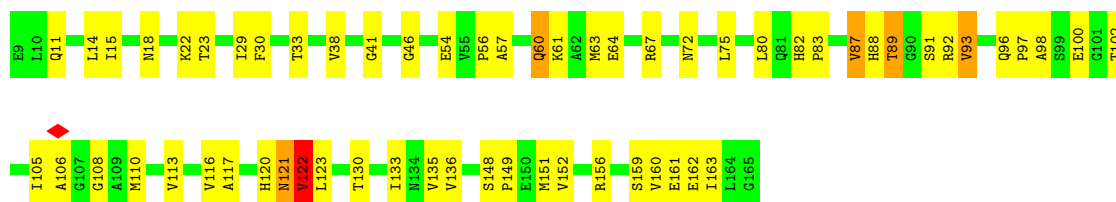


• Molecule 33: 30S ribosomal protein S4



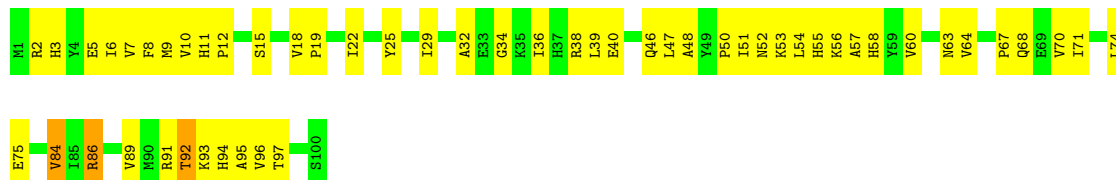
• Molecule 34: 30S ribosomal protein S5





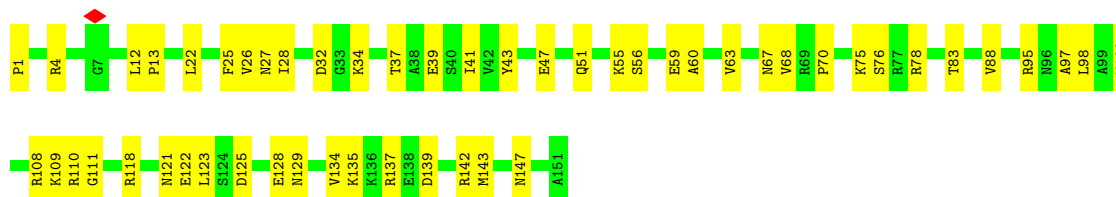
- Molecule 35: 30S ribosomal protein S6

Chain K: 47% 50% .



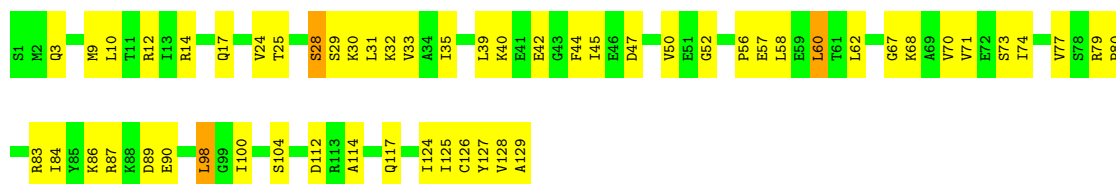
- Molecule 36: 30S ribosomal protein S7

Chain L: 66% 34% .



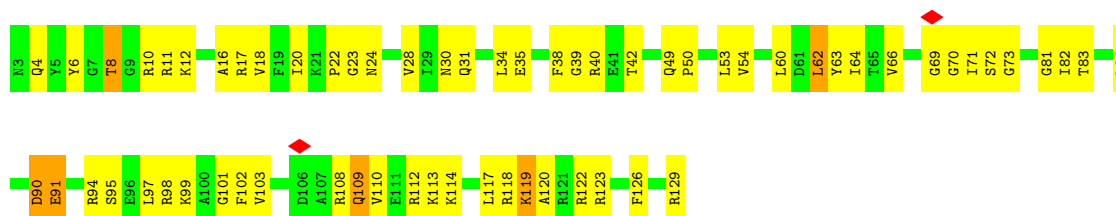
- Molecule 37: 30S ribosomal protein S8

Chain M: 57% 40% .

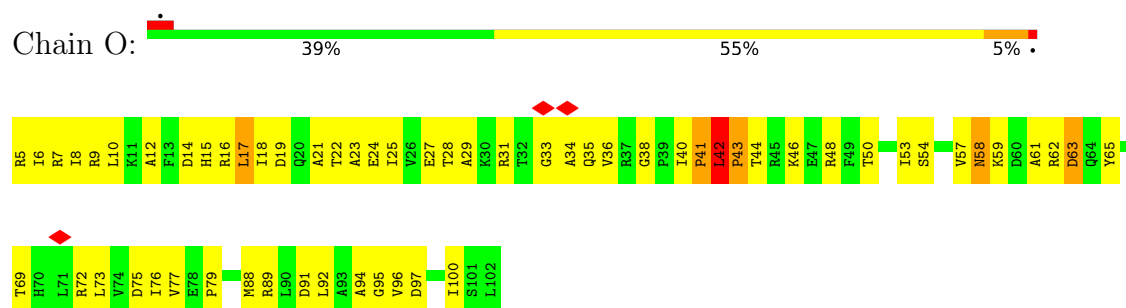


- Molecule 38: 30S ribosomal protein S9

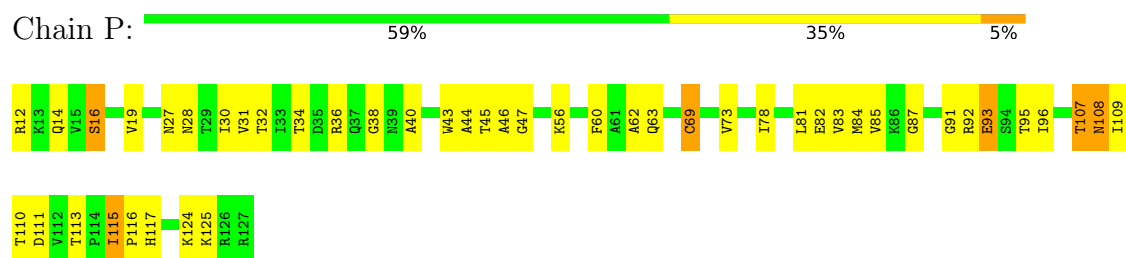
Chain N: 50% 46% 5% .



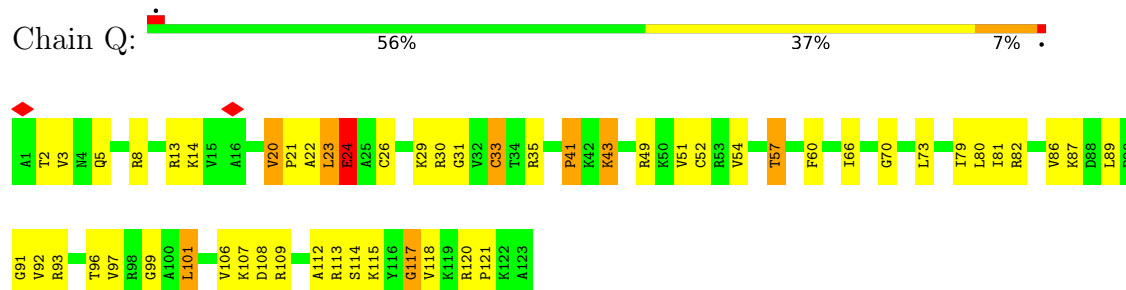
- Molecule 39: 30S ribosomal protein S10



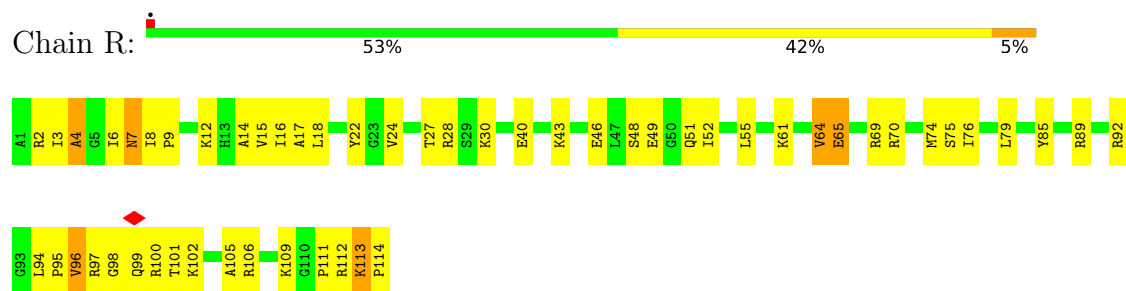
- Molecule 40: 30S ribosomal protein S11



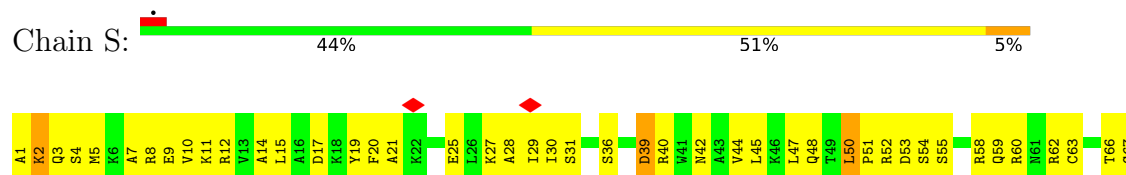
- Molecule 41: 30S ribosomal protein S12

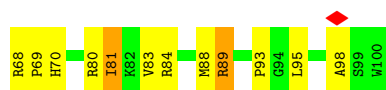


- Molecule 42: 30S ribosomal protein S13

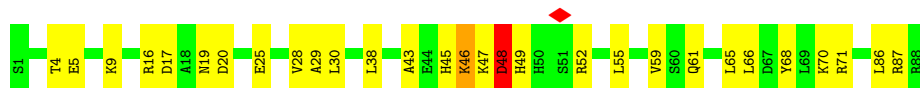


- Molecule 43: 30S ribosomal protein S14





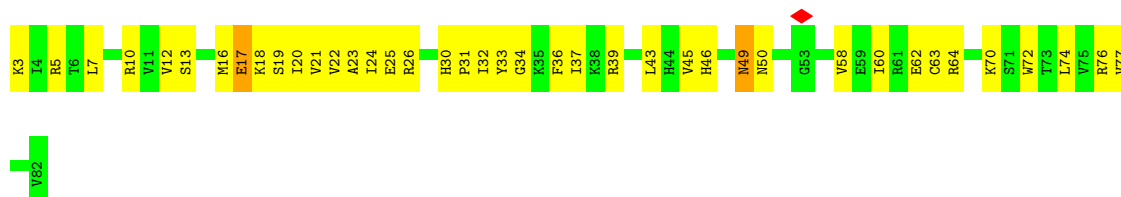
- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18

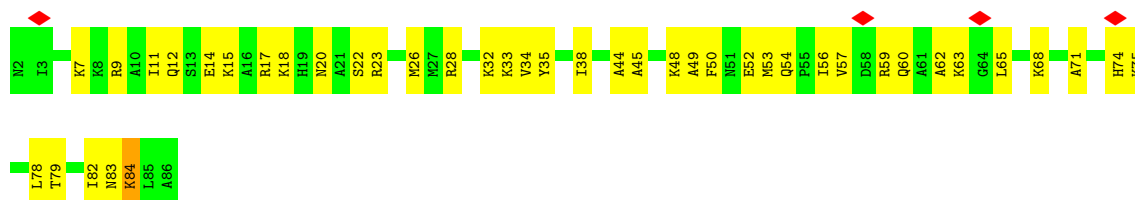


- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

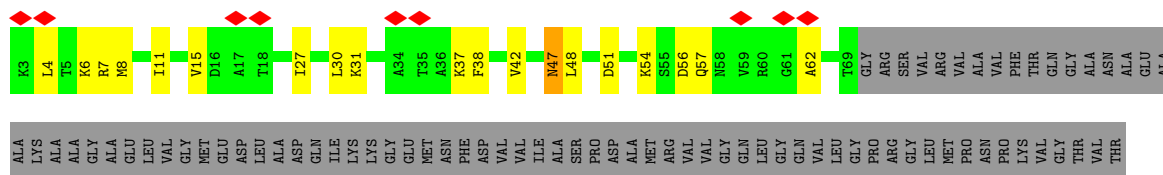




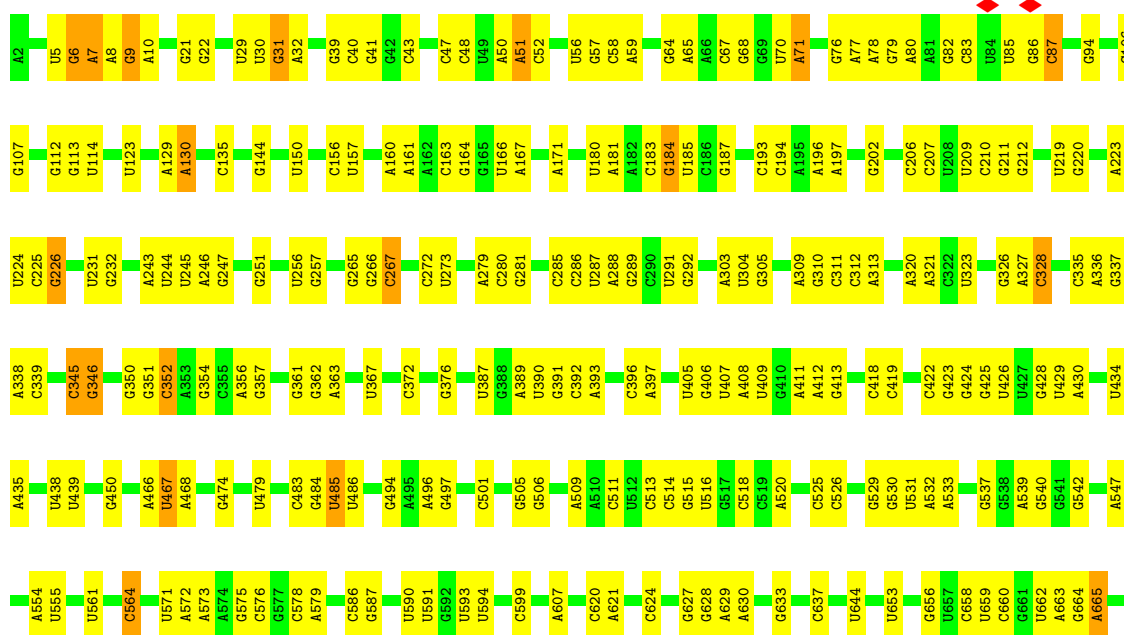
- Molecule 50: 30S ribosomal protein S21

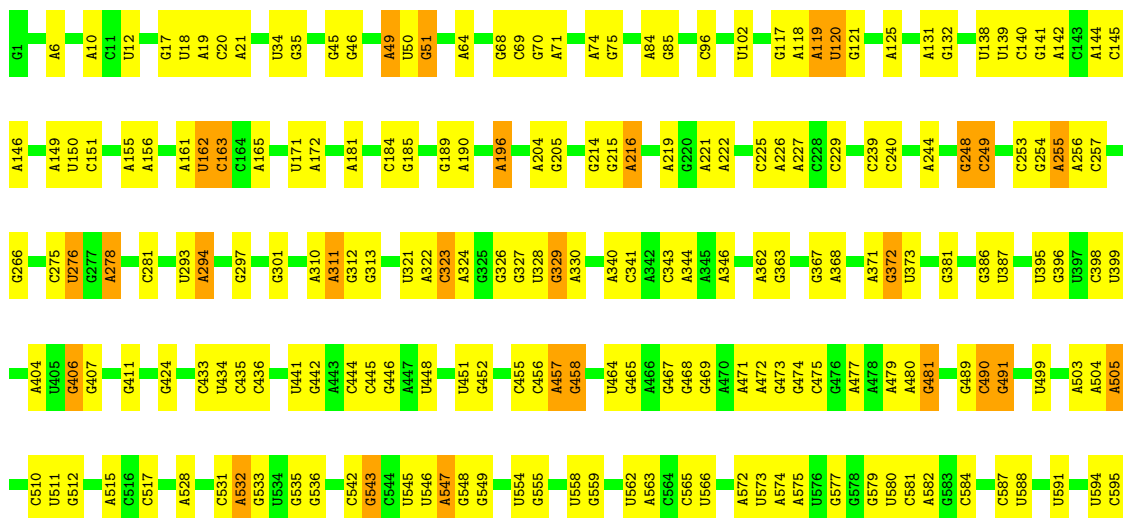
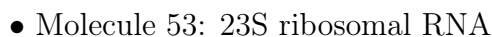


- Molecule 51: 50S ribosomal protein L1

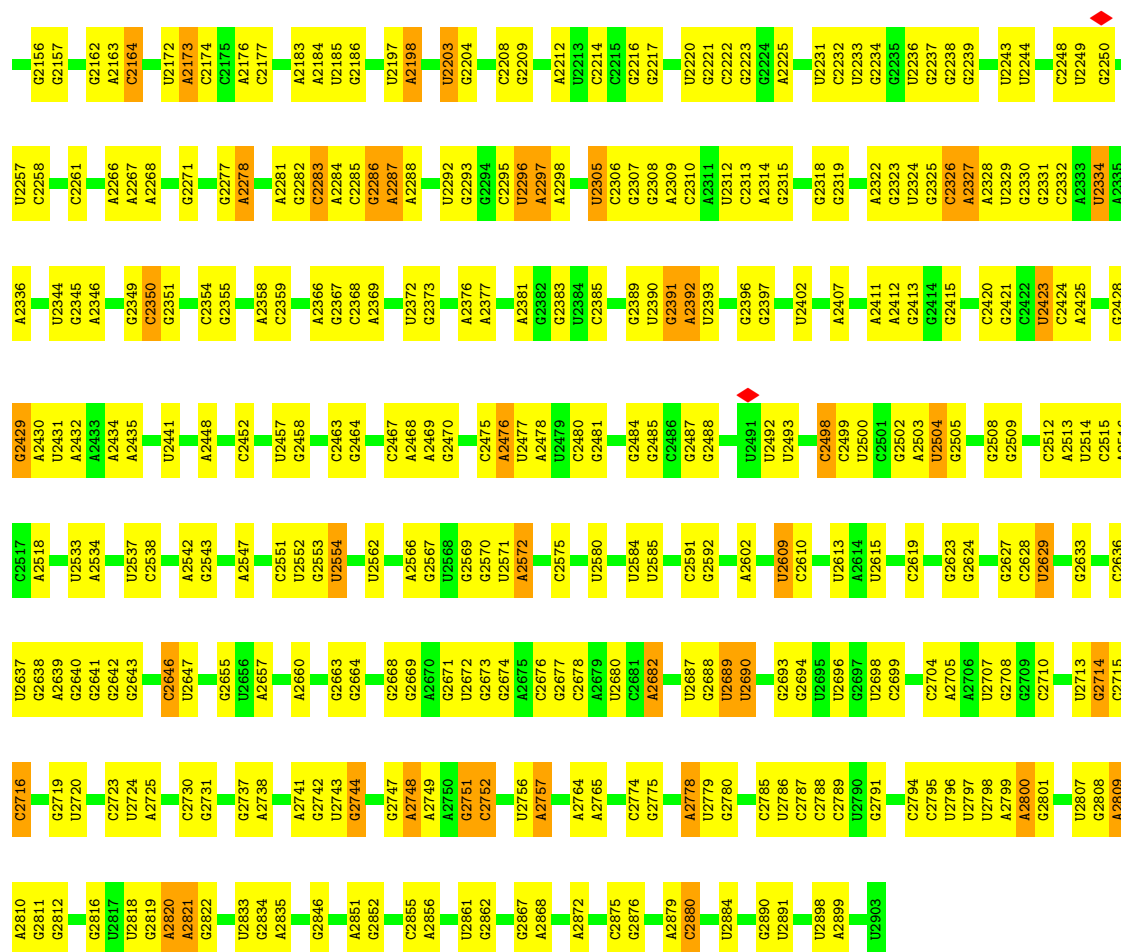


- Molecule 52: 16S ribosomal RNA



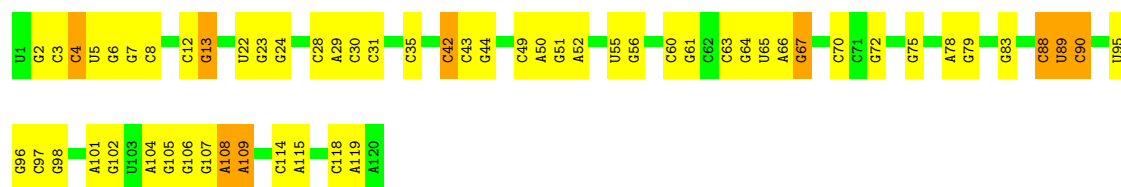


G2061	C1962	G1873	U1636	A1528	A1413	A1301	U1180	U1082	G994	U894	A781	U896
A2062	U1963	C1874	A1637	G1529	C1414	C1306	U1181	U1083	C995	U895	A782	G597
C2063	C1967	G1875	C1638	A1535	U1415	A1307	G1182	A1084	C996	A896	A783	G651
G2066	A1970	A1876	G1645	C1536	C1416	A1308	U1183	A1085	G997	A910	A784	A603
U2068	U1971	G1877	C1646	G1537	C1417	G1309	G1186	A1088	C1005	A911	A785	U606
G2069	G1972	A1878	U1647	G1538	A1418	U1313	G1187	A1089	C1006	C912	A792	U607
A2070	U1882	U1781	U1648	U1539	A1419	U1314	U1201	A1090	C1007	G913	A793	C611
C2071	U1883	U1782	G1651	G1540	A1420	U1315	G1202	G1093	U1012	C914	A796	G612
A2072	A1884	A1786	A1652	U1542	G1424	C1320	G1203	A1094	C1013	C915	A797	A613
C2073	A1885	A1787	G1653	G1543	G1425	A1322	A1205	A1095	G916	G916	A798	A614
A2082	U1888	U1790	U1662	G1547	G1430	C1323	G1212	A1098	A1019	A917	A799	U615
G2083	A1889	A1791	G1663	A1548	A1431	U1326	U1216	U1098	U1020	A918	A800	A616
U2086	A1890	A1792	A1664	A1549	A1432	C1327	G1217	C1104	A1021	C922	A801	G617
C2087	G1891	C1795	A1665	C1550	A1433	A1328	G1218	U1105	G1022	G923	A802	G618
A2088	C1892	G1796	G1666	C1551	A1434	U1329	U1224	G1106	U1023	G924	A803	G619
G2093	C1893	U1797	U1667	U1552	A1435	C1330	U1225	G1107	G1024	G925	A804	G620
C2094	C1894	U1798	G1668	U1553	G1436	C1331	U1226	G1108	G1025	G926	A805	A621
A2095	U1895	U1799	U1669	U1554	U1437	G1332	U1227	G1109	G1026	U927	A806	G622
C2096	A1896	U1800	A1670	G1555	A1438	C1333	U1228	G1110	A1027	C928	A807	A623
G2104	U1897	A1801	G1671	U1556	U1439	G1334	U1229	A1111	A1028	G929	A808	A624
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G2110	G1906	C1806	G1673	U1558	U1441	U1336	U1231	G1113	G1030	G931	A810	A626
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G2113	U1909	U1809	G1676	U1561	U1444	C1339	U1234	G1115	G1033	G934	A813	A629
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A2115	G1911	A1811	A1678	U1563	C1446	U1341	U1236	A1117	U1035	G936	A815	A631
C2116	U1912	U1812	G1679	C1564	C1447	U1342	U1237	G1118	U1036	G937	A816	A632
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G2118	C1914	G1814	U1681	U1566	U1449	U1344	U1239	G1120	U1038	G939	A818	A634
A2119	U1915	A1815	G1682	U1567	U1450	U1345	U1240	G1121	G1039	G940	A819	A635
C2120	G1916	U1816	U1683	U1568	U1451	U1346	U1241	A1122	G1040	G941	A820	A636
U2121	A1917	G1817	G1684	U1569	U1452	U1347	U1242	G1123	U1041	G942	A821	A637
G2122	U1918	A1818	U1685	U1570	U1453	U1348	U1243	A1124	G1042	G943	A822	A638
C2123	A1919	U1819	G1686	U1571	U1454	U1349	U1244	G1125	G1043	G944	A823	A639
U2124	C1920	G1820	U1687	U1572	U1455	U1350	U1245	G1126	G1044	G945	A824	A640
G2125	U1921	U1821	G1688	U1573	U1456	U1351	U1246	A1127	U1045	G946	A825	A641
A2126	G1922	A1822	U1689	U1574	U1457	U1352	U1247	G1128	U1046	G947	A826	A642
C2127	U1923	U1823	G1690	U1575	U1458	U1353	U1248	A1129	U1047	G948	A827	A643
U2128	A1924	G1824	U1691	U1576	U1459	U1354	U1249	G1130	G1048	G949	A828	A644
G2129	C1925	U1825	G1692	U1577	U1460	U1355	U1250	A1131	U1049	G950	A829	A645
U2130	U1926	A1826	U1693	U1578	U1461	U1356	U1251	G1132	U1050	G951	A830	A646
C2131	A1927	U1827	U1694	U1579	U1462	U1357	U1252	A1133	G1051	G952	A831	U647
U2132	U1928	G1828	G1695	U1580	U1463	U1358	U1253	G1134	U1052	G953	A832	U648
A2133	C1929	U1829	U1696	U1581	U1464	U1359	U1254	A1135	U1053	G954	A833	U649
G2134	U1930	A1830	U1697	U1582	U1465	U1360	U1255	G1136	U1054	G955	A834	U650
U2135	A1931	U1831	G1698	U1583	U1466	U1361	U1256	A1137	U1055	G956	A835	A651
G2136	C1932	G1832	U1699	U1584	U1467	U1362	U1257	G1138	U1056	G957	A836	A652
U2137	U1933	U1833	G1700	U1585	U1468	U1363	U1258	A1139	U1057	G958	A837	A653
C2138	A1934	A1834	U1701	U1586	U1469	U1364	U1259	G1140	U1058	G959	A838	A654
U2139	U1935	U1835	G1702	U1587	U1470	U1365	U1260	A1141	U1059	G960	A839	A655
G2140	C1936	G1836	U1703	U1588	U1471	U1366	U1261	G1142	U1060	G961	A840	A656
U2141	U1937	A1837	G1704	U1589	U1472	U1367	U1262	A1143	U1061	G962	A841	U657
C2142	A1938	U1838	U1705	U1590	U1473	U1368	U1263	G1144	U1062	G963	A842	U658
U2143	U1939	A1839	G1706	U1591	U1474	U1369	U1264	A1145	U1063	G964	A843	U659
G2144	C1940	G1840	U1707	U1592	U1475	U1370	U1265	G1146	U1064	G965	A844	U660
U2145	U1941	U1841	G1708	U1593	U1476	U1371	U1266	A1147	U1065	G966	A845	U661
C2146	A1942	A1842	U1709	U1594	U1477	U1372	U1267	G1148	U1066	G967	A846	U662
U2147	U1943	U1843	G1710	U1595	U1478	U1373	U1268	A1149	U1067	G968	A847	U663
G2148	C1944	G1844	U1711	U1596	U1479	U1374	U1269	G1150	U1068	G969	A848	U664
U2149	U1945	A1845	U1712	U1597	U1480	U1375	U1270	A1151	U1069	G970	A849	U665
C2150	C1946	U1846	G1713	U1598	U1481	U1376	U1271	G1152	U1070	G971	A850	U666
U2151	U1947	G1847	U1714	U1599	U1482	U1377	U1272	A1153	U1071	G972	A851	U667



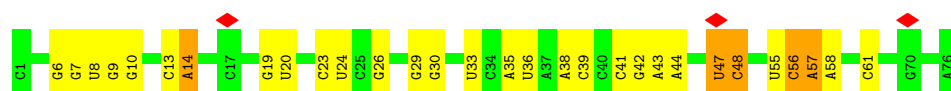
• Molecule 54: 5S ribosomal RNA

Chain 2: 52% 41% 8%



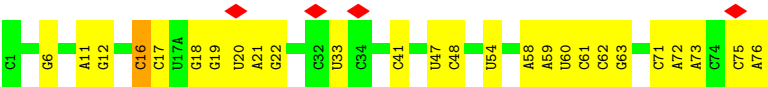
• Molecule 55: tRNAfMet

Chain 5: 61% 32% 6%

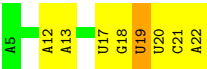


• Molecule 55: tRNAfMet

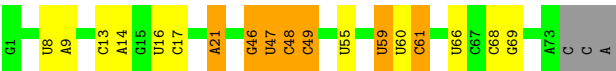
Chain 6: 5% 66% 32%



● Molecule 56: mRNA



● Molecule 57: tRNAPhe



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1707	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.917	Depositor
Minimum map value	-11.939	Depositor
Average map value	0.125	Depositor
Map value standard deviation	0.927	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.31	0/2122	0.99	14/2852 (0.5%)
2	c	0.30	0/1586	0.91	2/2134 (0.1%)
3	d	0.30	0/1571	0.96	7/2113 (0.3%)
4	e	0.31	0/1435	0.91	3/1926 (0.2%)
5	f	0.30	0/1343	0.92	3/1816 (0.2%)
6	g	0.31	0/1122	0.99	7/1515 (0.5%)
7	h	0.33	0/1002	1.00	4/1350 (0.3%)
8	i	0.34	0/1046	1.02	4/1410 (0.3%)
9	j	0.30	0/1152	1.00	7/1551 (0.5%)
10	k	0.30	0/948	1.00	4/1268 (0.3%)
11	l	0.30	0/1054	1.05	6/1403 (0.4%)
12	m	0.32	0/1093	0.96	4/1460 (0.3%)
13	n	0.32	0/974	1.06	8/1301 (0.6%)
14	o	0.29	0/902	0.99	5/1209 (0.4%)
15	p	0.30	0/929	0.89	4/1242 (0.3%)
16	q	0.29	0/960	1.00	6/1278 (0.5%)
17	r	0.29	0/829	0.97	5/1107 (0.5%)
18	s	0.27	0/864	0.93	3/1156 (0.3%)
19	t	0.30	0/745	0.89	2/994 (0.2%)
20	u	0.29	0/788	0.99	2/1051 (0.2%)
21	v	0.30	0/766	0.94	3/1025 (0.3%)
22	w	0.27	0/582	0.91	2/769 (0.3%)
23	x	0.29	0/635	0.96	2/848 (0.2%)
24	y	0.28	0/510	0.90	3/677 (0.4%)
25	z	0.29	0/453	0.89	1/605 (0.2%)
26	B	0.29	0/450	0.99	2/599 (0.3%)
27	C	0.34	0/417	0.99	4/554 (0.7%)
28	D	0.32	0/380	1.10	4/498 (0.8%)
29	E	0.29	0/513	0.96	0/676
30	F	0.31	0/303	1.04	2/397 (0.5%)
31	G	0.30	0/1788	1.00	12/2408 (0.5%)
32	H	0.31	0/1652	0.93	4/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.94	5/2227 (0.2%)
34	J	0.31	0/1170	1.02	8/1573 (0.5%)
35	K	0.31	0/836	0.98	2/1128 (0.2%)
36	L	0.29	0/1196	1.00	2/1602 (0.1%)
37	M	0.30	0/989	1.00	5/1326 (0.4%)
38	N	0.31	0/1034	0.87	0/1375
39	O	0.33	0/797	0.99	5/1077 (0.5%)
40	P	0.32	0/886	1.01	8/1195 (0.7%)
41	Q	0.32	0/969	1.16	10/1300 (0.8%)
42	R	0.31	0/893	0.94	1/1193 (0.1%)
43	S	0.31	0/817	0.96	6/1088 (0.6%)
44	T	0.29	0/722	0.92	2/964 (0.2%)
45	U	0.34	0/659	1.04	7/884 (0.8%)
46	V	0.31	0/658	0.90	1/881 (0.1%)
47	W	0.32	0/545	0.88	0/731
48	X	0.33	0/653	1.10	7/877 (0.8%)
49	Y	0.29	0/671	1.01	3/888 (0.3%)
50	Z	0.33	0/551	1.04	5/728 (0.7%)
51	a	0.30	0/1034	0.95	5/1387 (0.4%)
52	3	0.40	0/36963	0.51	4/57662 (0.0%)
53	1	0.40	0/69796	0.51	1/108888 (0.0%)
54	2	0.40	0/2872	0.51	0/4479
55	5	0.40	0/1832	0.50	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.39	0/1740	0.49	0/2712
All	All	0.37	0/163130	0.66	226/243971 (0.1%)

There are no bond length outliers.

The worst 5 of 226 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	n	116	VAL	N-CA-C	11.17	118.17	106.21
41	Q	20	VAL	N-CA-C	10.90	119.78	107.89
28	D	4	THR	N-CA-C	10.23	124.39	112.93
51	a	31	LYS	N-CA-C	-9.92	101.18	113.28
1	b	87	SER	N-CA-C	-9.30	102.06	113.50

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	b	2083	0	2157	100	0
2	c	1565	0	1616	71	0
3	d	1552	0	1619	49	0
4	e	1411	0	1447	71	0
5	f	1323	0	1374	53	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	53	0
8	i	1032	0	1088	48	0
9	j	1129	0	1162	50	0
10	k	939	0	1012	42	0
11	l	1045	0	1117	49	0
12	m	1074	0	1157	53	0
13	n	961	0	1000	44	0
14	o	892	0	923	38	0
15	p	917	0	965	39	0
16	q	947	0	1022	28	0
17	r	816	0	839	22	0
18	s	857	0	922	39	0
19	t	739	0	807	44	0
20	u	780	0	834	19	0
21	v	753	0	780	29	0
22	w	575	0	592	31	0
23	x	625	0	655	23	0
24	y	509	0	543	18	0
25	z	449	0	491	13	0
26	B	444	0	461	14	0
27	C	410	0	440	15	0
28	D	377	0	418	16	0
29	E	504	0	574	20	0
30	F	302	0	343	23	0
31	G	1757	0	1787	71	0
32	H	1625	0	1699	65	0
33	I	1643	0	1710	75	0
34	J	1157	0	1199	45	0
35	K	818	0	808	43	0
36	L	1182	0	1240	32	0
37	M	979	0	1034	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	60	0
39	O	787	0	828	42	0
40	P	870	0	878	39	0
41	Q	955	0	1019	50	0
42	R	884	0	944	55	0
43	S	805	0	847	55	0
44	T	714	0	737	23	0
45	U	649	0	666	27	0
46	V	649	0	691	35	0
47	W	536	0	552	23	0
48	X	638	0	665	31	0
49	Y	665	0	714	41	0
50	Z	545	0	579	36	0
51	a	1027	0	1092	31	0
52	3	33012	0	16618	492	0
53	1	62317	0	31346	835	0
54	2	2568	0	1303	66	0
55	5	1640	0	836	22	0
55	6	1640	0	837	17	0
56	4	388	0	196	6	0
57	7	1557	0	789	12	0
58	5	10	0	10	1	0
All	All	150149	0	101225	2989	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 12.

The worst 5 of 2989 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.32	1.12
8:i:25:PRO:HB2	53:1:1095:A:H61	1.17	1.04
55:5:13:C:H2'	55:5:14:A:H5''	1.40	1.02
19:t:2:ILE:HD11	53:1:144:A:H4'	1.39	1.00
43:S:60:ARG:HH21	52:3:981:U:H1'	1.27	0.97

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	224 (83%)	36 (13%)	9 (3%)	3	21
2	c	207/209 (99%)	174 (84%)	33 (16%)	0	100	100
3	d	199/201 (99%)	171 (86%)	26 (13%)	2 (1%)	12	47
4	e	175/177 (99%)	150 (86%)	22 (13%)	3 (2%)	7	35
5	f	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	11	45
6	g	147/149 (99%)	124 (84%)	20 (14%)	3 (2%)	6	32
7	h	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	19
8	i	139/141 (99%)	125 (90%)	11 (8%)	3 (2%)	5	29
9	j	140/142 (99%)	121 (86%)	15 (11%)	4 (3%)	3	24
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	21
11	l	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	18	54
12	m	134/136 (98%)	114 (85%)	17 (13%)	3 (2%)	5	29
13	n	118/120 (98%)	103 (87%)	14 (12%)	1 (1%)	16	52
14	o	114/116 (98%)	102 (90%)	8 (7%)	4 (4%)	3	21
15	p	112/114 (98%)	89 (80%)	22 (20%)	1 (1%)	14	49
16	q	115/117 (98%)	103 (90%)	10 (9%)	2 (2%)	7	35
17	r	101/103 (98%)	80 (79%)	20 (20%)	1 (1%)	12	47
18	s	108/110 (98%)	91 (84%)	15 (14%)	2 (2%)	6	32
19	t	91/93 (98%)	75 (82%)	16 (18%)	0	100	100
20	u	100/102 (98%)	82 (82%)	17 (17%)	1 (1%)	12	47
21	v	92/94 (98%)	77 (84%)	13 (14%)	2 (2%)	5	29
22	w	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
23	x	75/77 (97%)	67 (89%)	6 (8%)	2 (3%)	4	26
24	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	37
25	z	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	34 (77%)	10 (23%)	0	100	100
29	E	62/64 (97%)	50 (81%)	7 (11%)	5 (8%)	1	9
30	F	36/38 (95%)	26 (72%)	9 (25%)	1 (3%)	4	25
31	G	223/225 (99%)	207 (93%)	15 (7%)	1 (0%)	30	66
32	H	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	24	62
33	I	203/205 (99%)	174 (86%)	27 (13%)	2 (1%)	12	47
34	J	155/157 (99%)	126 (81%)	24 (16%)	5 (3%)	3	22
35	K	98/100 (98%)	77 (79%)	16 (16%)	5 (5%)	1	16
36	L	149/151 (99%)	123 (83%)	24 (16%)	2 (1%)	9	41
37	M	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	4	28
38	N	125/127 (98%)	101 (81%)	17 (14%)	7 (6%)	1	15
39	O	96/98 (98%)	70 (73%)	18 (19%)	8 (8%)	0	9
40	P	114/116 (98%)	91 (80%)	20 (18%)	3 (3%)	4	26
41	Q	121/123 (98%)	91 (75%)	23 (19%)	7 (6%)	1	14
42	R	112/114 (98%)	96 (86%)	12 (11%)	4 (4%)	2	21
43	S	98/100 (98%)	81 (83%)	16 (16%)	1 (1%)	12	47
44	T	86/88 (98%)	74 (86%)	10 (12%)	2 (2%)	5	29
45	U	80/82 (98%)	64 (80%)	14 (18%)	2 (2%)	4	27
46	V	78/80 (98%)	63 (81%)	13 (17%)	2 (3%)	4	26
47	W	63/65 (97%)	55 (87%)	6 (10%)	2 (3%)	3	22
48	X	77/79 (98%)	64 (83%)	12 (16%)	1 (1%)	9	41
49	Y	83/85 (98%)	75 (90%)	8 (10%)	0	100	100
50	Z	63/65 (97%)	42 (67%)	17 (27%)	4 (6%)	1	13
51	a	130/223 (58%)	122 (94%)	8 (6%)	0	100	100
All	All	5919/6112 (97%)	5009 (85%)	785 (13%)	125 (2%)	8	30

5 of 125 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	107	LYS
1	b	131	MET

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Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
7	h	81	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	80
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	73
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	78
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/100 (100%)	96 (96%)	4 (4%)	28	49
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	67
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	66
11	l	102/102 (100%)	99 (97%)	3 (3%)	37	58
12	m	109/109 (100%)	107 (98%)	2 (2%)	51	66
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	82 (98%)	2 (2%)	43	63
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	66
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	66
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	65
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	80
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	67
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	77
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	102 (98%)	2 (2%)	50	66
38	N	105/105 (100%)	101 (96%)	4 (4%)	29	51
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	73
43	S	83/83 (100%)	81 (98%)	2 (2%)	43	63
44	T	76/76 (100%)	75 (99%)	1 (1%)	61	71
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	70
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	108 (98%)	2 (2%)	51	66
All	All	4908/4972 (99%)	4852 (99%)	56 (1%)	63	73

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	w	17	LEU
51	a	47	ASN
33	I	168	THR
51	a	4	LEU
43	S	50	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
44	T	39	GLN
45	U	29	ASN
13	n	107	ASN
13	n	73	ASN
47	W	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	2 (0%)
53	1	2902/2903 (99%)	323 (11%)	9 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	10 (13%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	72/76 (94%)	13 (18%)	0
All	All	4800/4810 (99%)	508 (10%)	12 (0%)

5 of 508 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	31	G
52	3	32	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2286	G
53	1	2296	U
54	2	88	C
53	1	2326	C
53	1	859	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
58	FME	5	101	55	8,9,10	0.50	0	8,9,11	1.05	1 (12%)

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	FME	5	101	55	-	0/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
58	5	101	FME	O-C-CA	-2.00	119.62	124.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	5	101	FME	1	0

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.

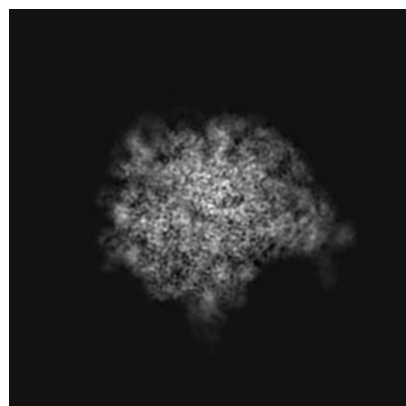
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21631. These allow visual inspection of the internal detail of the map and identification of artifacts.

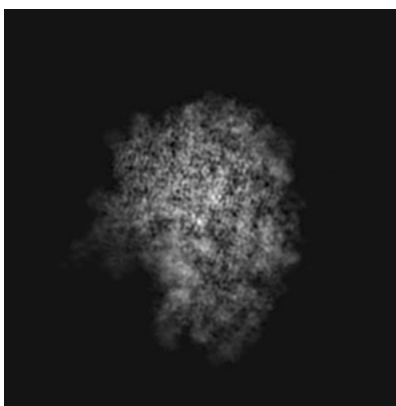
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

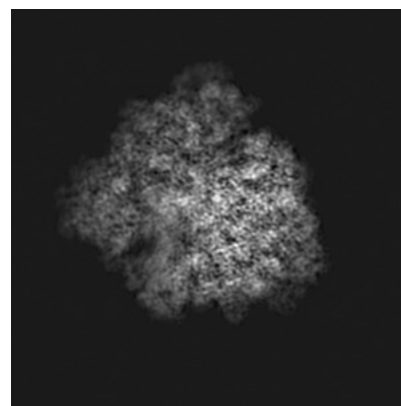
6.1.1 Primary map



X

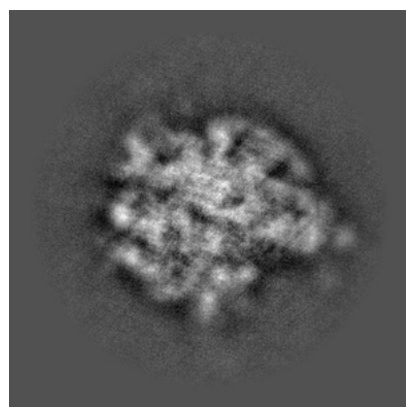


Y

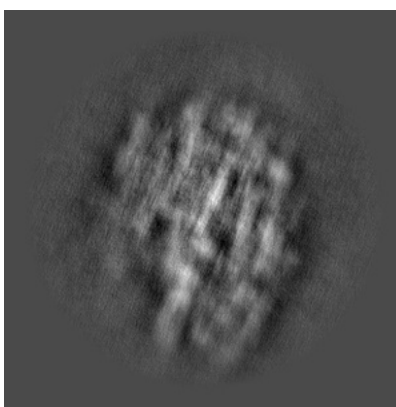


Z

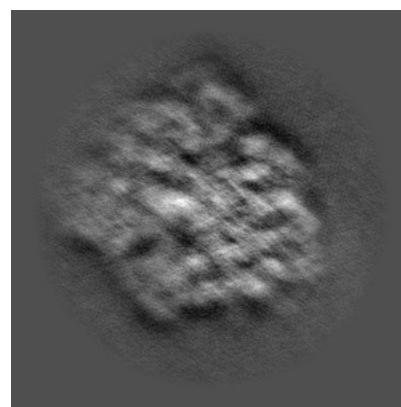
6.1.2 Raw map



X



Y

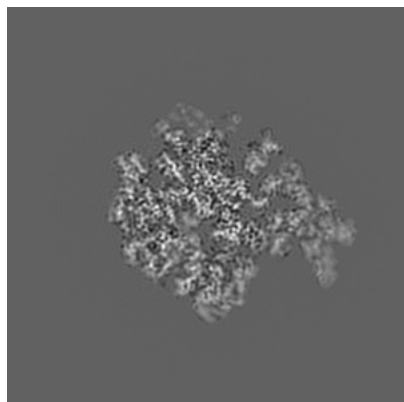


Z

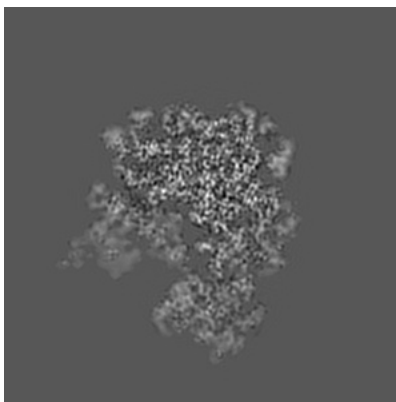
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

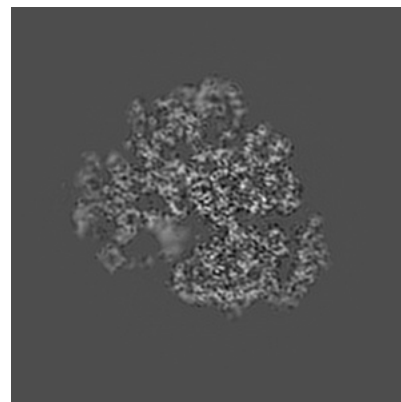
6.2.1 Primary map



X Index: 144

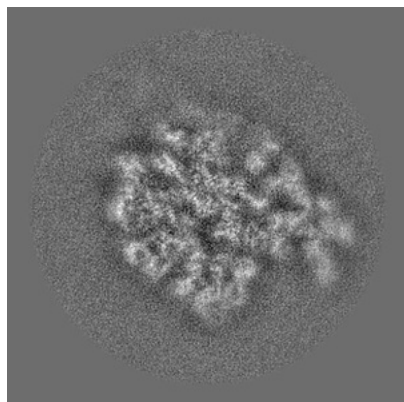


Y Index: 144

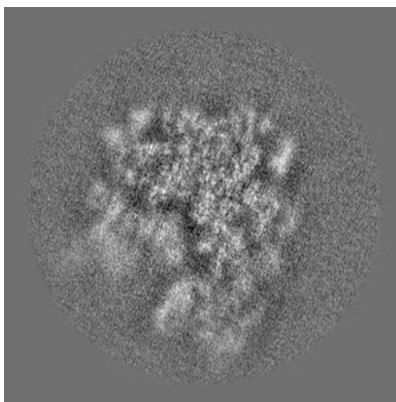


Z Index: 144

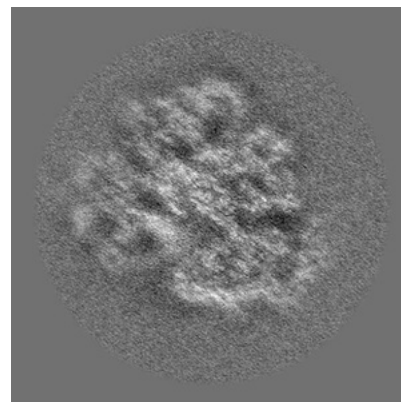
6.2.2 Raw map



X Index: 144



Y Index: 144

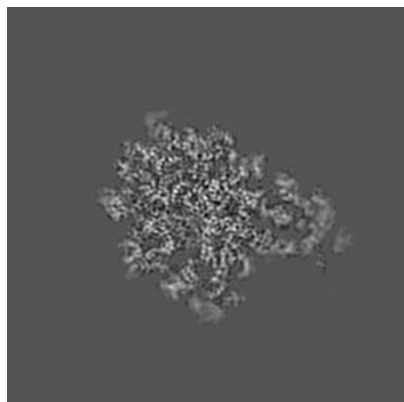


Z Index: 144

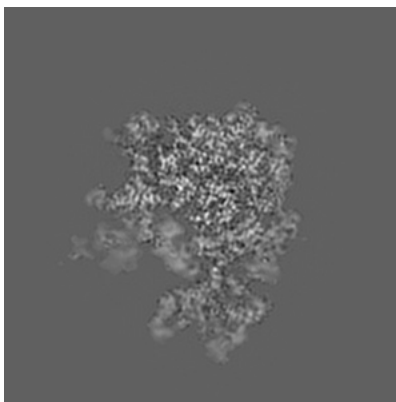
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

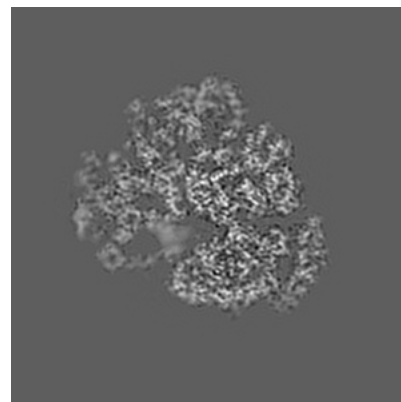
6.3.1 Primary map



X Index: 153

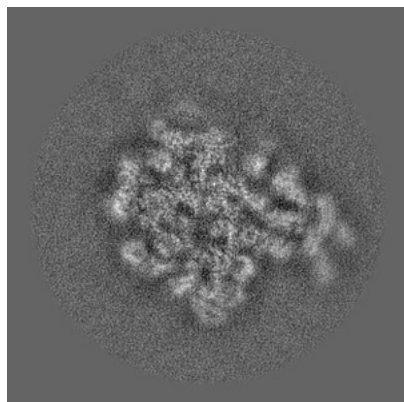


Y Index: 150

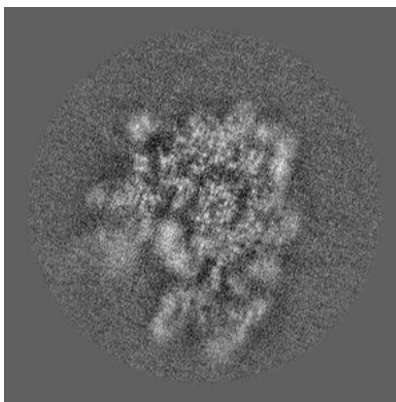


Z Index: 143

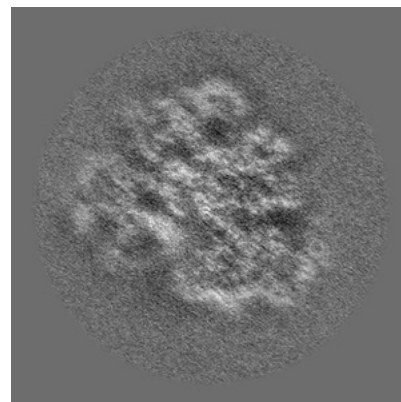
6.3.2 Raw map



X Index: 148



Y Index: 150

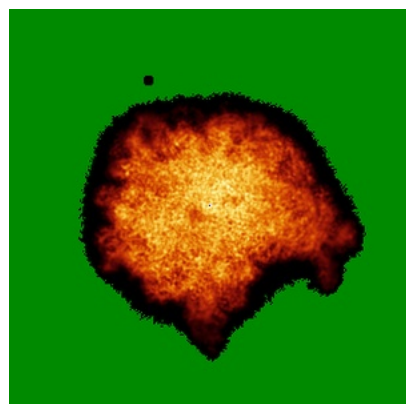


Z Index: 145

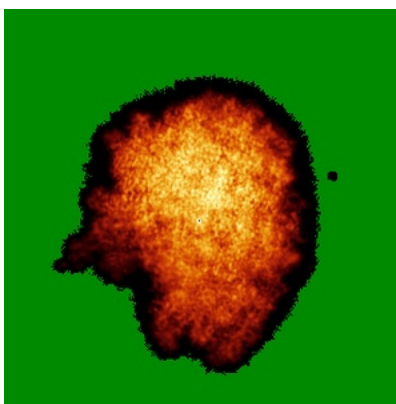
The images above show the largest variance slices of the map in three orthogonal directions.

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

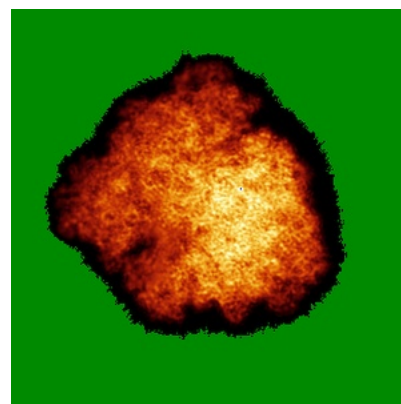
6.4.1 Primary map



X

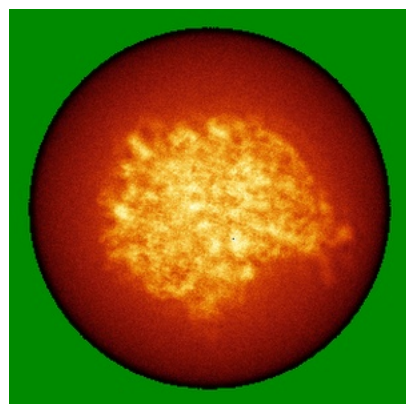


Y

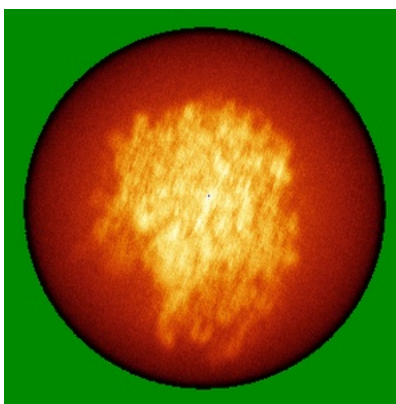


Z

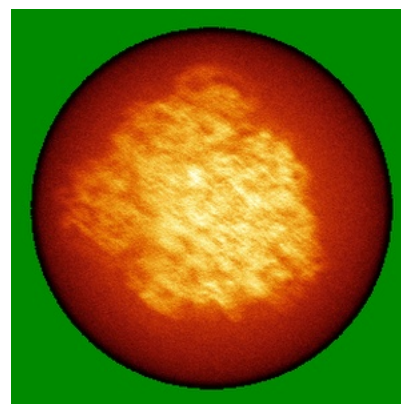
6.4.2 Raw map



X



Y

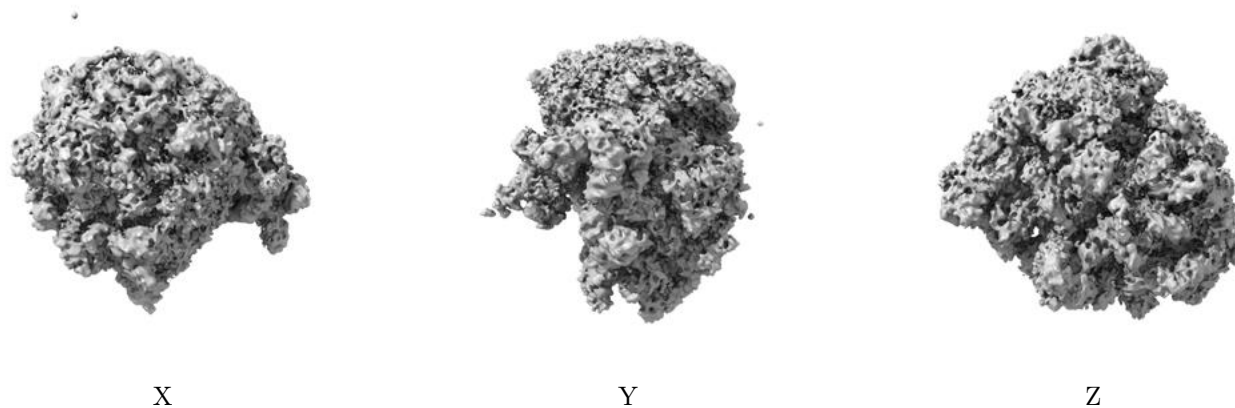


Z

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.

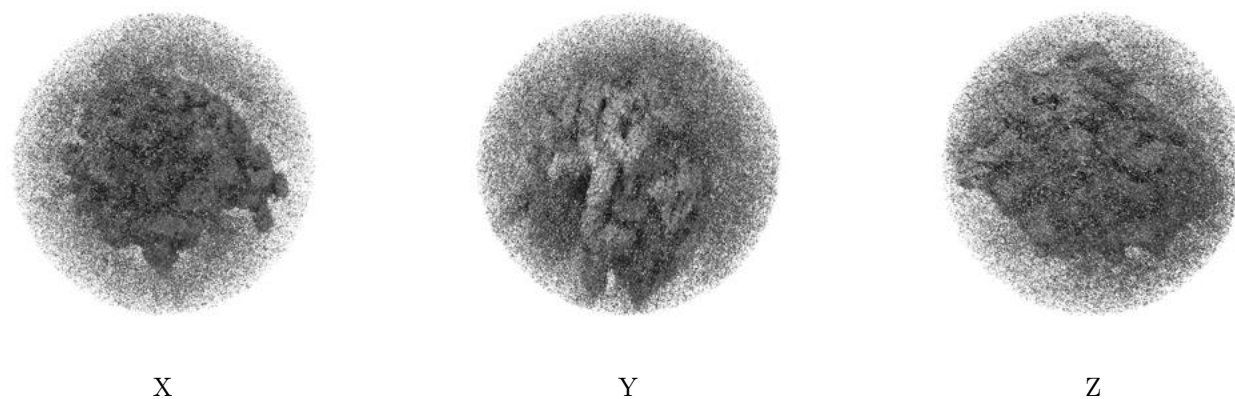
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

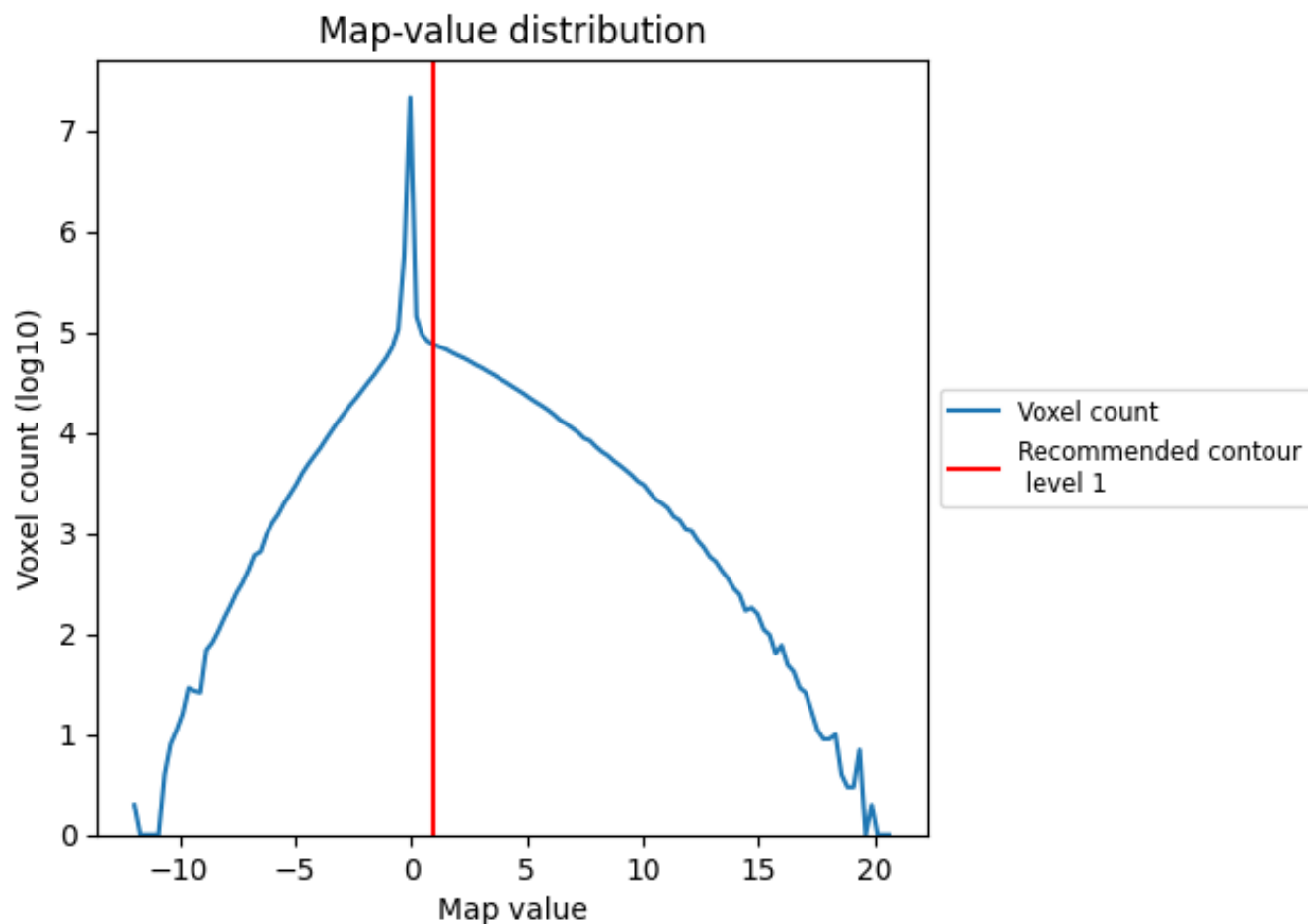
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

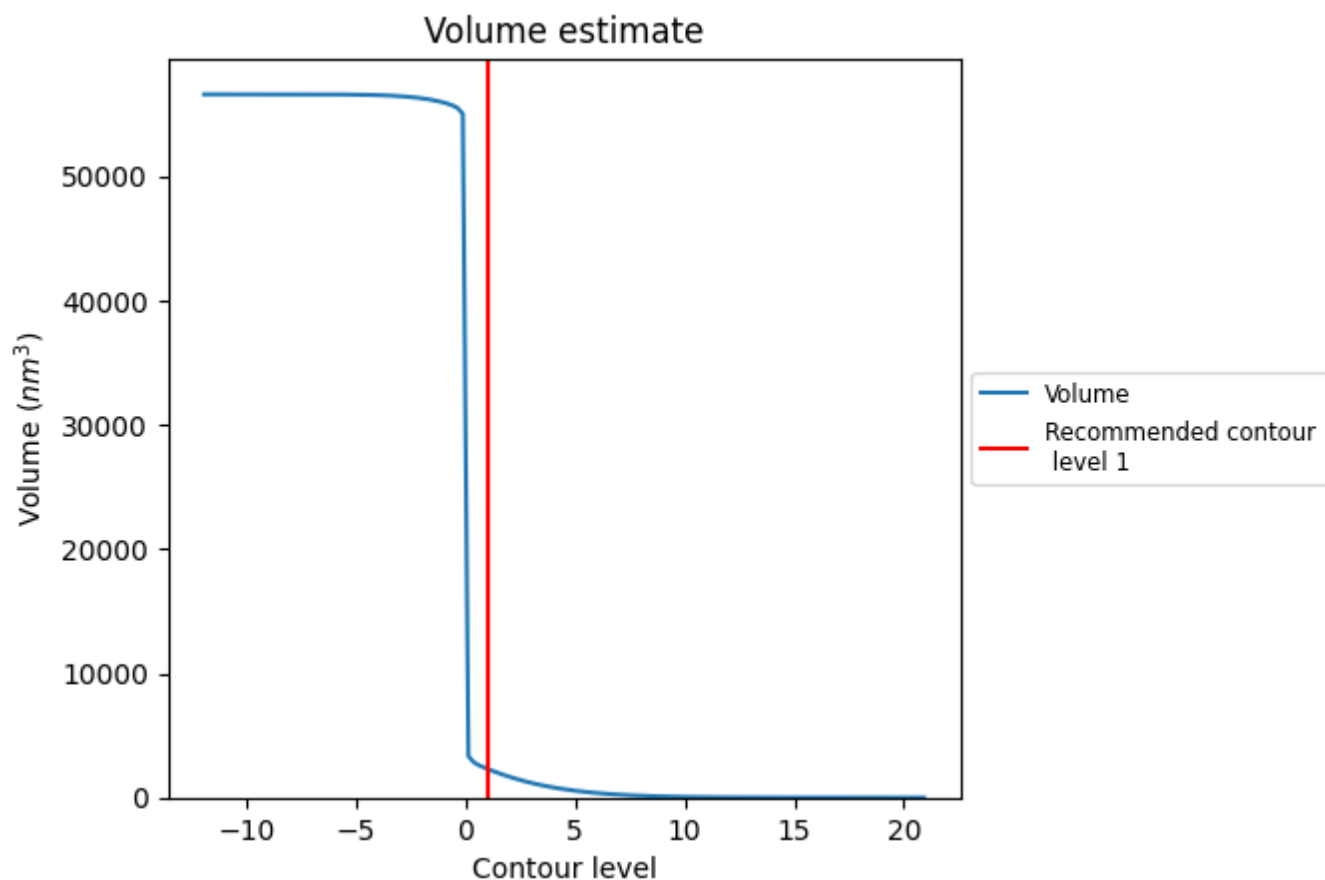
This section contains the results of statistical analysis of the map.

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.

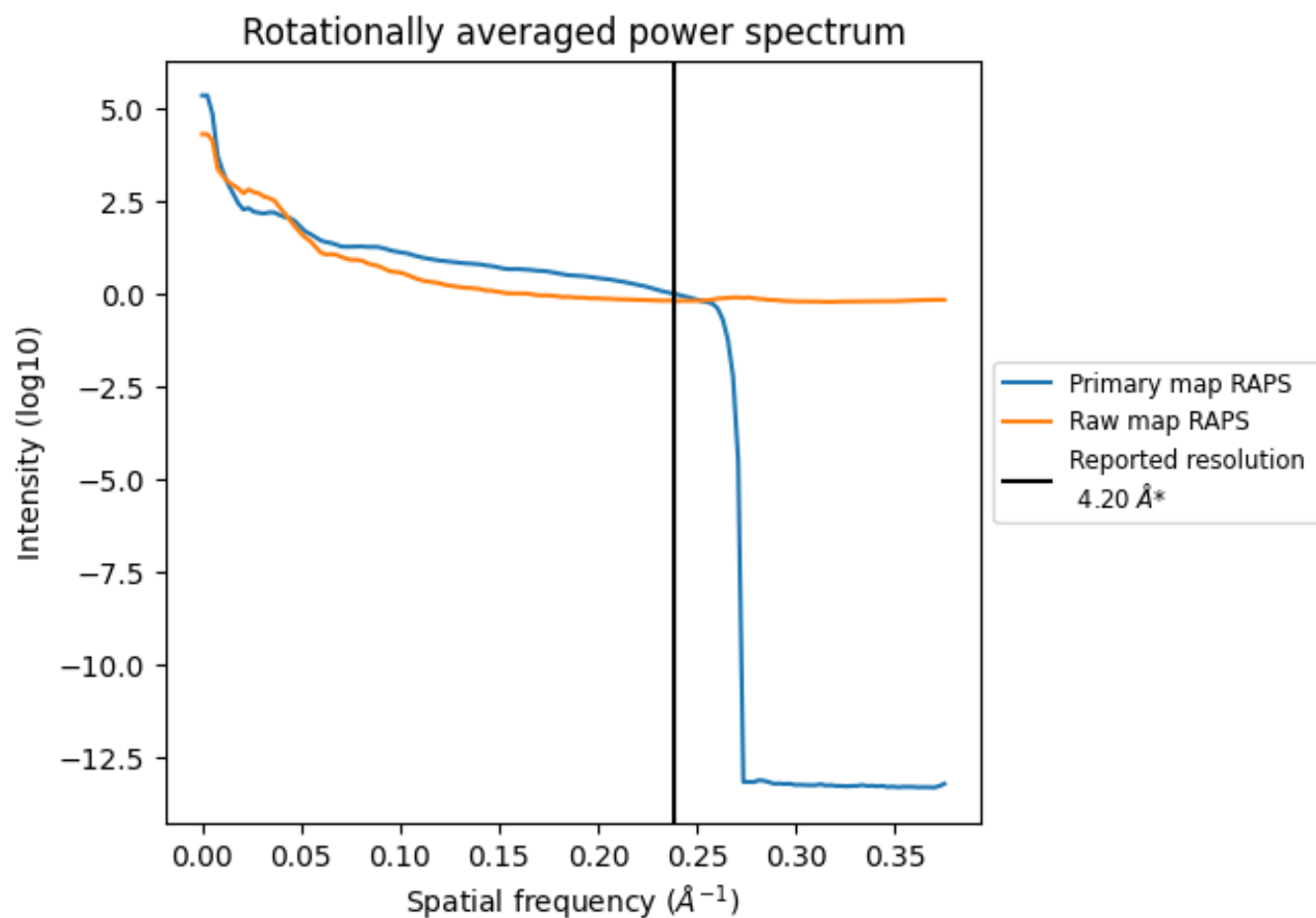
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2300 nm^3 ; this corresponds to an approximate mass of 2077 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 ⓘ

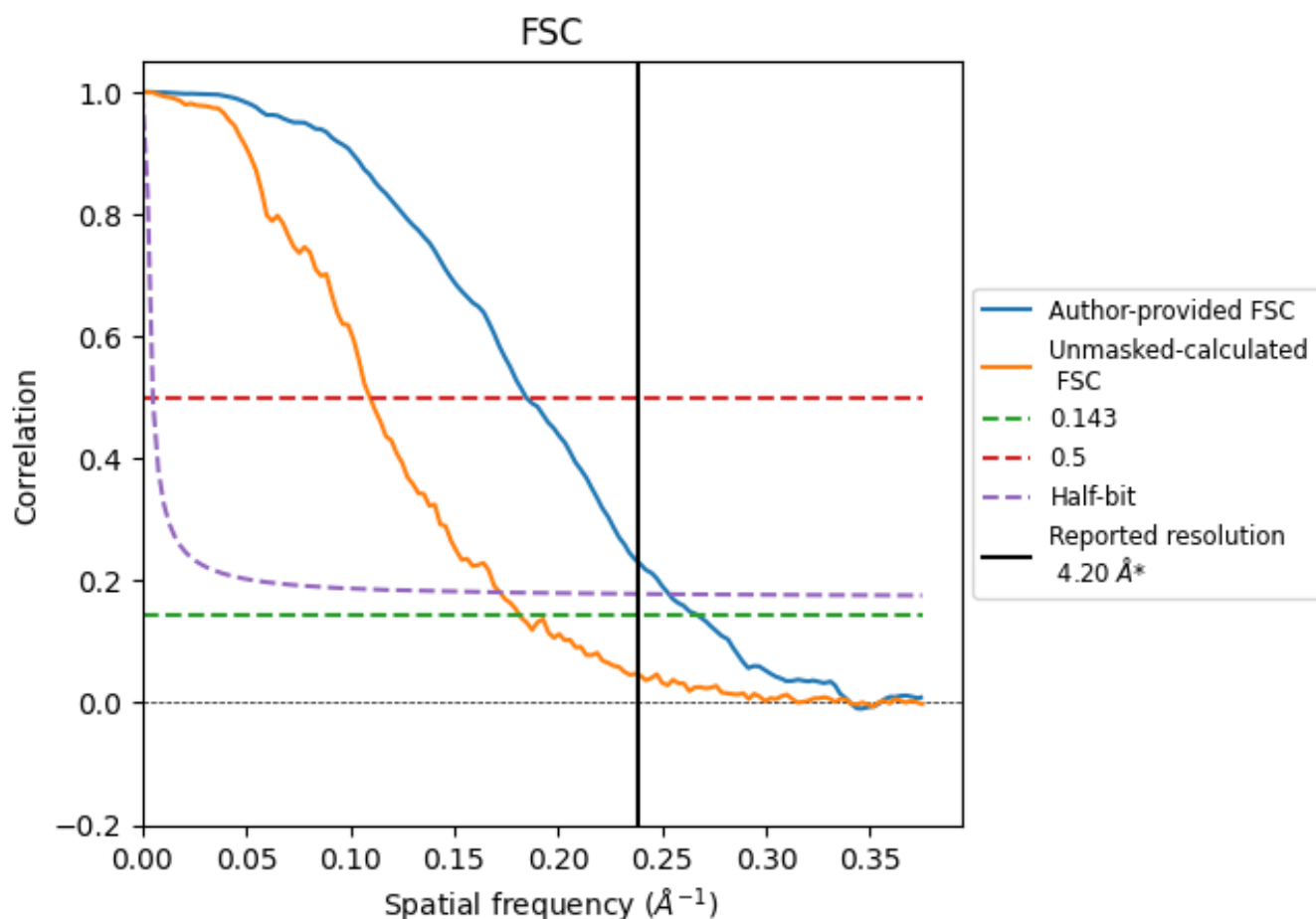


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

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 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	3.74	5.42	3.95
Unmasked-calculated*	5.51	9.13	5.81

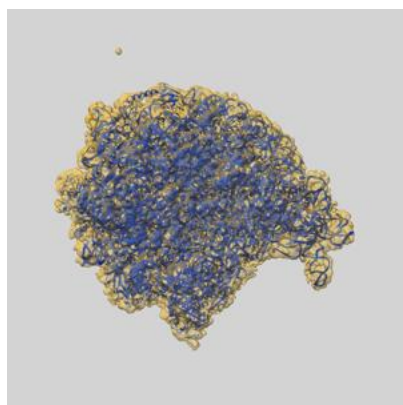
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 4.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.51 differs from the reported value 4.2 by more than 10 %

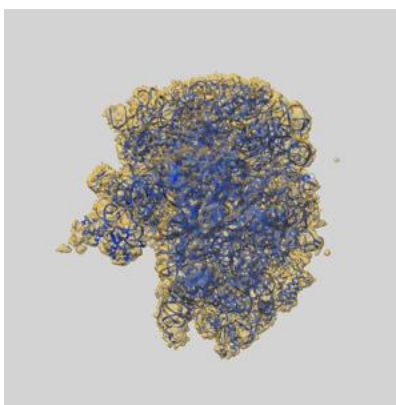
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21631 and PDB model 6WDC. Per-residue inclusion information can be found in section [3](#) on page [15](#).

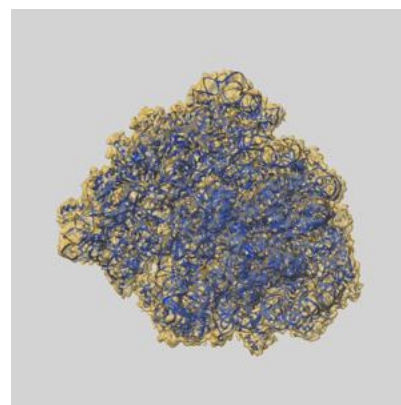
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0 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](#)

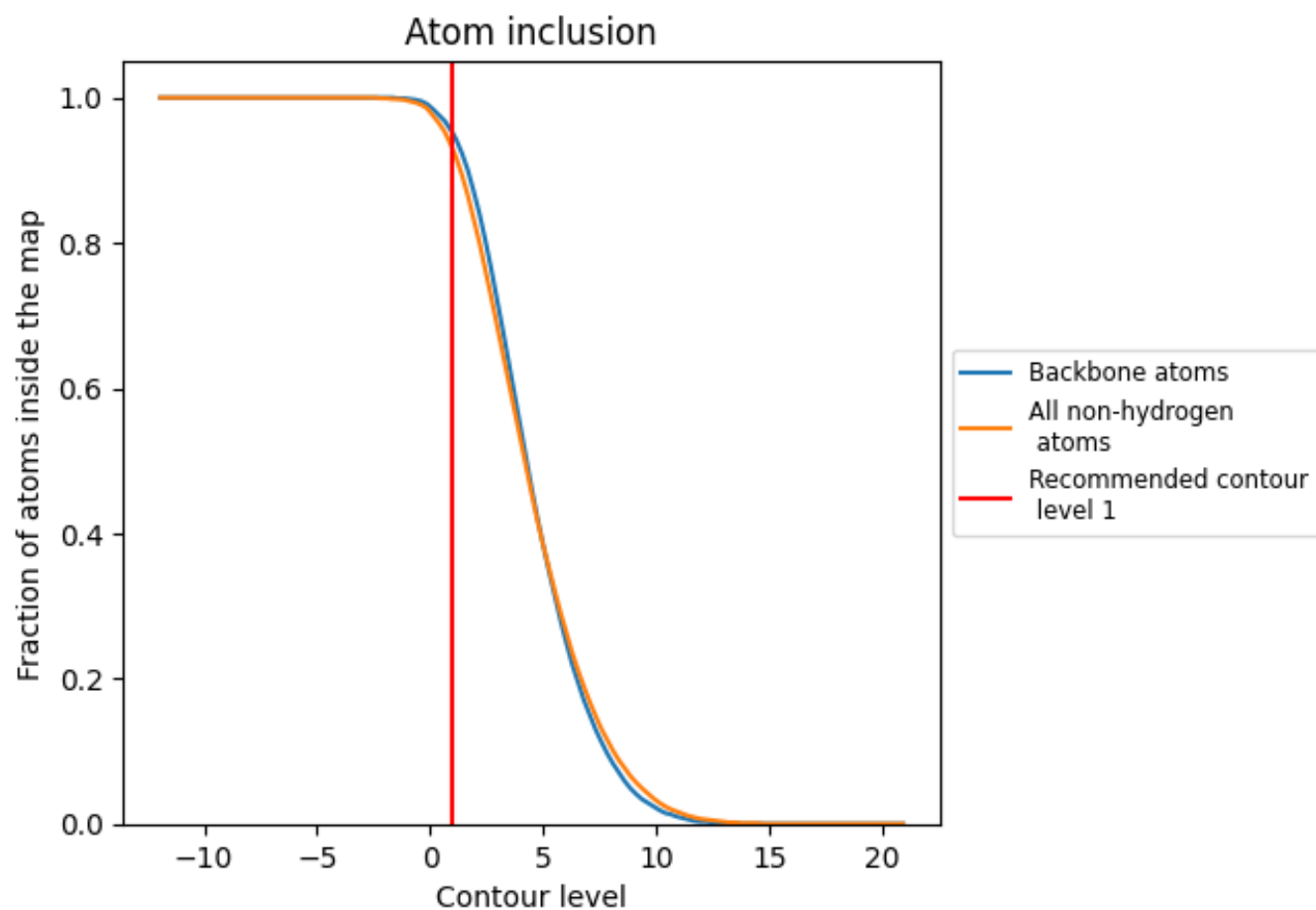


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.2880
1	 0.9590	 0.3110
2	 0.9580	 0.2350
3	 0.9500	 0.2550
4	 0.9120	 0.2280
5	 0.8150	 0.1090
6	 0.7950	 0.1030
7	 0.8630	 0.1290
B	 0.8990	 0.3780
C	 0.6970	 0.2550
D	 0.9320	 0.4350
E	 0.9330	 0.4230
F	 0.8870	 0.3390
G	 0.8740	 0.2710
H	 0.8700	 0.2710
I	 0.8380	 0.2340
J	 0.9000	 0.3300
K	 0.9550	 0.2910
L	 0.9070	 0.2490
M	 0.9110	 0.3210
N	 0.8880	 0.2430
O	 0.8440	 0.2440
P	 0.9430	 0.3120
Q	 0.9140	 0.3400
R	 0.9080	 0.2370
S	 0.8510	 0.2620
T	 0.9460	 0.3070
U	 0.8820	 0.2750
V	 0.9340	 0.2890
W	 0.8830	 0.2620
X	 0.9200	 0.2390
Y	 0.8490	 0.2400
Z	 0.8730	 0.2710
a	 0.8180	 0.1550
b	 0.9370	 0.4110



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Chain	Atom inclusion	Q-score
c	 0.9400	 0.3970
d	 0.9180	 0.3440
e	 0.9240	 0.1990
f	 0.9410	 0.2530
g	 0.6250	 0.2100
h	 0.6030	 0.0930
i	 0.5900	 0.1090
j	 0.9460	 0.3960
k	 0.9340	 0.3970
l	 0.9300	 0.3550
m	 0.6530	 0.2910
n	 0.9210	 0.3930
o	 0.9270	 0.2960
p	 0.9400	 0.3570
q	 0.9370	 0.3900
r	 0.9490	 0.3650
s	 0.9270	 0.3790
t	 0.9310	 0.3680
u	 0.9400	 0.3310
v	 0.9050	 0.2830
w	 0.9430	 0.4090
x	 0.9420	 0.3800
y	 0.9520	 0.3090
z	 0.9500	 0.3710