



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:59 AM UTC

PDB ID : 9FY3 / pdb_00009fy3
EMDB ID : EMD-50858
Title : Structure of CliM-stalled Bacillus subtilis 70S ribosome with tRNA-Tyr in the A-site
Authors : Gersteuer, F.; Wilson, D.N.
Deposited on : 2024-07-02
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

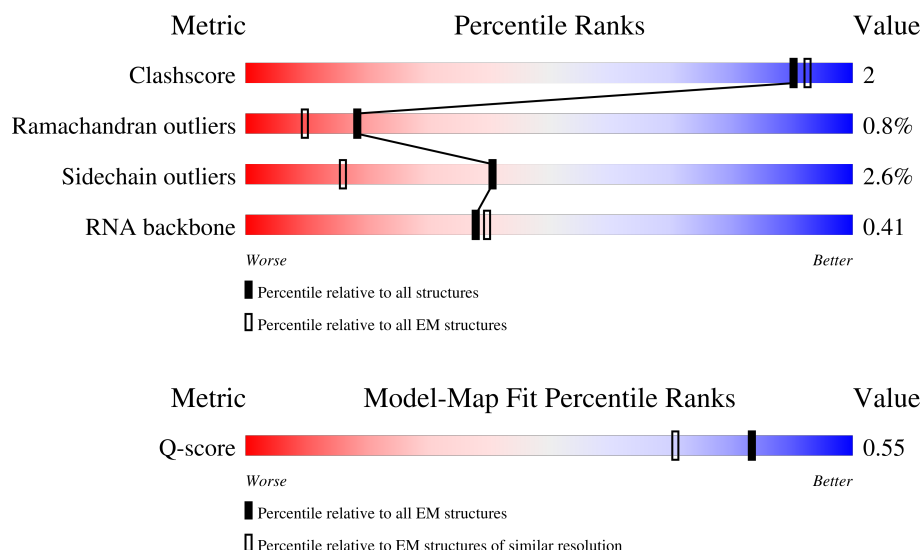
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 Å.

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





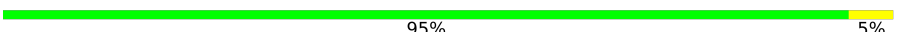





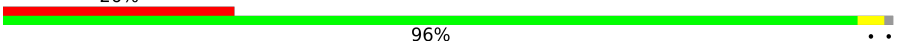













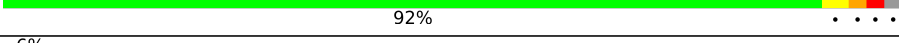
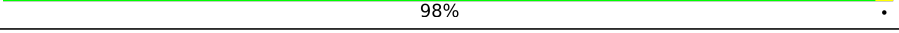

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	0	59	
2	1	49	
3	2	44	

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Mol	Chain	Length	Quality of chain
4	3	66	 88% 9% .
5	4	37	 89% 11%
6	5	38	 95% 5%
7	6	66	 50% 64% 6% 30%
8	B	112	 66% 29% .
9	C	277	 84% 13% ..
10	D	209	 82% 17% .
11	E	207	 5% 89% 11%
12	F	179	 26% 96% . .
13	G	179	 25% 92% 6% .
14	J	145	 83% 14% ..
15	K	122	 85% 13% .
16	L	146	 93% 7%
17	M	144	 89% 5% 6%
18	N	120	 84% 14% ..
19	O	120	 13% 87% 12% .
20	P	115	 5% 90% 8% ..
21	Q	119	 86% 12% ..
22	R	102	 5% 91% 8% .
23	S	113	 81% 15% . .
24	T	95	 91% 5% .
25	U	103	 8% 89% 9% ..
26	X	62	 13% 92%
27	Y	66	 6% 98% .
28	Z	59	 92% 7% .

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Mol	Chain	Length	Quality of chain
29	c	218	
30	e	166	
31	f	95	
32	g	156	
33	h	132	
34	i	130	
35	j	102	
36	k	131	
37	l	138	
38	m	121	
39	n	61	
40	o	89	
41	p	90	
42	q	87	
43	r	79	
44	t	88	
45	v	76	
46	A	2928	
47	b	246	
48	s	92	
49	7	9	
50	9	85	
51	a	1554	
52	W	94	
53	d	200	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 139157 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 Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	54	Total	C	N	O	S	0	0
			425	262	86	71	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	11	VAL	MET	conflict	UNP O34687

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O	S	0	0
			403	245	81	74	3		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

- Molecule 6 is a protein called Nascent Chain CliM.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	38	Total	C	N	O	S	0	0
			346	232	56	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	46	Total	C	N	O	S	0	0
			356	222	63	66	5		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 9 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	273	Total	C	N	O	S	0	0
			2093	1301	412	374	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	216	VAL	ILE	conflict	UNP P42919

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	206	Total	C	N	O	S	0	0
			1567	983	290	292	2		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	178	Total	C	N	O	S	0	0
			1405	893	245	260	7		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	144	Total	C	N	O	S	0	0
			1142	720	211	206	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	119	Total	C	N	O	S	0	0
			954	583	186	181	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- 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
			933	593	184	156			

- Molecule 21 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	118	Total	C	N	O	S	0	0
			950	597	191	158	4		

- Molecule 22 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	101	Total	C	N	O	S	0	0
			789	503	139	146	1		

- 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
			850	530	165	151	4		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	91	Total	C	N	O	S	0	0
			733	458	135	137	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	102	Total	C	N	O	S	0	0
			770	482	143	141	4		

- Molecule 26 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	61	Total	C	N	O	S	0	0
			467	288	98	79	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	33	VAL	LEU	conflict	UNP P37807

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	66	Total	C	N	O	S	0	0
			540	334	104	100	2		

- Molecule 28 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

- Molecule 29 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	204	Total	C	N	O	S	0	0
			1608	1004	302	299	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	148	ILE	VAL	conflict	UNP P21465

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	164	Total	C	N	O	S	0	0
			1219	767	225	225	2		

- Molecule 31 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	93	Total	C	N	O	S	0	0
			765	482	136	145	2		

- Molecule 32 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	151	Total	C	N	O	S	0	0
			1199	751	225	217	6		

- Molecule 33 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	130	Total	C	N	O	S	0	0
			1030	650	190	187	3		

- Molecule 34 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	128	Total	C	N	O	S	0	0
			997	618	198	180	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
i	72	PHE	LEU	conflict	UNP P21470

- Molecule 35 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	97	Total	C	N	O	S	0	0
			779	491	143	143	2		

- Molecule 36 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	115	Total	C	N	O	S	0	0
			847	520	166	159	2		

- Molecule 37 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	134	Total	C	N	O	S	0	0
			1036	642	208	184	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	2	ALA	PRO	conflict	UNP P21472

- Molecule 38 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	m	118	Total	C	N	O	0	0
			943	579	194	170		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	33	ILE	VAL	conflict	UNP P20282

- Molecule 39 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	60	Total	C	N	O	S	0	0
			498	317	98	78	5		

- Molecule 40 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	87	Total	C	N	O	S	0	0
			730	448	149	132	1		

- Molecule 41 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	87	Total	C	N	O	S	0	0
			691	439	127	123	2		

- Molecule 42 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	84	Total	C	N	O	S	0	0
			693	438	128	125	2		

- Molecule 43 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	65	Total	C	N	O	S	0	0
			522	334	97	89	2		

- Molecule 44 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	86	Total	C	N	O	S	0	0
			658	402	134	121	1		

- Molecule 45 is a RNA chain called P-site tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 46 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	2724	Total	C	N	O	P	0	0
			58523	26110	10840	18851	2722		

- Molecule 47 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	b	195	Total	C	N	O	S	0	0
			1564	996	277	285	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	83	Total	C	N	O	S	0	0
			668	429	122	115	2		

- Molecule 49 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	9	Total	C	N	O	P	0	0
			189	85	30	65	9		

- Molecule 50 is a RNA chain called A-site tRNA-Tyr.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	9	74	Total	C	N	O	P	0	0
			1581	705	288	514	74		

- Molecule 51 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 52 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	W	83	Total	C	N	O	0	0
			639	395	125	119		

- Molecule 53 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	d	199	Total	C	N	O	S	0	0
			1604	1013	298	291	2		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

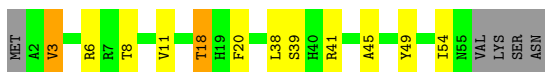
Mol	Chain	Residues	Atoms		AltConf
54	0	1	Total	Zn	0
			1	1	
54	4	1	Total	Zn	0
			1	1	
54	6	1	Total	Zn	0
			1	1	
54	n	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)


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

- Molecule 1: Large ribosomal subunit protein bL32

Chain 0:  71% 17% • 8%



- Molecule 2: 50S ribosomal protein L33 1

Chain 1:  82% 14% • •




- Molecule 3: 50S ribosomal protein L34

Chain 2:  93% 7%




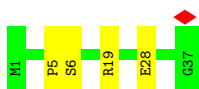
- Molecule 4: 50S ribosomal protein L35

Chain 3:  88% 9% •



- Molecule 5: 50S ribosomal protein L36

Chain 4:  89% 11%



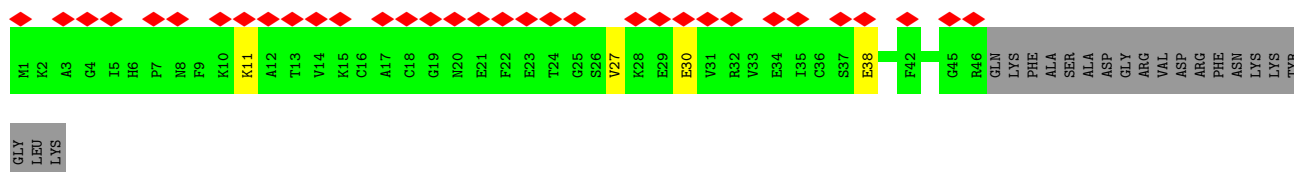
- Molecule 6: Nascent Chain CliM

Chain 5:  95% 5%



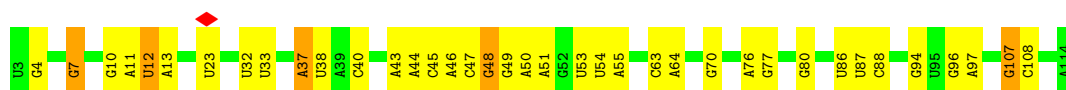
- Molecule 7: 50S ribosomal protein L31

Chain 6:  50% 64% 6% 30%




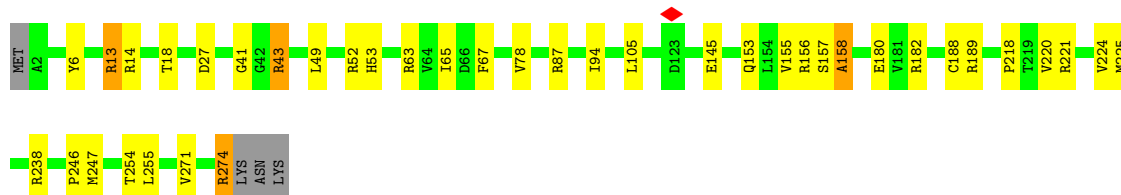
- Molecule 8: 5S rRNA

Chain B:  66% 29%




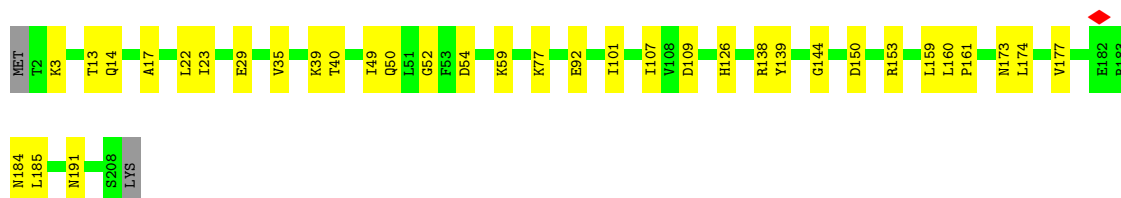
- Molecule 9: Large ribosomal subunit protein uL2

Chain C:  84% 13%




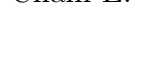
- Molecule 10: 50S ribosomal protein L3

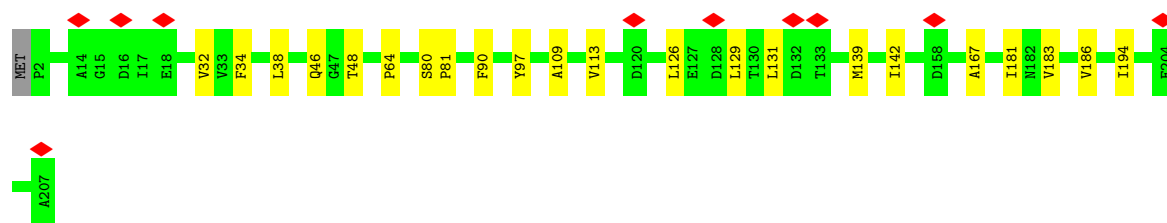
Chain D:  82% 17%



- Molecule 11: 50S ribosomal protein L4

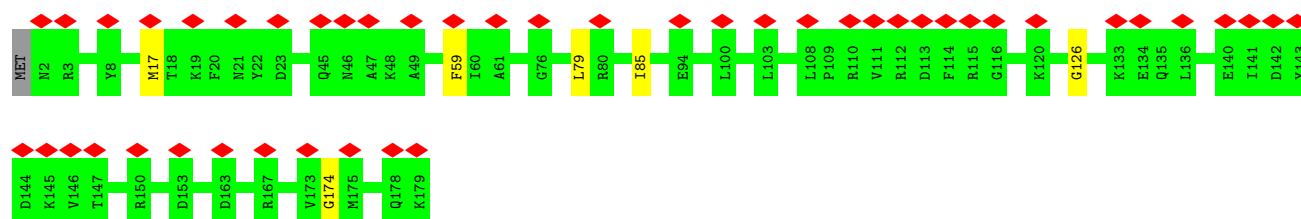
Chain E:  5% 89% 11%





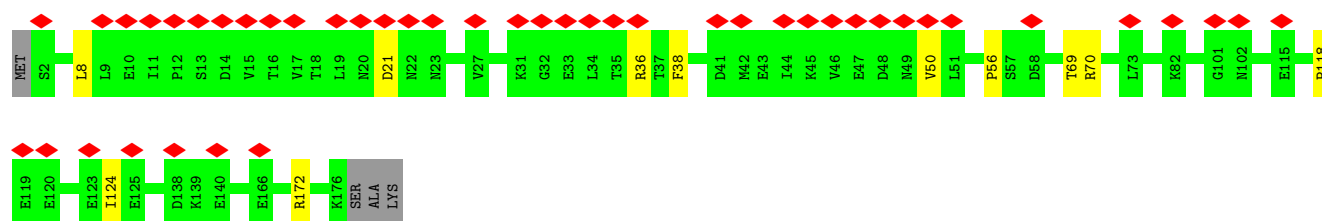
- Molecule 12: 50S ribosomal protein L5

Chain F: 26% 96%



- Molecule 13: Large ribosomal subunit protein uL6

Chain G: 25% 92% 6%



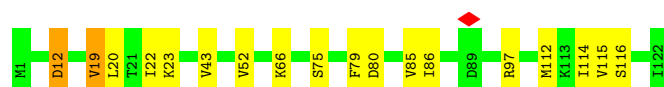
- Molecule 14: 50S ribosomal protein L13

Chain J: 83% 14%



- Molecule 15: 50S ribosomal protein L14

Chain K: 85% 13%

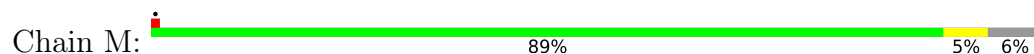


- Molecule 16: 50S ribosomal protein L15

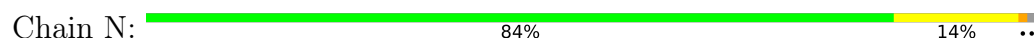
Chain L: 93% 7%



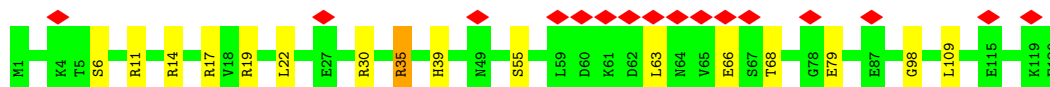
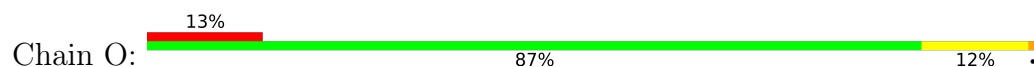
- Molecule 17: 50S ribosomal protein L16



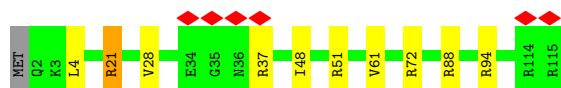
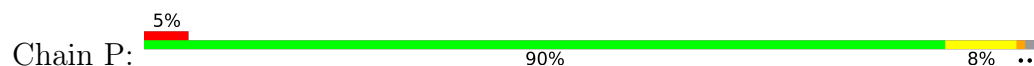
- Molecule 18: 50S ribosomal protein L17



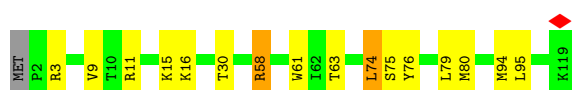
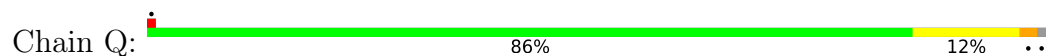
- Molecule 19: 50S ribosomal protein L18



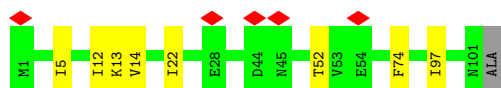
- Molecule 20: 50S ribosomal protein L19




- Molecule 21: Large ribosomal subunit protein bL20

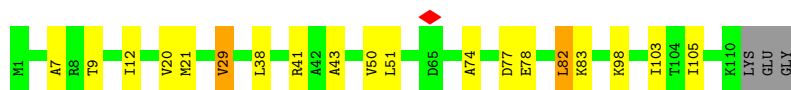


- Molecule 22: 50S ribosomal protein L21




- Molecule 23: 50S ribosomal protein L22

Chain S:  81% 15% . .




- Molecule 24: Large ribosomal subunit protein uL23

Chain T:  91% 5% .



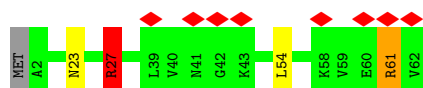
- Molecule 25: 50S ribosomal protein L24

Chain U:  8% 89% 9% ..



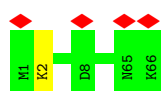
- Molecule 26: Large ribosomal subunit protein bL28

Chain X:  13% 92% . . .




- Molecule 27: 50S ribosomal protein L29

Chain Y:  6% 98% .




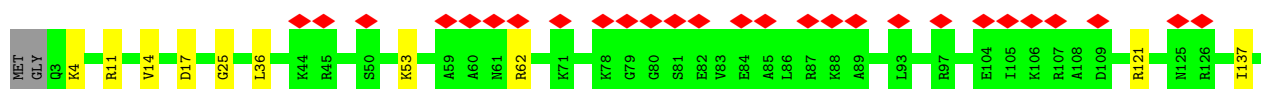
- Molecule 28: Large ribosomal subunit protein uL30

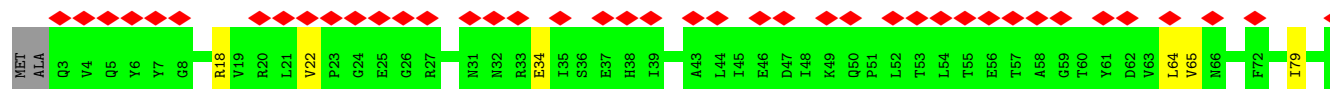
Chain Z:  92% 7% .

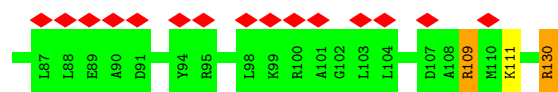


- Molecule 29: Small ribosomal subunit protein uS3

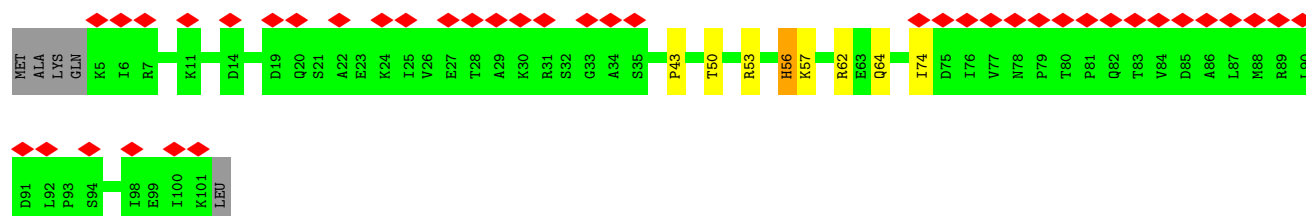
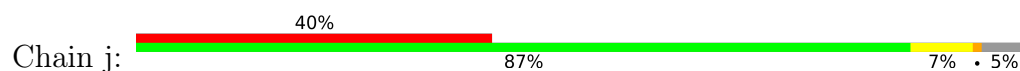
Chain c:  15% 88% 6% 6%



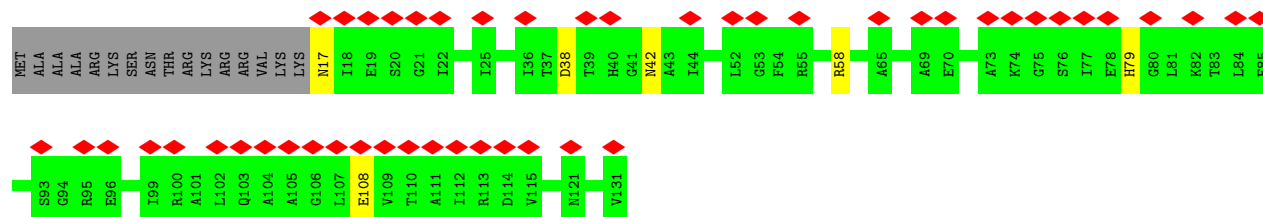
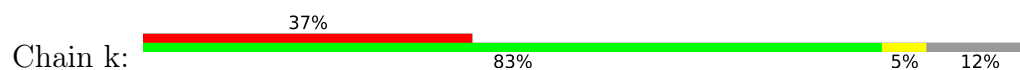




- Molecule 35: 30S ribosomal protein S10



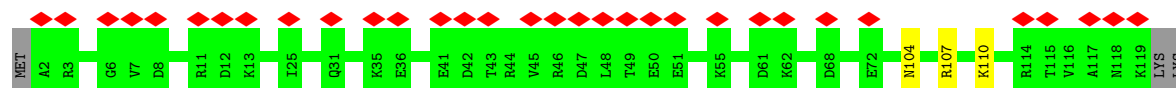
- Molecule 36: 30S ribosomal protein S11



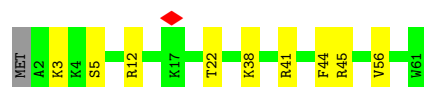
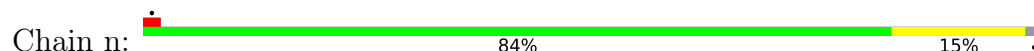
- Molecule 37: Small ribosomal subunit protein uS12



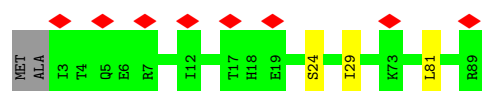
- Molecule 38: Small ribosomal subunit protein uS13



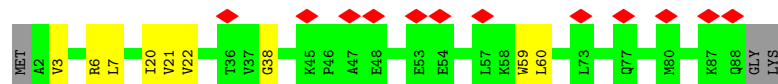
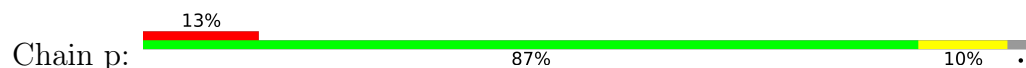
- Molecule 39: 30S ribosomal protein S14



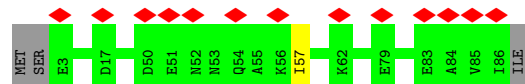
- Molecule 40: 30S ribosomal protein S15



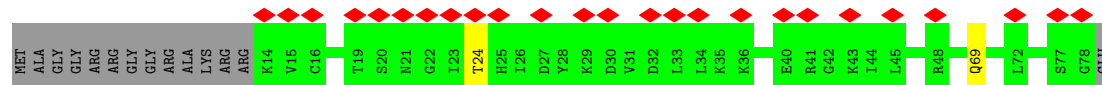
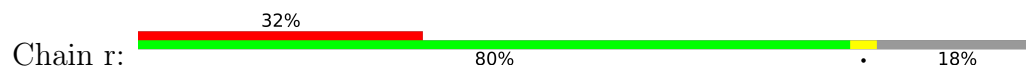
- Molecule 41: 30S ribosomal protein S16



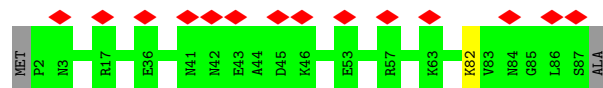
- Molecule 42: 30S ribosomal protein S17



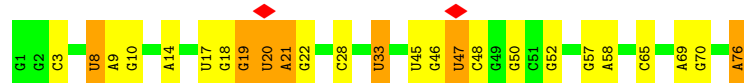
- Molecule 43: 30S ribosomal protein S18



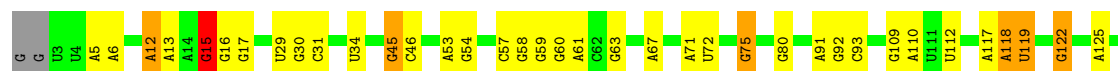
- Molecule 44: 30S ribosomal protein S20

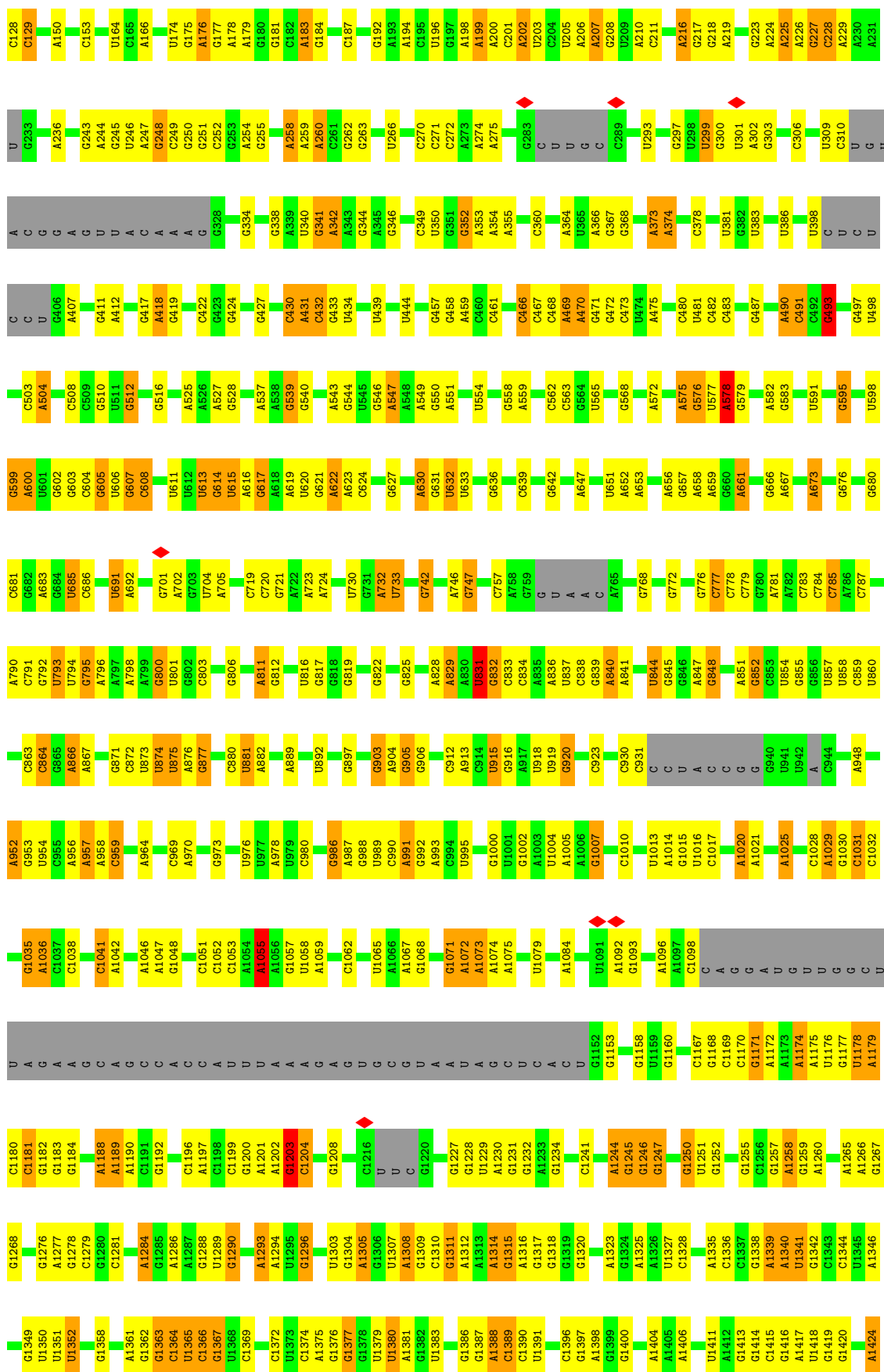


- Molecule 45: P-site tRNA-Phe

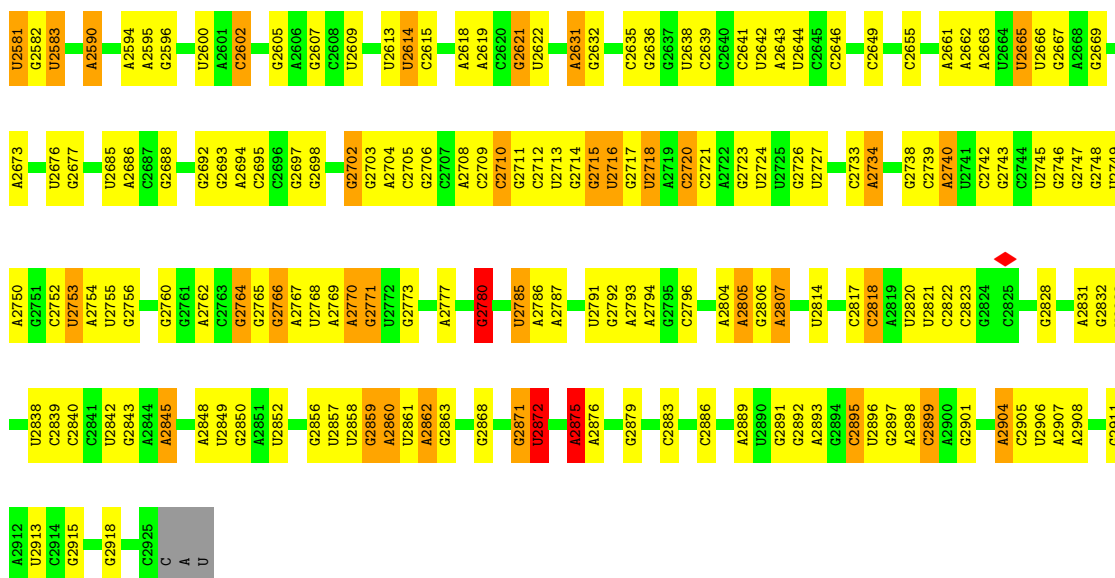


- Molecule 46: 23S rRNA

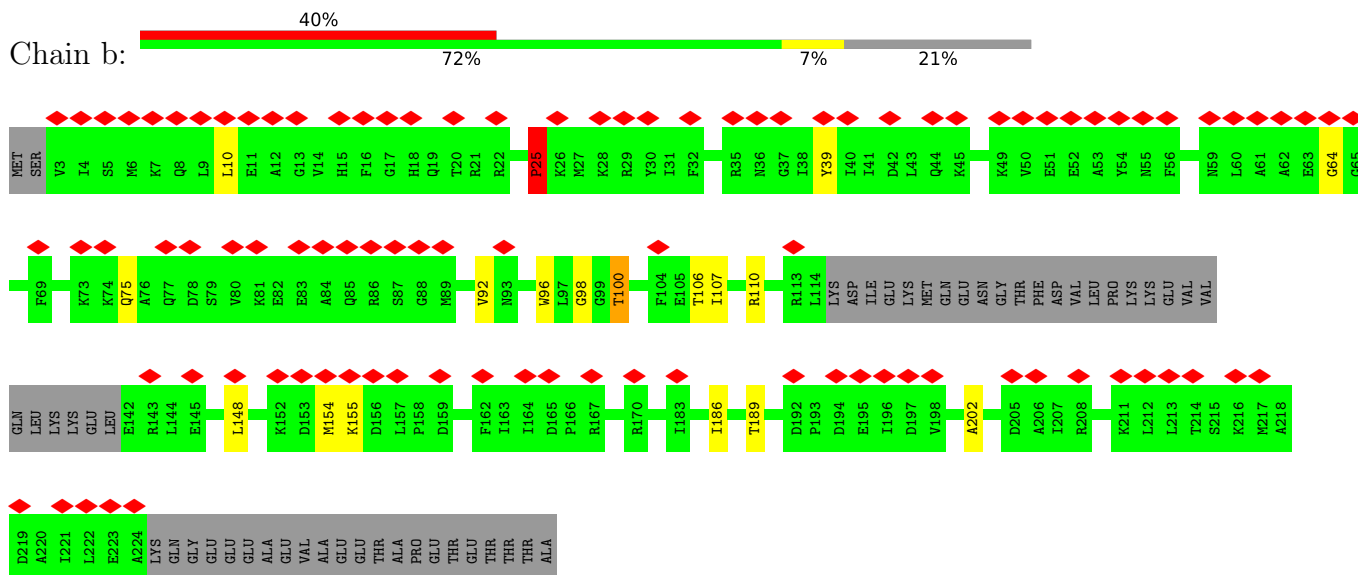




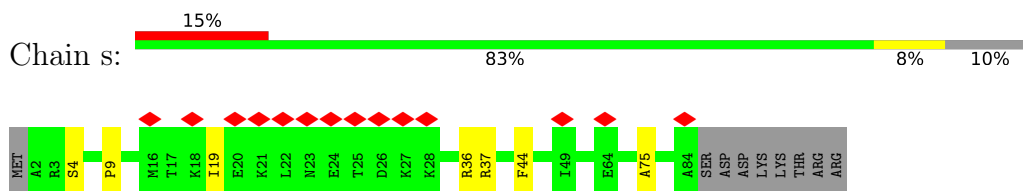
C2503	C2424	A2343	G2267	A	U2127	A2043	A1961	C1866	G1799	U1704	U1603	G1521	C1425
C2506	C2431	U2344	G2268	G	U2128	A2044	G1962	C1867	C1800	C1705	U1606	G1525	A1426
U2508	C2432	C2347	U2271	C	G2129	U2048	A1966	C1872	A1801	U1708	C1607	G1526	G1427
C2509	A2348	A2349	U2272	A	U2130	A2049	U1967	U1873	A1802	A1709	A1608	G1527	A1432
G2510	C2350	C2350	U2273	U	G2131	U2050	U1968	G1874	U1806	U1713	U1528	U1529	U1435
C2513	A2351	C2351	U2274	C	A	U2051	U1969	G1875	U1807	U1717	U1530	U1531	U1436
U2518	U2352	U2352	U2275	G	C	C2052	G1974	A1876	U1808	U1719	A1614	G1534	C1443
G2519	U2353	U2353	A2276	G	C	C2053	G1978	A1877	A1809	G1718	A1615	U1535	C1444
U2522	U2354	U2354	U2277	G	C	U2054	G1979	U1883	G1810	G1719	A1616	U1536	C1445
G2523	U2355	U2355	U2278	G	U	G2055	G1978	A1884	C1811	C1720	A1617	U1537	C1446
C2524	U2356	U2356	G2282	G	U	U2056	A1981	G1885	A1812	U1721	A1618	A1534	C1447
C2525	A2357	A2357	C2283	A	G	G2057	A1982	G1886	A1813	U1724	U1626	A1535	U1448
A2526	A2358	A2358	U2286	U	U	A2059	G1983	G1887	A1814	A1724	U1627	A1536	C1449
C2527	C2363	C2363	C2287	A	C	A2060	U1984	G1888	A1815	G1742	G1630	A1540	C1450
U2528	A2364	A2364	U2290	C	A	C2061	U1985	A1889	A1816	A1743	A1631	A1541	U
C2529	A2365	A2365	U2291	U	C	A2062	G1986	U1892	C1817	G1744	G1632	A1542	U
U2530	G2366	G2366	U2292	A	G	U2063	G1987	U1893	A1818	U1745	G1633	U1543	U
C2531	C2370	C2370	A2296	C	A	C2064	G1988	U1894	C1819	G1746	U1634	C1544	U
A2532	U2371	U2371	A2297	U	U	U2065	A1989	A1895	A1820	U1747	G1635	U	U
U2533	C2372	C2372	G2300	G	C	U2070	C1990	G1898	G1821	G1748	G1640	A1460	U
G2534	U2373	U2373	U2301	G	G	C2071	C1992	U1899	U1823	G1749	U1641	A1461	U
C2539	G2374	G2374	A2302	C	U	C2072	A1995	A1901	C1824	G1750	C1644	A1556	G1462
U2540	A2375	A2375	U2303	U	A	G2077	C1996	G1902	U1825	U1751	G1557	G1558	A1465
A2541	C2376	C2376	C2304	G	G	A2078	G1997	C1903	U1827	G1752	G1559	U1560	U1466
U2542	U2377	U2377	G2305	A	A	C2079	A1998	U1903	G1828	C1753	A1648	G1564	U1473
C2543	G2378	G2378	C2306	C	C	A2080	A1999	G1904	C1829	U1754	C1649	G1565	C1474
U2544	C2379	C2379	A2307	C	C	G2081	A2000	A1905	G1830	C1755	C1650	U1567	G1475
C2545	G2380	G2380	C2310	U	U	C2082	G2002	G1911	A1831	U1756	G1562	C1563	A1480
A2546	A2381	A2381	U2219	C	C	G2085	G2003	G1912	G1836	U1758	A1653	U1565	U1474
C2547	C2382	C2382	A2220	U	U	A2087	G2004	A1914	U1837	A1760	A1654	G1566	U1475
U2548	A2383	A2383	C2225	G	G	U2011	U2011	A1925	U1838	U1767	C1657	A1569	G1481
C2549	U2392	U2392	U2226	A	A	A2089	G2015	A1929	A1839	C1770	G1658	U1570	G1482
U2550	C2393	C2393	A2227	A	A	G2090	G2016	A1930	G1840	C1771	C1662	C1573	A1485
C2551	G2394	G2394	A2228	C	C	A2091	U2020	G1935	C1841	U1776	G1665	G1576	U1486
U2552	A2395	A2395	C2229	C	C	C2092	U2021	G1936	G1842	G1777	U1498	C1577	A1490
C2553	C2402	C2402	U2230	G	G	U2097	G2021	U1939	A1844	U1778	A	G	U1499
U2554	G2403	G2403	G2231	C	C	G2098	U2022	G1940	A1845	G1779	A	A	U1500
C2555	U2320	U2320	C2232	A	A	G2099	C2023	A1941	G1846	G1782	U1501	U1502	U1501
U2556	A2405	A2405	C2233	C	C	A2100	U2024	U1847	U1849	A1677	U1503	G1502	U1502
C2557	C2406	C2406	C2234	G	G	G2101	C2025	A1848	A1850	G1678	U1681	U1505	U1505
U2558	A2407	A2407	G2235	C	C	C2102	A2026	A1942	G1851	U1682	C1682	A1506	U1506
C2559	C2324	C2324	C2236	C	C	U2103	G2029	U1944	G1852	U1789	C1683	U1507	U1507
U2563	U2325	U2325	C2237	C	C	U2104	A2030	U1945	G1853	G1792	G1684	C1508	U1508
C2568	G2411	G2411	U2240	A	A	U2105	G2031	U1946	G1854	G1793	G1690	U1513	U1513
C2569	U2412	U2412	A2241	C	C	A2106	A2032	U1947	U1851	A1691	U1692	C1600	C1514
U2413	C2413	C2413	G2248	U	U	C2107	G2033	U1948	G1852	U1693	U1694	A1601	C1515
A2414	U2414	U2414	G2249	C	C	U2108	A2034	U1949	G1853	G1794	G1691	C1516	U1516
C2415	U2415	U2415	G2249	C	C	U2109	C2035	U1955	A1858	U1797	U1692	U1602	U1516
U2416	A2416	A2416	G2253	C	C	U2121	U2036	U1958	C1859	G1798	G1694	U1602	U1516
C2417	U2417	U2417	A2254	G	G	C2122	C2037	U1959	U1863	U1798	U1694	U1602	U1516
U2418	U2418	U2418	C2255	U	U	A2123	A2042	U1960	G1864	U1798	U1694	U1602	U1516
U2419	U2419	U2419	G2255	U	U	A2123	A2042	U1960	C1865	U1798	U1694	U1602	U1516
G2499	G2499	G2499	G2255	G	G	A2123	A2042	U1960	C1865	U1798	U1694	U1602	U1516
C2580	C2580	C2580	G2255	G	G	A2123	A2042	U1960	C1865	U1798	U1694	U1602	U1516



• Molecule 47: 30S ribosomal protein S2



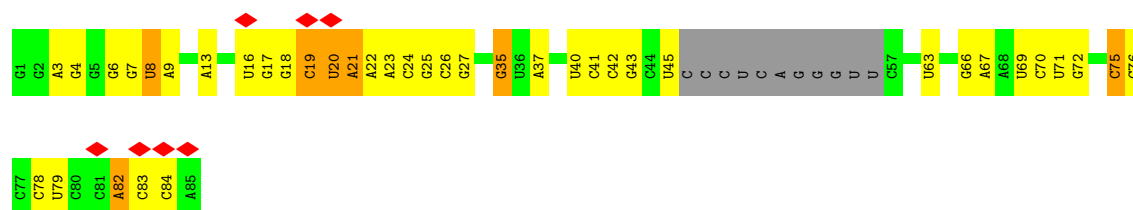
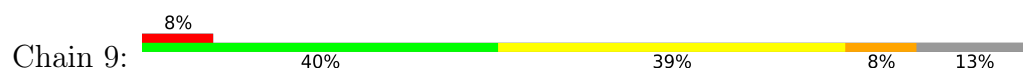
• Molecule 48: 30S ribosomal protein S19



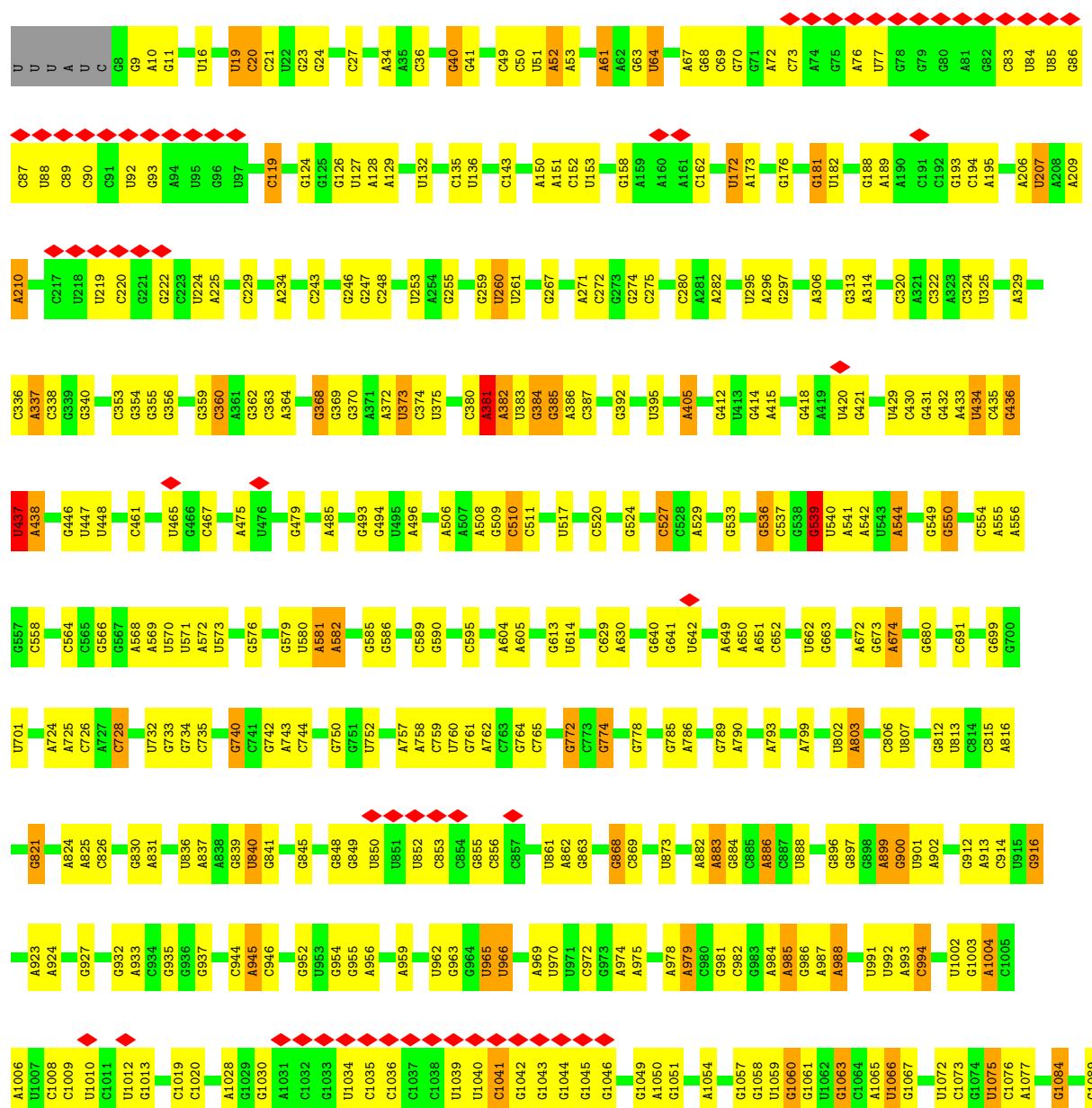
• Molecule 49: mRNA

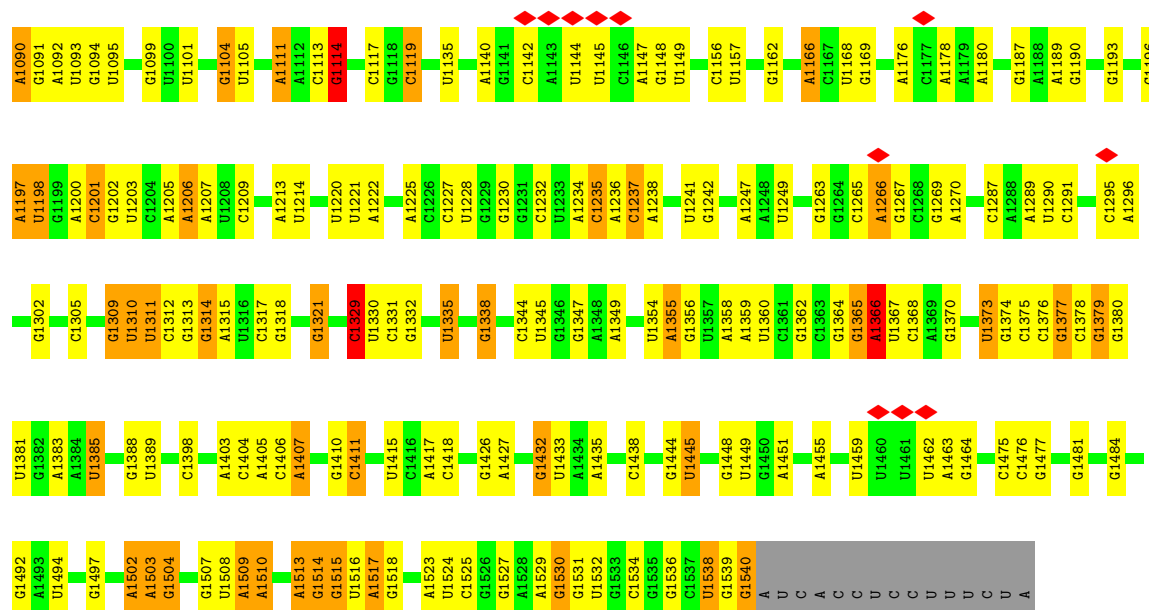


- Molecule 50: A-site tRNA-Tyr

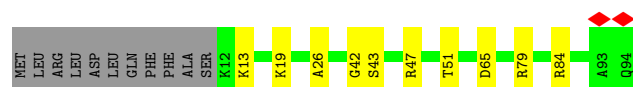
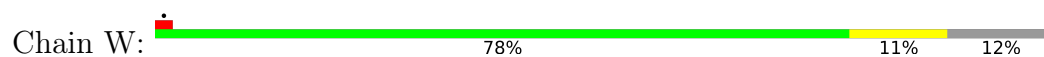


- Molecule 51: 16S rRNA

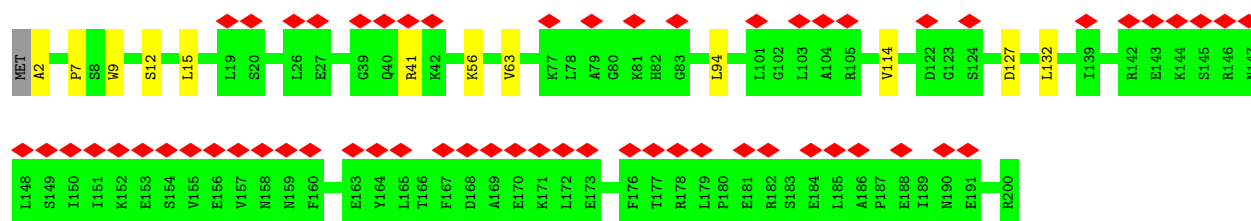




- Molecule 52: Large ribosomal subunit protein bL27



- Molecule 53: 30S ribosomal protein S4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47146	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.14	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.046	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	319.104, 319.104, 319.104	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83100003, 0.83100003, 0.83100003	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, PSU, ZN

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	0	0.67	0/432	1.24	1/574 (0.2%)
2	1	0.50	0/408	1.03	0/541
3	2	0.72	0/371	1.17	0/483
4	3	0.68	0/519	1.16	0/680
5	4	0.57	0/300	1.17	1/393 (0.3%)
6	5	0.50	0/356	1.11	1/481 (0.2%)
7	6	0.54	0/363	1.01	0/485
8	B	0.62	0/2675	1.13	16/4170 (0.4%)
9	C	0.65	1/2130 (0.0%)	1.13	3/2858 (0.1%)
10	D	0.64	0/1597	1.21	4/2140 (0.2%)
11	E	0.56	0/1586	1.09	4/2139 (0.2%)
12	F	0.50	0/1424	1.05	0/1910
13	G	0.52	0/1360	1.02	0/1832
14	J	0.62	0/1165	1.17	1/1566 (0.1%)
15	K	0.60	0/928	1.16	1/1245 (0.1%)
16	L	0.55	0/1094	1.10	0/1457
17	M	0.56	0/1099	1.09	0/1468
18	N	0.61	0/961	1.22	3/1284 (0.2%)
19	O	0.53	0/922	1.01	0/1236
20	P	0.57	0/946	1.09	1/1264 (0.1%)
21	Q	0.68	0/962	1.17	0/1277
22	R	0.54	0/800	0.98	1/1073 (0.1%)
23	S	0.64	0/859	1.19	3/1156 (0.3%)
24	T	0.52	0/739	1.12	2/985 (0.2%)
25	U	0.54	0/780	1.01	1/1043 (0.1%)
26	X	0.57	0/471	1.17	1/626 (0.2%)
27	Y	0.46	0/541	1.05	0/718
28	Z	0.50	0/458	1.04	1/613 (0.2%)
29	c	0.51	0/1630	1.04	0/2193
30	e	0.53	0/1231	1.06	1/1655 (0.1%)
31	f	0.52	0/776	1.08	0/1043
32	g	0.51	0/1215	1.10	0/1629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.53	0/1042	1.03	0/1397
34	i	0.53	0/1011	1.06	1/1356 (0.1%)
35	j	0.55	0/791	1.06	1/1066 (0.1%)
36	k	0.56	0/861	0.97	0/1164
37	l	0.52	0/1052	1.00	0/1413
38	m	0.53	0/949	1.09	0/1268
39	n	0.53	0/508	1.05	1/672 (0.1%)
40	o	0.48	0/738	1.11	0/985
41	p	0.49	0/704	1.09	0/945
42	q	0.49	0/701	0.96	0/936
43	r	0.49	0/530	1.11	0/710
44	t	0.50	0/661	1.25	0/882
45	v	0.66	0/1812	1.16	12/2823 (0.4%)
46	A	0.63	0/65501	1.36	937/102165 (0.9%)
47	b	0.50	0/1586	1.13	1/2130 (0.0%)
48	s	0.52	0/685	1.05	0/920
49	7	0.70	0/210	1.31	3/324 (0.9%)
50	9	0.66	0/1766	1.08	13/2749 (0.5%)
51	a	0.62	0/36826	1.16	261/57450 (0.5%)
52	W	0.56	0/647	1.10	1/858 (0.1%)
53	d	0.51	0/1635	1.09	1/2196 (0.0%)
All	All	0.61	1/151314 (0.0%)	1.24	1278/226626 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	3
3	2	0	2
9	C	0	7
10	D	0	1
13	G	0	1
14	J	0	3
16	L	0	3
17	M	0	1
18	N	0	1
19	O	0	4
20	P	0	3
21	Q	0	2
23	S	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
25	U	0	2
26	X	0	1
29	c	0	2
31	f	0	1
33	h	0	1
34	i	0	2
35	j	0	2
36	k	0	1
38	m	0	1
39	n	0	3
46	A	0	3
52	W	0	2
All	All	0	53

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	53	HIS	CG-CD2	-6.17	1.29	1.35

The worst 5 of 1278 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	A	732	A	O3'-P-O5'	-18.68	75.98	104.00
46	A	1375	A	O3'-P-O5'	-15.29	81.06	104.00
46	A	2904	A	C2'-C3'-O3'	15.28	132.42	109.50
46	A	621	G	O3'-P-O5'	-13.96	83.05	104.00
46	A	373	A	O3'-P-O5'	-13.93	83.11	104.00

There are no chirality outliers.

5 of 53 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	20	PHE	Peptide
1	0	41	ARG	Sidechain
1	0	6	ARG	Sidechain
3	2	12	ARG	Sidechain
3	2	28	ARG	Sidechain

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	0	425	0	441	5	0
2	1	403	0	414	4	0
3	2	368	0	410	0	0
4	3	512	0	564	2	0
5	4	297	0	339	2	0
6	5	346	0	345	2	0
7	6	356	0	346	1	0
8	B	2392	0	1213	1	0
9	C	2093	0	2179	16	0
10	D	1575	0	1642	16	0
11	E	1567	0	1652	7	0
12	F	1405	0	1467	2	0
13	G	1342	0	1388	3	0
14	J	1142	0	1182	10	0
15	K	921	0	977	8	0
16	L	1082	0	1132	4	0
17	M	1076	0	1145	3	0
18	N	954	0	983	8	0
19	O	913	0	947	4	0
20	P	933	0	1004	2	0
21	Q	950	0	1018	8	0
22	R	789	0	833	2	0
23	S	850	0	911	8	0
24	T	733	0	781	2	0
25	U	770	0	825	2	0
26	X	467	0	512	2	0
27	Y	540	0	581	0	0
28	Z	456	0	491	2	0
29	c	1608	0	1646	1	0
30	e	1219	0	1300	3	0
31	f	765	0	765	1	0
32	g	1199	0	1256	5	0
33	h	1030	0	1086	1	0
34	i	997	0	1033	4	0
35	j	779	0	821	3	0
36	k	847	0	860	2	0
37	l	1036	0	1091	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	943	0	1008	1	0
39	n	498	0	529	2	0
40	o	730	0	759	1	0
41	p	691	0	718	5	0
42	q	693	0	734	0	0
43	r	522	0	558	0	0
44	t	658	0	715	0	0
45	v	1622	0	820	1	0
46	A	58523	0	29464	179	0
47	b	1564	0	1625	5	0
48	s	668	0	682	3	0
49	7	189	0	95	1	0
50	9	1581	0	804	2	0
51	a	32891	0	16559	79	0
52	W	639	0	652	2	0
53	d	1604	0	1638	5	0
54	0	1	0	0	0	0
54	4	1	0	0	0	0
54	6	1	0	0	0	0
54	n	1	0	0	0	0
All	All	139157	0	92940	378	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 2.

The worst 5 of 378 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)
46:A:1808:U:H5	46:A:1813:A:N7	1.80	0.80
46:A:1709:A:H61	46:A:2025:C:H5	1.32	0.75
46:A:1411:U:HO2'	46:A:2241:A:H8	1.37	0.69
32:g:148:ASN:HD22	36:k:58:ARG:HH22	1.44	0.65
51:a:437:U:H3'	53:d:9:TRP:CD2	2.31	0.64

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	0	52/59 (88%)	47 (90%)	3 (6%)	2 (4%)	2	9
2	1	46/49 (94%)	43 (94%)	3 (6%)	0	100	100
3	2	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
4	3	62/66 (94%)	56 (90%)	6 (10%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	5	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	6	44/66 (67%)	38 (86%)	6 (14%)	0	100	100
9	C	271/277 (98%)	253 (93%)	16 (6%)	2 (1%)	18	47
10	D	205/209 (98%)	188 (92%)	15 (7%)	2 (1%)	12	38
11	E	204/207 (99%)	187 (92%)	17 (8%)	0	100	100
12	F	176/179 (98%)	160 (91%)	14 (8%)	2 (1%)	11	36
13	G	173/179 (97%)	150 (87%)	21 (12%)	2 (1%)	10	34
14	J	142/145 (98%)	133 (94%)	8 (6%)	1 (1%)	18	47
15	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
16	L	144/146 (99%)	134 (93%)	9 (6%)	1 (1%)	18	47
17	M	133/144 (92%)	129 (97%)	4 (3%)	0	100	100
18	N	117/120 (98%)	107 (92%)	8 (7%)	2 (2%)	7	25
19	O	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
20	P	112/115 (97%)	103 (92%)	7 (6%)	2 (2%)	6	23
21	Q	116/119 (98%)	110 (95%)	5 (4%)	1 (1%)	14	41
22	R	99/102 (97%)	94 (95%)	5 (5%)	0	100	100
23	S	108/113 (96%)	103 (95%)	3 (3%)	2 (2%)	6	22
24	T	89/95 (94%)	79 (89%)	10 (11%)	0	100	100
25	U	100/103 (97%)	91 (91%)	8 (8%)	1 (1%)	12	38
26	X	59/62 (95%)	55 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Y	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
28	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
29	c	202/218 (93%)	180 (89%)	19 (9%)	3 (2%)	8	28
30	e	162/166 (98%)	153 (94%)	9 (6%)	0	100	100
31	f	91/95 (96%)	77 (85%)	14 (15%)	0	100	100
32	g	149/156 (96%)	135 (91%)	13 (9%)	1 (1%)	18	47
33	h	128/132 (97%)	116 (91%)	10 (8%)	2 (2%)	7	27
34	i	126/130 (97%)	112 (89%)	13 (10%)	1 (1%)	16	44
35	j	95/102 (93%)	86 (90%)	9 (10%)	0	100	100
36	k	113/131 (86%)	105 (93%)	8 (7%)	0	100	100
37	l	132/138 (96%)	123 (93%)	8 (6%)	1 (1%)	16	44
38	m	116/121 (96%)	105 (90%)	11 (10%)	0	100	100
39	n	58/61 (95%)	53 (91%)	4 (7%)	1 (2%)	7	25
40	o	85/89 (96%)	78 (92%)	7 (8%)	0	100	100
41	p	85/90 (94%)	73 (86%)	12 (14%)	0	100	100
42	q	82/87 (94%)	74 (90%)	7 (8%)	1 (1%)	10	34
43	r	63/79 (80%)	61 (97%)	1 (2%)	1 (2%)	7	27
44	t	84/88 (96%)	83 (99%)	1 (1%)	0	100	100
47	b	191/246 (78%)	172 (90%)	13 (7%)	6 (3%)	3	12
48	s	81/92 (88%)	74 (91%)	5 (6%)	2 (2%)	4	16
52	W	81/94 (86%)	77 (95%)	3 (4%)	1 (1%)	10	34
53	d	197/200 (98%)	176 (89%)	21 (11%)	0	100	100
All	All	5244/5556 (94%)	4806 (92%)	398 (8%)	40 (1%)	18	44

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	P	37	ARG
33	h	79	ARG
47	b	100	THR
47	b	154	MET
10	D	184	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	48/53 (91%)	45 (94%)	3 (6%)	16	45
2	1	46/47 (98%)	43 (94%)	3 (6%)	15	43
3	2	39/39 (100%)	38 (97%)	1 (3%)	40	75
4	3	54/56 (96%)	52 (96%)	2 (4%)	30	65
5	4	35/35 (100%)	34 (97%)	1 (3%)	37	73
6	5	38/38 (100%)	38 (100%)	0	100	100
7	6	39/55 (71%)	36 (92%)	3 (8%)	12	36
9	C	221/225 (98%)	213 (96%)	8 (4%)	31	66
10	D	168/170 (99%)	164 (98%)	4 (2%)	43	77
11	E	169/170 (99%)	164 (97%)	5 (3%)	36	72
12	F	153/154 (99%)	152 (99%)	1 (1%)	76	91
13	G	148/151 (98%)	146 (99%)	2 (1%)	59	85
14	J	122/123 (99%)	117 (96%)	5 (4%)	27	62
15	K	101/101 (100%)	95 (94%)	6 (6%)	18	48
16	L	110/110 (100%)	109 (99%)	1 (1%)	70	89
17	M	109/116 (94%)	108 (99%)	1 (1%)	70	89
18	N	99/100 (99%)	97 (98%)	2 (2%)	48	80
19	O	93/93 (100%)	86 (92%)	7 (8%)	12	37
20	P	98/100 (98%)	95 (97%)	3 (3%)	35	70
21	Q	97/98 (99%)	95 (98%)	2 (2%)	47	79
22	R	84/84 (100%)	81 (96%)	3 (4%)	31	66
23	S	91/93 (98%)	89 (98%)	2 (2%)	45	78
24	T	82/85 (96%)	82 (100%)	0	100	100
25	U	86/87 (99%)	83 (96%)	3 (4%)	32	67
26	X	49/50 (98%)	47 (96%)	2 (4%)	27	62
27	Y	57/57 (100%)	56 (98%)	1 (2%)	51	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Z	52/53 (98%)	51 (98%)	1 (2%)	50	81
29	c	167/178 (94%)	162 (97%)	5 (3%)	36	72
30	e	128/130 (98%)	127 (99%)	1 (1%)	73	90
31	f	82/84 (98%)	80 (98%)	2 (2%)	43	77
32	g	127/132 (96%)	125 (98%)	2 (2%)	55	83
33	h	110/112 (98%)	108 (98%)	2 (2%)	51	82
34	i	101/102 (99%)	100 (99%)	1 (1%)	68	88
35	j	88/92 (96%)	86 (98%)	2 (2%)	44	78
36	k	87/100 (87%)	85 (98%)	2 (2%)	44	78
37	l	112/115 (97%)	107 (96%)	5 (4%)	24	58
38	m	101/104 (97%)	100 (99%)	1 (1%)	68	88
39	n	53/54 (98%)	52 (98%)	1 (2%)	50	81
40	o	82/83 (99%)	81 (99%)	1 (1%)	63	87
41	p	74/76 (97%)	71 (96%)	3 (4%)	27	62
42	q	77/80 (96%)	77 (100%)	0	100	100
43	r	56/64 (88%)	55 (98%)	1 (2%)	51	82
44	t	69/70 (99%)	68 (99%)	1 (1%)	59	85
47	b	167/212 (79%)	161 (96%)	6 (4%)	31	66
48	s	72/81 (89%)	71 (99%)	1 (1%)	59	85
52	W	64/74 (86%)	61 (95%)	3 (5%)	23	57
53	d	172/173 (99%)	168 (98%)	4 (2%)	44	78
All	All	4477/4659 (96%)	4361 (97%)	116 (3%)	41	75

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	P	88	ARG
52	W	19	LYS
28	Z	30	LYS
52	W	13	LYS
41	p	60	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
23	S	73	GLN
25	U	99	GLN
53	d	115	ASN
43	r	21	ASN
23	S	95	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	v	75/76 (98%)	19 (25%)	0
46	A	2710/2928 (92%)	526 (19%)	103 (3%)
49	7	8/9 (88%)	2 (25%)	0
50	9	72/85 (84%)	33 (45%)	8 (11%)
51	a	1532/1554 (98%)	312 (20%)	0
8	B	111/112 (99%)	27 (24%)	9 (8%)
All	All	4508/4764 (94%)	919 (20%)	120 (2%)

5 of 919 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	B	4	G
8	B	7	G
8	B	10	G
8	B	11	A
8	B	12	U

5 of 120 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	A	1296	G
46	A	2898	A
46	A	1602	U
46	A	2892	G
50	9	78	C

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

2 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
46	OMG	A	2280	46,45	23,26,27	0.40	0	32,38,41	0.60	0
46	PSU	A	2718	46	18,21,22	0.97	2 (11%)	21,30,33	0.97	2 (9%)

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
46	OMG	A	2280	46,45	-	0/9/27/28	0/3/3/3
46	PSU	A	2718	46	-	1/7/25/26	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	A	2718	PSU	C4-C5	-2.57	1.37	1.44
46	A	2718	PSU	C6-C5	2.48	1.38	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	A	2718	PSU	O2'-C2'-C3'	2.29	119.16	111.82
46	A	2718	PSU	C4-N3-C2	-2.10	123.48	126.37

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	A	2718	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

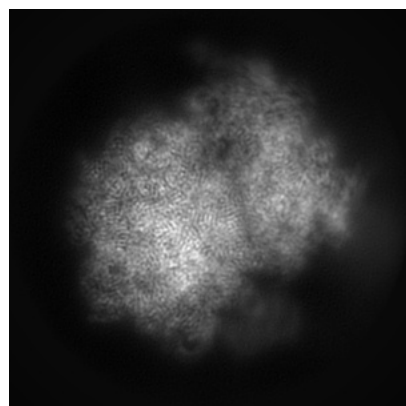
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50858. These allow visual inspection of the internal detail of the map and identification of artifacts.

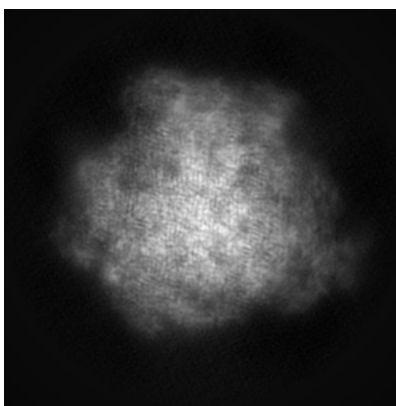
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

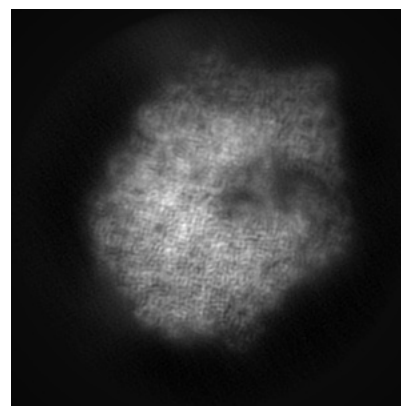
6.1.1 Primary map



X

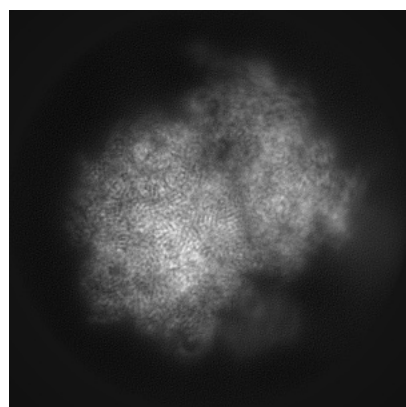


Y

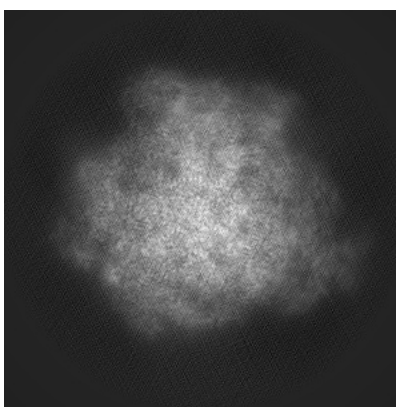


Z

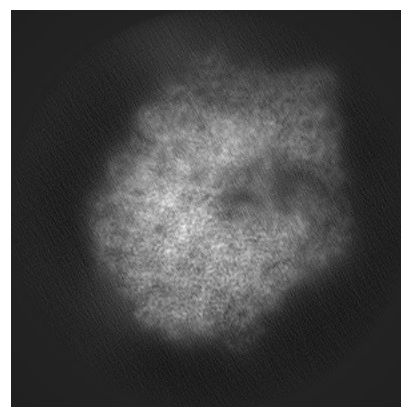
6.1.2 Raw map



X



Y

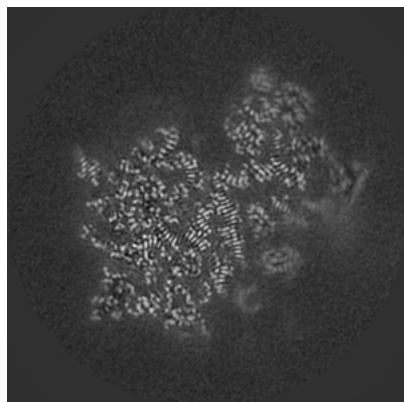


Z

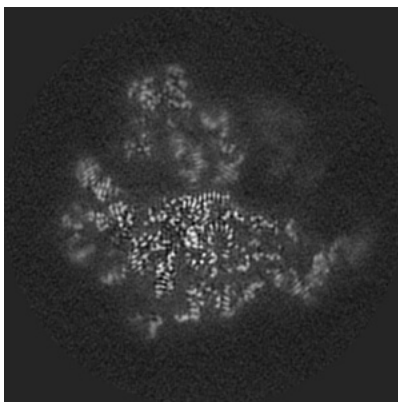
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

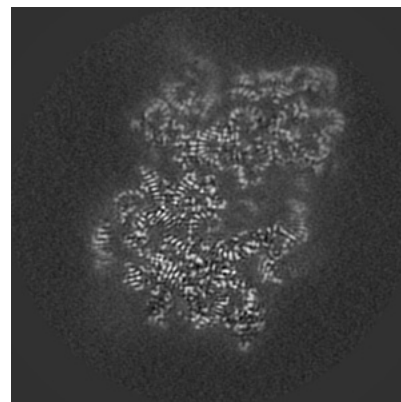
6.2.1 Primary map



X Index: 192

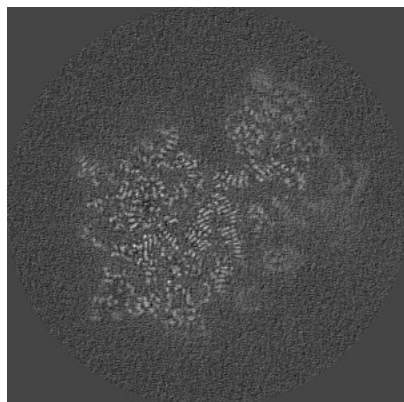


Y Index: 192

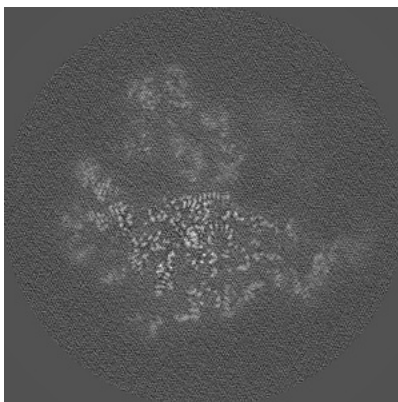


Z Index: 192

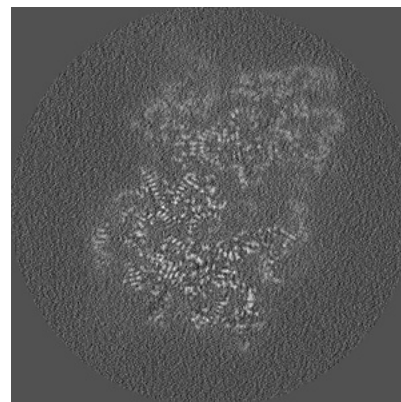
6.2.2 Raw map



X Index: 192



Y Index: 192

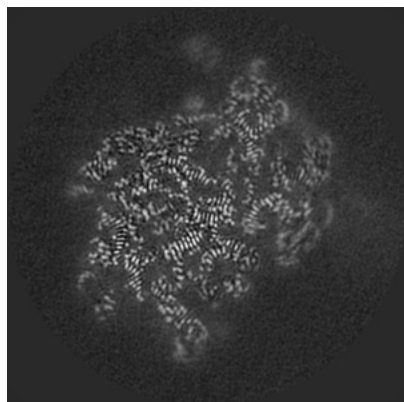


Z Index: 192

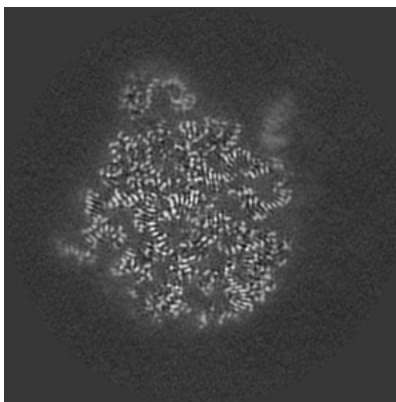
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

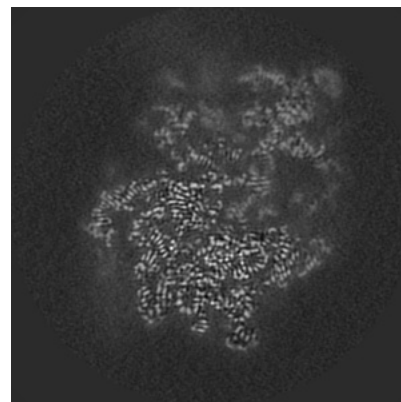
6.3.1 Primary map



X Index: 163

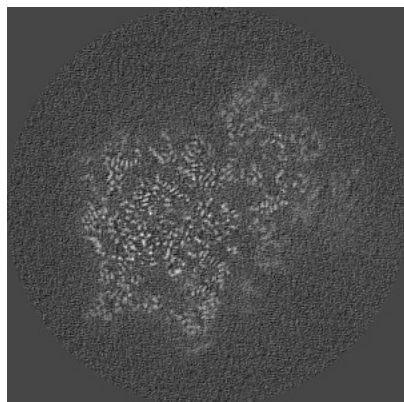


Y Index: 157

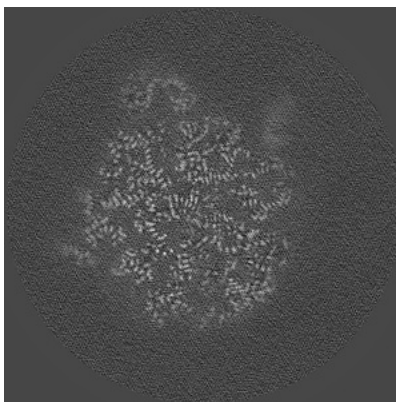


Z Index: 179

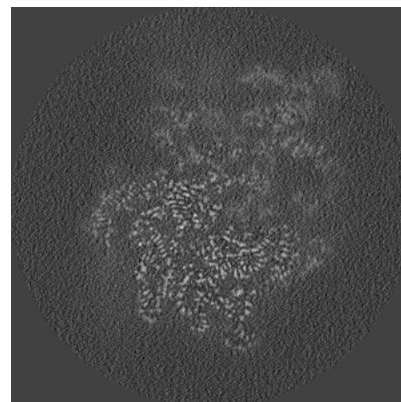
6.3.2 Raw map



X Index: 183



Y Index: 156

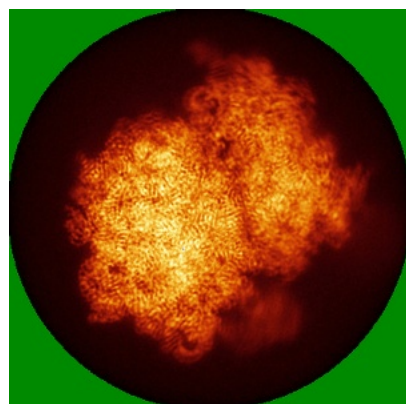


Z Index: 178

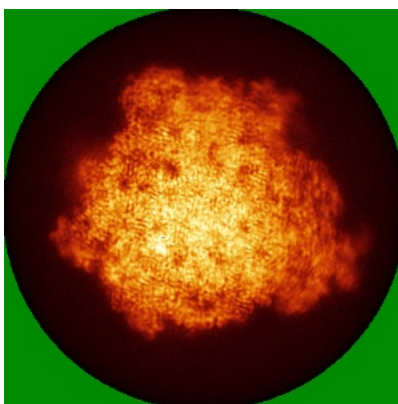
The images above show the largest variance slices of the map in three orthogonal directions.

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

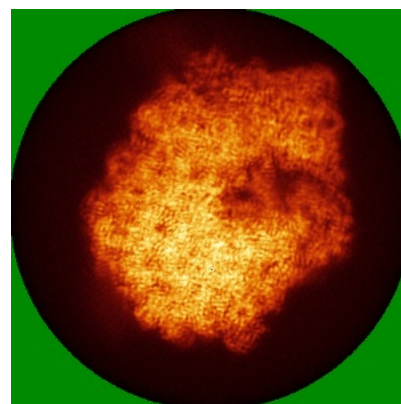
6.4.1 Primary map



X

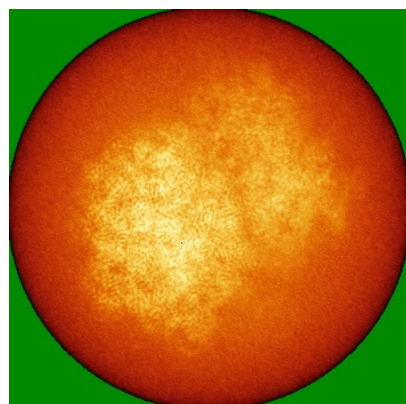


Y

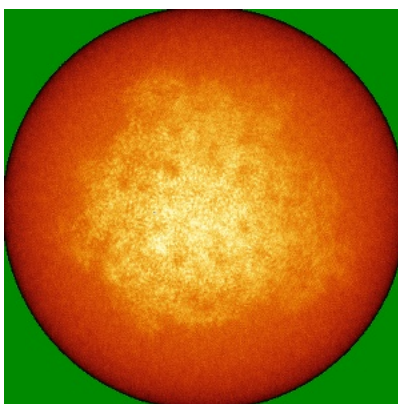


Z

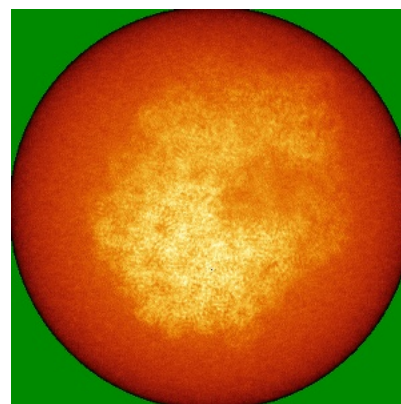
6.4.2 Raw map



X



Y

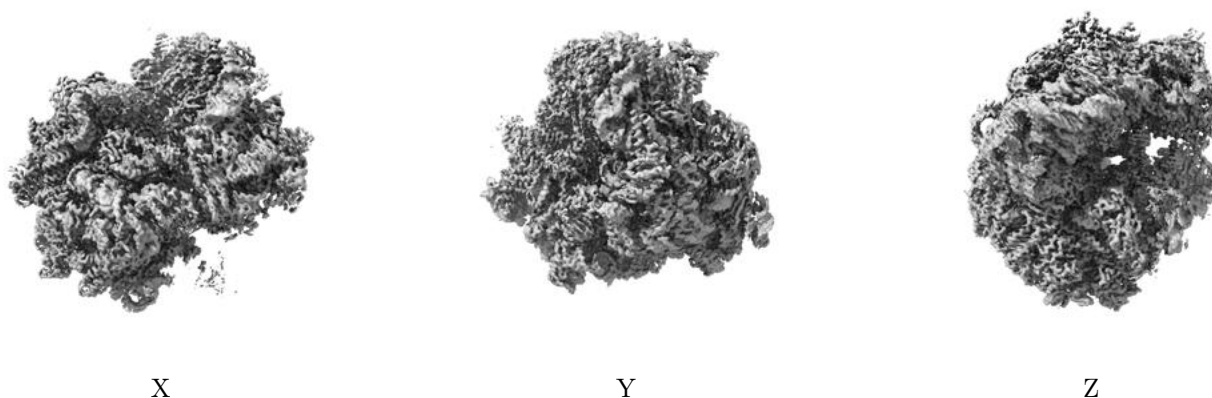


Z

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.

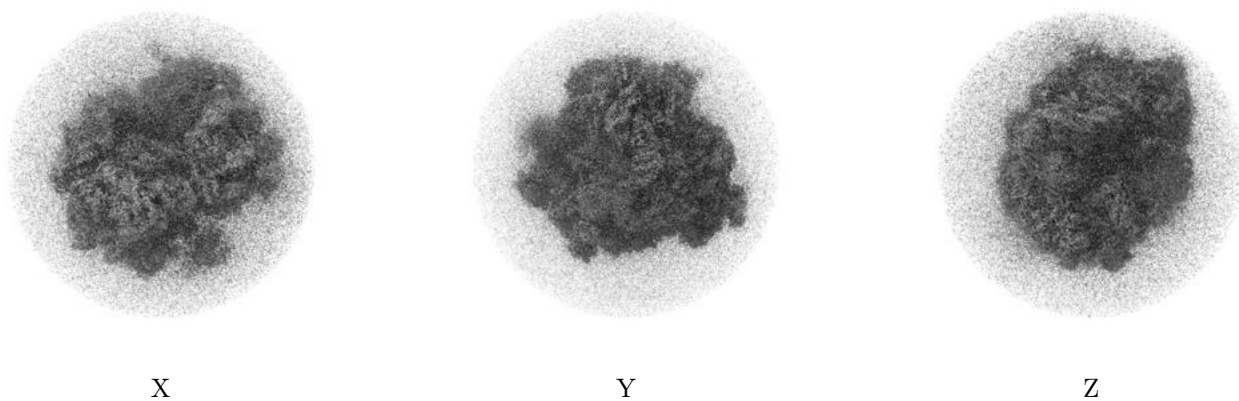
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

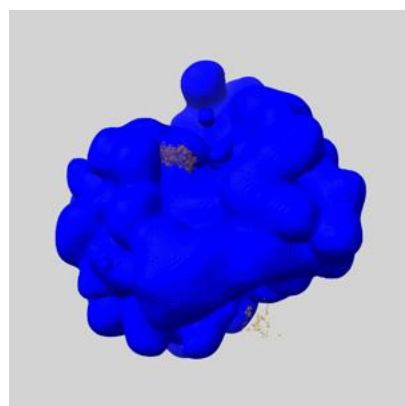
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

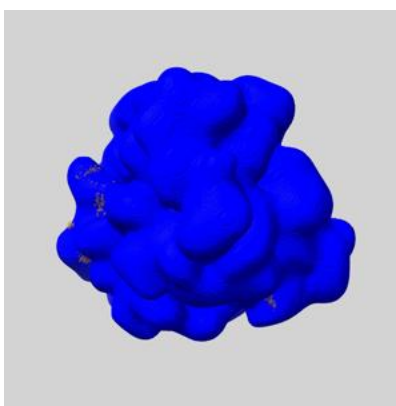
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

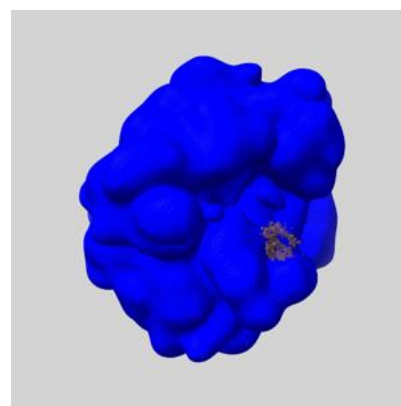
6.6.1 emd_50858_msk_1.map [i](#)



X



Y

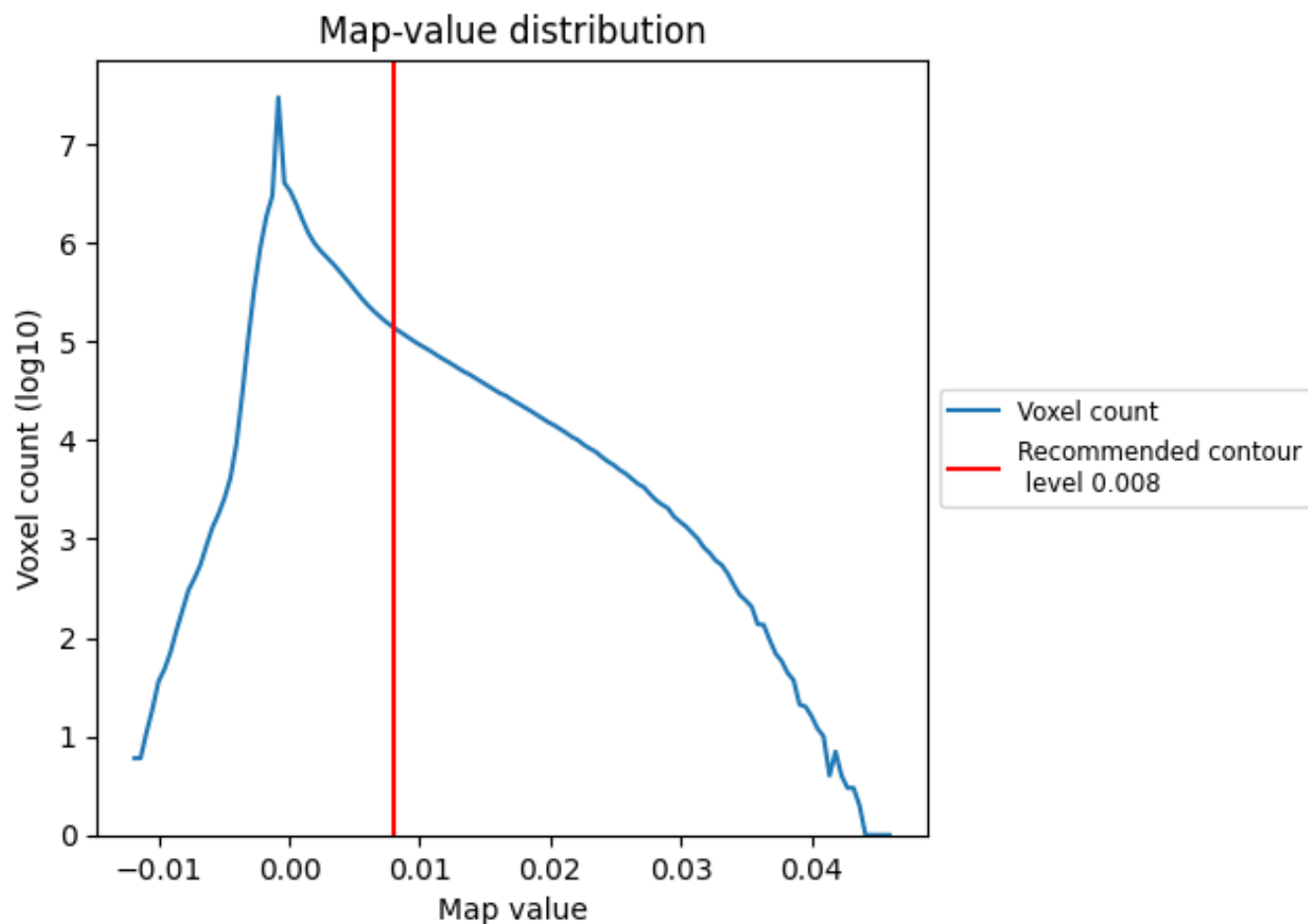


Z

7 Map analysis [i](#)

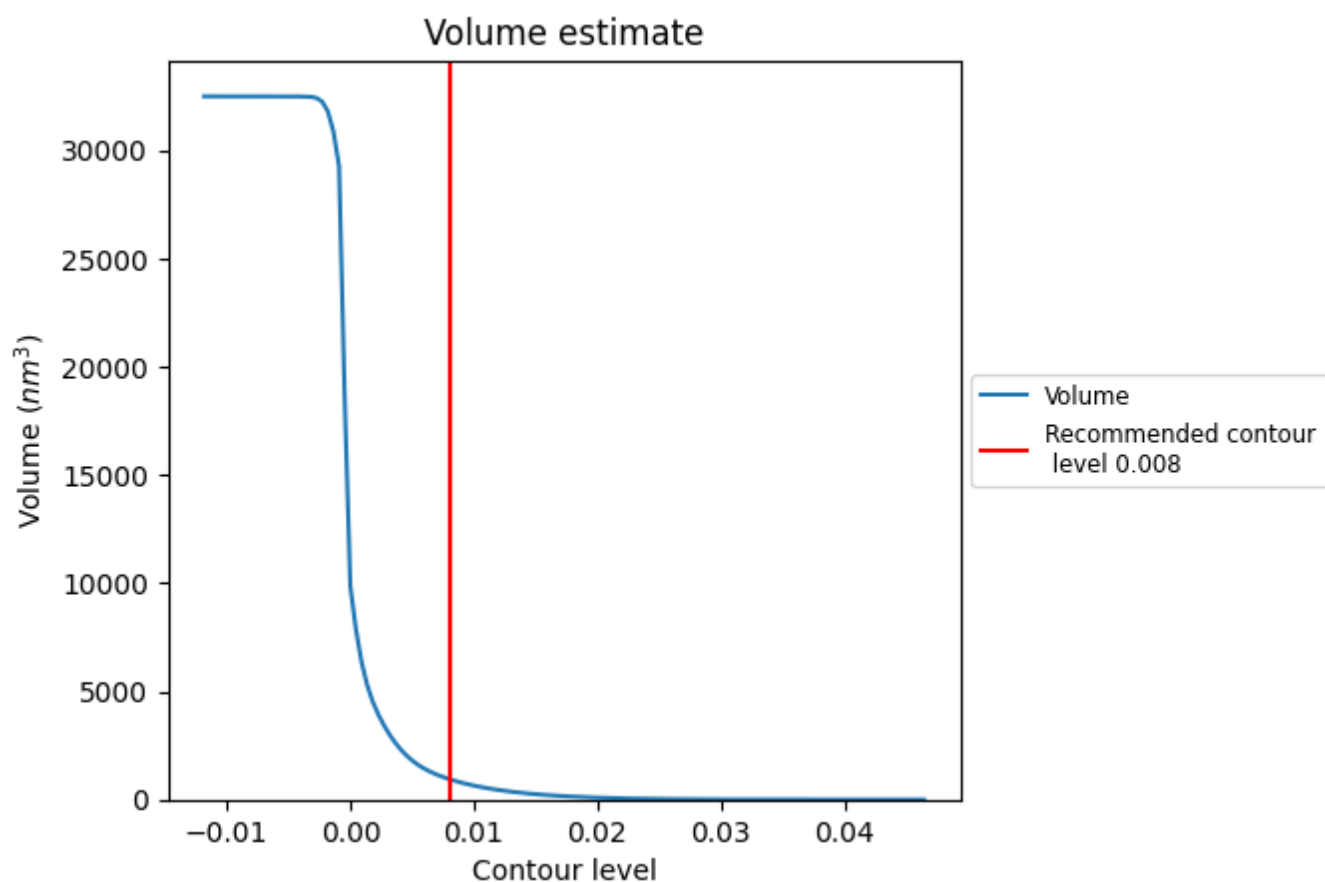
This section contains the results of statistical analysis of the map.

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.

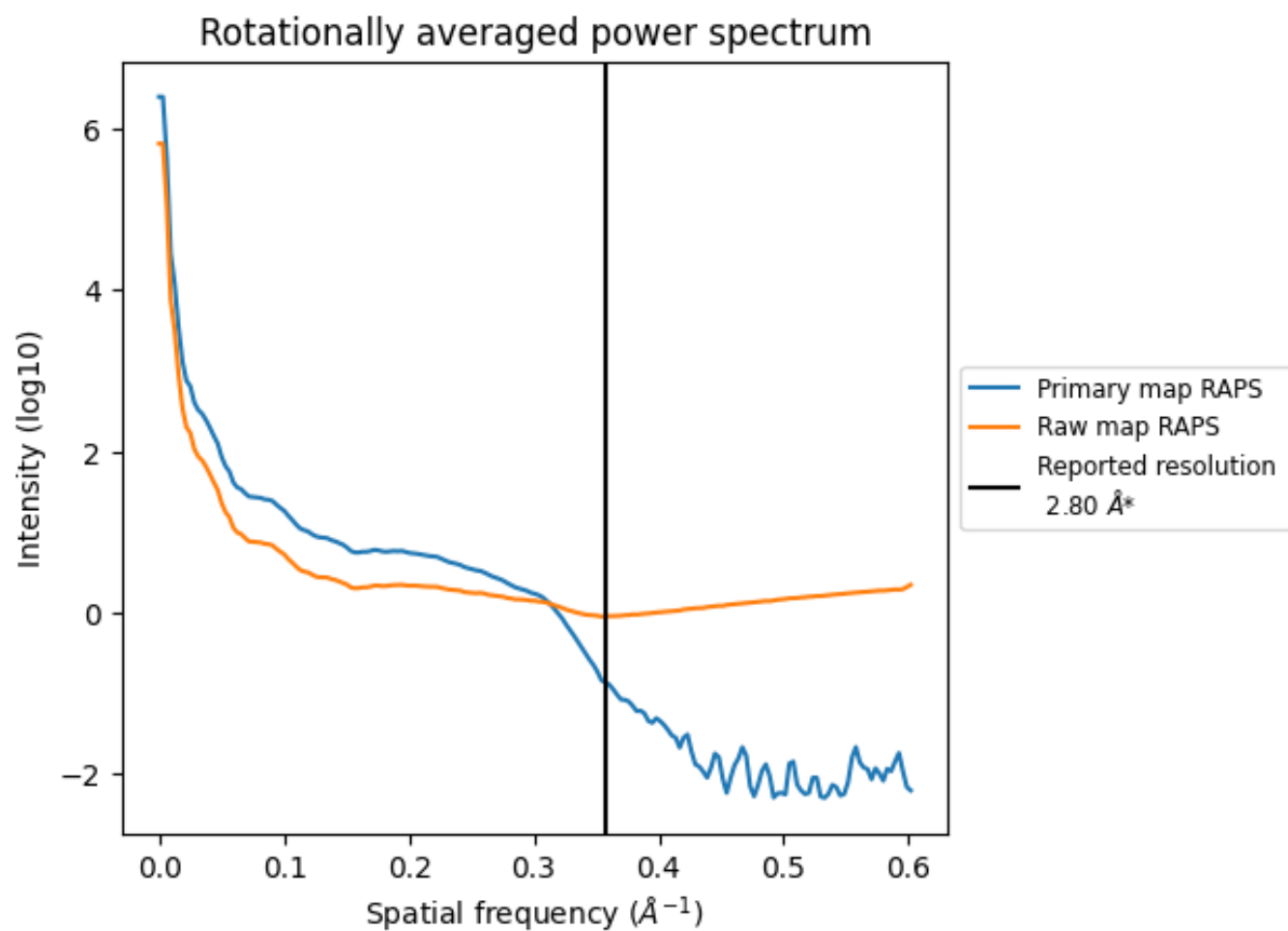
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 946 nm³; this corresponds to an approximate mass of 855 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 ⓘ

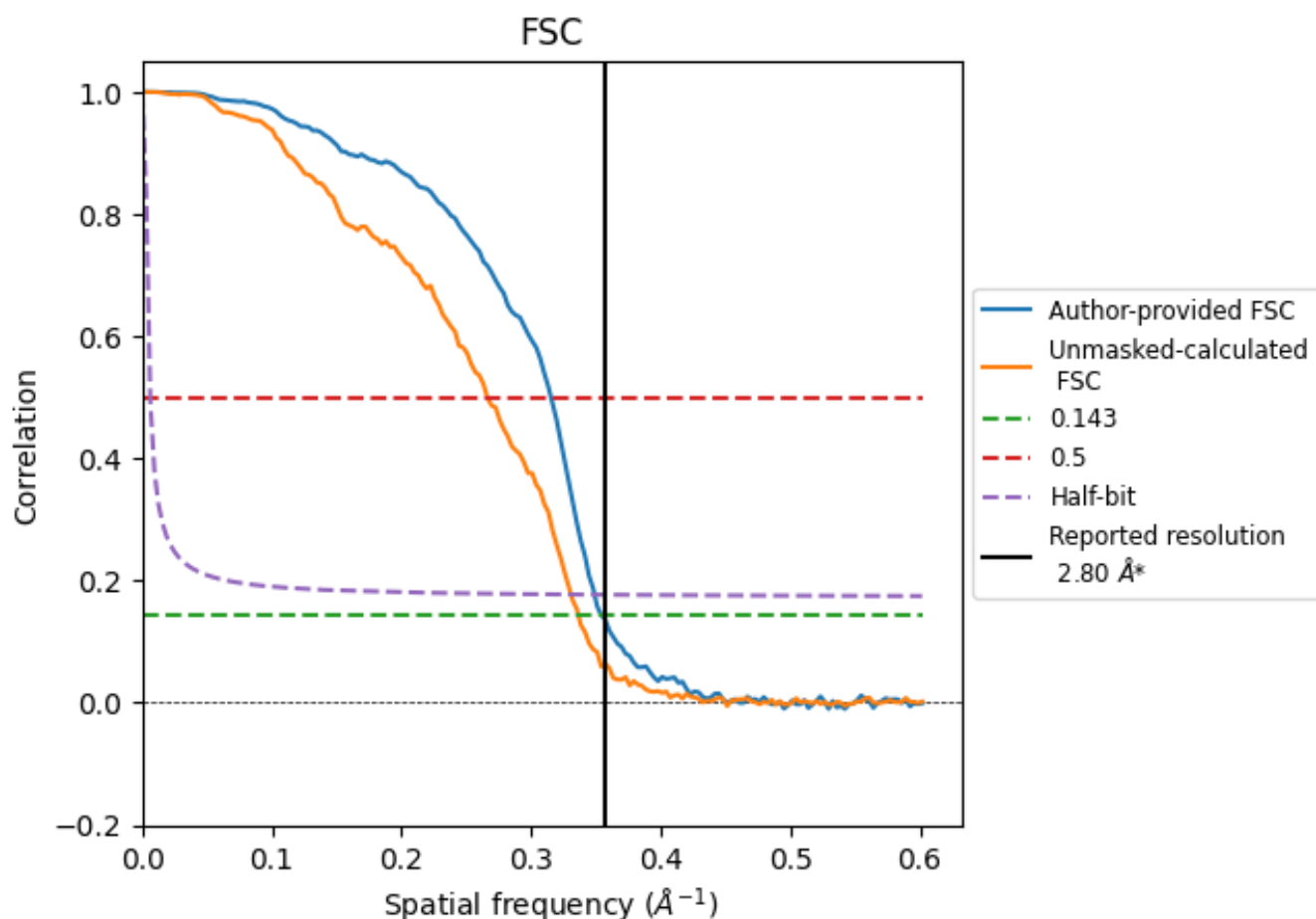


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

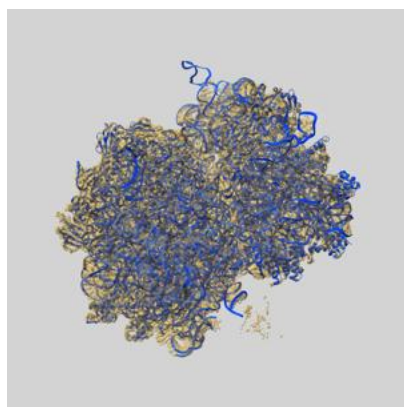
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.82	3.17	2.87
Unmasked-calculated*	2.97	3.76	3.02

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

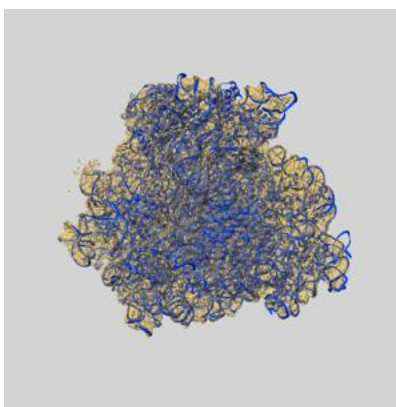
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50858 and PDB model 9FY3. Per-residue inclusion information can be found in section [3](#) on page [14](#).

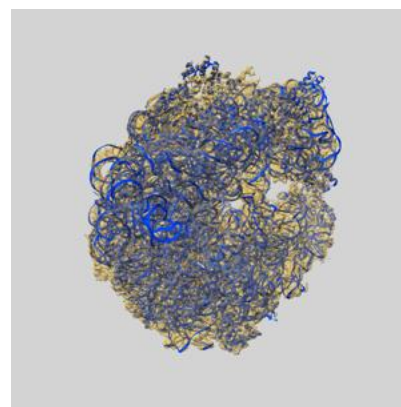
9.1 Map-model overlay [i](#)



X



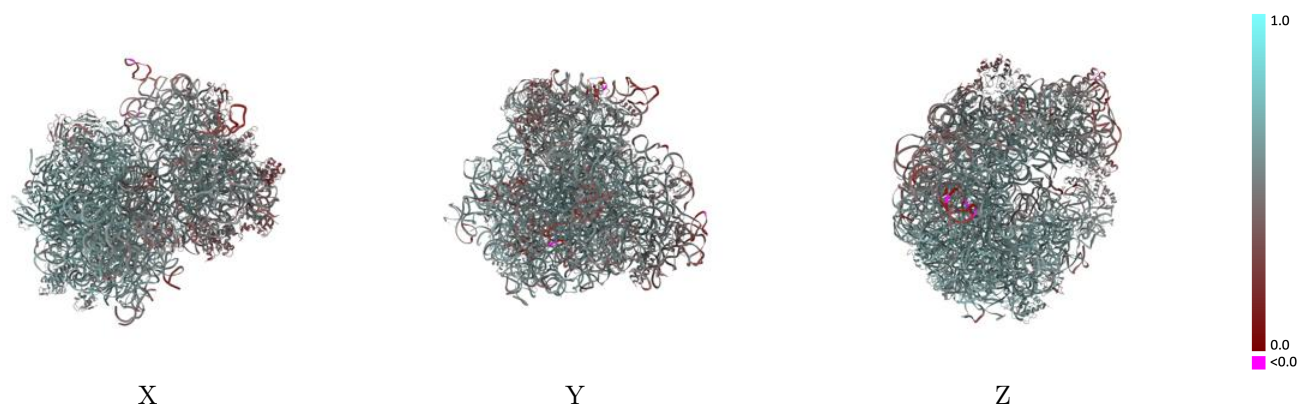
Y



Z

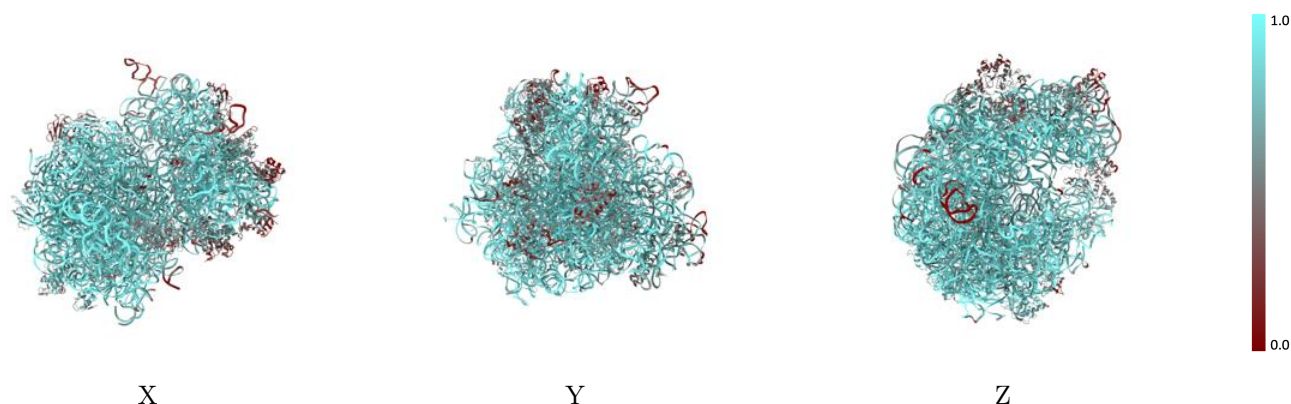
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



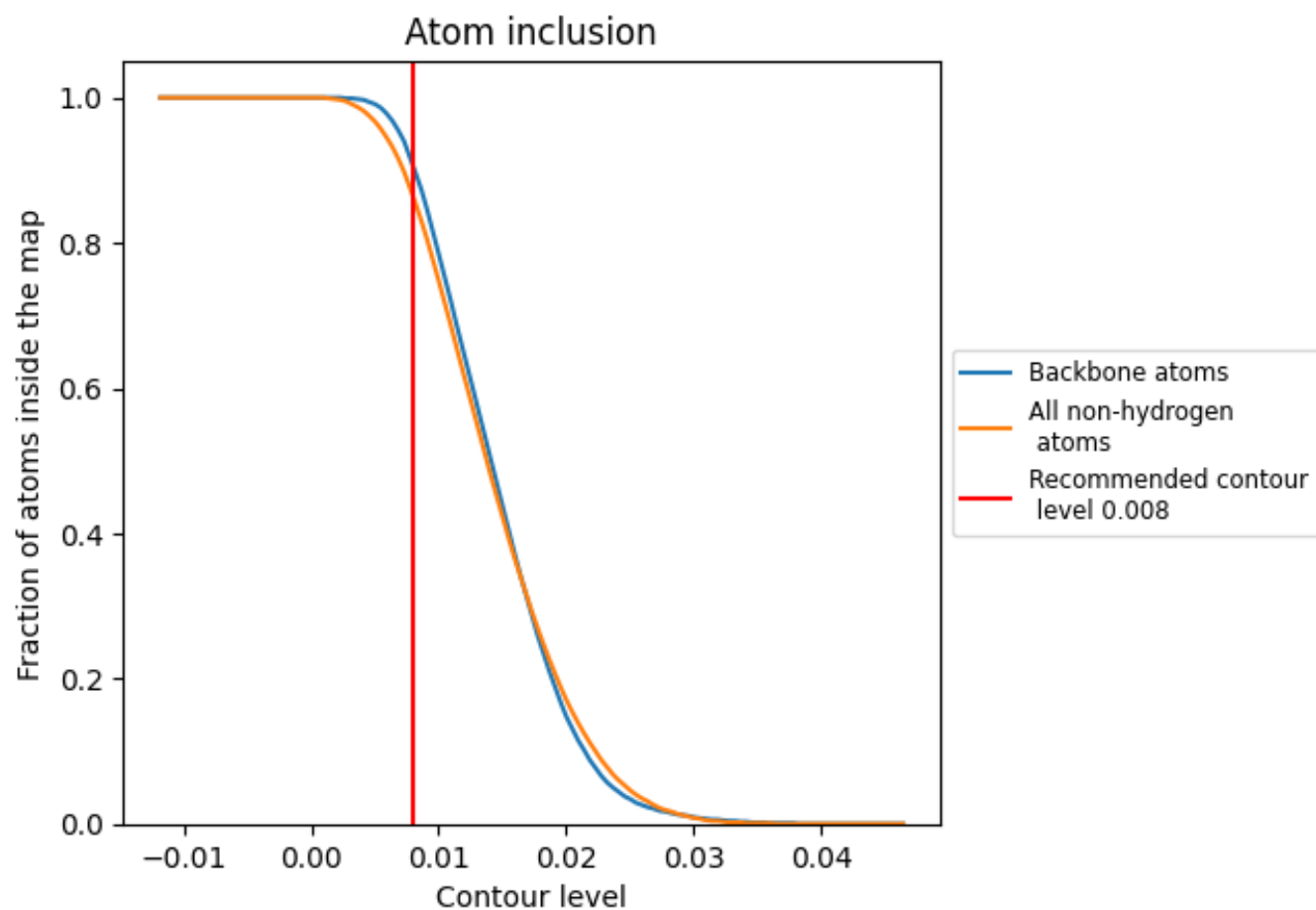
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.008).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ







































The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.5500
0	 0.8740	 0.5870
1	 0.7840	 0.5600
2	 0.9710	 0.6360
3	 0.9300	 0.6150
4	 0.8970	 0.5890
5	 0.8490	 0.5700
6	 0.3010	 0.3820
7	 0.9470	 0.5760
9	 0.7770	 0.4730
A	 0.9660	 0.6000
B	 0.9080	 0.5320
C	 0.8960	 0.6000
D	 0.8540	 0.6000
E	 0.7930	 0.5730
F	 0.5190	 0.4360
G	 0.5880	 0.4850
J	 0.8550	 0.5920
K	 0.8790	 0.5970
L	 0.8080	 0.5790
M	 0.8950	 0.6000
N	 0.8730	 0.5860
O	 0.6520	 0.5010
P	 0.7930	 0.5660
Q	 0.8860	 0.6080
R	 0.7930	 0.5920
S	 0.8740	 0.6000
T	 0.8230	 0.5710
U	 0.7270	 0.5560
W	 0.8770	 0.5930
X	 0.7150	 0.5510
Y	 0.7200	 0.5220
Z	 0.8270	 0.5760
a	 0.8800	 0.5060
b	 0.4130	 0.4040



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Chain	Atom inclusion	Q-score
c	 0.6540	 0.4870
d	 0.5420	 0.4510
e	 0.6930	 0.5190
f	 0.3660	 0.3530
g	 0.5050	 0.4150
h	 0.6730	 0.4840
i	 0.5100	 0.4270
j	 0.4850	 0.4110
k	 0.4960	 0.3980
l	 0.8400	 0.5840
m	 0.6020	 0.4540
n	 0.7990	 0.5370
o	 0.6910	 0.4840
p	 0.6250	 0.4590
q	 0.6460	 0.4840
r	 0.4880	 0.3870
s	 0.6470	 0.4710
t	 0.5890	 0.4590
v	 0.8910	 0.5130