



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:47 PM UTC

PDB ID : 6O8X / pdb_00006o8x
EMDB ID : EMD-0657
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class02
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.68 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

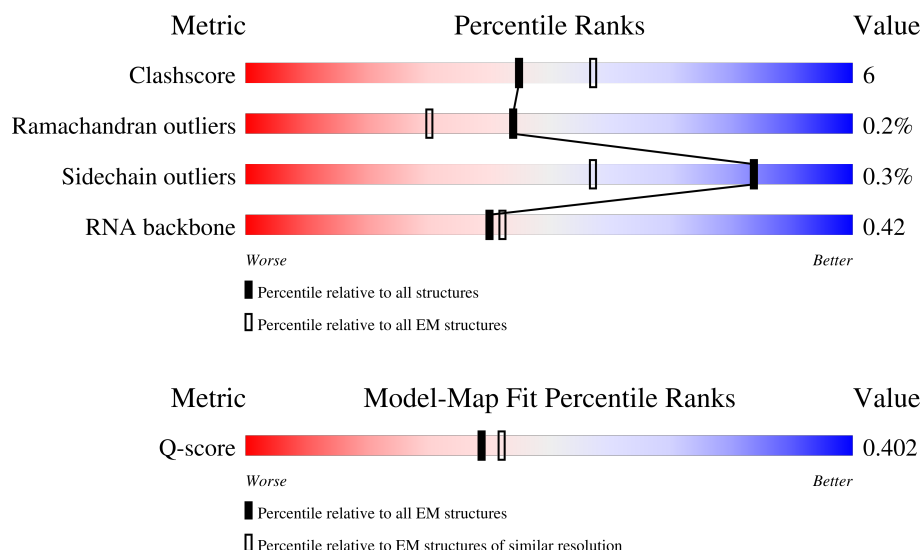
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.68 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	11376 (3.18 - 4.18)

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	

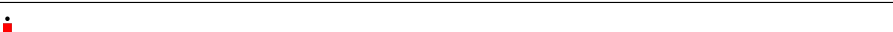
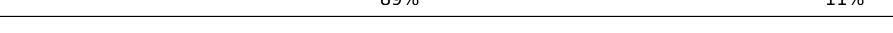
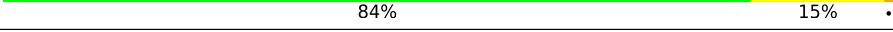
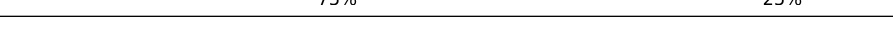
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Mol	Chain	Length	Quality of chain
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	A	2903	
21	B	116	
22	C	275	
23	D	207	
24	E	206	
25	F	177	
26	G	176	
27	K	145	
28	L	122	

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Mol	Chain	Length	Quality of chain
29	M	146	 82% 16%
30	N	141	 7% 76% 24%
31	O	123	 89% 11%
32	P	117	 84% 15%
33	Q	114	 78% 22%
34	R	118	 86% 12%
35	S	102	 75% 25%
36	T	112	 89% 11%
37	U	89	 69% 28%
38	V	101	 82% 15%
39	W	94	 67% 82% 17%
40	X	76	 83% 17%
41	Y	54	 81% 17%
42	Z	61	 80% 20%
43	0	58	 86% 14%
44	1	60	 5% 82% 18%
45	2	56	 84% 16%
46	3	49	 82% 18%
47	4	44	 80% 18%
48	5	64	 84% 16%
49	6	38	 79% 21%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 138230 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	1528	Total	C	N	O	P	0	0
			32746	14609	5979	10630	1528		

- 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	2898	Total	C	N	O	P	0	0
			62196	27761	11436	20101	2898		

- 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
			2478	1105	444	813	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
			2114	1310	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
			1578	993	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
			1572	984	289	297	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
			1391	886	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
			1344	841	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
			1129	713	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
			1094	676	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
			1117	709	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
			978	603	189	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
			898	555	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	115	Total	C	N	O	S	0	0
			913	580	172	157	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
			783	500	138	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
			719	457	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
			757	478	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	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
			424	265	86	71	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	60	Total	C	N	O	S	0	0
			475	301	75	97	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
			373	226	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		

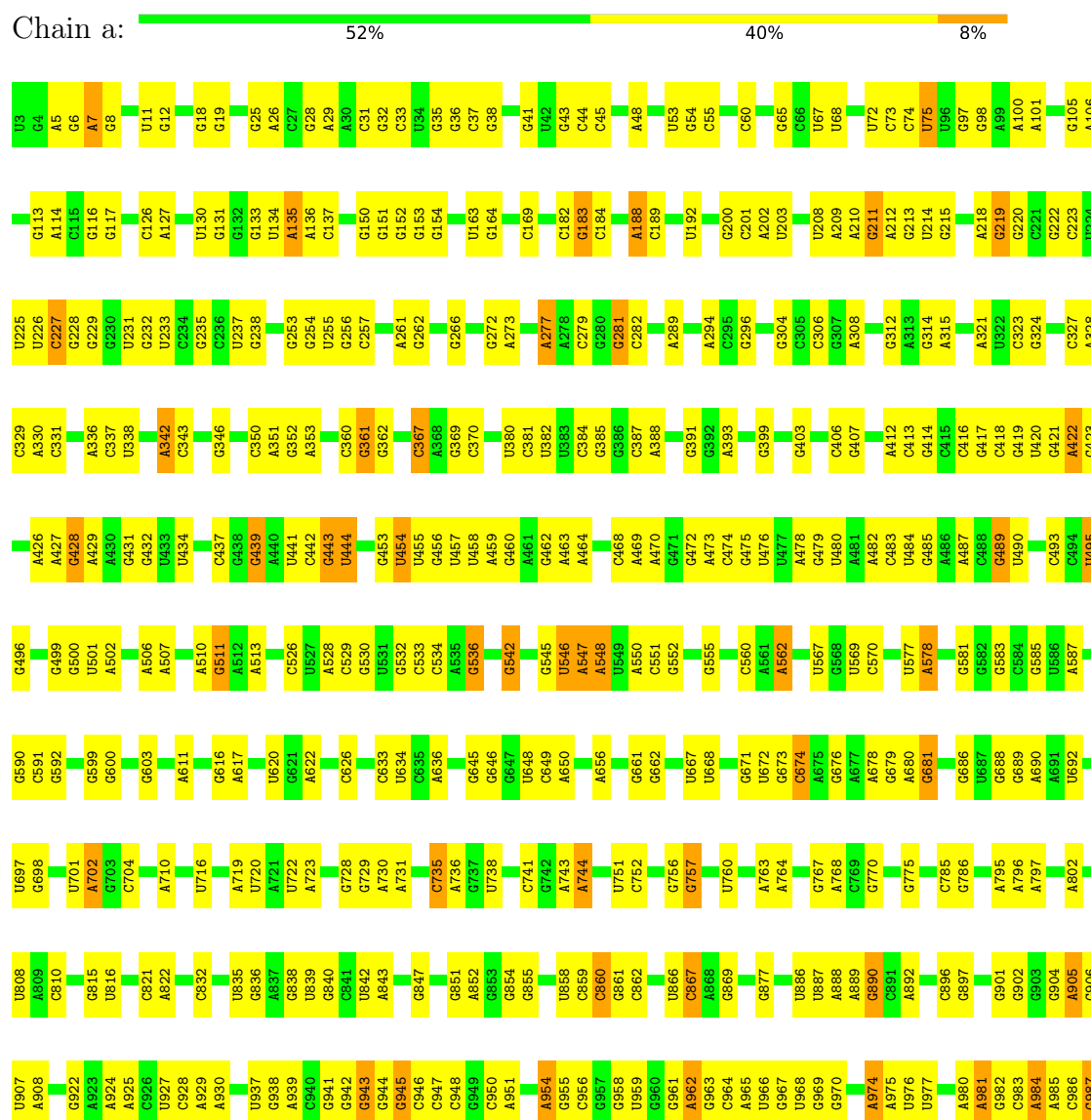
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

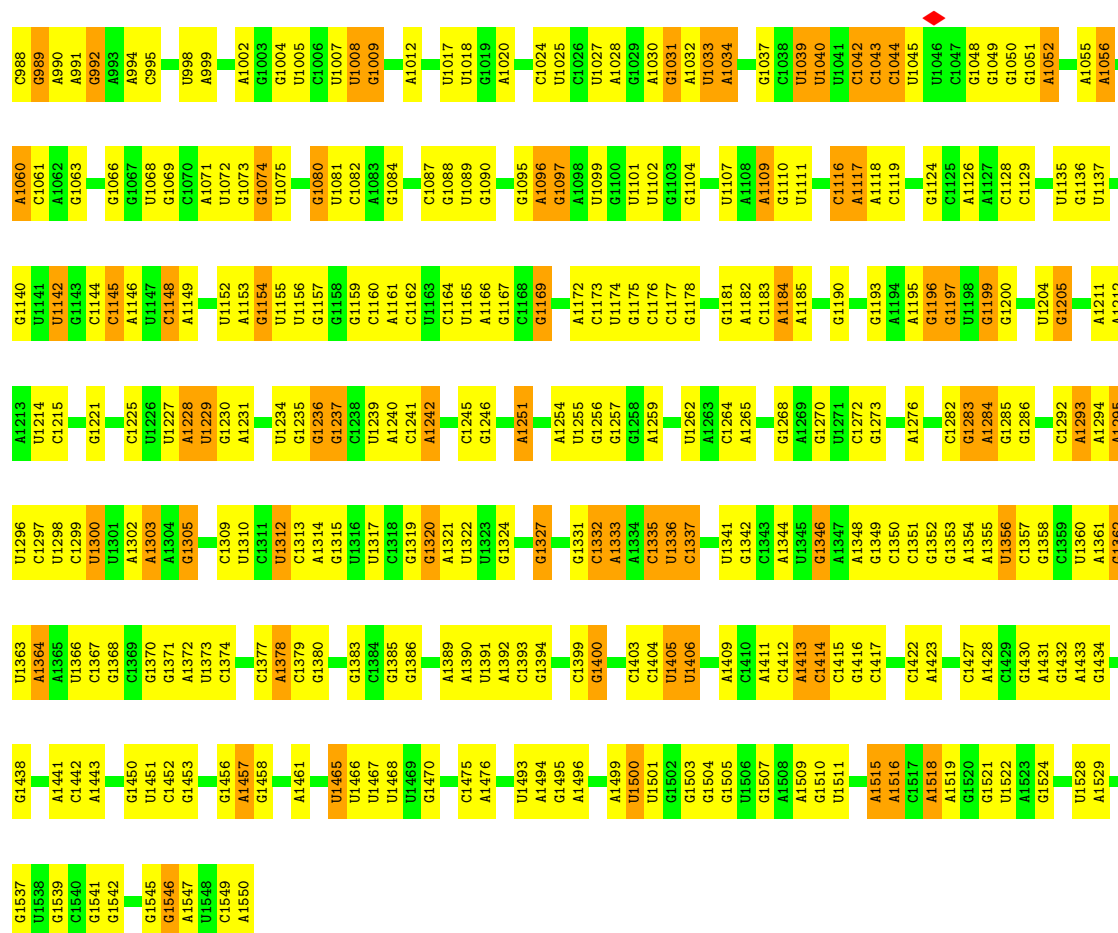
Mol	Chain	Residues	Atoms		AltConf
50	n	1	Total	Zn	0
			1	1	
50	2	1	Total	Zn	0
			1	1	
50	3	1	Total	Zn	0
			1	1	
50	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

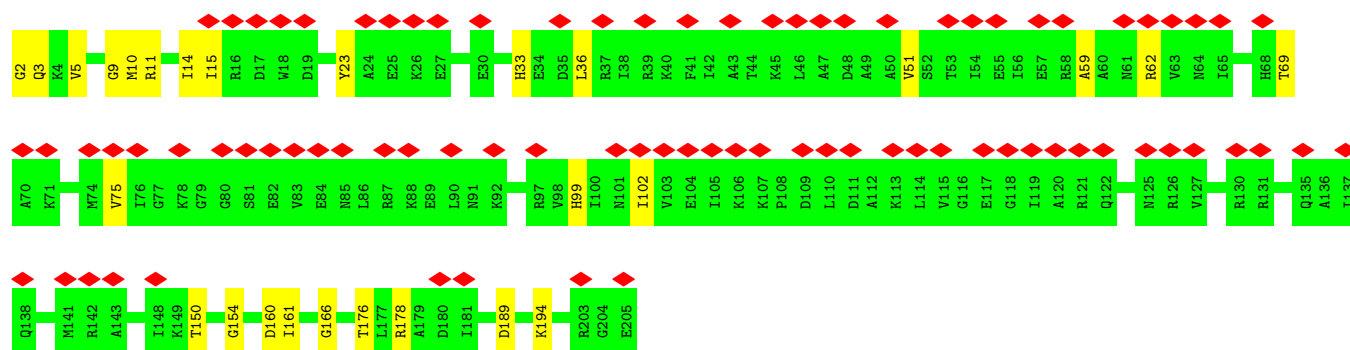
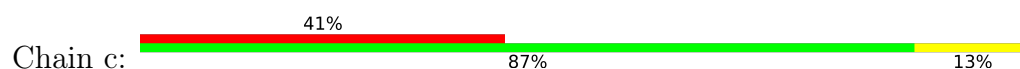
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

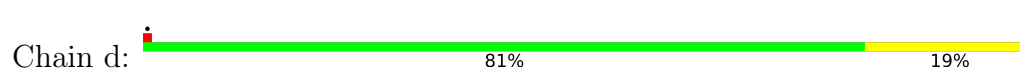




• Molecule 2: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S4





- Molecule 4: 30S ribosomal protein S5

Chain e: 85% 15%



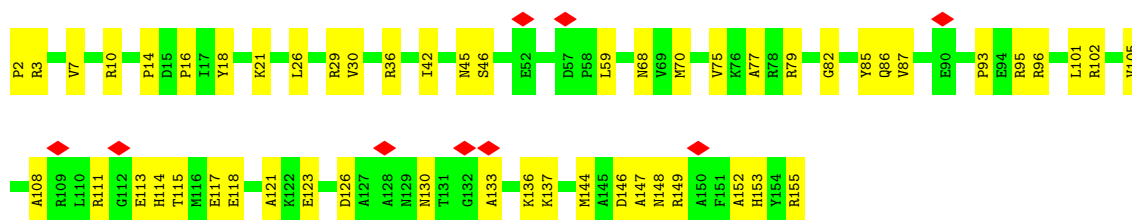
- Molecule 5: 30S ribosomal protein S6

Chain f: 77% 23%



- Molecule 6: 30S ribosomal protein S7

Chain g: 6% 66% 34%



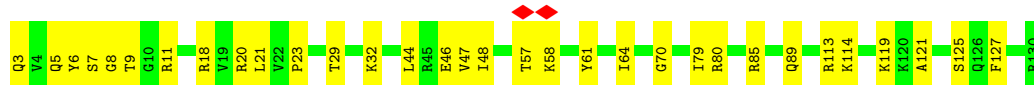
- Molecule 7: 30S ribosomal protein S8

Chain h: 84% 16%



- Molecule 8: 30S ribosomal protein S9

Chain i: 75% 25%

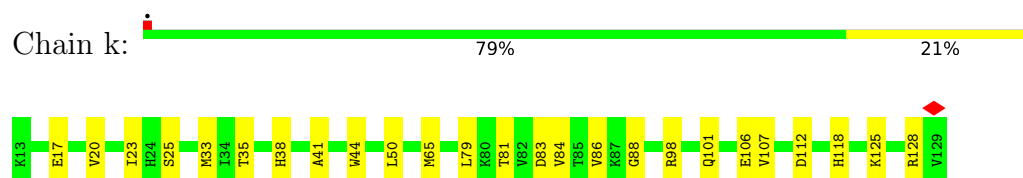


- Molecule 9: 30S ribosomal protein S10

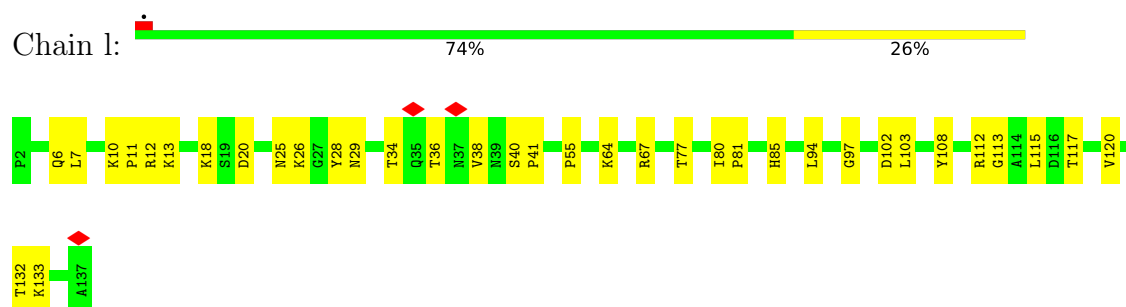
Chain j: 8% 79% 21%



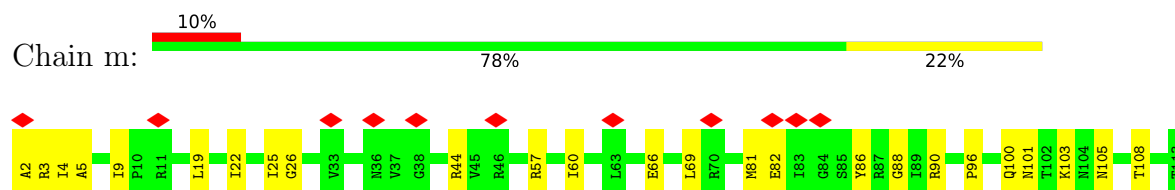
- Molecule 10: 30S ribosomal protein S11



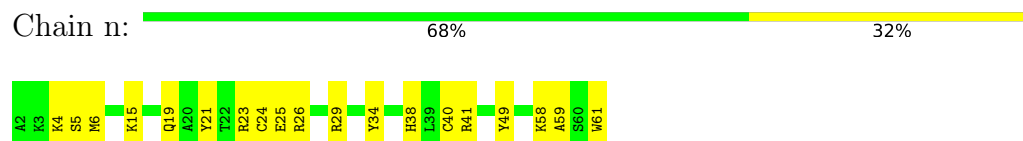
- Molecule 11: 30S ribosomal protein S12



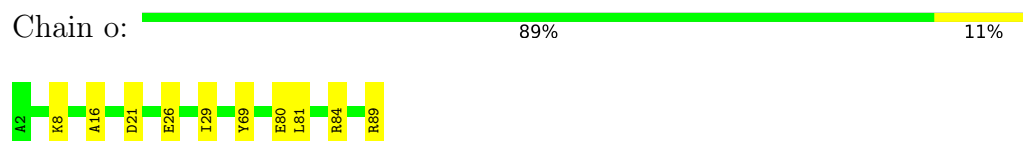
- Molecule 12: 30S ribosomal protein S13



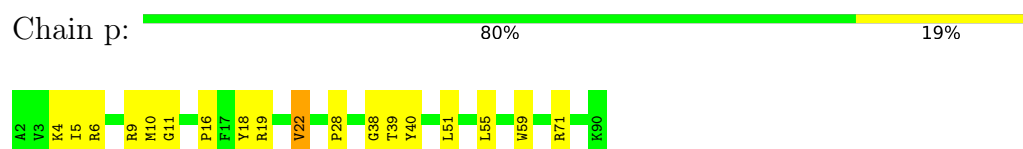
- Molecule 13: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S16



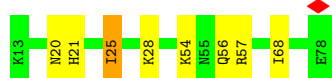
- Molecule 16: 30S ribosomal protein S17

Chain q:  83% 17%



- Molecule 17: 30S ribosomal protein S18

Chain r:  88% 11%



- Molecule 18: 30S ribosomal protein S19

Chain s:  6% 71% 29%



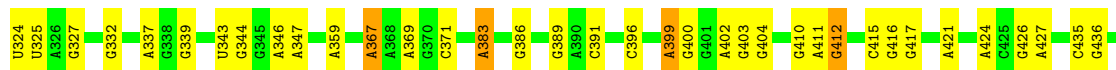
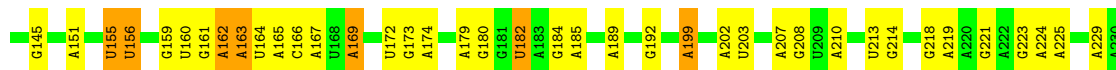
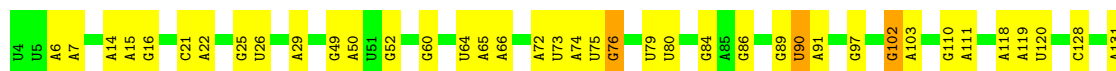
- Molecule 19: 30S ribosomal protein S20

Chain t:  85% 12%

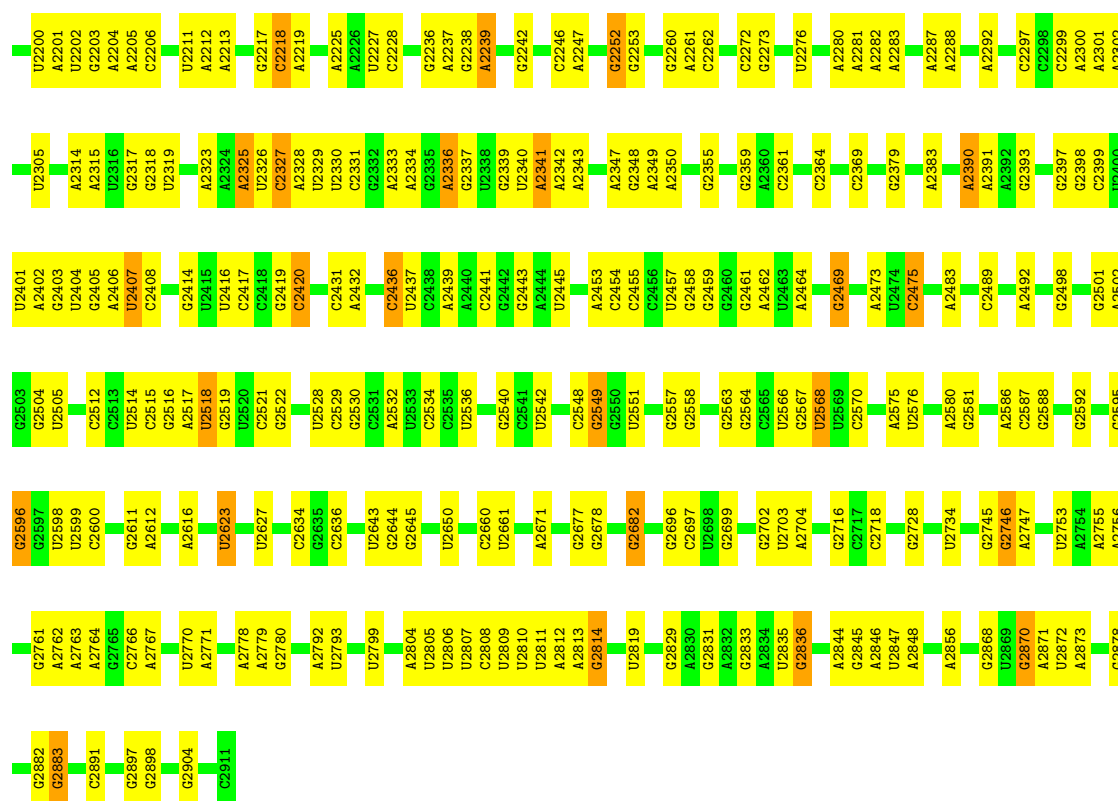


- Molecule 20: 23S rRNA

Chain A:  61% 32% 6%

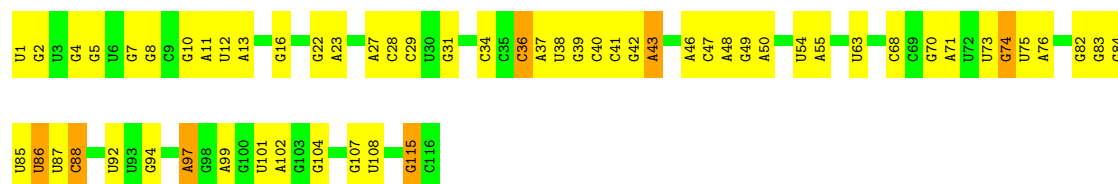


U2123	G2006	C1882	G1770	A1516	U1436	G1335	A1196	U1123	U1039	U943	A860	A660
G2124	U2007	U1883	A1774	G1519	C1441	U1336	C1208	A1124	U1042	A946	A861	G661
U2125	C2008	G1886	U1775	A1520	A1442	U1337	C1210	A1125	G1042	A947	U867	C662
A2126	U2009	G1886	U1775	G1521	A1443	U1338	C1211	A1126	G1043	U949	U868	G663
C2127	C2010	A1896	G1776	U1525	U1444	G1345	C1212	A1128	G1047	A950	G871	G664
A2128	U2025	U1900	G1778	U1530	U1445	U1346	U1213	G1129	A1048	A951	G872	G669
G2130	G2026	A1832	A1782	A1530	U1448	U1347	U1214	U1130	A1049	A952	U874	A670
A2131	A2027	A1913	A1783	A1532	U1449	U1348	U1215	C1132	A1050	C953	C873	G673
A2132	A2034	C1635	A1787	A1532	U1450	U1349	G1216	G1133	U1051	C957	A875	C674
A2133					U1451	C1350	G1217	U1134	A1052			G675
G2134	A2037	G1640	G1790	A1536	U1452	G1357	U1218	A1135	A1053	U960	A883	G676
G2139	C2038	U1925		U1539	U1453	A1387	G1219	A1136	A1061	G961	A884	G677
A2140	C2039	A	U1793	U1539	U1454	A1388		A1137	G1062	C962	U885	G678
C2143	U2042	A	A1794	U1540	U1455	A1389		A1138	G1063	C963	U886	U678
G2144	G2043	C	U1795	A1545	U1456	A1390		G1139	G1065	A964	A887	C679
A2145	A2044	U	C1796	A1545	U1457	G1360	G1256	C1140	A1066	U965	A888	U680
A2146	A2045	A	A1797	U1548	A1457	G1361	U1257	U1141	A1067	U966	A889	G681
U2147	G2046	U1931	A1798	U1549	A1461	U1365	U1258	U1142	A1068	C967	A890	A682
A2148	A2047	A1651		U1550	U1462	C1366		A1143	A1069	A968	A891	U683
G2149	U2048	A1652	C1814	A1551	G1463	G1375	G1262	C1144	U1073	G978	U892	G684
A2150	G2049	A1653	A1815	U1552	U1464	U1376	G1272	U1145	U1081	G979	A894	A685
C2151	A2050		A1816		G1465	U1377	G1273	A1146		G980	A894	G686
C2152	A2051	U1937	A1817	A1559	U1466	U1377	A1274	U1147				U693
G2153	U1940	G1689	G1821	G1560	A1469	U1388	G1275	U1148	C1085	A985	G897	A694
C2154	A1941	U1677	A1822	U1566	C1470	A1389	C1276	A1151	A1086	G986	A898	G696
U2155	U2055	U1677	A1823	G1567	G1471	A1390	G1277	U1152	A1087		A899	U697
C2156	A2056	C1691	A1824	U1568	G1471	G1391		U1153	A1088	A993	G900	U699
G2157	C2057	A1683	A1825	U1572	U1475	G1394	A1284	G1154	A1089	G996	A904	U701
C2158	C2061	U1689	A1826	A1573	U1487	A1395	G1285	A1155	A1094	A997	G905	A702
U2159	G2062	G1690	U1827	G1573	G1488	A1396		C1156	G1095	U998	C906	G703
A2160	U2063	C1955	G1828	A1576	C1489	G1397	U1288	G1162	A1096	A999	A907	A708
C2161	G2066	U1957	A1830	U1577	U1490	G1397	A1290	U1163	A1097	U913	G914	G709
U2162	C2069	U1958	U1831	A1578	U1491	G1400	U1291	A1167				A710
C2163	G2070	U1958	U1832	U1579	G1492	A1401	U1292	A1168	U1100	G1001	U928	C711
U2165					C1493				U1101	G1006	G931	G722
G2168	A2074	U1969	A1833	A1583	G1494	G1404	G1293	G1171	G1102	U1007	A919	A828
A2169	G2075	U1970	U1834	U1584	C1494	G1405	C1294	U1172	G1103	A1008	G922	A829
G2170	U2082	G1974	A1835	U1585	A1495	G1406	G1301	A1173	C1104	G1009	G923	A830
C2171	G2083	C1975	G1841	G1587	U1496	G1407	A1302	U1174	U1105	U1010	G924	G831
G2172	U2084	C1976	G1842	U1588	U1497	G1407	G1303	C1175	A1106	G1012	C925	G832
C2173	A2085	U1977	A1843	G1589	G1499				A1107	A1013	C926	A833
G2174	G2086	G1978	C1844	U1590	A1500				A1108	A1014	C927	A834
C2175					A1501				A1109	A1015	U928	C835
G2176	U2090	A1741	A1862	G1600	G1502	A1420	C1307	U1178	G1111	G1016	G931	U836
G2179	G2107	A1744	A1867	G1601	U1503	A1421	G1308	U1181	G1112	A1023	G932	A840
U2180	A2108	U1752	A1868	U1602	G1504	C1422	A1310	C1180	A1113	G1024	G933	G845
G2181	C2109	G1753	C1603	C1603	A1506	A1423	A1311	A1184	G1114	A1029	G934	C846
C2183	U2114	A1754	A1606	U1509	C1510	G1428		C1185	C1115	U935	U935	G849
G2184	G2115	U1755	A1611	C1511	C1511	U1430	G1319	A1186	C1116	A1030	U936	U754
A2185	U2116	U1757	A1612	A1512	A1512	U1431	A1320	U1187	A1117	C1031	A857	U755
U2186	A2117	G1767	A1613	A1513	A1513	U1432	G1321	A1188	C1118	G1032	U938	A756
A2187				G1514	G1514	U1433	A1322	C1193	C1119	C1035	C939	A757
				A1615	C1515	C1435	U1324	G1194	U1121	A1036	A941	A758
								A1195	U1122		A942	C759



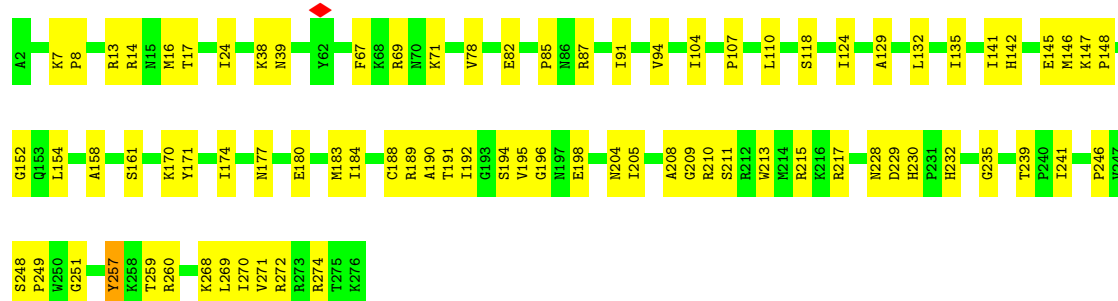
• Molecule 21: 5S rRNA

Chain B: 50% 44% 6%

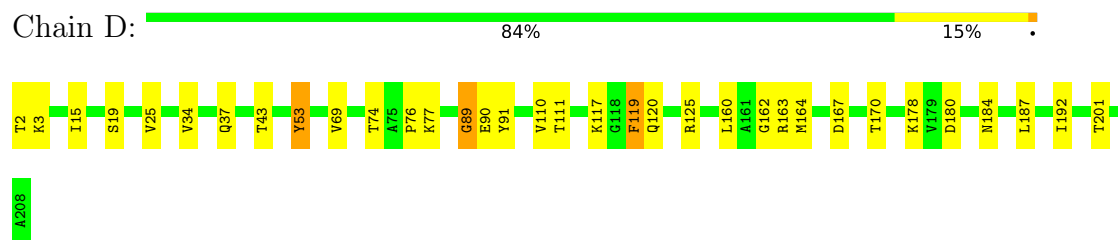


• Molecule 22: 50S ribosomal protein L2

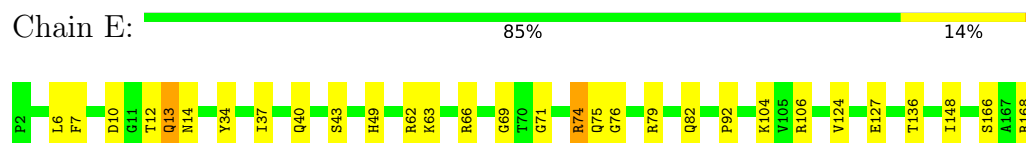
Chain C: 71% 29%



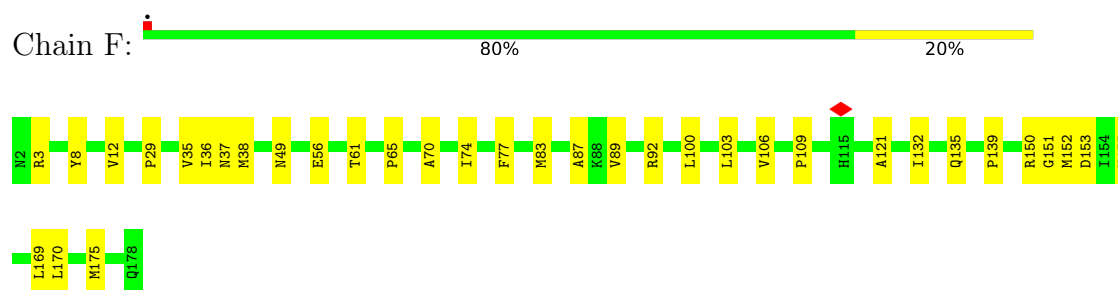
• Molecule 23: 50S ribosomal protein L3



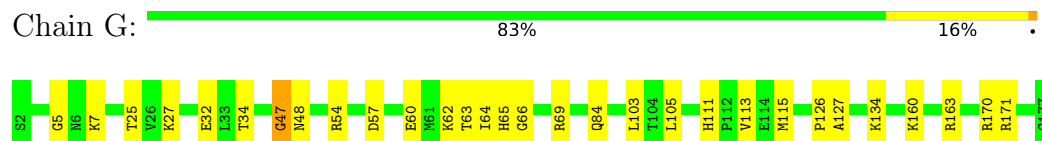
- Molecule 24: 50S ribosomal protein L4



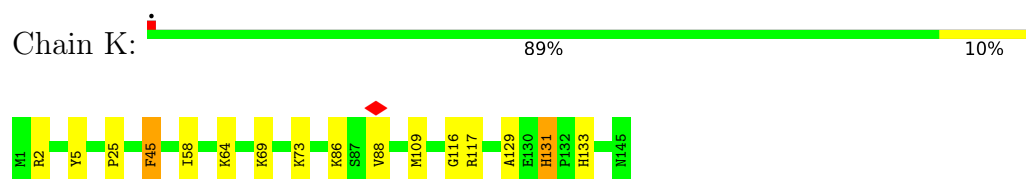
- Molecule 25: 50S ribosomal protein L5



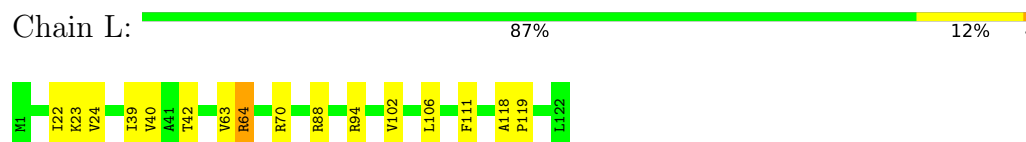
- Molecule 26: 50S ribosomal protein L6



- Molecule 27: 50S ribosomal protein L13



- Molecule 28: 50S ribosomal protein L14



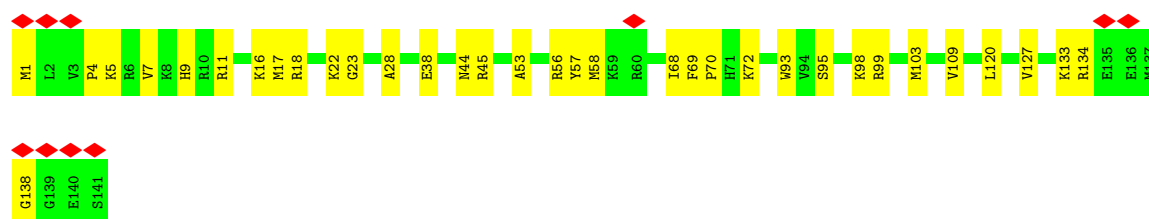
- Molecule 29: 50S ribosomal protein L15

Chain M:  82% 16%



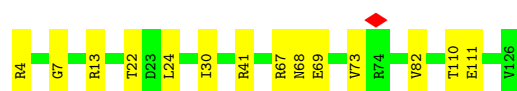
- Molecule 30: 50S ribosomal protein L16

Chain N:  7% 76% 24%



- Molecule 31: 50S ribosomal protein L17

Chain O:  89% 11%



- Molecule 32: 50S ribosomal protein L18

Chain P:  84% 15%



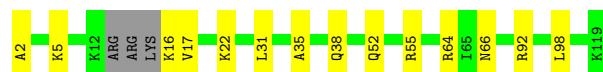
- Molecule 33: 50S ribosomal protein L19

Chain Q:  78% 22%



- Molecule 34: 50S ribosomal protein L20

Chain R:  86% 12%

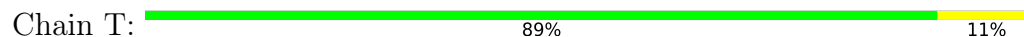


- Molecule 35: 50S ribosomal protein L21

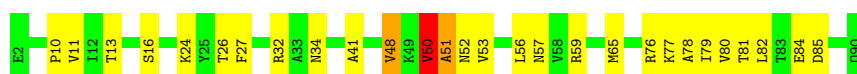
Chain S:  75% 25%



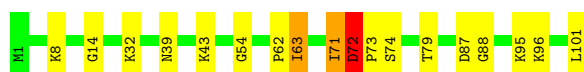
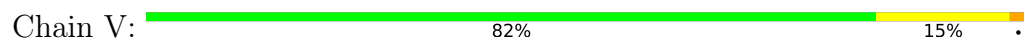
- Molecule 36: 50S ribosomal protein L22



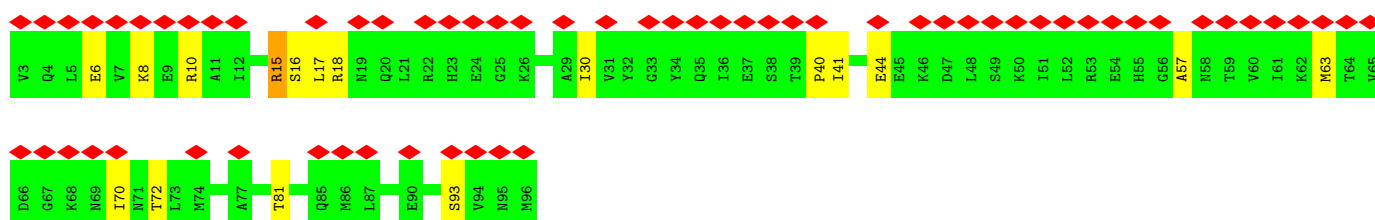
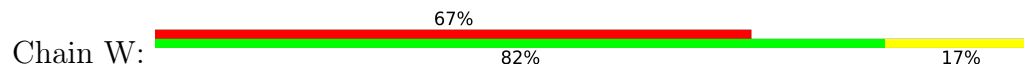
- Molecule 37: 50S ribosomal protein L23



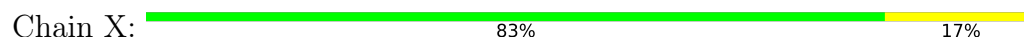
- Molecule 38: 50S ribosomal protein L24



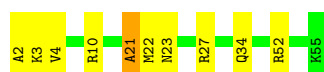
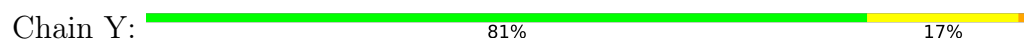
- Molecule 39: 50S ribosomal protein L25



- Molecule 40: 50S ribosomal protein L27



- Molecule 41: 50S ribosomal protein L28



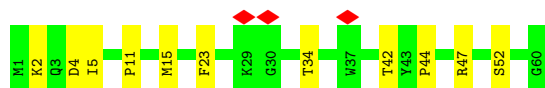
• Molecule 42: 50S ribosomal protein L29

Chain Z:  80% 20%

• Molecule 43: 50S ribosomal protein L30

Chain 0:  86% 14%

• Molecule 44: 50S ribosomal protein L31 type B

Chain 1:  5% 82% 18%

• Molecule 45: 50S ribosomal protein L32

Chain 2:  84% 16%

• Molecule 46: 50S ribosomal protein L33

Chain 3:  82% 18%

• Molecule 47: 50S ribosomal protein L34

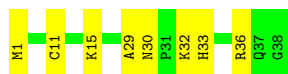
Chain 4:  80% 18% .

• Molecule 48: 50S ribosomal protein L35

Chain 5:  84% 16%

- Molecule 49: 50S ribosomal protein L36

Chain 6:  79% 21%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32689	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	1.890	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.238	Depositor
Map size (Å)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.097, 1.097, 1.097	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.31	0/36657	0.43	0/57173
2	c	0.21	0/1635	0.57	0/2197
3	d	0.27	0/1650	0.61	0/2217
4	e	0.27	0/1217	0.60	0/1641
5	f	0.29	0/807	0.54	0/1087
6	g	0.25	0/1249	0.58	0/1682
7	h	0.32	0/1054	0.55	0/1417
8	i	0.22	0/1003	0.57	0/1343
9	j	0.24	0/812	0.60	0/1093
10	k	0.29	0/878	0.60	2/1185 (0.2%)
11	l	0.30	0/1082	0.69	0/1453
12	m	0.23	0/890	0.58	0/1195
13	n	0.22	0/504	0.66	0/669
14	o	0.34	0/751	0.58	0/1001
15	p	0.35	0/720	0.65	0/966
16	q	0.31	0/689	0.60	0/920
17	r	0.32	0/544	0.61	0/728
18	s	0.23	0/650	0.55	0/872
19	t	0.30	0/612	0.53	0/818
20	A	0.41	0/69661	0.48	2/108645 (0.0%)
21	B	0.34	0/2769	0.46	0/4310
22	C	0.46	0/2147	0.76	0/2885
23	D	0.46	0/1598	0.77	0/2145
24	E	0.41	0/1594	0.63	0/2155
25	F	0.30	0/1408	0.58	0/1890
26	G	0.32	0/1362	0.66	2/1833 (0.1%)
27	K	0.47	0/1148	0.73	0/1549
28	L	0.45	0/929	0.70	1/1247 (0.1%)
29	M	0.40	0/1103	0.82	4/1470 (0.3%)
30	N	0.42	0/1140	0.75	2/1518 (0.1%)
31	O	0.44	0/985	0.84	2/1318 (0.2%)
32	P	0.40	0/907	0.66	0/1214

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Q	0.45	0/938	0.67	0/1262
34	R	0.46	0/923	0.63	0/1227
35	S	0.39	0/794	0.65	0/1064
36	T	0.41	0/858	0.66	0/1157
37	U	0.39	0/724	0.82	4/966 (0.4%)
38	V	0.33	0/772	0.79	2/1035 (0.2%)
39	W	0.23	0/766	0.61	0/1030
40	X	0.45	0/578	0.66	0/773
41	Y	0.28	0/430	0.57	0/573
42	Z	0.34	0/505	0.61	0/672
43	0	0.42	0/437	0.64	0/589
44	1	0.28	0/487	0.74	0/662
45	2	0.43	0/436	0.62	0/578
46	3	0.27	0/423	0.53	0/563
47	4	0.42	0/374	0.76	0/485
48	5	0.41	0/528	0.69	0/689
49	6	0.42	0/309	0.61	0/409
All	All	0.37	0/150437	0.52	21/225570 (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	2
7	h	0	1
16	q	0	1
19	t	0	1
22	C	0	2
23	D	0	2
24	E	0	1
25	F	0	1
26	G	0	2
27	K	0	2
29	M	0	2
30	N	0	1
32	P	0	1
35	S	0	1
37	U	0	2
38	V	0	2
39	W	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	X	0	2
41	Y	0	1
47	4	0	1
All	All	0	29

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	V	71	ILE	CA-C-N	6.42	137.46	121.80
38	V	71	ILE	C-N-CA	6.42	137.46	121.80
31	O	41	ARG	CA-CB-CG	6.09	126.29	114.10
29	M	15	VAL	CA-C-N	5.91	132.83	121.54
29	M	15	VAL	C-N-CA	5.91	132.83	121.54

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	d	189	GLU	Peptide
3	d	29	ARG	Peptide
7	h	22	HIS	Peptide
16	q	73	THR	Peptide
19	t	66	ILE	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	32746	0	16491	369	0
2	c	1610	0	1653	19	0
3	d	1620	0	1641	25	0
4	e	1204	0	1280	15	0
5	f	795	0	789	13	0
6	g	1229	0	1259	38	0
7	h	1041	0	1092	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	i	990	0	1035	23	0
9	j	800	0	846	17	0
10	k	863	0	882	18	0
11	l	1065	0	1133	24	0
12	m	884	0	932	19	0
13	n	492	0	510	16	0
14	o	741	0	756	7	0
15	p	708	0	746	15	0
16	q	681	0	719	11	0
17	r	537	0	572	8	0
18	s	634	0	649	18	0
19	t	610	0	640	10	0
20	A	62196	0	31247	463	0
21	B	2478	0	1246	34	0
22	C	2114	0	2201	56	0
23	D	1578	0	1655	25	0
24	E	1572	0	1619	22	0
25	F	1391	0	1450	23	0
26	G	1344	0	1373	19	0
27	K	1129	0	1166	13	0
28	L	922	0	985	13	0
29	M	1094	0	1144	13	0
30	N	1117	0	1175	21	0
31	O	978	0	1017	8	0
32	P	898	0	928	13	0
33	Q	924	0	979	18	0
34	R	913	0	955	12	0
35	S	783	0	823	17	0
36	T	849	0	906	11	0
37	U	719	0	767	24	0
38	V	763	0	824	10	0
39	W	757	0	775	18	0
40	X	572	0	580	7	0
41	Y	424	0	457	7	0
42	Z	504	0	538	8	0
43	0	435	0	472	5	0
44	1	475	0	441	9	0
45	2	429	0	446	8	0
46	3	419	0	435	7	0
47	4	373	0	418	9	0
48	5	522	0	576	9	0
49	6	304	0	338	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	2	1	0	0	0	0
50	3	1	0	0	0	0
50	6	1	0	0	0	0
50	n	1	0	0	0	0
All	All	138230	0	91561	1363	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 6.

The worst 5 of 1363 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:994:A:H2	1:a:1331:G:N2	1.35	1.25
20:A:2596:G:C4	20:A:2596:G:C2	2.23	1.21
1:a:994:A:C2	1:a:1331:G:N2	2.07	1.19
20:A:2536:U:C6	20:A:2536:U:C2	2.38	1.05
1:a:1321:A:N6	1:a:1346:G:C2	2.25	1.04

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%)	175 (88%)	24 (12%)	0	100	100
4	e	161/163 (99%)	146 (91%)	15 (9%)	0	100	100
5	f	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
6	g	152/154 (99%)	138 (91%)	14 (9%)	0	100	100
7	h	129/131 (98%)	119 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	i	126/128 (98%)	107 (85%)	19 (15%)	0	100	100
9	j	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
10	k	115/117 (98%)	93 (81%)	22 (19%)	0	100	100
11	l	134/136 (98%)	107 (80%)	27 (20%)	0	100	100
12	m	110/112 (98%)	90 (82%)	20 (18%)	0	100	100
13	n	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
14	o	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
15	p	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
16	q	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
17	r	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
18	s	76/78 (97%)	69 (91%)	7 (9%)	0	100	100
19	t	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
22	C	271/275 (98%)	228 (84%)	43 (16%)	0	100	100
23	D	205/207 (99%)	177 (86%)	27 (13%)	1 (0%)	24	56
24	E	204/206 (99%)	170 (83%)	34 (17%)	0	100	100
25	F	174/177 (98%)	153 (88%)	21 (12%)	0	100	100
26	G	172/176 (98%)	147 (86%)	23 (13%)	2 (1%)	10	39
27	K	141/145 (97%)	123 (87%)	18 (13%)	0	100	100
28	L	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
29	M	144/146 (99%)	109 (76%)	33 (23%)	2 (1%)	9	36
30	N	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
31	O	119/123 (97%)	94 (79%)	25 (21%)	0	100	100
32	P	115/117 (98%)	98 (85%)	17 (15%)	0	100	100
33	Q	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
34	R	110/118 (93%)	104 (94%)	6 (6%)	0	100	100
35	S	98/102 (96%)	88 (90%)	10 (10%)	0	100	100
36	T	110/112 (98%)	94 (86%)	16 (14%)	0	100	100
37	U	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	5	29
38	V	99/101 (98%)	75 (76%)	21 (21%)	3 (3%)	3	25
39	W	92/94 (98%)	71 (77%)	20 (22%)	1 (1%)	11	41
40	X	74/76 (97%)	62 (84%)	12 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	Y	52/54 (96%)	41 (79%)	11 (21%)	0	100	100
42	Z	59/61 (97%)	54 (92%)	5 (8%)	0	100	100
43	0	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
44	1	58/60 (97%)	39 (67%)	19 (33%)	0	100	100
45	2	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
46	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
47	4	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
48	5	62/64 (97%)	53 (86%)	9 (14%)	0	100	100
49	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5102/5212 (98%)	4375 (86%)	716 (14%)	11 (0%)	44	71

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	G	48	ASN
26	G	47	GLY
29	M	95	VAL
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%)	162 (100%)	0	100	100
3	d	175/175 (100%)	175 (100%)	0	100	100
4	e	126/126 (100%)	126 (100%)	0	100	100
5	f	86/86 (100%)	86 (100%)	0	100	100
6	g	131/131 (100%)	131 (100%)	0	100	100
7	h	112/112 (100%)	112 (100%)	0	100	100
8	i	101/101 (100%)	101 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	j	90/90 (100%)	90 (100%)	0	100	100
10	k	91/91 (100%)	91 (100%)	0	100	100
11	l	118/118 (100%)	118 (100%)	0	100	100
12	m	95/95 (100%)	95 (100%)	0	100	100
13	n	51/51 (100%)	51 (100%)	0	100	100
14	o	78/78 (100%)	78 (100%)	0	100	100
15	p	79/79 (100%)	78 (99%)	1 (1%)	61	70
16	q	76/76 (100%)	76 (100%)	0	100	100
17	r	57/57 (100%)	56 (98%)	1 (2%)	51	66
18	s	68/68 (100%)	68 (100%)	0	100	100
19	t	62/62 (100%)	61 (98%)	1 (2%)	55	67
22	C	225/225 (100%)	224 (100%)	1 (0%)	84	81
23	D	169/170 (99%)	167 (99%)	2 (1%)	63	71
24	E	172/172 (100%)	171 (99%)	1 (1%)	78	79
25	F	153/154 (99%)	153 (100%)	0	100	100
26	G	146/146 (100%)	146 (100%)	0	100	100
27	K	122/122 (100%)	121 (99%)	1 (1%)	73	76
28	L	98/98 (100%)	97 (99%)	1 (1%)	68	74
29	M	111/112 (99%)	110 (99%)	1 (1%)	70	75
30	N	111/112 (99%)	110 (99%)	1 (1%)	70	75
31	O	104/105 (99%)	104 (100%)	0	100	100
32	P	91/91 (100%)	91 (100%)	0	100	100
33	Q	97/97 (100%)	97 (100%)	0	100	100
34	R	88/94 (94%)	88 (100%)	0	100	100
35	S	83/83 (100%)	82 (99%)	1 (1%)	63	71
36	T	95/95 (100%)	95 (100%)	0	100	100
37	U	80/80 (100%)	78 (98%)	2 (2%)	42	60
38	V	85/85 (100%)	84 (99%)	1 (1%)	63	71
39	W	84/85 (99%)	84 (100%)	0	100	100
40	X	61/61 (100%)	61 (100%)	0	100	100
41	Y	46/47 (98%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Z	55/55 (100%)	55 (100%)	0	100	100
43	0	49/49 (100%)	49 (100%)	0	100	100
44	1	54/55 (98%)	54 (100%)	0	100	100
45	2	46/46 (100%)	46 (100%)	0	100	100
46	3	49/49 (100%)	49 (100%)	0	100	100
47	4	38/39 (97%)	38 (100%)	0	100	100
48	5	51/51 (100%)	51 (100%)	0	100	100
49	6	35/35 (100%)	35 (100%)	0	100	100
All	All	4356/4371 (100%)	4341 (100%)	15 (0%)	84	83

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

Mol	Chain	Res	Type
27	K	45	PHE
37	U	50	VAL
28	L	24	VAL
38	V	63	ILE
35	S	22	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
35	S	90	GLN
46	3	26	ASN
36	T	66	ASN
43	0	52	HIS
48	5	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1528 (99%)	392 (25%)	0
20	A	2889/2903 (99%)	708 (24%)	24 (0%)
21	B	113/116 (97%)	30 (26%)	1 (0%)
All	All	4528/4547 (99%)	1130 (24%)	25 (0%)

5 of 1130 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A
1	a	6	G
1	a	7	A
1	a	11	U
1	a	12	G

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	1502	G
20	A	1585	U
21	B	101	U
20	A	1584	G
20	A	1604	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](#)

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	A	2
1	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	928:U	O3'	931:C	P	12.58
1	a	75:U	O3'	96:U	P	12.00
1	A	1579:U	O3'	1583:A	P	10.23

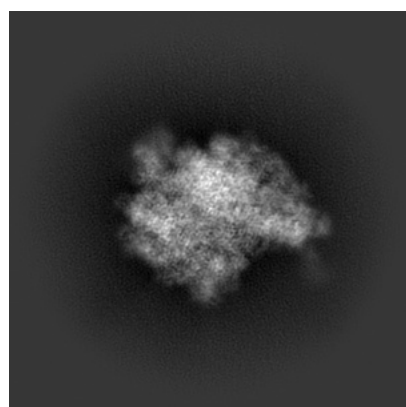
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0657. These allow visual inspection of the internal detail of the map and identification of artifacts.

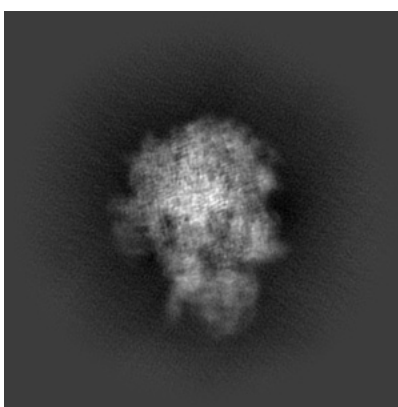
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

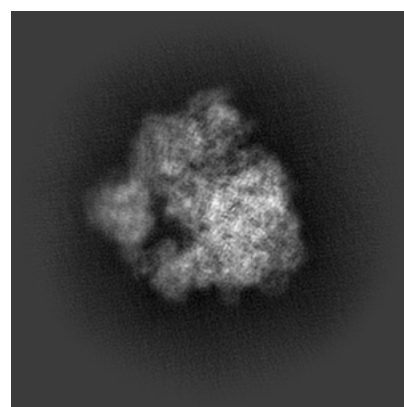
6.1.1 Primary map



X



Y

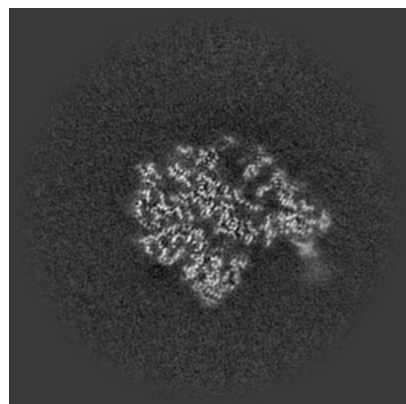


Z

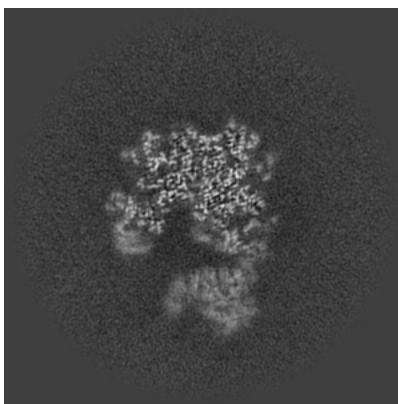
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

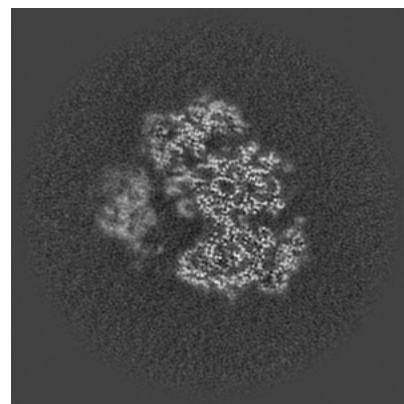
6.2.1 Primary map



X Index: 220



Y Index: 220

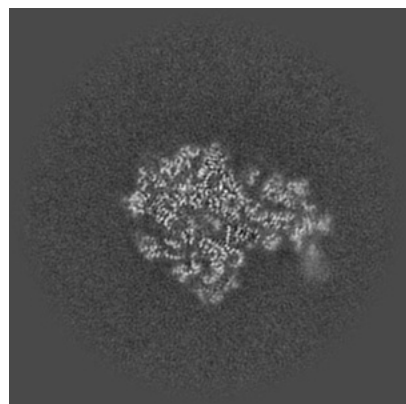


Z Index: 220

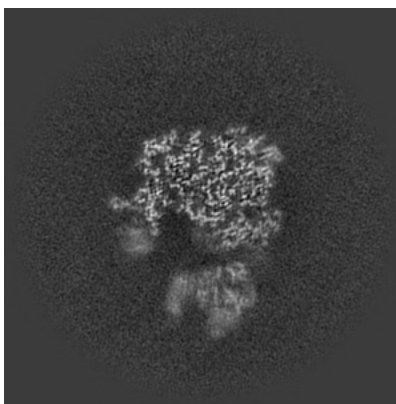
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

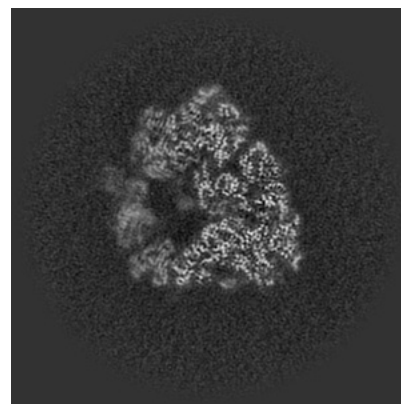
6.3.1 Primary map



X Index: 228



Y Index: 231

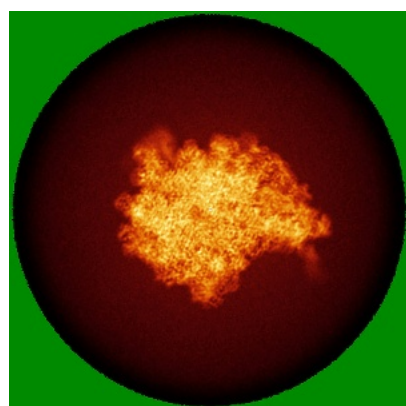


Z Index: 209

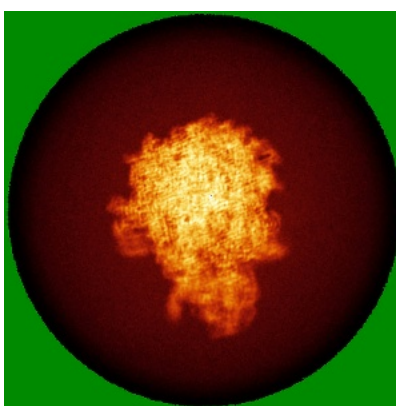
The images above show the largest variance slices of the map in three orthogonal directions.

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

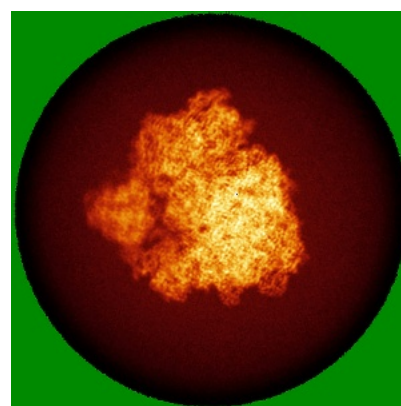
6.4.1 Primary map



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.

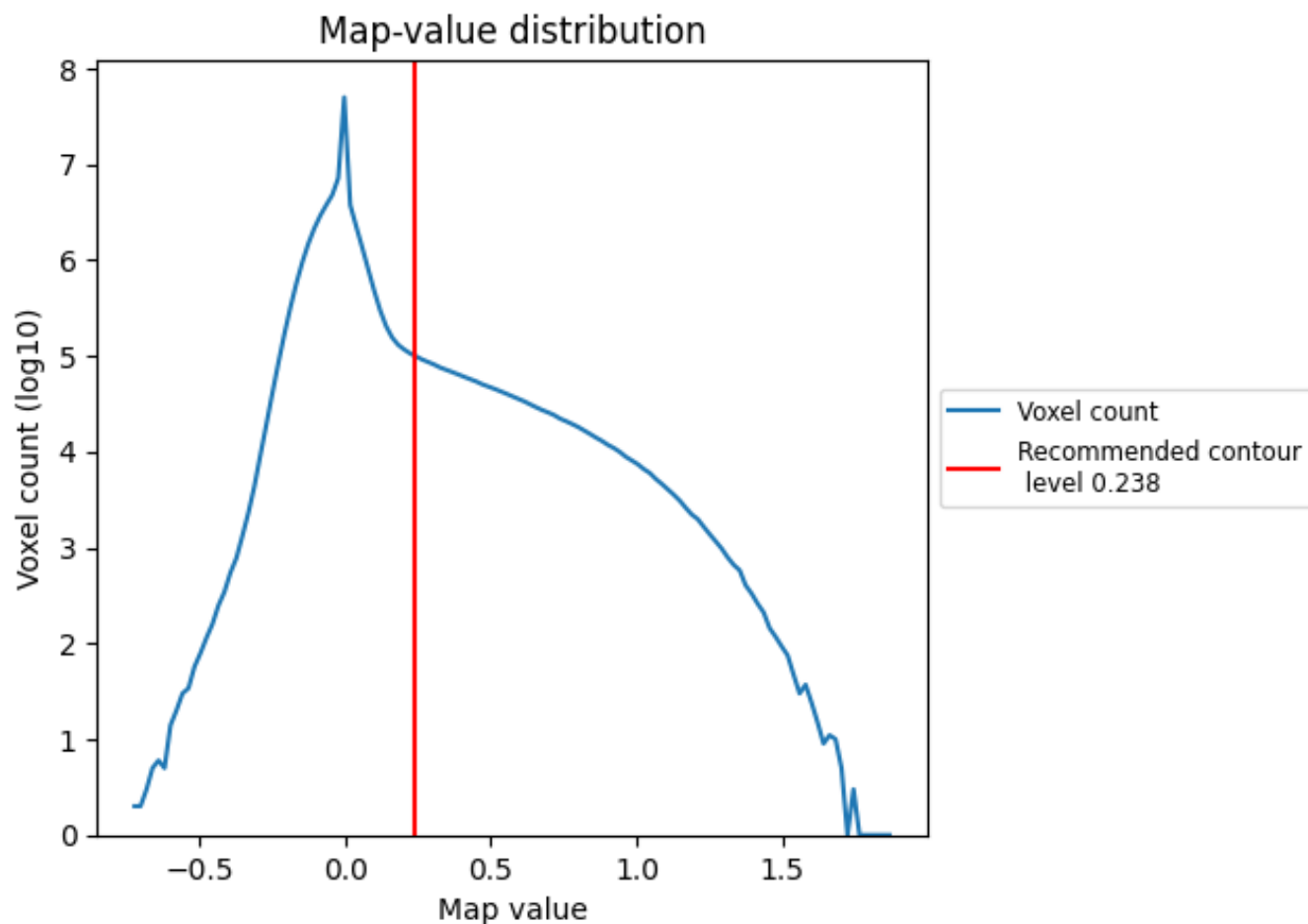
6.6 Mask visualisation

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

7 Map analysis [i](#)

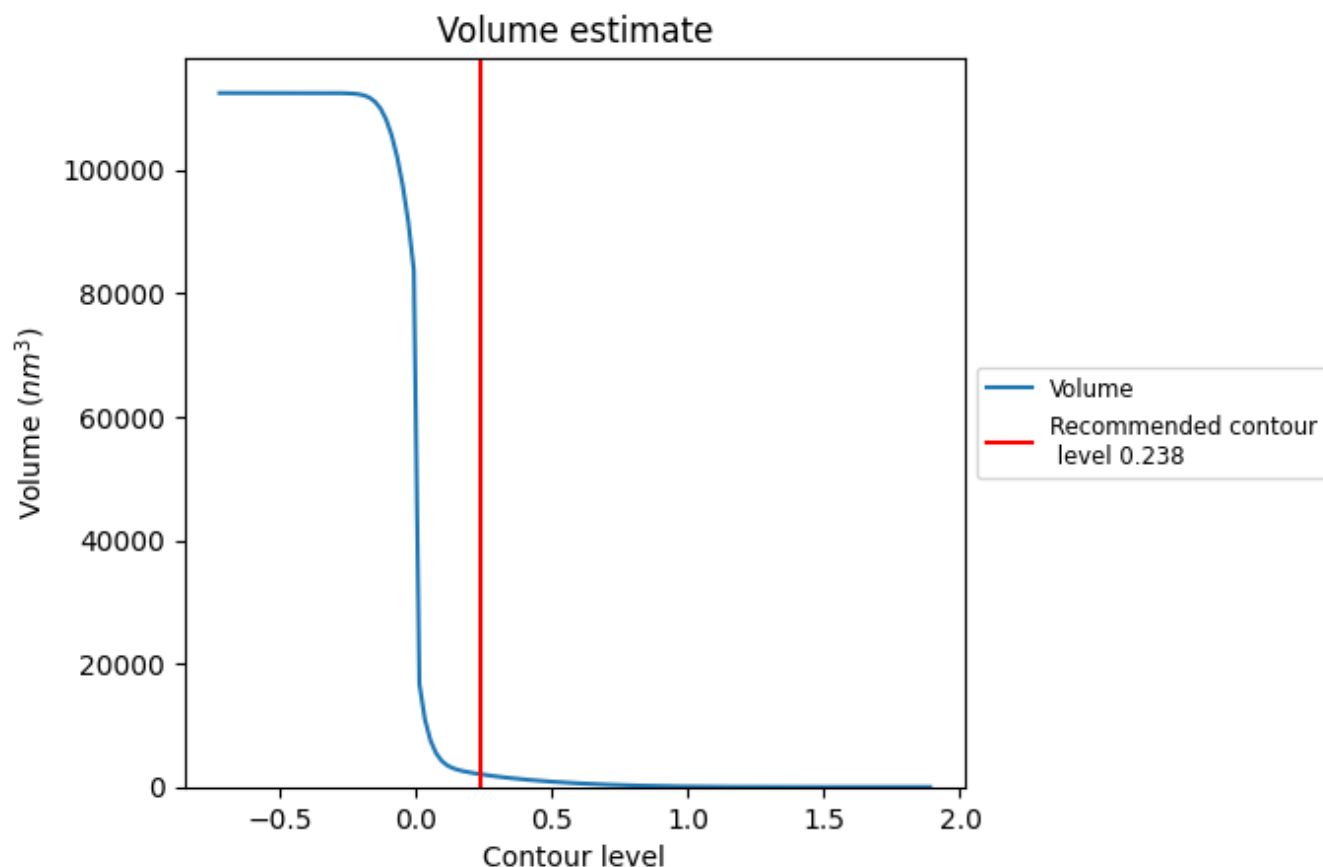
This section contains the results of statistical analysis of the map.

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.

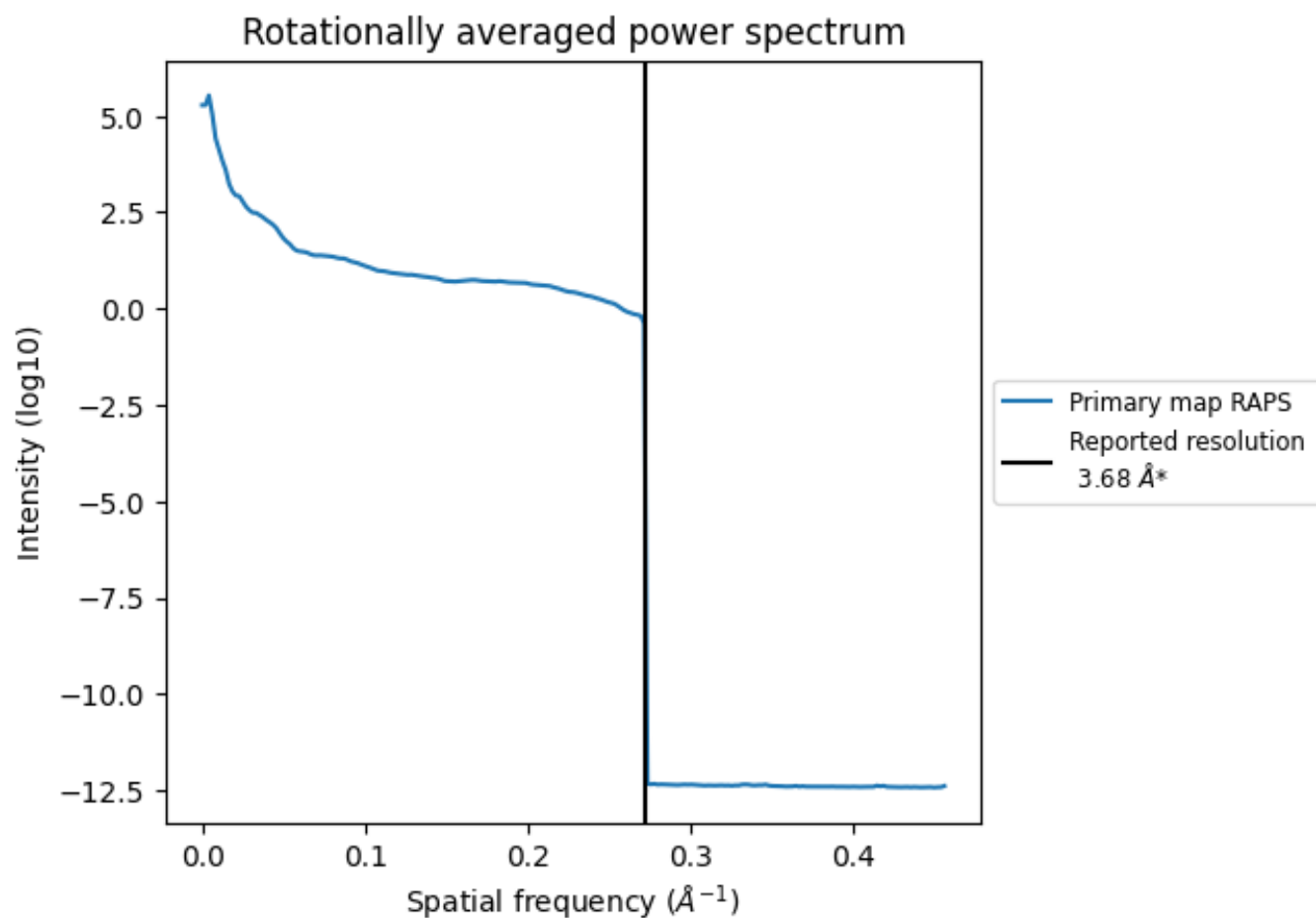
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2048 nm³; this corresponds to an approximate mass of 1850 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 0.272 Å⁻¹

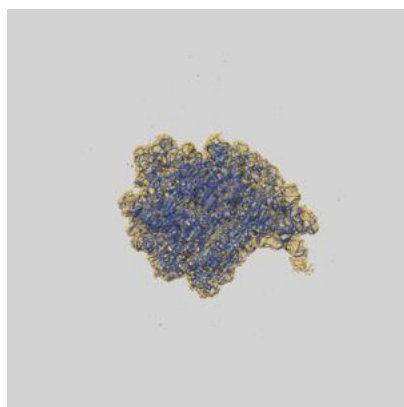
8 Fourier-Shell correlation

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

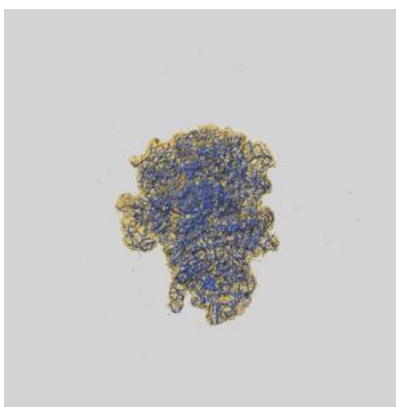
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0657 and PDB model 6O8X. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

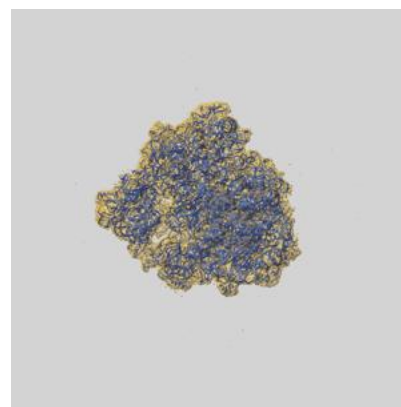
9.1 Map-model overlay [i](#)



X



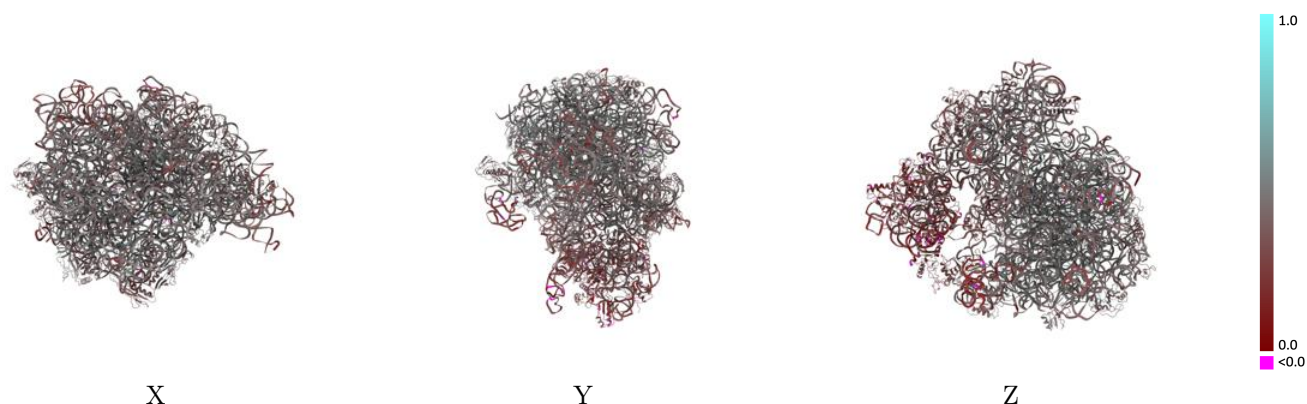
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.238 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](#)

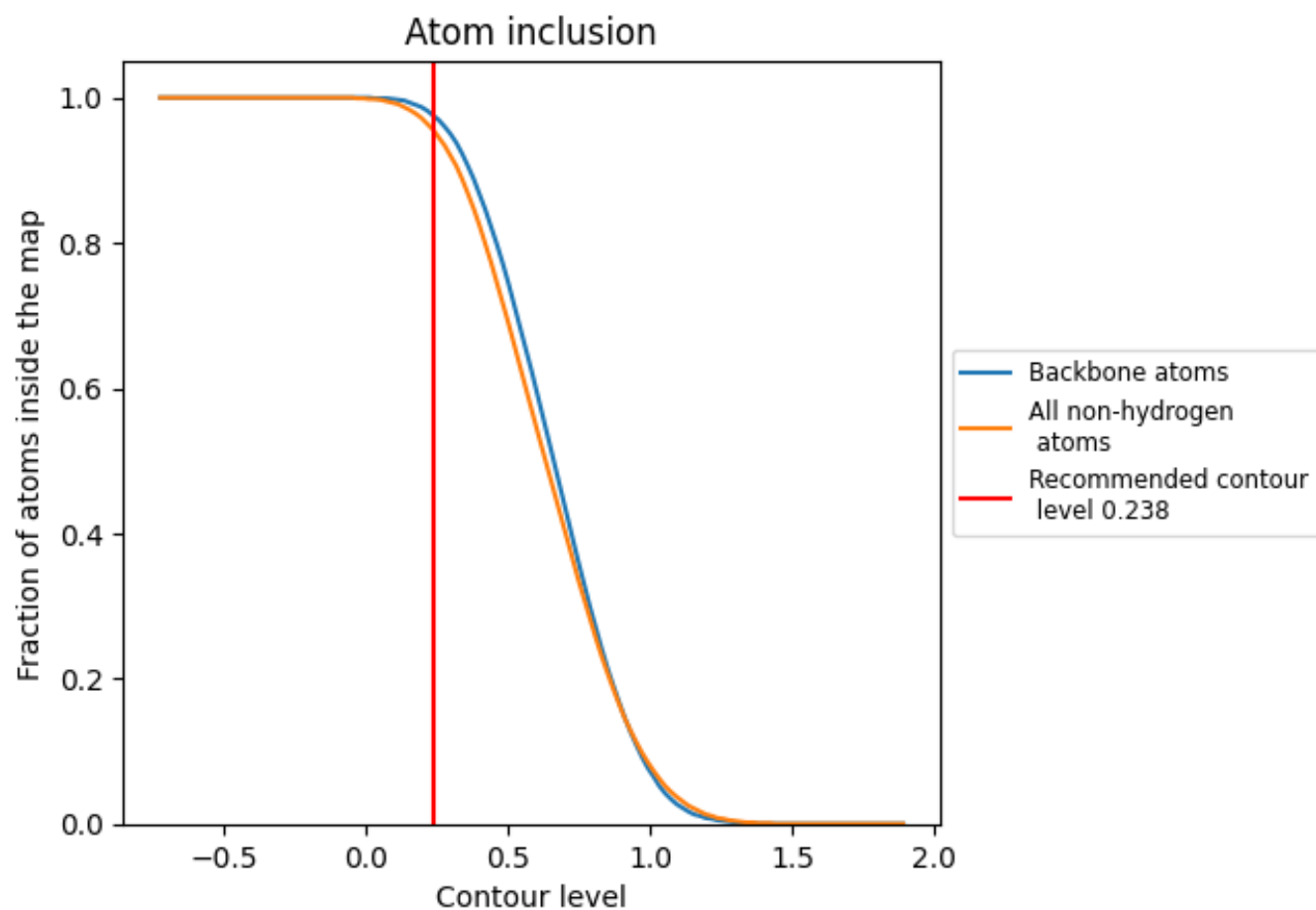


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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	 0.9550	 0.4020
0	 0.9090	 0.4630
1	 0.8830	 0.2890
2	 0.9570	 0.4650
3	 0.8760	 0.4560
4	 0.9230	 0.4470
5	 0.9130	 0.4770
6	 0.9560	 0.4600
A	 0.9900	 0.4290
B	 0.9960	 0.4020
C	 0.9260	 0.4520
D	 0.9300	 0.4690
E	 0.9220	 0.4370
F	 0.8600	 0.3250
G	 0.8870	 0.3780
K	 0.9300	 0.4550
L	 0.9040	 0.4720
M	 0.9320	 0.4460
N	 0.8180	 0.4070
O	 0.9180	 0.4350
P	 0.8920	 0.3700
Q	 0.9150	 0.4560
R	 0.9020	 0.4120
S	 0.9240	 0.4500
T	 0.9230	 0.4500
U	 0.9150	 0.4240
V	 0.8650	 0.3960
W	 0.3150	 0.2990
X	 0.9460	 0.4660
Y	 0.8910	 0.4570
Z	 0.9040	 0.3750
a	 0.9880	 0.3700
c	 0.5310	 0.2820
d	 0.8960	 0.3340
e	 0.8850	 0.3640



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Chain	Atom inclusion	Q-score
f	 0.8810	 0.3990
g	 0.8560	 0.2080
h	 0.9150	 0.4090
i	 0.8960	 0.2830
j	 0.8100	 0.2520
k	 0.9090	 0.3700
l	 0.8570	 0.3950
m	 0.7680	 0.2210
n	 0.8930	 0.2790
o	 0.8820	 0.4010
p	 0.9290	 0.3920
q	 0.8760	 0.4040
r	 0.8940	 0.3900
s	 0.8480	 0.2450
t	 0.8860	 0.3680