



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 11:16 PM UTC

PDB ID : 8V9K / pdb_00008v9k
EMDB ID : EMD-43075
Title : Cryo-EM structure of the Mycobacterium smegmatis 70S ribosome in complex with hibernation factor Rv2629 (Balon) (Structure 5)
Authors : Rybak, M.Y.; Helena-Bueno, K.; Hill, C.H.; Melnikov, S.V.; Gagnon, M.G.
Deposited on : 2023-12-08
Resolution : 3.10 Å(reported)
Based on initial model : 5o60

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

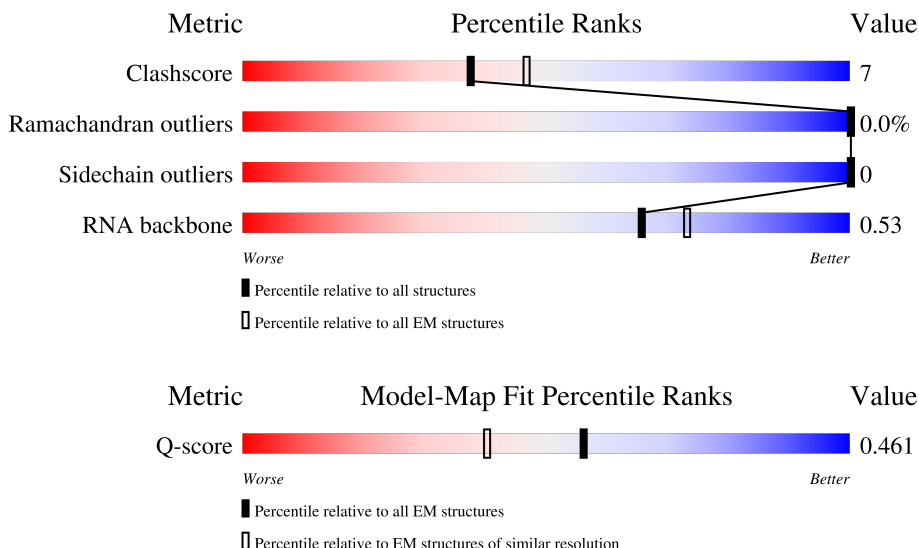
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



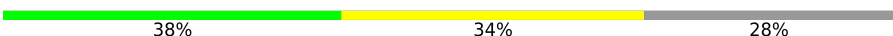
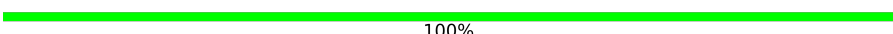
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	a	1528	
2	b	277	
3	c	275	

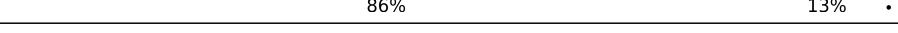
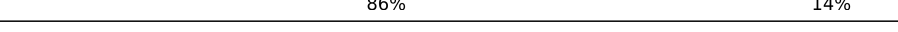
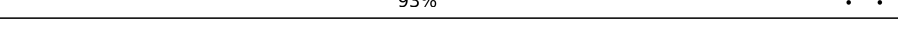
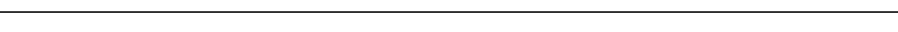
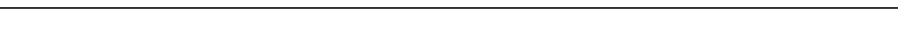
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Mol	Chain	Length	Quality of chain
4	d	201	
5	e	214	
6	f	96	
7	g	156	
8	h	132	
9	i	150	
10	j	101	
11	k	138	
12	l	124	
13	m	124	
14	n	61	
15	o	89	
16	p	156	
17	q	98	
18	r	84	
19	s	93	
20	t	86	
21	u	33	
22	v	3	
23	y	76	
24	z	374	
25	A	3164	
26	B	118	
27	C	278	
28	D	217	

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Mol	Chain	Length	Quality of chain
29	E	215	
30	F	187	
31	G	179	
32	H	151	
33	I	175	
34	J	142	
35	K	235	
36	L	147	
37	M	122	
38	N	147	
39	O	137	
40	P	199	
41	Q	127	
42	R	113	
43	S	129	
44	T	103	
45	U	153	
46	V	100	
47	W	105	
48	X	215	
49	Y	88	
50	Z	64	
51	1	77	
52	2	61	
53	3	75	

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Mol	Chain	Length	Quality of chain
54	4	57	 82%12%5%
55	5	55	 84%5%11%
56	6	47	 91%6%.
57	7	64	 75%23%.
58	8	37	 78%22%
59	9	24	 75%21%.

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153253 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	126	Total	C	N	O	S	0	0
			994	630	194	170			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O		0	0
			720	449	147	124			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	113	Total	C	N	O		0	0
			891	570	162	159			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			650	418	122	109	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 21 is a protein called 30S Ribosomal Protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called poly-U mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	3	Total	C	N	O	P	0	0
			60	27	6	24	3		

- Molecule 23 is a RNA chain called pe/E deacylated phenylalanine-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	y	74	Total	C	N	O	P	S	0	0
			1581	707	285	515	73	1		

- Molecule 24 is a protein called Ribosome hibernation factor Balon (Rv2629).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	364	Total	C	N	O	S	0	0
			2800	1740	511	543	6		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	3081	Total	C	N	O	P	0	0
			66171	29494	12172	21424	3081		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 29 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 30 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 35 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	K	102	Total	C	N	O	0	0
			531	316	109	106		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	L	146	Total	C	N	O	S	0
			1130	722	207	200	1	0

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	M	122	Total	C	N	O	S	0
			938	586	179	170	3	0

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	N	145	Total	C	N	O	S	0
			1078	676	205	194	3	0

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	O	136	Total	C	N	O	S	0
			1092	690	213	187	2	0

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	P	118	Total	C	N	O	S	0
			928	583	180	163	2	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Q	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	97	Total	C	N	O		0	0
			756	479	138	139			

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	192	Total	C	N	O		0	0
			1428	881	255	292			

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	Y	85	Total	C	N	O	0	0
			628	387	133	108		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 53 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	59	Total	C	N	O	S	0	0
			432	269	73	85	5		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 55 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	63	Total	C	N	O		0	0
			502	302	115	85			

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 59 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	9	23	Total	C	N	O		0	0
			189	111	50	28			

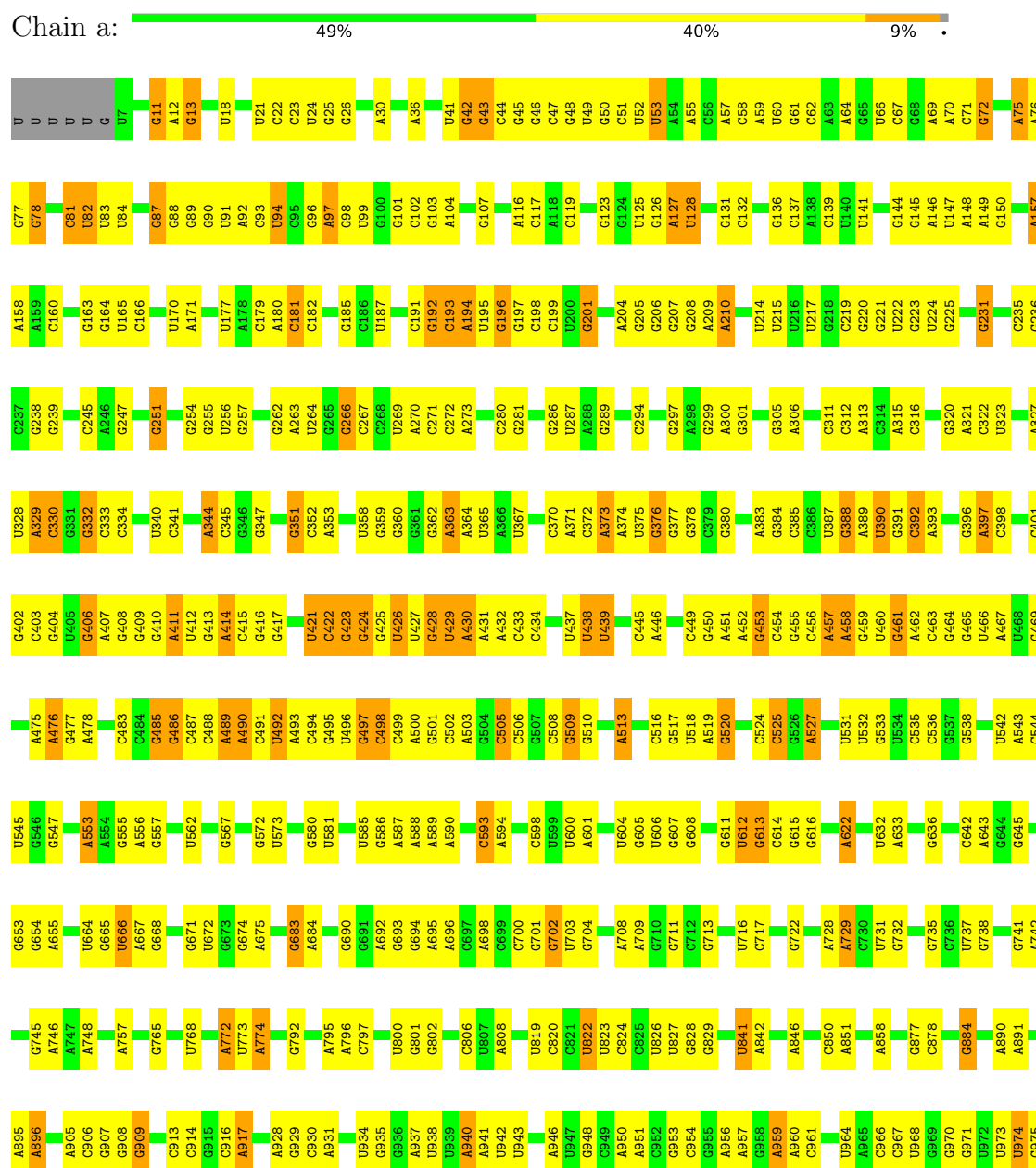
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

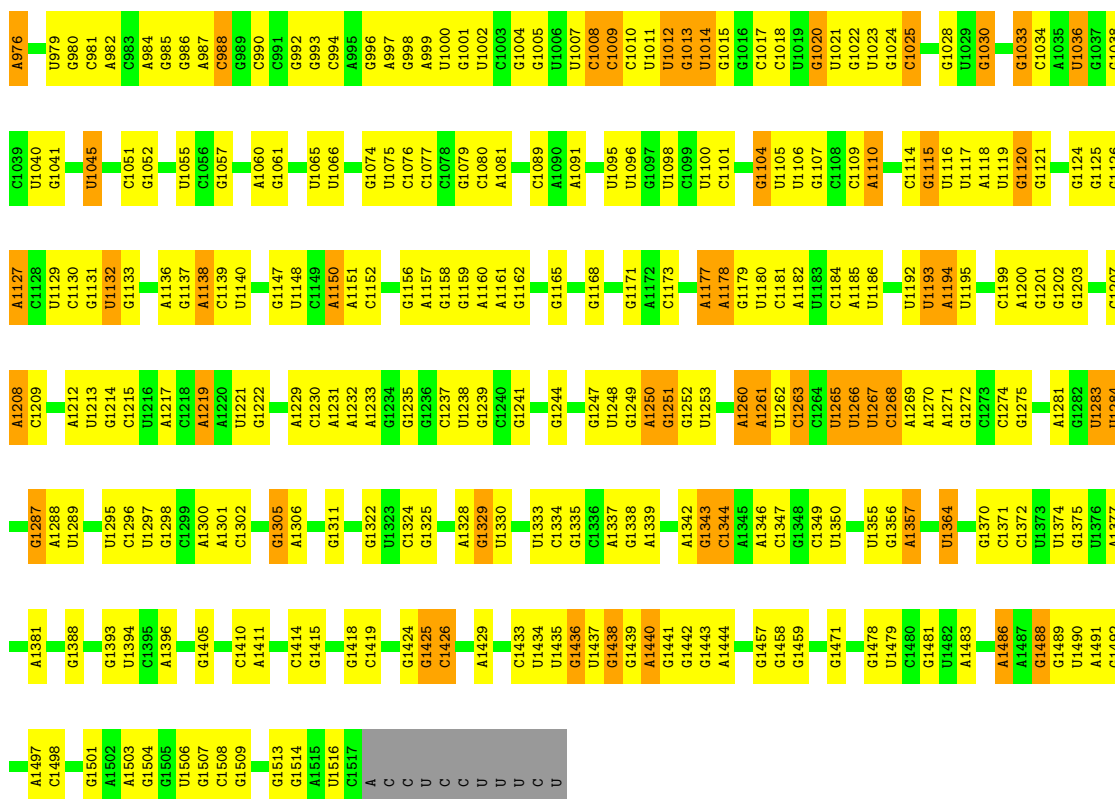
Mol	Chain	Residues	Atoms		AltConf
60	Z	1	Total	Zn	0
			1	1	
60	5	1	Total	Zn	0
			1	1	

3 Residue-property plots

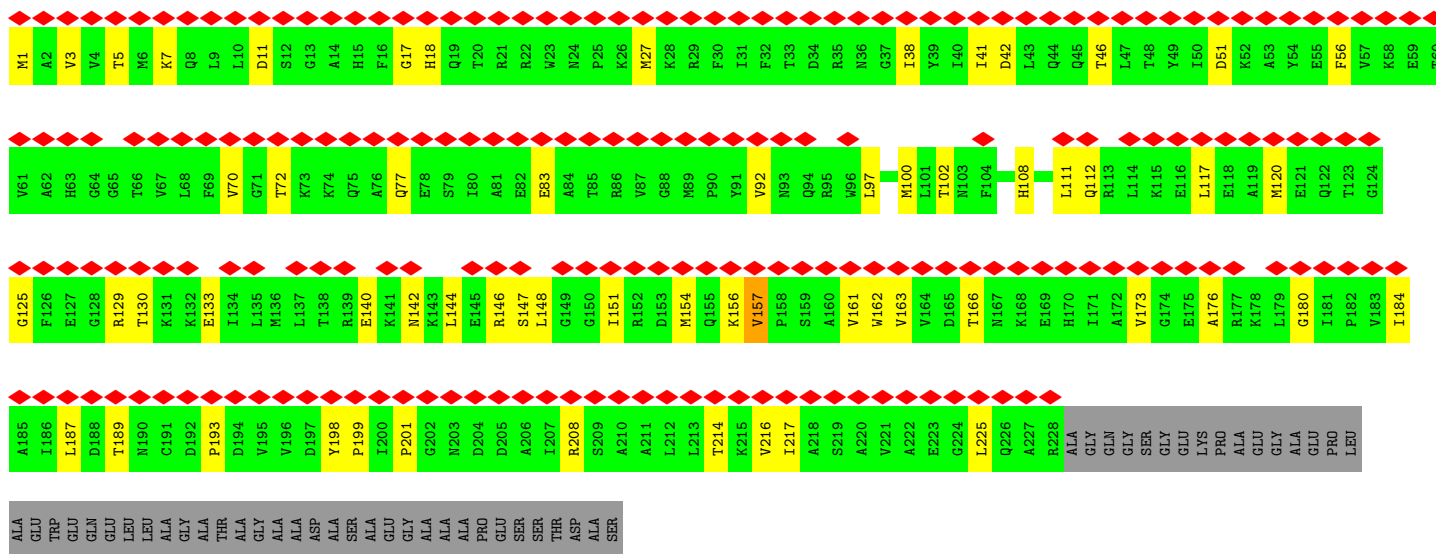
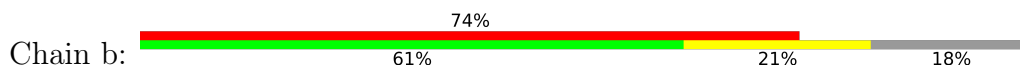
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA





• Molecule 2: 30S Ribosomal Protein S2

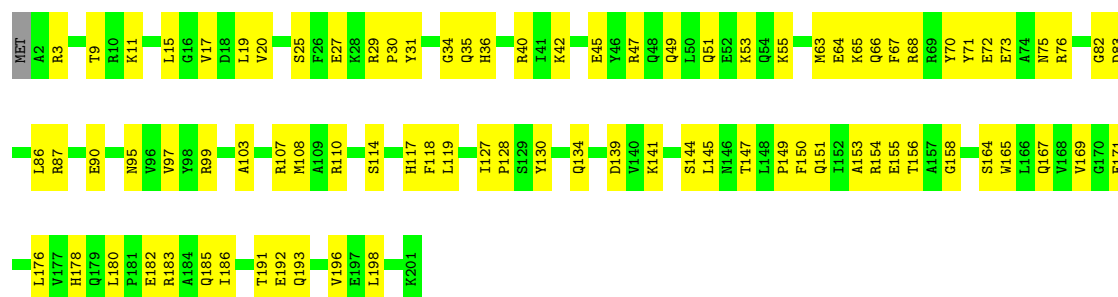


• Molecule 3: 30S ribosomal protein S3

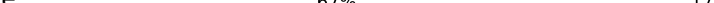


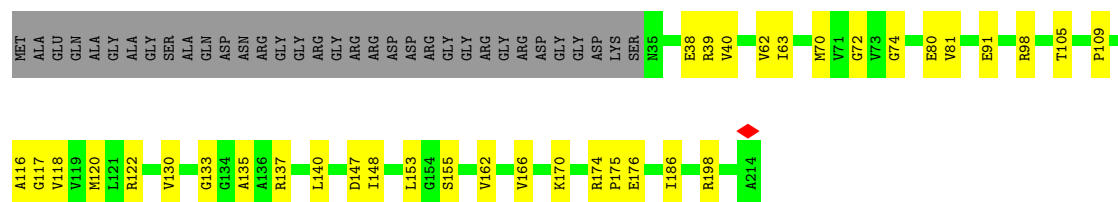
- Molecule 4: 30S ribosomal protein S4

Chain d: 57% 42%



- Molecule 5: Small ribosomal subunit protein uS5

Chain e:  67% 17% 16%



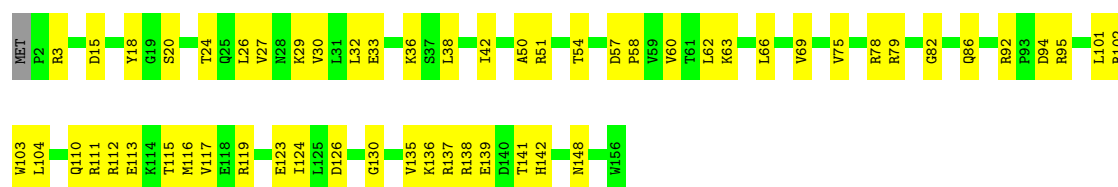
- Molecule 6: 30S ribosomal protein S6

Chain f: 73% 27%



- Molecule 7: 30S ribosomal protein S7

Chain g: 63% 36%



- Molecule 8: Small ribosomal subunit protein uS8

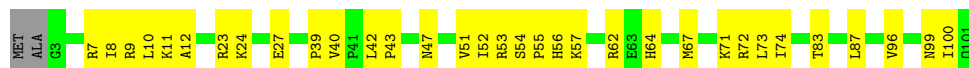
Chain h: 77% 22%



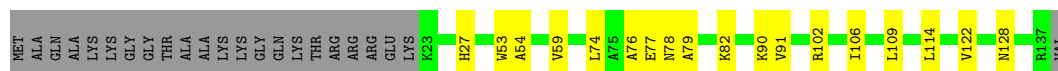
- Molecule 9: 30S ribosomal protein S9



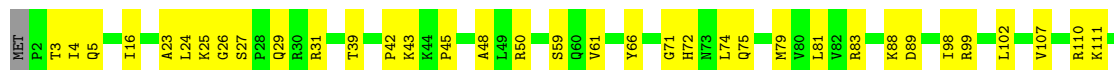
- Molecule 10: 30S ribosomal protein S10



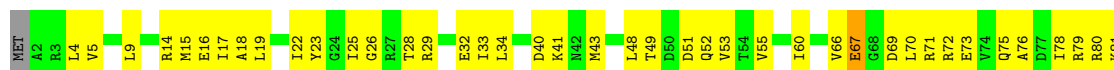
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13



- Molecule 14: Small ribosomal subunit protein uS14B

Chain n:  70% 28% .



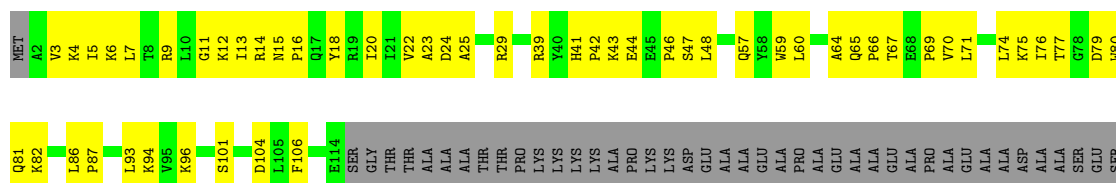
- Molecule 15: Small ribosomal subunit protein uS15

Chain o:  79% 20% .



- Molecule 16: 30S ribosomal protein S16

Chain p:  38% 34% 28%



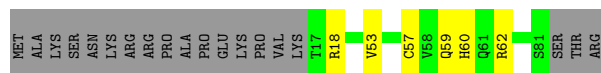
- Molecule 17: 30S ribosomal protein S17

Chain q:  77% 19% .



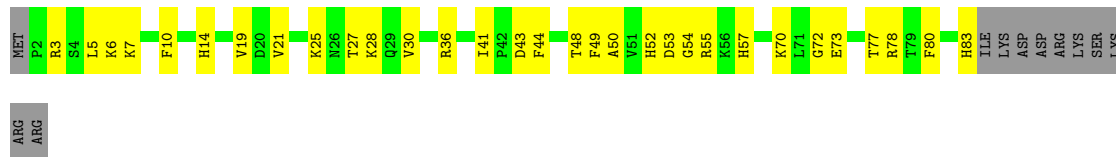
- Molecule 18: Small ribosomal subunit protein bS18B

Chain r:  70% 7% 23%



- Molecule 19: 30S ribosomal protein S19

Chain s:  55% 33% 12%

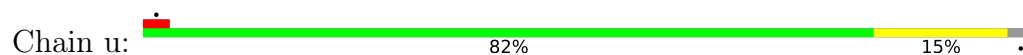


- Molecule 20: 30S ribosomal protein S20

Chain t:  66% 33% .



- Molecule 21: 30S Ribosomal Protein S22

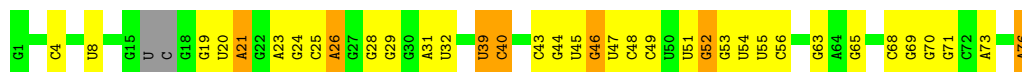


- Molecule 22: poly-U mRNA

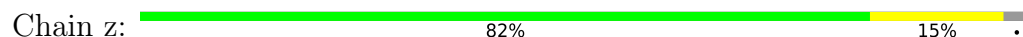


There are no outlier residues recorded for this chain.

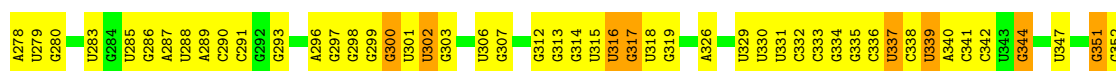
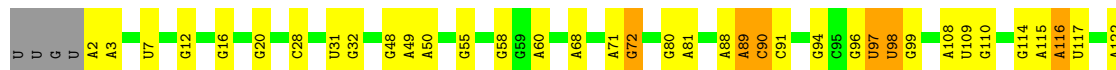
- Molecule 23: pe/E deacylated phenylalanine-tRNA



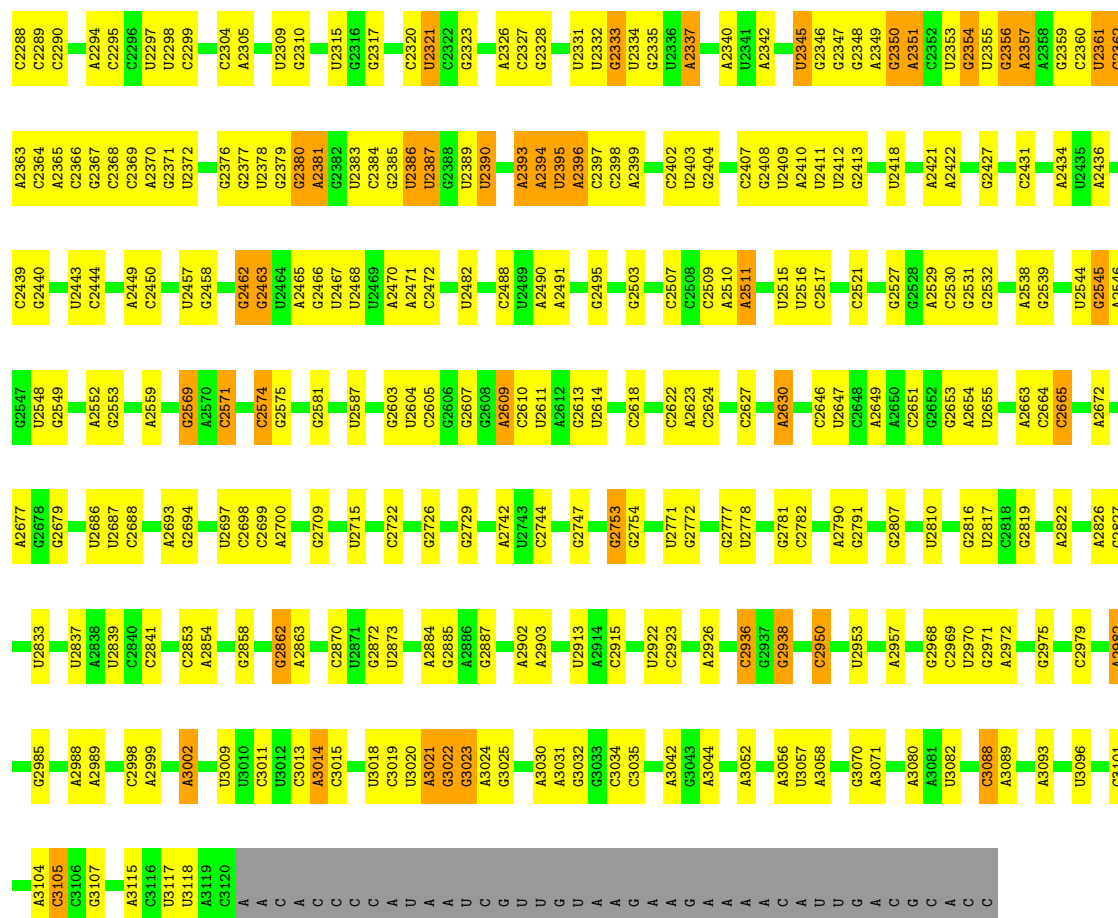
- Molecule 24: Ribosome hibernation factor Balon (Rv2629)



- Molecule 25: 23S Ribosomal RNA

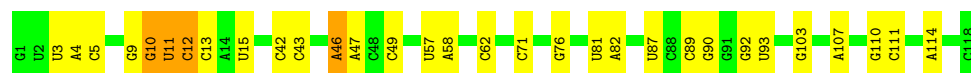


U2167	G2034	G1885	A1737	G1626	A1566	C1472	G1306	A1204	G1087	U966	A830	U709	G474
U2168	U2035	G1886	G1738	U1627	C	A1473	G1307	G1205	U1088	G967	A831	C718	U487
G2178	A2042	G1892	G1746	A1628	C	A1474	C1311	A1206	G1092	A972	G832	C719	G488
U2179	C2043	G1893	G1755	G1629	A	G1475	C1312	G1209	A1093	G973	U839	C720	A489
U2180	G2046	C1900	G1754	U1630	C	G1476	U1313	G1212	G1094	G974	C845	C721	G494
A2184	G2046	C1901	A1755	G1632	G	C1477	C1314	U1212	A1099	U975	C846	C722	G499
G2188	U2061	C1904	G1756	G1637	U	C1478	G1335	A1213	A1099	A978	U857	C723	G499
G2188	G2062	G1905	G1758	G1637	G	G1479	G1336	A1214	G1100	G979	A858	A726	C619
C2191	A2065	C1906	A1759	U1640	A	A1480	G1337	U1215	G1101	C980	C618	A727	C502
A2194	G2075	C1927	G1762	U1641	C	U1494	G1338	G1220	G1107	U981	U862	C728	A503
U2195	G2075	G1938	G1763	G1642	G	A1499	A1344	A1221	G1107	A982	C868	G730	G512
G2196	U2086	U1939	G1767	A1648	C	A1500	G1353	C1222	G1114	A994	U871	A731	A517
C2087	C2087	C1944	U1767	C1649	A	C1501	G1354	G1223	U995	G996	G872	U733	G634
C2088	C2088	U1945	G1768	G1653	C	G1502	G1365	G1225	A1118	G997	G873	C734	G635
A2212	C2089	U1946	G1769	U1654	U	U1507	G1371	U1226	A1119	G998	G875	U735	U529
U2090	U2090	U1947	G1780	A1655	U	A1508	G1372	C1227	C1122	C999	U876	G736	G530
U2091	A1948	U1948	C1784	G1658	C	U1509	G1373	A1228	A1127	C1000	U877	C737	A537
U2092	C1949	C1949	C1785	G1659	G	A1510	A1380	G1230	A1128	C1001	G878	A738	G538
G2093	C1952	C1953	G1786	G1670	G	U1511	G1384	U1231	G1129	C1002	A879	A739	U641
G2094	C1954	C1955	G1787	G1671	C	G1524	G1385	G1232	C1130	A1003	G880	A740	G642
G2095	U1949	U1950	G1788	U1674	G	G1525	G1386	G1233	G1131	C1004	G644	G741	G643
G2096	U1951	U1952	U1675	U1675	U	G1526	G1387	G1234	G1132	A1005	G645	C742	U544
U2097	A1956	U1957	U1676	U1676	G	G1527	U1388	A1246	G1140	G1006	G646	U743	A545
U2098	G1961	A1962	A1790	G1677	U	U1528	U1389	G1249	U1141	G1007	U647	A744	G546
G2099	C1963	G1964	A1791	U1678	C	G1529	G1390	U1250	A1144	A998	U648	C745	U547
A2106	U1965	U1966	A1792	A1679	G	C1531	G1391	G1251	A1145	U1009	G649	C746	G551
G2107	U1967	U1968	U1681	U1680	C	G1532	C1392	U1252	A1146	U1010	G650	C747	A554
A2238	A2238	C1801	G1688	U1688	U	U1533	C1393	G1253	U1151	A1011	A663	A753	G557
A2239	A2239	A1803	G1689	U1689	C	C1534	A1394	G1254	G1152	C1012	A664	C754	G561
U2240	U2240	G1804	A1691	A1691	U	A1535	G1395	G1255	U1153	U1013	A665	C755	G562
A2244	A2244	G1805	G1703	G1703	G	U1536	U1397	G1256	G1162	C1022	A666	U760	A566
C2245	A2114	A1808	U1704	U1704	C	U1537	G1400	G1257	A1163	G1023	A667	C761	G569
U2246	C2129	U1809	C1705	C1705	G	U1538	A1415	C1260	A1164	A1025	A668	G762	A579
A2247	G2130	A1810	A1706	A1706	U	U1539	A1416	A1261	G1165	C1030	U669	U763	G580
C2248	G2131	G1805	G1707	G1707	C	A1540	C1421	G1272	U1178	A1033	C921	G764	G582
G2249	C2138	C1825	A1710	A1710	C	U1541	A1422	A1274	G1180	C1045	C927	G765	A579
A2250	C2138	A1826	G1711	G1711	C	G1542	G1426	A1275	U1183	C1046	U928	U772	G580
A2255	U2141	A1827	G1712	G1712	C	A1543	G1434	C1283	A1188	A1047	C929	G773	G581
G2256	A2142	A1828	U1713	U1713	U	U1544	C1435	A1284	A1189	A1048	A935	G774	G582
A2257	C2144	C1829	A1714	A1714	C	C1551	G1443	G1285	A1191	G1049	U942	C781	U566
G2263	C2148	C1830	A1715	A1715	U	C1552	G1444	G1286	G1192	A1063	U947	U782	G567
C2267	G2016	G1840	U1716	U1716	C	A1553	U1455	C1287	G1193	A1064	G948	G783	A588
G2270	C2017	G1841	C1718	C1718	C	A1554	G1456	A1288	G1194	C1065	C949	A785	A589
A2275	G2018	A2019	G1719	G1719	U	A1555	U1457	A1289	A1195	A1076	A950	U801	A592
C2279	A2020	U1864	G1720	G1720	C	U1560	G1468	U1292	U1199	A1077	G951	C784	G593
G2280	A2026	A1865	G1721	G1721	C	C1561	U1469	G1293	U1200	G1078	C705	U785	A594
A2284	U2163	C1866	G1724	G1724	C	C1562	G1470	G1296	G1201	G1079	G706	C786	A595
G2285	U2164	U1870	A1731	A1731	U	A1563	A1468	G1297	G1202	G1085	C596	U818	A596
A2286	C2165	A1871	G1872	G1872	C	A1564	A1469	C1298	A1203	C1086	U951	G819	C597
C2287	C2166	A1872	G1873	G1873	C	A1565	A1470	G1299	A1204	C1087	G707	U820	C598



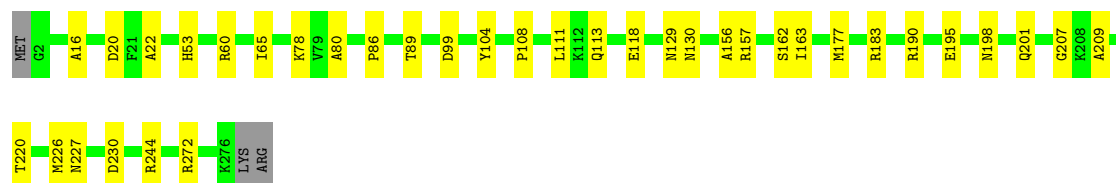
• Molecule 26: 5S Ribosomal RNA

Chain B: 74% 23%



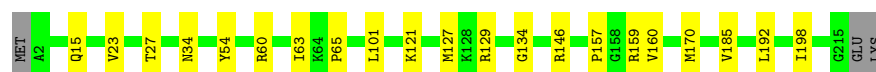
• Molecule 27: 50S ribosomal protein L2

Chain C: 86% 13%



• Molecule 28: 50S ribosomal protein L3

Chain D: 89% 10%



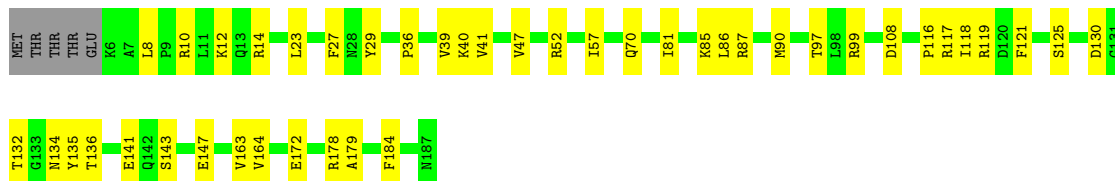
- Molecule 29: Large ribosomal subunit protein uL4

Chain E:  87% 11%



- Molecule 30: Large ribosomal subunit protein uL5

Chain F:  74% 23%



- Molecule 31: 50S ribosomal protein L6

Chain G:  84% 14%



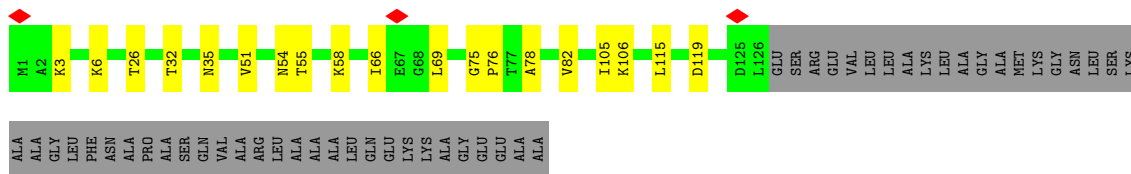
- Molecule 32: 50S ribosomal protein L9

Chain H:  89% 11%



- Molecule 33: 50S ribosomal protein L10

Chain I:  61% 11% 28%

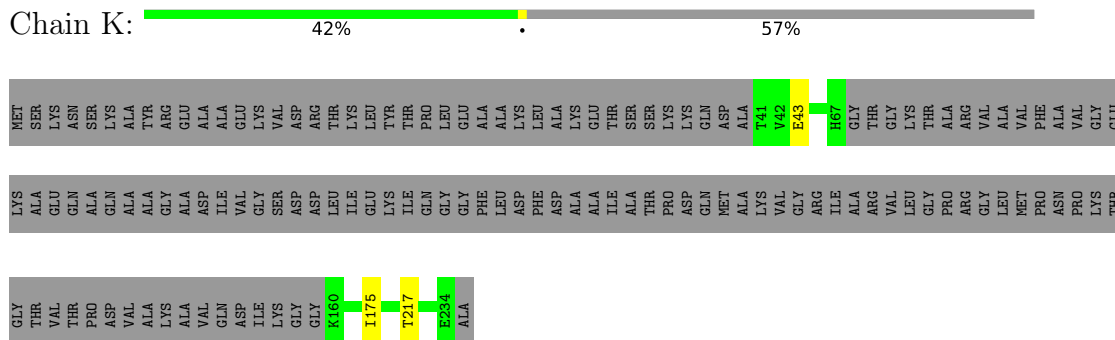


- Molecule 34: 50S ribosomal protein L11

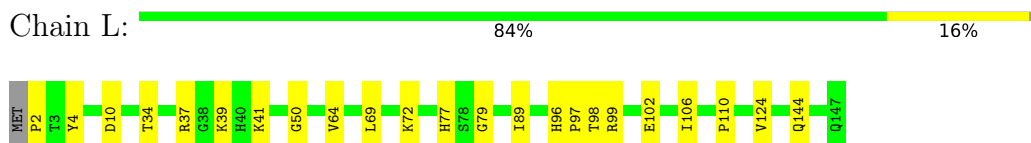
Chain J:  75% 19% 6%



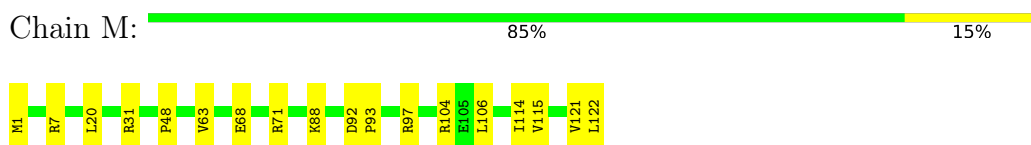
- Molecule 35: Large ribosomal subunit protein uL1



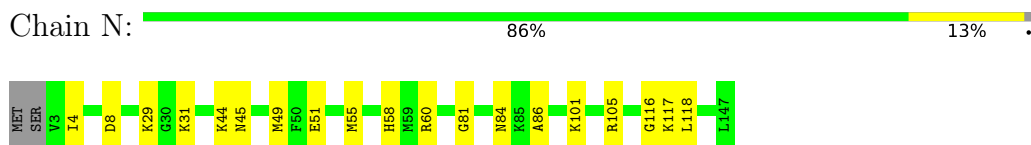
- Molecule 36: Large ribosomal subunit protein uL13



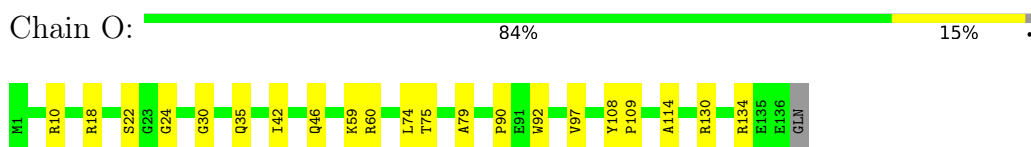
- Molecule 37: 50S ribosomal protein L14



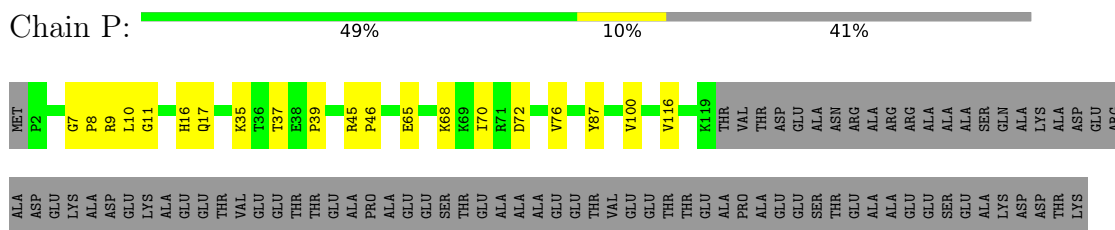
- Molecule 38: 50S ribosomal protein L15



- Molecule 39: Large ribosomal subunit protein uL16



- Molecule 40: 50S ribosomal protein L17



- Molecule 41: Large ribosomal subunit protein uL18

Chain Q:  86% 13%



- Molecule 42: 50S ribosomal protein L19

Chain R:  86% 14%



- Molecule 43: Large ribosomal subunit protein bL20

Chain S:  88% 9%



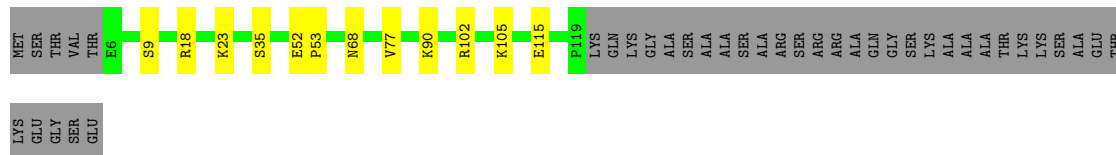
- Molecule 44: Large ribosomal subunit protein bL21

Chain T:  93%



- Molecule 45: Large ribosomal subunit protein uL22

Chain U:  67% 8% 25%



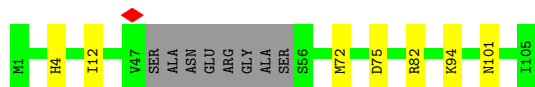
- Molecule 46: Large ribosomal subunit protein uL23

Chain V:  83% 14%



- Molecule 47: 50S ribosomal protein L24

Chain W:  86% 7% 8%



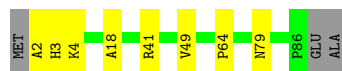
- Molecule 48: 50S ribosomal protein L25

Chain X:  76% 13% 11%



- Molecule 49: 50S ribosomal protein L27

Chain Y:  88% 9% .



- Molecule 50: Large ribosomal subunit protein bL28

Chain Z:  75% 23% .



- Molecule 51: 50S ribosomal protein L29

Chain 1:  70% 13% 17%



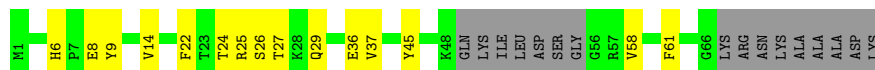
- Molecule 52: 50S ribosomal protein L30

Chain 2:  95% . .



- Molecule 53: Large ribosomal subunit protein bL31

Chain 3:  59% 20% 21%

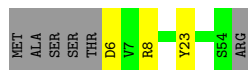
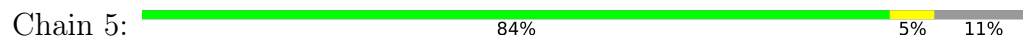


- Molecule 54: 50S ribosomal protein L32

Chain 4:  82% 12% 5%



- Molecule 55: Large ribosomal subunit protein bL33A



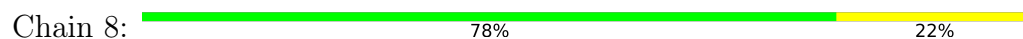
- Molecule 56: 50S ribosomal protein L34



- Molecule 57: 50S ribosomal protein L35



- Molecule 58: 50S ribosomal protein L36



- Molecule 59: 50S Ribosomal Protein L37



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	147778	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 ($e^-/\text{\AA}^2$)	40.18	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.418	Depositor
Minimum map value	-0.439	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	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: 4SU, ZN, PSU, 5MU, 7MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	a	0.11	0/36309	0.26	0/56657
2	b	0.11	0/1822	0.31	0/2457
3	c	0.13	0/1684	0.34	0/2261
4	d	0.14	0/1672	0.39	0/2251
5	e	0.13	0/1312	0.32	0/1772
6	f	0.13	0/782	0.32	0/1059
7	g	0.13	0/1252	0.38	0/1690
8	h	0.13	0/1025	0.30	0/1385
9	i	0.13	0/1012	0.37	0/1362
10	j	0.12	0/802	0.37	0/1086
11	k	0.13	0/873	0.33	0/1180
12	l	0.17	0/969	0.37	0/1294
13	m	0.16	0/942	0.53	1/1260 (0.1%)
14	n	0.13	0/488	0.35	0/650
15	o	0.17	0/729	0.34	0/977
16	p	0.17	0/908	0.46	0/1226
17	q	0.10	0/759	0.31	0/1016
18	r	0.10	0/518	0.28	0/693
19	s	0.10	0/668	0.29	0/901
20	t	0.16	0/663	0.36	0/882
21	u	0.15	0/280	0.34	0/359
22	v	0.08	0/65	0.14	0/98
23	y	0.18	1/1628 (0.1%)	0.23	0/2536
24	z	0.13	0/2848	0.32	0/3874
25	A	0.14	0/74096	0.28	0/115613
26	B	0.12	0/2821	0.26	0/4396
27	C	0.14	0/2153	0.29	0/2895
28	D	0.15	0/1609	0.32	0/2165
29	E	0.13	0/1592	0.27	0/2153
30	F	0.12	0/1467	0.30	0/1973
31	G	0.12	0/1369	0.28	0/1848
32	H	0.10	0/1027	0.32	0/1398

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.09	0/925	0.28	0/1246
34	J	0.11	0/1006	0.30	0/1364
35	K	0.08	0/530	0.22	0/731
36	L	0.16	0/1157	0.30	1/1567 (0.1%)
37	M	0.12	0/946	0.26	0/1268
38	N	0.15	0/1091	0.37	0/1457
39	O	0.13	0/1118	0.29	0/1506
40	P	0.14	0/945	0.27	0/1267
41	Q	0.12	0/966	0.24	0/1298
42	R	0.14	0/921	0.32	0/1236
43	S	0.15	0/1000	0.24	0/1341
44	T	0.12	0/764	0.25	0/1030
45	U	0.13	0/887	0.28	0/1204
46	V	0.14	0/766	0.28	0/1030
47	W	0.12	0/738	0.27	0/987
48	X	0.12	0/1443	0.28	0/1970
49	Y	0.13	0/638	0.24	0/854
50	Z	0.15	0/478	0.29	0/641
51	1	0.12	0/534	0.21	0/713
52	2	0.13	0/477	0.23	0/640
53	3	0.10	0/441	0.27	0/597
54	4	0.14	0/427	0.28	0/572
55	5	0.14	0/413	0.33	0/553
56	6	0.14	0/380	0.24	0/500
57	7	0.14	0/507	0.27	0/672
58	8	0.13	0/303	0.29	0/401
59	9	0.14	0/191	0.31	0/247
All	All	0.13	1/166136 (0.0%)	0.28	2/248259 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	8	4SU	O3'-P	6.08	1.62	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	L	2	PRO	CA-N-CD	-5.68	104.05	112.00
13	m	67	GLU	CB-CA-C	-5.23	108.98	115.89

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	a	32439	0	16321	567	0
2	b	1793	0	1839	37	0
3	c	1660	0	1707	31	0
4	d	1641	0	1668	77	0
5	e	1296	0	1360	22	0
6	f	771	0	797	20	0
7	g	1232	0	1282	46	0
8	h	1010	0	1046	19	0
9	i	994	0	1050	33	0
10	j	788	0	819	31	0
11	k	855	0	863	13	0
12	l	958	0	1045	28	0
13	m	935	0	986	45	0
14	n	477	0	503	13	0
15	o	720	0	760	13	0
16	p	891	0	935	57	0
17	q	748	0	795	17	0
18	r	513	0	540	3	0
19	s	650	0	656	27	0
20	t	660	0	712	20	0
21	u	280	0	342	4	0
22	v	60	0	31	0	0
23	y	1581	0	808	24	0
24	z	2800	0	2769	35	0
25	A	66171	0	33292	540	0
26	B	2522	0	1285	14	0
27	C	2110	0	2165	26	0
28	D	1587	0	1630	15	0
29	E	1569	0	1607	14	0
30	F	1445	0	1476	32	0
31	G	1348	0	1399	16	0
32	H	1018	0	988	13	0
33	I	918	0	959	14	0
34	J	990	0	1021	21	0
35	K	531	0	271	2	0
36	L	1130	0	1167	13	0
37	M	938	0	1000	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1078	0	1151	15	0
39	O	1092	0	1128	18	0
40	P	928	0	972	11	0
41	Q	956	0	991	13	0
42	R	907	0	938	11	0
43	S	988	0	1038	8	0
44	T	754	0	802	2	0
45	U	873	0	909	8	0
46	V	756	0	802	11	0
47	W	732	0	782	5	0
48	X	1428	0	1443	18	0
49	Y	628	0	647	8	0
50	Z	470	0	480	12	0
51	1	531	0	541	9	0
52	2	474	0	500	1	0
53	3	432	0	392	11	0
54	4	423	0	463	8	0
55	5	405	0	407	3	0
56	6	377	0	411	3	0
57	7	502	0	541	11	0
58	8	299	0	324	4	0
59	9	189	0	205	4	0
60	5	1	0	0	0	0
60	Z	1	0	0	0	0
All	All	153253	0	103761	1878	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 7.

The worst 5 of 1878 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:177:U:H3	1:a:209:A:N6	1.57	1.03
25:A:337:U:H3	25:A:344:G:H1	1.00	0.96
1:a:1244:G:H1	1:a:1253:U:H3	1.04	0.95
1:a:49:U:H3	1:a:396:G:H1	1.10	0.94
23:y:51:U:H3	23:y:63:G:H1	1.06	0.94

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	
2	b	226/277 (82%)	212 (94%)	13 (6%)	1 (0%)	30	61
3	c	206/275 (75%)	192 (93%)	14 (7%)	0	100	100
4	d	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
5	e	178/214 (83%)	169 (95%)	9 (5%)	0	100	100
6	f	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
7	g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
8	h	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
9	i	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
10	j	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
11	k	113/138 (82%)	104 (92%)	9 (8%)	0	100	100
12	l	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
13	m	114/124 (92%)	104 (91%)	9 (8%)	1 (1%)	14	44
14	n	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	111/156 (71%)	106 (96%)	5 (4%)	0	100	100
17	q	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
18	r	63/84 (75%)	62 (98%)	1 (2%)	0	100	100
19	s	80/93 (86%)	78 (98%)	2 (2%)	0	100	100
20	t	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
21	u	30/33 (91%)	30 (100%)	0	0	100	100
24	z	362/374 (97%)	348 (96%)	14 (4%)	0	100	100
27	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
28	D	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
29	E	207/215 (96%)	202 (98%)	5 (2%)	0	100	100
30	F	180/187 (96%)	175 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	G	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
32	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
33	I	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
34	J	131/142 (92%)	121 (92%)	10 (8%)	0	100	100
35	K	98/235 (42%)	90 (92%)	8 (8%)	0	100	100
36	L	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
37	M	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
38	N	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
39	O	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
40	P	116/199 (58%)	113 (97%)	3 (3%)	0	100	100
41	Q	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
42	R	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
43	S	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
44	T	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
45	U	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
46	V	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
47	W	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
48	X	190/215 (88%)	184 (97%)	6 (3%)	0	100	100
49	Y	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
50	Z	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
51	1	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
52	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
53	3	55/75 (73%)	53 (96%)	2 (4%)	0	100	100
54	4	52/57 (91%)	52 (100%)	0	0	100	100
55	5	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
56	6	44/47 (94%)	44 (100%)	0	0	100	100
57	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
58	8	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
59	9	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	6445/7287 (88%)	6164 (96%)	279 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	157	VAL
13	m	5	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	191/218 (88%)	191 (100%)	0	100	100
3	c	170/212 (80%)	170 (100%)	0	100	100
4	d	175/176 (99%)	175 (100%)	0	100	100
5	e	127/147 (86%)	127 (100%)	0	100	100
6	f	85/85 (100%)	85 (100%)	0	100	100
7	g	131/132 (99%)	131 (100%)	0	100	100
8	h	107/108 (99%)	107 (100%)	0	100	100
9	i	102/125 (82%)	102 (100%)	0	100	100
10	j	89/90 (99%)	89 (100%)	0	100	100
11	k	89/105 (85%)	89 (100%)	0	100	100
12	l	103/105 (98%)	103 (100%)	0	100	100
13	m	99/104 (95%)	99 (100%)	0	100	100
14	n	49/50 (98%)	49 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	92/118 (78%)	92 (100%)	0	100	100
17	q	80/83 (96%)	80 (100%)	0	100	100
18	r	55/72 (76%)	55 (100%)	0	100	100
19	s	70/84 (83%)	70 (100%)	0	100	100
20	t	69/70 (99%)	69 (100%)	0	100	100
21	u	30/31 (97%)	30 (100%)	0	100	100
24	z	290/298 (97%)	290 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	D	160/163 (98%)	160 (100%)	0	100	100
29	E	169/173 (98%)	169 (100%)	0	100	100
30	F	151/156 (97%)	151 (100%)	0	100	100
31	G	148/150 (99%)	148 (100%)	0	100	100
32	H	90/116 (78%)	90 (100%)	0	100	100
33	I	89/120 (74%)	89 (100%)	0	100	100
34	J	102/108 (94%)	102 (100%)	0	100	100
35	K	6/184 (3%)	6 (100%)	0	100	100
36	L	119/120 (99%)	119 (100%)	0	100	100
37	M	100/100 (100%)	100 (100%)	0	100	100
38	N	112/114 (98%)	112 (100%)	0	100	100
39	O	114/115 (99%)	114 (100%)	0	100	100
40	P	97/158 (61%)	97 (100%)	0	100	100
41	Q	93/94 (99%)	93 (100%)	0	100	100
42	R	100/100 (100%)	100 (100%)	0	100	100
43	S	97/99 (98%)	97 (100%)	0	100	100
44	T	81/83 (98%)	81 (100%)	0	100	100
45	U	90/117 (77%)	90 (100%)	0	100	100
46	V	83/85 (98%)	83 (100%)	0	100	100
47	W	81/86 (94%)	81 (100%)	0	100	100
48	X	155/168 (92%)	155 (100%)	0	100	100
49	Y	61/63 (97%)	61 (100%)	0	100	100
50	Z	50/51 (98%)	50 (100%)	0	100	100
51	1	58/66 (88%)	58 (100%)	0	100	100
52	2	52/54 (96%)	52 (100%)	0	100	100
53	3	46/63 (73%)	46 (100%)	0	100	100
54	4	43/46 (94%)	43 (100%)	0	100	100
55	5	47/52 (90%)	47 (100%)	0	100	100
56	6	35/36 (97%)	35 (100%)	0	100	100
57	7	53/54 (98%)	53 (100%)	0	100	100
58	8	35/35 (100%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	9	18/19 (95%)	18 (100%)	0	100	100
All	All	5229/5856 (89%)	5229 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
31	G	23	ASN
42	R	76	HIS
57	7	31	HIS
31	G	144	GLN
36	L	132	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1510/1528 (98%)	292 (19%)	0
22	v	2/3 (66%)	0	0
23	y	72/76 (94%)	12 (16%)	0
25	A	3079/3164 (97%)	500 (16%)	13 (0%)
26	B	117/118 (99%)	15 (12%)	1 (0%)
All	All	4780/4889 (97%)	819 (17%)	14 (0%)

5 of 819 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	18	U
1	a	36	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	980	C
25	A	981	U
26	B	10	G
25	A	1510	A

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Mol	Chain	Res	Type
25	A	2094	G

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

6 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
23	PSU	y	32	23	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
23	PSU	y	39	23	18,21,22	1.33	2 (11%)	21,30,33	2.30	3 (14%)
23	4SU	y	8	23	18,21,22	1.86	4 (22%)	25,30,33	2.21	4 (16%)
23	5MU	y	54	23	19,22,23	1.41	6 (31%)	27,32,35	2.01	6 (22%)
23	PSU	y	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)
23	7MG	y	46	23	23,26,27	1.34	3 (13%)	27,39,42	2.74	7 (25%)

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
23	PSU	y	32	23	-	0/7/25/26	0/2/2/2
23	PSU	y	39	23	-	0/7/25/26	0/2/2/2
23	4SU	y	8	23	-	0/7/25/26	0/2/2/2
23	5MU	y	54	23	-	0/7/25/26	0/2/2/2
23	PSU	y	55	23	-	0/7/25/26	0/2/2/2
23	7MG	y	46	23	-	6/7/37/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	8	4SU	C4-S4	-5.05	1.59	1.68
23	y	8	4SU	C4-N3	-3.42	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	46	7MG	C5-C4	3.40	1.48	1.37
23	y	55	PSU	C6-C5	3.33	1.39	1.35
23	y	32	PSU	C6-C5	3.23	1.38	1.35

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	y	46	7MG	N9-C4-N3	9.79	139.81	125.46
23	y	39	PSU	N1-C2-N3	7.07	122.62	115.17
23	y	8	4SU	C4-N3-C2	-6.59	121.00	127.31
23	y	55	PSU	N1-C2-N3	6.45	121.97	115.17
23	y	32	PSU	N1-C2-N3	6.43	121.95	115.17

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	y	46	7MG	O4'-C4'-C5'-O5'
23	y	46	7MG	C3'-C4'-C5'-O5'
23	y	46	7MG	C2'-C1'-N9-C8
23	y	46	7MG	O4'-C1'-N9-C4
23	y	46	7MG	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	y	39	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

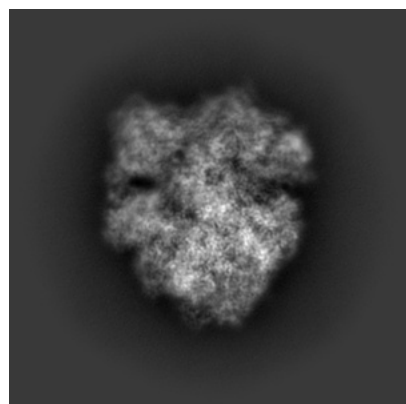
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43075. These allow visual inspection of the internal detail of the map and identification of artifacts.

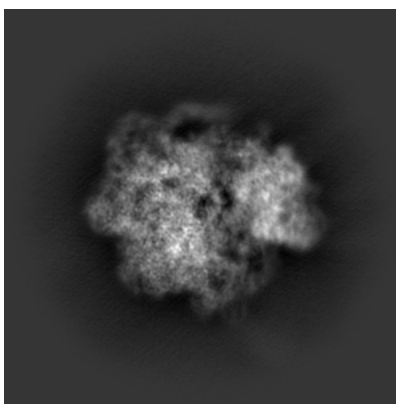
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

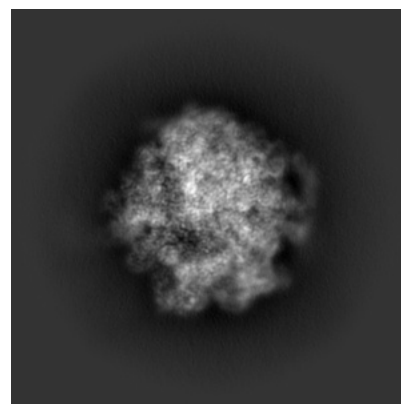
6.1.1 Primary map



X

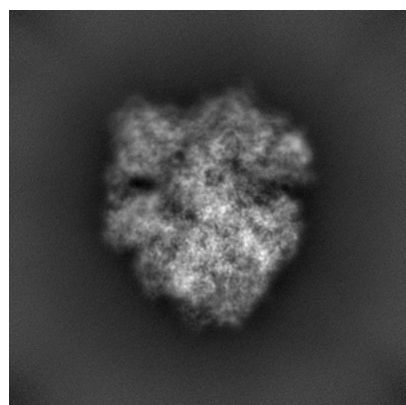


Y

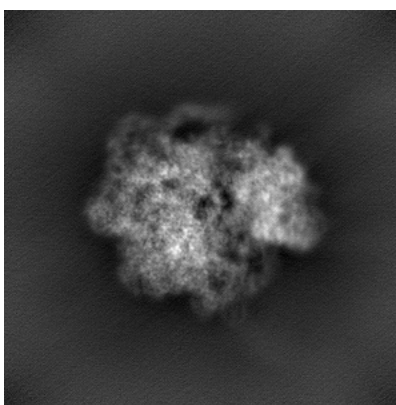


Z

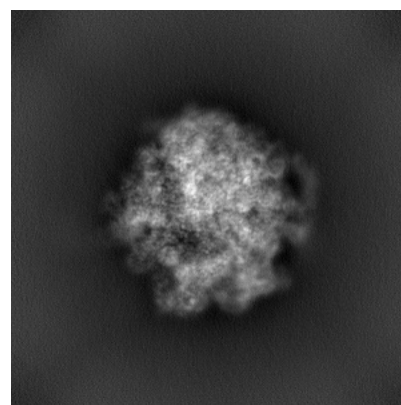
6.1.2 Raw map



X



Y

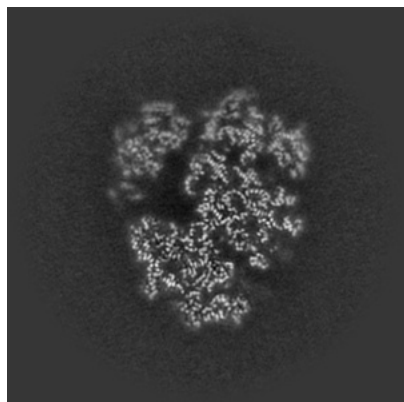


Z

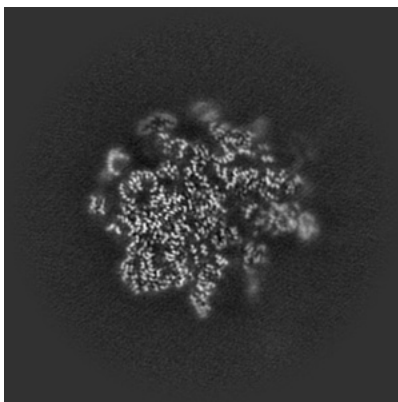
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

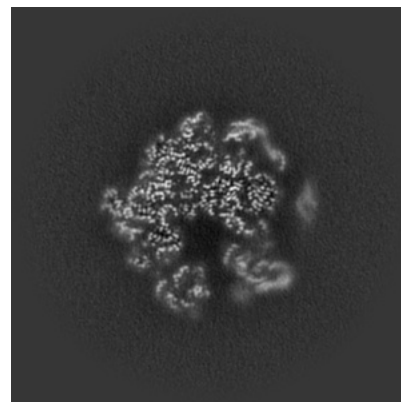
6.2.1 Primary map



X Index: 256

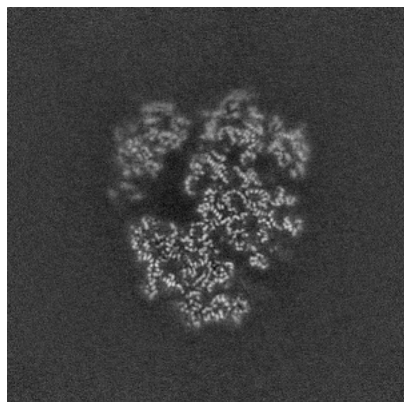


Y Index: 256

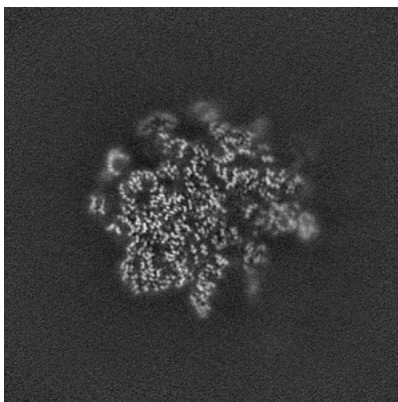


Z Index: 256

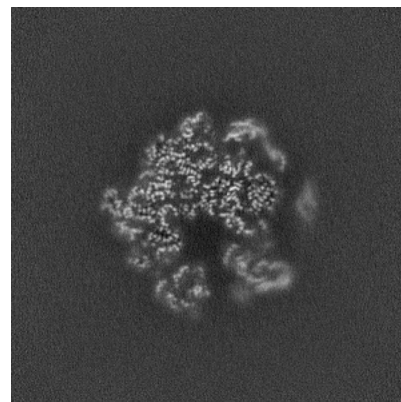
6.2.2 Raw map



X Index: 256



Y Index: 256

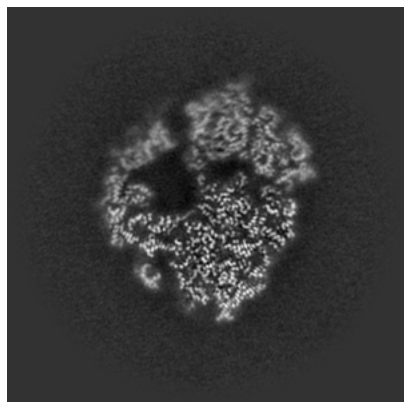


Z Index: 256

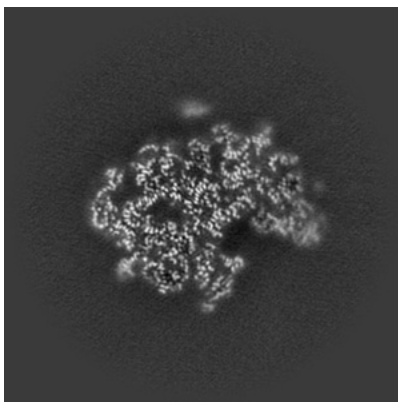
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

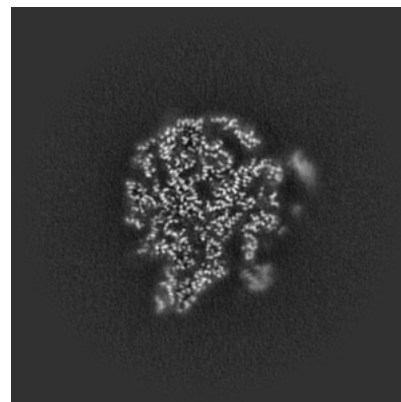
6.3.1 Primary map



X Index: 233

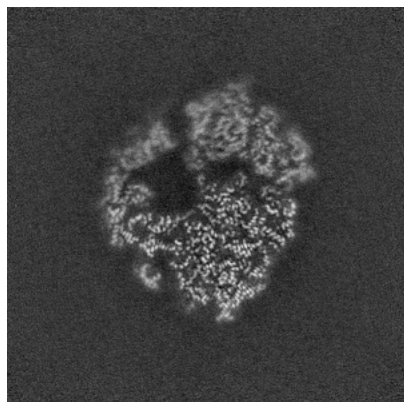


Y Index: 278

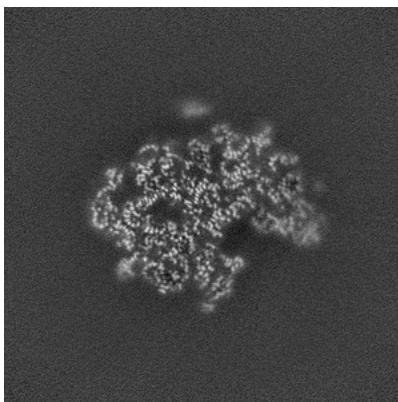


Z Index: 219

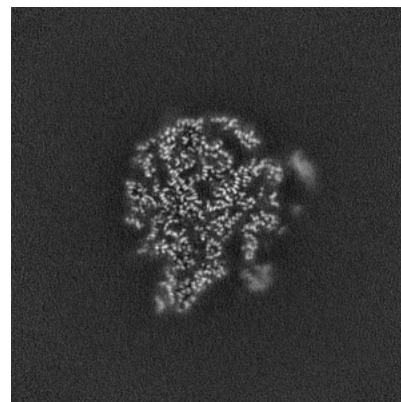
6.3.2 Raw map



X Index: 233



Y Index: 278

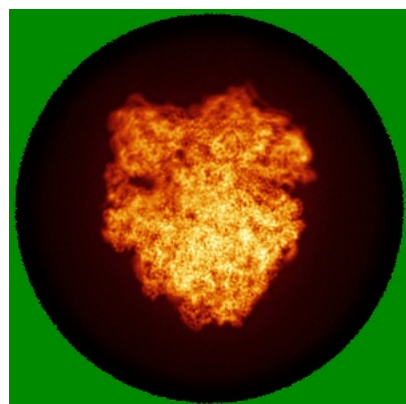


Z Index: 219

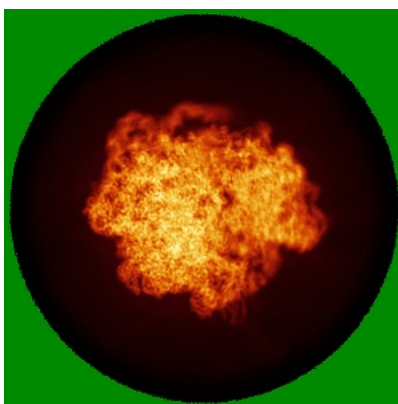
The images above show the largest variance slices of the map in three orthogonal directions.

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

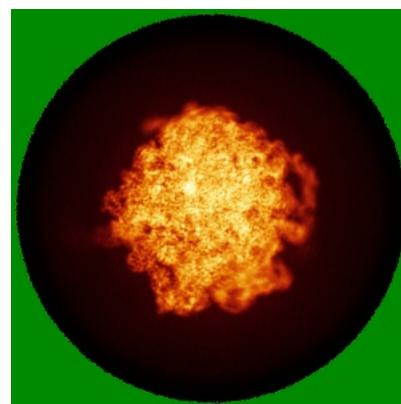
6.4.1 Primary map



X

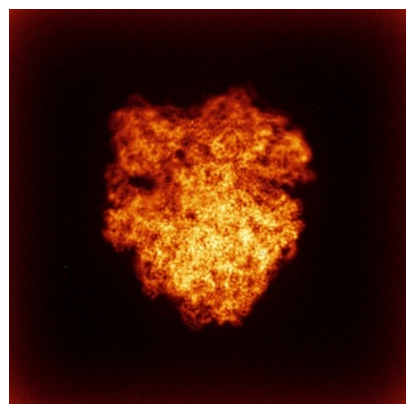


Y

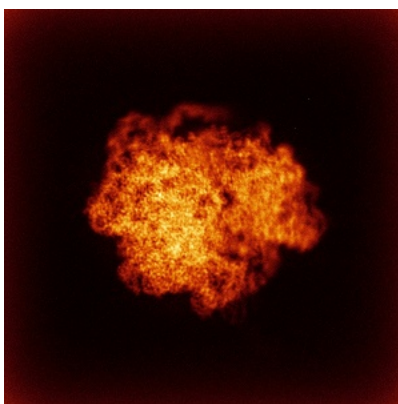


Z

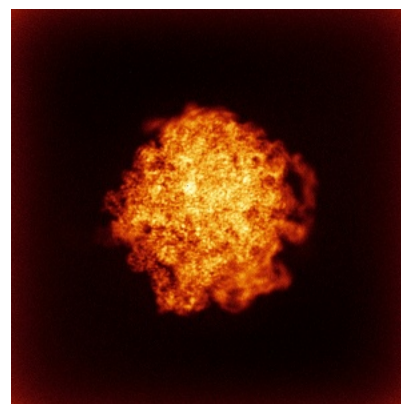
6.4.2 Raw map



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



X



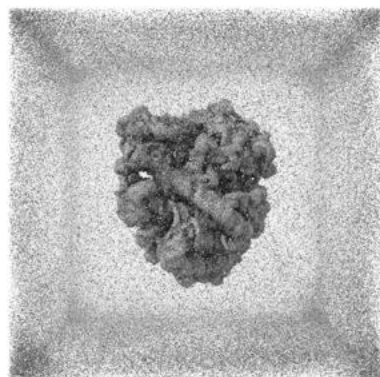
Y



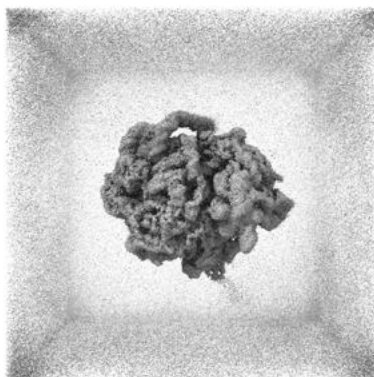
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

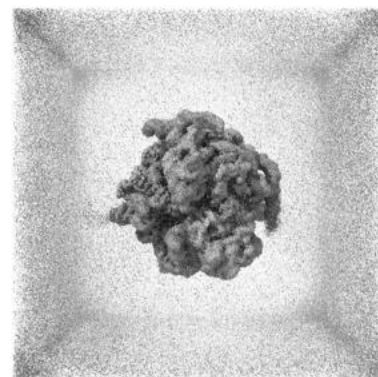
6.5.2 Raw map



X



Y



Z

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.

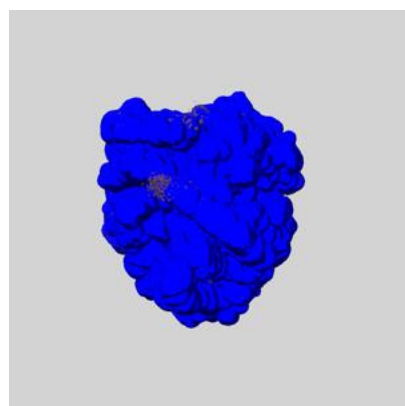
6.6 Mask visualisation [i](#)

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

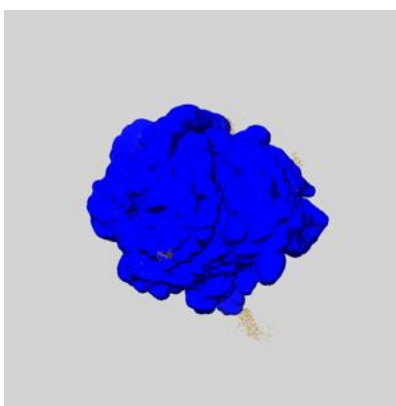
A mask typically either:

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

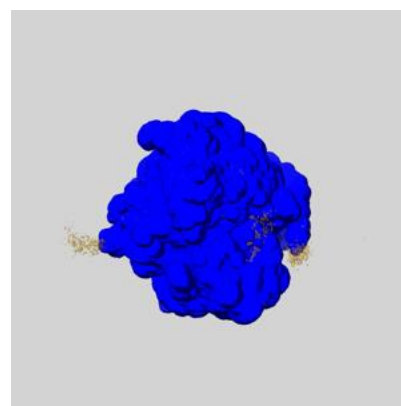
6.6.1 emd_43075_msk_1.map [i](#)



X



Y

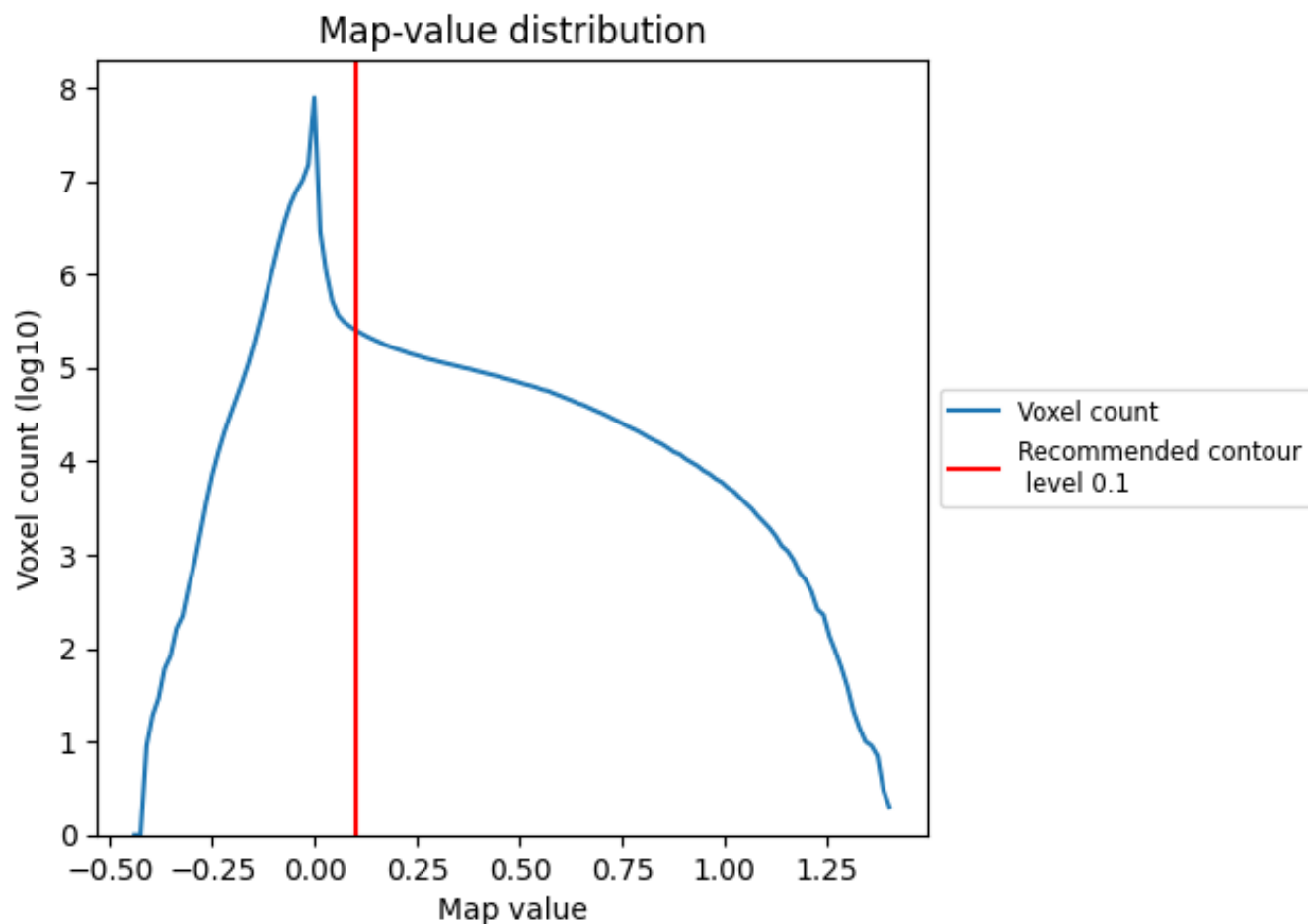


Z

7 Map analysis [i](#)

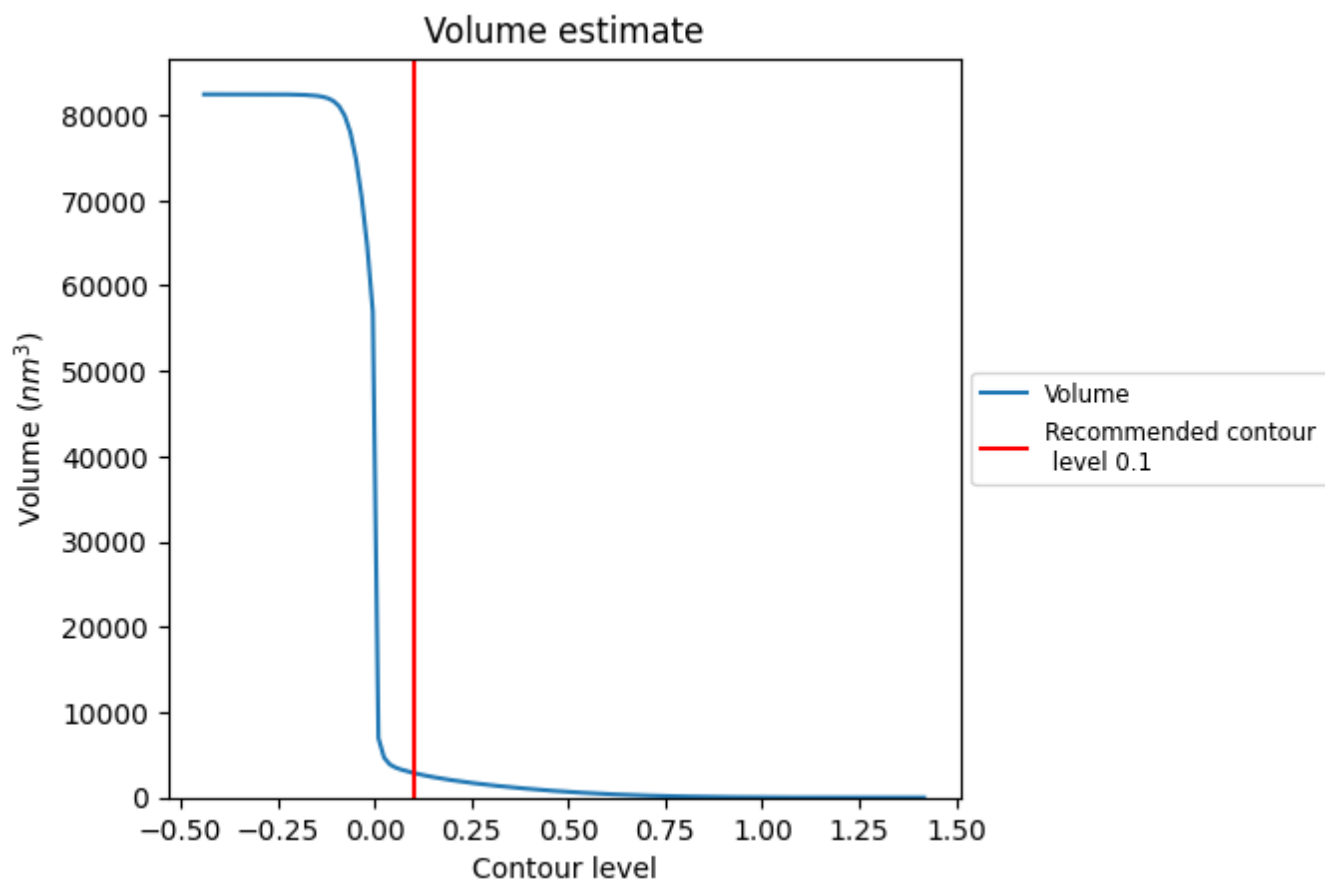
This section contains the results of statistical analysis of the map.

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.

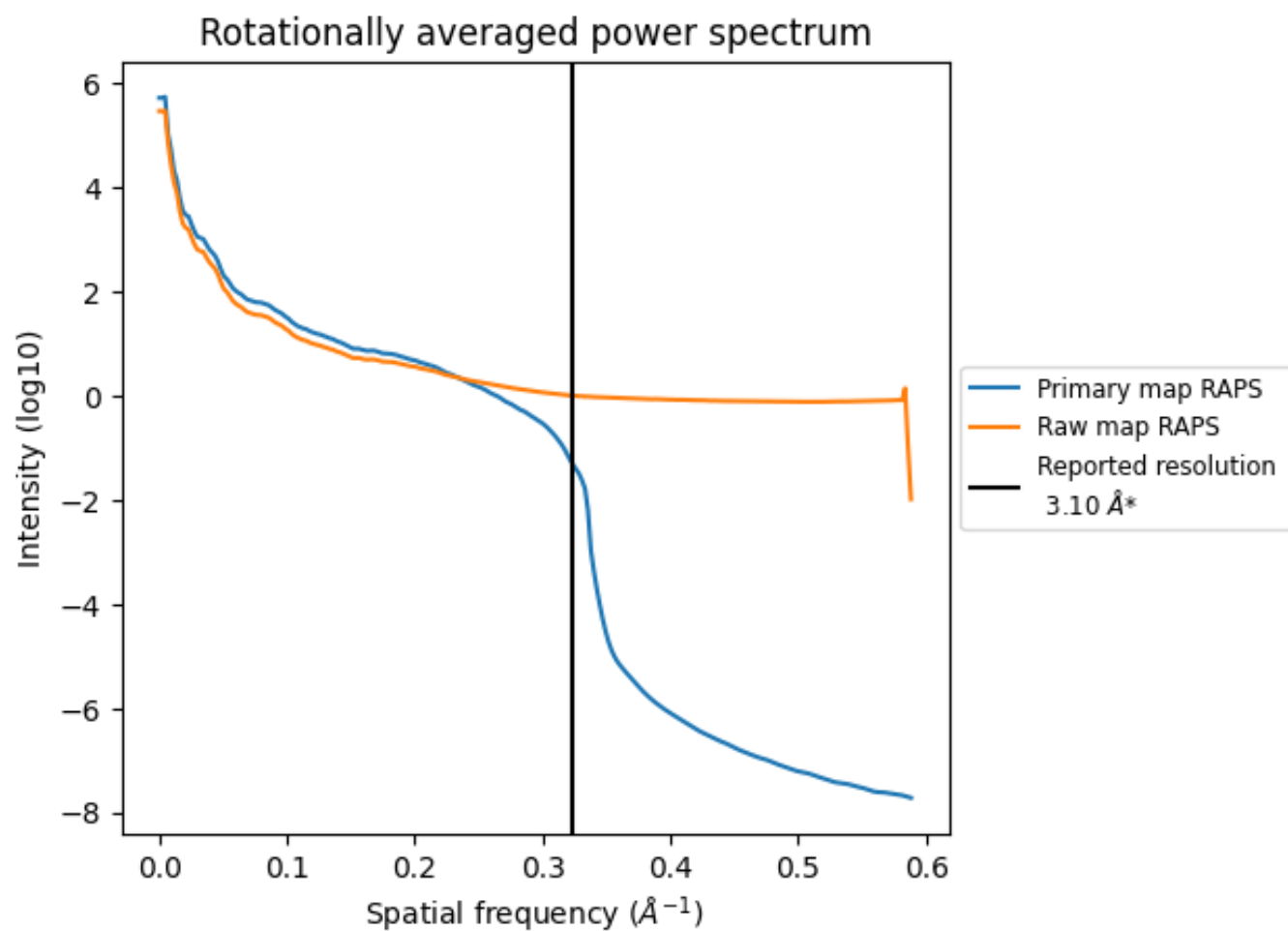
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2897 nm³; this corresponds to an approximate mass of 2617 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

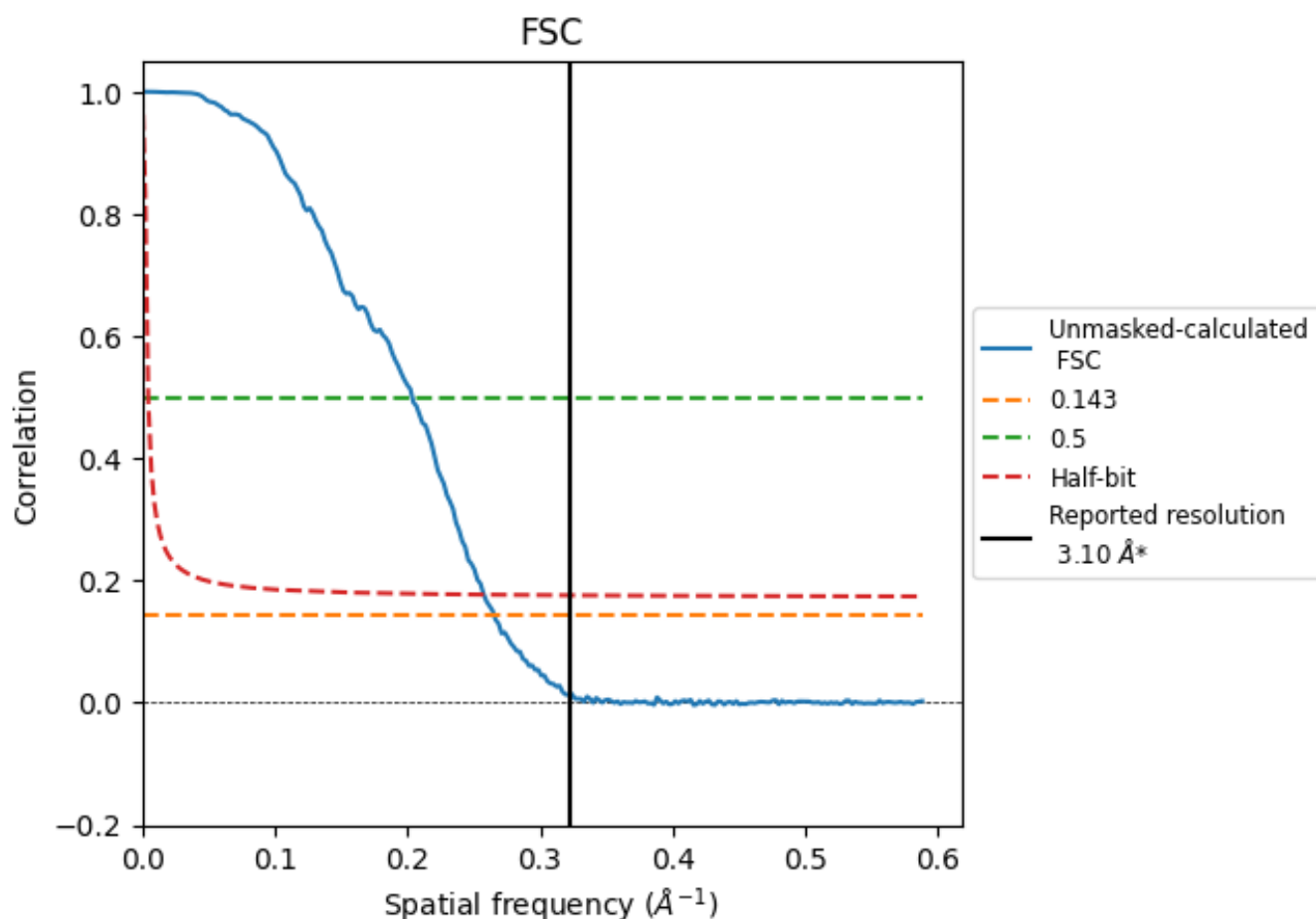


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

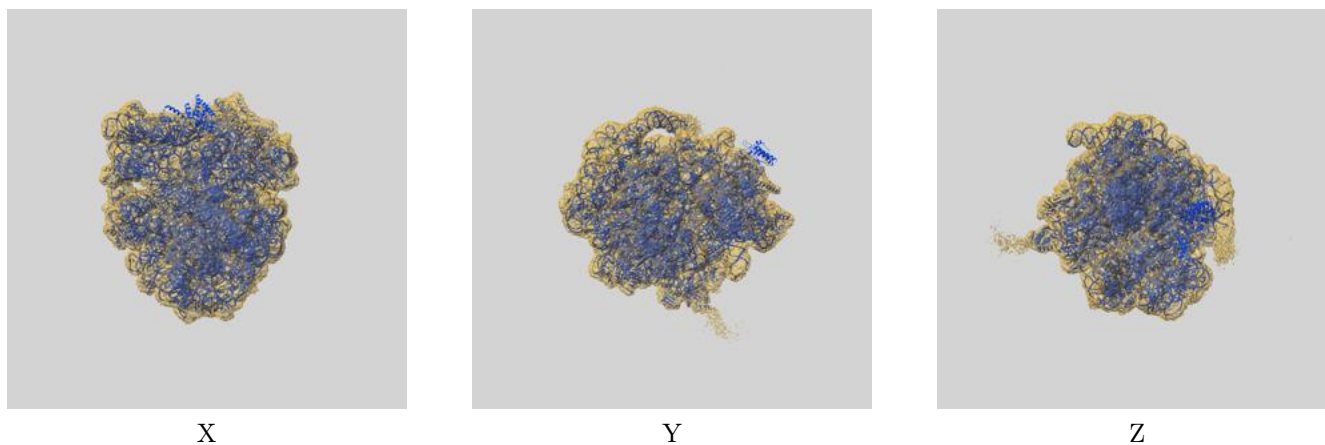
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.77	4.91	3.88

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.77 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

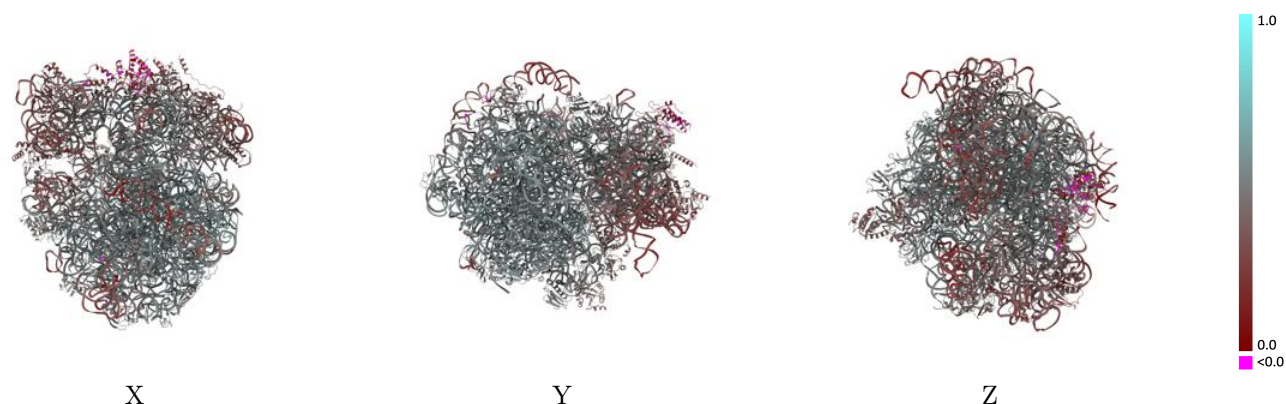
This section contains information regarding the fit between EMDB map EMD-43075 and PDB model 8V9K. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



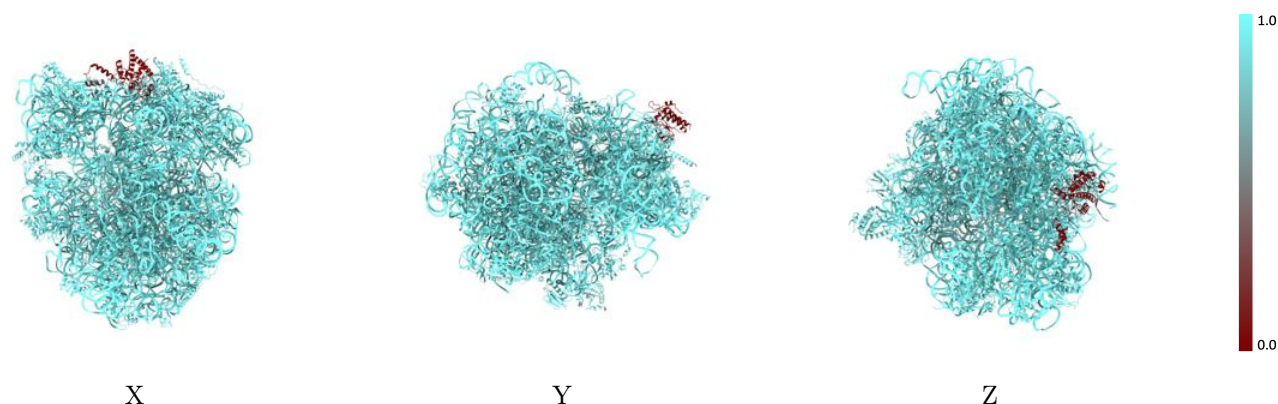
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



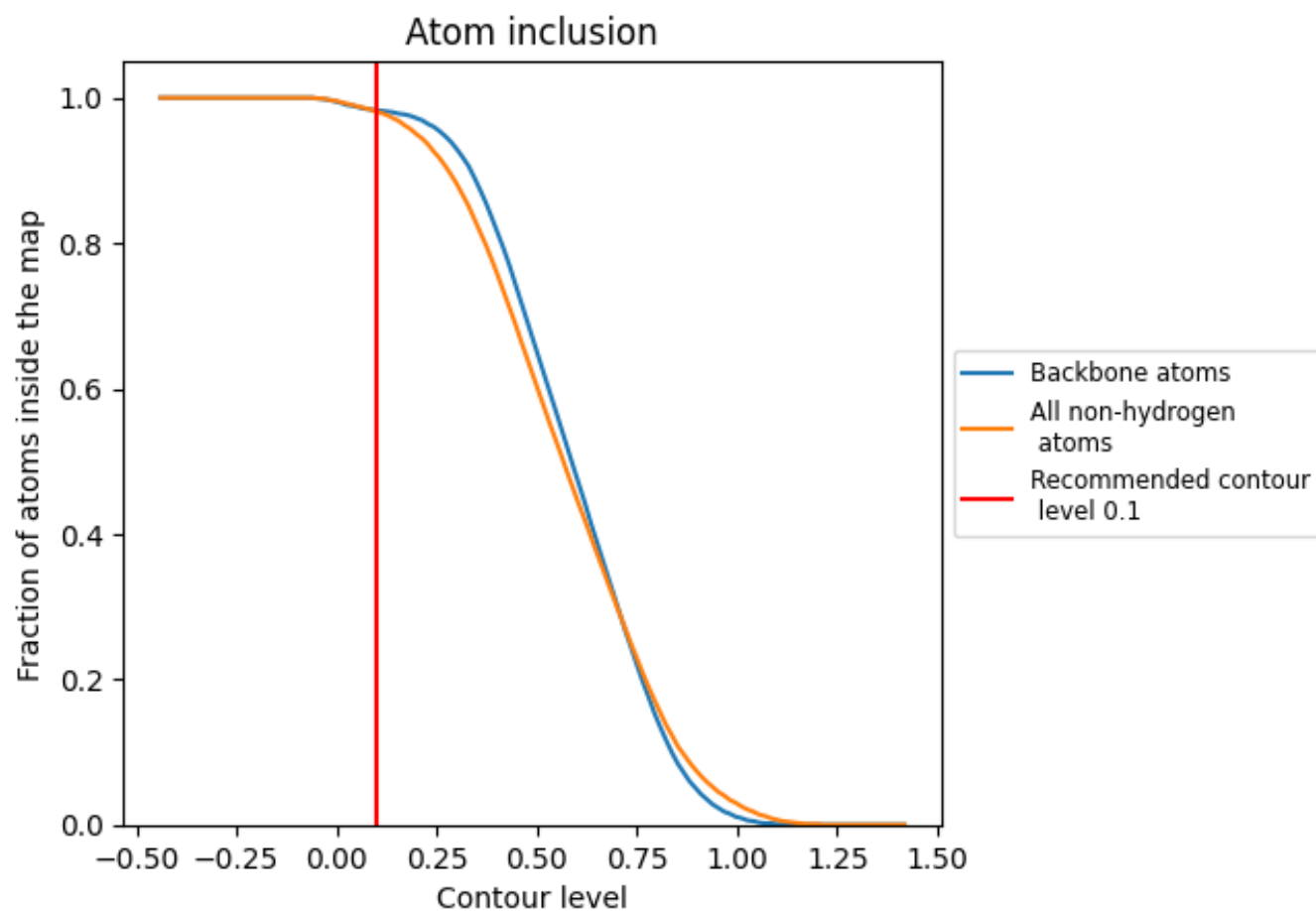
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9810	 0.4610
1	 0.9920	 0.4880
2	 0.9890	 0.5390
3	 0.9950	 0.4110
4	 0.9900	 0.5400
5	 0.9950	 0.5310
6	 0.9740	 0.5480
7	 0.9850	 0.5530
8	 0.9860	 0.5330
9	 0.9780	 0.5510
A	 0.9980	 0.4950
B	 0.9990	 0.4900
C	 0.9700	 0.5390
D	 0.9900	 0.5320
E	 0.9930	 0.5210
F	 0.9850	 0.4420
G	 0.9880	 0.4800
H	 0.9190	 0.4480
I	 0.8580	 0.3500
J	 0.9930	 0.3880
K	 0.9960	 0.4240
L	 0.9860	 0.5300
M	 0.9540	 0.5260
N	 0.9880	 0.5330
O	 0.9720	 0.5280
P	 0.9910	 0.5390
Q	 0.9960	 0.4940
R	 0.9670	 0.5190
S	 0.9920	 0.5310
T	 0.9990	 0.5480
U	 0.9870	 0.5360
V	 0.9850	 0.5210
W	 0.9850	 0.4940
X	 0.9730	 0.4900
Y	 0.9840	 0.5380



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Chain	Atom inclusion	Q-score
Z	 0.9930	 0.5440
a	 0.9990	 0.4080
b	 0.1040	 0.1510
c	 0.9830	 0.3880
d	 0.9890	 0.3370
e	 0.9740	 0.4480
f	 0.9770	 0.4600
g	 0.9810	 0.3220
h	 0.9960	 0.4740
i	 0.9920	 0.3620
j	 0.9820	 0.3780
k	 0.9810	 0.4800
l	 0.9420	 0.4130
m	 0.9840	 0.3260
n	 0.9760	 0.4230
o	 0.9830	 0.4650
p	 0.9850	 0.3610
q	 0.9790	 0.4200
r	 0.9960	 0.4630
s	 0.9910	 0.3550
t	 0.9750	 0.3360
u	 0.8850	 0.4780
v	 1.0000	 0.4870
y	 0.9980	 0.4330
z	 0.9610	 0.4600