



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 04:40 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:

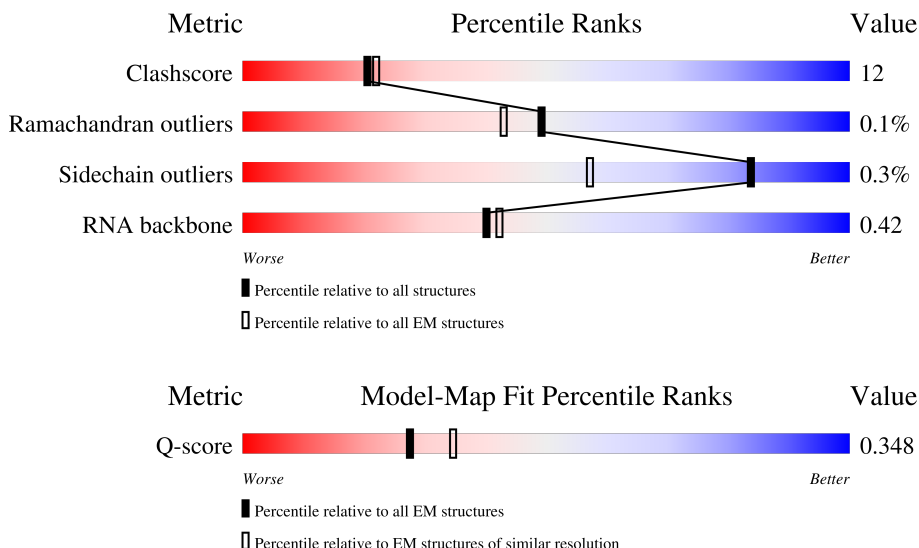
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 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.



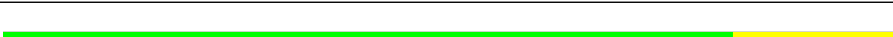
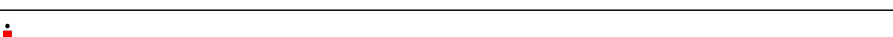
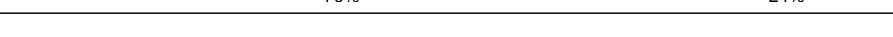
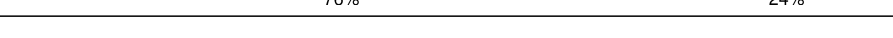
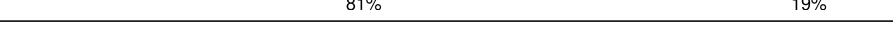
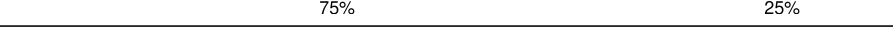
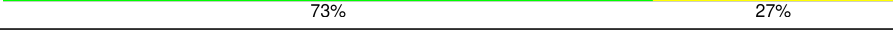
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

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

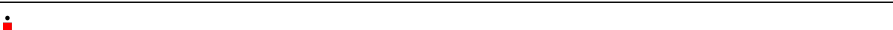
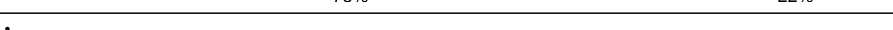
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Mol	Chain	Length	Quality of chain
4	4	9	
5	B	271	
6	C	209	
7	D	201	
8	E	177	
9	F	175	
10	G	149	
11	J	142	
12	K	123	
13	L	144	
14	M	136	
15	N	119	
16	O	116	
17	P	114	
18	Q	117	
19	R	103	
20	S	110	
21	T	94	
22	U	103	
23	V	94	
24	W	76	
25	X	77	
26	Y	62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

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Mol	Chain	Length	Quality of chain
29	b	56	 70%30%
30	c	52	 73%27%
31	d	46	 74%26%
32	e	64	 88%9%
33	f	38	 82%18%
34	g	225	 79%20%
35	h	208	 74%26%
36	i	205	 76%24%
37	j	156	 76%24%
38	k	104	 66%34%
39	l	151	 74%26%
40	m	129	 81%19%
41	n	127	 76%24%
42	o	99	 78%22%
43	p	117	 82%18%
44	q	87	 82%18%
45	r	116	 80%20%
46	s	100	 78%22%
47	t	88	 57%33%8%
48	u	82	 68%32%
49	v	80	 79%21%
50	w	66	 77%23%
51	x	83	 70%30%
52	y	86	 91%9%
53	z	70	 91%9%

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Mol	Chain	Length	Quality of chain
54	5	76	49% 38% 9%
55	A	357	69% 31%
56	6	3	67% 33%

2 Entry composition

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
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

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

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

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

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

- Molecule 4 is a RNA chain called mRNA.

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

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

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

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

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

- 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	S	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	S	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	C	N	O	S	0	0
			790	495	151	143	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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 Peptide chain release factor 2.

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

- 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	

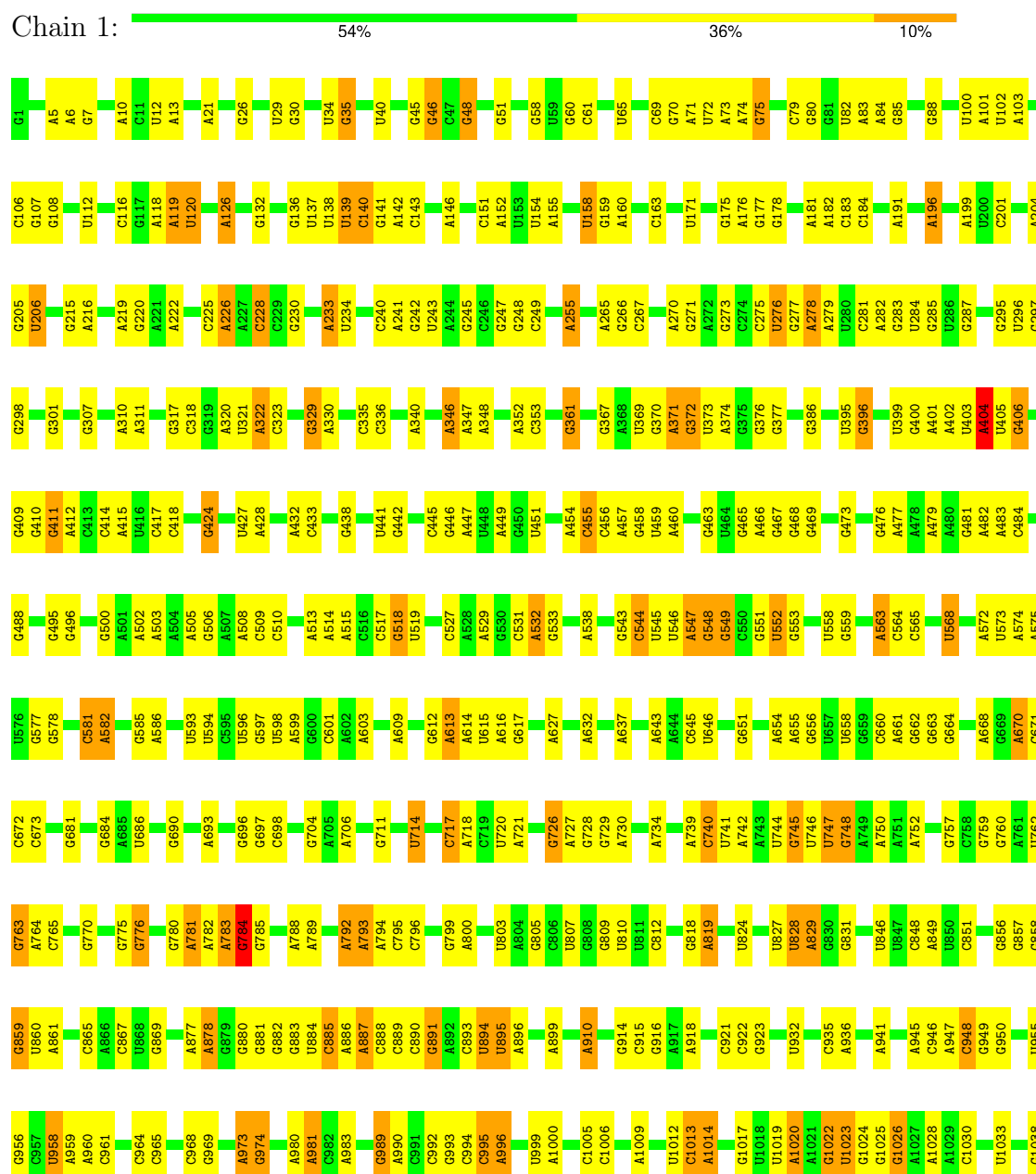
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

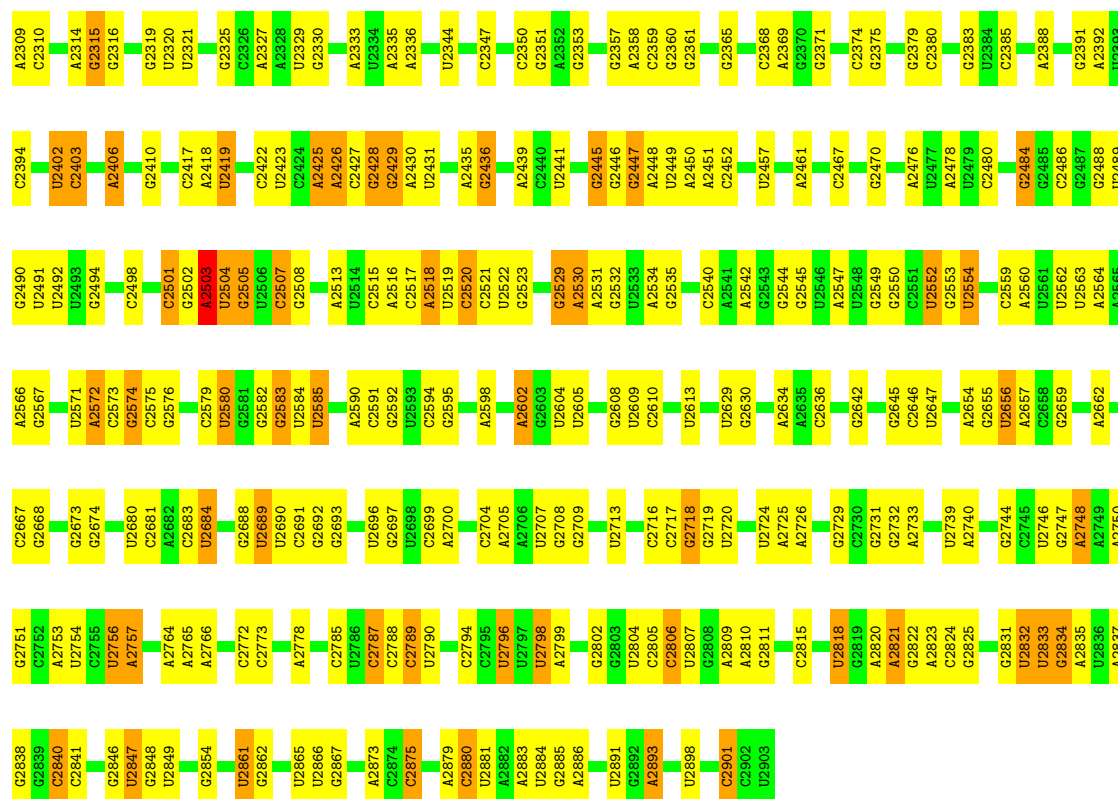
3 Residue-property plots

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.

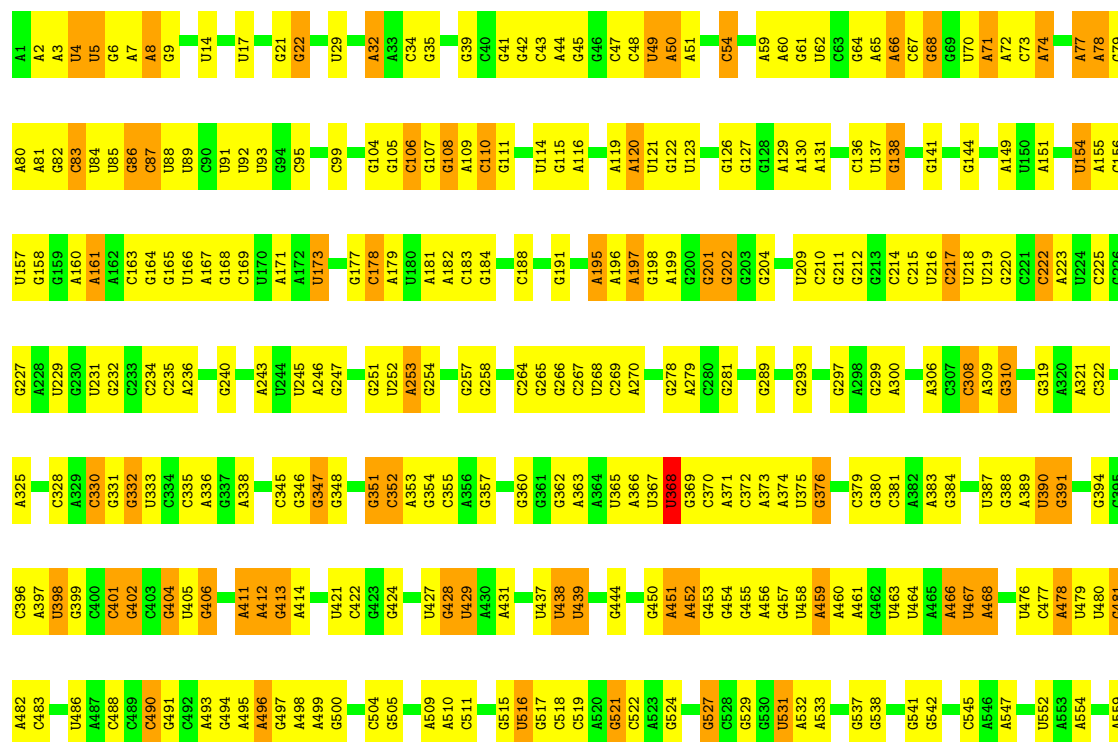
• Molecule 1: 23S ribosomal RNA

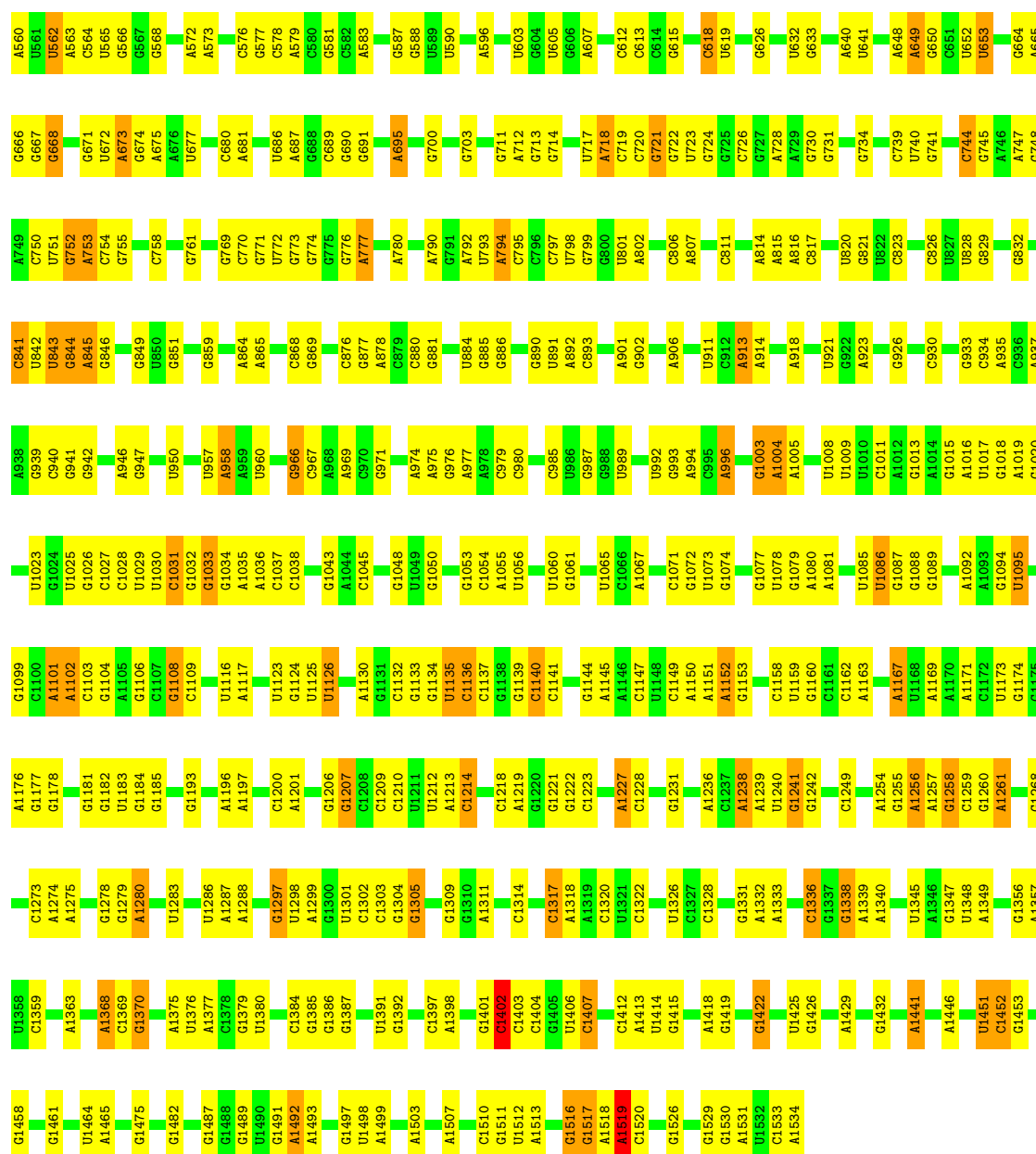


A2212	G2136	G2056	G1972	G1884	G1799	A1700	A1593	A1496	G1408	G1311	G1212	G1116	A1039
U2213	U2137	G2057	G1980	G1888	C1800	A1701	A1593	U1497	U1409	U1312	U1217	U1119	A1040
C2214	U2138	A2060	G1980	A1888	A1801	U1712	U1602	C1498	U1410	G1324	G1218	G1119	G1041
G2215	U2139	A2061	U1982	A1889	A1802	U1713	U1602	G1501	U1412	U1325	G1123	G1124	G1042
G2216	G2140	A2062	A1987	A1899	G1807	U1714	C1607	G1502	A1413	U1326	U1222	G1125	C1043
G2217	G2141	C2063	G1988	A1900	A1808	G1715	A1608	A1503	C1414	U1329	G1223	A1126	C1044
G2223	A2142	C2064	A1987	A1901	A1809	U1716	A1609	A1504	U1415	U1329	G1227	A1127	C1045
G2224	C2145	G2069	U1991	G1902	A1810	G1721	A1610	U1416	U1416	G1332	G1227	G1128	A1046
A2225	A2146	U2081	G1992	G1903	C1816	U1722	C1612	C1417	C1417	U1231	U1231	G1129	G1056
G2226	A2147	A2082	U1993	G1906	G1817	G1723	G1613	U1508	A1418	G1338	G1232	U1130	U1057
G2228	C2153	G1995	U1911	U1911	U1818	G1724	A1614	A1514	A1419	G1339	G1236	U1131	U1058
G2233	G2166	U2086	U1912	A1912	U1820	U1725	C1615	A1515	G1421	U1340	G1237	U1132	G1059
U2233	G2167	G2087	A1913	A1913	U1821	U1729	C1617	A1522	G1425	G1339	G1238	A1133	U1060
G2234	A2158	A2088	C1914	C1914	G1822	G1730	A1618	U1523	A1426	U1342	G1238	U1134	U1061
G2237	G2159	G2093	G2002	A1916	G1823	G1731	G1619	G1524	A1427	U1344	A1247	G1136	G1062
G2238	C2160	A2094	G2002	U1917	G1824	C1732	A1626	A1525	C1428	C1345	G1248	G1137	C1064
G2238	C2161	A2095	C2006	U1918	U1825	G1733	A1626	A1525	C1437	C1351	U1249	G1138	U1065
G2238	A2162	A2096	C2006	A1919	U1826	G1738	G1631	A1528	U1438	U1352	G1250	G1139	U1066
U2240	C2163	C2096	G2010	U1919	U1827	U1738	G1631	G1529	U1438	G1352	G1251	U1140	A1067
A2241	A2164	A2097	G2010	U1919	U1828	U1738	G1631	G1530	A1439	G1353	G1252	U1141	G1068
G2242	C2165	U2098	G2011	U1923	A1829	A1744	A1634	C1531	U1443	A1354	A1253	A1142	A1070
U2243	U2166	U2099	G2012	C1924	A1830	U1751	C1639	A1532	G1444	G1355	U1255	A1151	G1071
G2250	U2167	G2102	A2013	G1925	C1833	U1751	C1639	C1533	G1449	G1358	G1256	G1152	C1072
G2250	G2168	C2103	U2022	U1926	U1834	A1754	C1646	U1534	G1449	G1359	U1263	C1153	A1073
A2251	A2169	G2104	C2023	A1927	G1835	U1756	U1647	A1535	G1455	G1360	U1263	G1154	G1074
G2252	A2170	U2105	G2024	A1928	C1836	G1756	U1648	C1536	G1455	G1361	U1263	A1155	C1075
G2253	A2171	U2106	G2025	G1930	C1837	U1757	G1649	G1537	U1458	C1362	G1266	G1158	C1076
C2264	U2172	C2107	U2026	G1930	C1837	U1758	A1650	U1458	U1458	C1363	U1267	G1158	A1077
U2265	A2173	A2108	G2027	C1934	C1844	A1759	G1651	G1543	C1461	G1364	U1268	C1161	U1077
A2266	C2174	G1935	U2028	A1936	G1845	C1760	G1652	C1550	C1462	A1365	A1269	G1162	C1079
A2267	C2175	A1937	G2029	A1937	G1846	U1765	G1653	C1559	G1463	A1366	G1270	G1168	U1082
A2268	A2176	U2111	A2030	A1937	A1847	C1764	U1657	U1559	G1464	A1367	G1271	A1169	A1084
G2269	C2177	G2112	A2031	A1938	A1848	U1765	C1658	G1560	G1465	G1368	A1272	C1170	A1085
A2270	C2178	U2113	G2032	U1939	G1849	U1773	G1659	U1466	U1466	U1372	A1275	G1171	A1086
G2271	U2181	A2114	A2033	U1940	G1850	C1774	G1660	A1566	U1467	A1378	G1278	U1176	G1087
U2272	U2182	G2115	U2034	C1941	A1854	U1775	G1667	G1567	U1468	U1379	C1278	G1177	U1094
A2273	A2183	G2116	G2035	U1942	G1854	G1776	G1668	G1568	A1469	U1379	G1279	U1174	A1088
G2277	A2184	A2118	C2036	U1943	G1857	U1777	A1669	A1569	G1475	G1380	A1287	A1175	A1089
A2278	U2188	A2119	G2037	G1948	A1858	U1778	A1669	A1570	U1476	A1383	U1294	U1176	A1090
G2279	U2189	G2120	U2039	G1954	U1859	U1779	C1670	A1571	U1477	A1384	U1294	G1177	U1094
C2283	G2190	U2122	G2040	U1955	G1860	U1780	U1671	A1572	G1478	C1385	C1296	C1178	A1095
G2286	G2193	G2123	C2043	U1956	G1862	U1781	U1671	U1578	G1479	C1386	G1296	G1179	A1096
A2287	U2194	G2124	C2044	A1960	G1863	A1784	G1674	A1579	G1482	A1387	G1297	G1182	U1097
G2291	A2198	G2125	C2045	C1961	U1864	A1785	G1682	A1580	G1483	G1388	C1297	U1101	U1101
U2292	A2199	A2126	G2046	C1962	U1865	A1786	G1682	A1581	U1484	G1388	G1300	G1186	C1102
G2293	C2200	G2128	G2047	U1963	G1869	U1787	U1688	C1582	U1484	U1394	G1300	G1187	A1103
G2296	G2204	C2129	G2049	U1963	G1870	A1788	C1691	A1583	C1489	U1396	A1302	U1188	G1110
U2305	U2301	U2130	C2050	A1966	C1871	G1790	U1692	C1586	U1490	U1397	C1305	A1189	G1112
G2308	U2305	U2132	A2052	G1968	A1871	A1791	U1693	A1586	G1491	U1398	G1306	G1206	A1111
G2308	U2305	G2208	A2053	A1969	A1872	U1796	G1694	G1587	G1492	C1399	A1307	G1113	G1112
G2308	U2305	A2134	A2054	A1970	G1873	U1797	G1695	U1588	C1493	A1403	G1310	C1114	G1115
G2308	A2211	A2135	C2055	U1971	G1878	U1798	G1699	A1590	A1495				



• Molecule 2: 16S ribosomal RNA

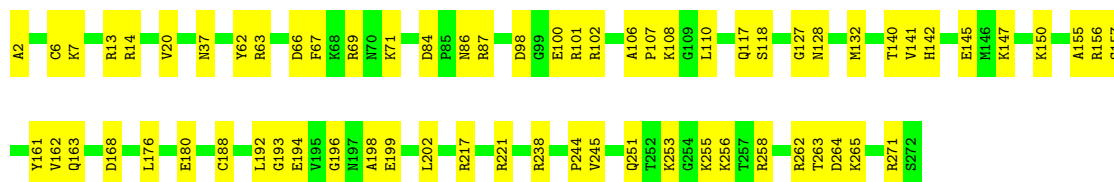






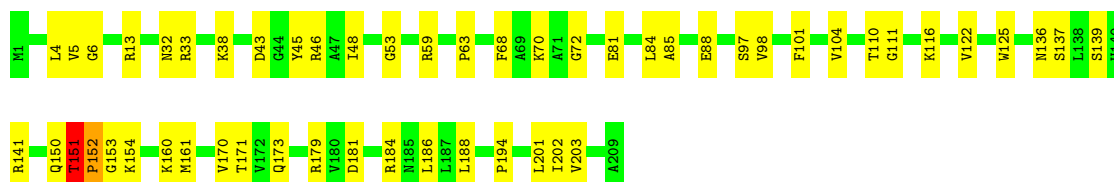
- Molecule 5: 50S ribosomal protein L2

Chain B: 75% 25%



- Molecule 6: 50S ribosomal protein L3

Chain C: 75% 24%



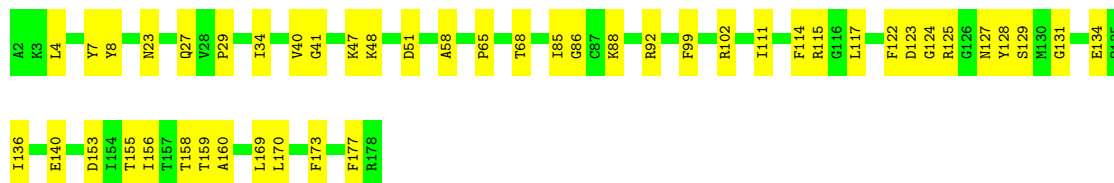
- Molecule 7: 50S ribosomal protein L4

Chain D: 78% 22%



- Molecule 8: 50S ribosomal protein L5

Chain E: 74% 26%



- Molecule 9: 50S ribosomal protein L6

Chain F: 79% 21%

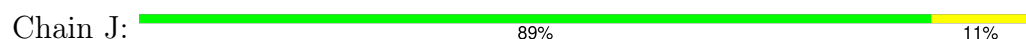




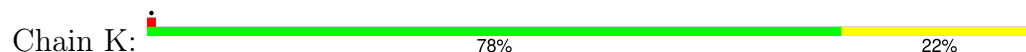
- Molecule 10: 50S ribosomal protein L9



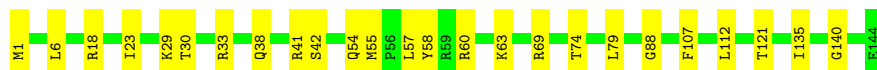
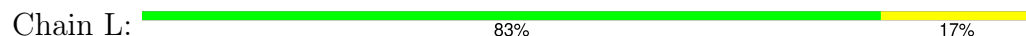
- Molecule 11: 50S ribosomal protein L13



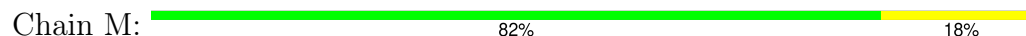
- Molecule 12: 50S ribosomal protein L14



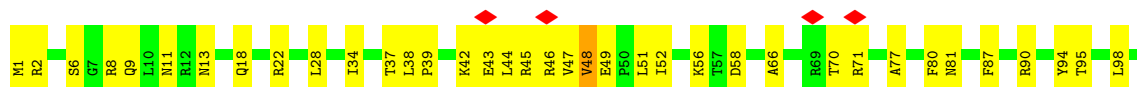
- Molecule 13: 50S ribosomal protein L15



- Molecule 14: 50S ribosomal protein L16



- Molecule 15: 50S ribosomal protein L17





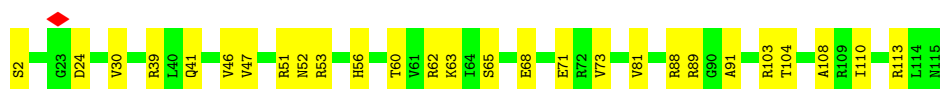
- Molecule 16: 50S ribosomal protein L18

Chain O: 77% 23%



- Molecule 17: 50S ribosomal protein L19

Chain P: 76% 24%



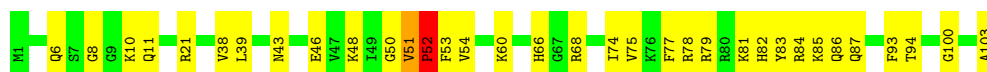
- Molecule 18: 50S ribosomal protein L20

Chain Q: 76% 24%



- Molecule 19: 50S ribosomal protein L21

Chain R: 67% 31% ..



- Molecule 20: 50S ribosomal protein L22

Chain S: 81% 19%



- Molecule 21: 50S ribosomal protein L23

Chain T: 78% 22%

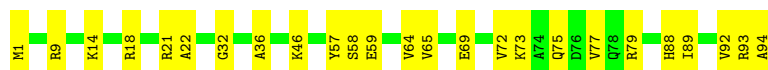


- Molecule 22: 50S ribosomal protein L24

Chain U: 75% 25%



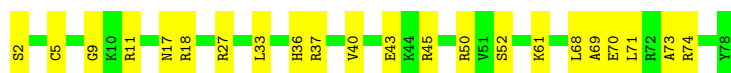
- Molecule 23: 50S ribosomal protein L25



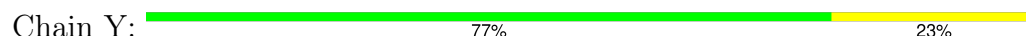
- Molecule 24: 50S ribosomal protein L27



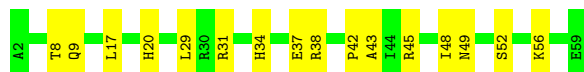
- Molecule 25: 50S ribosomal protein L28



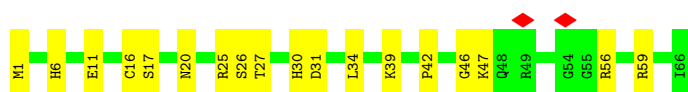
- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32





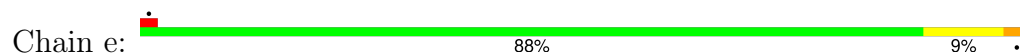
- Molecule 30: 50S ribosomal protein L33



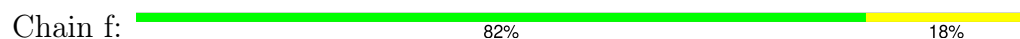
- Molecule 31: 50S ribosomal protein L34



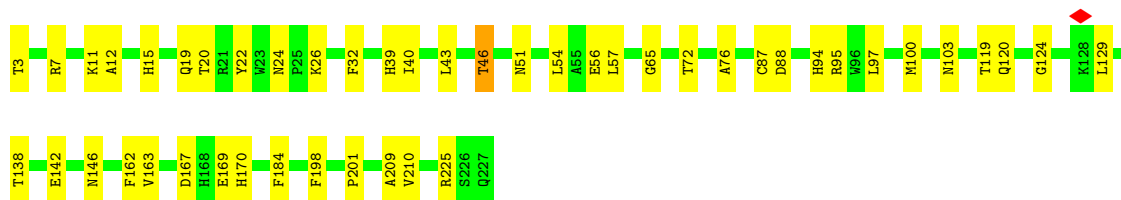
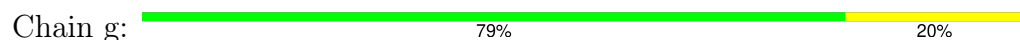
- Molecule 32: 50S ribosomal protein L35



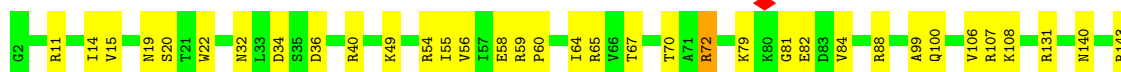
- Molecule 33: 50S ribosomal protein L36



- Molecule 34: 30S ribosomal protein S2



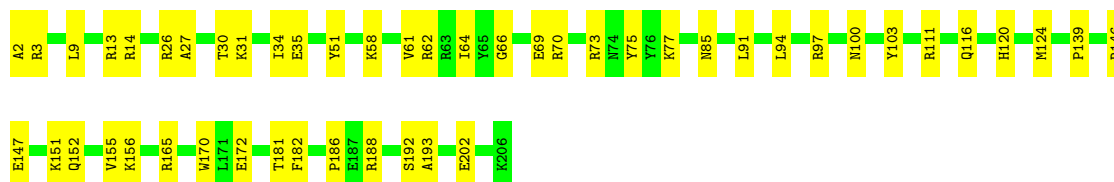
- Molecule 35: 30S ribosomal protein S3





- Molecule 36: 30S ribosomal protein S4

Chain i: 76% 24%



- Molecule 37: 30S ribosomal protein S5

Chain j: 76% 24%



- Molecule 38: 30S ribosomal protein S6

Chain k: 66% 34%



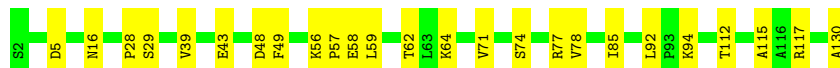
- Molecule 39: 30S ribosomal protein S7

Chain l: 74% 26%



- Molecule 40: 30S ribosomal protein S8

Chain m: 81% 19%



- Molecule 41: 30S ribosomal protein S9

Chain n:  76% 24%



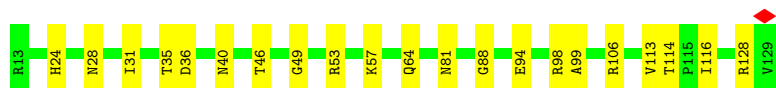
- Molecule 42: 30S ribosomal protein S10

Chain o:  78% 22%



- Molecule 43: 30S ribosomal protein S11

Chain p:  82% 18%



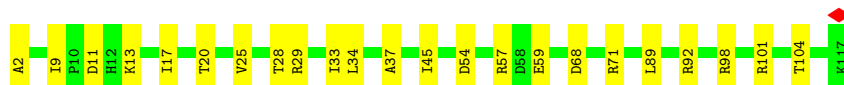
- Molecule 44: 30S ribosomal protein S12

Chain q:  82% 18%



- Molecule 45: 30S ribosomal protein S13

Chain r:  80% 20%



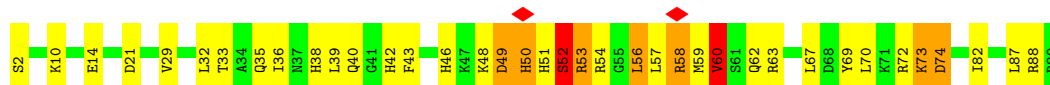
- Molecule 46: 30S ribosomal protein S14

Chain s:  78% 22%



- Molecule 47: 30S ribosomal protein S15

Chain t:  57% 33% 8%



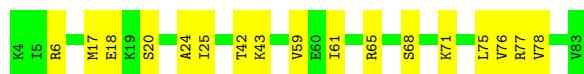
- Molecule 48: 30S ribosomal protein S16

Chain u:  68% 32%



- Molecule 49: 30S ribosomal protein S17

Chain v:  79% 21%



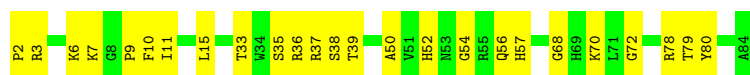
- Molecule 50: 30S ribosomal protein S18

Chain w:  77% 23%



- Molecule 51: 30S ribosomal protein S19

Chain x:  70% 30%



- Molecule 52: 30S ribosomal protein S20

Chain y:  91% 9%



- Molecule 53: 30S ribosomal protein S21

Chain z:  91% 9%

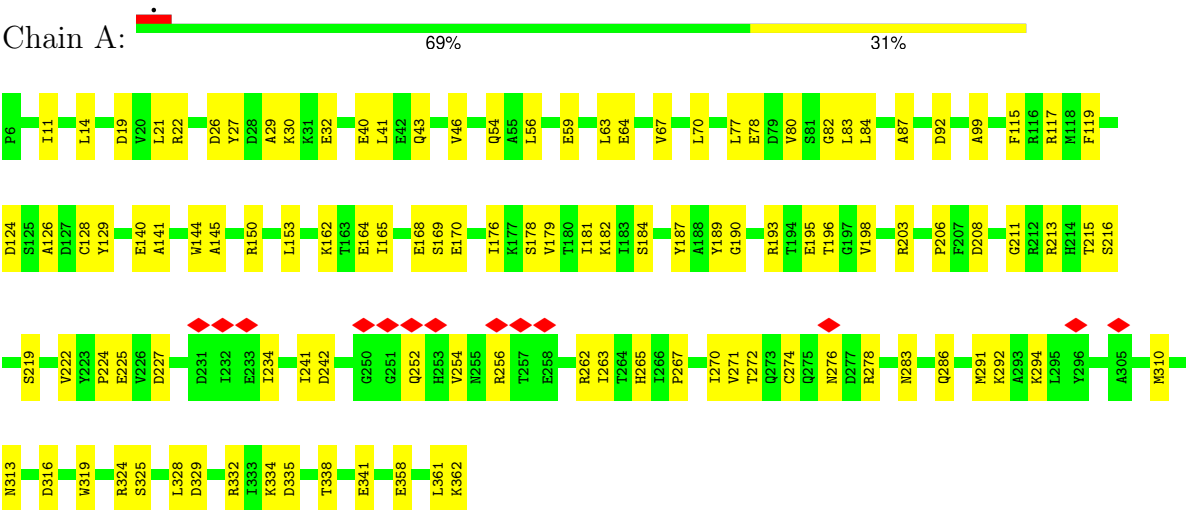


- Molecule 54: P-tRNA

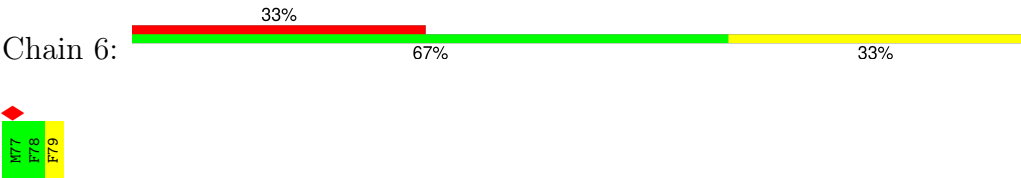
Chain 5:  49% 38% 9%



- Molecule 55: Peptide chain release factor 2



● Molecule 56: FME-PHE-PHE



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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	0.066	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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.36	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(°)	Ideal(°)
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

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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	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 ⓘ

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 ⓘ

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 ⓘ

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	2MG	1	2445	1	23,26,27	2.94	6 (26%)	33,38,41	2.27	7 (21%)
54	PSU	5	55	54	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
1	2MA	1	2503	1	22,25,26	3.71	8 (36%)	32,37,40	2.44	7 (21%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.12	3 (11%)
1	PSU	1	1911	1	18,21,22	1.13	2 (11%)	21,30,33	2.16	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%)
2	4OC	2	1402	2	20,23,24	3.00	8 (40%)	25,32,35	1.25	4 (16%)
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.02	6 (28%)
1	PSU	1	2605	1	18,21,22	1.12	2 (11%)	21,30,33	2.10	5 (23%)
1	PSU	1	746	1	18,21,22	1.08	2 (11%)	21,30,33	1.81	4 (19%)
1	OMG	1	2251	54,1	23,26,27	2.40	8 (34%)	32,38,41	1.95	8 (25%)
2	5MC	2	967	2	19,22,23	3.83	8 (42%)	26,32,35	0.99	1 (3%)
2	PSU	2	516	2	18,21,22	1.02	1 (5%)	21,30,33	1.95	5 (23%)
1	G7M	1	2069	1	23,26,27	2.58	8 (34%)	34,39,42	2.51	11 (32%)
2	2MG	2	1207	2	23,26,27	2.88	7 (30%)	33,38,41	2.34	9 (27%)
54	5MU	5	54	54	19,22,23	4.81	7 (36%)	27,32,35	3.52	8 (29%)
1	5MC	1	1962	1	19,22,23	3.79	8 (42%)	26,32,35	1.02	2 (7%)
2	2MG	2	966	2	23,26,27	2.99	7 (30%)	33,38,41	2.30	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	1	1835	1	23,26,27	2.89	7 (30%)	33,38,41	2.20	10 (30%)
1	6MZ	1	1618	1	22,25,26	2.85	6 (27%)	29,36,39	4.45	14 (48%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
2	G7M	2	527	2	23,26,27	3.59	12 (52%)	34,39,42	1.57	7 (20%)
54	4OC	5	32	54	20,23,24	3.00	8 (40%)	25,32,35	1.02	1 (4%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.07	5 (23%)
1	1MG	1	745	1	23,26,27	2.83	7 (30%)	33,39,42	2.07	9 (27%)
1	6MZ	1	2030	1	22,25,26	2.89	6 (27%)	29,36,39	4.47	13 (44%)
2	MA6	2	1518	2	23,26,27	1.56	5 (21%)	33,38,41	2.71	12 (36%)
2	UR3	2	1498	2	19,22,23	2.53	7 (36%)	26,32,35	1.56	3 (11%)
54	4SU	5	8	54	18,21,22	3.69	7 (38%)	25,30,33	2.22	5 (20%)
54	H2U	5	20	54	18,21,22	3.38	5 (27%)	19,30,33	1.55	4 (21%)
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%)
1	5MU	1	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.82	10 (37%)
1	3TD	1	1915	1	19,22,23	4.25	5 (26%)	23,32,35	2.02	4 (17%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	2.77	13 (39%)
1	5MU	1	747	1	19,22,23	4.82	7 (36%)	27,32,35	3.92	9 (33%)
1	OMU	1	2552	1	19,22,23	2.88	8 (42%)	25,31,34	1.92	5 (20%)
1	OMC	1	2498	1	19,22,23	2.91	7 (36%)	25,31,34	0.91	1 (4%)

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	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
1	2MA	1	2503	1	-	5/7/25/26	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	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
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	746	1	-	2/7/25/26	0/2/2/2
1	OMG	1	2251	54,1	-	0/9/27/28	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
54	4SU	5	8	54	-	3/7/25/26	0/2/2/2
54	H2U	5	20	54	-	4/7/38/39	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
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	OMC	1	2498	1	-	0/9/27/28	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($^{\circ}$)	Ideal($^{\circ}$)
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
54	5	55	PSU	1	0
1	1	2503	2MA	4	0
2	2	1407	5MC	2	0
2	2	1516	2MG	1	0
2	2	1402	4OC	1	0
1	1	2251	OMG	2	0
54	5	54	5MU	1	0
1	1	1962	5MC	1	0
54	5	32	4OC	1	0
1	1	2580	PSU	1	0
1	1	745	1MG	1	0
1	1	2030	6MZ	1	0
54	5	8	4SU	1	0
54	5	20	H2U	1	0
1	1	1915	3TD	4	0
2	2	1519	MA6	1	0
1	1	2552	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

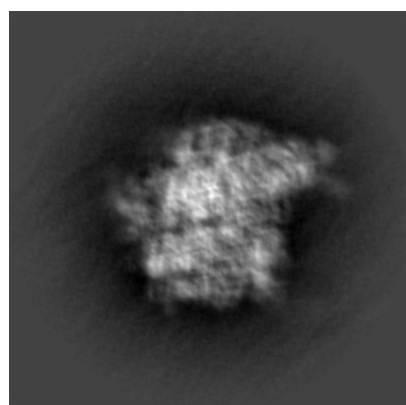
6 Map visualisation [i](#)

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

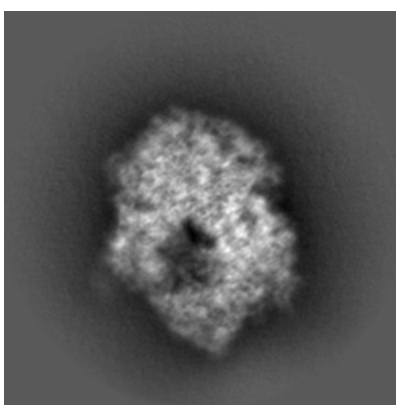
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

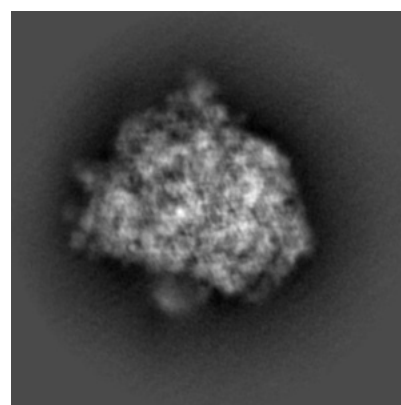
6.1.1 Primary map



X



Y

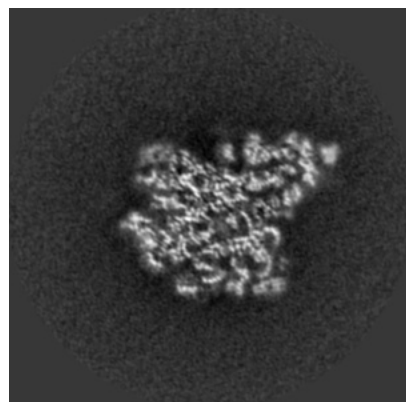


Z

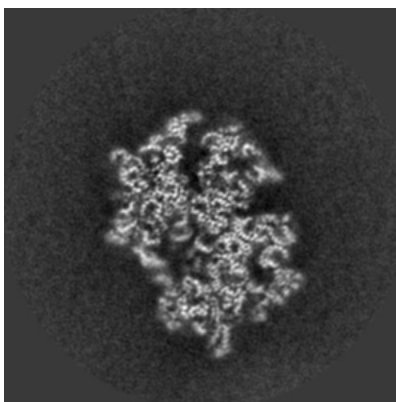
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

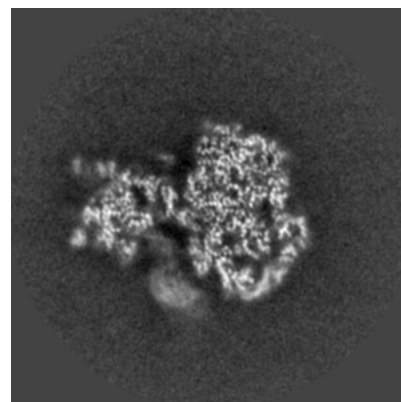
6.2.1 Primary map



X Index: 128



Y Index: 128

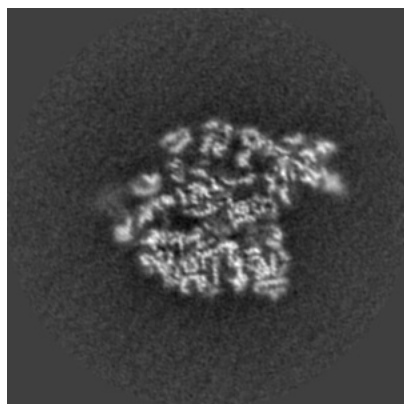


Z Index: 128

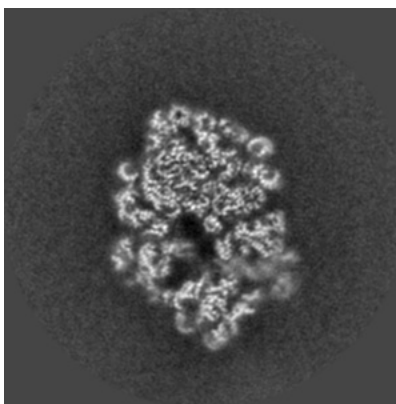
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

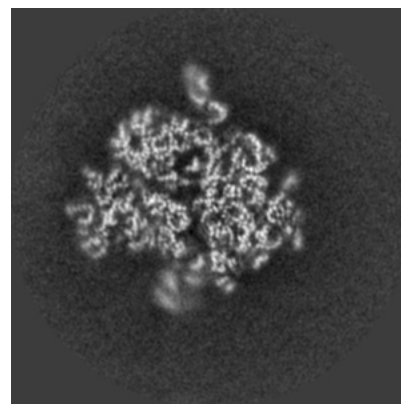
6.3.1 Primary map



X Index: 122



Y Index: 114

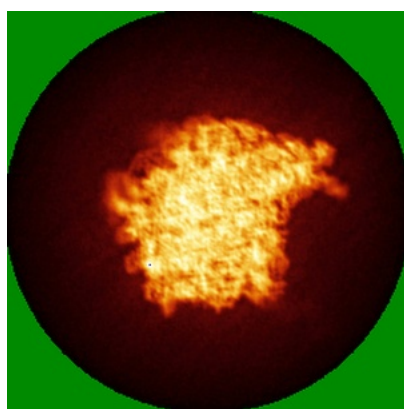


Z Index: 143

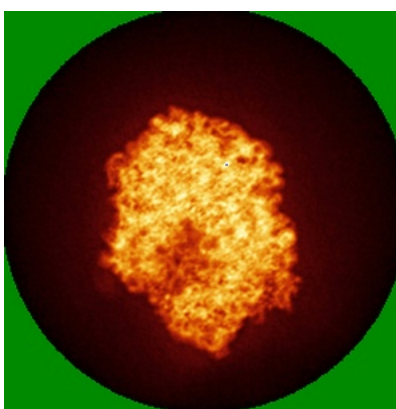
The images above show the largest variance slices of the map in three orthogonal directions.

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

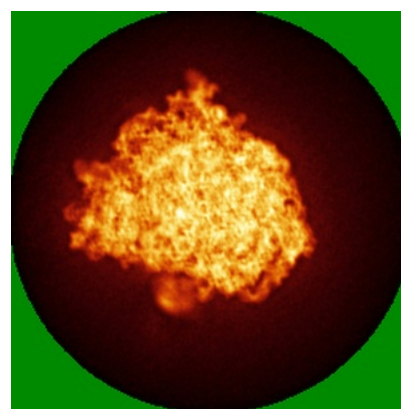
6.4.1 Primary map



X



Y

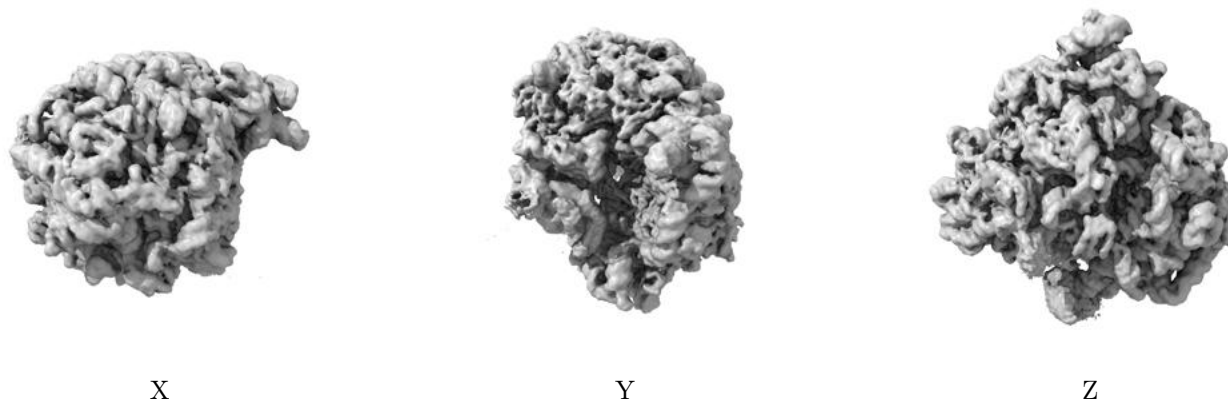


Z

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



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.

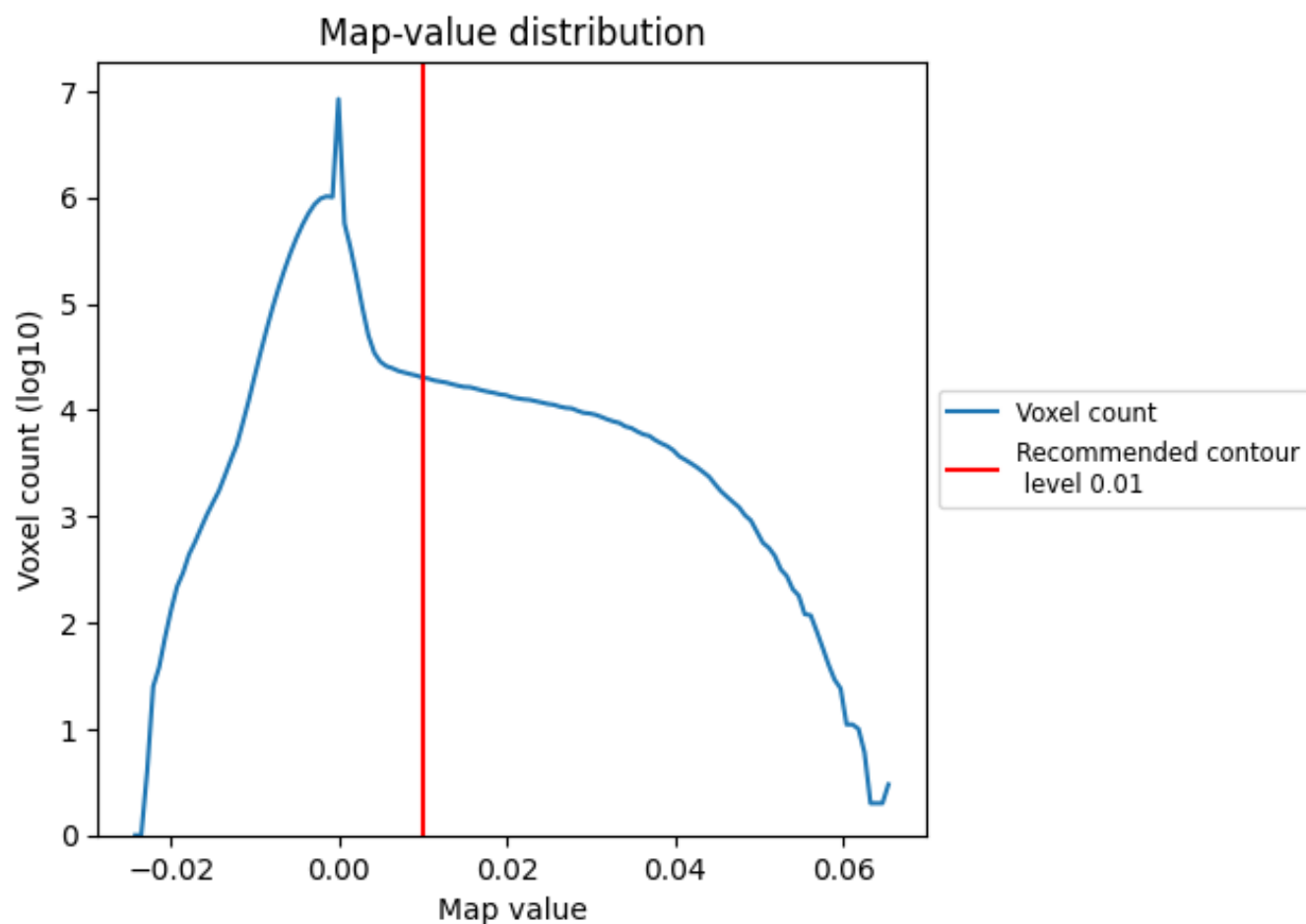
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

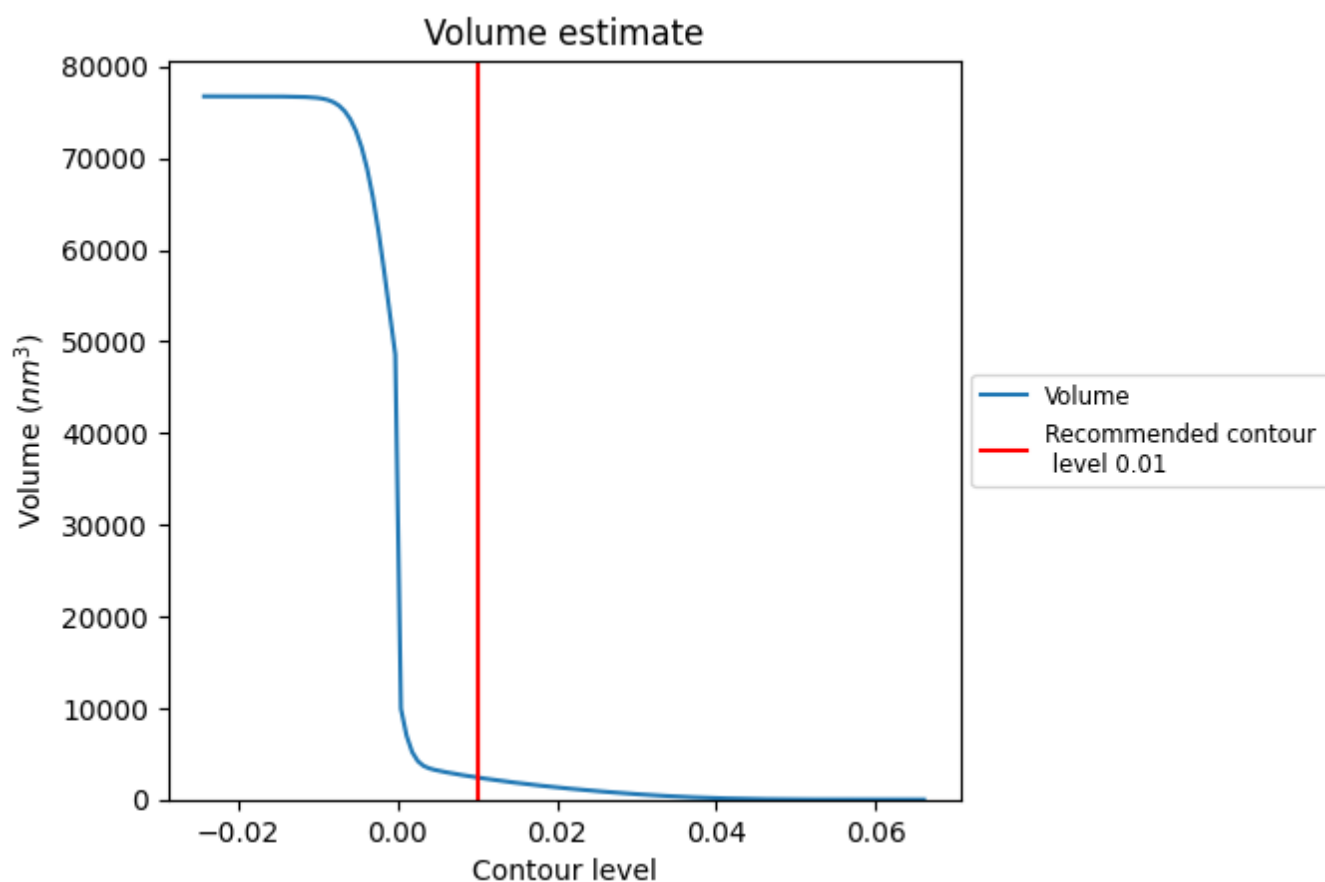
This section contains the results of statistical analysis of the map.

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.

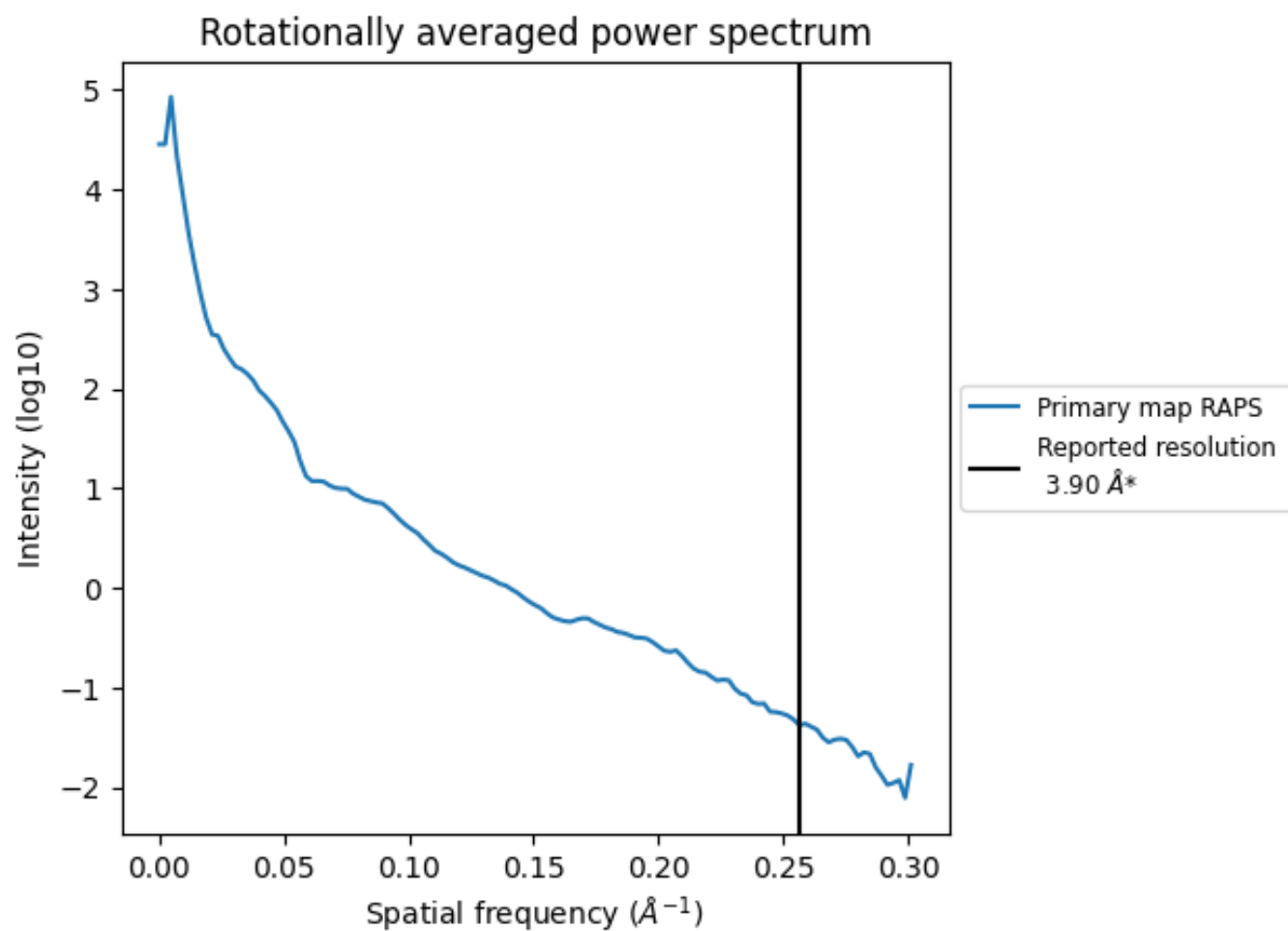
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2414 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

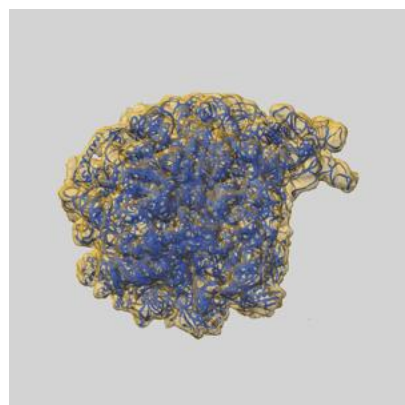
8 Fourier-Shell correlation

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

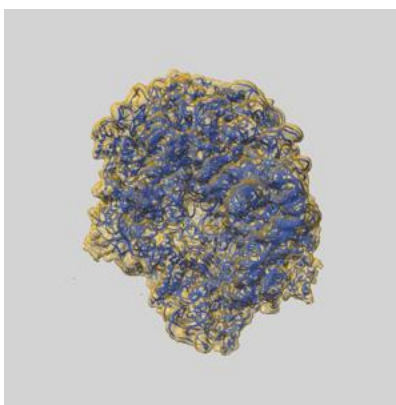
9 Map-model fit [i](#)

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

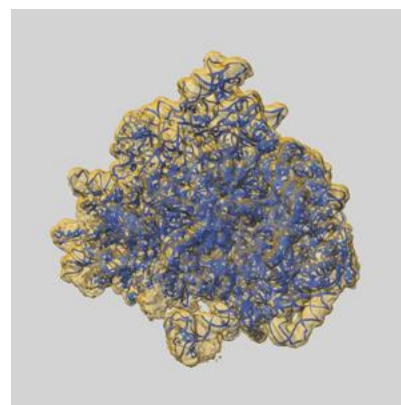
9.1 Map-model overlay [i](#)



X



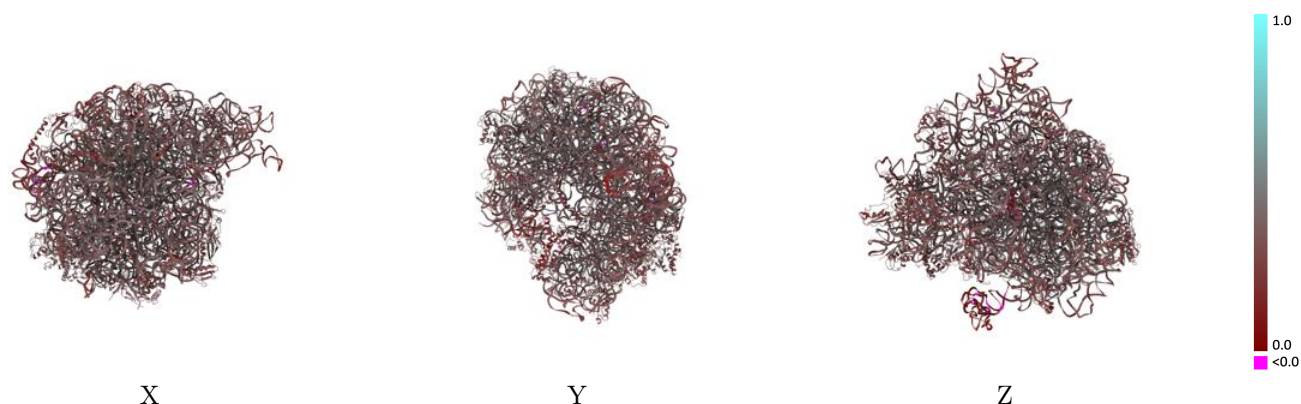
Y



Z

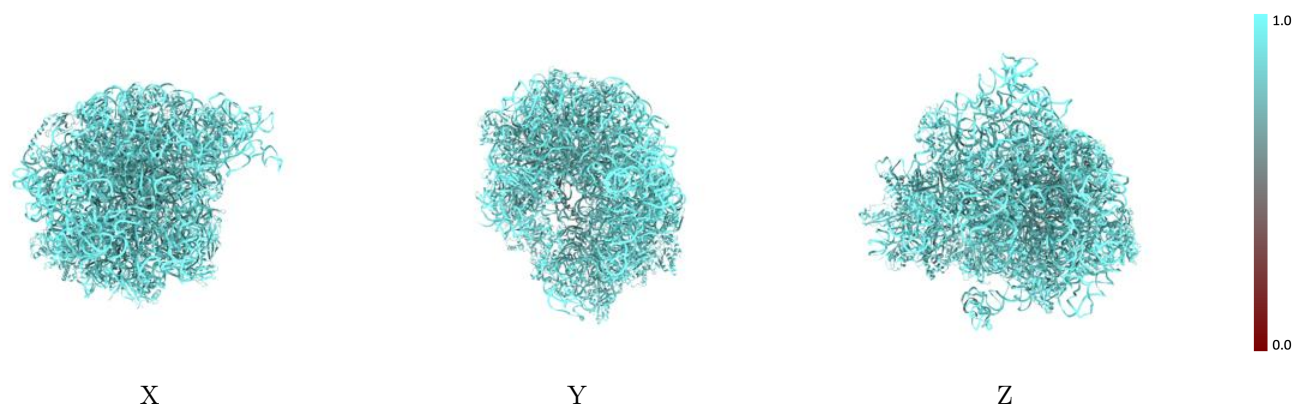
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



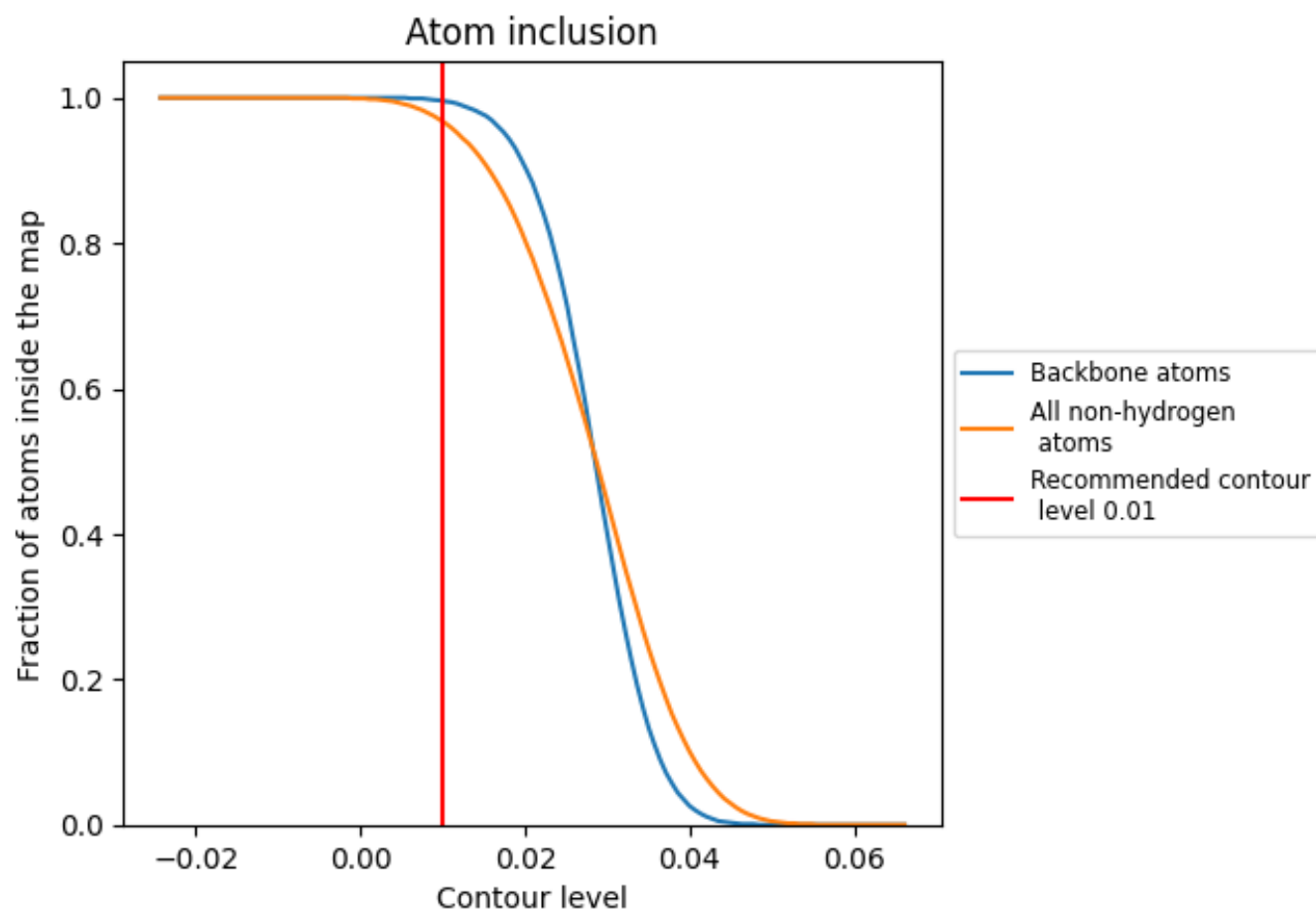
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

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