



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:14 AM UTC

PDB ID : 6O8W / pdb_00006o8w
EMDB ID : EMD-0656
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class01
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.53 Å (reported)
Based on initial models : 5LI0, 4YBB

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:

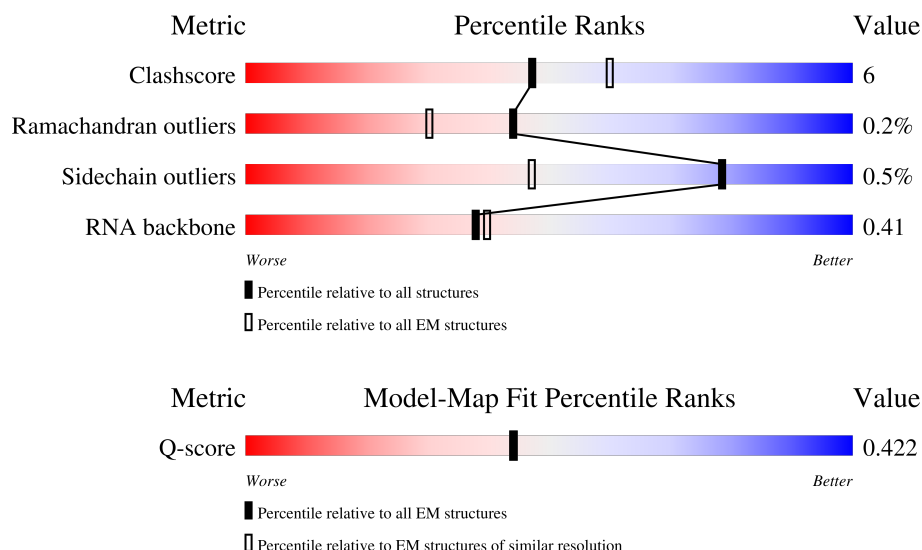
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.53 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	12947 (3.03 - 4.02)

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	1523	
2	c	204	
3	d	201	

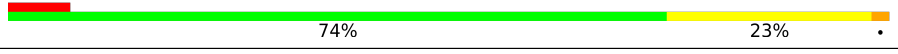
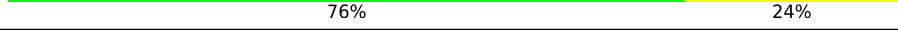
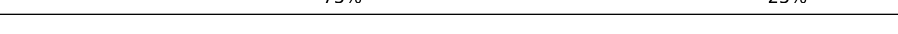
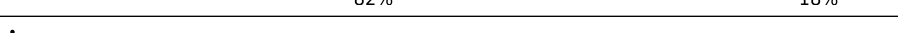
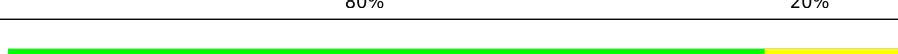
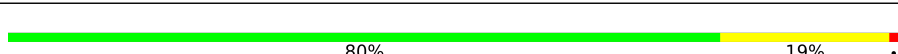
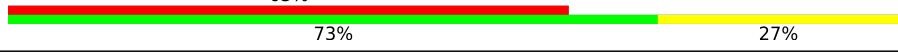
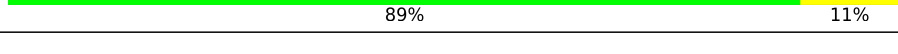
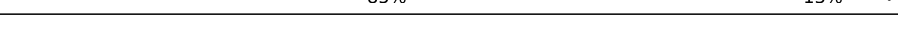
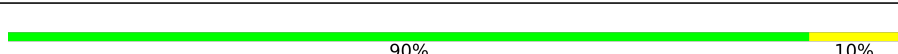
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Mol	Chain	Length	Quality of chain
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	u	76	
21	v	5	
22	A	2903	
23	B	116	
24	C	275	
25	D	207	
26	E	206	
27	F	177	
28	G	176	

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Mol	Chain	Length	Quality of chain
29	K	145	
30	L	122	
31	M	146	
32	N	141	
33	O	123	
34	P	117	
35	Q	114	
36	R	118	
37	S	102	
38	T	112	
39	U	89	
40	V	101	
41	W	94	
42	X	76	
43	Y	54	
44	Z	61	
45	0	58	
46	1	59	
47	2	56	
48	3	49	
49	4	44	
50	5	64	
51	6	38	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 139953 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 tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 21 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	5	Total	C	N	O	P	0	0
			100	45	11	39	5		

- Molecule 22 is a RNA chain called 50S subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	A	2903	Total	C	N	O	P	0	0
			62301	27808	11456	20134	2903		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B	116	Total	C	N	O	P	0	0
			2478	1106	442	814	116		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	275	Total	C	N	O	S	0	0
			2113	1310	415	381	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	207	Total	C	N	O	S	0	0
			1578	993	292	289	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	206	Total	C	N	O	S	0	0
			1573	983	290	298	2		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	177	Total	C	N	O	S	0	0
			1391	886	239	260	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	176	Total	C	N	O	S	0	0
			1344	841	244	255	4		

- Molecule 29 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	K	145	Total	C	N	O	S	0	0
			1129	713	205	207	4		

- Molecule 30 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L	122	Total	C	N	O	S	0	0
			921	573	176	170	2		

- Molecule 31 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	146	Total	C	N	O	S	0	0
			1094	676	212	205	1		

- Molecule 32 is a protein called 50S ribosomal protein L16.

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

- Molecule 33 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	O	123	Total	C	N	O	S	0	0
			978	602	190	183	3		

- Molecule 34 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P	112	Total	C	N	O	S	0	0
			862	533	169	159	1		

- Molecule 35 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Q	114	Total	C	N	O	0	0
			923	581	185	157		

- Molecule 36 is a protein called 50S ribosomal protein L20.

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

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	S	102	Total	C	N	O	S	0
			783	499	139	143	2	0

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	T	112	Total	C	N	O	S	0
			848	531	156	159	2	0

- Molecule 39 is a protein called 50S ribosomal protein L23.

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

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	V	101	Total	C	N	O	S	0
			762	485	135	140	2	0

- Molecule 41 is a protein called 50S ribosomal protein L25.

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

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	X	76	Total	C	N	O	0	0
			571	350	109	112		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	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 44 is a protein called 50S ribosomal protein L29.

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

- Molecule 45 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	0	58	Total	C	N	O	S	0	0
			434	270	81	82	1		

- Molecule 46 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	59	Total	C	N	O	S	0	0
			472	300	74	96	2		

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	56	Total	C	N	O	S	0	0
			428	261	88	73	6		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	4	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	5	64	Total	C	N	O	S	0	0
			521	320	122	77	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

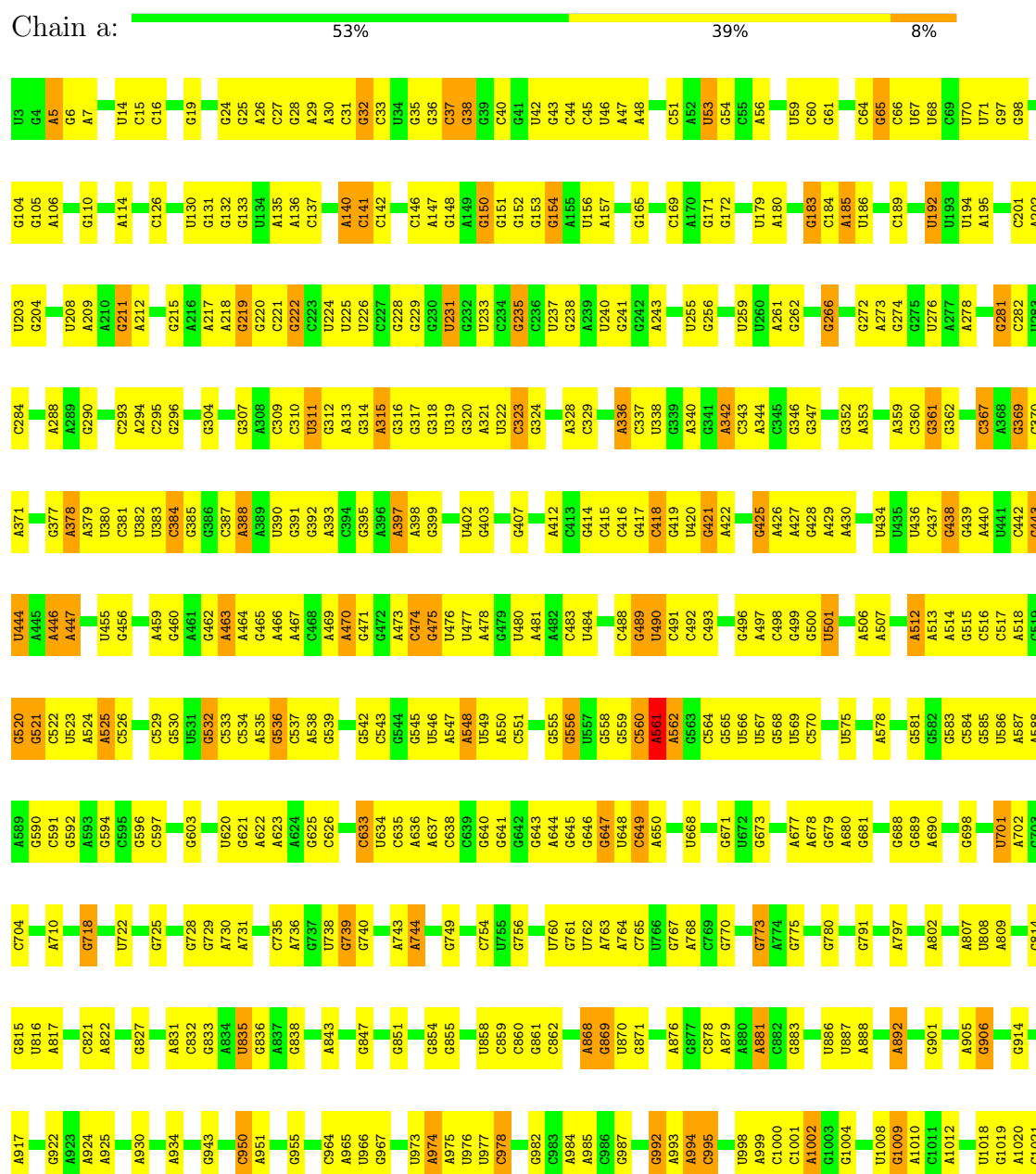
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

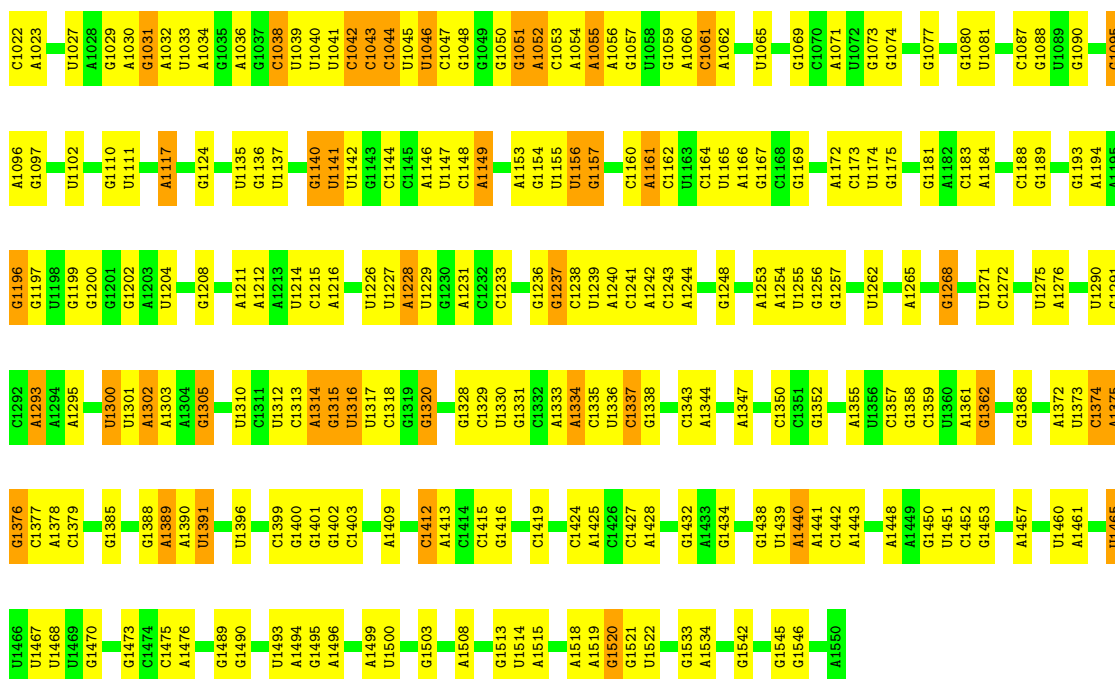
Mol	Chain	Residues	Atoms		AltConf
52	n	1	Total	Zn	0
			1	1	
52	2	1	Total	Zn	0
			1	1	
52	3	1	Total	Zn	0
			1	1	
52	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

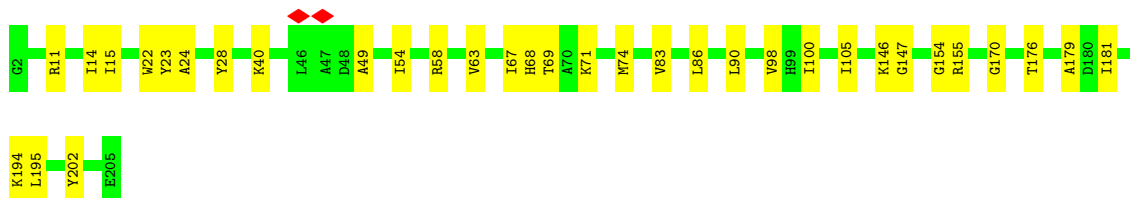
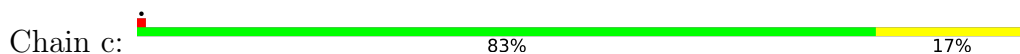
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

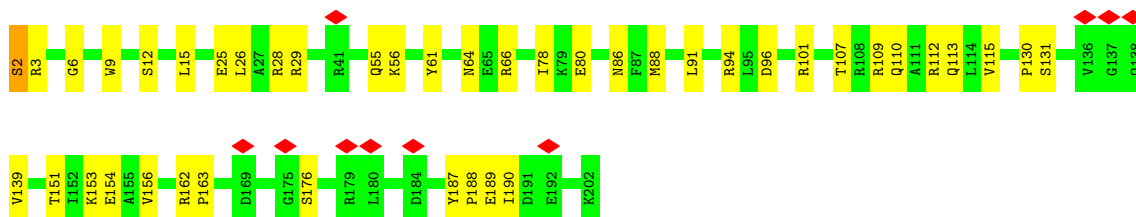
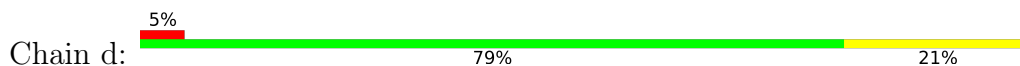




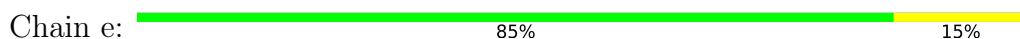
• Molecule 2: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S5



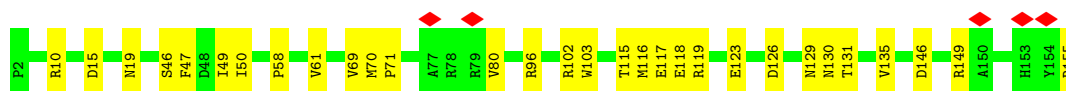
• Molecule 5: 30S ribosomal protein S6

Chain f:  90% 10%



- Molecule 6: 30S ribosomal protein S7

Chain g:  81% 19%



- Molecule 7: 30S ribosomal protein S8

Chain h:  85% 15%



- Molecule 8: 30S ribosomal protein S9

Chain i:  75% 25%



- Molecule 9: 30S ribosomal protein S10

Chain j:  81% 19%



- Molecule 10: 30S ribosomal protein S11

Chain k:  88% 12%



- Molecule 11: 30S ribosomal protein S12

Chain l:  71% 28%





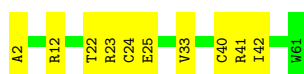
- Molecule 12: 30S ribosomal protein S13

Chain m: 82% 18%



- Molecule 13: 30S ribosomal protein S14 type Z

Chain n: 83% 17%



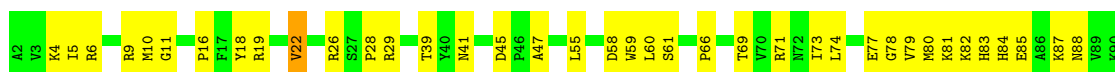
- Molecule 14: 30S ribosomal protein S15

Chain o: 85% 15%



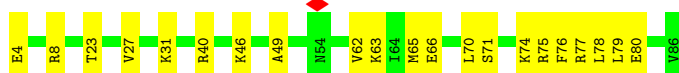
- Molecule 15: 30S ribosomal protein S16

Chain p: 57% 42%



- Molecule 16: 30S ribosomal protein S17

Chain q: 75% 25%



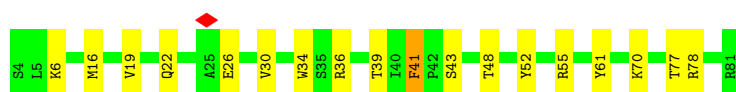
- Molecule 17: 30S ribosomal protein S18

Chain r: 86% 14%

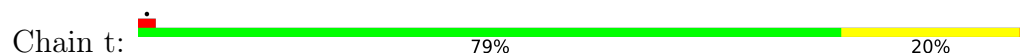


- Molecule 18: 30S ribosomal protein S19

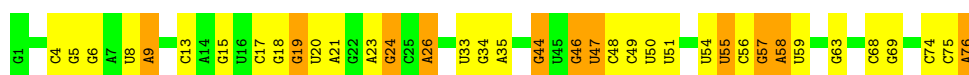
Chain s: 77% 22%



- Molecule 19: 30S ribosomal protein S20



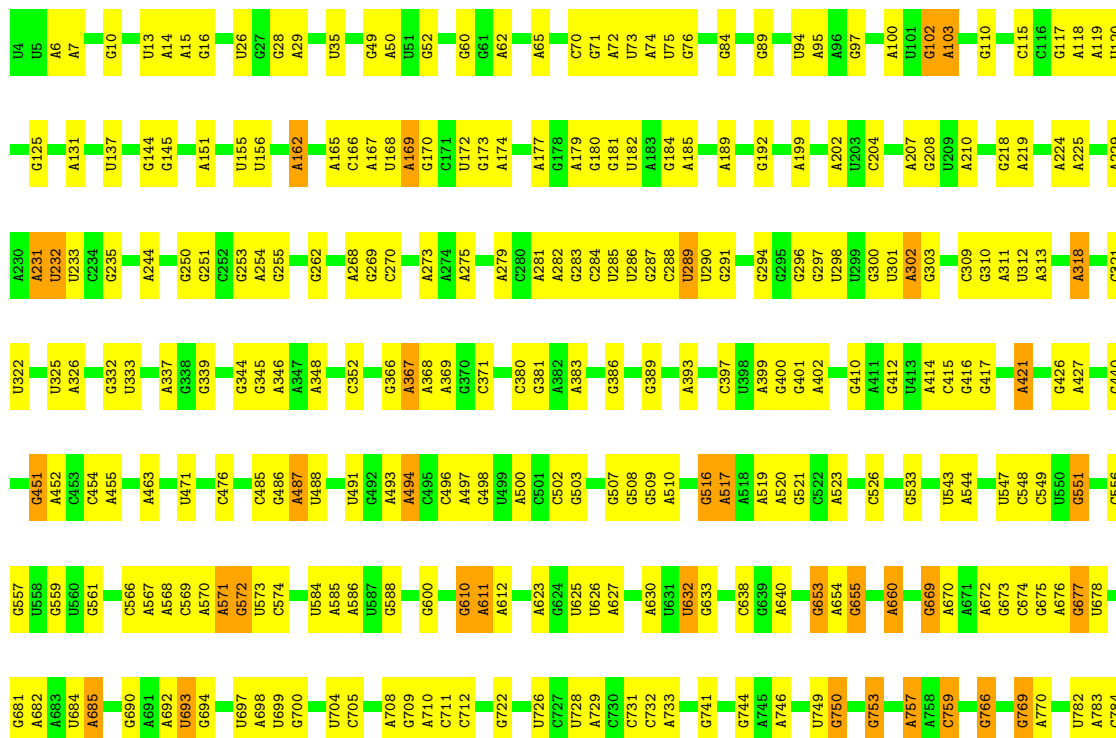
- Molecule 20: tRNA



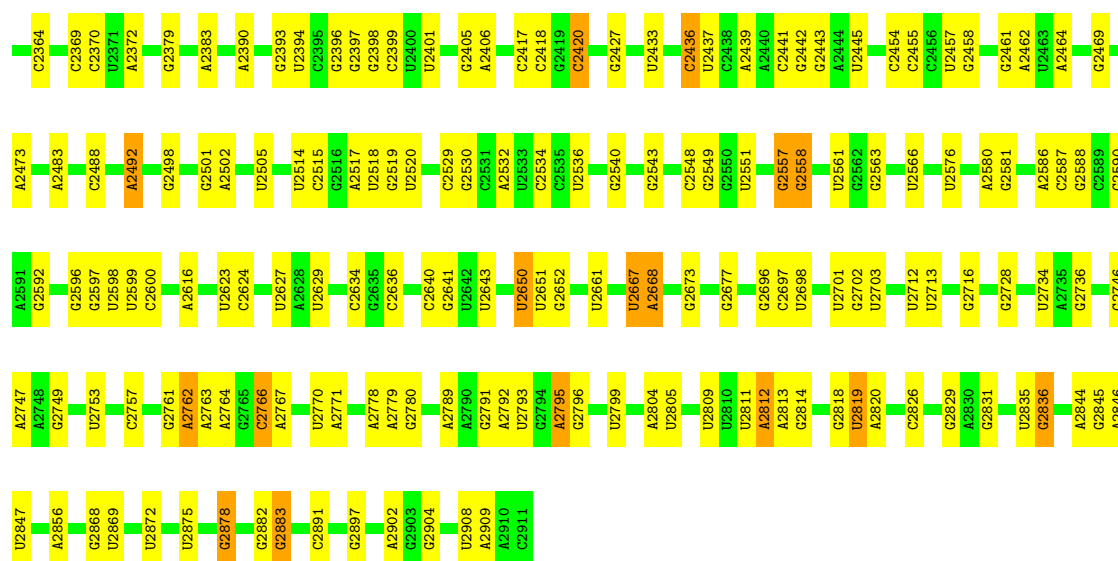
- Molecule 21: mRNA



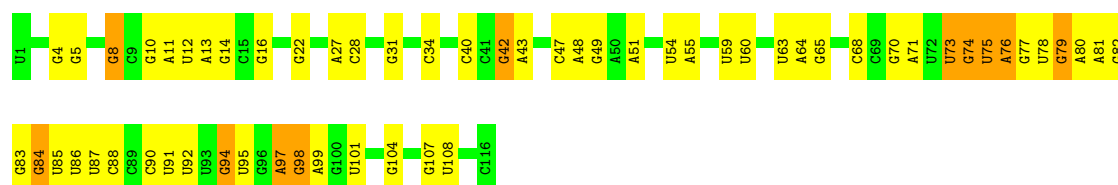
- Molecule 22: 50S subunit



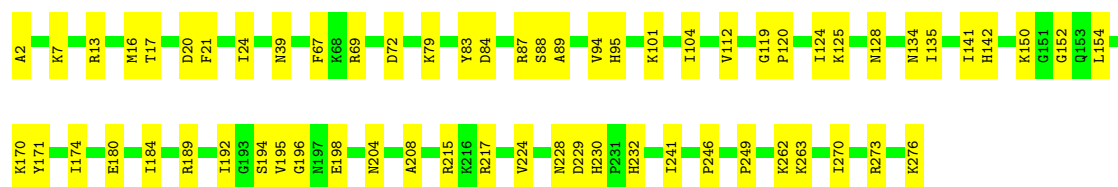
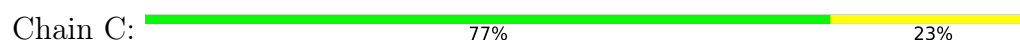
C2272	A2155	A1927	A1787	U1535	C1440	C1330	U1214	U1123	U1052	U965	G893	G785
U2276	A2156	C1928	G1790	A1536	C1441	U1336	A1215	A1124	A1053	U966	A894	U786
U2279	G2157	U1931	G1793	U1539	G1443	U1338	G1217	A1125	G1057	C967	G898	U787
A2280	G2158	U1943	U1794	U1542	U1448	G1345	G1224	G1127	A1060	U969	G899	U788
A2281	A2055	G1944	U1795	U1543	U1449	G1346	U1225	G1128	A1061	U970	G900	U789
A2282	C2056	G1945	U1796	U1551	U1450	C1350	C1234	G1129	A1062	U971	A901	U791
A2283	C2057	C1948	U1797	A1552	U1451	U1357	G1235	G1130	U1063	A902	A902	U792
A2284	C2058	G1949	U1798	U1553	U1452	A1357	G1236	G1131	G982	A903	A903	A804
G2290	C2059	A1951	U1799	A1559	U1453	A1358	U1237	G1132	G983	G905	G905	G805
C2297	C2060	G1952	A1801	U1565	U1454	A1359	U1238	U1134	A1066	C984	C906	G808
C2298	A2074	U1953	G1813	G1566	U1455	U1365	U1239	A1135	A985	C907	A907	G808
C2299	C2075	C1955	C1814	C1567	U1456	U1366	A1240	A1136	A1068	C908	C908	G815
A2301	A2076	U1969	A1815	G1568	A1457	U1367	A1241	U1137	A1069	A987	C909	G816
A2302	U2082	U1970	G1821	A1572	U1461	G1373	G1244	A1071	G1070	C988	G910	G817
G2305	C2083	C1971	U1822	G1573	U1462	G1374	G1249	A1072	A1072	C991	A919	G820
C2306	G2084	U1972	A1823	A1576	A1469	G1375	U1254	U1079	G992	A993	G920	A821
C2307	C2085	C1976	G1825	A1577	C1470	U1376	C1255	U1143	G994	G994	G921	A822
G2317	G2086	C1977	U1826	G1584	G1471	U1377	G1256	U1144	U1080	U995	G922	A823
G2318	U2090	U1978	U1827	U1585	U1475	U1388	A1257	A1146	U1081	A997	G923	U824
G2319	G2107	C1979	G1828	A1586	U1487	U1394	G1262	U1148	C1085	U998	C924	U825
G2320	U2114	A1980	A1829	G1589	C1488	A1395	U1268	C1149	A1086	G1001	C925	G832
G2321	G2115	G1831	A1830	A1590	C1489	G1396	G1269	A1150	A1087	U1007	A927	A833
G2322	U2116	A1832	U1831	A1591	U1490	G1397	U1270	G1151	C1092	U1008	G928	U836
G2323	A2117	C1986	U1833	U1593	U1491	G1400	G1272	G1152	U1093	A1008	C931	A840
G2324	U2123	G1989	G1842	C1600	G1494	A1401	G1273	C1157	A1094	U1010	G933	G845
G2325	U2125	U1990	A1843	U1602	A1495	G1404	A1274	A1166	G1095	A1014	G934	C846
G2326	C2126	U1996	A1867	A1603	U1496	G1405	C1275	A1167	G1096	A1015	U935	G849
G2327	C2127	U1997	A1868	A1604	U1497	C1406	G1277	A1168	A1097	G1016	U936	U850
G2328	U2128	U2005	G1871	C1605	A1500	G1411	G1285	G1171	U1100	A1023	C939	U851
G2329	G2129	G2006	G1872	A1606	A1501	U1415	U1286	U1172	U1101	C1024	A941	C852
G2330	A2130	U2007	G1881	A1612	G1502	U1416	G1287	A1173	G1102	C1025	A942	U853
G2331	U2132	U2007	G1882	A1613	U1503	G1417	A1288	C1174	G1103	C1026	U943	C854
G2332	G2133	A2011	G1886	G1614	G1504	G1417	G1289	C1175	C1104	G1027	U944	A860
G2333	C2134	U2025	G1887	A1615	U1507	A1420	A1290	G1178	U1106	G1028	C945	A860
G2334	G2143	G2035	G1888	A1616	G1508	A1421	U1292	G1179	A1107	G1029	A946	U867
G2335	C2144	U2036	G1889	A1630	U1509	C1422	G1293	C1180	G1108	A1030	A948	U868
G2336	U2145	G2043	G1890	A1632	C1510	G1424	A1302	A1182	A1109	C1032	U949	G872
G2337	G2146	A2044	U1913	A1633	G1519	G1425	A1303	A1183	G1111	A1033	A951	U874
G2338	A2147	A2045	G1917	A1634	G1521	U1431	G1307	C1192	G1112	A1036	A952	A875
G2339	G2148	A2046	G1918	C1635	G1525	U1432	U1308	C1193	G1113	G1037	C955	U885
G2340	G2149	G2047	G1919	A1636	U1645	U1436	G1309	C1194	G1114	U1038	C956	U886
G2341	A2150	U2048	G1920	U1645	G1532	U1436	A1310	A1195	C1115	U1039	G957	U887
G2342	G2154	G2049	A1926	U1646	A1646	A1439	A1311	A1196	C1116	C1045	A958	A888
G2343	G2252	C2253	G2254	A2255	G2256	U2259	G1319	C1208	C1118	A1048	U960	G889
G2344	G2253	C2254	A2255	G2256	U2259	G2260	A1322	A1209	C1119	A1049	G961	A890
G2345	G2254	A2255	G2256	U2259	G2260	C2361	A1322	A1212	U1121	A1050	C962	A891
G2346	G2255	A2256	U2259	G2260	C2361	U2261	A1322	U1213	U1122	A1051	C963	U892



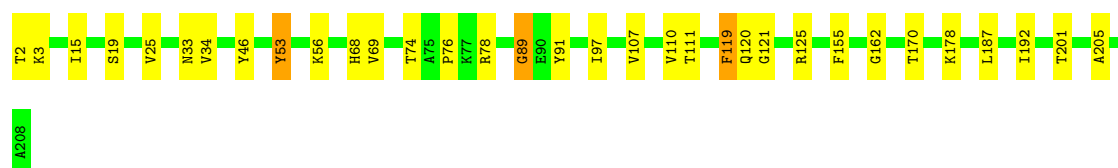
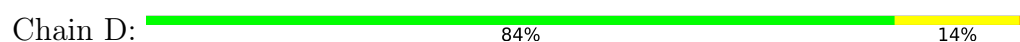
- Molecule 23: 5S rRNA



- Molecule 24: 50S ribosomal protein L2



- Molecule 25: 50S ribosomal protein L3



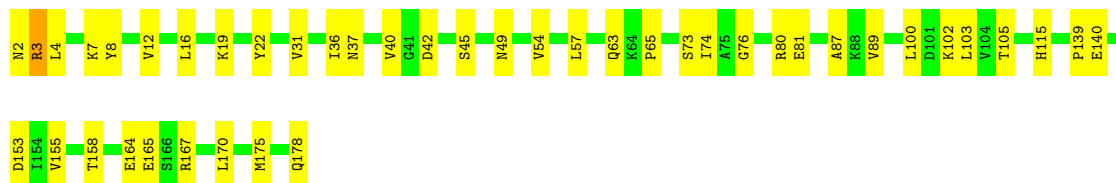
- Molecule 26: 50S ribosomal protein L4





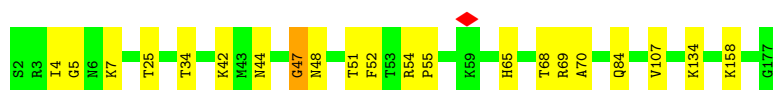
- Molecule 27: 50S ribosomal protein L5

Chain F: 76% 24%



- Molecule 28: 50S ribosomal protein L6

Chain G: 88% 11%



- Molecule 29: 50S ribosomal protein L13

Chain K: 84% 15%



- Molecule 30: 50S ribosomal protein L14

Chain L: 93% 7%



- Molecule 31: 50S ribosomal protein L15

Chain M: 85% 14%



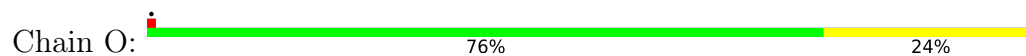
- Molecule 32: 50S ribosomal protein L16

Chain N: 7% 74% 23%

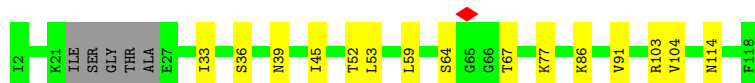
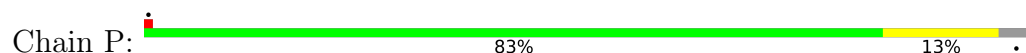




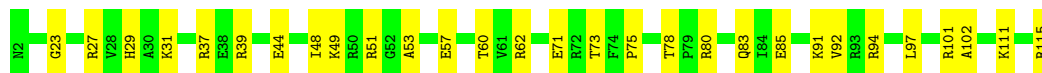
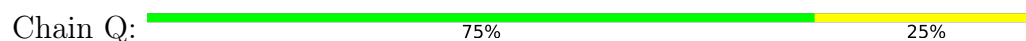
- Molecule 33: 50S ribosomal protein L17



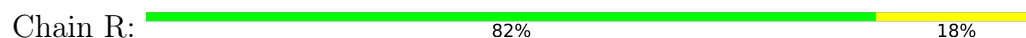
- Molecule 34: 50S ribosomal protein L18



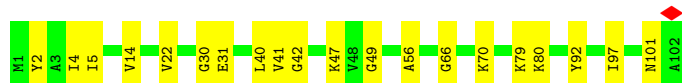
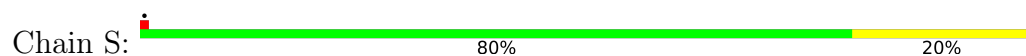
- Molecule 35: 50S ribosomal protein L19



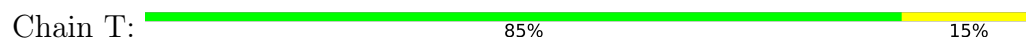
- Molecule 36: 50S ribosomal protein L20



- Molecule 37: 50S ribosomal protein L21

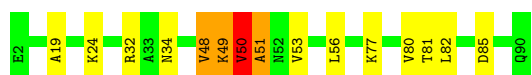


- Molecule 38: 50S ribosomal protein L22



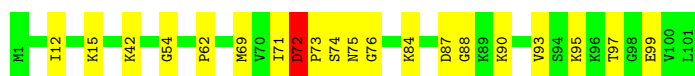
- Molecule 39: 50S ribosomal protein L23

Chain U:  83% 12% . .



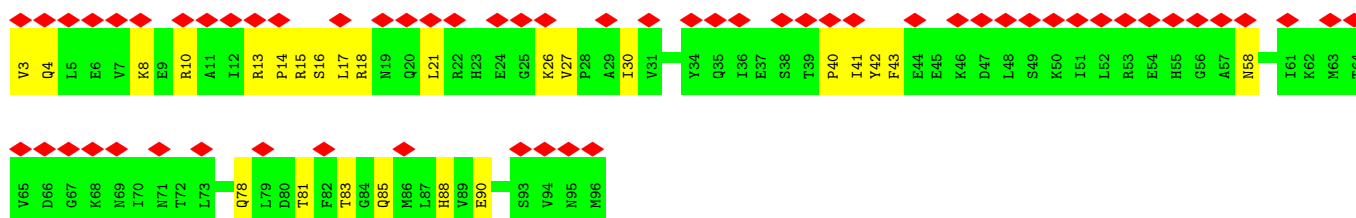
- Molecule 40: 50S ribosomal protein L24

Chain V:  80% 19% .



- Molecule 41: 50S ribosomal protein L25

Chain W:  63% 73% 27%



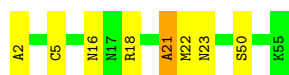
- Molecule 42: 50S ribosomal protein L27

Chain X:  89% 11%



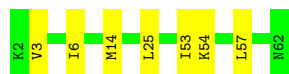
- Molecule 43: 50S ribosomal protein L28

Chain Y:  85% 13% .



- Molecule 44: 50S ribosomal protein L29

Chain Z:  89% 11%

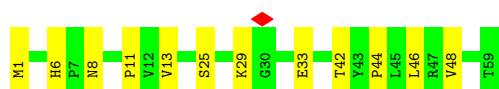
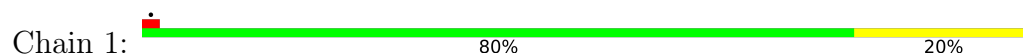


- Molecule 45: 50S ribosomal protein L30

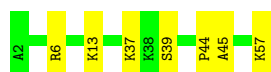
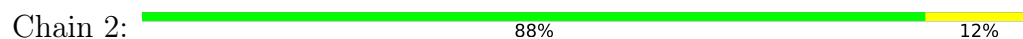
Chain 0:  79% 21%



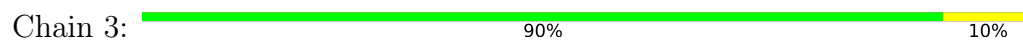
- Molecule 46: 50S ribosomal protein L31 type B



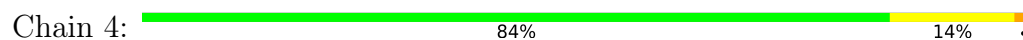
- Molecule 47: 50S ribosomal protein L32



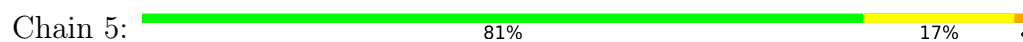
- Molecule 48: 50S ribosomal protein L33



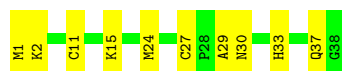
- Molecule 49: 50S ribosomal protein L34



- Molecule 50: 50S ribosomal protein L35



- Molecule 51: 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	35466	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	2.098	Depositor
Minimum map value	-0.790	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.092	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 [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	0.60	6/36545 (0.0%)	0.45	2/56995 (0.0%)
2	c	0.29	0/1635	0.57	0/2197
3	d	2.50	1/1650 (0.1%)	0.70	2/2217 (0.1%)
4	e	0.33	0/1217	0.62	0/1641
5	f	0.30	0/807	0.54	0/1087
6	g	0.26	0/1249	0.59	1/1682 (0.1%)
7	h	0.32	0/1054	0.61	0/1417
8	i	0.27	0/1003	0.64	0/1343
9	j	0.29	0/812	0.69	0/1093
10	k	0.30	0/878	0.61	2/1185 (0.2%)
11	l	0.31	0/1082	0.74	0/1453
12	m	0.26	0/890	0.63	0/1195
13	n	0.28	0/504	0.65	0/669
14	o	0.32	0/751	0.62	0/1001
15	p	0.32	0/720	0.66	0/966
16	q	0.28	0/689	0.59	0/920
17	r	0.32	0/544	0.63	0/728
18	s	0.26	0/650	0.58	0/872
19	t	0.25	0/612	0.58	0/818
20	u	0.31	0/1813	0.46	0/2823
21	v	0.26	0/109	1.39	3/166 (1.8%)
22	A	0.46	0/69780	0.49	3/108830 (0.0%)
23	B	0.38	0/2769	0.53	1/4311 (0.0%)
24	C	0.54	0/2145	0.80	1/2881 (0.0%)
25	D	0.52	0/1599	0.79	0/2145
26	E	0.45	0/1594	0.66	0/2156
27	F	0.31	0/1409	0.64	0/1894
28	G	0.35	0/1362	0.65	0/1833
29	K	0.52	0/1148	0.72	0/1548
30	L	0.51	0/928	0.74	1/1245 (0.1%)
31	M	0.45	0/1102	0.85	2/1470 (0.1%)
32	N	0.46	0/1141	0.84	2/1519 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	O	0.52	0/985	0.87	3/1320 (0.2%)
34	P	0.40	0/870	0.66	0/1163
35	Q	0.49	0/935	0.69	0/1256
36	R	0.54	0/963	0.78	0/1280
37	S	0.46	0/793	0.72	0/1063
38	T	0.47	0/857	0.73	0/1156
39	U	0.46	0/727	0.87	4/972 (0.4%)
40	V	0.39	0/769	0.81	3/1027 (0.3%)
41	W	0.27	0/769	0.70	0/1034
42	X	0.51	0/576	0.68	0/770
43	Y	0.40	0/431	0.67	0/574
44	Z	0.37	0/505	0.61	0/672
45	0	0.46	0/434	0.66	0/583
46	1	0.29	0/486	0.72	0/661
47	2	0.51	0/434	0.66	0/575
48	3	0.36	0/423	0.57	0/563
49	4	0.52	0/377	0.71	0/491
50	5	0.47	0/527	0.77	0/687
51	6	0.48	0/309	0.65	0/409
All	All	0.54	7/152361 (0.0%)	0.54	30/228556 (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
2	c	0	1
3	d	0	3
11	l	0	2
18	s	0	1
19	t	0	1
24	C	0	3
25	D	0	2
26	E	0	1
27	F	0	1
28	G	0	1
29	K	0	1
31	M	0	2
32	N	0	5
33	O	0	1
35	Q	0	1

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	S	0	1
40	V	0	3
42	X	0	1
43	Y	0	1
46	1	0	1
49	4	0	1
All	All	0	34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	2	SER	CA-CB	101.01	3.55	1.53
1	a	561	A	C6-N1	41.74	2.19	1.35
1	a	561	A	N3-C4	40.47	2.15	1.34
1	a	561	A	C2-N3	40.27	2.14	1.33
1	a	561	A	N1-C2	40.13	2.14	1.34

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	v	18	U	O3'-P-O5'	-15.42	80.87	104.00
3	d	2	SER	CB-CA-C	10.32	129.71	110.10
3	d	2	SER	CA-CB-OG	8.02	127.14	111.10
39	U	49	LYS	CA-C-N	7.45	135.37	121.97
39	U	49	LYS	C-N-CA	7.45	135.37	121.97

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	22	TRP	Peptide
3	d	187	TYR	Peptide
3	d	188	PRO	Peptide
3	d	189	GLU	Peptide
11	l	37	ASN	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32646	0	16441	355	0
2	c	1610	0	1653	19	0
3	d	1620	0	1641	43	0
4	e	1204	0	1280	17	0
5	f	795	0	789	6	0
6	g	1229	0	1259	20	0
7	h	1041	0	1092	14	0
8	i	990	0	1035	24	0
9	j	800	0	846	13	0
10	k	863	0	882	8	0
11	l	1065	0	1133	28	0
12	m	884	0	932	13	0
13	n	492	0	509	8	0
14	o	741	0	756	9	0
15	p	708	0	746	29	0
16	q	681	0	719	13	0
17	r	537	0	572	6	0
18	s	634	0	649	12	0
19	t	610	0	640	13	0
20	u	1623	0	821	25	0
21	v	100	0	52	0	0
22	A	62301	0	31306	415	0
23	B	2478	0	1246	24	0
24	C	2113	0	2195	39	0
25	D	1578	0	1658	21	0
26	E	1573	0	1617	19	0
27	F	1391	0	1449	28	0
28	G	1344	0	1373	15	0
29	K	1129	0	1167	16	0
30	L	921	0	981	4	0
31	M	1094	0	1145	15	0
32	N	1118	0	1180	20	0
33	O	978	0	1010	17	0
34	P	862	0	884	7	0
35	Q	923	0	977	22	0
36	R	950	0	1009	17	0
37	S	783	0	823	13	0
38	T	848	0	901	12	0
39	U	720	0	772	11	0
40	V	762	0	821	14	0
41	W	758	0	780	20	0
42	X	571	0	575	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	Y	425	0	460	5	0
44	Z	504	0	538	5	0
45	0	434	0	470	9	0
46	1	472	0	440	8	0
47	2	428	0	445	6	0
48	3	419	0	435	4	0
49	4	374	0	424	5	0
50	5	521	0	576	12	0
51	6	304	0	338	7	0
52	2	1	0	0	0	0
52	3	1	0	0	0	0
52	6	1	0	0	0	0
52	n	1	0	0	0	0
All	All	139953	0	92442	1283	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 1283 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:561:A:C4	1:a:561:A:C5	2.07	1.32
1:a:561:A:C5	1:a:561:A:C6	2.19	1.31
22:A:2818:G:C2	22:A:2818:G:C4	2.20	1.25
1:a:561:A:C2	1:a:561:A:N1	2.14	1.16
1:a:561:A:C4	1:a:561:A:N3	2.15	1.15

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	c	202/204 (99%)	178 (88%)	24 (12%)	0	100	100
3	d	199/201 (99%)	169 (85%)	30 (15%)	0	100	100
4	e	161/163 (99%)	142 (88%)	19 (12%)	0	100	100
5	f	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
6	g	152/154 (99%)	137 (90%)	15 (10%)	0	100	100
7	h	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
8	i	126/128 (98%)	109 (86%)	16 (13%)	1 (1%)	16	50
9	j	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
10	k	115/117 (98%)	95 (83%)	20 (17%)	0	100	100
11	l	134/136 (98%)	103 (77%)	30 (22%)	1 (1%)	18	52
12	m	110/112 (98%)	85 (77%)	25 (23%)	0	100	100
13	n	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
14	o	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
15	p	87/89 (98%)	72 (83%)	15 (17%)	0	100	100
16	q	81/83 (98%)	67 (83%)	14 (17%)	0	100	100
17	r	64/66 (97%)	52 (81%)	12 (19%)	0	100	100
18	s	76/78 (97%)	59 (78%)	17 (22%)	0	100	100
19	t	79/81 (98%)	70 (89%)	9 (11%)	0	100	100
24	C	269/275 (98%)	241 (90%)	28 (10%)	0	100	100
25	D	205/207 (99%)	178 (87%)	27 (13%)	0	100	100
26	E	204/206 (99%)	174 (85%)	30 (15%)	0	100	100
27	F	175/177 (99%)	150 (86%)	25 (14%)	0	100	100
28	G	172/176 (98%)	141 (82%)	29 (17%)	2 (1%)	10	42
29	K	141/145 (97%)	124 (88%)	17 (12%)	0	100	100
30	L	120/122 (98%)	104 (87%)	16 (13%)	0	100	100
31	M	144/146 (99%)	102 (71%)	40 (28%)	2 (1%)	9	38
32	N	139/141 (99%)	115 (83%)	24 (17%)	0	100	100
33	O	121/123 (98%)	96 (79%)	25 (21%)	0	100	100
34	P	108/117 (92%)	92 (85%)	16 (15%)	0	100	100
35	Q	110/114 (96%)	101 (92%)	9 (8%)	0	100	100
36	R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
37	S	98/102 (96%)	89 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	T	110/112 (98%)	98 (89%)	12 (11%)	0	100	100
39	U	87/89 (98%)	68 (78%)	18 (21%)	1 (1%)	11	44
40	V	98/101 (97%)	71 (72%)	24 (24%)	3 (3%)	3	24
41	W	92/94 (98%)	73 (79%)	18 (20%)	1 (1%)	11	44
42	X	74/76 (97%)	64 (86%)	10 (14%)	0	100	100
43	Y	52/54 (96%)	42 (81%)	10 (19%)	0	100	100
44	Z	59/61 (97%)	56 (95%)	3 (5%)	0	100	100
45	0	54/58 (93%)	50 (93%)	4 (7%)	0	100	100
46	1	57/59 (97%)	42 (74%)	15 (26%)	0	100	100
47	2	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
48	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
49	4	42/44 (96%)	37 (88%)	5 (12%)	0	100	100
50	5	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	36
51	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5097/5211 (98%)	4343 (85%)	742 (15%)	12 (0%)	44	73

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	G	48	ASN
40	V	73	PRO
8	i	41	HIS
28	G	47	GLY
31	M	95	VAL

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	111 (99%)	1 (1%)	70	76
8	i	101/101 (100%)	100 (99%)	1 (1%)	68	75
9	j	90/90 (100%)	90 (100%)	0	100	100
10	k	91/91 (100%)	90 (99%)	1 (1%)	65	74
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%)	77 (98%)	2 (2%)	42	63
16	q	76/76 (100%)	76 (100%)	0	100	100
17	r	57/57 (100%)	57 (100%)	0	100	100
18	s	68/68 (100%)	67 (98%)	1 (2%)	57	71
19	t	62/62 (100%)	62 (100%)	0	100	100
24	C	225/225 (100%)	225 (100%)	0	100	100
25	D	169/170 (99%)	167 (99%)	2 (1%)	63	73
26	E	171/172 (99%)	170 (99%)	1 (1%)	78	80
27	F	153/154 (99%)	153 (100%)	0	100	100
28	G	146/146 (100%)	145 (99%)	1 (1%)	76	78
29	K	122/122 (100%)	121 (99%)	1 (1%)	73	77
30	L	98/98 (100%)	98 (100%)	0	100	100
31	M	111/112 (99%)	110 (99%)	1 (1%)	70	76
32	N	112/112 (100%)	109 (97%)	3 (3%)	39	62
33	O	104/105 (99%)	103 (99%)	1 (1%)	68	75
34	P	86/91 (94%)	84 (98%)	2 (2%)	44	64
35	Q	97/97 (100%)	97 (100%)	0	100	100
36	R	94/94 (100%)	94 (100%)	0	100	100
37	S	83/83 (100%)	82 (99%)	1 (1%)	63	73
38	T	94/95 (99%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	U	80/80 (100%)	78 (98%)	2 (2%)	42	63
40	V	84/85 (99%)	84 (100%)	0	100	100
41	W	85/85 (100%)	85 (100%)	0	100	100
42	X	60/61 (98%)	60 (100%)	0	100	100
43	Y	47/47 (100%)	47 (100%)	0	100	100
44	Z	55/55 (100%)	54 (98%)	1 (2%)	51	69
45	0	49/49 (100%)	49 (100%)	0	100	100
46	1	55/55 (100%)	55 (100%)	0	100	100
47	2	46/46 (100%)	46 (100%)	0	100	100
48	3	49/49 (100%)	49 (100%)	0	100	100
49	4	39/39 (100%)	39 (100%)	0	100	100
50	5	51/51 (100%)	51 (100%)	0	100	100
51	6	35/35 (100%)	35 (100%)	0	100	100
All	All	4358/4371 (100%)	4336 (100%)	22 (0%)	78	81

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	N	94	VAL
34	P	103	ARG
34	P	91	VAL
37	S	22	VAL
25	D	53	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
39	U	52	ASN
48	3	26	ASN
40	V	49	GLN
43	Y	23	ASN
51	6	30	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1520/1523 (99%)	414 (27%)	0
20	u	75/76 (98%)	26 (34%)	0
21	v	4/5 (80%)	1 (25%)	0
22	A	2900/2903 (99%)	714 (24%)	21 (0%)
23	B	115/116 (99%)	38 (33%)	3 (2%)
All	All	4614/4623 (99%)	1193 (25%)	24 (0%)

5 of 1193 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A
1	a	6	G
1	a	7	A
1	a	19	G
1	a	24	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	A	1431	A
22	A	1604	A
22	A	1585	U
22	A	1605	C
22	A	890	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	a	3
22	A	2

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	13.85
1	a	71:U	O3'	97:G	P	13.64
1	A	1579:U	O3'	1583:A	P	5.91
1	a	465:G	O3'	466:A	P	5.38
1	a	519:C	O3'	520:G	P	3.31

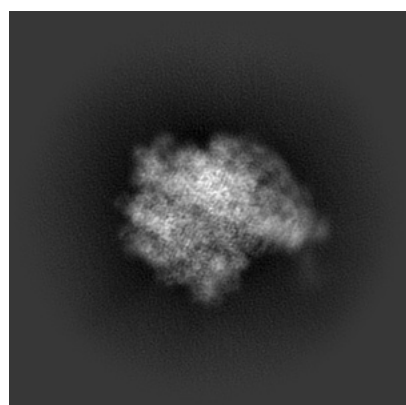
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0656. These allow visual inspection of the internal detail of the map and identification of artifacts.

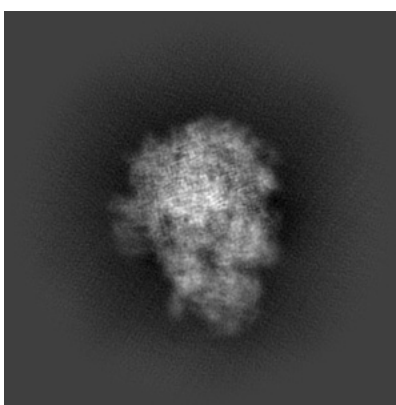
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

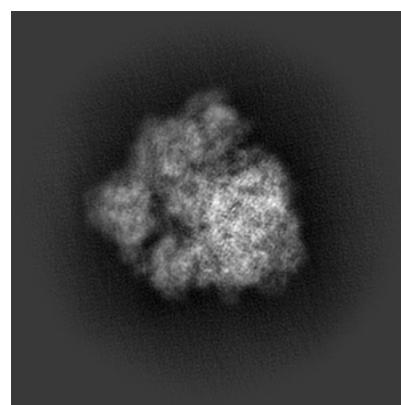
6.1.1 Primary map



X



Y

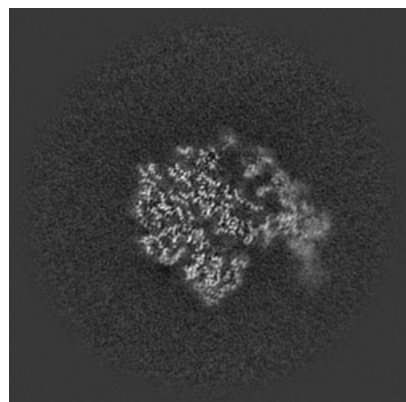


Z

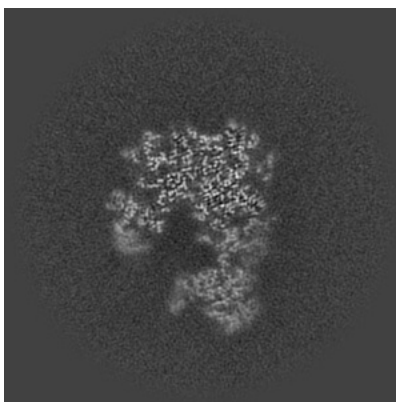
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

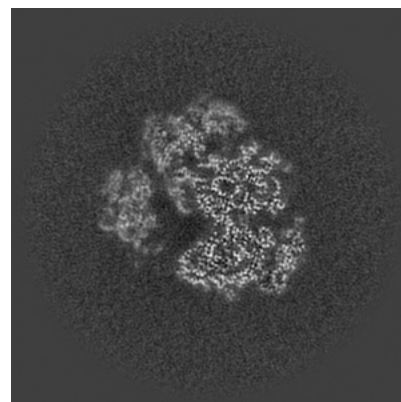
6.2.1 Primary map



X Index: 220



Y Index: 220

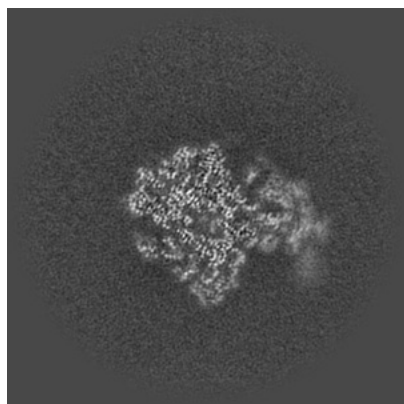


Z Index: 220

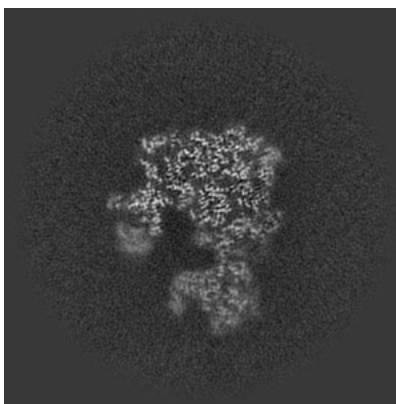
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

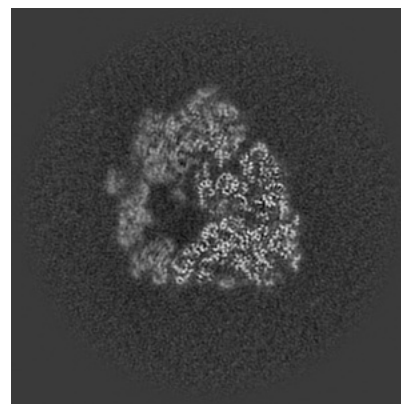
6.3.1 Primary map



X Index: 226



Y Index: 228

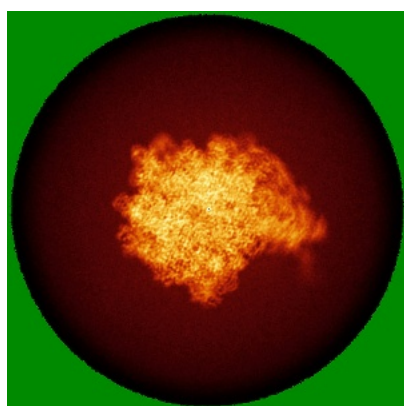


Z Index: 209

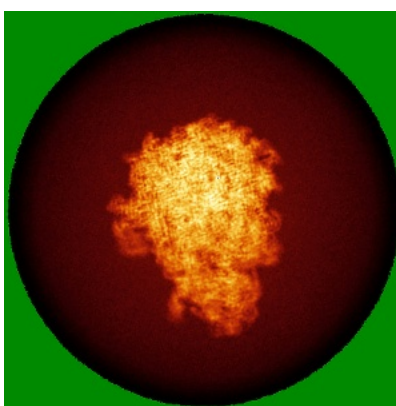
The images above show the largest variance slices of the map in three orthogonal directions.

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

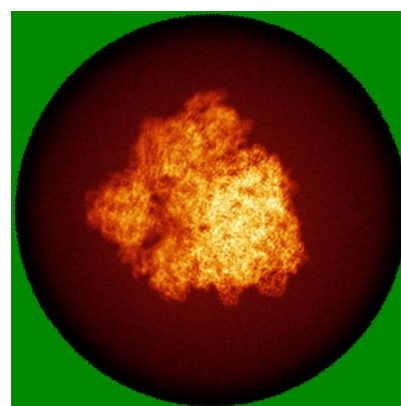
6.4.1 Primary map



X



Y

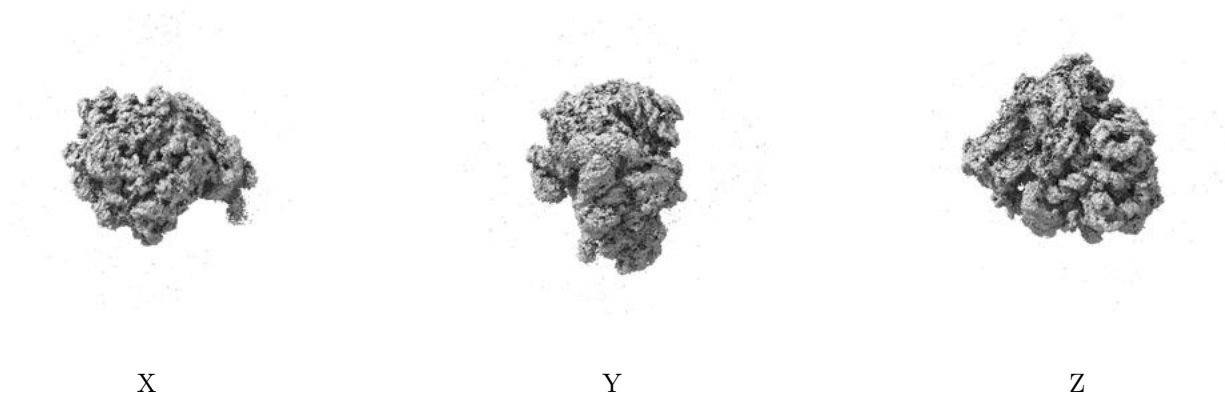


Z

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 [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.

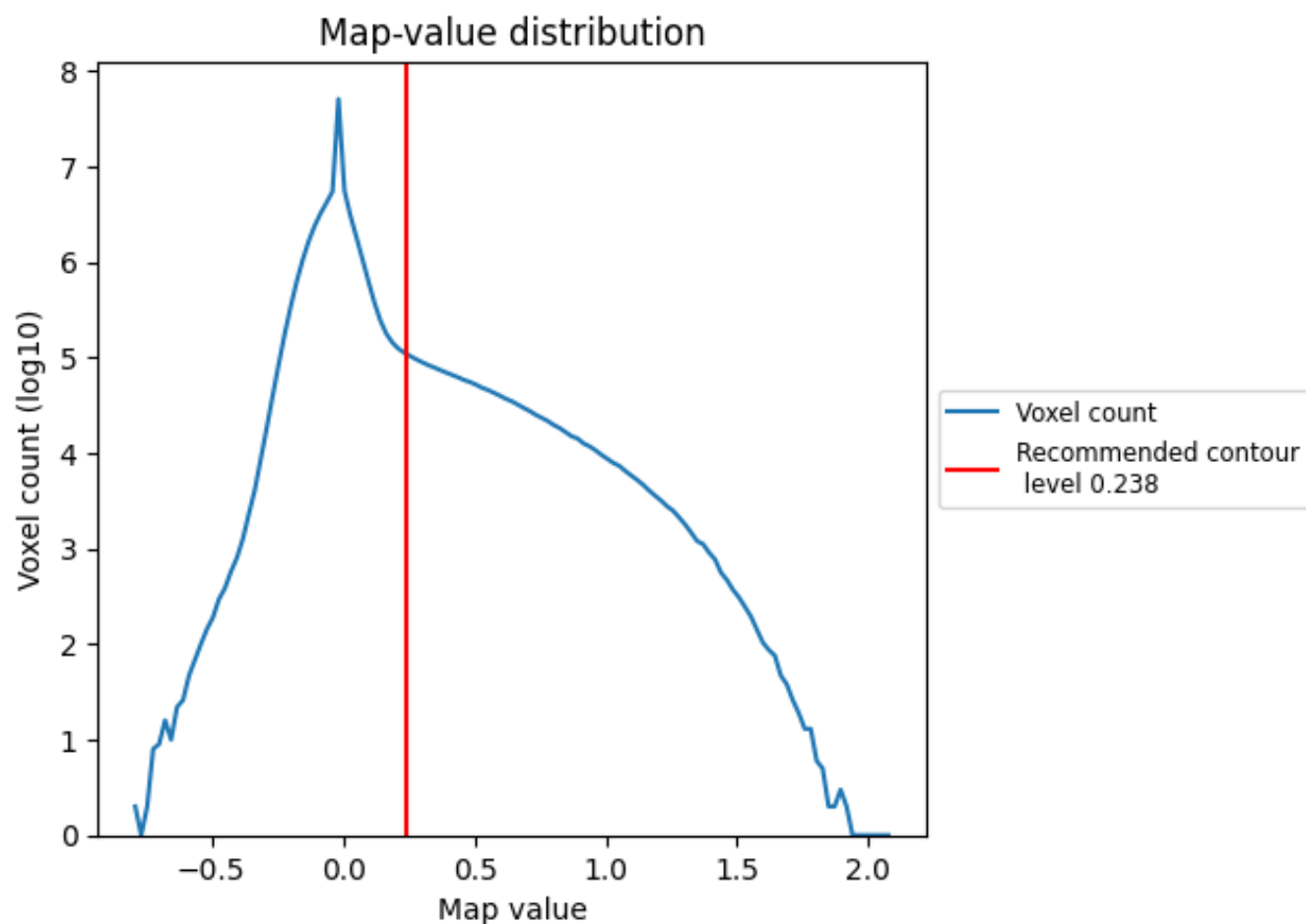
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

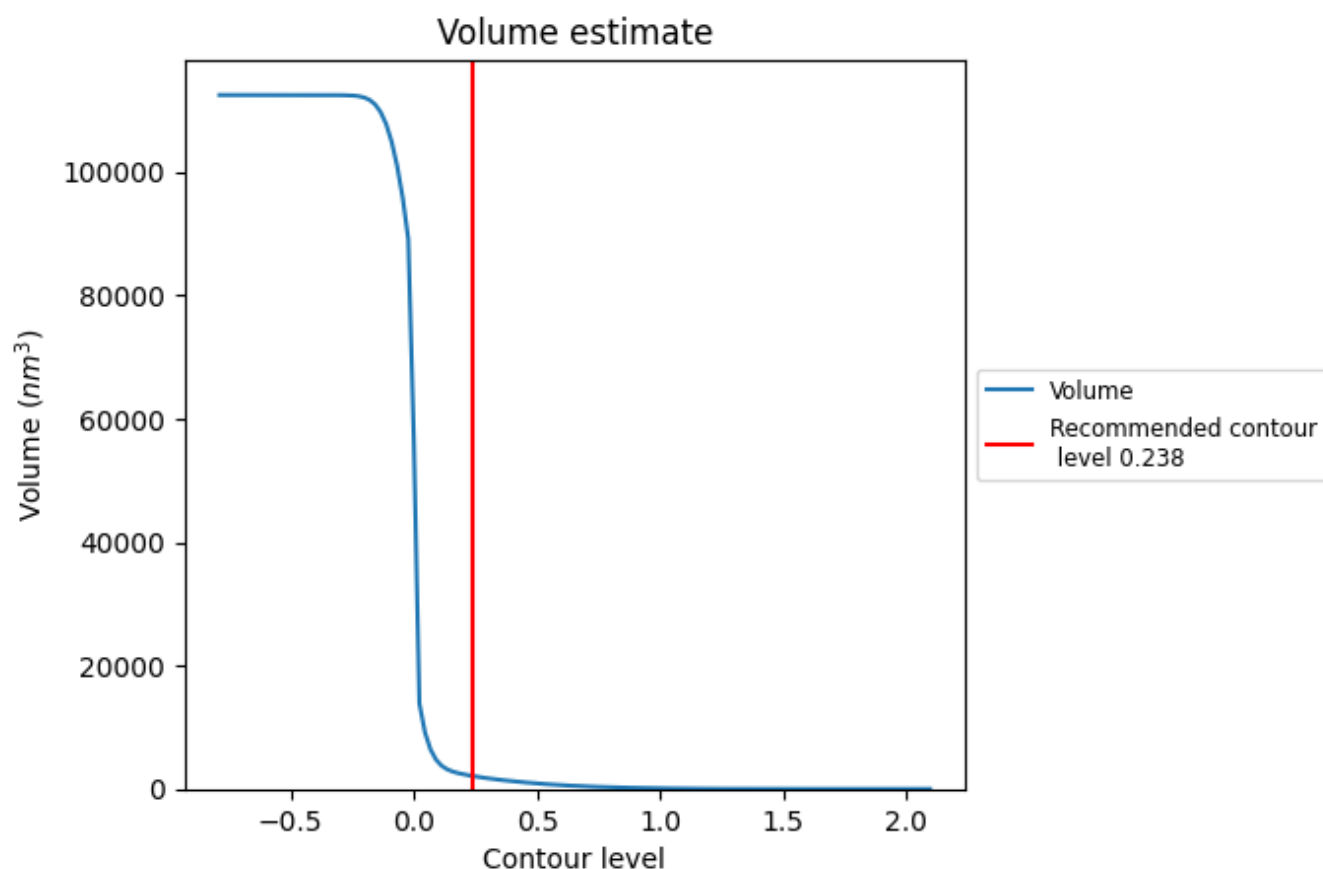
This section contains the results of statistical analysis of the map.

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.

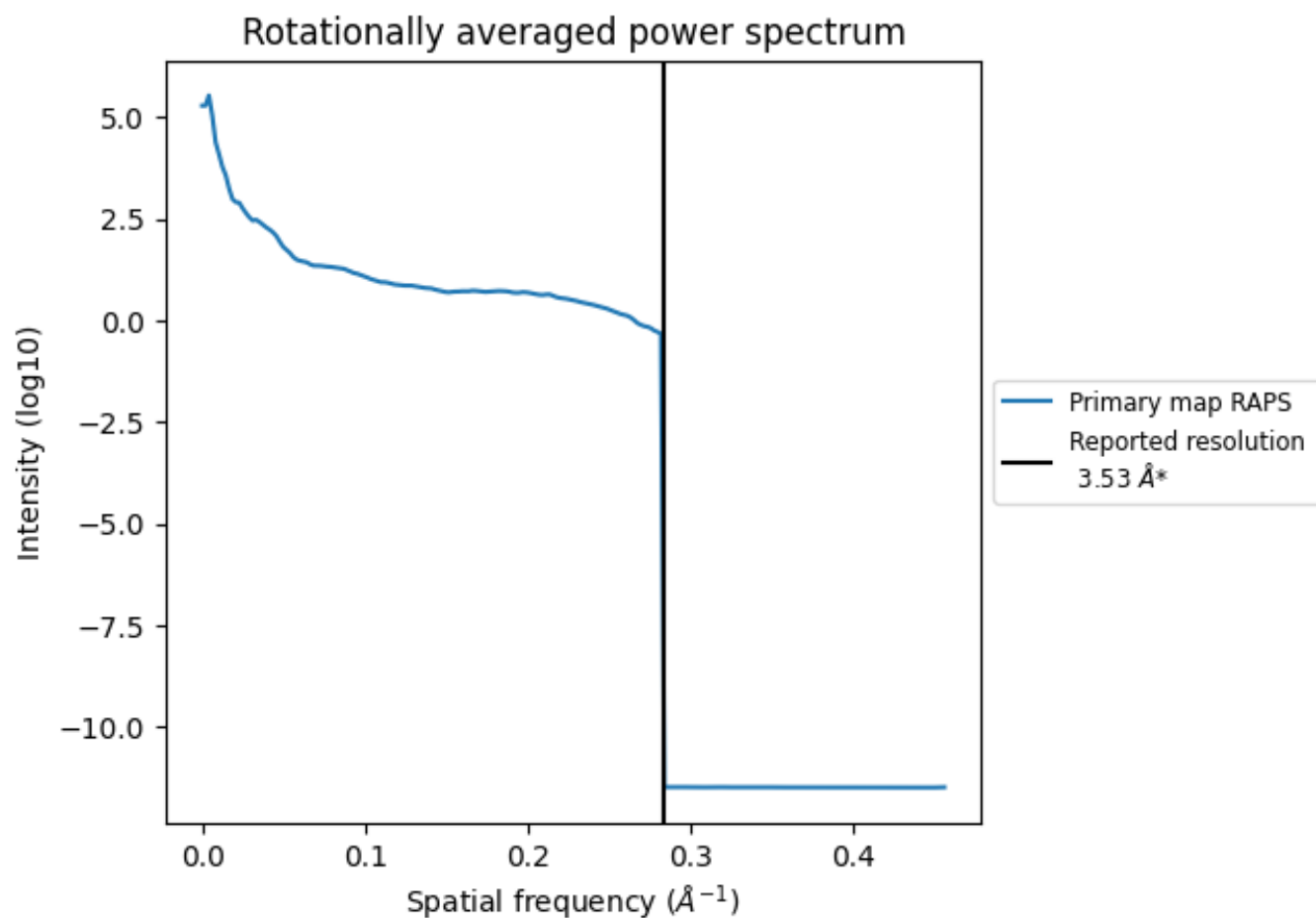
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2103 nm³; this corresponds to an approximate mass of 1899 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 0.283 Å⁻¹

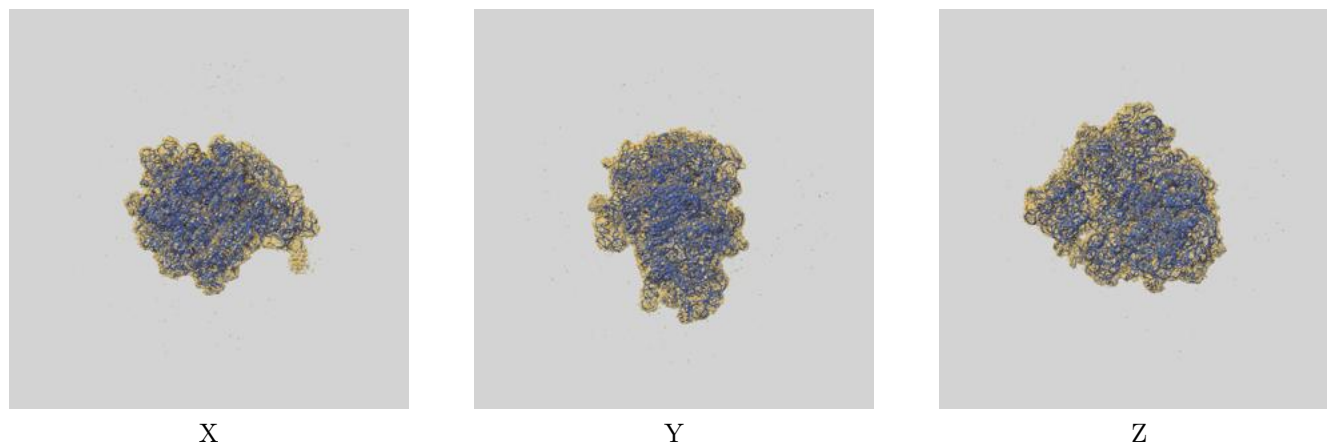
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

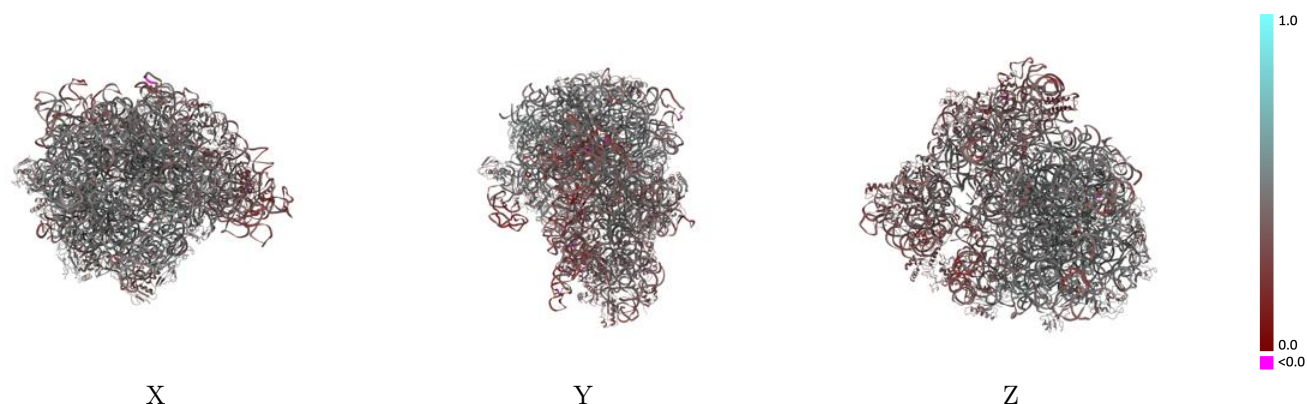
This section contains information regarding the fit between EMDB map EMD-0656 and PDB model 6O8W. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



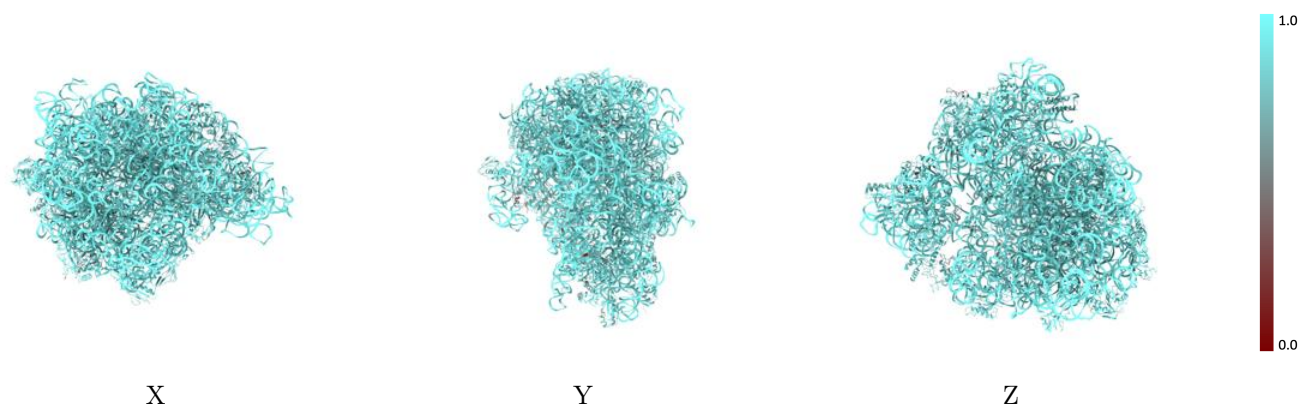
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



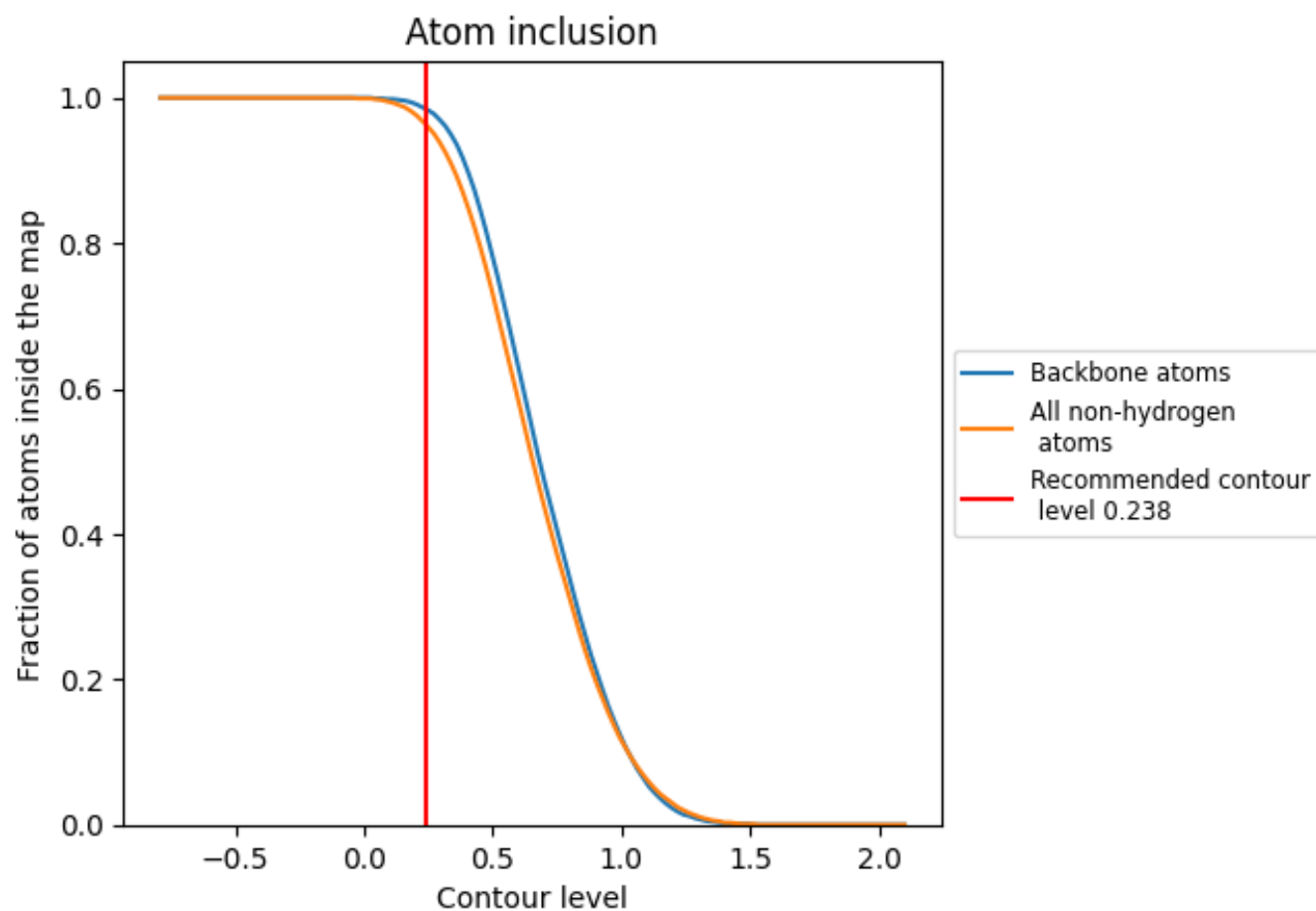
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.9640	 0.4220
0	 0.9250	 0.4750
1	 0.9010	 0.2830
2	 0.9570	 0.4810
3	 0.9360	 0.4750
4	 0.9290	 0.4550
5	 0.9330	 0.4840
6	 0.9700	 0.4810
A	 0.9920	 0.4520
B	 0.9940	 0.4030
C	 0.9310	 0.4740
D	 0.9390	 0.4820
E	 0.9420	 0.4600
F	 0.8580	 0.3350
G	 0.9060	 0.4000
K	 0.9350	 0.4660
L	 0.9130	 0.4900
M	 0.9500	 0.4780
N	 0.8220	 0.4190
O	 0.9340	 0.4600
P	 0.9080	 0.3870
Q	 0.9130	 0.4650
R	 0.9120	 0.4460
S	 0.9230	 0.4770
T	 0.9460	 0.4730
U	 0.9300	 0.4470
V	 0.9070	 0.4290
W	 0.3690	 0.3130
X	 0.9400	 0.4890
Y	 0.9710	 0.4960
Z	 0.9040	 0.4170
a	 0.9910	 0.3860
c	 0.9000	 0.3740
d	 0.8350	 0.3200
e	 0.9020	 0.4160



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Chain	Atom inclusion	Q-score
f	 0.8760	 0.4240
g	 0.8500	 0.3170
h	 0.9150	 0.3940
i	 0.9400	 0.3680
j	 0.8680	 0.3610
k	 0.8820	 0.4040
l	 0.8670	 0.3440
m	 0.8920	 0.3050
n	 0.9580	 0.3810
o	 0.8850	 0.3800
p	 0.9030	 0.3150
q	 0.8540	 0.3660
r	 0.8790	 0.3940
s	 0.9000	 0.2810
t	 0.8380	 0.2850
u	 0.9900	 0.3890
v	 0.9800	 0.4700