



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 12:09 am BST

PDB ID : 7ACJ / pdb_00007acj
EMDB ID : EMD-11717
Title : Structure of translocated trans-translation complex on E. coli stalled ribosome.
Authors : Guyomar, C.; D'Urso, G.; Chat, S.; Giudice, E.; Gillet, R.
Deposited on : 2020-09-11
Resolution : 3.20 Å(reported)
Based on initial model : 4YBB

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 : 1.8.4, CSD as541be (2020)
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

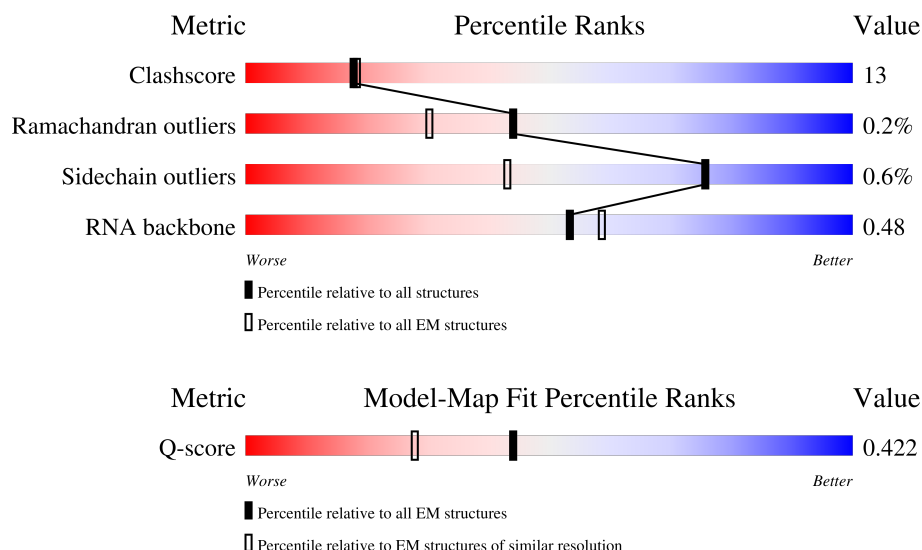
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



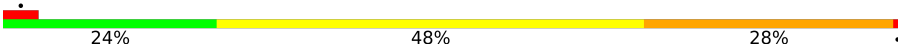
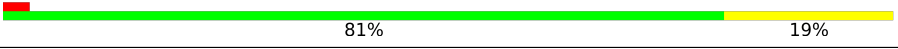
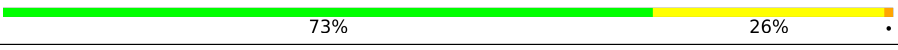
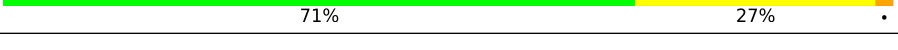
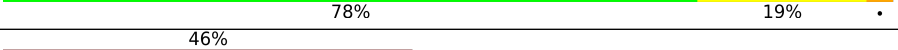
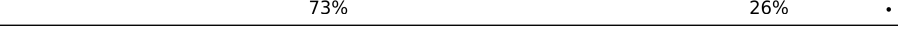
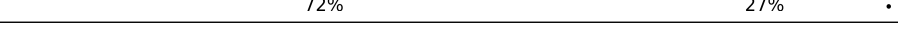
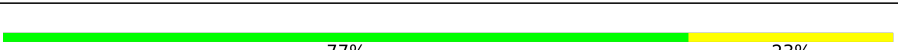
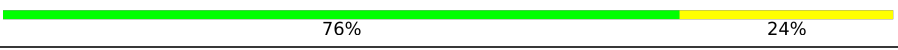
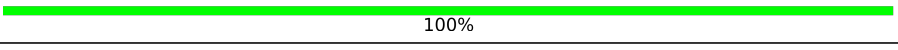
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	1	2903	
2	2	1534	
3	3	120	

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Mol	Chain	Length	Quality of chain
4	4	363	
5	5	150	
6	A	79	
7	B	271	
8	C	209	
9	D	201	
10	E	177	
11	F	175	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	119	
18	O	116	
19	P	114	
20	Q	117	
21	R	103	
22	S	110	
23	T	94	
24	U	103	
25	V	94	
26	W	2	
27	X	77	
28	Y	62	

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Mol	Chain	Length	Quality of chain
29	Z	58	
30	a	65	
31	b	56	
32	c	52	
33	d	46	
34	e	64	
35	f	38	
36	g	225	
37	h	212	
38	i	205	
39	j	156	
40	k	104	
41	l	151	
42	m	129	
43	n	127	
44	o	99	
45	p	117	
46	q	122	
47	r	112	
48	s	100	
49	t	88	
50	u	82	
51	v	80	
52	w	67	
53	x	86	

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Mol	Chain	Length	Quality of chain
54	y	86	 74%26%
55	z	70	 80%20%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 151803 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	363	Total	C	N	O	P	0	0
			7756	3466	1410	2518	362		

- Molecule 5 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	150	Total	C	N	O	S	0	0
			1209	763	226	216	4		

- Molecule 6 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	79	Total	C	N	O	S	0	0
			595	367	120	107	1		

- Molecule 7 is a protein called 50S ribosomal protein L2.

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

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

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

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

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

- Molecule 15 is a protein called 50S ribosomal protein L15.

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

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	W	2	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	65	Total	C	N	O	S	0	0
			514	317	98	93	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

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

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	212	Total	C	N	O	S	0	0
			1658	1049	311	294	4		

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 42 is a protein called 30S ribosomal protein S8.

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

- Molecule 43 is a protein called 30S ribosomal protein S9.

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

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

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

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	122	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	112	Total	C	N	O	S	0	0
			867	535	175	154	3		

- Molecule 48 is a protein called 30S ribosomal protein S14.

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

- Molecule 49 is a protein called 30S ribosomal protein S15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called 30S ribosomal protein S17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	67	Total	C	N	O	S	0	0
			553	350	104	98	1		

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	86	Total	C	N	O	S	0	0
			685	437	130	116	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	237	Total 237	Mg 237	0
56	2	57	Total 57	Mg 57	0
56	3	7	Total 7	Mg 7	0
56	5	1	Total 1	Mg 1	0
56	B	4	Total 4	Mg 4	0
56	b	1	Total 1	Mg 1	0
56	i	1	Total 1	Mg 1	0

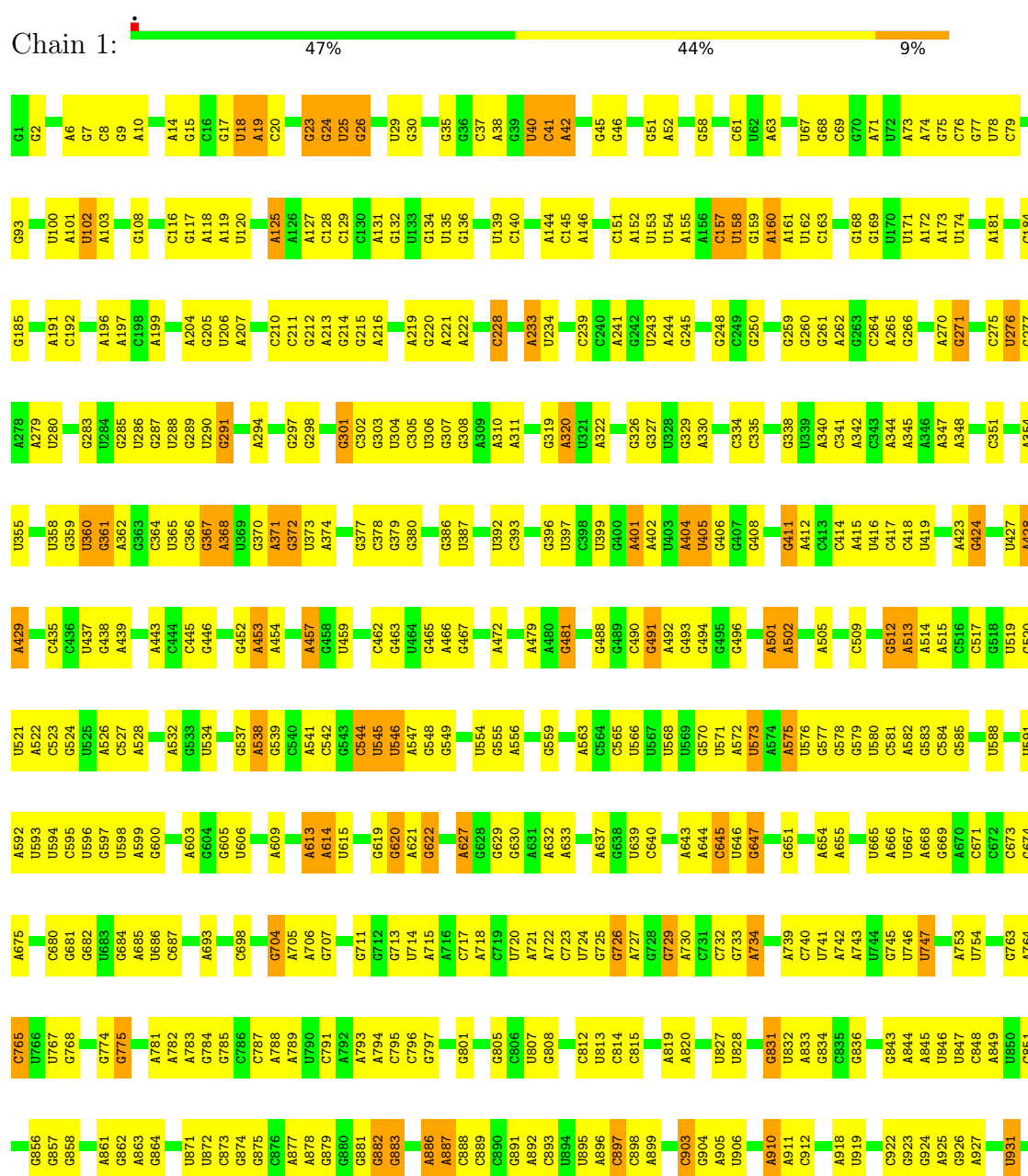
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	a	1	Total 1	Zn 1	0
57	f	1	Total 1	Zn 1	0

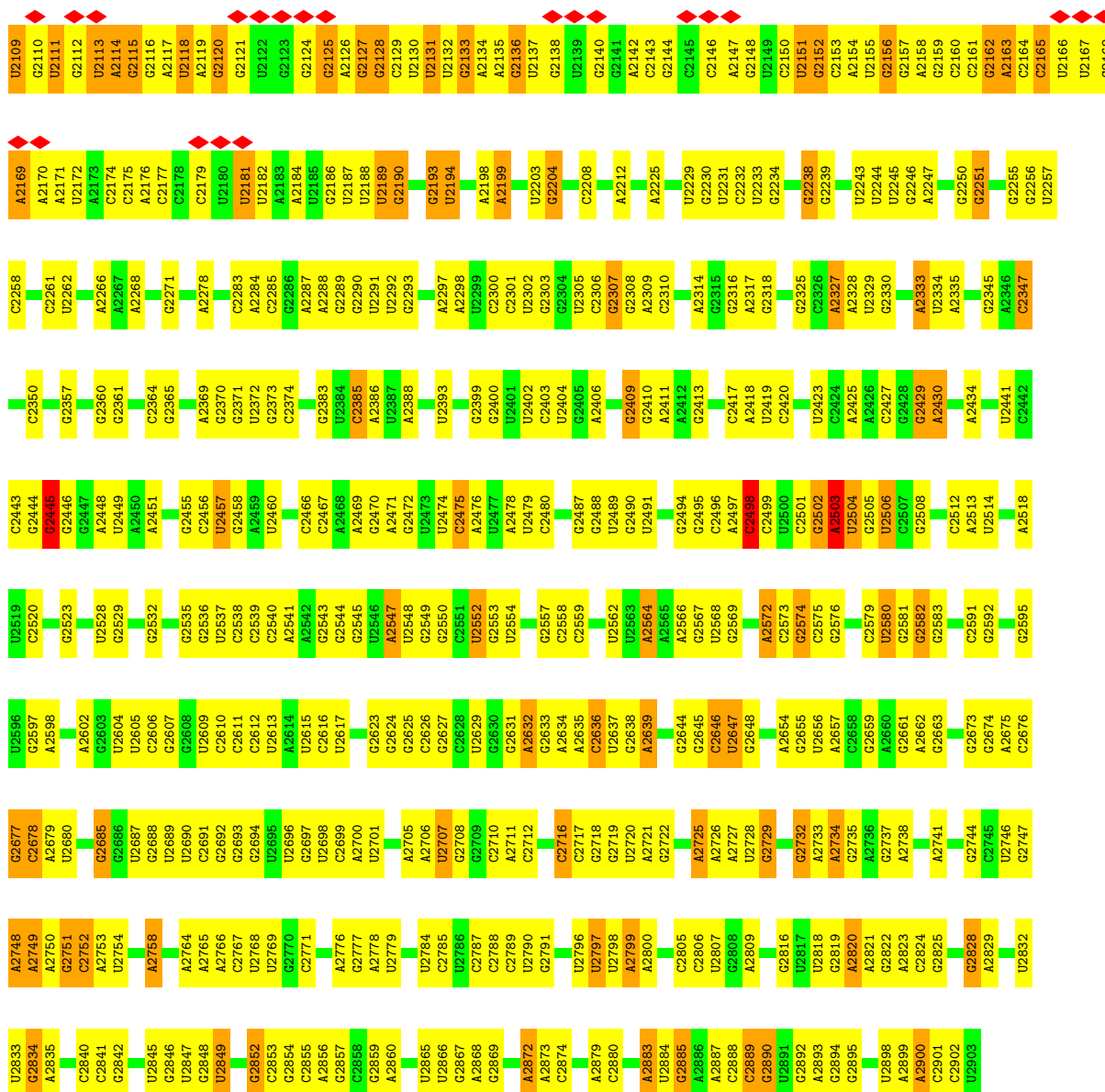
3 Residue-property plots

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 ribosomal RNA

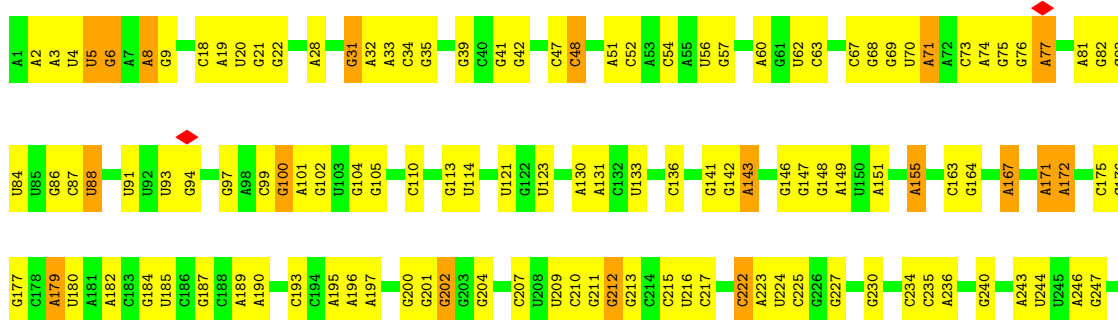


A2033	G1954	A1866	U1781	A1700	G1537	G1421	C1233	A1144	U1078	C1013	U934
U2034	U1955	G1869	U1782	A1701	G1538	G1422	U1234	C1145	C1079	G1016	C937
G2035	U1956	G1870	A1783	C1704	U1539	G1423	G1235	C1146	A1080	G1016	G938
A2037	C1957	A1871	A1784	A1705	G1540	G1424	G1236	A1147	U1081	G1016	G939
G2038	C1958	A1872	C1788	A1708	C1541	G1425	A1237	U1148	U1082	A1020	G940
U2039	G1962	G1873	A1789	C1709	C1542	G1426	G1238	G1149	U1083	A1020	A941
G2040	U1963	G1874	C1790	A1709	A1543	A1427	C1238	C1150	A1084	G1022	
C2043	C1966	G1875	A1791	G1710	A1544	G1428	A1247	C1151	A1085	G1022	
G2044	C1967	C1881	A1794	A1713	A1545	A1431	G1248	A1152	A1086	U1023	C946
C2045	U1968	U1882	C1795	U1714	C1547	G1432	U1249	C1153	G1087	G1024	A947
G2048	A1969	U1883	C1796	G1715	A1548	A1433	G1250	G1154	A1088	G1025	C948
G2049	A1970	G1884	G1797	U1716	A1549	A1434	C1251	A1155	A1089	G1026	G949
A2051	U1971	A1885	U1798	A1717	C1550	A1438	G1252	A1156	A1090	A1027	G950
C2055	G1972	U1889	G1799	G1718	A1551	A1439	A1253	G1157	G1091	A1028	
G2056	U1975	A1890	C1800	U1719	C1557	A1447	U1254	C1167	C1092	A1029	G954
C2057	U1976	A1896	A1801	G1720	U1558	G1448	G1256	U1173	G1093	C1030	U955
G2058	C1977	G1899	A1802	G1721	U1559	G1458	G1260	U1174	U1094	G1031	G956
A2059	U1979	A1899	A1805	G1724	G1561	U1466	A1261	C1172	A1095	G1033	C957
G2060	G1980	G1899	G1806	U1725	U1562	U1467	A1262	U1175	A1096	G1034	U958
A2061	C1983	G1903	G1807	C1726	U1563	U1468	A1263	U1176	C1100	G1036	C961
G2062	U1983	G1906	A1808	C1727	C1564	U1469	A1264	A1176	U1101	A1039	C965
C2066	C1986	U1906	A1809	U1728	C1565	U1470	G1265	G1177	C1102	A1040	G966
A1987	A1987		A1810	U1729	A1566	A1476	G1266	U1178	U1101	G1041	U967
G2069	U1991	C1909	U1811	G1730	G1567	U1477	U1267	U1179	U1101	G1042	C968
A2070	C1992	U1910	G1812	G1731	G1568	U1478	A1268	G1179	G1102	G1043	G969
C2072	U1993	A1912	G1813	C1732	U1569	U1479	A1269	G1186	U1107	G1044	U970
U2074	C1996	A1913	G1814	A1735	A1570	U1476	G1270	G1187	U1108	C1045	G971
U2075	C1997	G1914	G1815	U1736	A1571	U1482	G1271	U1188	G1110	A1046	A972
U2076	C1998	3TD1915	G1816	G1737	A1572	G1483	A1272	U1189	A1111	A1046	A973
A2077	C1999	U1916	A1817	U1738	U1578	U1484	A1275	G1190	G1112	G1049	G974
C2078	C2006	U1917	A1818	G1740	A1580	U1485	A1276	G1191	U1113	A1050	G976
U2081	G2010	A1918	G1826	C1741	G1581	C1489	C1278	G1196	C1114	G1051	A980
A2082	U2011	A1919	U1827	A1744	C1582	A1490	G1279	C1197	G1115	C1052	A983
U2086	G2012	G1920	G1828	A1745	U1583	C1493	G1283	U1201	U1119	C1053	A983
G2087	A2015	G1921	A1829	A1746	U1584	A1494	A1286	G1202	G1120	A1054	C987
C2089	C2018	U1922	C1830	U1746	C1585	A1508	A1287	G1206	C1121	G1056	C987
A2090	G2019	U1923	G1831	A1751	A1586	A1509	G1288	G1206	G1122	A1057	A988
C2091	U2020	A1936	U1834	C1752	G1587	A1509	C1289	G1212	G1125	U1060	A990
U2092	C2021	U1936	G1835	G1753	U1588	G1510	G1296	A1213	U1061	G1061	C991
G2093	U2022	U1939	G1844	G1754	A1589	G1514	C1297	A1214	A1127	G1062	C994
U2098	C2023	U1940	G1845	C1764	U1590	A1515	C1298	G1215	G1128	G1063	C995
G2099	G2100	C1941	G1857	U1769	A1591	A1515	C1299	G1216	G1131	C1064	A996
A2101	U2026	G1942	A1858	U1773	A1592	G1519	G1300	U1222	U1132	U1065	C997
G2102	G2027	U1944	G1862	A1773	A1593	U1594	A1301	G1223	A1133	U1066	C998
U2105	G2029	G1945	G1863	U1779	A1595	U1523	A1304	U1224	A1134	A1067	U999
C2106	A2030	A1952	U1864	U1779	C1598	U1527	G1309	G1225	C1135	A1070	C1007
A2108	G2032	A1953	U1865	A1780	A1598	G1532	G1316	A1226	G1137	A1073	A1008
					A1603	G1533	U1316	G1227	G1138	G1074	A1009
					C1604	U1534	G1317	G1228		C1075	A1010
					C1605	A1535	A1321	G1416	U1141	C1076	U1012
					C1606	A1536		G1417	A1142		
					C1607	C1536		G1418			
					A1608			G1420			



• Molecule 2: 16S ribosomal RNA

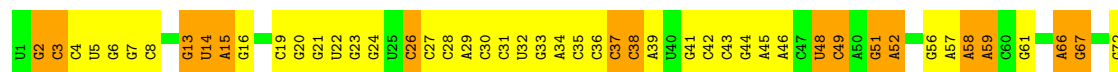
Chain 2: 46% 46% 8%



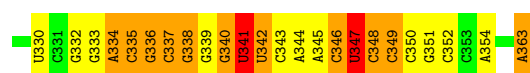
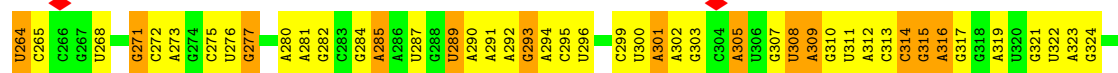
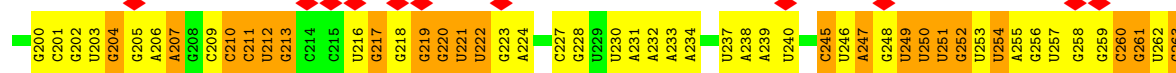
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U1315	G1316	C1317	A1318	A1319	C1320	G1323	A1324	U1325	U1326	C1327	C1328	A1329	A1333	G1334	U1335	C1336	G1343	C1344	G1347	U1348	A1349	A1350	U1351	G1352	G1353	U1354	G1355	G1356	A1357	C1358	C1359	A1360	G1361	A1362	A1363	U1364	G1365	C1366	C1367	G1370	U1371	U1372	G1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	C1382	G1386	
G1241	G1242	C1243	G1244	A1245	A1246	U1247	A1250	A1251	A1252	G1253	C1254	G1255	A1256	A1257	G1258	G1259	G1260	A1261	C1265	G1266	C1267	A1268	A1269	G1270	A1271	A1274	C1279	A1280	C1281	C1282	U1286	A1287	A1288	A1289	G1290	U1291	G1292	C1293	G1294	G1297	U1298	A1299	G1300	U1301	C1302	G1303	G1304	G1305	U1308	A1311				
U1168	A1169	A1170	U1171	U1173	G1174	G1175	A1176	A1180	G1181	G1182	U1183	G1184	G1185	G1190	A1191	C1192	A1196	A1197	G1198	A1201	U1202	C1265	G1266	A1268	A1269	G1270	A1271	A1274	C1279	A1280	C1281	C1282	U1286	A1287	A1288	A1289	G1290	U1291	G1292	C1293	G1294	G1297	U1298	A1299	G1300	U1301	C1302	G1303	G1304	G1305	U1308	A1311		
A1092	A1093	G1094	U1095	U1096	C1097	A1101	A1102	A1106	G1107	G1108	C1109	U1115	U1116	A1117	U1118	C1119	C1120	G1121	U1122	U1123	G1124	U1125	U1126	G1127	A1130	G1133	G1134	U1135	U1136	C1137	G1138	A1139	C1140	C1141	G1142	G1143	G1144	A1145	C1146	C1147	A1150	G1156	A1157	C1158	G1159	G1160	C1161	A1167						
U1023	G1024	U1025	C1028	U1029	U1030	C1031	G1032	G1033	G1034	A1035	A1036	C1037	C1038	G1039	U1040	G1041	A1042	A1043	A1044	C1045	A1046	G1047	G1048	U1049	G1050	C1051	U1052	G1053	C1054	A1055	U1056	C1064	U1065	G1068	C1069	U1070	C1071	U1072	G1074	G1077	U1078	A1081	A1082	U1083	G1084	G1087	G1088	G1089						
U961	C962	G963	A964	U965	G966	C967	A968	A969	C970	G971	G973	A974	A975	A977	A978	C979	C980	U981	U982	A983	C984	C985	U986	G987	G988	G989	C990	G993	A994	C995	A996	U997	C998	C999	A1000	G1003	A1004	A1005	G1006	U1007	U1008	U1009	U1010	C1011	A1012	A1014	G1015	U1016	U1017	G1018	A1019	G1020	A1021	
U875	C876	C879	C880	A889	C890	A891	A892	A893	C894	G898	A901	A909	C910	U911	A912	A913	A914	G917	A918	U921	G922	U923	C924	G925	C932	G933	C934	A935	C936	A937	A938	G939	C940	A941	G942	U943	G944	G945	C948	A949	U950	G951	U952	G953	G954	U955	A958	U959	U960					
G791	A792	U793	A794	G799	G800	U801	A802	A807	C808	G809	C810	G811	U813	A814	A815	A816	C817	G818	G821	U822	C823	A824	A825	G734	U735	G736	G741	G742	A743	C744	G745	A746	A747	G748	U751	G752	G755	G763	C764	G765	G766	A673	G674	A675	A676	U677	C680	A681	G682	G683	U684	G685	U686	A687
U692	G693	A694	A695	A696	U697	G700	A701	A702	G711	A712	G713	A715	A716	U717	A718	G721	U625	G626	G627	G633	C634	A635	G734	U735	G736	G741	G742	A743	C744	G745	A746	A747	G748	U751	G752	G755	G763	C764	G765	G766	A673	G674	A675	A676	U677	C680	A681	G682	G683	U684	G685	U686	A687	
G597	U598	C599	A600	G601	A602	U603	G604	A607	A608	A609	U610	C613	G614	C618	A621	U625	G626	G627	G633	C634	A635	G734	U735	G736	G741	G742	A743	C744	G745	A746	A747	G748	U751	G752	G755	G763	C764	G765	G766	A673	G674	A675	A676	U677	C680	A681	G682	G683	U684	G685	U686	A687		
G350	G351	C352	A353	G354	C355	A356	G357	U358	C359	G360	A363	A366	U367	C370	A371	C372	A373	A374	U375	C379	G380	C381	A382	A383	G384	G388	A389	U390	G391	C392	A393	G394	U398	G399	C400	C401	U405	A406	U407	A408	U409	G410	A411	A412	G413	A414	U421	C422	G423	A424	G425			
G251	G254	G255	U256	G257	U261	A262	A263	C264	G265	G266	C267	U268	C269	A270	A274	G275	C285	C286	G289	G294	C295	U296	G297	A300	A306	A309	G310	C311	C312	A313	G318	G319	A320	A321	C322	G324	A327	C328	G332	U333	C334	G335	A336	G337	A338									



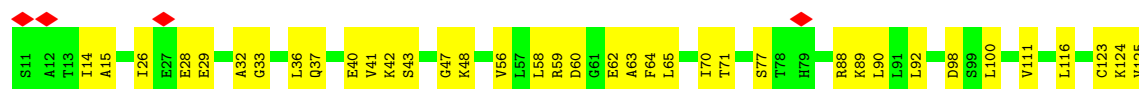
• Molecule 3: 5S ribosomal RNA



• Molecule 4: transfer-messenger RNA (tmRNA)

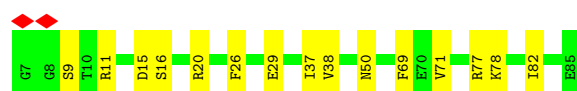


• Molecule 5: SsrA-binding protein



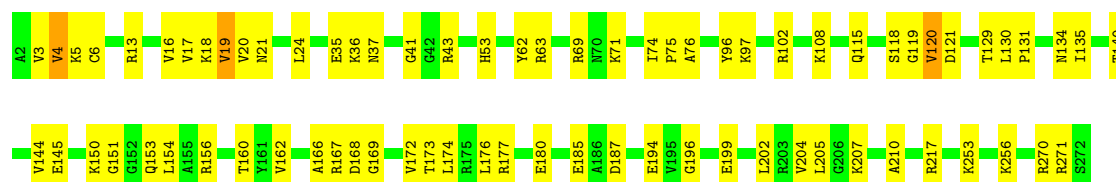
• Molecule 6: 50S ribosomal protein L27

Chain A:  81% 19%



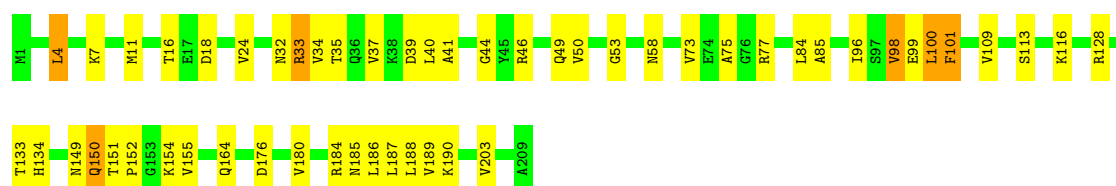
- Molecule 7: 50S ribosomal protein L2

Chain B:  73% 26%



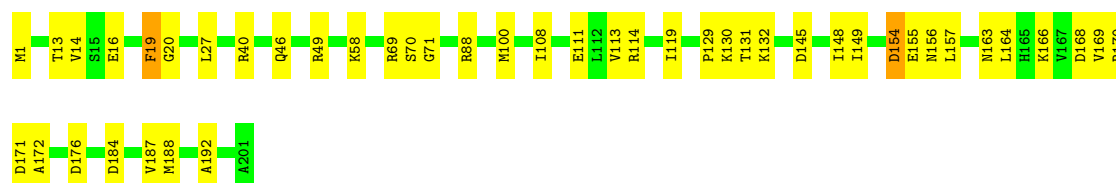
- Molecule 8: 50S ribosomal protein L3

Chain C:  75% 22%



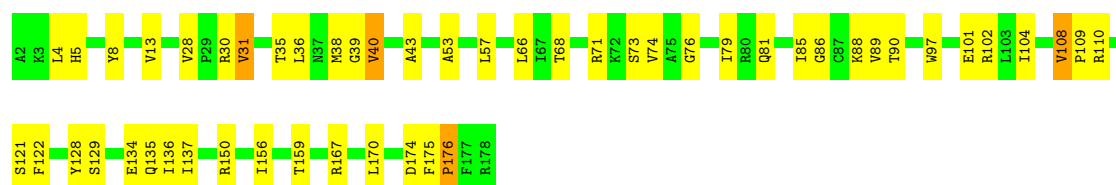
- Molecule 9: 50S ribosomal protein L4

Chain D:  78% 21%



- Molecule 10: 50S ribosomal protein L5

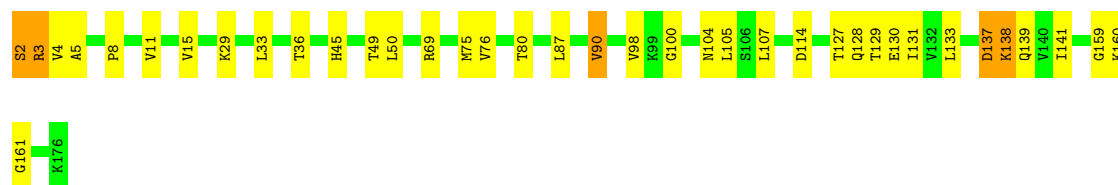
Chain E:  71% 27%



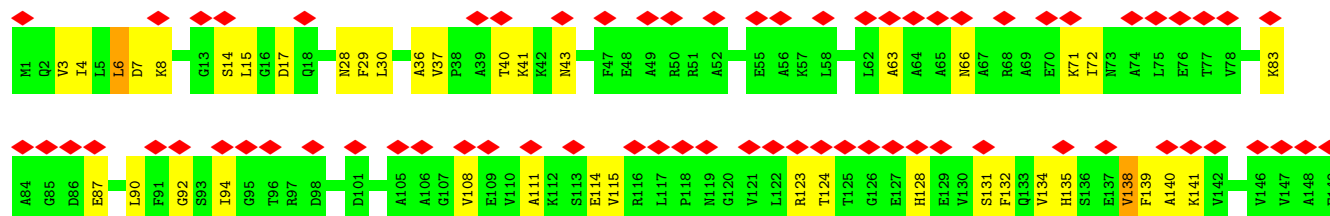
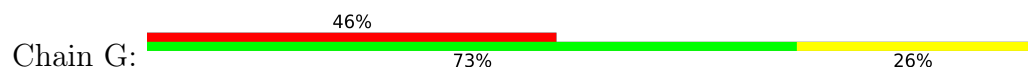
- Molecule 11: 50S ribosomal protein L6

Chain F:  78% 19%

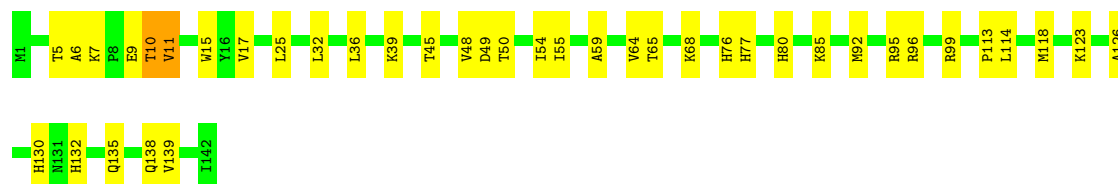




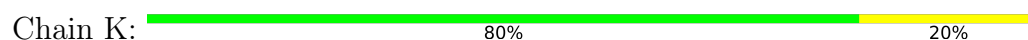
- Molecule 12: 50S ribosomal protein L9



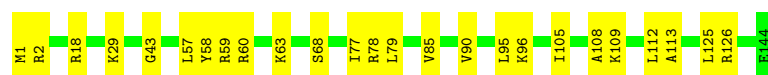
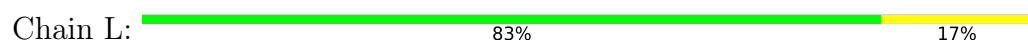
- Molecule 13: 50S ribosomal protein L13



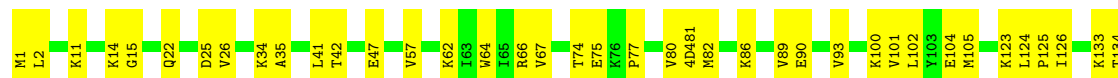
- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16



V135
M136

- Molecule 17: 50S ribosomal protein L17

Chain N:  77% 21%

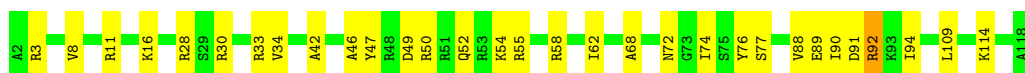

- Molecule 18: 50S ribosomal protein L18

Chain O:  76% 22%

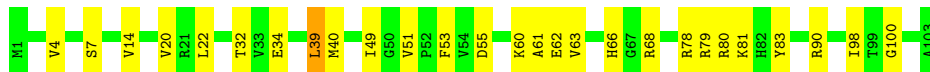

- Molecule 19: 50S ribosomal protein L19

Chain P:  77% 23%


- Molecule 20: 50S ribosomal protein L20

Chain Q:  74% 26%


- Molecule 21: 50S ribosomal protein L21

Chain R:  74% 25%


- Molecule 22: 50S ribosomal protein L22

Chain S:  75% 25%

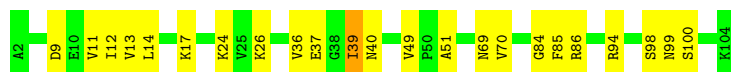

- Molecule 23: 50S ribosomal protein L23

Chain T:  79% 21%



- Molecule 24: 50S ribosomal protein L24

Chain U: 78% 21%



- Molecule 25: 50S ribosomal protein L25

Chain V: 76% 24%



- Molecule 26: Nascent peptide

Chain W: 100%

There are no outlier residues recorded for this chain.

- Molecule 27: 50S ribosomal protein L28

Chain X: 77% 23%



- Molecule 28: 50S ribosomal protein L29

Chain Y: 81% 19%



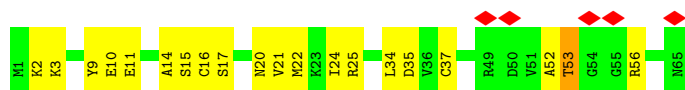
- Molecule 29: 50S ribosomal protein L30

Chain Z: 83% 17%



- Molecule 30: 50S ribosomal protein L31

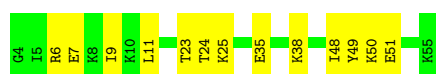
Chain a: 8% 69% 29%



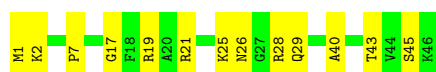
- Molecule 31: 50S ribosomal protein L32



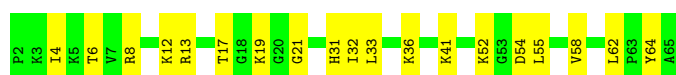
- Molecule 32: 50S ribosomal protein L33



- Molecule 33: 50S ribosomal protein L34



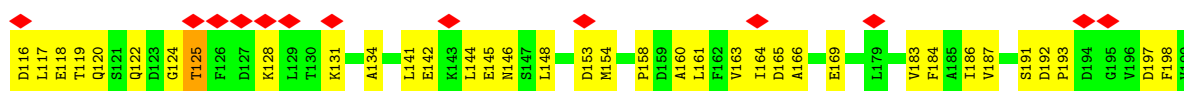
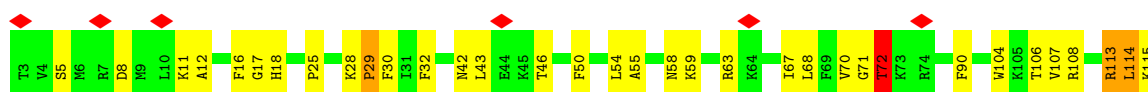
- Molecule 34: 50S ribosomal protein L35

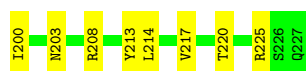


- Molecule 35: 50S ribosomal protein L36



- Molecule 36: 30S ribosomal protein S2





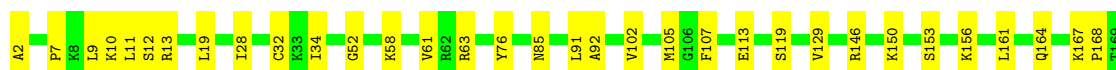
- Molecule 37: 30S ribosomal protein S3

Chain h: 71% 27% .



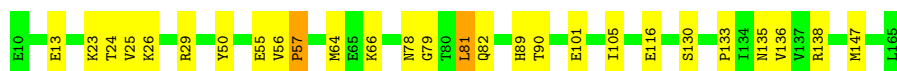
- Molecule 38: 30S ribosomal protein S4

Chain i: 74% 26% .



- Molecule 39: 30S ribosomal protein S5

Chain j: 83% 16% .



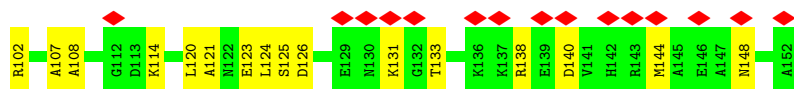
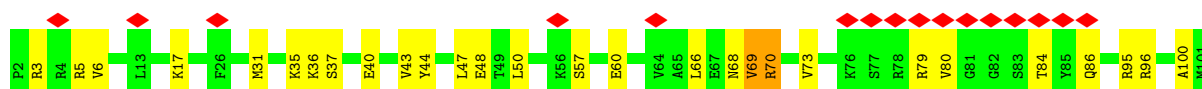
- Molecule 40: 30S ribosomal protein S6

Chain k: 75% 23% .



- Molecule 41: 30S ribosomal protein S7

Chain l: 21% 71% 28% .



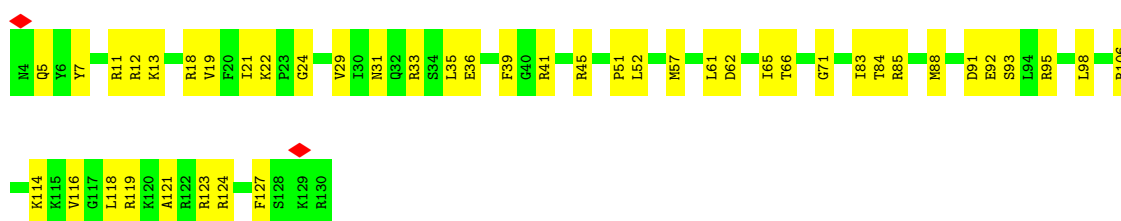
- Molecule 42: 30S ribosomal protein S8

Chain m:  80% 19% .



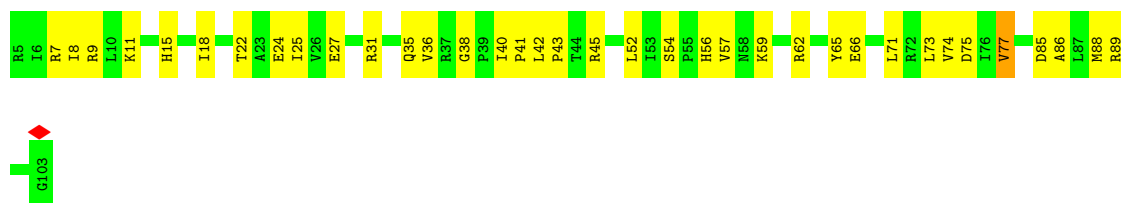
- Molecule 43: 30S ribosomal protein S9

Chain n:  65% 35% .



- Molecule 44: 30S ribosomal protein S10

Chain o:  64% 35% .



- Molecule 45: 30S ribosomal protein S11

Chain p:  68% 32% .



- Molecule 46: 30S ribosomal protein S12

Chain q:  81% 18% .



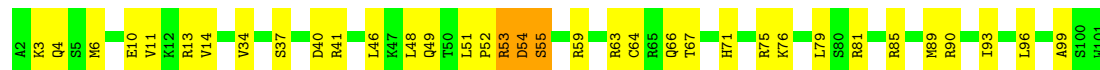
- Molecule 47: 30S ribosomal protein S13

Chain r:  61% 32% 7% .



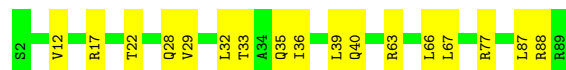
- Molecule 48: 30S ribosomal protein S14

Chain s: 65% 32% .



- Molecule 49: 30S ribosomal protein S15

Chain t: 81% 19% .



- Molecule 50: 30S ribosomal protein S16

Chain u: 74% 24% .



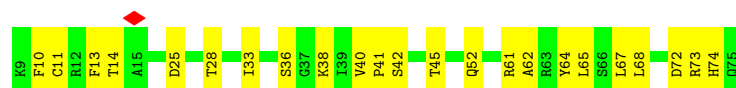
- Molecule 51: 30S ribosomal protein S17

Chain v: 75% 24% .



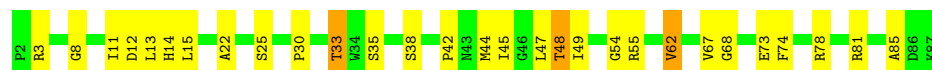
- Molecule 52: 30S ribosomal protein S18

Chain w: 66% 34% .

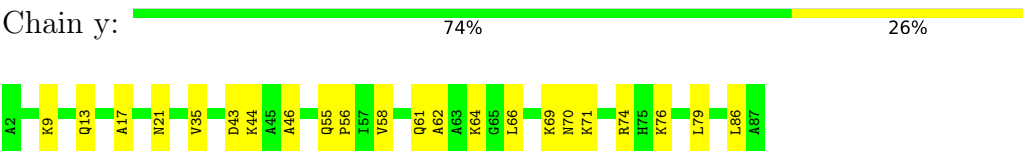


- Molecule 53: 30S ribosomal protein S19

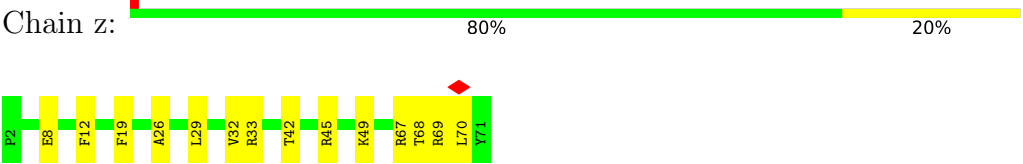
Chain x: 66% 30% .



● Molecule 54: 30S ribosomal protein S20



● Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14192	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	24.173	Depositor
Minimum map value	-10.824	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	499.19998, 499.19998, 499.19998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 1MG, 5MC, OMU, MG, 3TD, 2MG, OMG, 4OC, ZN, 4D4, 6MZ, G7M, MA6, PSU, 0TD, UR3, OMC, 2MA

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	1	0.08	0/69286	0.22	0/108087
2	2	0.09	1/36590 (0.0%)	0.20	0/57074
3	3	0.11	0/2872	0.31	0/4478
4	4	0.15	0/8612	0.34	1/13426 (0.0%)
5	5	0.17	0/1231	0.58	1/1655 (0.1%)
6	A	0.13	0/602	0.42	0/797
7	B	0.27	2/2121 (0.1%)	0.61	10/2852 (0.4%)
8	C	0.54	3/1586 (0.2%)	0.86	12/2134 (0.6%)
9	D	0.13	0/1571	0.45	4/2113 (0.2%)
10	E	0.38	1/1434 (0.1%)	0.63	5/1926 (0.3%)
11	F	0.25	1/1333 (0.1%)	0.69	9/1805 (0.5%)
12	G	0.25	1/1121 (0.1%)	0.66	2/1515 (0.1%)
13	J	0.18	0/1152	0.54	3/1551 (0.2%)
14	K	0.12	0/955	0.37	0/1279
15	L	0.13	0/1062	0.39	0/1413
16	M	0.17	0/1081	0.40	0/1443
17	N	0.31	0/964	0.66	4/1289 (0.3%)
18	O	0.12	0/902	0.56	2/1209 (0.2%)
19	P	0.18	0/929	0.50	3/1242 (0.2%)
20	Q	0.12	0/960	0.43	1/1278 (0.1%)
21	R	0.22	0/829	0.58	2/1107 (0.2%)
22	S	0.12	0/864	0.41	0/1156
23	T	0.12	0/752	0.34	0/1005
24	U	0.24	1/796 (0.1%)	0.62	2/1062 (0.2%)
25	V	0.12	0/766	0.37	0/1025
26	W	0.06	0/16	0.04	0/20
27	X	0.12	0/635	0.39	0/848
28	Y	0.13	0/502	0.35	0/667
29	Z	0.12	0/452	0.34	0/605
30	a	0.17	0/523	0.48	0/698
31	b	0.11	0/450	0.35	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.13	0/433	0.41	0/576
33	d	0.13	0/380	0.44	0/498
34	e	0.13	0/513	0.41	0/676
35	f	0.11	0/303	0.35	0/397
36	g	0.35	3/1791 (0.2%)	0.67	12/2413 (0.5%)
37	h	0.19	1/1685 (0.1%)	0.59	7/2270 (0.3%)
38	i	0.12	0/1665	0.41	1/2227 (0.0%)
39	j	0.24	1/1165 (0.1%)	0.44	0/1568
40	k	0.20	0/867	0.62	3/1171 (0.3%)
41	l	0.20	1/1195 (0.1%)	0.54	3/1602 (0.2%)
42	m	0.13	0/989	0.46	2/1326 (0.2%)
43	n	0.14	0/1034	0.53	0/1375
44	o	0.18	0/800	0.56	1/1082 (0.1%)
45	p	0.12	0/893	0.36	0/1205
46	q	0.13	0/954	0.43	0/1279
47	r	0.59	3/875 (0.3%)	0.96	9/1170 (0.8%)
48	s	0.26	1/817 (0.1%)	0.60	3/1088 (0.3%)
49	t	0.14	0/722	0.45	1/964 (0.1%)
50	u	0.11	0/659	0.36	0/884
51	v	0.23	0/657	0.55	2/881 (0.2%)
52	w	0.43	1/562 (0.2%)	0.52	2/754 (0.3%)
53	x	0.25	0/702	0.72	4/944 (0.4%)
54	y	0.12	0/675	0.41	0/895
55	z	0.12	0/597	0.43	0/792
All	All	0.15	21/163882 (0.0%)	0.34	111/245395 (0.0%)

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	r	96	PRO	N-CD	-13.87	1.28	1.47
8	C	33	ARG	C-O	-13.31	1.08	1.24
10	E	176	PRO	N-CD	-12.92	1.29	1.47
52	w	41	PRO	N-CD	9.69	1.61	1.47
36	g	193	PRO	N-CD	7.51	1.58	1.47

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	r	73	ILE	N-CA-C	12.27	123.14	110.62
47	r	103	LYS	N-CA-C	11.69	125.15	111.71
8	C	100	LEU	N-CA-C	11.19	126.19	112.54
24	U	39	ILE	N-CA-C	11.18	121.85	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	J	10	THR	N-CA-C	10.46	123.96	109.11

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	1	62336	0	31371	1053	0
2	2	32929	0	16586	606	0
3	3	2569	0	1301	56	0
4	4	7756	0	3922	163	0
5	5	1209	0	1228	48	0
6	A	595	0	610	12	0
7	B	2082	0	2154	64	0
8	C	1565	0	1616	55	0
9	D	1552	0	1619	51	0
10	E	1410	0	1443	63	0
11	F	1313	0	1355	69	0
12	G	1110	0	1148	65	0
13	J	1129	0	1162	52	0
14	K	946	0	1023	24	0
15	L	1053	0	1129	20	0
16	M	1075	0	1154	35	0
17	N	951	0	994	31	0
18	O	892	0	923	28	0
19	P	917	0	962	17	0
20	Q	947	0	1019	31	0
21	R	816	0	839	27	0
22	S	857	0	922	34	0
23	T	746	0	811	18	0
24	U	788	0	844	45	0
25	V	753	0	780	17	0
26	W	16	0	16	0	0
27	X	625	0	652	14	0
28	Y	501	0	531	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	Z	448	0	488	6	0
30	a	514	0	509	31	0
31	b	444	0	458	17	0
32	c	426	0	464	36	0
33	d	377	0	415	24	0
34	e	504	0	572	19	0
35	f	302	0	340	12	0
36	g	1760	0	1787	73	0
37	h	1658	0	1732	57	0
38	i	1643	0	1707	60	0
39	j	1152	0	1196	25	0
40	k	848	0	845	28	0
41	l	1181	0	1238	85	0
42	m	979	0	1031	38	0
43	n	1022	0	1070	117	0
44	o	790	0	831	42	0
45	p	877	0	887	31	0
46	q	951	0	1012	18	0
47	r	867	0	921	55	0
48	s	805	0	844	52	0
49	t	714	0	734	14	0
50	u	649	0	666	16	0
51	v	648	0	691	27	0
52	w	553	0	573	17	0
53	x	685	0	710	47	0
54	y	669	0	719	16	0
55	z	589	0	629	15	0
56	1	237	0	0	0	0
56	2	57	0	0	0	0
56	3	7	0	0	0	0
56	5	1	0	0	0	0
56	B	4	0	0	0	0
56	b	1	0	0	0	0
56	i	1	0	0	0	0
57	a	1	0	0	0	0
57	f	1	0	0	0	0
All	All	151803	0	101183	3266	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 13.

The worst 5 of 3266 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)
13:J:130:HIS:CE1	13:J:132:HIS:HB2	1.38	1.56
43:n:35:LEU:HD21	43:n:45:ARG:CD	1.34	1.56
43:n:19:VAL:CG1	43:n:65:ILE:HD13	1.41	1.50
24:U:36:VAL:HG12	24:U:39:ILE:CD1	1.04	1.49
37:h:21:THR:CG2	37:h:58:GLU:HG3	1.44	1.48

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	
5	5	148/150 (99%)	132 (89%)	16 (11%)	0	100	100
6	A	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
7	B	269/271 (99%)	255 (95%)	14 (5%)	0	100	100
8	C	207/209 (99%)	188 (91%)	17 (8%)	2 (1%)	12	45
9	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
10	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	56
11	F	173/175 (99%)	154 (89%)	19 (11%)	0	100	100
12	G	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
13	J	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
14	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
15	L	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
16	M	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
17	N	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
19	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
20	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	R	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
22	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
23	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
24	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
25	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
27	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
28	Y	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
29	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	a	63/65 (97%)	56 (89%)	6 (10%)	1 (2%)	7	36
31	b	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
32	c	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
33	d	44/46 (96%)	44 (100%)	0	0	100	100
34	e	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
35	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
36	g	223/225 (99%)	210 (94%)	11 (5%)	2 (1%)	14	47
37	h	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
38	i	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
39	j	154/156 (99%)	146 (95%)	8 (5%)	0	100	100
40	k	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
41	l	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
42	m	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
43	n	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
44	o	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
45	p	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
46	q	119/122 (98%)	115 (97%)	4 (3%)	0	100	100
47	r	110/112 (98%)	96 (87%)	11 (10%)	3 (3%)	4	25
48	s	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
49	t	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
50	u	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
51	v	78/80 (98%)	75 (96%)	2 (3%)	1 (1%)	9	40
52	w	65/67 (97%)	62 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	x	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
54	y	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
55	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
All	All	5760/5862 (98%)	5457 (95%)	293 (5%)	10 (0%)	44	73

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	a	53	THR
8	C	149	ASN
47	r	67	GLY
51	v	51	ASN
36	g	72	THR

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	
5	5	125/125 (100%)	125 (100%)	0	100	100
6	A	59/59 (100%)	59 (100%)	0	100	100
7	B	216/216 (100%)	216 (100%)	0	100	100
8	C	164/164 (100%)	162 (99%)	2 (1%)	63	79
9	D	165/165 (100%)	165 (100%)	0	100	100
10	E	148/148 (100%)	147 (99%)	1 (1%)	76	83
11	F	136/136 (100%)	136 (100%)	0	100	100
12	G	114/114 (100%)	113 (99%)	1 (1%)	70	81
13	J	116/116 (100%)	116 (100%)	0	100	100
14	K	104/104 (100%)	102 (98%)	2 (2%)	50	73
15	L	103/103 (100%)	103 (100%)	0	100	100
16	M	108/108 (100%)	108 (100%)	0	100	100
17	N	99/99 (100%)	97 (98%)	2 (2%)	48	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	O	86/86 (100%)	85 (99%)	1 (1%)	63	79
19	P	99/99 (100%)	98 (99%)	1 (1%)	68	80
20	Q	89/89 (100%)	88 (99%)	1 (1%)	65	79
21	R	84/84 (100%)	83 (99%)	1 (1%)	63	79
22	S	93/93 (100%)	91 (98%)	2 (2%)	45	71
23	T	81/81 (100%)	78 (96%)	3 (4%)	30	63
24	U	84/84 (100%)	84 (100%)	0	100	100
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	1/1 (100%)	1 (100%)	0	100	100
27	X	67/67 (100%)	67 (100%)	0	100	100
28	Y	54/54 (100%)	54 (100%)	0	100	100
29	Z	48/48 (100%)	48 (100%)	0	100	100
30	a	58/58 (100%)	58 (100%)	0	100	100
31	b	47/47 (100%)	46 (98%)	1 (2%)	47	71
32	c	47/47 (100%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/51 (100%)	51 (100%)	0	100	100
35	f	34/34 (100%)	34 (100%)	0	100	100
36	g	187/187 (100%)	187 (100%)	0	100	100
37	h	172/172 (100%)	172 (100%)	0	100	100
38	i	172/172 (100%)	172 (100%)	0	100	100
39	j	119/119 (100%)	118 (99%)	1 (1%)	73	82
40	k	91/91 (100%)	89 (98%)	2 (2%)	45	71
41	l	124/124 (100%)	123 (99%)	1 (1%)	73	82
42	m	104/104 (100%)	102 (98%)	2 (2%)	50	73
43	n	105/105 (100%)	104 (99%)	1 (1%)	68	80
44	o	86/86 (100%)	86 (100%)	0	100	100
45	p	90/90 (100%)	89 (99%)	1 (1%)	65	79
46	q	102/102 (100%)	102 (100%)	0	100	100
47	r	90/90 (100%)	89 (99%)	1 (1%)	65	79
48	s	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	t	76/76 (100%)	76 (100%)	0	100	100
50	u	65/65 (100%)	64 (98%)	1 (2%)	57	76
51	v	74/74 (100%)	74 (100%)	0	100	100
52	w	58/58 (100%)	58 (100%)	0	100	100
53	x	74/74 (100%)	73 (99%)	1 (1%)	59	77
54	y	65/65 (100%)	65 (100%)	0	100	100
55	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4793/4793 (100%)	4764 (99%)	29 (1%)	76	84

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	T	10	VAL
50	u	71	VAL
31	b	30	VAL
43	n	92	GLU
23	T	58	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
36	g	58	ASN
53	x	14	HIS
41	l	68	ASN
43	n	75	GLN
54	y	75	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	588 (20%)	30 (1%)
2	2	1532/1534 (99%)	308 (20%)	11 (0%)
3	3	119/120 (99%)	32 (26%)	7 (5%)
4	4	362/363 (99%)	207 (57%)	19 (5%)
All	All	4915/4920 (99%)	1135 (23%)	67 (1%)

5 of 1135 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	C
1	1	9	G
1	1	10	A
1	1	15	G
1	1	19	A

5 of 67 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	4	153	U
4	4	178	G
4	4	348	C
1	1	2402	U
1	1	2308	G

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

38 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	$\# Z > 2$
2	5MC	2	967	2	18,22,23	3.75	7 (38%)	26,32,35	0.98	1 (3%)
1	G7M	1	2069	1	23,26,27	2.66	8 (34%)	35,39,42	2.43	10 (28%)
1	6MZ	1	2030	1	22,25,26	2.74	3 (13%)	30,36,39	2.40	11 (36%)
2	MA6	2	1519	2	23,26,27	1.76	4 (17%)	34,38,41	3.99	14 (41%)
46	0TD	q	89	46	7,9,10	1.46	0	6,11,13	2.15	2 (33%)
1	6MZ	1	1618	1	22,25,26	2.73	3 (13%)	30,36,39	2.35	11 (36%)
4	PSU	4	342	4	18,21,22	1.11	1 (5%)	22,30,33	1.76	5 (22%)
1	3TD	1	1915	1	18,22,23	4.20	6 (33%)	22,32,35	1.57	2 (9%)
2	2MG	2	1516	2	23,26,27	3.04	8 (34%)	32,38,41	2.71	12 (37%)
4	PSU	4	347	4	18,21,22	1.09	1 (5%)	22,30,33	1.84	5 (22%)
1	1MG	1	745	1	22,26,27	2.65	5 (22%)	33,39,42	1.76	8 (24%)
2	5MC	2	1407	2	18,22,23	3.75	7 (38%)	26,32,35	1.02	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1	1911	1	18,21,22	1.11	1 (5%)	22,30,33	1.76	4 (18%)
1	OMG	1	2251	4,1	23,26,27	2.66	6 (26%)	33,38,41	3.32	10 (30%)
1	PSU	1	2457	1	18,21,22	1.06	1 (5%)	22,30,33	1.78	4 (18%)
1	5MC	1	1962	1	18,22,23	3.74	7 (38%)	26,32,35	1.05	2 (7%)
1	5MU	1	747	1	19,22,23	5.27	5 (26%)	28,32,35	3.60	9 (32%)
1	2MG	1	2445	1	23,26,27	3.04	8 (34%)	32,38,41	2.74	13 (40%)
1	2MA	1	2503	1	22,25,26	3.87	7 (31%)	33,37,40	3.65	9 (27%)
2	MA6	2	1518	2	23,26,27	1.75	4 (17%)	34,38,41	3.96	13 (38%)
1	PSU	1	1917	1	18,21,22	1.07	1 (5%)	22,30,33	1.71	4 (18%)
2	PSU	2	516	2	18,21,22	1.11	1 (5%)	22,30,33	1.72	5 (22%)
2	2MG	2	966	2	23,26,27	3.07	8 (34%)	32,38,41	2.77	12 (37%)
16	4D4	M	81	16	9,11,12	2.04	2 (22%)	8,13,15	1.86	3 (37%)
1	OMU	1	2552	1	19,22,23	2.99	8 (42%)	26,31,34	1.68	5 (19%)
4	5MU	4	341	4	19,22,23	5.26	5 (26%)	28,32,35	3.56	9 (32%)
1	PSU	1	955	1	18,21,22	1.10	1 (5%)	22,30,33	1.75	4 (18%)
2	2MG	2	1207	2	23,26,27	3.08	8 (34%)	32,38,41	2.82	12 (37%)
1	PSU	1	2504	1	18,21,22	1.13	1 (5%)	22,30,33	1.69	4 (18%)
2	4OC	2	1402	2	20,23,24	3.22	8 (40%)	26,32,35	0.88	1 (3%)
1	PSU	1	2605	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	5MU	1	1939	1	19,22,23	5.25	5 (26%)	28,32,35	3.61	9 (32%)
1	OMC	1	2498	1	19,22,23	3.40	8 (42%)	26,31,34	0.72	0
1	PSU	1	2580	1	18,21,22	1.08	2 (11%)	22,30,33	2.01	6 (27%)
1	PSU	1	746	1,56	18,21,22	1.07	1 (5%)	22,30,33	1.69	4 (18%)
2	G7M	2	527	2	23,26,27	2.64	8 (34%)	35,39,42	2.42	10 (28%)
2	UR3	2	1498	2	19,22,23	3.01	8 (42%)	26,32,35	1.29	2 (7%)
1	2MG	1	1835	1	23,26,27	3.07	8 (34%)	32,38,41	2.82	12 (37%)

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
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MA6	2	1519	2	-	5/11/29/30	0/3/3/3
46	0TD	q	89	46	-	1/7/12/14	-
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3
4	PSU	4	342	4	-	1/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
4	PSU	4	347	4	-	3/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	4,1	-	1/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	4/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	3/9/27/28	0/3/3/3
1	2MA	1	2503	1	-	2/7/25/26	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	6/7/25/26	0/2/2/2
2	2MG	2	966	2	-	3/9/27/28	0/3/3/3
16	4D4	M	81	16	-	4/11/12/14	-
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
4	5MU	4	341	4	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
1	PSU	1	2504	1	-	3/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	2/7/25/26	0/2/2/2
1	OMC	1	2498	1	-	3/9/27/28	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	746	1,56	-	2/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	0/9/27/28	0/3/3/3

The worst 5 of 176 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1939	5MU	C6-N1	12.72	1.59	1.38
4	4	341	5MU	C6-N1	12.72	1.59	1.38
1	1	747	5MU	C6-N1	12.69	1.59	1.38
1	1	1915	3TD	C6-C5	12.42	1.49	1.35
4	4	341	5MU	C2-N1	12.18	1.58	1.38

The worst 5 of 253 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-15.44	100.20	117.08
2	2	1518	MA6	N1-C6-N6	-15.25	100.41	117.08
1	1	2503	2MA	C1'-N9-C8	-13.18	97.37	127.14
1	1	747	5MU	C5-C4-N3	12.01	125.56	115.31
1	1	1939	5MU	C5-C4-N3	11.99	125.54	115.31

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	C2'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	C2'-C1'-C5-C6
2	2	516	PSU	O4'-C1'-C5-C6
2	2	516	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

18 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	967	5MC	2	0
2	2	1519	MA6	1	0
46	q	89	0TD	1	0
2	2	1516	2MG	3	0
4	4	347	PSU	1	0
1	1	2251	OMG	1	0
1	1	2457	PSU	1	0
1	1	2445	2MG	1	0
1	1	2503	2MA	1	0
2	2	1518	MA6	4	0
2	2	966	2MG	1	0
1	1	2552	OMU	1	0
4	4	341	5MU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1207	2MG	2	0
1	1	1939	5MU	1	0
1	1	2498	OMC	2	0
1	1	2580	PSU	4	0
1	1	1835	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 310 ligands modelled in this entry, 310 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

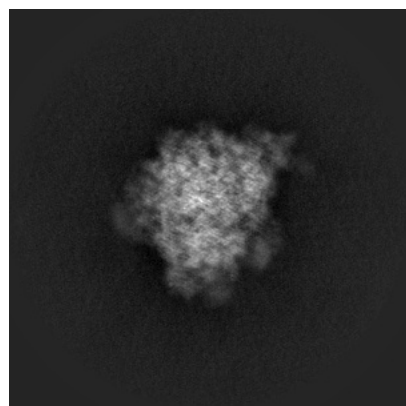
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11717. These allow visual inspection of the internal detail of the map and identification of artifacts.

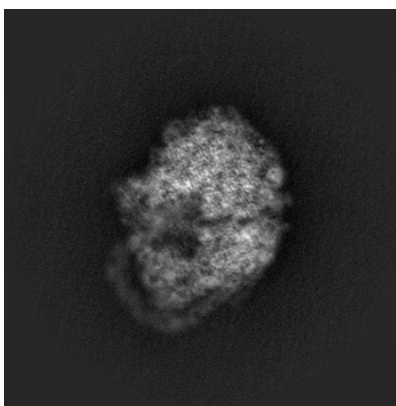
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

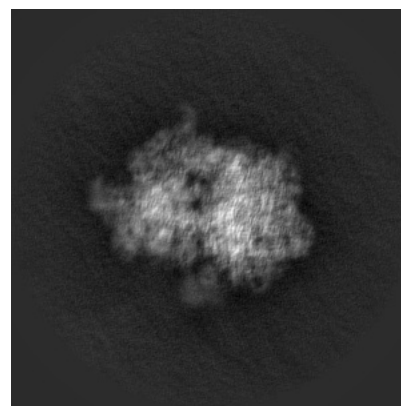
6.1.1 Primary map



X

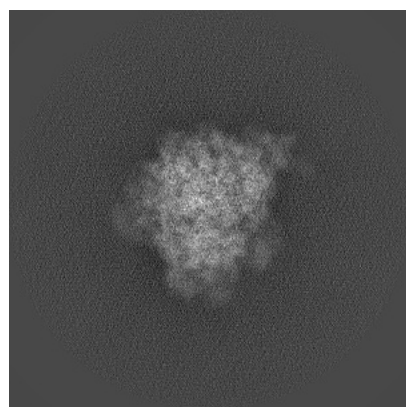


Y

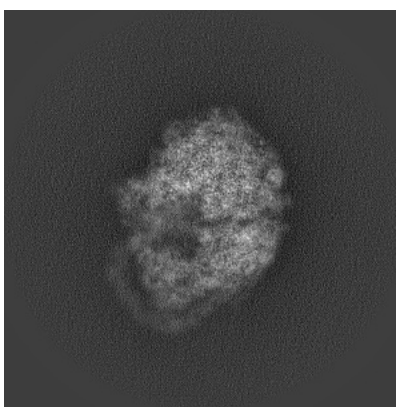


Z

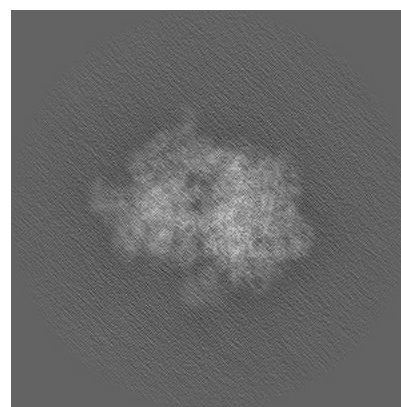
6.1.2 Raw map



X



Y

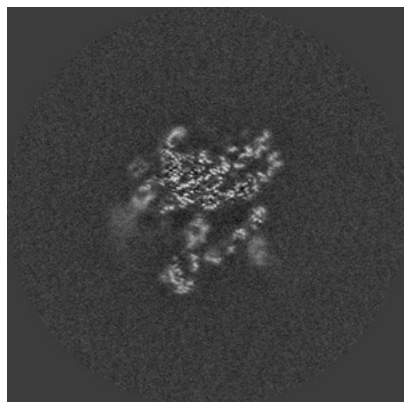


Z

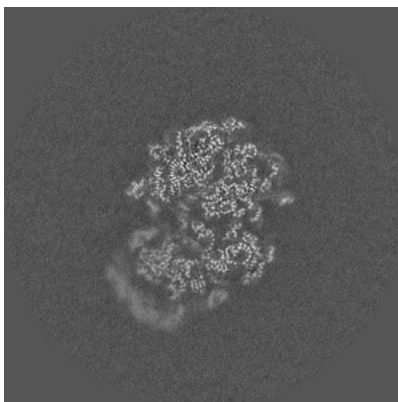
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

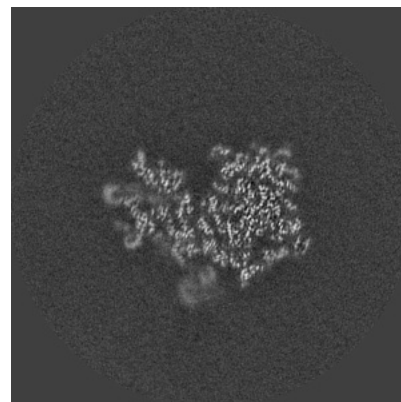
6.2.1 Primary map



X Index: 240

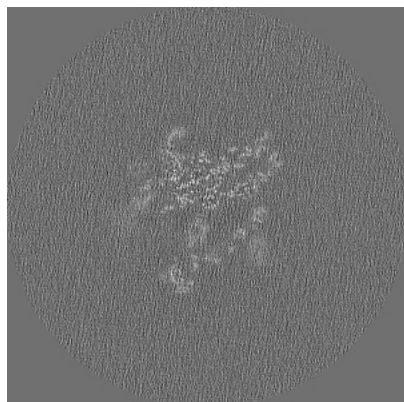


Y Index: 240

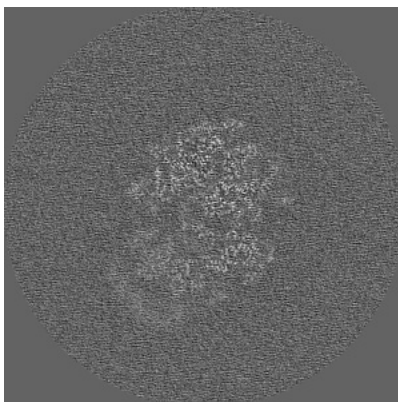


Z Index: 240

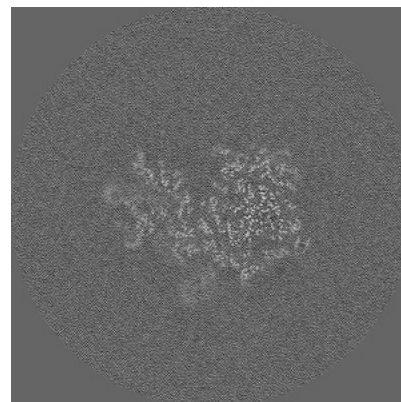
6.2.2 Raw map



X Index: 240



Y Index: 240

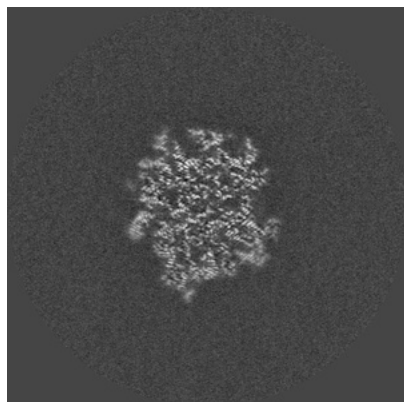


Z Index: 240

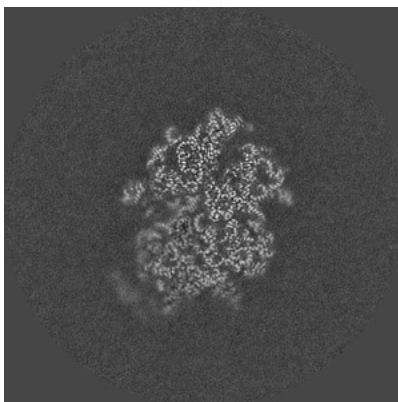
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

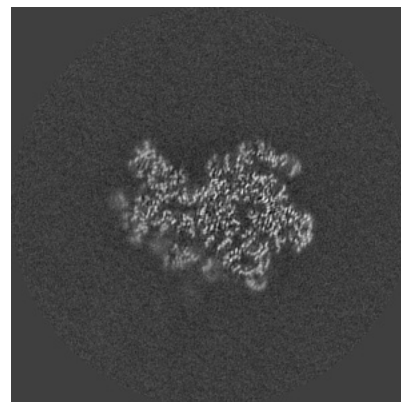
6.3.1 Primary map



X Index: 267

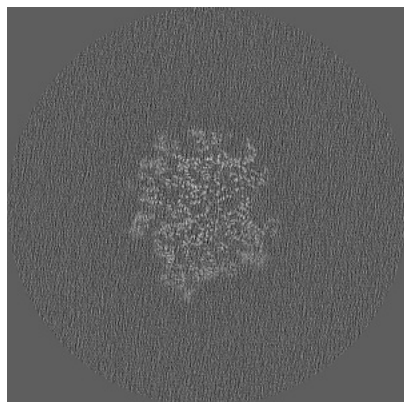


Y Index: 231

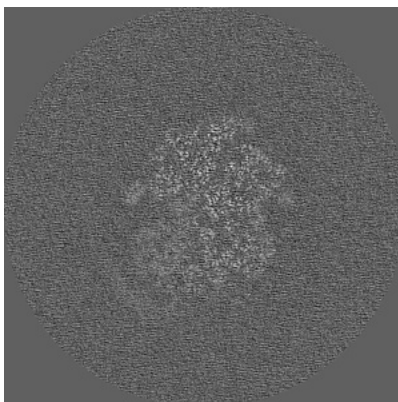


Z Index: 254

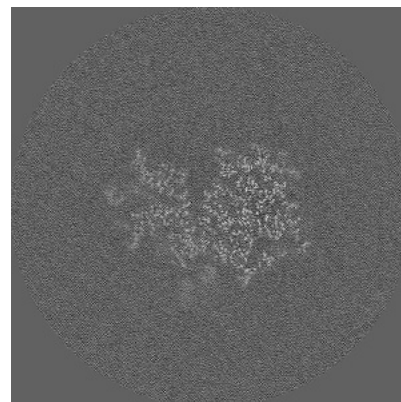
6.3.2 Raw map



X Index: 266



Y Index: 234

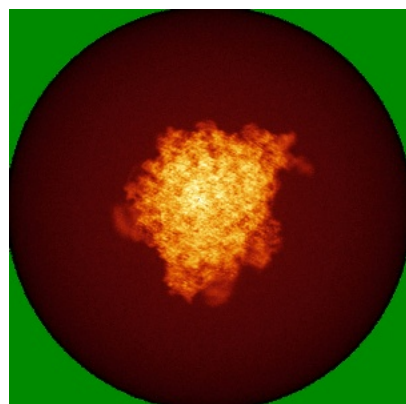


Z Index: 243

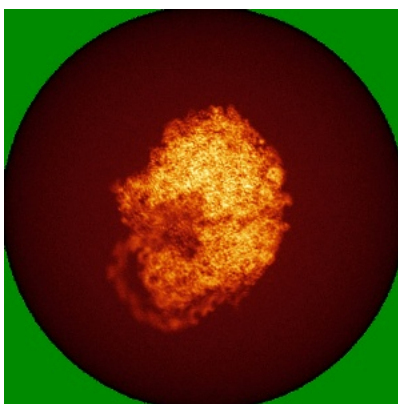
The images above show the largest variance slices of the map in three orthogonal directions.

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

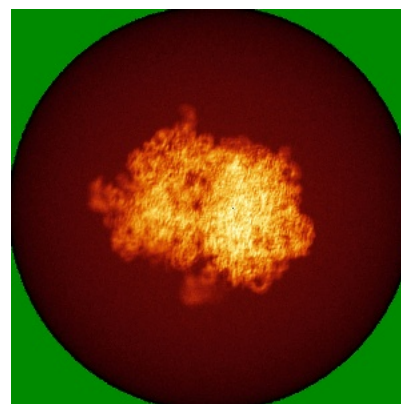
6.4.1 Primary map



X

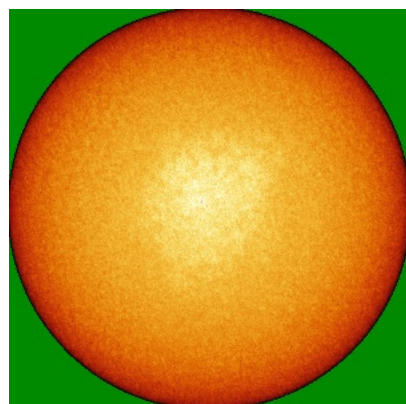


Y

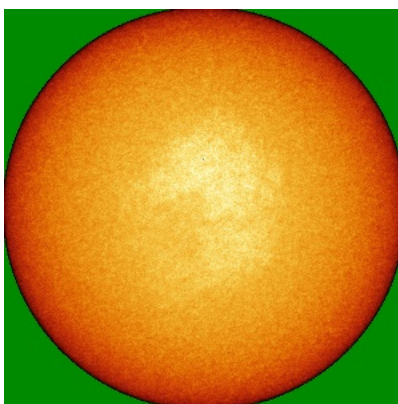


Z

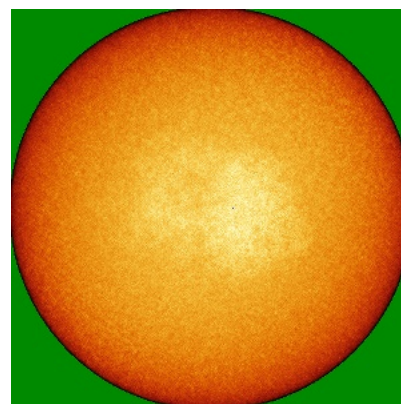
6.4.2 Raw map



X



Y

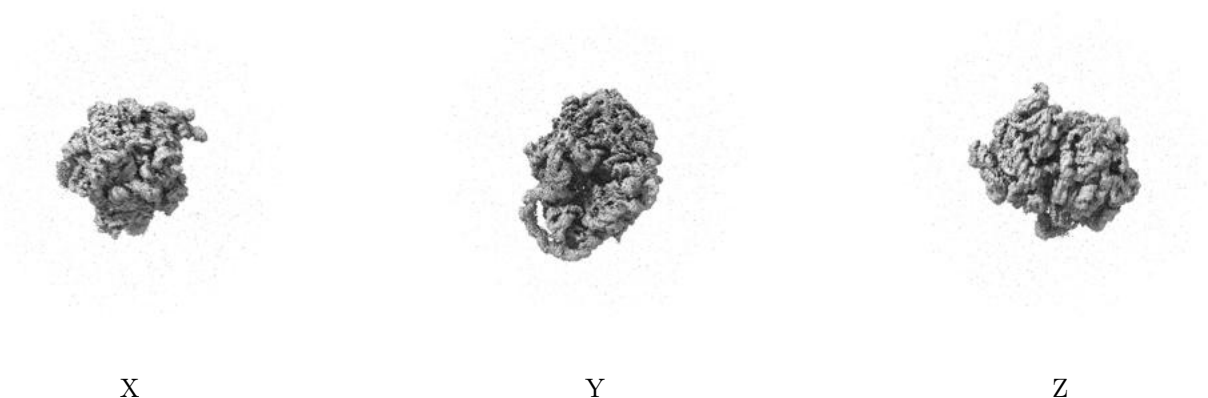


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

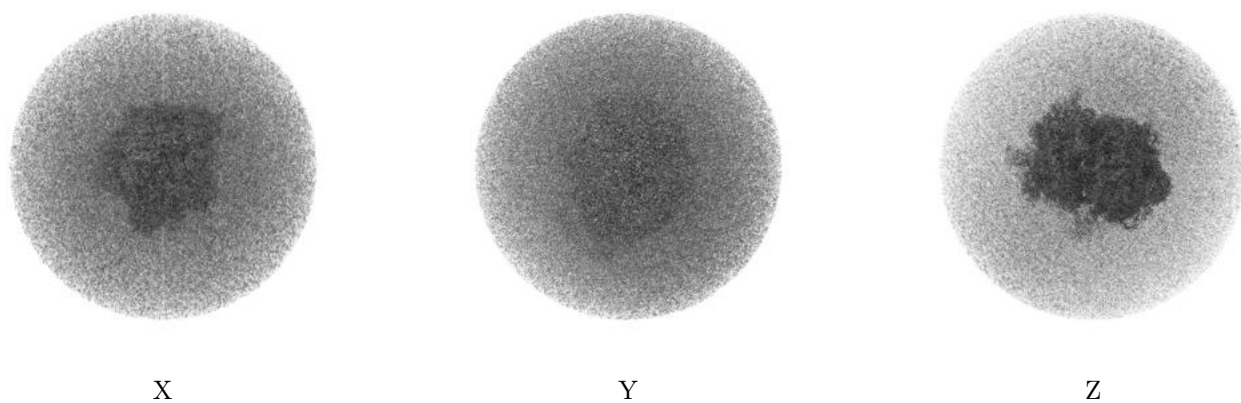
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

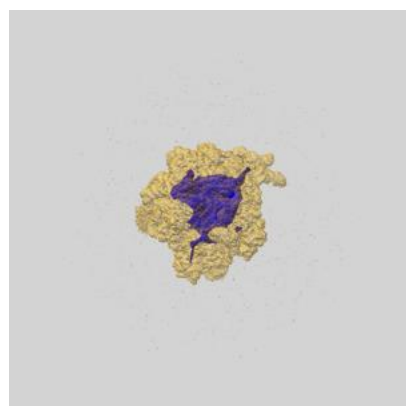
6.6 Mask visualisation [i](#)

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

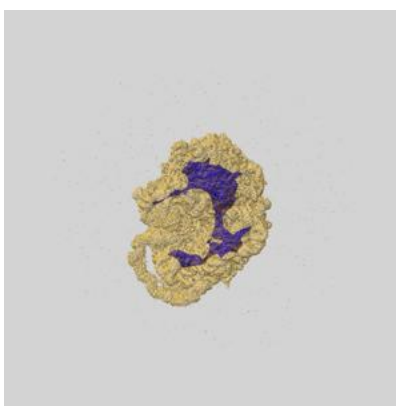
A mask typically either:

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

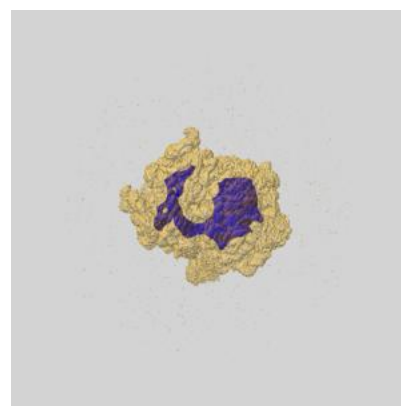
6.6.1 emd_11717_msk_1.map [i](#)



X



Y

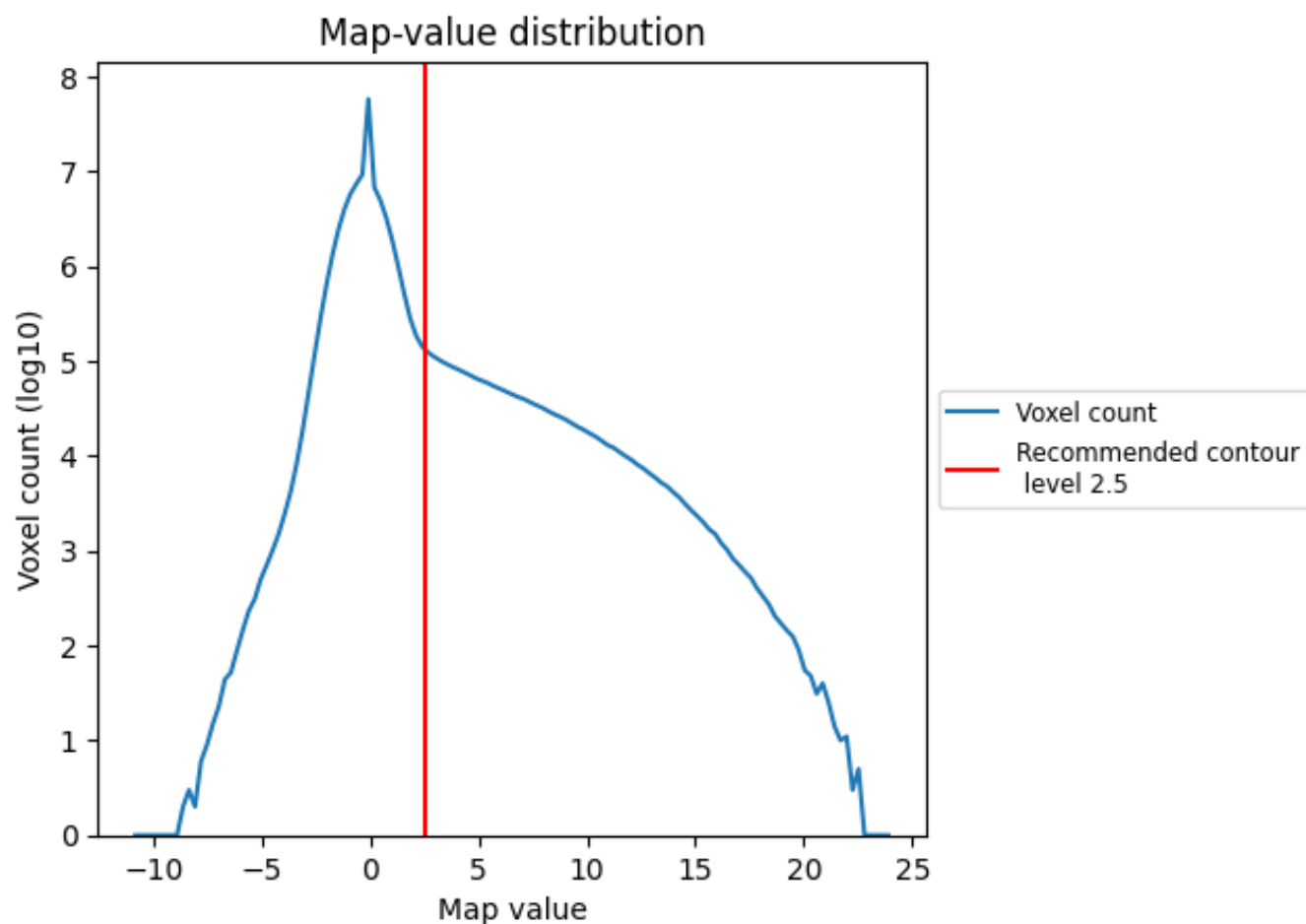


Z

7 Map analysis [i](#)

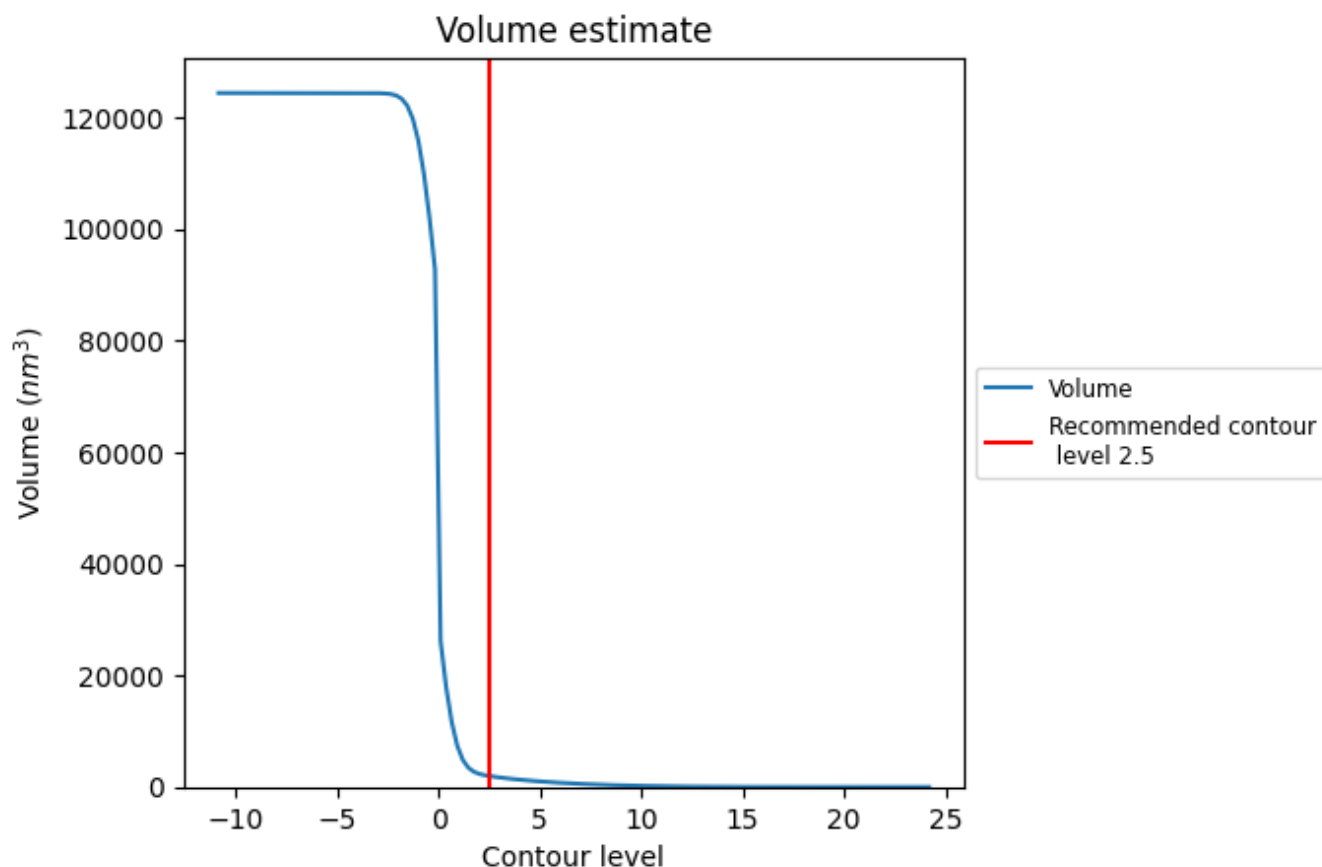
This section contains the results of statistical analysis of the map.

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.

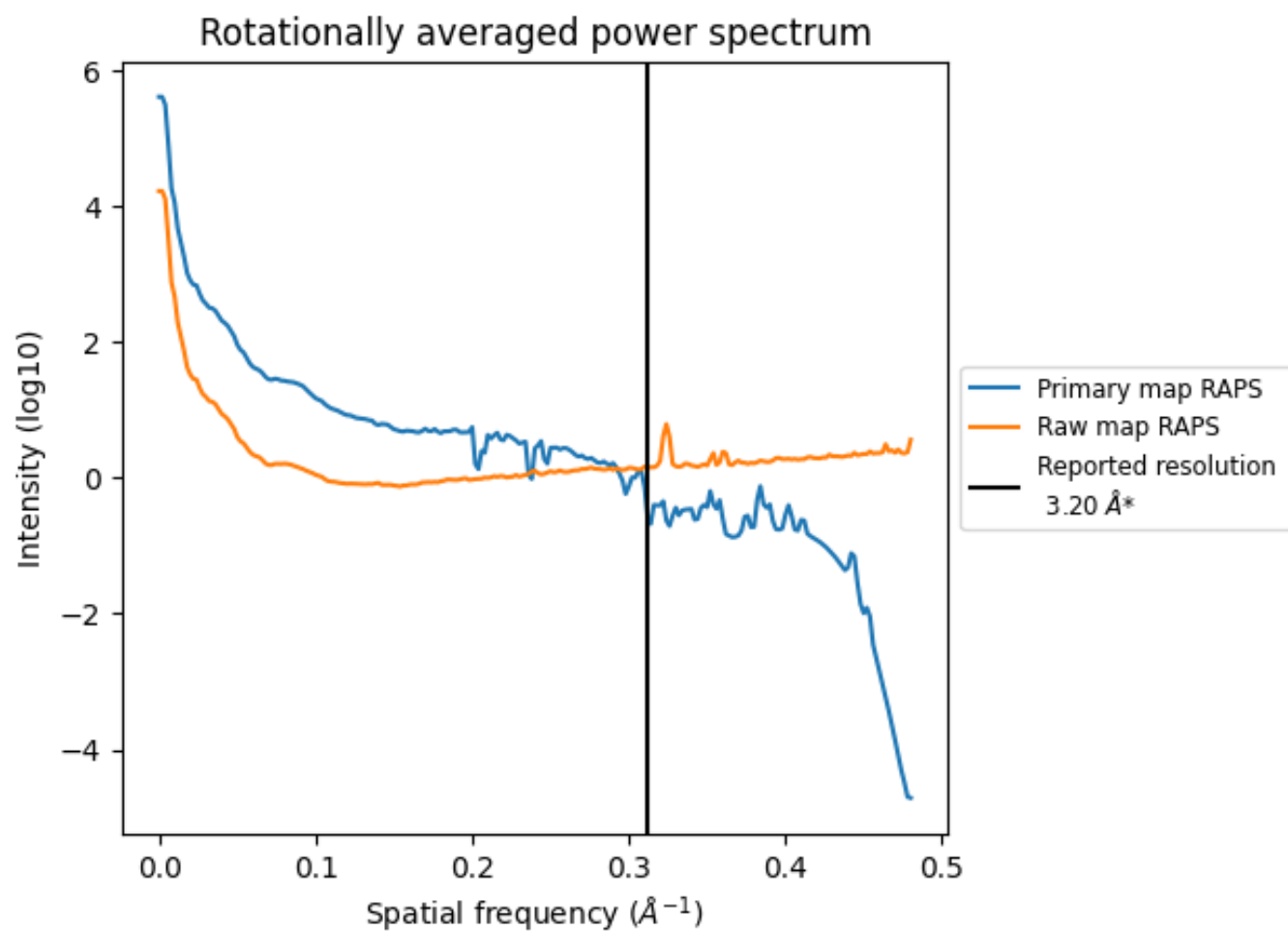
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1971 nm^3 ; this corresponds to an approximate mass of 1781 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 ⓘ

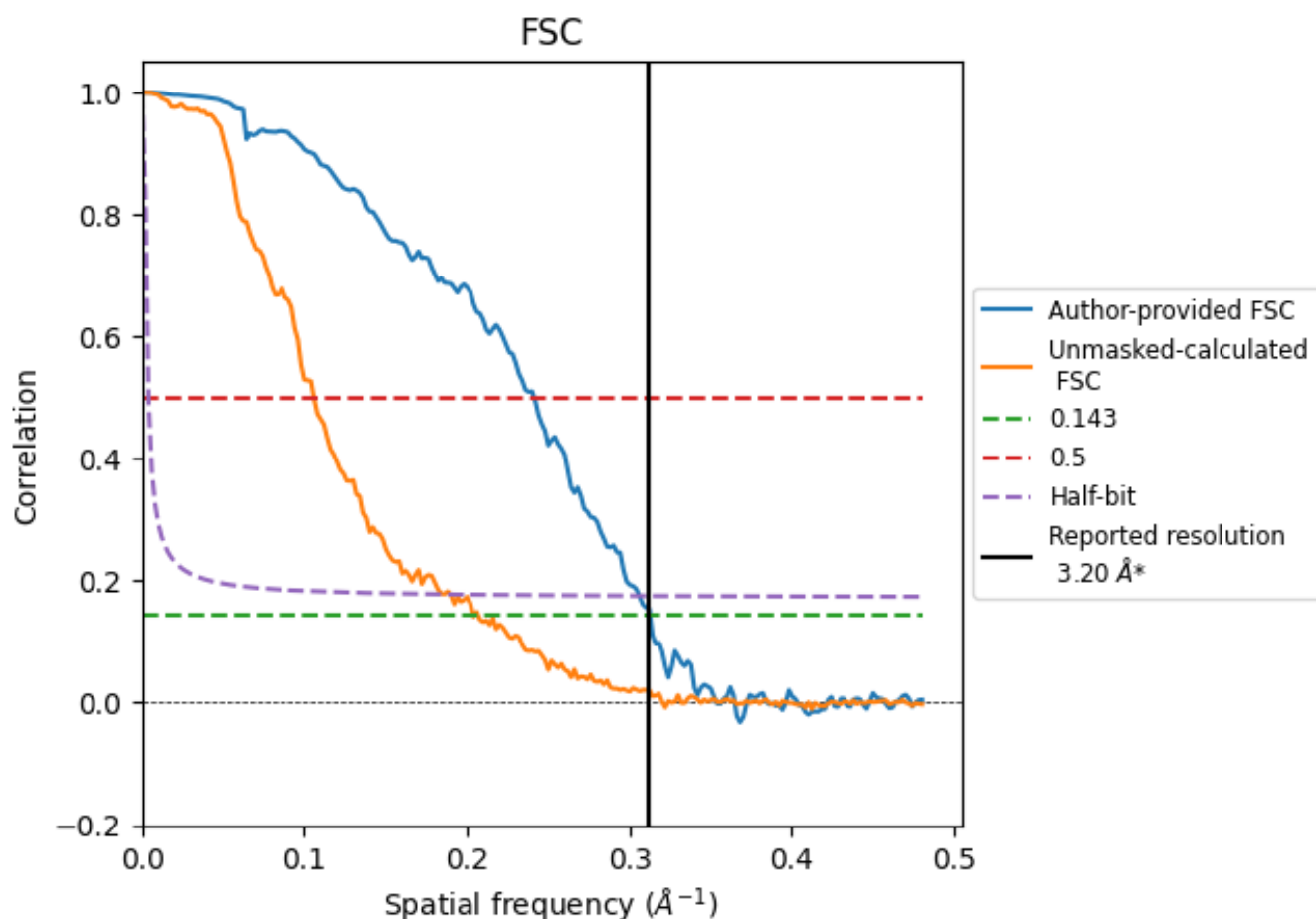


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

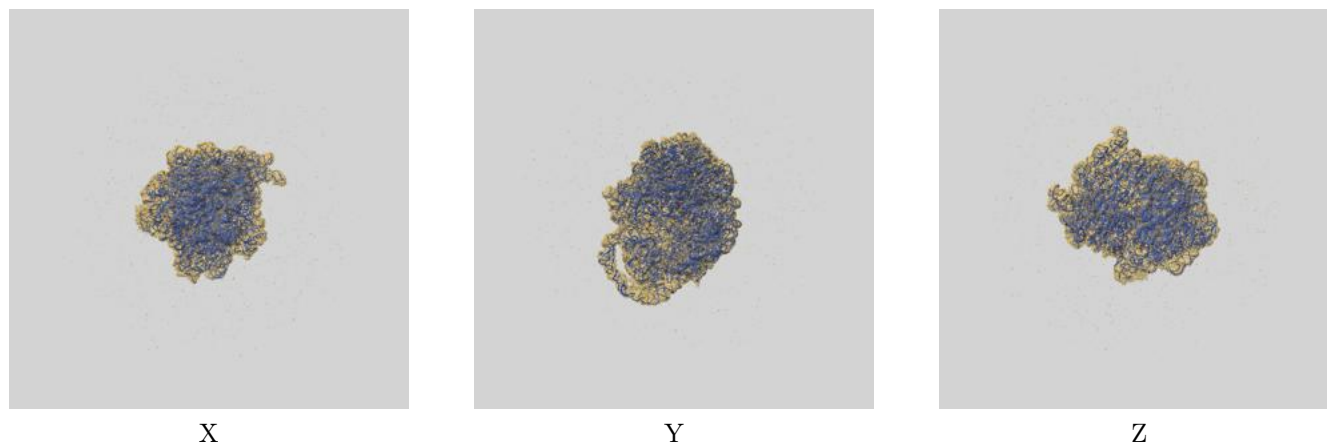
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.19	4.14	3.26
Unmasked-calculated*	4.90	9.43	5.27

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.90 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

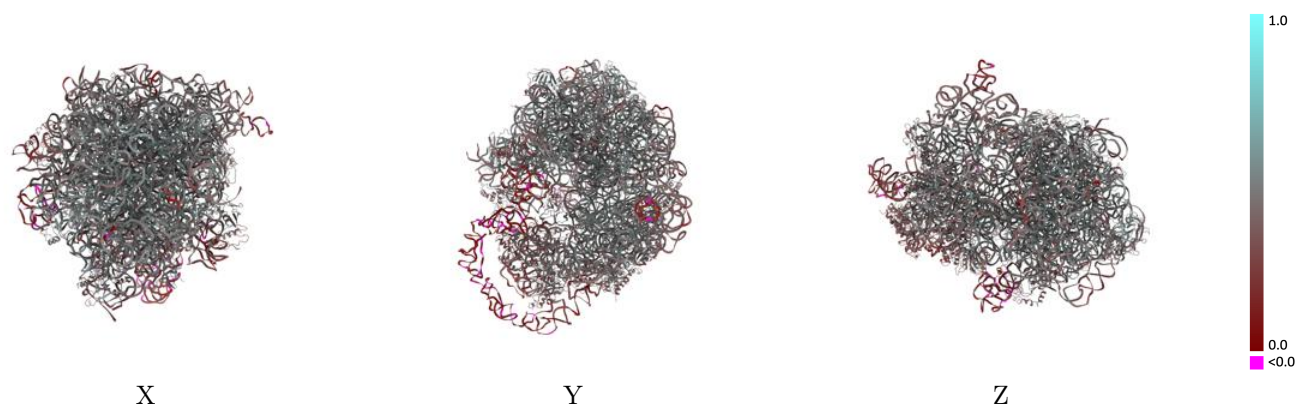
This section contains information regarding the fit between EMDB map EMD-11717 and PDB model 7ACJ. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



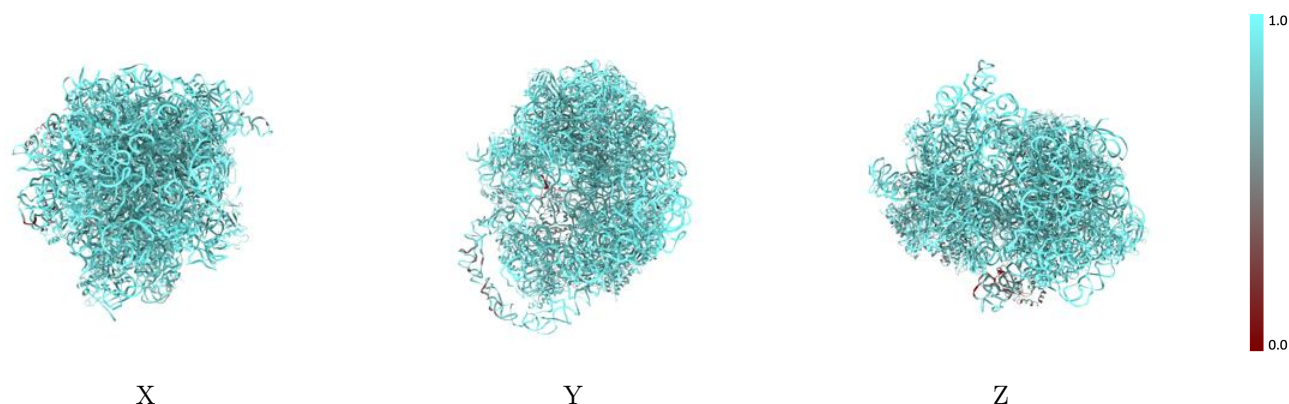
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



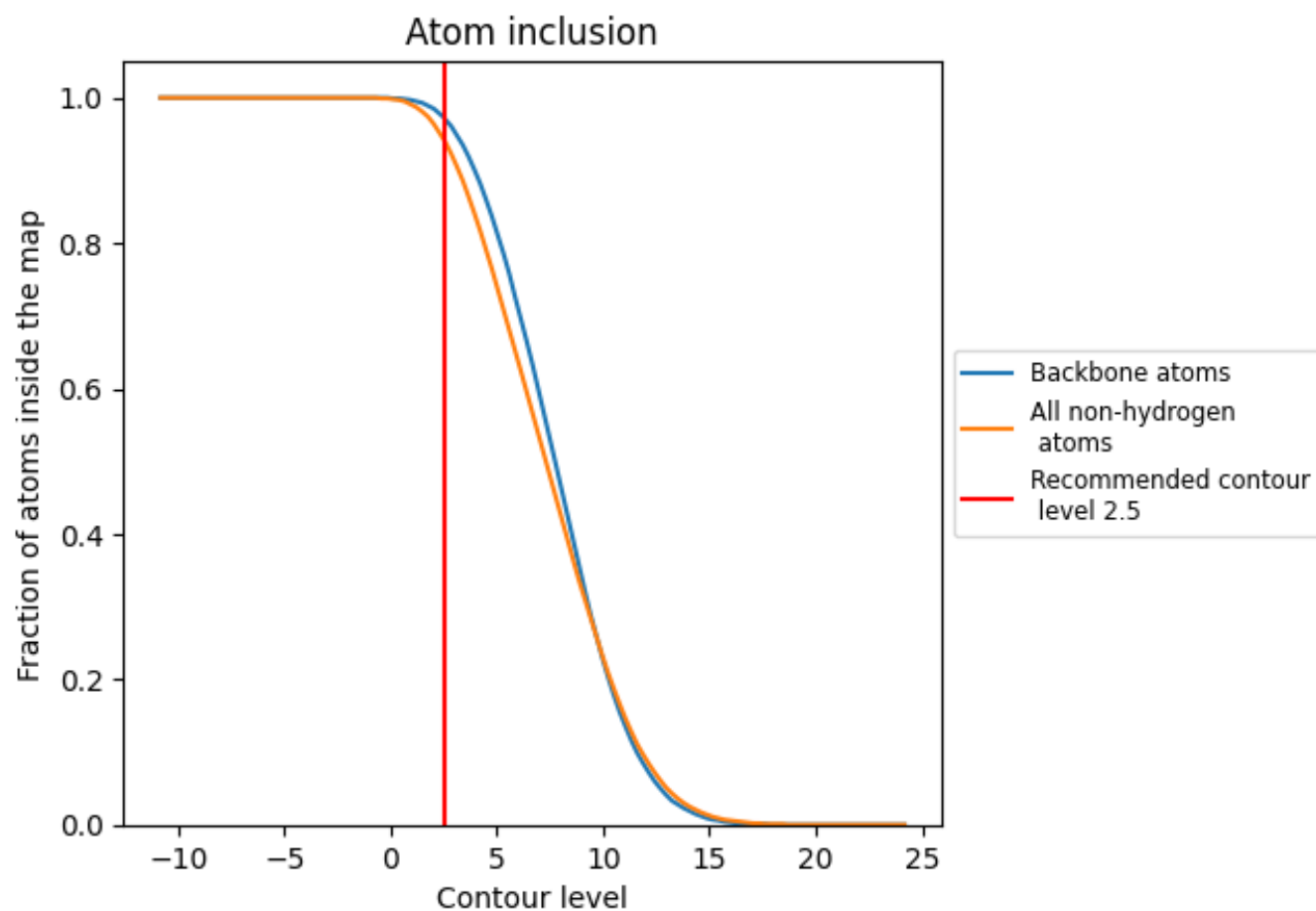
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.4220
1	 0.9700	 0.4430
2	 0.9800	 0.4200
3	 0.9780	 0.4190
4	 0.8650	 0.1850
5	 0.8320	 0.3960
A	 0.9240	 0.4960
B	 0.9400	 0.5040
C	 0.9210	 0.4710
D	 0.9400	 0.4890
E	 0.8740	 0.3550
F	 0.9140	 0.4030
G	 0.4510	 0.3110
J	 0.9250	 0.4660
K	 0.9240	 0.4970
L	 0.9410	 0.4960
M	 0.9290	 0.4890
N	 0.9380	 0.4760
O	 0.9410	 0.4400
P	 0.9150	 0.4880
Q	 0.9440	 0.4830
R	 0.9370	 0.4940
S	 0.9220	 0.4850
T	 0.9160	 0.4710
U	 0.9290	 0.4620
V	 0.9360	 0.4610
W	 0.8750	 0.4590
X	 0.9370	 0.4880
Y	 0.9060	 0.4180
Z	 0.9220	 0.4950
a	 0.8250	 0.2930
b	 0.9210	 0.4800
c	 0.9280	 0.4850
d	 0.9490	 0.5160
e	 0.9290	 0.5020



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Chain	Atom inclusion	Q-score
f	 0.9420	 0.4710
g	 0.7030	 0.3680
h	 0.8910	 0.4170
i	 0.9250	 0.4400
j	 0.9220	 0.4630
k	 0.9040	 0.4110
l	 0.6420	 0.2640
m	 0.9280	 0.4770
n	 0.8700	 0.2960
o	 0.8850	 0.3680
p	 0.9270	 0.4290
q	 0.9290	 0.4790
r	 0.8580	 0.3020
s	 0.9160	 0.4070
t	 0.9360	 0.4370
u	 0.9250	 0.4650
v	 0.9460	 0.4450
w	 0.8610	 0.4030
x	 0.8690	 0.3430
y	 0.9010	 0.4330
z	 0.7980	 0.3680