



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:35 PM UTC

PDB ID : 8VK7 / pdb_00008vk7
EMDB ID : EMD-43305
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX:50S-HflX-B
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-08
Resolution : 3.09 Å (reported)
Based on initial models : 6DZI, 5O61

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:

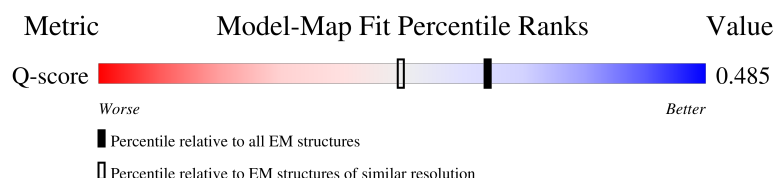
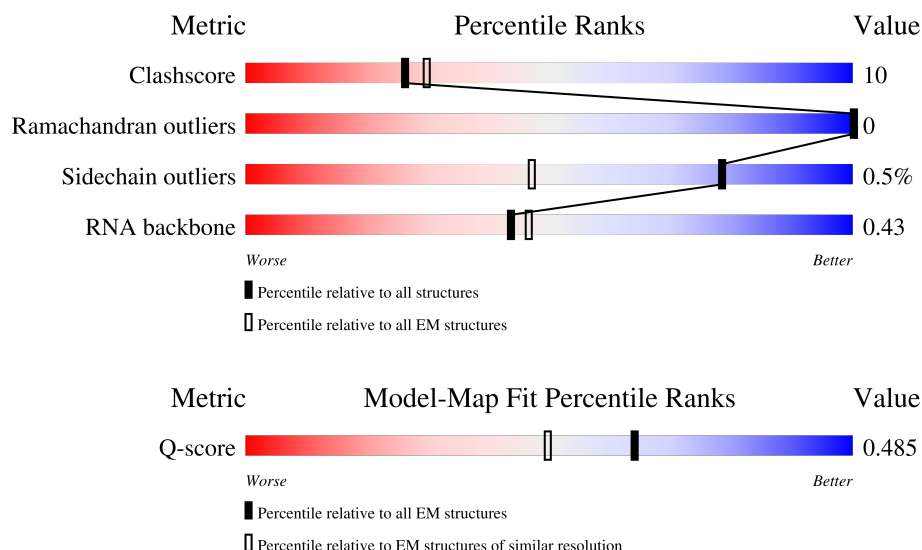
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.09 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	14003 (2.59 - 3.59)

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	2	61	5% 70% 26% .
2	3	24	88% 8% .

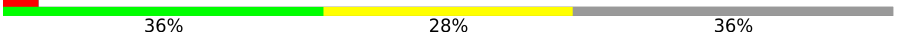
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Mol	Chain	Length	Quality of chain
3	4	470	
4	A	3120	
5	B	118	
6	C	278	
7	D	217	
8	E	215	
9	F	187	
10	G	179	
11	H	151	
12	I	175	
13	J	142	
14	K	147	
15	L	122	
16	M	147	
17	N	138	
18	O	199	
19	P	127	
20	Q	113	
21	R	129	
22	S	103	
23	T	153	
24	U	100	
25	V	105	
26	W	215	
27	X	88	

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Mol	Chain	Length	Quality of chain
28	Y	64	
29	Z	77	
30	b	57	
31	c	55	
32	d	47	
33	e	64	
34	f	37	
35	g	75	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	GCP	4	501	-	-	X	-

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 96832 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 protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	468	Total	C	N	O	S	0	0
			3539	2187	651	694	7		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2950	Total	C	N	O	P	0	0
			63364	28241	11658	20515	2950		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	114	Total	C	N	O	P	0	0
			2438	1088	452	784	114		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 8 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 9 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 13 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 14 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 17 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 19 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 21 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 22 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 23 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 24 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	95	Total	C	N	O	S	0	0
			719	448	135	134	2		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	W	95	Total	C	N	O	0	0
			735	452	149	134		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 28 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 31 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	e	63	Total	C	N	O	0	0
			502	302	115	85		

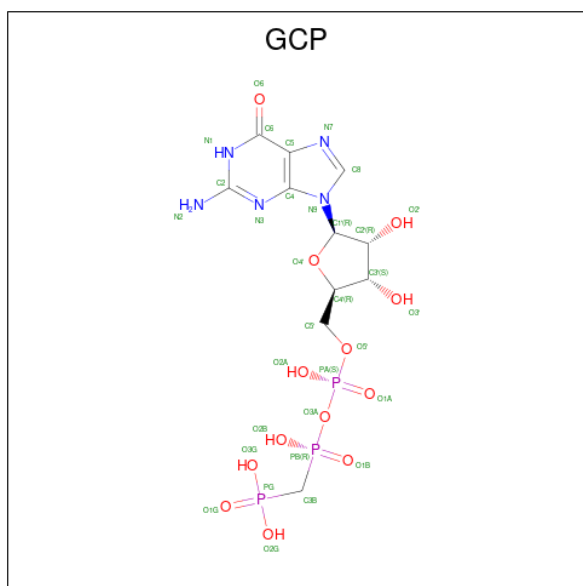
- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 35 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 36 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

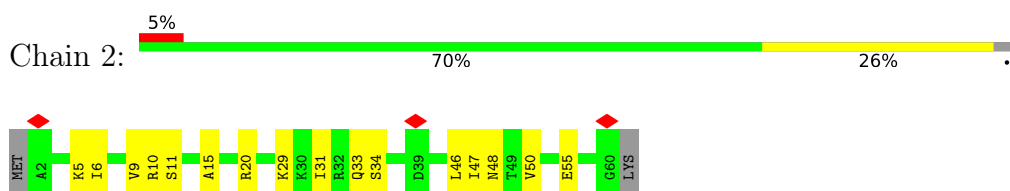


Mol	Chain	Residues	Atoms					AltConf
36	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

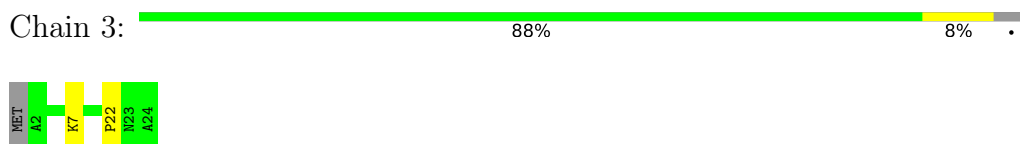
3 Residue-property plots

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.

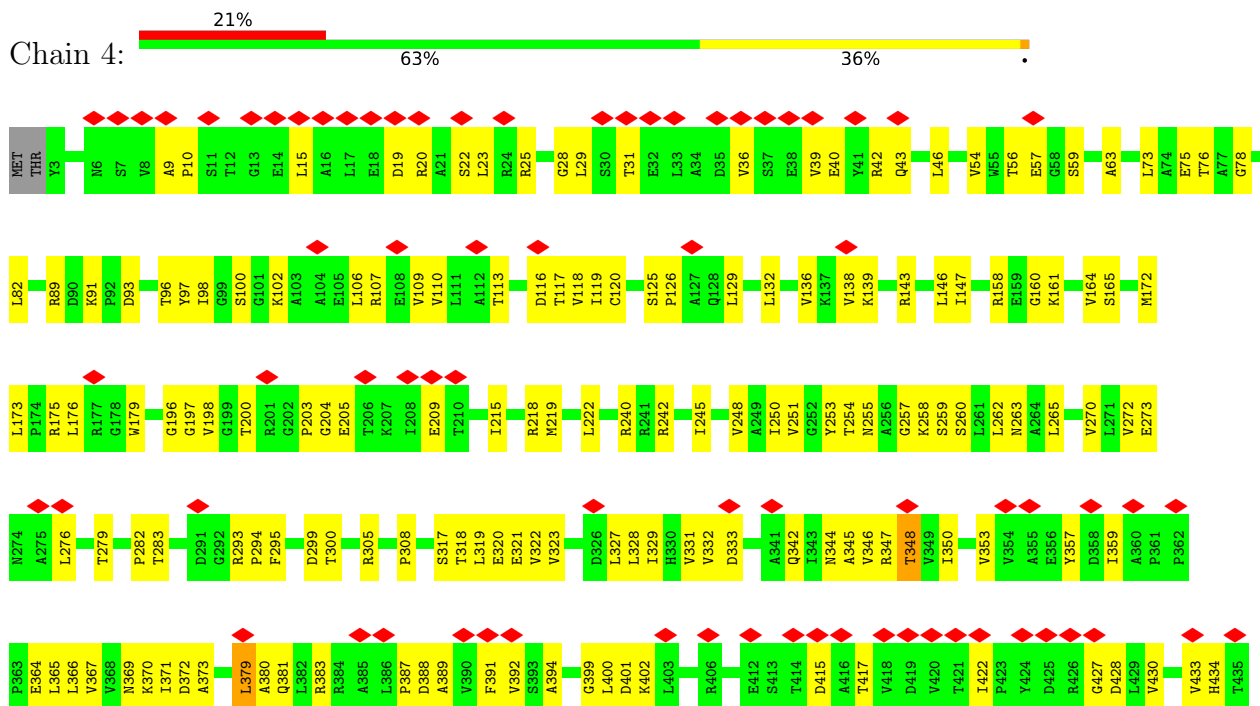
- Molecule 1: 50S ribosomal protein L30

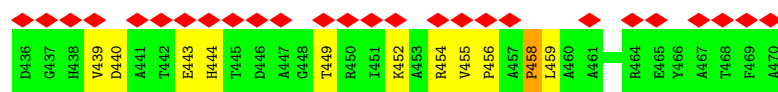


- Molecule 2: 50S Ribosomal Protein L37



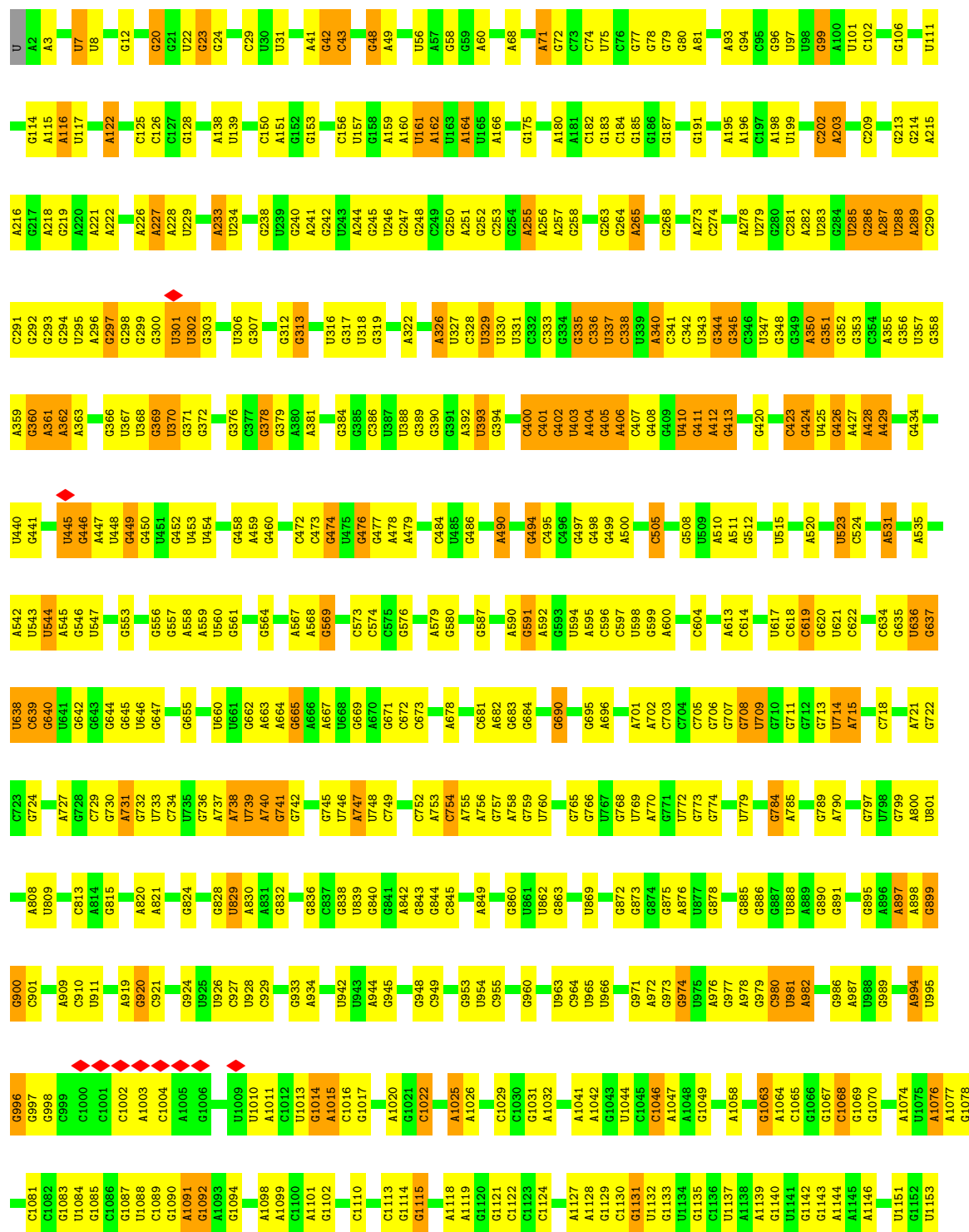
- Molecule 3: GTPase HflX



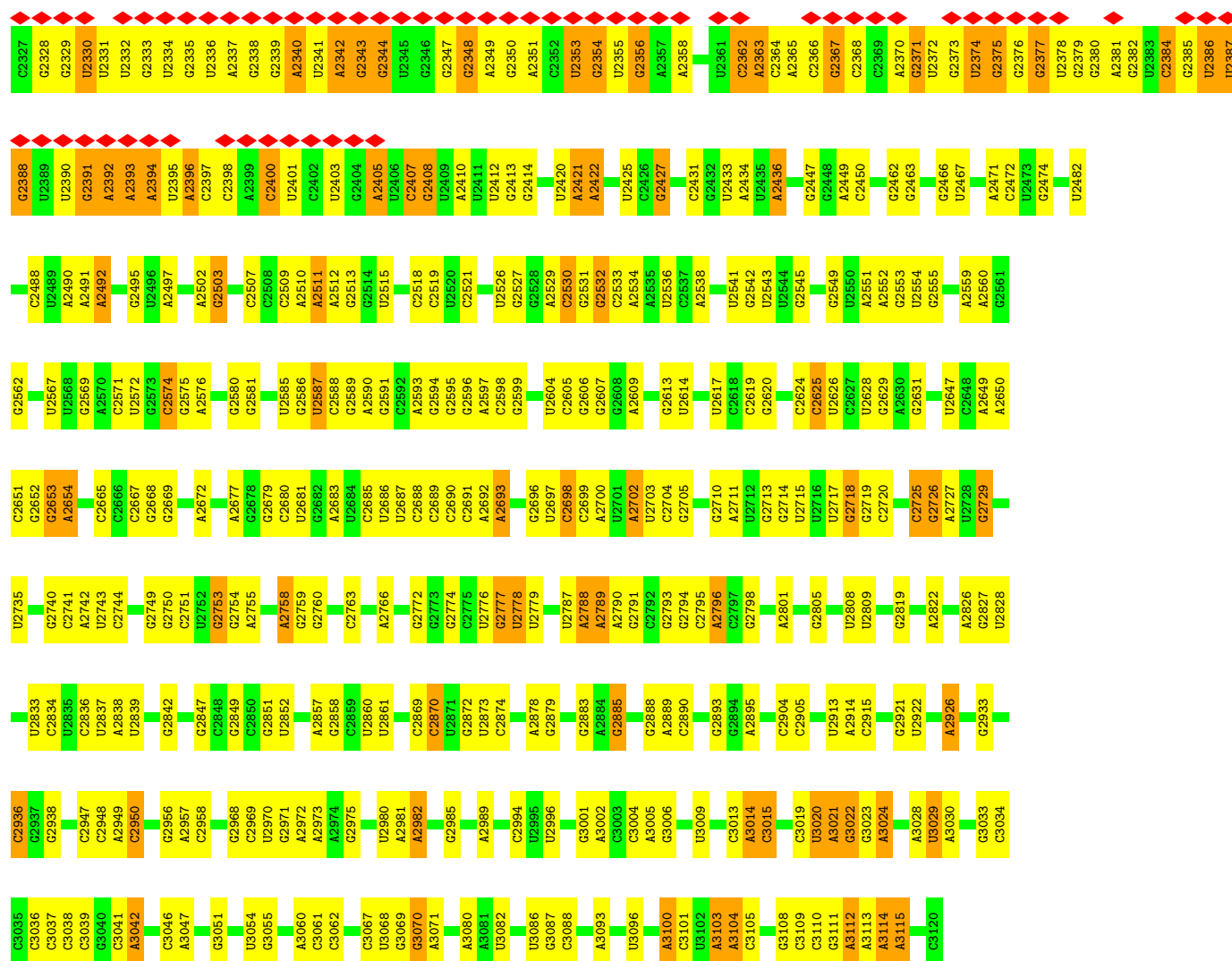


• Molecule 4: 23S ribosomal RNA

Chain A: 49% 35% 10% 5%

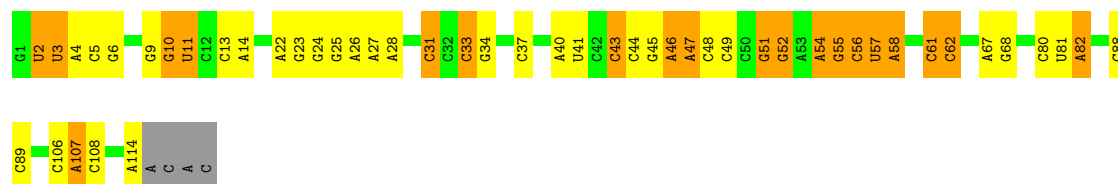


C2224	A2151	C2023	G1917	A1832	G1726	U1641	G1507	G1411	C1321	U1223	G1154
A2225	A2152	G2024	G1921	C1833	A1727	G1642	A1510	A1415	C1322	G1224	C1155
G2228	G2153	C2025	G1921	C1834	U1728	G1643	U1511	A1416	G1323	G1225	A1156
G2234	G2154	A2026	G1927	C1835	A1729	G1644	U1512	A1417	G1324	U1226	G1157
G2235	U2155	G2031	C1927	G1837	U1731	G1645	C1513	A1418	G1326	G1227	U1158
G2236	A2156	A2032	C1930	G1845	U1732	A1648	C1514	A1419	A1327	A1228	G1159
C2243	G2157	U2033	C1930	G1846	U1735	C1649	G1515	G1425	A1328	A1229	G1160
A2244	U2158	G2034	U1931	G1847	G1736	G1650	G1516	A1426	G1329	A1230	C1161
C2245	G2159	A2035	U1932	A1848	A1737	C1651	A1517	U1427	C1330	G1230	G1162
U2246	A2160	U2037	G1933	A1849	U1737	G1653	A1518	G1428	C1331	U1235	G1165
G2251	A2161	A2038	U1937	G1850	G1743	G1654	G1522	C1429	U1335	G1236	A1166
A2254	A2162	C2043	G1938	G1851	A1744	A1655	G1529	G1430	A1336	U1237	C1167
A2255	U2163	G2044	U1945	A1852	C1753	G1657	U1530	G1434	G1337	G1238	A1168
G2256	C2164	A2045	U1946	U1853	G1754	U1665	G1531	A1435	U1338	G1239	A1169
A2257	U2167	A2046	U1947	U1854	A1755	U1669	C1532	G1436	G1339	G1240	A1172
U2261	G2168	C2049	G1950	C1856	G1756	G1670	U1533	A1437	A1340	G1243	G1173
G2262	G2169	U2051	C1954	U1857	U1757	A1673	C1534	G1438	U1341	U1244	G1174
G2263	U2170	C2052	A1955	G1858	G1758	U1674	C1535	G1442	G1342	U1245	A1175
C2267	C2171	C2053	A1956	G1859	A1759	G1675	U1536	G1443	A1344	A1246	G1176
A2274	U2175	C2054	G1957	G1860	G1762	U1676	U1537	U1444	G1350	U1247	U1177
A2275	A2176	C2055	U1972	U1864	G1763	G1677	G1538	G1449	G1351	U1248	U1178
C2276	C2177	C2056	C1973	A1865	U1767	G1678	G1541	G1453	A1352	U1250	U1179
A2277	U2178	C2057	C1974	G1866	C1768	A1679	A1542	G1454	G1357	U1251	G1180
C2278	U2179	C2058	A1974	G1867	G1769	A1680	U1543	G1455	U1358	G1252	G1181
A2279	G2180	C2059	A1975	U1870	G1770	U1681	U1544	U1455	G1359	G1253	C1182
G2280	C2181	C2060	A1976	C1871	U1771	A1682	C1545	G1456	U1360	G1254	U1184
A2284	U2182	C2061	C1977	A1872	G1772	C1683	A	A1457	A1362	G1255	A1187
G2285	G2183	C2062	U1981	U1873	U1780	G1687	G	G1458	G1363	G1256	A1188
A2286	C2184	C2063	G1984	U1874	G1786	A1691	C	U1459	U1364	U1259	G1189
C2287	U2185	C2064	A1985	G1875	A1787	G1692	C	G1365	A1366	G1260	G1190
G2288	C2186	C2065	U1986	U1876	G1788	C1693	G	A1464	G1367	A1261	A1191
C2289	A2187	C2066	G1987	G1877	A1789	U1694	U	G1465	A1368	G1268	G1192
G2290	C2188	C2067	C1988	G1878	G1797	C1695	C	G1466	U1369	C1269	C1193
A2294	U2189	C2068	U1989	U1879	U1798	U1696	C	U1467	G1370	G1270	C1194
C2295	C2190	C2069	A1990	U1880	C1797	G1697	A	A1468	U1371	C1271	C1195
U2301	A2191	C2070	C1991	A1881	U1798	U1697	C	G1473	G1379	C1272	C1197
G2302	U2192	C2071	U1996	A1882	A1803	G1703	C	G1478	A1380	A1274	G1198
U2303	G2193	C2072	U1996	G1883	G1804	U1704	C	G1479	G1381	A1275	U1199
U2304	U2194	C2073	A2001	G1884	G1805	C1705	A	A1480	U1386	G1287	A1202
G2305	C2195	C2074	A2002	G1885	A1806	U1706	C	C1481	A1387	C1287	A1203
U2306	U2196	C2075	A2003	A1886	C1807	A1710	C	G1485	C1393	G1291	G1205
G2307	C2197	C2076	A2004	A1887	G1813	G1711	C	U1486	A1394	U1292	A1206
U2308	U2198	C2077	A2005	G1892	C1823	U1712	C	U1487	G1295	G1293	G1207
G2309	C2199	C2078	A2006	C1893	C1824	G1713	C	G1488	G1400	U1294	U1208
U2310	U2200	C2079	A2007	G1894	C1825	U1714	C	U1489	C1403	G1296	G1209
G2311	C2201	C2080	A2008	G1895	C1826	A1715	C	U1493	U1404	A1304	C1211
U2312	U2202	C2081	A2009	C1896	C1827	U1716	C	U1494	U1405	G1305	U1212
G2313	C2203	C2082	A2010	A1897	A1828	U1717	C	G1499	U1406	A1213	A1214
U2314	U2204	C2083	A2011	U1908	C1829	G1724	C	A1500	C1407	C1314	U1215
G2315	C2205	C2084	A2012	U1909	C1830	G1725	C	G1639	U1216	G1217	A1216
U2316	U2206	C2085	A2013	U1910	A1831	G1726	C	A1640	G1217	G1218	G1219
G2317	C2207	C2086	A2014	U1911	A1832	G1727	C				
U2318	U2208	C2087	A2015	U1912	A1833	G1728	C				
G2319	C2209	C2088	A2016	U1913	A1834	G1729	C				
U2320	U2210	C2089	A2017	U1914	A1835	G1730	C				
G2321	C2211	C2090	A2018	U1915	A1836	G1731	C				
U2322	U2212	C2091	A2019	U1916	A1837	G1732	C				
G2323	C2213	C2092	A2020	U1917	A1838	G1733	C				
U2324	U2214	C2093	A2021	U1918	A1839	G1734	C				
G2325	C2215	C2094	A2022	U1919	A1840	G1735	C				
A2326	U2216	C2095	A2023	U1920	A1841	G1736	C				



• Molecule 5: 5S ribosomal RNA

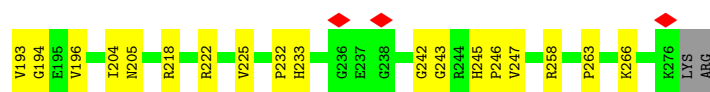
Chain B: 54% 25% 17%



• Molecule 6: 50S ribosomal protein L2

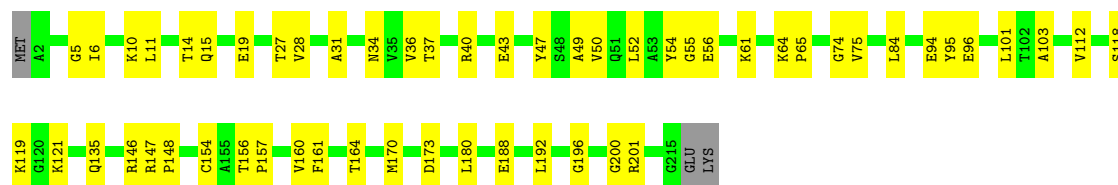
Chain C: 81% 18%





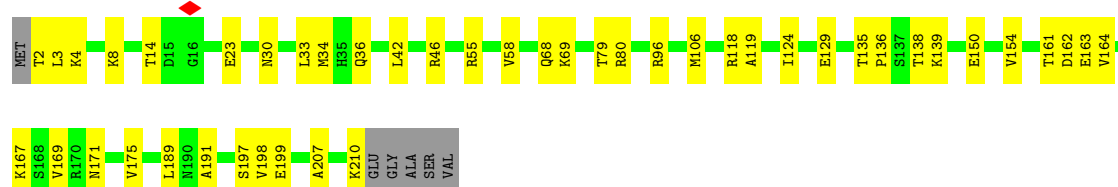
• Molecule 7: 50S ribosomal protein L3

Chain D: 73% 25%



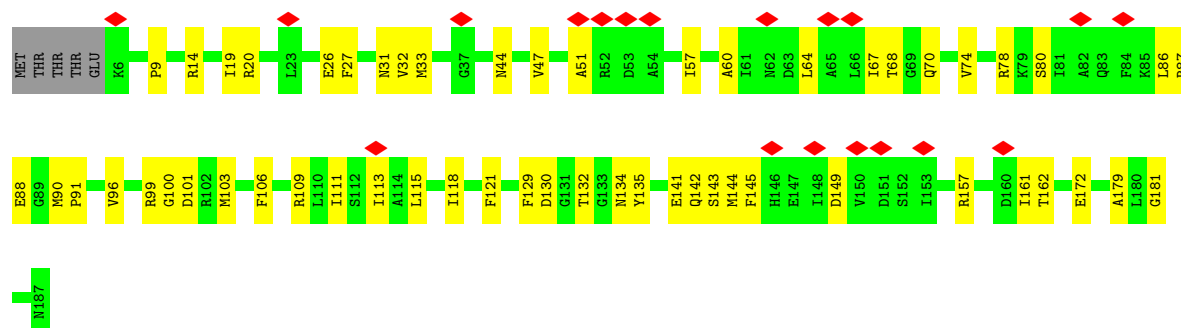
• Molecule 8: 50S Ribosomal Protein L4

Chain E: 76% 21%



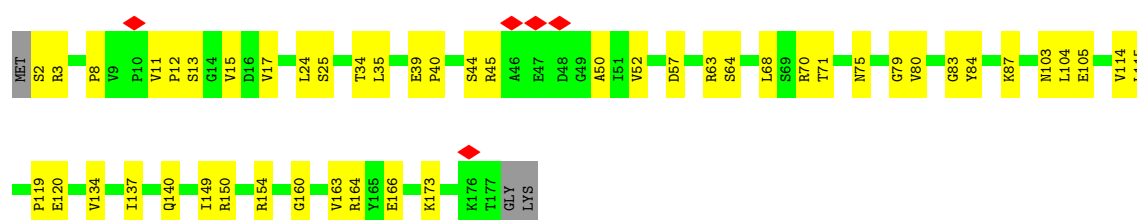
• Molecule 9: 50S Ribosomal Protein L5

Chain F: 10% 68% 29%

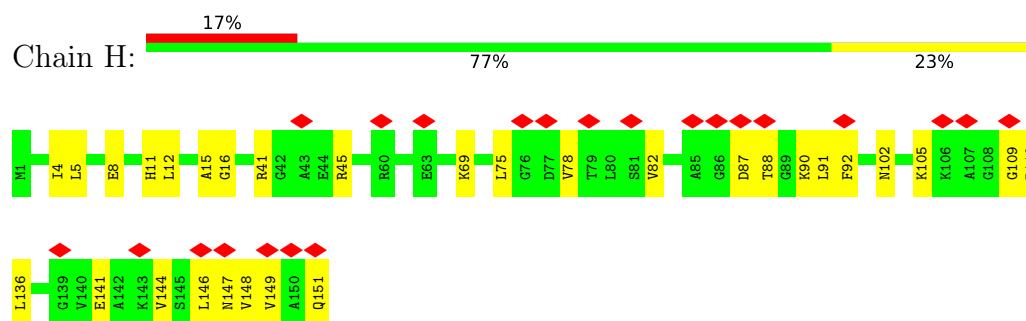


• Molecule 10: 50S ribosomal protein L6

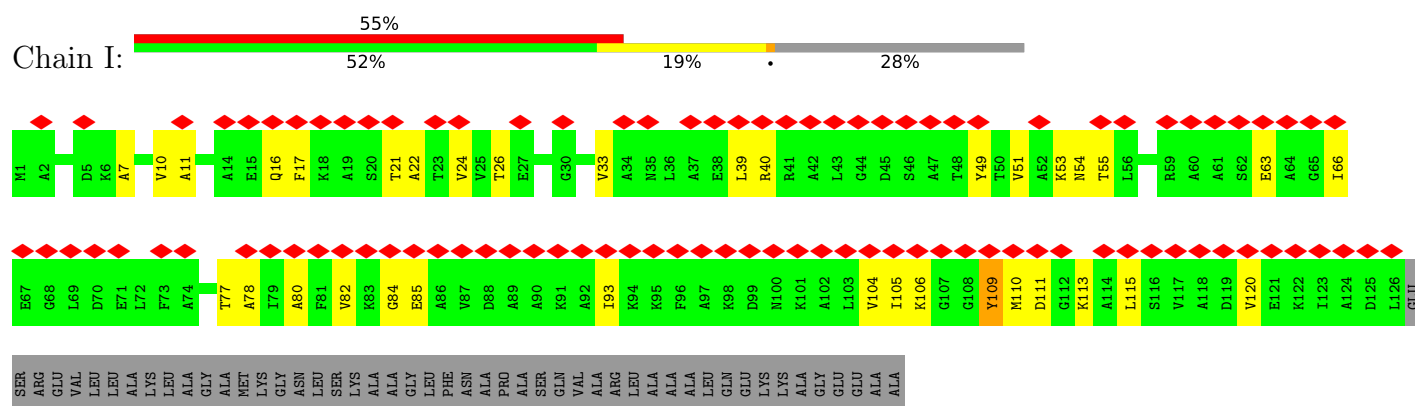
Chain G: 72% 27%



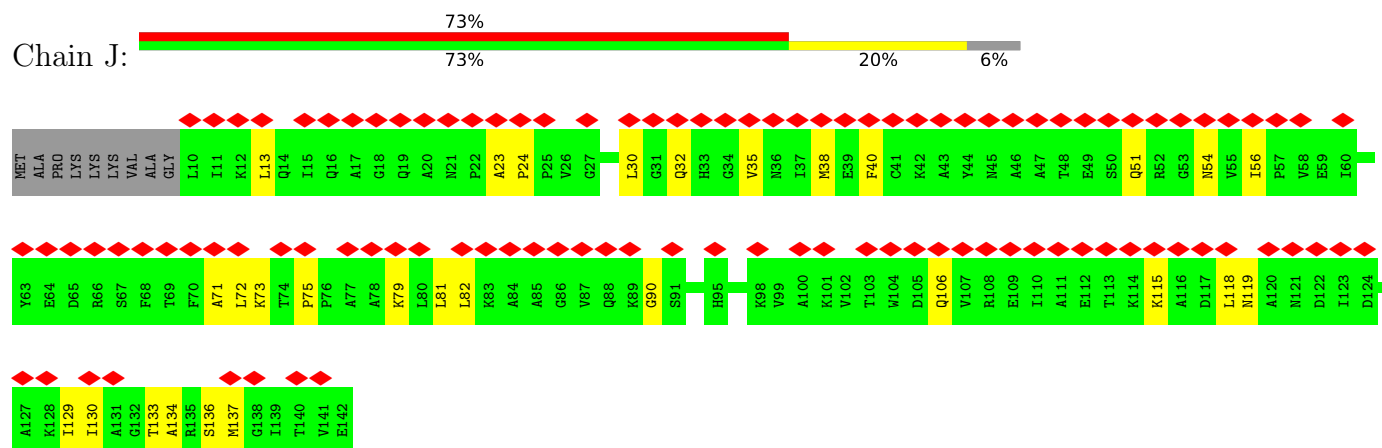
- Molecule 11: 50S ribosomal protein L9



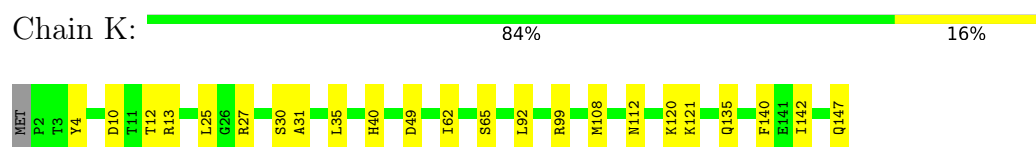
- Molecule 12: 50S ribosomal protein L10



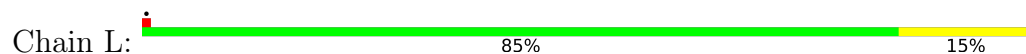
- Molecule 13: 50S ribosomal protein L11



- Molecule 14: 50S Ribosomal Protein L13



- Molecule 15: 50S ribosomal protein L14





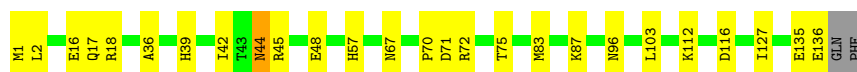
- Molecule 16: 50S ribosomal protein L15

Chain M: 77% 22%



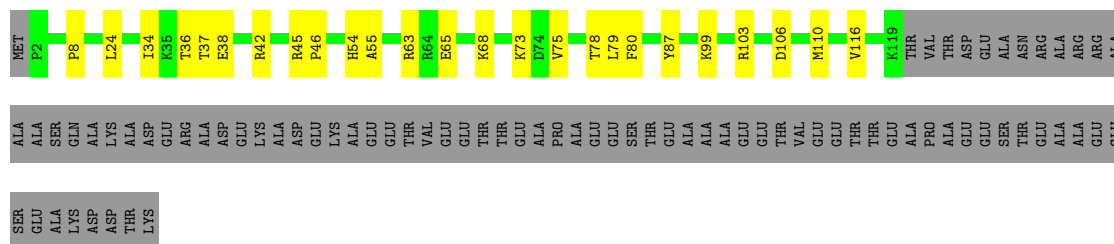
- Molecule 17: Large ribosomal subunit protein uL16

Chain N: 80% 18%



- Molecule 18: 50S ribosomal protein L17

Chain O: 47% 13% 41%



- Molecule 19: 50S Ribosomal Protein L18

Chain P: 70% 29%

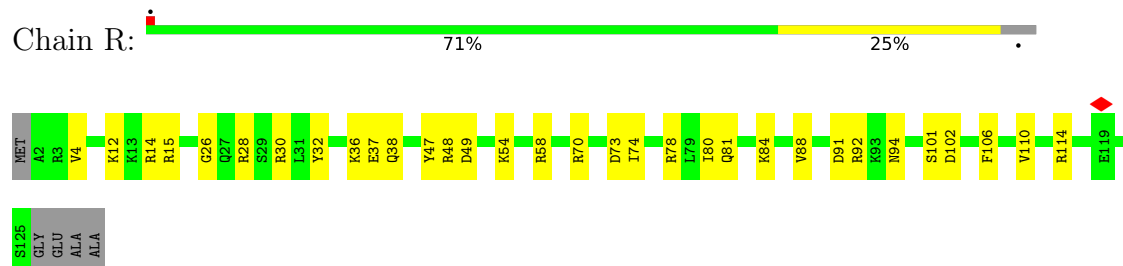


- Molecule 20: 50S ribosomal protein L19

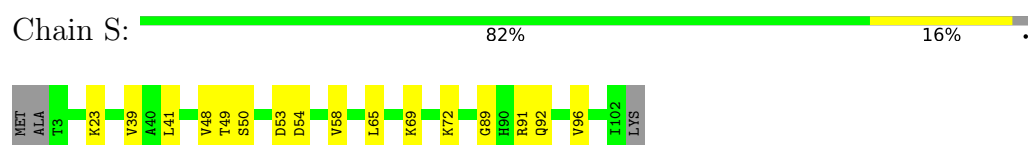
Chain Q: 64% 36%



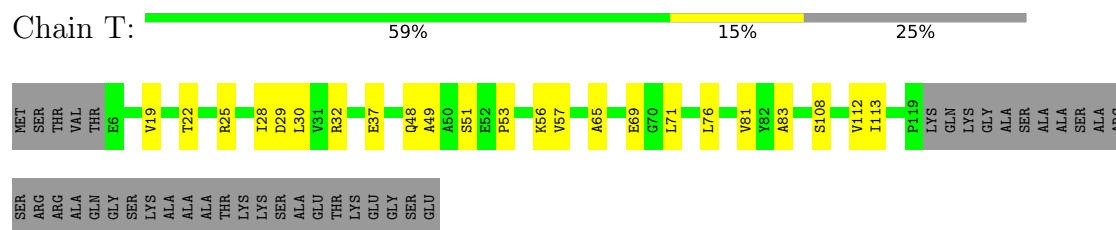
- Molecule 21: 50S Ribosomal Protein L20



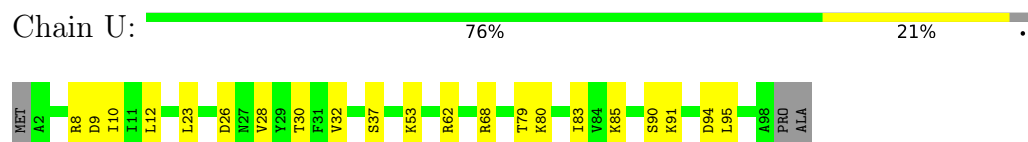
- Molecule 22: 50S Ribosomal Protein L21



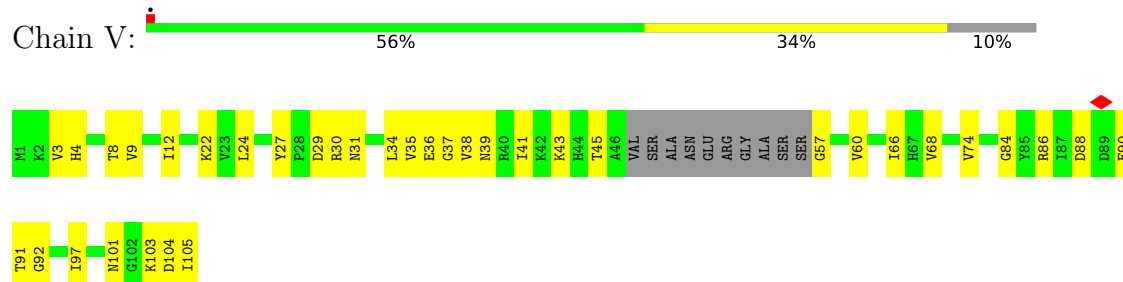
- Molecule 23: 50S Ribosomal Protein L22



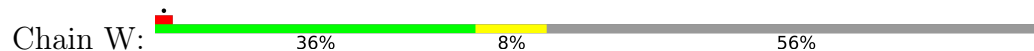
- Molecule 24: 50S Ribosomal Protein L23



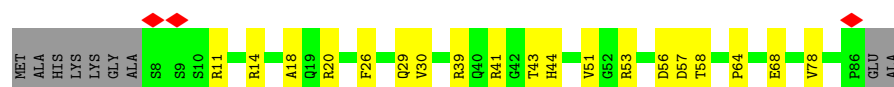
- Molecule 25: 50S ribosomal protein L24



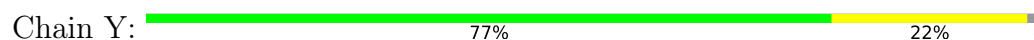
- Molecule 26: 50S ribosomal protein L25



- Molecule 27: 50S ribosomal protein L27



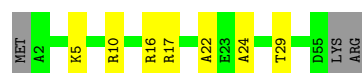
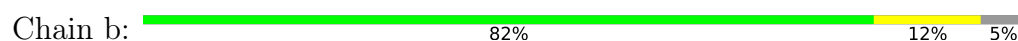
- Molecule 28: 50S Ribosomal Protein L28



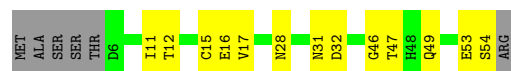
- Molecule 29: 50S ribosomal protein L29



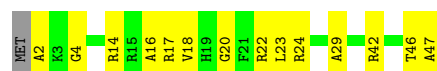
- Molecule 30: 50S ribosomal protein L32



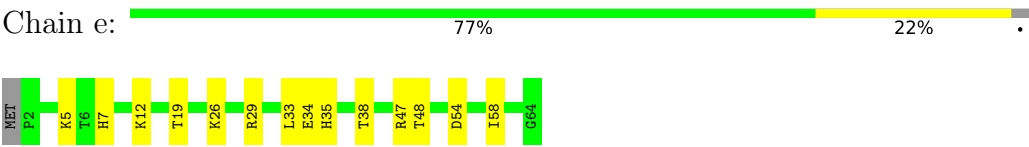
- Molecule 31: 50S Ribosomal Protein L33



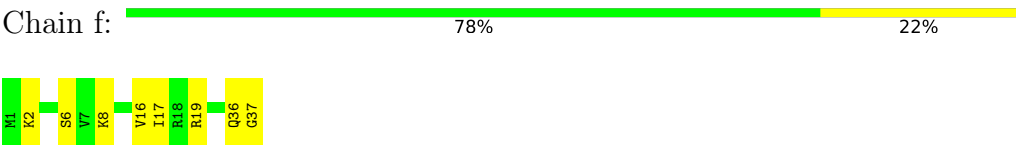
- Molecule 32: 50S ribosomal protein L34



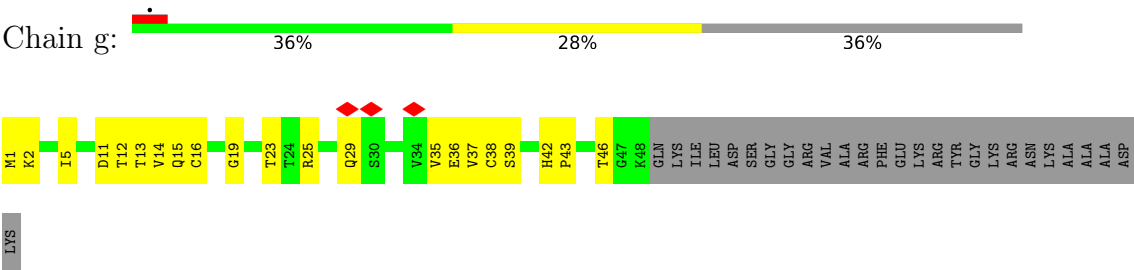
● Molecule 33: 50S ribosomal protein L35



● Molecule 34: 50S ribosomal protein L36



● Molecule 35: 50S Ribosomal Protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.85	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.755	Depositor
Minimum map value	-0.985	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	430.4, 430.4, 430.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.076, 1.076, 1.076	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP

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	2	0.26	0/477	0.36	0/640
2	3	0.29	0/191	0.34	0/247
3	4	0.46	2/3583 (0.1%)	0.59	5/4857 (0.1%)
4	A	0.34	0/70952	0.32	0/110707
5	B	0.26	0/2727	0.32	0/4250
6	C	0.29	0/2153	0.43	0/2895
7	D	0.30	0/1609	0.41	0/2165
8	E	0.29	0/1592	0.38	0/2153
9	F	0.24	0/1467	0.49	2/1973 (0.1%)
10	G	0.22	0/1369	0.38	0/1848
11	H	0.21	0/1027	0.42	0/1398
12	I	0.17	0/925	0.38	0/1246
13	J	0.17	0/1006	0.39	0/1364
14	K	0.29	0/1157	0.39	0/1567
15	L	0.28	0/946	0.41	0/1268
16	M	0.28	0/1091	0.43	0/1457
17	N	0.30	0/1118	0.39	0/1506
18	O	0.30	0/945	0.38	0/1267
19	P	0.23	0/966	0.38	0/1298
20	Q	0.27	0/921	0.40	0/1236
21	R	0.31	0/1000	0.37	0/1341
22	S	0.27	0/764	0.36	0/1030
23	T	0.28	0/887	0.39	0/1204
24	U	0.27	0/766	0.38	0/1030
25	V	0.25	0/725	0.39	0/969
26	W	0.22	0/745	0.39	0/1008
27	X	0.31	0/595	0.40	0/798
28	Y	0.29	0/478	0.38	0/641
29	Z	0.24	0/534	0.34	0/713
30	b	0.28	0/427	0.34	0/572
31	c	0.26	0/413	0.35	0/553
32	d	0.33	0/380	0.36	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.32	0/507	0.40	0/672
34	f	0.28	0/303	0.37	0/401
35	g	0.17	0/372	0.32	0/503
All	All	0.32	2/105118 (0.0%)	0.35	7/157277 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	458	PRO	CG-CD	-21.28	0.78	1.50
3	4	458	PRO	N-CD	9.82	1.61	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	458	PRO	N-CD-CG	-20.42	72.57	103.20
3	4	458	PRO	CA-CB-CG	-11.04	83.52	104.50
3	4	458	PRO	CA-N-CD	-9.32	98.95	112.00
9	F	9	PRO	N-CD-CG	-7.30	92.24	103.20
9	F	9	PRO	CA-CB-CG	-6.87	91.45	104.50

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	2	474	0	500	8	0
2	3	189	0	205	2	0
3	4	3539	0	3584	147	0
4	A	63364	0	31879	899	0
5	B	2438	0	1241	38	0
6	C	2110	0	2165	41	0
7	D	1587	0	1630	41	0
8	E	1569	0	1607	37	0
9	F	1445	0	1476	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	G	1348	0	1399	42	0
11	H	1018	0	988	29	0
12	I	918	0	959	30	0
13	J	990	0	1021	28	0
14	K	1130	0	1167	20	0
15	L	938	0	1000	14	0
16	M	1078	0	1151	27	0
17	N	1092	0	1128	20	0
18	O	928	0	972	16	0
19	P	956	0	991	32	0
20	Q	907	0	938	32	0
21	R	988	0	1038	26	0
22	S	754	0	802	12	0
23	T	873	0	909	20	0
24	U	756	0	802	17	0
25	V	719	0	768	30	0
26	W	735	0	756	11	0
27	X	586	0	601	17	0
28	Y	470	0	484	9	0
29	Z	531	0	541	11	0
30	b	423	0	463	7	0
31	c	405	0	411	8	0
32	d	377	0	411	10	0
33	e	502	0	541	18	0
34	f	299	0	324	7	0
35	g	364	0	350	13	0
36	4	32	0	14	15	0
All	All	96832	0	65216	1602	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 10.

The worst 5 of 1602 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)
4:A:287:A:O2'	4:A:288:U:O5'	1.81	0.97
4:A:1543:A:N7	4:A:1627:U:O2	1.98	0.95
5:B:10:G:O2'	5:B:11:U:O5'	1.84	0.94
4:A:1211:G:N2	4:A:1217:G:O6	1.99	0.94
3:4:143:ARG:NH2	3:4:305:ARG:O	2.01	0.93

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	
1	2	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
3	4	466/470 (99%)	369 (79%)	97 (21%)	0	100	100
6	C	273/278 (98%)	248 (91%)	25 (9%)	0	100	100
7	D	212/217 (98%)	200 (94%)	12 (6%)	0	100	100
8	E	207/215 (96%)	185 (89%)	22 (11%)	0	100	100
9	F	180/187 (96%)	156 (87%)	24 (13%)	0	100	100
10	G	174/179 (97%)	160 (92%)	14 (8%)	0	100	100
11	H	149/151 (99%)	126 (85%)	23 (15%)	0	100	100
12	I	124/175 (71%)	110 (89%)	14 (11%)	0	100	100
13	J	131/142 (92%)	113 (86%)	18 (14%)	0	100	100
14	K	144/147 (98%)	127 (88%)	17 (12%)	0	100	100
15	L	120/122 (98%)	108 (90%)	12 (10%)	0	100	100
16	M	143/147 (97%)	127 (89%)	16 (11%)	0	100	100
17	N	134/138 (97%)	120 (90%)	14 (10%)	0	100	100
18	O	116/199 (58%)	109 (94%)	7 (6%)	0	100	100
19	P	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
20	Q	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
21	R	122/129 (95%)	114 (93%)	8 (7%)	0	100	100
22	S	98/103 (95%)	92 (94%)	6 (6%)	0	100	100
23	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
24	U	95/100 (95%)	86 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	V	91/105 (87%)	80 (88%)	11 (12%)	0	100	100
26	W	93/215 (43%)	87 (94%)	6 (6%)	0	100	100
27	X	77/88 (88%)	74 (96%)	3 (4%)	0	100	100
28	Y	61/64 (95%)	56 (92%)	5 (8%)	0	100	100
29	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
30	b	52/57 (91%)	46 (88%)	6 (12%)	0	100	100
31	c	47/55 (86%)	44 (94%)	3 (6%)	0	100	100
32	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
33	e	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
34	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
35	g	46/75 (61%)	33 (72%)	13 (28%)	0	100	100
All	All	3982/4461 (89%)	3559 (89%)	423 (11%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	2	52/54 (96%)	51 (98%)	1 (2%)	50	73
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	370/372 (100%)	368 (100%)	2 (0%)	81	85
6	C	215/218 (99%)	214 (100%)	1 (0%)	81	85
7	D	160/163 (98%)	159 (99%)	1 (1%)	78	83
8	E	169/173 (98%)	168 (99%)	1 (1%)	78	83
9	F	151/156 (97%)	151 (100%)	0	100	100
10	G	148/150 (99%)	148 (100%)	0	100	100
11	H	90/116 (78%)	89 (99%)	1 (1%)	65	78
12	I	89/120 (74%)	88 (99%)	1 (1%)	65	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	J	102/108 (94%)	102 (100%)	0	100	100
14	K	119/120 (99%)	119 (100%)	0	100	100
15	L	100/100 (100%)	99 (99%)	1 (1%)	68	79
16	M	112/114 (98%)	112 (100%)	0	100	100
17	N	114/116 (98%)	112 (98%)	2 (2%)	51	73
18	O	97/158 (61%)	97 (100%)	0	100	100
19	P	93/94 (99%)	93 (100%)	0	100	100
20	Q	100/100 (100%)	100 (100%)	0	100	100
21	R	97/99 (98%)	97 (100%)	0	100	100
22	S	81/83 (98%)	81 (100%)	0	100	100
23	T	90/117 (77%)	89 (99%)	1 (1%)	65	78
24	U	83/85 (98%)	83 (100%)	0	100	100
25	V	79/86 (92%)	78 (99%)	1 (1%)	61	77
26	W	77/168 (46%)	76 (99%)	1 (1%)	61	77
27	X	58/63 (92%)	58 (100%)	0	100	100
28	Y	50/51 (98%)	50 (100%)	0	100	100
29	Z	58/66 (88%)	58 (100%)	0	100	100
30	b	43/46 (94%)	43 (100%)	0	100	100
31	c	47/52 (90%)	47 (100%)	0	100	100
32	d	35/36 (97%)	35 (100%)	0	100	100
33	e	53/54 (98%)	53 (100%)	0	100	100
34	f	35/35 (100%)	35 (100%)	0	100	100
35	g	43/63 (68%)	40 (93%)	3 (7%)	14	41
All	All	3228/3555 (91%)	3211 (100%)	17 (0%)	78	85

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	g	5	ILE
35	g	23	THR
12	I	109	TYR
15	L	28	SER
17	N	44	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
19	P	50	GLN
22	S	13	GLN
26	W	64	ASN
23	T	67	ASN
21	R	122	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	2947/3120 (94%)	675 (22%)	20 (0%)
5	B	113/118 (95%)	32 (28%)	6 (5%)
All	All	3060/3238 (94%)	707 (23%)	26 (0%)

5 of 707 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	7	U
4	A	12	G
4	A	20	G
4	A	23	G
4	A	31	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	2155	U
4	A	2362	C
5	B	57	U
4	A	2343	G
4	A	2374	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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
36	GCP	4	501	-	32,34,34	1.39	7 (21%)	49,54,54	1.80	8 (16%)

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
36	GCP	4	501	-	-	1/19/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	4	501	GCP	C5-C4	2.88	1.46	1.38
36	4	501	GCP	C6-N1	-2.71	1.33	1.38
36	4	501	GCP	PG-O3G	2.70	1.61	1.55
36	4	501	GCP	PG-O2G	2.61	1.60	1.55
36	4	501	GCP	C5-N7	-2.16	1.34	1.39

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	4	501	GCP	C5-C4-N3	-5.66	119.38	128.39
36	4	501	GCP	PB-O3A-PA	-4.62	117.30	132.37
36	4	501	GCP	C2-N3-C4	4.39	119.86	112.30
36	4	501	GCP	N9-C4-N3	4.30	134.55	125.95
36	4	501	GCP	C6-C5-N7	3.09	135.92	130.29

There are no chirality outliers.

All (1) torsion outliers are listed below:

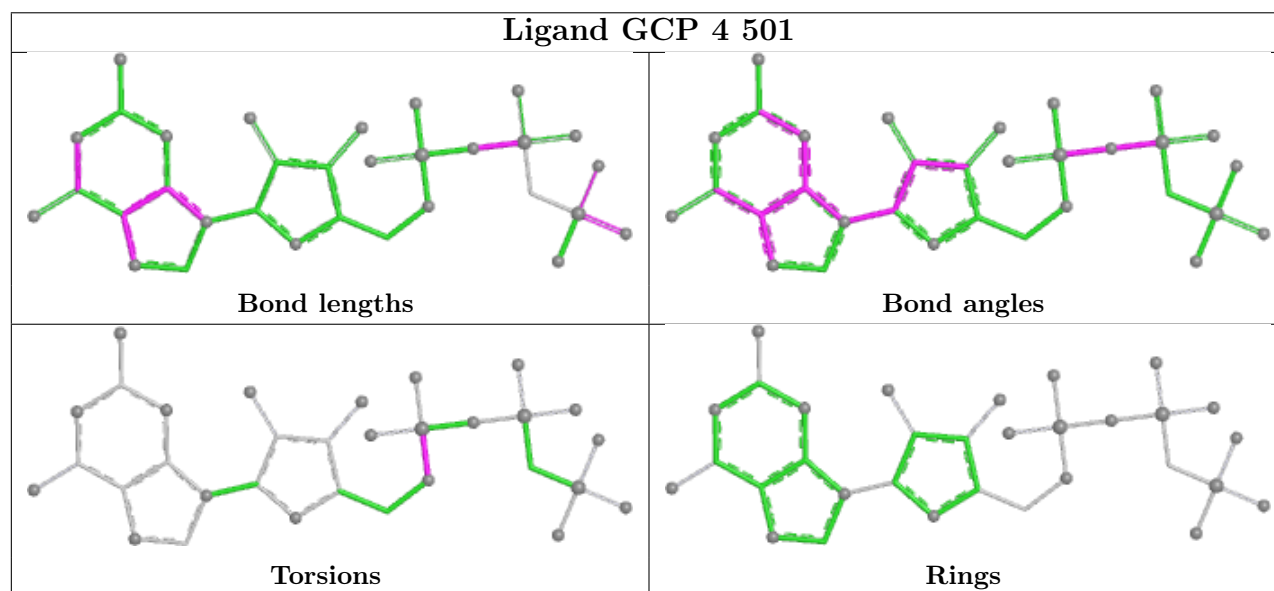
Mol	Chain	Res	Type	Atoms
36	4	501	GCP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	4	501	GCP	15	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

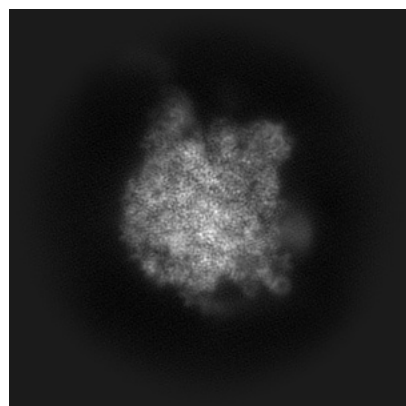
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43305. These allow visual inspection of the internal detail of the map and identification of artifacts.

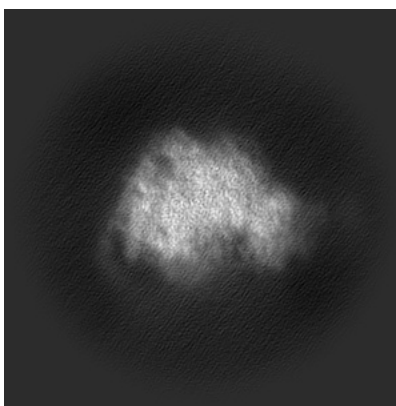
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

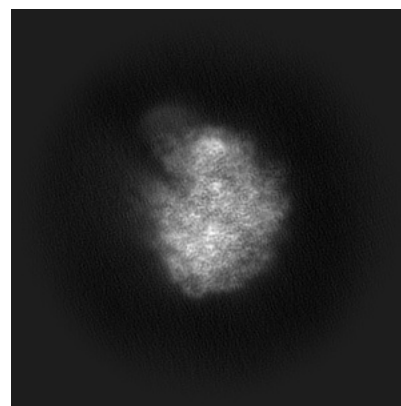
6.1.1 Primary map



X

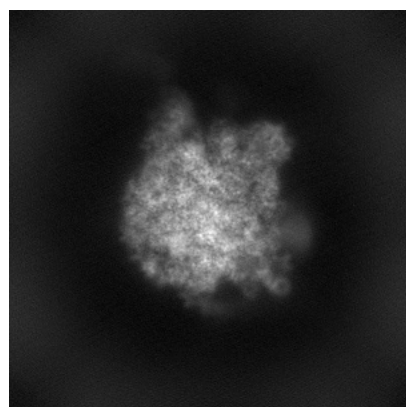


Y

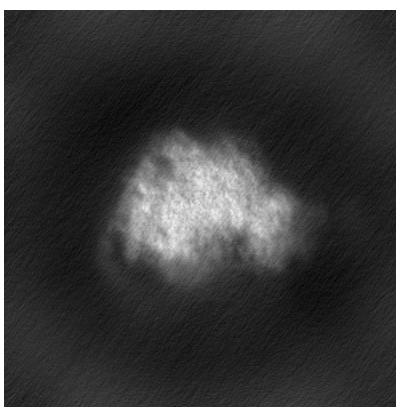


Z

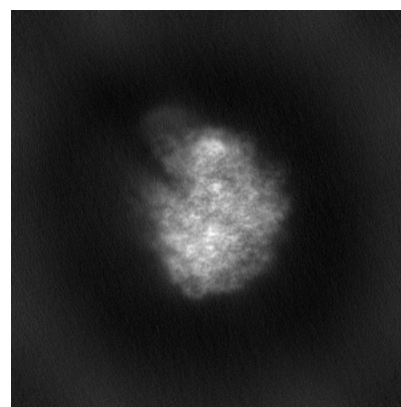
6.1.2 Raw map



X



Y

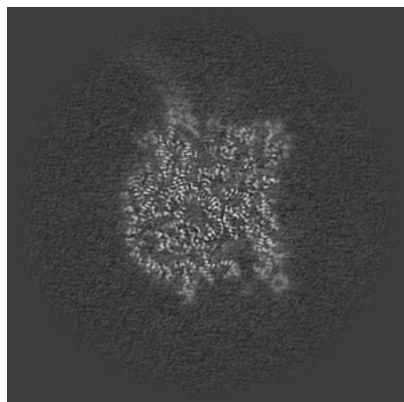


Z

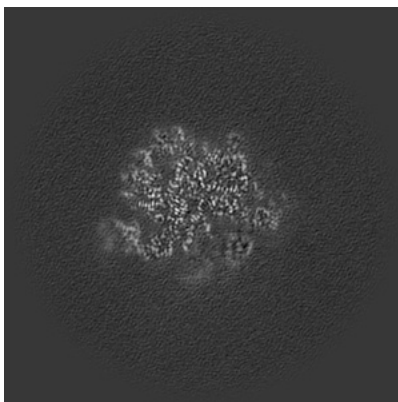
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

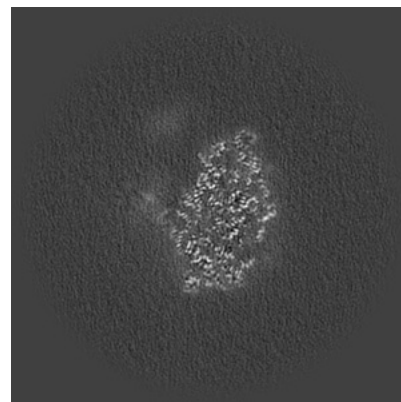
6.2.1 Primary map



X Index: 200

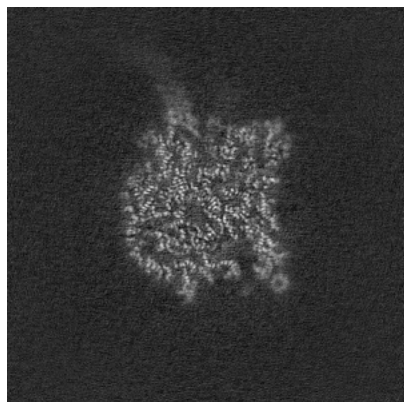


Y Index: 200

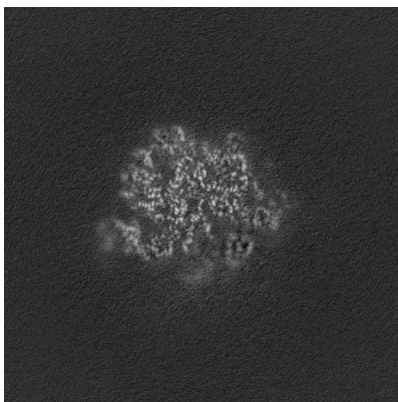


Z Index: 200

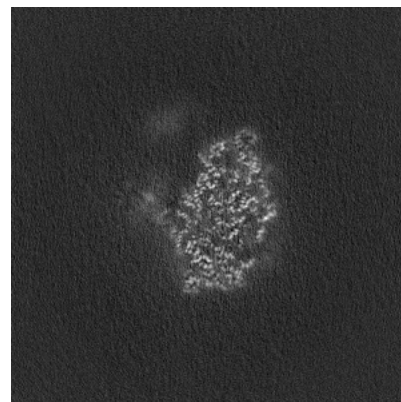
6.2.2 Raw map



X Index: 200



Y Index: 200

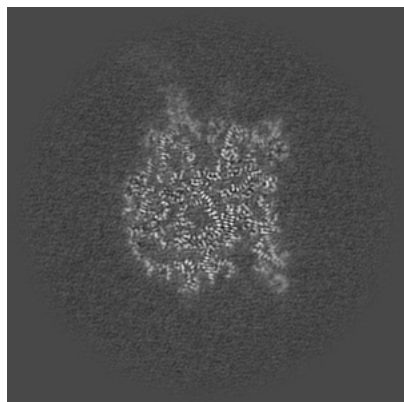


Z Index: 200

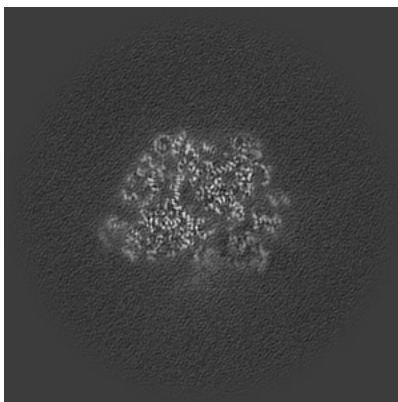
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

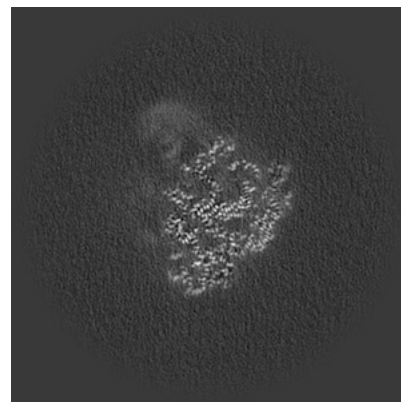
6.3.1 Primary map



X Index: 203

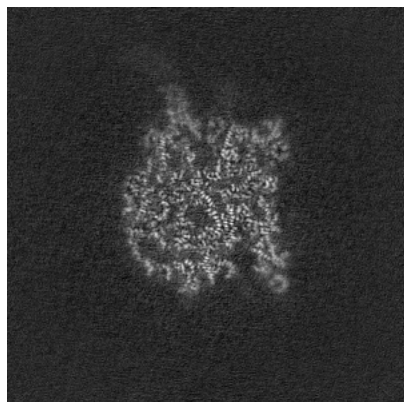


Y Index: 192

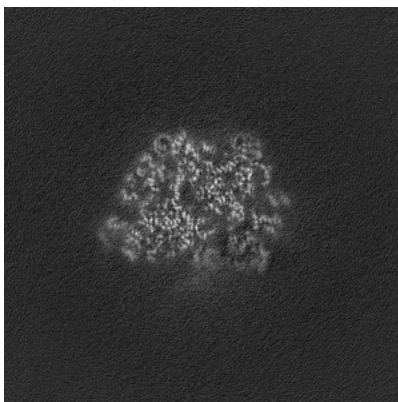


Z Index: 173

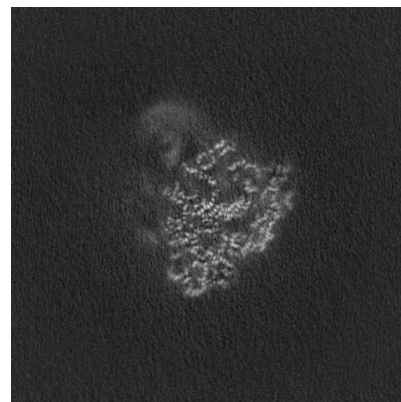
6.3.2 Raw map



X Index: 203



Y Index: 192

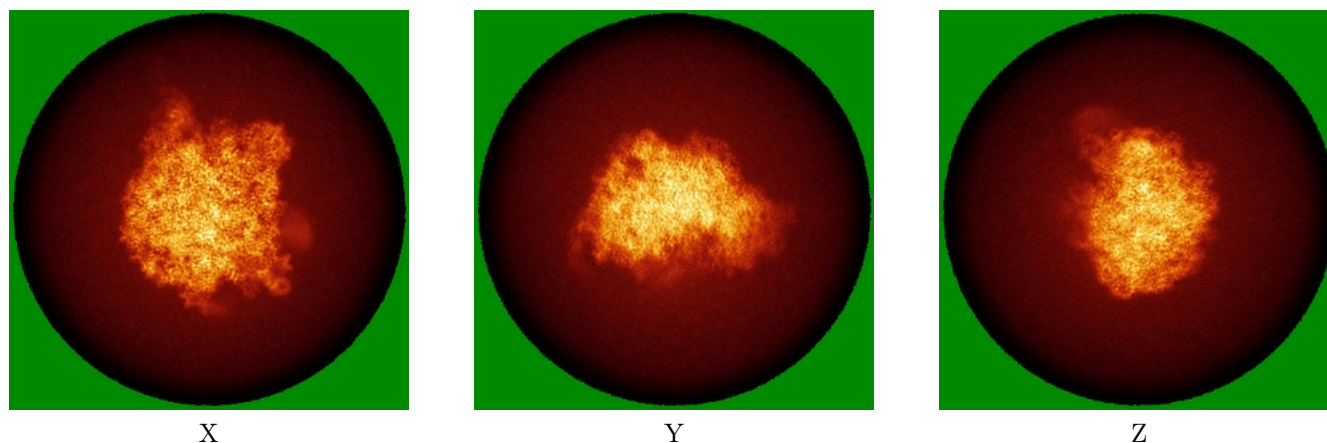


Z Index: 172

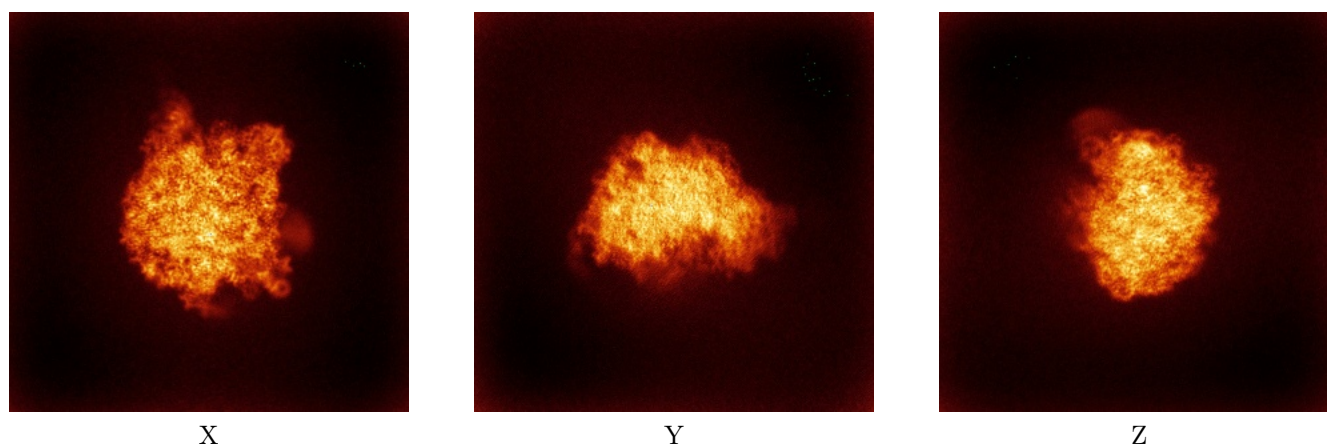
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

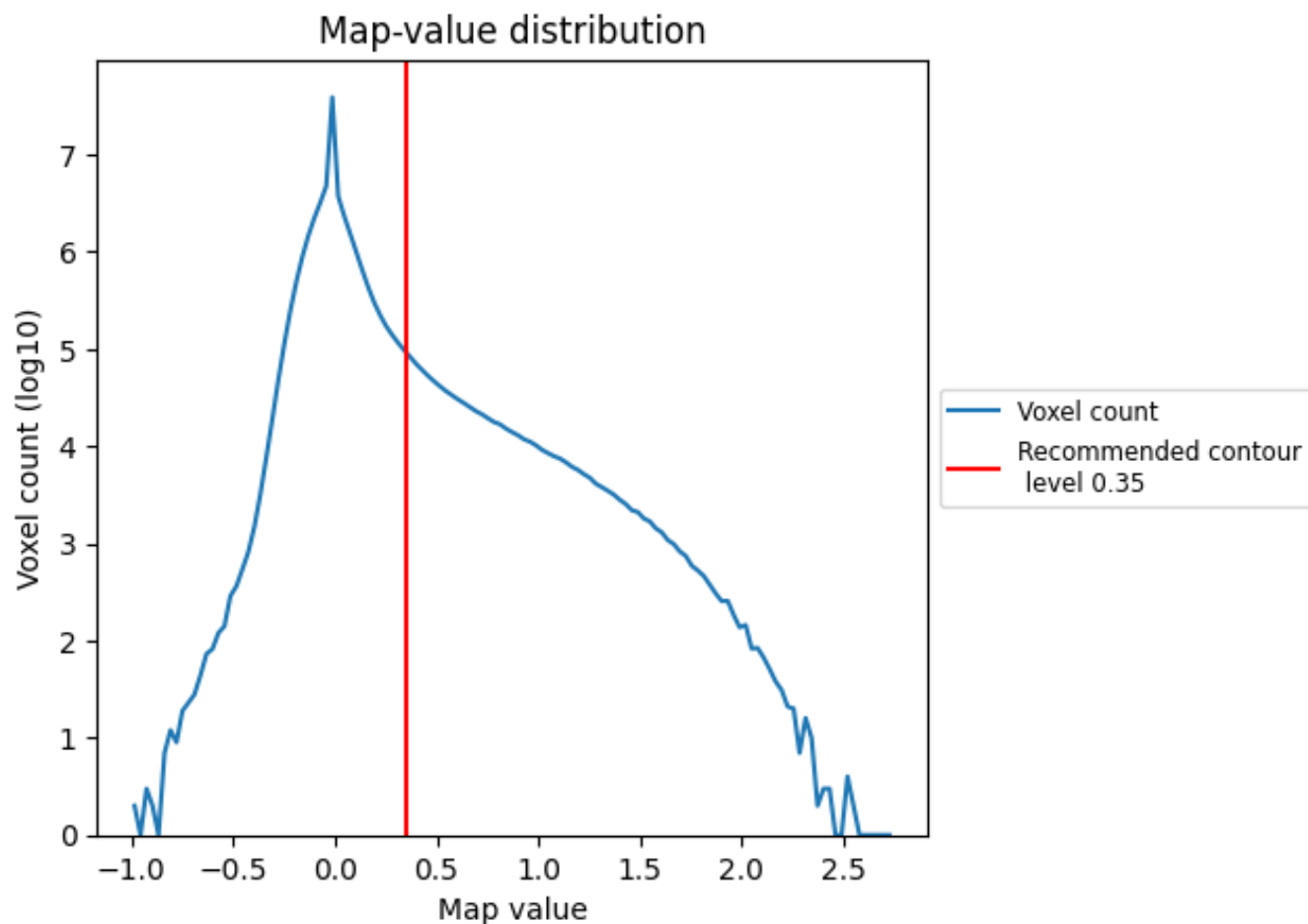
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

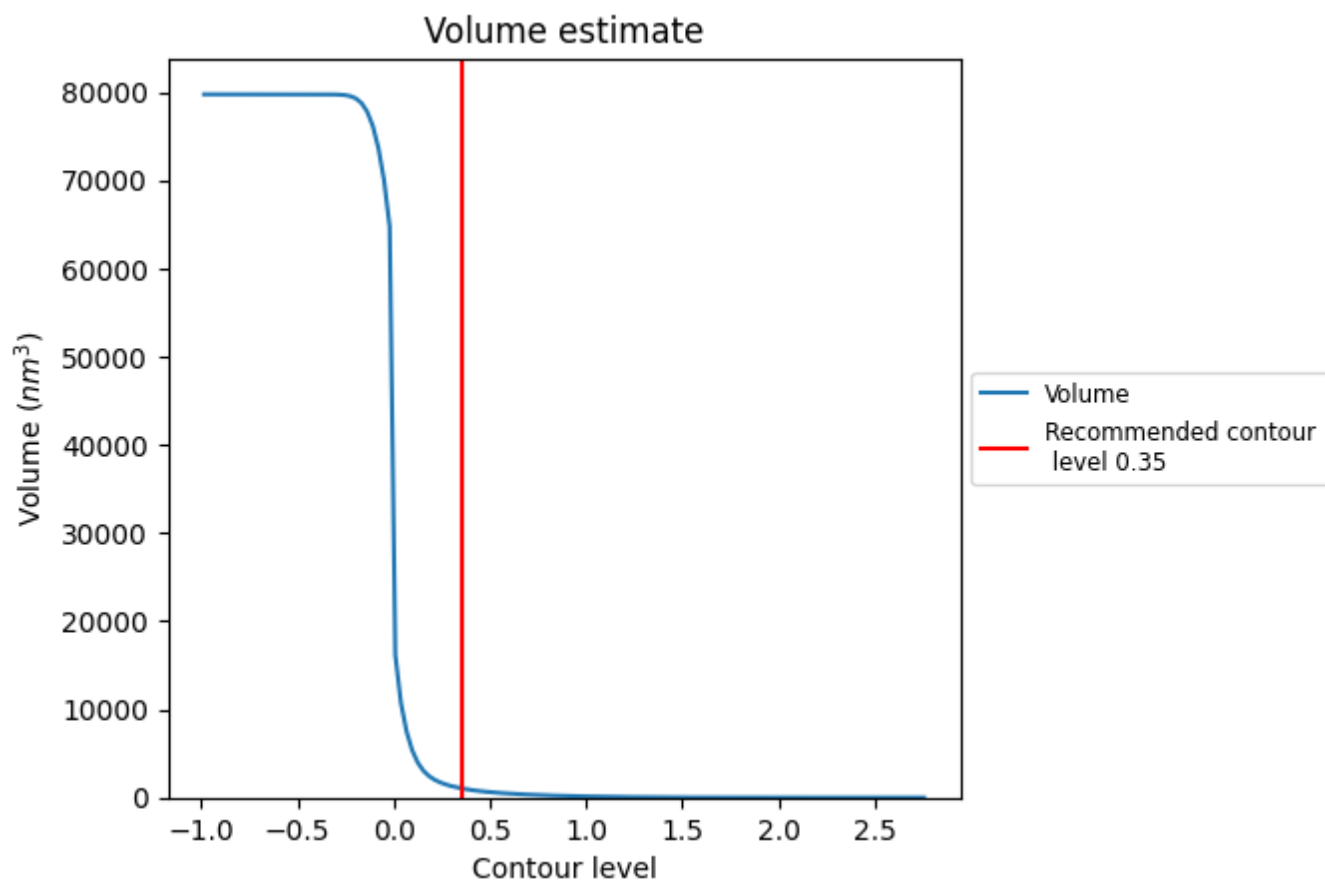
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

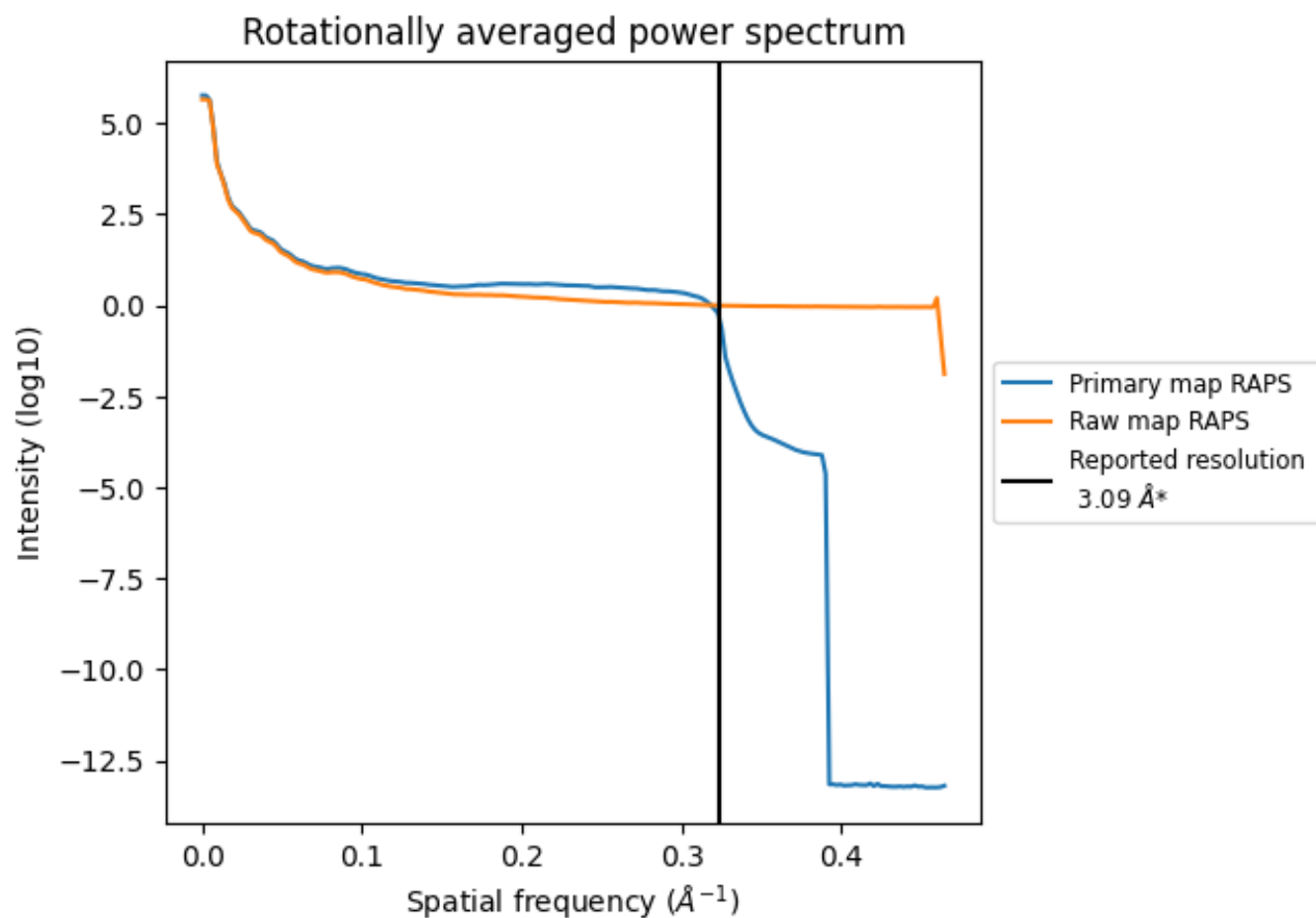
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1055 nm³; this corresponds to an approximate mass of 953 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 ⓘ

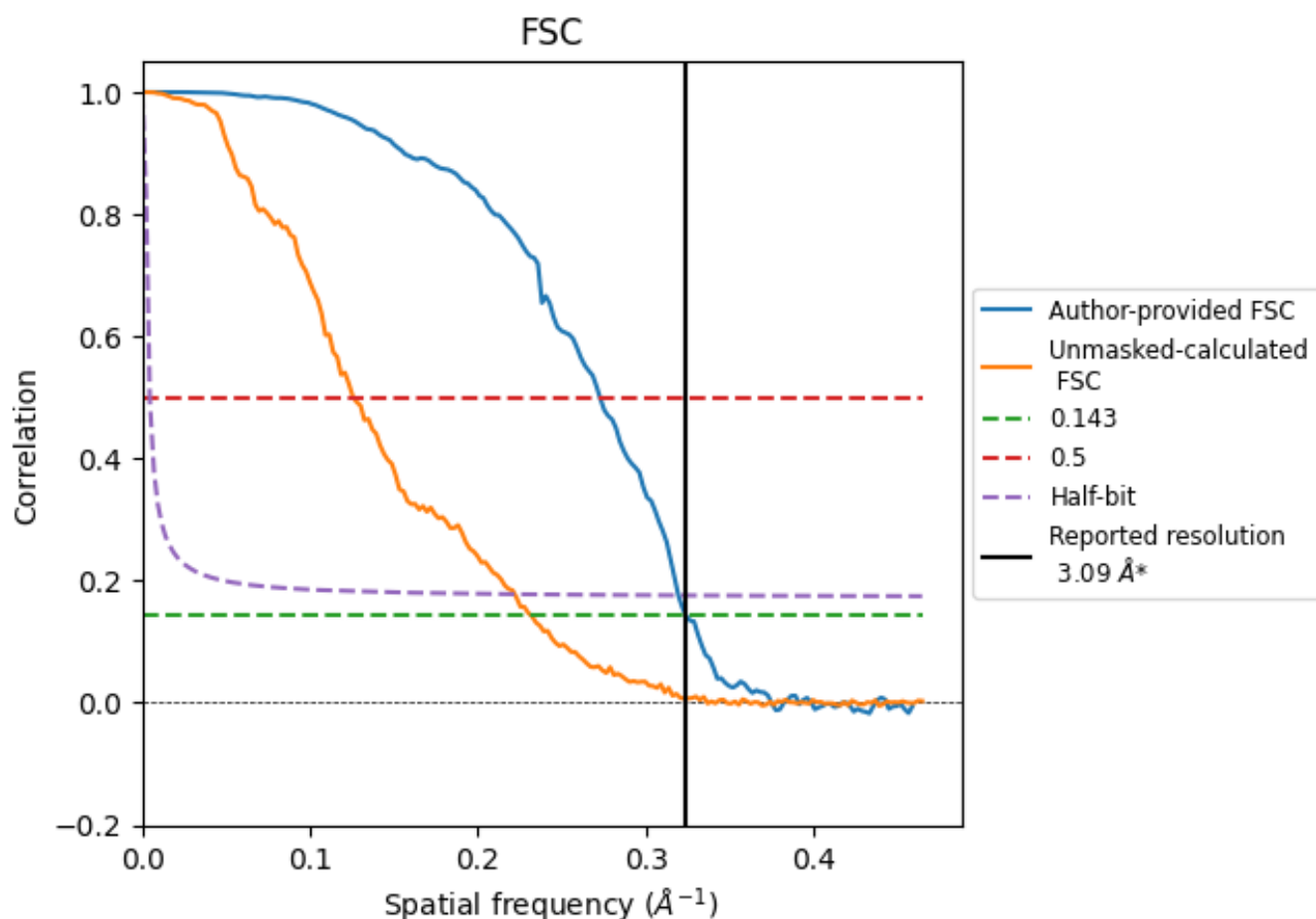


*Reported resolution corresponds to spatial frequency of 0.324 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.324 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	3.09	3.67	3.13
Unmasked-calculated*	4.32	7.95	4.50

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.32 differs from the reported value 3.09 by more than 10 %

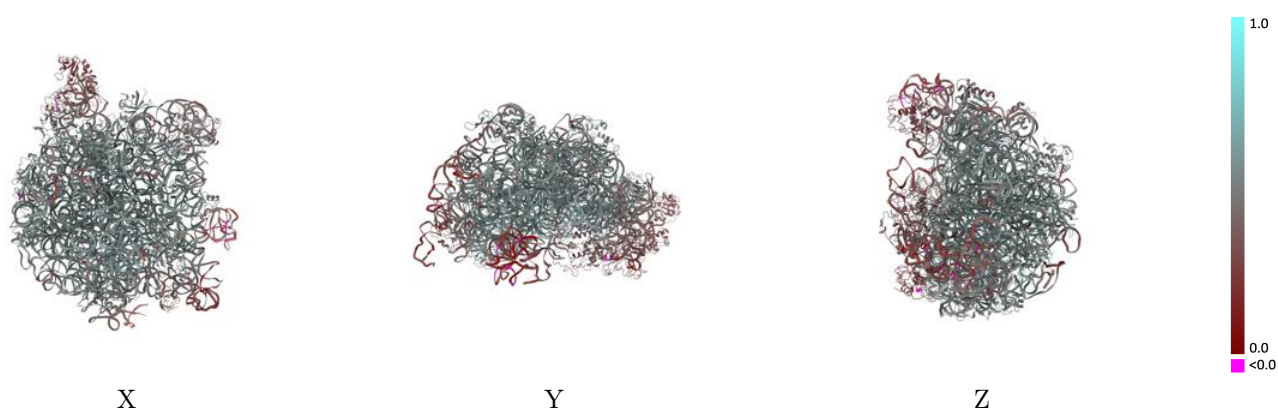
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43305 and PDB model 8VK7. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

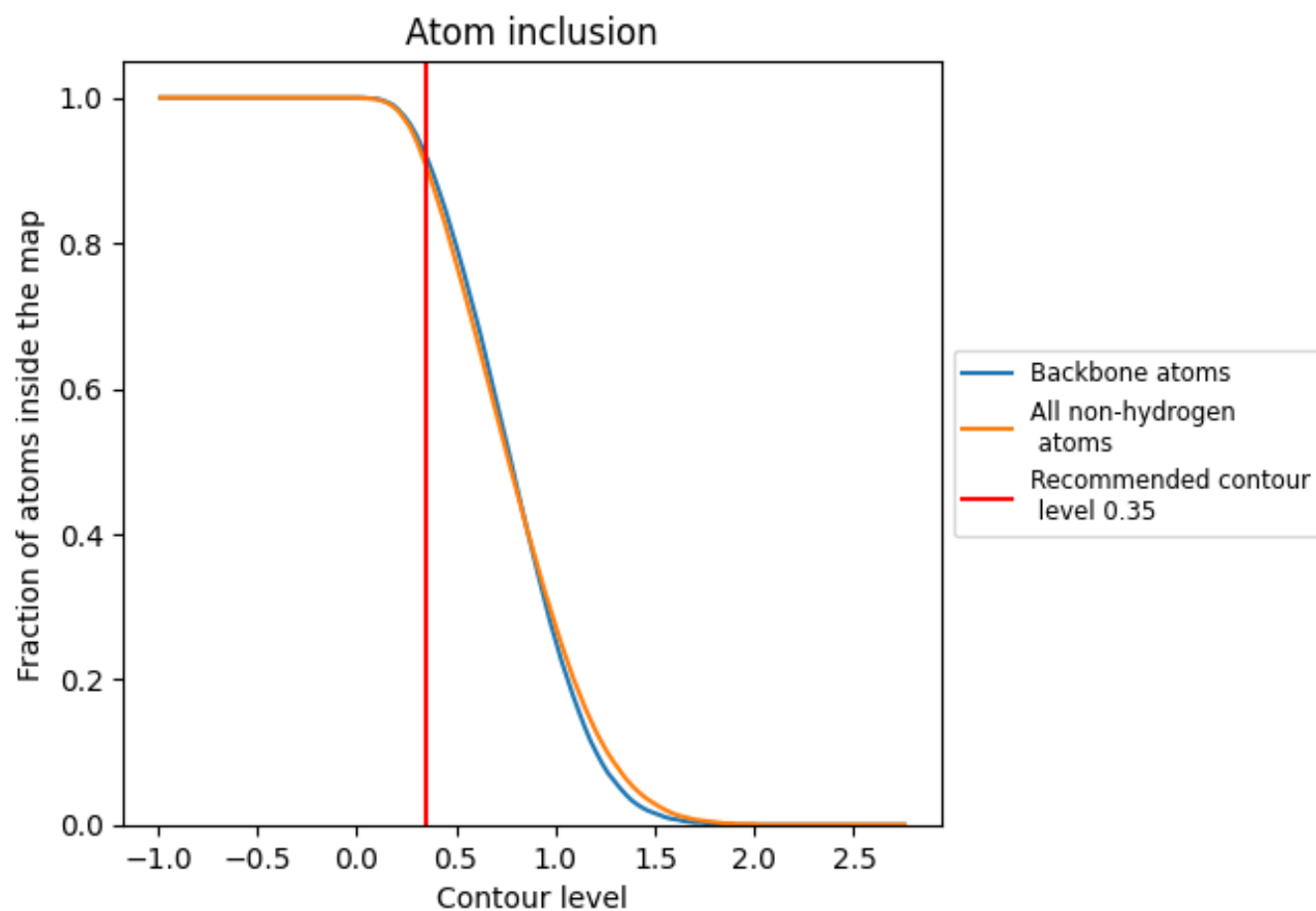


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9070	 0.4850
2	 0.8950	 0.5340
3	 0.9890	 0.5670
4	 0.6310	 0.3740
A	 0.9420	 0.4910
B	 0.9730	 0.4640
C	 0.9250	 0.5360
D	 0.9450	 0.5340
E	 0.9220	 0.5180
F	 0.7480	 0.3540
G	 0.8360	 0.4420
H	 0.6990	 0.4140
I	 0.2450	 0.2810
J	 0.2290	 0.2680
K	 0.9490	 0.5390
L	 0.9330	 0.5200
M	 0.9310	 0.5280
N	 0.9350	 0.5170
O	 0.9390	 0.5360
P	 0.8950	 0.4620
Q	 0.9100	 0.5010
R	 0.9440	 0.5360
S	 0.9100	 0.5370
T	 0.9530	 0.5390
U	 0.9410	 0.5140
V	 0.8980	 0.4800
W	 0.8110	 0.4810
X	 0.9440	 0.5450
Y	 0.9630	 0.5500
Z	 0.9040	 0.4950
b	 0.9400	 0.5490
c	 0.9520	 0.5440
d	 0.9660	 0.5650
e	 0.9670	 0.5480
f	 0.9620	 0.5510
g	 0.6610	 0.3260

