



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:51 AM UTC

PDB ID : 9P4I / pdb_00009p4i
EMDB ID : EMD-71268
Title : YsxC-GTP treated 44.5SYsxC particles. Class 5.
Authors : Ortega, J.; Seffouh, A.
Deposited on : 2025-06-16
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

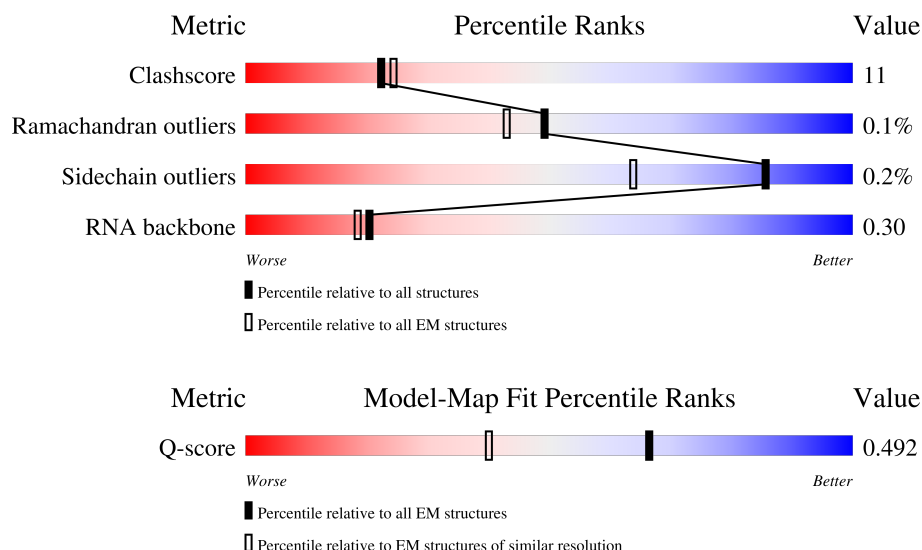
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 Å.

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



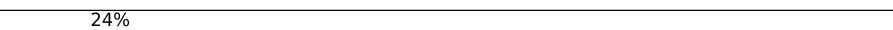
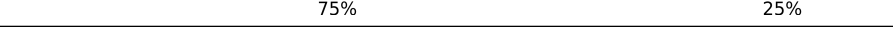
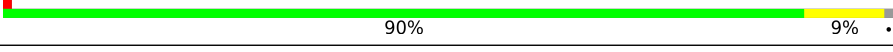
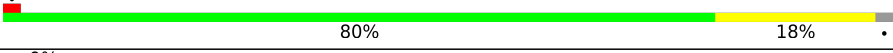
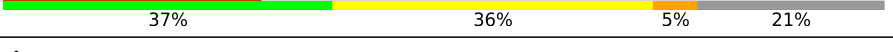
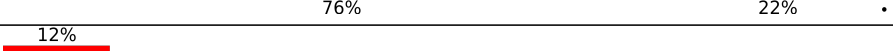
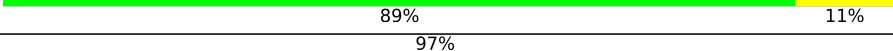
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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

Mol	Chain	Length	Quality of chain
1	A	2927	
2	B	119	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	209	 82% 17% .
5	E	207	 7% 82% 16% .
6	G	179	 50% 63% 34% ..
7	J	145	 81% 17% .
8	K	122	 77% 23% .
9	L	146	 24% 75% 25%
10	N	120	 85% 13% ..
11	O	120	 40% 59% 35% . .
12	P	115	 10% 75% 23% ..
13	Q	118	 90% 9% .
14	R	102	 87% 12% .
15	S	113	 80% 17% .
16	T	95	 80% 18% .
17	U	103	 9% 81% 17% .
18	V	94	 29% 37% 36% 5% 21%
19	Y	66	 68% 30% .
20	Z	59	 76% 22% .
21	b	59	 12% 69% 22% 8%
22	d	44	 89% 11%
23	f	37	 97% 76% 22% .

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 82115 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2818	Total	C	N	O	P	0	0
			60508	26994	11168	19528	2818		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	C	U	conflict	GB 2210155072
A	1558	C	G	conflict	GB 2210155072

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

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

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L6.

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

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	118	Total	C	N	O	S	0	0
			892	549	173	169	1		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	74	Total	C	N	O		0	0
			578	359	113	106			

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 22 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

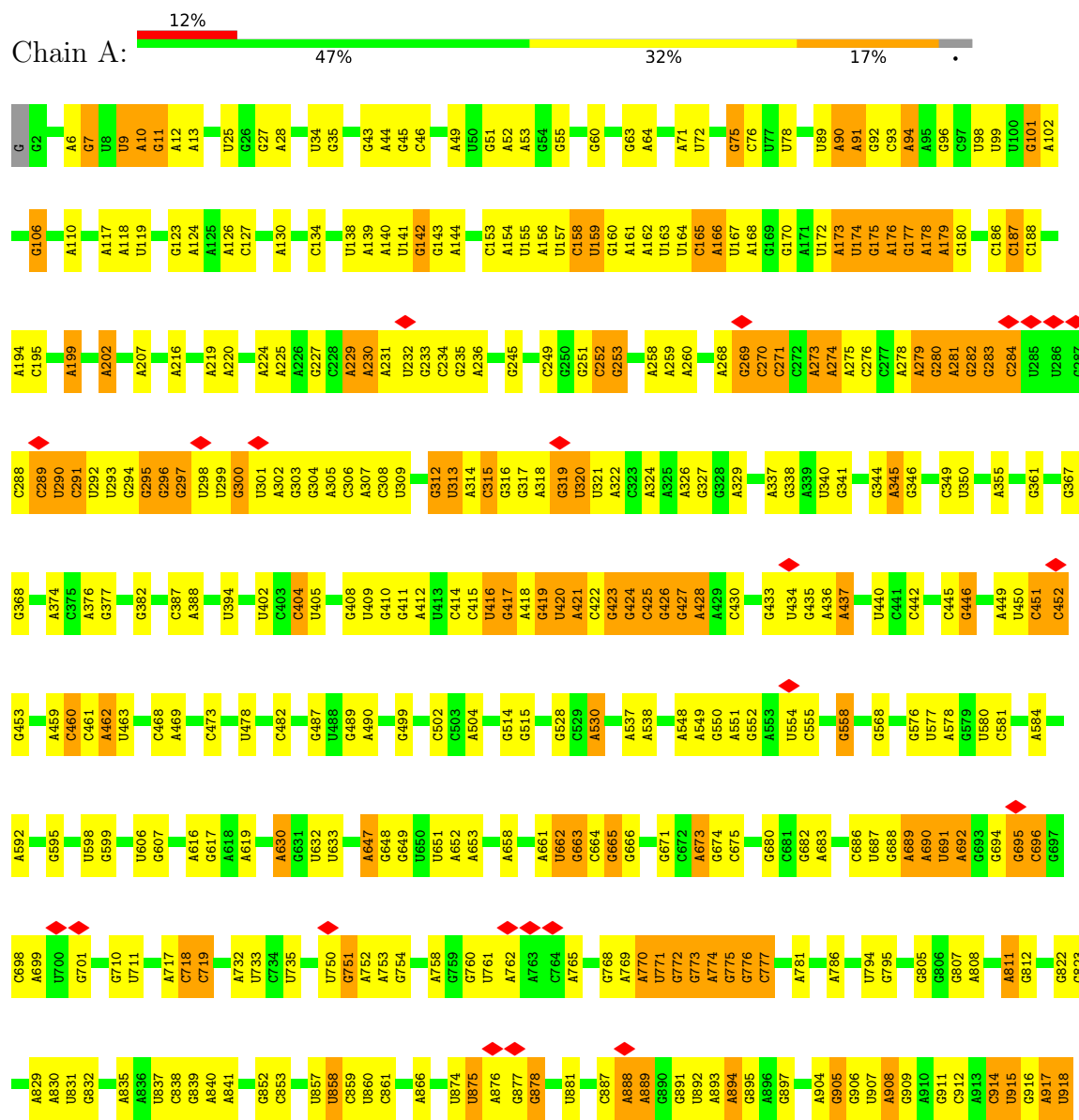
- Molecule 23 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

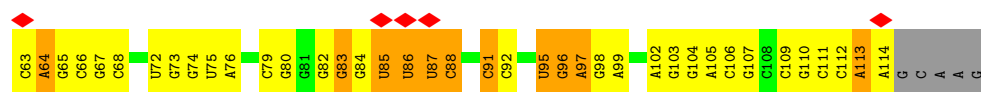
3 Residue-property plots

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

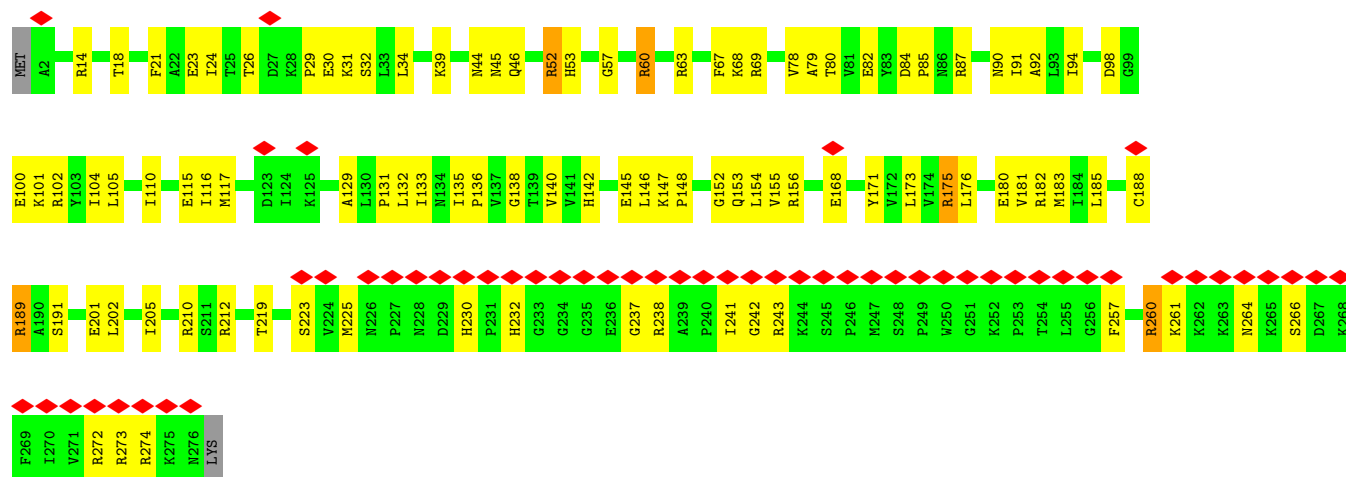
• Molecule 1: 23S rRNA



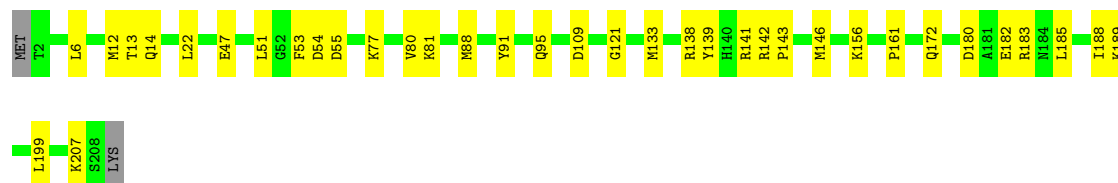
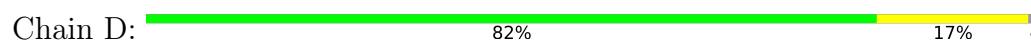
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A2000	U	A1814	C1726	A1615	U1535	U1486	G1250	A1157	A1097	G920
G2001	A	A1815	G1616	G1616	G1457	G1457	G1251	U1158	C1098	G921
G2002	A	A1816	A1734	A1617	G1537	G1468	G1252	U1159	C1099	A922
C2003	C	C1817	A1735	A1618	G1538	G1469	G1253	G1160	A1006	A923
G2004	U	A1818	G1744	A1619	G1539	G1470	A1260	G1161	G1007	C923
C2005	A	G1821	A1745	A1620	A1540	G1471	C1261	C1162	A1008	U924
A2006	U	G1822	A1746	G1621	G1546	G1472	G1264	U1163	U1009	A925
A2007	A	U1823	C1622	C1623	G1551	C1473	A1265	G1015	G1015	G926
C2008	A	U1824	C1623	C1624	C1552	C1474	A1266	G1016	U1016	G927
A2009	G	G1825	C1624	A1627	A1553	C1475	A1267	G1017	G1017	G928
A2010	C	U1826	U1754	G1628	U1554	C1476	G1276	G1018	U1018	G929
U2011	C	U1827	G1757	G1629	A1555	U1477	A1277	G1019	A1019	C930
U2020	C	G1828	U1758	G1630	A1556	G1478	G1278	G1100	A1020	C931
G2021	U	C1829	U1759	A1631	A1557	A1480	C1279	U1101	A1026	C932
U2022	U	G1830	A1760	G1632	G1561	A1485	G1280	C1102	A1027	C933
C2023	A	A1831	G1761	G1633	G1562	G1488	U1289	U1103	C1028	U934
U2024	A	A1832	G1762	G1634	G1563	U1489	G1290	A1104	G1029	A935
C2025	G	U1833	U1763	G1635	G1564	A1490	A1291	G1105	G1030	C936
A2026	U	G1834	G1765	G1636	U1565	A1491	G1292	U1106	A1031	C937
A2052	C	C1841	C1766	G1640	G1566	G1492	A1293	G1107	A1036	G938
A2060	C	A1844	A1767	U1641	U1567	C1493	G1296	U1108	C1041	G939
G2061	G	A1845	A1768	G1642	G1568	G1494	A1308	G1109	A1042	G940
A2062	A	G1846	C1769	G1642	A1569	C1495	G1309	G1110	A1046	U941
G2068	A	A1847	C1770	G1651	U1570	G1496	G1311	U1111	A1047	U942
U2070	G	U1848	C1771	C1652	G1571	U1497	A1312	U1112	A1055	A943
C2072	U	A1849	C1772	A1653	G1572	U1498	A1313	U1113	A1056	C944
U2074	U	U1850	A1773	A1654	C1573	A1499	A1314	A1114	G1057	C945
C2075	C	G1851	A1774	A1655	U1500	U1500	G1315	G1115	U1058	G946
A2080	C	G1852	G1775	A1655	G1574	U1501	A1316	A1116	A1059	A947
U2084	G	G1853	A1776	G1664	G1575	G1502	G1317	A1117	U1065	A948
C2084	A	G1854	A1777	G1667	G1576	G1503	A1323	U1118	A1066	U949
A2087	A	C1855	A1778	A1667	G1577	A1504	G1324	U1119	A1067	U950
G2088	U	U1856	C1779	A1667	G1578	U1505	A1201	U1120	G1068	C951
A2089	U	G1857	C1780	G1673	A1579	A1506	A1325	U1121	A1072	A952
G2090	A	U1858	G1781	G1674	A1580	A1507	A1326	U1122	A1073	G953
A2091	G	C1859	C1783	G1679	A1581	C1508	U1214	U1123	A1074	U954
C2092	C	G1860	A1784	A1679	U1582	G1512	U1215	U1124	A1075	C955
C2093	C	C1861	G1785	A1680	A1583	G1513	C1328	U1125	G1076	A956
C2094	C	U1862	U1786	U1681	A1584	C1514	G1331	A1126	G1077	A957
G2095	C	U1863	G1787	C1682	A1585	G1515	U1332	U1127	A1078	A958
U2096	A	G1864	A1791	U1689	G1586	A1516	A1339	U1128	U1079	C959
U2097	C	C1865	G1792	G1690	U1587	A1517	A1340	U1129	U1080	A964
G2098	U	U1866	G1793	A1691	A1588	A1518	U1341	A1130	U1081	G973
C2099	A	C	U1867	U1692	A1593	A1519	G1344	A1131	C1089	A974
A2100	A	G	G1801	G1693	G1594	G1525	U1345	A1132	A1092	G975
G2101	A	U1868	A1802	C1694	U1595	C1526	A1346	G1133	U1093	U976
C2102	C	C	C1803	G1695	U1596	G1527	A1347	U1134	A1094	U977
U2103	C	U	U1804	A1697	C1597	U1528	G1348	G1135	A1095	A978
U2104	C	G	G1805	A1697	U1598	G1529	U1349	U1136	C1082	U979
A2105	C	U	U1806	G1712	U1599	G1530	G1350	U1137	U1082	C980
U2106	G	G	U1807	G1719	G1600	A1531	U1351	C1138	U1081	C981
C2107	G	A	U1808	G1720	A1606	A1532	U1352	U1139	A1092	G985
U2108	C	C	A	C	C1607	A1533	A1461	U1140	G1093	A987
G2109	C	A	A	A	A1608	A1534	A1464	A1141	A1094	C992
C2110	C	C	A	C	A1609	A1535	A1465	A1142	U1095	A991
								A1143	C1095	G992
								G1145		
								C1146		
								U1147		
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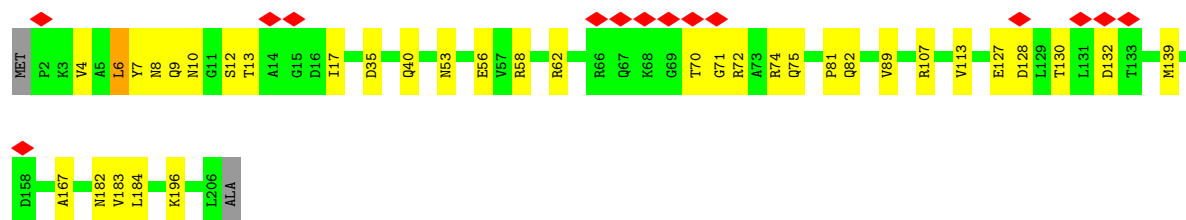
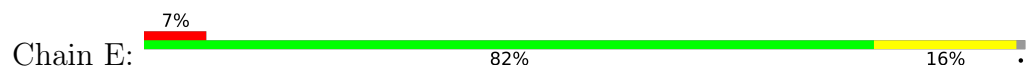
• Molecule 3: 50S ribosomal protein L2



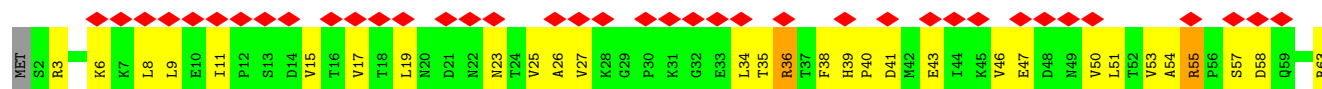
• Molecule 4: 50S ribosomal protein L3

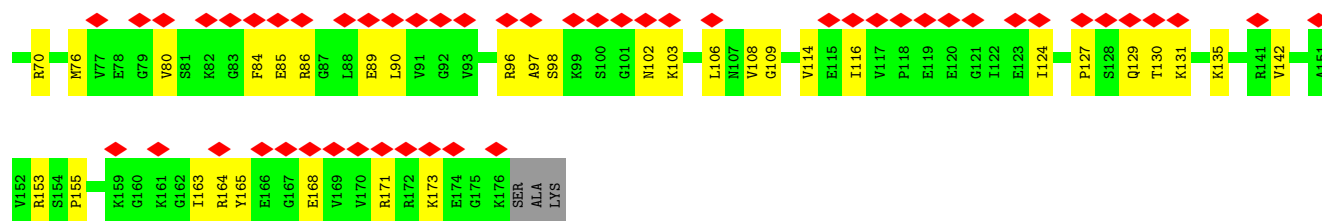


• Molecule 5: 50S ribosomal protein L4

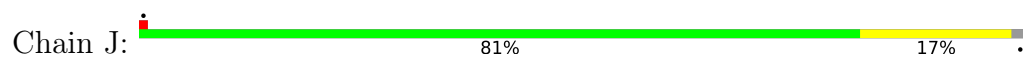


• Molecule 6: 50S ribosomal protein L6

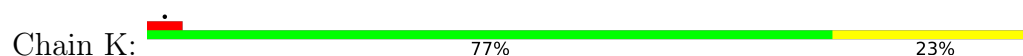




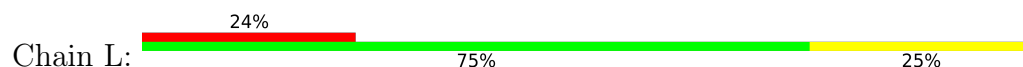
• Molecule 7: 50S ribosomal protein L13



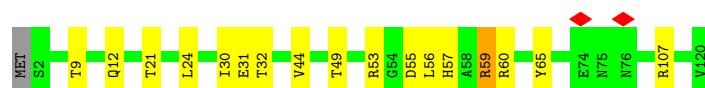
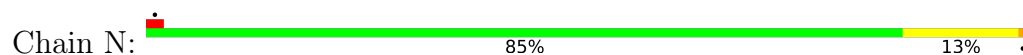
• Molecule 8: 50S ribosomal protein L14



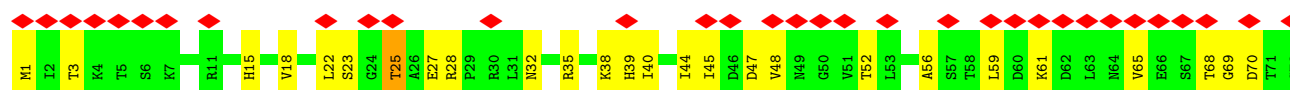
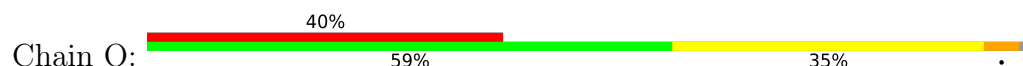
• Molecule 9: 50S ribosomal protein L15

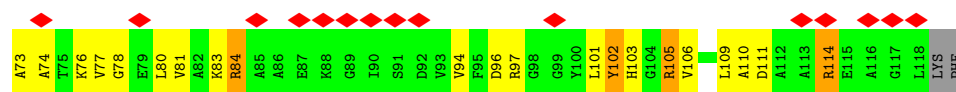


• Molecule 10: 50S ribosomal protein L17

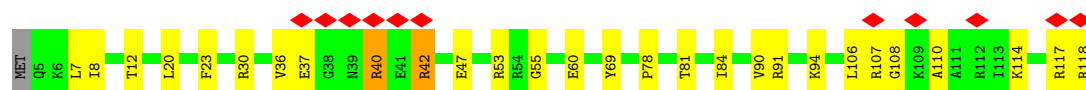
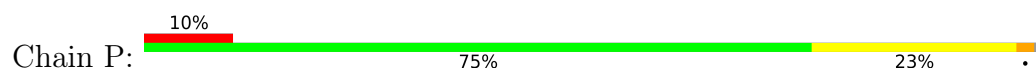


• Molecule 11: 50S ribosomal protein L18

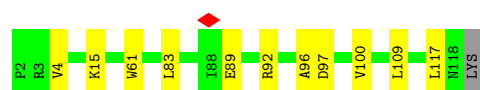




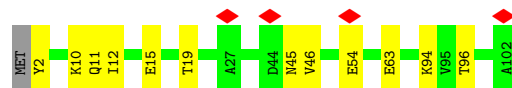
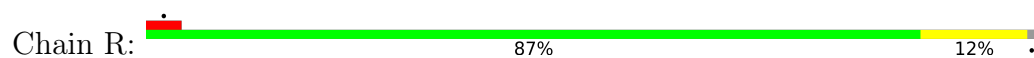
- Molecule 12: 50S ribosomal protein L19



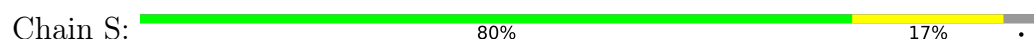
- Molecule 13: 50S ribosomal protein L20



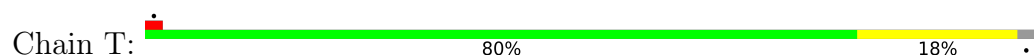
- Molecule 14: 50S ribosomal protein L21



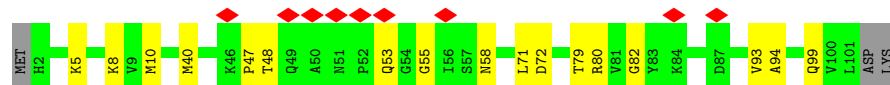
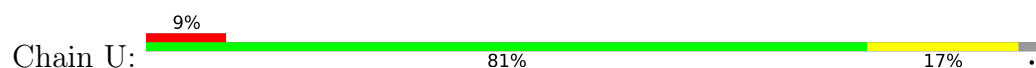
- Molecule 15: 50S ribosomal protein L22



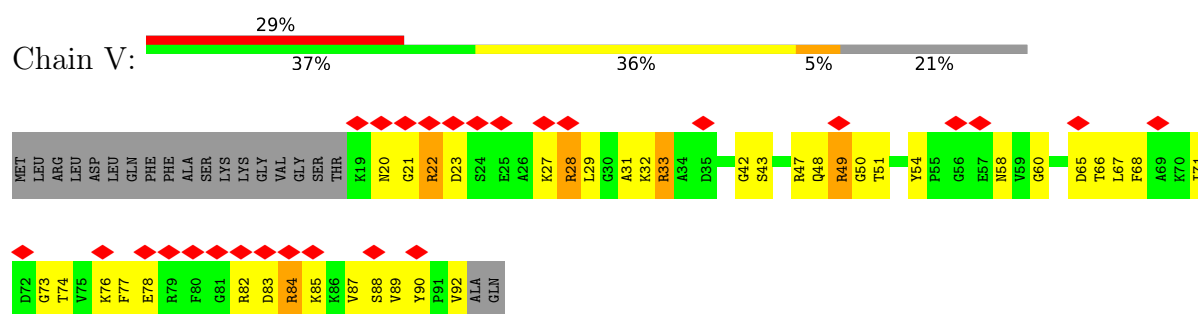
- Molecule 16: 50S ribosomal protein L23



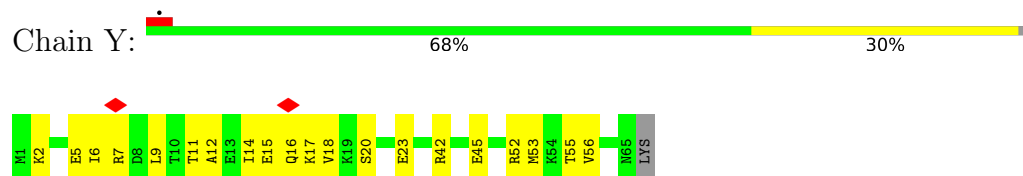
- Molecule 17: 50S ribosomal protein L24



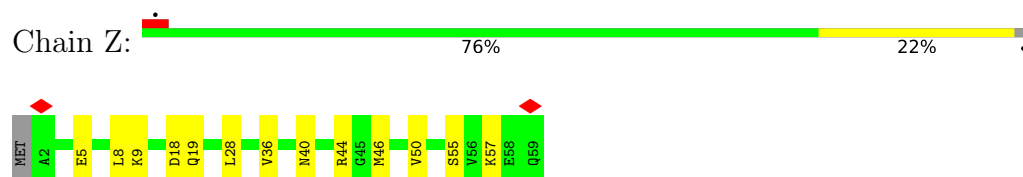
- Molecule 18: 50S ribosomal protein L27



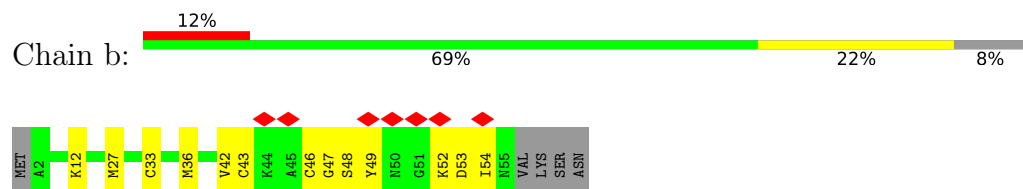
- Molecule 19: 50S ribosomal protein L29



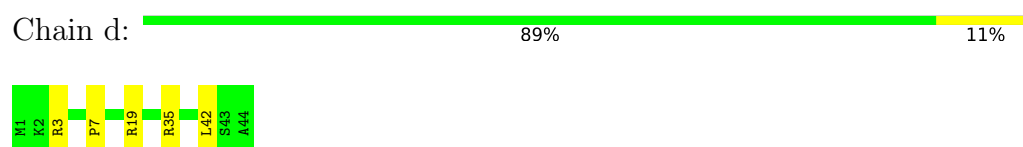
- Molecule 20: 50S ribosomal protein L30



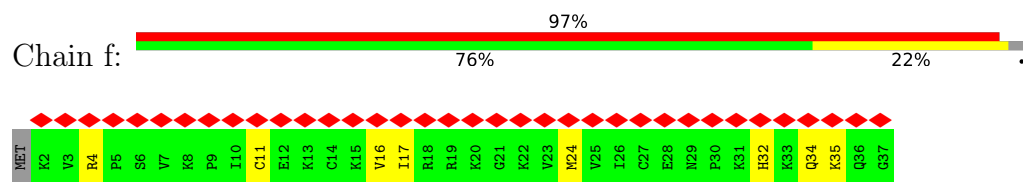
- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L34



- Molecule 23: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113285	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	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.314	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.066	Depositor
Map size (Å)	383.04, 383.04, 383.04	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.42	0/67774	0.57	6/105732 (0.0%)
2	B	0.72	0/2678	0.93	0/4174
3	C	0.96	0/2148	1.12	0/2881
4	D	0.40	0/1597	0.54	0/2140
5	E	0.52	0/1580	0.65	0/2132
6	G	0.48	0/1360	0.64	0/1832
7	J	0.30	0/1146	0.37	0/1542
8	K	0.39	0/927	0.56	0/1245
9	L	0.32	0/1093	0.60	0/1457
10	N	0.45	0/960	0.61	0/1284
11	O	0.64	0/900	0.91	1/1209 (0.1%)
12	P	0.38	0/949	0.54	0/1269
13	Q	0.34	0/952	0.47	0/1266
14	R	0.42	0/797	0.59	0/1070
15	S	0.35	0/851	0.51	0/1146
16	T	0.44	0/759	0.69	0/1011
17	U	0.31	0/764	0.57	0/1022
18	V	0.70	0/586	0.96	0/779
19	Y	0.39	0/531	0.71	0/707
20	Z	0.23	0/457	0.38	0/613
21	b	0.27	0/433	0.44	0/574
22	d	0.29	0/370	0.32	0/483
23	f	0.15	0/291	0.39	0/383
All	All	0.45	0/89903	0.61	7/135951 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	13
4	D	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	2
6	G	0	2
7	J	0	1
10	N	0	3
11	O	0	3
12	P	0	2
15	S	0	1
18	V	0	7
All	All	0	37

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2380	G	C3'-C2'-C1'	-6.61	94.89	101.50
1	A	2620	C	O3'-P-O5'	6.09	113.14	104.00
1	A	1863	U	C1'-O4'-C4'	-5.85	103.85	109.70
1	A	2348	C	C2'-C3'-O3'	5.36	117.53	109.50
1	A	2621	G	C3'-C2'-C1'	-5.27	96.23	101.50

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	14	ARG	Sidechain
3	C	52	ARG	Sidechain
3	C	60	ARG	Sidechain
3	C	63	ARG	Sidechain
3	C	87	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	60508	0	30450	854	0
2	B	2395	0	1212	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2111	0	2200	122	0
4	D	1575	0	1642	31	0
5	E	1561	0	1647	42	0
6	G	1342	0	1388	72	0
7	J	1123	0	1162	17	0
8	K	920	0	977	38	0
9	L	1081	0	1132	35	0
10	N	953	0	983	14	0
11	O	892	0	925	93	0
12	P	936	0	1008	32	0
13	Q	940	0	1005	13	0
14	R	786	0	826	9	0
15	S	842	0	899	16	0
16	T	752	0	802	17	0
17	U	754	0	809	19	0
18	V	578	0	586	42	0
19	Y	530	0	568	29	0
20	Z	455	0	491	13	0
21	b	426	0	445	12	0
22	d	367	0	410	5	0
23	f	288	0	327	4	0
All	All	82115	0	51894	1496	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 11.

The worst 5 of 1496 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)
6:G:46:VAL:CA	6:G:51:LEU:HD22	1.08	1.55
6:G:46:VAL:C	6:G:51:LEU:CD2	1.90	1.43
6:G:46:VAL:C	6:G:51:LEU:HD22	1.42	1.40
6:G:46:VAL:CA	6:G:51:LEU:CD2	2.00	1.36
6:G:47:GLU:N	6:G:51:LEU:CD2	1.89	1.35

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	
3	C	273/277 (99%)	227 (83%)	45 (16%)	1 (0%)	30	60
4	D	205/209 (98%)	191 (93%)	14 (7%)	0	100	100
5	E	203/207 (98%)	179 (88%)	24 (12%)	0	100	100
6	G	173/179 (97%)	155 (90%)	18 (10%)	0	100	100
7	J	140/145 (97%)	128 (91%)	12 (9%)	0	100	100
8	K	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
9	L	144/146 (99%)	119 (83%)	25 (17%)	0	100	100
10	N	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
11	O	116/120 (97%)	92 (79%)	24 (21%)	0	100	100
12	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
13	Q	115/118 (98%)	107 (93%)	8 (7%)	0	100	100
14	R	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
15	S	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
16	T	91/95 (96%)	87 (96%)	4 (4%)	0	100	100
17	U	98/103 (95%)	83 (85%)	15 (15%)	0	100	100
18	V	72/94 (77%)	54 (75%)	17 (24%)	1 (1%)	9	30
19	Y	63/66 (96%)	59 (94%)	4 (6%)	0	100	100
20	Z	56/59 (95%)	56 (100%)	0	0	100	100
21	b	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
22	d	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
23	f	34/37 (92%)	27 (79%)	7 (21%)	0	100	100
All	All	2432/2530 (96%)	2146 (88%)	284 (12%)	2 (0%)	49	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	V	31	ALA
3	C	155	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	
3	C	223/225 (99%)	222 (100%)	1 (0%)	84	94
4	D	168/170 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	168 (99%)	1 (1%)	78	92
6	G	148/151 (98%)	147 (99%)	1 (1%)	76	91
7	J	120/123 (98%)	120 (100%)	0	100	100
8	K	101/101 (100%)	101 (100%)	0	100	100
9	L	110/110 (100%)	110 (100%)	0	100	100
10	N	99/100 (99%)	98 (99%)	1 (1%)	68	88
11	O	91/93 (98%)	90 (99%)	1 (1%)	65	87
12	P	99/100 (99%)	99 (100%)	0	100	100
13	Q	96/97 (99%)	96 (100%)	0	100	100
14	R	83/84 (99%)	83 (100%)	0	100	100
15	S	90/93 (97%)	90 (100%)	0	100	100
16	T	84/85 (99%)	84 (100%)	0	100	100
17	U	84/87 (97%)	84 (100%)	0	100	100
18	V	58/74 (78%)	58 (100%)	0	100	100
19	Y	56/57 (98%)	56 (100%)	0	100	100
20	Z	52/53 (98%)	52 (100%)	0	100	100
21	b	48/53 (91%)	48 (100%)	0	100	100
22	d	39/39 (100%)	39 (100%)	0	100	100
23	f	34/35 (97%)	34 (100%)	0	100	100
All	All	2052/2100 (98%)	2047 (100%)	5 (0%)	85	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	18	THR
5	E	6	LEU
6	G	84	PHE
10	N	57	HIS
11	O	102	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
11	O	32	ASN
12	P	15	GLN
11	O	43	GLN
15	S	95	GLN
4	D	140	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2816/2927 (96%)	1077 (38%)	82 (2%)
2	B	111/119 (93%)	64 (57%)	8 (7%)
All	All	2927/3046 (96%)	1141 (38%)	90 (3%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	10	A
1	A	11	G
1	A	13	A

5 of 90 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2116	G
1	A	2435	C
1	A	2143	A
1	A	2348	C
1	A	2581	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

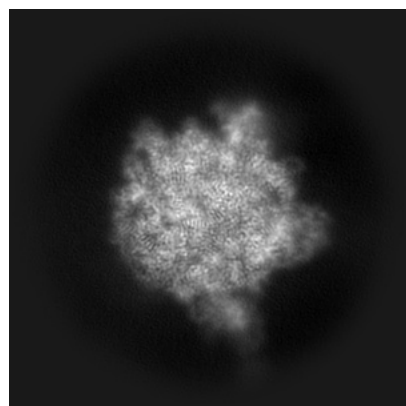
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71268. These allow visual inspection of the internal detail of the map and identification of artifacts.

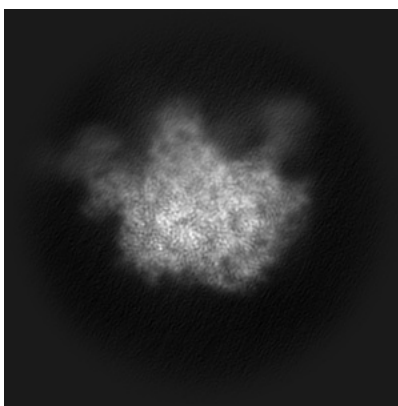
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

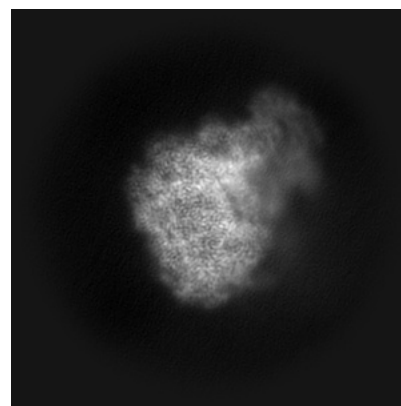
6.1.1 Primary map



X

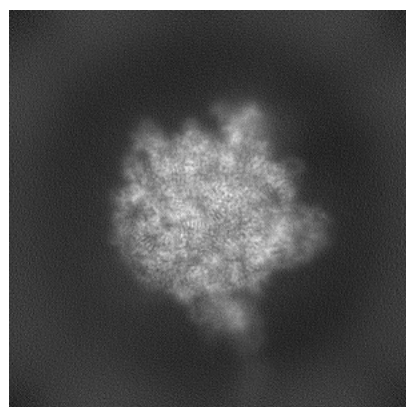


Y

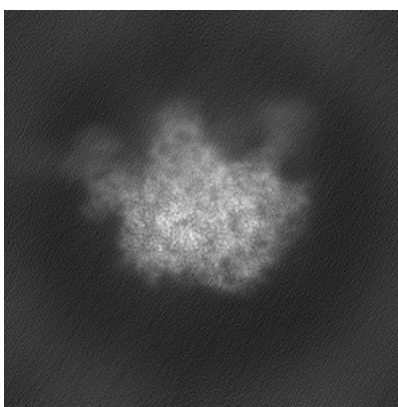


Z

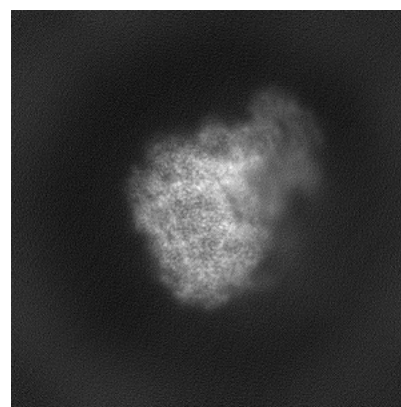
6.1.2 Raw map



X



Y

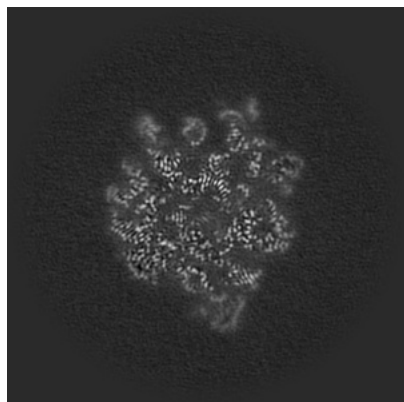


Z

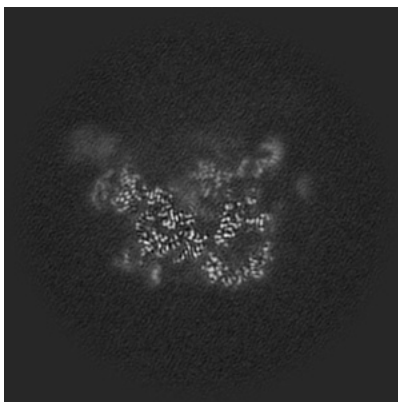
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

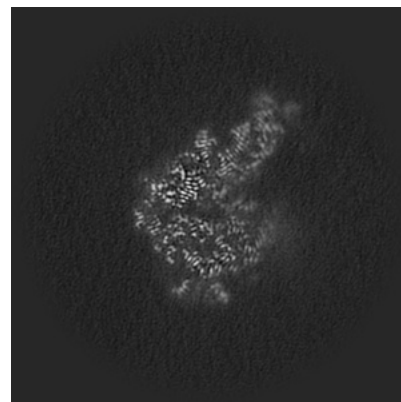
6.2.1 Primary map



X Index: 224

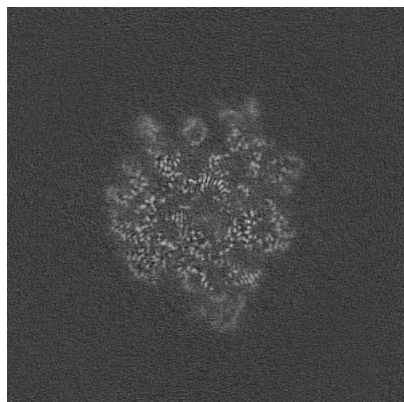


Y Index: 224

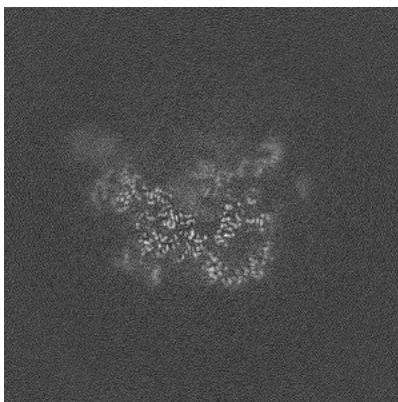


Z Index: 224

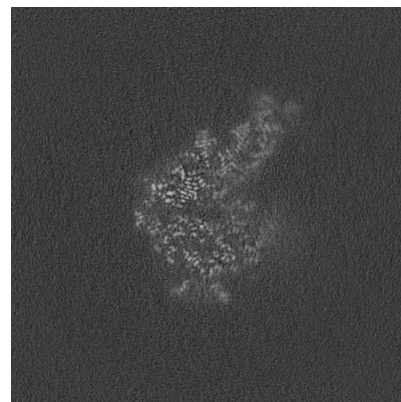
6.2.2 Raw map



X Index: 224



Y Index: 224

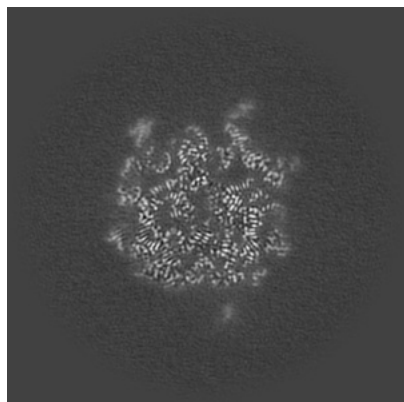


Z Index: 224

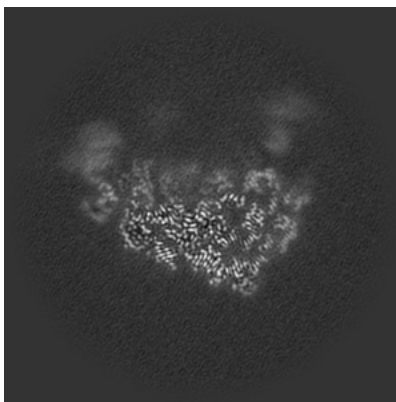
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

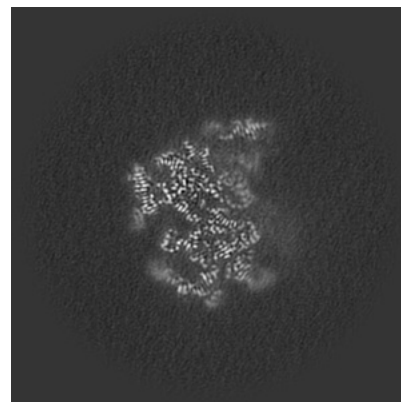
6.3.1 Primary map



X Index: 212

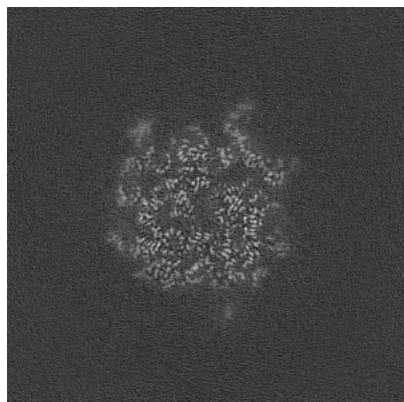


Y Index: 248

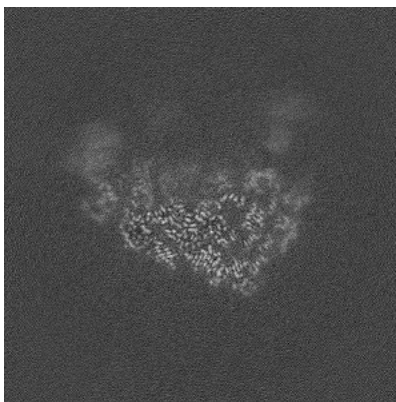


Z Index: 241

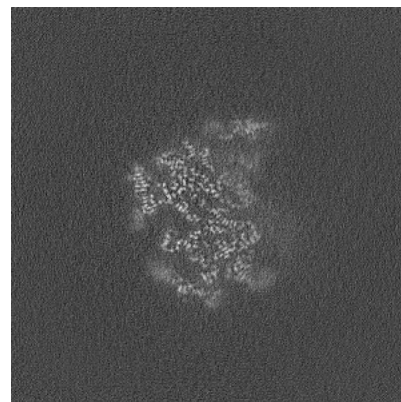
6.3.2 Raw map



X Index: 211



Y Index: 248

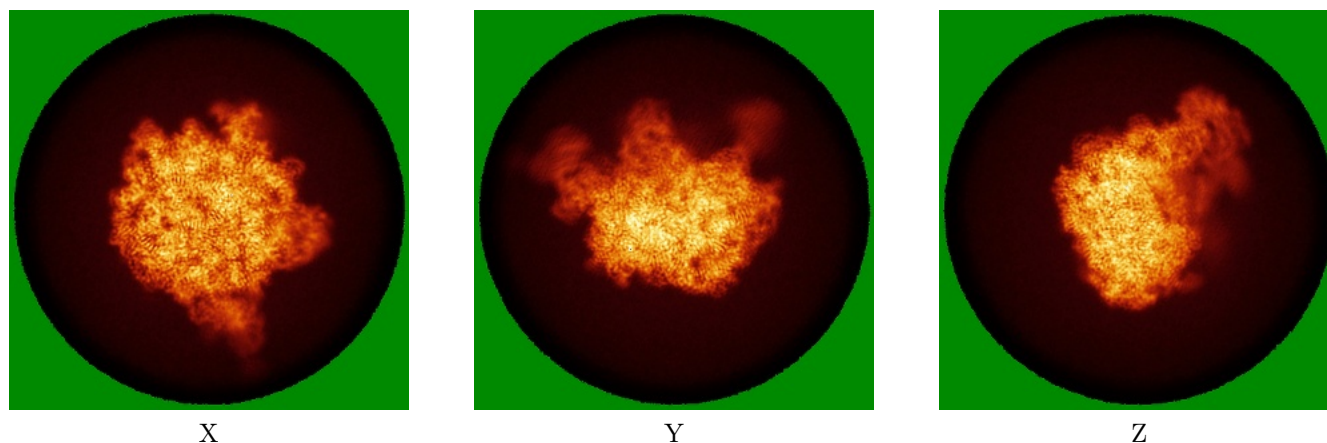


Z Index: 241

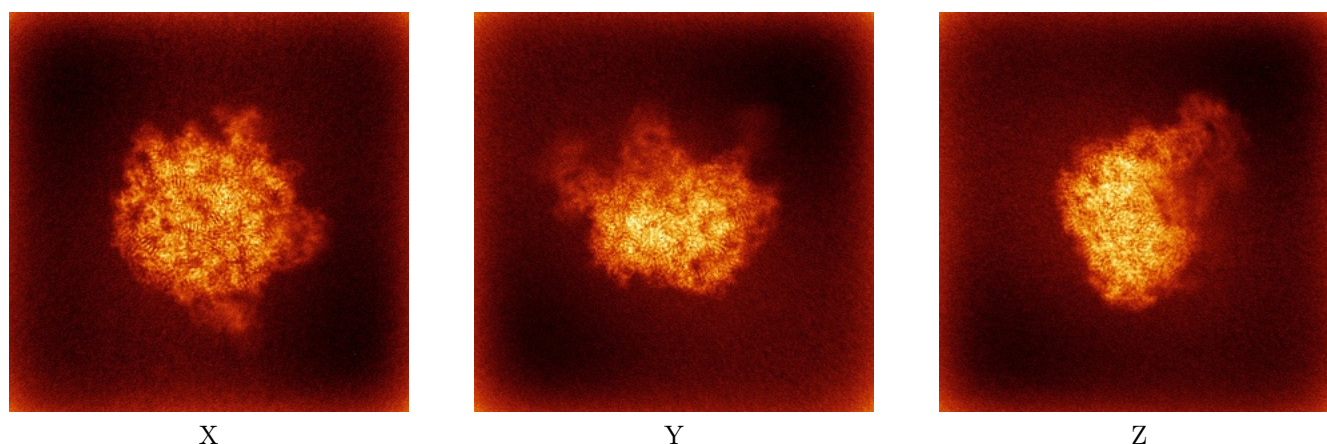
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

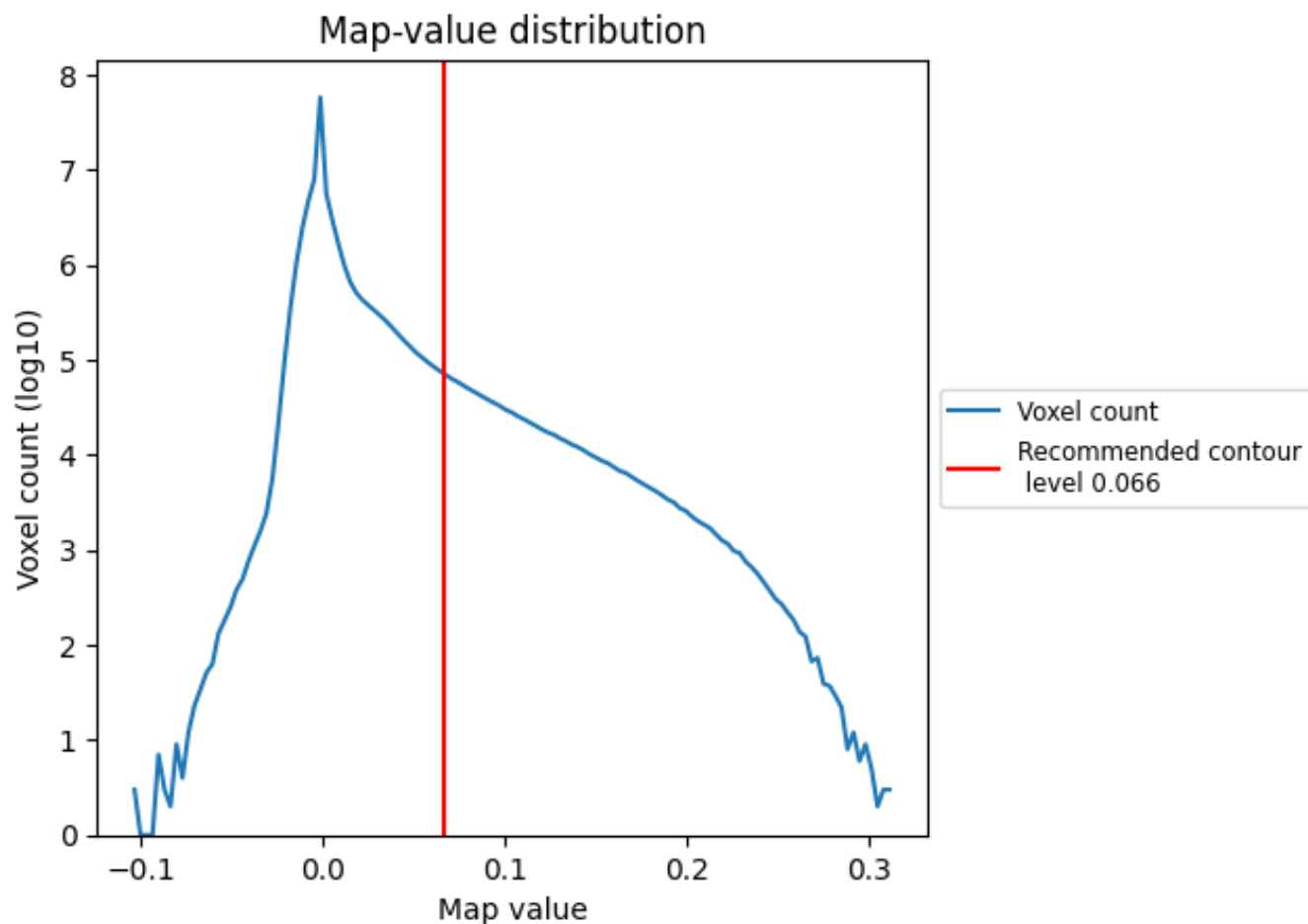
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

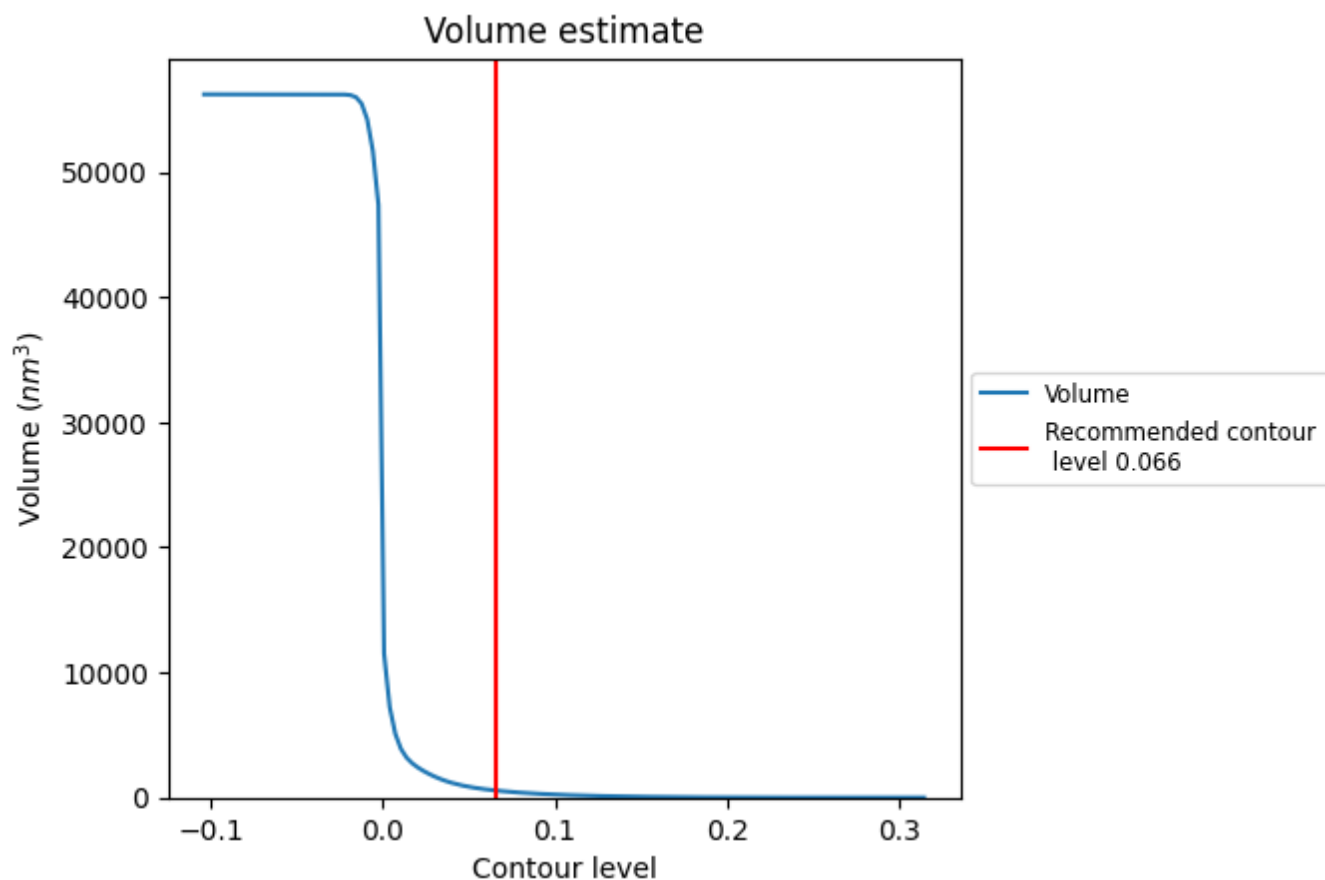
This section contains the results of statistical analysis of the map.

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.

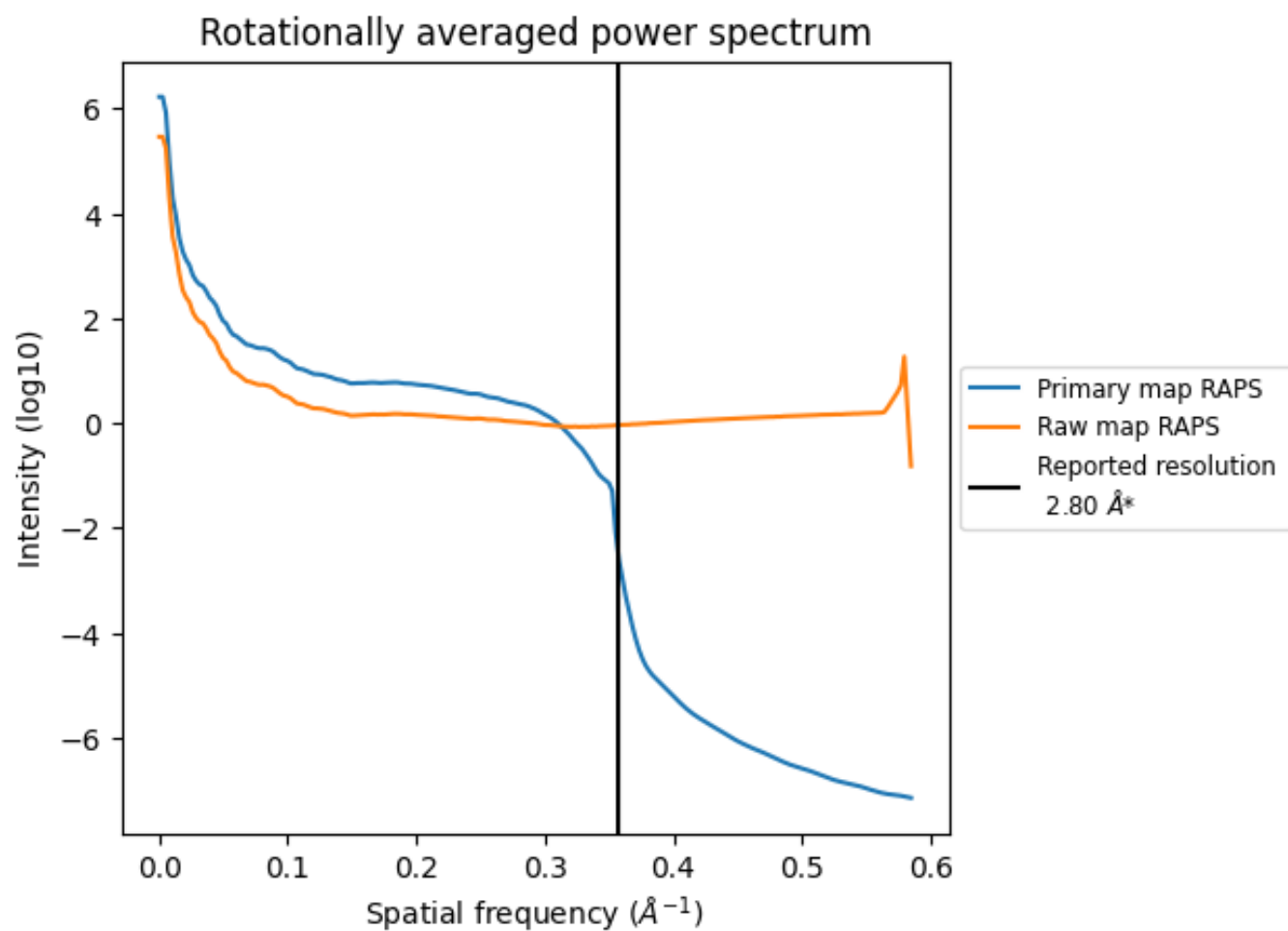
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 558 nm³; this corresponds to an approximate mass of 504 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

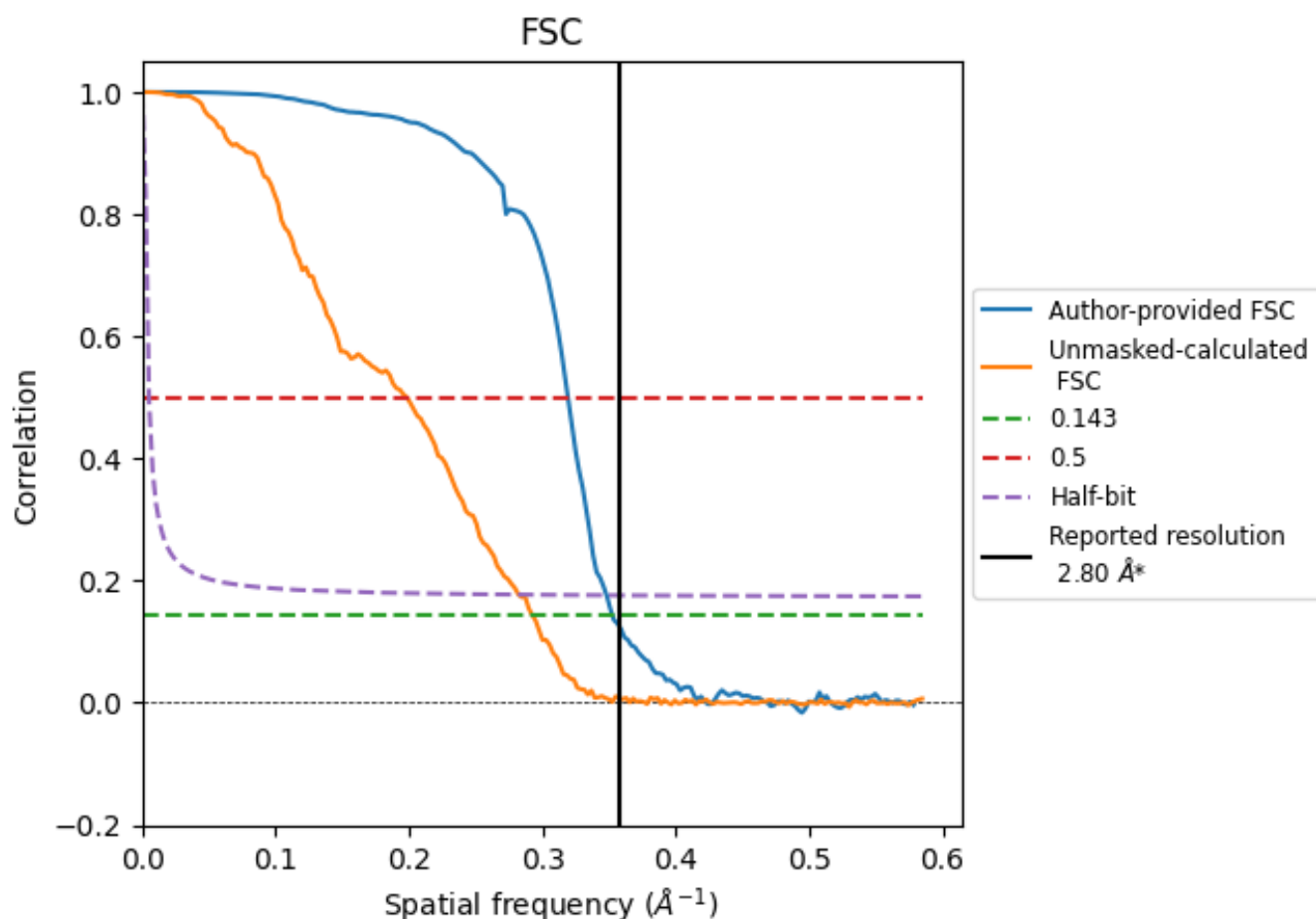


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

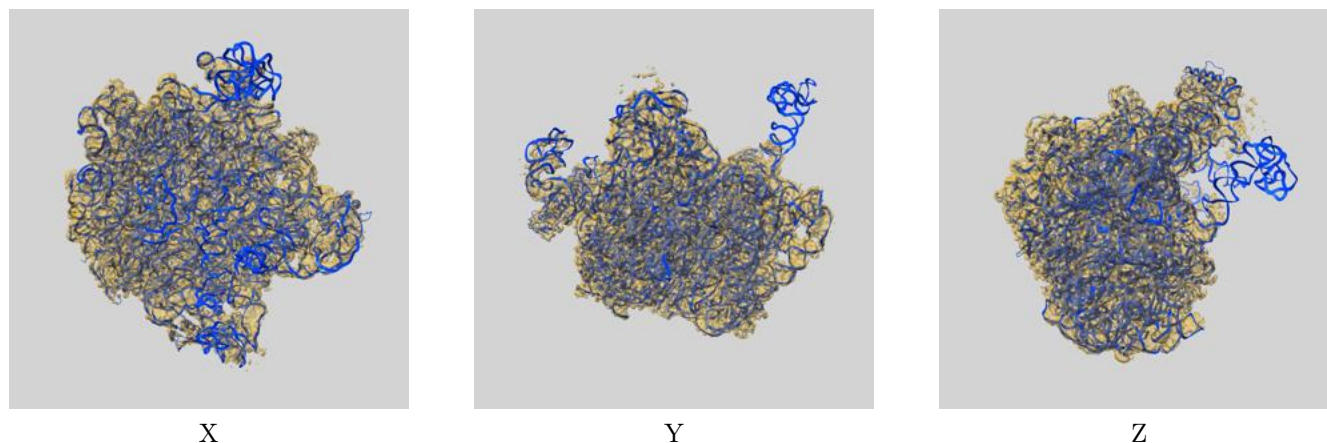
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.13	2.87
Unmasked-calculated*	3.42	5.04	3.54

*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 3.42 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

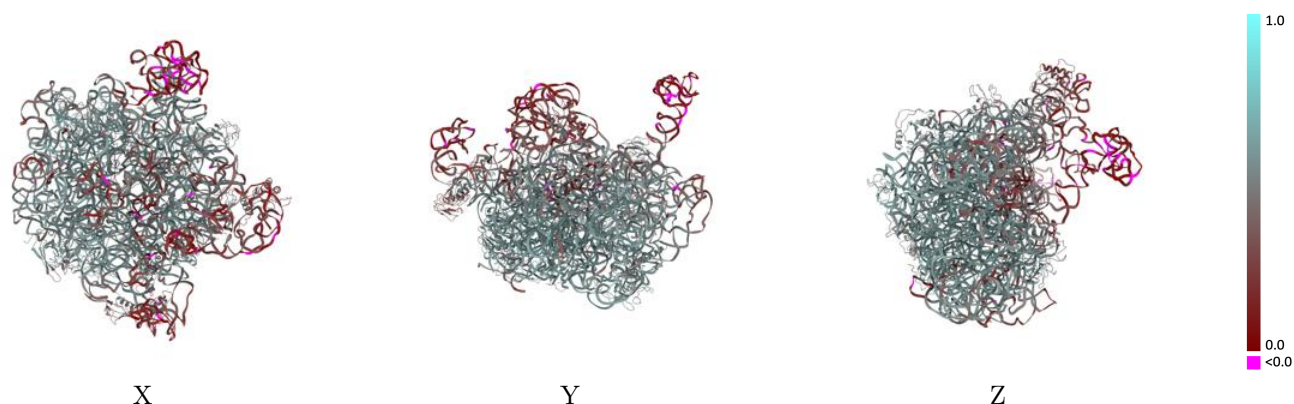
This section contains information regarding the fit between EMDB map EMD-71268 and PDB model 9P4I. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



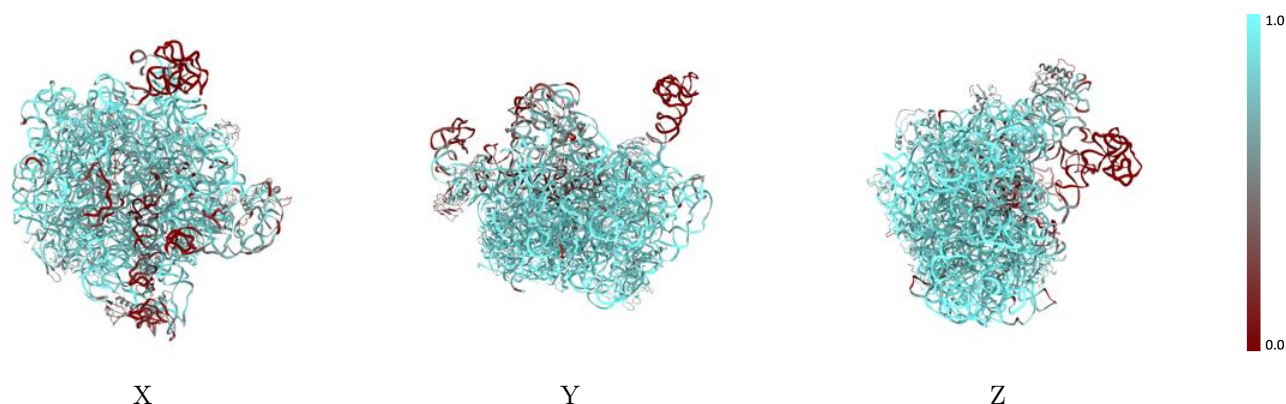
The images above show the 3D surface view of the map at the recommended contour level 0.066 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



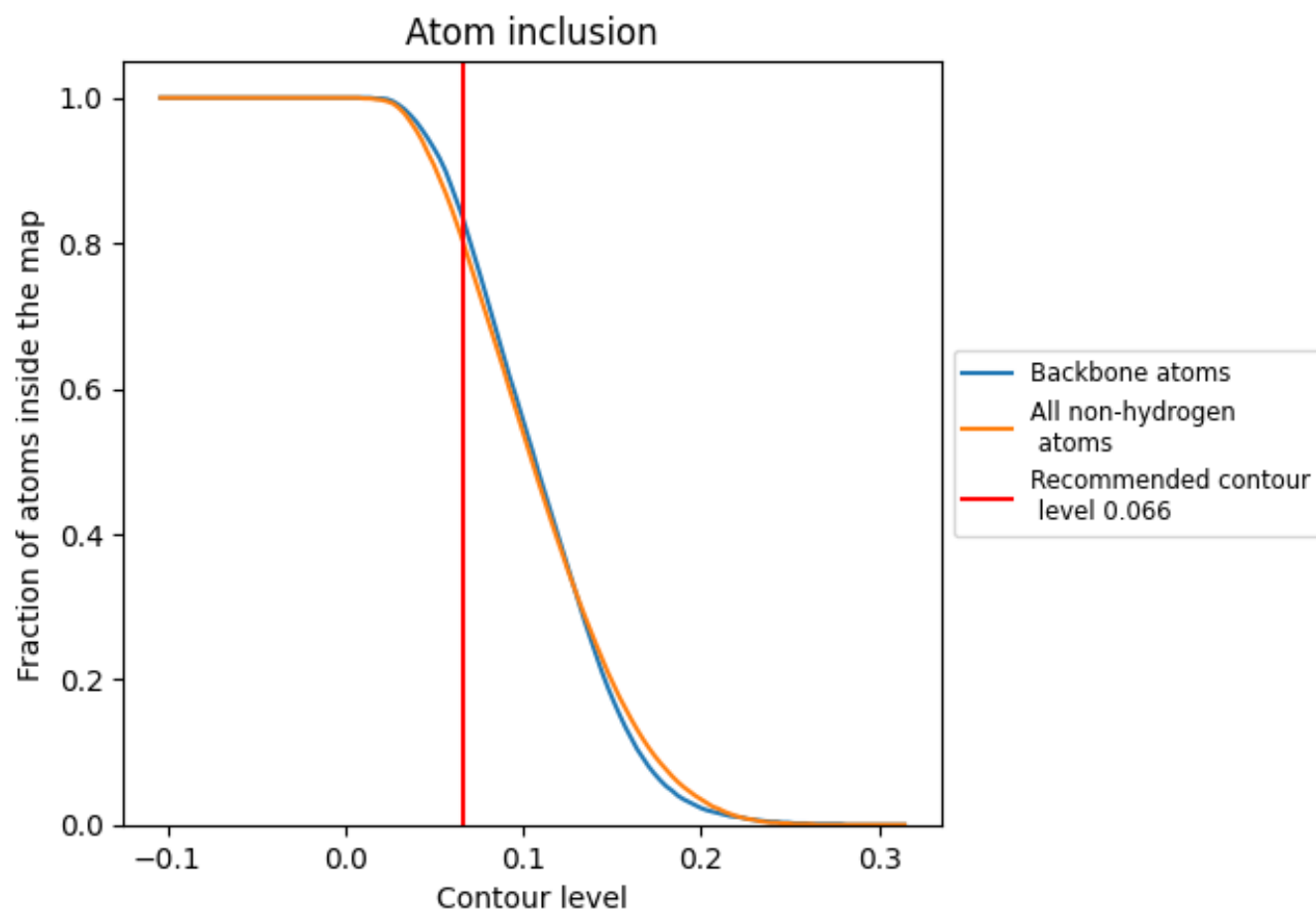
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.066).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.066) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.4920
A	 0.8320	 0.4920
B	 0.6550	 0.2850
C	 0.6520	 0.4910
D	 0.8600	 0.5710
E	 0.7890	 0.5330
G	 0.3900	 0.3820
J	 0.8990	 0.5770
K	 0.7450	 0.5270
L	 0.6200	 0.4730
N	 0.8750	 0.5670
O	 0.4290	 0.3540
P	 0.7460	 0.5300
Q	 0.8970	 0.5720
R	 0.8470	 0.5710
S	 0.9020	 0.5880
T	 0.8450	 0.5640
U	 0.7540	 0.5310
V	 0.4540	 0.4620
Y	 0.7840	 0.5110
Z	 0.8290	 0.5570
b	 0.7940	 0.5180
d	 0.9330	 0.6170
f	 0.0960	 0.4660

