



wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 02:25 pm BST

PDB ID : 6HTQ
EMDB ID : EMD-0270
Title : Stringent response control by a bifunctional RelA enzyme in the presence and absence of the ribosome
Authors : Wilson, D.N.; Abdelshahid, M.
Deposited on : 2018-10-04
Resolution : 4.50 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:

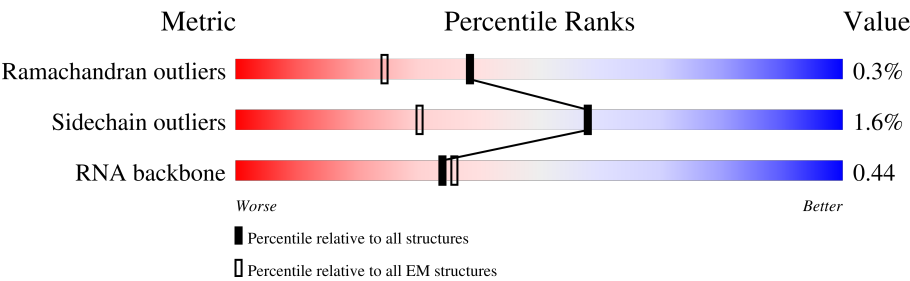
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.50 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.



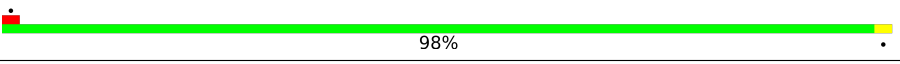
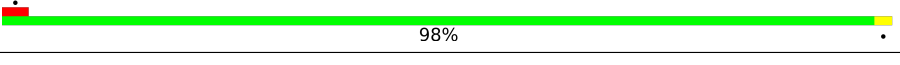
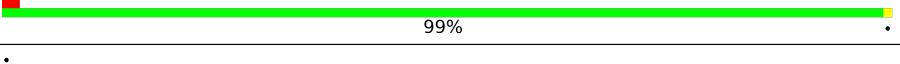
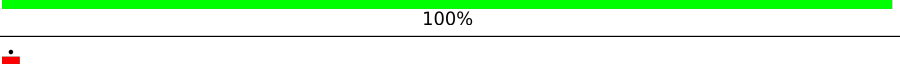
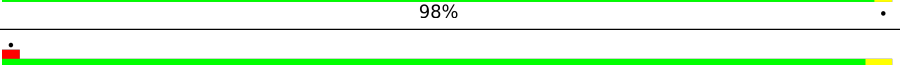
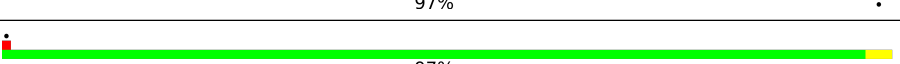
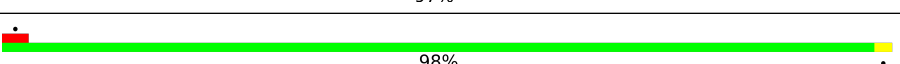
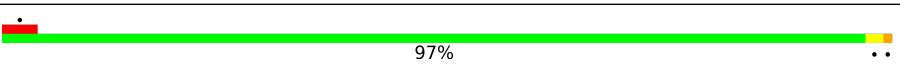
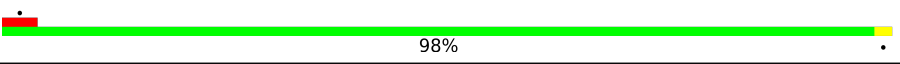
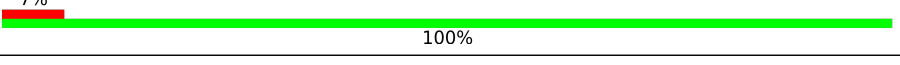
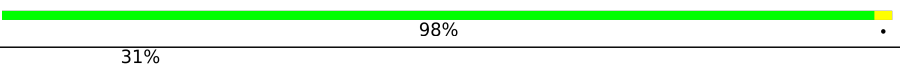
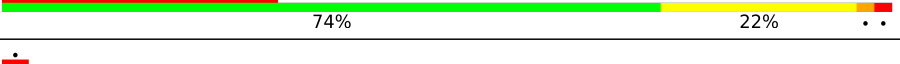
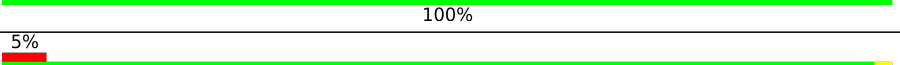
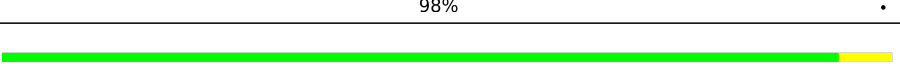
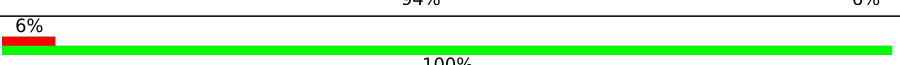
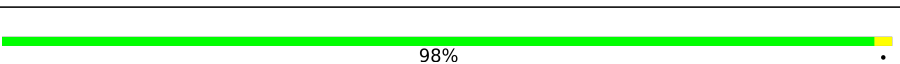
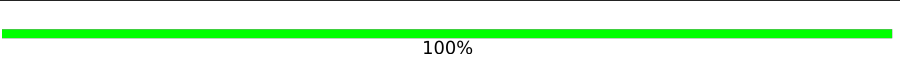
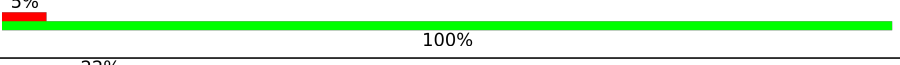
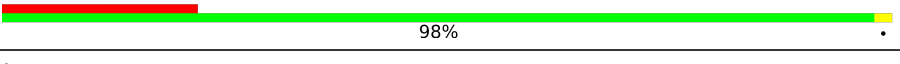

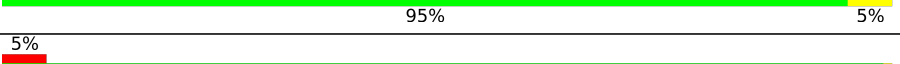
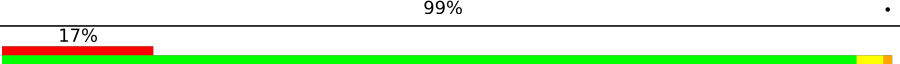
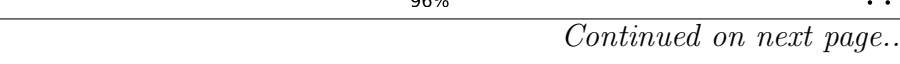


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	2925	<div><div>63%</div><div>33%</div><div>..</div></div>
2	B	112	<div><div>64%</div><div>34%</div><div>.</div></div>
3	C	272	<div><div>99%</div><div>.</div></div>
4	D	206	<div><div>99%</div><div>.</div></div>
5	E	205	<div><div>99%</div><div>.</div></div>
6	F	176	<div><div>97%</div><div>.</div></div>
7	G	175	<div><div>6%</div><div>100%</div></div>
8	J	142	<div><div>99%</div><div>..</div></div>

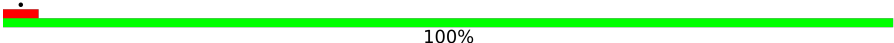

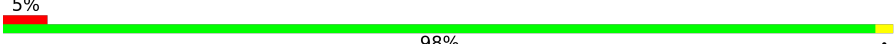
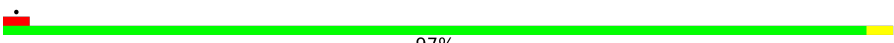
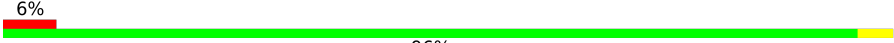



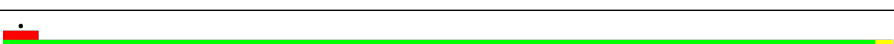
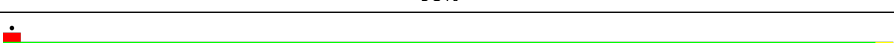
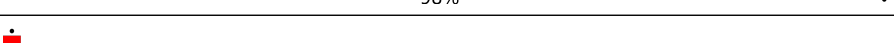
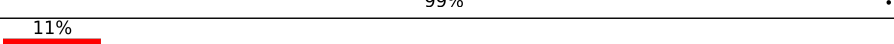
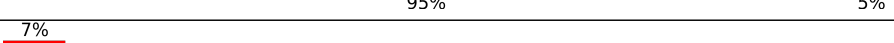
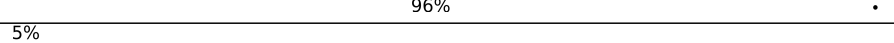
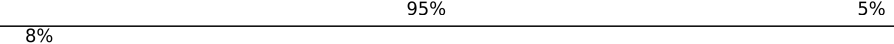
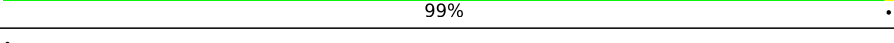
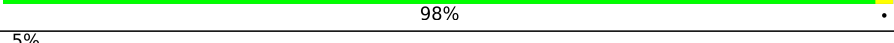

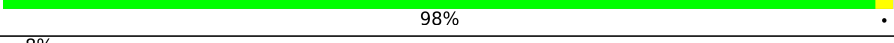
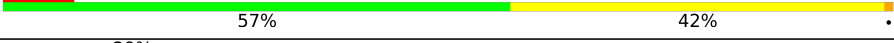
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Mol	Chain	Length	Quality of chain
9	K	122	
10	L	146	
11	M	135	
12	N	119	
13	O	120	
14	P	115	
15	Q	117	
16	R	101	
17	S	109	
18	T	90	
19	U	101	
20	V	82	
21	W	58	
22	X	65	
23	Y	58	
24	1	54	
25	2	48	
26	3	44	
27	4	64	
28	5	37	
29	Z	63	
30	a	1533	
31	b	218	
32	c	206	
33	d	195	

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Mol	Chain	Length	Quality of chain
34	e	164	 100%
35	f	92	 99%
36	g	149	 98%
37	h	131	 97%
38	i	125	 96%
39	j	95	 100%
40	k	114	 99%
41	l	136	 97%
42	m	108	 98%
43	n	60	 98%
44	o	85	 99%
45	p	88	 95%
46	q	84	 96%
47	r	64	 95%
48	s	78	 99%
49	t	83	 98%
50	v	87	 74%
51	x	341	 98%
52	u	76	 57%
53	w	75	 63%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146680 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	A	2887	Total	C	N	O	P	0	0
			61997	27661	11460	19992	2884		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 25 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

- Molecule 30 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	218	Total	C	N	O	S	0	0
			1757	1119	309	323	6		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	149	Total	C	N	O	S	0	0
			1181	740	220	215	6		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	125	Total	C	N	O	S	0	0
			966	599	191	175	1		

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	114	Total	C	N	O	S	0	0
			838	516	164	156	2		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	m	108	Total	C	N	O	0	0
			868	534	176	158		

- Molecule 43 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	78	Total	C	N	O	S	0	0
			633	409	112	110	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 50 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	87	Total	C	N	O	P	0	0
			1861	829	333	612	87		

- Molecule 51 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	341	Total	C	N	O	S	0	0
			2752	1717	504	524	7		

- Molecule 52 is a RNA chain called A/R-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	76	Total	C	N	O	P	0	0
			1623	723	289	535	76		

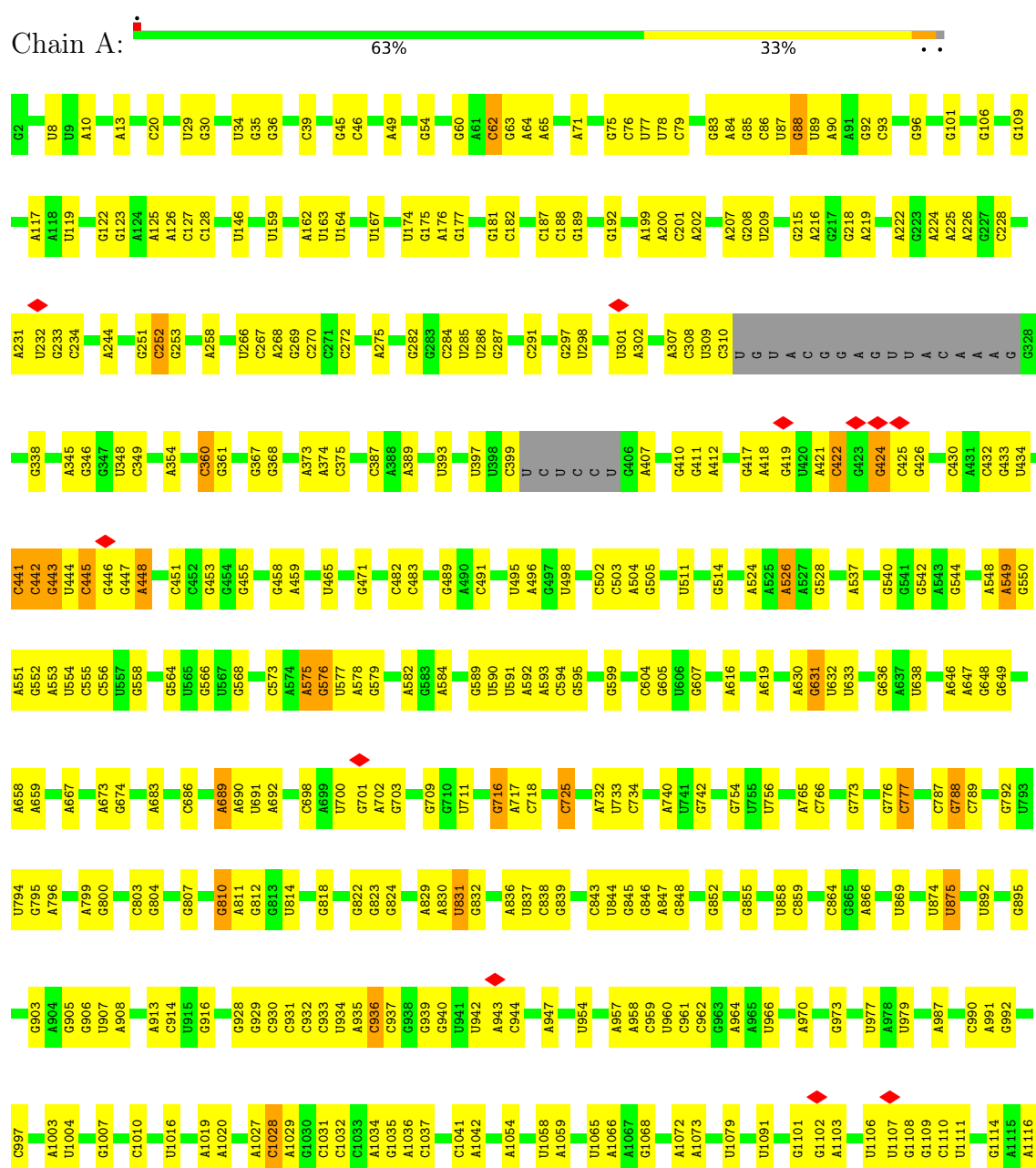
- Molecule 53 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	75	Total	C	N	O	P	0	0
			1599	713	285	526	75		

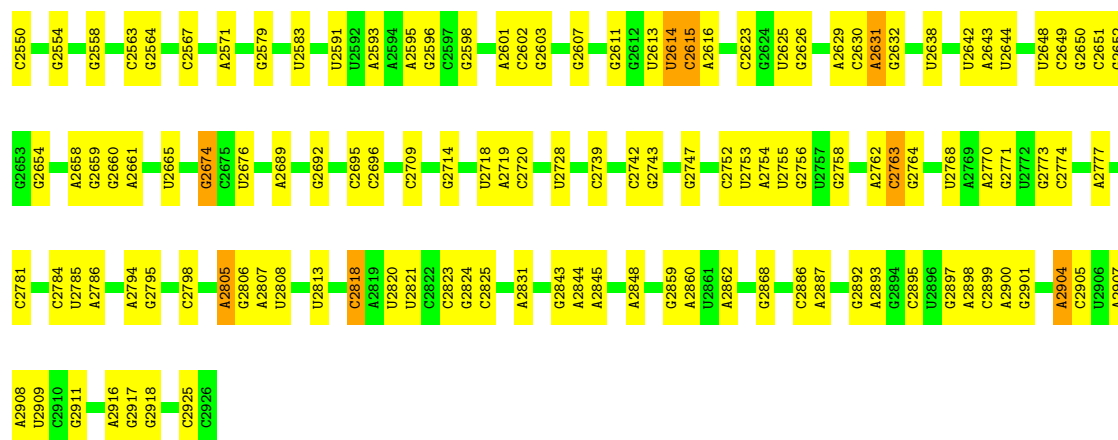
3 Residue-property plots

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

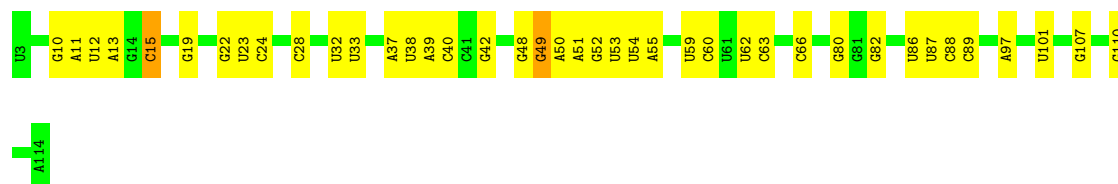


A2454	G2337	U2213	C2114	G2021	A1913	U1804	G1719	C1604	A1516	C1409	G1323	U1229	G1117
A2455	A2338	G2219	A2119	U2022	A1928	G1805	C1720	G1521	G1521	U1411	A1323	G1236	C1118
C2456	A2339	G2220	U2120	C2023	A1929	A1809	A1721	A1608	A1608	U1412	G1324	G1237	A1119
G2457	A2340	U2024	G1810	U2025	A1930	G1810	A1723	G1526	G1526	C1415	A1325	A1243	C1120
A2458	C2341	C2222	U2121	A2026	G1931	C1811	A1724	C1527	C1527	G1416	U1327	A1244	C1121
G2459	A2342	G2122	G2122	A2026	G1932	A1812	A1734	U1528	U1528	U1417	C1328	G1245	G1122
U2460	A2343	A2227	A2123	G2033	G1935	A1813	A1616	G1616	G1616	G1419	G1330	C1248	A1123
A2464	U2345	C2231	G2126	G2038	G1943	A1814	U1738	U1626	U1626	C1422	C1333	U1249	C1124
A2468	C2348	G2232	U2127	G2038	U1944	C1817	G1740	U1631	U1631	A1423	A1339	G1250	A1125
A2469	A2349	C2233	U2128	A2044	A1945	G1828	G1741	G1632	G1632	A1424	A1340	U1251	A1126
C2470	G2350	U2240	U2131	A2047	C1963	C1829	G1744	U1634	U1634	A1425	U1341	G1252	U1128
C2471	A2351	A2241	A2132	U2051	C1963	A1831	G1745	G1634	G1634	A1426	U1350	A1268	A1134
G2474	G2352	G2245	G2133	A2052	A1956	G1830	G1746	U1645	U1645	G1427	U1351	G1269	G1137
A2477	U2353	G2246	A2134	C2053	A1957	C1834	G1747	C1645	C1645	G1431	U1352	A1266	G1139
U2478	G2355	G2249	G2135	C2054	G1959	G1835	G1748	C1652	C1652	U1432	C1353	G1267	U1140
A2479	A2356	G2250	U2140	U2055	G1959	G1836	U1756	C1653	C1653	U1433	G1359	A1268	A1141
A2480	G2360	A2254	A2141	G2068	G1963	U1837	G1757	A1654	U1546	A1434	A1360	A1269	A1142
C2481	C2255	A2255	G2145	U2070	G1964	G1840	U1758	G1658	G1658	U1435	A1361	C1270	U1143
G2490	A2363	G2256	A2146	A2062	A1965	G1841	G1766	C1550	C1550	C1437	C1364	U1274	C1146
U2491	A2364	U2260	A2148	G2063	A1966	C1842	C1767	C1551	C1551	A1442	U1365	G1275	U1147
C2494	G2374	A2261	A2152	C2064	A1967	G1843	A1767	C1552	C1552	U1448	C1366	G1276	C1148
A2497	C2376	A2262	G2152	C2065	U1968	A1845	A1768	U1553	U1553	C1449	G1367	A1278	G1158
C2503	G2379	G2268	A2155	U2069	U1972	G1846	C1771	C1555	C1555	U1458	U1368	A1278	U1159
C2504	A2383	C2277	G2156	U2070	U1973	A1847	A1774	G1678	G1678	U1459	C1370	U1282	G1160
A2505	U2385	U2278	U2159	A2071	G1977	U1856	G1775	A1679	C1559	G1460	G1371	A1287	A1172
C2506	G2387	G2281	G2160	C2072	G1978	G1857	A1776	A1680	C1560	U1464	U1372	G1288	A1173
A2507	G2387	G2281	G2162	G2075	A1981	A1858	G1777	C1683	G1561	A1465	C1374	G1292	G1177
G2510	U2390	G2288	C2166	C2079	U1981	G1871	G1779	A1691	U1565	U1466	U1375	A1293	U1178
G2514	C2393	A2295	C2174	G2081	U1984	C1872	G1780	U1692	G1566	G1472	U1379	U1295	A1179
G2516	G2401	A2296	C2175	C2084	C1985	A1877	C1781	C1693	U1567	A1473	U1380	G1296	C1180
U2520	G2412	A2297	G2176	G2085	C1986	G1878	G1782	G1696	A1569	C1474	G1381	C1297	C1181
G2523	G2413	G2308	G2177	G2086	A1989	A1882	C1783	A1697	G1571	G1475	U1383	G1298	G1182
C2527	C2414	C2312	G2185	A2089	C1990	G1884	G1785	G1698	G1576	C1476	C1384	G1300	G1185
G2531	U2415	A2316	U2192	G2090	C1991	A1883	U1786	A1699	C1577	U1489	A1388	U1301	A1188
A2532	G2420	A2317	G2192	A2091	C1992	G1886	G1787	C1701	G	A1490	C1389	A1302	A1189
U2533	G2425	G2318	A2200	C2093	C1993	A1887	U1790	U1702	A	A1491	G1397	A1306	G1203
G2534	C2431	C2324	U2201	C2094	A1995	A1889	A1791	C1705	A	U1498	A1398	U1307	A1203
U2535	U2432	U2325	A2202	C2095	A2000	G1890	G1792	U1708	U	A1499	G1399	A1308	A1210
G2536	C2432	C2326	U2203	G2096	G2001	G1891	G1793	U1708	A	U1500	G1399	A1308	A1210
A2542	U2435	U2331	A2205	G2098	G2002	G1898	A1797	G1712	G1502	U1501	C1402	G1311	C1216
G2547	G2439	G2332	C2207	U2105	C2003	U1899	G1798	A1713	G	U1502	G1403	A1312	U
U2548	G2333	G2332	C2207	G2109	A2010	G1902	G1799	A1714	U	U1505	A1404	A1313	U
G2549	U2452	U2335	C2208	G2109	U2011	G1905	G1800	C1715	A	U1506	A1405	A1314	C
C2549	G2453	U2336	U2209	G2110	C2012	A1905	G1801	G1716	G1589	U1507	G1407	G1315	G1220
			G2211	C2113			C1803	G1718	G1594	U1508	G1408	G1319	G1227
			C2212										G1228



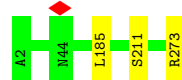
• Molecule 2: 5S ribosomal RNA

Chain B: 64% 34%



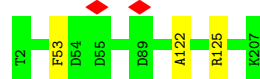
• Molecule 3: 50S ribosomal protein L2

Chain C: 99%



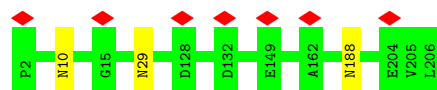
• Molecule 4: 50S ribosomal protein L3

Chain D: 99%



• Molecule 5: 50S ribosomal protein L4

Chain E: 99%

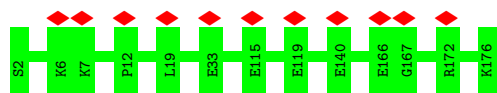


• Molecule 6: 50S ribosomal protein L5

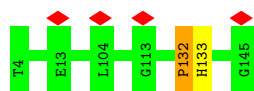
Chain F: 97%



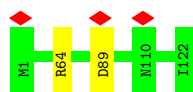
- Molecule 7: 50S ribosomal protein L6



- Molecule 8: 50S ribosomal protein L13



- Molecule 9: 50S ribosomal protein L14



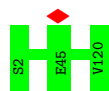
- Molecule 10: 50S ribosomal protein L15



- Molecule 11: 50S ribosomal protein L16

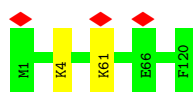


- Molecule 12: 50S ribosomal protein L17



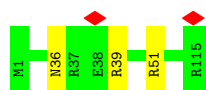
- Molecule 13: 50S ribosomal protein L18

Chain O:  98%



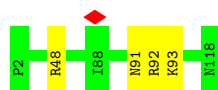
- Molecule 14: 50S ribosomal protein L19

Chain P:  97%



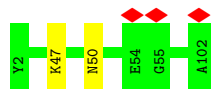
- Molecule 15: 50S ribosomal protein L20

Chain Q:  97%



- Molecule 16: 50S ribosomal protein L21

Chain R:  98%



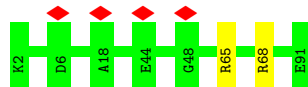
- Molecule 17: 50S ribosomal protein L22

Chain S:  97%



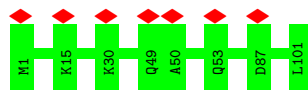
- Molecule 18: 50S ribosomal protein L23

Chain T:  98%



- Molecule 19: 50S ribosomal protein L24

Chain U:  7% 100%



-

- Chain W:

Figure 1: A horizontal bar chart showing the distribution of 1000 samples across 100 categories. The categories are labeled R3, K4, C5, V6, I7, T8, G9, T13, A14, G15, N16, N17, R18, A21, M22, N23, A24, R27, T28, W29, G30, A31, N32, L33, Q34, K35, V36, R37, I38, L39, P44, K55, V59, and F60. The bars are colored in a repeating pattern of green, yellow, and red. Red diamonds are placed above the bars for categories R3, K4, C5, V6, I7, T8, G9, T13, A14, G15, N16, N17, R18, M22, N23, A24, W29, G30, A31, N32, L33, Q34, K35, V36, R37, I38, L39, P44, K55, V59, and F60.

- Chain X:  100%

A diagram showing a 4x4 grid with columns labeled M1, R7, R44, and N65. Red diamonds are placed above the R7 and R44 columns.

- Chain Y:  5% 98%

A diagram of a 3D protein structure. A yellow bar highlights a specific region of the protein, labeled 'K9'. To the left of this bar is a green bar labeled 'A2', and to the right is a green bar labeled 'E58' and 'Q59'. Red diamond shapes are positioned above the 'A2' and 'E58/Q59' bars, indicating specific residues or interactions.

- Chain 1:  94% 6%

A schematic diagram of a protein structure, likely a beta-barrel, represented by a series of vertical bars. Five specific residues are highlighted in yellow: A2, L38, N50, G51, and N55. The residues are connected by horizontal lines, indicating their sequential order in the protein chain. The background is black, and the highlighted residues are yellow.

- Chain 2:  6% 100%

M1	E11	R24	T48

- Chain 3: 98%



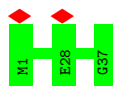
- Molecule 27: 50S ribosomal protein L35

Chain 4: 100%

There are no outlier residues recorded for this chain.

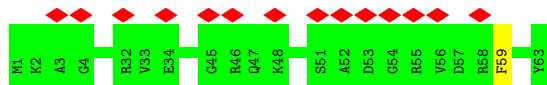
- Molecule 28: 50S ribosomal protein L36

Chain 5: 5% 100%



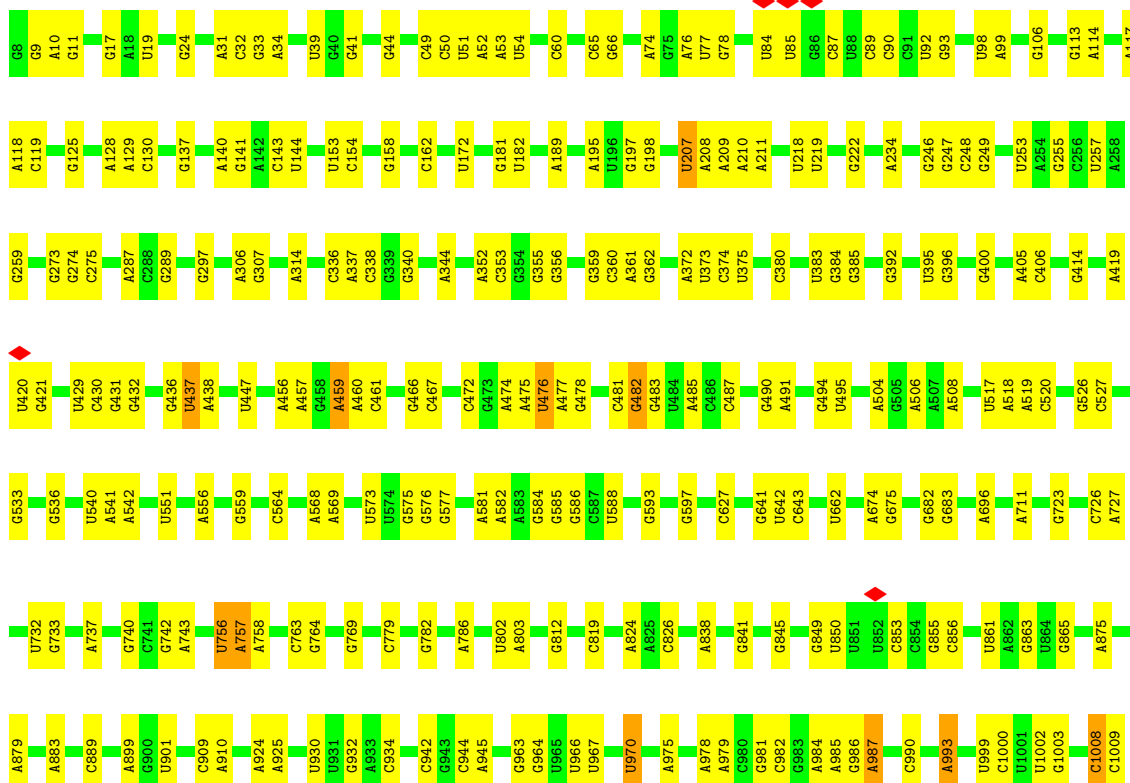
- Molecule 29: 50S ribosomal protein L31

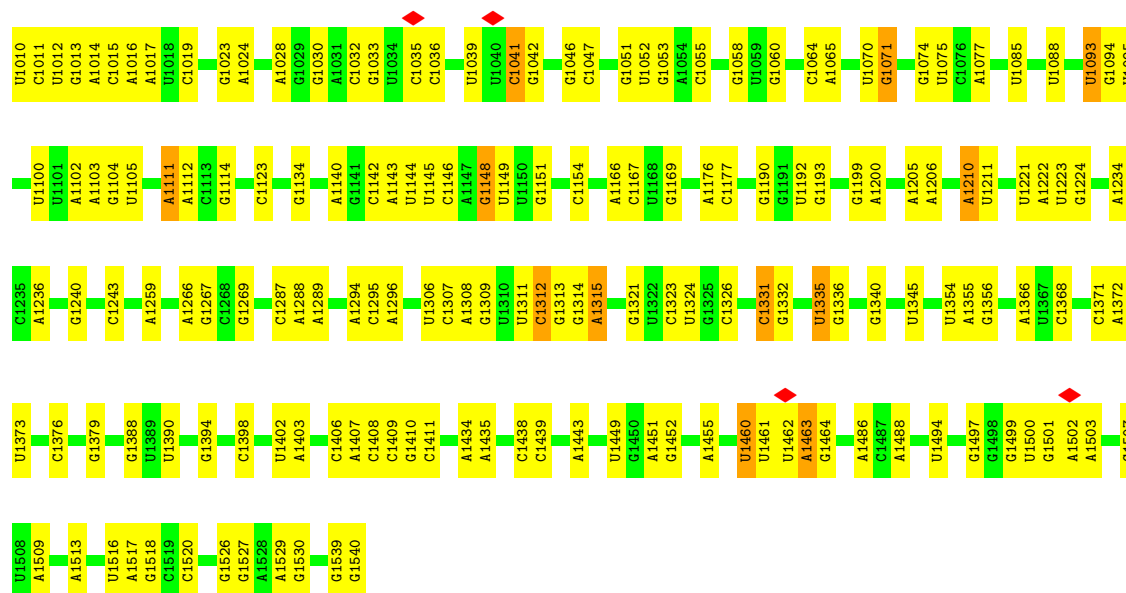
Chain Z: 22% 98%



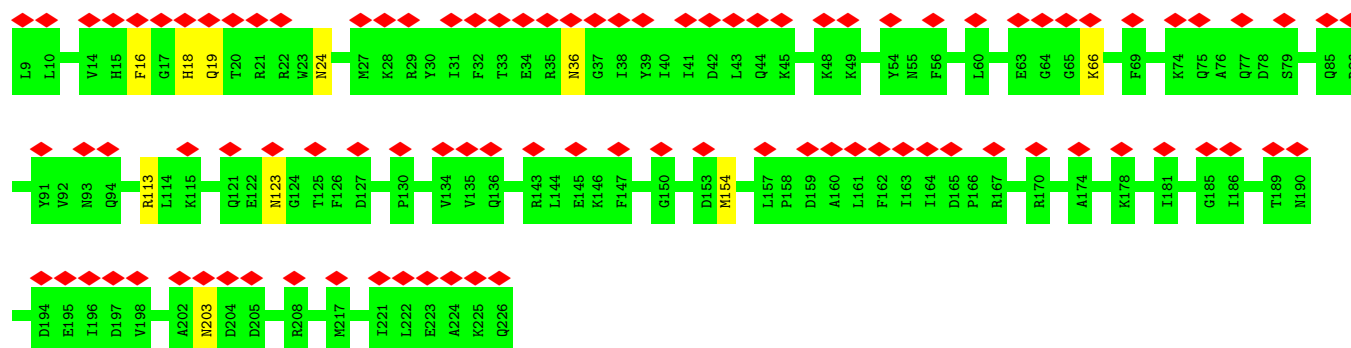
- Molecule 30: 16S rRNA

Chain a: 72% 27%

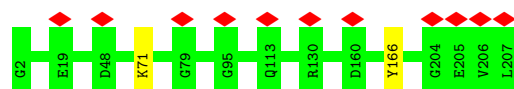




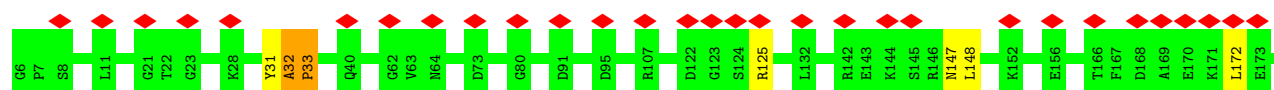
• Molecule 31: 30S ribosomal protein S2

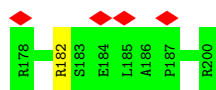


• Molecule 32: 30S ribosomal protein S3

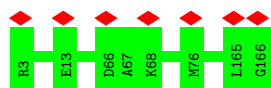


• Molecule 33: 30S ribosomal protein S4

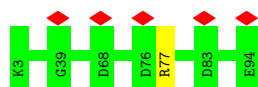




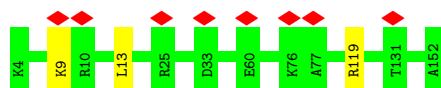
- Molecule 34: 30S ribosomal protein S5



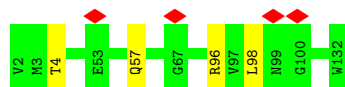
- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7



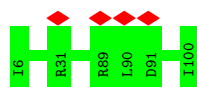
- Molecule 37: 30S ribosomal protein S8



- Molecule 38: 30S ribosomal protein S9

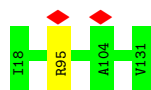


- Molecule 39: 30S ribosomal protein S10



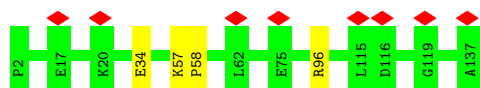
- Molecule 40: 30S ribosomal protein S11

Chain k:  99%



- Molecule 41: 30S ribosomal protein S12

Chain l:  97%



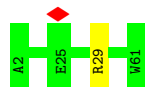
- Molecule 42: 30S ribosomal protein S13

Chain m:  98%



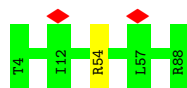
- Molecule 43: 30S ribosomal protein S14

Chain n:  98%



- Molecule 44: 30S ribosomal protein S15

Chain o:  99%



- Molecule 45: 30S ribosomal protein S16

Chain p:  95% 5%

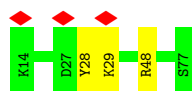


- Molecule 46: 30S ribosomal protein S17

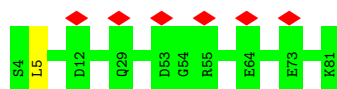
Chain q:  96%



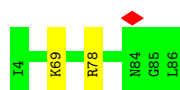
- Molecule 47: 30S ribosomal protein S18



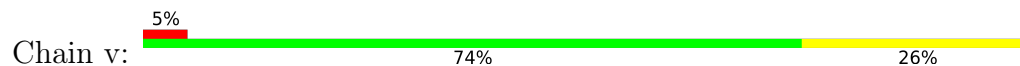
- Molecule 48: 30S ribosomal protein S19



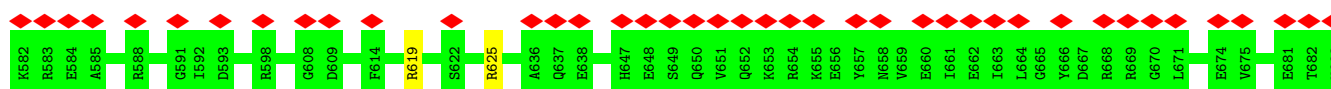
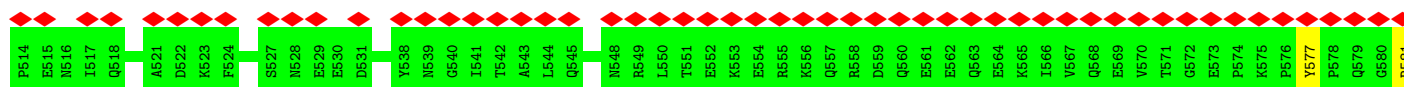
- Molecule 49: 30S ribosomal protein S20

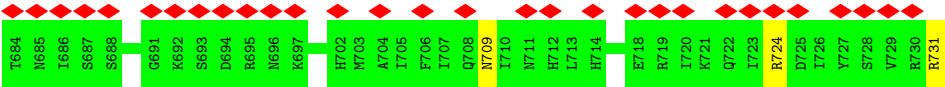


- Molecule 50: P-tRNA



- Molecule 51: GTP pyrophosphokinase





• Molecule 52: A/R-tRNA



• Molecule 53: E-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	650054	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 ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.465	Depositor
Minimum map value	-0.311	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.0471	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A	1.01	9/69438 (0.0%)	1.08	261/108311 (0.2%)
2	B	0.41	0/2675	0.97	7/4170 (0.2%)
3	C	0.43	0/2120	0.64	1/2845 (0.0%)
4	D	0.40	0/1591	0.64	0/2132
5	E	0.34	0/1580	0.57	0/2132
6	F	0.30	0/1405	0.60	0/1887
7	G	0.26	0/1360	0.50	0/1832
8	J	0.34	0/1146	0.63	0/1542
9	K	0.42	0/927	0.64	1/1245 (0.1%)
10	L	0.34	0/1093	0.60	2/1457 (0.1%)
11	M	0.35	0/1099	0.51	0/1468
12	N	0.33	0/960	0.60	0/1284
13	O	0.27	0/921	0.57	0/1236
14	P	0.37	0/957	0.61	0/1279
15	Q	0.39	0/952	0.61	0/1266
16	R	0.34	0/797	0.61	0/1070
17	S	0.35	0/851	0.68	1/1146 (0.1%)
18	T	0.31	0/731	0.50	0/974
19	U	0.29	0/772	0.59	0/1032
20	V	0.36	0/638	0.66	0/847
21	W	3.43	2/448 (0.4%)	1.27	4/596 (0.7%)
22	X	0.27	0/531	0.51	0/707
23	Y	0.31	0/457	0.60	0/613
24	1	0.37	0/433	0.63	0/574
25	2	0.32	0/406	0.57	0/540
26	3	0.37	0/370	0.58	0/483
27	4	0.35	0/519	0.58	0/680
28	5	0.31	0/299	0.50	0/393
29	Z	0.30	0/509	0.50	0/678
30	a	0.54	0/36826	0.98	55/57450 (0.1%)
31	b	0.27	0/1782	0.57	0/2392
32	c	0.30	0/1641	0.55	0/2208
33	d	0.32	0/1598	0.59	1/2147 (0.0%)
34	e	0.35	0/1230	0.59	0/1655

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	f	0.29	0/766	0.46	0/1031
36	g	0.28	0/1196	0.57	0/1604
37	h	0.33	0/1048	0.59	0/1407
38	i	0.29	0/979	0.60	0/1315
39	j	0.31	0/773	0.58	0/1044
40	k	0.29	0/852	0.54	0/1153
41	l	0.33	0/1069	0.61	0/1435
42	m	0.30	0/873	0.61	0/1166
43	n	0.36	0/507	0.62	0/672
44	o	0.27	0/718	0.53	0/960
45	p	0.31	0/708	0.57	0/950
46	q	0.31	0/699	0.60	0/933
47	r	0.27	0/526	0.54	0/705
48	s	0.31	0/649	0.59	0/872
49	t	0.25	0/639	0.51	0/852
50	v	0.43	0/2080	0.98	3/3242 (0.1%)
51	x	0.28	0/2794	0.55	0/3757
52	u	0.39	1/1813 (0.1%)	0.98	4/2823 (0.1%)
53	w	0.32	0/1786	1.00	7/2782 (0.3%)
All	All	0.76	12/159537 (0.0%)	0.95	347/238974 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	1
4	D	0	2
8	J	0	1
15	Q	0	2
16	R	0	1
17	S	0	1
21	W	0	9
29	Z	0	1
31	b	0	3
32	c	0	1
33	d	0	3
36	g	0	1
37	h	0	1
41	l	0	2
45	p	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
51	x	0	1
All	All	0	31

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2120	U	C2-N3	107.16	2.12	1.37
1	A	2120	U	N3-C4	80.91	2.11	1.38
1	A	2120	U	N1-C2	78.44	2.09	1.38
1	A	2120	U	N1-C6	74.52	2.05	1.38
21	W	34	GLN	CD-NE2	71.67	3.12	1.32

The worst 5 of 347 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	445	C	N1-C2-O2	13.25	126.85	118.90
1	A	2079	C	N1-C2-O2	12.62	126.47	118.90
1	A	2260	U	O4'-C1'-N1	11.68	117.54	108.20
1	A	2079	C	N3-C2-O2	-11.21	114.06	121.90
1	A	445	C	C6-N1-C2	-10.54	116.08	120.30

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	211	SER	Peptide
4	D	122	ALA	Peptide
4	D	53	PHE	Peptide
8	J	132	PRO	Peptide
15	Q	91	ASN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
3	C	270/272 (99%)	239 (88%)	31 (12%)	0	100	100
4	D	204/206 (99%)	180 (88%)	24 (12%)	0	100	100
5	E	203/205 (99%)	180 (89%)	23 (11%)	0	100	100
6	F	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
7	G	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
8	J	140/142 (99%)	119 (85%)	19 (14%)	2 (1%)	9	40
9	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
10	L	144/146 (99%)	134 (93%)	10 (7%)	0	100	100
11	M	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
12	N	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
13	O	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
14	P	113/115 (98%)	104 (92%)	9 (8%)	0	100	100
15	Q	115/117 (98%)	107 (93%)	7 (6%)	1 (1%)	14	51
16	R	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
17	S	107/109 (98%)	91 (85%)	14 (13%)	2 (2%)	6	33
18	T	88/90 (98%)	86 (98%)	2 (2%)	0	100	100
19	U	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
20	V	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
21	W	56/58 (97%)	34 (61%)	22 (39%)	0	100	100
22	X	63/65 (97%)	60 (95%)	3 (5%)	0	100	100
23	Y	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
24	1	52/54 (96%)	43 (83%)	8 (15%)	1 (2%)	6	33
25	2	46/48 (96%)	41 (89%)	5 (11%)	0	100	100
26	3	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
27	4	62/64 (97%)	58 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	5	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
29	Z	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
31	b	216/218 (99%)	191 (88%)	24 (11%)	1 (0%)	25	64
32	c	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
33	d	193/195 (99%)	179 (93%)	12 (6%)	2 (1%)	13	49
34	e	162/164 (99%)	150 (93%)	12 (7%)	0	100	100
35	f	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
36	g	147/149 (99%)	132 (90%)	15 (10%)	0	100	100
37	h	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	54
38	i	123/125 (98%)	111 (90%)	11 (9%)	1 (1%)	16	54
39	j	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
40	k	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
41	l	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	19	56
42	m	106/108 (98%)	95 (90%)	10 (9%)	1 (1%)	14	51
43	n	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
44	o	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
45	p	86/88 (98%)	77 (90%)	7 (8%)	2 (2%)	5	29
46	q	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
47	r	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	8	37
48	s	76/78 (97%)	67 (88%)	9 (12%)	0	100	100
49	t	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	11	44
51	x	339/341 (99%)	292 (86%)	47 (14%)	0	100	100
All	All	5546/5640 (98%)	4959 (89%)	570 (10%)	17 (0%)	38	72

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	S	40	PRO
8	J	133	HIS
15	Q	93	LYS
45	p	47	ALA
49	t	69	LYS

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	
3	C	220/220 (100%)	219 (100%)	1 (0%)	86	89
4	D	167/167 (100%)	166 (99%)	1 (1%)	84	88
5	E	169/169 (100%)	166 (98%)	3 (2%)	54	71
6	F	151/151 (100%)	146 (97%)	5 (3%)	33	54
7	G	148/148 (100%)	148 (100%)	0	100	100
8	J	120/120 (100%)	120 (100%)	0	100	100
9	K	101/101 (100%)	100 (99%)	1 (1%)	73	81
10	L	110/110 (100%)	109 (99%)	1 (1%)	75	83
11	M	109/109 (100%)	108 (99%)	1 (1%)	75	83
12	N	99/99 (100%)	99 (100%)	0	100	100
13	O	93/93 (100%)	91 (98%)	2 (2%)	47	65
14	P	100/100 (100%)	97 (97%)	3 (3%)	36	56
15	Q	96/96 (100%)	95 (99%)	1 (1%)	73	81
16	R	83/83 (100%)	82 (99%)	1 (1%)	67	79
17	S	90/90 (100%)	90 (100%)	0	100	100
18	T	81/81 (100%)	79 (98%)	2 (2%)	42	62
19	U	85/85 (100%)	85 (100%)	0	100	100
20	V	64/64 (100%)	62 (97%)	2 (3%)	35	55
21	W	47/47 (100%)	41 (87%)	6 (13%)	3	15
22	X	56/56 (100%)	56 (100%)	0	100	100
23	Y	52/52 (100%)	51 (98%)	1 (2%)	52	69
24	1	48/48 (100%)	46 (96%)	2 (4%)	25	47
25	2	46/46 (100%)	46 (100%)	0	100	100
26	3	39/39 (100%)	38 (97%)	1 (3%)	41	61
27	4	54/54 (100%)	54 (100%)	0	100	100
28	5	35/35 (100%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Z	53/53 (100%)	53 (100%)	0	100	100
31	b	189/189 (100%)	183 (97%)	6 (3%)	34	55
32	c	168/168 (100%)	167 (99%)	1 (1%)	84	88
33	d	169/169 (100%)	165 (98%)	4 (2%)	44	63
34	e	128/128 (100%)	128 (100%)	0	100	100
35	f	81/81 (100%)	80 (99%)	1 (1%)	67	79
36	g	125/125 (100%)	123 (98%)	2 (2%)	58	74
37	h	111/111 (100%)	109 (98%)	2 (2%)	54	71
38	i	98/98 (100%)	94 (96%)	4 (4%)	26	48
39	j	86/86 (100%)	86 (100%)	0	100	100
40	k	86/86 (100%)	85 (99%)	1 (1%)	67	79
41	l	114/114 (100%)	113 (99%)	1 (1%)	75	83
42	m	94/94 (100%)	93 (99%)	1 (1%)	70	80
43	n	53/53 (100%)	52 (98%)	1 (2%)	52	69
44	o	80/80 (100%)	79 (99%)	1 (1%)	65	77
45	p	74/74 (100%)	73 (99%)	1 (1%)	62	75
46	q	77/77 (100%)	74 (96%)	3 (4%)	27	49
47	r	56/56 (100%)	54 (96%)	2 (4%)	30	52
48	s	70/70 (100%)	69 (99%)	1 (1%)	62	75
49	t	66/66 (100%)	65 (98%)	1 (2%)	60	75
51	x	307/307 (100%)	300 (98%)	7 (2%)	45	64
All	All	4748/4748 (100%)	4674 (98%)	74 (2%)	58	74

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	n	29	ARG
51	x	709	ASN
45	p	32	ARG
48	s	5	LEU
21	W	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
16	R	45	ASN
44	o	46	HIS
24	1	40	HIS
44	o	42	HIS
51	x	518	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2876/2925 (98%)	976 (33%)	54 (1%)
2	B	111/112 (99%)	37 (33%)	3 (2%)
30	a	1532/1533 (99%)	420 (27%)	0
50	v	86/87 (98%)	20 (23%)	0
52	u	75/76 (98%)	32 (42%)	0
53	w	74/75 (98%)	27 (36%)	0
All	All	4754/4808 (98%)	1512 (31%)	57 (1%)

5 of 1512 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	10	A
1	A	13	A
1	A	20	C
1	A	29	U

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1339	A
2	B	48	G
1	A	1631	A
2	B	37	A
1	A	2454	A

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	182:C	O3'	183:A	P	6.24
1	A	1449:C	O3'	1450:C	P	4.30
1	A	1452:C	O3'	1453:A	P	4.27
1	A	183:A	O3'	184:G	P	3.36
1	A	1451:U	O3'	1452:C	P	3.33

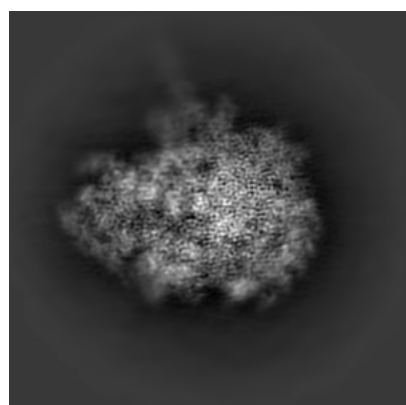
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0270. These allow visual inspection of the internal detail of the map and identification of artifacts.

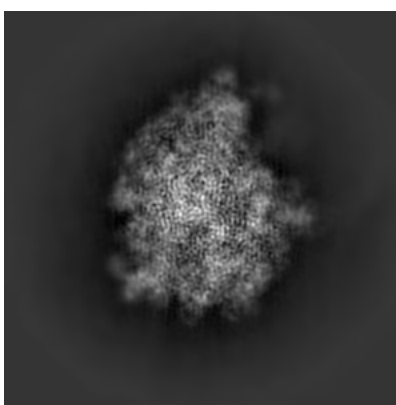
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

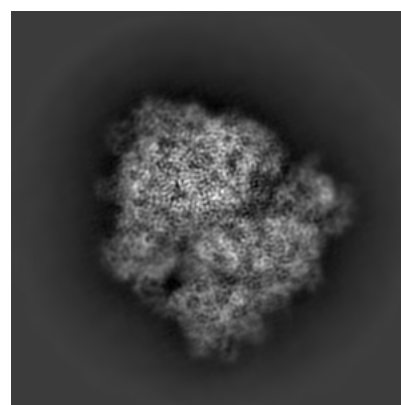
6.1.1 Primary map



X



Y

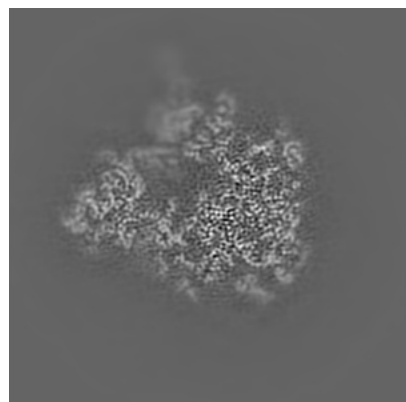


Z

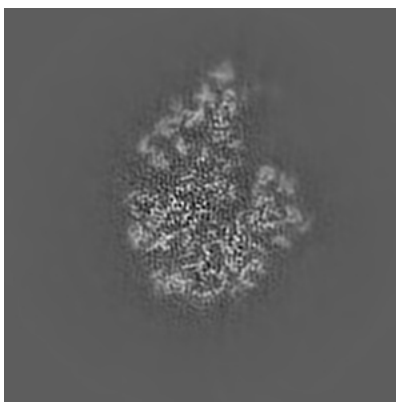
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

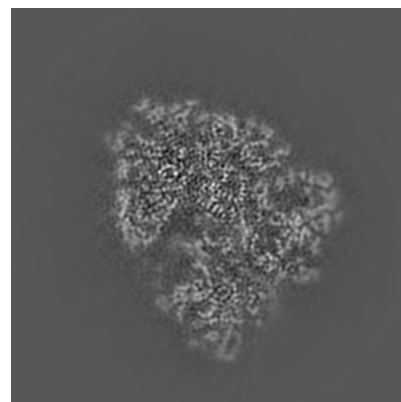
6.2.1 Primary map



X Index: 180



Y Index: 180

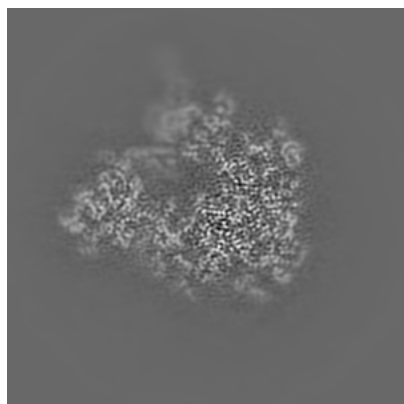


Z Index: 180

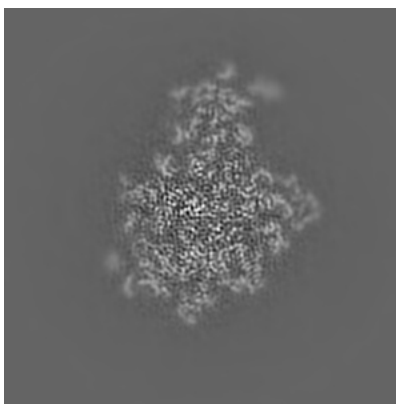
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

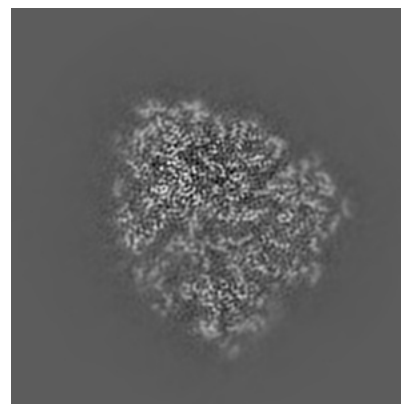
6.3.1 Primary map



X Index: 179



Y Index: 195

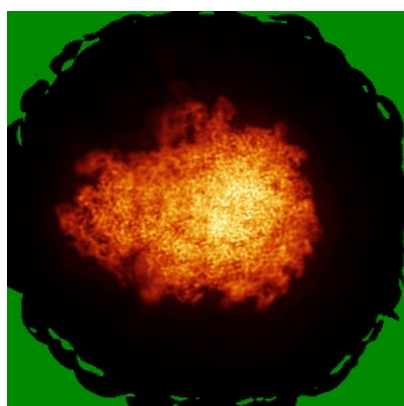


Z Index: 186

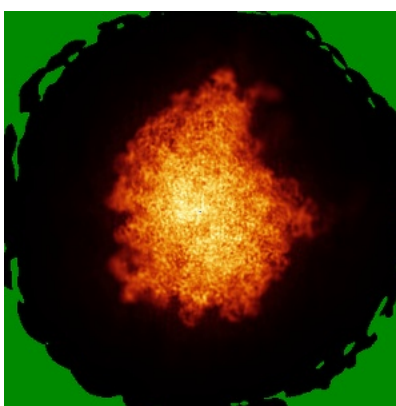
The images above show the largest variance slices of the map in three orthogonal directions.

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

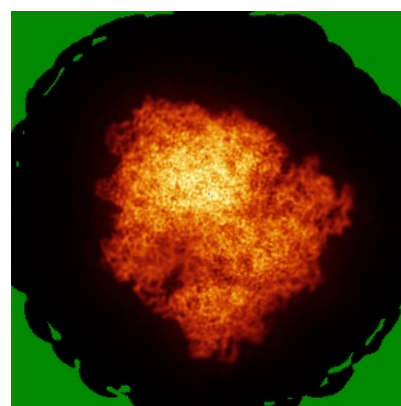
6.4.1 Primary map



X



Y

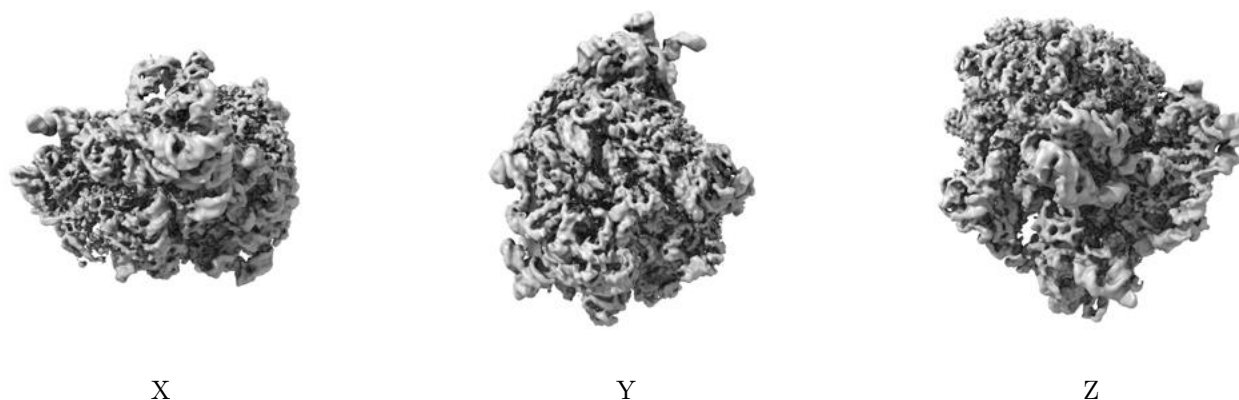


Z

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 0.0471. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

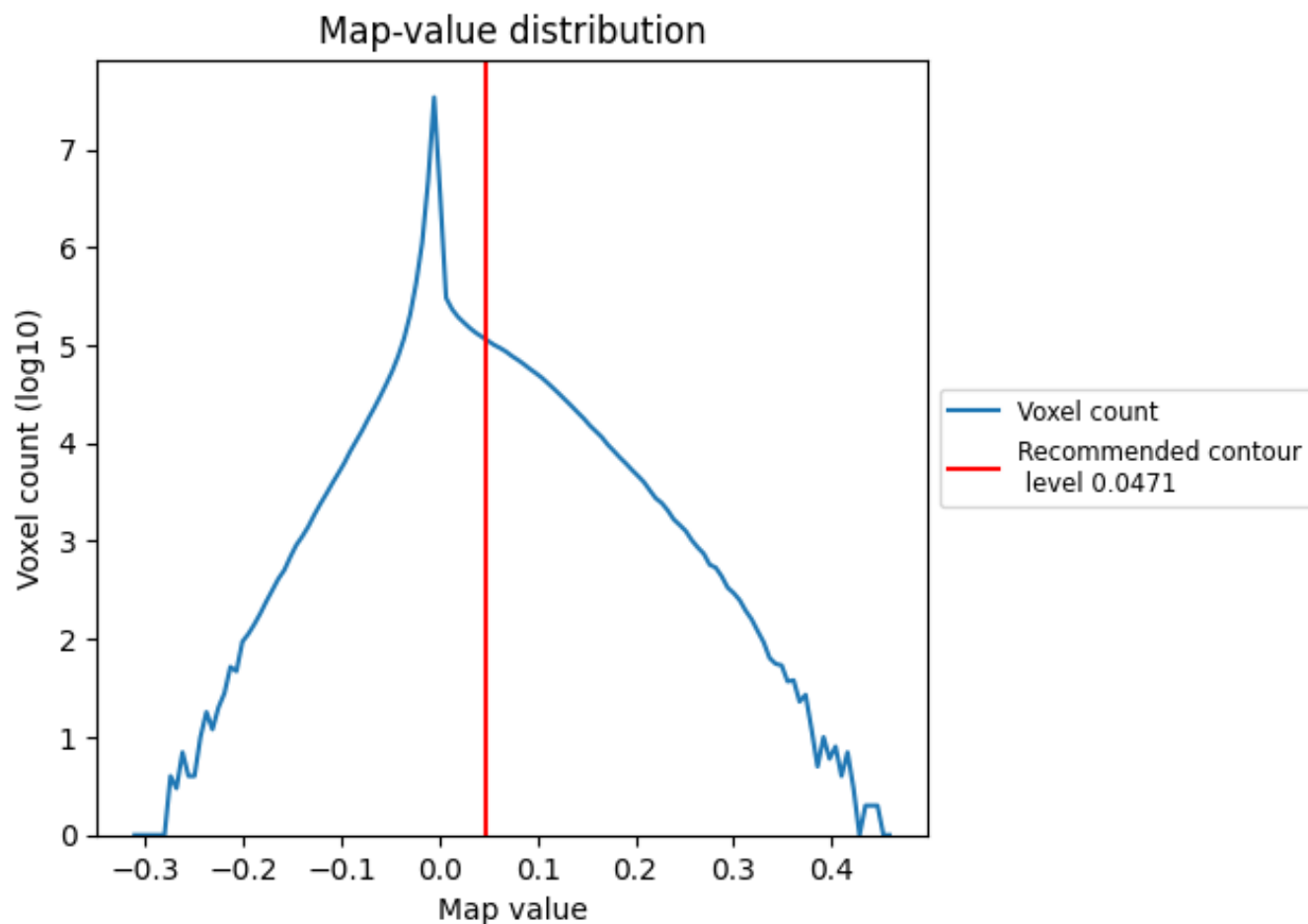
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

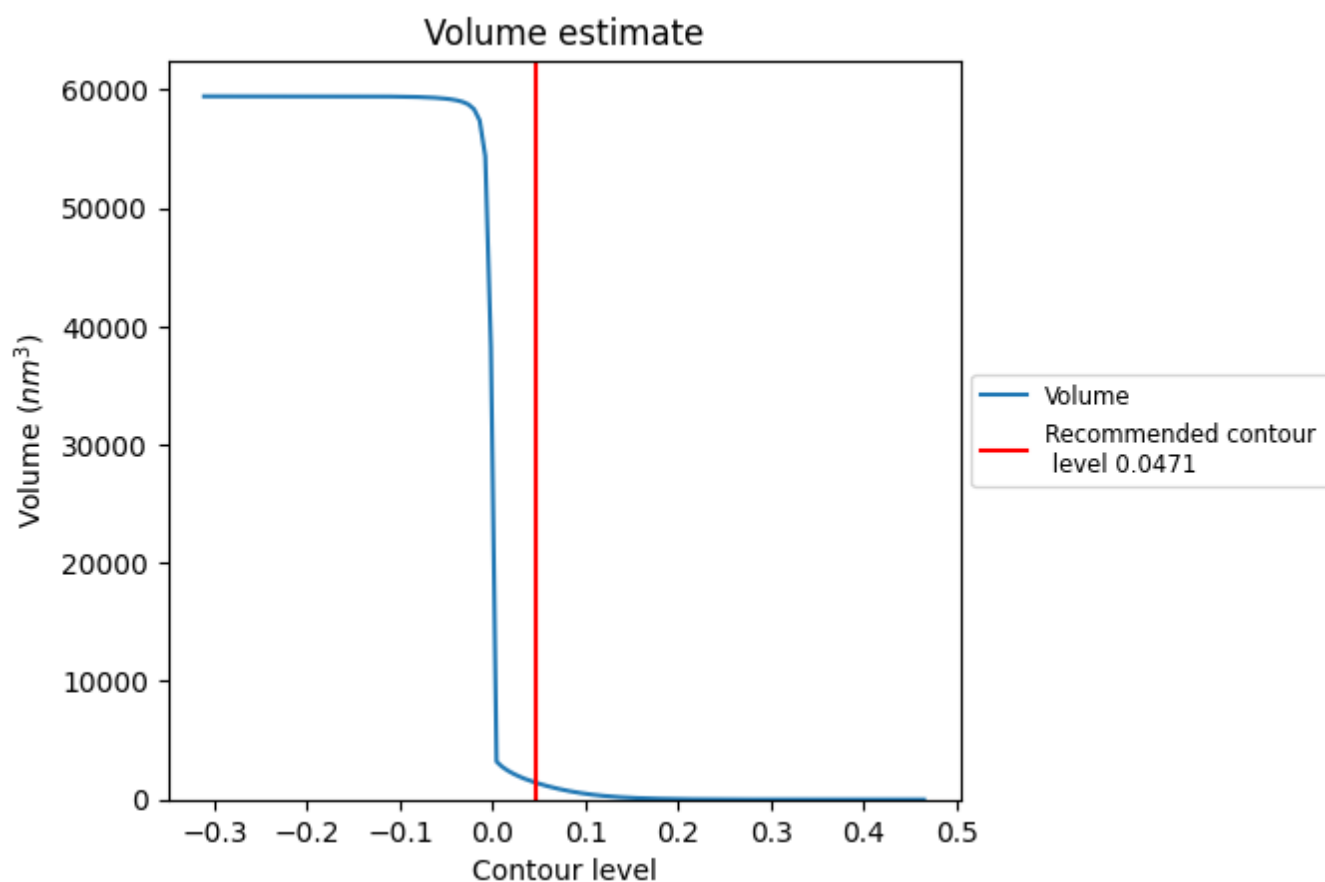
This section contains the results of statistical analysis of the map.

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.

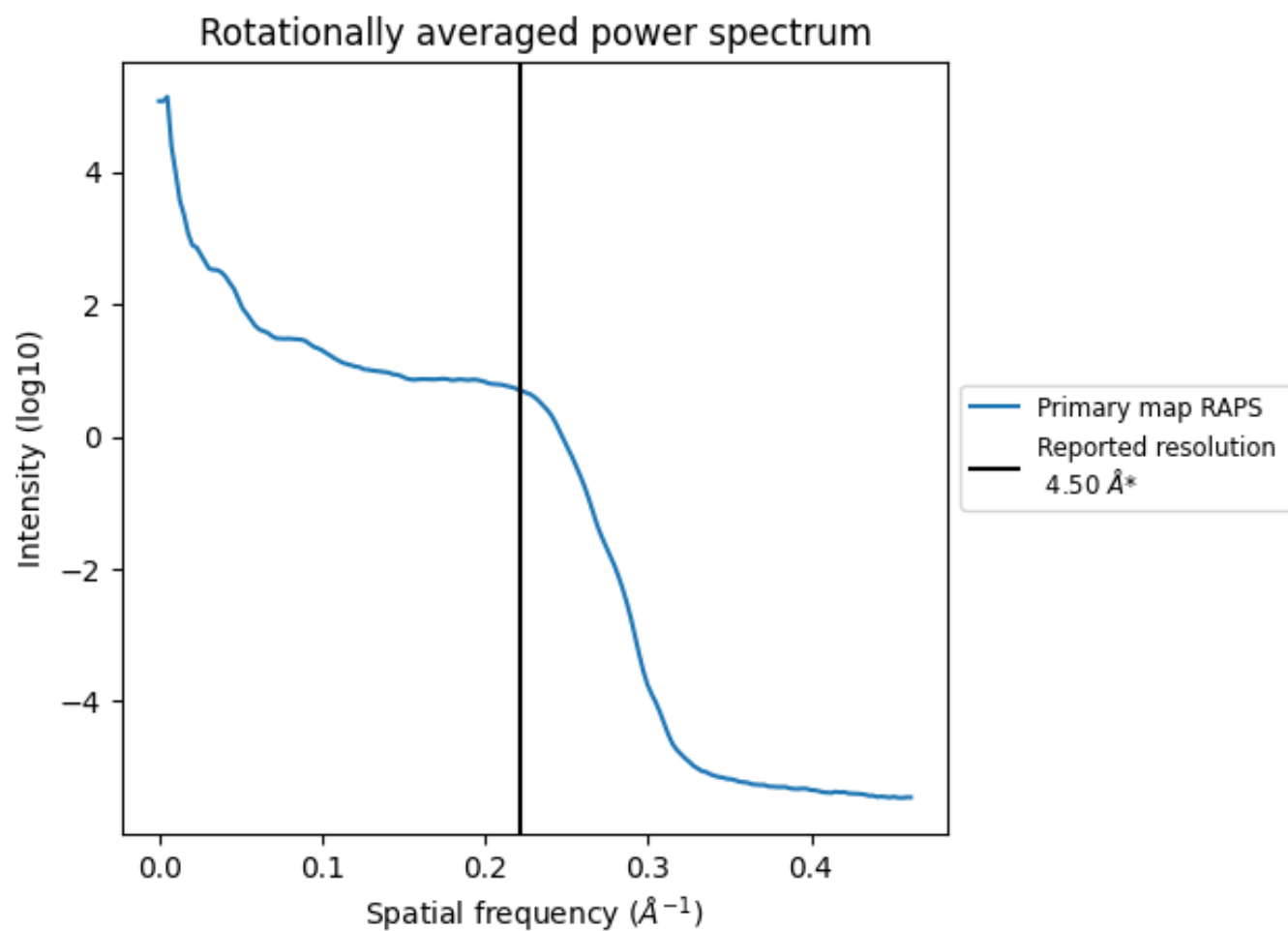
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1411 nm³; this corresponds to an approximate mass of 1274 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 0.222 Å⁻¹

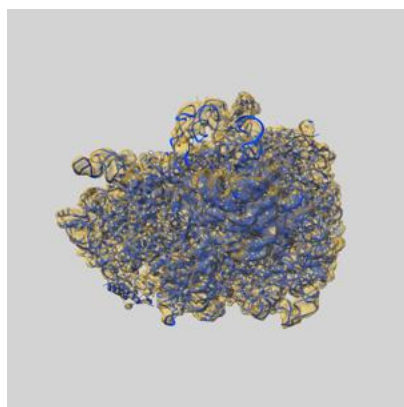
8 Fourier-Shell correlation

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

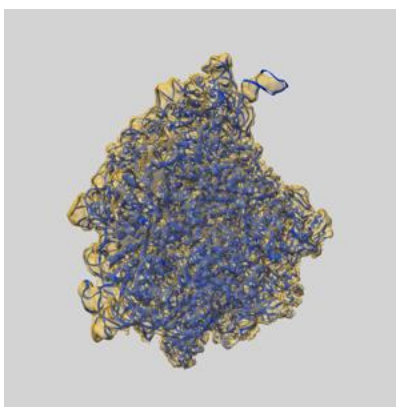
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0270 and PDB model 6HTQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

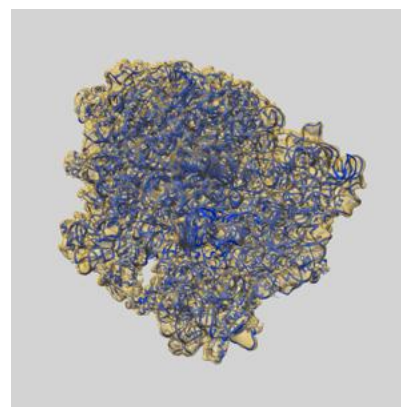
9.1 Map-model overlay [i](#)



X



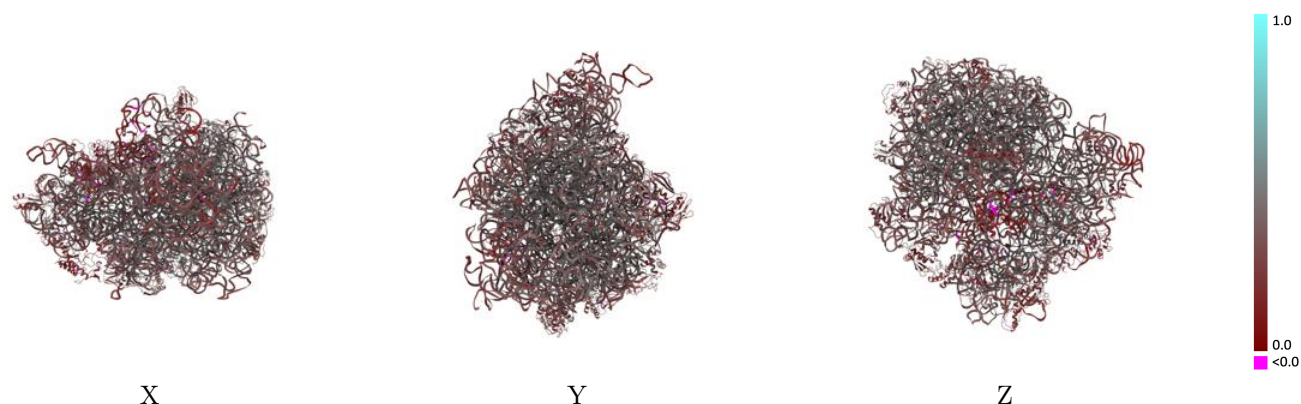
Y



Z

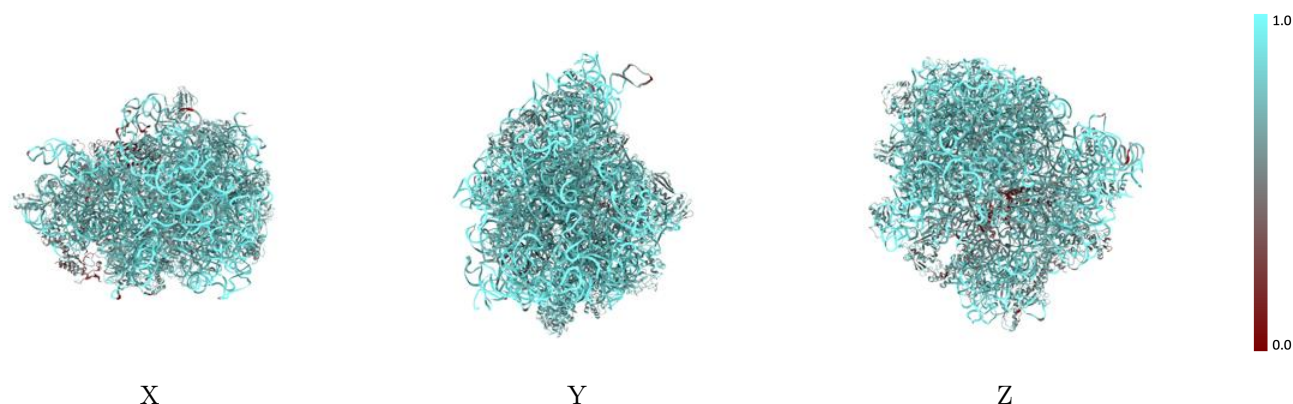
The images above show the 3D surface view of the map at the recommended contour level 0.0471 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



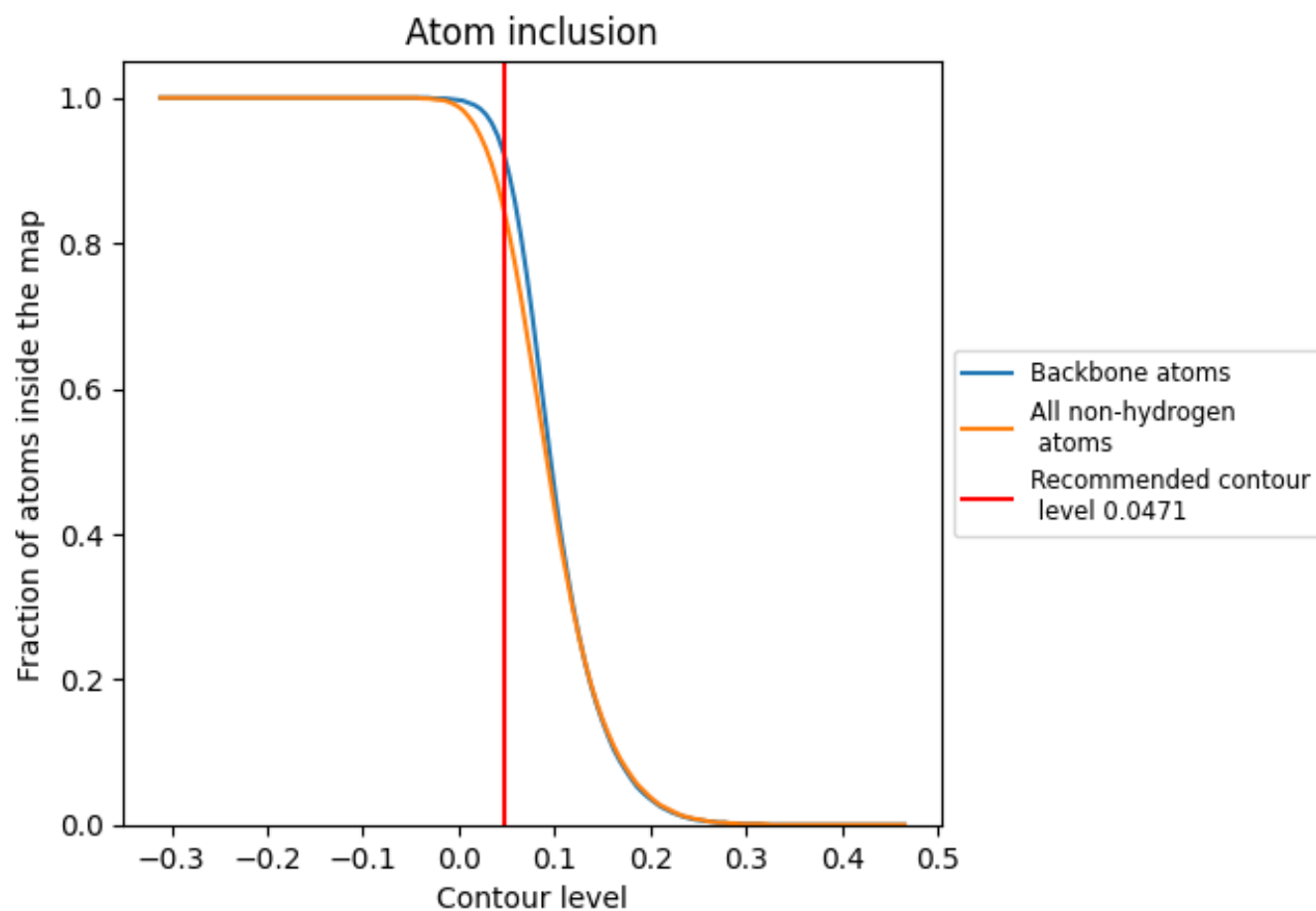
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0471).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (0.0471) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.3550
1	 0.8450	 0.4240
2	 0.7490	 0.3660
3	 0.8550	 0.4380
4	 0.8000	 0.4360
5	 0.7170	 0.3800
A	 0.9220	 0.3790
B	 0.9570	 0.3490
C	 0.7940	 0.4330
D	 0.7780	 0.4050
E	 0.7340	 0.3460
F	 0.6590	 0.2610
G	 0.6590	 0.2660
J	 0.7800	 0.3980
K	 0.7590	 0.4160
L	 0.7550	 0.3880
M	 0.7440	 0.3800
N	 0.7630	 0.3790
O	 0.7040	 0.2730
P	 0.7540	 0.4020
Q	 0.7940	 0.3940
R	 0.6920	 0.3380
S	 0.7660	 0.3940
T	 0.7190	 0.3430
U	 0.7050	 0.3110
V	 0.7630	 0.3870
W	 0.5950	 0.1450
X	 0.6690	 0.2590
Y	 0.7170	 0.3590
Z	 0.5830	 0.2530
a	 0.9300	 0.3620
b	 0.4160	 0.2330
c	 0.6800	 0.3170
d	 0.6220	 0.2600
e	 0.7210	 0.3720



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Chain	Atom inclusion	Q-score
f	 0.7070	 0.3340
g	 0.6800	 0.2890
h	 0.7300	 0.3540
i	 0.7180	 0.3110
j	 0.6730	 0.3070
k	 0.7060	 0.3240
l	 0.7120	 0.3800
m	 0.6850	 0.2850
n	 0.7310	 0.3650
o	 0.7210	 0.3140
p	 0.6960	 0.2910
q	 0.6450	 0.3110
r	 0.6790	 0.3250
s	 0.6740	 0.2810
t	 0.6830	 0.2700
u	 0.6990	 0.2190
v	 0.8400	 0.3330
w	 0.5290	 0.1910
x	 0.3800	 0.1860