



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:47 AM UTC

PDB ID : 6HTQ / pdb_00006htq
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:

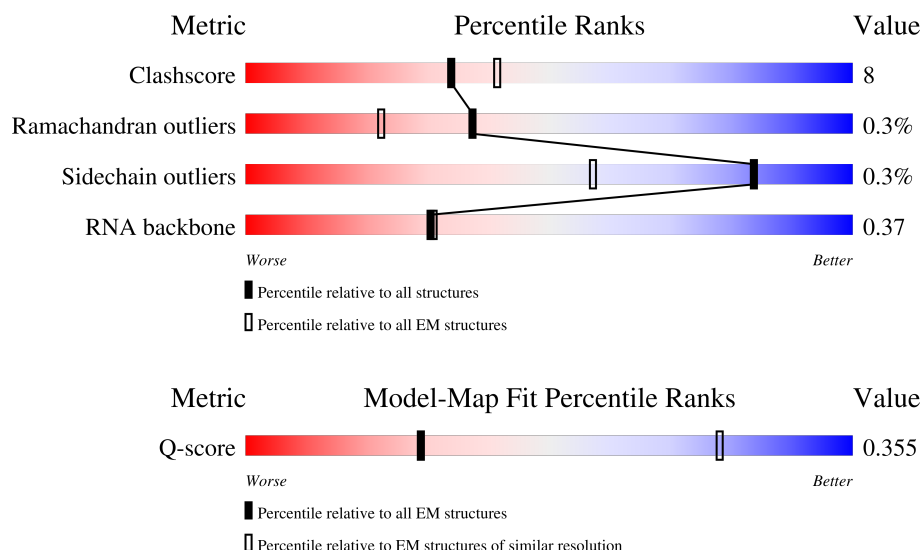
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 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.



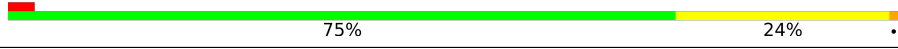
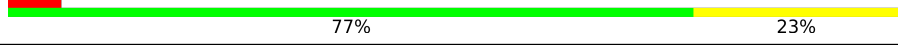
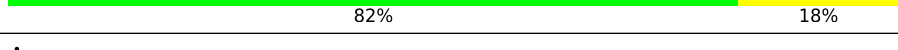
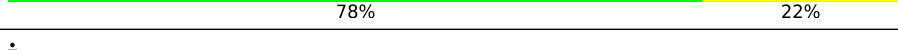
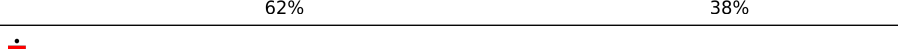
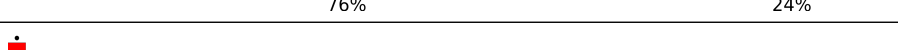
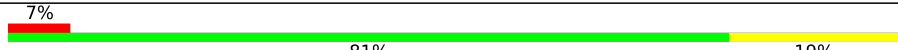
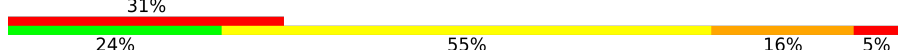
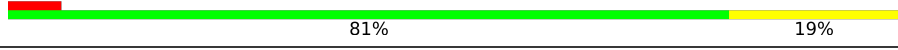
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	
2	B	112	
3	C	272	

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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	205	
6	F	176	
7	G	175	
8	J	142	
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	

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Mol	Chain	Length	Quality of chain
29	Z	63	
30	a	1533	
31	b	218	
32	c	206	
33	d	195	
34	e	164	
35	f	92	
36	g	149	
37	h	131	
38	i	125	
39	j	95	
40	k	114	
41	l	136	
42	m	108	
43	n	60	
44	o	85	
45	p	88	
46	q	84	
47	r	64	
48	s	78	
49	t	83	
50	v	87	
51	x	341	
52	u	76	
53	w	75	

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		

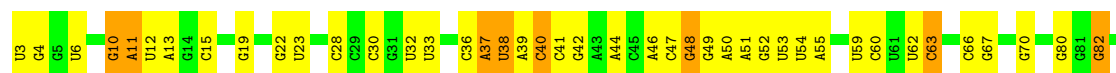
- Molecule 53 is a RNA chain called E-tRNA.

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

G1898	G1899	G1902	G1905	A1913	A1914	A1928	A1929	A1930	G1931	G1932	G1935	C1938	C1939	U1940	A1941	A1942	C1943	A1944	A1945	A1946	A1947	A1948	A1949	G1950	G1951	U1952	C1953	A1956	A1957	G1958	G1959	G1962	C1963	G1964	A1965	A1966	U1967	U1968	U1969	U1972	U1973	G1977	G1978	A1981	A1982	G1983	U1984	U1985								
U1826	C1826	U1827	C1828	C1829	G1830	A1831	A1832	C1833	C1834	A1835	A1836	U1837	A1838	A1839	G1840	C1841	C1842	A1843	A1844	A1845	G1846	U1847	A1848	U1849	A1850	G1851	G1852	G1853	G1854	C1855	U1856	G1857	A1858	C1859	G1866	G1867	G1868	G1869	U1870	G1871	G1872	A1877	A1878	A1882	A1883	A1884	A1885	A1886	A1887	A1888	C1889	C1890	A1891	G1892	G1893	U1893
U1756	G1757	U1758	U1759	A1760	U1764	G1765	G1766	A1767	A1768	A1769	A1680	C1771	A1774	G1775	A1776	G1777	A1778	G1779	C1780	C1781	G1782	C1783	A1784	G1785	U1786	G1787	A1788	A1789	U1790	A1791	G1792	G1793	A1797	G1798	G1799	C1800	G1801	A1802	G1803	U1804	G1805	U1806	U1807	A1808	A1809	G1810	C1811	A1812	A1813	A1814	A1815	A1816	C1817	A1820	G1821	
U1666	G1671	A1672	G1673	G1674	A1675	A1676	A1677	A1678	A1679	A1680	C1683	A1686	G1687	A1691	U1692	C1693	G1696	A1697	G1698	A1699	A1700	U1704	U1708	A1709	G1712	A1713	A1714	G1715	U1716	G1719	C1720	A1721	G1722	A1723	A1724	A1734	U1738	C1739	G1740	G1741	G1742	A1743	A1744	A1745	A1746	G1747	G1748									
A	A	A	U	U	U	A	G	U	A	G1589	A1592	A1593	G1594	U1595	U1596	C1597	C1598	C1604	A1608	A1614	A1615	G1616	A1617	A1618	A1619	A1620	G1621	U1626	A1627	G1628	A1631	G1632	G1633	U1634	G1639	G1640	U1641	C1644	C1645	C1649	C1652	A1653	A1654	A1655	G1658	A1661										
U1505	A1506	U1507	C1508	U1513	C1514	C1515	A1516	U1521	G1525	C1526	U1527	U1528	U1529	G1530	G1531	A1532	A1533	G1537	G1538	C1539	A1540	A1541	A1542	U1543	C1544	U1547	C1550	C1551	C1552	A1553	U	A1555	A1556	G1557	G1558	C1559	U1560	G1561	U1565	A1566	U1567	G1568	A1569	U1570	G1571	C1572	A1573	G1574	A1575	G1576	G1577	G				
A1417	U1418	U1419	U1419	U1422	A1423	A1424	C1425	A1426	G1427	G1431	A1432	U1433	U1434	U1435	U1436	C1437	A1442	U1448	C1449	A1453	U1457	U1458	U1459	G1460	C1463	A1464	A1465	U1466	G1467	G1472	A1473	C1474	G1475	C1476	A1477	G1478	G1479	G1482	U1489	A1490	A1491	U1498	A1499	U1500	U1501	G1502	G1503	A1504								
G1338	A1339	U1340	U1341	G1349	U1350	U1351	U1352	C1353	G1359	A1360	A1361	G1362	G1363	C1364	U1365	C1366	C1367	U1368	C1369	G1370	G1371	C1372	A1375	G1376	G1377	G1378	U1379	A1380	A1381	G1382	U1383	C1384	G1385	G1386	G1387	A1388	C1389	G1394	G1397	A1398	G1400	C1402	G1403	A1404	A1405	A1406	G1407	G1408	U1411	A1412						
A1260	C1261	G1262	G1263	A1266	G1267	G1268	A1269	C1270	G1275	G1276	A1277	G1278	U1282	A1287	U1288	U1289	G1292	A1293	U1295	G1296	C1297	G1298	G1299	G1300	U1301	A1302	U1303	G1304	A1305	G1306	U1307	A1308	G1311	A1312	A1313	A1314	G1315	G1319	U1320	U1321	G1322	A1323	G1324	A1325	A1326	U1327	C1328	C1333	C1337							
U1178	A1179	C1180	C1181	G1182	G1183	G1184	G1185	A1188	A1189	A1190	C1191	G1192	U1195	A1196	C1197	C1198	C1199	G1200	A1202	C1203	C1204	U1205	G1206	C1207	G1208	G1209	A1210	C1216	U	C	G1220	G1227	U1228	A1230	G1231	G1232	G1236	U1242	A1243	A1244	G1245	C1248	U1249	G1250	U1251	G1252	A1258	G1259								
G1102	A1103	U1104	G1105	U1106	U1107	G1108	C1109	C1110	U1111	G1114	A1115	G1116	C1117	C1118	G1119	G1120	C1121	G1122	C1123	C1124	C1125	A1126	U1127	U1128	G1133	A1134	G1137	C1138	G1139	U1140	A1141	A1142	U1143	G1144	G1145	C1146	U1147	G1156	A1157	G1158	U1159	G1160	A1161	U1165	G1166	C1167	G1168	A1172	A1173	A1174	U1175	G1176	G1177			
A1006	G1007	C1011	G1012	U1013	A1014	G1015	U1016	C1017	G1018	A1019	A1020	A1026	A1027	C1028	A1029	G1030	C1031	C1032	C1033	A1034	G1035	A1036	C1037	G1038	C1039	C1040	C1041	A1042	G1043	A1054	A1055	A1056	G1057	U1058	A1059	U1065	A1066	A1067	G1068	U1069	G1070	G1071	G1072	A1073	U1076	U1079	U1090	U1091	A1092	G1093	A1094	G1101				
A851	G852	C853	U854	G855	U858	C859	U860	C864	G865	A866	A867	A868	U869	A870	U874	U875	A876	G877	G878	U881	U886	U891	U892	G895	U901	G902	G903	A904	G905	G906	U907	A908	G909	A910	G911	C912	A913	C914	U915	G916	G920	G921	A925	G926	G927	G928	G929	C930	C931							

- Molecule 2: 5S ribosomal RNA

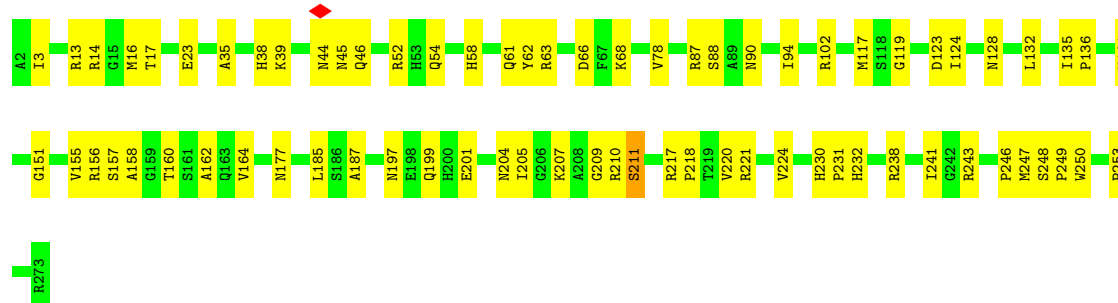
Chain B:





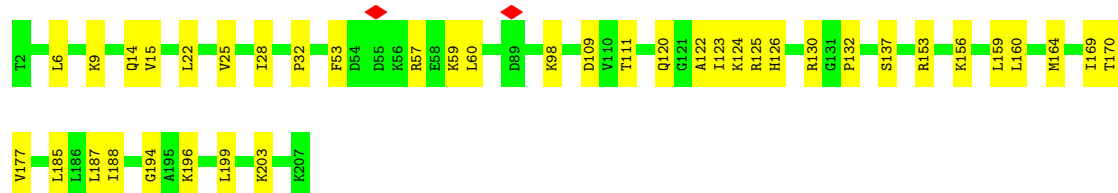
• Molecule 3: 50S ribosomal protein L2

Chain C: 74% 26%



• Molecule 4: 50S ribosomal protein L3

Chain D: 81% 19%



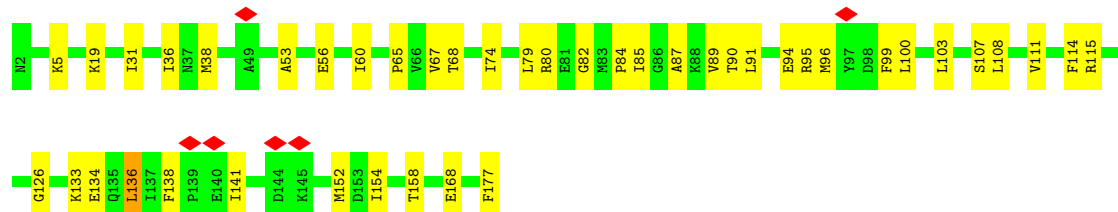
• Molecule 5: 50S ribosomal protein L4

Chain E: 80% 20%

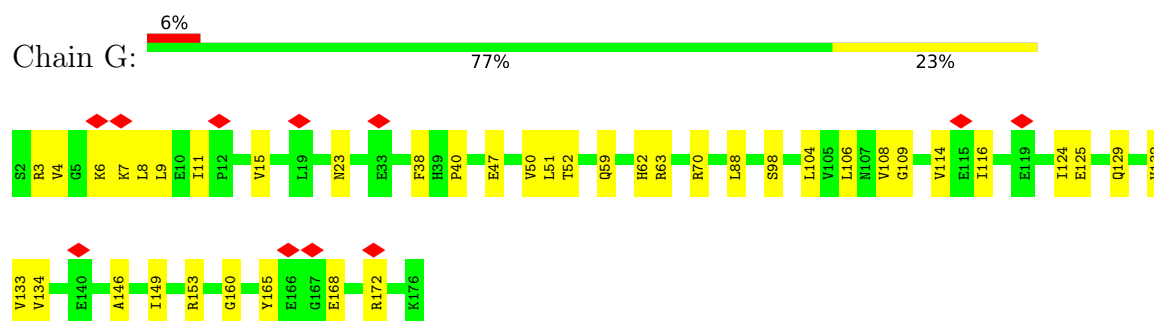


• Molecule 6: 50S ribosomal protein L5

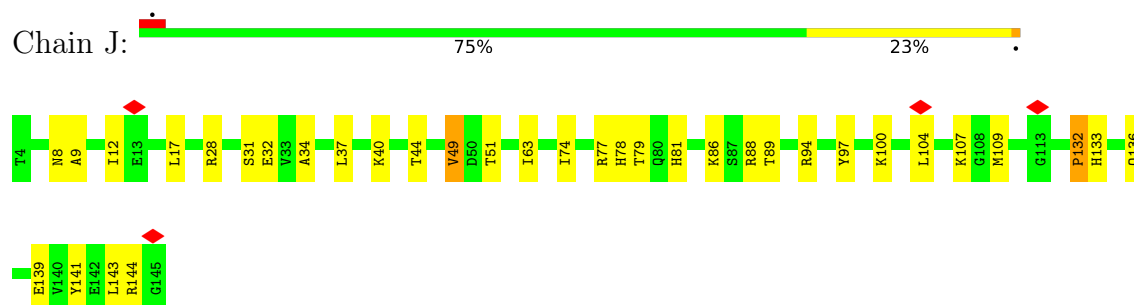
Chain F: 75% 24%



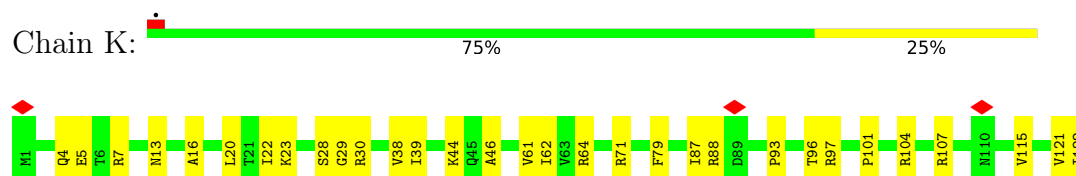
- Molecule 7: 50S ribosomal protein L6



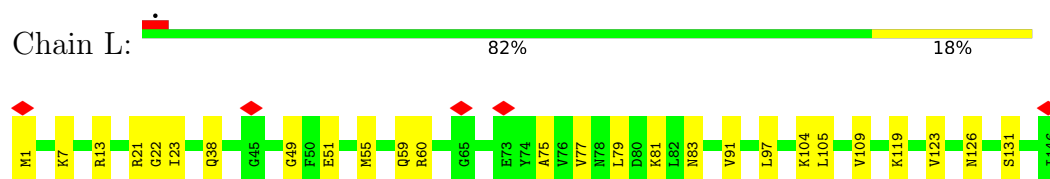
- Molecule 8: 50S ribosomal protein L13



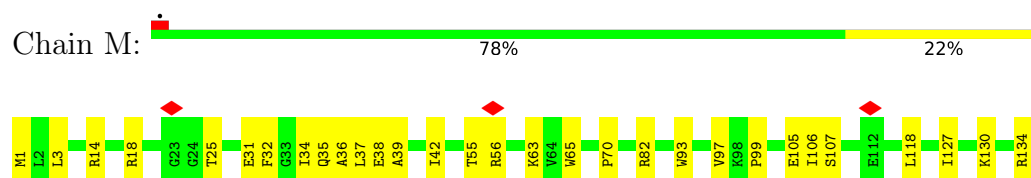
- Molecule 9: 50S ribosomal protein L14



- Molecule 10: 50S ribosomal protein L15

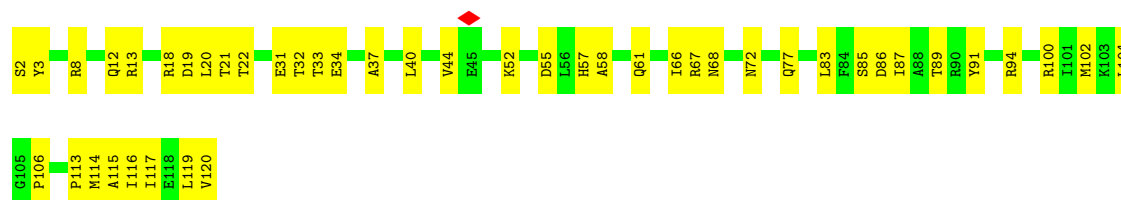


- Molecule 11: 50S ribosomal protein L16

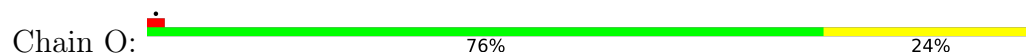


- Molecule 12: 50S ribosomal protein L17





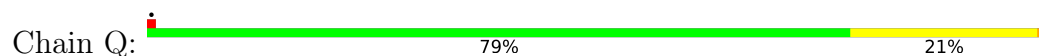
- Molecule 13: 50S ribosomal protein L18



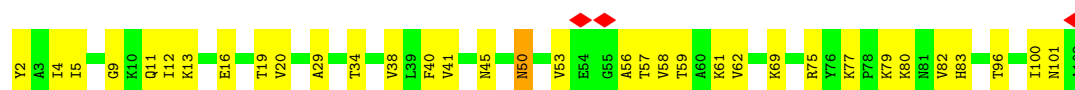
- Molecule 14: 50S ribosomal protein L19



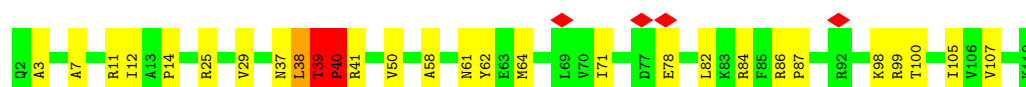
- Molecule 15: 50S ribosomal protein L20



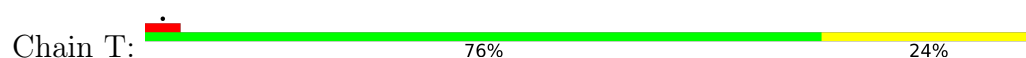
- Molecule 16: 50S ribosomal protein L21



- Molecule 17: 50S ribosomal protein L22

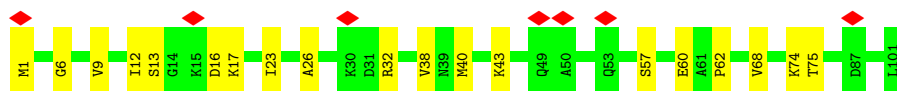
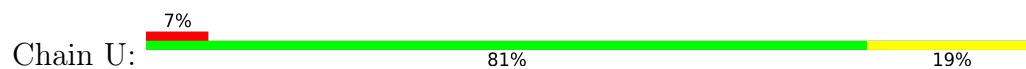


- Molecule 18: 50S ribosomal protein L23





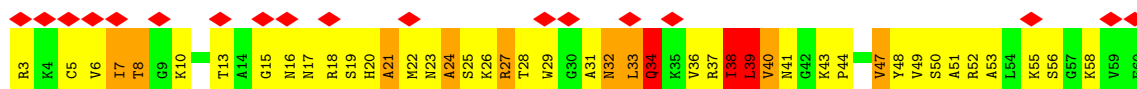
- Molecule 19: 50S ribosomal protein L24



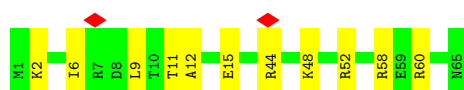
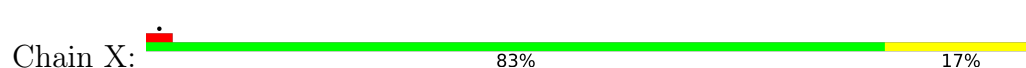
- Molecule 20: 50S ribosomal protein L27



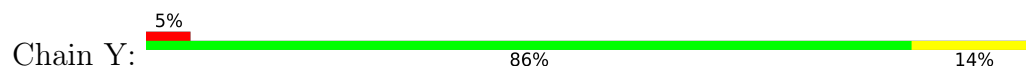
- Molecule 21: 50S ribosomal protein L28



- Molecule 22: 50S ribosomal protein L29



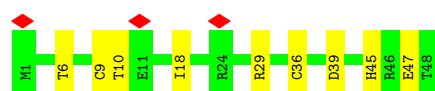
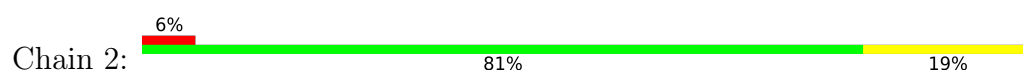
- Molecule 23: 50S ribosomal protein L30



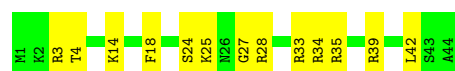
- Molecule 24: 50S ribosomal protein L32



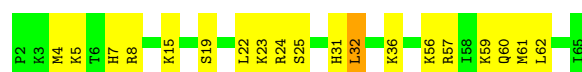
- Molecule 25: 50S ribosomal protein L33 1



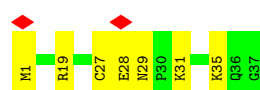
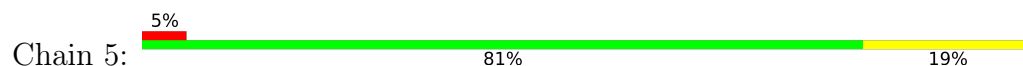
- Molecule 26: 50S ribosomal protein L34



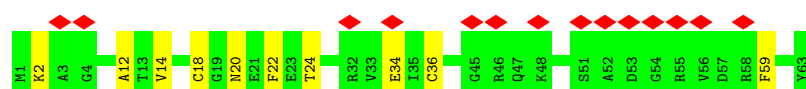
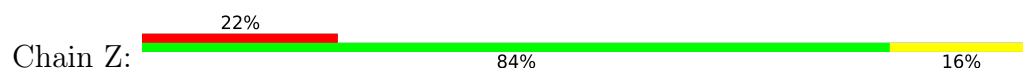
- Molecule 27: 50S ribosomal protein L35



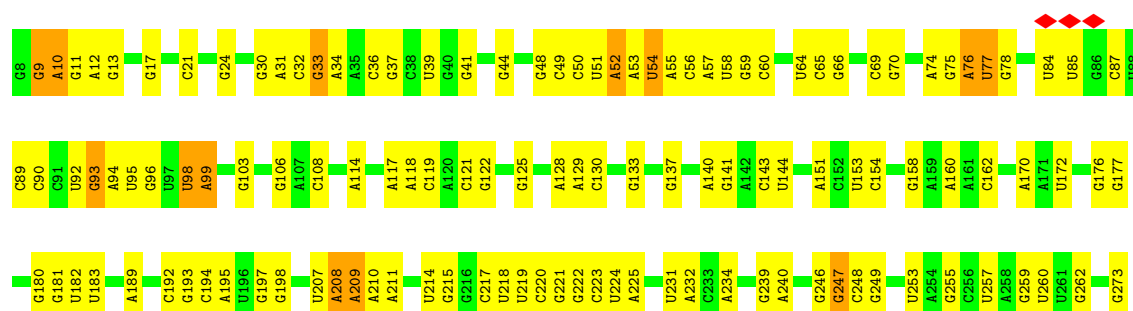
- Molecule 28: 50S ribosomal protein L36

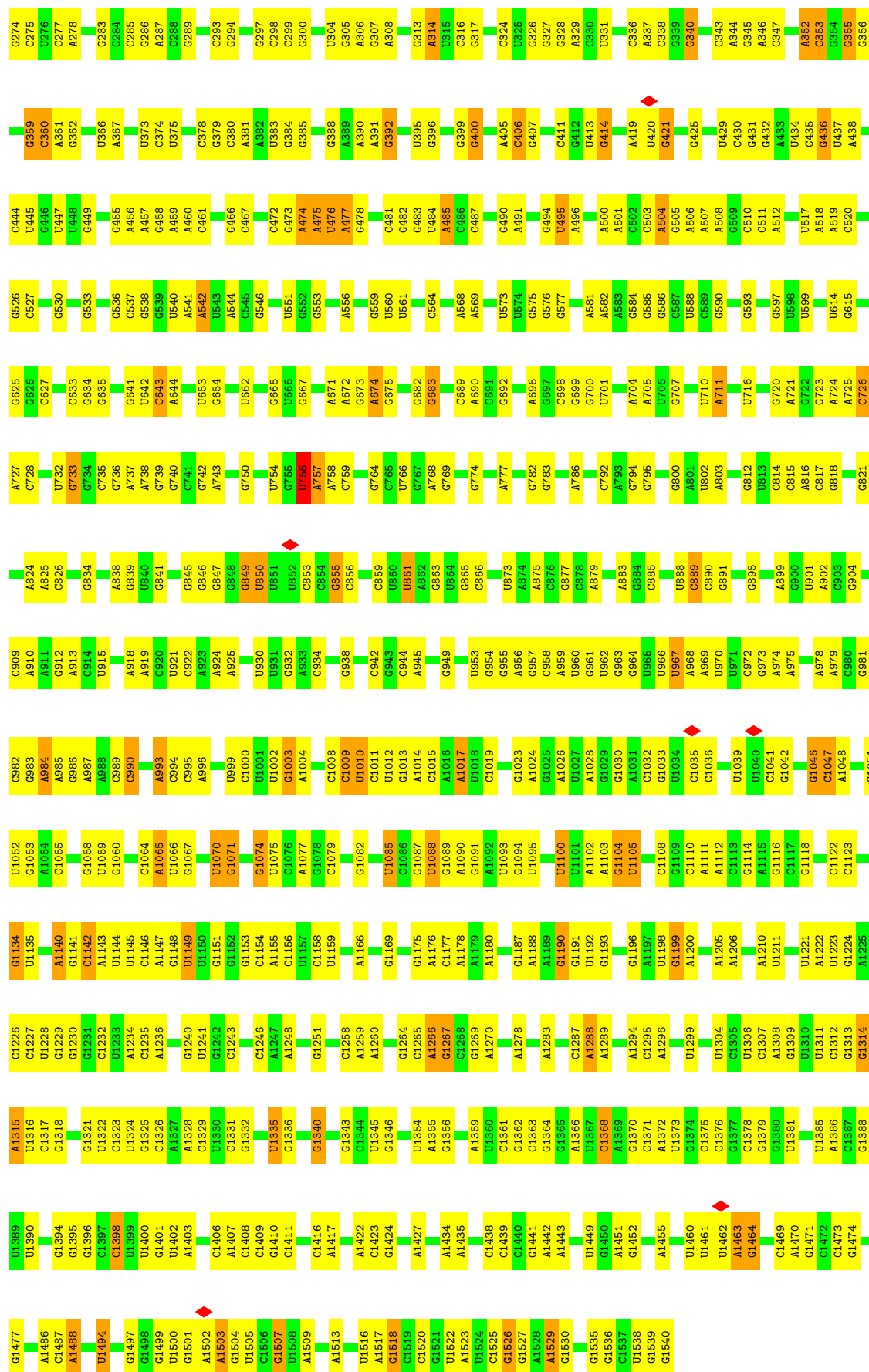


- Molecule 29: 50S ribosomal protein L31

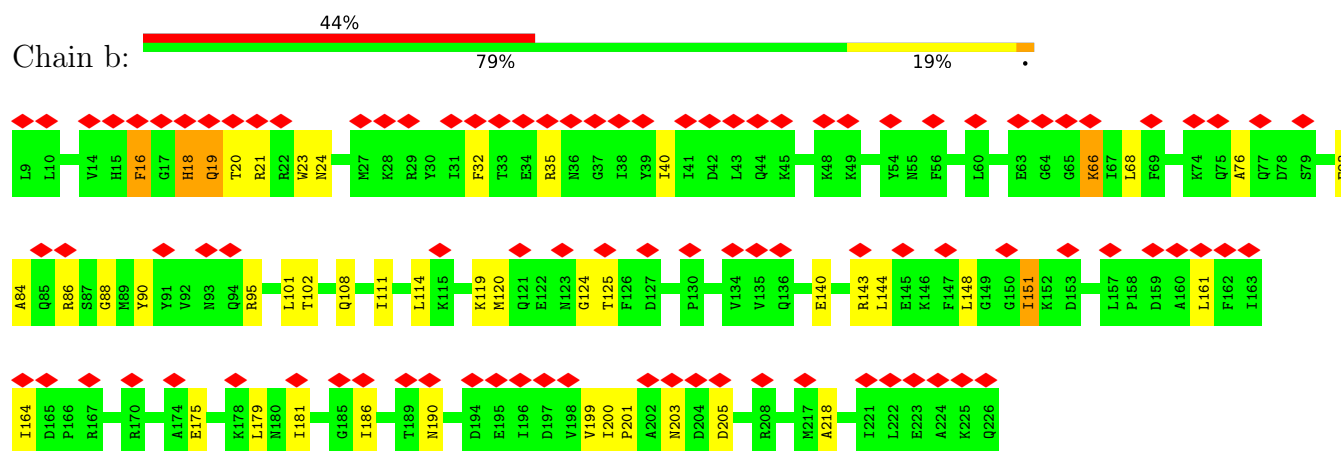


- Molecule 30: 16S rRNA

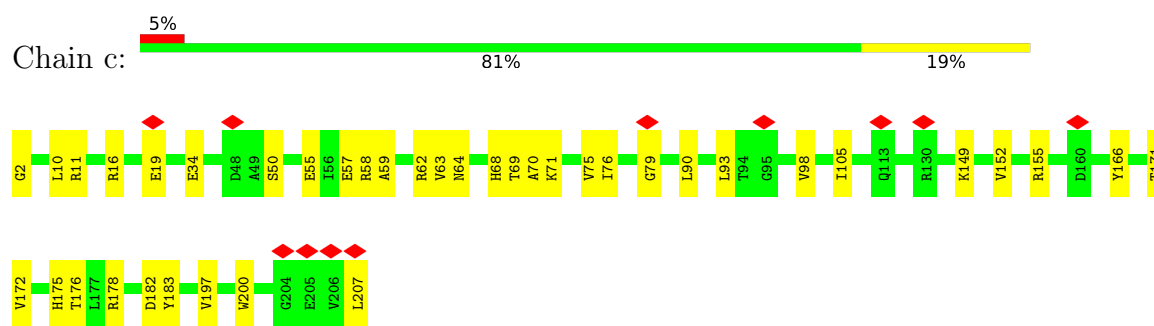




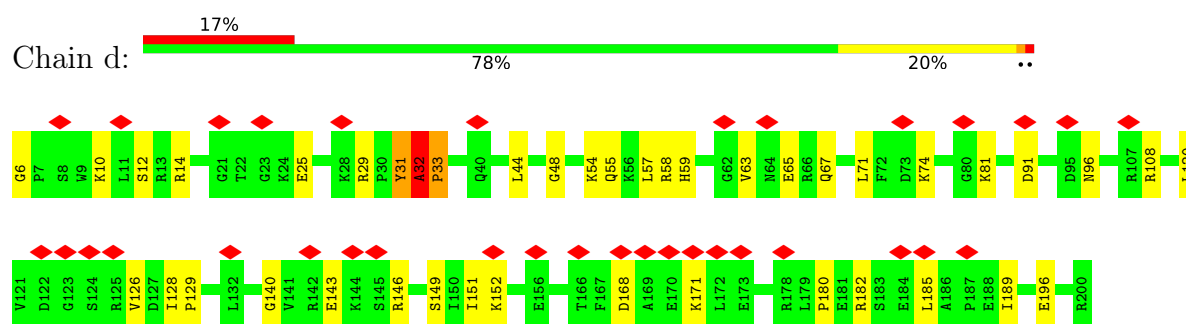
- Molecule 31: 30S ribosomal protein S2



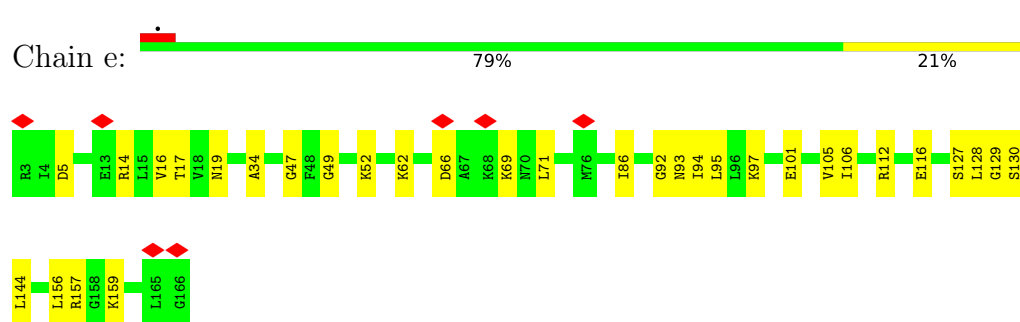
- Molecule 32: 30S ribosomal protein S3



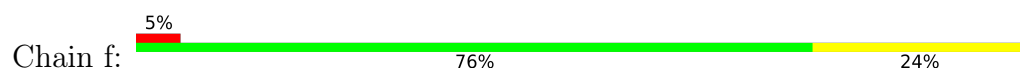
- Molecule 33: 30S ribosomal protein S4



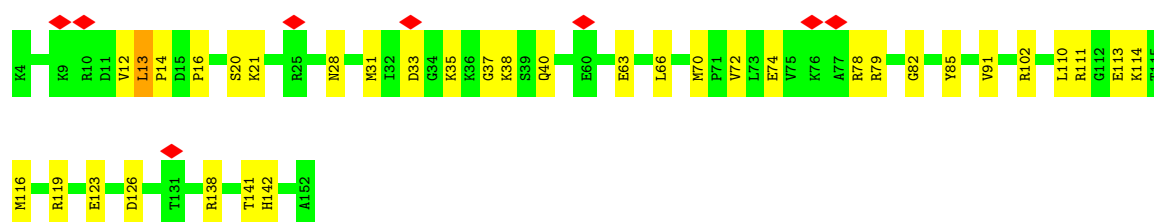
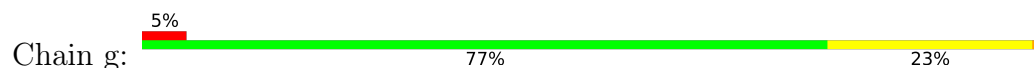
- Molecule 34: 30S ribosomal protein S5



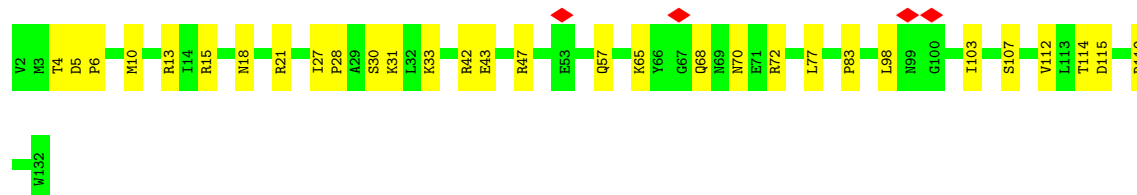
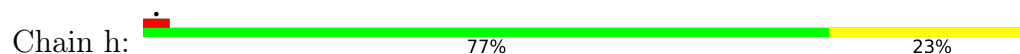
- Molecule 35: 30S ribosomal protein S6



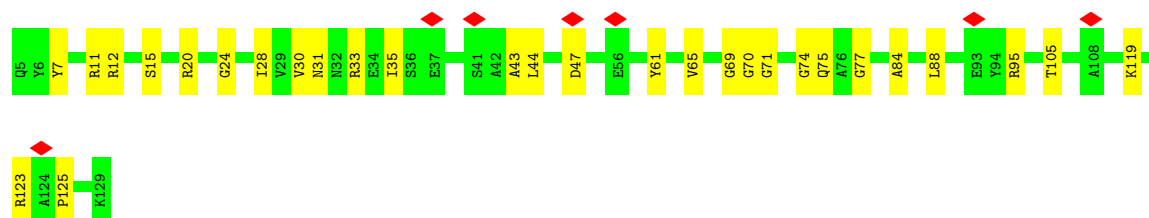
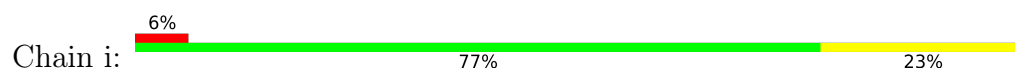
- Molecule 36: 30S ribosomal protein S7



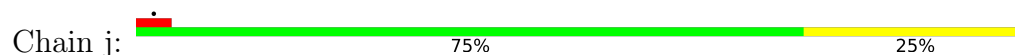
- Molecule 37: 30S ribosomal protein S8



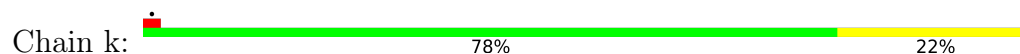
- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10

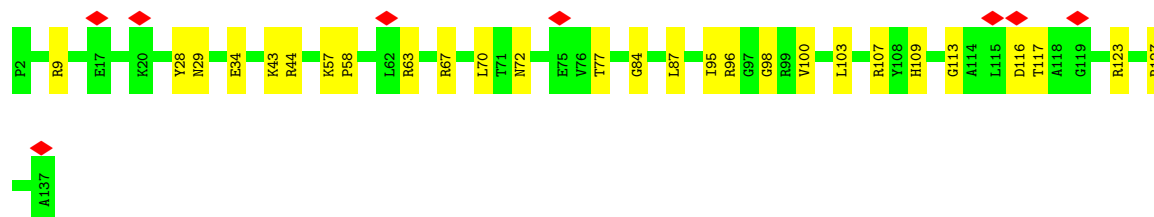
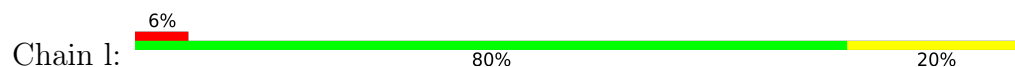


- Molecule 40: 30S ribosomal protein S11

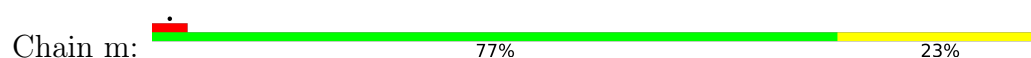




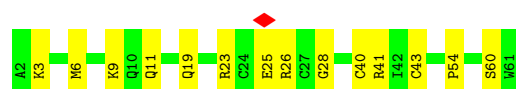
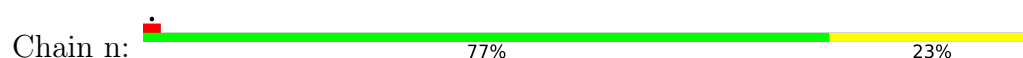
- Molecule 41: 30S ribosomal protein S12



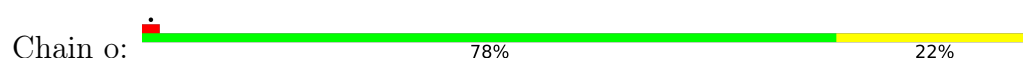
- Molecule 42: 30S ribosomal protein S13



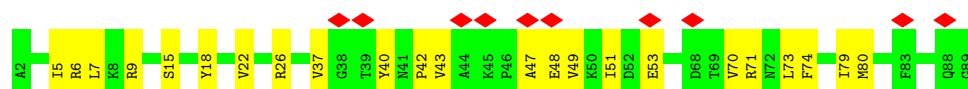
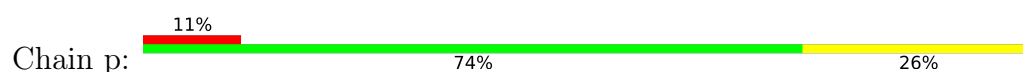
- Molecule 43: 30S ribosomal protein S14



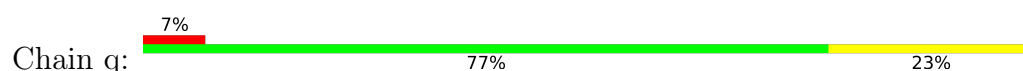
- Molecule 44: 30S ribosomal protein S15

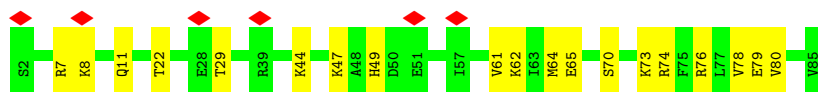


- Molecule 45: 30S ribosomal protein S16

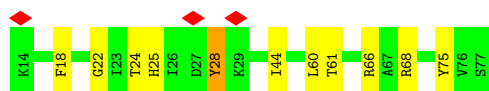
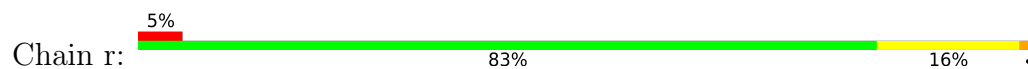


- Molecule 46: 30S ribosomal protein S17

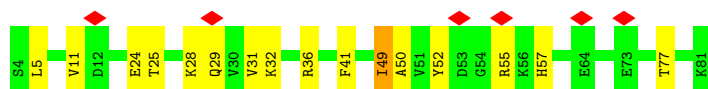




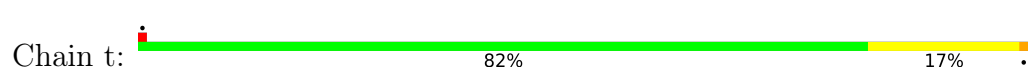
- Molecule 47: 30S ribosomal protein S18



- Molecule 48: 30S ribosomal protein S19



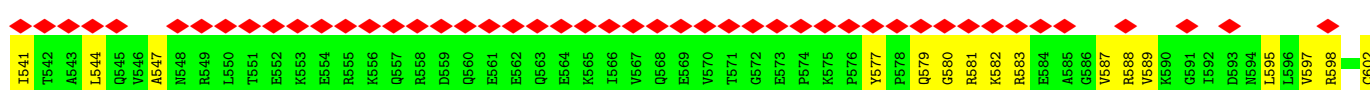
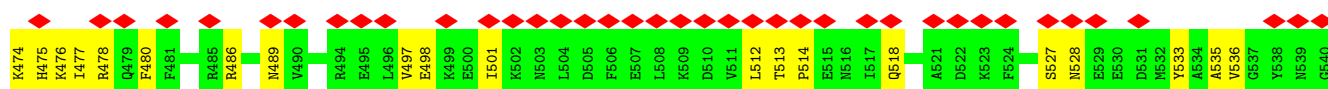
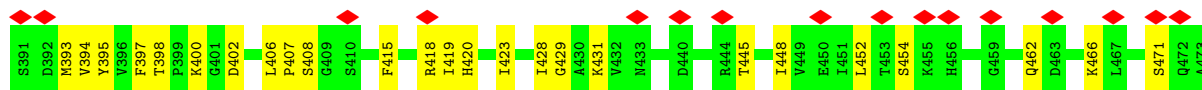
- Molecule 49: 30S ribosomal protein S20

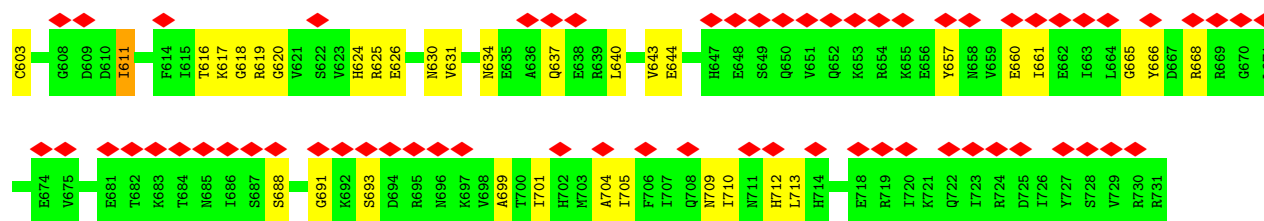


- Molecule 50: P-tRNA

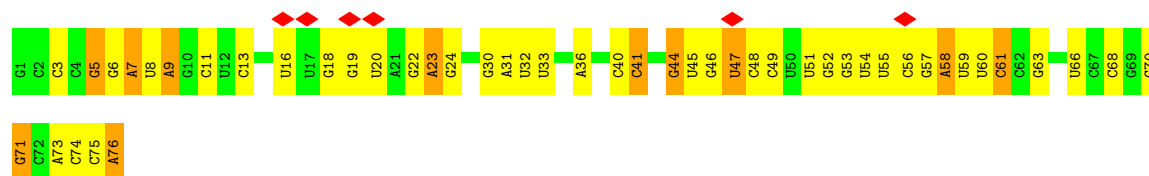


- Molecule 51: GTP pyrophosphokinase

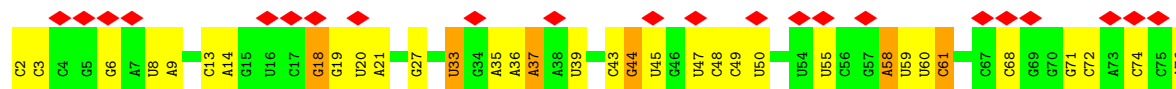




• Molecule 52: A/R-tRNA



• 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 ($\text{\AA}$)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.45	6/69438 (0.0%)	0.43	3/108311 (0.0%)
2	B	0.20	0/2675	0.34	0/4170
3	C	0.38	0/2120	0.70	1/2845 (0.0%)
4	D	0.35	0/1591	0.64	0/2132
5	E	0.28	0/1580	0.58	0/2132
6	F	0.22	0/1405	0.59	1/1887 (0.1%)
7	G	0.17	0/1360	0.42	0/1832
8	J	0.30	0/1146	0.61	0/1542
9	K	0.36	0/927	0.65	2/1245 (0.2%)
10	L	0.28	0/1093	0.57	0/1457
11	M	0.27	0/1099	0.53	0/1468
12	N	0.30	0/960	0.60	0/1284
13	O	0.20	0/921	0.55	0/1236
14	P	0.30	0/957	0.59	0/1279
15	Q	0.36	0/952	0.67	0/1266
16	R	0.25	0/797	0.59	0/1070
17	S	0.32	0/851	0.75	3/1146 (0.3%)
18	T	0.23	0/731	0.49	0/974
19	U	0.21	0/772	0.55	0/1032
20	V	0.30	0/638	0.73	2/847 (0.2%)
21	W	4.07	2/448 (0.4%)	1.58	7/596 (1.2%)
22	X	0.17	0/531	0.47	0/707
23	Y	0.26	0/457	0.58	0/613
24	1	0.33	0/433	0.68	0/574
25	2	0.22	0/406	0.56	0/540
26	3	0.36	0/370	0.56	0/483
27	4	0.31	0/519	0.61	0/680
28	5	0.23	0/299	0.46	0/393
29	Z	0.21	0/509	0.50	0/678
30	a	0.26	0/36826	0.37	2/57450 (0.0%)
31	b	0.19	0/1782	0.62	5/2392 (0.2%)
32	c	0.23	0/1641	0.52	0/2208
33	d	0.26	0/1598	0.63	0/2147
34	e	0.28	0/1230	0.60	0/1655

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	f	0.19	0/766	0.43	0/1031
36	g	0.22	0/1196	0.56	0/1604
37	h	0.28	0/1048	0.61	0/1407
38	i	0.24	0/979	0.64	0/1315
39	j	0.25	0/773	0.55	0/1044
40	k	0.22	0/852	0.50	0/1153
41	l	0.28	0/1069	0.64	0/1435
42	m	0.26	0/873	0.66	0/1166
43	n	0.29	0/507	0.71	0/672
44	o	0.22	0/718	0.56	0/960
45	p	0.22	0/708	0.60	0/950
46	q	0.22	0/699	0.57	0/933
47	r	0.21	0/526	0.61	0/705
48	s	0.22	0/649	0.51	0/872
49	t	0.20	0/639	0.56	0/852
50	v	0.21	0/2080	0.33	0/3242
51	x	0.21	0/2794	0.58	2/3757 (0.1%)
52	u	0.15	0/1813	0.31	0/2823
53	w	0.16	0/1786	0.33	0/2782
All	All	0.41	8/159537 (0.0%)	0.46	28/238974 (0.0%)

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 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	W	34	GLN	CD-NE2	85.13	3.12	1.33
1	A	2120	U	C2-N3	37.51	2.12	1.37
1	A	2120	U	N3-C4	36.41	2.11	1.38
1	A	2120	U	N1-C2	35.30	2.09	1.38
1	A	2120	U	N1-C6	33.53	2.05	1.38

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	W	34	GLN	CG-CD-NE2	10.47	132.10	116.40
21	W	34	GLN	CG-CD-OE1	-9.23	102.35	120.80
17	S	38	LEU	CA-C-N	6.06	136.58	121.80
17	S	38	LEU	C-N-CA	6.06	136.58	121.80
1	A	2260	U	O4'-C1'-N1	6.03	117.54	108.50

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

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	A	61997	0	31214	577	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2392	0	1213	17	0
3	C	2083	0	2168	52	0
4	D	1569	0	1637	25	0
5	E	1561	0	1647	30	0
6	F	1386	0	1446	27	0
7	G	1342	0	1388	25	0
8	J	1123	0	1162	22	0
9	K	920	0	977	20	0
10	L	1081	0	1132	19	0
11	M	1076	0	1145	18	0
12	N	953	0	983	34	0
13	O	912	0	947	20	0
14	P	944	0	1020	24	0
15	Q	940	0	1005	20	0
16	R	786	0	826	24	0
17	S	842	0	899	20	0
18	T	725	0	770	15	0
19	U	762	0	821	10	0
20	V	630	0	644	20	0
21	W	444	0	487	64	0
22	X	530	0	568	8	0
23	Y	455	0	491	8	0
24	1	426	0	441	14	0
25	2	401	0	413	6	0
26	3	367	0	410	12	0
27	4	512	0	564	14	0
28	5	296	0	342	5	0
29	Z	499	0	491	7	0
30	a	32891	0	16559	315	0
31	b	1757	0	1830	29	0
32	c	1619	0	1658	25	0
33	d	1568	0	1604	30	0
34	e	1218	0	1300	26	0
35	f	755	0	746	14	0
36	g	1181	0	1235	25	0
37	h	1036	0	1095	20	0
38	i	966	0	1005	21	0
39	j	761	0	795	15	0
40	k	838	0	854	18	0
41	l	1052	0	1112	20	0
42	m	868	0	925	17	0
43	n	497	0	531	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	o	710	0	735	13	0
45	p	695	0	721	15	0
46	q	691	0	728	13	0
47	r	518	0	555	7	0
48	s	633	0	649	13	0
49	t	637	0	696	12	0
50	v	1861	0	938	14	0
51	x	2752	0	2789	64	0
52	u	1623	0	820	22	0
53	w	1599	0	810	8	0
All	All	146680	0	97941	1573	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 8.

The worst 5 of 1573 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2120:U:C5	1:A:2120:U:C6	1.95	1.53
1:A:2120:U:C5	1:A:2120:U:C4	2.06	1.41
1:A:2120:U:C6	1:A:2120:U:N1	2.05	1.25
1:A:2120:U:N1	1:A:2120:U:C2	2.09	1.20
1:A:2120:U:C4	1:A:2120:U:N3	2.11	1.19

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	270/272 (99%)	239 (88%)	31 (12%)	0	100	100
4	D	204/206 (99%)	180 (88%)	24 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	39
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	49
16	R	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
17	S	107/109 (98%)	91 (85%)	14 (13%)	2 (2%)	6	32
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	32
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
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%)	24	63
32	c	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
33	d	193/195 (99%)	179 (93%)	12 (6%)	2 (1%)	12	47
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	h	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	53
38	i	123/125 (98%)	111 (90%)	11 (9%)	1 (1%)	16	53
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%)	18	55
42	m	106/108 (98%)	95 (90%)	10 (9%)	1 (1%)	14	49
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	28
46	q	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
47	r	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	37
48	s	76/78 (97%)	67 (88%)	9 (12%)	0	100	100
49	t	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	10	43
51	x	339/341 (99%)	292 (86%)	47 (14%)	0	100	100
All	All	5546/5640 (98%)	4959 (89%)	570 (10%)	17 (0%)	37	71

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%)	220 (100%)	0	100	100
4	D	167/167 (100%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	169/169 (100%)	169 (100%)	0	100	100
6	F	151/151 (100%)	150 (99%)	1 (1%)	76	79
7	G	148/148 (100%)	147 (99%)	1 (1%)	76	79
8	J	120/120 (100%)	119 (99%)	1 (1%)	73	77
9	K	101/101 (100%)	101 (100%)	0	100	100
10	L	110/110 (100%)	110 (100%)	0	100	100
11	M	109/109 (100%)	109 (100%)	0	100	100
12	N	99/99 (100%)	99 (100%)	0	100	100
13	O	93/93 (100%)	93 (100%)	0	100	100
14	P	100/100 (100%)	100 (100%)	0	100	100
15	Q	96/96 (100%)	96 (100%)	0	100	100
16	R	83/83 (100%)	83 (100%)	0	100	100
17	S	90/90 (100%)	90 (100%)	0	100	100
18	T	81/81 (100%)	80 (99%)	1 (1%)	63	73
19	U	85/85 (100%)	85 (100%)	0	100	100
20	V	64/64 (100%)	64 (100%)	0	100	100
21	W	47/47 (100%)	42 (89%)	5 (11%)	6	22
22	X	56/56 (100%)	56 (100%)	0	100	100
23	Y	52/52 (100%)	52 (100%)	0	100	100
24	1	48/48 (100%)	47 (98%)	1 (2%)	47	65
25	2	46/46 (100%)	46 (100%)	0	100	100
26	3	39/39 (100%)	39 (100%)	0	100	100
27	4	54/54 (100%)	53 (98%)	1 (2%)	50	66
28	5	35/35 (100%)	35 (100%)	0	100	100
29	Z	53/53 (100%)	53 (100%)	0	100	100
31	b	189/189 (100%)	189 (100%)	0	100	100
32	c	168/168 (100%)	168 (100%)	0	100	100
33	d	169/169 (100%)	168 (99%)	1 (1%)	78	80
34	e	128/128 (100%)	128 (100%)	0	100	100
35	f	81/81 (100%)	81 (100%)	0	100	100
36	g	125/125 (100%)	124 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	h	111/111 (100%)	111 (100%)	0	100	100
38	i	98/98 (100%)	98 (100%)	0	100	100
39	j	86/86 (100%)	86 (100%)	0	100	100
40	k	86/86 (100%)	86 (100%)	0	100	100
41	l	114/114 (100%)	114 (100%)	0	100	100
42	m	94/94 (100%)	94 (100%)	0	100	100
43	n	53/53 (100%)	53 (100%)	0	100	100
44	o	80/80 (100%)	80 (100%)	0	100	100
45	p	74/74 (100%)	74 (100%)	0	100	100
46	q	77/77 (100%)	77 (100%)	0	100	100
47	r	56/56 (100%)	56 (100%)	0	100	100
48	s	70/70 (100%)	69 (99%)	1 (1%)	59	71
49	t	66/66 (100%)	66 (100%)	0	100	100
51	x	307/307 (100%)	306 (100%)	1 (0%)	86	84
All	All	4748/4748 (100%)	4733 (100%)	15 (0%)	84	84

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	W	39	LEU
48	s	49	ILE
21	W	47	VAL
51	x	611	ILE
33	d	151	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
40	k	121	ASN
51	x	518	GLN
42	m	100	GLN
47	r	69	GLN
16	R	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2878/2925 (98%)	977 (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	4756/4808 (98%)	1513 (31%)	57 (1%)

5 of 1513 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 [i](#)

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

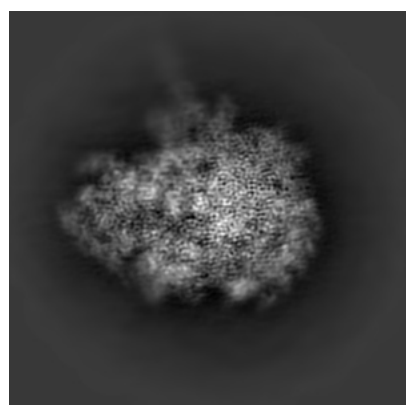
6 Map visualisation [i](#)

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.

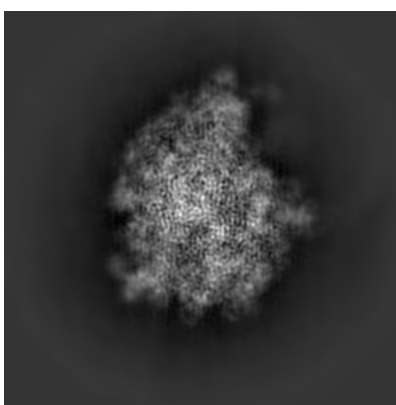
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

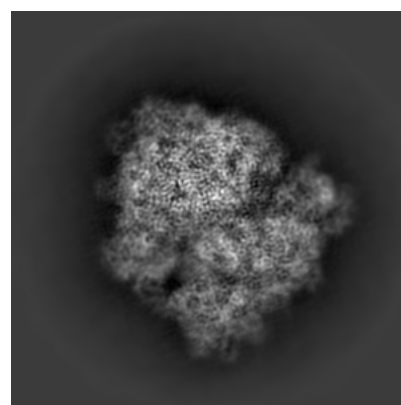
6.1.1 Primary map



X



Y

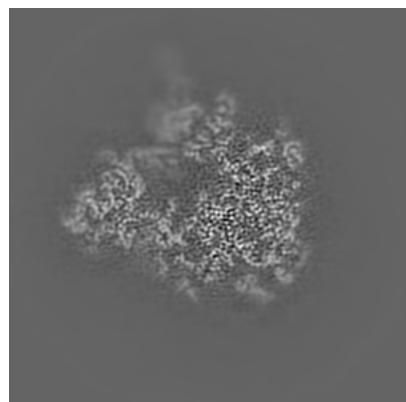


Z

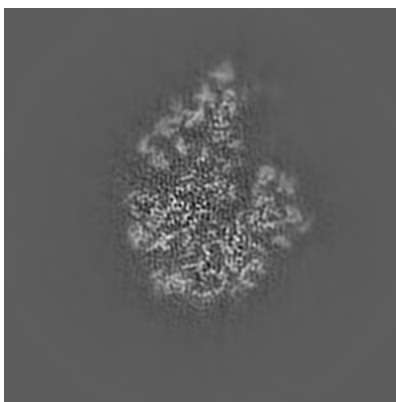
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

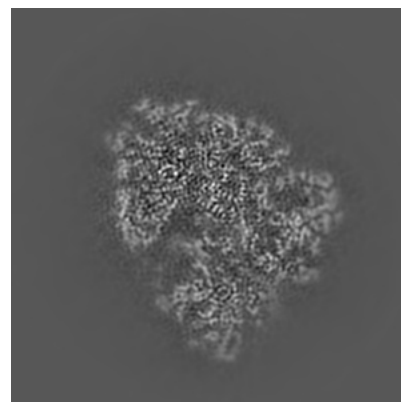
6.2.1 Primary map



X Index: 180



Y Index: 180

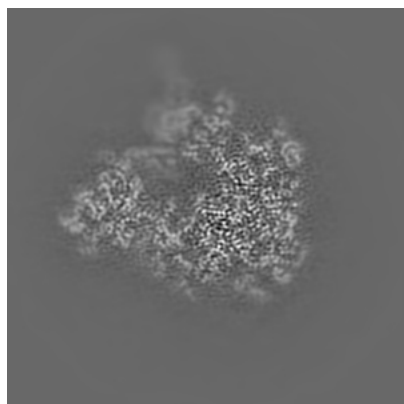


Z Index: 180

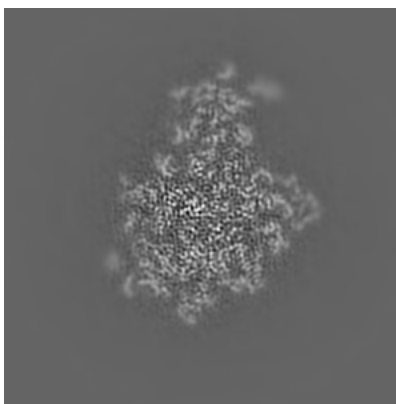
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

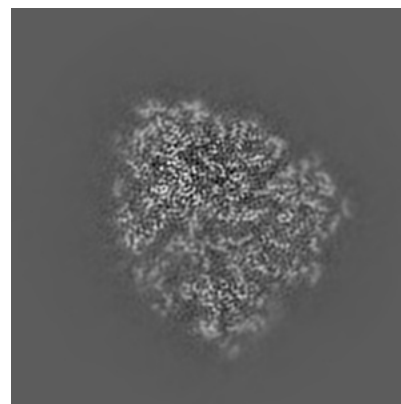
6.3.1 Primary map



X Index: 179



Y Index: 195

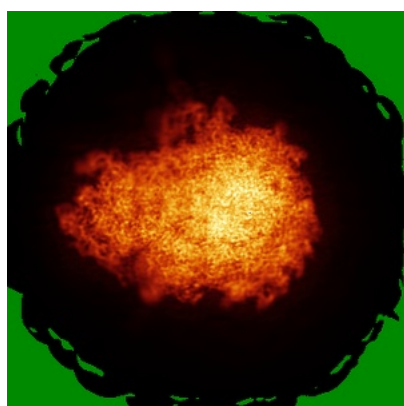


Z Index: 186

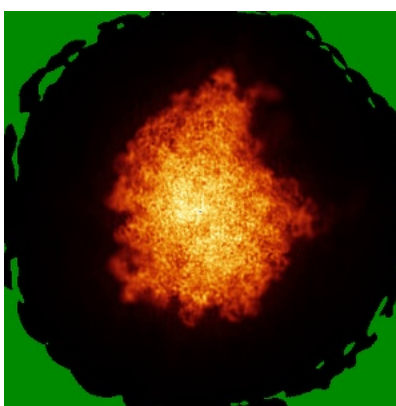
The images above show the largest variance slices of the map in three orthogonal directions.

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

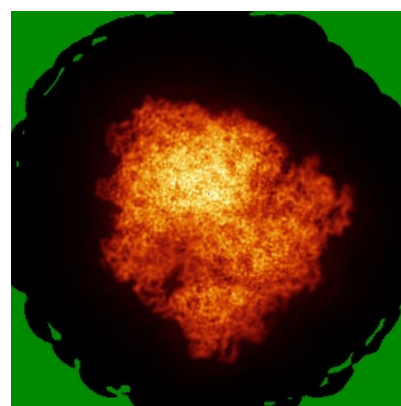
6.4.1 Primary map



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

This section was not generated.

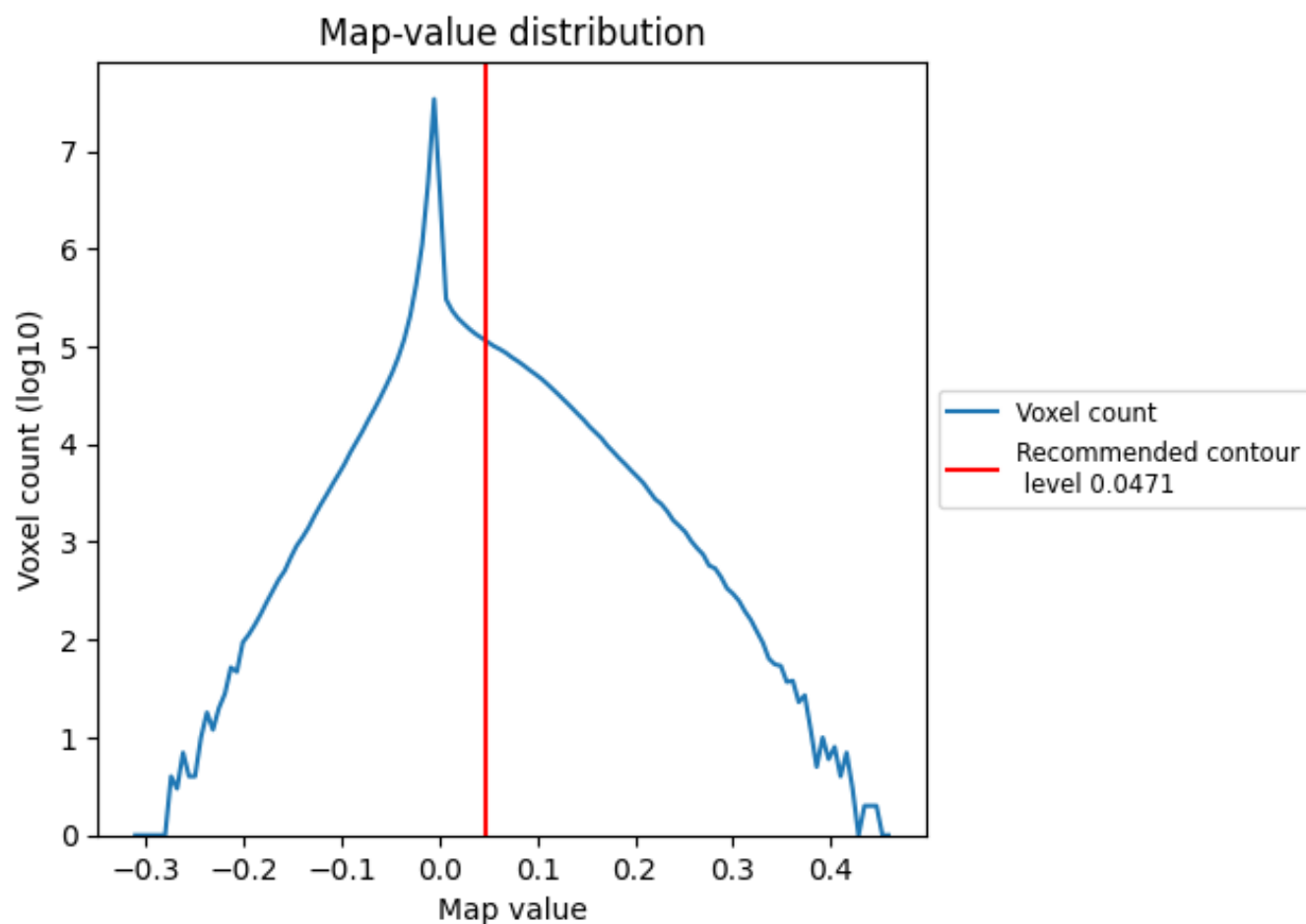
6.6 Mask visualisation

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

7 Map analysis [i](#)

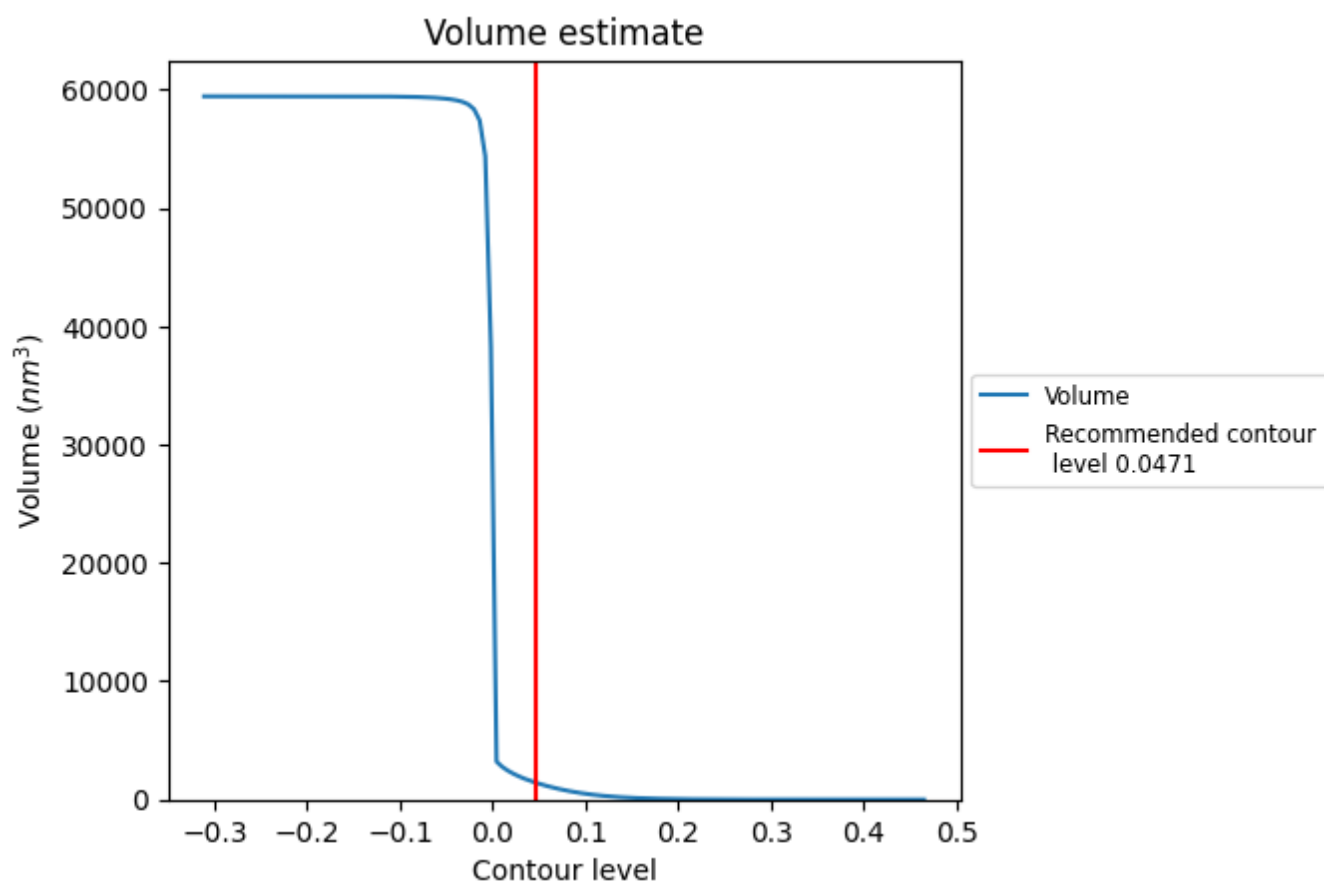
This section contains the results of statistical analysis of the map.

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.

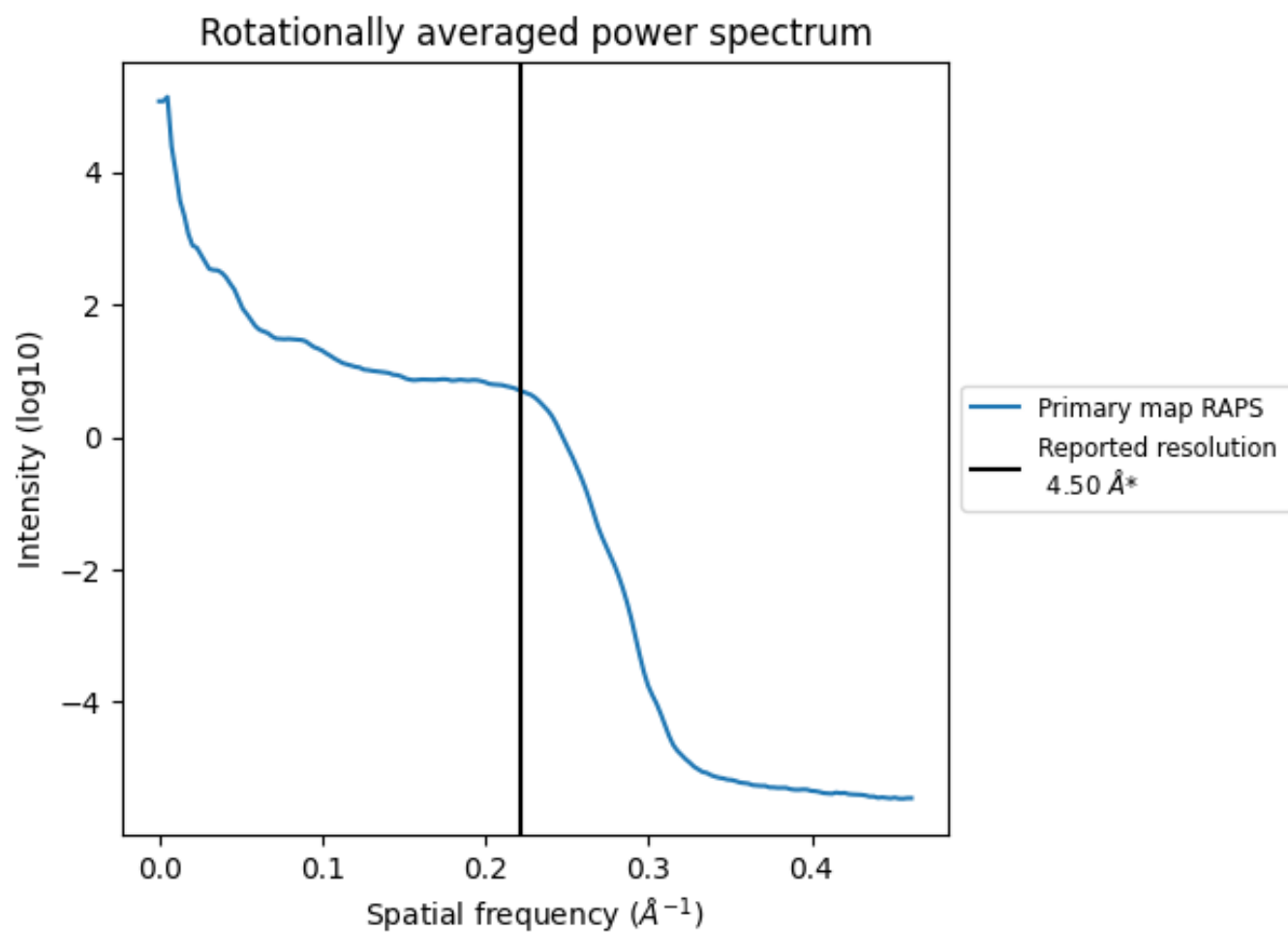
7.2 Volume estimate [i](#)



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.

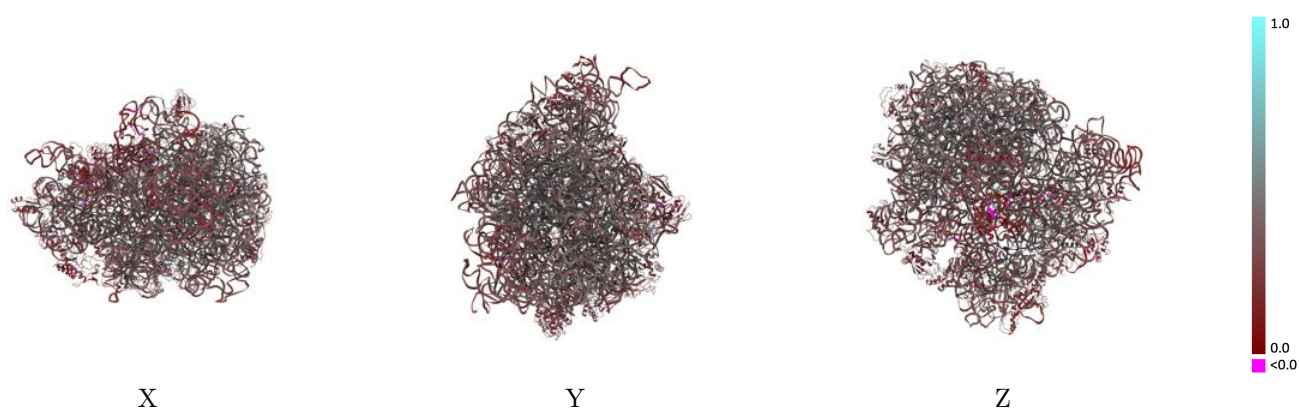
9 Map-model fit [i](#)

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](#)

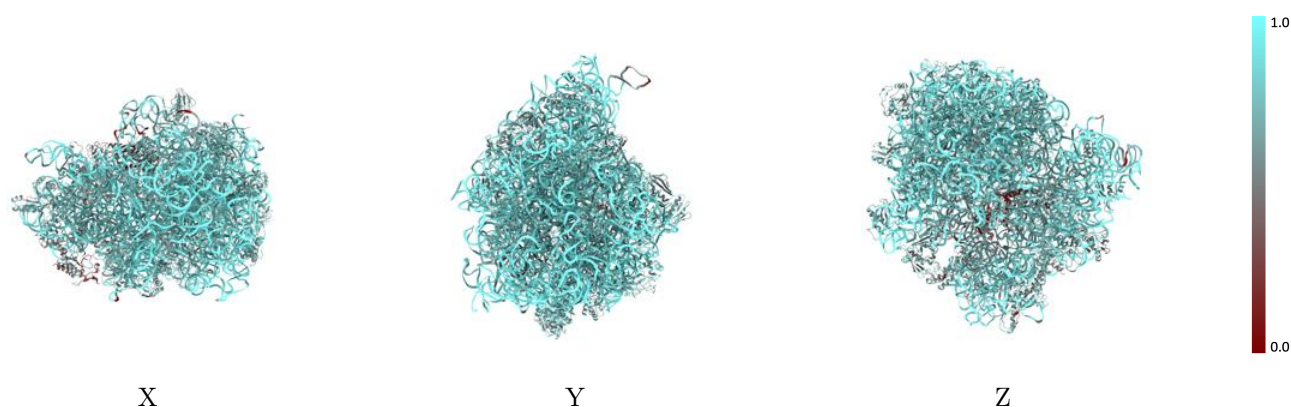
This section was not generated.

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



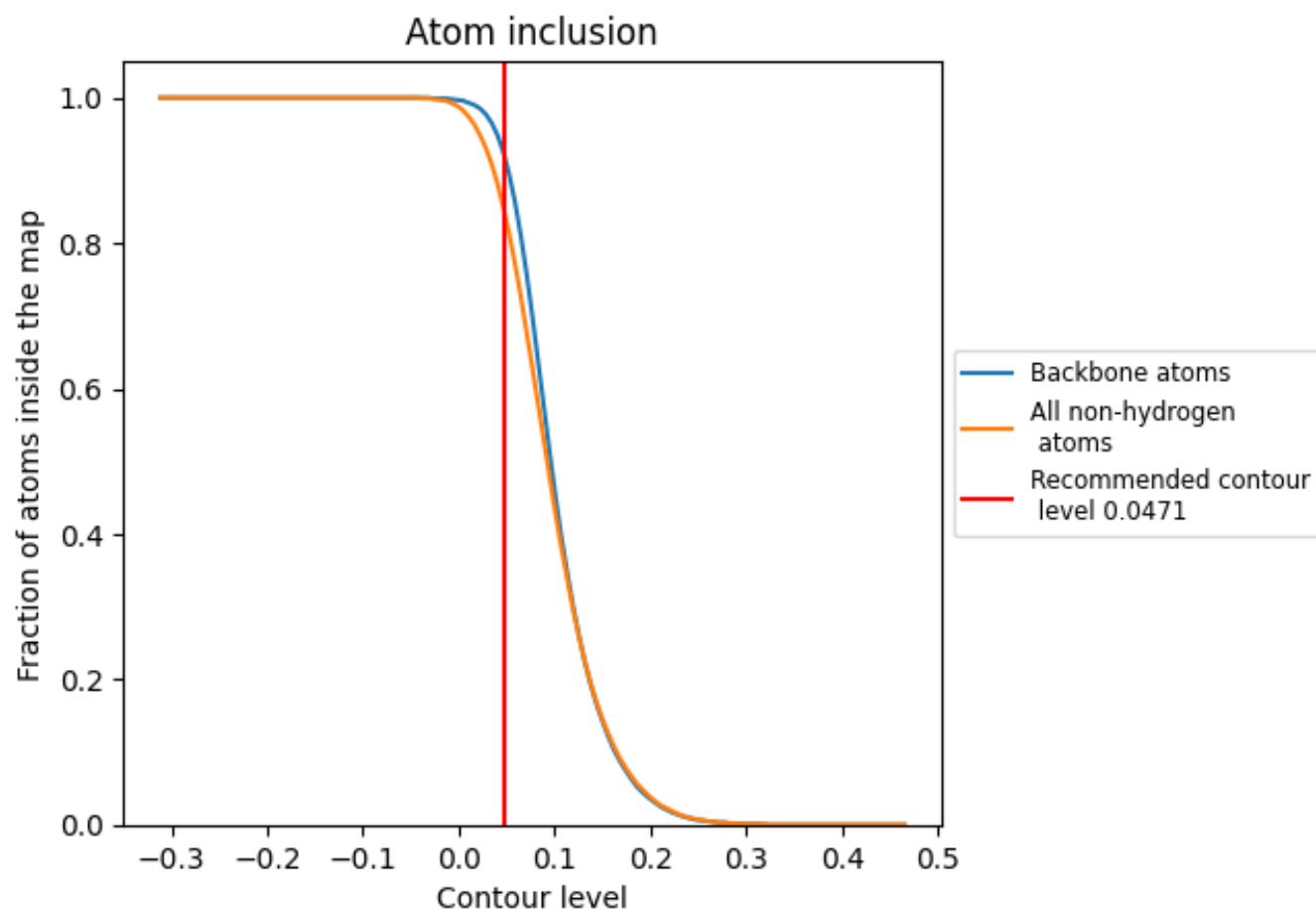
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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