wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 08:21 PM EDT

PDB ID	:	6OT3 / pdb_00006ot3
EMDB ID	:	EMD-20193
Title	:	RF2 accommodated state bound Release complex 70S at 24 ms
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	:	3.90 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:

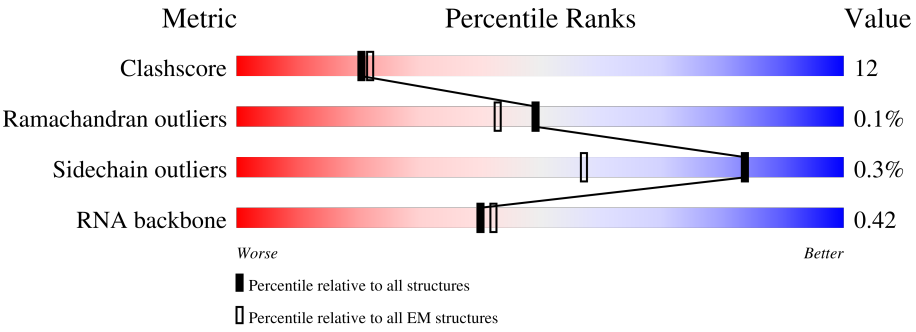
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

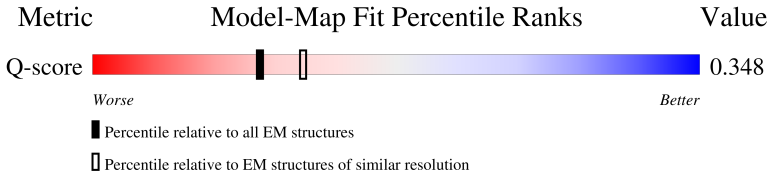
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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 <=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	54% 36% 10%
2	2	1534	51% 40% 8%
3	3	120	61% 32% 8%

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Mol	Chain	Length	Quality of chain
4	4	9	78% 11% 11%
5	B	271	75% 25%
6	C	209	75% 24%
7	D	201	78% 22%
8	E	177	74% 26%
9	F	175	79% 21%
10	G	149	70% 30%
11	J	142	89% 11%
12	K	123	78% 22%
13	L	144	83% 17%
14	M	136	82% 18%
15	N	119	65% 34%
16	O	116	77% 23%
17	P	114	76% 24%
18	Q	117	76% 24%
19	R	103	67% 31%
20	S	110	81% 19%
21	T	94	78% 22%
22	U	103	75% 25%
23	V	94	73% 27%
24	W	76	74% 26%
25	X	77	71% 29%
26	Y	62	77% 23%
27	Z	58	72% 28%
28	a	66	73% 27%

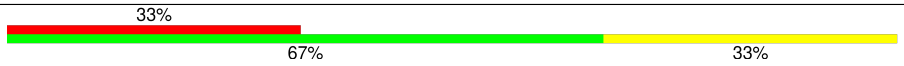
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Mol	Chain	Length	Quality of chain
29	b	56	
30	c	52	
31	d	46	
32	e	64	
33	f	38	
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	87	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	

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Mol	Chain	Length	Quality of chain
54	5	76	
55	A	357	
56	6	3	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 146899 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
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

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

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

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

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

- Molecule 4 is a RNA chain called mRNA.

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

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

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

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

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

- Molecule 27 is a protein called 50S ribosomal protein L30.

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

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

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

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

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

- Molecule 35 is a protein called 30S ribosomal protein S3.

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

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

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

- Molecule 38 is a protein called 30S ribosomal protein S6.

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

- Molecule 39 is a protein called 30S ribosomal protein S7.

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

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

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

- Molecule 42 is a protein called 30S ribosomal protein S10.

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

- Molecule 43 is a protein called 30S ribosomal protein S11.

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

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	87	Total 673	C 417	N 137	O 116	S 3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S13.

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

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

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

- Molecule 49 is a protein called 30S ribosomal protein S17.

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

- Molecule 50 is a protein called 30S ribosomal protein S18.

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

- Molecule 51 is a protein called 30S ribosomal protein S19.

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

- Molecule 52 is a protein called 30S ribosomal protein S20.

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

- Molecule 53 is a protein called 30S ribosomal protein S21.

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

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

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

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A	357	Total 2833	C 1742	N 498	O 583	S 10	0	0

- Molecule 56 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	1	2	Total	Mg	0
			2	2	
57	2	1	Total	Mg	0
			1	1	
57	3	8	Total	Mg	0
			8	8	
57	i	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

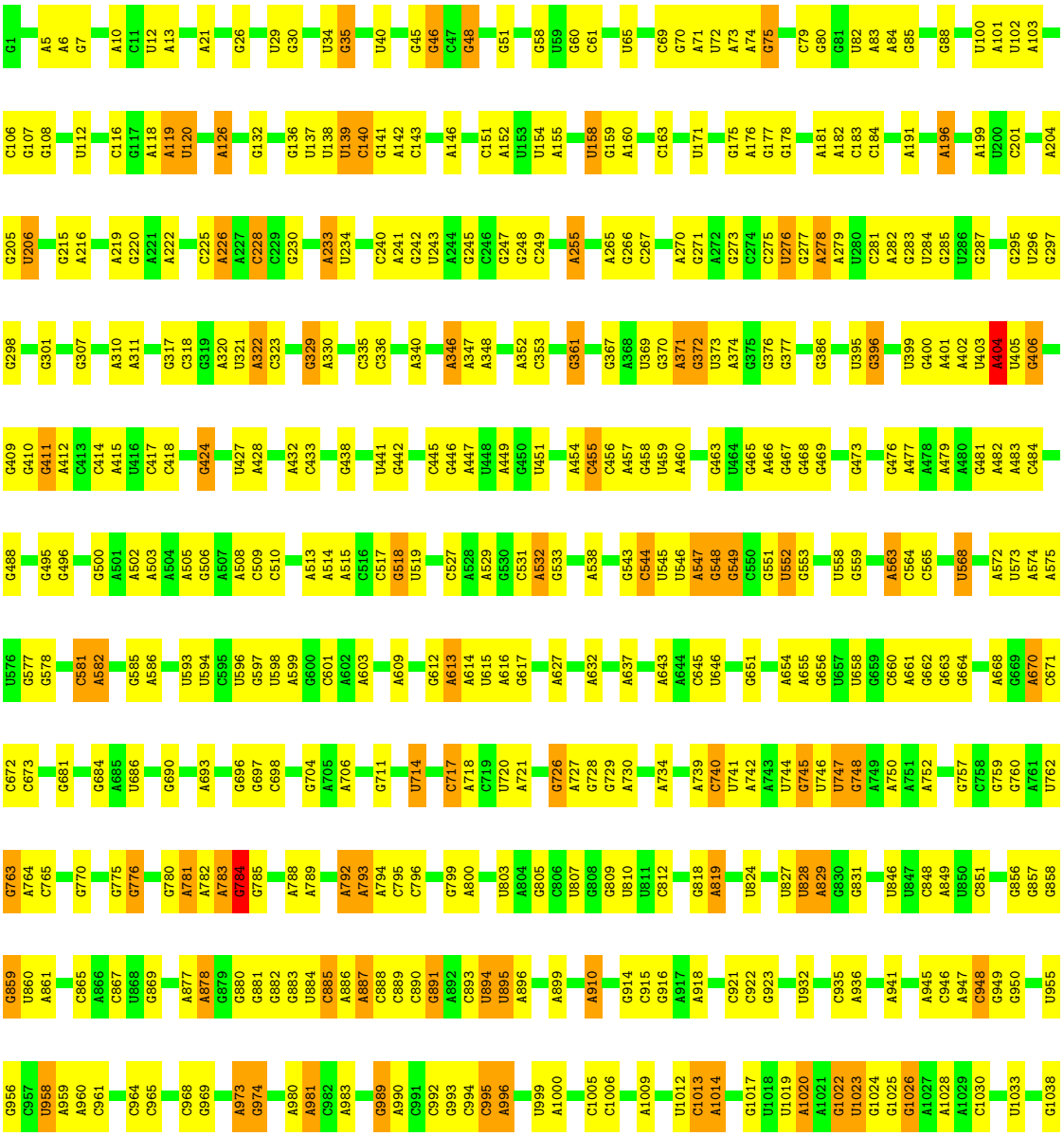
3 Residue-property plots (i)

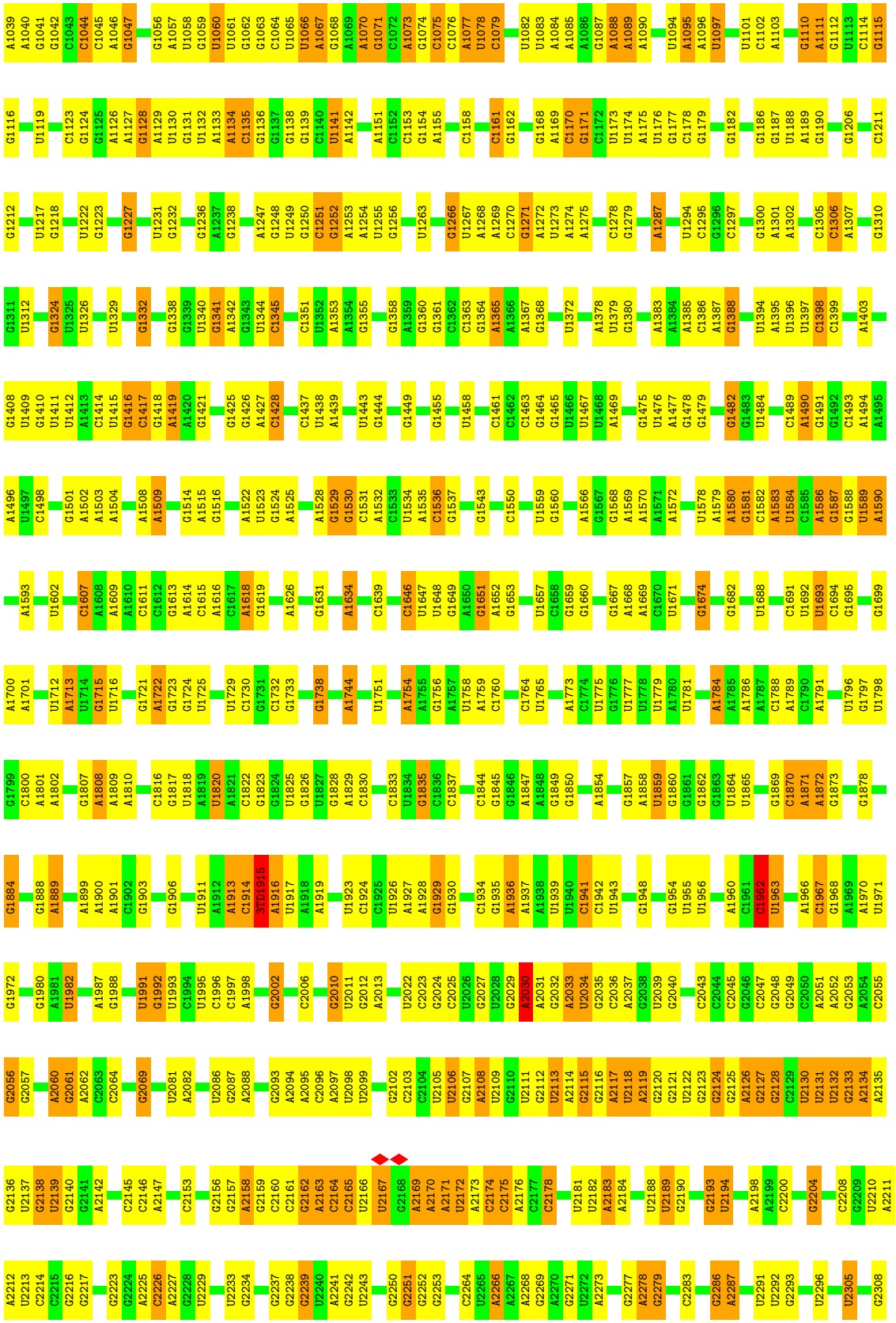
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

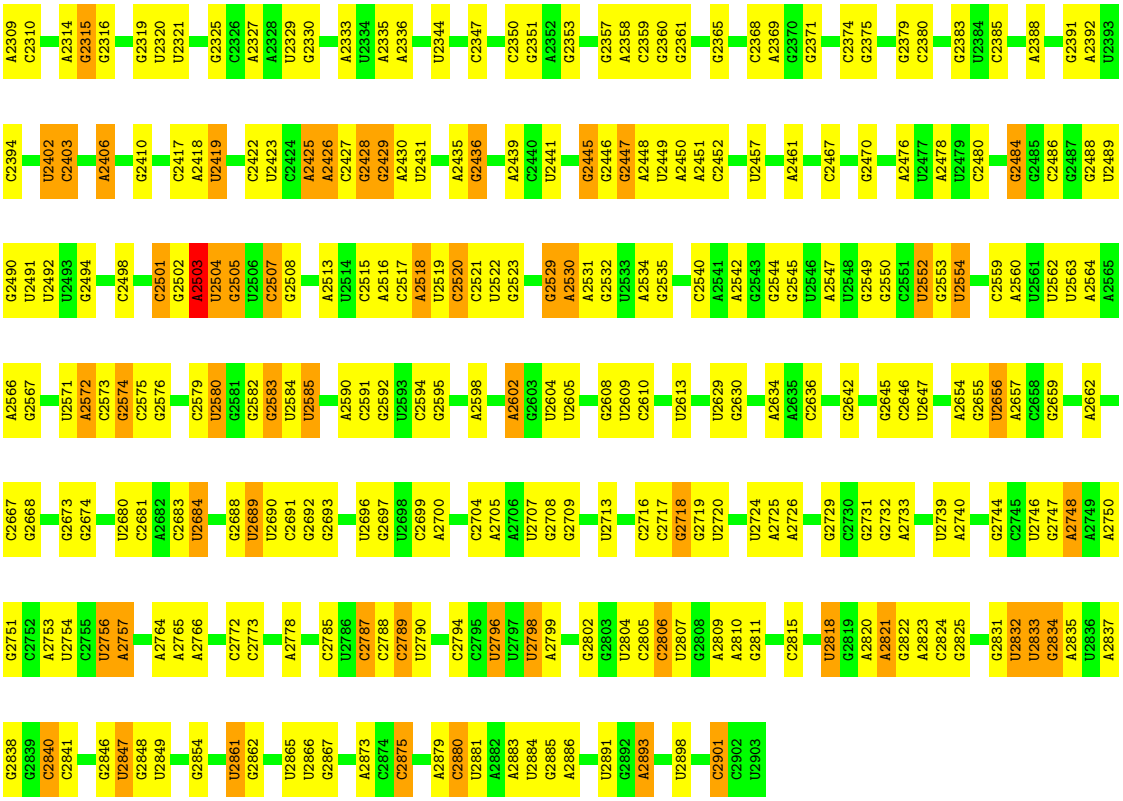
- Molecule 1: 23S ribosomal RNA

Chain 1:





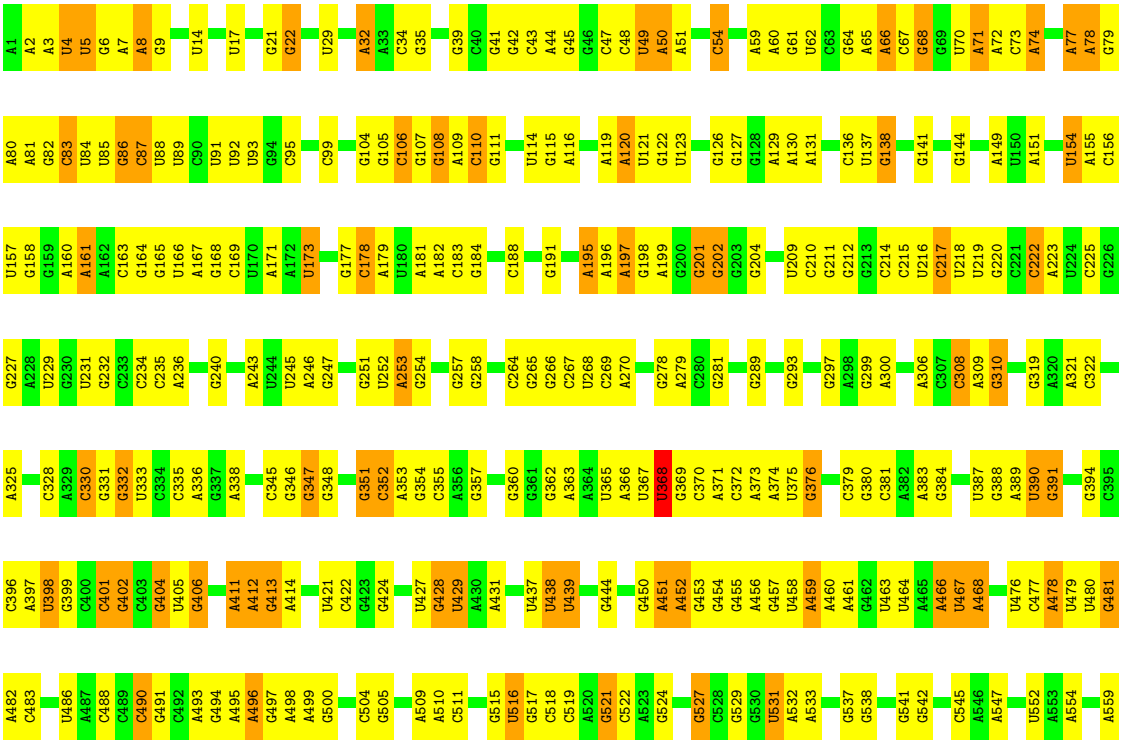

A1039 A1040 G1041 G1042 C1043 C1044 C1045 A1046 G1047 G1056 A1057 U1058 G1059 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075 C1076 A1077 U1078 C1079 U1082 U1083 A1084 A1085 A1086 G1087 A1088 A1089 A1090 U1094 A1095 A1096 U1097 U1101 C1102 A1103 G1110 A1111 G1112 U1113 C1114 G1115
G1116 U1119 C1123 G1124 G1125 A1126 A1127 G1128 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 G1138 G1139 C1140 U1141 A1142 A1151 C1152 C1153 G1154 A1155 C1158 C1161 G1162 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 G1182 G1186 G1187 U1188 A1189 G1190 G1206 C1211
G1212 U1217 G1218 U1222 G1223 G1227 U1231 G1232 G1236 A1237 G1238 A1247 G1248 U1249 G1250 C1251 G1252 A1253 A1254 U1255 G1256 U1263 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1274 A1275 C1278 G1279 A1287 U1294 C1295 G1296 C1297 G1300 A1301 A1302 C1305 C1306 A1307 G1310
G1311 U1312 G1324 U1325 U1326 U1329 G1332 G1338 G1339 U1340 G1341 A1342 G1343 U1344 C1345 C1351 U1352 A1353 A1354 G1355 G1358 A1359 G1360 G1361 C1362 C1363 G1364 A1365 A1366 A1367 G1368 U1372 A1378 U1379 G1380 A1383 A1384 A1385 C1386 A1387 G1388 U1394 A1395 U1396 U1397 C1398 C1399 A1403
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A1496 U1497 C1498 G1501 A1502 A1503 A1504 A1508 A1509 G1514 A1515 G1516 A1522 U1523 G1524 A1525 A1528 G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1543 C1550 U1559 G1560 A1566 G1567 G1568 A1569 A1570 A1571 A1572 U1578 A1579 A1580 G1581 C1582 A1583 U1584 C1585 A1586 G1587 G1588 U1589 A1590
A1593 U1602 C1607 A1608 A1609 A1610 C1611 C1612 G1613 A1614 C1615 A1616 C1617 A1618 G1619 A1626 G1631 A1634 C1639 C1646 U1647 U1648 G1649 A1650 G1651 A1652 G1653 U1657 C1658 G1659 G1660 G1667 A1668 A1669 C1670 U1671 G1674 G1682 U1688 C1691 U1692 U1693 C1694 G1695 G1699
A1700 A1701 U1712 A1713 U1714 G1715 U1716 G1721 A1722 G1723 G1724 U1725 U1729 C1730 C1731 C1732 G1733 G1738 A1744 U1751 A1754 A1755 G1756 A1757 U1758 A1759 C1760 C1764 U1765 A1773 C1774 U1775 G1776 U1777 U1778 U1779 A1780 U1781 A1784 A1785 A1786 A1787 C1788 A1789 C1790 A1791 U1796 G1797 U1798
G1799 C1800 A1801 A1802 G1807 A1808 A1809 A1810 C1816 G1817 U1818 A1819 U1820 A1821 C1822 G1823 G1824 U1825 G1826 U1827 G1828 A1829 C1830 C1833 U1834 G1835 C1836 C1837 C1844 G1845 G1846 A1847 A1848 G1849 G1850 A1854 G1857 A1858 U1859 G1860 G1861 G1862 G1863 U1864 U1865 G1869 C1870 A1871 A1872 G1873 G1878
G1884 G1888 A1889 A1899 A1900 A1901 C1902 G1903 G1906 U1911 A1912 A1913 C1914 3TD1915 A1916 U1917 A1918 A1919 U1923 C1924 C1925 U1926 A1927 A1928 G1929 G1930 C1934 G1935 A1936 A1937 A1938 U1939 U1940 C1941 C1942 U1943 G1948 G1954 U1955 U1956 A1960 C1961 C1962 U1963 A1966 C1967 G1968 A1969 A1970 U1971
G1972 G1980 A1981 U1982 A1987 G1988 U1991 G1992 U1993 C1994 U1995 C1996 C1997 A1998 G2002 C2006 G2010 U2011 G2012 A2013 U2022 C2023 G2024 C2025 U2026 G2027 U2028 G2029 A2030 A2031 G2032 A2033 U2034 G2035 C2036 A2037 G2038 U2039 G2040 C2043 C2044 C2045 G2046 C2047 G2048 G2049 C2050 A2051 A2052 G2053 A2054 C2055
G2056 G2057 A2060 G2061 A2062 C2063 C2064 G2069 U2081 A2082 U2086 G2087 A2088 G2093 A2094 A2095 C2096 A2097 U2098 U2099 G2102 C2103 C2104 U2105 U2106 C2107 A2108 U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135
G2136 U2137 G2138 U2139 G2140 G2141 A2142 C2145 C2146 A2147 C2153 G2156 G2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 U2181 U2182 A2183 A2184 U2188 U2189 G2190 G2193 U2194 A2198 A2199 C2200 G2204 C2208 G2209 U2210 A2211
A2212 U2213 C2214 C2215 G2216 G2217 G2223 G2224 A2225 C2226 A2227 G2228 U2229 U2233 G2234 G2237 G2238 G2239 U2240 A2241 G2242 U2243 G2250 G2251 G2252 G2253 C2264 U2265 A2266 A2267 A2268 G2269 A2270 G2271 U2272 A2273 G2277 A2278 G2279 C2283 G2286 A2287 U2291 U2292 G2293 U2296 U2305 G2308

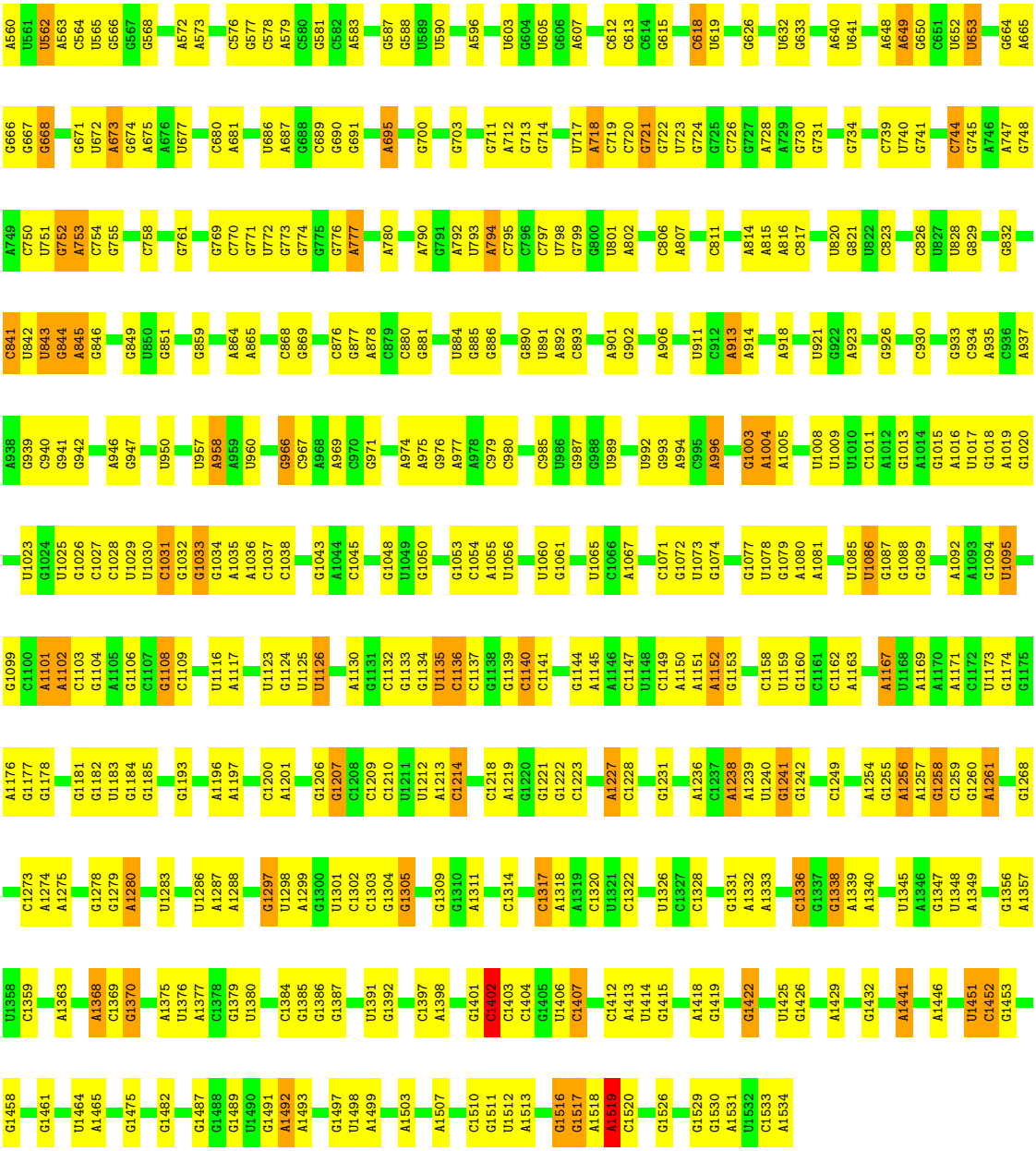


• Molecule 2: 16S ribosomal RNA

Chain 2:



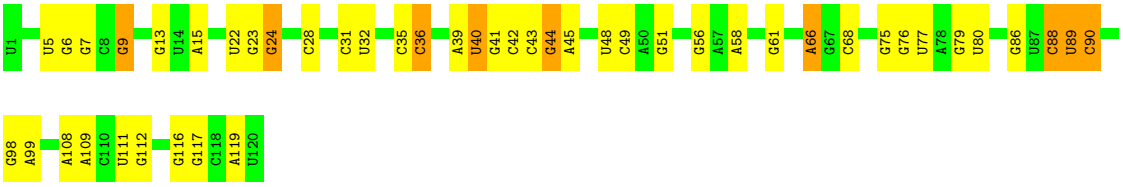




• Molecule 3: 5S ribosomal RNA

Chain 3:





• Molecule 4: mRNA

Chain 4:

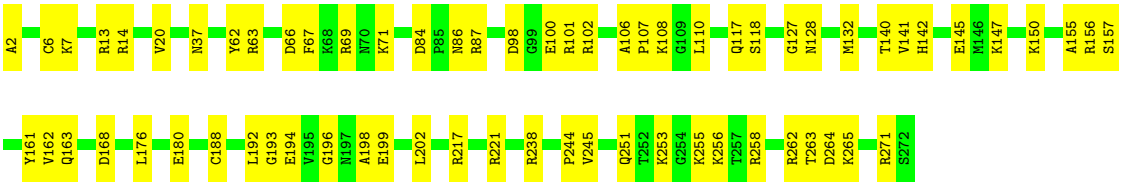




• Molecule 5: 50S ribosomal protein L2

Chain B:

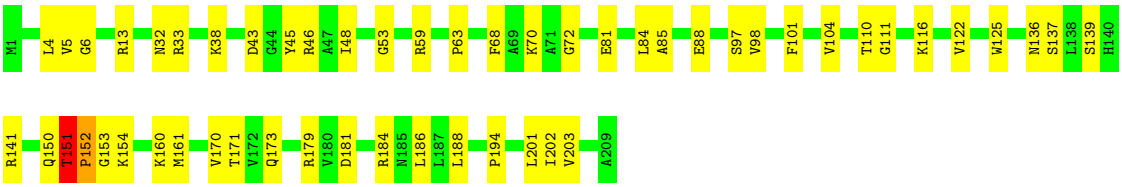




• Molecule 6: 50S ribosomal protein L3

Chain C:

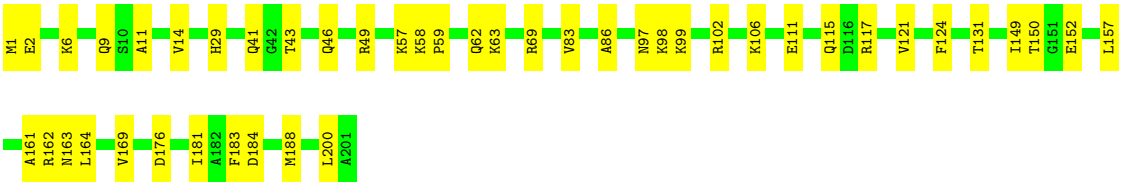




• Molecule 7: 50S ribosomal protein L4

Chain D:

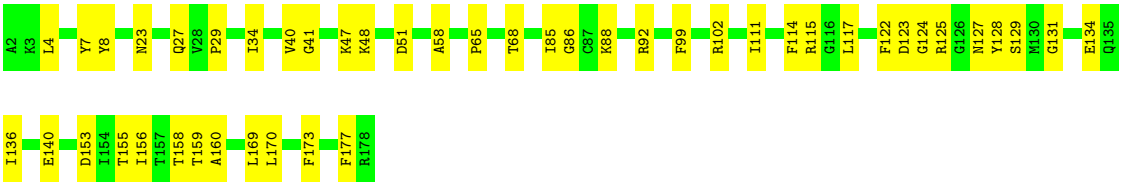




• Molecule 8: 50S ribosomal protein L5

Chain E:





• Molecule 9: 50S ribosomal protein L6

Chain F:





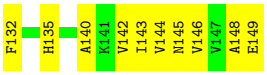


• Molecule 10: 50S ribosomal protein L9

Chain G:



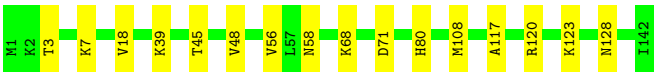




• Molecule 11: 50S ribosomal protein L13

Chain J:

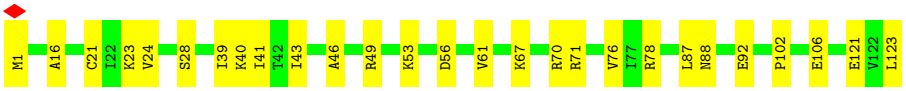




• Molecule 12: 50S ribosomal protein L14

Chain K:

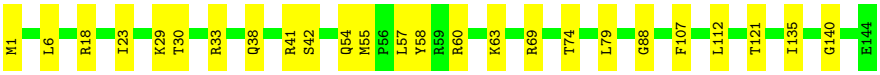




• Molecule 13: 50S ribosomal protein L15

Chain L:





• Molecule 14: 50S ribosomal protein L16

Chain M:

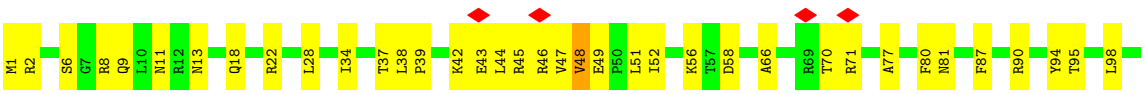


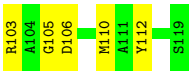


• Molecule 15: 50S ribosomal protein L17

Chain N:



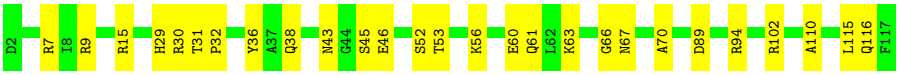




• Molecule 16: 50S ribosomal protein L18

Chain O:

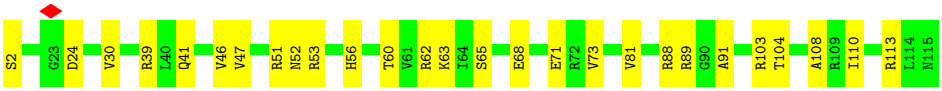




• Molecule 17: 50S ribosomal protein L19

Chain P:

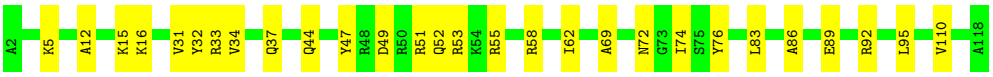




• Molecule 18: 50S ribosomal protein L20

Chain Q:

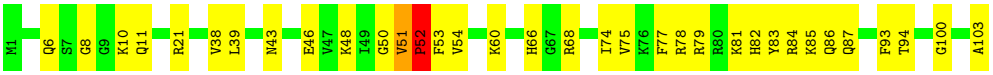




• Molecule 19: 50S ribosomal protein L21

Chain R:

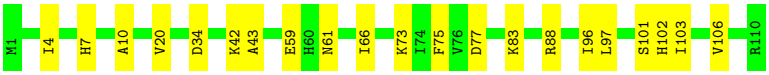




• Molecule 20: 50S ribosomal protein L22

Chain S:

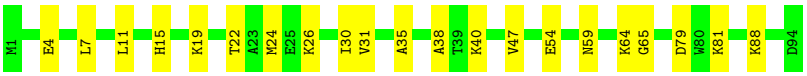




• Molecule 21: 50S ribosomal protein L23

Chain T:

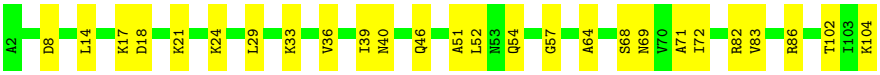




• Molecule 22: 50S ribosomal protein L24

Chain U:

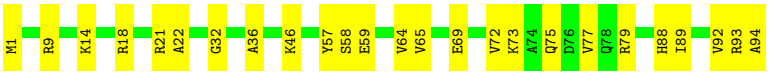




• Molecule 23: 50S ribosomal protein L25

Chain V:





• Molecule 24: 50S ribosomal protein L27

Chain W:

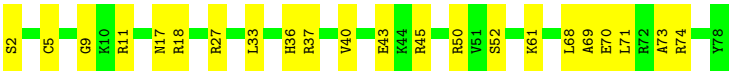




• Molecule 25: 50S ribosomal protein L28

Chain X:

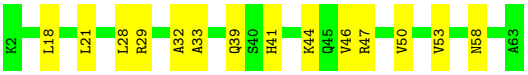




• Molecule 26: 50S ribosomal protein L29

Chain Y:





• Molecule 27: 50S ribosomal protein L30

Chain Z:

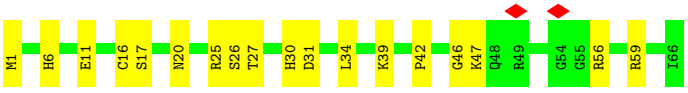




• Molecule 28: 50S ribosomal protein L31

Chain a:

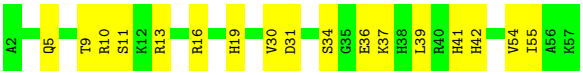




• Molecule 29: 50S ribosomal protein L32

Chain b:

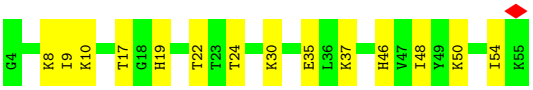




• Molecule 30: 50S ribosomal protein L33

Chain c:

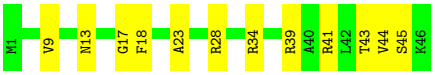




• Molecule 31: 50S ribosomal protein L34

Chain d:

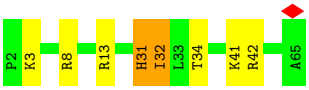




• Molecule 32: 50S ribosomal protein L35

Chain e:





• Molecule 33: 50S ribosomal protein L36

Chain f:

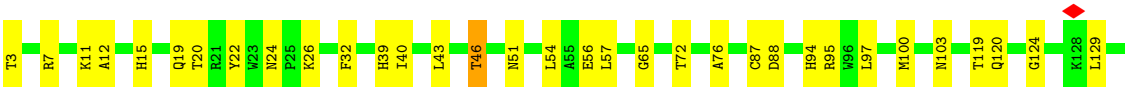


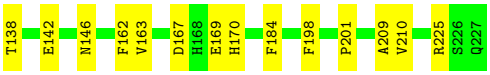


• Molecule 34: 30S ribosomal protein S2

Chain g:



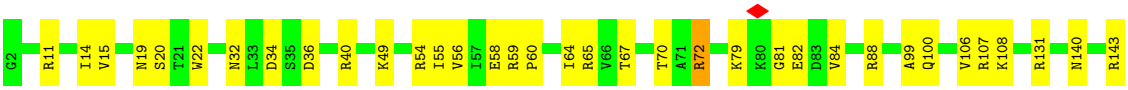




• Molecule 35: 30S ribosomal protein S3

Chain h:



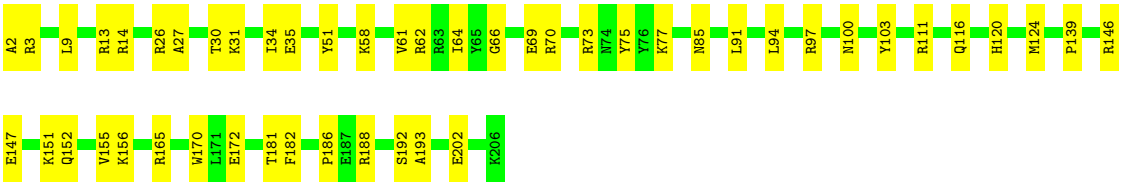




• Molecule 36: 30S ribosomal protein S4

Chain i:

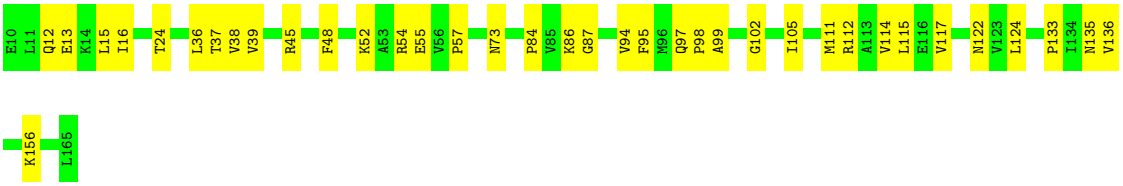




• Molecule 37: 30S ribosomal protein S5

Chain j:





• Molecule 38: 30S ribosomal protein S6

Chain k:

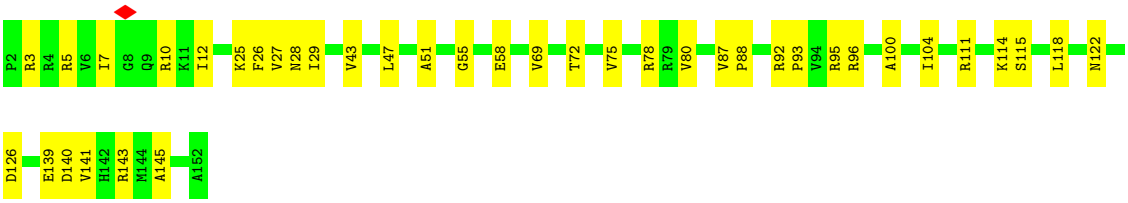




• Molecule 39: 30S ribosomal protein S7

Chain l:

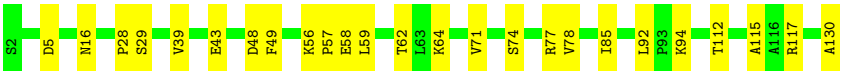




• Molecule 40: 30S ribosomal protein S8

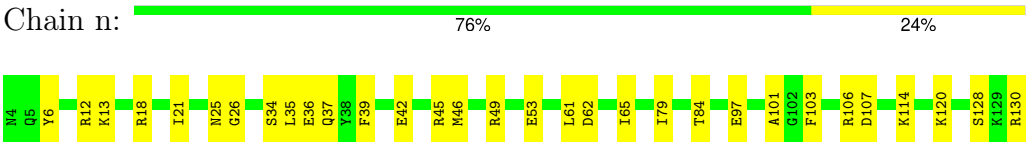
Chain m:





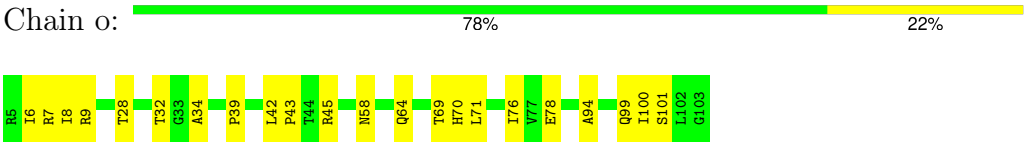
• Molecule 41: 30S ribosomal protein S9

Chain n:



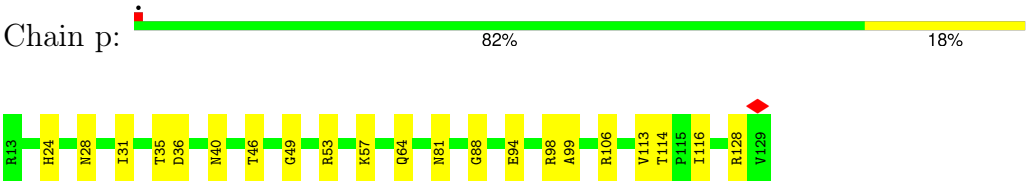
• Molecule 42: 30S ribosomal protein S10

Chain o:



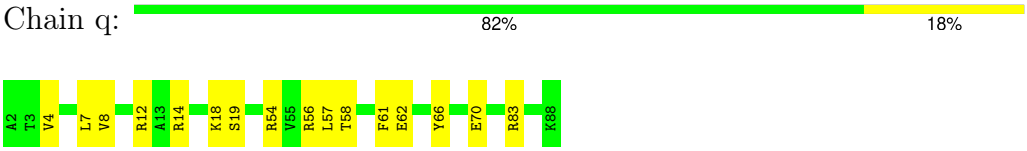
• Molecule 43: 30S ribosomal protein S11

Chain p:



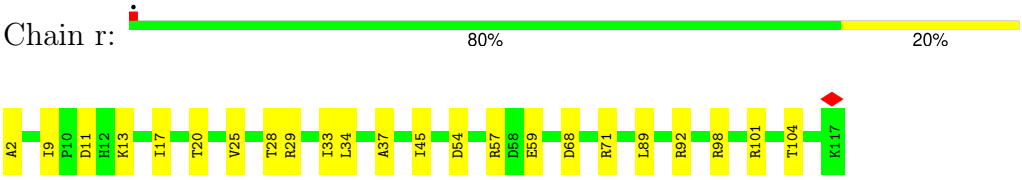
• Molecule 44: 30S ribosomal protein S12

Chain q:



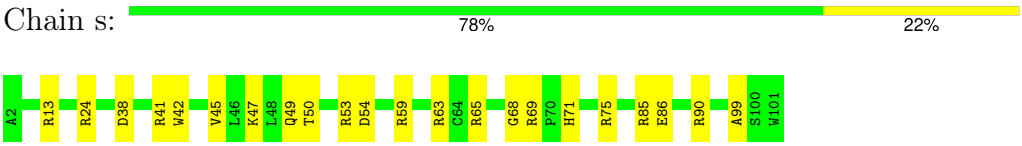
• Molecule 45: 30S ribosomal protein S13

Chain r:



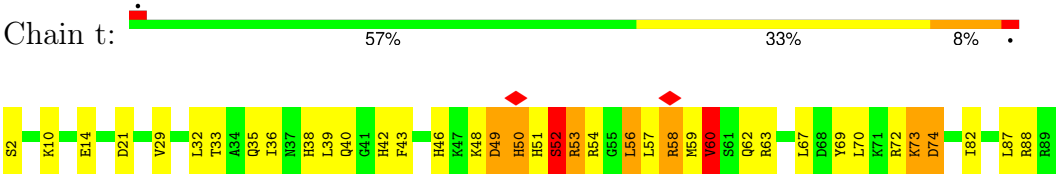
• Molecule 46: 30S ribosomal protein S14

Chain s:



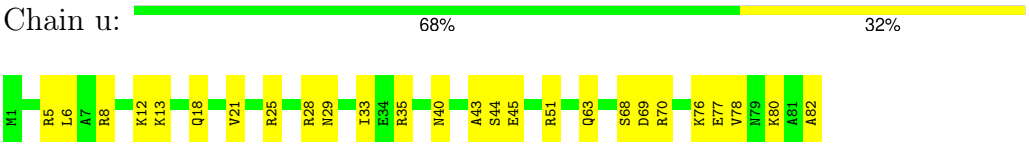
• Molecule 47: 30S ribosomal protein S15

Chain t:



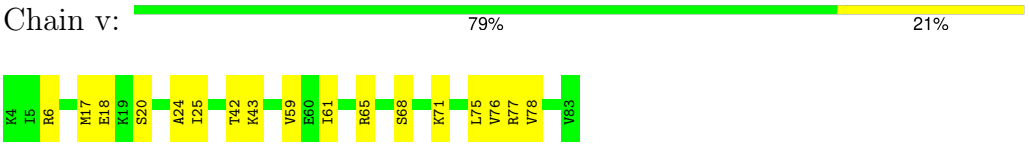
• Molecule 48: 30S ribosomal protein S16

Chain u:



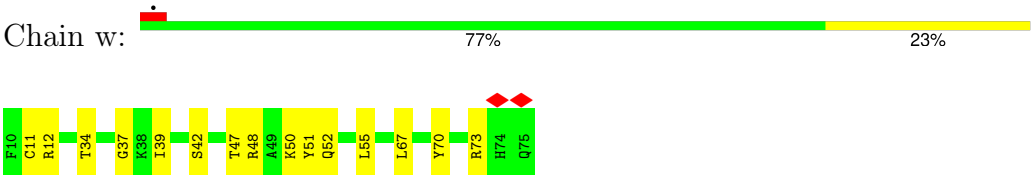
• Molecule 49: 30S ribosomal protein S17

Chain v:



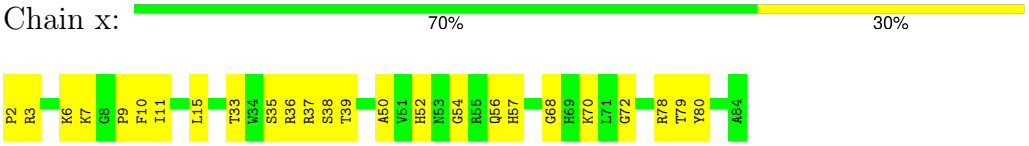
• Molecule 50: 30S ribosomal protein S18

Chain w:



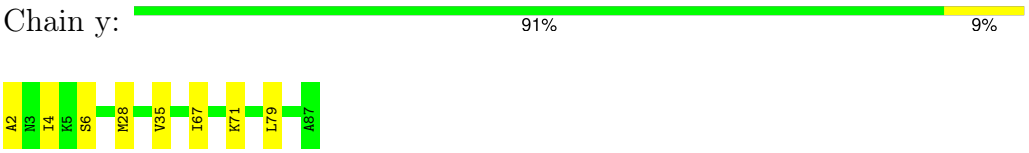
• Molecule 51: 30S ribosomal protein S19

Chain x:



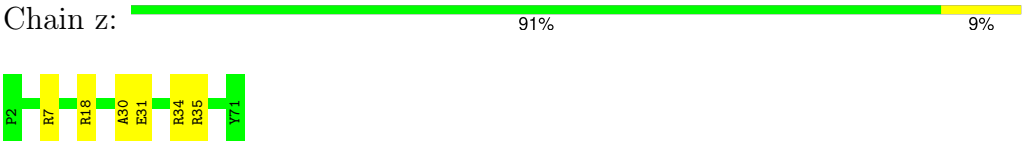
• Molecule 52: 30S ribosomal protein S20

Chain y:



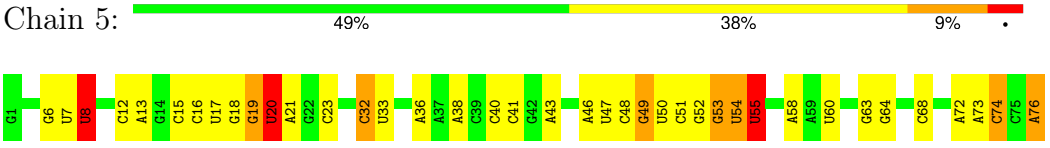
• Molecule 53: 30S ribosomal protein S21

Chain z:



• Molecule 54: P-tRNA

Chain 5:



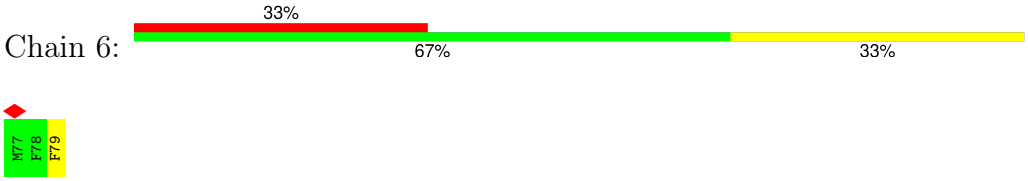
• Molecule 55: Peptide chain release factor 2

Chain A:



• Molecule 56: FME-PHE-PHE

Chain 6:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193636	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 ($e^-/Å^2$)	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	0.066	Depositor
Minimum map value	-0.024	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1	0.36	0/69286	0.37	4/108087 (0.0%)
2	2	0.35	0/36590	0.37	1/57074 (0.0%)
3	3	0.33	0/2872	0.34	0/4478
4	4	0.29	0/203	0.36	0/312
5	B	0.36	0/2121	0.60	0/2852
6	C	0.38	0/1586	0.65	1/2134 (0.0%)
7	D	0.34	0/1571	0.56	0/2113
8	E	0.33	0/1434	0.57	0/1926
9	F	0.31	0/1333	0.52	0/1805
10	G	0.28	0/1122	0.62	1/1515 (0.1%)
11	J	0.34	0/1152	0.57	0/1551
12	K	0.34	0/955	0.61	0/1279
13	L	0.33	0/1062	0.59	0/1413
14	M	0.34	0/1093	0.57	0/1460
15	N	0.38	0/964	0.79	0/1289
16	O	0.30	0/902	0.56	0/1209
17	P	0.38	0/929	0.66	0/1242
18	Q	0.35	0/960	0.57	0/1278
19	R	0.43	1/829 (0.1%)	0.65	1/1107 (0.1%)
20	S	0.34	0/864	0.58	0/1156
21	T	0.33	0/752	0.57	0/1005
22	U	0.36	0/796	0.63	0/1062
23	V	0.32	0/766	0.51	0/1025
24	W	0.33	0/589	0.51	0/779
25	X	0.39	0/635	0.56	0/848
26	Y	0.32	0/502	0.57	0/667
27	Z	0.30	0/452	0.55	0/605
28	a	0.31	0/531	0.58	0/709
29	b	0.34	0/450	0.57	0/599
30	c	0.30	0/433	0.56	0/576
31	d	0.37	0/380	0.62	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	e	0.41	0/513	0.67	1/676 (0.1%)
33	f	0.30	0/303	0.60	0/397
34	g	0.32	0/1791	0.66	2/2413 (0.1%)
35	h	0.32	0/1663	0.59	0/2241
36	i	0.30	0/1665	0.55	0/2227
37	j	0.35	0/1165	0.61	0/1568
38	k	0.33	0/867	0.63	0/1171
39	l	0.29	0/1195	0.56	0/1602
40	m	0.32	0/989	0.55	0/1326
41	n	0.29	0/1034	0.61	0/1375
42	o	0.29	0/800	0.59	0/1082
43	p	0.31	0/893	0.53	0/1205
44	q	0.33	0/682	0.57	0/918
45	r	0.31	0/909	0.63	0/1215
46	s	0.30	0/817	0.53	0/1088
47	t	0.38	0/722	0.95	4/964 (0.4%)
48	u	0.33	0/659	0.66	0/884
49	v	0.32	0/657	0.64	0/881
50	w	0.30	0/553	0.54	0/743
51	x	0.29	0/680	0.55	0/915
52	y	0.34	0/675	0.54	0/895
53	z	0.29	0/597	0.56	0/792
54	5	0.32	0/1704	0.35	0/2654
55	A	0.32	0/2873	0.65	4/3870 (0.1%)
56	6	0.43	0/23	0.44	0/29
All	All	0.35	1/158543 (0.0%)	0.45	19/236784 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	52	PRO	N-CA	-6.09	1.39	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	t	52	SER	N-CA-C	-8.02	101.31	112.45
47	t	60	VAL	N-CA-C	-7.78	103.27	110.82
47	t	58	ARG	N-CA-C	-7.00	103.64	111.28
32	e	31	HIS	O-C-N	6.44	130.59	123.25
1	1	784	G	C4'-C3'-O3'	5.80	121.70	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62336	0	31370	692	0
2	2	32929	0	16587	369	0
3	3	2569	0	1301	34	0
4	4	184	0	95	1	0
5	B	2082	0	2154	51	0
6	C	1565	0	1616	50	0
7	D	1552	0	1619	32	0
8	E	1410	0	1444	34	0
9	F	1313	0	1358	23	0
10	G	1111	0	1148	28	0
11	J	1129	0	1162	12	0
12	K	946	0	1023	20	0
13	L	1053	0	1129	21	0
14	M	1074	0	1157	17	0
15	N	951	0	994	36	0
16	O	892	0	923	21	0
17	P	917	0	962	25	0
18	Q	947	0	1019	22	0
19	R	816	0	839	36	0
20	S	857	0	922	18	0
21	T	746	0	811	14	0
22	U	788	0	844	19	0
23	V	753	0	780	18	0
24	W	582	0	599	13	0
25	X	625	0	652	18	0
26	Y	501	0	531	9	0
27	Z	448	0	488	9	0
28	a	522	0	520	14	0
29	b	444	0	458	14	0
30	c	426	0	464	10	0
31	d	377	0	418	8	0
32	e	504	0	572	10	0
33	f	302	0	340	6	0
34	g	1760	0	1787	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	h	1636	0	1710	34	0
36	i	1643	0	1707	37	0
37	j	1152	0	1196	27	0
38	k	848	0	846	25	0
39	l	1181	0	1238	27	0
40	m	979	0	1031	15	0
41	n	1022	0	1070	21	0
42	o	790	0	831	17	0
43	p	877	0	887	13	0
44	q	673	0	720	13	0
45	r	900	0	965	18	0
46	s	805	0	844	19	0
47	t	714	0	734	53	0
48	u	649	0	666	22	0
49	v	648	0	691	13	0
50	w	544	0	560	10	0
51	x	663	0	688	23	0
52	y	669	0	719	5	0
53	z	589	0	629	4	0
54	5	1627	0	832	22	0
55	A	2833	0	2729	76	0
56	6	32	0	28	1	0
57	1	2	0	0	0	0
57	2	1	0	0	0	0
57	3	8	0	0	0	0
57	i	1	0	0	0	0
58	a	1	0	0	0	0
58	f	1	0	0	0	0
All	All	146899	0	99407	1880	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 12.

The worst 5 of 1880 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)
19:R:51:VAL:HG13	19:R:52:PRO:CD	1.51	1.40
19:R:51:VAL:CG1	19:R:52:PRO:HD3	1.55	1.36
1:1:402:A:C8	1:1:403:U:C6	2.18	1.30
6:C:151:THR:OG1	6:C:152:PRO:HD3	1.34	1.27
6:C:151:THR:HG23	6:C:152:PRO:CD	1.76	1.15

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	198 (96%)	7 (3%)	2 (1%)	12	45
7	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	55
9	F	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
10	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
11	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
12	K	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
13	L	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	N	117/119 (98%)	106 (91%)	11 (9%)	0	100	100
16	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	R	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	45
20	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
21	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
23	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
25	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
28	a	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
29	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
30	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	d	44/46 (96%)	44 (100%)	0	0	100	100
32	e	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	36
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
35	h	206/208 (99%)	189 (92%)	17 (8%)	0	100	100
36	i	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
37	j	154/156 (99%)	142 (92%)	12 (8%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
40	m	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
41	n	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
44	q	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
45	r	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
46	s	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	t	86/88 (98%)	79 (92%)	5 (6%)	2 (2%)	5	30
48	u	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
49	v	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
50	w	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	x	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
52	y	84/86 (98%)	84 (100%)	0	0	100	100
53	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	A	355/357 (99%)	331 (93%)	24 (7%)	0	100	100
56	6	1/3 (33%)	1 (100%)	0	0	100	100
All	All	5929/6031 (98%)	5627 (95%)	295 (5%)	7 (0%)	49	80

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	151	THR
47	t	50	HIS
47	t	74	ASP
19	R	52	PRO
32	e	32	ILE

5.3.2 Protein sidechains (i)

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	B	216/216 (100%)	216 (100%)	0	100 100
6	C	164/164 (100%)	163 (99%)	1 (1%)	78 80
7	D	165/165 (100%)	165 (100%)	0	100 100
8	E	148/148 (100%)	147 (99%)	1 (1%)	76 78
9	F	136/136 (100%)	136 (100%)	0	100 100
10	G	114/114 (100%)	114 (100%)	0	100 100
11	J	116/116 (100%)	116 (100%)	0	100 100
12	K	104/104 (100%)	104 (100%)	0	100 100
13	L	103/103 (100%)	103 (100%)	0	100 100
14	M	109/109 (100%)	109 (100%)	0	100 100
15	N	99/99 (100%)	97 (98%)	2 (2%)	48 65
16	O	86/86 (100%)	86 (100%)	0	100 100
17	P	99/99 (100%)	99 (100%)	0	100 100
18	Q	89/89 (100%)	89 (100%)	0	100 100
19	R	84/84 (100%)	83 (99%)	1 (1%)	63 72
20	S	93/93 (100%)	93 (100%)	0	100 100
21	T	81/81 (100%)	81 (100%)	0	100 100
22	U	84/84 (100%)	84 (100%)	0	100 100
23	V	78/78 (100%)	77 (99%)	1 (1%)	61 71
24	W	58/58 (100%)	58 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	54/54 (100%)	54 (100%)	0	100	100
27	Z	48/48 (100%)	48 (100%)	0	100	100
28	a	59/59 (100%)	59 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/51 (100%)	51 (100%)	0	100	100
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	186 (100%)	1 (0%)	81	82
35	h	171/171 (100%)	169 (99%)	2 (1%)	63	72
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	119 (100%)	0	100	100
38	k	91/91 (100%)	91 (100%)	0	100	100
39	l	124/124 (100%)	124 (100%)	0	100	100
40	m	104/104 (100%)	104 (100%)	0	100	100
41	n	105/105 (100%)	105 (100%)	0	100	100
42	o	86/86 (100%)	86 (100%)	0	100	100
43	p	90/90 (100%)	90 (100%)	0	100	100
44	q	74/74 (100%)	74 (100%)	0	100	100
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	71 (93%)	5 (7%)	15	41
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	72 (100%)	0	100	100
52	y	65/65 (100%)	65 (100%)	0	100	100
53	z	60/60 (100%)	60 (100%)	0	100	100
55	A	304/305 (100%)	304 (100%)	0	100	100
56	6	2/2 (100%)	2 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4946/4947 (100%)	4932 (100%)	14 (0%)	84 85

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	h	72	ARG
35	h	179	ARG
47	t	73	LYS
47	t	53	ARG
47	t	60	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
37	j	121	HIS
48	u	26	ASN
38	k	63	ASN
44	q	5	ASN
52	y	48	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	759 (26%)	16 (0%)
2	2	1532/1534 (99%)	415 (27%)	5 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	2 (25%)	0
54	5	75/76 (98%)	19 (25%)	0
All	All	4636/4642 (99%)	1218 (26%)	21 (0%)

5 of 1218 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	34	U
1	1	35	G
1	1	40	U
1	1	46	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2425	A
2	2	210	C
2	2	1109	C
2	2	496	A
2	2	83	C

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

39 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	$\#\|Z\| > 2$
1	1MG	1	745	1	23,26,27	2.83	7 (30%)	33,39,42	2.07	9 (27%)
1	G7M	1	2069	1	23,26,27	2.58	8 (34%)	34,39,42	2.51	11 (32%)
54	5MU	5	54	54	19,22,23	4.81	7 (36%)	27,32,35	3.52	8 (29%)
1	5MU	1	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.82	10 (37%)
1	5MU	1	747	1	19,22,23	4.82	7 (36%)	27,32,35	3.92	9 (33%)
1	PSU	1	1911	1	18,21,22	1.13	2 (11%)	21,30,33	2.16	5 (23%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.12	3 (11%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	2.77	13 (39%)
54	4OC	5	32	54	20,23,24	3.00	8 (40%)	25,32,35	1.02	1 (4%)
1	6MZ	1	2030	1	22,25,26	2.89	6 (27%)	29,36,39	4.47	13 (44%)
2	G7M	2	527	2	23,26,27	3.59	12 (52%)	34,39,42	1.57	7 (20%)
1	3TD	1	1915	1	19,22,23	4.25	5 (26%)	23,32,35	2.02	4 (17%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.07	5 (23%)
1	PSU	1	2605	1	18,21,22	1.12	2 (11%)	21,30,33	2.10	5 (23%)
1	PSU	1	2504	1	18,21,22	1.22	2 (11%)	21,30,33	1.93	4 (19%)
2	2MG	2	1516	2	23,26,27	2.95	8 (34%)	33,38,41	2.14	10 (30%)
1	2MG	1	2445	1	23,26,27	2.94	6 (26%)	33,38,41	2.27	7 (21%)
54	4SU	5	8	54	18,21,22	3.69	7 (38%)	25,30,33	2.22	5 (20%)
2	5MC	2	967	2	19,22,23	3.83	8 (42%)	26,32,35	0.99	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	6MZ	1	1618	1	22,25,26	2.85	6 (27%)	29,36,39	4.45	14 (48%)
1	2MA	1	2503	1	22,25,26	3.71	8 (36%)	32,37,40	2.44	7 (21%)
1	OMC	1	2498	1	19,22,23	2.91	7 (36%)	25,31,34	0.91	1 (4%)
2	4OC	2	1402	2	20,23,24	3.00	8 (40%)	25,32,35	1.25	4 (16%)
54	H2U	5	20	54	18,21,22	3.38	5 (27%)	19,30,33	1.55	4 (21%)
2	PSU	2	516	2	18,21,22	1.02	1 (5%)	21,30,33	1.95	5 (23%)
1	OMU	1	2552	1	19,22,23	2.88	8 (42%)	25,31,34	1.92	5 (20%)
56	FME	6	77	56	8,9,10	0.92	0	8,9,11	0.73	0
1	PSU	1	955	1	18,21,22	1.04	1 (5%)	21,30,33	1.80	3 (14%)
2	MA6	2	1518	2	23,26,27	1.56	5 (21%)	33,38,41	2.71	12 (36%)
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.02	6 (28%)
1	2MG	1	1835	1	23,26,27	2.89	7 (30%)	33,38,41	2.20	10 (30%)
1	PSU	1	746	1	18,21,22	1.08	2 (11%)	21,30,33	1.81	4 (19%)
54	PSU	5	55	54	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
2	2MG	2	966	2	23,26,27	2.99	7 (30%)	33,38,41	2.30	7 (21%)
1	OMG	1	2251	1,54	23,26,27	2.40	8 (34%)	32,38,41	1.95	8 (25%)
1	5MC	1	1962	1	19,22,23	3.79	8 (42%)	26,32,35	1.02	2 (7%)
2	2MG	2	1207	2	23,26,27	2.88	7 (30%)	33,38,41	2.34	9 (27%)
2	UR3	2	1498	2	19,22,23	2.53	7 (36%)	26,32,35	1.56	3 (11%)

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
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
54	4SU	5	8	54	-	3/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
1	2MA	1	2503	1	-	5/7/25/26	0/3/3/3
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
54	H2U	5	20	54	-	4/7/38/39	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
56	FME	6	77	56	-	3/7/9/11	-
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	PSU	1	746	1	-	2/7/25/26	0/2/2/2
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2

The worst 5 of 216 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.15	1.49	1.35
1	1	2503	2MA	C4-N3	11.48	1.49	1.34
1	1	2030	6MZ	C6-N6	11.32	1.47	1.34
1	1	747	5MU	C2-N1	11.29	1.56	1.38
54	5	20	H2U	C2-N1	11.13	1.51	1.35

The worst 5 of 242 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	1618	6MZ	C4-N9-C8	14.23	120.68	105.74
1	1	2030	6MZ	C4-N9-C8	13.98	120.42	105.74
1	1	747	5MU	C5-C4-N3	12.88	126.52	115.32
1	1	1939	5MU	C5-C4-N3	12.51	126.19	115.32
54	5	54	5MU	C5-C4-N3	11.98	125.74	115.32

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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
1	1	2504	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

17 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	745	1MG	1	0
54	5	54	5MU	1	0
2	2	1407	5MC	2	0
2	2	1519	MA6	1	0
54	5	32	4OC	1	0
1	1	2030	6MZ	1	0
1	1	1915	3TD	4	0
1	1	2580	PSU	1	0
2	2	1516	2MG	1	0
54	5	8	4SU	1	0
1	1	2503	2MA	4	0
2	2	1402	4OC	1	0
54	5	20	H2U	1	0
1	1	2552	OMU	2	0
54	5	55	PSU	1	0
1	1	2251	OMG	2	0
1	1	1962	5MC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

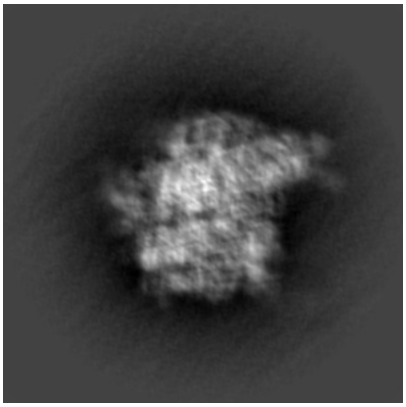
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20193. These allow visual inspection of the internal detail of the map and identification of artifacts.

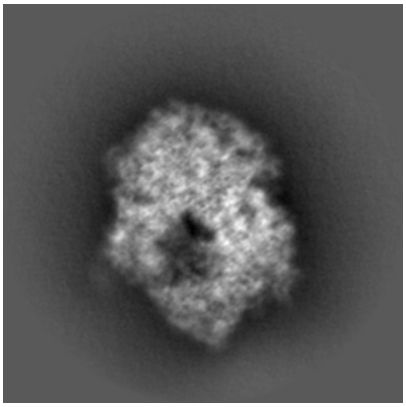
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

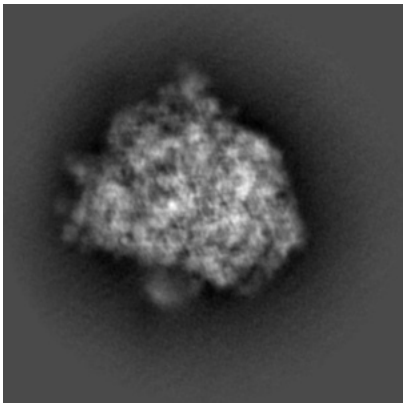
6.1.1 Primary map



X



Y

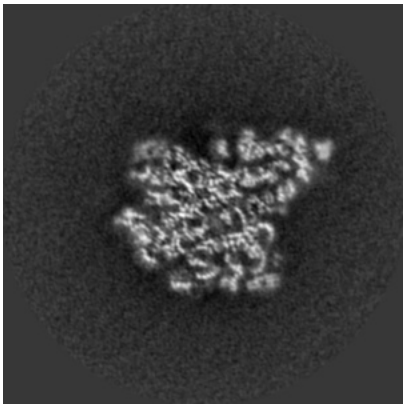


Z

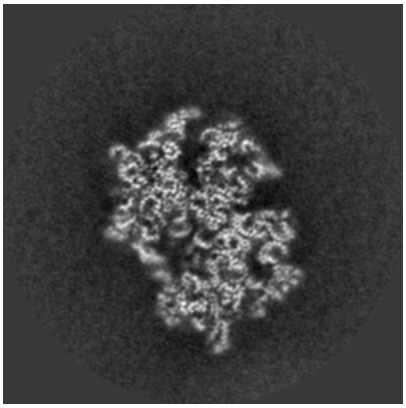
The images above show the map projected in three orthogonal directions.

6.2 Central slices

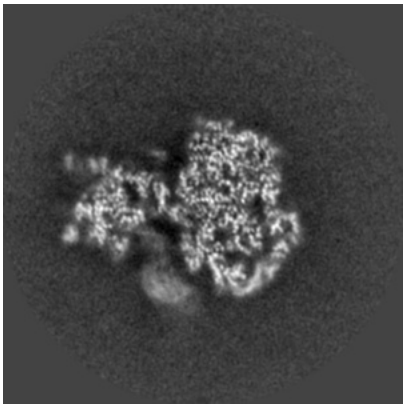
6.2.1 Primary map



X Index: 128



Y Index: 128

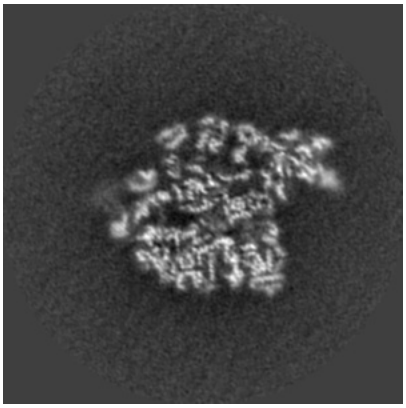


Z Index: 128

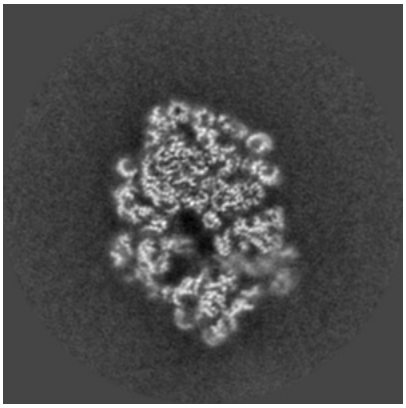
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

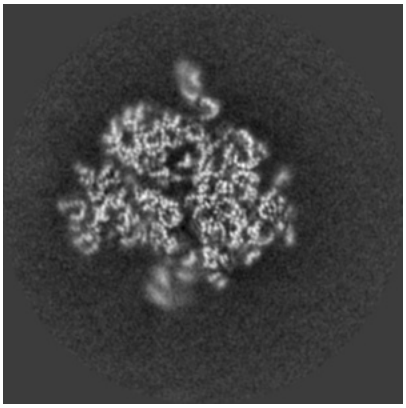
6.3.1 Primary map



X Index: 122



Y Index: 114

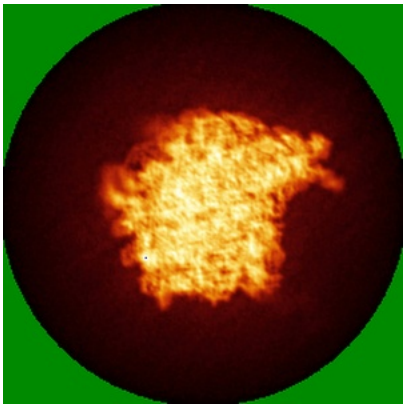


Z Index: 143

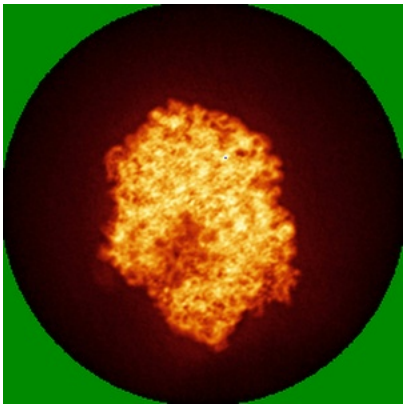
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

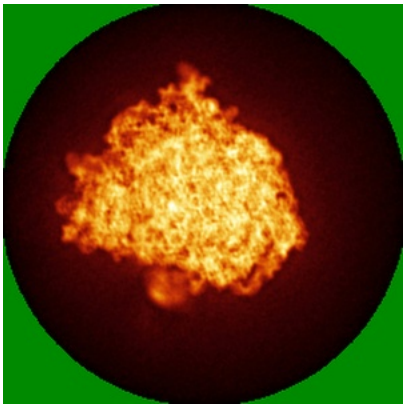
6.4.1 Primary map



X



Y

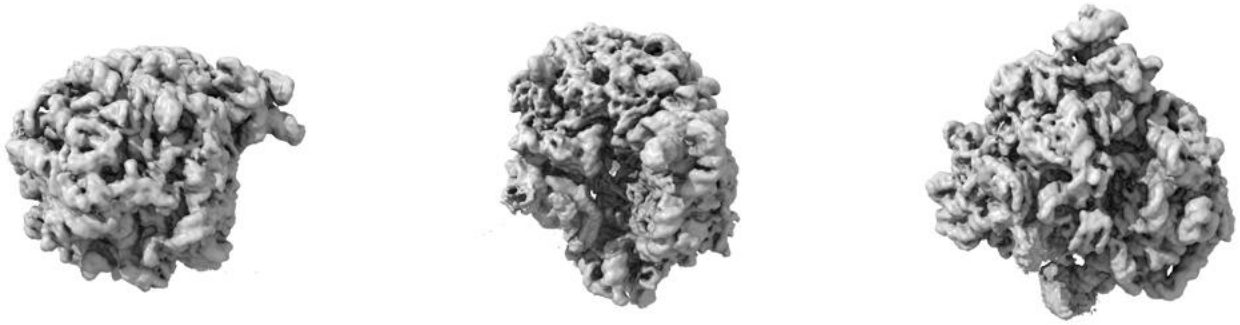


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

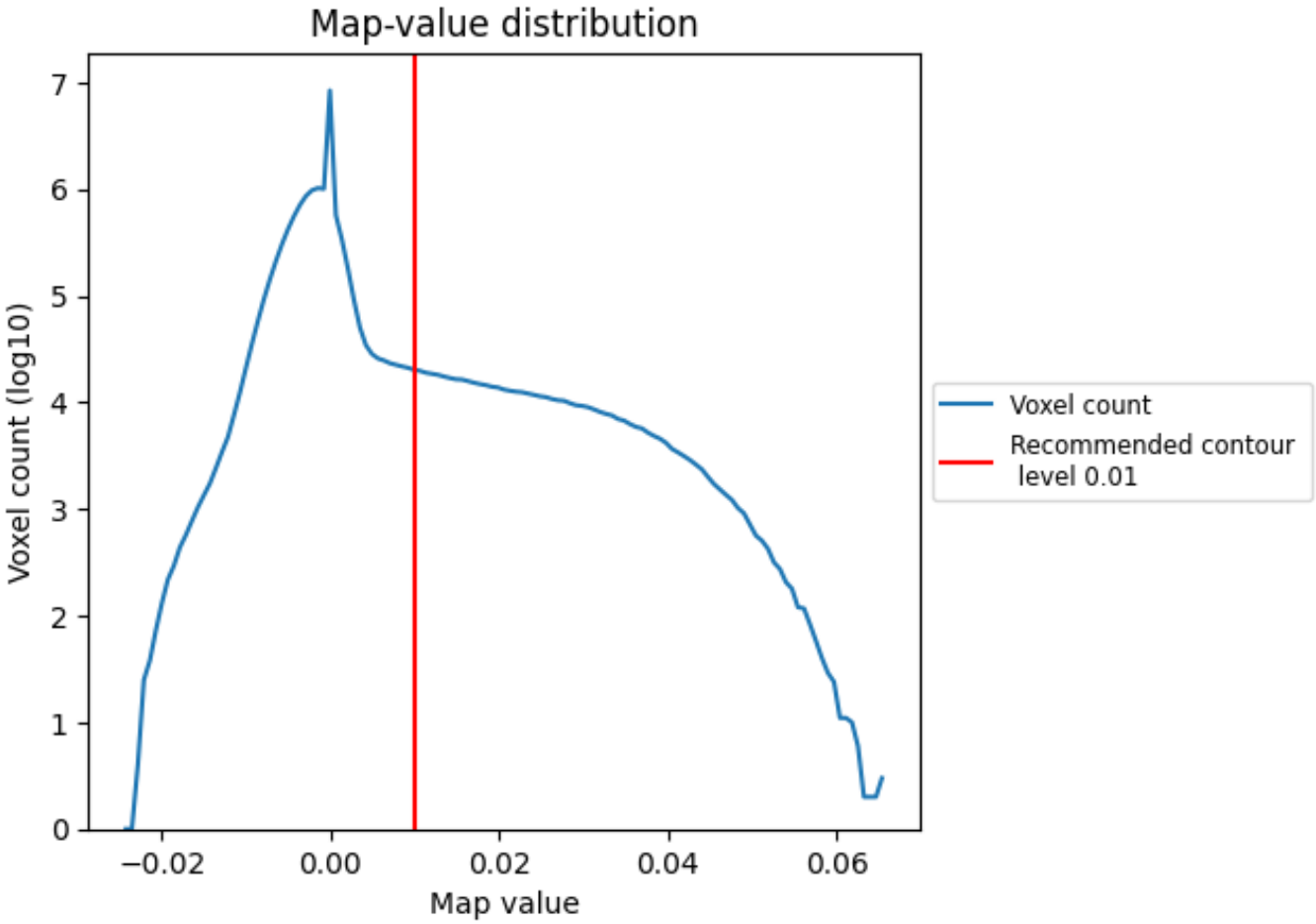
6.6 Mask visualisation (i)

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

7 Map analysis

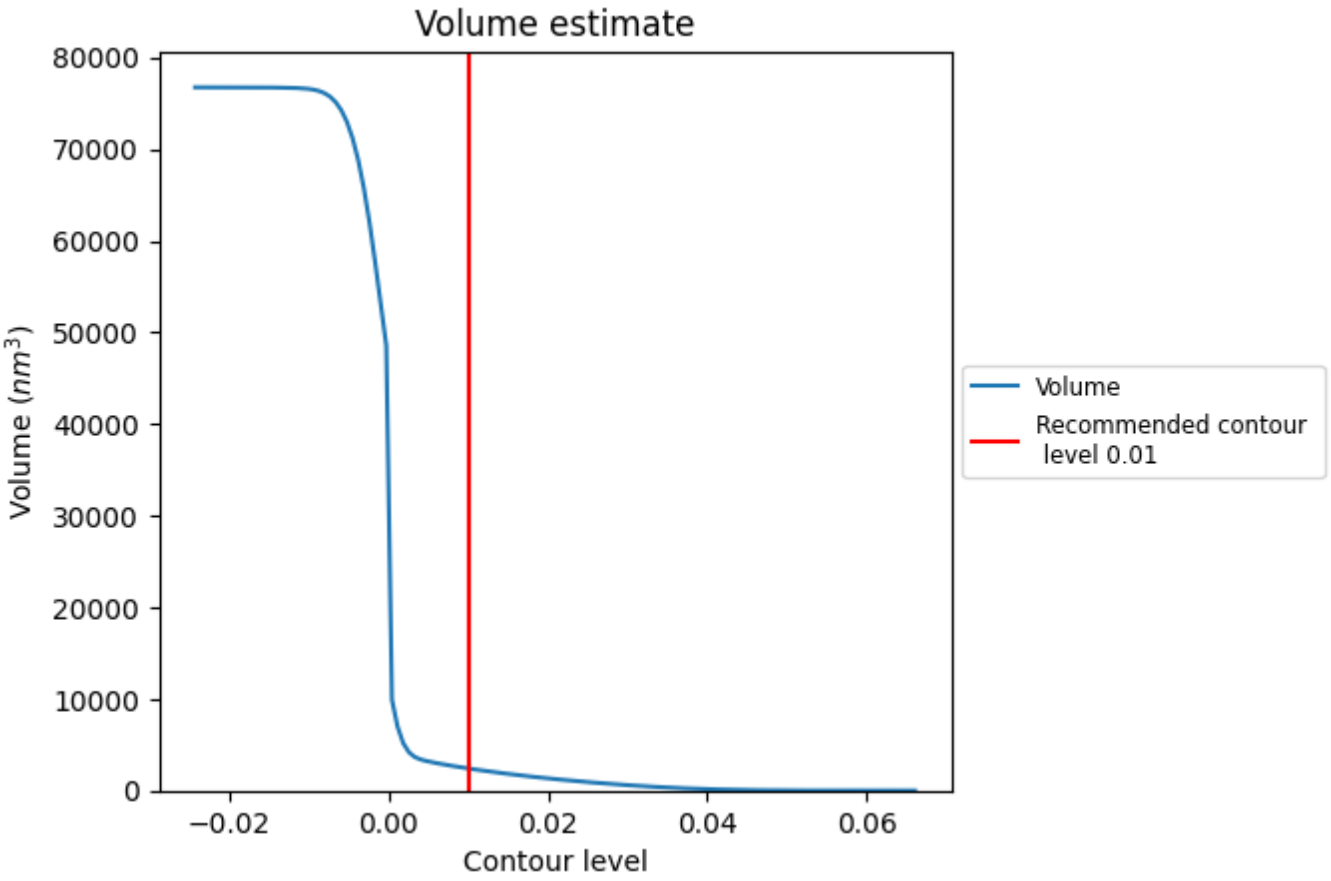
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

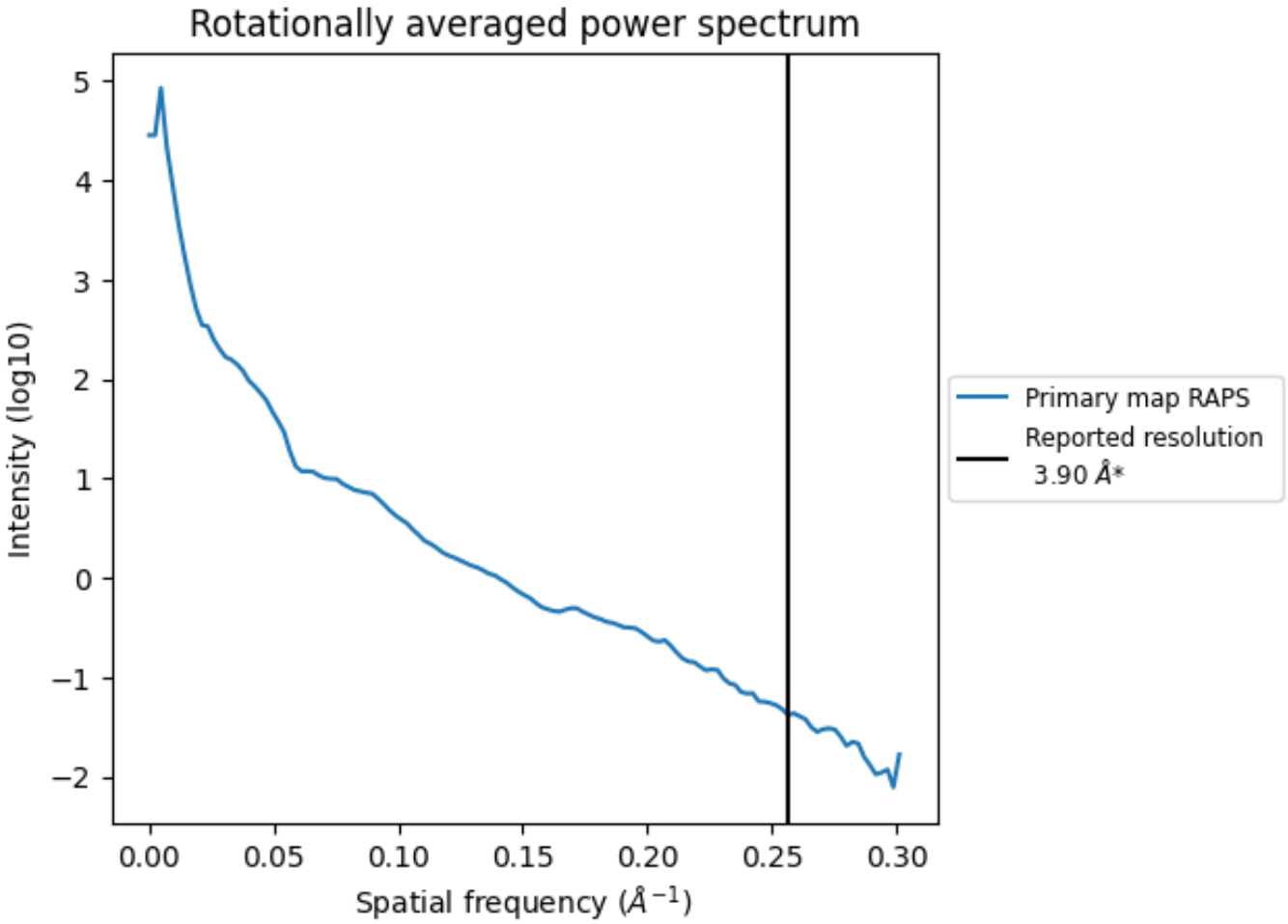
7.2 Volume estimate (i)



The volume at the recommended contour level is 2414 nm^3; this corresponds to an approximate mass of 2180 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 (i)



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

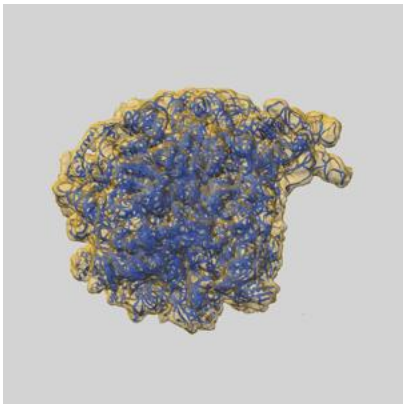
8 Fourier-Shell correlation (i)

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

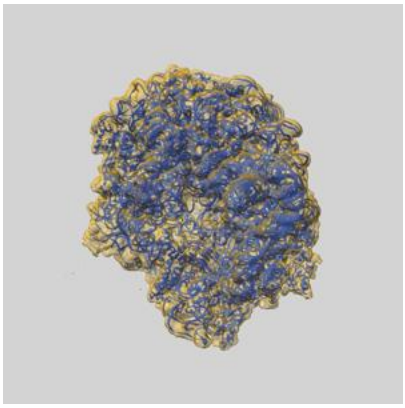
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20193 and PDB model 6OT3. Per-residue inclusion information can be found in section 3 on page 15.

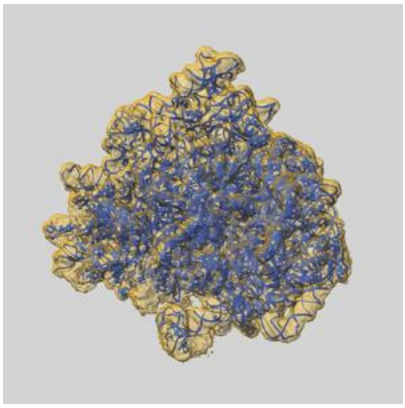
9.1 Map-model overlay



X



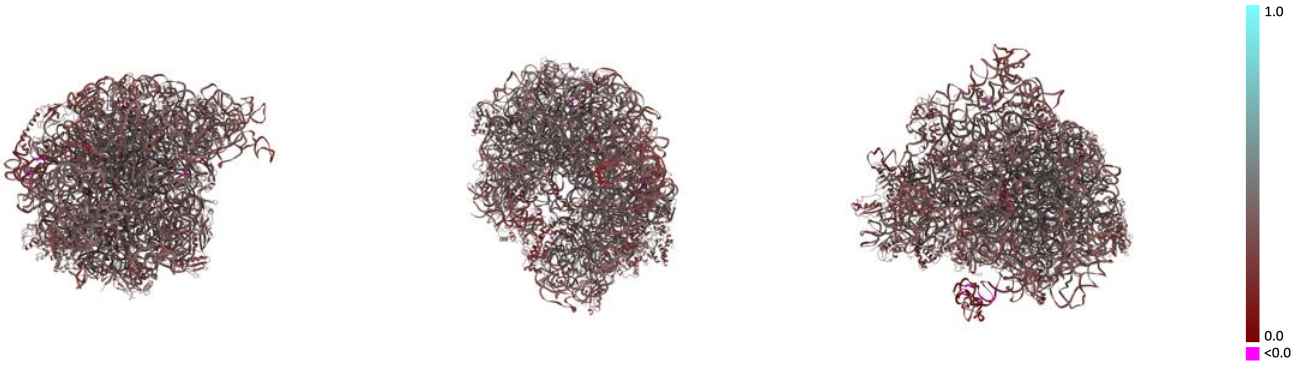
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

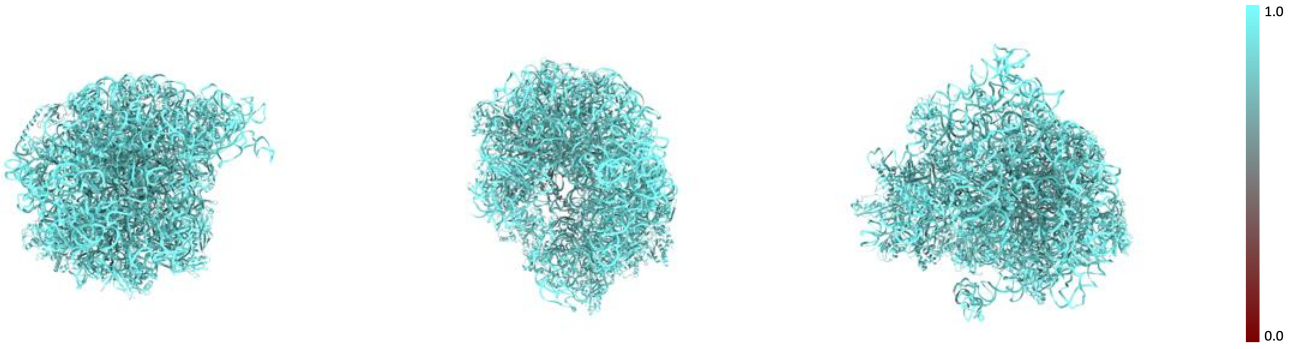
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

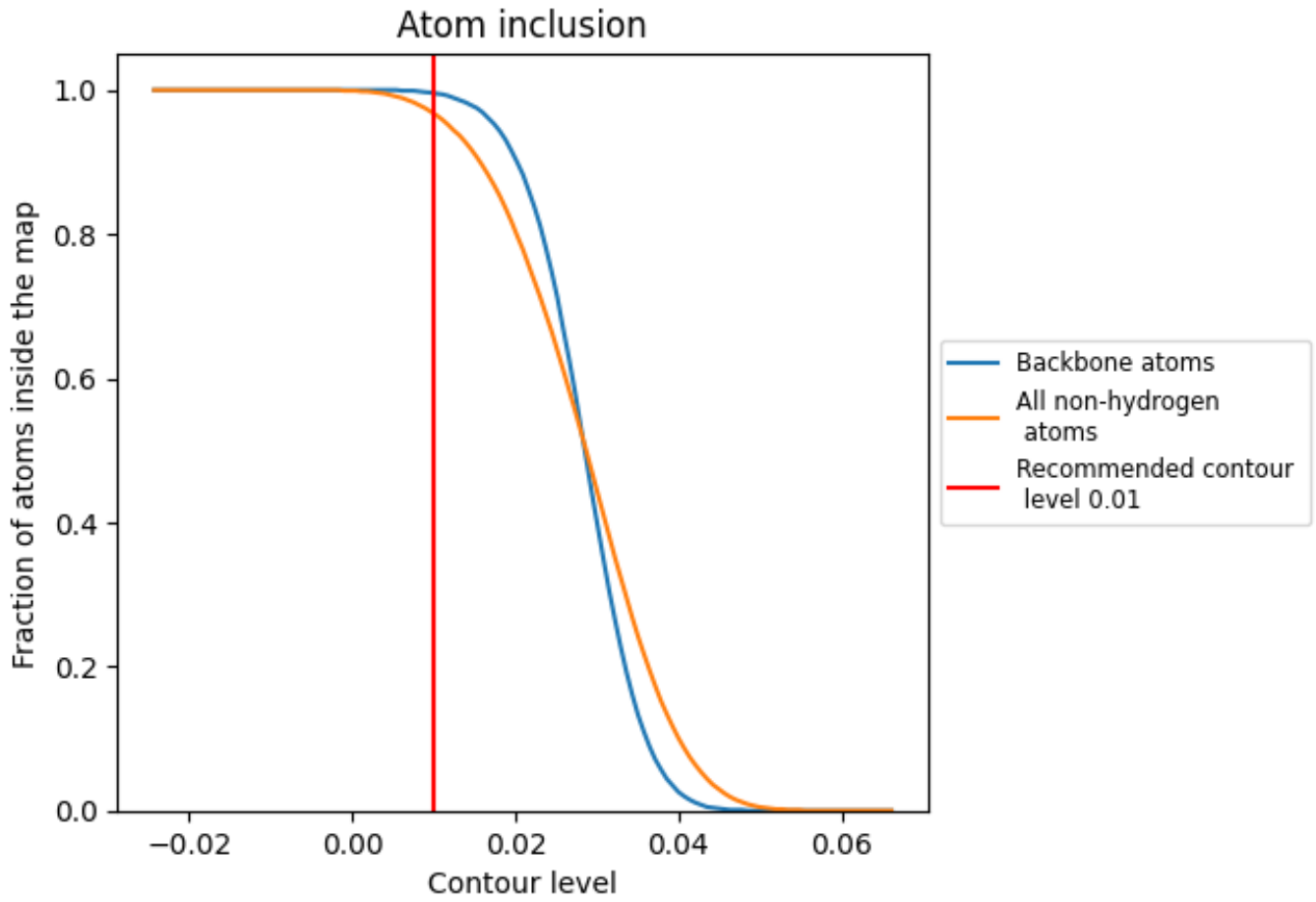
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9670	0.3480
1	0.9960	0.3640
2	0.9980	0.3560
3	0.9990	0.3490
4	0.9950	0.3690
5	0.9740	0.3360
6	0.7190	0.2220
A	0.8140	0.2480
B	0.8930	0.3790
C	0.9180	0.3550
D	0.9160	0.3480
E	0.9160	0.2980
F	0.9440	0.3200
G	0.8460	0.2660
J	0.9140	0.3540
K	0.8350	0.3410
L	0.9240	0.3660
M	0.8970	0.3630
N	0.9070	0.2820
O	0.9590	0.3270
P	0.8960	0.3220
Q	0.9220	0.3150
R	0.9280	0.3610
S	0.8740	0.3610
T	0.8990	0.3340
U	0.9500	0.3290
V	0.9550	0.3380
W	0.9130	0.3650
X	0.9000	0.3440
Y	0.9490	0.2730
Z	0.9130	0.3570
a	0.8980	0.2840
b	0.9250	0.3540
c	0.9280	0.3520
d	0.8930	0.3530



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Chain	Atom inclusion	Q-score
e	0.8840	0.3580
f	0.9250	0.3470
g	0.9020	0.2960
h	0.8910	0.3320
i	0.9350	0.3090
j	0.9200	0.3470
k	0.8980	0.3010
l	0.9080	0.2950
m	0.9270	0.3470
n	0.9350	0.3150
o	0.9050	0.3120
p	0.9070	0.3450
q	0.8620	0.3460
r	0.9170	0.2960
s	0.9330	0.3170
t	0.8970	0.2190
u	0.9520	0.3230
v	0.9290	0.3360
w	0.8720	0.3110
x	0.9300	0.3120
y	0.9250	0.2880
z	0.8300	0.2790