



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2024 – 12:28 am GMT

PDB ID : 7PJZ
EMDB ID : EMD-13465
Title : Structure of the 70S-EF-G-GDP ribosome complex with tRNAs in chimeric state 2 (CHI2-EF-G-GDP)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.; Fischer, N.
Deposited on : 2021-08-24
Resolution : 6.00 Å (reported)
Based on initial models : 4AQY, 6YSS, 5LZD, 5J9Z

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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

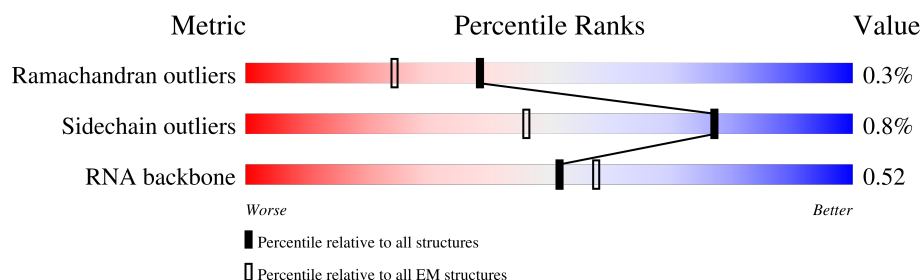
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 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.




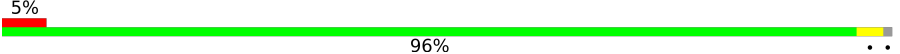
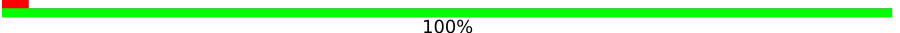
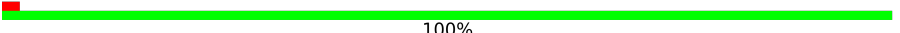
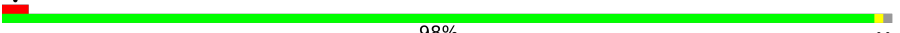
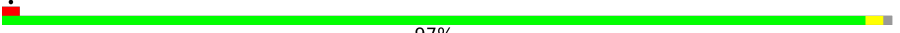
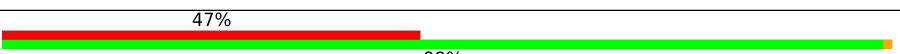
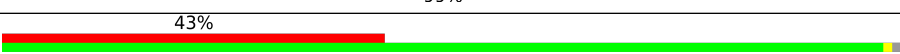
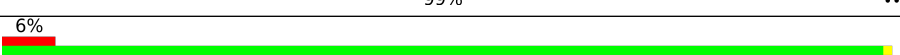
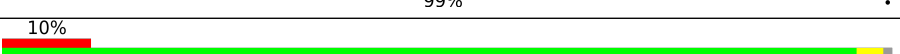
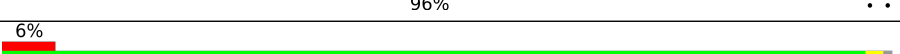
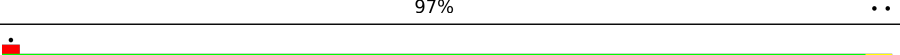
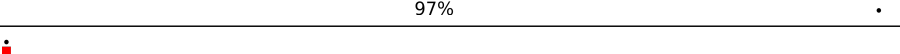
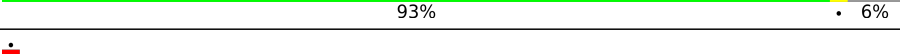
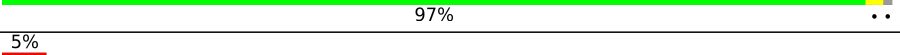
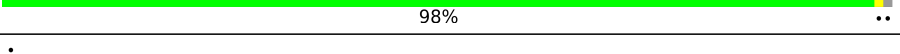
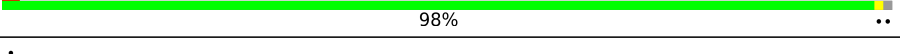
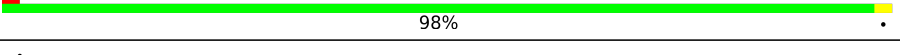
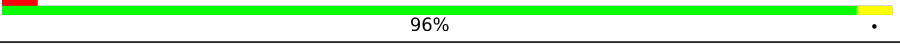
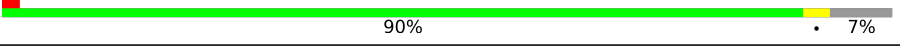
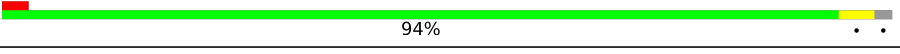
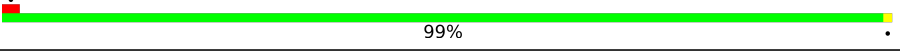

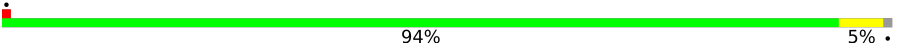
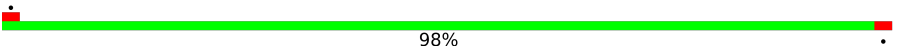
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	0	57	<div> <div>5%</div> <div>98%</div> <div>.</div> </div>
2	1	55	<div> <div>91%</div> <div>9%</div> </div>
3	2	46	<div> <div>96%</div> <div>.</div> </div>
4	3	65	<div> <div>95%</div> <div>..</div> </div>
5	4	38	<div> <div>100%</div> </div>
6	5	165	<div> <div>65%</div> <div>79%</div> <div>21%</div> </div>
7	6	70	<div> <div>9%</div> <div>90%</div> <div>.</div> <div>6%</div> </div>
8	A	2903	<div> <div>39%</div> <div>52%</div> <div>9%</div> </div>

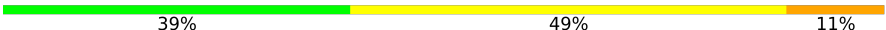

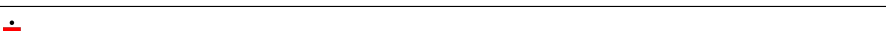
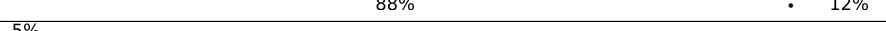
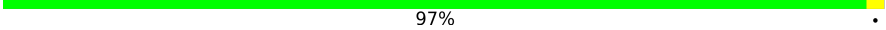


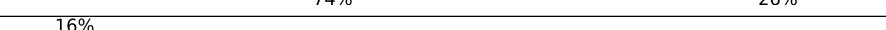

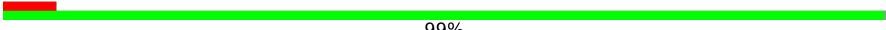

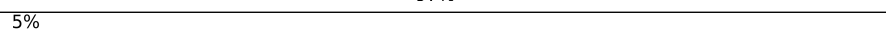
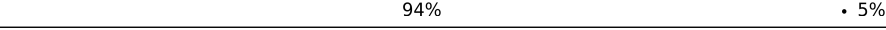


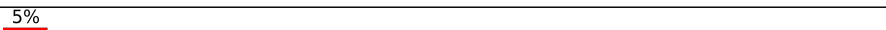
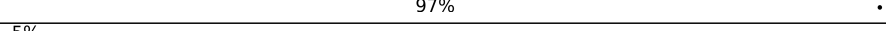
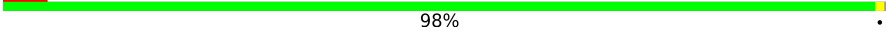


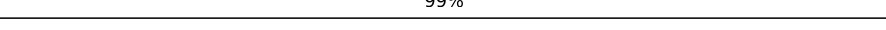
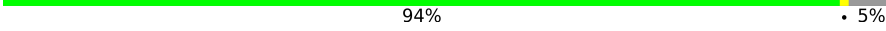



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Mol	Chain	Length	Quality of chain
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	


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Mol	Chain	Length	Quality of chain
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	
53	t	87	
54	u	71	
55	v	77	
56	w	76	
57	x	704	
58	y	2	

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Mol	Chain	Length	Quality of chain
59	z	33	 A horizontal bar chart showing the quality of chain 59. The bar is divided into three segments: a green segment on the left labeled '21%', a yellow segment in the middle labeled '9%', and a grey segment on the right labeled '70%'. The total length of the bar represents 100%.

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 152440 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62338	27816	11471	20148	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 12 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 15 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a RNA chain called P-site tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	77	Total	C	N	O	P	S	0	0
			1642	733	297	534	77	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	x	669	Total	C	N	O	S		1	0
			5192	3275	900	994	23			

- Molecule 58 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	2	Total	C	N	O	S	0	0
			21	15	2	3	1		

- Molecule 59 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	10	Total	C	N	O	P	0	0
			208	93	29	76	10		

- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	6	1	Total	Zn	0
			1	1	

- Molecule 61 is APRAMYCIN (three-letter code: AM2) (formula: C₂₁H₄₁N₅O₁₁).



Mol	Chain	Residues	Atoms				AltConf
61	a	1	Total	C	N	O	0
			37	21	5	11	

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$).

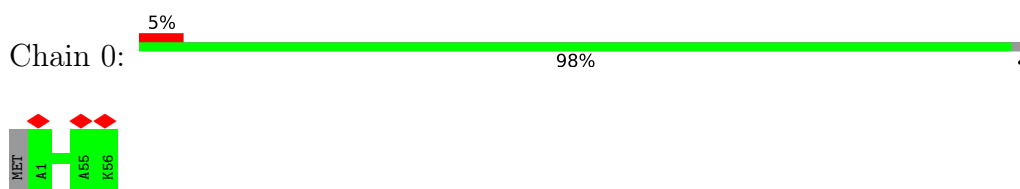


Mol	Chain	Residues	Atoms					AltConf
62	x	1	Total	C	N	O	P	0
			28	10	5	11	2	

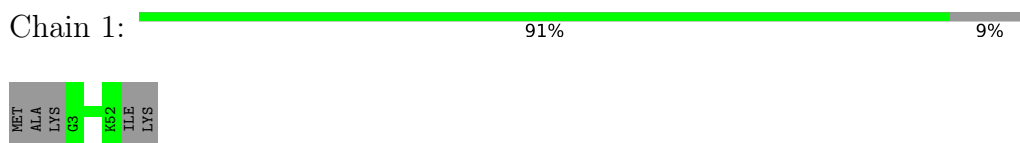
3 Residue-property plots [i](#)

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.

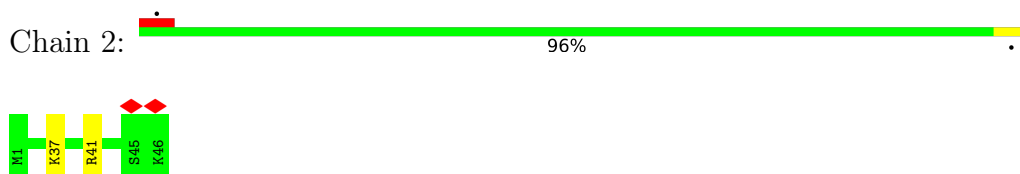
- Molecule 1: 50S ribosomal protein L32



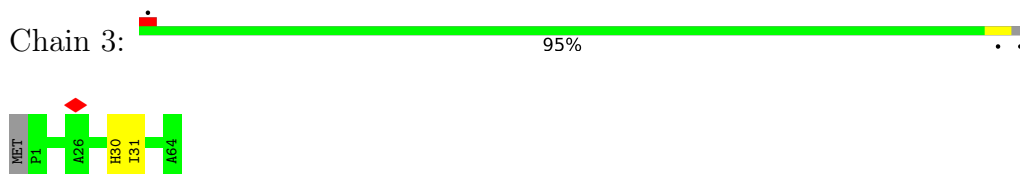
- Molecule 2: 50S ribosomal protein L33



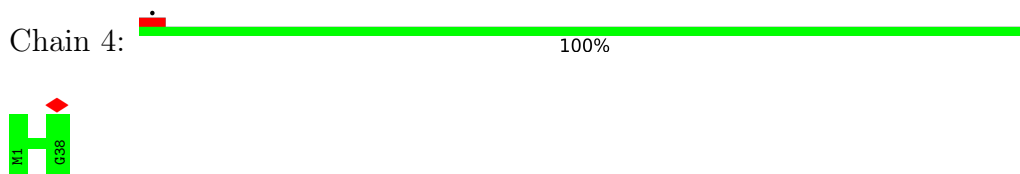
- Molecule 3: 50S ribosomal protein L34



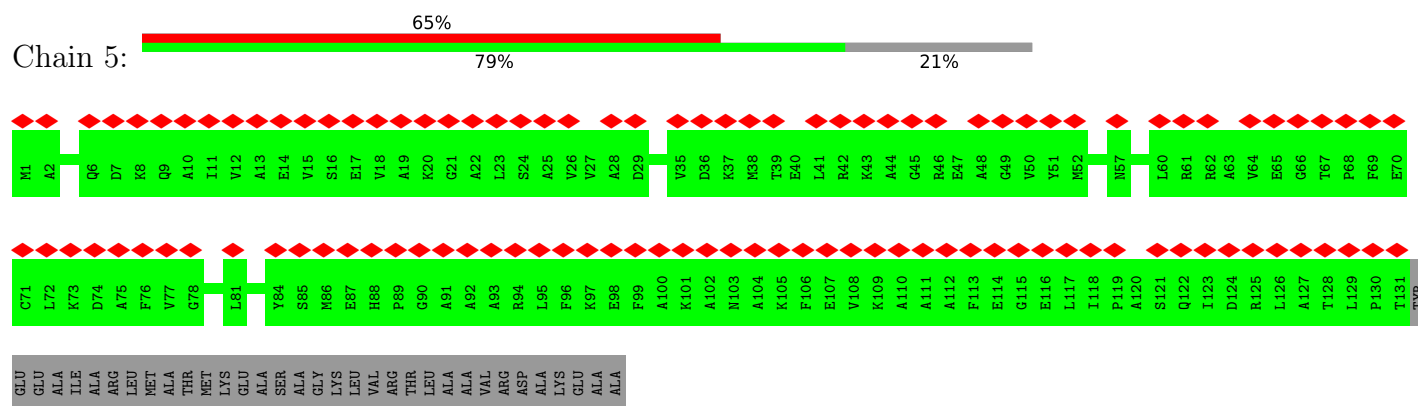
- Molecule 4: 50S ribosomal protein L35



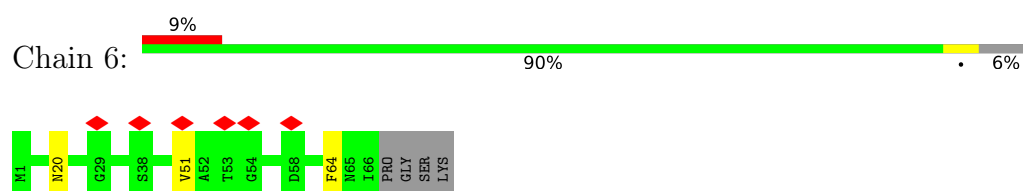
- Molecule 5: 50S ribosomal protein L36



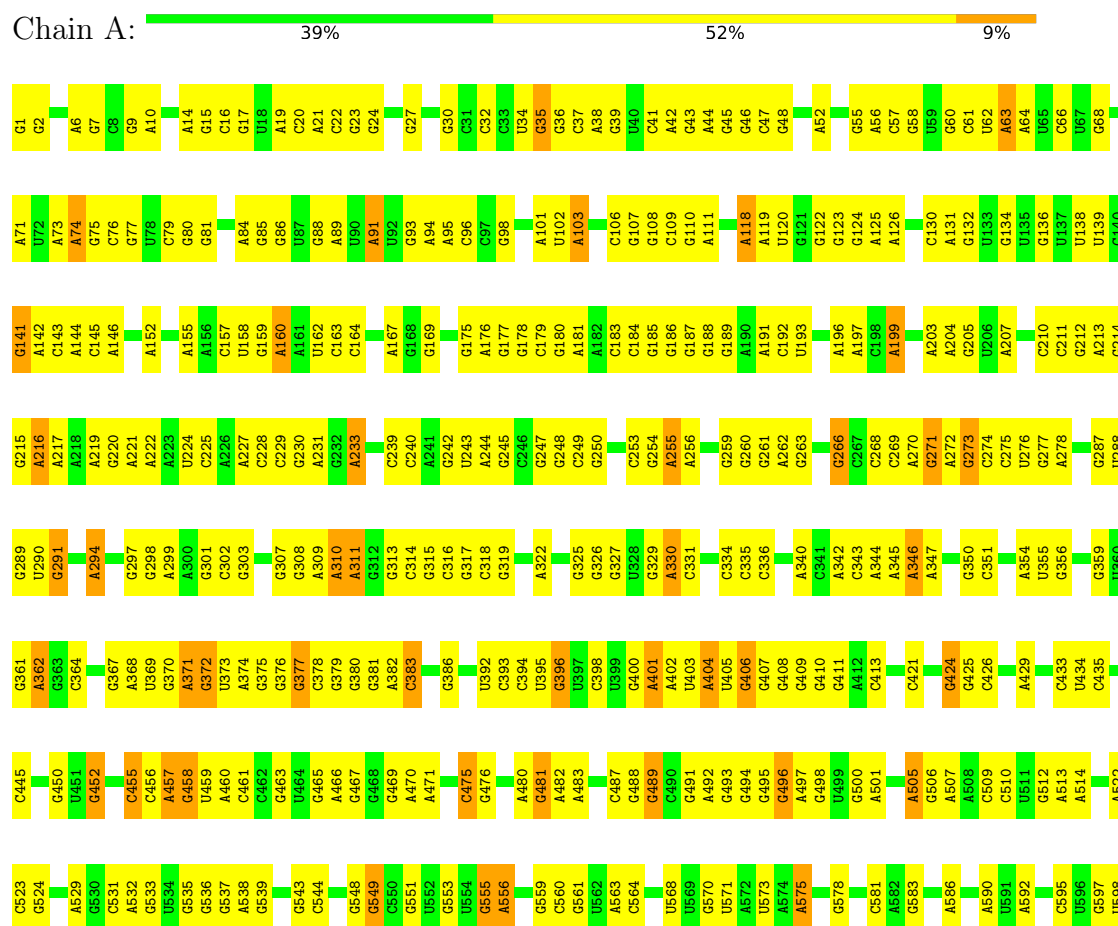
- Molecule 6: 50S ribosomal protein L10



- Molecule 7: 50S ribosomal protein L31



- Molecule 8: 23S ribosomal RNA



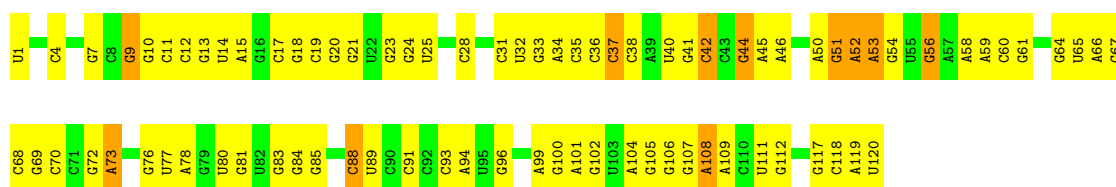
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G1472	G1473	A1395	U1312	U1313	G1317	C1320	G1323	G1332	G1333	G1334	C1335	A1336	G1337	G1338	U1415	U1416	C1417	G1418	A1419	A1420	G1421	G1422	G1423	G1424	G1425	A1426	A1427	G1428	G1429	G1430	A1433	A1434	G1435	G1436	G1445	G1448	G1449	G1450	C1451	G1452	C1453	C1454	G1455	G1456	U1457	U1458	U1539	G1540	C1541	U1542	A1544	A1548	A1549							
A1551	A1552	A1553	C1556	C1557	C1558	C1561	A1566	A1567	G1568	A1569	A1570	A1571	A1572	C1573	C1574	C1577	U1578	A1579	A1580	A1583	U1584	C1585	A1586	G1587	C1588	U1589	A1590	A1591	C1592	A1593	A1596	C1600	A1603	C1604	C1606	C1607	A1608	A1609	A1610	C1615	A1616	C1617	A1618	G1619	A1626	G1627														
G1395	C1398	C1399	U1400	G1401	U1402	A1403	C1404	G1407	G1408	U1409	G1410	U1415	U1416	C1417	G1418	A1419	A1420	G1421	G1422	G1423	G1424	G1425	A1426	A1427	G1428	G1429	G1430	A1433	A1434	G1435	G1436	G1445	G1448	G1449	G1450	C1451	G1452	C1453	C1454	G1455	G1456	U1457	U1458	G1459	U1460	C1461	A1465	A1469	A1470	G1471										
U1312	U1313	G1317	C1320	G1323	G1332	G1333	G1334	C1335	A1336	G1337	G1338	G1341	A1342	C1345	G1346	A1347	C1348	C1349	A1359	G1360	G1361	C1362	A1365	A1366	A1367	G1368	C1370	G1371	U1372	A1373	G1374	G1377	A1378	U1379	G1380	G1381	G1382	A1383	A1384	C1385	G1386	A1387	G1388	G1389																
G1227	G1228	C1229	U1231	U1232	C1233	A1237	G1238	G1239	U1240	A1241	A1244	A1247	C1251	G1252	A1253	A1254	U1255	G1256	A1280	C1281	G1285	G1286	G1287	H1291	G1292	U1294	G1295	G1296	G1300	A1301	A1302	G1303	G1304	C1305	C1306	A1307	A1308	G1311																						
G1161	G1162	G1163	A1164	A1165	G1166	G1167	G1168	A1169	G1170	G1171	C1172	U1173	U1174	A1175	G1176	G1177	G1178	G1179	U1180	U1181	G1182	G1186	G1187	U1188	A1189	G1190	G1191	G1192	G1193	A1194	G1197	C1200	H1201	G1202	U1203	A1204	C1207	G1208	U1209	G1210	C1211	U1212	A1213	A1214	G1215	G1216	U1217	G1218	U1219	A1220	U1221	U1222	G1225	U1226						
A1098	G1099	C1100	U1101	C1102	G1103	C1104	U1105	G1106	G1107	G1110	G1111	G1112	U1113	C1114	G1115	G1116	G1117	C1118	U1119	G1120	C1121	G1122	G1123	G1124	G1125	A1126	G1127	G1128	A1129	U1130	G1131	U1132	A1133	A1134	C1135	G1136	G1137	G1138	G1139	C1140	U1141	A1142	A1143	A1147	U1148	G1149	C1150	A1151	C1152	C1153	U1154	A1155	A1156	G1157	C1158	U1159	G1160			
G1037	G1038	A1039	G966	G971	G972	A973	G974	A975	G976	G977	G978	A979	C982	A983	A984	A988	G989	A990	C991	C992	C995	A996	U997	C998	A999	C999	C999	A1000	A1001	C1005	C1006	C1007	A1008	A1009	G938	G939	G940	A941	G942	A943	C944	A945	C946	G949	G950	C951	G952	G953	A1027	A1028	U954	U955	C956	A959	A960	C961	G962			
U963	C964	C965	A899	A900	C903	G904	G907	G908	A909	A910	A911	C912	U913	G914	C915	G916	C917	U918	A919	U919	A920	C921	C922	G923	G924	A925	A926	A927	A928	U929	C930	U931	A936	C937	G938	G939	G940	A941	G942	A943	C944	A945	C946	G949	G950	C951	G952	G953	A1027	A1028	U954	U955	C956	A959	A960	C961	G962			
G831	U832	A833	G834	G835	C836	C837	G841	U842	G843	A844	A845	U846	U847	G848	G849	U850	C851	U852	C853	C854	G855	C921	C922	G856	G857	G858	C859	U860	A861	G862	A863	C864	C865	A866	C867	G868	G869	U870	U871	G874	G875	C876	A877	G881	G882	G883	U884	C885	A886	A887	G888	A889	A1028	U954	U955	C956	A959	A960	C961	G962
C758	G759	G760	A761	U762	G763	A764	C765	G770	G771	G772	G773	G774	G775	G776	G777	G778	U779	G780	A781	A782	A783	G784	G785	C786	C787	C791	A792	A793	A794	C795	C796	A797	G798	G799	A800	G801	A802	G805	G808	C812	U813	C814	C815	C816	C817	G818	A819	A820	G823	U827	U828	A829	G830							
A677	C678	C679	C680	G681	G682	U683	G684	A685	U686	G690	A693	U694	G695	G696	G697	G701	G704	A705	A706	G707	G708	G712	G713	A718	C719	U720	A721	A722	G726	A727	G728	G729	A730	C731	G732	G733	A734	A735	G739	C740	G745	U746	C747	G748	A749	A750	A751	A752	G757											
A603	A609	G612	A613	A614	U615	G617	G618	A621	G622	C623	A627	G628	G629	A631	A632	A633	G634	G635	G636	A637	G638	U639	C640	C645	U646	G647	G651	U652	U653	A654	A655	G656	G659	C660	A661	G664	U665	A666	U667	G668	G669	A670	C671	C672	C673	G674	A675	A676												





• Molecule 9: 5S ribosomal RNA

Chain B: 32% 59% 9%



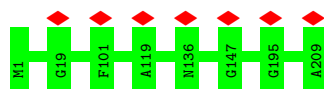
• Molecule 10: 50S ribosomal protein L2

Chain C: 5% 96% ..



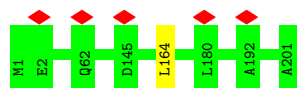
• Molecule 11: 50S ribosomal protein L3

Chain D: 100%



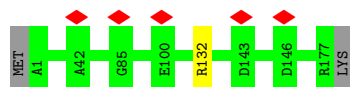
• Molecule 12: 50S ribosomal protein L4

Chain E: 100%



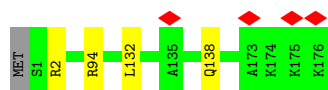
• Molecule 13: 50S ribosomal protein L5

Chain F: 98% ..



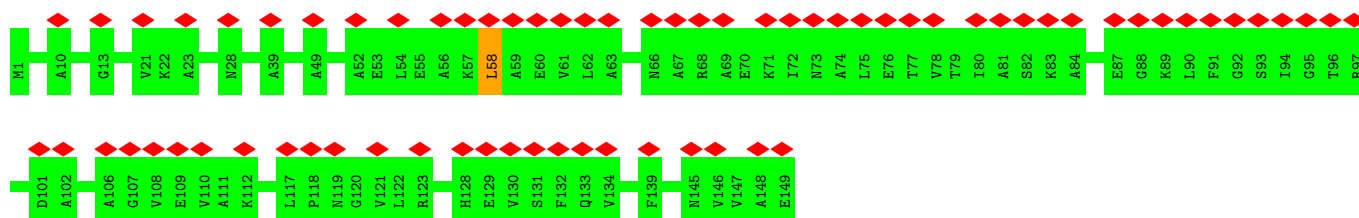
- Molecule 14: 50S ribosomal protein L6

Chain G:  97%




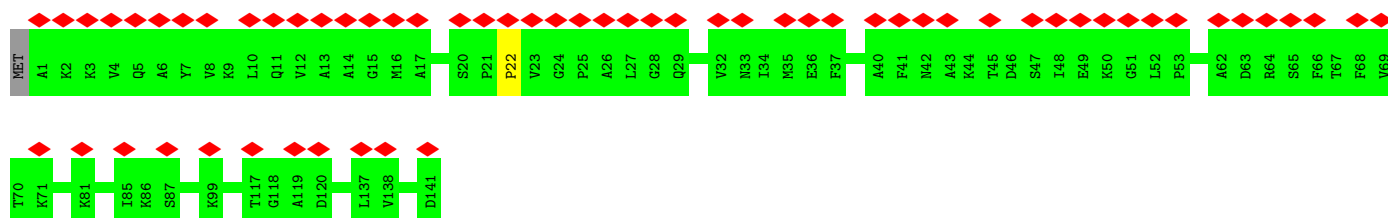
- Molecule 15: 50S ribosomal protein L9

Chain H:  47% 99%



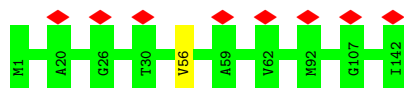
- Molecule 16: 50S ribosomal protein L11

Chain I:  43% 99%



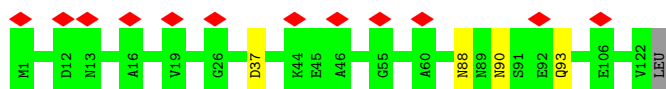
- Molecule 17: 50S ribosomal protein L13

Chain J:  6% 99%



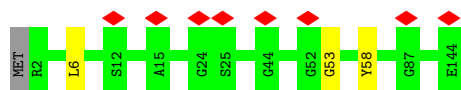
- Molecule 18: 50S ribosomal protein L14

Chain K:  10% 96%

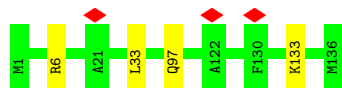


- Molecule 19: 50S ribosomal protein L15

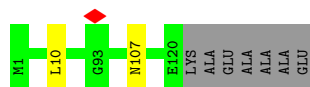
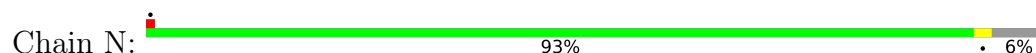
Chain L:  6% 97%



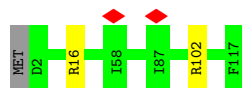
- Molecule 20: 50S ribosomal protein L16



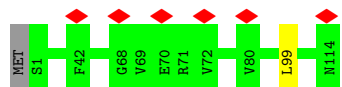
- Molecule 21: 50S ribosomal protein L17



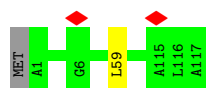
- Molecule 22: 50S ribosomal protein L18



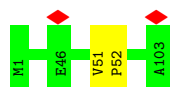
- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20

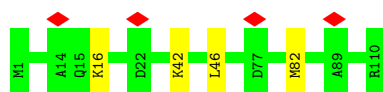


- Molecule 25: 50S ribosomal protein L21




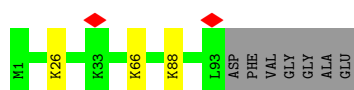
- Molecule 26: 50S ribosomal protein L22

Chain S:  96%



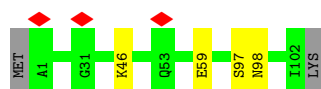
- Molecule 27: 50S ribosomal protein L23

Chain T:  90%



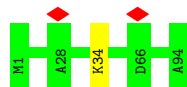
- Molecule 28: 50S ribosomal protein L24

Chain U:  94%



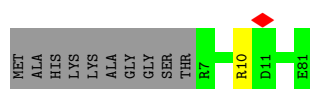
- Molecule 29: 50S ribosomal protein L25

Chain V:  99%



- Molecule 30: 50S ribosomal protein L27

Chain W:  87%



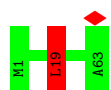
- Molecule 31: 50S ribosomal protein L28

Chain X:  94%



- Molecule 32: 50S ribosomal protein L29

Chain Y:  98%



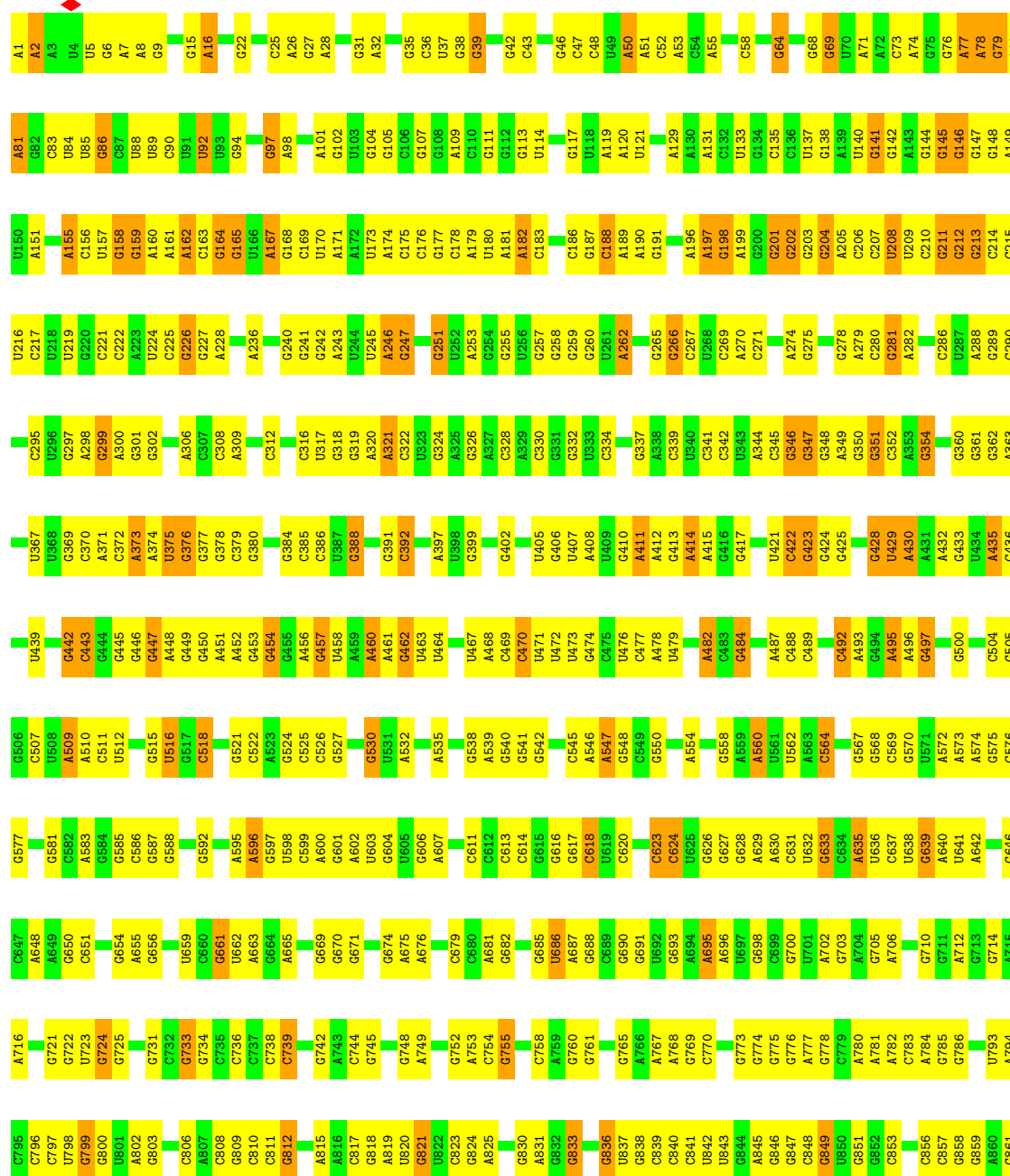
- Molecule 33: 50S ribosomal protein L30

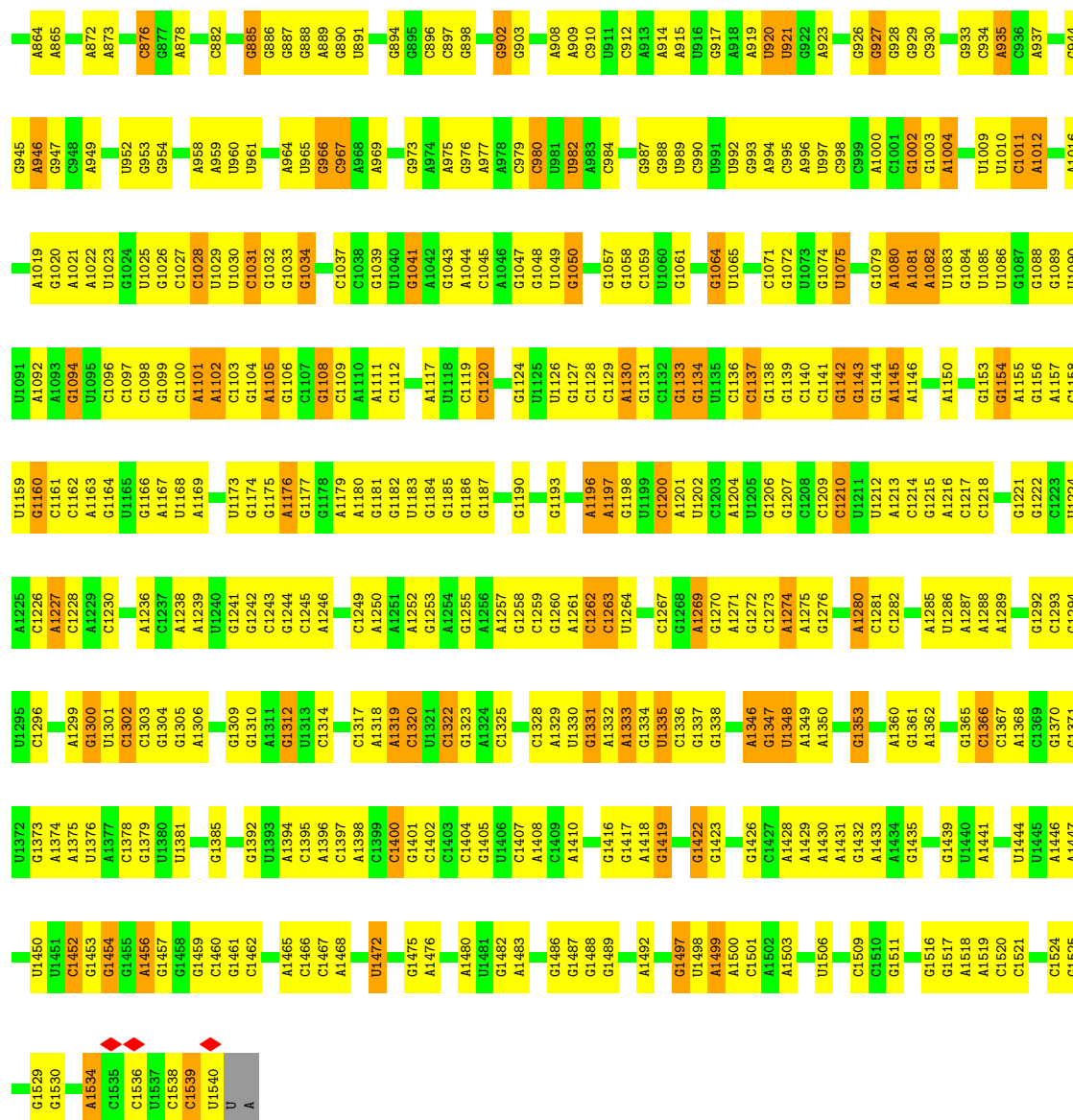
Chain Z:  98%



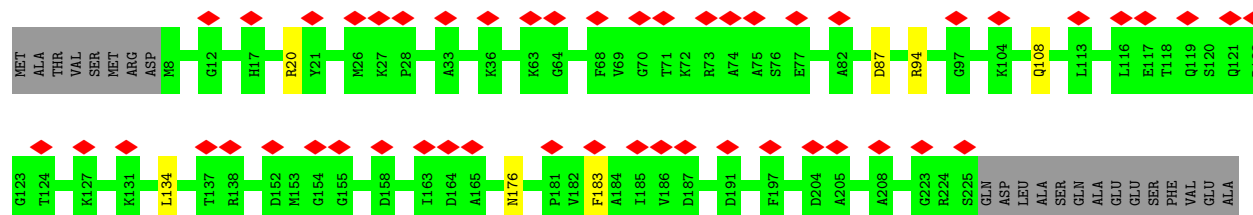
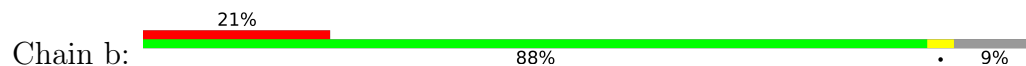
- Molecule 34: 16S ribosomal RNA

Chain a:  39% 49% 11%

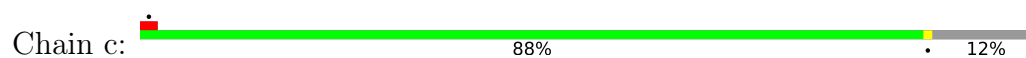


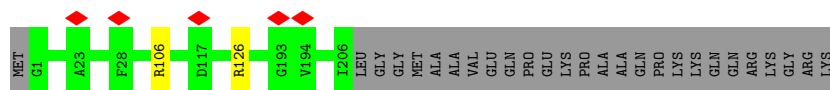


• Molecule 35: 30S ribosomal protein S2

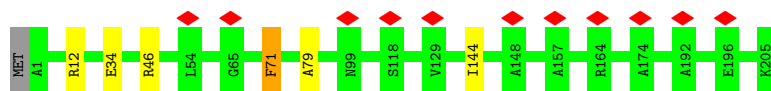


• Molecule 36: 30S ribosomal protein S3

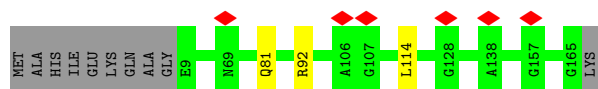




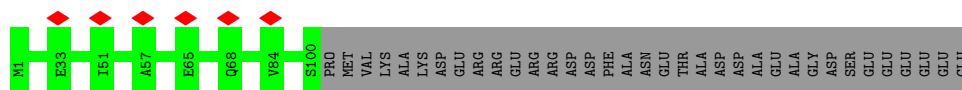
- Molecule 37: 30S ribosomal protein S4



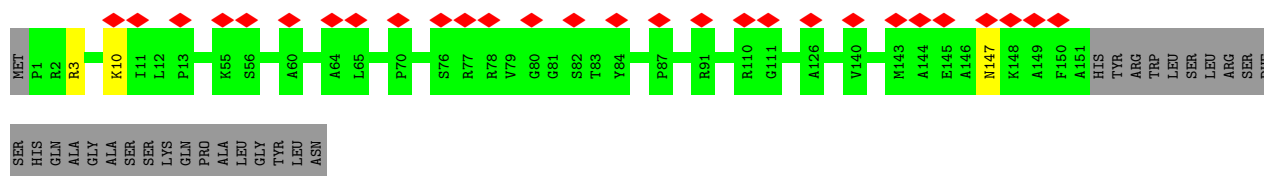
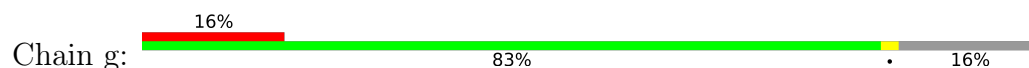
- Molecule 38: 30S ribosomal protein S5



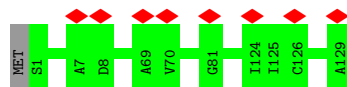
- Molecule 39: 30S ribosomal protein S6



- Molecule 40: 30S ribosomal protein S7

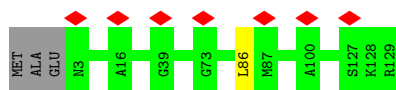


- Molecule 41: 30S ribosomal protein S8

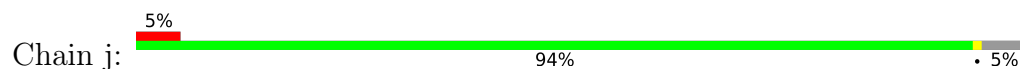


- Molecule 42: 30S ribosomal protein S9

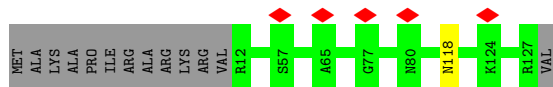
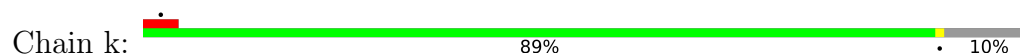




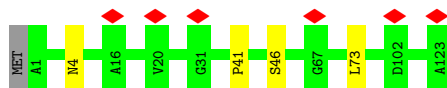
- Molecule 43: 30S ribosomal protein S10



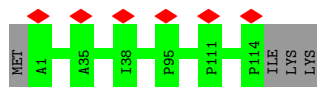
- Molecule 44: 30S ribosomal protein S11



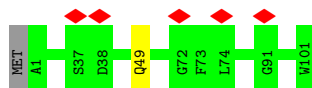
- Molecule 45: 30S ribosomal protein S12



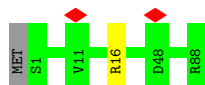
- Molecule 46: 30S ribosomal protein S13



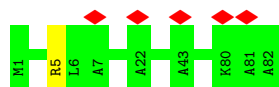
- Molecule 47: 30S ribosomal protein S14



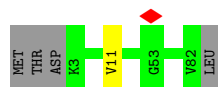
- Molecule 48: 30S ribosomal protein S15



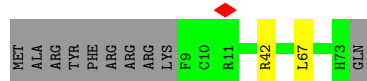
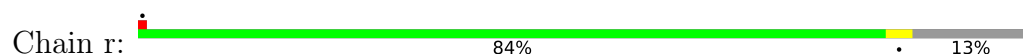
- Molecule 49: 30S ribosomal protein S16



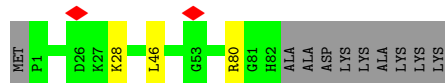
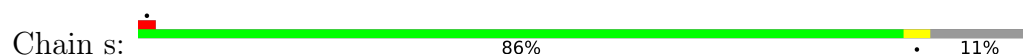
- Molecule 50: 30S ribosomal protein S17



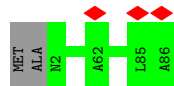
- Molecule 51: 30S ribosomal protein S18



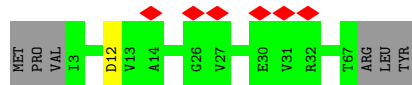
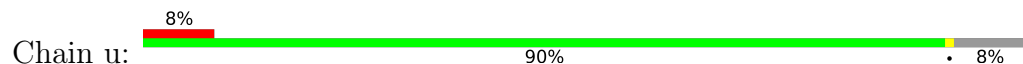
- Molecule 52: 30S ribosomal protein S19



- Molecule 53: 30S ribosomal protein S20

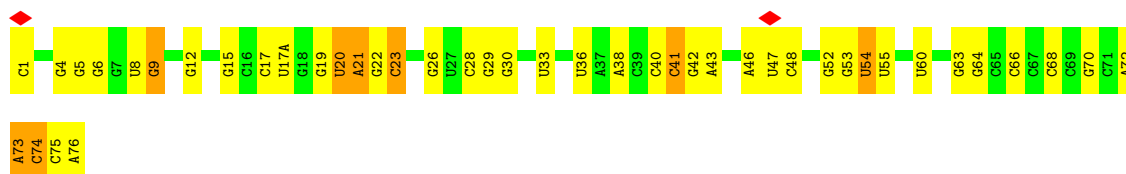


- Molecule 54: 30S ribosomal protein S21

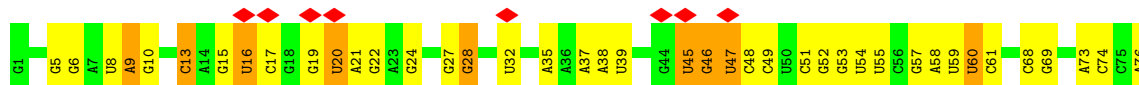


- Molecule 55: P-site tRNA(fMet)

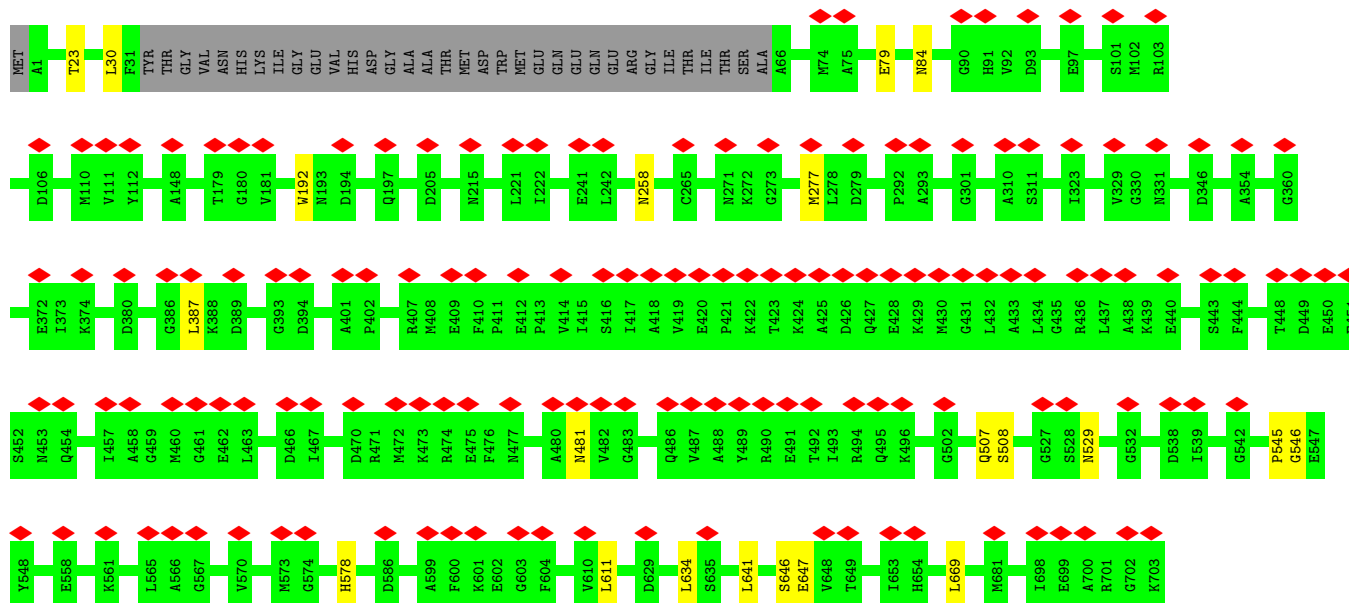




• Molecule 56: P-site fMet-Phe-tRNA(Phe)



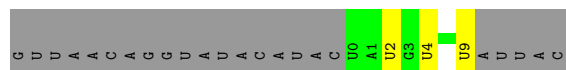
• Molecule 57: Elongation factor G



• Molecule 58: Dipeptide (FME-PHE)



• Molecule 59: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6168	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	10.963	Depositor
Minimum map value	-5.358	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (\AA)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 6MZ, OMG, MIA, FME, 2MG, 5MU, H2U, 4OC, 1MG, MA6, PSU, 3TD, 5MC, 2MA, OMU, UR3, GDP, AM2, G7M, ZN, 4SU, OMC

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	0	0.81	0/450	1.06	0/599
2	1	0.71	0/416	1.15	0/554
3	2	0.82	0/380	1.08	1/498 (0.2%)
4	3	0.81	0/513	1.07	0/676
5	4	0.77	0/303	1.17	0/397
6	5	0.31	0/646	0.62	0/898
7	6	0.76	0/531	1.04	0/709
8	A	1.65	635/69266 (0.9%)	1.90	2790/108055 (2.6%)
9	B	1.68	28/2873 (1.0%)	2.02	154/4478 (3.4%)
10	C	0.78	1/2121 (0.0%)	1.05	4/2852 (0.1%)
11	D	0.76	0/1586	0.99	0/2134
12	E	0.74	0/1571	0.99	1/2113 (0.0%)
13	F	0.79	0/1434	0.99	1/1926 (0.1%)
14	G	0.76	0/1343	0.98	2/1816 (0.1%)
15	H	0.62	0/1122	0.87	1/1515 (0.1%)
16	I	0.37	0/692	0.66	0/960
17	J	0.82	0/1152	1.03	1/1551 (0.1%)
18	K	0.73	0/947	1.01	0/1268
19	L	0.72	0/1054	1.17	2/1403 (0.1%)
20	M	0.83	0/1093	1.08	3/1460 (0.2%)
21	N	0.77	1/973 (0.1%)	1.14	1/1301 (0.1%)
22	O	0.73	0/902	0.94	2/1209 (0.2%)
23	P	0.81	0/929	1.02	1/1242 (0.1%)
24	Q	0.82	0/960	1.04	1/1278 (0.1%)
25	R	0.81	0/829	1.04	0/1107
26	S	0.79	0/864	1.10	4/1156 (0.3%)
27	T	0.82	0/744	1.10	1/994 (0.1%)
28	U	0.93	1/787 (0.1%)	1.12	1/1051 (0.1%)
29	V	0.93	0/766	0.99	0/1025
30	W	0.76	0/582	1.02	0/769
31	X	0.87	2/635 (0.3%)	1.17	2/848 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.77	0/510	1.08	1/677 (0.1%)
33	Z	0.78	0/453	1.12	0/605
34	a	1.52	254/36725 (0.7%)	1.85	1350/57285 (2.4%)
35	b	0.62	0/1735	0.86	2/2338 (0.1%)
36	c	0.73	0/1651	0.93	1/2225 (0.0%)
37	d	0.70	0/1665	0.96	1/2227 (0.0%)
38	e	0.73	0/1154	1.00	1/1554 (0.1%)
39	f	0.71	0/835	0.89	0/1128
40	g	0.63	0/1195	0.86	1/1602 (0.1%)
41	h	0.66	0/989	0.86	0/1326
42	i	0.65	0/1034	0.93	1/1375 (0.1%)
43	j	0.66	0/796	0.94	1/1077 (0.1%)
44	k	0.65	0/885	0.94	0/1195
45	l	0.75	0/969	1.09	1/1300 (0.1%)
46	m	0.65	0/892	0.95	0/1193
47	n	0.68	0/811	0.97	0/1081
48	o	0.66	0/722	0.97	0/964
49	p	0.70	0/659	0.96	1/884 (0.1%)
50	q	0.81	0/657	1.00	1/881 (0.1%)
51	r	0.73	1/544 (0.2%)	0.98	1/731 (0.1%)
52	s	0.66	0/675	1.02	2/908 (0.2%)
53	t	0.79	0/671	0.90	0/888
54	u	0.59	0/512	0.91	0/683
55	v	1.45	16/1745 (0.9%)	1.88	65/2716 (2.4%)
56	w	1.09	2/1650 (0.1%)	1.48	27/2569 (1.1%)
57	x	0.72	1/5288 (0.0%)	0.95	6/7152 (0.1%)
58	y	0.29	0/11	0.79	0/13
59	z	0.89	0/230	1.17	0/355
All	All	1.39	942/164127 (0.6%)	1.68	4436/244774 (1.8%)

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
4	3	0	1
25	R	0	1
28	U	0	1
32	Y	0	1
35	b	0	1
37	d	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
54	u	0	1
57	x	0	1
All	All	0	10

The worst 5 of 942 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1	G	OP3-P	-10.75	1.48	1.61
9	B	1	U	OP3-P	-10.72	1.48	1.61
55	v	1	C	OP3-P	-10.66	1.48	1.61
8	A	1055	G	N9-C4	-10.60	1.29	1.38
34	a	640	A	N9-C4	-9.66	1.32	1.37

The worst 5 of 4436 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1055	G	N3-C4-C5	16.27	136.74	128.60
34	a	921	U	C6-N1-C2	-14.36	112.39	121.00
8	A	1055	G	N3-C4-N9	-14.11	117.53	126.00
34	a	201	G	N3-C4-C5	12.85	135.03	128.60
34	a	604	G	N3-C4-C5	12.82	135.01	128.60

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	3	30	HIS	Peptide
25	R	51	VAL	Peptide
28	U	97	SER	Peptide
32	Y	19	LEU	Peptide
35	b	87	ASP	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
1	0	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	8	38
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	107 (83%)	22 (17%)	0	100	100
7	6	64/70 (91%)	57 (89%)	5 (8%)	2 (3%)	3	22
10	C	269/273 (98%)	245 (91%)	24 (9%)	0	100	100
11	D	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
12	E	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
13	F	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
14	G	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
15	H	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
16	I	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	19	57
17	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
18	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
19	L	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
20	M	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
21	N	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	O	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
23	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	91 (90%)	9 (9%)	1 (1%)	13	49
26	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
27	T	91/100 (91%)	81 (89%)	9 (10%)	1 (1%)	12	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	89 (89%)	10 (10%)	1 (1%)	13	49
29	V	92/94 (98%)	92 (100%)	0	0	100	100
30	W	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
31	X	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
32	Y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	8	38
33	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
35	b	216/240 (90%)	180 (83%)	35 (16%)	1 (0%)	25	65
36	c	204/233 (88%)	193 (95%)	11 (5%)	0	100	100
37	d	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	25	65
38	e	155/167 (93%)	140 (90%)	15 (10%)	0	100	100
39	f	98/135 (73%)	89 (91%)	9 (9%)	0	100	100
40	g	149/179 (83%)	134 (90%)	15 (10%)	0	100	100
41	h	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
42	i	125/130 (96%)	106 (85%)	19 (15%)	0	100	100
43	j	96/103 (93%)	78 (81%)	18 (19%)	0	100	100
44	k	114/129 (88%)	103 (90%)	11 (10%)	0	100	100
45	l	121/124 (98%)	104 (86%)	16 (13%)	1 (1%)	16	55
46	m	112/118 (95%)	100 (89%)	12 (11%)	0	100	100
47	n	99/102 (97%)	90 (91%)	9 (9%)	0	100	100
48	o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
49	p	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
50	q	78/84 (93%)	65 (83%)	13 (17%)	0	100	100
51	r	63/75 (84%)	54 (86%)	9 (14%)	0	100	100
52	s	80/92 (87%)	72 (90%)	8 (10%)	0	100	100
53	t	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
54	u	63/71 (89%)	51 (81%)	12 (19%)	0	100	100
57	x	666/704 (95%)	588 (88%)	71 (11%)	7 (1%)	12	47
All	All	6516/6924 (94%)	5877 (90%)	621 (10%)	18 (0%)	38	73

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	6	64	PHE

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Mol	Chain	Res	Type
57	x	387	LEU
57	x	545	PRO
57	x	546	GLY
4	3	31	ILE

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	
1	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	37 (97%)	1 (3%)	41	59
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	58 (98%)	1 (2%)	56	72
10	C	216/218 (99%)	213 (99%)	3 (1%)	62	75
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	135 (98%)	2 (2%)	60	75
15	H	114/114 (100%)	113 (99%)	1 (1%)	75	83
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	99 (96%)	4 (4%)	27	48
19	L	102/103 (99%)	101 (99%)	1 (1%)	73	82
20	M	109/109 (100%)	108 (99%)	1 (1%)	75	83
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	R	84/84 (100%)	84 (100%)	0	100	100
26	S	93/93 (100%)	92 (99%)	1 (1%)	70	80
27	T	80/84 (95%)	79 (99%)	1 (1%)	65	77
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	77 (99%)	1 (1%)	65	77
30	W	57/63 (90%)	56 (98%)	1 (2%)	54	71
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	177 (98%)	3 (2%)	56	72
36	c	170/190 (90%)	169 (99%)	1 (1%)	84	88
37	d	172/173 (99%)	170 (99%)	2 (1%)	67	79
38	e	114/126 (90%)	112 (98%)	2 (2%)	54	71
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	122 (98%)	2 (2%)	58	74
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	86 (100%)	0	100	100
44	k	89/99 (90%)	88 (99%)	1 (1%)	70	80
45	l	103/104 (99%)	101 (98%)	2 (2%)	52	69
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	78 (99%)	1 (1%)	65	77
48	o	76/77 (99%)	75 (99%)	1 (1%)	65	77
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	74 (100%)	0	100	100
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	71 (99%)	1 (1%)	62	75
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
57	x	551/578 (95%)	545 (99%)	6 (1%)	70	80
58	y	1/1 (100%)	1 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5178/5408 (96%)	5138 (99%)	40 (1%)	77 85

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	k	118	ASN
57	x	84	ASN
45	l	4	ASN
48	o	16	ARG
57	x	481	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	l	44	GLN
38	e	81	GLN
44	k	21	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1536/1542 (99%)	447 (29%)	0
55	v	76/77 (98%)	20 (26%)	0
56	w	74/76 (97%)	23 (31%)	0
59	z	9/33 (27%)	3 (33%)	0
8	A	2898/2903 (99%)	593 (20%)	39 (1%)
9	B	119/120 (99%)	21 (17%)	3 (2%)
All	All	4712/4751 (99%)	1107 (23%)	42 (0%)

5 of 1107 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	34	U
8	A	35	G
8	A	46	G
8	A	62	U

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	2287	A
8	A	2406	A
8	A	2308	G
8	A	2346	A
8	A	2750	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

46 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
8	PSU	A	2457	8	18,21,22	3.52	8 (44%)	22,30,33	2.16	4 (18%)
34	5MC	a	967	34	18,22,23	3.28	7 (38%)	26,32,35	1.29	4 (15%)
56	PSU	w	55	56	18,21,22	1.43	3 (16%)	22,30,33	1.91	5 (22%)
34	G7M	a	527	34	20,26,27	2.07	4 (20%)	17,39,42	1.44	3 (17%)
56	MIA	w	37	56	24,31,32	2.44	4 (16%)	26,44,47	2.74	10 (38%)
34	MA6	a	1518	34	18,26,27	1.53	3 (16%)	19,38,41	3.38	3 (15%)
34	4OC	a	1402	34	20,23,24	3.16	8 (40%)	26,32,35	1.13	3 (11%)
8	PSU	A	955	8	18,21,22	3.55	7 (38%)	22,30,33	1.98	4 (18%)
8	2MA	A	2503	8	17,25,26	2.33	5 (29%)	17,37,40	1.51	4 (23%)
8	PSU	A	2580	8	18,21,22	3.28	7 (38%)	22,30,33	2.54	6 (27%)
8	OMU	A	2552	8	19,22,23	2.66	5 (26%)	26,31,34	2.07	6 (23%)
8	6MZ	A	1618	8	18,25,26	1.72	6 (33%)	16,36,39	2.94	4 (25%)
8	2MG	A	1835	8	18,26,27	2.08	7 (38%)	16,38,41	2.13	4 (25%)
8	2MG	A	2445	8	18,26,27	1.89	5 (27%)	16,38,41	1.36	2 (12%)
8	PSU	A	746	8	18,21,22	3.74	6 (33%)	22,30,33	1.68	5 (22%)
8	5MC	A	747	8	18,22,23	3.41	7 (38%)	26,32,35	1.39	2 (7%)
55	PSU	v	55	55	18,21,22	3.82	6 (33%)	22,30,33	1.89	5 (22%)
56	4SU	w	8	56	18,21,22	1.89	5 (27%)	26,30,33	2.11	6 (23%)
34	2MG	a	1207	34	18,26,27	2.13	7 (38%)	16,38,41	1.50	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	2605	8	18,21,22	3.48	7 (38%)	22,30,33	2.27	6 (27%)
8	3TD	A	1915	8	18,22,23	7.27	11 (61%)	22,32,35	1.73	2 (9%)
34	UR3	a	1498	34	19,22,23	2.46	6 (31%)	26,32,35	1.12	2 (7%)
56	PSU	w	32	56	18,21,22	3.91	6 (33%)	22,30,33	1.85	6 (27%)
34	2MG	a	1516	34	18,26,27	2.32	7 (38%)	16,38,41	1.40	3 (18%)
34	PSU	a	516	34	18,21,22	3.65	7 (38%)	22,30,33	1.90	5 (22%)
55	5MU	v	54	55	19,22,23	4.60	7 (36%)	28,32,35	3.73	10 (35%)
56	PSU	w	39	56	18,21,22	3.75	6 (33%)	22,30,33	2.22	5 (22%)
8	PSU	A	2604	8	18,21,22	3.51	8 (44%)	22,30,33	2.41	6 (27%)
8	PSU	A	2504	8	18,21,22	3.85	7 (38%)	22,30,33	1.84	4 (18%)
56	5MU	w	54	56	19,22,23	1.38	6 (31%)	28,32,35	2.21	9 (32%)
8	PSU	A	1911	8	18,21,22	3.58	7 (38%)	22,30,33	1.96	5 (22%)
8	G7M	A	2069	8	20,26,27	1.78	6 (30%)	17,39,42	1.85	4 (23%)
8	5MC	A	1962	8	18,22,23	2.96	7 (38%)	26,32,35	1.34	2 (7%)
8	PSU	A	1917	8	18,21,22	3.68	6 (33%)	22,30,33	1.92	5 (22%)
34	MA6	a	1519	34	18,26,27	1.53	3 (16%)	19,38,41	3.54	5 (26%)
8	6MZ	A	2030	8	18,25,26	1.80	6 (33%)	16,36,39	2.37	5 (31%)
8	1MG	A	745	8	18,26,27	2.35	6 (33%)	19,39,42	1.58	5 (26%)
55	H2U	v	20	55	18,21,22	3.58	3 (16%)	21,30,33	2.03	5 (23%)
8	5MU	A	1939	8	19,22,23	4.63	7 (36%)	28,32,35	3.83	9 (32%)
34	5MC	a	1407	34	18,22,23	3.16	7 (38%)	26,32,35	1.09	2 (7%)
55	4SU	v	8	55	18,21,22	3.41	8 (44%)	26,30,33	2.15	4 (15%)
8	OMC	A	2498	8	19,22,23	3.08	8 (42%)	26,31,34	0.84	0
56	G7M	w	46	56	20,26,27	4.39	14 (70%)	17,39,42	2.21	3 (17%)
8	OMG	A	2251	8,56	18,26,27	2.49	8 (44%)	19,38,41	1.52	5 (26%)
34	2MG	a	966	34	18,26,27	0.99	1 (5%)	16,38,41	1.40	3 (18%)
58	FME	y	101	58	8,9,10	1.03	1 (12%)	7,9,11	1.05	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
34	5MC	a	967	34	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
34	G7M	a	527	34	-	2/3/25/26	0/3/3/3
56	MIA	w	37	56	-	3/11/33/34	0/3/3/3
34	MA6	a	1518	34	-	0/7/29/30	0/3/3/3
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
8	2MA	A	2503	8	-	2/3/25/26	0/3/3/3
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
8	OMU	A	2552	8	-	2/9/27/28	0/2/2/2
8	6MZ	A	1618	8	-	2/5/27/28	0/3/3/3
8	2MG	A	1835	8	-	2/5/27/28	0/3/3/3
8	2MG	A	2445	8	-	2/5/27/28	0/3/3/3
8	PSU	A	746	8	-	1/7/25/26	0/2/2/2
8	5MC	A	747	8	-	2/7/25/26	0/2/2/2
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/5/27/28	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	2/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/5/27/28	0/3/3/3
34	PSU	a	516	34	-	0/7/25/26	0/2/2/2
55	5MU	v	54	55	-	3/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	1/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/3/25/26	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	4/7/29/30	0/3/3/3
8	6MZ	A	2030	8	-	3/5/27/28	0/3/3/3
8	1MG	A	745	8	-	0/3/25/26	0/3/3/3
55	H2U	v	20	55	-	1/7/38/39	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
8	OMC	A	2498	8	-	2/9/27/28	0/2/2/2
56	G7M	w	46	56	-	1/3/25/26	0/3/3/3
8	OMG	A	2251	8,56	-	0/5/27/28	0/3/3/3
34	2MG	a	966	34	-	3/5/27/28	0/3/3/3
58	FME	y	101	58	-	4/7/9/11	-

The worst 5 of 286 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	O4'-C1'	17.31	1.67	1.43
8	A	1915	3TD	C2'-C1'	-15.67	1.33	1.53
8	A	1915	3TD	C6-C5	13.05	1.50	1.35
55	v	20	H2U	C2-N1	12.16	1.53	1.35
8	A	1939	5MU	C2-N1	10.72	1.55	1.38

The worst 5 of 205 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1939	5MU	C5-C4-N3	13.01	126.41	115.31
34	a	1519	MA6	N1-C6-N6	-12.93	103.44	117.06
34	a	1518	MA6	N1-C6-N6	-12.58	103.82	117.06
55	v	54	5MU	C5-C4-N3	12.04	125.59	115.31
8	A	1939	5MU	C5-C6-N1	-10.62	112.41	123.34

There are no chirality outliers.

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	967	5MC	O4'-C4'-C5'-O5'
34	a	967	5MC	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C6
34	a	1498	UR3	O4'-C1'-N1-C2
34	a	1519	MA6	C5-C6-N6-C9

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
62	GDP	x	801	-	24,30,30	5.24	12 (50%)	30,47,47	1.86	11 (36%)
61	AM2	a	2001	-	40,40,40	0.24	0	53,60,60	0.60	2 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	GDP	x	801	-	-	7/12/32/32	0/3/3/3
61	AM2	a	2001	-	-	4/12/84/84	0/4/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	x	801	GDP	C2'-C1'	-17.38	1.27	1.53
62	x	801	GDP	O4'-C1'	10.27	1.55	1.41
62	x	801	GDP	C3'-C4'	-10.01	1.27	1.53
62	x	801	GDP	C2-N2	4.96	1.46	1.34
62	x	801	GDP	O4'-C4'	4.81	1.55	1.45

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	N2-C2-N1	4.60	126.50	116.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	C3'-C2'-C1'	3.21	105.81	100.98
62	x	801	GDP	N2-C2-N3	-3.20	113.50	119.74
62	x	801	GDP	C2'-C3'-C4'	2.63	107.75	102.64
62	x	801	GDP	PA-O3A-PB	-2.62	123.84	132.83

There are no chirality outliers.

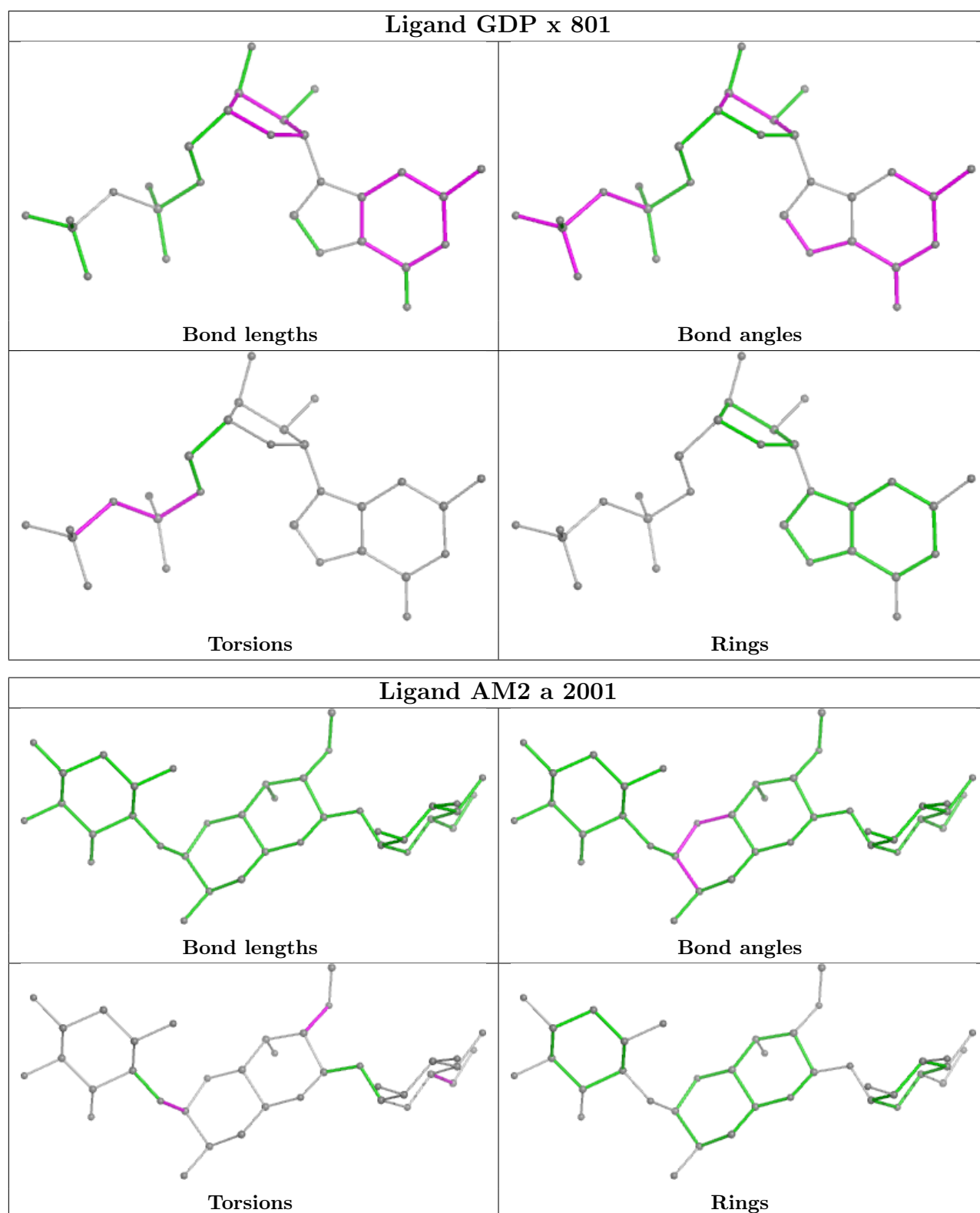
5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	a	2001	AM2	CA8-CA7-NA7-CA9
62	x	801	GDP	C5'-O5'-PA-O3A
61	a	2001	AM2	OB1-CB5-CB6-OB6
62	x	801	GDP	PA-O3A-PB-O3B
61	a	2001	AM2	OA4-CA1-OA1-CC1

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

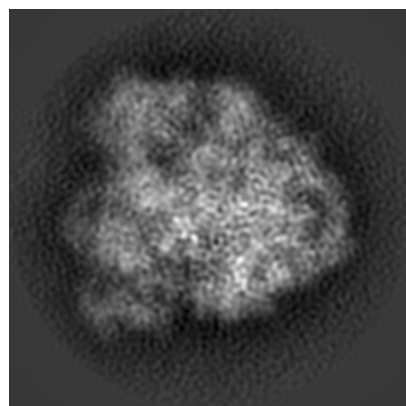
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13465. These allow visual inspection of the internal detail of the map and identification of artifacts.

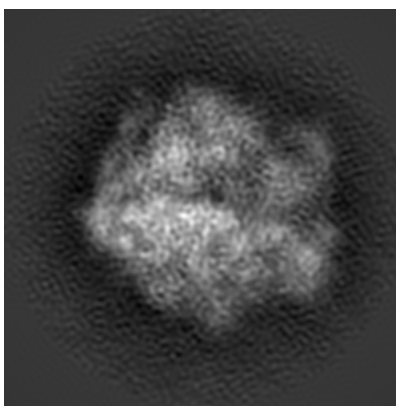
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

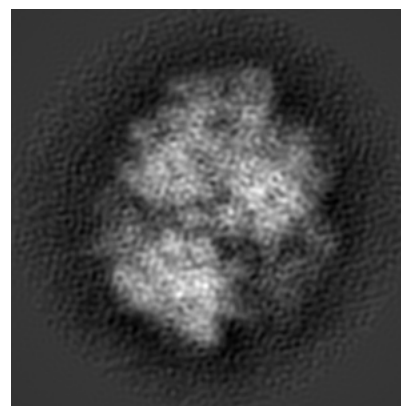
6.1.1 Primary map



X

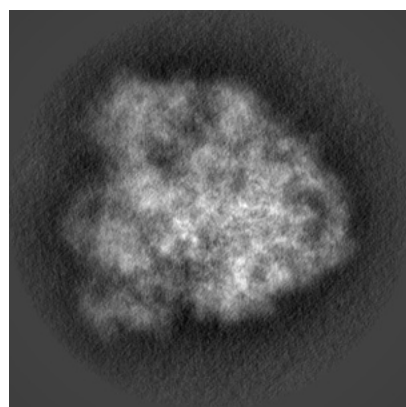


Y

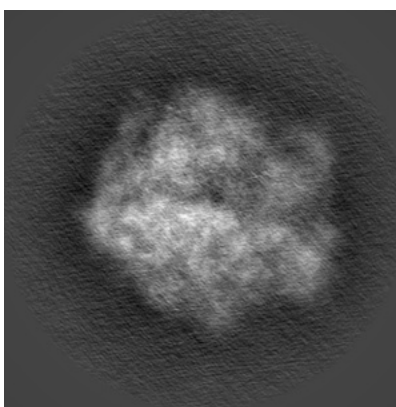


Z

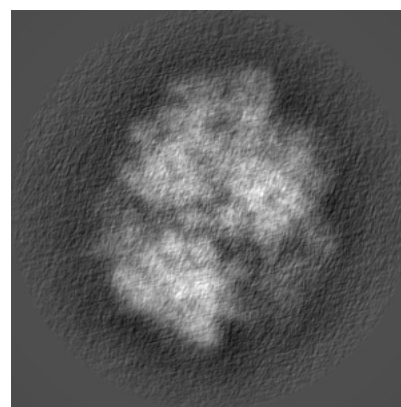
6.1.2 Raw map



X



Y

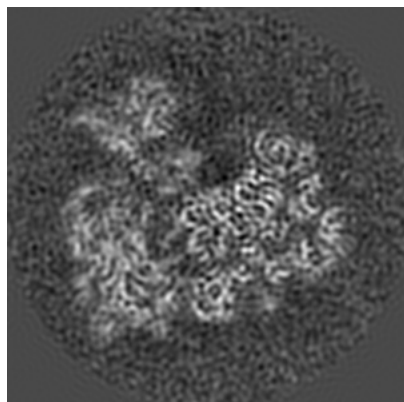


Z

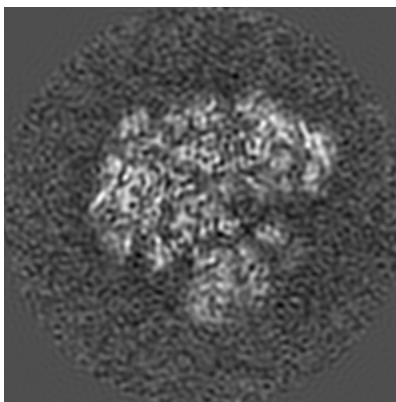
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

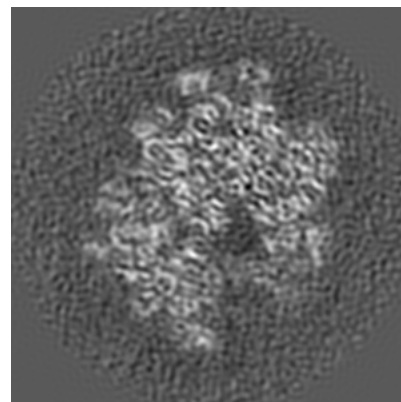
6.2.1 Primary map



X Index: 144

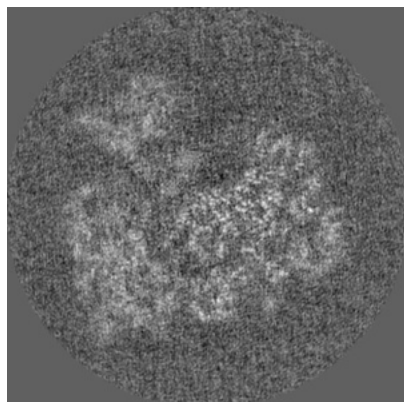


Y Index: 144

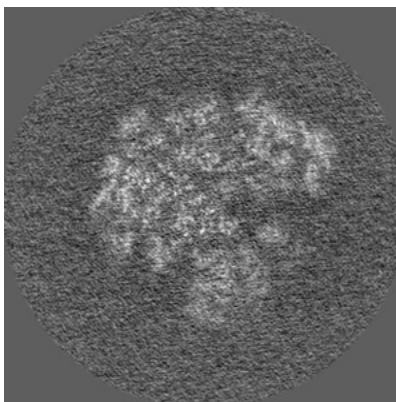


Z Index: 144

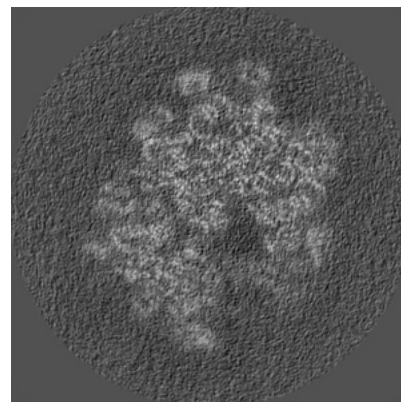
6.2.2 Raw map



X Index: 144



Y Index: 144

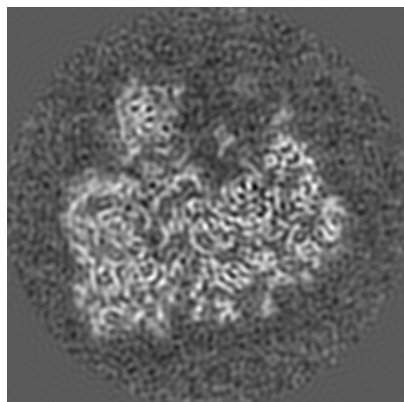


Z Index: 144

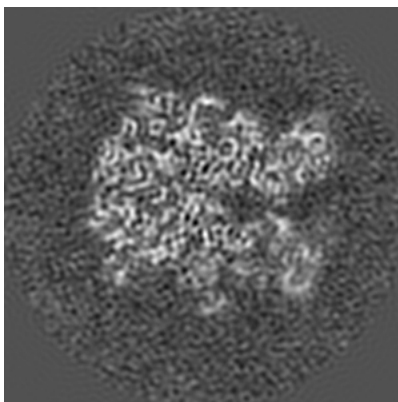
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

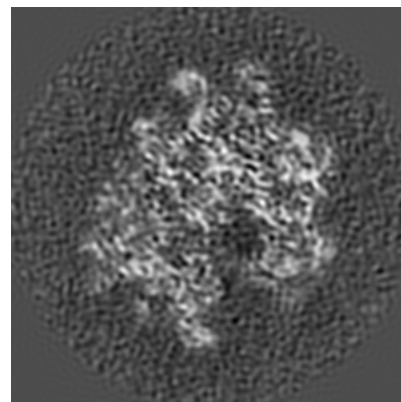
6.3.1 Primary map



X Index: 138

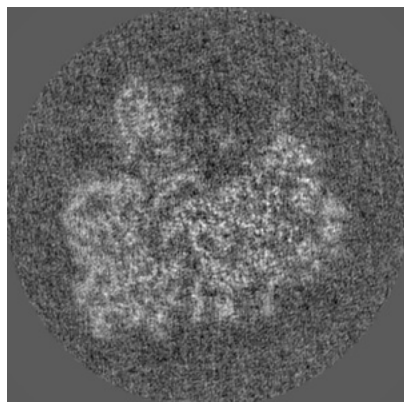


Y Index: 159

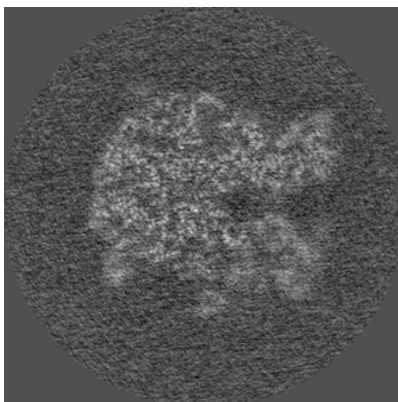


Z Index: 147

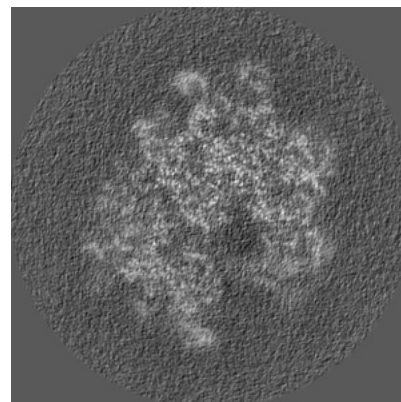
6.3.2 Raw map



X Index: 139



Y Index: 157

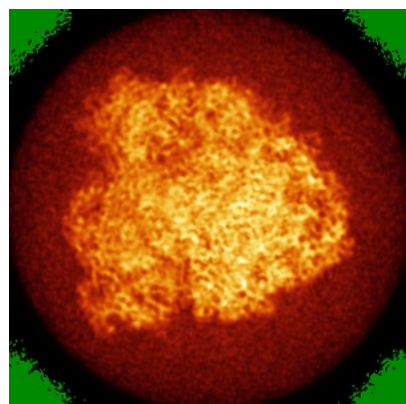


Z Index: 146

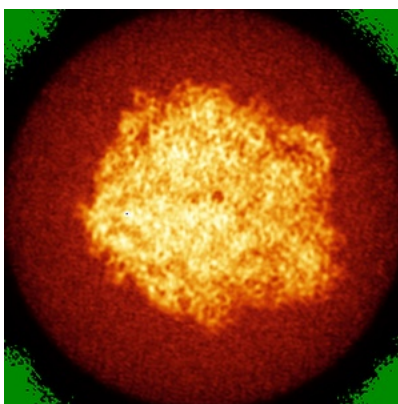
The images above show the largest variance slices of the map in three orthogonal directions.

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

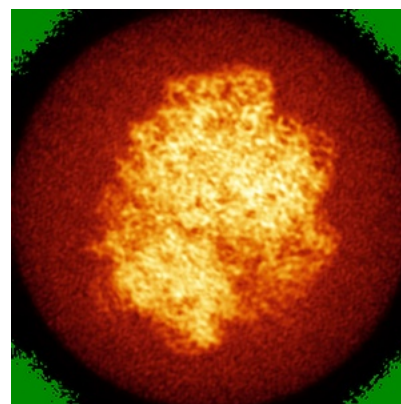
6.4.1 Primary map



X

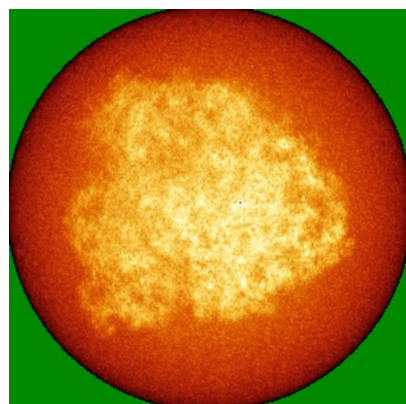


Y

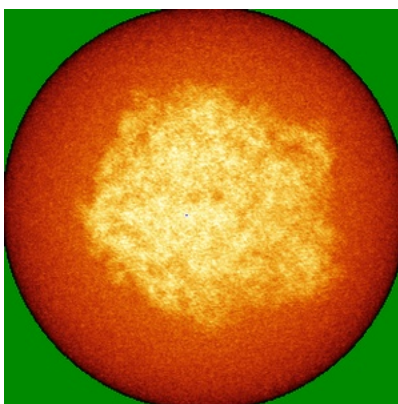


Z

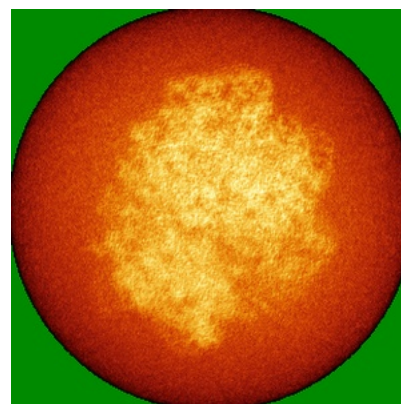
6.4.2 Raw map



X



Y

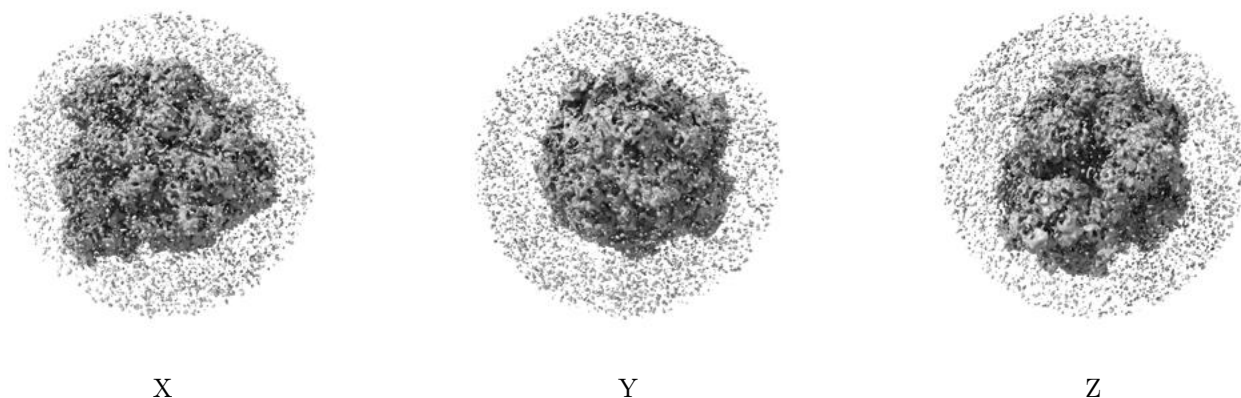


Z

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.

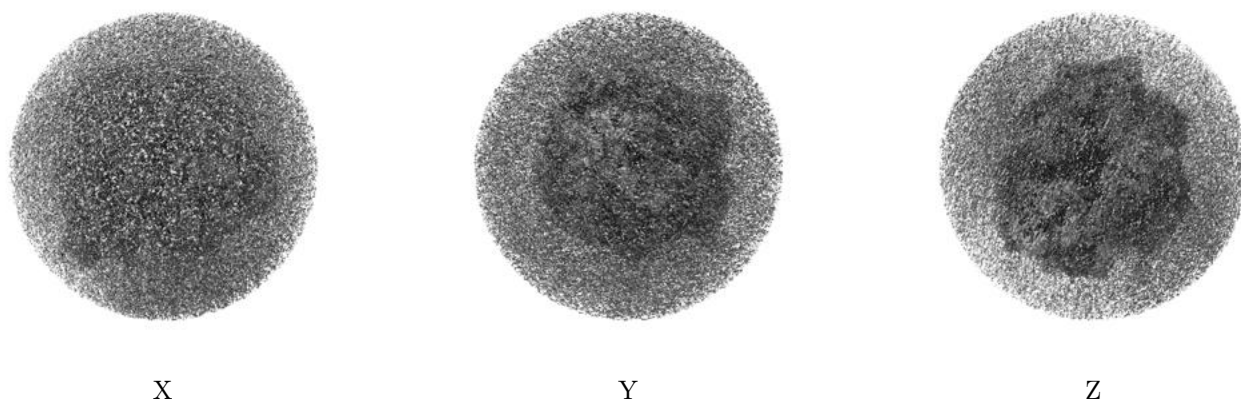
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

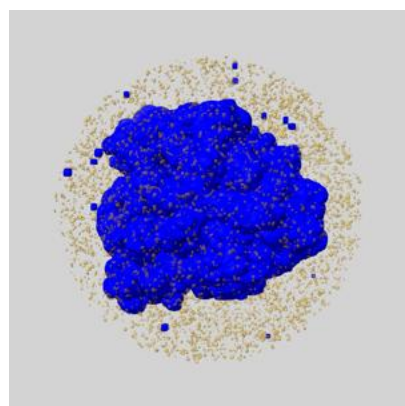
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

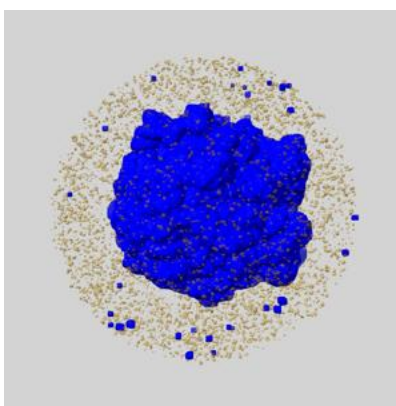
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

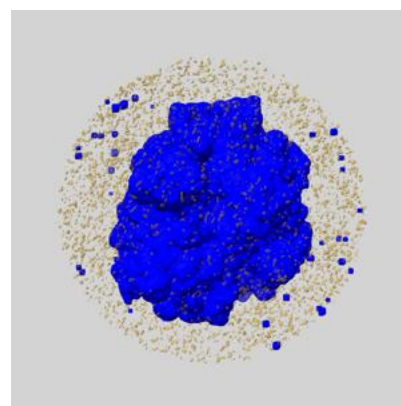
6.6.1 emd_13465_msk_1.map [i](#)



X



Y

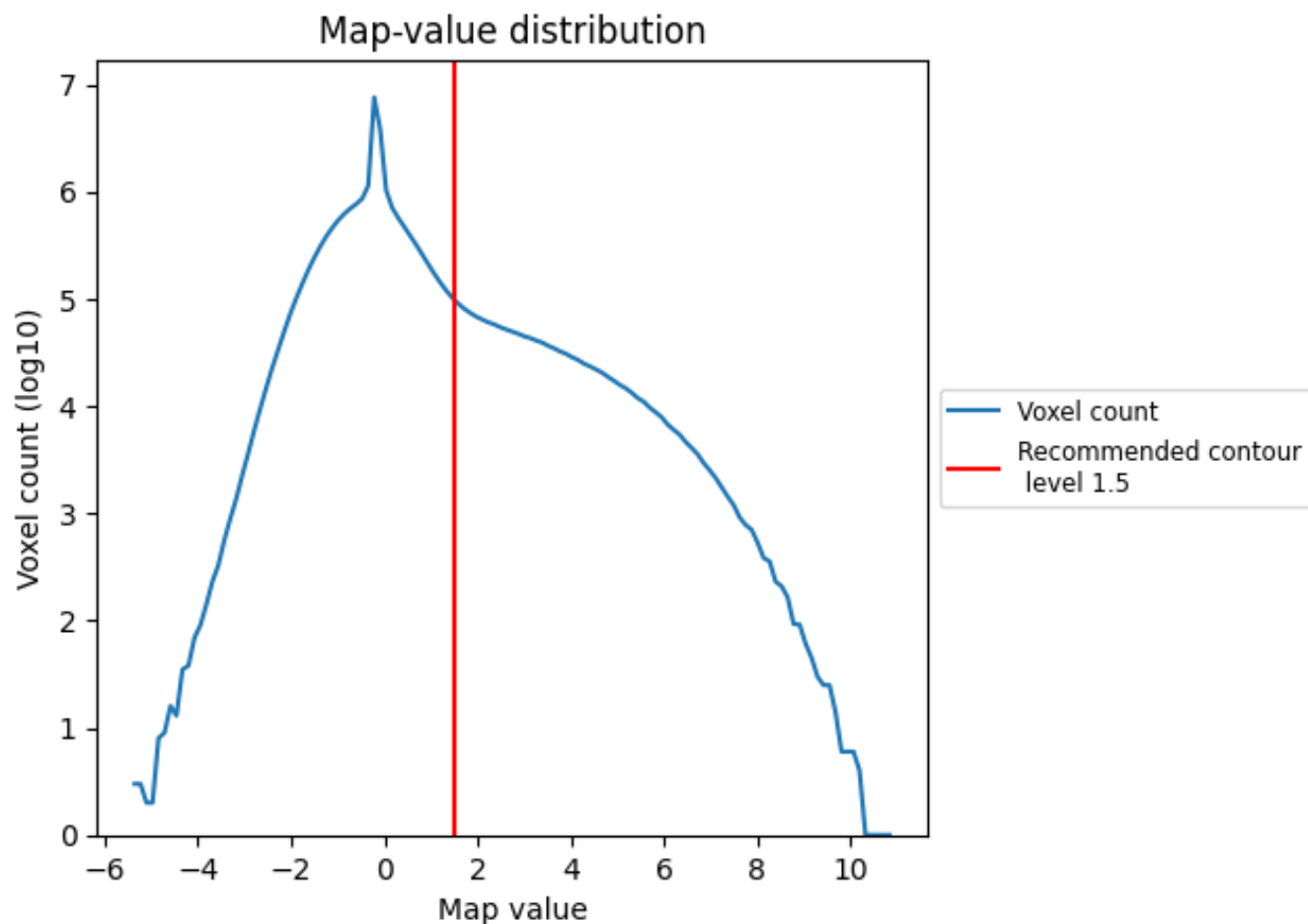


Z

7 Map analysis [i](#)

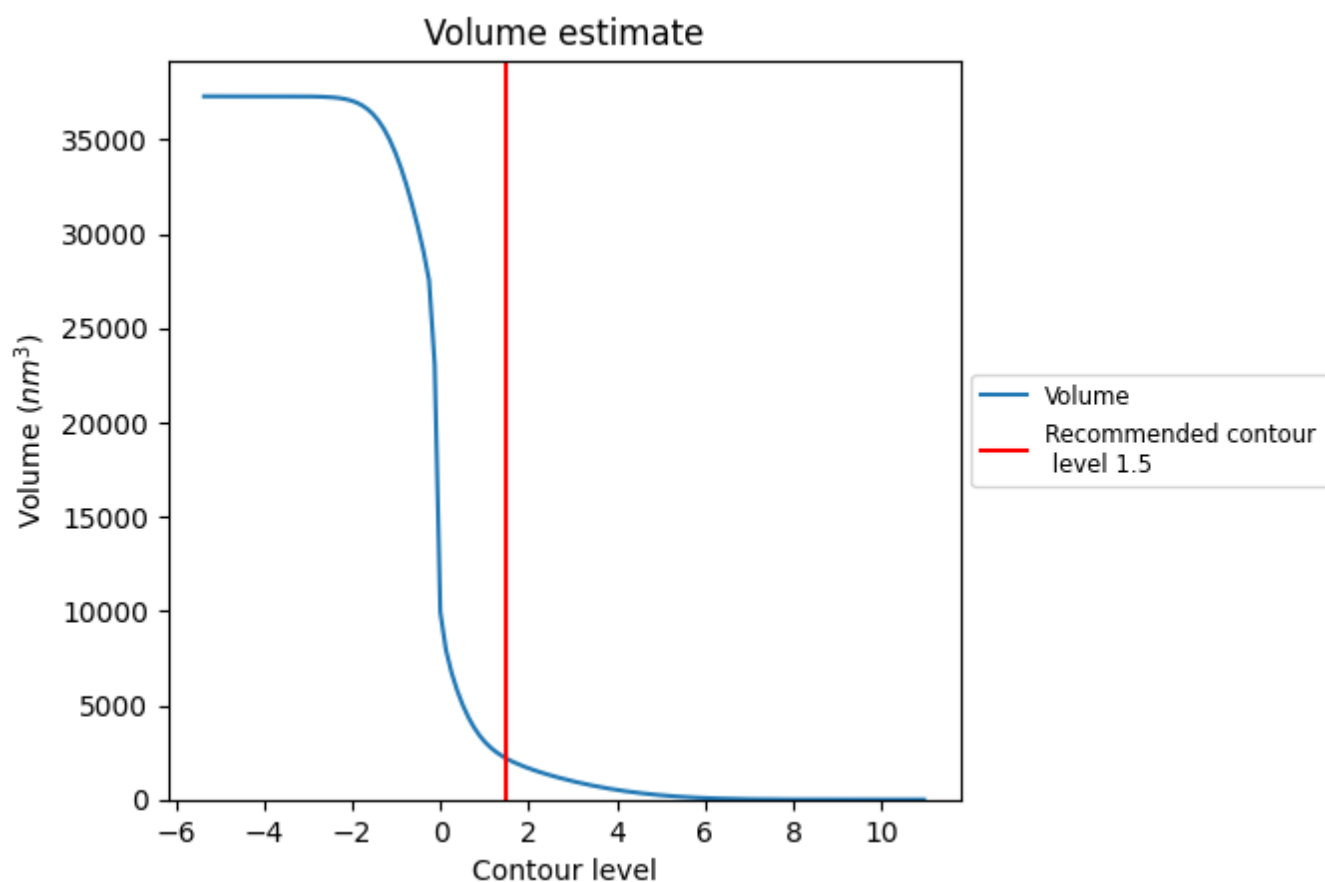
This section contains the results of statistical analysis of the map.

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.

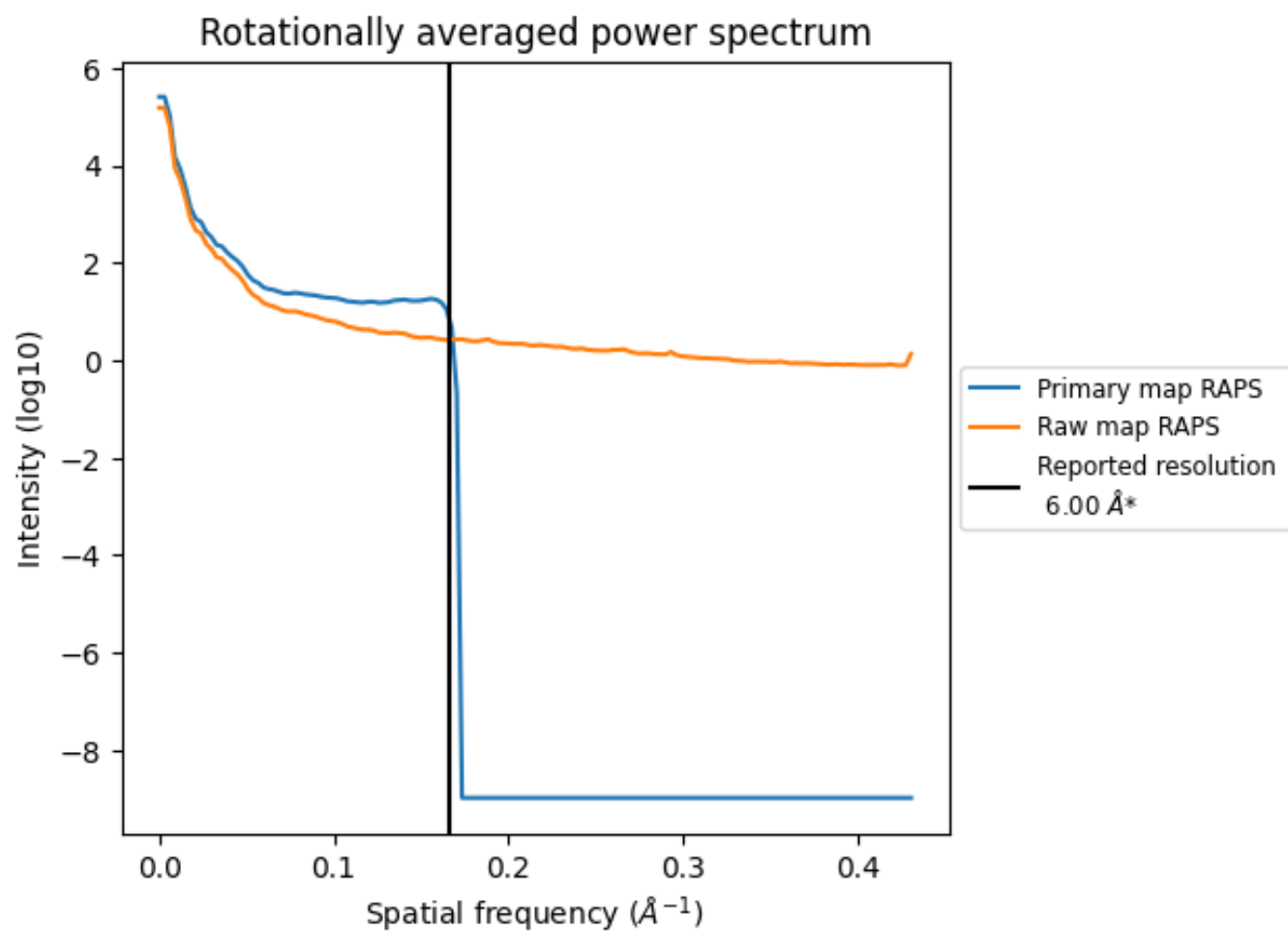
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2172 nm³; this corresponds to an approximate mass of 1962 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 ⓘ

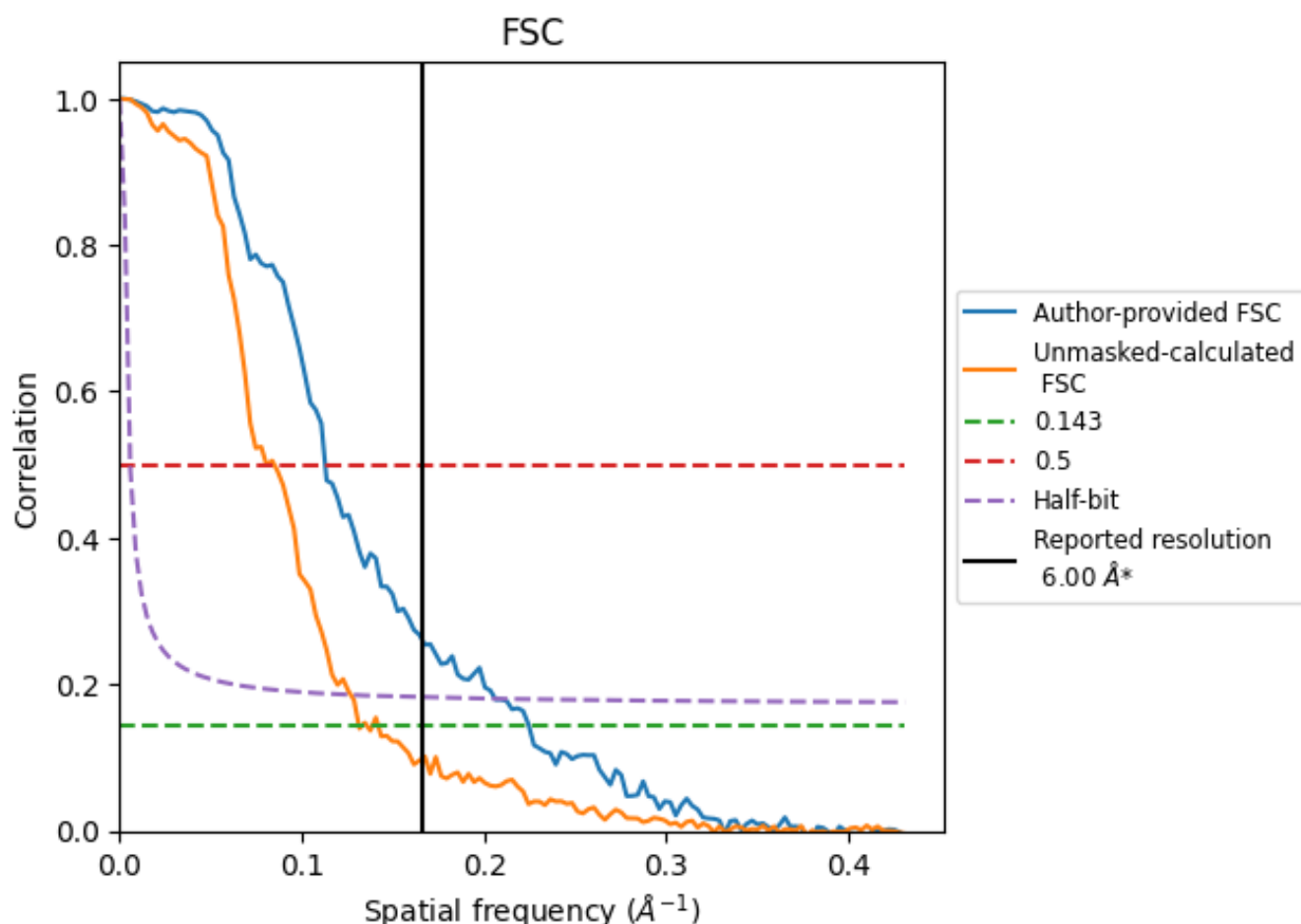


*Reported resolution corresponds to spatial frequency of 0.167 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.167 Å⁻¹

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.00	-	-
Author-provided FSC curve	4.45	8.86	4.85
Unmasked-calculated*	7.61	12.39	7.87

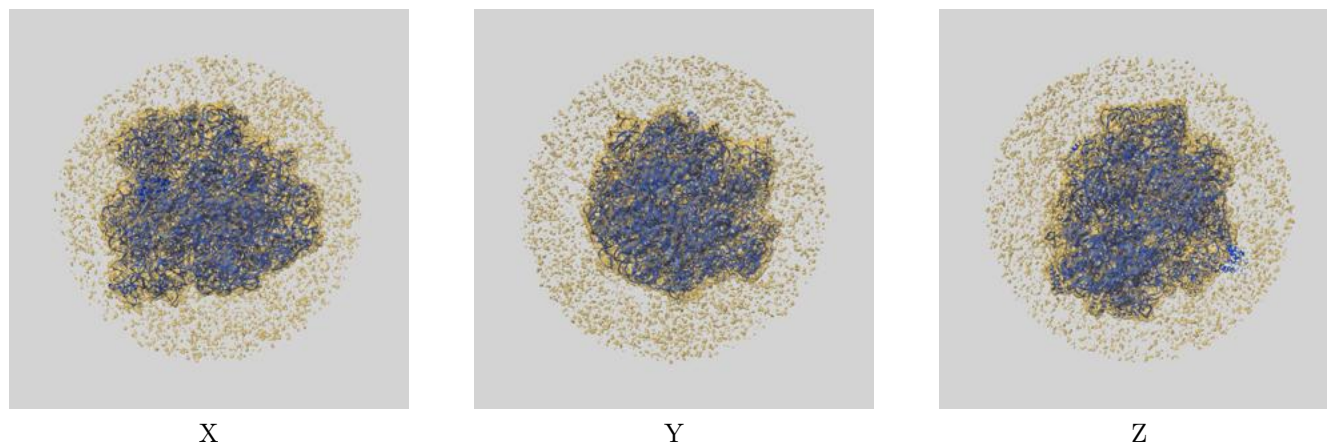
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.45 differs from the reported value 6.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.61 differs from the reported value 6.0 by more than 10 %

9 Map-model fit [i](#)

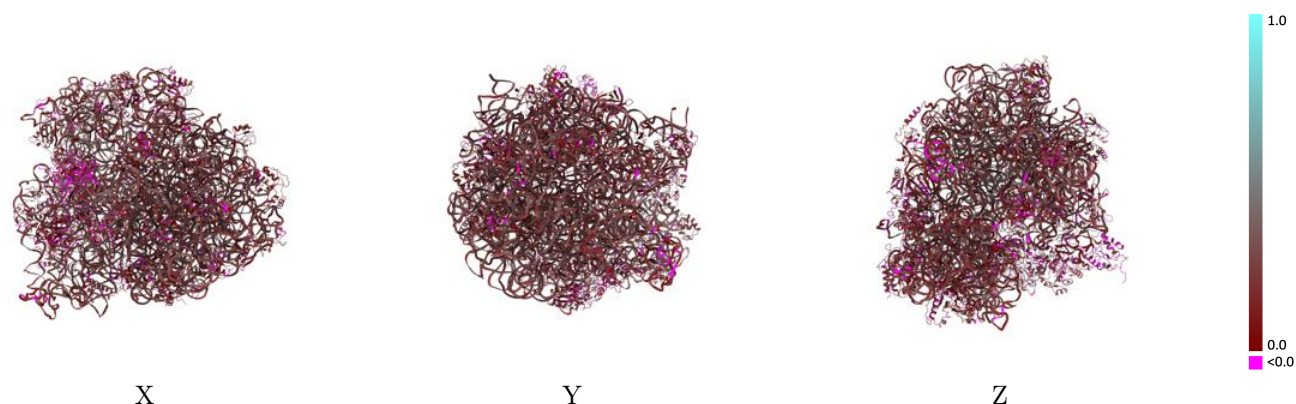
This section contains information regarding the fit between EMDB map EMD-13465 and PDB model 7PJZ. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



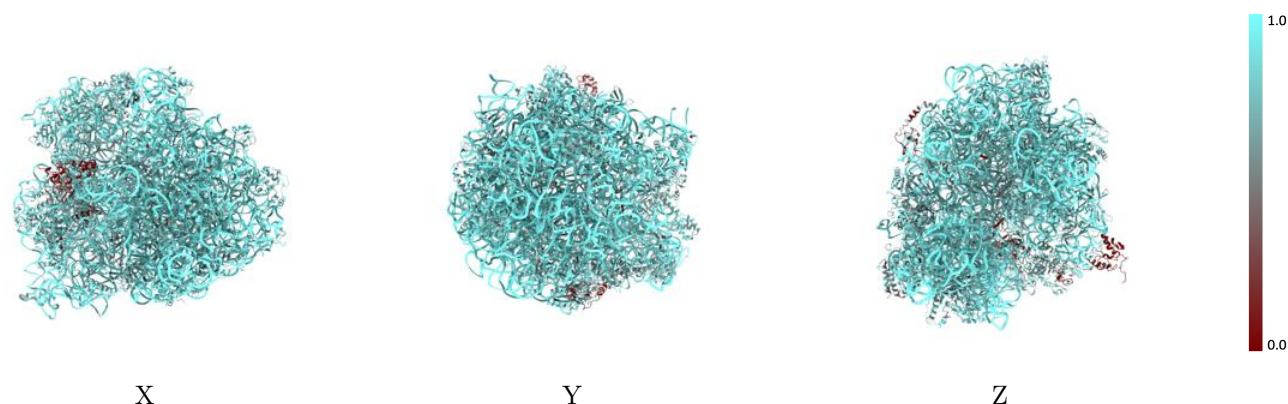
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



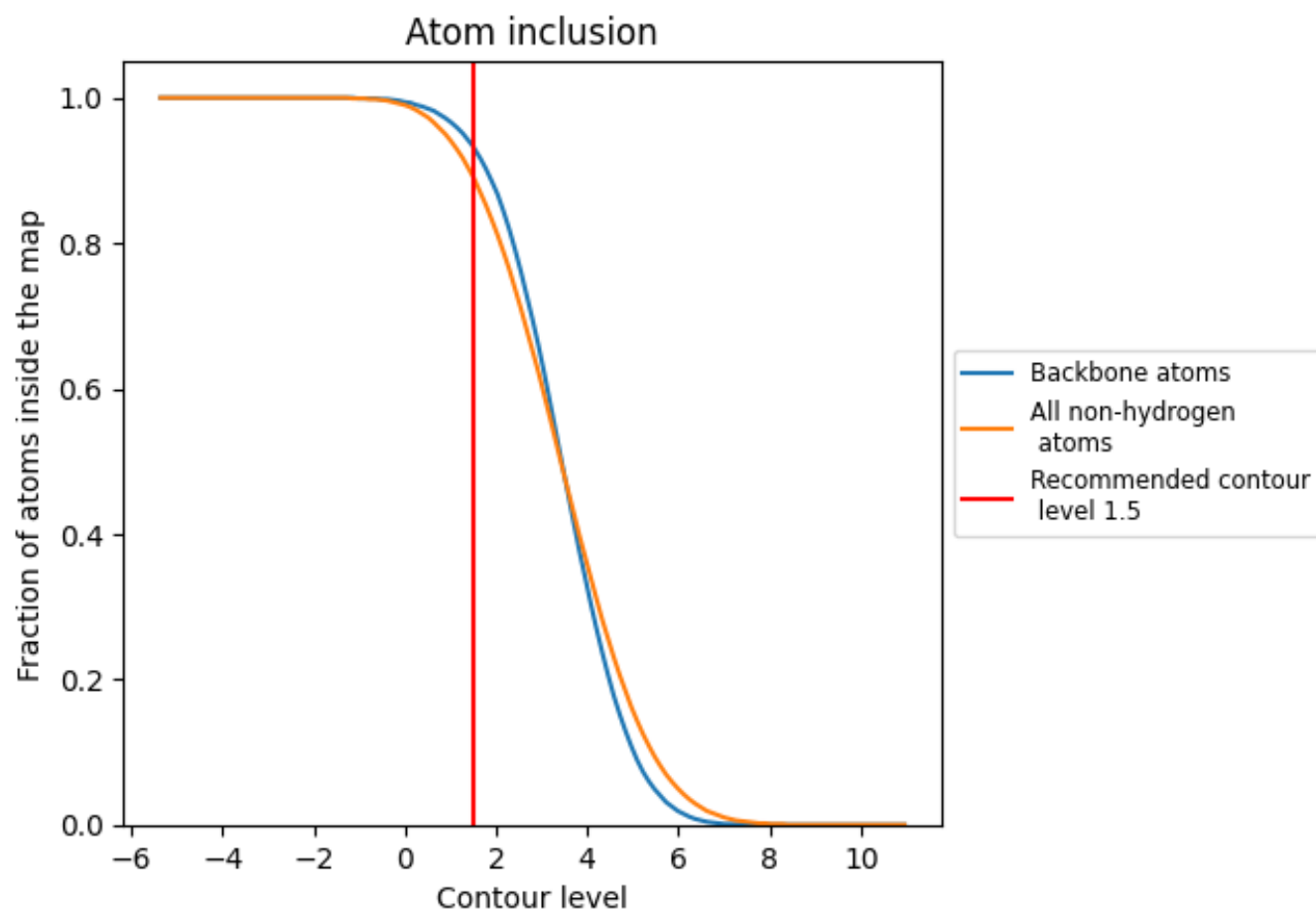
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 89% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.2290
0	 0.8200	 0.2180
1	 0.8030	 0.1790
2	 0.8170	 0.2260
3	 0.7900	 0.1990
4	 0.7910	 0.1960
5	 0.2040	 0.0550
6	 0.7750	 0.1830
A	 0.9630	 0.2580
B	 0.9830	 0.2580
C	 0.7770	 0.2080
D	 0.7790	 0.1960
E	 0.8000	 0.2120
F	 0.8140	 0.1870
G	 0.8280	 0.2000
H	 0.4640	 0.1680
I	 0.5470	 0.0990
J	 0.7740	 0.1970
K	 0.7310	 0.2030
L	 0.7960	 0.2050
M	 0.7970	 0.2110
N	 0.8210	 0.1900
O	 0.8780	 0.1880
P	 0.7810	 0.1970
Q	 0.8120	 0.1760
R	 0.8190	 0.1980
S	 0.7420	 0.1830
T	 0.8350	 0.2030
U	 0.8540	 0.1950
V	 0.8390	 0.1850
W	 0.8530	 0.1850
X	 0.8090	 0.2120
Y	 0.8290	 0.1740
Z	 0.8420	 0.2060
a	 0.9620	 0.2400



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Chain	Atom inclusion	Q-score
b	 0.5880	 0.1850
c	 0.7970	 0.1980
d	 0.8110	 0.1770
e	 0.7740	 0.1860
f	 0.7760	 0.1750
g	 0.6770	 0.1790
h	 0.7950	 0.1910
i	 0.8110	 0.1880
j	 0.7780	 0.1740
k	 0.7740	 0.1880
l	 0.7760	 0.2030
m	 0.7630	 0.1710
n	 0.8400	 0.1760
o	 0.7830	 0.1800
p	 0.8180	 0.1890
q	 0.7960	 0.1760
r	 0.7900	 0.1640
s	 0.8080	 0.1830
t	 0.8050	 0.1780
u	 0.7460	 0.1970
v	 0.9020	 0.2410
w	 0.7110	 0.2060
x	 0.6490	 0.1570
y	 0.9050	 0.3130
z	 0.8650	 0.2590