



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 12:46 AM UTC

PDB ID : 6O8Z / pdb_00006o8z
EMDB ID : EMD-0659
Title : Cryo-EM image reconstruction of the 70S Ribosome Enterococcus faecalis Class04
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.49 Å (reported)
Based on initial models : 4YBB, 5LI0

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

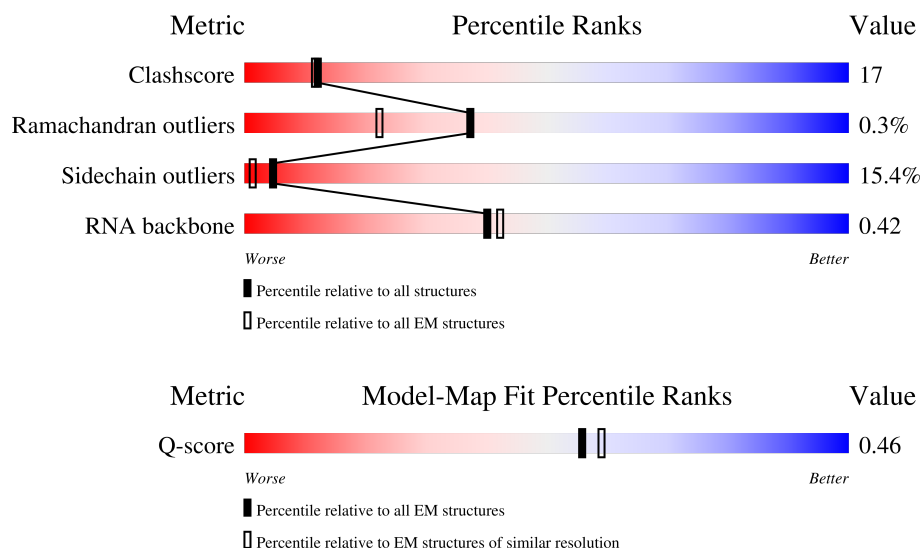
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.49 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.



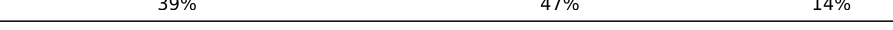
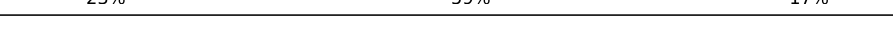
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13600 (2.99 - 3.99)

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	1528	
2	c	204	
3	d	201	

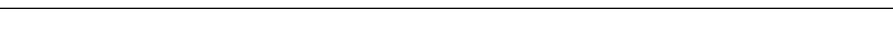
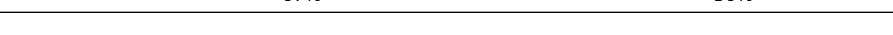
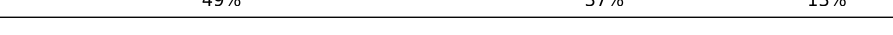
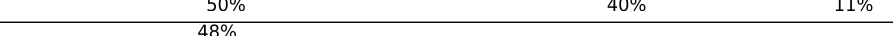
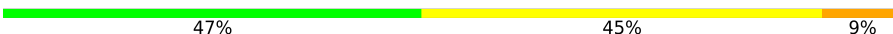
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Mol	Chain	Length	Quality of chain
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	A	2909	
21	B	116	
22	C	275	
23	D	207	
24	E	206	
25	F	177	
26	G	176	
27	K	145	
28	L	122	

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Mol	Chain	Length	Quality of chain
29	M	146	
30	N	141	
31	O	123	
32	P	117	
33	Q	114	
34	R	118	
35	S	102	
36	T	112	
37	U	89	
38	V	101	
39	W	94	
40	X	76	
41	Y	54	
42	Z	61	
43	0	58	
44	1	83	
45	2	56	
46	3	49	
47	4	44	
48	5	64	
49	6	38	

2 Entry composition [i](#)

There are 50 unique types of molecules in this entry. The entry contains 138498 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1523	Total	C	N	O	P	0	0
			32646	14564	5967	10592	1523		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	204	Total	C	N	O	S	0	0
			1610	1012	303	292	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1620	1016	303	297	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	97	Total	C	N	O	S	0	0
			795	501	137	154	3		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	154	Total	C	N	O	S	0	0
			1229	765	236	222	6		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	128	Total	C	N	O	S	0	0
			990	615	197	177	1		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	99	Total	C	N	O	S	0	0
			800	504	147	147	2		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			863	533	165	161	4		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	136	Total	C	N	O	S	0	0
			1065	661	214	188	2		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	112	Total	C	N	O	S	0	0
			884	540	180	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	88	Total	C	N	O	S	0	0
			741	455	152	133	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	89	Total	C	N	O	S	0	0
			708	448	131	127	2		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	83	Total	C	N	O	S	0	0
			681	427	127	124	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	66	Total	C	N	O	S	0	0
			537	343	99	94	1		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	78	Total	C	N	O	S	0	0
			634	410	113	109	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	81	Total	C	N	O	S	0	0
			610	372	119	117	2		

- Molecule 20 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A	2903	Total	C	N	O	P	0	0
			62311	27813	11458	20137	2903		

- Molecule 21 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B	116	Total	C	N	O	P	0	0
			2480	1106	444	814	116		

- Molecule 22 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	C	275	Total	C	N	O	S	0	0
			2115	1311	416	381	7		

- Molecule 23 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	207	Total	C	N	O	S	0	0
			1579	994	292	289	4		

- Molecule 24 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E	206	Total	C	N	O	S	0	0
			1574	984	290	298	2		

- Molecule 25 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F	177	Total	C	N	O	S	0	0
			1392	887	239	260	6		

- Molecule 26 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	G	176	Total	C	N	O	S	0	0
			1345	842	244	255	4		

- Molecule 27 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	145	Total	C	N	O	S	0	0
			1130	714	205	207	4		

- Molecule 28 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	122	Total	C	N	O	S	0	0
			922	574	176	170	2		

- Molecule 29 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	M	146	Total	C	N	O	S	0	0
			1095	677	212	205	1		

- Molecule 30 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	141	Total	C	N	O	S	0	0
			1118	710	216	185	7		

- Molecule 31 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O	123	Total	C	N	O	S	0	0
			979	603	190	183	3		

- Molecule 32 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	117	Total	C	N	O	S	0	0
			899	556	175	167	1		

- Molecule 33 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	114	Total	C	N	O	0	0
			924	582	185	157		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	R	118	Total	C	N	O	S	0	0
			950	602	184	160	4		

- Molecule 35 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	S	102	Total	C	N	O	S	0	0
			784	500	139	143	2		

- Molecule 36 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	T	112	Total	C	N	O	S	0	0
			849	532	156	159	2		

- Molecule 37 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	89	Total	C	N	O	S	0	0
			720	458	127	132	3		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 39 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	W	94	Total	C	N	O	S	0	0
			758	479	135	140	4		

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	X	76	Total	C	N	O	S	0	0
			572	351	109	112			

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Y	54	Total	C	N	O	S	0	0
			425	265	86	72	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	51	ALA	THR	conflict	UNP A0A1B4XRZ8

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	61	Total	C	N	O	S	0	0
			504	314	94	95	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	0	58	Total	C	N	O	S	0	0
			435	271	81	82	1		

- Molecule 44 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	83	Total	C	N	O	S	0	0
			673	424	114	133	2		

- Molecule 45 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	56	Total	C	N	O	S	0	0
			429	262	88	73	6		

- Molecule 46 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 47 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	4	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

- Molecule 48 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 49 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

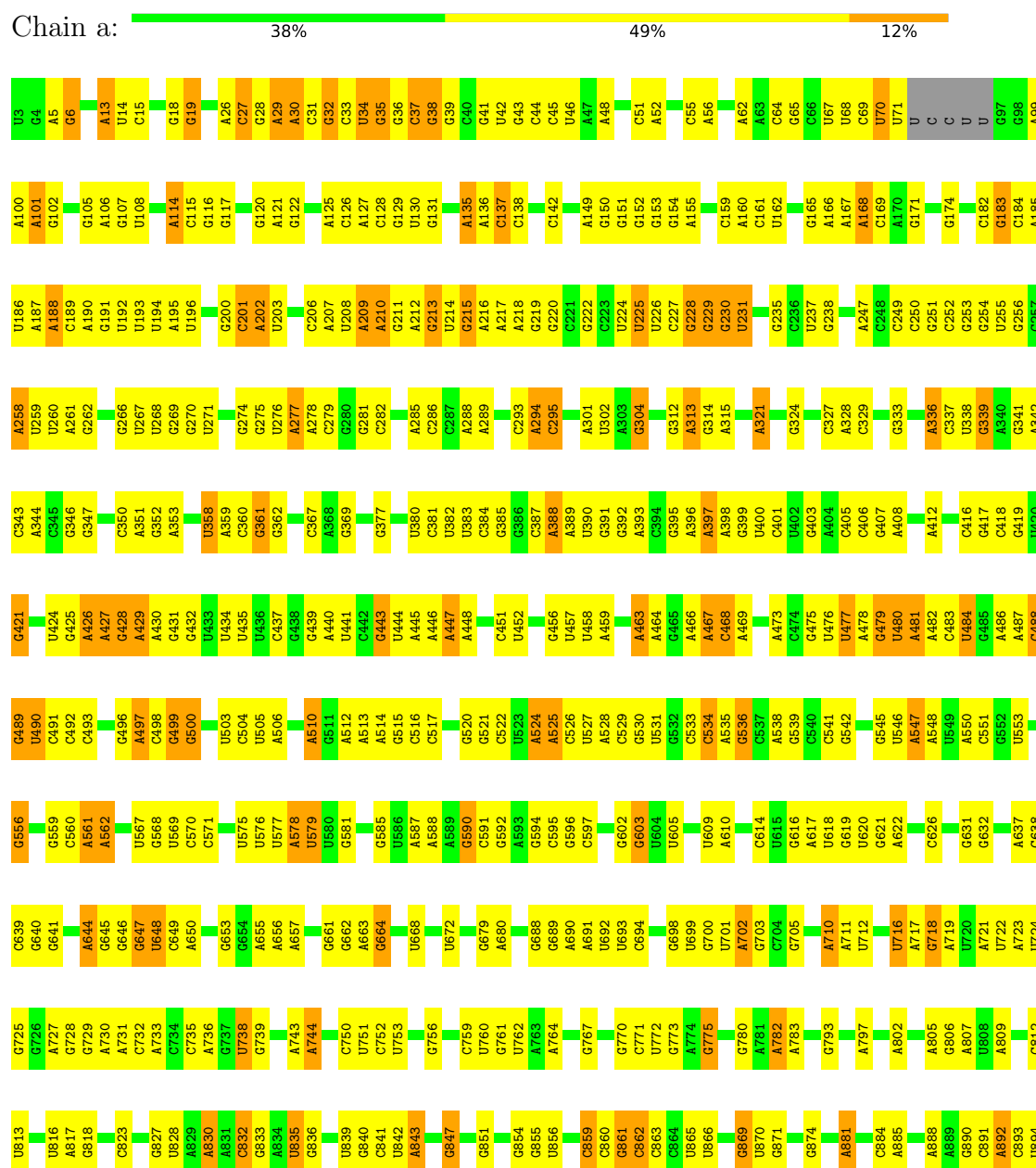
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

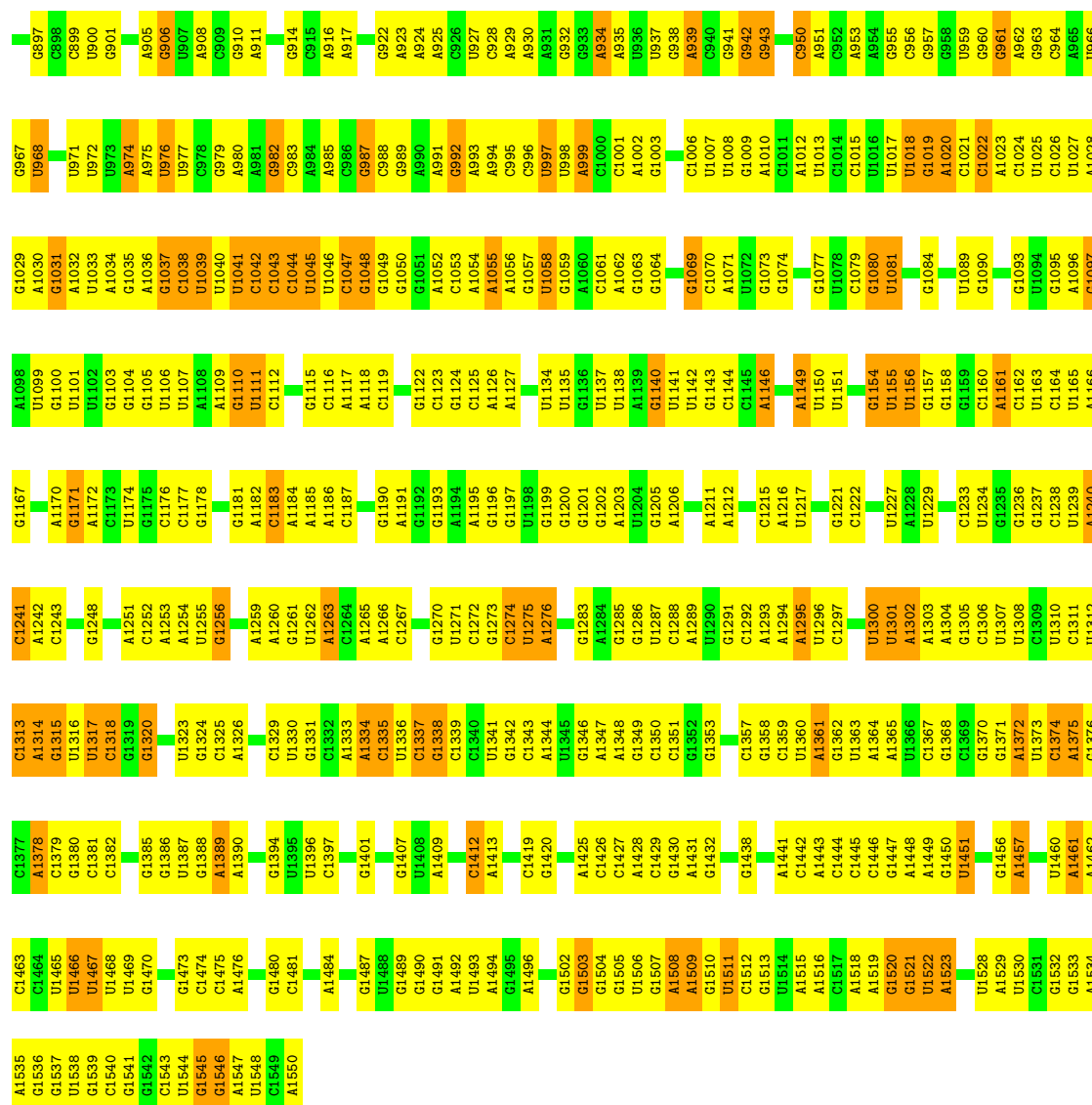
Mol	Chain	Residues	Atoms		AltConf
50	n	1	Total	Zn	0
			1	1	
50	2	1	Total	Zn	0
			1	1	
50	3	1	Total	Zn	0
			1	1	
50	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

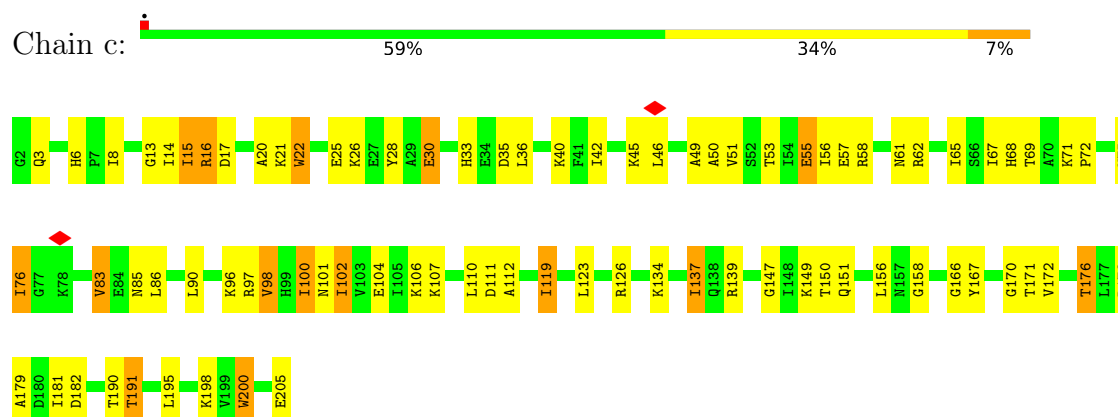
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA



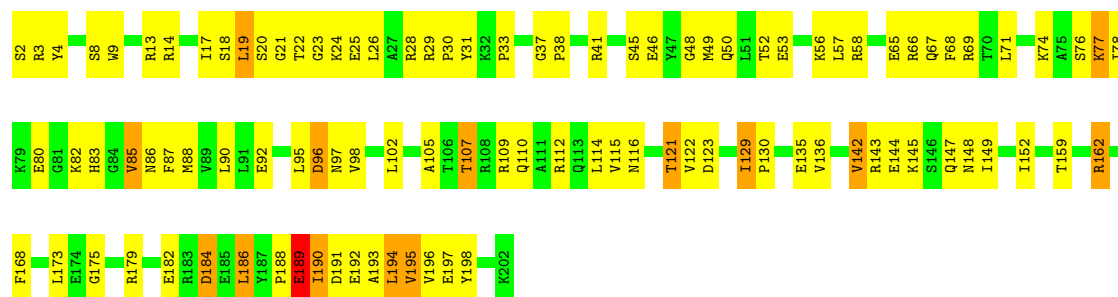


• Molecule 2: 30S ribosomal protein S3



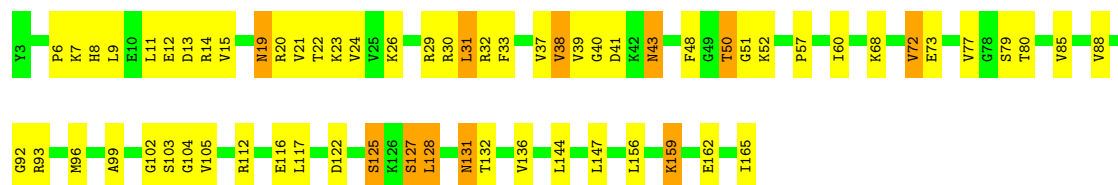
• Molecule 3: 30S ribosomal protein S4





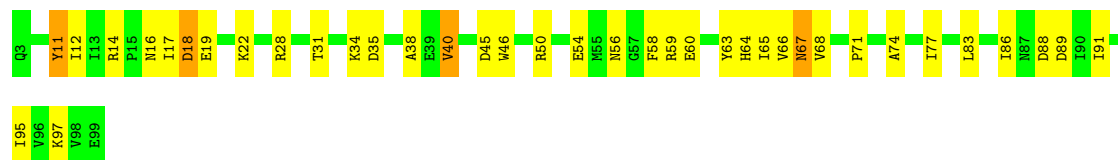
• Molecule 4: 30S ribosomal protein S5

Chain e: 60% 33% 7%



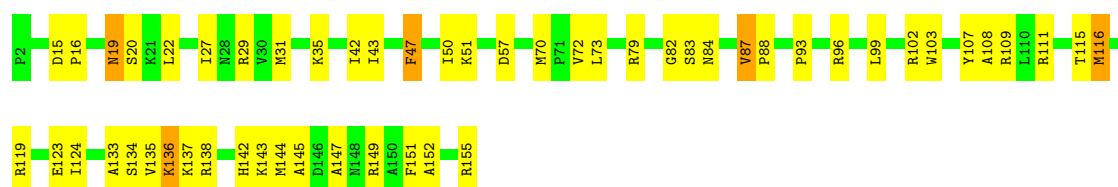
• Molecule 5: 30S ribosomal protein S6

Chain f: 61% 35% 4%



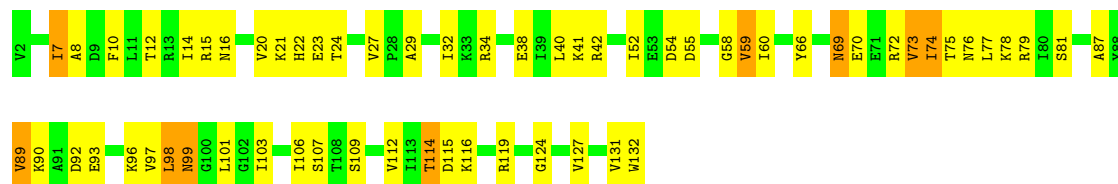
• Molecule 6: 30S ribosomal protein S7

Chain g: 66% 31% 3%

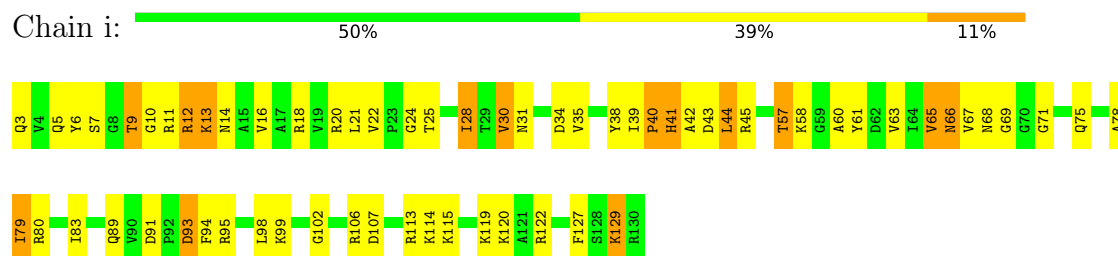


• Molecule 7: 30S ribosomal protein S8

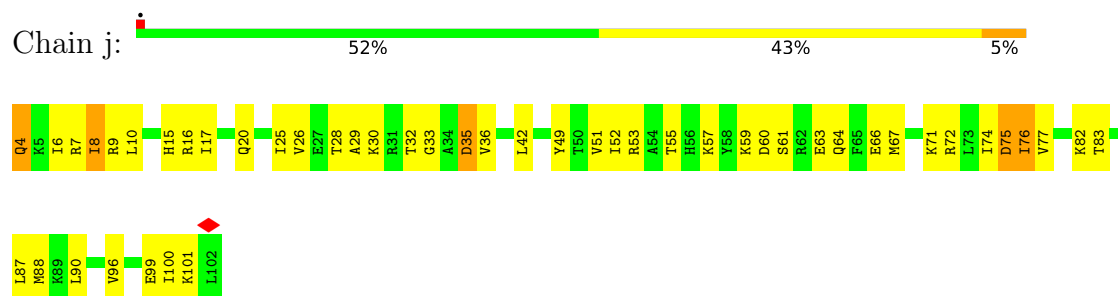
Chain h: 53% 40% 7%



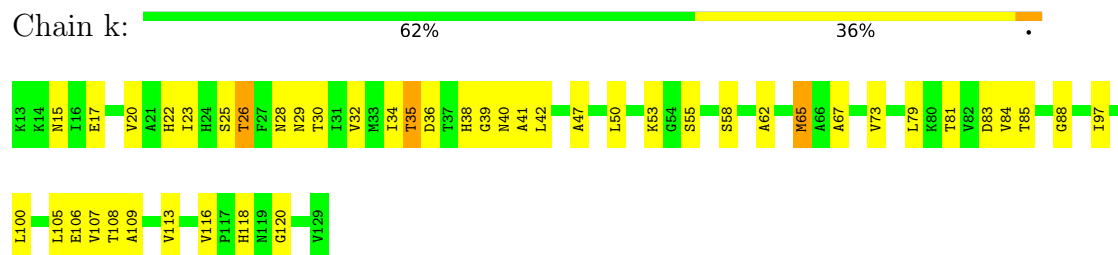
- Molecule 8: 30S ribosomal protein S9



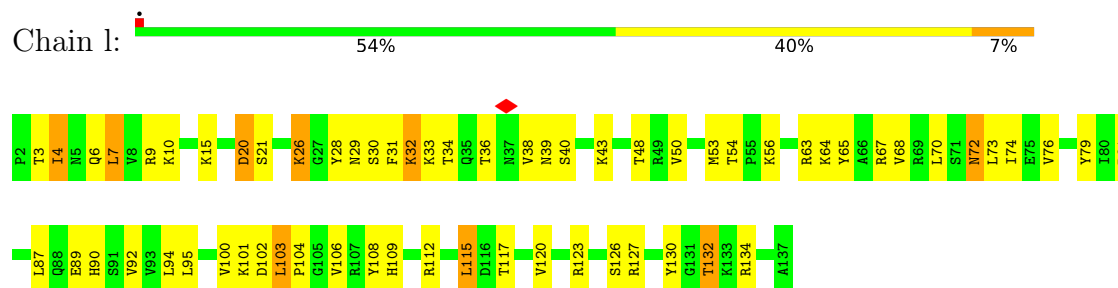
- Molecule 9: 30S ribosomal protein S10



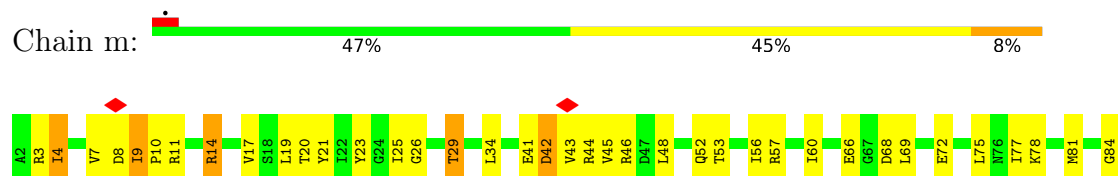
- Molecule 10: 30S ribosomal protein S11

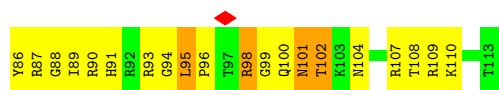


- Molecule 11: 30S ribosomal protein S12

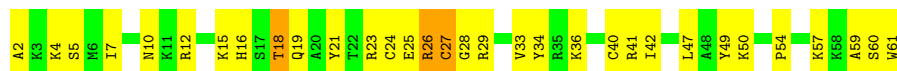


- Molecule 12: 30S ribosomal protein S13





- Molecule 13: 30S ribosomal protein S14 type Z



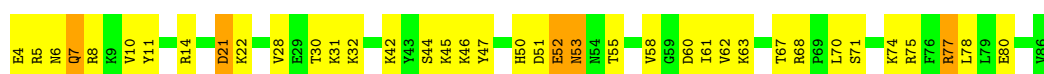
- Molecule 14: 30S ribosomal protein S15



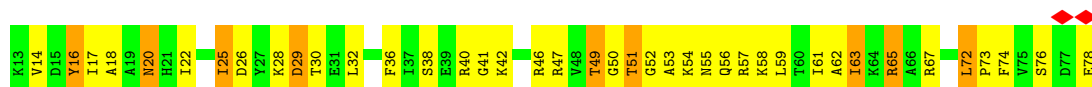
- Molecule 15: 30S ribosomal protein S16



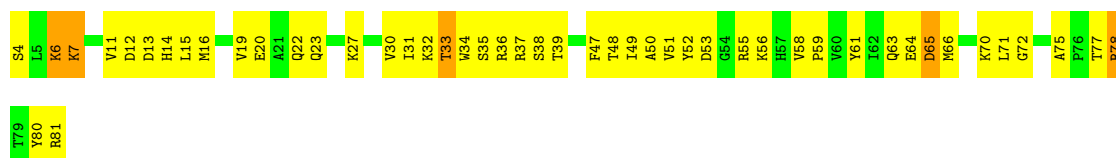
- Molecule 16: 30S ribosomal protein S17



- Molecule 17: 30S ribosomal protein S18

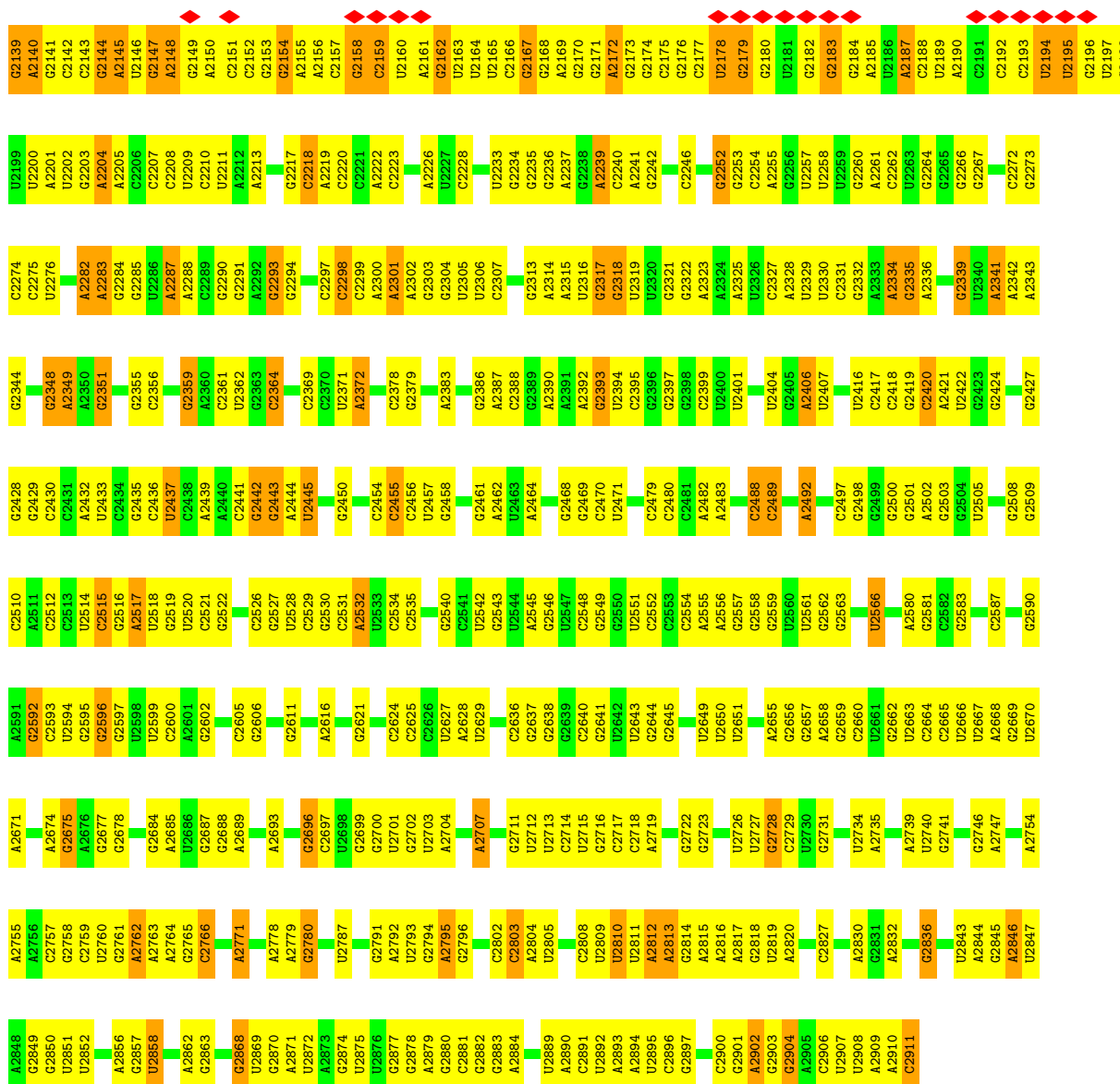


- Molecule 18: 30S ribosomal protein S19



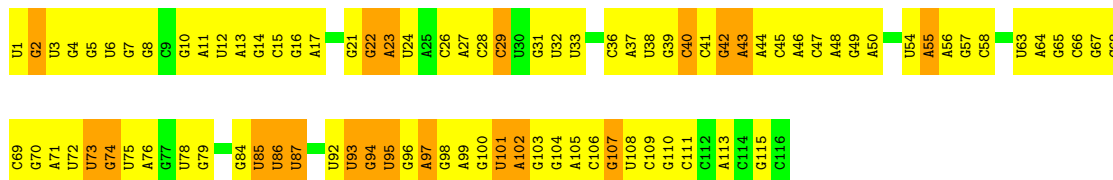
- Molecule 19: 30S ribosomal protein S20

C2061	C1977	G1871	C1605	U1535	G1463	G1397	A1320	A1241	G1165	G1096	C1022
G2062	G1978	U1793	A1606	A1536	G1464	C1398	G1321	G1242	A1166	A1097	A1023
G2066	C1979	A1794	C1607	A1537	G1465	C1399	A1322	G1243	A1167	U1098	G1024
C2069	C1981	U1795	C1611	A1538	G1466	A1401	A1323	G1246	A1168	G1099	C1025
G2070	G1982	G1796	A1612	U1539	G1467	U1402	G1328	U1247	U1172	U1100	C1026
A1963	A1797	C1797	A1613	G1540	G1468	A1403	U1329	U1248	A1173	G1102	A1028
A1964	A1798	C1798	A1614	C1541	A1469	G1404	U1330	G1249	A1174	G1103	G1029
A1984	C1802	U1799	G1614	U1542	C1470	A1405	C1331	A1251	G1176	C1104	A1030
A1986	C1803	U1800	A1615	U1543	A1473	G1406	C1332	G1254	G1177	U1105	C1031
A1988	C1804	G1709	A1616	A1544	G1474	U1407	C1333	U1255	U1178	A1107	A1033
A1989	A1805	G1710	A1617	A1545	A1475	A1408	C1334	C1256	G1179	G1108	C1034
A1990	G1806	A1711	A1618	C1546	U1475	A1409	G1335	A1257	A1181	A1109	C1035
A1991	G1807	C1713	C1623	U1547	G1478	G1410	U1336	G1262	U1182	A1110	A1036
A1992	U1808	U1714	A1624	U1551	C1479	G1411	U1337	G1263	A1183	G1112	G1037
A1993	C1809	G1715	A1625	A1552	C1480	A1414	U1338	A1264	A1184	G1113	U1039
A1994	U1810	G1716	G1626	A1553	A1481	U1415	G1346	G1268	U1190	G1114	A1040
A1995	C1811	G1717	U1627	A1558	G1488	A1420	U1347	G1269	U1191	C1115	A1041
A1996	U1812	C1718	G1628	A1559	C1489	A1421	U1348	C1270	C1192	A1116	G1042
A1997	G1813	U1721	A1629	G1560	U1490	A1422	U1349	U1271	C1193	C1117	U1043
A2002	C1814	U1722	G1630	U1561	U1491	A1423	U1352	G1275	G1194	C1119	C1045
A2003	A1815	U1723	A1631	G1562	G1492	A1424	G1353	C1276	A1195	A1120	C1046
A2004	A1816	G1724	A1632	U1563	C1493	G1425	G1354	C1277	U1201	U1122	A1048
C2005	A1817	A1725	A1633	G1564	G1494	U1426	G1355	U1278	G1202	U1123	A1049
G2006	A1818	C1726	C1635	A1565	A1495	U1427	G1356	G1282	G1210	A1124	A1050
G2007	U1819	C1727	A1536	C1566	U1496	A1428	G1357	G1285	C1211	G1131	A1051
C2008	A1823	U1735	G1640	G1568	U1497	A1429	A1357	U1292	A1212	U1132	U1056
U2009	A1824	U1736	C1641	G1569	G1498	U1430	C1358	A1288	U1213	U1130	G1057
C2010	G1825	U1737	A1642	G1570	U1499	A1431	G1359	G1289	U1214	G1132	A1061
A2011	A1826	C1737	C1643	G1571	A1500	U1432	C1360	A1290	A1215	G1133	G1062
C2016	U1827	G1738	G1644	A1572	A1501	U1433	C1361	A1293	G1216	U1134	A1066
A2017	A1830	U1742	U1645	G1573	G1502	G1437	C1362	U1294	G1217	A1135	A1067
U2032	G1831	G1746	U1650	A1574	U1503	U1438	C1363	C1294	U1218	A1136	A1068
U2033	U1832	C1746	A1651	A1575	G1504	A1439	U1365	G1297	G1219	U1137	A1069
A2034	A1833	U1752	A1652	A1576	U1505	G1440	C1366	U1298	U1222	G1139	G1070
G2035	U1834	U1753	A1653	A1577	U1506	C1441	G1373	A1306	U1223	C1140	U1073
U2036	A1835	G1754	A1657	A1578	U1507	A1442	G1374	G1307	G1224	U1141	U1081
A2037	G1836	A1754	A1657	U1579	U1508	G1443	G1375	G1308	G1225	A1142	C1085
C2038	U1837	C1755	A1657	N	U1509	U1444	U1376	A1309	U1226	G1143	A1086
C2039	G1837	G1756	G1669	N	C1510	U1445	U1377	G1312	A1227	U1144	G1087
U2042	A1843	U1757	A1669	G1584	A1512	U1447	A1378	A1310	G1228	A1145	A1088
G2043	C1851	C1758	A1673	U1585	C1515	U1448	G1379	G1307	G1229	A1146	A1089
A2044	C1852	G1759	G1674	A1586	A1516	U1449	U1380	G1308	G1230	G1147	A1090
A2045	G1853	G1760	A1675	U1589	A1517	N	C1381	A1311	A1231	U1148	C1089
G2046	U1854	G1767	U1676	G1589	U1518	U1450	G1382	G1307	A1232	C1149	A1091
A2047	U1855	G1768	U1677	A1590	G1519	U1451	G1383	G1307	G1233	G1150	C1092
U2048	G1856	C1768	A1678	A1591	U1520	G1452	G1384	A1310	G1234	A1151	U1093
U2049	C1857	A1769	U1679	G1592	G1521	U1453	A1385	A1315	G1235	G1152	G1094
G2052	U1858	G1770	A1683	U1593	U1525	U1454	U1388	U1318	U1236	C1157	G1095
A1952	C1861	U1776	A1684	U1594	U1526	U1455	U1389	G1319	A1240		
A1966	A1862	G1777	G1695	C1595	U1529	G1456	A1390				
U1969	G1863	G1778	G1696	C1600	U1530	A1457	A1391				
U1970	G1864	C1778	U1687	G1601	A1530	G1458	G1391				
C2056	U1867	A1787	G1688	U1602	G1531	C1459	G1394				
C2057	A1867	G1790	A1689	C1603	A1532	A1460	A1395				
G2060	A1868		G1690	A1604	U1534	U1462	G1396				
U2123											
G2124											
U2125											
A2126											
C2127											
U2048											
G2049											
G2129											
G2130											
A2131											
U2132											
A2133											
G2134											
G2135											
U2136											
A2137											
G2138											



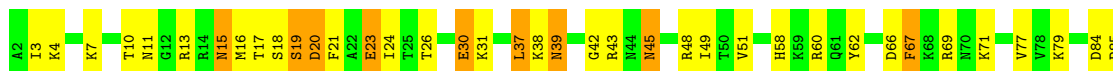
• Molecule 21: 5S rRNA

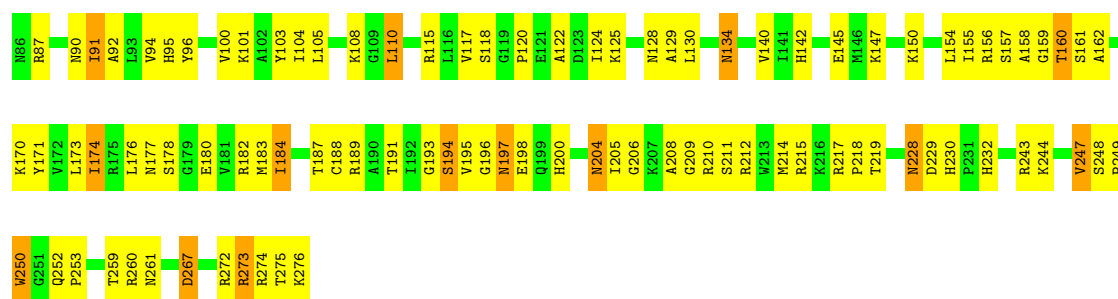
Chain B: 23% 59% 17%



• Molecule 22: 50S ribosomal protein L2

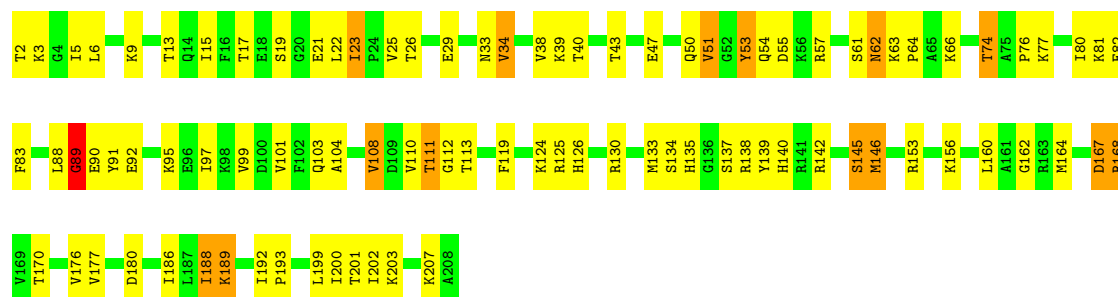
Chain C: 52% 40% 8%





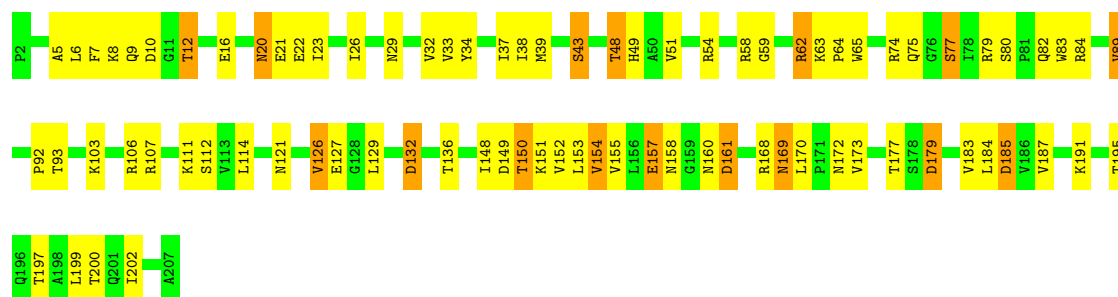
- Molecule 23: 50S ribosomal protein L3

Chain D: 55% 38% 7%



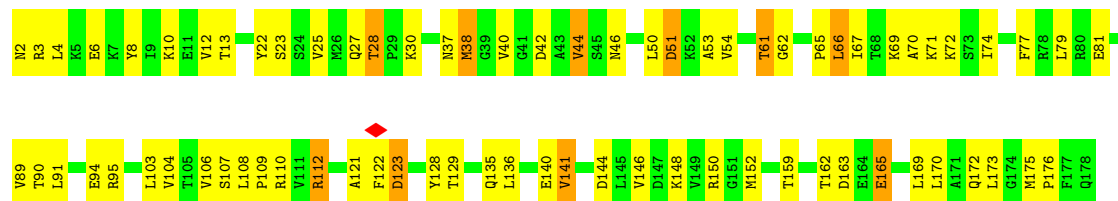
- Molecule 24: 50S ribosomal protein L4

Chain E: 60% 33% 8%



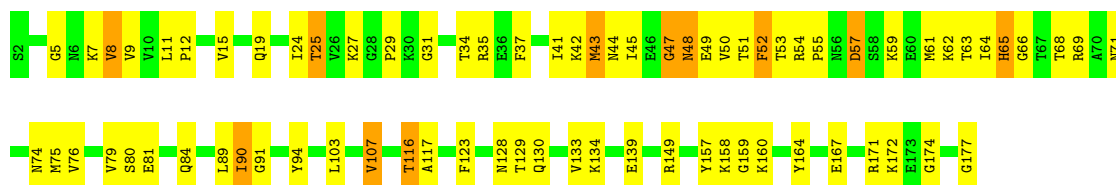
- Molecule 25: 50S ribosomal protein L5

Chain F: 58% 36% 6%



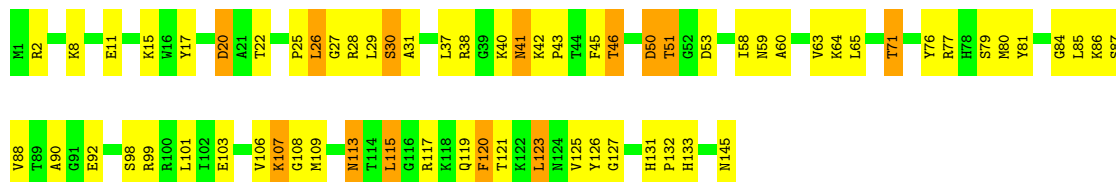
- Molecule 26: 50S ribosomal protein L6

Chain G: 58% 36% 6%



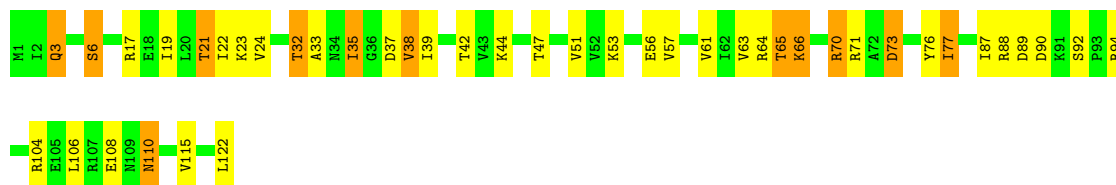
• Molecule 27: 50S ribosomal protein L13

Chain K: 54% 37% 9%



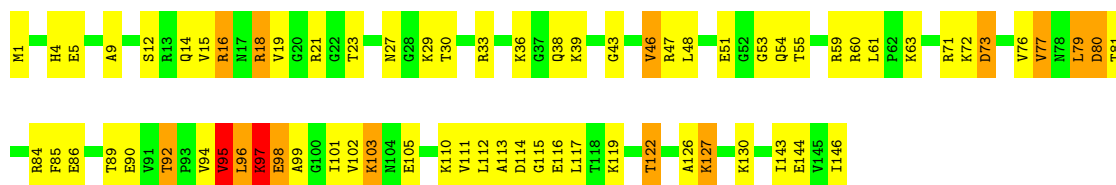
• Molecule 28: 50S ribosomal protein L14

Chain L: 65% 25% 10%



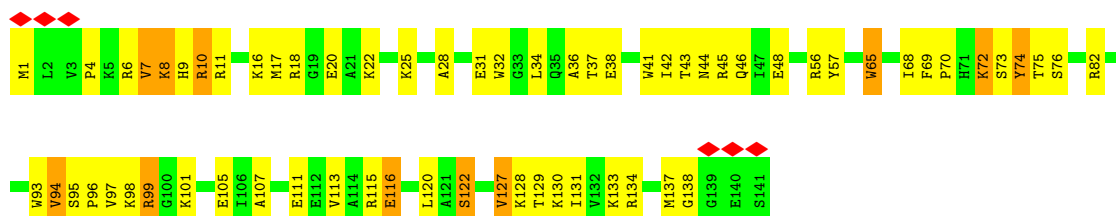
• Molecule 29: 50S ribosomal protein L15

Chain M: 51% 38% 9%

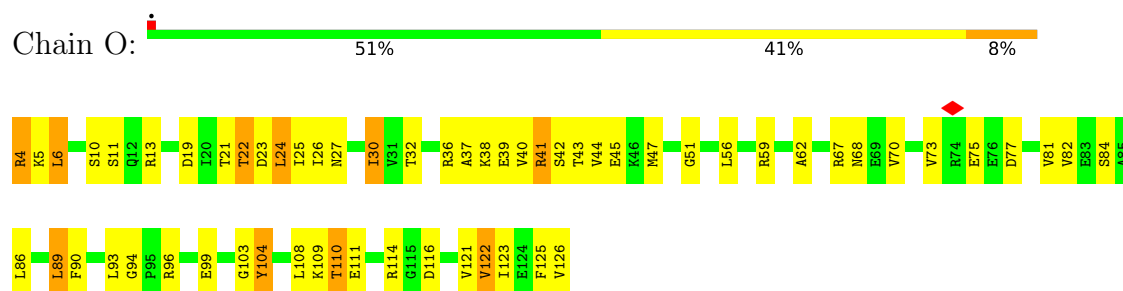


• Molecule 30: 50S ribosomal protein L16

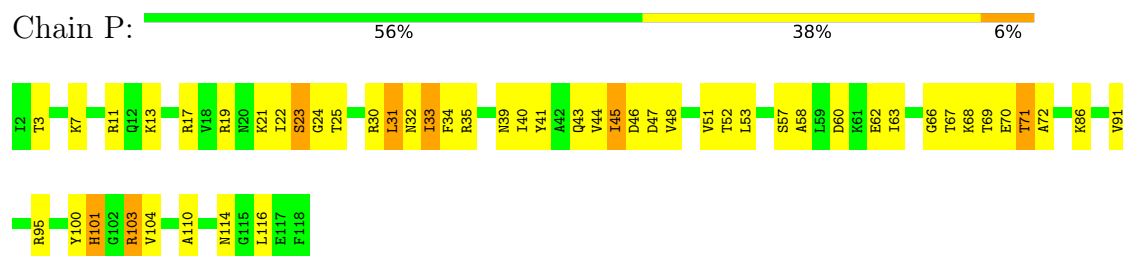
Chain N: 53% 39% 8%



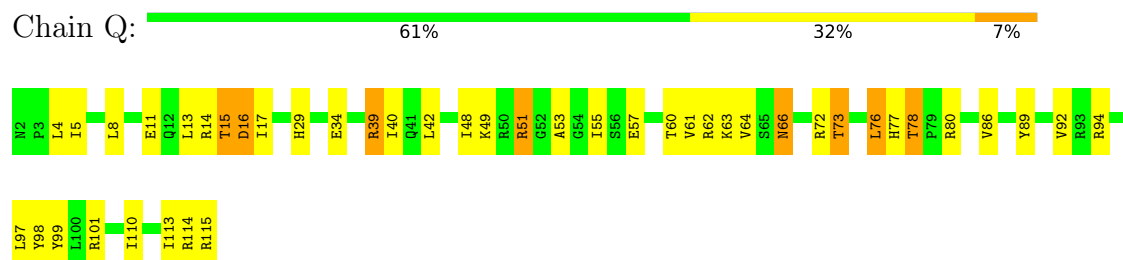
• Molecule 31: 50S ribosomal protein L17



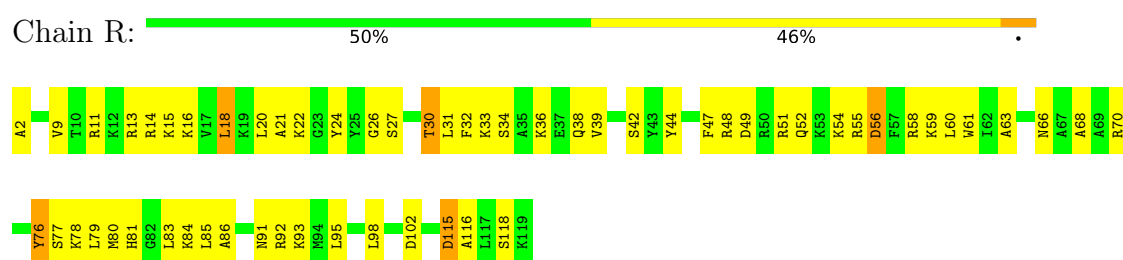
- Molecule 32: 50S ribosomal protein L18



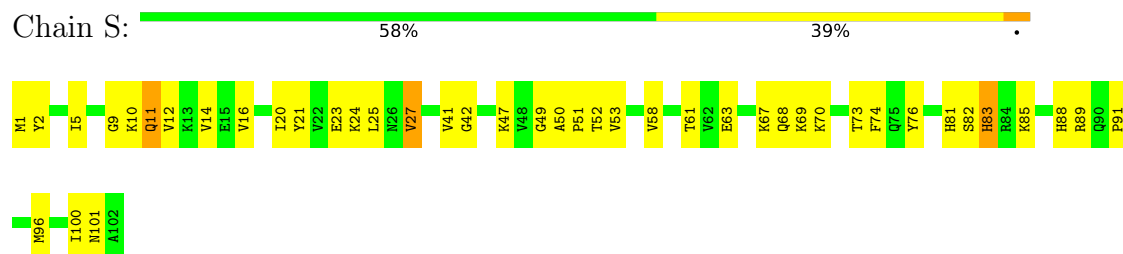
- Molecule 33: 50S ribosomal protein L19



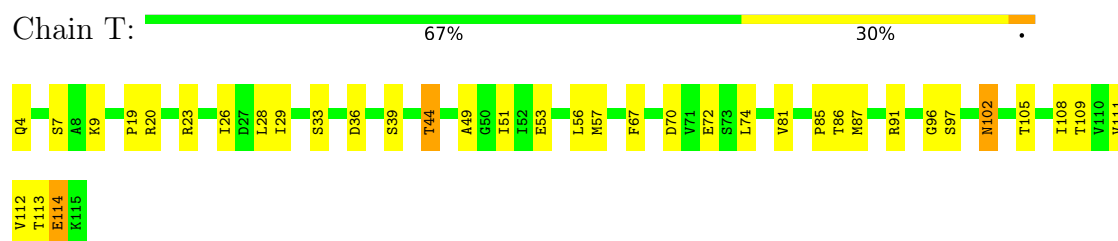
- Molecule 34: 50S ribosomal protein L20



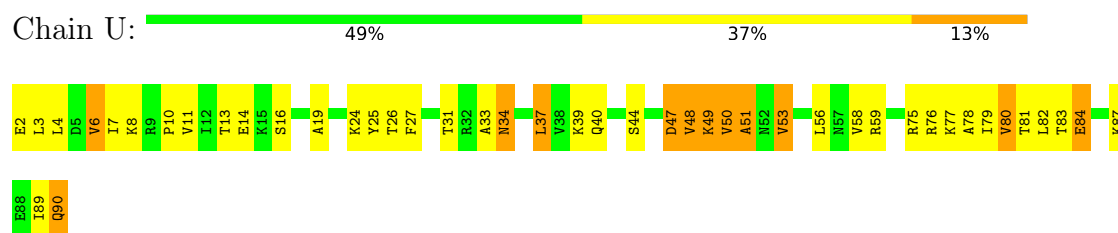
- Molecule 35: 50S ribosomal protein L21



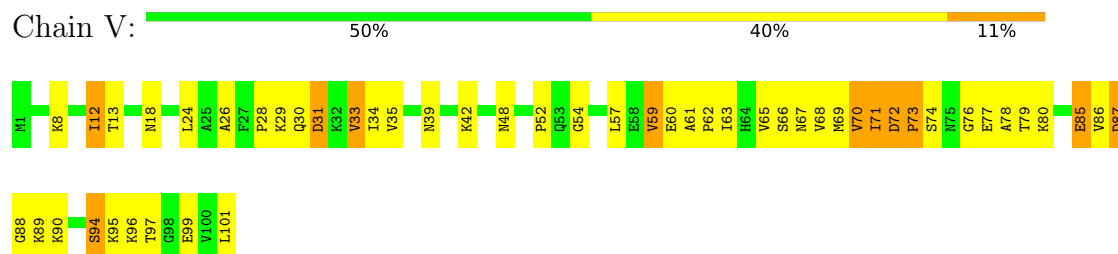
- Molecule 36: 50S ribosomal protein L22



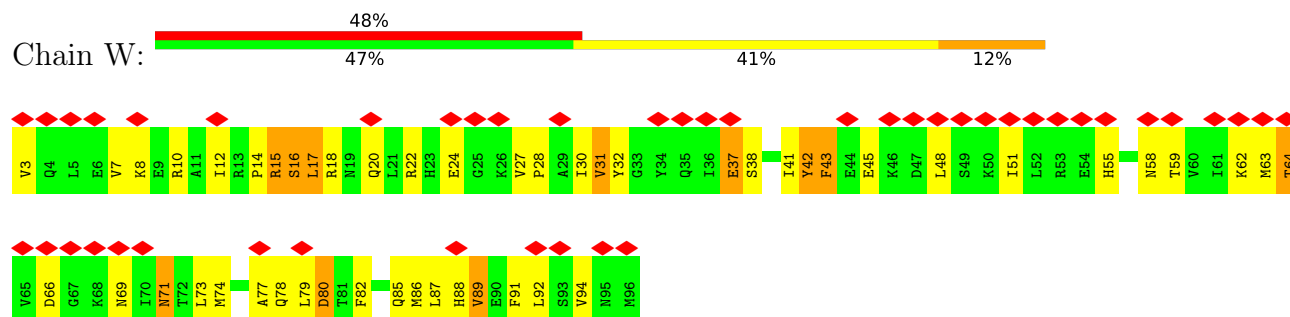
- Molecule 37: 50S ribosomal protein L23



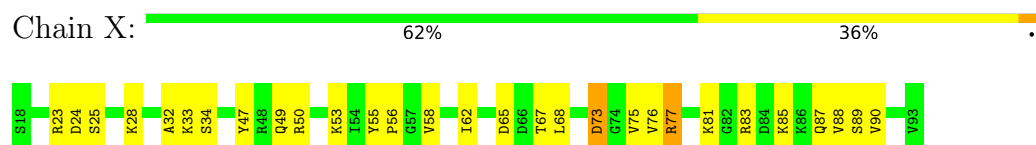
- Molecule 38: 50S ribosomal protein L24



- Molecule 39: 50S ribosomal protein L25



- Molecule 40: 50S ribosomal protein L27



- Molecule 41: 50S ribosomal protein L28

Chain Y:  50% 43% 7%



- Molecule 42: 50S ribosomal protein L29

Chain Z:  70% 26% 0%



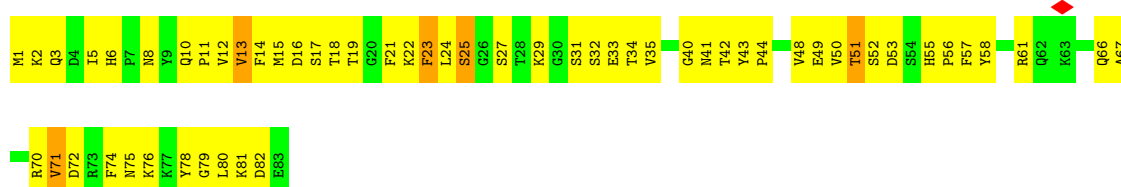
- Molecule 43: 50S ribosomal protein L30

Chain 0:  47% 45% 9%



- Molecule 44: 50S ribosomal protein L31 type B

Chain 1:  31% 63% 6%



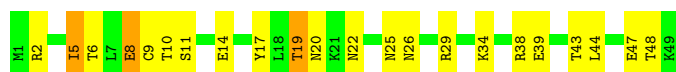
- Molecule 45: 50S ribosomal protein L32

Chain 2:  66% 30% 0%



- Molecule 46: 50S ribosomal protein L33

Chain 3:  55% 39% 6%

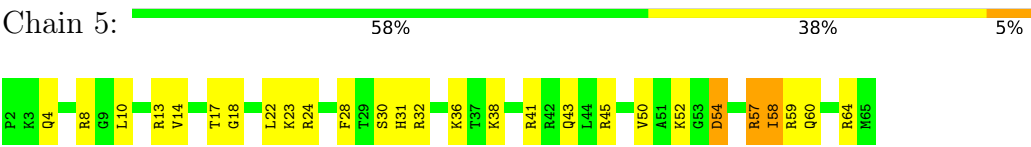


- Molecule 47: 50S ribosomal protein L34

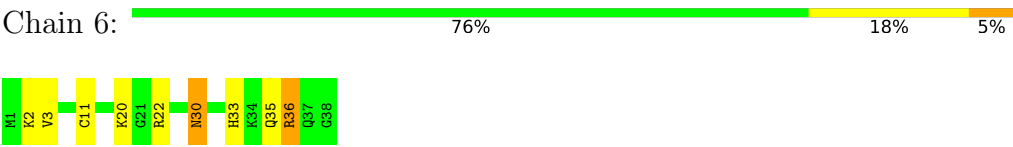
Chain 4:  50% 39% 11%



● Molecule 48: 50S ribosomal protein L35



● Molecule 49: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37183	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.100	Depositor
Minimum map value	-0.938	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.238	Depositor
Map size ($\text{\AA}$)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.097, 1.097, 1.097	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.40	0/36547	0.40	0/57003
2	c	0.32	0/1635	0.46	0/2197
3	d	0.33	0/1650	0.49	0/2217
4	e	0.37	0/1217	0.47	0/1641
5	f	0.38	0/807	0.47	0/1087
6	g	0.27	0/1249	0.45	0/1682
7	h	0.39	0/1054	0.50	0/1417
8	i	0.29	0/1003	0.46	0/1343
9	j	0.29	0/812	0.45	0/1093
10	k	0.32	0/878	0.45	0/1185
11	l	0.36	0/1082	0.55	0/1453
12	m	0.28	0/890	0.56	0/1195
13	n	0.34	0/504	0.50	0/669
14	o	0.41	0/751	0.52	0/1001
15	p	0.39	0/720	0.49	0/966
16	q	0.38	0/689	0.51	0/920
17	r	0.36	0/544	0.51	0/728
18	s	0.27	0/650	0.51	0/872
19	t	0.32	0/612	0.52	0/818
20	A	0.49	0/69799	0.45	2/108874 (0.0%)
21	B	0.40	0/2773	0.41	0/4320
22	C	0.52	0/2150	0.60	0/2892
23	D	0.51	0/1601	0.58	0/2150
24	E	0.46	0/1596	0.52	0/2159
25	F	0.34	0/1411	0.45	0/1897
26	G	0.33	0/1365	0.50	0/1839
27	K	2.09	7/1151 (0.6%)	0.63	2/1554 (0.1%)
28	L	0.52	0/929	0.54	0/1247
29	M	0.46	0/1105	0.68	0/1474
30	N	0.41	0/1141	0.55	0/1519
31	O	0.52	0/987	0.62	0/1323
32	P	0.40	0/908	0.55	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Q	0.49	0/938	0.51	0/1262
34	R	0.50	0/963	0.53	0/1280
35	S	0.45	0/796	0.51	0/1068
36	T	0.48	0/858	0.50	0/1157
37	U	0.44	0/727	0.60	2/972 (0.2%)
38	V	0.34	0/772	0.59	2/1035 (0.2%)
39	W	0.23	0/769	0.52	0/1034
40	X	0.47	0/578	0.54	0/773
41	Y	0.37	0/431	0.53	0/574
42	Z	0.36	0/505	0.46	0/672
43	0	0.45	0/437	0.47	0/589
44	1	0.29	0/690	0.56	0/930
45	2	0.47	0/436	0.48	0/578
46	3	0.33	0/423	0.43	0/563
47	4	0.46	0/377	0.58	0/491
48	5	0.45	0/528	0.56	0/689
49	6	0.46	0/309	0.54	0/409
All	All	0.48	7/150747 (0.0%)	0.46	8/226027 (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	d	0	1
19	t	0	1
23	D	0	2
26	G	0	1
29	M	0	2
30	N	0	1
31	O	0	2
37	U	0	1
38	V	0	2
39	W	0	1
All	All	0	14

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	K	107	LYS	CD-CE	52.85	3.11	1.52
27	K	120	PHE	CE1-CZ	19.86	1.98	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	K	120	PHE	CD1-CE1	19.82	1.98	1.38
27	K	120	PHE	CD2-CE2	19.82	1.98	1.38
27	K	120	PHE	CE2-CZ	18.91	1.95	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	K	107	LYS	CG-CD-CE	8.96	131.92	111.30
20	A	956	C	N3-C4-N4	-6.69	97.93	118.00
27	K	107	LYS	CD-CE-NZ	6.22	131.81	111.90
37	U	49	LYS	CA-C-N	5.82	132.44	121.97
37	U	49	LYS	C-N-CA	5.82	132.44	121.97

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	D	53	TYR	Peptide
23	D	89	GLY	Peptide
26	G	47	GLY	Peptide
3	d	189	GLU	Peptide
19	t	66	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32646	0	16439	867	0
2	c	1610	0	1653	48	0
3	d	1620	0	1641	74	0
4	e	1204	0	1280	43	0
5	f	795	0	789	24	0
6	g	1229	0	1259	40	0
7	h	1041	0	1092	42	0
8	i	990	0	1035	50	0
9	j	800	0	846	41	0
10	k	863	0	882	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	l	1065	0	1133	47	0
12	m	884	0	932	60	0
13	n	492	0	509	28	0
14	o	741	0	756	23	0
15	p	708	0	746	26	0
16	q	681	0	719	35	0
17	r	537	0	572	31	0
18	s	634	0	649	49	0
19	t	610	0	640	16	0
20	A	62311	0	31312	1495	0
21	B	2480	0	1249	107	0
22	C	2115	0	2202	108	0
23	D	1579	0	1661	59	0
24	E	1574	0	1621	55	0
25	F	1392	0	1454	55	0
26	G	1345	0	1375	52	0
27	K	1130	0	1169	82	0
28	L	922	0	985	27	0
29	M	1095	0	1149	64	0
30	N	1118	0	1180	49	0
31	O	979	0	1019	36	0
32	P	899	0	932	48	0
33	Q	924	0	979	29	0
34	R	950	0	1009	48	0
35	S	784	0	826	32	0
36	T	849	0	906	20	0
37	U	720	0	772	30	0
38	V	763	0	824	39	0
39	W	758	0	780	55	0
40	X	572	0	580	21	0
41	Y	425	0	460	17	0
42	Z	504	0	538	13	0
43	0	435	0	472	21	0
44	1	673	0	639	51	0
45	2	429	0	446	16	0
46	3	419	0	436	13	0
47	4	374	0	424	24	0
48	5	522	0	576	26	0
49	6	304	0	337	6	0
50	2	1	0	0	0	0
50	3	1	0	0	0	0
50	6	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	n	1	0	0	0	0
All	All	138498	0	91884	3892	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 17.

The worst 5 of 3892 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)
27:K:120:PHE:CZ	27:K:120:PHE:CE2	1.95	1.55
27:K:120:PHE:CD1	27:K:120:PHE:CE1	1.98	1.52
27:K:120:PHE:CE2	27:K:120:PHE:CD2	1.98	1.51
27:K:120:PHE:CZ	27:K:120:PHE:CE1	1.98	1.50
1:a:1019:G:C2	1:a:1052:A:N6	2.00	1.28

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	
2	c	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
3	d	199/201 (99%)	159 (80%)	39 (20%)	1 (0%)	24	57
4	e	161/163 (99%)	140 (87%)	21 (13%)	0	100	100
5	f	95/97 (98%)	79 (83%)	16 (17%)	0	100	100
6	g	152/154 (99%)	129 (85%)	23 (15%)	0	100	100
7	h	129/131 (98%)	106 (82%)	23 (18%)	0	100	100
8	i	126/128 (98%)	109 (86%)	15 (12%)	2 (2%)	7	36
9	j	97/99 (98%)	76 (78%)	21 (22%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	k	115/117 (98%)	93 (81%)	22 (19%)	0	100	100
11	l	134/136 (98%)	105 (78%)	29 (22%)	0	100	100
12	m	110/112 (98%)	81 (74%)	29 (26%)	0	100	100
13	n	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
14	o	86/88 (98%)	75 (87%)	10 (12%)	1 (1%)	10	41
15	p	87/89 (98%)	72 (83%)	15 (17%)	0	100	100
16	q	81/83 (98%)	68 (84%)	13 (16%)	0	100	100
17	r	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
18	s	76/78 (97%)	60 (79%)	16 (21%)	0	100	100
19	t	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
22	C	273/275 (99%)	219 (80%)	54 (20%)	0	100	100
23	D	205/207 (99%)	163 (80%)	40 (20%)	2 (1%)	12	44
24	E	204/206 (99%)	167 (82%)	37 (18%)	0	100	100
25	F	175/177 (99%)	144 (82%)	31 (18%)	0	100	100
26	G	174/176 (99%)	133 (76%)	39 (22%)	2 (1%)	11	43
27	K	143/145 (99%)	112 (78%)	31 (22%)	0	100	100
28	L	120/122 (98%)	97 (81%)	23 (19%)	0	100	100
29	M	144/146 (99%)	101 (70%)	40 (28%)	3 (2%)	5	31
30	N	139/141 (99%)	111 (80%)	28 (20%)	0	100	100
31	O	121/123 (98%)	92 (76%)	29 (24%)	0	100	100
32	P	115/117 (98%)	90 (78%)	25 (22%)	0	100	100
33	Q	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
34	R	116/118 (98%)	102 (88%)	14 (12%)	0	100	100
35	S	100/102 (98%)	85 (85%)	15 (15%)	0	100	100
36	T	110/112 (98%)	94 (86%)	16 (14%)	0	100	100
37	U	87/89 (98%)	66 (76%)	19 (22%)	2 (2%)	5	30
38	V	99/101 (98%)	68 (69%)	29 (29%)	2 (2%)	6	32
39	W	92/94 (98%)	67 (73%)	23 (25%)	2 (2%)	5	30
40	X	74/76 (97%)	63 (85%)	11 (15%)	0	100	100
41	Y	52/54 (96%)	39 (75%)	13 (25%)	0	100	100
42	Z	59/61 (97%)	54 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	0	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
44	1	81/83 (98%)	52 (64%)	29 (36%)	0	100	100
45	2	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
46	3	47/49 (96%)	40 (85%)	7 (15%)	0	100	100
47	4	42/44 (96%)	36 (86%)	6 (14%)	0	100	100
48	5	62/64 (97%)	47 (76%)	15 (24%)	0	100	100
49	6	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
All	All	5143/5235 (98%)	4173 (81%)	953 (18%)	17 (0%)	37	67

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	G	48	ASN
29	M	95	VAL
29	M	98	GLU
38	V	73	PRO
39	W	16	SER

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	
2	c	162/162 (100%)	134 (83%)	28 (17%)	2	11
3	d	175/175 (100%)	154 (88%)	21 (12%)	5	23
4	e	126/126 (100%)	105 (83%)	21 (17%)	2	13
5	f	86/86 (100%)	76 (88%)	10 (12%)	5	24
6	g	131/131 (100%)	120 (92%)	11 (8%)	10	34
7	h	112/112 (100%)	89 (80%)	23 (20%)	1	7
8	i	101/101 (100%)	81 (80%)	20 (20%)	1	7
9	j	90/90 (100%)	78 (87%)	12 (13%)	4	20
10	k	91/91 (100%)	79 (87%)	12 (13%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	l	118/118 (100%)	99 (84%)	19 (16%)	2	14
12	m	95/95 (100%)	81 (85%)	14 (15%)	3	17
13	n	51/51 (100%)	42 (82%)	9 (18%)	2	11
14	o	78/78 (100%)	69 (88%)	9 (12%)	5	24
15	p	79/79 (100%)	66 (84%)	13 (16%)	2	13
16	q	76/76 (100%)	64 (84%)	12 (16%)	2	15
17	r	57/57 (100%)	44 (77%)	13 (23%)	1	5
18	s	68/68 (100%)	60 (88%)	8 (12%)	5	23
19	t	62/62 (100%)	56 (90%)	6 (10%)	8	30
22	C	225/225 (100%)	180 (80%)	45 (20%)	1	7
23	D	170/170 (100%)	140 (82%)	30 (18%)	2	11
24	E	172/172 (100%)	135 (78%)	37 (22%)	1	6
25	F	154/154 (100%)	138 (90%)	16 (10%)	7	27
26	G	146/146 (100%)	132 (90%)	14 (10%)	8	30
27	K	122/122 (100%)	106 (87%)	16 (13%)	4	20
28	L	98/98 (100%)	78 (80%)	20 (20%)	1	7
29	M	112/112 (100%)	90 (80%)	22 (20%)	1	8
30	N	112/112 (100%)	92 (82%)	20 (18%)	2	10
31	O	105/105 (100%)	83 (79%)	22 (21%)	1	6
32	P	91/91 (100%)	77 (85%)	14 (15%)	2	16
33	Q	97/97 (100%)	79 (81%)	18 (19%)	1	9
34	R	94/94 (100%)	81 (86%)	13 (14%)	3	19
35	S	83/83 (100%)	73 (88%)	10 (12%)	5	23
36	T	95/95 (100%)	84 (88%)	11 (12%)	5	24
37	U	80/80 (100%)	66 (82%)	14 (18%)	2	11
38	V	85/85 (100%)	74 (87%)	11 (13%)	4	21
39	W	85/85 (100%)	75 (88%)	10 (12%)	5	23
40	X	61/61 (100%)	55 (90%)	6 (10%)	7	30
41	Y	47/47 (100%)	36 (77%)	11 (23%)	1	4
42	Z	55/55 (100%)	48 (87%)	7 (13%)	4	21
43	0	49/49 (100%)	38 (78%)	11 (22%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	1	75/75 (100%)	64 (85%)	11 (15%)	3	17
45	2	46/46 (100%)	41 (89%)	5 (11%)	6	26
46	3	49/49 (100%)	41 (84%)	8 (16%)	2	14
47	4	39/39 (100%)	33 (85%)	6 (15%)	2	16
48	5	51/51 (100%)	46 (90%)	5 (10%)	7	30
49	6	35/35 (100%)	33 (94%)	2 (6%)	18	45
All	All	4391/4391 (100%)	3715 (85%)	676 (15%)	5	16

5 of 676 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	N	20	GLU
37	U	14	GLU
30	N	113	VAL
30	N	10	ARG
33	Q	39	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
33	Q	83	GLN
42	Z	36	GLN
34	R	91	ASN
38	V	44	HIS
48	5	4	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1521/1528 (99%)	312 (20%)	0
20	A	2899/2909 (99%)	654 (22%)	27 (0%)
21	B	115/116 (99%)	30 (26%)	3 (2%)
All	All	4535/4553 (99%)	996 (21%)	30 (0%)

5 of 996 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A

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Mol	Chain	Res	Type
1	a	6	G
1	a	13	A
1	a	19	G
1	a	27	C

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	1101	U
21	B	32	U
20	A	1584	G
21	B	101	U
20	A	2144	G

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

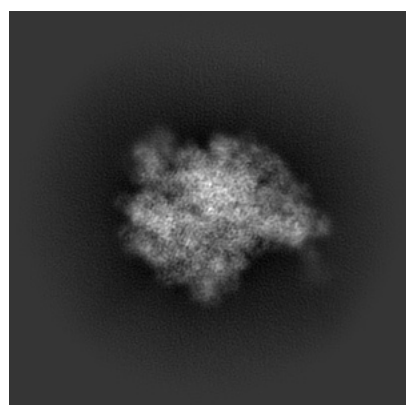
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0659. These allow visual inspection of the internal detail of the map and identification of artifacts.

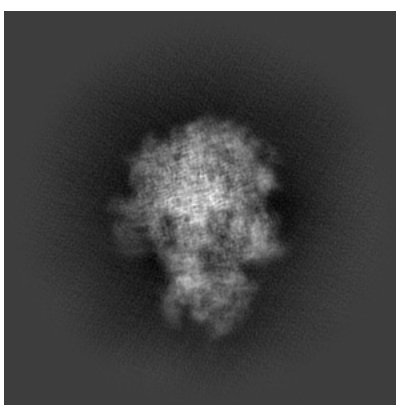
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

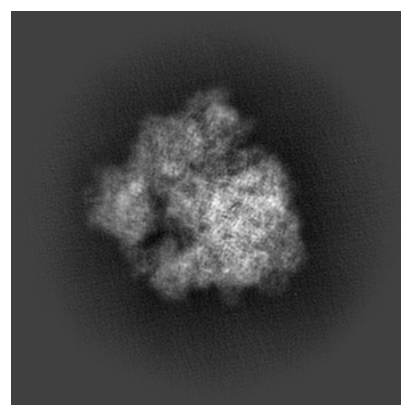
6.1.1 Primary map



X



Y

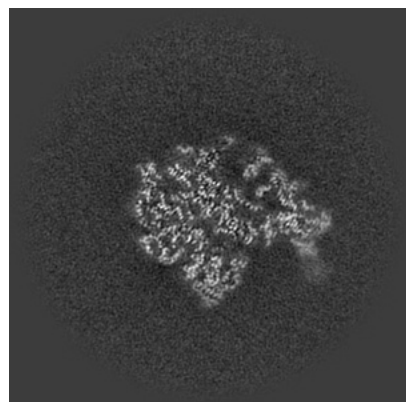


Z

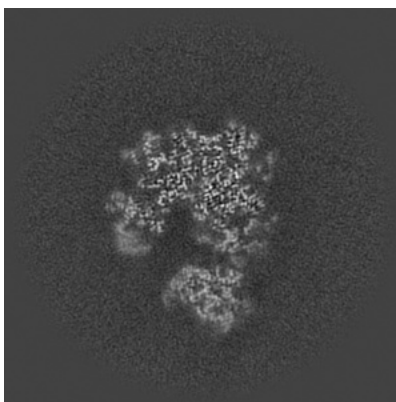
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

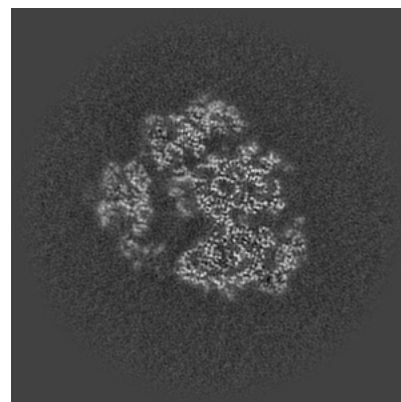
6.2.1 Primary map



X Index: 220



Y Index: 220

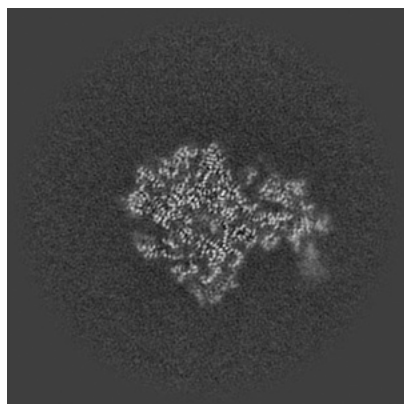


Z Index: 220

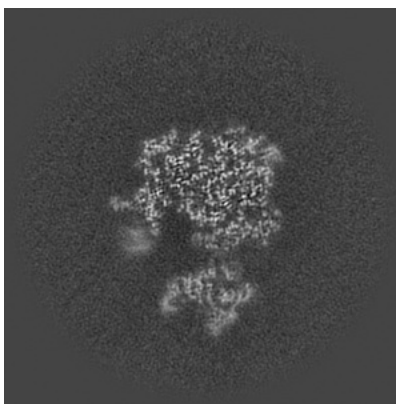
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

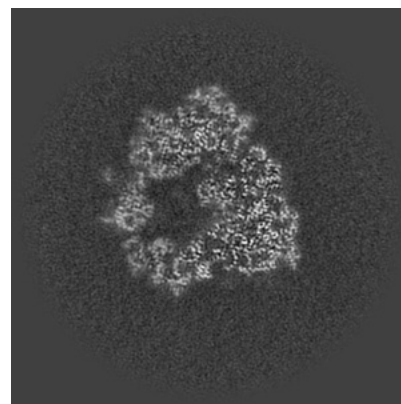
6.3.1 Primary map



X Index: 227



Y Index: 231

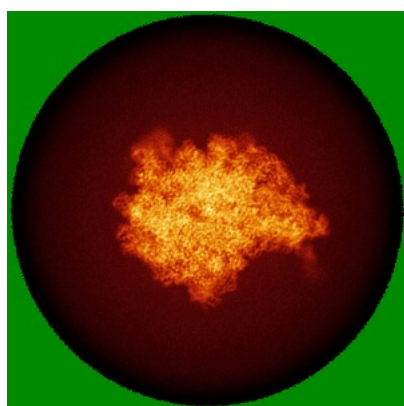


Z Index: 205

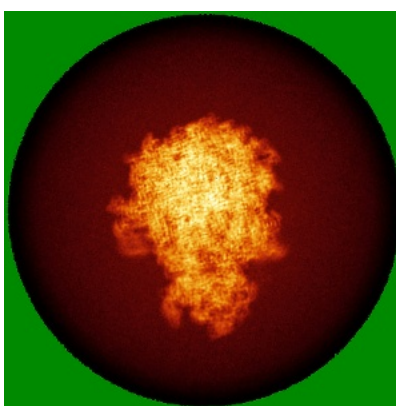
The images above show the largest variance slices of the map in three orthogonal directions.

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

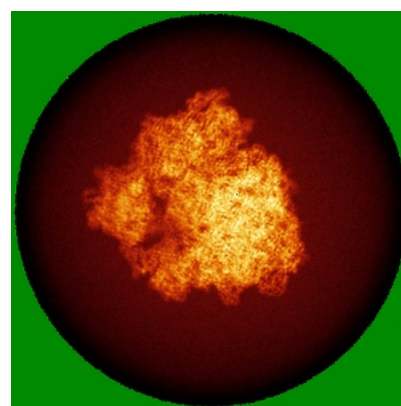
6.4.1 Primary map



X



Y

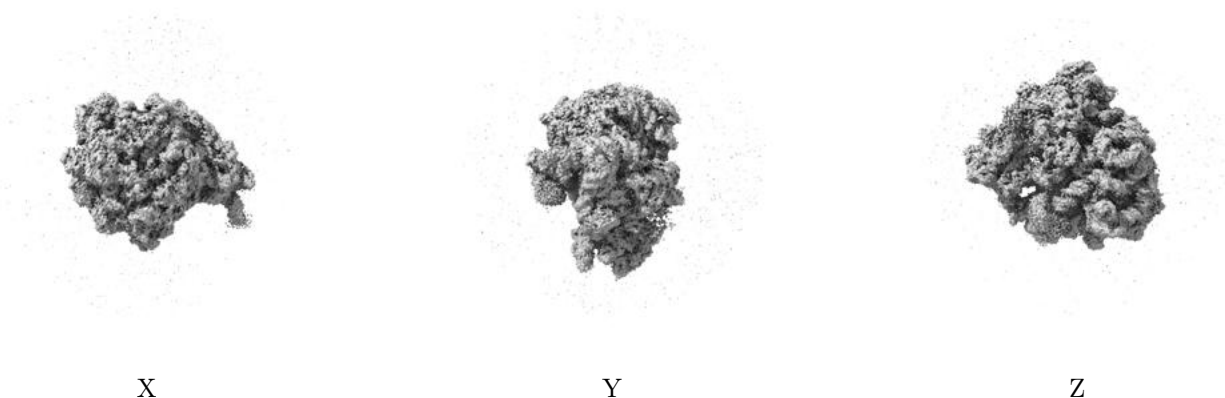


Z

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

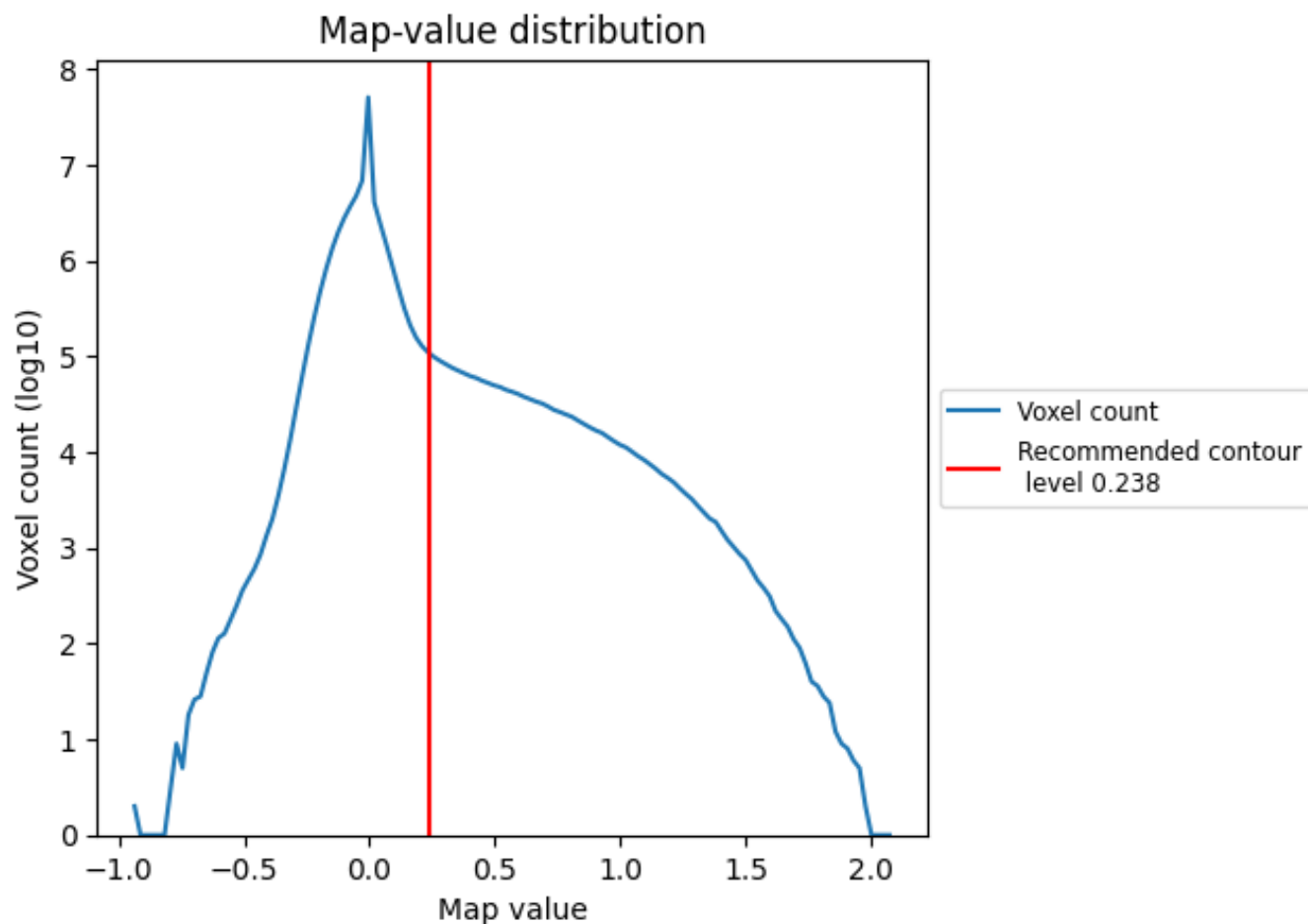
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

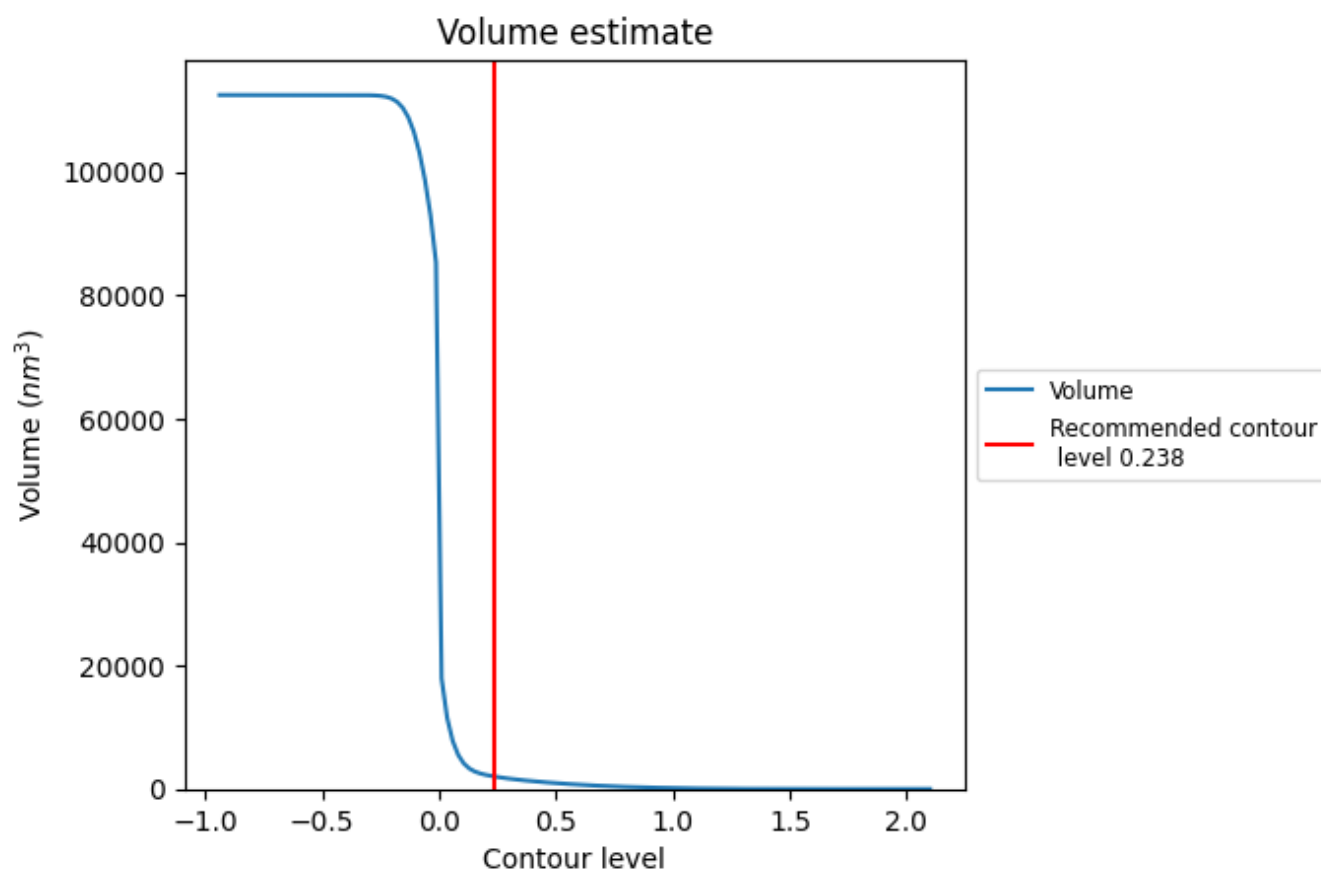
This section contains the results of statistical analysis of the map.

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.

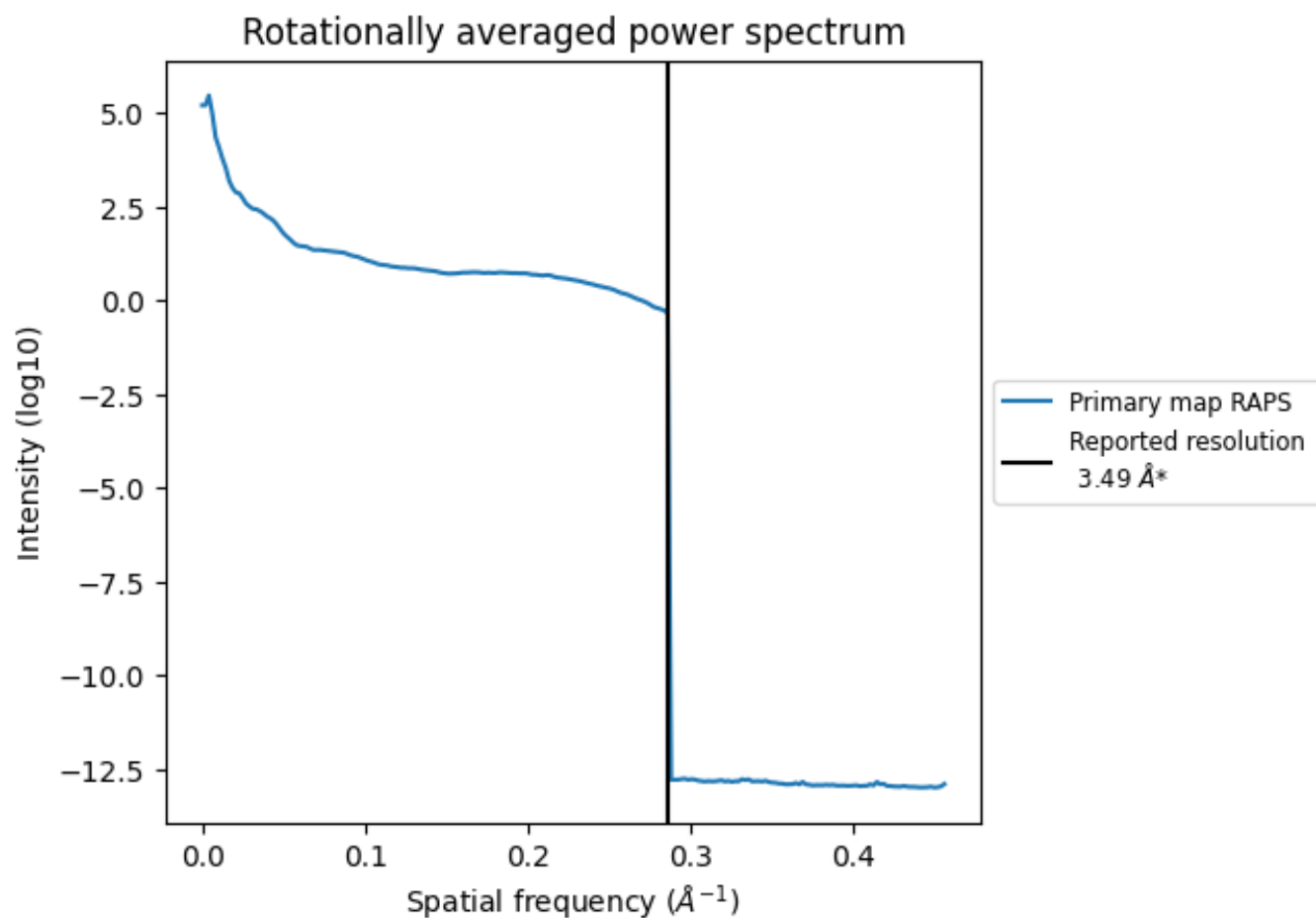
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2013 nm^3 ; this corresponds to an approximate mass of 1818 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 0.287 Å⁻¹

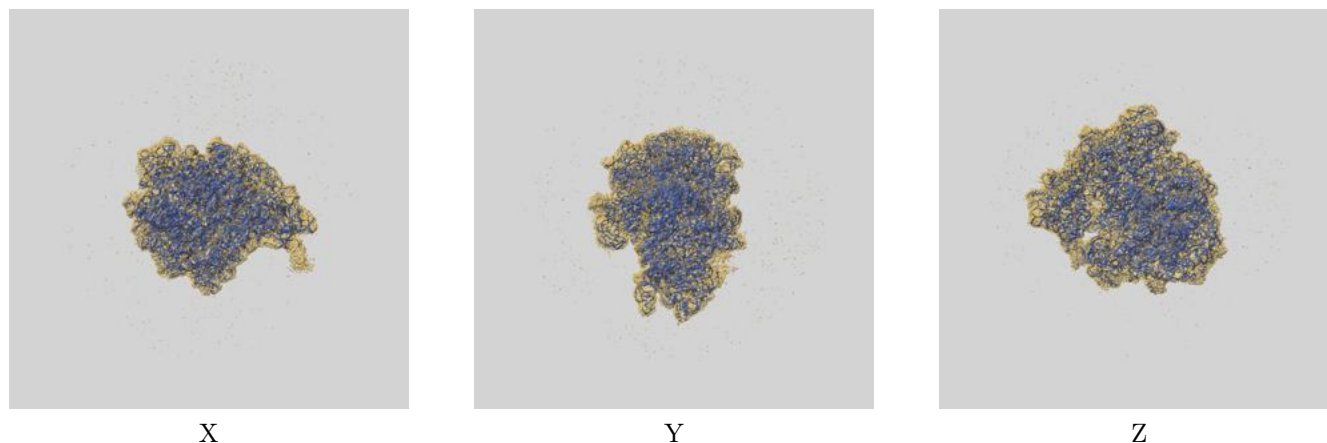
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

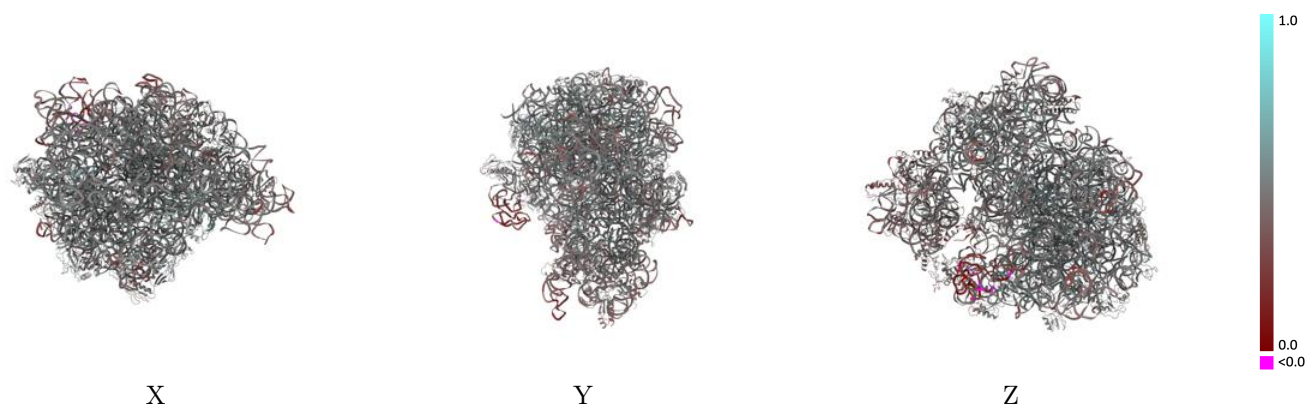
This section contains information regarding the fit between EMDB map EMD-0659 and PDB model 6O8Z. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



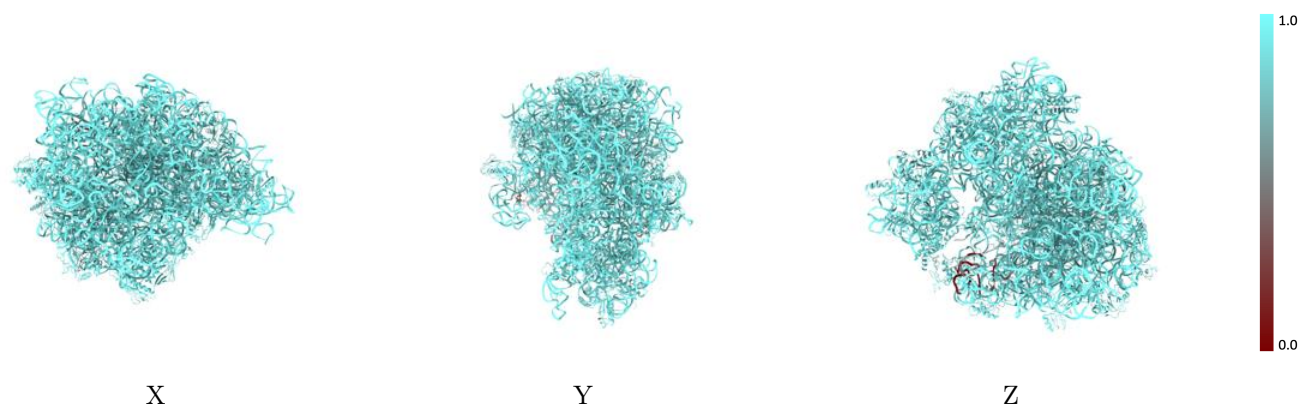
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



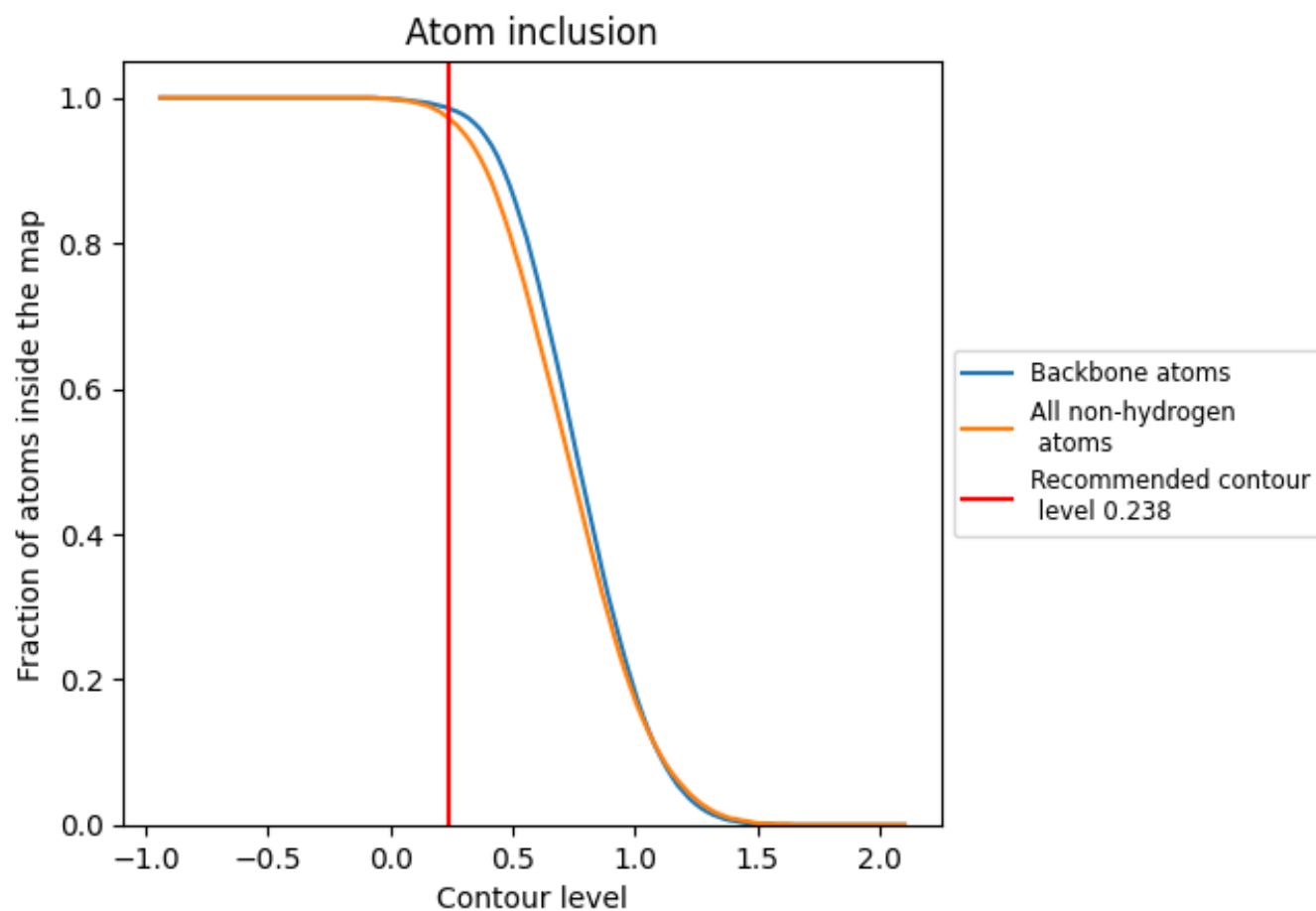
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.238).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9720	 0.4600
0	 0.9530	 0.5030
1	 0.9230	 0.3680
2	 0.9790	 0.5270
3	 0.9380	 0.5030
4	 0.9520	 0.5090
5	 0.9600	 0.5370
6	 0.9760	 0.5230
A	 0.9810	 0.4600
B	 0.9960	 0.4360
C	 0.9640	 0.5140
D	 0.9630	 0.5210
E	 0.9700	 0.4940
F	 0.9360	 0.4430
G	 0.9270	 0.4420
K	 0.9670	 0.5100
L	 0.9510	 0.5260
M	 0.9680	 0.5020
N	 0.8910	 0.4780
O	 0.9640	 0.5020
P	 0.9440	 0.4500
Q	 0.9680	 0.5210
R	 0.9470	 0.4850
S	 0.9340	 0.5040
T	 0.9680	 0.5110
U	 0.9570	 0.4850
V	 0.9250	 0.4600
W	 0.4090	 0.3400
X	 0.9530	 0.5130
Y	 0.9440	 0.5060
Z	 0.9450	 0.4550
a	 0.9970	 0.4490
c	 0.9270	 0.4390
d	 0.9510	 0.4530
e	 0.9470	 0.4780



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Chain	Atom inclusion	Q-score
f	 0.9420	 0.4790
g	 0.9230	 0.4170
h	 0.9670	 0.4840
i	 0.9620	 0.4250
j	 0.9240	 0.4220
k	 0.9260	 0.4530
l	 0.9260	 0.4840
m	 0.9020	 0.3860
n	 0.9750	 0.4660
o	 0.9430	 0.4710
p	 0.9700	 0.4780
q	 0.9350	 0.4860
r	 0.9230	 0.4630
s	 0.9570	 0.4100
t	 0.9530	 0.4440