



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:22 PM UTC

PDB ID : 6O8Y / pdb_00006o8y
EMDB ID : EMD-0658
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class03
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 4.14 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:

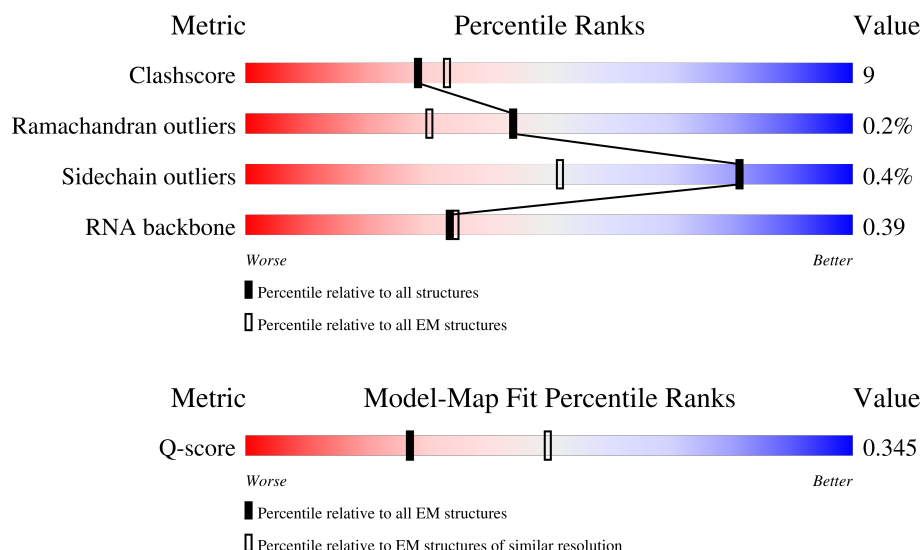
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.14 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.



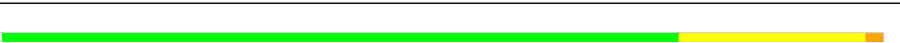
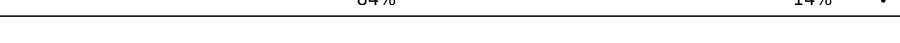
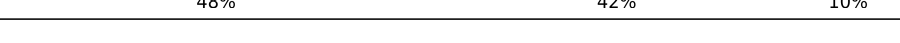
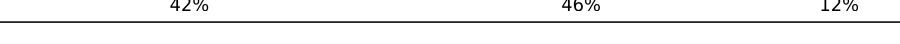
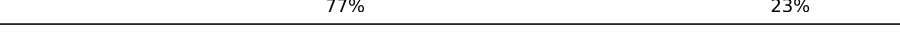
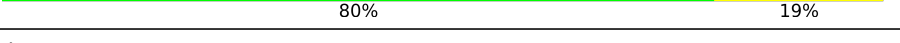
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5577 (3.64 - 4.64)

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	13% 46% 43% 11%
2	c	204	81% 19%
3	d	201	75% 24% .

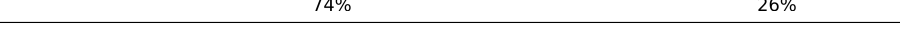
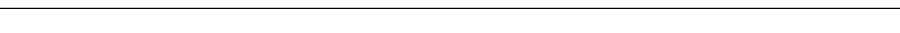
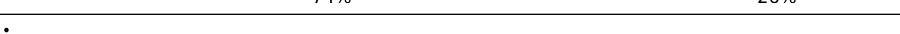
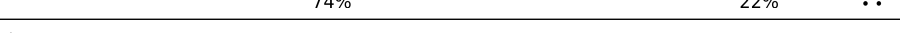
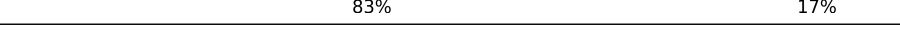
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Mol	Chain	Length	Quality of chain
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	A	2903	
21	B	116	
22	C	275	
23	D	207	
24	E	206	
25	F	177	
26	G	176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

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Mol	Chain	Length	Quality of chain
29	M	146	 78%20%..
30	N	141	 8%74%26%
31	O	123	 74%24%. .
32	P	117	 73%26%. .
33	Q	114	 74%26%
34	R	118	 77%20%. .
35	S	102	 74%26%
36	T	112	 88%12%. .
37	U	89	 74%22%..
38	V	101	 73%25%..
39	W	94	 63%83%17%
40	X	76	 68%30%. .
41	Y	54	 83%17%
42	Z	61	 84%16%
43	0	58	 78%22%
44	1	60	 68%32%
45	2	56	 68%32%
46	3	49	 73%27%
47	4	44	 82%16%. .
48	5	64	 80%20%
49	6	38	 66%34%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 138210 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	2897	Total	C	N	O	P	0	0
			62176	27750	11434	20095	2897		

- 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	982	290	298	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F	177	Total	C	N	O	S	0	0
			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	602	190	183	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	117	Total	C	N	O	S	0	0
			898	556	175	166	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	1
			913	578	175	156	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	499	139	143	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	89	Total	C	N	O	S	0	0
			719	458	126	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	479	134	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	85	72	2		

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	60	Total	C	N	O	S	0	0
			475	302	74	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		

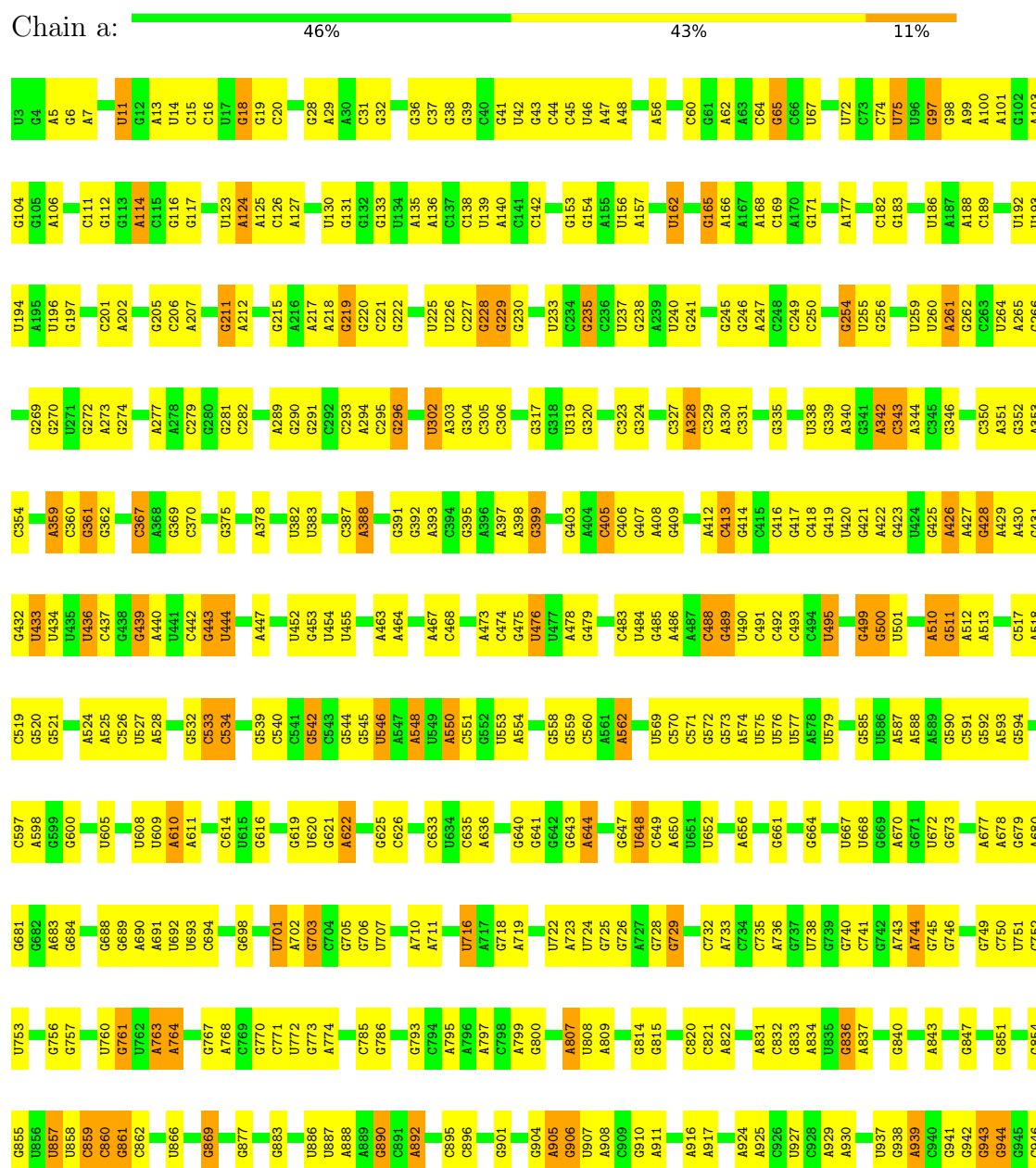
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

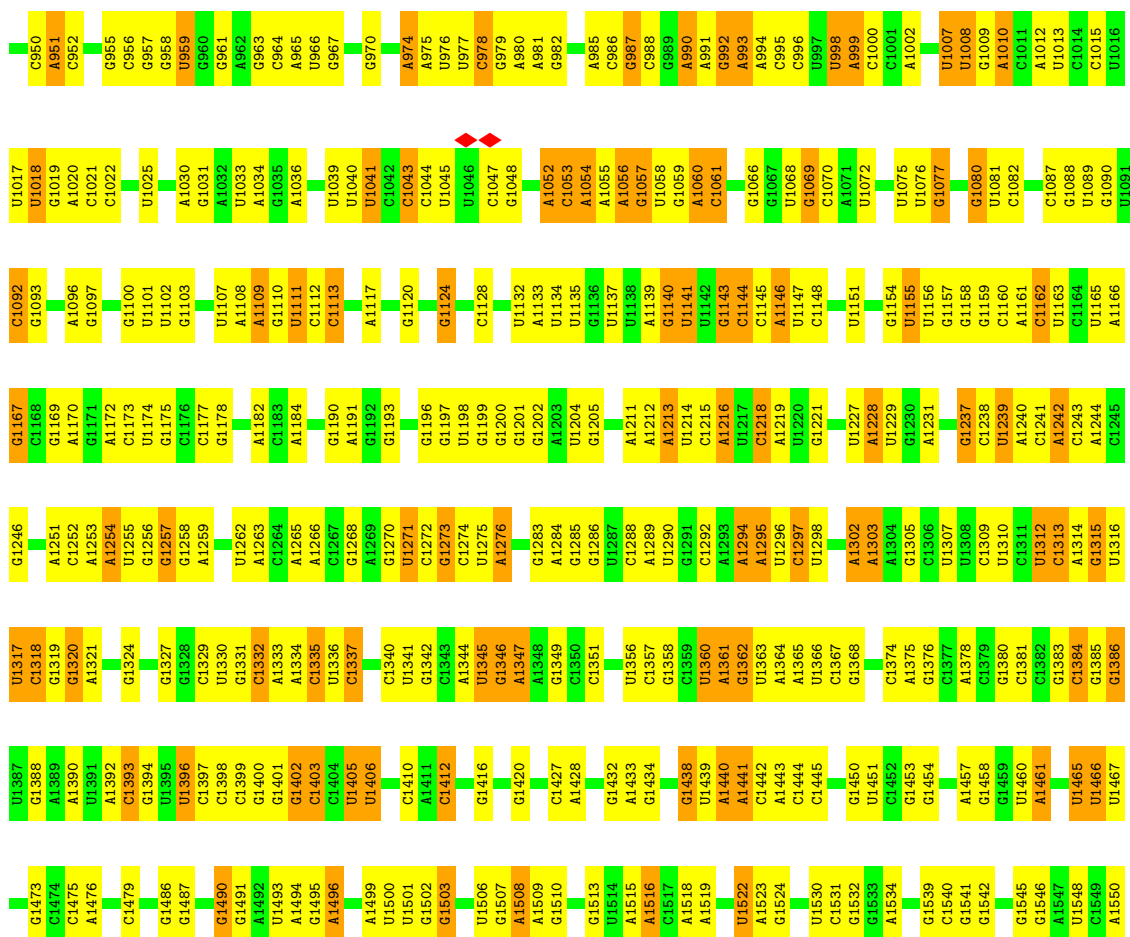
Mol	Chain	Residues	Atoms		AltConf
50	n	1	Total	Zn	0
			1	1	
50	2	1	Total	Zn	0
			1	1	
50	3	1	Total	Zn	0
			1	1	
50	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

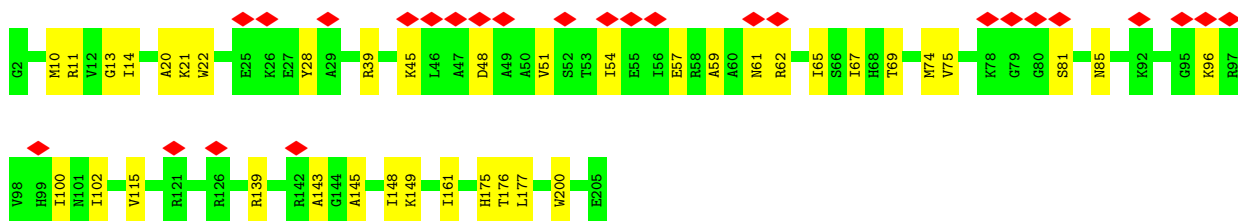
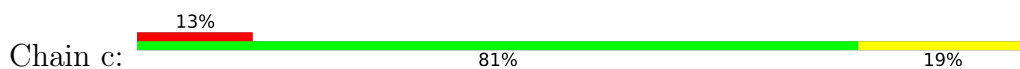
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

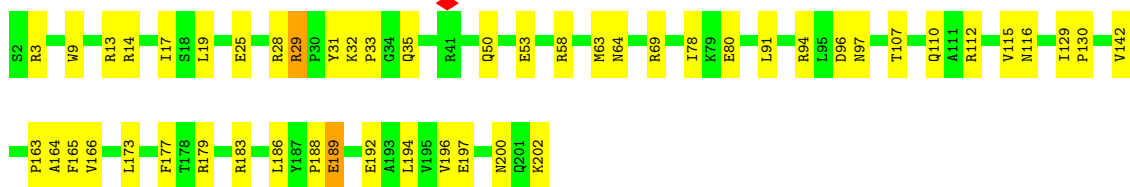




• Molecule 2: 30S ribosomal protein S3

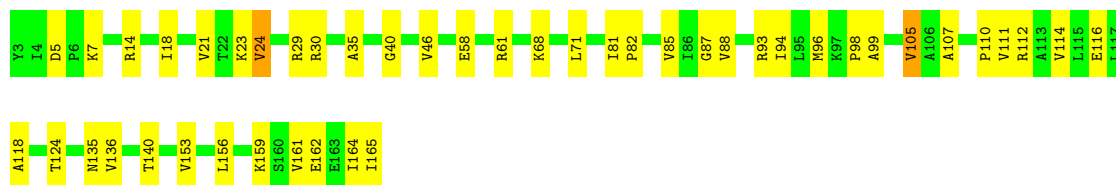


• Molecule 3: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S5

Chain e:  72% 26% .



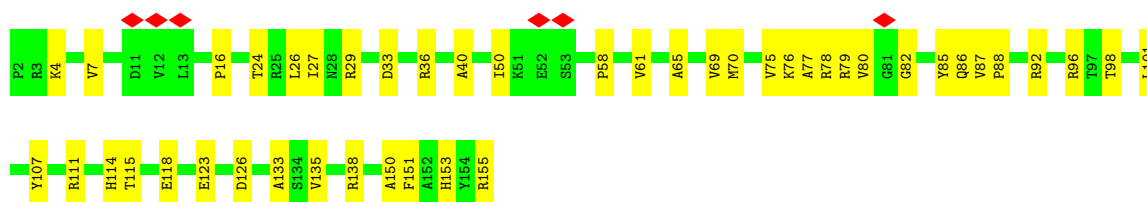
- Molecule 5: 30S ribosomal protein S6

Chain f:  70% 30%



- Molecule 6: 30S ribosomal protein S7

Chain g:  71% 29%



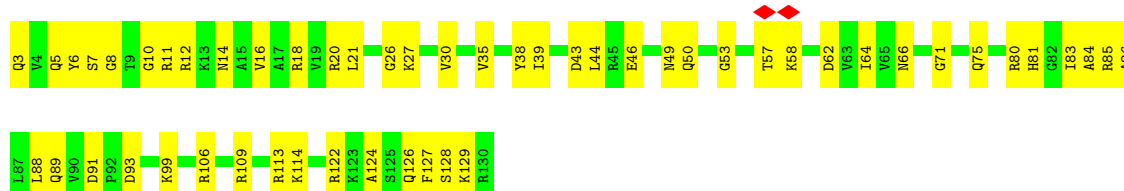
- Molecule 7: 30S ribosomal protein S8

Chain h:  78% 21% .



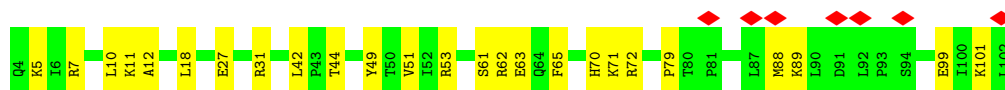
- Molecule 8: 30S ribosomal protein S9

Chain i:  59% 41%

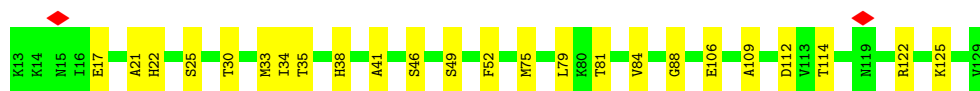
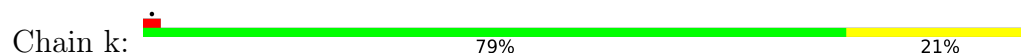


- Molecule 9: 30S ribosomal protein S10

Chain j:  7% 75% 25%



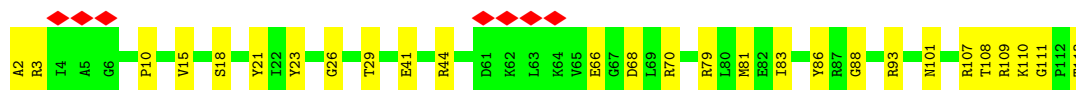
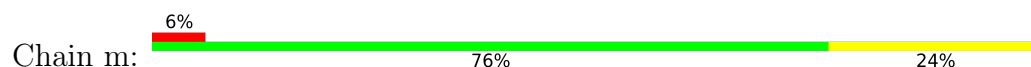
- Molecule 10: 30S ribosomal protein S11



- Molecule 11: 30S ribosomal protein S12



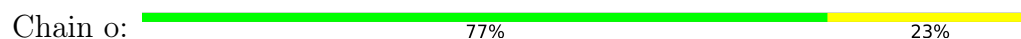
- Molecule 12: 30S ribosomal protein S13



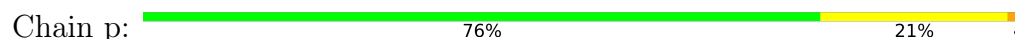
- Molecule 13: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S17



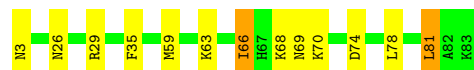
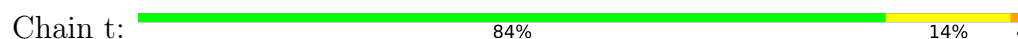
- Molecule 17: 30S ribosomal protein S18



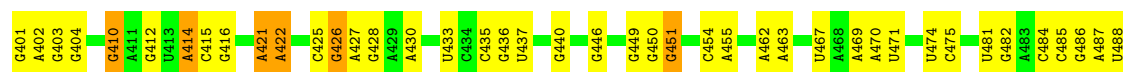
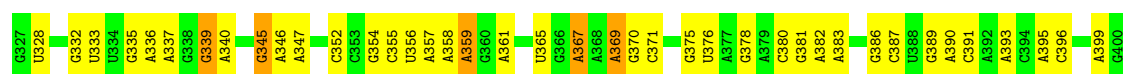
- Molecule 18: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S20



- Molecule 20: 23S rRNA



C1605	G1446	U1518	C1369	A1281	C1192	U1121	U1052	U965	G897	G820	C732	A489
A1606	U1447	G1519	G1373	A1284	C1193	U1122	A1053	U966	A896	A821	A733	A492
C1607	U1448	G1520	G1374	A1285	C1194	U1123	U1059	U969	G899	A822	A739	A493
G1609	U1449	G1521	A1286	A1288	A1195	U1124	A1060	U970	G900	U823	G740	A494
U1525	U1450	U1376	U1377	A1289	C1198	A1125	A1061	U971	A902	U824	G741	C495
G1526	U1451	U1377	A1378	A1290	C1198	G1127	G1062	A972	G903	C674	A585	C496
U1529	U1452	U1378	A1379	A1291	U1206	A1128	A1066	G979	A904	G675	U587	U499
A1613	U1453	U1379	A1380	A1292	A1207	G1129	A1067	G980	G905	A828	G744	A500
G1614	U1454	U1380	C1385	U1293	C1208	U1130	A1068	A981	G906	A829	A745	G503
A1615	U1455	G1530	C1386	U1294	A1209	G1131	A1069	G982	A907	A830	A746	U504
U1616	A1457	A1532	C1387	C1294	C1210	C1132	C1068	A985	G910	G832	A755	G505
G1533	G1458	G1533	C1295	G1296	C1211	C1133	A1069	G986	U911	A833	A756	G506
U1622	A1461	A1536	A1389	G1297	A1212	U1134	G1070	G987	U912	A834	A757	G507
C1623	U1462	A1537	A1390	G1297	U1213	A1135	G1071	G988	U913	C835	A758	G508
G1624	G1463	A1538	G1391	U1297	U1214	U1136	U1073	C988	U914	U837	C759	G509
A1625	G1464	U1539	G1396	A1302	G1216	A1137	G1074	G989	G917	G838	A762	A510
U1627	U1465	U1542	G1397	G1303	C1217	C1139	U1075	G990	C918	A840	A763	G516
G1628	G1468	U1543	A1401	C1307	U1218	U1140	C1085	A993	U919	A841	C764	G517
A1629	A1469	A1545	A1402	A1308	G1219	U1141	U1087	G994	A927	A842	U764	A518
G1630	C1470	G1551	G1404	A1309	U1220	A1142	C1088	U995	U928	G920	G765	A519
A1631	A1473	A1552	G1405	A1310	U1226	C1144	G1083	A997	U929	A843	G766	A520
C1632	G1474	A1553	G1406	A1311	A1227	U1145	A1084	A998	A930	A844	A767	G521
A1633	U1475	G1554	G1407	G1312	G1228	A1146	G1085	U999	C934	G845	G768	A522
A1634	U1476	G1555	A1408	A1313	G1229	G1147	U1086	G1001	A931	C846	A770	C523
U1639	G1478	A1556	U1409	C1314	U1235	U1148	G1087	A1000	A932	U851	A774	C526
C1640	A1479	A1559	G1410	A1315	U1236	A1151	C1088	G1008	U933	U852	C776	G622
G1642	A1481	G1560	G1411	G1319	U1239	U1152	C1089	G1009	G934	U853	A698	A623
U1650	A1485	U1561	A1414	A1322	U1240	U1153	C1092	G1010	G935	U854	U782	G633
A1651	A1486	G1565	U1415	A1323	A1241	G1154	U1093	U1010	A863	A630	U626	U631
A1652	U1487	A1566	G1416	U1324	A1242	C1155	A1094	U935	C784	U701	A627	U544
C1653	G1488	C1567	A1417	U1325	U1247	U1156	G1095	A1014	G785	A702	A640	A645
G1654	C1489	G1568	A1418	C1326	U1247	U1157	G1096	A1015	U786	G703	U632	U547
U1665	A1490	U1573	A1419	C1327	U1248	U1158	A1097	G1016	U787	C705	U633	C548
C1574	U1491	C1574	A1420	U1327	G1253	G1159	U1098	A1020	G788	G706	U634	C549
C1575	U1492	G1575	A1421	G1328	U1254	G1160	G1099	A1023	A789	U707	U644	U550
A1576	G1493	A1576	A1422	C1329	A1257	U1161	U1101	G1024	A941	A708	A645	A551
A1577	G1494	U1577	G1423	C1330	U1258	A1166	G1102	G1025	A942	A791	U644	A552
A1584	A1495	A1584	G1424	C1331	C1259	A1167	G1103	C1026	A943	C873	A645	A553
A1585	U1496	U1585	G1425	C1332	U1259	A1168	C1104	A1036	U944	C711	A645	A554
A1586	U1497	A1586	C1333	C1334	G1265	G1171	U1105	G1038	C945	C712	C556	C555
A1590	G1498	U1588	G1335	G1336	G1266	U1172	U1106	C1032	A948	C713	U648	C556
G1592	A1500	A1592	U1430	A1337	A1267	U1173	A1107	A1033	U949	G714	C649	G561
U1593	G1502	U1593	A1431	A1337	G1268	C1174	G1108	G1034	A884	A715	G653	C562
U1594	U1503	G1594	G1436	G1345	G1269	C1175	A1109	C1035	U885	A716	G654	A565
A1697	G1504	A1697	U1437	U1346	G1270	G1176	A1110	A1036	C887	G722	G655	C566
U1698	U1507	U1698	U1438	U1347	U1271	G1179	C1112	C1038	U888	U721	A656	A567
C1699	U1508	G1600	G1439	C1350	G1272	U1180	A1113	G1038	A890	A725	G657	A568
G1601	C1440	A1601	C1441	G1359	A1274	U1181	C1114	C1047	U891	C727	A660	A570
U1700	U1509	U1700	A1441	U1365	G1275	A1182	C1115	A1048	A959	U728	G661	A571
C1701	C1510	C1701	A1442	U1365	G1276	A1183	A1117	A1049	U960	U729	C662	G572
U1604	C1511	U1604	U1443	U1366	G1277	A1184	C1118	A1050	G961	C730	C663	U573
A1604	C1512	A1604	U1444	G1368	U1280	A1186	C1119	A1051	A964	C731	G664	C574

G2863	G2864	G2865	G2868	A2871	U2872	A2873	G2874	U2875	U2876	G2877	G2878	A2879	G2880	G2881	G2882	G2883	U2889	A2890	C2891	U2895	G2896	G2897	G2898	U2899	C2900	G2901	A2902	G2903	G2904	U2908	A2909	A2910	C2911																														
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G2590	A2591	G2592	C2593	U2594	G2595	G2596	U2597	U2598	U2599	C2600	A2601	A2604	C2605	G2606	A2616	U2623	C2624	C2625	C2626	U2627	A2628	U2629	C2630	U2633	G2634	G2635	C2636	C2640	G2641	U2642	U2643	G2644	G2645	U2649	U2650	A2658	G2659	C2660	U2661	U2666	U2667	A2668	G2669	A2671	U2670	A2671	A2677	G2678	G2682	G2683													
A2496	C2497	G2498	A2502	G2503	G2504	U2505	G2508	A2511	C2515	G2516	U2517	U2518	G2519	U2520	C2521	U2528	C2529	G2530	C2531	A2532	C2533	C2534	G2537	G2540	C2541	U2542	G2543	U2544	A2545	C2548	G2549	G2550	U2551	G2558	G2559	U2560	U2561	G2562	G2563	U2564	G2565	U2566	C2570	A2580	G2581	C2587																	
U2401	A2402	G2403	U2404	G2405	A2406	U2407	C2408	G2411	U2415	U2416	C2417	C2418	G2419	C2420	A2425	C2431	A2432	U2433	C2436	U2437	C2438	A2439	C2441	C2442	G2443	A2444	U2445	A2453	C2454	C2455	C2456	U2457	G2458	G2459	G2460	A2461	A2462	U2463	A2464	C2465	C2466	A2467	U2476	A2482	C2489	A2492	G2495																
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G2235	A2239	G2242	G2243	G2244	G2245	U2246	U2248	G2252	G2253	U2257	U2258	U2259	G2265	C2272	C2273	G2274	C2275	U2276	C2277	C2278	C2279	A2280	A2281	A2282	A2283	A2287	A2288	C2289	G2290	G2291	A2292	C2297	C2298	C2299	A2300	A2301	A2302	U2305	U2306	G2313	U2316	U2317	G2318	U2319	U2320	G2321	G2322																
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C1893	U1894	A1898	A1899	A1898	U1900	U1906	U1997	G1911	U1912	U1913	A1914	G1917	U2007	G1920	G1921	G1922	G1923	U1924	U1925	A	A	A1823	C	U	A	U	C1932	A1933	U1937	C1938	C1939	G1943	G1944	A1950	A1951	A1952	U1953	C1955	C1956	C1961	U1962	G1963	G1968	U1969	U1970	G1971	C1972	G1973	C1977	G1978	U1979	C1980	A1891	C1982									
U1706	U1707	A1708	C1796	G1709	A1797	A1798	A1799	A1711	A1712	C1802	A1803	C1804	A1805	U1810	C1811	U2017	G1812	U1813	U1814	A1815	G1821	U1731	A1732	A1823	A1824	A1741	U1827	U1828	A1829	U1762	G1753	A1754	G1755	U1756	U1757	G1837	G1759	G1760	U1761	C1842	A1843	G1844	G1845	A1867	C1868	U1871	G1872	U1771	A1774	U1775	A1776	U1877	G1778	G1786	A1787	G1886	U1788	U1789	G1790	A1890	C2080	A1891	C1982

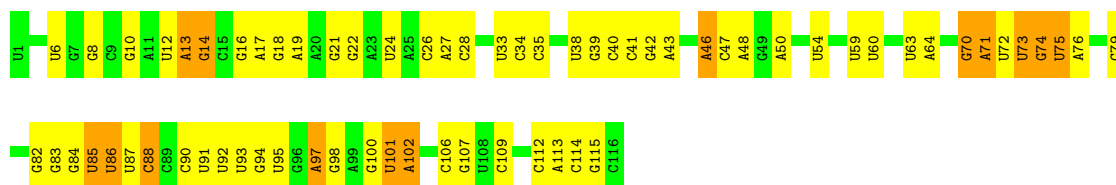
● Molecule 21: 5S rRNA

Chain B:

42%

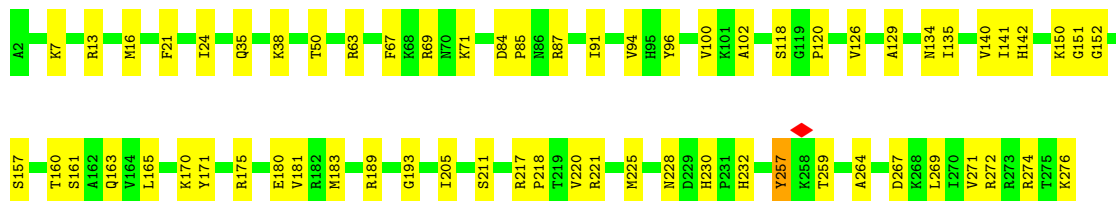
46%

12%



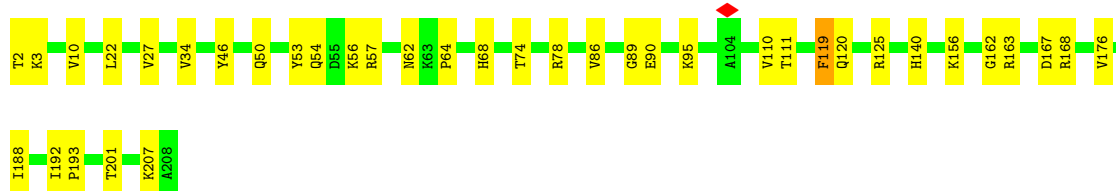
- Molecule 22: 50S ribosomal protein L2

Chain C: 77% 23%



- Molecule 23: 50S ribosomal protein L3

Chain D: 82% 18%



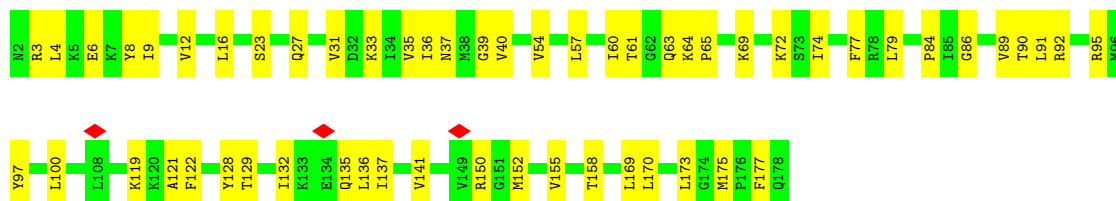
- Molecule 24: 50S ribosomal protein L4

Chain E: 80% 19%



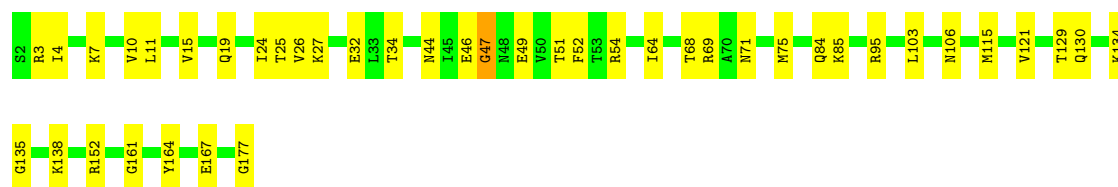
- Molecule 25: 50S ribosomal protein L5

Chain F: 68% 32%



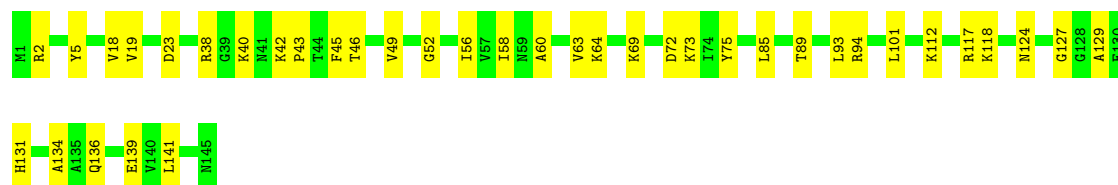
- Molecule 26: 50S ribosomal protein L6

Chain G:  76% 23% .



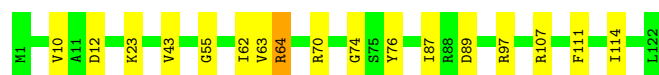
- Molecule 27: 50S ribosomal protein L13

Chain K:  74% 26%



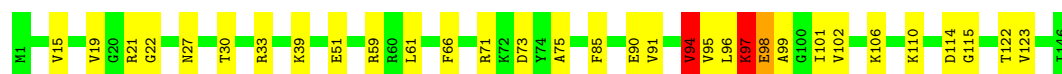
- Molecule 28: 50S ribosomal protein L14

Chain L:  86% 13% .



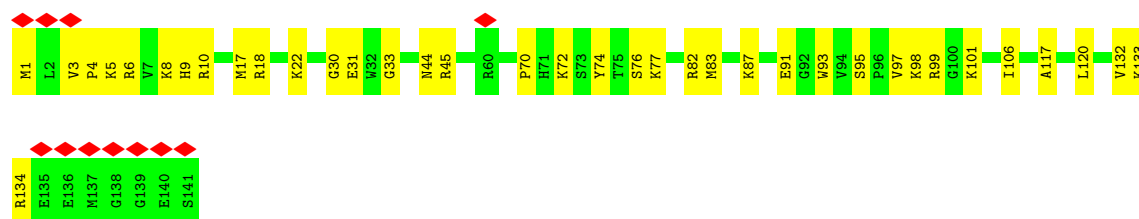
- Molecule 29: 50S ribosomal protein L15

Chain M:  78% 20% ..



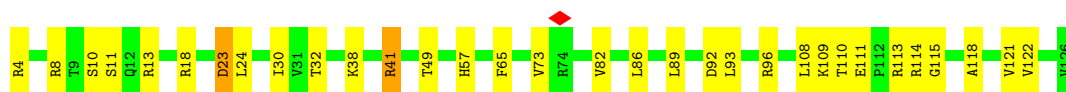
- Molecule 30: 50S ribosomal protein L16

Chain N:  8% 74% 26%



- Molecule 31: 50S ribosomal protein L17

Chain O:  8% 74% 24% .



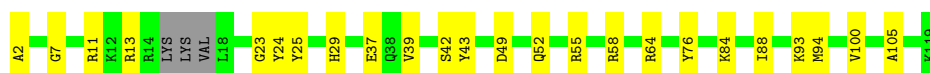
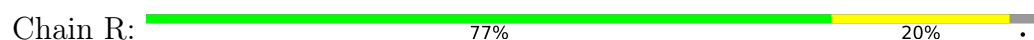
- Molecule 32: 50S ribosomal protein L18



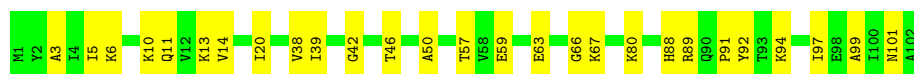
- Molecule 33: 50S ribosomal protein L19



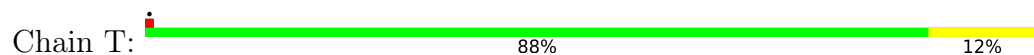
- Molecule 34: 50S ribosomal protein L20



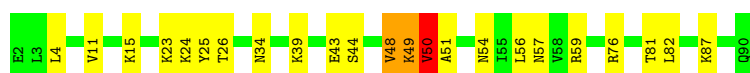
- Molecule 35: 50S ribosomal protein L21



- Molecule 36: 50S ribosomal protein L22



- Molecule 37: 50S ribosomal protein L23

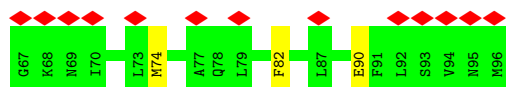
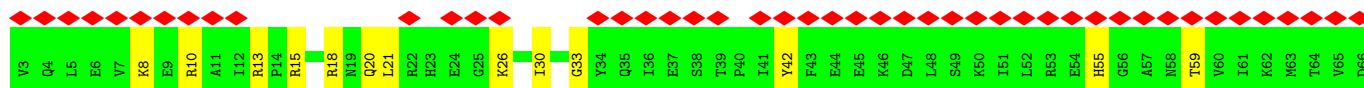
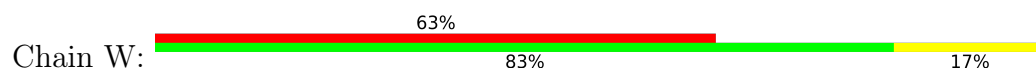


- Molecule 38: 50S ribosomal protein L24





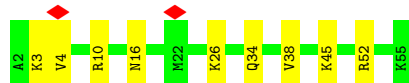
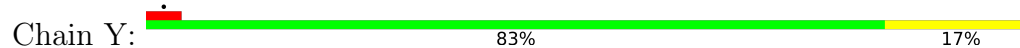
- Molecule 39: 50S ribosomal protein L25



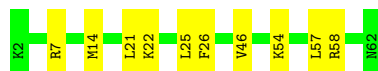
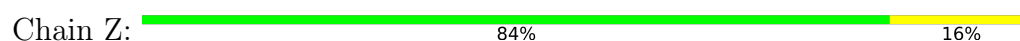
- Molecule 40: 50S ribosomal protein L27



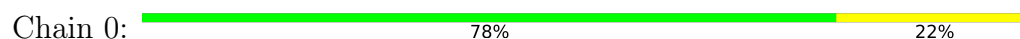
- Molecule 41: 50S ribosomal protein L28



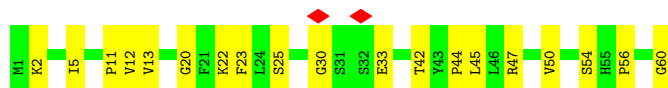
- Molecule 42: 50S ribosomal protein L29



- Molecule 43: 50S ribosomal protein L30

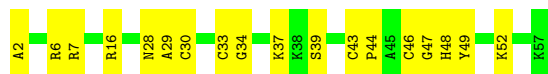


- Molecule 44: 50S ribosomal protein L31 type B



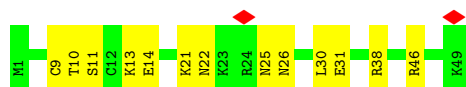
- Molecule 45: 50S ribosomal protein L32

Chain 2:  68% 32%



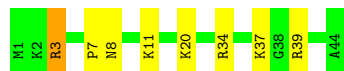
- Molecule 46: 50S ribosomal protein L33

Chain 3:  73% 27%



- Molecule 47: 50S ribosomal protein L34

Chain 4:  82% 16%



- Molecule 48: 50S ribosomal protein L35

Chain 5:  80% 20%



- Molecule 49: 50S ribosomal protein L36

Chain 6:  66% 34%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18979	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	1.406	Depositor
Minimum map value	-0.456	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.078	Depositor
Recommended contour level	0.238	Depositor
Map size ($\text{\AA}$)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.097, 1.097, 1.097	Depositor

5 Model quality

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	0.32	0/36657	0.45	0/57173
2	c	0.22	0/1635	0.57	0/2197
3	d	0.32	1/1650 (0.1%)	0.66	0/2217
4	e	0.28	0/1217	0.61	0/1641
5	f	0.31	0/807	0.50	0/1087
6	g	0.24	0/1249	0.58	0/1682
7	h	0.35	0/1054	0.57	0/1417
8	i	0.27	0/1003	0.62	0/1343
9	j	0.26	0/812	0.66	0/1093
10	k	0.29	0/878	0.62	2/1185 (0.2%)
11	l	0.30	0/1082	0.67	0/1453
12	m	0.25	0/890	0.64	0/1195
13	n	0.23	0/504	0.60	0/669
14	o	0.33	0/751	0.60	0/1001
15	p	0.36	0/720	0.67	0/966
16	q	0.30	0/689	0.65	0/920
17	r	0.30	0/544	0.62	0/728
18	s	0.26	0/650	0.60	0/872
19	t	0.28	0/612	0.58	0/818
20	A	0.40	0/69635	0.50	3/108600 (0.0%)
21	B	0.36	0/2769	0.47	0/4311
22	C	0.42	0/2147	0.71	0/2886
23	D	0.41	0/1598	0.72	0/2144
24	E	0.38	0/1593	0.64	0/2154
25	F	0.29	0/1408	0.59	0/1891
26	G	0.30	0/1362	0.65	0/1833
27	K	0.43	0/1149	0.67	0/1552
28	L	0.42	0/929	0.67	1/1247 (0.1%)
29	M	0.37	0/1102	0.86	4/1468 (0.3%)
30	N	0.40	0/1139	0.76	2/1515 (0.1%)
31	O	0.40	0/986	0.80	2/1321 (0.2%)
32	P	0.36	0/907	0.68	0/1214

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Q	0.41	0/938	0.67	0/1262
34	R	0.43	0/922	0.74	0/1223
35	S	0.36	0/794	0.59	0/1065
36	T	0.37	0/858	0.65	0/1157
37	U	0.37	0/725	0.79	4/967 (0.4%)
38	V	0.33	0/772	0.79	2/1035 (0.2%)
39	W	0.26	0/767	0.66	0/1029
40	X	0.39	0/578	0.61	0/773
41	Y	0.30	0/430	0.56	0/572
42	Z	0.33	0/505	0.60	0/672
43	0	0.39	0/437	0.68	0/589
44	1	0.25	0/488	0.66	0/663
45	2	0.41	0/436	0.61	0/578
46	3	0.27	0/423	0.54	0/563
47	4	0.42	0/375	0.70	0/487
48	5	0.34	0/528	0.67	0/689
49	6	0.38	0/309	0.61	0/409
All	All	0.36	1/150413 (0.0%)	0.53	20/225526 (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	1
17	r	0	2
19	t	0	2
23	D	0	2
25	F	0	1
26	G	0	2
29	M	0	4
30	N	0	2
31	O	0	1
32	P	0	2
34	R	0	1
35	S	0	1
36	T	0	1
37	U	0	1
38	V	0	2
39	W	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	X	0	1
47	4	0	2
All	All	0	30

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	29	ARG	C-N	6.40	1.40	1.34

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	V	71	ILE	CA-C-N	6.31	137.21	121.80
38	V	71	ILE	C-N-CA	6.31	137.21	121.80
29	M	15	VAL	CA-C-N	6.14	133.27	121.54
29	M	15	VAL	C-N-CA	6.14	133.27	121.54
31	O	41	ARG	CB-CG-CD	-5.88	97.78	111.30

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	161	ILE	Peptide
3	d	189	GLU	Peptide
17	r	19	ALA	Peptide
17	r	26	ASP	Peptide
19	t	66	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32746	0	16491	524	0
2	c	1610	0	1653	24	0
3	d	1620	0	1641	33	0
4	e	1204	0	1280	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	f	795	0	789	18	0
6	g	1229	0	1259	31	0
7	h	1041	0	1092	18	0
8	i	990	0	1035	42	0
9	j	800	0	846	21	0
10	k	863	0	882	16	0
11	l	1065	0	1133	18	0
12	m	884	0	932	20	0
13	n	492	0	511	13	0
14	o	741	0	756	14	0
15	p	708	0	746	15	0
16	q	681	0	719	20	0
17	r	537	0	572	15	0
18	s	634	0	649	27	0
19	t	610	0	640	11	0
20	A	62176	0	31231	818	0
21	B	2478	0	1245	39	0
22	C	2114	0	2200	50	0
23	D	1578	0	1657	31	0
24	E	1572	0	1614	32	0
25	F	1391	0	1444	40	0
26	G	1344	0	1373	26	0
27	K	1129	0	1162	27	0
28	L	922	0	985	11	0
29	M	1094	0	1147	23	0
30	N	1117	0	1175	24	0
31	O	978	0	1015	22	0
32	P	898	0	932	22	0
33	Q	924	0	979	26	0
34	R	913	0	951	25	0
35	S	783	0	821	22	0
36	T	849	0	906	10	0
37	U	719	0	770	18	0
38	V	763	0	824	18	0
39	W	757	0	778	14	0
40	X	572	0	580	21	0
41	Y	424	0	458	7	0
42	Z	504	0	538	9	0
43	0	435	0	472	9	0
44	1	475	0	441	12	0
45	2	429	0	445	13	0
46	3	419	0	437	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	4	373	0	419	9	0
48	5	522	0	576	13	0
49	6	304	0	338	9	0
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	138210	0	91539	2021	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 9.

The worst 5 of 2021 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:797:A:H62	1:a:815:G:N2	1.54	1.05
20:A:2597:G:C2	20:A:2597:G:C6	2.43	1.05
1:a:673:G:C2	1:a:764:A:N1	2.25	1.04
20:A:1100:U:N3	20:A:1128:A:C8	2.25	1.04
1:a:702:A:N6	1:a:718:G:C2	2.26	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%)	170 (85%)	29 (15%)	0	100	100
4	e	161/163 (99%)	148 (92%)	13 (8%)	0	100	100
5	f	95/97 (98%)	81 (85%)	14 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	g	152/154 (99%)	137 (90%)	15 (10%)	0	100	100
7	h	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
8	i	126/128 (98%)	113 (90%)	13 (10%)	0	100	100
9	j	97/99 (98%)	78 (80%)	19 (20%)	0	100	100
10	k	115/117 (98%)	93 (81%)	22 (19%)	0	100	100
11	l	134/136 (98%)	105 (78%)	28 (21%)	1 (1%)	18	54
12	m	110/112 (98%)	91 (83%)	19 (17%)	0	100	100
13	n	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
14	o	86/88 (98%)	74 (86%)	12 (14%)	0	100	100
15	p	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
16	q	81/83 (98%)	65 (80%)	16 (20%)	0	100	100
17	r	64/66 (97%)	54 (84%)	10 (16%)	0	100	100
18	s	76/78 (97%)	64 (84%)	12 (16%)	0	100	100
19	t	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
22	C	271/275 (98%)	229 (84%)	42 (16%)	0	100	100
23	D	205/207 (99%)	167 (82%)	37 (18%)	1 (0%)	24	61
24	E	204/206 (99%)	170 (83%)	34 (17%)	0	100	100
25	F	175/177 (99%)	155 (89%)	20 (11%)	0	100	100
26	G	172/176 (98%)	148 (86%)	23 (13%)	1 (1%)	21	58
27	K	143/145 (99%)	122 (85%)	21 (15%)	0	100	100
28	L	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
29	M	142/146 (97%)	108 (76%)	31 (22%)	3 (2%)	5	32
30	N	139/141 (99%)	116 (84%)	23 (16%)	0	100	100
31	O	121/123 (98%)	93 (77%)	28 (23%)	0	100	100
32	P	115/117 (98%)	98 (85%)	17 (15%)	0	100	100
33	Q	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
34	R	110/118 (93%)	105 (96%)	5 (4%)	0	100	100
35	S	100/102 (98%)	86 (86%)	14 (14%)	0	100	100
36	T	110/112 (98%)	93 (84%)	17 (16%)	0	100	100
37	U	85/89 (96%)	68 (80%)	16 (19%)	1 (1%)	10	42
38	V	99/101 (98%)	75 (76%)	22 (22%)	2 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	W	90/94 (96%)	65 (72%)	24 (27%)	1 (1%)	11	44
40	X	74/76 (97%)	60 (81%)	14 (19%)	0	100	100
41	Y	52/54 (96%)	46 (88%)	6 (12%)	0	100	100
42	Z	59/61 (97%)	56 (95%)	3 (5%)	0	100	100
43	0	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
44	1	58/60 (97%)	43 (74%)	15 (26%)	0	100	100
45	2	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
46	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
47	4	42/44 (96%)	36 (86%)	6 (14%)	0	100	100
48	5	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
49	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5104/5212 (98%)	4340 (85%)	754 (15%)	10 (0%)	44	76

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	M	95	VAL
29	M	98	GLU
26	G	47	GLY
38	V	73	PRO
23	D	54	GLN

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%)	124 (98%)	2 (2%)	55	69
5	f	86/86 (100%)	86 (100%)	0	100	100
6	g	131/131 (100%)	131 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	112/112 (100%)	111 (99%)	1 (1%)	70	76
8	i	101/101 (100%)	100 (99%)	1 (1%)	68	76
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%)	77 (98%)	2 (2%)	42	62
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%)	68 (100%)	0	100	100
19	t	62/62 (100%)	61 (98%)	1 (2%)	55	69
22	C	225/225 (100%)	224 (100%)	1 (0%)	84	83
23	D	169/170 (99%)	167 (99%)	2 (1%)	63	73
24	E	172/172 (100%)	170 (99%)	2 (1%)	63	73
25	F	153/154 (99%)	153 (100%)	0	100	100
26	G	146/146 (100%)	146 (100%)	0	100	100
27	K	121/122 (99%)	121 (100%)	0	100	100
28	L	98/98 (100%)	98 (100%)	0	100	100
29	M	112/112 (100%)	112 (100%)	0	100	100
30	N	111/112 (99%)	110 (99%)	1 (1%)	70	76
31	O	105/105 (100%)	104 (99%)	1 (1%)	68	76
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	82/83 (99%)	82 (100%)	0	100	100
36	T	95/95 (100%)	95 (100%)	0	100	100
37	U	79/80 (99%)	77 (98%)	2 (2%)	42	62
38	V	85/85 (100%)	85 (100%)	0	100	100
39	W	84/85 (99%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	X	61/61 (100%)	61 (100%)	0	100	100
41	Y	47/47 (100%)	47 (100%)	0	100	100
42	Z	55/55 (100%)	55 (100%)	0	100	100
43	0	49/49 (100%)	49 (100%)	0	100	100
44	1	55/55 (100%)	55 (100%)	0	100	100
45	2	46/46 (100%)	45 (98%)	1 (2%)	45	64
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	4357/4371 (100%)	4340 (100%)	17 (0%)	81	83

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	U	48	VAL
45	2	49	TYR
22	C	257	TYR
23	D	86	VAL
23	D	119	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
42	Z	36	GLN
43	0	40	ASN
48	5	34	HIS
16	q	54	ASN
16	q	6	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1528 (99%)	423 (27%)	0
20	A	2890/2903 (99%)	844 (29%)	24 (0%)
21	B	115/116 (99%)	38 (33%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4531/4547 (99%)	1305 (28%)	24 (0%)

5 of 1305 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	13	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	1530	A
20	A	1604	A
20	A	1585	U
20	A	1605	C
20	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
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	16.85
1	A	1579:U	O3'	1583:A	P	12.96
1	a	75:U	O3'	96:U	P	8.17

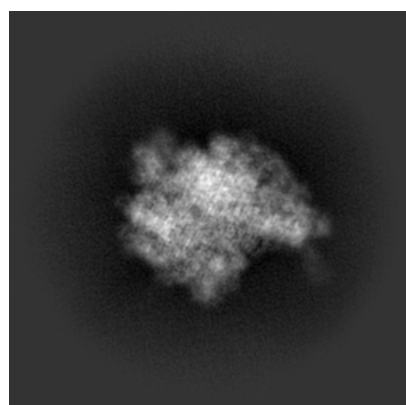
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0658. These allow visual inspection of the internal detail of the map and identification of artifacts.

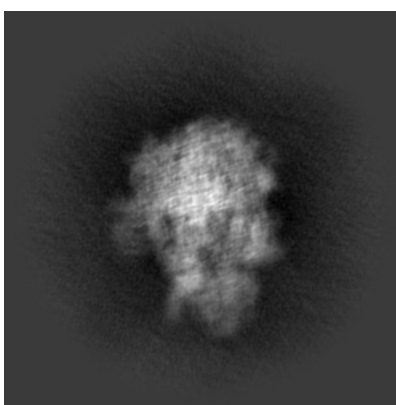
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

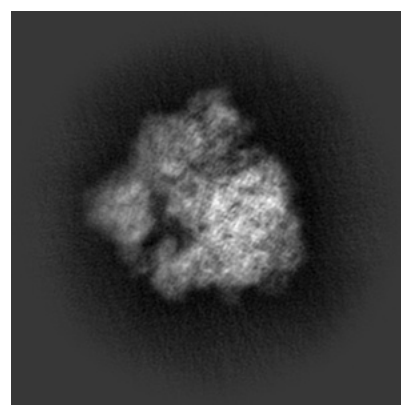
6.1.1 Primary map



X



Y

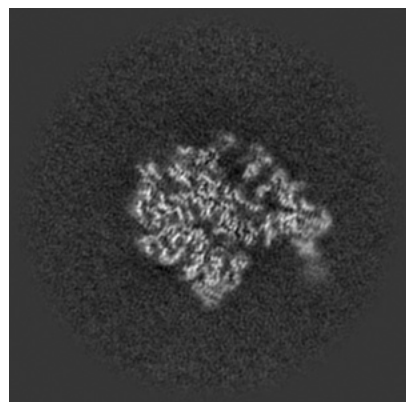


Z

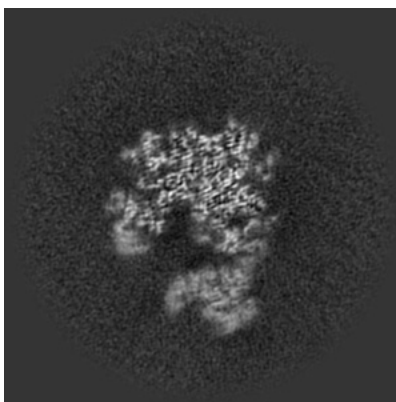
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

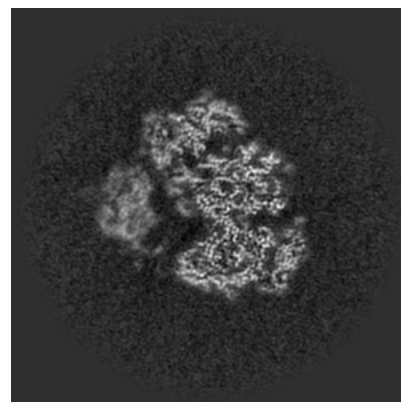
6.2.1 Primary map



X Index: 220



Y Index: 220

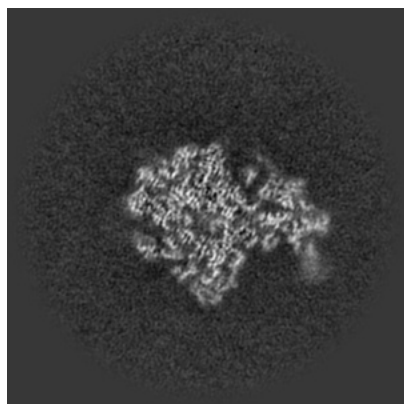


Z Index: 220

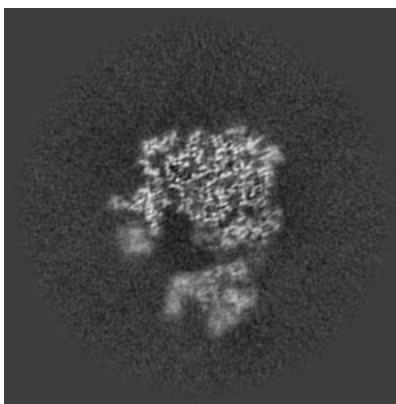
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

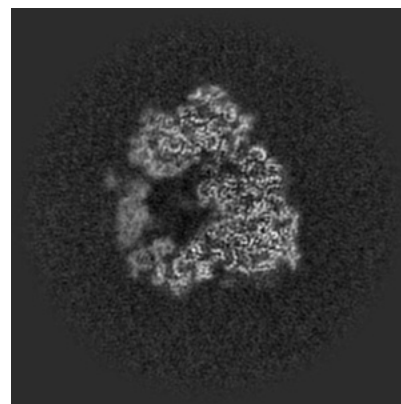
6.3.1 Primary map



X Index: 226



Y Index: 230

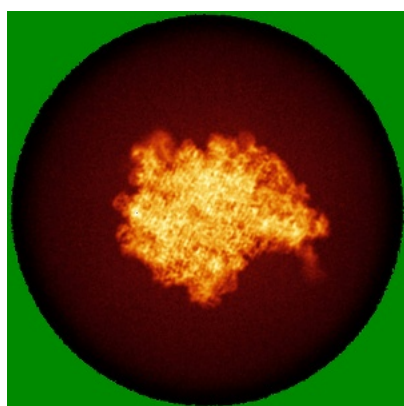


Z Index: 205

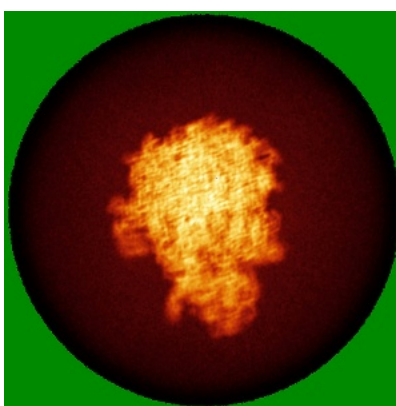
The images above show the largest variance slices of the map in three orthogonal directions.

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

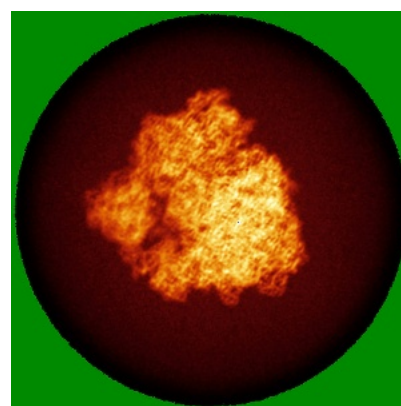
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

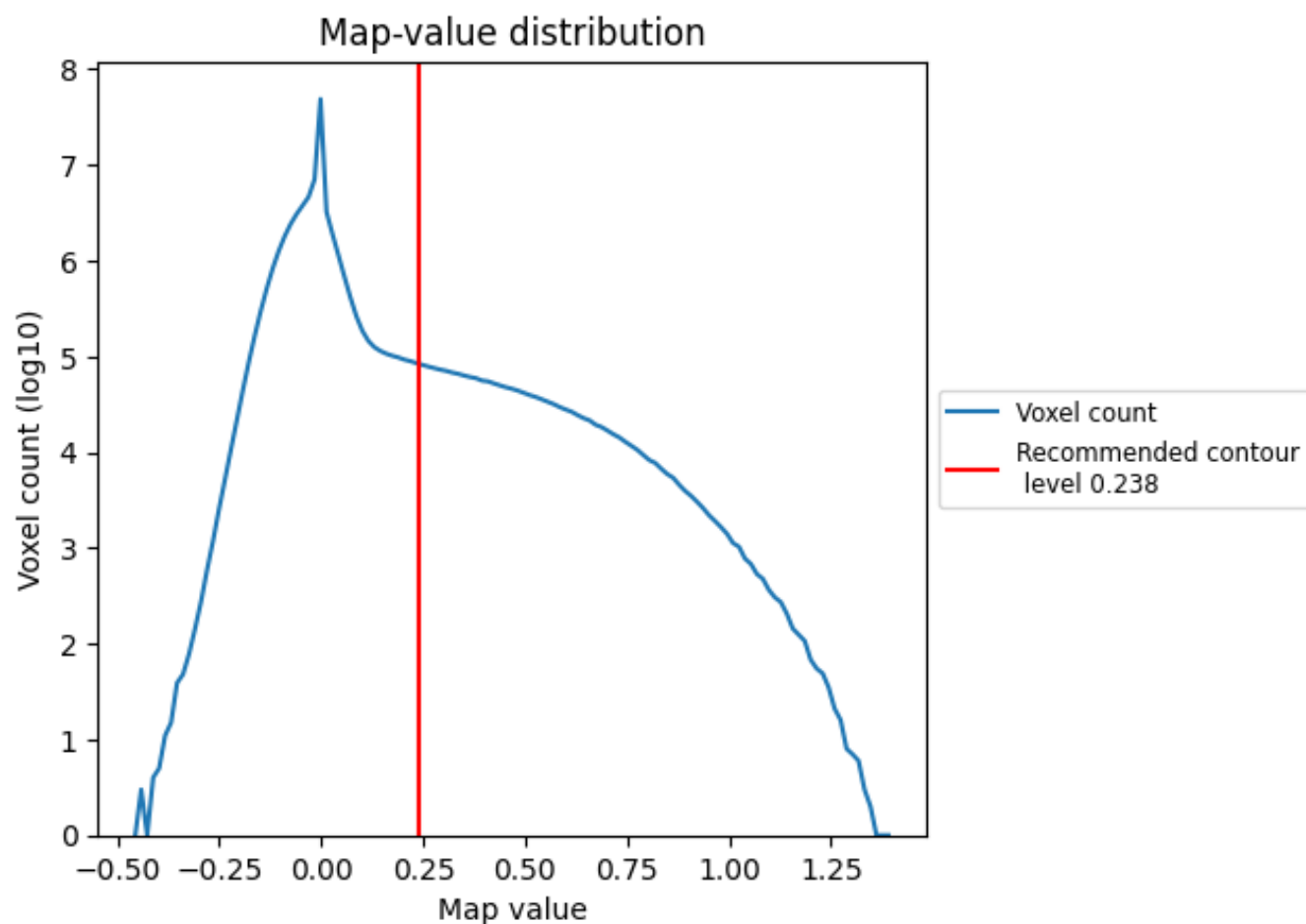
6.6 Mask visualisation

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

7 Map analysis [i](#)

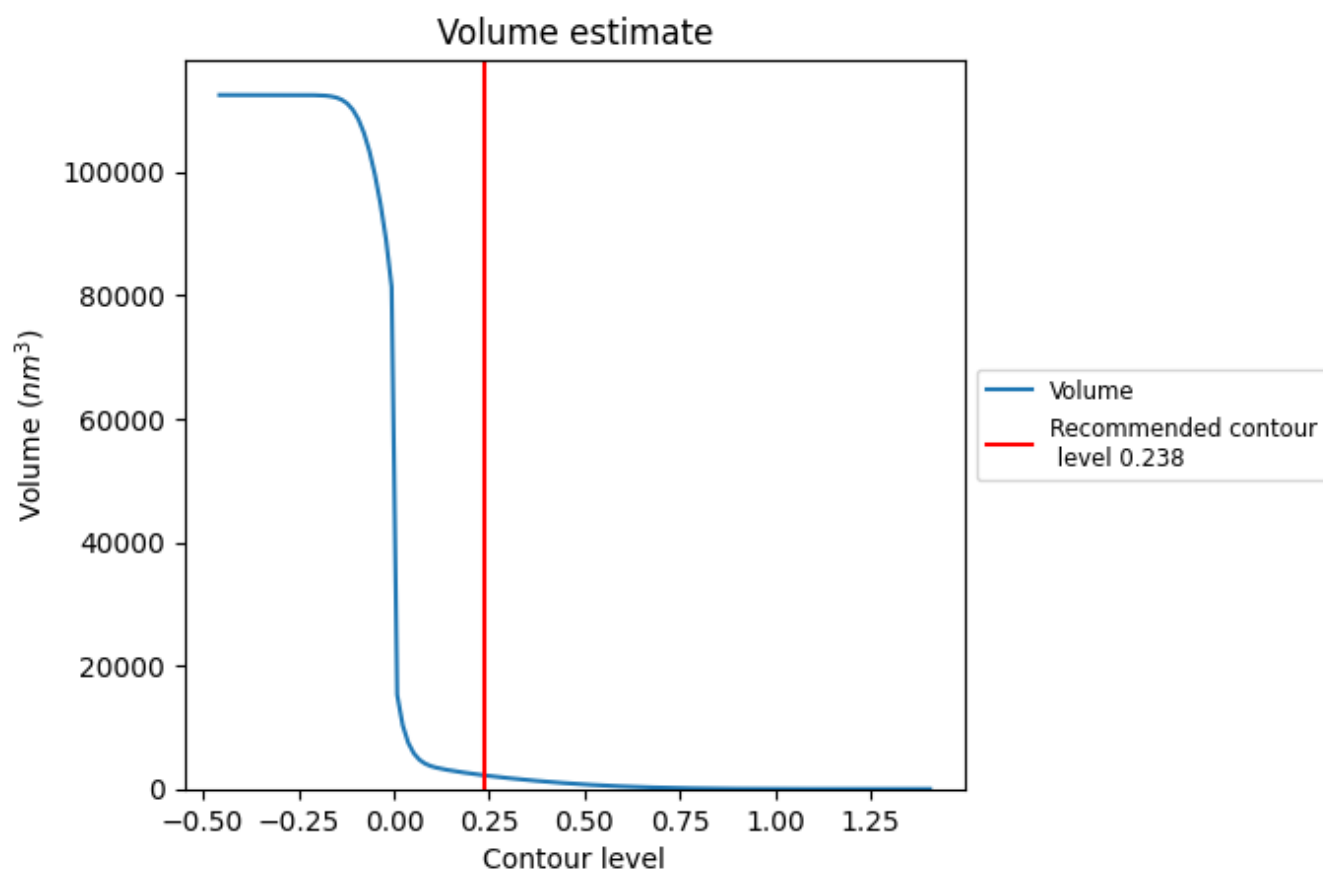
This section contains the results of statistical analysis of the map.

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.

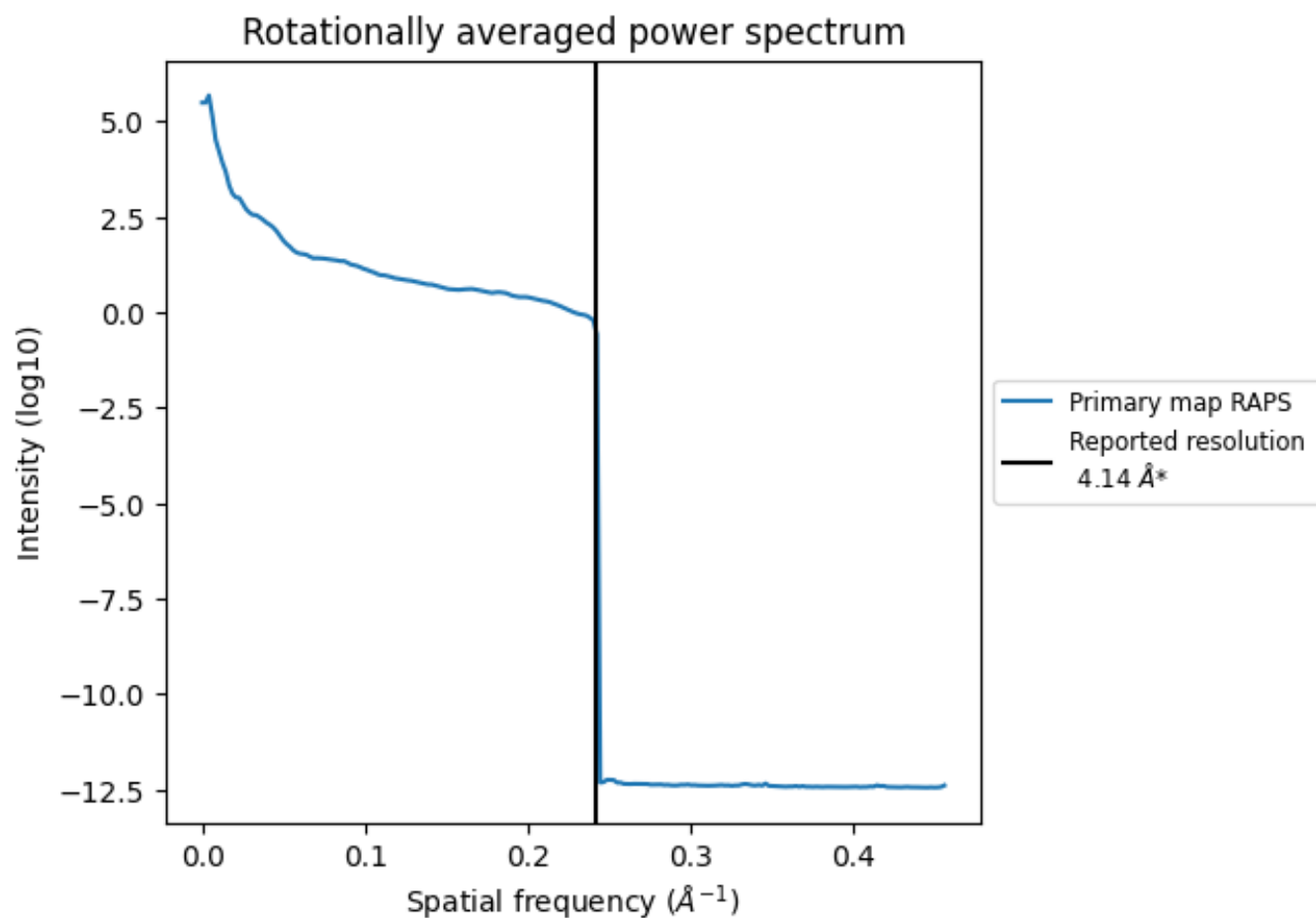
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2203 nm³; this corresponds to an approximate mass of 1990 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 0.242 Å⁻¹

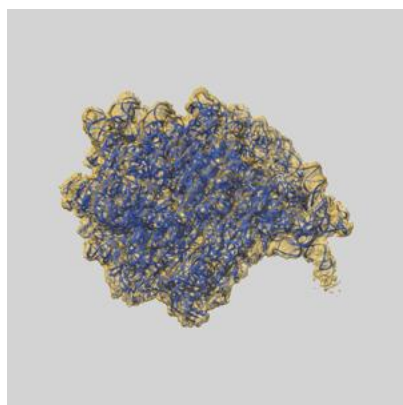
8 Fourier-Shell correlation

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

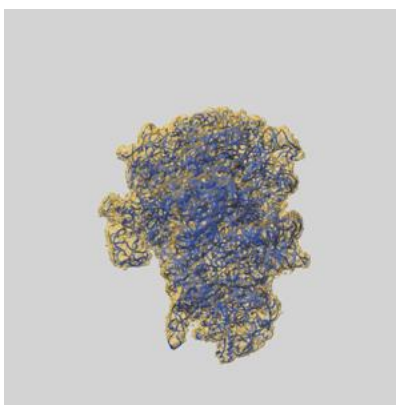
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0658 and PDB model 6O8Y. Per-residue inclusion information can be found in section 3 on page 13.

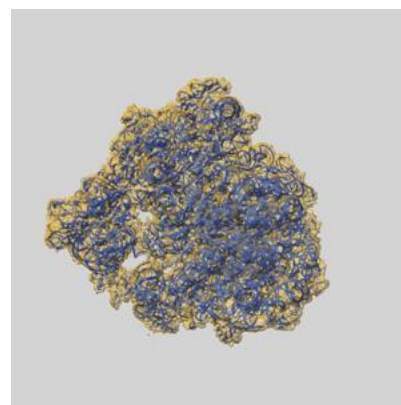
9.1 Map-model overlay [i](#)



X



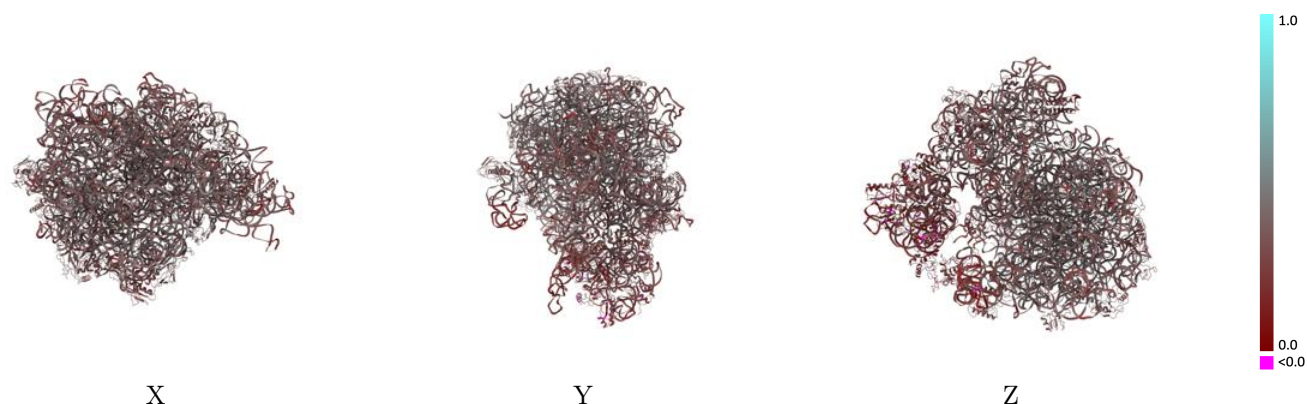
Y



Z

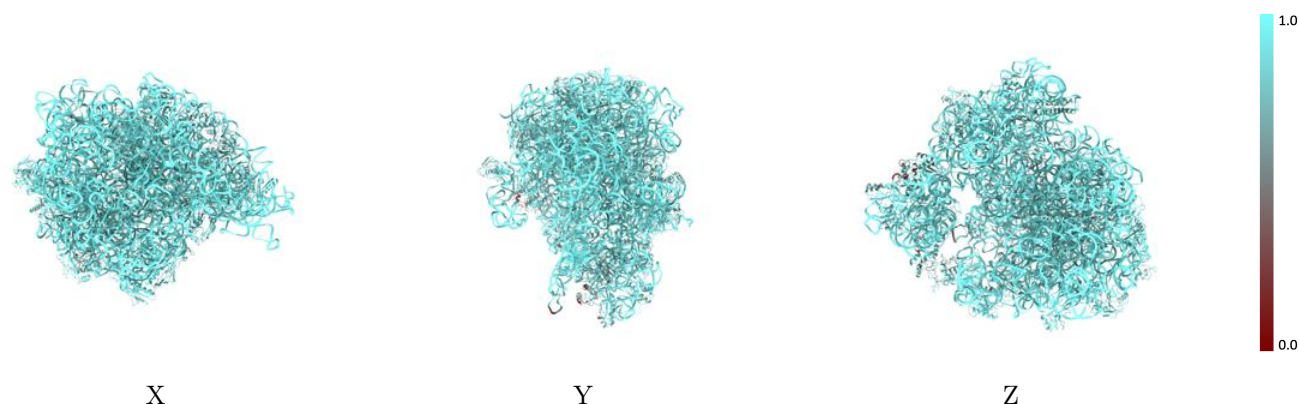
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



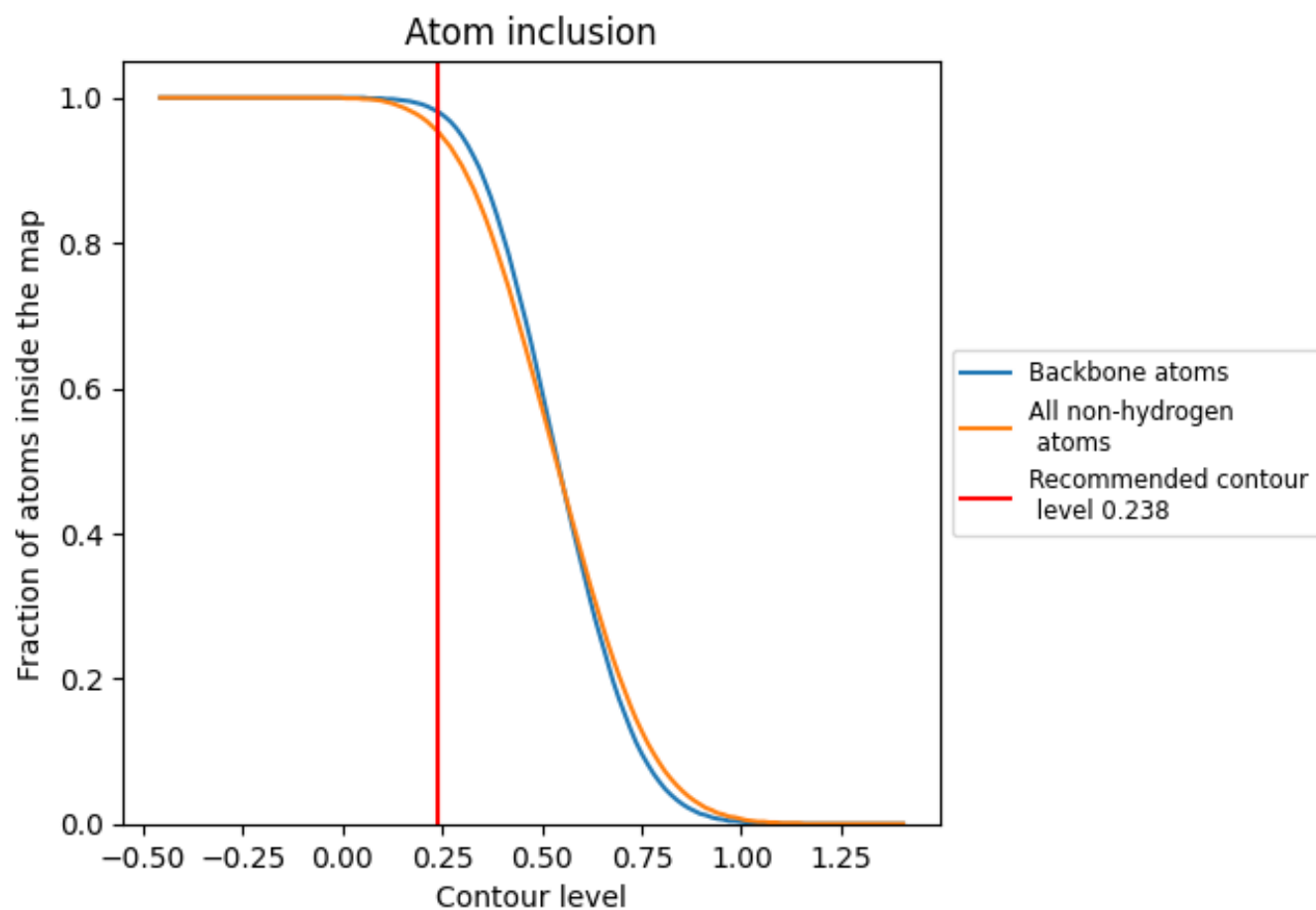
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.238).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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	 0.9540	 0.3450
0	 0.8810	 0.3710
1	 0.8440	 0.2370
2	 0.9430	 0.3970
3	 0.8960	 0.3450
4	 0.8800	 0.3650
5	 0.8630	 0.3710
6	 0.9360	 0.3490
A	 0.9910	 0.3680
B	 0.9930	 0.3230
C	 0.9030	 0.3850
D	 0.8730	 0.4030
E	 0.9020	 0.3600
F	 0.8320	 0.2500
G	 0.8860	 0.3290
K	 0.9060	 0.3820
L	 0.8470	 0.3990
M	 0.9130	 0.3770
N	 0.8210	 0.3520
O	 0.9200	 0.3640
P	 0.9120	 0.3040
Q	 0.8730	 0.3890
R	 0.9050	 0.3260
S	 0.9030	 0.3820
T	 0.9050	 0.3680
U	 0.9130	 0.3530
V	 0.8820	 0.3370
W	 0.3100	 0.2650
X	 0.9330	 0.3830
Y	 0.8590	 0.3670
Z	 0.9040	 0.3160
a	 0.9920	 0.3260
c	 0.7190	 0.2500
d	 0.8990	 0.2930
e	 0.8730	 0.3290



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Chain	Atom inclusion	Q-score
f	 0.8360	 0.3430
g	 0.8550	 0.2060
h	 0.9000	 0.3400
i	 0.8950	 0.2400
j	 0.8400	 0.2380
k	 0.8550	 0.3310
l	 0.8270	 0.3200
m	 0.7940	 0.1960
n	 0.9120	 0.2590
o	 0.8600	 0.3400
p	 0.9190	 0.3480
q	 0.8360	 0.3320
r	 0.8190	 0.3310
s	 0.8980	 0.1550
t	 0.8460	 0.2930