



wwPDB EM Validation Summary Report ⓘ

Jun 27, 2026 – 12:52 PM EDT

PDB ID : 6OST / pdb_00006ost
EMDB ID : EMD-20188
Title : RF2 pre-accommodated state bound Release complex 70S at 24ms
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-05-02
Resolution : 4.20 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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

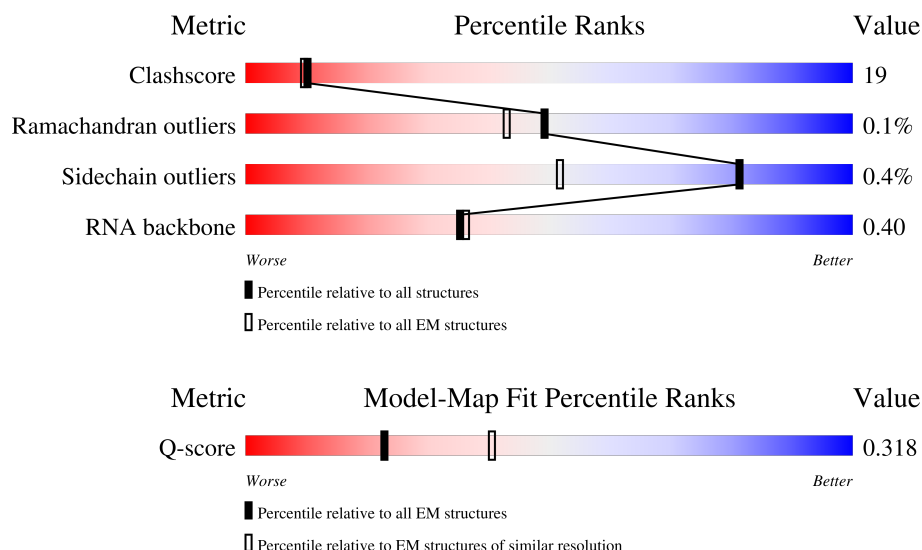
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



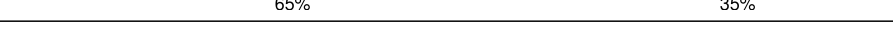
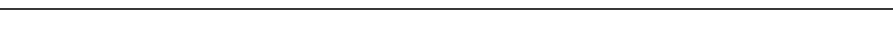
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	42% 44% 14%
2	2	1534	40% 46% 13%
3	3	120	42% 49% 9%

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Mol	Chain	Length	Quality of chain
4	B	271	
5	C	209	
6	D	201	
7	E	177	
8	F	175	
9	G	149	
10	J	142	
11	K	123	
12	L	144	
13	M	136	
14	N	119	
15	O	116	
16	P	114	
17	Q	117	
18	R	103	
19	S	110	
20	T	94	
21	U	103	
22	V	94	
23	W	76	
24	X	77	
25	Y	62	
26	Z	58	
27	b	56	
28	c	52	

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Mol	Chain	Length	Quality of chain
29	d	46	
30	e	64	
31	f	38	
32	g	225	
33	h	208	
34	i	205	
35	j	156	
36	k	104	
37	l	151	
38	m	129	
39	n	127	
40	o	99	
41	p	117	
42	q	123	
43	r	116	
44	s	100	
45	t	88	
46	u	82	
47	v	80	
48	w	66	
49	x	83	
50	y	86	
51	z	70	
52	4	9	
53	7	362	

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Mol	Chain	Length	Quality of chain
54	5	76	41% 38% 18%
55	6	3	33% 67%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146620 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 protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 10 is a protein called 50S ribosomal protein L13.

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

- Molecule 11 is a protein called 50S ribosomal protein L14.

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

- Molecule 12 is a protein called 50S ribosomal protein L15.

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

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

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

- Molecule 15 is a protein called 50S ribosomal protein L18.

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

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

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

- Molecule 18 is a protein called 50S ribosomal protein L21.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.

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

- Molecule 20 is a protein called 50S ribosomal protein L23.

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

- Molecule 21 is a protein called 50S ribosomal protein L24.

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

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	76	Total	C	N	O	S	
			582	360	117	104	1	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

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

- Molecule 26 is a protein called 50S ribosomal protein L30.

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

- Molecule 27 is a protein called 50S ribosomal protein L32.

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

- Molecule 28 is a protein called 50S ribosomal protein L33.

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

- Molecule 29 is a protein called 50S ribosomal protein L34.

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

- Molecule 30 is a protein called 50S ribosomal protein L35.

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

- Molecule 31 is a protein called 50S ribosomal protein L36.

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

- Molecule 32 is a protein called 30S ribosomal protein S2.

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

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

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

- Molecule 36 is a protein called 30S ribosomal protein S6.

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

- Molecule 37 is a protein called 30S ribosomal protein S7.

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

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

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

- Molecule 41 is a protein called 30S ribosomal protein S11.

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

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

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

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

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

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

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

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	9	Total	C	N	O	P	0	0
			184	83	26	66	9		

- Molecule 53 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	352	Total	C	N	O	S	0	0
			2793	1722	484	577	10		

- Molecule 54 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 55 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

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

Mol	Chain	Residues	Atoms		AltConf
56	1	1	Total 1	Mg 1	0
56	2	1	Total 1	Mg 1	0
56	3	8	Total 8	Mg 8	0
56	b	1	Total 1	Mg 1	0
56	i	1	Total 1	Mg 1	0

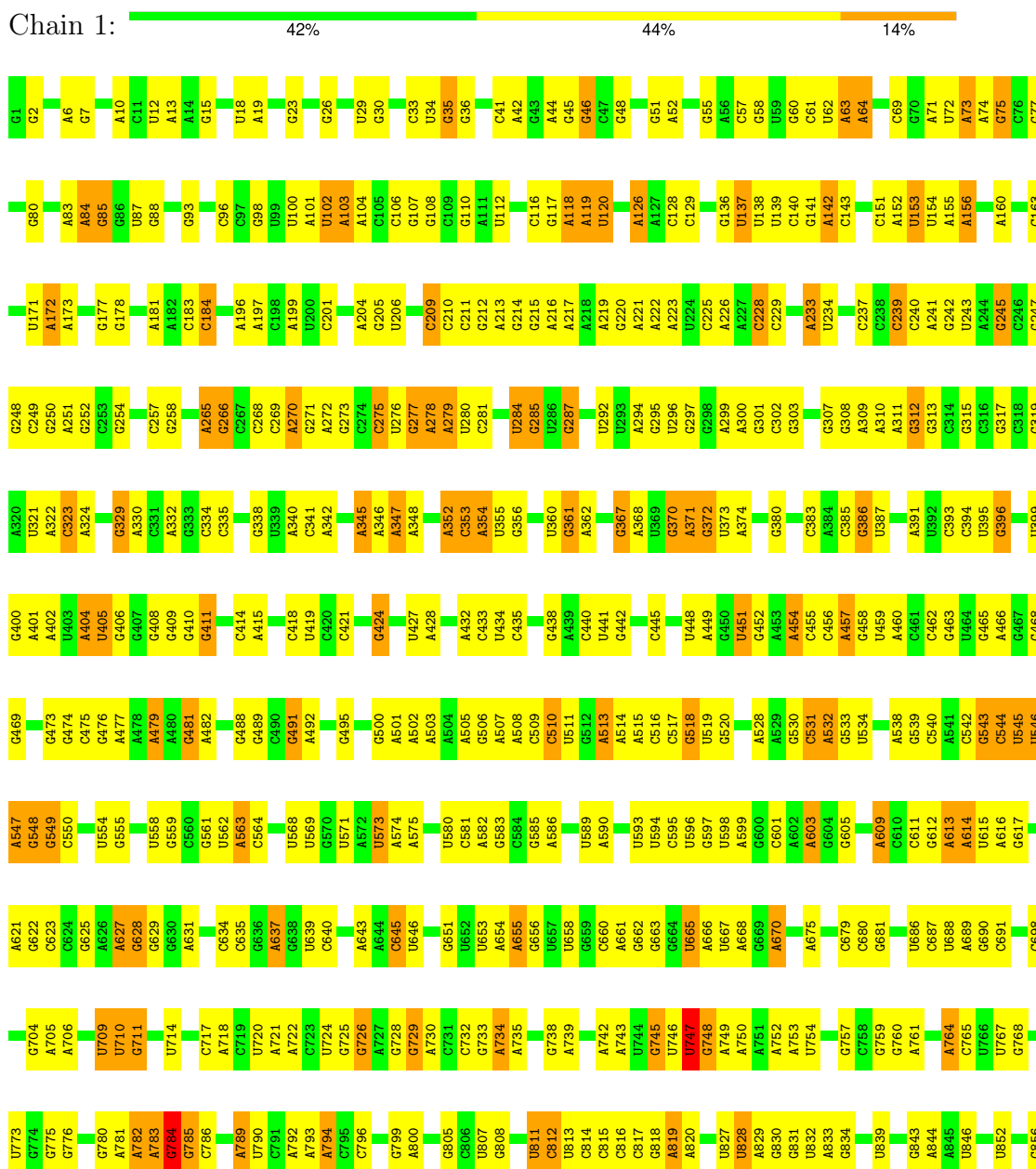
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

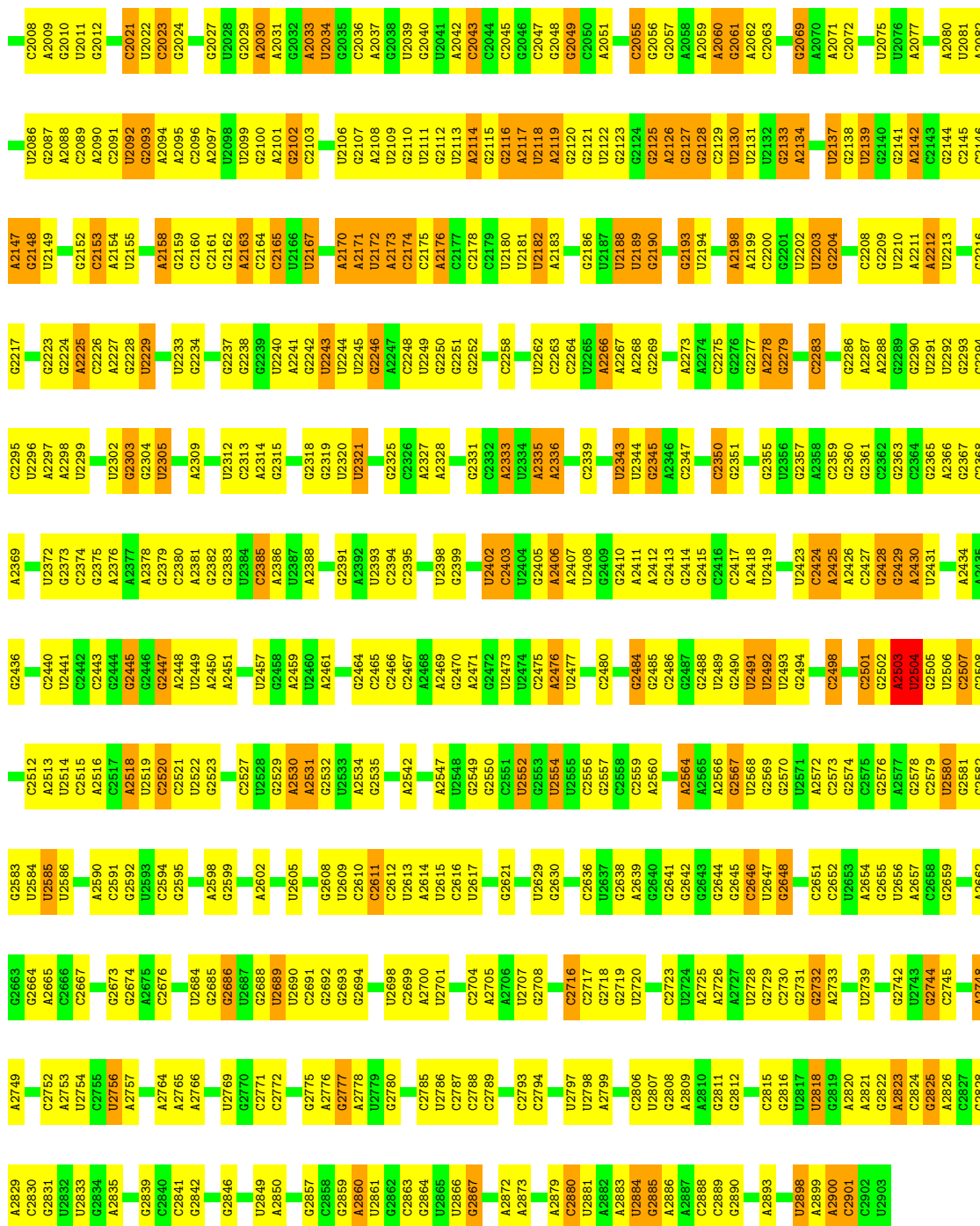
3 Residue-property plots

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



U1931	A1858	A1791	U1716	G1633	A1392	A1307	U1231	A1156	A1085	U1012	A933	G857
C1934	U1869	G1792	A1717	A1634	A1395	A1308	G1252	G1157	A1086	C1013	U934	G858
G1935	G1860	G1718	G1718	U1635	U1394	A1309	A1286	C1158	G1087	A1014	U935	G859
A1936	G1861	U1796	U1720	U1636	A1395	G1310	G1235	C1161	A1088	U1019	U936	U860
A1937	G1862	G1797	U1721	A1637	U1396	G1312	A1236	C1164	A1089	A1020	G939	A861
U1938	G1863	G1798	G1722	C1638	U1397	U1313	G1237	C1165	U1090	A1021	G940	C865
U1939	U1864	U1798	A1722	C1639	C1398	U1313	G1238	A1166	G1093	G1022	G941	A866
A1945	A1866	G1799	G1723	A1640	C1399	G1314	A1241	G1166	U1094	G1023	G942	C867
G1946	G1869	C1800	G1724	A1641	A1403	C1315	A1246	C1167	A1095	G1024	G943	U868
G1947	A1870	A1801	C1726	G1642	G1404	U1316	A1247	G1168	A1096	G1025	G944	G869
G1948	A1871	A1803	C1727	G1643	U1405	A1248	A1247	A1169	U1097	G1026	C946	U870
	A1872	C1804	C1728	G1644	U1406	G1248	G1238	C1170	A1098	A1027		
	A1873	A1805	U1729	G1645	G1407	U1249	U1239	G1171	G1099	A1028	G949	G874
U1951	G1874	C1806	G1730	C1646	U1482	G1407	G1250	C1172	C1100		G950	G875
A1952	G1875	G1807	G1731	U1647	U1483	U1408	G1251	U1173	U1101	U1033		C876
A1953	G1876	A1808	G1732	U1648	U1484	A1409	C1252	U1174	C1102	G1034	G954	A877
G1954	A1876	A1809	G1733	G1649	U1485	G1410	A1253	U1175	A1103	U1035	G955	A878
U1955	U1880	A1810	G1734	A1652	C1488	U1411	A1254	U1176	C1104	G1036	G956	G879
U1956	C1881	G1811	U1735	G1653	C1489	U1412	U1255	G1177	U1105		G957	G880
C1957		G1814	U1736	A1654	A1413	G1332	G1256	C1178	G1106	A1040	U958	G881
		A1815	U1737	U1655	C1414	U1340	G1259	G1179	U1107	G1041	G959	G882
C1962	G1884	C1816	A1739	G1656	G1415	G1341	A1260	U1180	U1108	G1042	A960	G883
U1963	A1885	G1817	G1740	C1657	G1416	U1342	A1261	U1181	C1109	G1043	C961	U884
U1964	U1886	U1818	G1741	G1660	G1417	G1343	U1262	G1182	G1110	C1044	G962	C885
C1965	C1887	A1919	C1742	U1661	A1418	U1344	U1263		A1111	C1045	U963	A886
A1966	A1888	U1820	G1743	A1665	A1420		A1264	G1186	G1112	A1046	C964	A887
C1967	A1889	G1821	U1744	G1666	G1421	C1351	A1265	G1187	U1113	G1047		C888
G1968	U1890	A1822	A1745	U1667	G1422	U1352	G1266	U1188	C1114	A1048	G968	C889
A1969	C1894	C1823	G1746	G1668	G1423	A1353	U1267	A1189	G1115	C1049	C969	C890
U1970	A1899	G1824	G1750	A1669	C1424	A1354	A1268	G1190	G1116	A1050	A972	G891
G1972	A1900	U1825	G1753	C1670	A1504	C1355	A1269	G1192	C1117	G1051	A973	A892
C1973	G1903	G1826	U1754	U1671	G1430	G1360	G1270	G1193	U1119	G1055	A974	C893
G1974	G1904	U1827	A1754	G1674	A1431	G1361	A1272	G1197	C1123	A1057	A975	U894
G1975	C1905	G1828	A1755	A1508	G1432	C1362	U1273	U1198	G1124	G1058	A976	A896
U1976	G1906	A1829	G1756	A1509	A1433	C1363	A1274		G1125	U1059	A979	C897
A1977	U1907	C1830	A1757	G1510	A1434	G1364	A1275	U1201	A1126	G1060	A980	C898
U1978	G1908	U1758	U1758			A1365	A1276	U1202	C1129	U1061	A981	A899
U1979	C1909	A1759	C1760	G1514	C1437	A1366	A1277	U1203	A1129	G1062	C982	
G1980	U1910	U1834	C1760	A1515	U1438	A1367	C1278	U1204	U1130		A983	C903
A1981	G1911	G1835	G1764	A1522	A1439	G1368	G1279	A1205	G1131	U1065		G904
U1982	U1912	C1836	C1764	A1523	G1447	G1369	G1283		U1132	U1066	G987	G907
	A1913	C1837		G1524	G1448	C1370		U1209	C1135	A1067	A988	
C1986	C1914	C1838	A1772	G1527	G1449	U1371	A1286	G1212	G1136	G1068	G989	A910
A1987	3TD1915	U1841	C1773	G1528	G1450	A1372	A1287	G1213	A1069	A1069	C991	A911
G1988	A1916		U1775	A1529	C1451	G1374	G1288		A1070	G1071	C992	C912
	U1917	C1844	G1776	G1530	G1452			U1219	A1072	G1072	G993	U913
U1991	A1918	G1845		G1531	A1453	U1378	U1294	G1220	G1141	A1073	C994	G914
G1992	U1923	A1847	U1779	C1532	C1454	U1379	C1297	G1221	A1142	G1074	C995	C915
U1993	C1924	U1781	A1780	A1535	U1458	G1380	C1298	G1222	A1143	C1075	A996	G916
U1994	U1995	G1849	U1782	G1536	U1459	G1381	G1299	G1223	A1144	G1076	U999	A917
C1996	C1925	G1850	A1783	G1537	U1460	A1382	G1299	G1223	A1144	C1077		A918
C1997	U1926	A1705	G1784	G1538	C1461	A1383	A1301	A1226	A1151	U1078	A1000	C922
A1998	A1927	U1709	G1788	U1539	C1462	A1385	A1302	G1227	C1152	C1079	G1006	G923
C1999	C2000	A1954	A1789	G1540	C1463	C1386	G1303	G1228	G1153	U1083	A1009	U931
C2001	G1929	G1857	C1790	C1541	G1464	A1387	C1306	A1230	A1155	A1084		U932

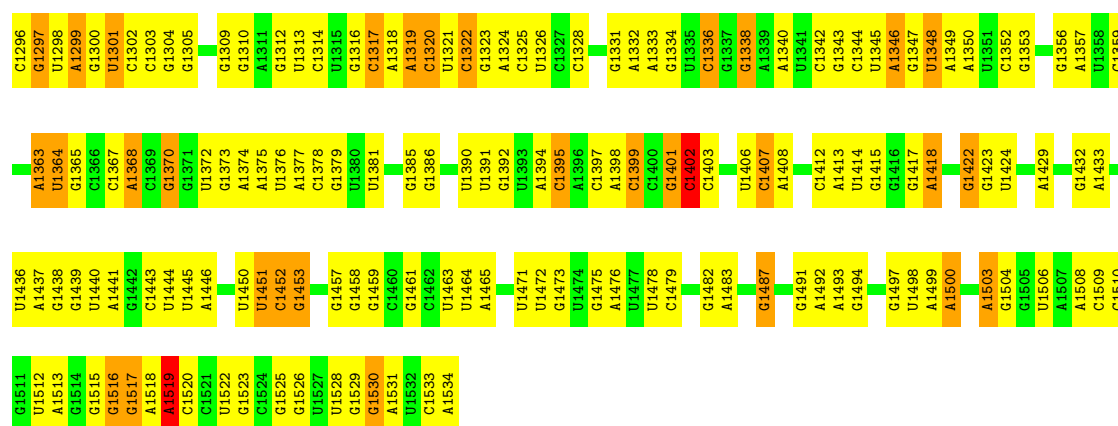


• Molecule 2: 16S Ribosomal RNA

Chain 2: 40% 46% 13%

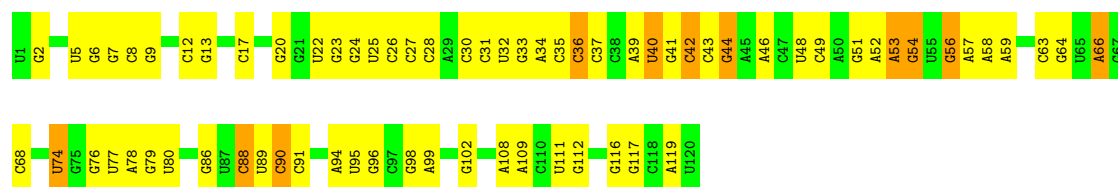


U1211	C1140	G1072	G1002	C924	U850	C770	A694	A607	G530	U458	C379	C307	G213	G145
U1212	C1141	U1073	G1003	G925	G851	A780	A695	U610	U531	U464	G380	C308	C214	G146
C1214	G1142	G1074	A1004	G926	U855		A696		A532	A465	C381	C309	C215	A149
	G1143		A1005	G927	C856	C783	G698	C613	A533	A466	A382	G310	U216	A151
G1218	G1144	G1077	U1007	G928	C857	A784	C699	G614	A535	U467	G383	C311	U219	U154
A1219	A1146	G1078	U1008		C858	G795	G700	G615	C536	A468	G384	A313	G220	U155
G1220	C1147	A1080	U1009	C932	C859	G786	U701	G616	G537	C469	U387	C314	C221	U156
G1221	U1148	A1081	U1010	G933	A860	A787	A702	G617	G538	C470	G388	A315	C222	A157
C1222	C1149		C1011	G934	G861	U788	G703	C618	A539	U471	A389	C316	U224	U157
C1223	A1150		A1012	A935	C862	U789	A704	U619		U472	U390		C225	G158
U1224	U1085	U1085	G1013		U863		G705	C620	G542	U473	G391	G319	C226	G159
C1226	A1151	U1086	A1014	G939	A864	A792	A706	A621	U543		C392	A320		A160
A1227	A1152	G1087	G1014		A865	U793			G544	U476	A393	A321	G232	A161
C1228	G1153	G1088	G1015	G945	C866	A794	G711	U625	G545	C477	G394	C322		A162
	G1156	U1089	U1016	A946	C867	A712	G713	G626	C546	A478	C395		G235	G163
G1233	A1157	U1091	G1018	G947	C868	C797	G714	G627	A547	U479	A396	A325	A236	G164
C1234	U1158	A1092	A1019	C948	C869	U798	G715	G628	A553	U480	A397	A327		C169
U1235	U1159	A1093	G1020	A949	U870	G799	A716	A629	A554	G481	C401	C328	G240	U170
A1236	C1161	U1094	A1021	U950	U871	G800	A717	G633	U555	A482	G402	A329	U244	A171
C1237	G1162	U1095	A1022	G951	A872	U801	U718			G483	G403	C330	U245	A172
A1238		C1096	U1023		A873	A802			G558	U484	G404	G331	U246	U173
U1239	G1166	C1100	G1024	A958	C876	C805	G721	A640	A560	C489	G405	G332		
U1240	A1167	A1101	U1025	A959	C879	C806	G722	U641	A559	C490	G406			
G1241	U1168	A1102	C1026	U960		A807	U723	A642	U561	U409		C335	G251	G176
G1242	A1169	C1103	C1027	U961	C882	C810	G724		U562	G410	G409	A336	U252	G177
	A1170		U1028	G962	C883	G725			U563	G411	G408	A337	U253	G178
A1250	A1171	G1107	U1030	G966	U884	C811	G726	C650	C564	A493	A412	A338	U254	U179
G1255	A1176	G1108	C1031	C967	C885	C812	G727	U652	U565	G494	A413	A339	G255	U180
A1256	G1177	C1109	G1032	A968	C886	A814	A728	U653	C567	A495	G414		U256	A181
G1258	A1178	A1110	G1033	C969	C887	A815			C568	A496	A415	C345	U257	A182
C1259	A1179	A1111	G1034	G970	C888	A816	G734	G657	U569	A497	G416	G346	G258	C183
G1260	G1181		A1035	C971	C889	C817	G735	C658	A572	A498	G417	G347		U185
A1261	G1182	U1115	A1036	G974	C890	G818	C736		A573	C418	C419	G348	A262	C186
	U1183	U1116	G1040	A975	U891	A819		G661	A574	C501	U420		A263	G187
G1266	G1184	A1117	G1041	G976	A892	U820	G740	U682	G575	A502		C352	C264	
C1267	G1185	U1118	A1042	A977	C899	G821	G741	A663	C576	U421	U429	G360	G278	A190
A1268	G1186	C1119	G1043	A978	A900	U822	G742	G664	G577	A422	G430	G361	A279	G191
A1269	G1187	C1120	A1044	C979	A901	C823	A743	A665	C578	G423	G431	G362	C280	A192
G1270		U1121	C1045	G980	G902	C824	G744	G666	C579	A510	G424	A363	G281	G201
	A1191	U1122	A1046	U981	G903	A825	G745		C580	U512	G425	A364	A282	G202
C1273	C1192	U1123	G1047	U982	G904	C826	G746	A673	C581	C513		U365	G203	G203
A1274	G1193	G1124	G1048	A983	U904	U827	A746	G674	C582	G514	G428	G366	G204	G204
A1275		U1125	U1049	C984	U905	U828	A747	A675	A583	G515	U429	G367	G205	A196
G1276		U1126	G1050	C985	A906	G829	G748	U677	G584	U516	U430	U368	C206	A197
C1277	A1196		C1054	C986	A907	G833	G750		G585	C517	A431		U294	
G1278	A1197	G1128	A1055	U989	A908		U751	G680	G586	C518	U437	A369	G289	
A1280	U1198	A1130			A909	U837	G752	A681	G587	C519	U438	U367		
C1281	C1200	G1131	C1059	U992	U911	G838	G753	G685	U591	A520	U439	U368		
C1282	A1201	C1132	U1060	G993	U912	A753	G754	G686	G592	G521	U439		U294	A205
U1283	U1202	G1133	G1061	A994	A913	U842	G755	A687	A522	G524	G450	C372	A298	C207
	C1203	G1134	A914	C995	A914	U843	G756	G688	A523	G525	A451	A373	G299	U208
		U1065	U1065	A996	A918	U844	G757	G689	A595	C526	G454	A374	A300	U209
	G1207	C1136	G1066	C999	G922	A845	G758	G690	A596	G527	G455	U375	G211	
A1288	C1208	C1137	A1067	A1000		G846		G691	G601	C528	A456	G376	G212	
	C1210	G1139	C1071	C1001	A923	G849	G769				G457		A306	



• Molecule 3: 5S Ribosomal RNA

Chain 3: 42% 49% 9%



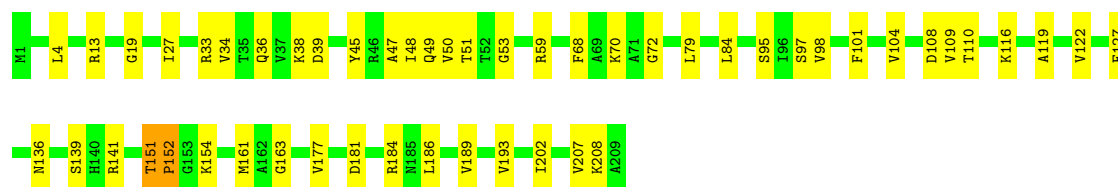
• Molecule 4: 50S ribosomal protein L2

Chain B: 60% 39%



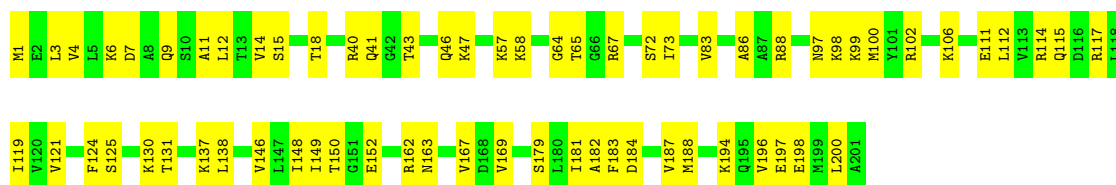
• Molecule 5: 50S ribosomal protein L3

Chain C: 76% 23%



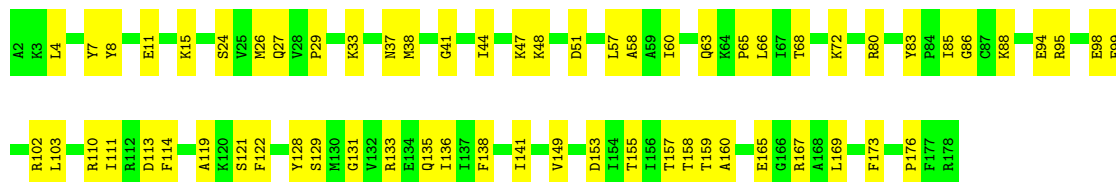
• Molecule 6: 50S ribosomal protein L4

Chain D: 67% 33%



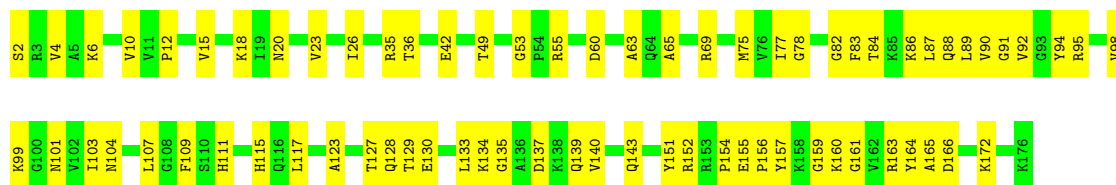
• Molecule 7: 50S ribosomal protein L5

Chain E: 64% 36%



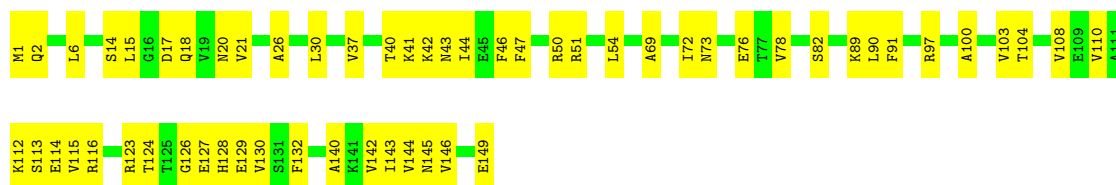
• Molecule 8: 50S ribosomal protein L6

Chain F: 59% 41%



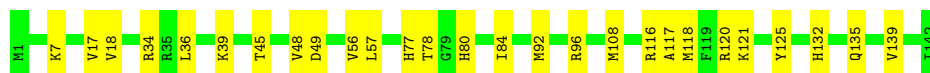
• Molecule 9: 50S ribosomal protein L9

Chain G: 62% 38%



• Molecule 10: 50S ribosomal protein L13

Chain J: 81% 19%



• Molecule 11: 50S ribosomal protein L14

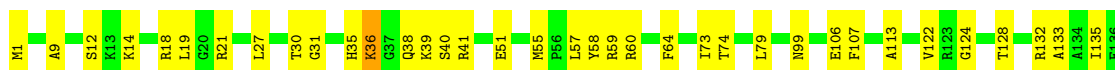
Chain K: 66% 34%





- Molecule 12: 50S ribosomal protein L15

Chain L: 73% 26%



- Molecule 13: 50S ribosomal protein L16

Chain M: 67% 33%



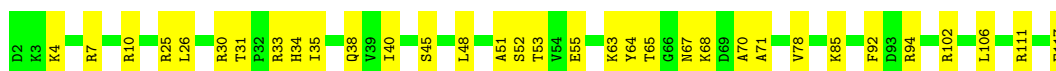
- Molecule 14: 50S ribosomal protein L17

Chain N: 74% 26%



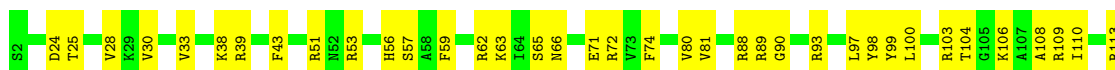
- Molecule 15: 50S ribosomal protein L18

Chain O: 72% 28%



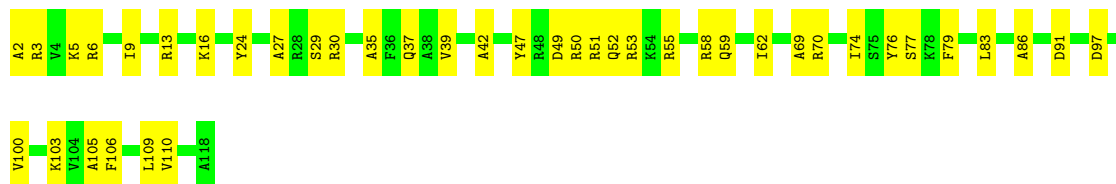
- Molecule 16: 50S ribosomal protein L19

Chain P: 67% 33%



- Molecule 17: 50S ribosomal protein L20

Chain Q:  65% 35%



- Molecule 18: 50S ribosomal protein L21

Chain R:  64% 34% .



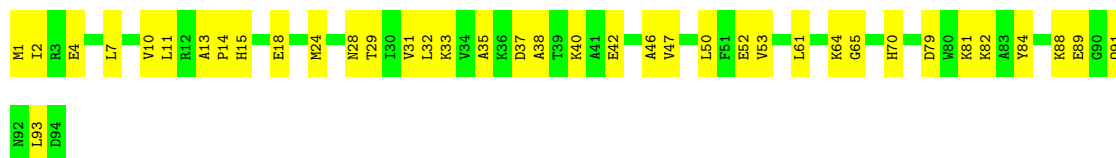
- Molecule 19: 50S ribosomal protein L22

Chain S:  72% 28%



- Molecule 20: 50S ribosomal protein L23

Chain T:  60% 40%



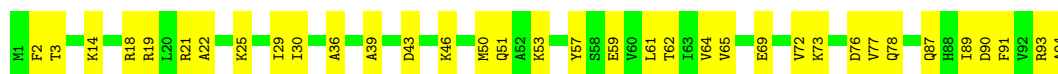
- Molecule 21: 50S ribosomal protein L24

Chain U:  66% 34%



- Molecule 22: 50S ribosomal protein L25

Chain V:  63% 37%

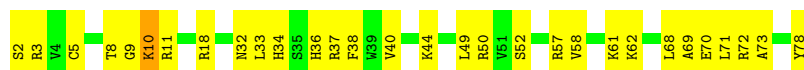


- Molecule 23: 50S ribosomal protein L27

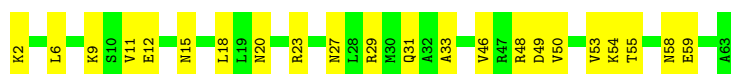
Chain W:  66% 34%



- Molecule 24: 50S ribosomal protein L28



- Molecule 25: 50S ribosomal protein L29



- Molecule 26: 50S ribosomal protein L30



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33

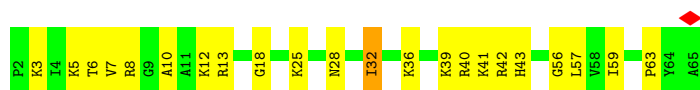


- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35





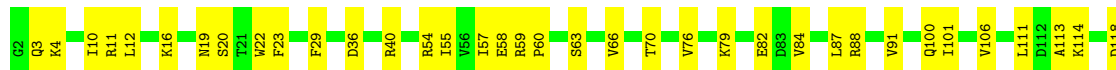
- Molecule 31: 50S ribosomal protein L36



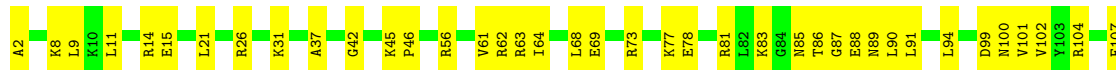
- Molecule 32: 30S ribosomal protein S2



- Molecule 33: 30S ribosomal protein S3



- Molecule 34: 30S ribosomal protein S4

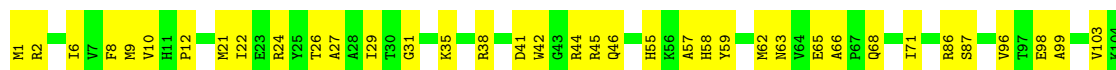


- Molecule 35: 30S ribosomal protein S5





- Molecule 36: 30S ribosomal protein S6



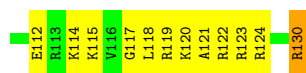
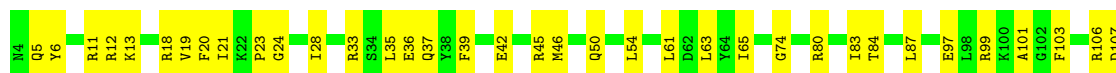
- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S9

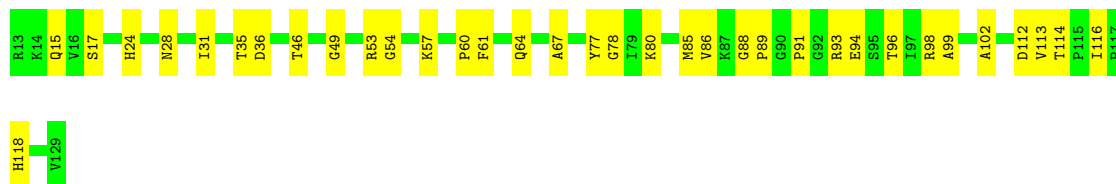


- Molecule 40: 30S ribosomal protein S10



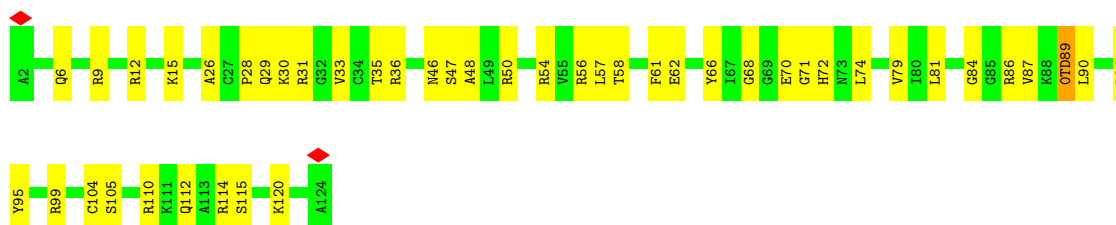
- Molecule 41: 30S ribosomal protein S11

Chain p:  70% 30%



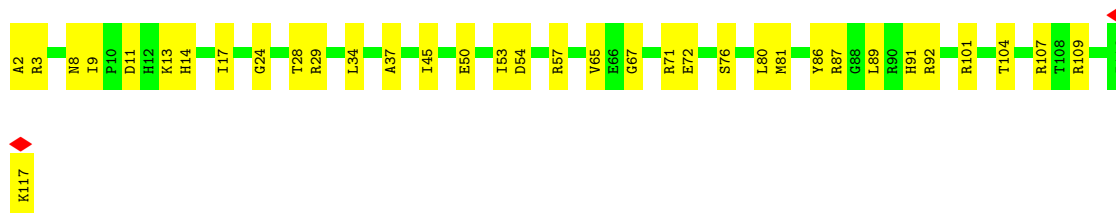
- Molecule 42: 30S ribosomal protein S12

Chain q:  63% 36%



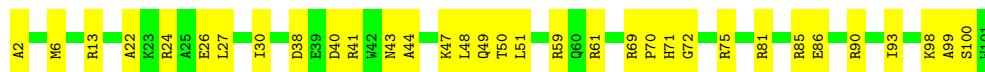
- Molecule 43: 30S ribosomal protein S13

Chain r:  70% 30%



- Molecule 44: 30S ribosomal protein S14

Chain s:  67% 33%



- Molecule 45: 30S ribosomal protein S15

Chain t:  84% 16%



- Molecule 46: 30S ribosomal protein S16

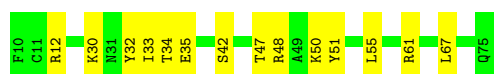
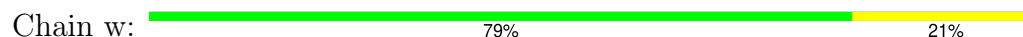
Chain u:  72% 28%



- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21

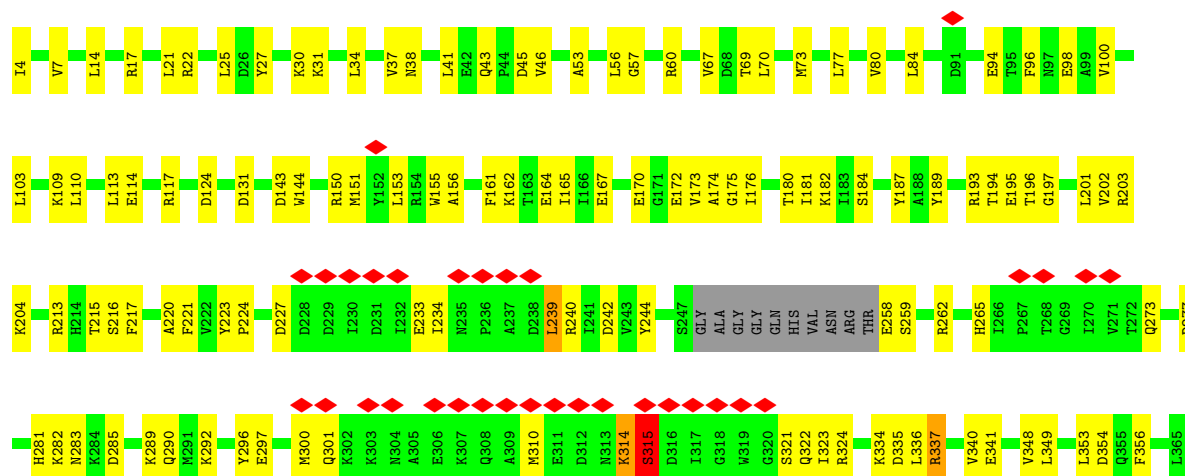


- Molecule 52: mRNA

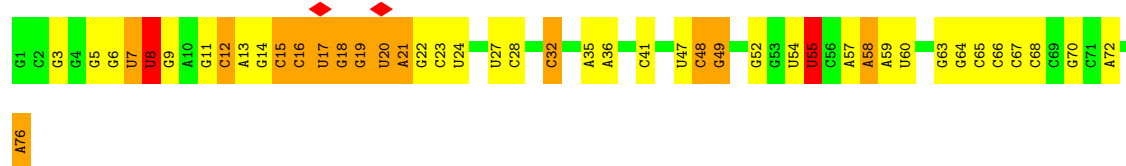


- Molecule 53: Peptide chain release factor 2





• Molecule 54: P-tRNA



• Molecule 55: FME-PHE-PHE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51221	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.027	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	421.12, 421.12, 421.12	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.645, 1.645, 1.645	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, OMC, FME, 3TD, PSU, 0TD, ZN, 4SU, 6MZ, UR3, 2MG, MA6, H2U, 5MU, OMU, 4OC, OMG, MG, 5MC, 2MA, G7M

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	0.51	0/69286	0.48	1/108087 (0.0%)
2	2	0.46	0/36590	0.45	1/57074 (0.0%)
3	3	0.47	0/2872	0.47	0/4478
4	B	0.49	1/2121 (0.0%)	0.68	1/2852 (0.0%)
5	C	0.46	0/1586	0.67	0/2134
6	D	0.44	0/1571	0.62	0/2113
7	E	0.43	0/1434	0.67	0/1926
8	F	0.43	0/1333	0.58	0/1805
9	G	0.38	0/1122	0.66	0/1515
10	J	0.48	0/1152	0.64	0/1551
11	K	0.43	0/955	0.66	0/1279
12	L	0.43	0/1062	0.64	0/1413
13	M	0.43	0/1093	0.63	0/1460
14	N	0.45	0/964	0.70	0/1289
15	O	0.40	0/902	0.60	0/1209
16	P	0.46	0/929	0.68	0/1242
17	Q	0.48	0/960	0.62	0/1278
18	R	0.48	0/829	0.69	0/1107
19	S	0.47	0/864	0.63	0/1156
20	T	0.44	0/752	0.63	0/1005
21	U	0.46	0/796	0.71	0/1062
22	V	0.46	0/766	0.61	0/1025
23	W	0.46	0/589	0.62	0/779
24	X	0.51	0/635	0.66	0/848
25	Y	0.47	0/502	0.62	0/667
26	Z	0.42	0/452	0.65	0/605
27	b	0.47	0/450	0.70	0/599
28	c	0.44	0/433	0.62	0/576
29	d	0.51	0/380	0.72	0/498
30	e	0.51	0/513	0.69	0/676
31	f	0.44	0/303	0.68	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	g	0.41	0/1791	0.66	0/2413
33	h	0.41	0/1663	0.61	0/2241
34	i	0.40	0/1665	0.63	1/2227 (0.0%)
35	j	0.43	0/1165	0.68	2/1568 (0.1%)
36	k	0.42	0/867	0.66	0/1171
37	l	0.38	0/1195	0.62	0/1602
38	m	0.41	0/989	0.60	0/1326
39	n	0.41	0/1034	0.66	0/1375
40	o	0.40	0/800	0.65	0/1082
41	p	0.38	0/893	0.59	0/1205
42	q	0.42	0/960	0.67	0/1286
43	r	0.40	0/909	0.65	0/1215
44	s	0.39	0/817	0.61	0/1088
45	t	0.41	0/722	0.60	0/964
46	u	0.37	0/659	0.57	0/884
47	v	0.40	0/657	0.71	0/881
48	w	0.41	0/553	0.57	0/743
49	x	0.34	0/680	0.55	0/915
50	y	0.43	0/675	0.61	0/895
51	z	0.38	0/597	0.61	0/792
52	4	0.34	0/203	0.49	0/312
53	7	0.37	0/2831	0.74	6/3815 (0.2%)
54	5	0.30	0/1704	0.39	0/2654
55	6	0.52	0/23	0.44	0/29
All	All	0.47	1/158248 (0.0%)	0.52	12/236388 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	223	THR	CA-C	-5.05	1.45	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	784	G	C4'-C3'-O3'	7.01	119.92	109.40
53	7	265	HIS	CA-C-N	6.06	125.18	120.33
53	7	265	HIS	C-N-CA	6.06	125.18	120.33
53	7	322	GLN	CA-C-N	5.55	131.97	121.97
53	7	322	GLN	C-N-CA	5.55	131.97	121.97

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	1302	0
2	2	32929	0	16587	623	0
3	3	2569	0	1301	50	0
4	B	2082	0	2154	105	0
5	C	1565	0	1616	39	0
6	D	1552	0	1619	52	0
7	E	1410	0	1444	54	0
8	F	1313	0	1358	47	0
9	G	1111	0	1148	40	0
10	J	1129	0	1162	23	0
11	K	946	0	1023	31	0
12	L	1053	0	1129	30	0
13	M	1074	0	1157	38	0
14	N	951	0	994	31	0
15	O	892	0	923	25	0
16	P	917	0	962	29	0
17	Q	947	0	1019	33	0
18	R	816	0	839	29	0
19	S	857	0	922	23	0
20	T	746	0	811	26	0
21	U	788	0	844	24	0
22	V	753	0	780	25	0
23	W	582	0	599	19	0
24	X	625	0	652	31	0
25	Y	501	0	531	17	0
26	Z	448	0	488	18	0
27	b	444	0	458	20	0
28	c	426	0	464	13	0
29	d	377	0	418	12	0
30	e	504	0	572	22	0
31	f	302	0	340	11	0
32	g	1760	0	1787	35	0
33	h	1636	0	1710	49	0
34	i	1643	0	1707	52	0
35	j	1152	0	1196	41	0
36	k	848	0	846	25	0
37	l	1181	0	1238	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	979	0	1031	31	0
39	n	1022	0	1070	44	0
40	o	790	0	831	44	0
41	p	877	0	887	22	0
42	q	957	0	1017	40	0
43	r	900	0	965	31	0
44	s	805	0	844	31	0
45	t	714	0	734	9	0
46	u	649	0	666	16	0
47	v	648	0	691	25	0
48	w	544	0	560	8	0
49	x	663	0	688	25	0
50	y	669	0	719	26	0
51	z	589	0	629	11	0
52	4	184	0	95	3	0
53	7	2793	0	2693	88	0
54	5	1627	0	831	32	0
55	6	32	0	28	9	0
56	1	1	0	0	0	0
56	2	1	0	0	0	0
56	3	8	0	0	0	0
56	b	1	0	0	0	0
56	i	1	0	0	0	0
57	f	1	0	0	0	0
All	All	146620	0	99148	3086	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 19.

The worst 5 of 3086 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:782:A:N3	4:B:225:MET:HG2	1.59	1.18
2:2:1146:A:O2'	2:2:1147:C:H6	1.28	1.16
2:2:1146:A:O2'	2:2:1147:C:C6	1.98	1.15
2:2:4:U:H3'	2:2:5:U:H5''	1.30	1.11
1:1:780:G:H2'	1:1:782:A:N7	1.67	1.08

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	
4	B	269/271 (99%)	243 (90%)	25 (9%)	1 (0%)	30	66
5	C	207/209 (99%)	197 (95%)	9 (4%)	1 (0%)	24	62
6	D	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
7	E	175/177 (99%)	157 (90%)	18 (10%)	0	100	100
8	F	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
9	G	147/149 (99%)	130 (88%)	17 (12%)	0	100	100
10	J	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
11	K	121/123 (98%)	112 (93%)	9 (7%)	0	100	100
12	L	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
13	M	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
14	N	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
15	O	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
16	P	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
19	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
20	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
21	U	101/103 (98%)	86 (85%)	15 (15%)	0	100	100
22	V	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
23	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
24	X	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
25	Y	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
26	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
27	b	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
28	c	50/52 (96%)	48 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	e	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7	37
31	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
32	g	223/225 (99%)	205 (92%)	18 (8%)	0	100	100
33	h	206/208 (99%)	194 (94%)	12 (6%)	0	100	100
34	i	203/205 (99%)	193 (95%)	10 (5%)	0	100	100
35	j	154/156 (99%)	138 (90%)	16 (10%)	0	100	100
36	k	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
37	l	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
38	m	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
39	n	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
40	o	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
41	p	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
42	q	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
43	r	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
44	s	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
45	t	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
46	u	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
47	v	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
48	w	64/66 (97%)	64 (100%)	0	0	100	100
49	x	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
50	y	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
51	z	68/70 (97%)	62 (91%)	6 (9%)	0	100	100
53	7	348/362 (96%)	326 (94%)	21 (6%)	1 (0%)	36	71
55	6	1/3 (33%)	1 (100%)	0	0	100	100
All	All	5893/6006 (98%)	5480 (93%)	409 (7%)	4 (0%)	49	82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	225	MET
53	7	315	SER
5	C	152	PRO

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Mol	Chain	Res	Type
30	e	32	ILE

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	
4	B	216/216 (100%)	215 (100%)	1 (0%)	81	81
5	C	164/164 (100%)	163 (99%)	1 (1%)	78	80
6	D	165/165 (100%)	165 (100%)	0	100	100
7	E	148/148 (100%)	148 (100%)	0	100	100
8	F	136/136 (100%)	136 (100%)	0	100	100
9	G	114/114 (100%)	113 (99%)	1 (1%)	70	75
10	J	116/116 (100%)	116 (100%)	0	100	100
11	K	104/104 (100%)	104 (100%)	0	100	100
12	L	103/103 (100%)	102 (99%)	1 (1%)	68	75
13	M	109/109 (100%)	109 (100%)	0	100	100
14	N	99/99 (100%)	99 (100%)	0	100	100
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	98 (99%)	1 (1%)	68	75
17	Q	89/89 (100%)	89 (100%)	0	100	100
18	R	84/84 (100%)	82 (98%)	2 (2%)	43	63
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	81/81 (100%)	81 (100%)	0	100	100
21	U	84/84 (100%)	84 (100%)	0	100	100
22	V	78/78 (100%)	77 (99%)	1 (1%)	61	71
23	W	58/58 (100%)	58 (100%)	0	100	100
24	X	67/67 (100%)	66 (98%)	1 (2%)	57	70
25	Y	54/54 (100%)	54 (100%)	0	100	100
26	Z	48/48 (100%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	b	47/47 (100%)	47 (100%)	0	100	100
28	c	47/47 (100%)	47 (100%)	0	100	100
29	d	38/38 (100%)	38 (100%)	0	100	100
30	e	51/51 (100%)	51 (100%)	0	100	100
31	f	34/34 (100%)	34 (100%)	0	100	100
32	g	187/187 (100%)	187 (100%)	0	100	100
33	h	171/171 (100%)	170 (99%)	1 (1%)	78	80
34	i	172/172 (100%)	172 (100%)	0	100	100
35	j	119/119 (100%)	119 (100%)	0	100	100
36	k	91/91 (100%)	91 (100%)	0	100	100
37	l	124/124 (100%)	123 (99%)	1 (1%)	73	77
38	m	104/104 (100%)	104 (100%)	0	100	100
39	n	105/105 (100%)	104 (99%)	1 (1%)	68	75
40	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
41	p	90/90 (100%)	90 (100%)	0	100	100
42	q	102/102 (100%)	102 (100%)	0	100	100
43	r	94/94 (100%)	94 (100%)	0	100	100
44	s	83/83 (100%)	83 (100%)	0	100	100
45	t	76/76 (100%)	76 (100%)	0	100	100
46	u	65/65 (100%)	65 (100%)	0	100	100
47	v	74/74 (100%)	74 (100%)	0	100	100
48	w	57/57 (100%)	57 (100%)	0	100	100
49	x	72/72 (100%)	72 (100%)	0	100	100
50	y	65/65 (100%)	65 (100%)	0	100	100
51	z	60/60 (100%)	60 (100%)	0	100	100
53	7	301/308 (98%)	298 (99%)	3 (1%)	68	75
55	6	2/2 (100%)	0	2 (100%)	0	0
All	All	4912/4919 (100%)	4894 (100%)	18 (0%)	81	82

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	7	314	LYS

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Mol	Chain	Res	Type
55	6	79	PHE
55	6	78	PHE
24	X	10	LYS
53	7	239	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
42	q	5	ASN
43	r	14	HIS
49	x	52	HIS
17	Q	81	ASN
16	P	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	773 (26%)	14 (0%)
2	2	1532/1534 (99%)	394 (25%)	6 (0%)
3	3	119/120 (99%)	29 (24%)	0
52	4	8/9 (88%)	2 (25%)	0
54	5	75/76 (98%)	24 (32%)	1 (1%)
All	All	4636/4642 (99%)	1222 (26%)	21 (0%)

5 of 1222 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	G
1	1	10	A
1	1	23	G
1	1	33	C
1	1	34	U

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	210	C
2	2	516	PSU
54	5	17	U
2	2	1109	C

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Mol	Chain	Res	Type
2	2	496	A

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

40 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	MA6	2	1519	2	23,26,27	1.56	4 (17%)	33,38,41	2.86	12 (36%)
1	PSU	1	2580	1	18,21,22	1.13	3 (16%)	21,30,33	2.34	6 (28%)
54	H2U	5	20	54	18,21,22	3.31	5 (27%)	19,30,33	1.36	3 (15%)
54	4OC	5	32	54	20,23,24	3.02	8 (40%)	25,32,35	1.00	2 (8%)
1	PSU	1	2605	1	18,21,22	1.11	2 (11%)	21,30,33	2.16	5 (23%)
1	OMG	1	2251	54,1	23,26,27	2.37	7 (30%)	32,38,41	1.88	7 (21%)
1	PSU	1	2457	1	18,21,22	1.19	3 (16%)	21,30,33	2.05	6 (28%)
1	6MZ	1	2030	1	22,25,26	2.88	6 (27%)	29,36,39	4.69	14 (48%)
2	5MC	2	1407	2	19,22,23	3.69	8 (42%)	26,32,35	1.12	2 (7%)
1	PSU	1	746	1	18,21,22	1.11	2 (11%)	21,30,33	1.85	5 (23%)
1	PSU	1	1917	1	18,21,22	1.09	1 (5%)	21,30,33	2.08	4 (19%)
1	PSU	1	1911	1	18,21,22	1.06	1 (5%)	21,30,33	2.19	4 (19%)
2	4OC	2	1402	2	20,23,24	2.92	8 (40%)	25,32,35	1.31	3 (12%)
1	5MU	1	747	1	19,22,23	4.70	7 (36%)	27,32,35	4.06	10 (37%)
1	2MA	1	2503	1	22,25,26	3.63	9 (40%)	32,37,40	2.27	8 (25%)
2	2MG	2	966	2	23,26,27	2.97	7 (30%)	33,38,41	2.44	8 (24%)
1	2MG	1	1835	1	23,26,27	2.86	8 (34%)	33,38,41	2.16	10 (30%)
1	1MG	1	745	1	23,26,27	2.76	6 (26%)	33,39,42	2.12	9 (27%)
2	5MC	2	967	2	19,22,23	3.72	8 (42%)	26,32,35	1.25	2 (7%)
54	5MU	5	54	54	19,22,23	4.82	7 (36%)	27,32,35	3.43	9 (33%)
2	MA6	2	1518	2	23,26,27	1.61	5 (21%)	33,38,41	2.65	12 (36%)
1	6MZ	1	1618	1	22,25,26	2.84	6 (27%)	29,36,39	4.37	11 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	1207	2	23,26,27	2.79	8 (34%)	33,38,41	2.61	13 (39%)
1	5MC	1	1962	1	19,22,23	3.56	8 (42%)	26,32,35	1.24	3 (11%)
1	PSU	1	2504	1	18,21,22	1.11	1 (5%)	21,30,33	1.97	4 (19%)
54	4SU	5	8	54	18,21,22	3.68	7 (38%)	25,30,33	2.20	5 (20%)
1	3TD	1	1915	1	19,22,23	4.31	5 (26%)	23,32,35	1.98	4 (17%)
1	G7M	1	2069	1	23,26,27	2.56	6 (26%)	34,39,42	2.52	12 (35%)
2	UR3	2	1498	2	19,22,23	2.39	6 (31%)	26,32,35	1.53	3 (11%)
2	G7M	2	527	2	23,26,27	3.54	10 (43%)	34,39,42	1.57	7 (20%)
42	0TD	q	89	42	8,9,10	1.47	0	6,11,13	3.05	3 (50%)
1	2MG	1	2445	1	23,26,27	2.89	6 (26%)	33,38,41	2.38	7 (21%)
1	OMC	1	2498	1	19,22,23	2.85	7 (36%)	25,31,34	0.89	0
54	PSU	5	55	54	18,21,22	1.18	1 (5%)	21,30,33	1.64	4 (19%)
1	5MU	1	1939	1	19,22,23	4.66	7 (36%)	27,32,35	3.98	10 (37%)
2	2MG	2	1516	2	23,26,27	2.98	7 (30%)	33,38,41	2.30	10 (30%)
2	PSU	2	516	2	18,21,22	1.04	2 (11%)	21,30,33	2.03	4 (19%)
1	PSU	1	955	1	18,21,22	1.00	1 (5%)	21,30,33	1.85	4 (19%)
1	OMU	1	2552	1	19,22,23	2.81	8 (42%)	25,31,34	2.10	5 (20%)
55	FME	6	77	55	8,9,10	0.70	0	8,9,11	1.27	1 (12%)

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	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
54	H2U	5	20	54	-	4/7/38/39	0/2/2/2
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	54,1	-	2/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	746	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4OC	2	1402	2	-	4/9/29/30	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1	-	3/7/25/26	0/3/3/3
2	2MG	2	966	2	-	3/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	1/11/29/30	0/3/3/3
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
54	4SU	5	8	54	-	4/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	0/7/25/26	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
42	0TD	q	89	42	-	3/7/12/14	-
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
1	OMC	1	2498	1	-	1/9/27/28	0/2/2/2
54	PSU	5	55	54	-	2/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
55	FME	6	77	55	-	2/7/9/11	-

The worst 5 of 211 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.54	1.50	1.35
54	5	54	5MU	C2-N1	11.31	1.56	1.38
1	1	1618	6MZ	C6-N6	10.94	1.46	1.34
1	1	2030	6MZ	C6-N6	10.82	1.46	1.34
1	1	2503	2MA	C4-N3	10.80	1.48	1.34

The worst 5 of 251 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2030	6MZ	C4-N9-C8	15.00	121.48	105.74
1	1	1618	6MZ	C4-N9-C8	13.24	119.64	105.74
1	1	747	5MU	C5-C4-N3	12.81	126.46	115.32
1	1	1939	5MU	C5-C4-N3	12.31	126.02	115.32
54	5	54	5MU	C5-C4-N3	11.65	125.44	115.32

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	q	89	0TD	CA-CB-SB-CSB
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

19 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1519	MA6	1	0
1	1	2580	PSU	2	0
54	5	32	4OC	2	0
1	1	2030	6MZ	1	0
2	2	1407	5MC	6	0
2	2	1402	4OC	3	0
1	1	747	5MU	1	0
1	1	2503	2MA	1	0
1	1	745	1MG	1	0
1	1	1962	5MC	1	0
1	1	2504	PSU	1	0
54	5	8	4SU	1	0
1	1	1915	3TD	1	0
2	2	527	G7M	2	0
42	q	89	0TD	3	0
54	5	55	PSU	1	0
2	2	1516	2MG	1	0
1	1	955	PSU	1	0
1	1	2552	OMU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 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.

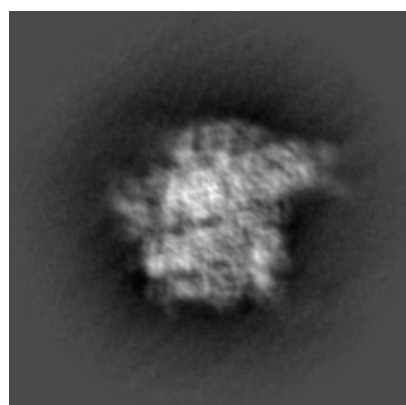
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20188. These allow visual inspection of the internal detail of the map and identification of artifacts.

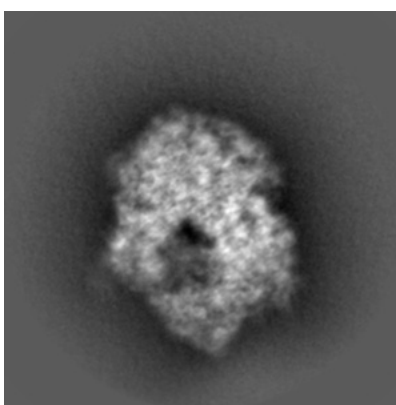
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

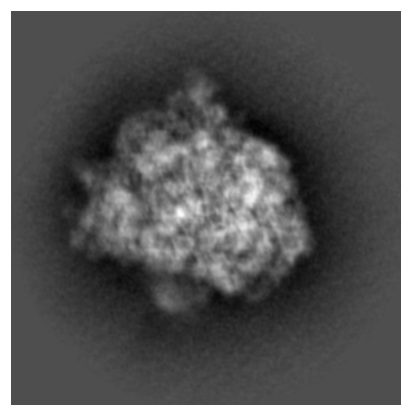
6.1.1 Primary map



X



Y

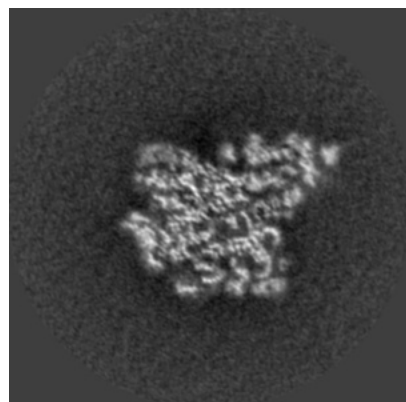


Z

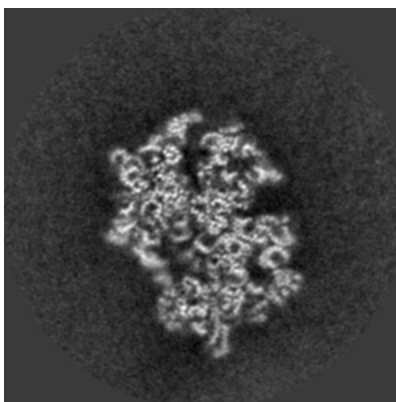
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

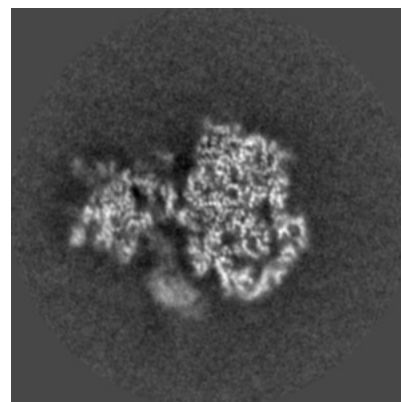
6.2.1 Primary map



X Index: 128



Y Index: 128

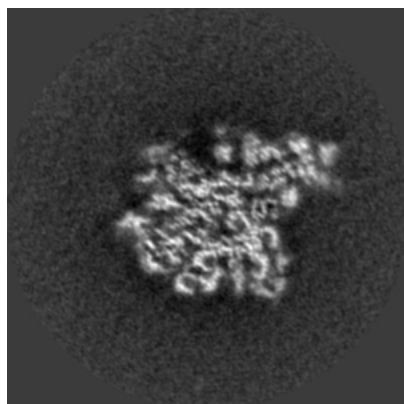


Z Index: 128

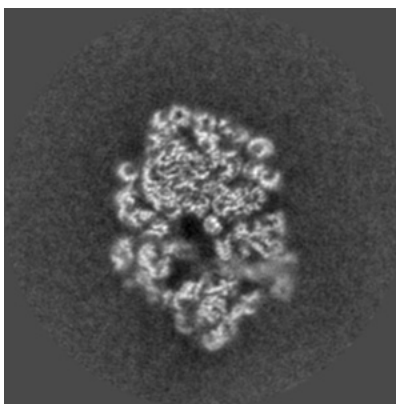
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

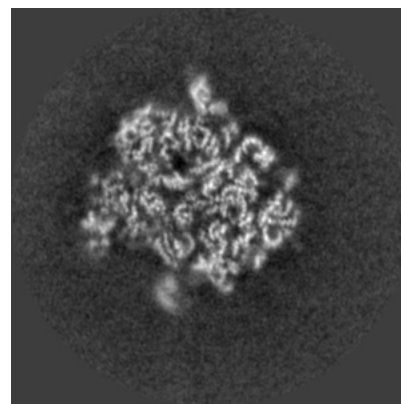
6.3.1 Primary map



X Index: 126



Y Index: 114

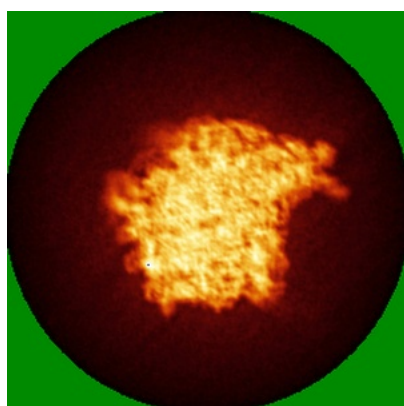


Z Index: 146

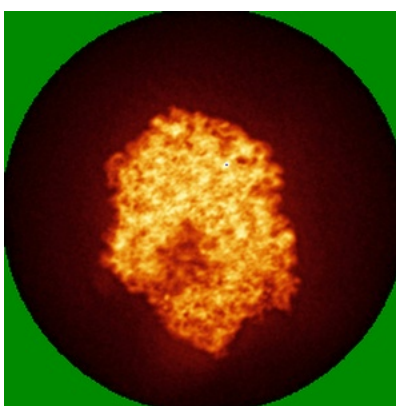
The images above show the largest variance slices of the map in three orthogonal directions.

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

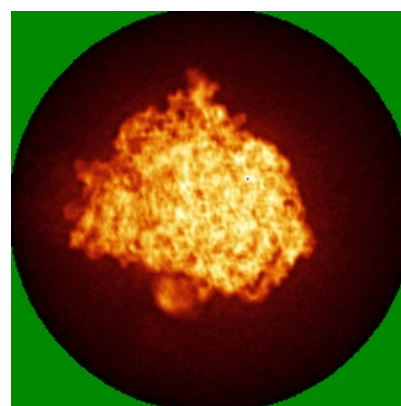
6.4.1 Primary map



X



Y

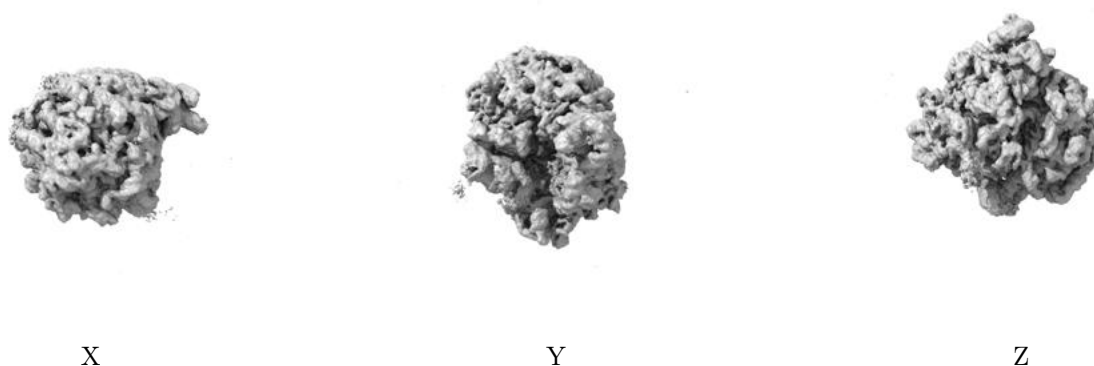


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

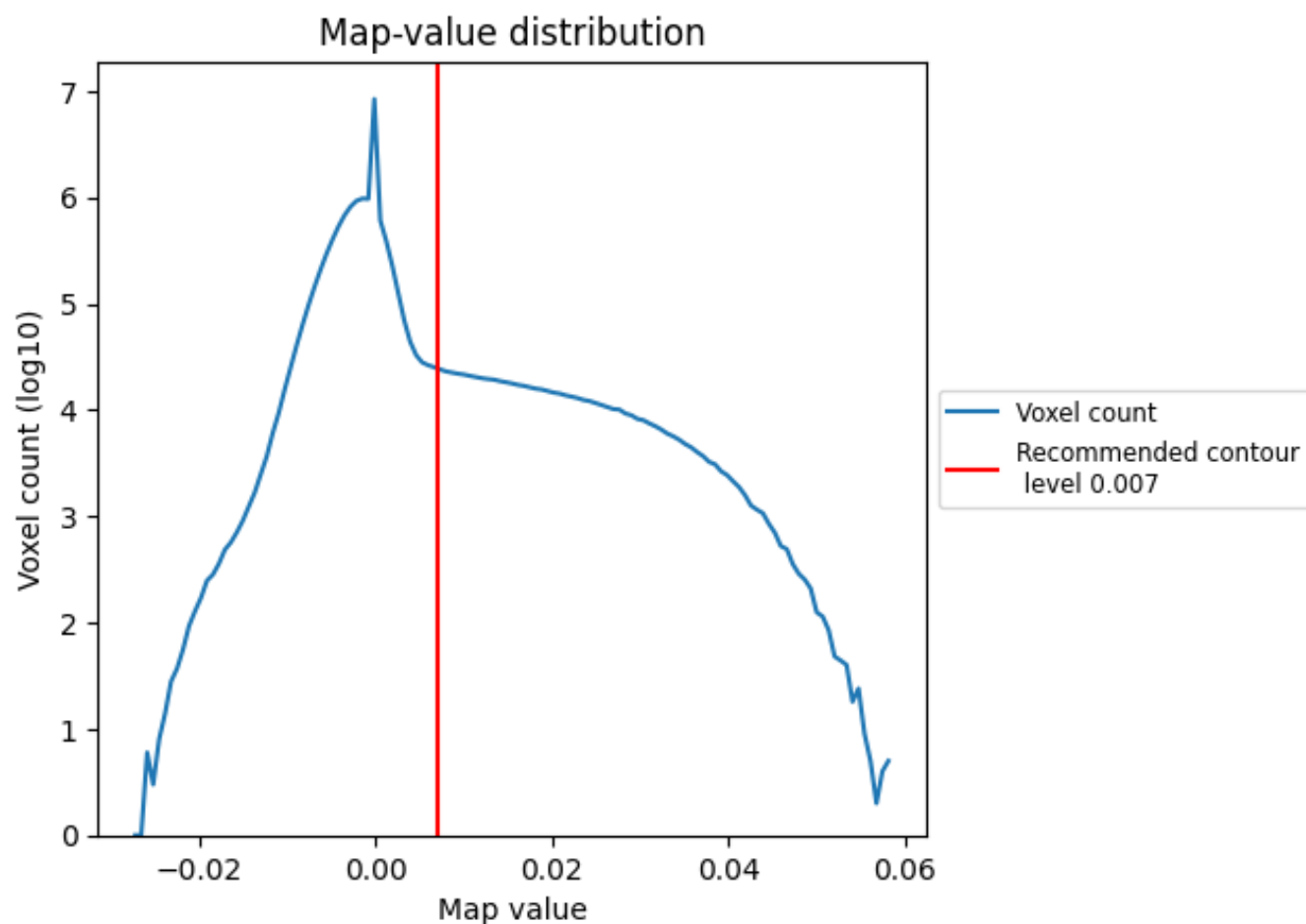
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

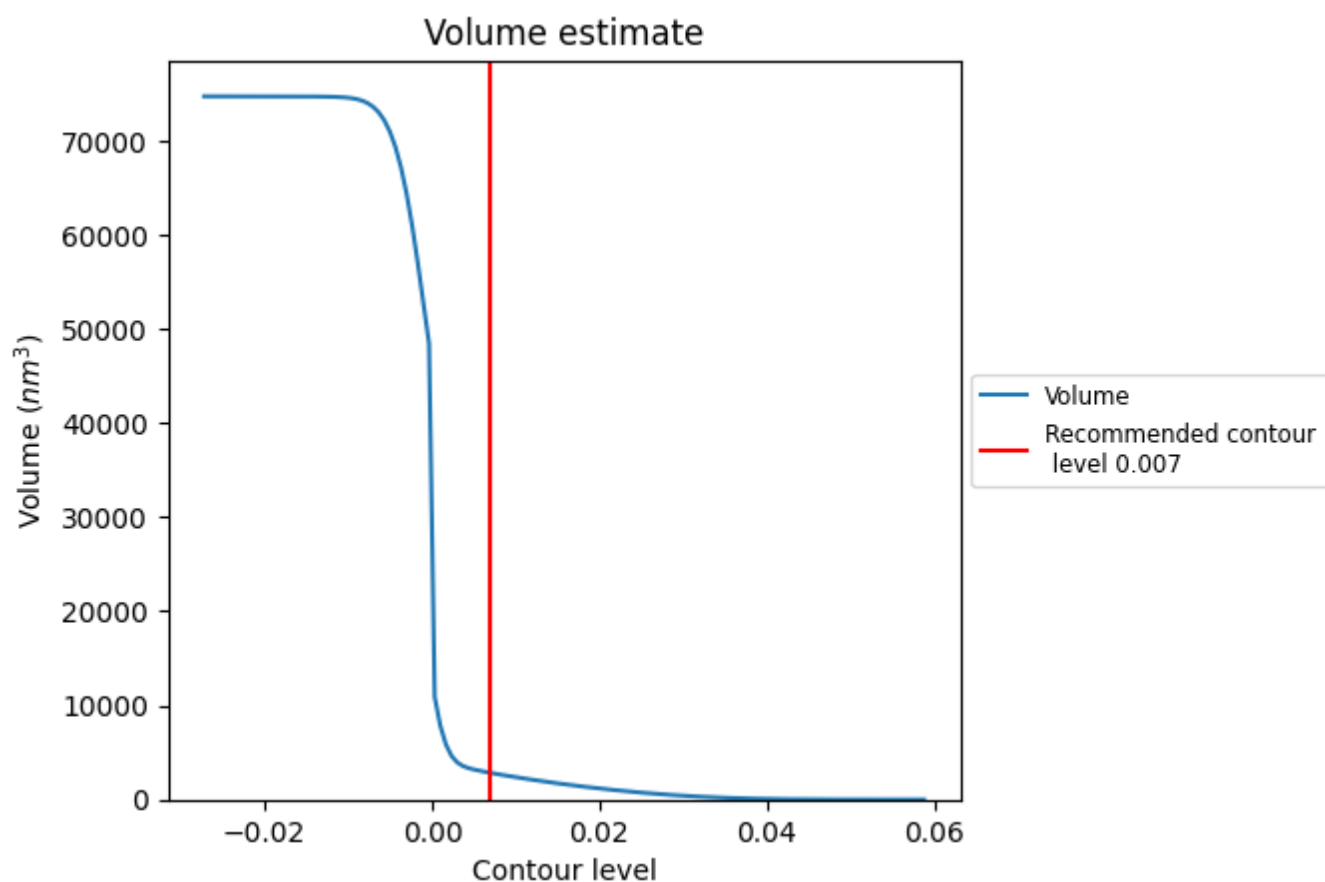
This section contains the results of statistical analysis of the map.

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.

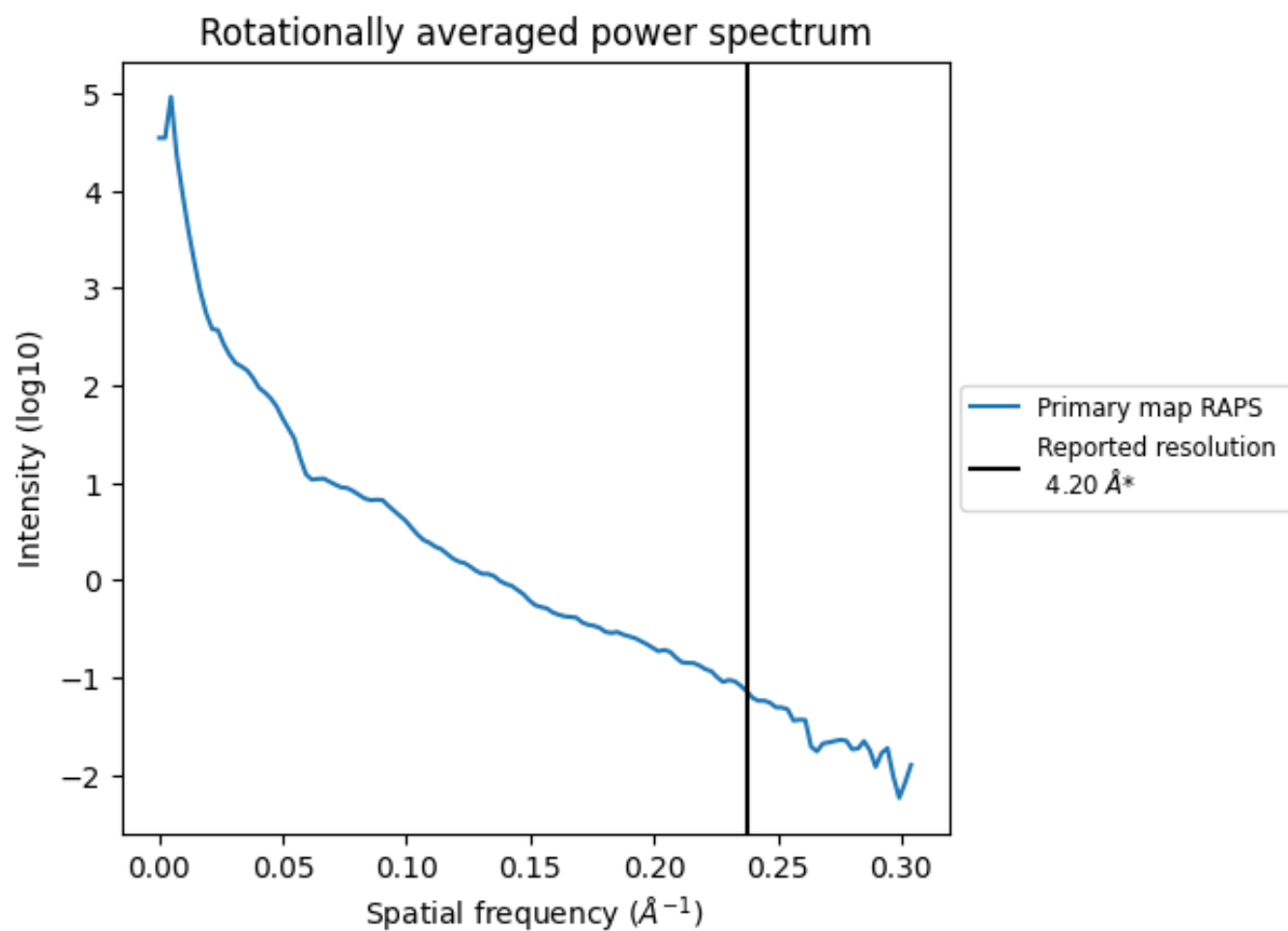
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2833 nm³; this corresponds to an approximate mass of 2559 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 0.238 Å⁻¹

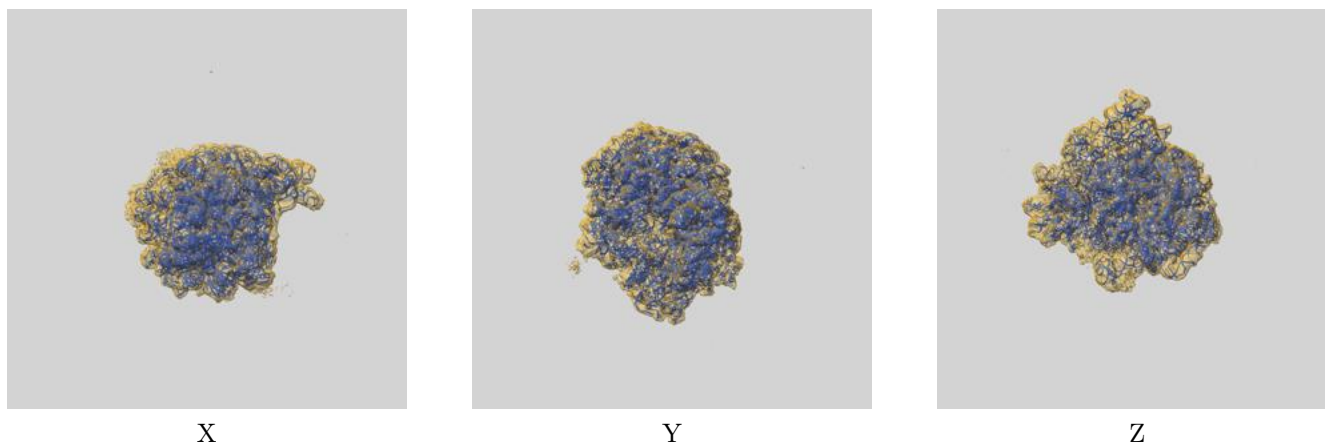
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

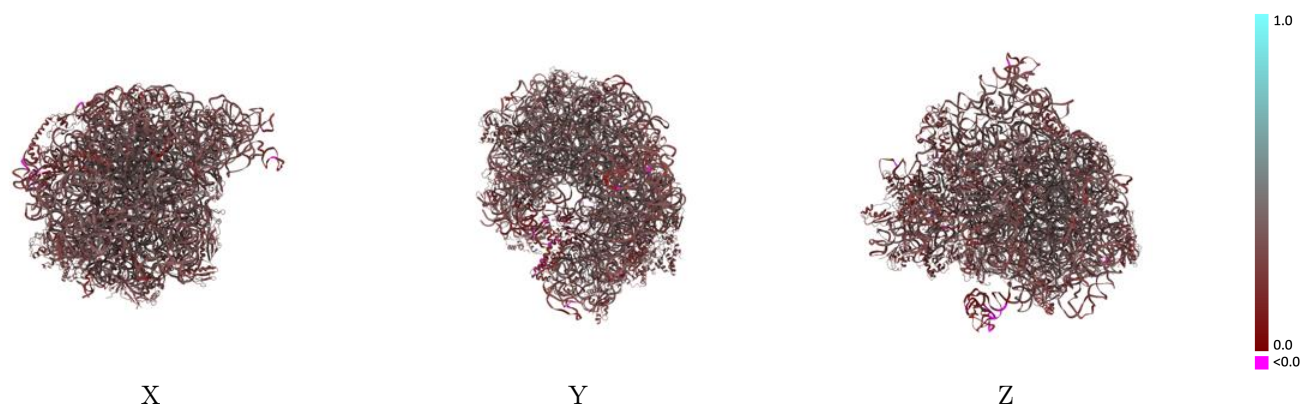
This section contains information regarding the fit between EMDB map EMD-20188 and PDB model 6OST. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



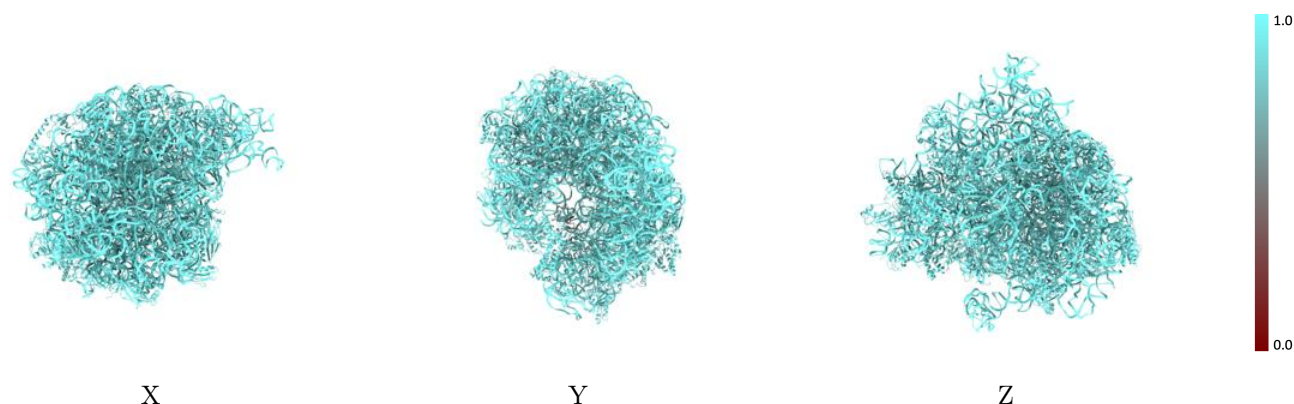
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



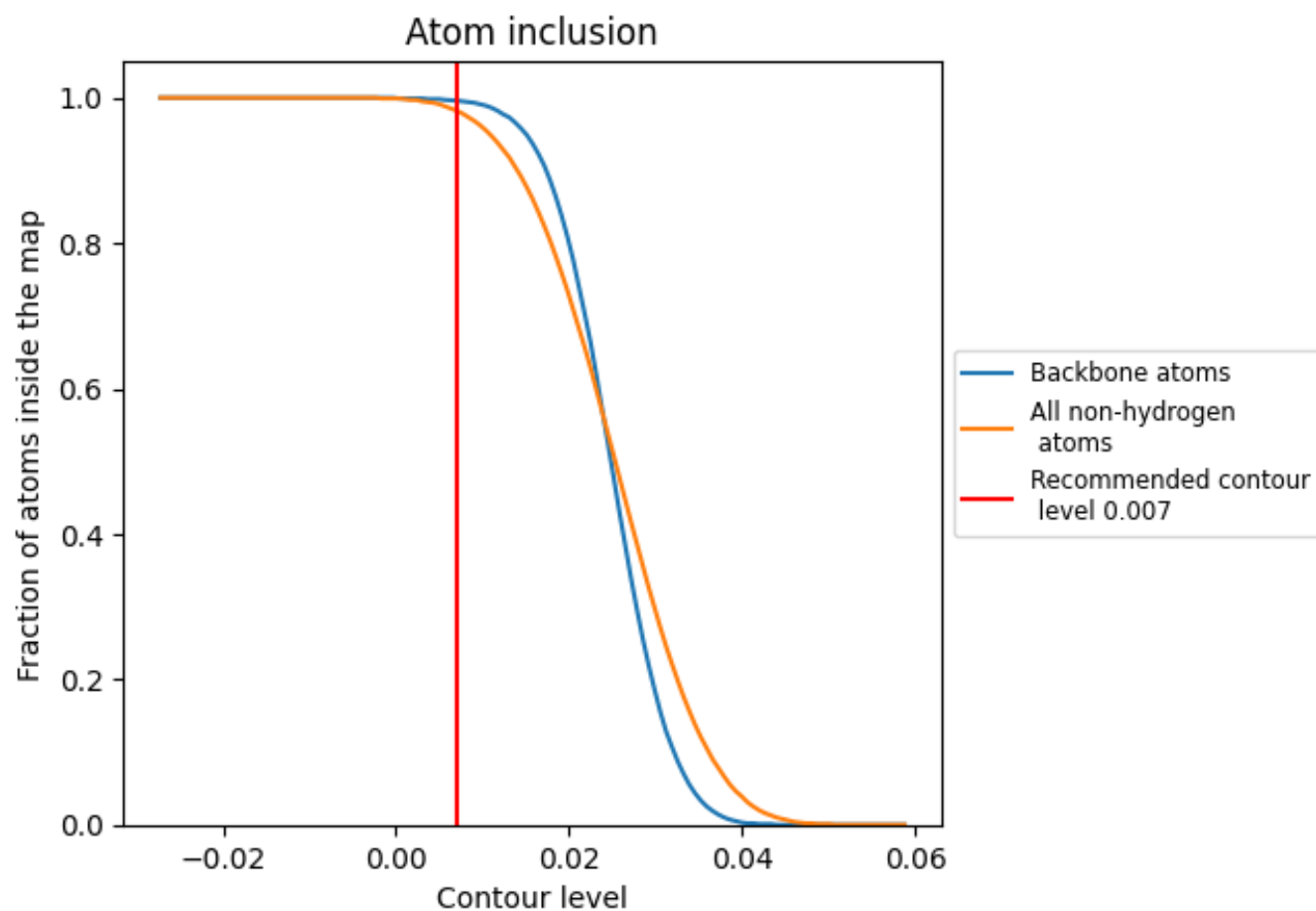
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9820	 0.3180
1	 0.9990	 0.3350
2	 0.9990	 0.3270
3	 1.0000	 0.3160
4	 0.9950	 0.3570
5	 0.9370	 0.2620
6	 0.7190	 0.1580
7	 0.8320	 0.1740
B	 0.9410	 0.3420
C	 0.9580	 0.3320
D	 0.9670	 0.3170
E	 0.9590	 0.2570
F	 0.9750	 0.2860
G	 0.9280	 0.2500
J	 0.9580	 0.3140
K	 0.9350	 0.3410
L	 0.9820	 0.3300
M	 0.9660	 0.3260
N	 0.9870	 0.3080
O	 0.9800	 0.2910
P	 0.9640	 0.3360
Q	 0.9650	 0.2790
R	 0.9670	 0.3250
S	 0.9450	 0.3330
T	 0.9510	 0.3130
U	 0.9870	 0.2940
V	 0.9850	 0.3050
W	 0.9630	 0.3140
X	 0.9480	 0.2990
Y	 0.9780	 0.2440
Z	 0.9630	 0.3160
b	 0.9720	 0.3160
c	 0.9640	 0.3100
d	 0.9520	 0.3280
e	 0.9310	 0.3200



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Chain	Atom inclusion	Q-score
f	 0.9760	 0.3020
g	 0.9350	 0.2730
h	 0.9250	 0.2980
i	 0.9690	 0.2670
j	 0.9510	 0.3080
k	 0.9300	 0.2770
l	 0.9440	 0.2730
m	 0.9570	 0.3140
n	 0.9770	 0.2750
o	 0.9390	 0.2790
p	 0.9310	 0.3070
q	 0.8960	 0.3160
r	 0.9370	 0.2600
s	 0.9630	 0.2830
t	 0.9520	 0.2850
u	 0.9840	 0.3230
v	 0.9640	 0.2900
w	 0.9500	 0.2820
x	 0.9610	 0.2750
y	 0.9600	 0.2660
z	 0.8770	 0.2590