



wwPDB EM Validation Summary Report ⓘ

Oct 19, 2025 – 01:41 AM JST

PDB ID : 9WNR / pdb_00009wnr
EMDB ID : EMD-66122
Title : Structure of E.coli ribosome in complex with an engineered arrest peptide and trigger factor
Authors : Sriramoju, M.K.; Ko, T.P.; Draczkowski, P.; Hsu, S.T.D.
Deposited on : 2025-09-05
Resolution : 2.76 Å(reported)
Based on initial model : 3JBU

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.dev129
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

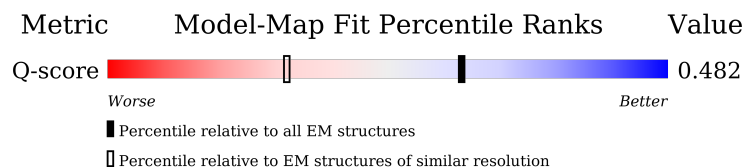
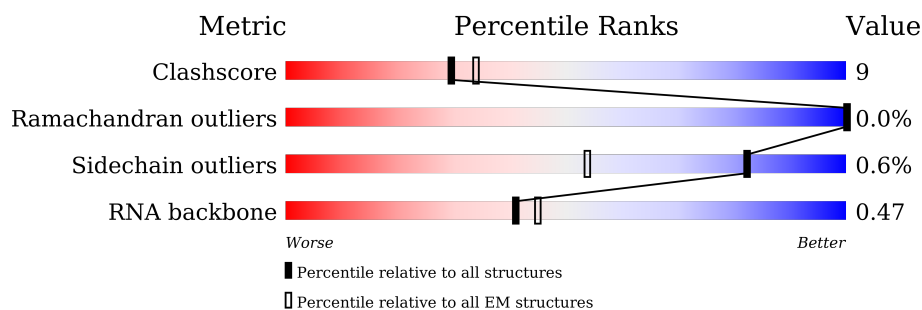
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.76 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.





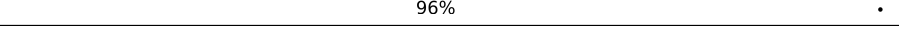
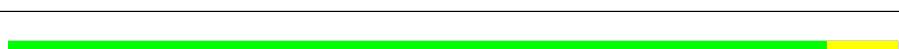
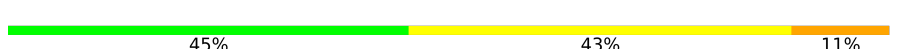


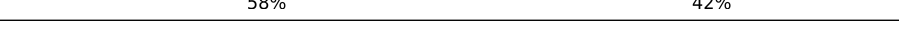



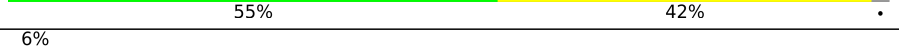

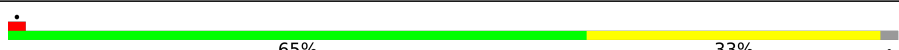


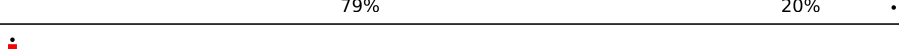







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	10642 (2.26 - 3.26)

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	78	85% 14% .
2	1	63	70% 27% .
3	2	59	76% 22% .



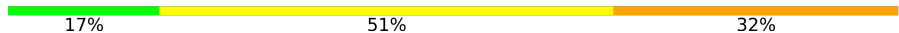
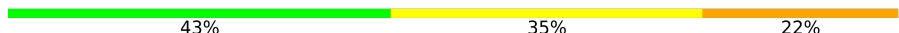
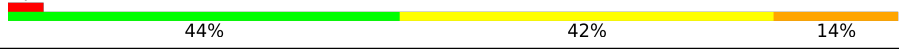















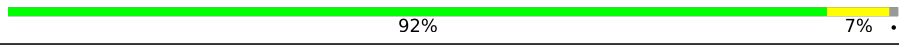
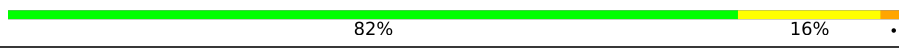
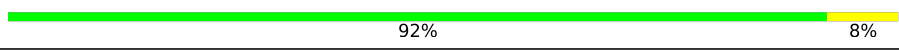


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Mol	Chain	Length	Quality of chain
4	4	57	
5	5	55	
6	6	46	
7	7	65	
8	8	38	
9	A	1533	
10	B	241	
11	C	233	
12	D	206	
13	E	167	
14	F	135	
15	G	179	
16	H	130	
17	I	130	
18	J	103	
19	K	129	
20	L	124	
21	M	118	
22	N	101	
23	O	89	
24	P	82	
25	Q	84	
26	R	75	
27	S	92	
28	T	87	




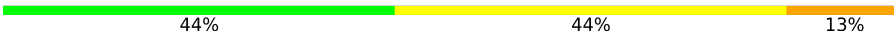
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Mol	Chain	Length	Quality of chain
29	U	71	
30	V	432	
31	X	76	
32	Y	77	
32	Z	77	
33	a	120	
34	b	2904	
35	c	273	
36	d	209	
37	e	201	
38	f	179	
39	g	177	
40	h	149	
41	k	142	
42	l	123	
43	m	144	
44	n	136	
45	o	127	
46	p	117	
47	q	115	
48	r	118	
49	s	103	
50	t	110	
51	u	100	
52	v	104	

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Mol	Chain	Length	Quality of chain
53	w	94	 88% 11% .
54	x	14	 50% 29% 21%
55	y	85	 7% 85% 14% .
56	z	39	 44% 44% 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	PRO	Z	101	-	-	X	-

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148018 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 bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 5 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 10 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 11 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	207	Total	C	N	O	S	0	0
			1632	1034	306	289	3		

- Molecule 12 is a protein called 30S ribosomal protein S4.

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

- Molecule 13 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 14 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 15 is a protein called 30S ribosomal protein S7.

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

- Molecule 16 is a protein called 30S ribosomal protein S8.

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

- Molecule 17 is a protein called 30S ribosomal protein S9.

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

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 21 is a protein called 30S ribosomal protein S13.

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

- Molecule 22 is a protein called 30S ribosomal protein S14.

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

- Molecule 23 is a protein called 30S ribosomal protein S15.

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

- Molecule 24 is a protein called 30S ribosomal protein S16.

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

- Molecule 25 is a protein called 30S ribosomal protein S17.

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

- Molecule 26 is a protein called 30S ribosomal protein S18.

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

- Molecule 27 is a protein called 30S ribosomal protein S19.

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

- Molecule 28 is a protein called 30S ribosomal protein S20.

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

- Molecule 29 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	64	Total	C	N	O	S	0	0
			529	329	110	89	1		

- Molecule 30 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	59	Total	C	N	O	S	0	0
			454	284	84	84	2		

- Molecule 31 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

- Molecule 32 is a RNA chain called P-tRNA(PRO), A-tRNA(PRO).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		
32	Z	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 33 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	120	Total	C	N	O	P	0	0
			2568	1144	468	837	119		

- Molecule 34 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 35 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 36 is a protein called 50S ribosomal protein L3.

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

- Molecule 37 is a protein called 50S ribosomal protein L4.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 39 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 40 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 41 is a protein called 50S ribosomal protein L13.

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

- Molecule 42 is a protein called 50S ribosomal protein L14.

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

- Molecule 43 is a protein called 50S ribosomal protein L15.

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

- Molecule 44 is a protein called 50S ribosomal protein L16.

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

- Molecule 45 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 46 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 47 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 48 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 49 is a protein called 50S ribosomal protein L21.

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

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

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	100	Total	C	N	O	S	0	0
			786	496	146	142	2		

- Molecule 52 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	103	Total	C	N	O	S	0	0
			788	498	148	142			

- Molecule 53 is a protein called 50S ribosomal protein L25.

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

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	14	Total	C	N	O	P	0	0
			299	133	55	97	14		

- Molecule 55 is a protein called Large ribosomal subunit protein bL27.

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

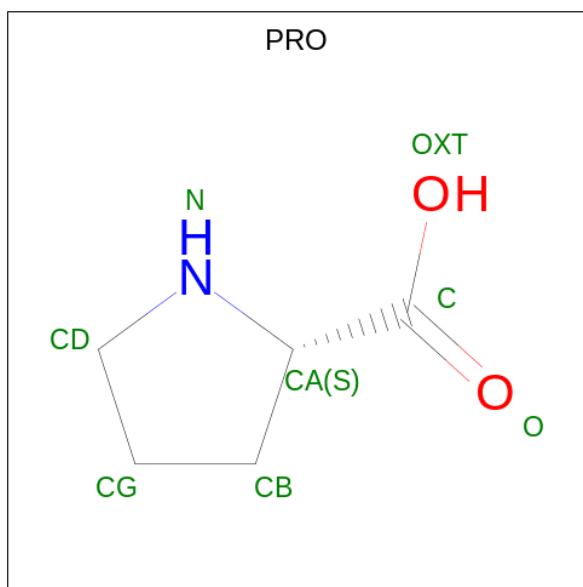
- Molecule 56 is a protein called eRAP-NC.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	39	Total	C	N	O	S	8	0
			397	259	72	64	2		

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

Mol	Chain	Residues	Atoms		AltConf
57	8	1	Total	Zn	0
			1	1	

- Molecule 58 is PROLINE (CCD ID: PRO) (formula: C₅H₉NO₂).




Mol	Chain	Residues	Atoms				AltConf
58	Z	1	Total	C	N	O	0
			7	5	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 bL28

Chain 0:  85% 14% .



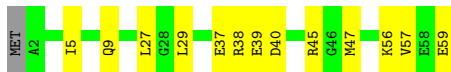
- Molecule 2: Large ribosomal subunit protein uL29

Chain 1:  70% 27% .



- Molecule 3: Large ribosomal subunit protein uL30

Chain 2:  76% 22% .




- Molecule 4: Large ribosomal subunit protein bL32

Chain 4:  75% 23% .



- Molecule 5: Large ribosomal subunit protein bL33

Chain 5:  84% 11% 5%




- Molecule 6: 50S ribosomal protein L34

Chain 6:  96% .



- Molecule 7: Large ribosomal subunit protein bL35

Chain 7:  89% 9% .



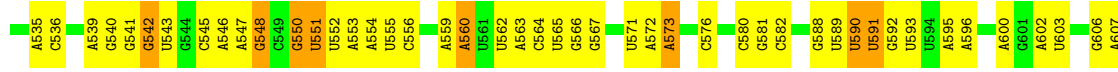
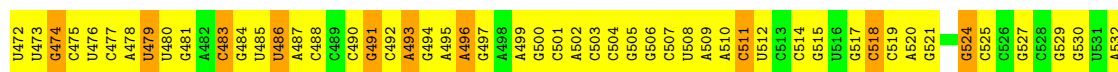
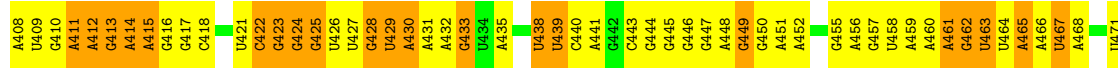
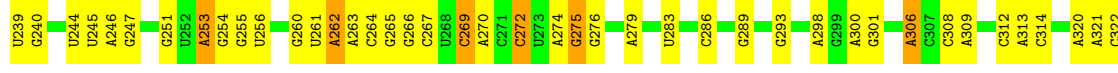
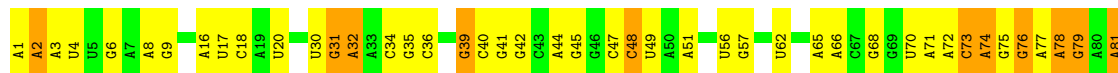
- Molecule 8: 50S ribosomal protein L36

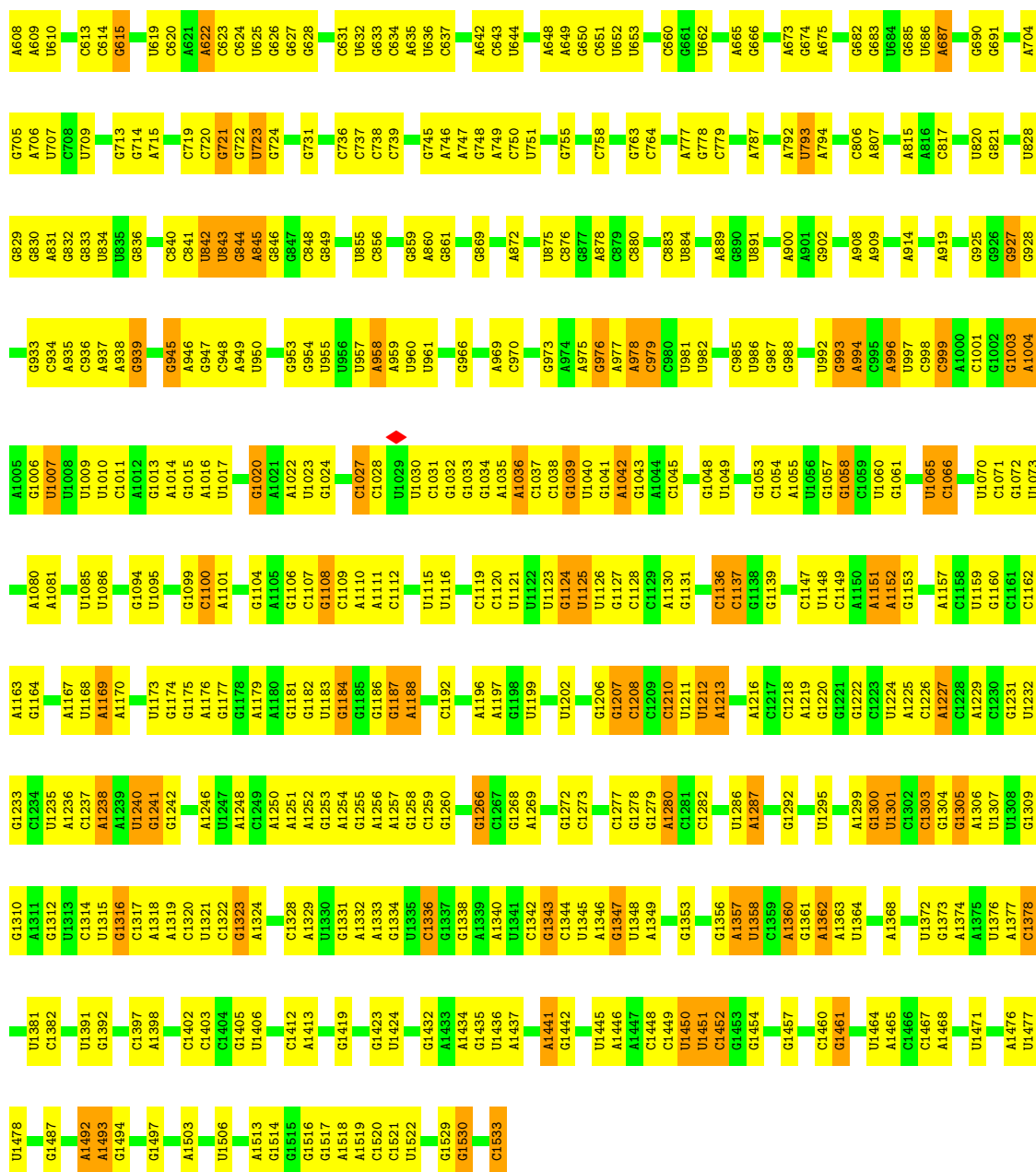
Chain 8:  92% 8% .



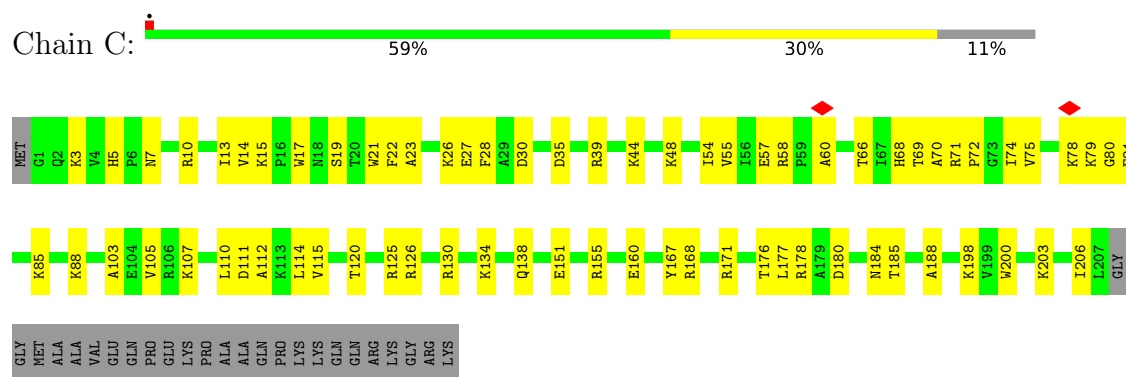
- Molecule 9: 16S rRNA

Chain A:  45% 43% 11% .

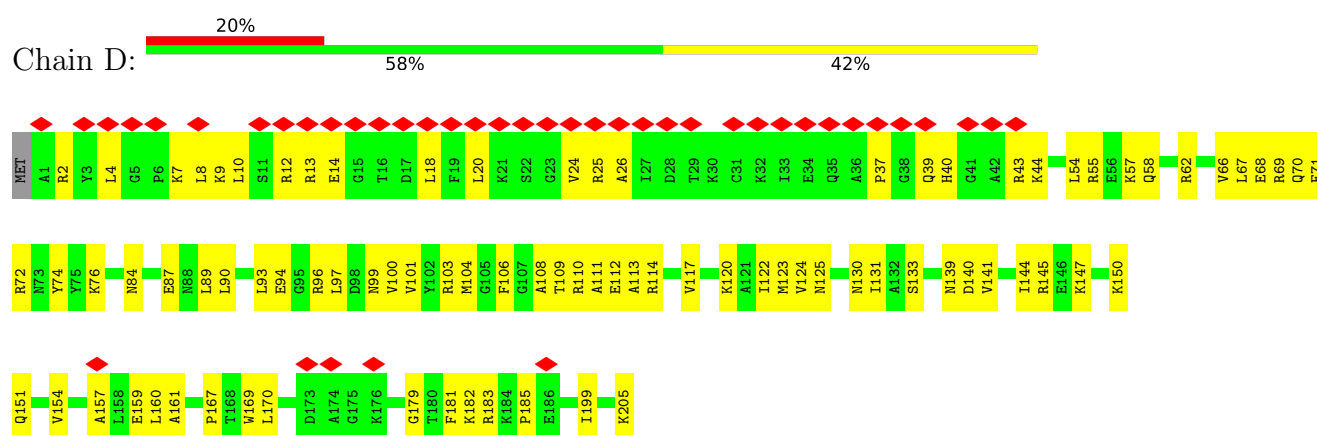




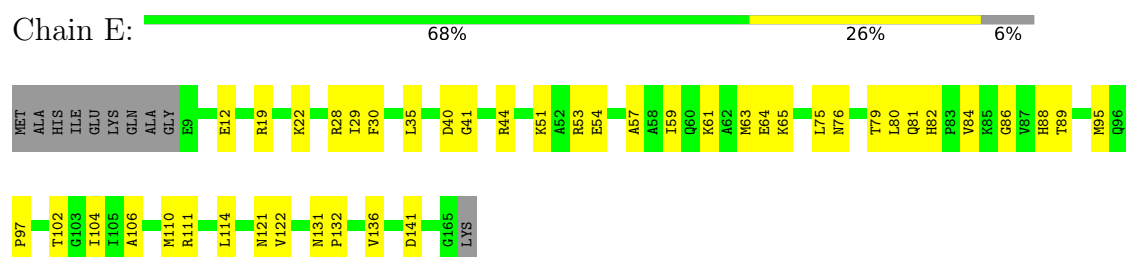
- Molecule 11: 30S ribosomal protein S3

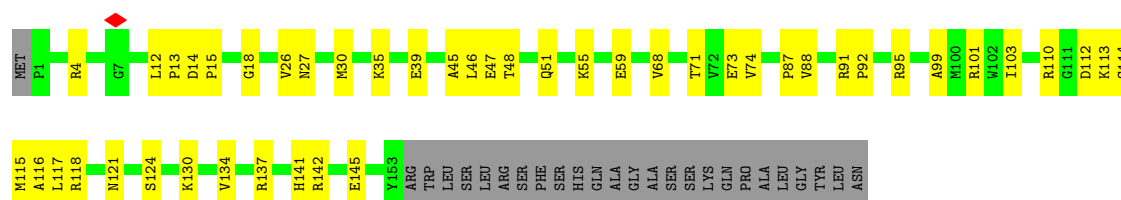


- Molecule 12: 30S ribosomal protein S4



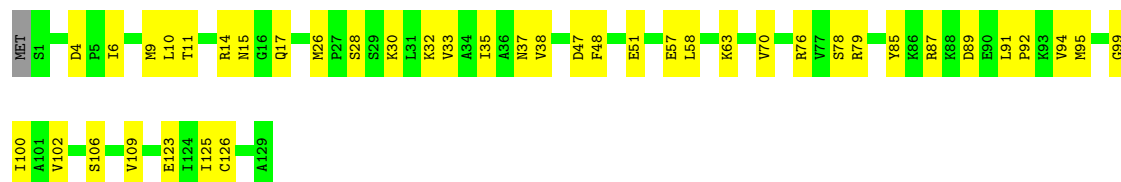
- Molecule 13: 30S ribosomal protein S5





• Molecule 16: 30S ribosomal protein S8

Chain H: 68% 32%



• Molecule 17: 30S ribosomal protein S9

Chain I: 55% 42%



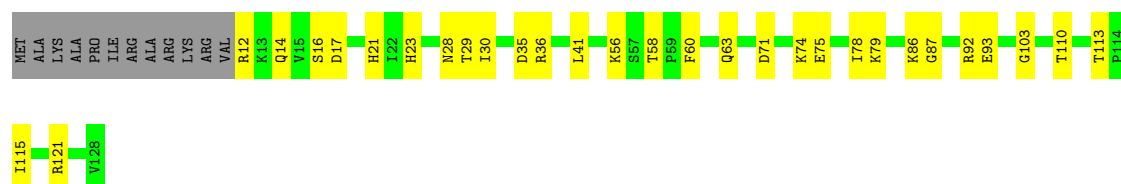
• Molecule 18: 30S ribosomal protein S10

Chain J: 6% 60% 37%

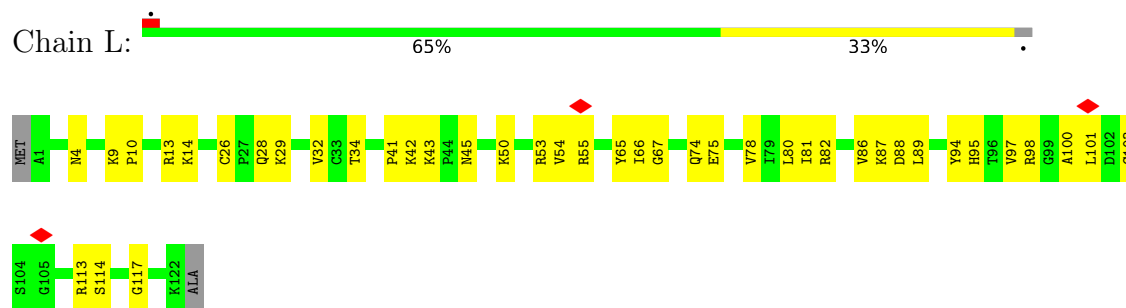


• Molecule 19: Small ribosomal subunit protein uS11

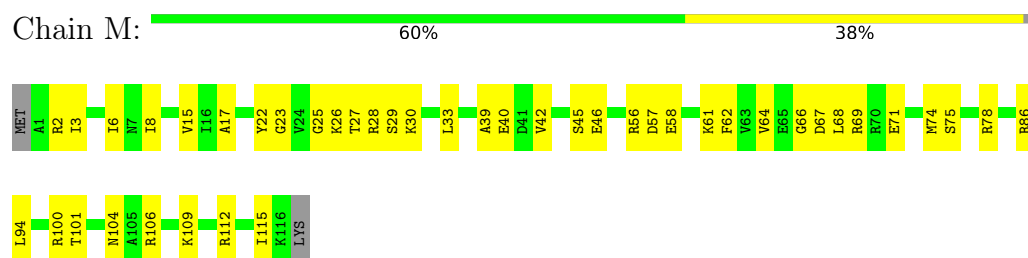
Chain K: 67% 23% 9%



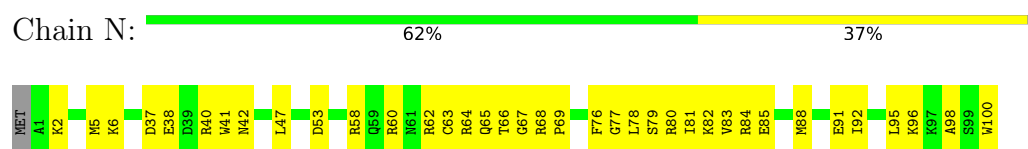
• Molecule 20: Small ribosomal subunit protein uS12



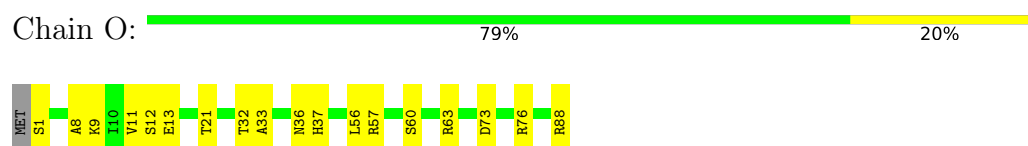
- Molecule 21: 30S ribosomal protein S13



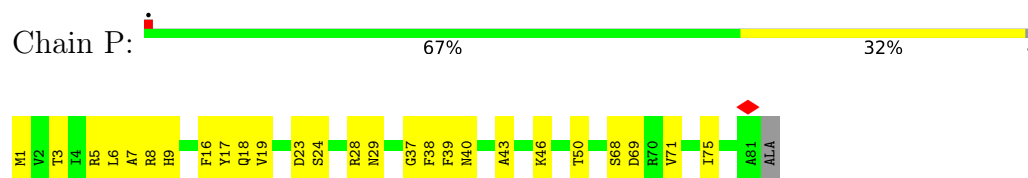
- Molecule 22: 30S ribosomal protein S14



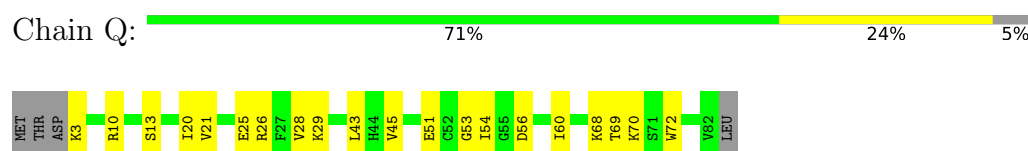
- Molecule 23: 30S ribosomal protein S15



- Molecule 24: 30S ribosomal protein S16



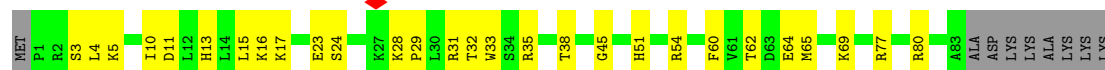
- Molecule 25: 30S ribosomal protein S17



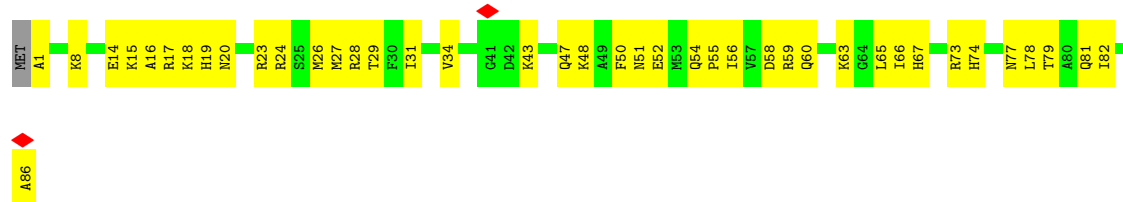
- Molecule 26: 30S ribosomal protein S18



- Molecule 27: 30S ribosomal protein S19



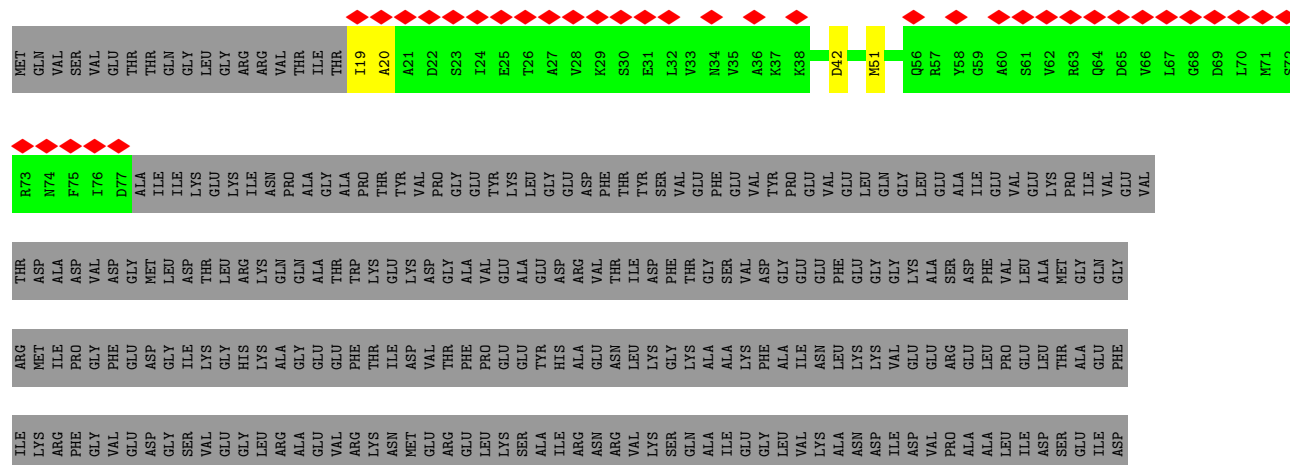
- Molecule 28: 30S ribosomal protein S20



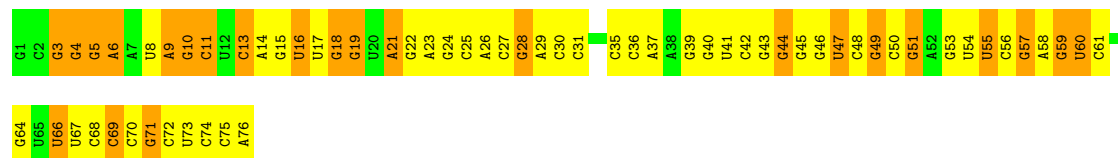
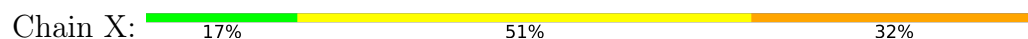
- Molecule 29: 30S ribosomal protein S21



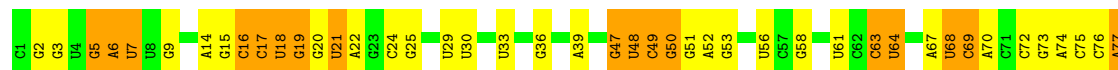
- Molecule 30: Trigger factor



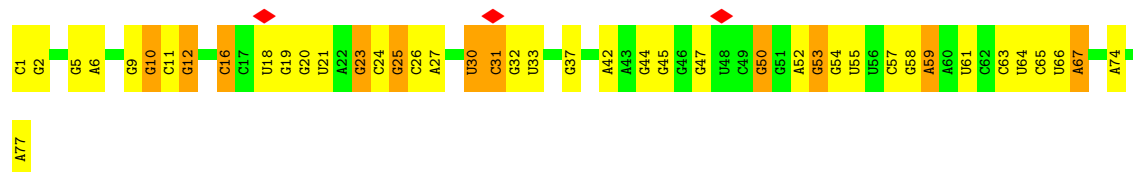
- Molecule 31: E-tRNA



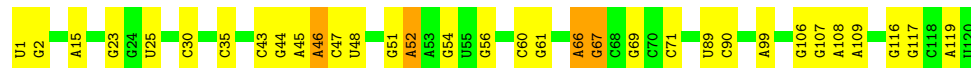
- Molecule 32: P-tRNA(PRO), A-tRNA(PRO)



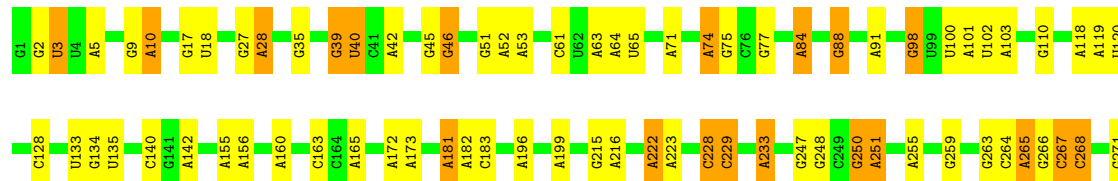
- Molecule 32: P-tRNA(PRO), A-tRNA(PRO)



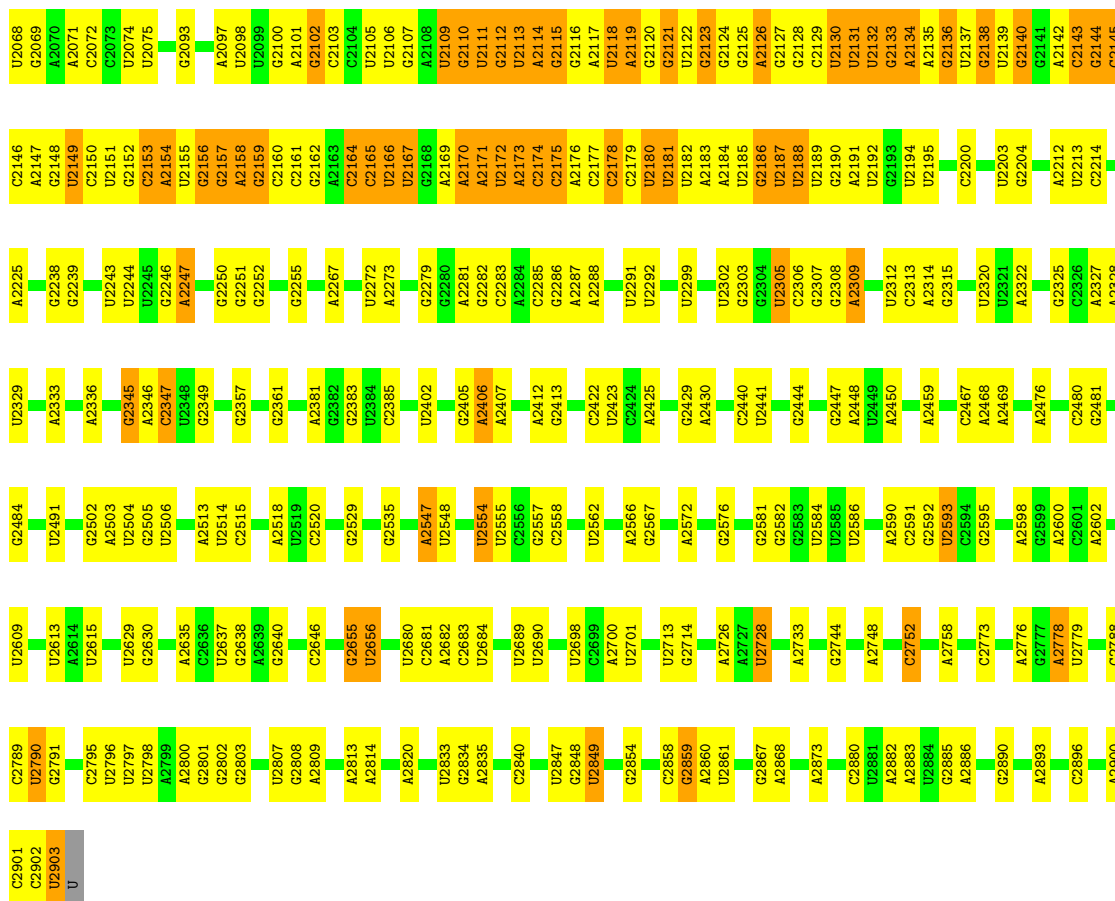
- Molecule 33: 5S rRNA



- Molecule 34: 23S rRNA

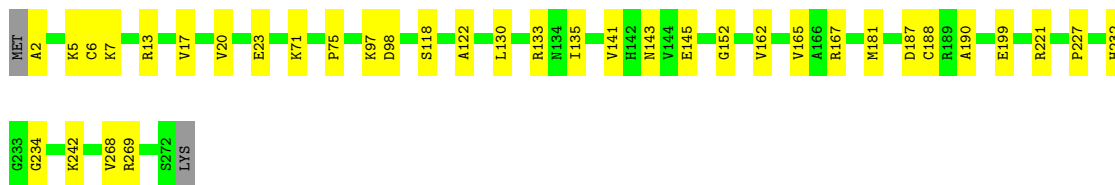


A1927	U1796	G1874	U1539	G1436	G1382	G1186	A1085	A1009	C890	A764	C640	A529	G400	A272
A1928	G1797	C1675	G1540	C1437	G1337	G1195	A1086	U1012	C891	C765	U641	G530	A401	G273
G1929	U1798	A1676	C1541	U1438	G1337	G1195	A1087	U1012	A892	U642	A643	C531	A402	U276
G1930	G1799	A1677	G1543	A1439	G1338	G1198	A1088	C1013	C893	A644	A643	A532	U403	G277
U1931	C1800	G1703	G1543	U1443	G1339	U1199	A1089	A1014	U894	G774	A644	U534	A404	A278
A1936	A1802	C1704	A1548	G1444	U1340	U1199	A1090	U1019	U895	G775	G645	U534	U405	A279
A1937	A1803	G1710	A1549	A1453	G1341	A1205	G1091	A1019	U896	G776	U646	A538	G411	U280
A1938	G1803	G1711	A1552	A1453	G1341	G1206	C1092	A1020	C897	G776	G647	A538	A412	C281
U1943	A1808	A1713	A1553	G1459	U1352	G1206	A1094	A1021	C898	A782	U653	U546	C413	A282
U1945	A1810	U1716	A1553	U1460	U1353	G1210	A1095	A1022	A900	A783	A654	A547	G414	G283
A1960	G1811	G1716	G1560	A1461	A1354	G1210	A1096	G1026	C901	A785	A655	G549	A415	U284
U1963	C1816	G1721	C1561	C1469	G1361	G1223	A1098	U1033	C902	A792	U657	C550	C417	U286
U1963	A1722	G1722	C1562	A1470	C1362	U1224	G1099	U1033	A910	G805	U658	G555	C418	G287
G1964	A1829	G1723	U1563	A1471	A1365	U1230	C1102	G1038	C912	C812	A668	A556	U419	U288
C1965	A1847	G1724	C1565	G1475	A1366	U1231	A1103	A1039	U913	U826	A669	C557	C420	U290
A1966	A1848	C1727	G1566	U1476	U1379	U1234	U1105	G1041	G914	U828	A670	A563	A429	G295
C1967	A1851	G1728	G1567	A1477	U1383	G1235	U1107	G1042	A927	U829	U686	A563	G424	G307
A1970	U1852	U1729	G1568	G1482	A1384	G1236	G1108	G1047	U932	U829	G701	U568	A428	A310
A1853	A1853	C1730	A1570	U1483	A1385	U1237	C1109	A1048	U932	U827	G704	G570	A430	A311
G1972	A1854	G1733	U1576	U1484	C1386	G1238	G1110	C1049	G938	U827	A705	A571	C445	A330
A1977	G1857	G1734	C1577	U1485	A1387	A1241	A1111	A1050	A941	U828	A706	A572	U451	A346
A1858	U1736	U1736	U1578	U1486	A1392	G1250	G1112	C1052	A941	U832	A706	A573	A461	A346
G1992	G1737	C1488	U1584	U1487	A1393	G1250	G1113	G1053	A941	U832	A706	A573	A461	A346
U1993	G1862	G1489	C1585	C1489	U1394	A1253	G1115	A1054	C946	A833	U709	A575	A467	A346
C1997	U1885	U1491	A1586	U1490	A1395	G1256	G1116	G1055	G952	A845	G713	U580	C461	U349
A1998	A1866	G1492	U1589	G1492	G1401	G1266	U1132	G1056	U955	U846	U714	A582	G465	G356
A2015	C1870	A1493	A1590	C1493	U1402	U1267	A1133	U1058	G956	G856	A716	C587	G466	C357
C2023	A1871	A1494	U1593	A1494	A1403	U1267	G1134	G1059	U970	U871	G726	A603	A479	C364
G2024	G1875	G1753	U1594	C1495	C1404	A1268	C1135	U1060	C971	U872	A727	G604	A480	U365
C2025	A1876	A1754	C1595	A1496	U1405	A1269	G1136	U1061	A959	U872	G728	A608	A481	C366
A2030	U1880	G1756	A1596	U1497	U1406	G1270	G1136	G1062	A960	C873	G729	A609	A482	G367
A2031	A1883	A1757	A1597	C1498	G1407	G1271	U1141	G1063	C961	C874	A730	A613	A483	A368
C2032	G1884	U1758	A1598	A1504	U1411	U1272	A1142	C1064	C964	A877	A730	A614	C487	U369
A2033	A1885	A1762	C1607	A1505	U1411	A1276	G1149	U1066	G969	A878	G738	U615	G491	A371
C2043	A1885	G1763	A1609	C1507	C1417	G1277	C1150	A1067	U970	A879	A739	A621	A492	G372
G2052	G1888	C1764	A1610	A1509	G1418	U1281	G1166	G1068	C972	C880	C740	A621	G493	G386
A2052	A1901	A1773	A1618	G1510	A1420	U1282	G1167	A1070	A984	C881	A730	A621	A493	U387
C2053	G1906	G1776	U1636	U1520	G1421	C1291	C1168	C1072	A981	A878	G738	U615	A492	G386
G2056	A1913	U1779	A1637	U1523	G1425	G1292	G1172	C1075	C982	G879	A739	A621	A493	U387
A2060	C1914	C1531	C1646	C1531	G1426	G1292	U1173	G1074	A984	C880	A739	A621	A493	U387
C2061	G1914	A1783	U1647	A1532	A1427	G1292	U1174	C1075	A984	C881	A739	A621	A493	U387
A2062	U1915	A1784	C1533	C1533	C1428	G1300	U1175	U1078	A990	G882	G745	A627	A505	G389
A2062	G1916	U1648	C1533	C1533	C1428	A1301	U1176	C1079	A990	U884	U746	A627	A505	G389
C2063	U1917	G1649	U1534	U1534	A1431	C1315	G1177	A1080	A996	C885	G748	A627	A505	U390
C2064	A1918	A1789	A1535	A1535	G1432	C1319	C1178	U1081	A996	A886	G748	A627	A505	A391
C2065	U1919	C1790	C1536	C1536	A1433	C1320	U1179	U1082	U999	A887	A752	A627	A505	G396
		U1791	U1656	U1538	G1435	A1321	U1181	A1084	A1000	C888	G757	A627	A505	G396



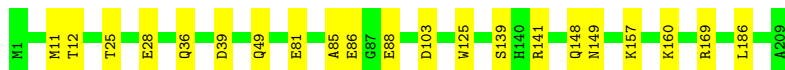
- Molecule 35: Large ribosomal subunit protein uL2

Chain c: 86% 13%



- Molecule 36: 50S ribosomal protein L3

Chain d: 90% 10%

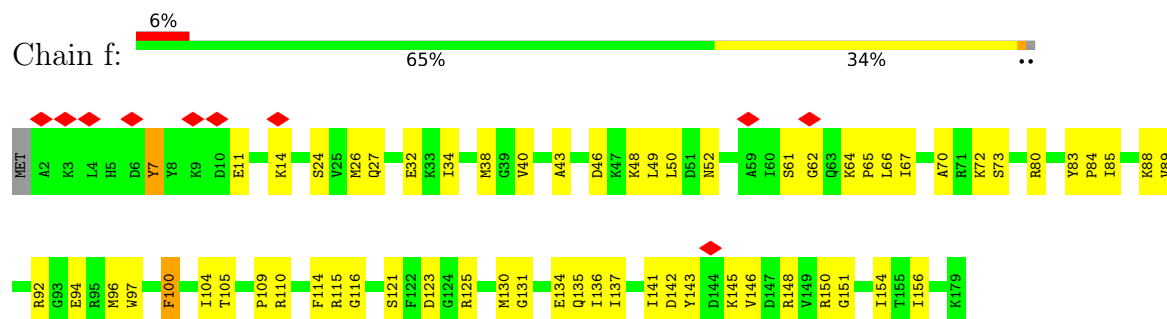


- Molecule 37: 50S ribosomal protein L4

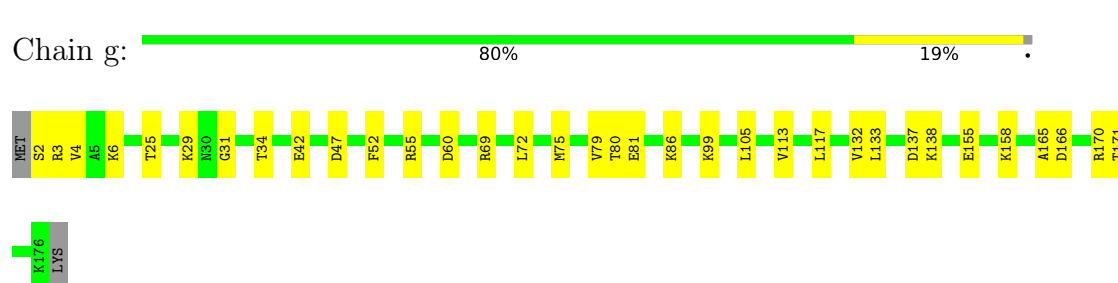
Chain e: 88% 12%



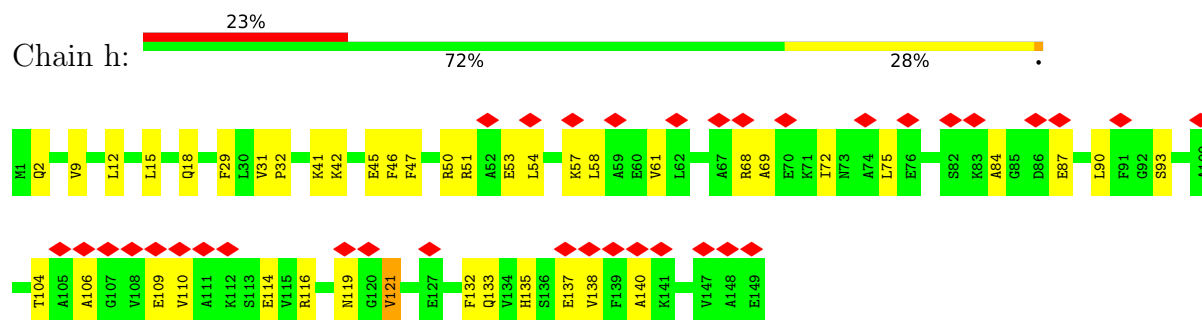
- Molecule 38: Large ribosomal subunit protein uL5



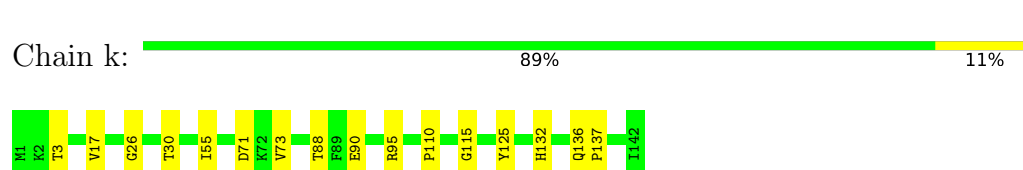
- Molecule 39: Large ribosomal subunit protein uL6



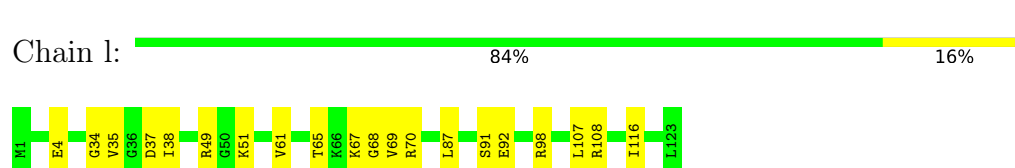
- Molecule 40: 50S ribosomal protein L9



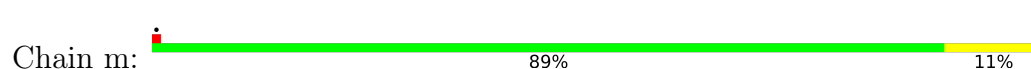
- Molecule 41: 50S ribosomal protein L13



- Molecule 42: 50S ribosomal protein L14



- Molecule 43: 50S ribosomal protein L15





- Molecule 44: 50S ribosomal protein L16

Chain n: 83% 15% ..



- Molecule 45: Large ribosomal subunit protein bL17

Chain o: 84% 10% 6%



- Molecule 46: Large ribosomal subunit protein uL18

Chain p: 85% 15% .



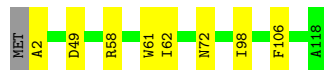
- Molecule 47: Large ribosomal subunit protein bL19

Chain q: 88% 11% .



- Molecule 48: Large ribosomal subunit protein bL20

Chain r: 92% 7% .



- Molecule 49: 50S ribosomal protein L21

Chain s: 82% 16% .

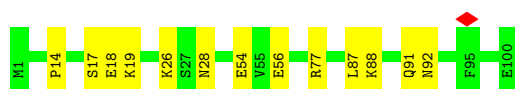
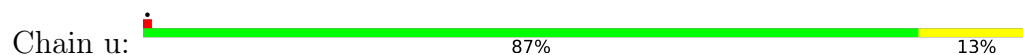


- Molecule 50: 50S ribosomal protein L22

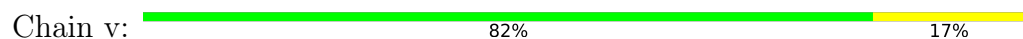
Chain t: 92% 8%



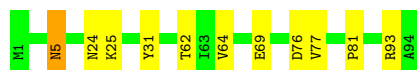
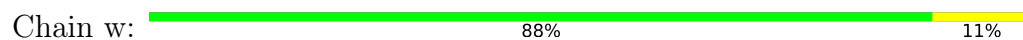
- Molecule 51: Large ribosomal subunit protein uL23



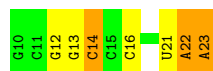
- Molecule 52: 50S ribosomal protein L24



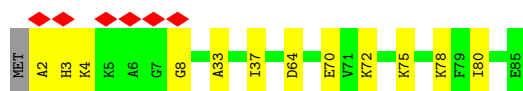
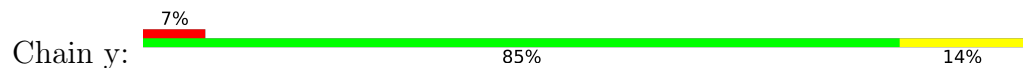
- Molecule 53: 50S ribosomal protein L25



- Molecule 54: mRNA



- Molecule 55: Large ribosomal subunit protein bL27



- Molecule 56: eRAP-NC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72313	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.235	Depositor
Minimum map value	-0.701	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	682.0, 682.0, 682.0	wwPDB
Map dimensions	620, 620, 620	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
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	0.19	0/635	0.30	0/848
2	1	0.18	0/496	0.29	0/660
3	2	0.21	0/453	0.29	0/605
4	4	0.22	0/450	0.33	0/599
5	5	0.18	0/433	0.28	0/576
6	6	0.23	0/380	0.32	0/498
7	7	0.22	0/513	0.27	0/676
8	8	0.24	0/303	0.24	0/397
9	A	0.15	0/36834	0.27	0/57462
10	B	0.12	0/1735	0.29	0/2338
11	C	0.13	0/1659	0.27	0/2236
12	D	0.11	0/1665	0.28	0/2227
13	E	0.16	0/1169	0.31	0/1573
14	F	0.16	0/881	0.31	0/1189
15	G	0.11	0/1219	0.25	0/1635
16	H	0.15	0/989	0.29	0/1326
17	I	0.12	0/1034	0.32	0/1375
18	J	0.13	0/813	0.35	0/1100
19	K	0.15	0/893	0.27	0/1205
20	L	0.15	0/963	0.33	0/1293
21	M	0.12	0/909	0.28	0/1215
22	N	0.12	0/817	0.24	0/1088
23	O	0.15	0/722	0.26	0/964
24	P	0.11	0/653	0.26	0/877
25	Q	0.13	0/657	0.31	0/881
26	R	0.14	0/553	0.27	0/742
27	S	0.12	0/680	0.33	0/915
28	T	0.16	0/676	0.28	0/895
29	U	0.12	0/536	0.35	0/711
30	V	0.15	0/457	0.42	0/612
31	X	0.12	0/1810	0.27	0/2820
32	Y	0.14	0/1840	0.27	0/2866

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.12	0/1840	0.25	0/2866
33	a	0.17	0/2869	0.26	0/4474
34	b	0.21	0/69800	0.30	0/108892
35	c	0.22	0/2121	0.30	0/2852
36	d	0.22	0/1586	0.33	0/2134
37	e	0.21	0/1571	0.28	0/2113
38	f	0.15	0/1443	0.36	0/1937
39	g	0.15	0/1333	0.26	0/1805
40	h	0.12	0/1121	0.26	0/1515
41	k	0.28	1/1152 (0.1%)	0.27	0/1551
42	l	0.20	0/955	0.34	0/1279
43	m	0.21	0/1062	0.31	0/1413
44	n	0.23	0/1093	0.49	2/1460 (0.1%)
45	o	0.22	0/973	0.30	0/1301
46	p	0.16	0/902	0.26	0/1209
47	q	0.21	0/929	0.27	0/1242
48	r	0.24	0/960	0.28	0/1278
49	s	0.22	0/829	0.35	0/1107
50	t	0.23	0/864	0.26	0/1156
51	u	0.19	0/793	0.29	0/1060
52	v	0.20	0/796	0.36	0/1062
53	w	0.18	0/766	0.30	0/1025
54	x	0.14	0/333	0.27	0/517
55	y	0.21	0/642	0.27	0/848
56	z	0.26	0/415	0.37	0/567
All	All	0.19	1/160975 (0.0%)	0.29	2/241067 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	k	136	GLN	C-O	-5.86	1.21	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	n	69	PRO	CA-N-CD	-9.77	98.32	112.00
44	n	68	PHE	C-N-CD	-5.81	101.18	125.00

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	0	625	0	652	9	0
2	1	495	0	526	13	0
3	2	449	0	488	8	0
4	4	444	0	458	11	0
5	5	426	0	464	4	0
6	6	377	0	418	1	0
7	7	504	0	572	3	0
8	8	302	0	341	2	0
9	A	32895	0	16553	612	0
10	B	1704	0	1732	53	0
11	C	1632	0	1710	58	0
12	D	1643	0	1710	85	0
13	E	1156	0	1199	32	0
14	F	862	0	864	30	0
15	G	1203	0	1256	40	0
16	H	979	0	1034	37	0
17	I	1022	0	1070	54	0
18	J	803	0	842	40	0
19	K	877	0	887	24	0
20	L	949	0	1014	37	0
21	M	900	0	968	38	0
22	N	805	0	847	40	0
23	O	714	0	737	19	0
24	P	643	0	661	28	0
25	Q	648	0	691	17	0
26	R	544	0	565	16	0
27	S	663	0	690	26	0
28	T	670	0	722	36	0
29	U	529	0	565	14	0
30	V	454	0	476	3	0
31	X	1621	0	820	56	0
32	Y	1647	0	832	42	0
32	Z	1647	0	832	26	0
33	a	2568	0	1302	21	0
34	b	62321	0	31344	518	0
35	c	2082	0	2154	23	0
36	d	1565	0	1616	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	e	1552	0	1619	18	0
38	f	1419	0	1457	56	0
39	g	1313	0	1358	22	0
40	h	1110	0	1148	28	0
41	k	1129	0	1162	11	0
42	l	946	0	1023	18	0
43	m	1053	0	1129	12	0
44	n	1074	0	1157	24	0
45	o	960	0	1000	19	0
46	p	892	0	923	15	0
47	q	917	0	962	10	0
48	r	947	0	1019	6	0
49	s	816	0	839	13	0
50	t	857	0	922	9	0
51	u	786	0	846	12	0
52	v	788	0	844	12	0
53	w	753	0	780	6	0
54	x	299	0	154	6	0
55	y	634	0	653	10	0
56	z	397	0	368	25	0
57	8	1	0	0	0	0
58	Z	7	0	7	4	0
All	All	148018	0	98982	2157	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 9.

The worst 5 of 2157 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)
36:d:11:MET:CG	36:d:25:THR:HG22	1.67	1.23
24:P:6:LEU:CD1	24:P:71:VAL:CG2	2.20	1.19
26:R:32:ILE:HG23	26:R:37:LYS:O	1.43	1.17
32:Y:77:A:O3'	56:z:162:PRO:C	1.90	1.14
24:P:6:LEU:HD13	24:P:71:VAL:CG2	1.80	1.10

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	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
3	2	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
4	4	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
5	5	50/55 (91%)	47 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
7	7	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
10	B	216/241 (90%)	197 (91%)	19 (9%)	0	100	100
11	C	205/233 (88%)	190 (93%)	15 (7%)	0	100	100
12	D	203/206 (98%)	183 (90%)	20 (10%)	0	100	100
13	E	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
14	F	104/135 (77%)	98 (94%)	6 (6%)	0	100	100
15	G	151/179 (84%)	143 (95%)	8 (5%)	0	100	100
16	H	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
17	I	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
18	J	98/103 (95%)	83 (85%)	15 (15%)	0	100	100
19	K	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
20	L	120/124 (97%)	105 (88%)	15 (12%)	0	100	100
21	M	114/118 (97%)	106 (93%)	8 (7%)	0	100	100
22	N	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
23	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
24	P	79/82 (96%)	68 (86%)	11 (14%)	0	100	100
25	Q	78/84 (93%)	71 (91%)	7 (9%)	0	100	100
26	R	64/75 (85%)	62 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	S	81/92 (88%)	73 (90%)	8 (10%)	0	100	100
28	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
29	U	62/71 (87%)	54 (87%)	8 (13%)	0	100	100
30	V	57/432 (13%)	54 (95%)	3 (5%)	0	100	100
35	c	269/273 (98%)	256 (95%)	13 (5%)	0	100	100
36	d	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
37	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
38	f	176/179 (98%)	159 (90%)	17 (10%)	0	100	100
39	g	173/177 (98%)	164 (95%)	9 (5%)	0	100	100
40	h	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
41	k	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
42	l	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
43	m	142/144 (99%)	125 (88%)	17 (12%)	0	100	100
44	n	134/136 (98%)	126 (94%)	7 (5%)	1 (1%)	19	32
45	o	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
46	p	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
47	q	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
48	r	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
49	s	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
50	t	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
51	u	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
52	v	101/104 (97%)	88 (87%)	13 (13%)	0	100	100
53	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
55	y	82/85 (96%)	82 (100%)	0	0	100	100
56	z	45/39 (115%)	37 (82%)	8 (18%)	0	100	100
All	All	5652/6314 (90%)	5264 (93%)	387 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
44	n	69	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	48/49 (98%)	48 (100%)	0	100	100
4	4	47/48 (98%)	47 (100%)	0	100	100
5	5	47/49 (96%)	46 (98%)	1 (2%)	48	69
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/34 (100%)	34 (100%)	0	100	100
10	B	180/199 (90%)	179 (99%)	1 (1%)	84	90
11	C	171/190 (90%)	171 (100%)	0	100	100
12	D	172/173 (99%)	172 (100%)	0	100	100
13	E	119/126 (94%)	119 (100%)	0	100	100
14	F	92/116 (79%)	92 (100%)	0	100	100
15	G	126/147 (86%)	126 (100%)	0	100	100
16	H	104/105 (99%)	104 (100%)	0	100	100
17	I	105/107 (98%)	105 (100%)	0	100	100
18	J	88/90 (98%)	88 (100%)	0	100	100
19	K	90/99 (91%)	90 (100%)	0	100	100
20	L	103/104 (99%)	103 (100%)	0	100	100
21	M	94/96 (98%)	94 (100%)	0	100	100
22	N	83/84 (99%)	83 (100%)	0	100	100
23	O	76/77 (99%)	76 (100%)	0	100	100
24	P	65/65 (100%)	65 (100%)	0	100	100
25	Q	74/78 (95%)	74 (100%)	0	100	100
26	R	57/65 (88%)	57 (100%)	0	100	100
27	S	72/79 (91%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	T	65/66 (98%)	65 (100%)	0	100	100
29	U	54/61 (88%)	54 (100%)	0	100	100
30	V	49/359 (14%)	49 (100%)	0	100	100
35	c	216/218 (99%)	216 (100%)	0	100	100
36	d	164/164 (100%)	164 (100%)	0	100	100
37	e	165/165 (100%)	165 (100%)	0	100	100
38	f	149/150 (99%)	147 (99%)	2 (1%)	65	80
39	g	136/138 (99%)	134 (98%)	2 (2%)	60	76
40	h	114/114 (100%)	112 (98%)	2 (2%)	54	72
41	k	116/116 (100%)	116 (100%)	0	100	100
42	l	104/104 (100%)	103 (99%)	1 (1%)	73	84
43	m	103/103 (100%)	103 (100%)	0	100	100
44	n	109/109 (100%)	109 (100%)	0	100	100
45	o	100/103 (97%)	100 (100%)	0	100	100
46	p	86/87 (99%)	86 (100%)	0	100	100
47	q	99/100 (99%)	97 (98%)	2 (2%)	50	70
48	r	89/90 (99%)	89 (100%)	0	100	100
49	s	84/84 (100%)	79 (94%)	5 (6%)	16	29
50	t	93/93 (100%)	93 (100%)	0	100	100
51	u	84/84 (100%)	83 (99%)	1 (1%)	67	81
52	v	84/85 (99%)	83 (99%)	1 (1%)	67	81
53	w	78/78 (100%)	76 (97%)	2 (3%)	41	63
55	y	62/63 (98%)	61 (98%)	1 (2%)	58	75
56	z	39/33 (118%)	29 (74%)	10 (26%)	0	0
All	All	4699/5160 (91%)	4668 (99%)	31 (1%)	82	89

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	s	54	VAL
56	z	153[A]	SER
52	v	66	GLN
56	z	156[A]	TRP
56	z	132	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
23	O	49	HIS
36	d	49	GLN
50	t	61	ASN
24	P	63	GLN
28	T	51	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	X	75/76 (98%)	39 (52%)	0
32	Y	76/77 (98%)	20 (26%)	2 (2%)
32	Z	76/77 (98%)	19 (25%)	0
33	a	119/120 (99%)	17 (14%)	0
34	b	2902/2904 (99%)	599 (20%)	0
54	x	13/14 (92%)	5 (38%)	0
9	A	1532/1533 (99%)	362 (23%)	12 (0%)
All	All	4793/4801 (99%)	1061 (22%)	14 (0%)

5 of 1061 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	2	A
9	A	4	U
9	A	6	G
9	A	9	G
9	A	16	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1003	G
9	A	1065	U
32	Y	16	C
9	A	1493	A
32	Y	6	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	PRO	Z	101	32	5,7,8	0.46	0	7,8,10	1.44	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PRO	Z	101	32	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Z	101	PRO	O-C-CA	-2.35	118.62	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Z	101	PRO	4	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.

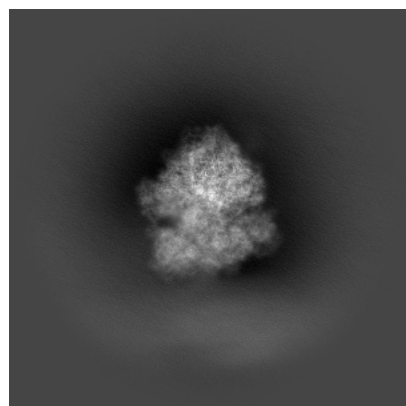
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66122. These allow visual inspection of the internal detail of the map and identification of artifacts.

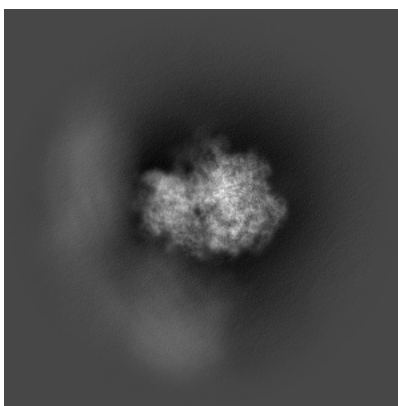
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

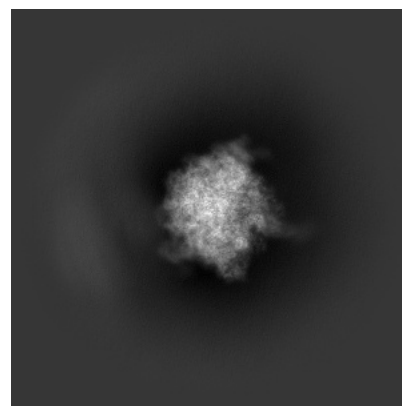
6.1.1 Primary map



X

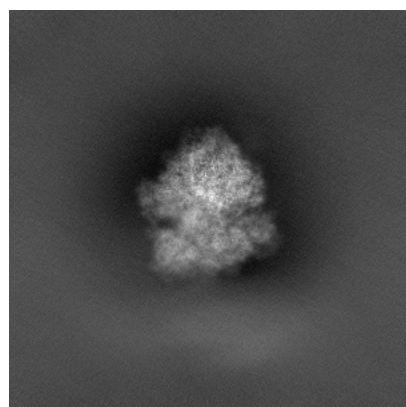


Y

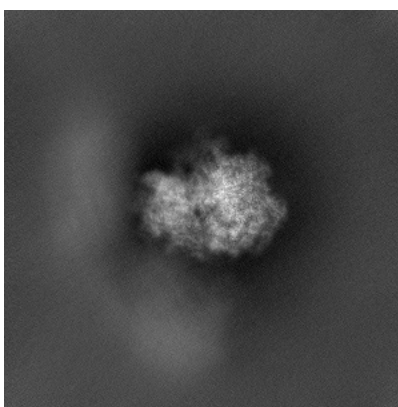


Z

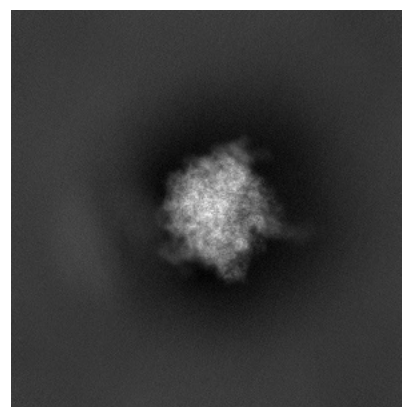
6.1.2 Raw map



X



Y

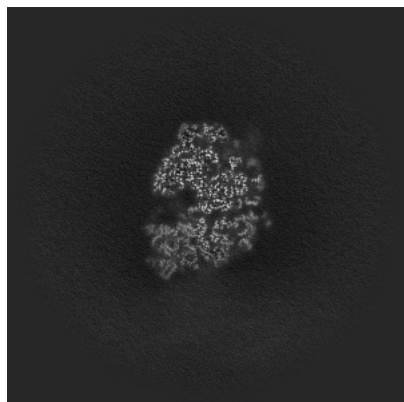


Z

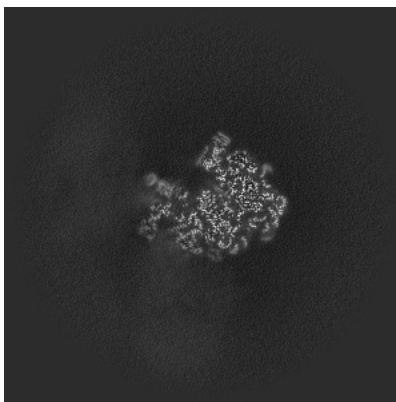
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

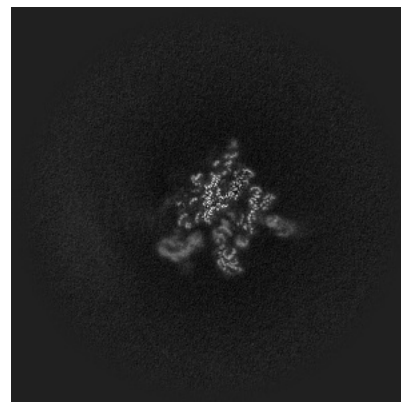
6.2.1 Primary map



X Index: 310

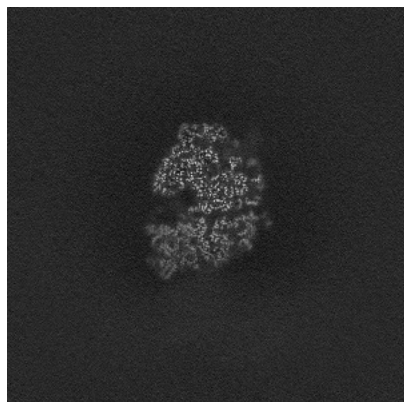


Y Index: 310

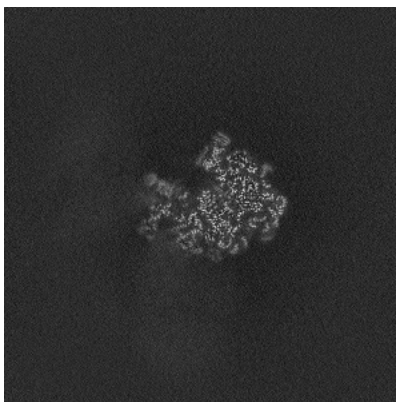


Z Index: 310

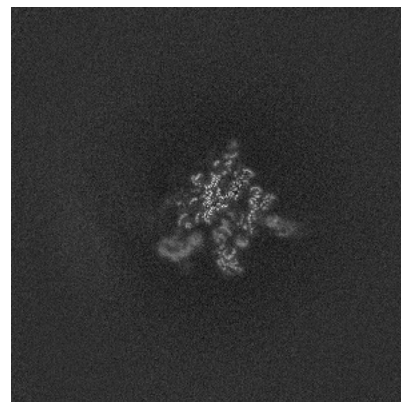
6.2.2 Raw map



X Index: 310



Y Index: 310

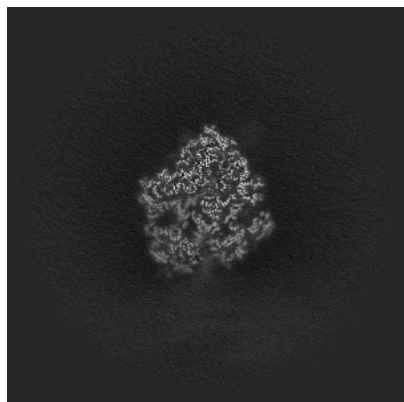


Z Index: 310

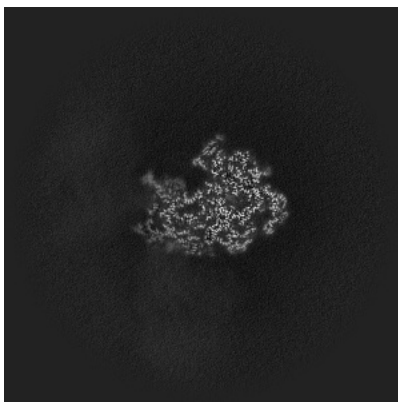
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

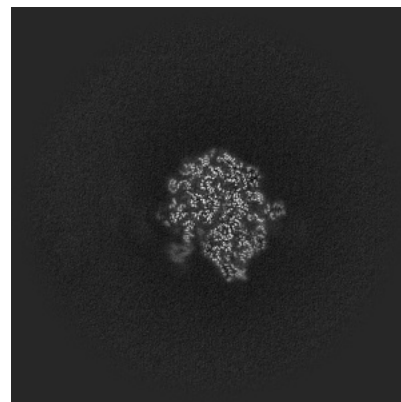
6.3.1 Primary map



X Index: 324

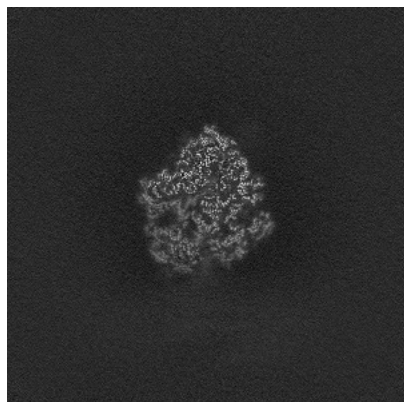


Y Index: 318

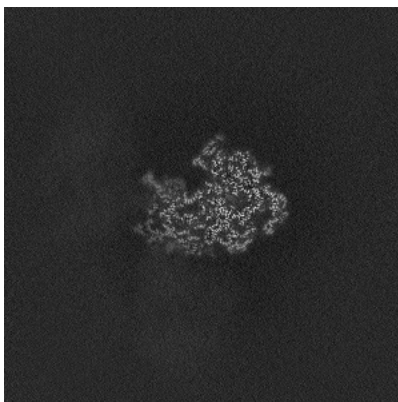


Z Index: 340

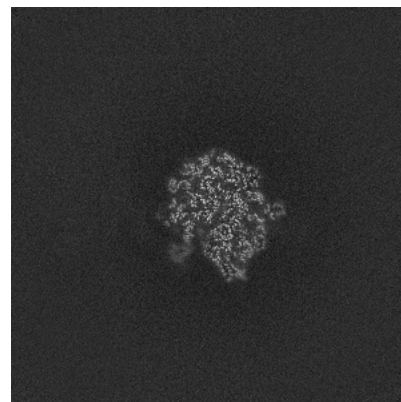
6.3.2 Raw map



X Index: 324



Y Index: 318

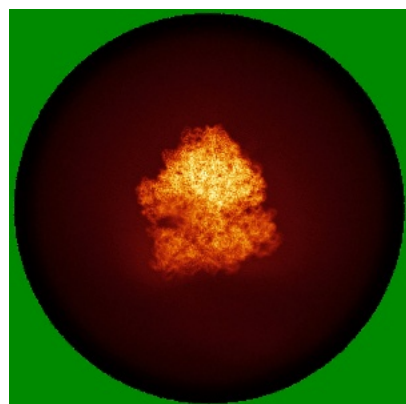


Z Index: 340

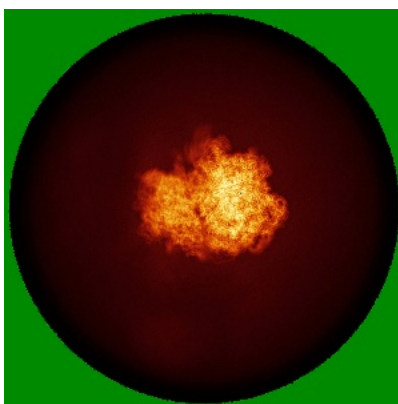
The images above show the largest variance slices of the map in three orthogonal directions.

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

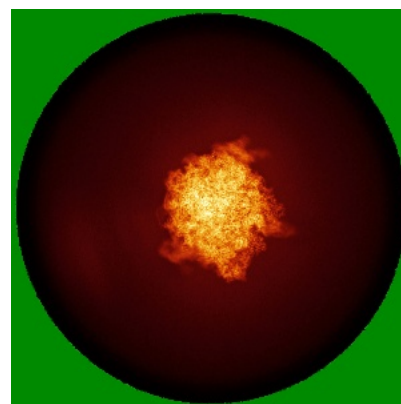
6.4.1 Primary map



X

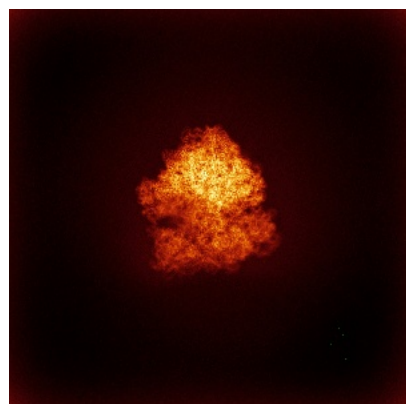


Y

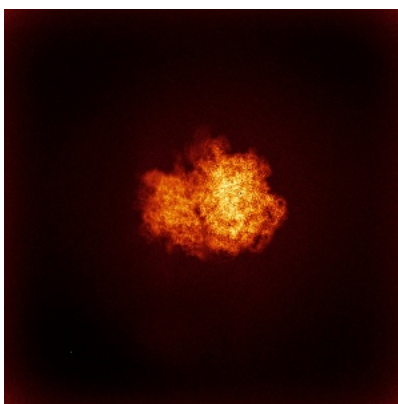


Z

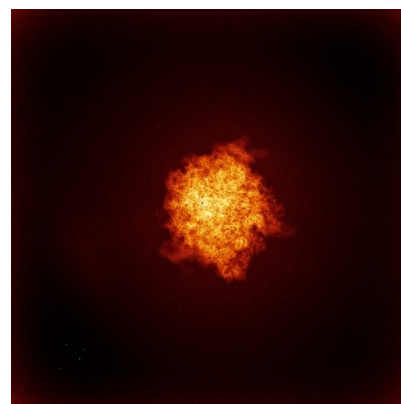
6.4.2 Raw map



X



Y

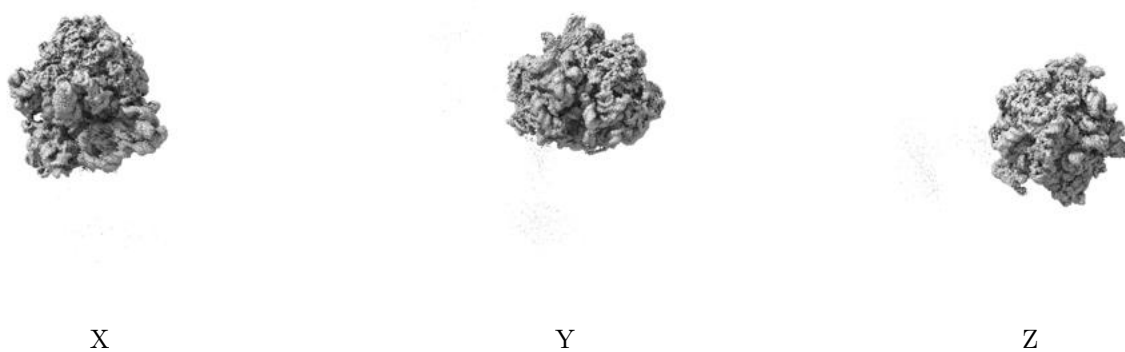


Z

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.

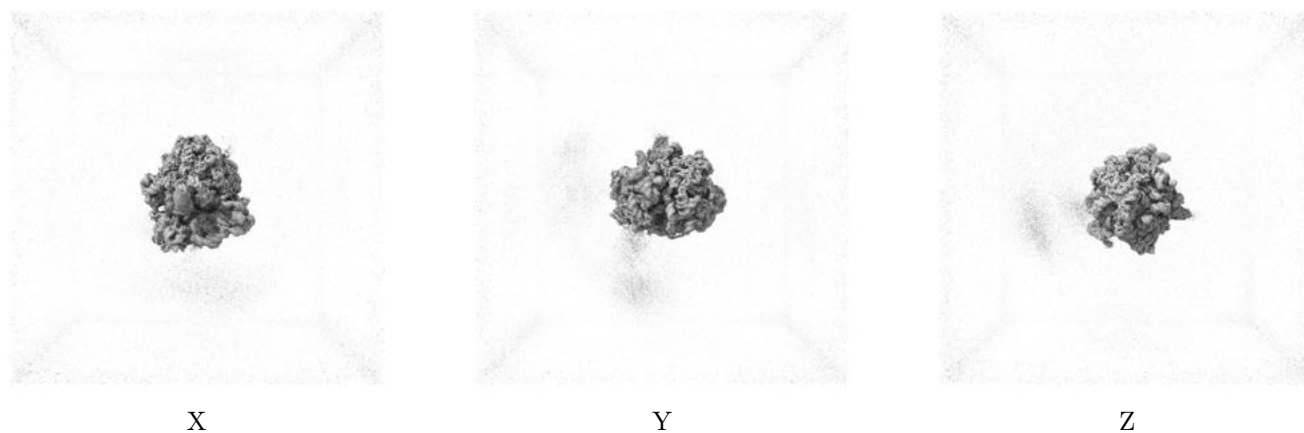
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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.

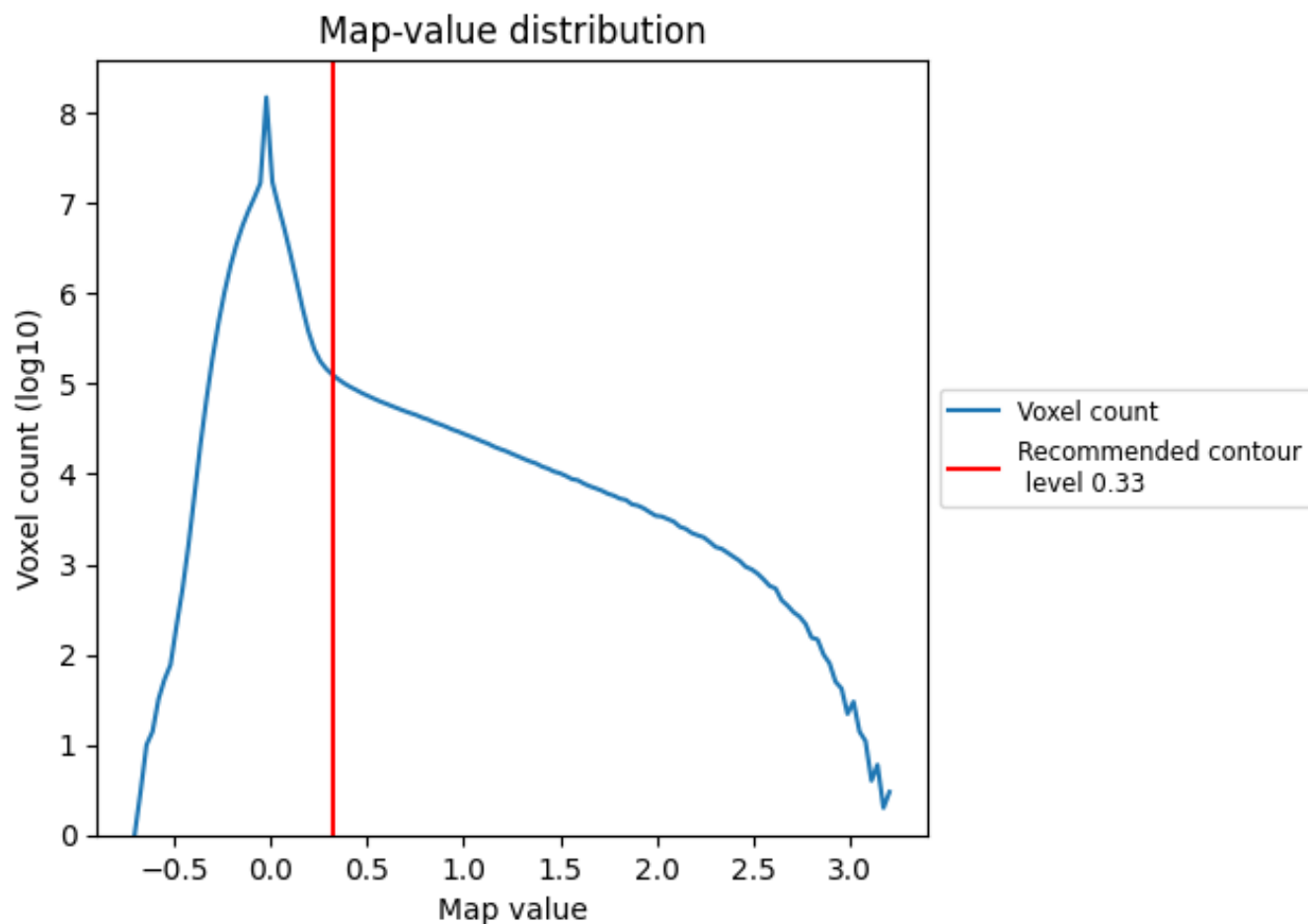
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

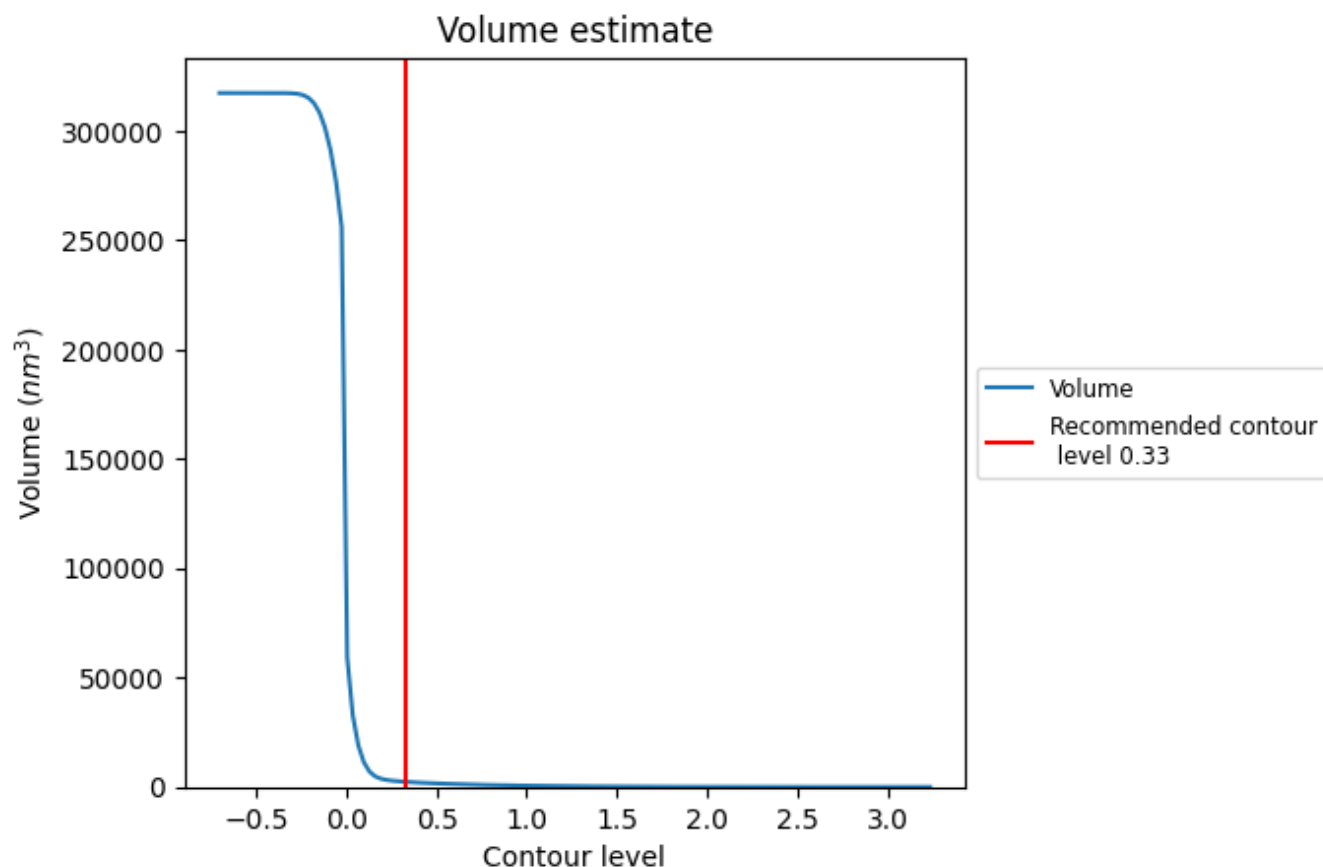
This section contains the results of statistical analysis of the map.

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.

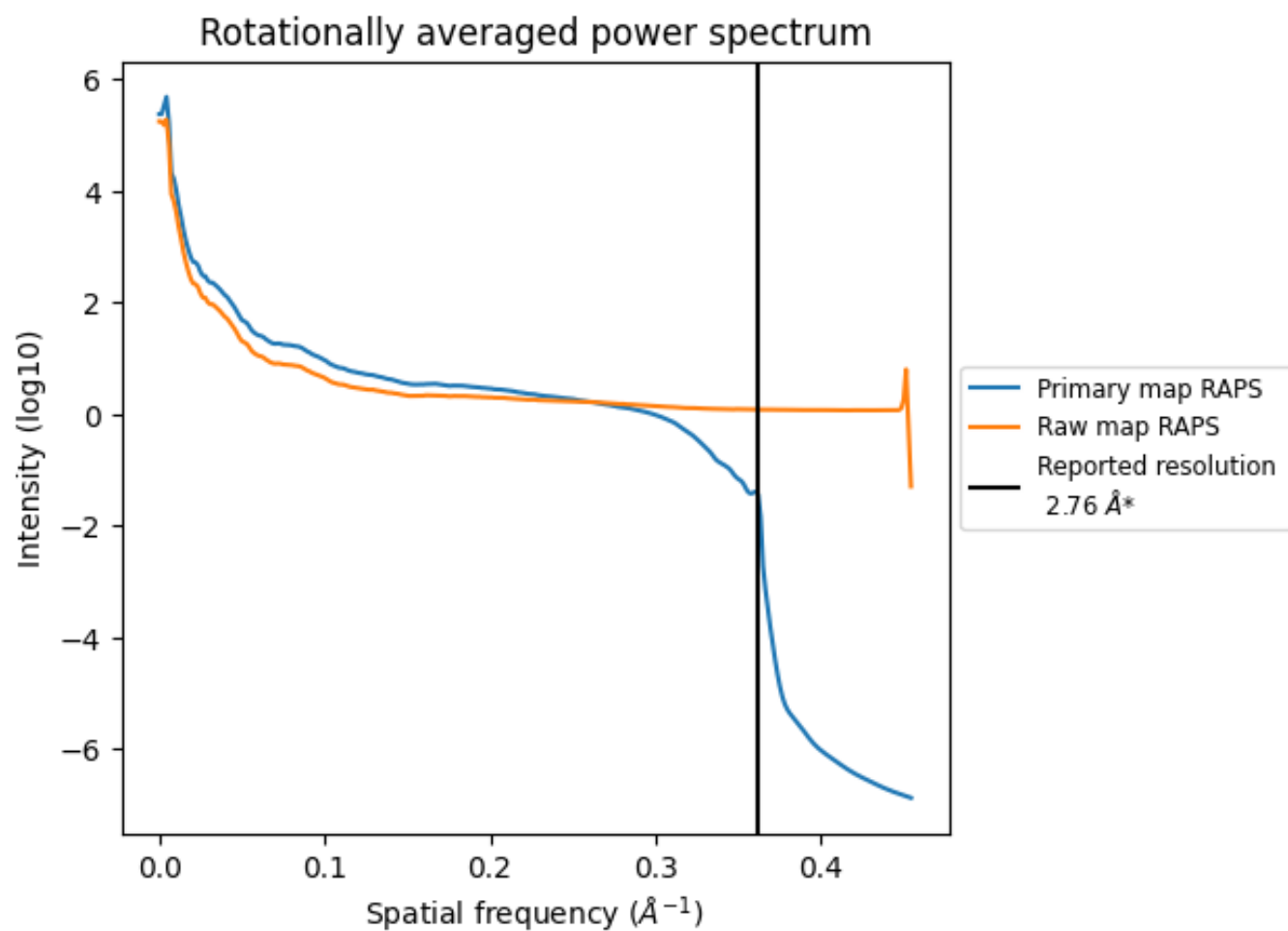
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2344 nm^3 ; this corresponds to an approximate mass of 2118 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 ⓘ

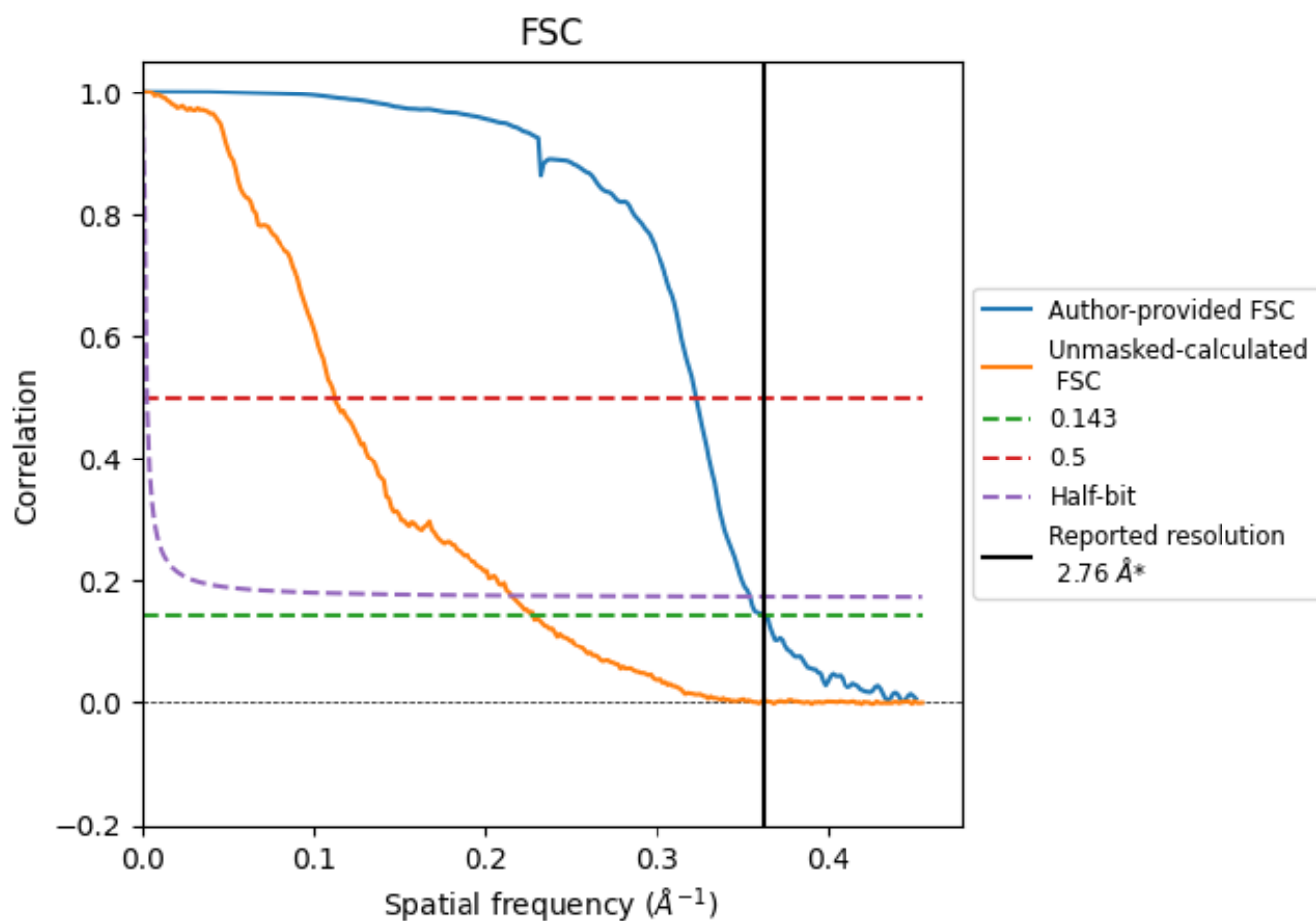


*Reported resolution corresponds to spatial frequency of 0.362 \AA^{-1}

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 0.362 \AA^{-1}

8.2 Resolution estimates [i](#)

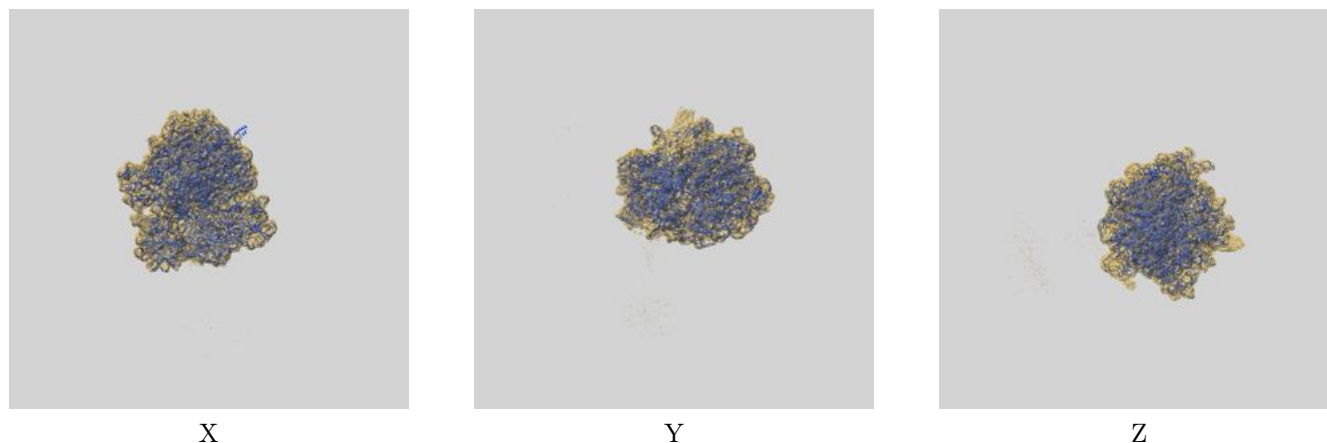
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.75	3.10	2.82
Unmasked-calculated*	4.39	8.90	4.64

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.39 differs from the reported value 2.76 by more than 10 %

9 Map-model fit [i](#)

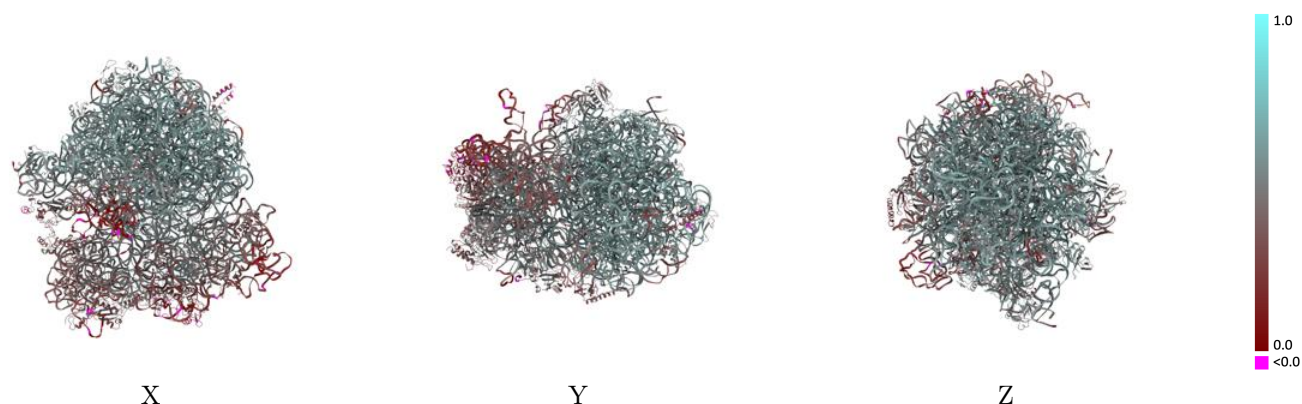
This section contains information regarding the fit between EMDB map EMD-66122 and PDB model 9WNR. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



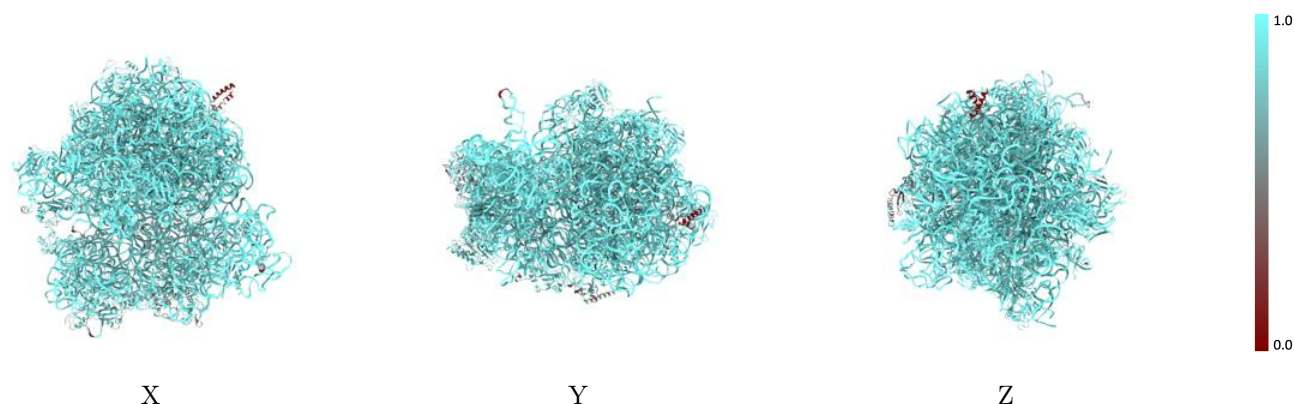
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



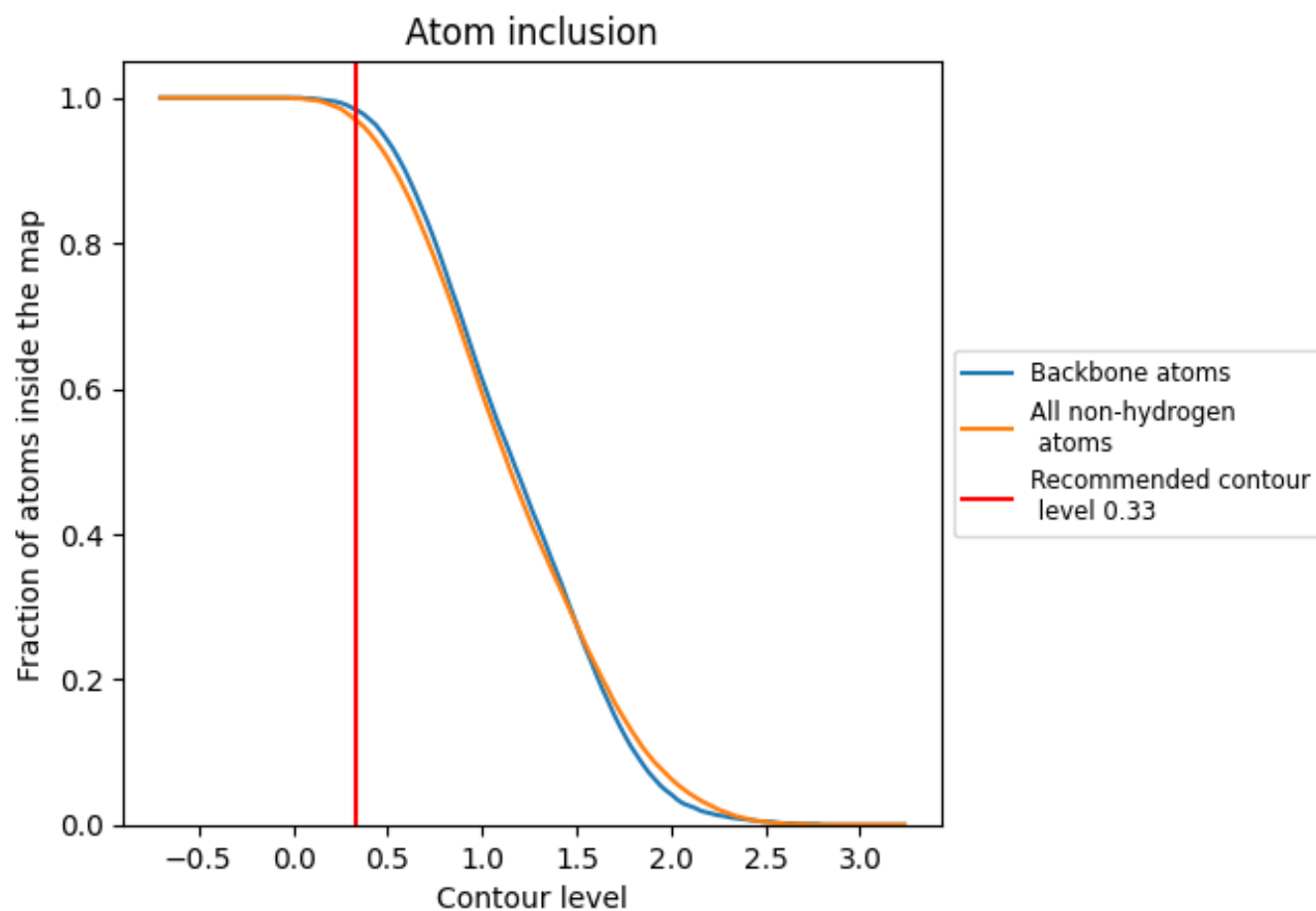
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.33).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4820
0	 0.9880	 0.5130
1	 0.9730	 0.4920
2	 0.9680	 0.5400
4	 0.9670	 0.5490
5	 0.9620	 0.5210
6	 0.9920	 0.5930
7	 0.9820	 0.5840
8	 0.9930	 0.5450
A	 0.9900	 0.4270
B	 0.8290	 0.3650
C	 0.8600	 0.3910
D	 0.6820	 0.1910
E	 0.9140	 0.4540
F	 0.9350	 0.4170
G	 0.9220	 0.3340
H	 0.9410	 0.4540
I	 0.9380	 0.3400
J	 0.8140	 0.3390
K	 0.9640	 0.4470
L	 0.8620	 0.3340
M	 0.9350	 0.3440
N	 0.9110	 0.3390
O	 0.9540	 0.4500
P	 0.9260	 0.3750
Q	 0.9160	 0.3730
R	 0.8890	 0.3790
S	 0.9260	 0.3200
T	 0.9330	 0.3290
U	 0.8360	 0.3610
V	 0.3210	 0.2590
X	 0.9800	 0.2460
Y	 0.9930	 0.3930
Z	 0.9360	 0.4260
a	 0.9990	 0.5180



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Chain	Atom inclusion	Q-score
b	 0.9960	 0.5430
c	 0.9870	 0.5740
d	 0.9800	 0.5530
e	 0.9690	 0.5350
f	 0.8800	 0.3300
g	 0.9650	 0.4550
h	 0.6750	 0.3620
k	 0.9790	 0.5600
l	 0.9670	 0.5410
m	 0.9760	 0.5500
n	 0.9720	 0.5410
o	 0.9860	 0.5710
p	 0.9630	 0.4900
q	 0.9630	 0.5280
r	 0.9860	 0.5730
s	 0.9620	 0.5520
t	 0.9710	 0.5530
u	 0.9550	 0.5050
v	 0.9700	 0.5130
w	 0.9660	 0.5120
x	 0.9830	 0.4290
y	 0.9130	 0.5190
z	 0.9120	 0.3920