



wwPDB EM Validation Summary Report ⓘ

Oct 15, 2021 – 01:50 am BST

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, 5J9Z, 5LZD, 6YSS

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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

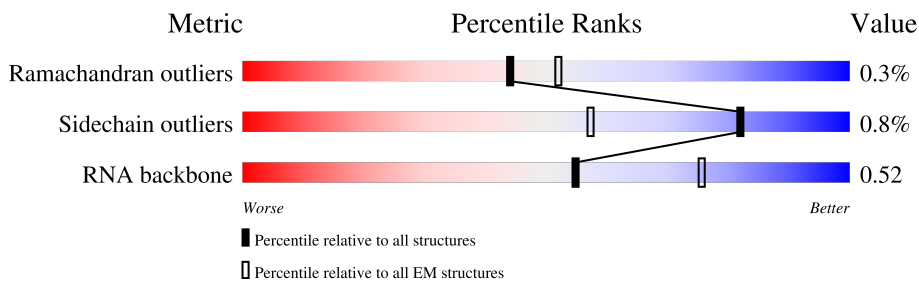
EMDB validation analysis : 0.0.0.dev97
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

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.





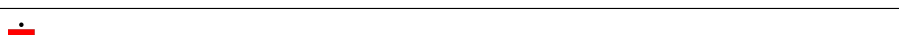
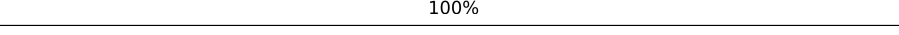
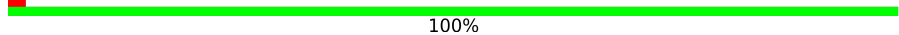

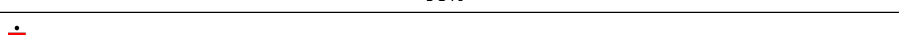
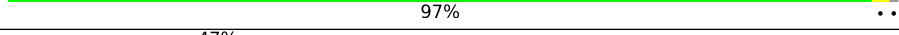


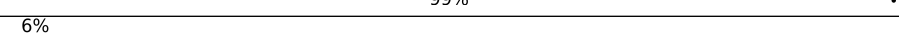
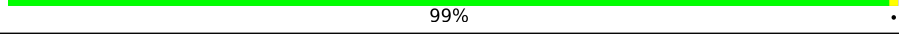
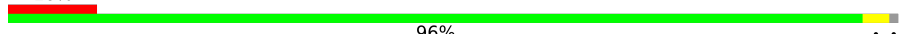
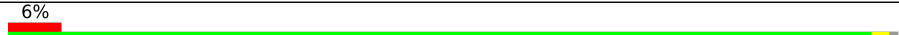
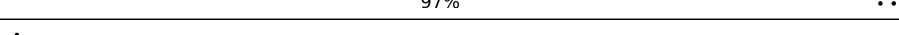
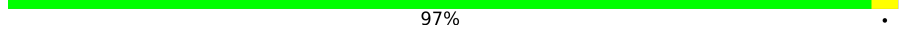


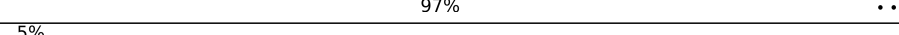
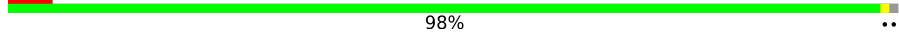

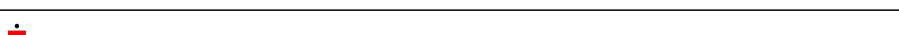
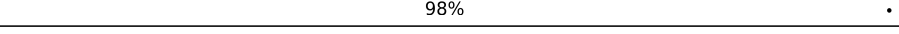
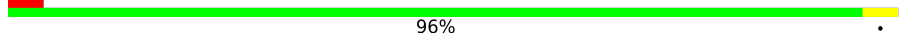

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
2	1	55	
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	

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Mol	Chain	Length	Quality of chain
9	B	120	 32% 59% 9%
10	C	273	 5% 96%
11	D	209	 100%
12	E	201	 100%
13	F	179	 98%
14	G	177	 97%
15	H	149	 47% 99%
16	I	142	 43% 99%
17	J	142	 6% 99%
18	K	123	 10% 96%
19	L	144	 6% 97%
20	M	136	 97%
21	N	127	 93% 6%
22	O	117	 97%
23	P	115	 5% 98%
24	Q	118	 98%
25	R	103	 98%
26	S	110	 96%
27	T	100	 90% 7%
28	U	104	 94%
29	V	94	 99%
30	W	85	 87% 12%
31	X	78	 94% 5%
32	Y	63	 98%
33	Z	59	 98%


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Mol	Chain	Length	Quality of chain
34	a	1542	39% 49% 11%
35	b	240	21% 88% 9%
36	c	233	88% 12%
37	d	206	5% 97%
38	e	167	92% 6%
39	f	135	74% 26%
40	g	179	16% 83% 16%
41	h	130	6% 99%
42	i	130	5% 97%
43	j	103	5% 94% 5%
44	k	129	89% 10%
45	l	124	5% 96%
46	m	118	5% 97%
47	n	102	5% 98%
48	o	89	98%
49	p	82	6% 99%
50	q	84	94% 5%
51	r	75	84% 13%
52	s	92	86% 11%
53	t	87	98%
54	u	71	8% 90% 8%
55	v	77	43% 47% 10%
56	w	76	11% 46% 42% 12%
57	x	704	21% 92% 5%
58	y	2	50% 50%

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Mol	Chain	Length	Quality of chain
59	z	33	 21% 9% 70%

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
			Total	C	N	O	S		
1	0	56	444	269	94	80	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
42	i	127	1022	634	206	179	3	0	0

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

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

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

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

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

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

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

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

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

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

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		

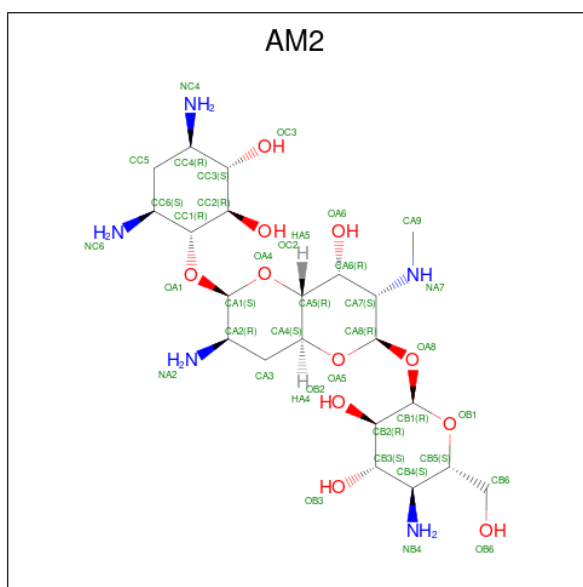
- Molecule 59 is a RNA chain called mRNA.

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).

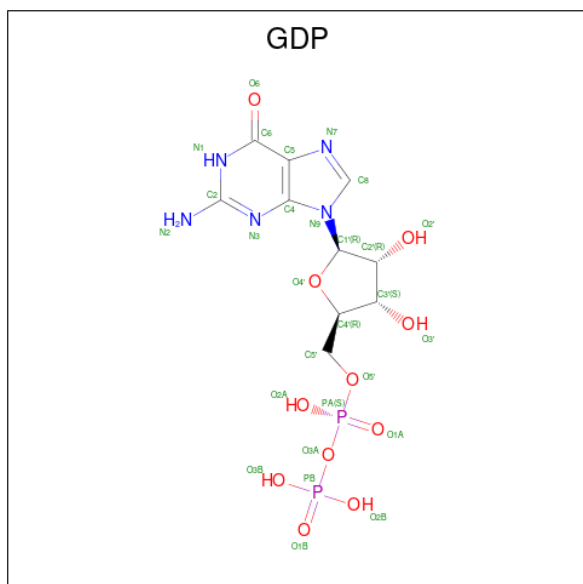
Mol	Chain	Residues	Atoms		AltConf
60	6	1	Total	Zn	0
			1	1	

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



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

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

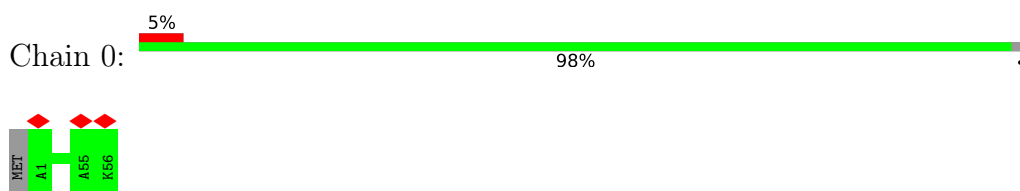


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
62	x	1	28	10	5	11	2	0

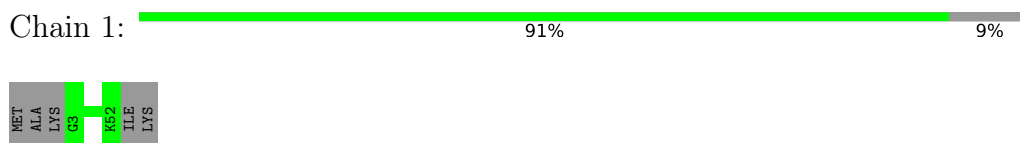
3 Residue-property plots [i](#)

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.

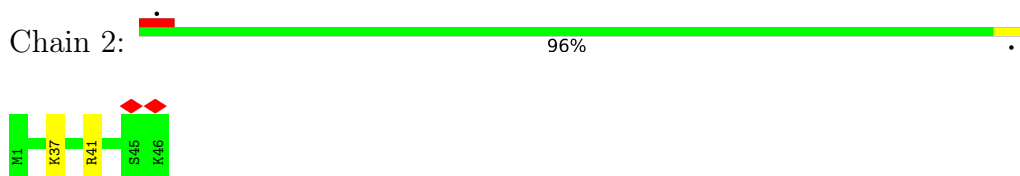
- Molecule 1: 50S ribosomal protein L32



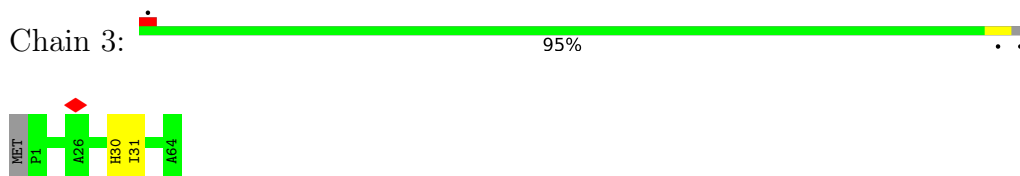
- Molecule 2: 50S ribosomal protein L33



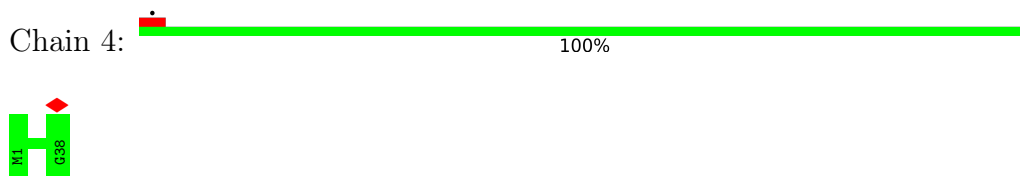
- Molecule 3: 50S ribosomal protein L34



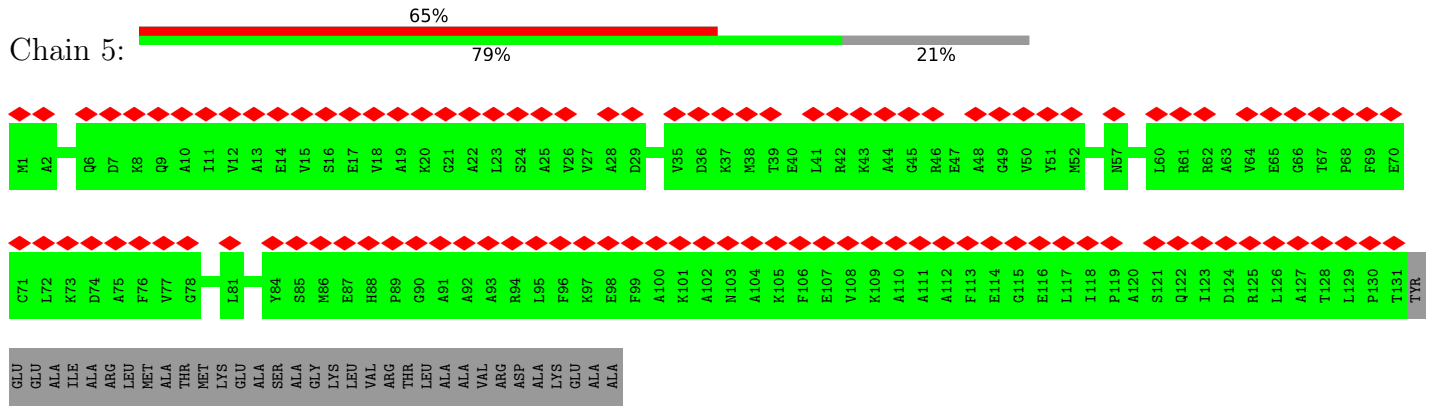
- Molecule 4: 50S ribosomal protein L35



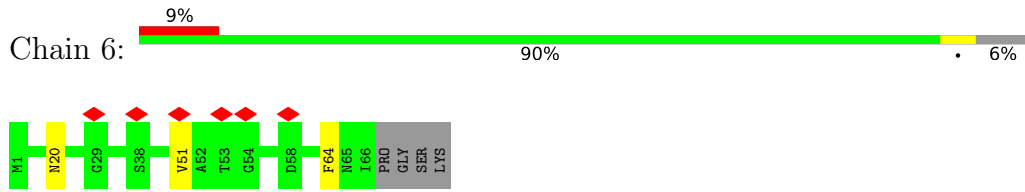
- Molecule 5: 50S ribosomal protein L36



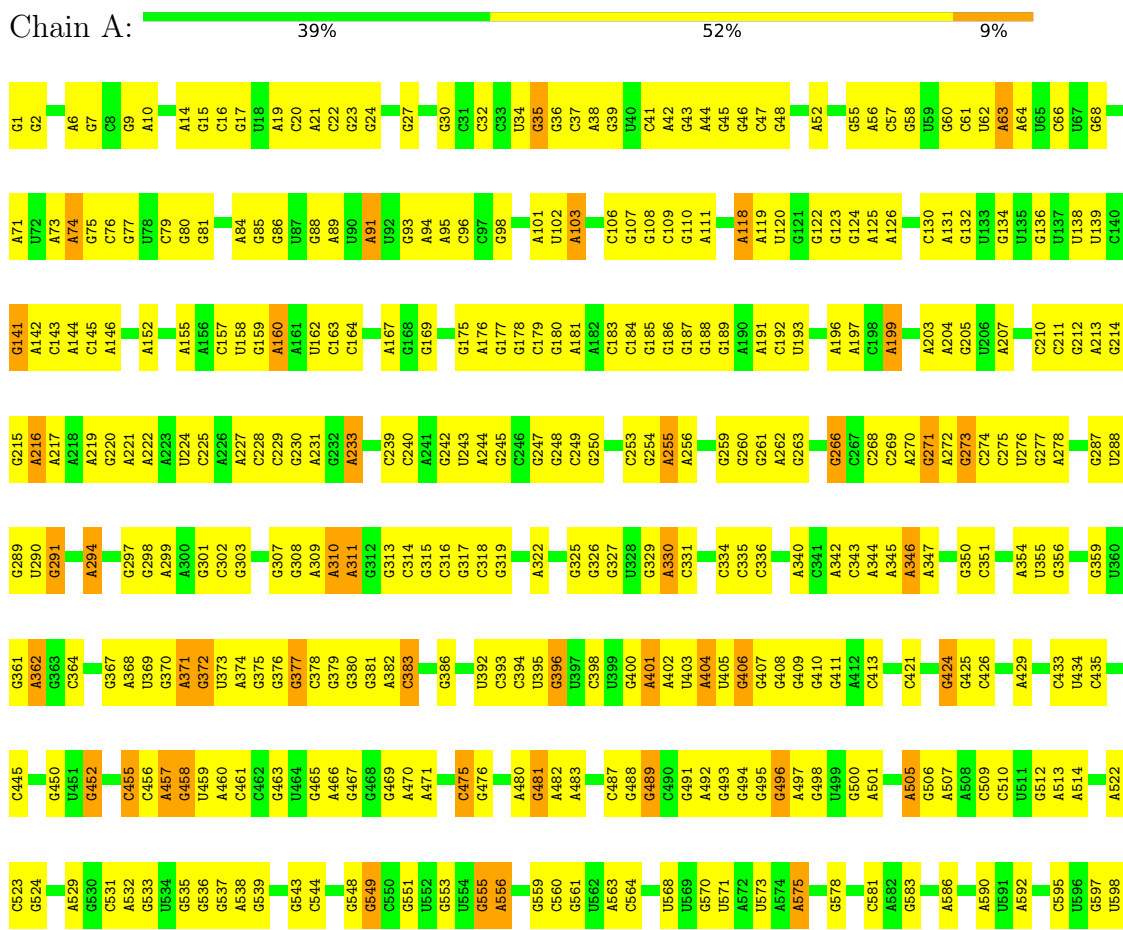
• Molecule 6: 50S ribosomal protein L10



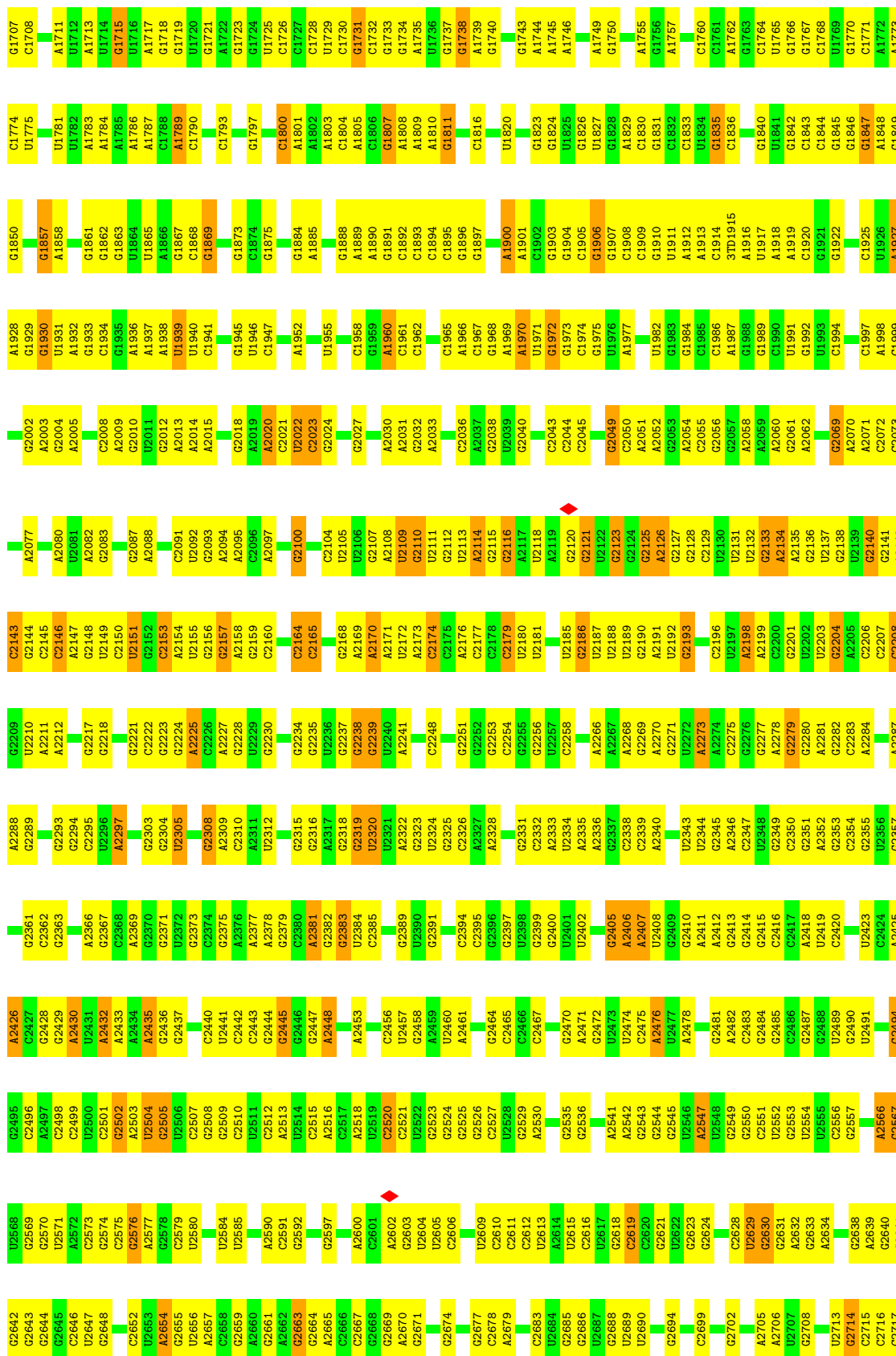
• Molecule 7: 50S ribosomal protein L31



• Molecule 8: 23S ribosomal RNA

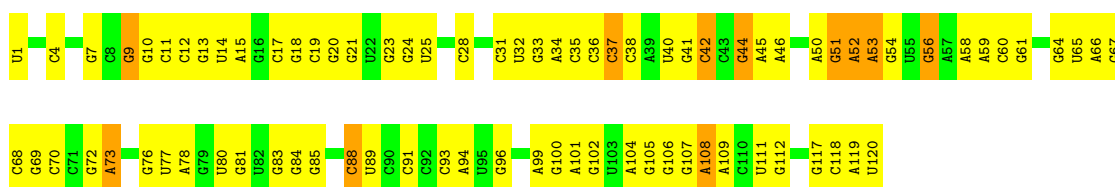


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G1472	G1473	U1474	G1475	U1476	U1477	U1478	G1479	G1482	A1490	C1491	G1492	C1493	U1497	C1498	G1501	A1502	A1503	G1511	G1512	U1513	G1514	A1515	G1516	G1517	C1518	G1519	U1520	G1521	A1522	U1523	G1524	A1525	C1526	G1527	A1528	G1529	G1530	C1531	A1532	C1533	C1534	C1535	C1536	G1537	G1538	U1539	G1540	C1541	U1542	C1543	A1544	A1548	A1549					
A1395	C1398	C1399	U1400	U1401	U1402	A1403	C1404	G1407	G1408	U1409	G1410	U1415	G1416	C1417	G1418	A1419	A1420	G1421	G1422	G1423	G1424	G1425	G1426	A1427	C1428	G1429	G1430	A1433	A1434	G1435	G1436	G1445	G1448	G1449	G1450	C1451	G1452	A1453	C1454	G1455	G1456	U1457	U1458	G1459	U1460	C1461	U1462	C1463	G1465	A1469	A1471							
U1312	U1313	G1317	C1320	C1323	G1332	G1333	C1334	C1335	A1336	G1337	G1338	G1341	A1342	C1345	G1346	A1347	C1348	C1349	A1354	G1355	G1356	C1357	G1358	A1359	G1360	C1361	C1362	A1365	A1366	A1367	G1368	C1369	C1370	G1371	U1372	A1373	G1374	G1377	A1378	U1379	G1380	G1381	G1382	A1383	A1384	A1385	G1386	A1387	G1388	G1389								
G1227	G1228	C1229	U1230	U1231	U1232	C1233	A1237	G1238	G1239	U1240	A1241	A1244	A1247	A1253	A1254	U1255	G1256	A1260	C1261	G1266	G1271	U1272	U1273	A1274	A1275	G1277	C1278	G1279	G1280	G1281	C1291	G1292	U1294	C1295	G1296	A1300	A1301	A1302	G1303	G1304	C1305	C1306	A1307	A1308	G1311													
C1161	G1162	G1163	A1164	A1165	G1166	G1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	G1176	G1177	C1178	G1179	U1180	U1181	G1182	G1186	G1187	U1188	A1189	G1190	G1191	C1192	G1193	A1194	G1197	C1200	H1201	U1202	U1203	A1204	C1207	C1208	H1209	G1210	C1211	A1212	A1213	A1214	G1215	G1216	U1217	G1218	U1219	G1220	A1221	U1222	G1225	A1226				
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G1037	G1038	A1039	U1040	G1041	G1042	C1043	C1044	C1045	A1046	G1047	A1048	C1049	C1052	U1053	A1054	G1055	U1056	A1057	U1058	G1059	U1060	U1061	G1062	G1063	C1064	A1065	U1066	U1067	G1068	A1069	U1070	C1071	C1072	A1073	G1074	C1075	C1076	U1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	U1090	C1091	C1092	G1093	U1094	A1095	U1097	
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C831	U832	A833	G834	C835	G836	C837	G841	U842	C843	A844	A845	U846	U847	C848	A849	U850	U851	C852	U853	C854	G855	C921	C922	G858	G859	G863	C864	C865	A866	C867	U868	G869	U870	U871	G874	G875	C876	A877	G881	U813	C814	C815	C816	C817	G818	A819	A820	C823	U827	U828	A829	U895						
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G758	G759	G760	A761	G762	G763	A764	C765	G770	G771	G774	G775	G776	G777	G778	U779	G780	A781	A782	A783	G784	A785	G786	C787	C791	G712	G713	A792	U793	A794	C795	U720	U721	A722	G726	A727	G728	G729	A730	C731	G732	G733	A734	A735	A739	C740	C741	C742	G745	U746	G747	G748	A749	C751	A751	A752	G757		

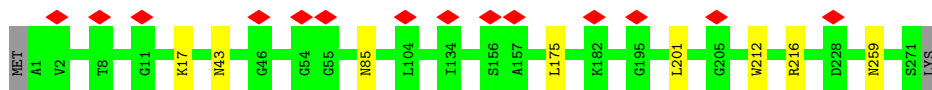




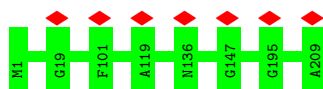
• Molecule 9: 5S ribosomal RNA



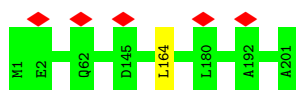
• Molecule 10: 50S ribosomal protein L2



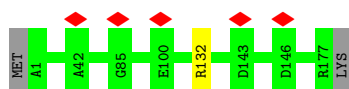
• Molecule 11: 50S ribosomal protein L3



• Molecule 12: 50S ribosomal protein L4

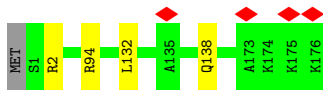


• Molecule 13: 50S ribosomal protein L5



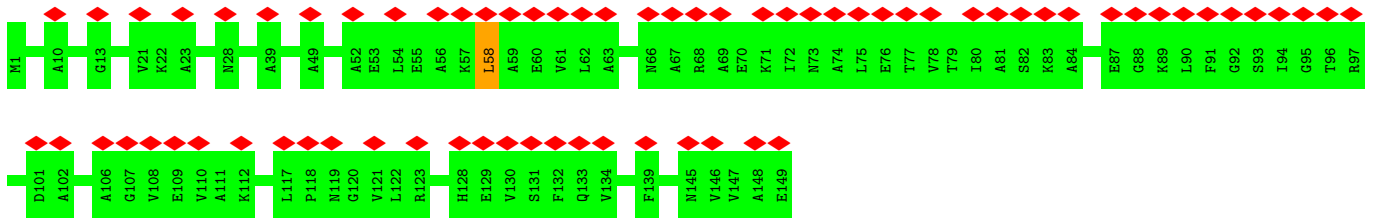
- Molecule 14: 50S ribosomal protein L6

Chain G:  97%

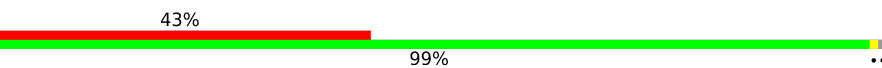


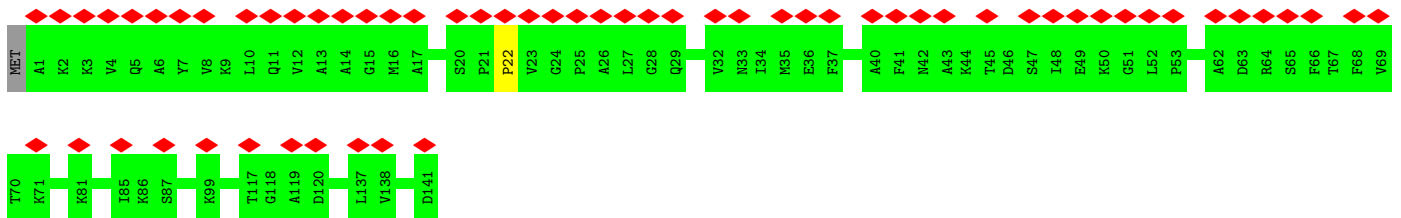
- Molecule 15: 50S ribosomal protein L9

Chain H:  47% 99%



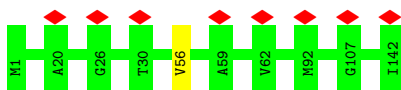
- Molecule 16: 50S ribosomal protein L11

Chain I:  43% 99%



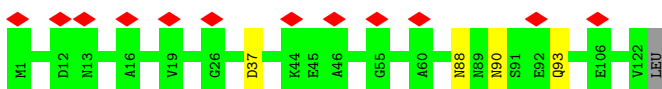
- Molecule 17: 50S ribosomal protein L13

Chain J:  6% 99%



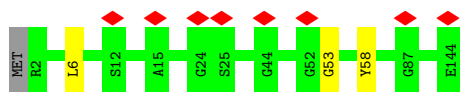
- Molecule 18: 50S ribosomal protein L14

Chain K:  10% 96%

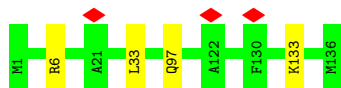


- Molecule 19: 50S ribosomal protein L15

Chain L:  6% 97%



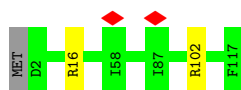
- Molecule 20: 50S ribosomal protein L16



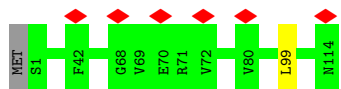
- Molecule 21: 50S ribosomal protein L17



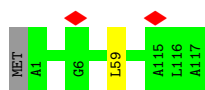
- Molecule 22: 50S ribosomal protein L18



- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20



- Molecule 25: 50S ribosomal protein L21




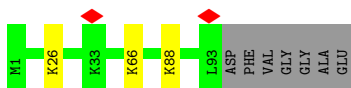
- Molecule 26: 50S ribosomal protein L22

Chain S:  96%



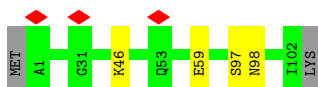
- Molecule 27: 50S ribosomal protein L23

Chain T:  90% 7%



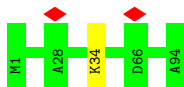
- Molecule 28: 50S ribosomal protein L24

Chain U:  94%



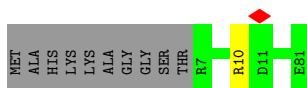
- Molecule 29: 50S ribosomal protein L25

Chain V:  99%



- Molecule 30: 50S ribosomal protein L27

Chain W:  87% 12%



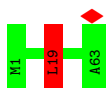
- Molecule 31: 50S ribosomal protein L28

Chain X:  94% 5%



- Molecule 32: 50S ribosomal protein L29

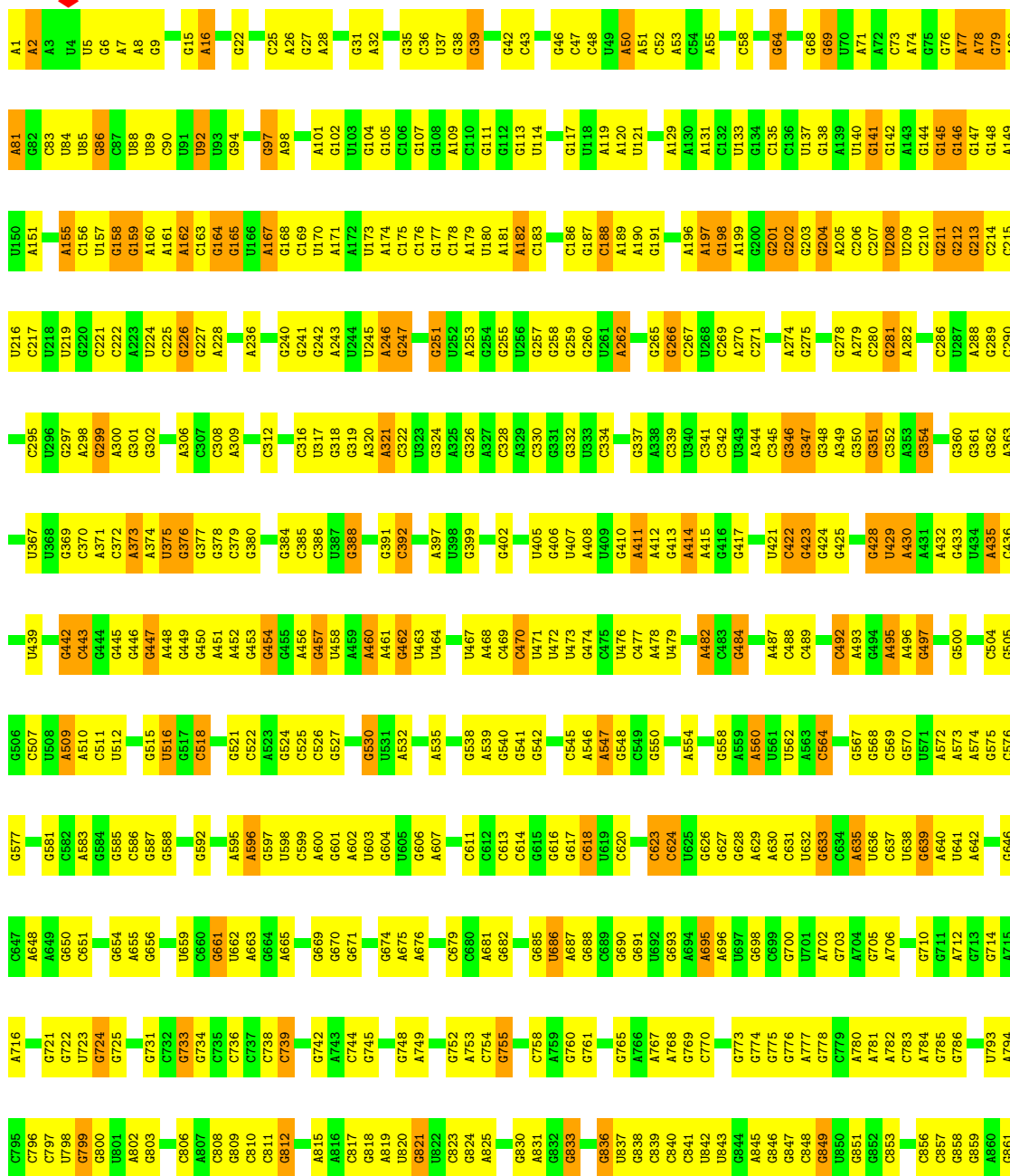
Chain Y:  98%

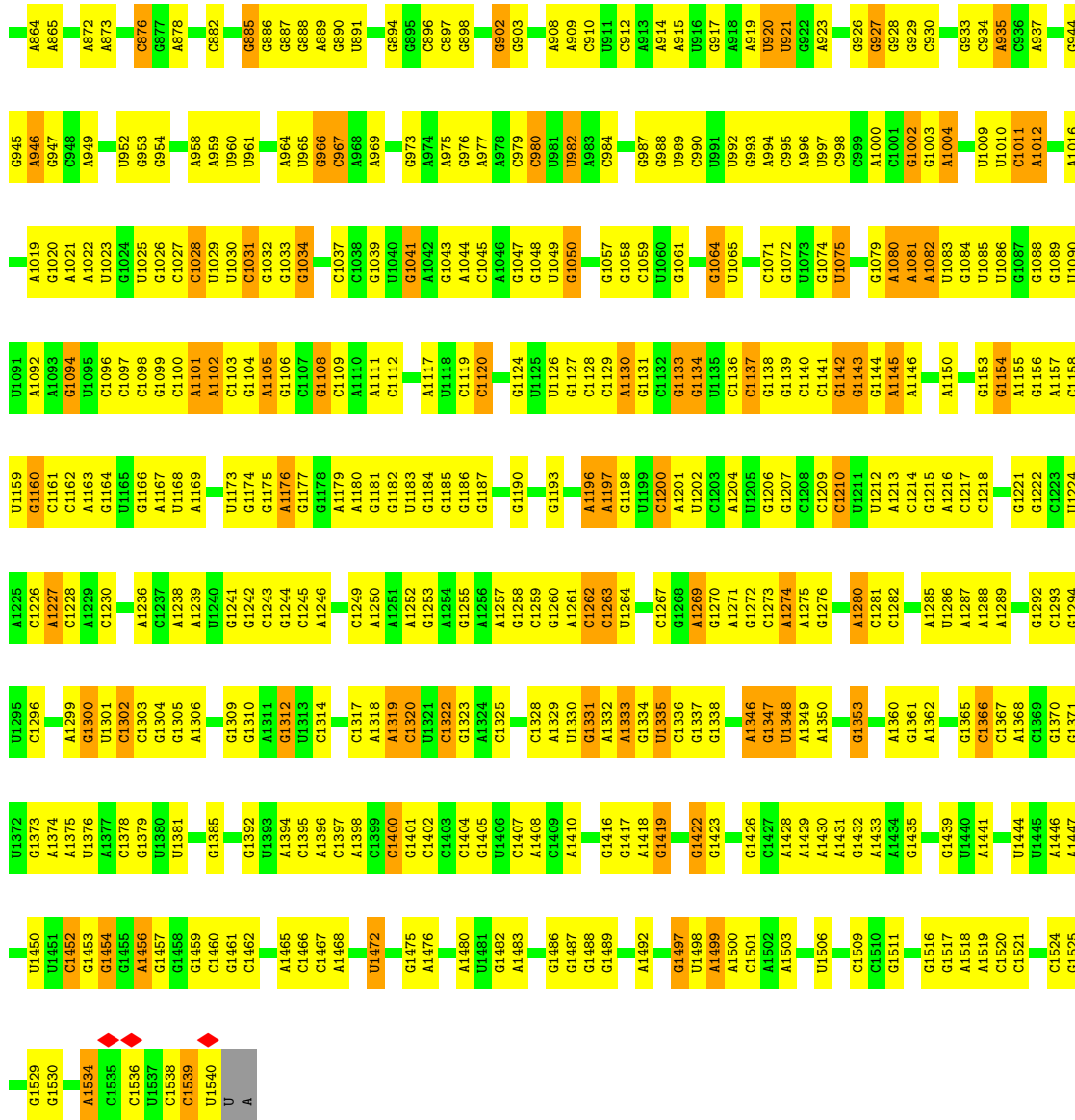


• Molecule 33: 50S ribosomal protein L30

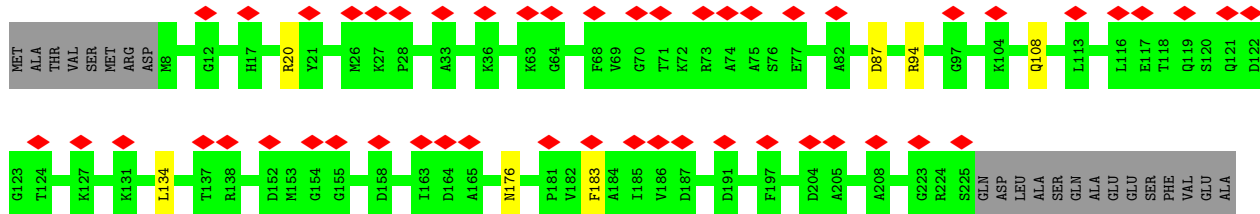
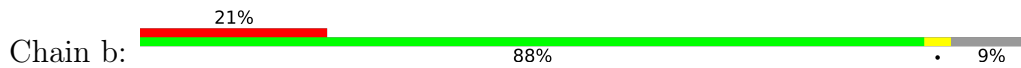


• Molecule 34: 16S ribosomal RNA

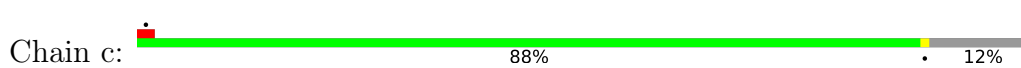


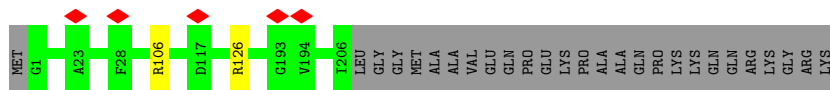


• Molecule 35: 30S ribosomal protein S2

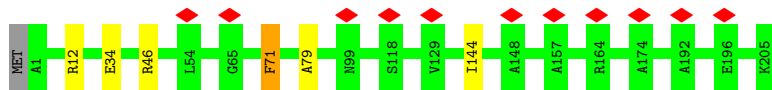


• Molecule 36: 30S ribosomal protein S3

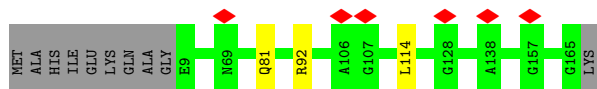
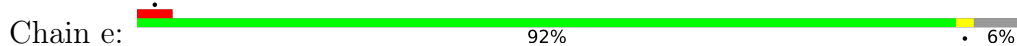




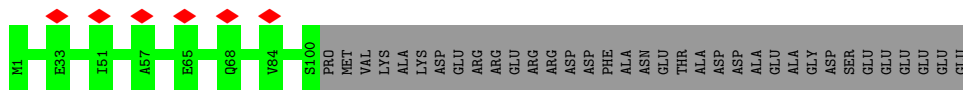
• Molecule 37: 30S ribosomal protein S4



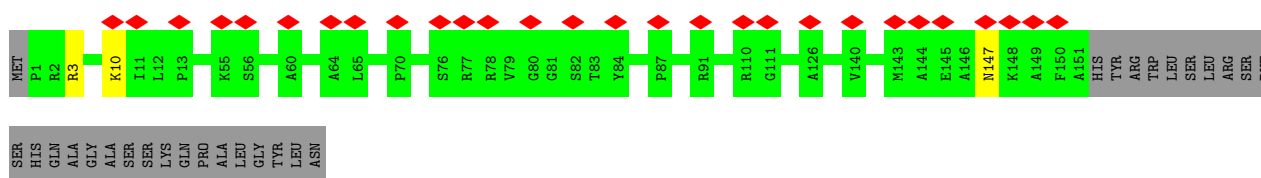
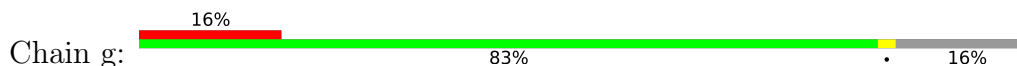
• Molecule 38: 30S ribosomal protein S5



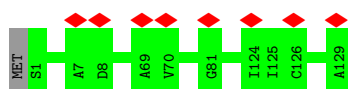
• Molecule 39: 30S ribosomal protein S6



• Molecule 40: 30S ribosomal protein S7

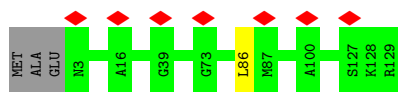


• Molecule 41: 30S ribosomal protein S8

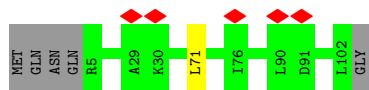
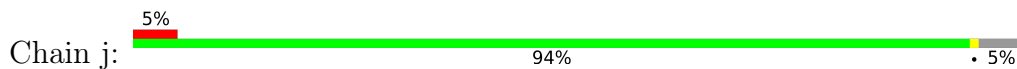


• Molecule 42: 30S ribosomal protein S9

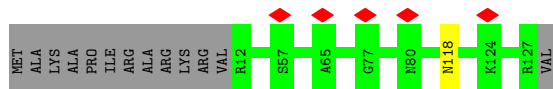
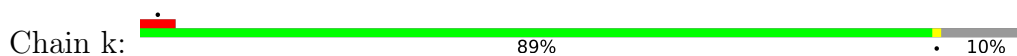




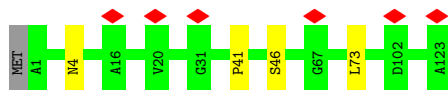
- Molecule 43: 30S ribosomal protein S10



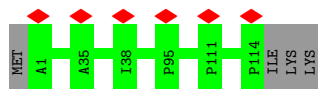
- Molecule 44: 30S ribosomal protein S11



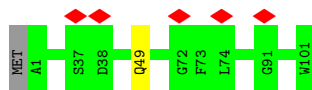
- Molecule 45: 30S ribosomal protein S12



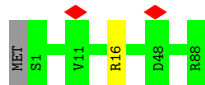
- Molecule 46: 30S ribosomal protein S13



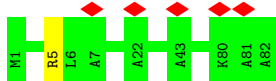
- Molecule 47: 30S ribosomal protein S14



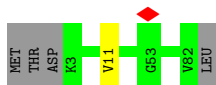
- Molecule 48: 30S ribosomal protein S15



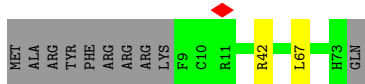
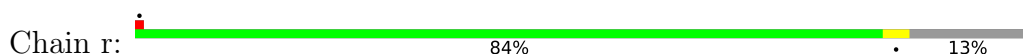
- Molecule 49: 30S ribosomal protein S16



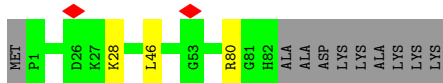
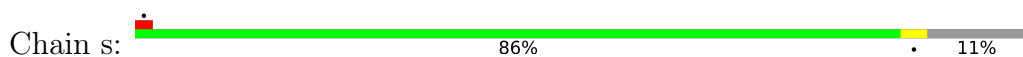
- Molecule 50: 30S ribosomal protein S17



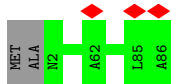
- Molecule 51: 30S ribosomal protein S18



- Molecule 52: 30S ribosomal protein S19



- Molecule 53: 30S ribosomal protein S20



- Molecule 54: 30S ribosomal protein S21

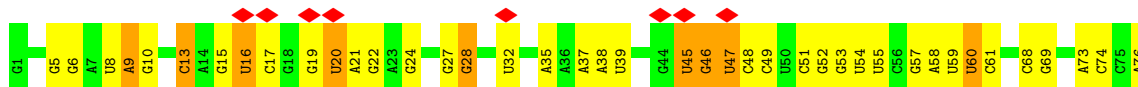


- Molecule 55: P-site tRNA(fMet)

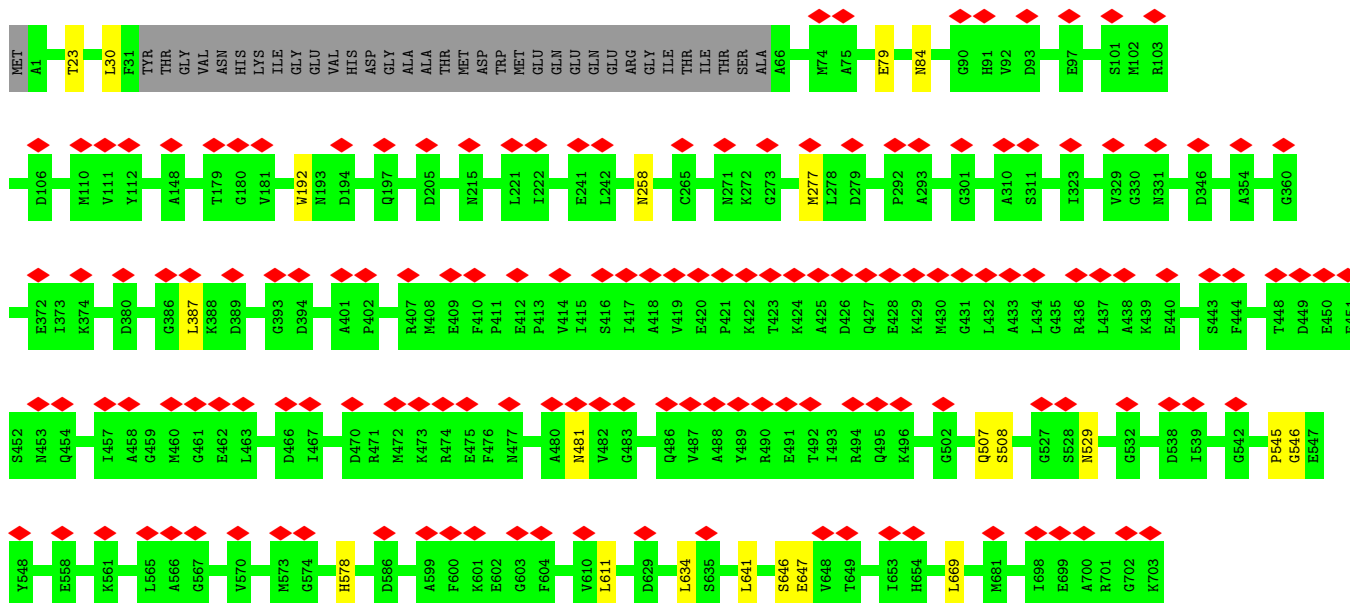
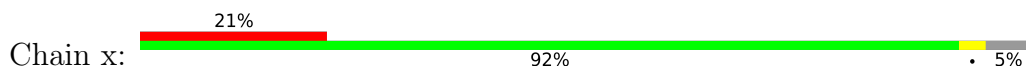




• Molecule 56: P-site fMet-Phe-tRNA(Phe)



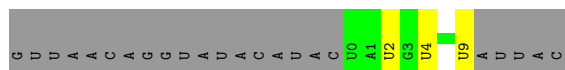
• Molecule 57: Elongation factor G



• 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 (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: AM2, OMC, 3TD, ZN, 4SU, 6MZ, PSU, 5MU, 4OC, 2MG, MA6, GDP, FME, OMG, OMU, 1MG, G7M, 2MA, 5MC, MIA, H2U, UR3

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%)	9	44
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%)	4	27
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%)	22	62
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%)	15	54
26	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
27	T	91/100 (91%)	81 (89%)	9 (10%)	1 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	89 (89%)	10 (10%)	1 (1%)	15	54
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%)	9	44
33	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
35	b	216/240 (90%)	180 (83%)	35 (16%)	1 (0%)	29	69
36	c	204/233 (88%)	193 (95%)	11 (5%)	0	100	100
37	d	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	29	69
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%)	19	60
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%)	14	52
All	All	6516/6924 (94%)	5877 (90%)	621 (10%)	18 (0%)	44	76

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 [i](#)

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%)	46	67
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%)	60	78
10	C	216/218 (99%)	213 (99%)	3 (1%)	67	80
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%)	65	80
15	H	114/114 (100%)	113 (99%)	1 (1%)	78	88
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	99 (96%)	4 (4%)	32	56
19	L	102/103 (99%)	101 (99%)	1 (1%)	76	86
20	M	109/109 (100%)	108 (99%)	1 (1%)	78	88
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%)	73	84
27	T	80/84 (95%)	79 (99%)	1 (1%)	69	82
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	77 (99%)	1 (1%)	69	82
30	W	57/63 (90%)	56 (98%)	1 (2%)	59	77
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%)	60	78
36	c	170/190 (90%)	169 (99%)	1 (1%)	86	92
37	d	172/173 (99%)	170 (99%)	2 (1%)	71	84
38	e	114/126 (90%)	112 (98%)	2 (2%)	59	77
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	122 (98%)	2 (2%)	62	79
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%)	73	84
45	l	103/104 (99%)	101 (98%)	2 (2%)	57	75
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	78 (99%)	1 (1%)	69	82
48	o	76/77 (99%)	75 (99%)	1 (1%)	69	82
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%)	67	80
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%)	73	84
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%)	82 89

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 [i](#)

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 [i](#)

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	1911	8	17,21,22	3.42	9 (52%)	20,30,33	3.24	6 (30%)
56	5MU	w	54	56	15,22,23	1.23	2 (13%)	16,32,35	2.15	2 (12%)
34	2MG	a	1207	34	19,26,27	3.53	7 (36%)	21,38,41	2.45	6 (28%)
34	G7M	a	527	34	20,26,27	3.10	6 (30%)	20,39,42	3.41	7 (35%)
34	MA6	a	1518	34	19,26,27	1.54	3 (15%)	18,38,41	3.47	3 (16%)
8	PSU	A	2604	8	17,21,22	3.56	9 (52%)	20,30,33	3.00	7 (35%)
56	PSU	w	32	56	17,21,22	3.49	9 (52%)	20,30,33	3.15	7 (35%)
56	4SU	w	8	56	14,21,22	1.46	3 (21%)	15,30,33	1.86	4 (26%)
55	PSU	v	55	55	17,21,22	3.55	9 (52%)	20,30,33	3.17	5 (25%)
8	3TD	A	1915	8	17,22,23	7.09	12 (70%)	19,32,35	2.22	5 (26%)
8	5MU	A	1939	8	15,22,23	2.84	3 (20%)	16,32,35	2.79	2 (12%)
56	MIA	w	37	56	24,31,32	2.44	4 (16%)	26,44,47	2.74	10 (38%)
8	OMG	A	2251	56,8	18,26,27	3.39	8 (44%)	20,38,41	3.22	7 (35%)
8	2MG	A	1835	8	19,26,27	3.64	7 (36%)	21,38,41	2.64	5 (23%)
34	5MC	a	1407	34	15,22,23	2.58	5 (33%)	19,32,35	1.30	2 (10%)
34	UR3	a	1498	34	14,22,23	2.63	4 (28%)	15,32,35	0.88	1 (6%)
56	G7M	w	46	56	20,26,27	4.99	14 (70%)	20,39,42	2.65	6 (30%)
8	OMC	A	2498	8	15,22,23	3.44	6 (40%)	17,31,34	1.25	1 (5%)
8	PSU	A	2457	8	17,21,22	3.67	9 (52%)	20,30,33	3.35	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	1MG	A	745	8	18,26,27	3.04	8 (44%)	19,39,42	2.67	3 (15%)
8	5MC	A	747	8	15,22,23	2.90	5 (33%)	19,32,35	1.32	3 (15%)
8	PSU	A	2504	8	17,21,22	3.57	9 (52%)	20,30,33	3.30	6 (30%)
8	5MC	A	1962	8	15,22,23	2.48	5 (33%)	19,32,35	1.09	2 (10%)
34	2MG	a	966	34	19,26,27	1.29	2 (10%)	21,38,41	2.43	9 (42%)
8	6MZ	A	1618	8	18,25,26	1.72	6 (33%)	16,36,39	2.94	4 (25%)
55	4SU	v	8	55	14,21,22	3.68	5 (35%)	15,30,33	1.32	2 (13%)
55	5MU	v	54	55	15,22,23	2.83	3 (20%)	16,32,35	2.84	3 (18%)
55	H2U	v	20	55	18,21,22	3.58	3 (16%)	21,30,33	2.03	5 (23%)
8	PSU	A	746	8	17,21,22	3.35	9 (52%)	20,30,33	3.52	7 (35%)
8	2MG	A	2445	8	19,26,27	3.27	8 (42%)	21,38,41	2.93	6 (28%)
58	FME	y	101	58	8,9,10	1.03	1 (12%)	7,9,11	1.05	1 (14%)
56	PSU	w	55	56	17,21,22	1.45	3 (17%)	20,30,33	3.17	8 (40%)
8	PSU	A	955	8	17,21,22	3.54	9 (52%)	20,30,33	3.33	6 (30%)
8	G7M	A	2069	8	20,26,27	2.78	6 (30%)	20,39,42	2.93	8 (40%)
34	2MG	a	1516	34	19,26,27	4.11	8 (42%)	21,38,41	2.43	8 (38%)
56	PSU	w	39	56	17,21,22	3.54	9 (52%)	20,30,33	3.05	7 (35%)
34	4OC	a	1402	34	16,23,24	3.25	6 (37%)	17,32,35	1.37	3 (17%)
34	5MC	a	967	34	15,22,23	2.80	5 (33%)	19,32,35	1.20	3 (15%)
34	PSU	a	516	34	17,21,22	3.41	9 (52%)	20,30,33	3.29	7 (35%)
8	6MZ	A	2030	8	18,25,26	1.80	6 (33%)	16,36,39	2.37	5 (31%)
8	OMU	A	2552	8	14,22,23	3.04	4 (28%)	14,31,34	1.15	1 (7%)
8	PSU	A	2580	8	17,21,22	3.68	9 (52%)	20,30,33	3.36	6 (30%)
8	PSU	A	1917	8	17,21,22	3.45	9 (52%)	20,30,33	3.15	6 (30%)
8	2MA	A	2503	8	17,25,26	3.55	6 (35%)	19,37,40	2.07	6 (31%)
8	PSU	A	2605	8	17,21,22	3.32	9 (52%)	20,30,33	2.79	6 (30%)
34	MA6	a	1519	34	19,26,27	1.53	3 (15%)	18,38,41	3.63	5 (27%)

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	1911	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/5/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	2MG	a	1207	34	-	0/5/27/28	0/3/3/3
34	G7M	a	527	34	-	2/3/25/26	0/3/3/3
34	MA6	a	1518	34	-	0/7/29/30	0/3/3/3
8	PSU	A	2604	8	-	2/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/5/25/26	0/2/2/2
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	2/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	4/5/25/26	0/2/2/2
56	MIA	w	37	56	-	3/11/33/34	0/3/3/3
8	OMG	A	2251	56,8	-	0/5/27/28	0/3/3/3
8	2MG	A	1835	8	-	2/5/27/28	0/3/3/3
34	5MC	a	1407	34	-	1/5/25/26	0/2/2/2
34	UR3	a	1498	34	-	0/5/25/26	0/2/2/2
56	G7M	w	46	56	-	1/3/25/26	0/3/3/3
8	OMC	A	2498	8	-	2/7/27/28	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/3/25/26	0/3/3/3
8	5MC	A	747	8	-	2/5/25/26	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	2/5/25/26	0/2/2/2
34	2MG	a	966	34	-	3/5/27/28	0/3/3/3
8	6MZ	A	1618	8	-	2/5/27/28	0/3/3/3
55	4SU	v	8	55	-	0/5/25/26	0/2/2/2
55	5MU	v	54	55	-	3/5/25/26	0/2/2/2
55	H2U	v	20	55	-	1/7/38/39	0/2/2/2
8	PSU	A	746	8	-	4/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/5/27/28	0/3/3/3
58	FME	y	101	58	-	4/7/9/11	-
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/3/25/26	0/3/3/3
34	2MG	a	1516	34	-	0/5/27/28	0/3/3/3
56	PSU	w	39	56	-	2/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
34	5MC	a	967	34	-	2/5/25/26	0/2/2/2
34	PSU	a	516	34	-	1/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	3/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	OMU	A	2552	8	-	0/7/27/28	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1917	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	2605	8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	4/7/29/30	0/3/3/3

The worst 5 of 294 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C2'-C1'	-17.95	1.33	1.54
8	A	1915	3TD	O4'-C1'	15.25	1.67	1.44
55	v	20	H2U	C2-N1	12.16	1.53	1.35
34	a	1516	2MG	C2-N2	12.01	1.44	1.34
8	A	2580	PSU	C5-C1'	-10.29	1.43	1.52

The worst 5 of 228 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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
34	a	527	G7M	C1'-N9-C4	12.34	148.33	126.64
8	A	2504	PSU	N1-C2-N3	-11.40	119.37	128.43
8	A	746	PSU	N1-C2-N3	-11.36	119.40	128.43

There are no chirality outliers.

5 of 61 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	1407	5MC	O4'-C1'-N1-C6
34	a	1519	MA6	C5-C6-N6-C9
34	a	1519	MA6	C5-C6-N6-C10

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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$
61	AM2	a	2001	-	40,40,40	0.24	0	53,60,60	0.60	2 (3%)
62	GDP	x	801	-	24,30,30	5.67	11 (45%)	31,47,47	2.22	12 (38%)

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
61	AM2	a	2001	-	-	4/12/84/84	0/4/4/4
62	GDP	x	801	-	-	7/12/32/32	0/3/3/3

The worst 5 of 11 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	C4-N3	7.50	1.47	1.35
62	x	801	GDP	C6-C5	6.13	1.51	1.41

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	N2-C2-N1	5.95	126.50	117.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	N3-C2-N1	-5.42	119.99	127.22
62	x	801	GDP	C5-C6-N1	-3.66	118.43	123.43
62	x	801	GDP	C3'-C2'-C1'	3.21	105.81	100.98
62	x	801	GDP	C6-N1-C2	3.20	121.01	115.93

There are no chirality outliers.

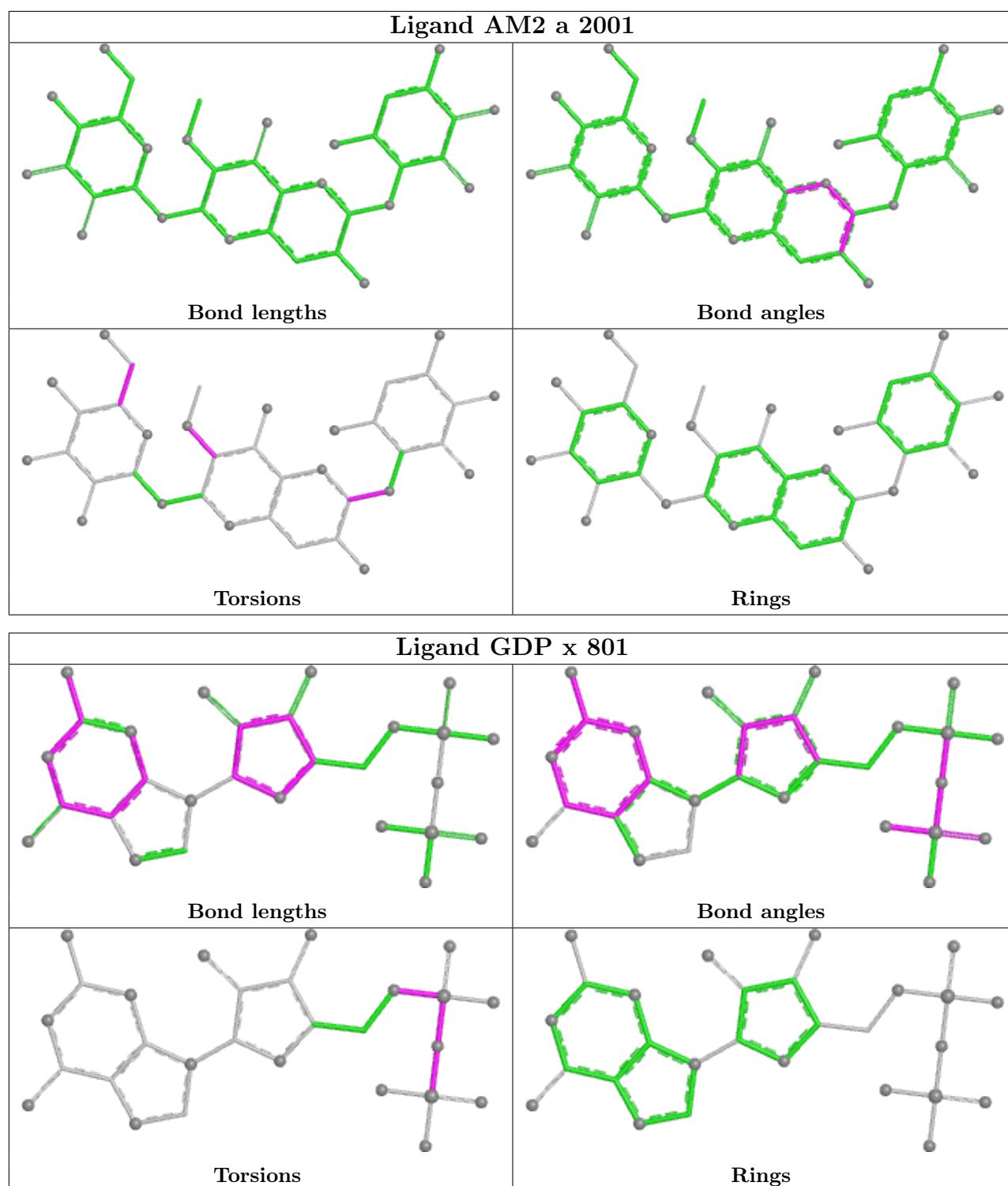
5 of 11 torsion outliers are listed below:

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.

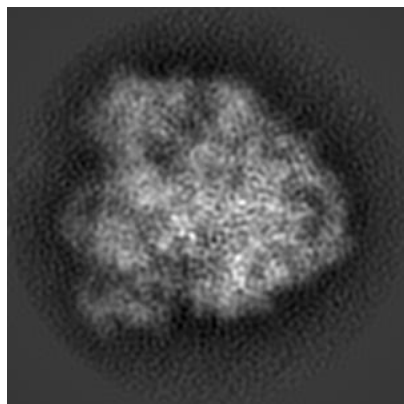
6 Map visualisation [i](#)

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.

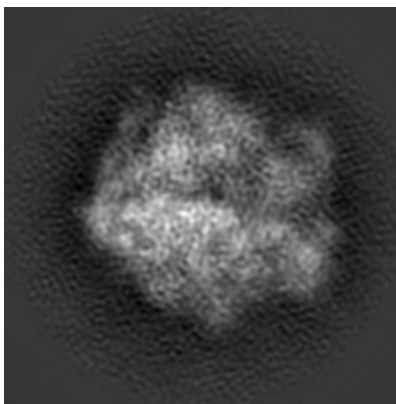
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

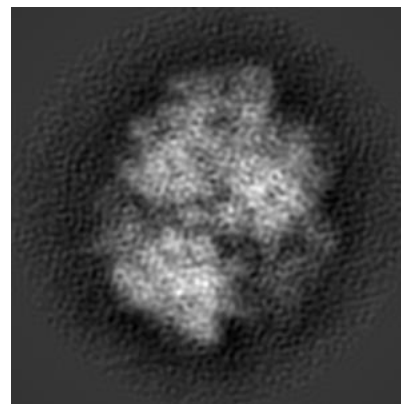
6.1.1 Primary map



X

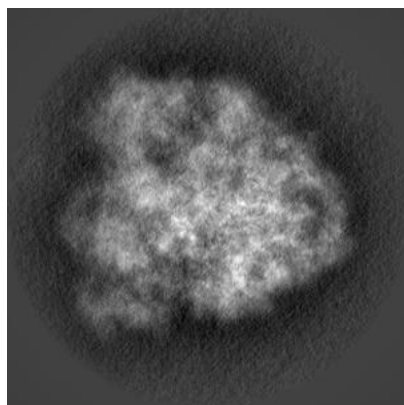


Y

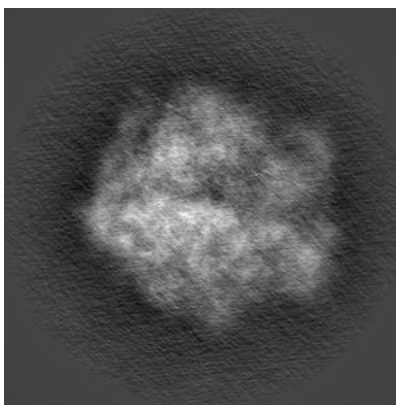


Z

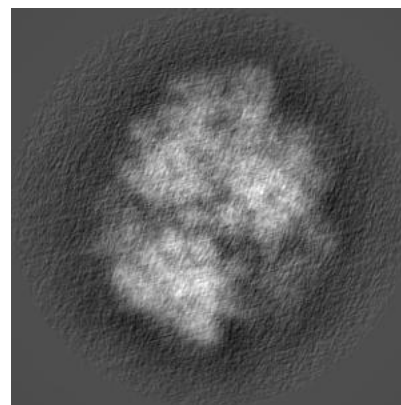
6.1.2 Raw map



X



Y

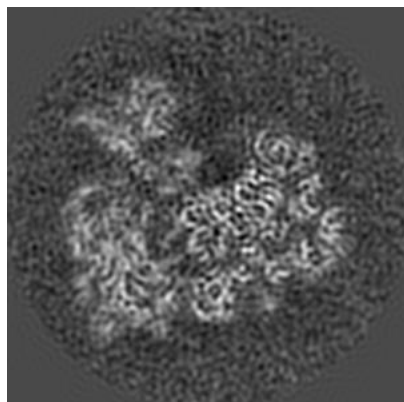


Z

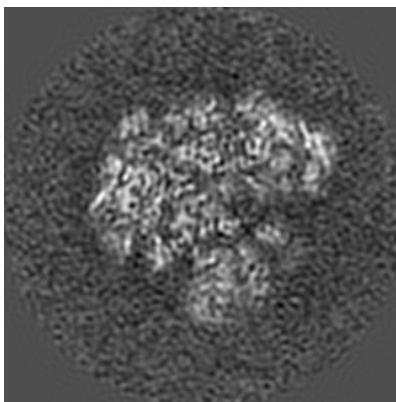
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

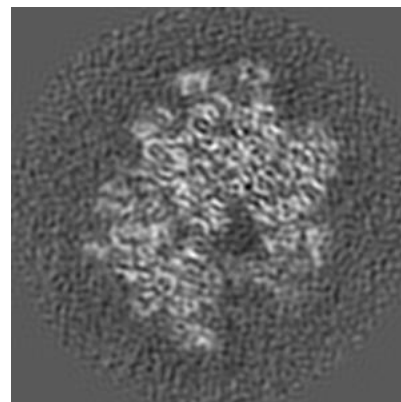
6.2.1 Primary map



X Index: 144

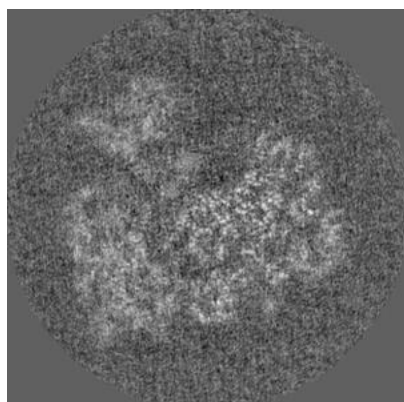


Y Index: 144

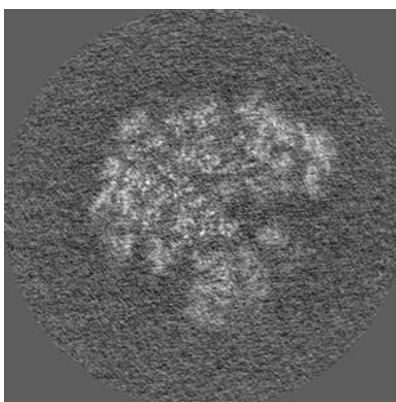


Z Index: 144

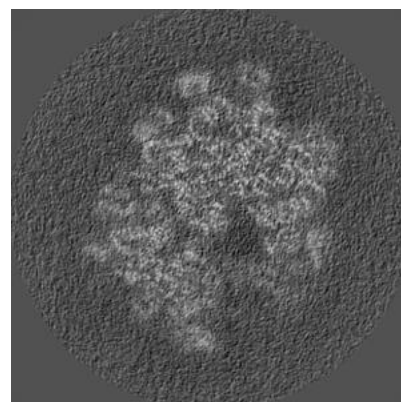
6.2.2 Raw map



X Index: 144



Y Index: 144

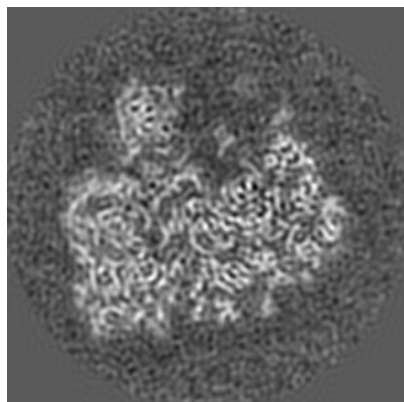


Z Index: 144

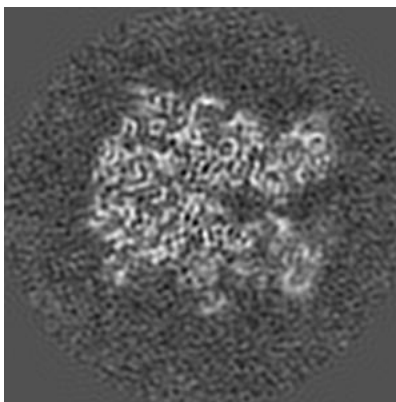
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

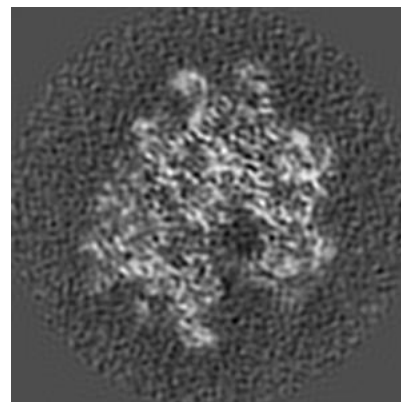
6.3.1 Primary map



X Index: 138

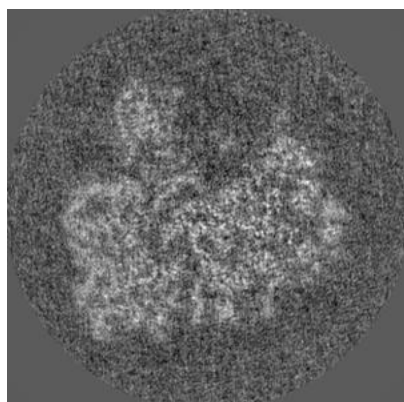


Y Index: 159

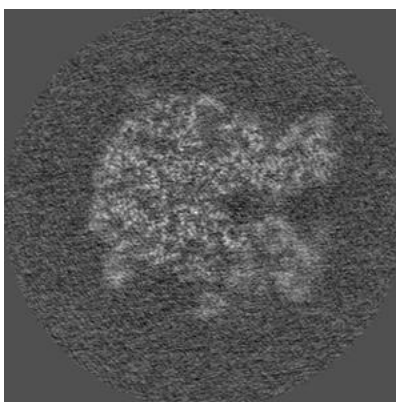


Z Index: 147

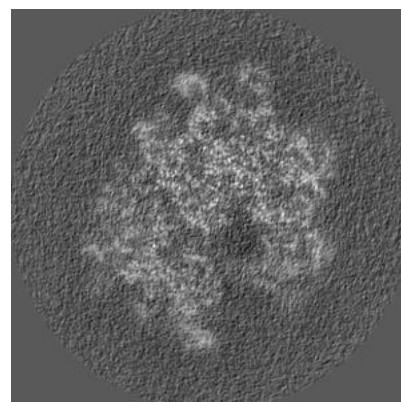
6.3.2 Raw map



X Index: 139



Y Index: 157

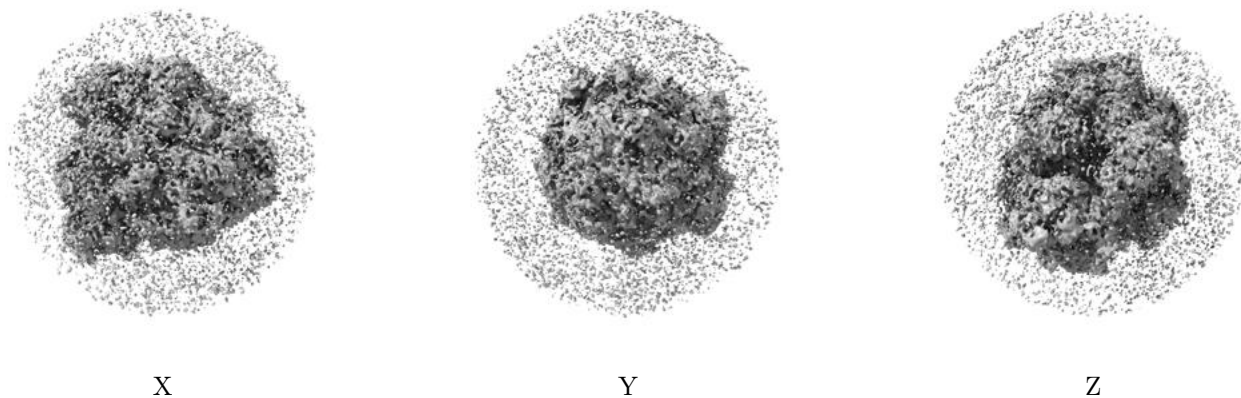


Z Index: 146

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

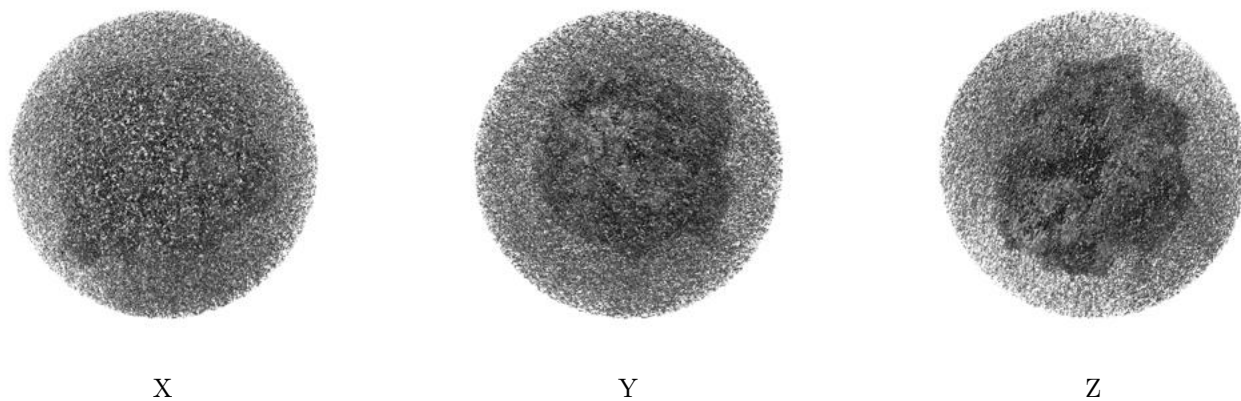
6.4 Orthogonal surface views [i](#)

6.4.1 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.

6.4.2 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.

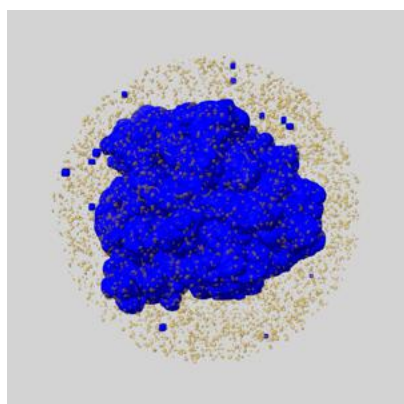
6.5 Mask visualisation [i](#)

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

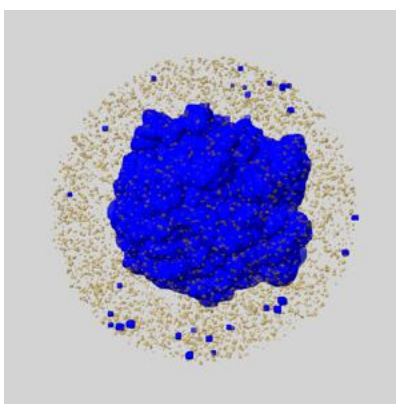
A mask typically either:

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

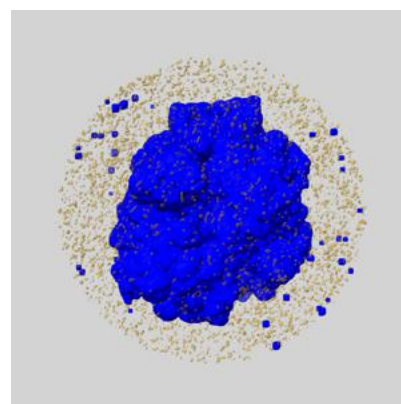
6.5.1 emd_13465_msk_1.map [i](#)



X



Y

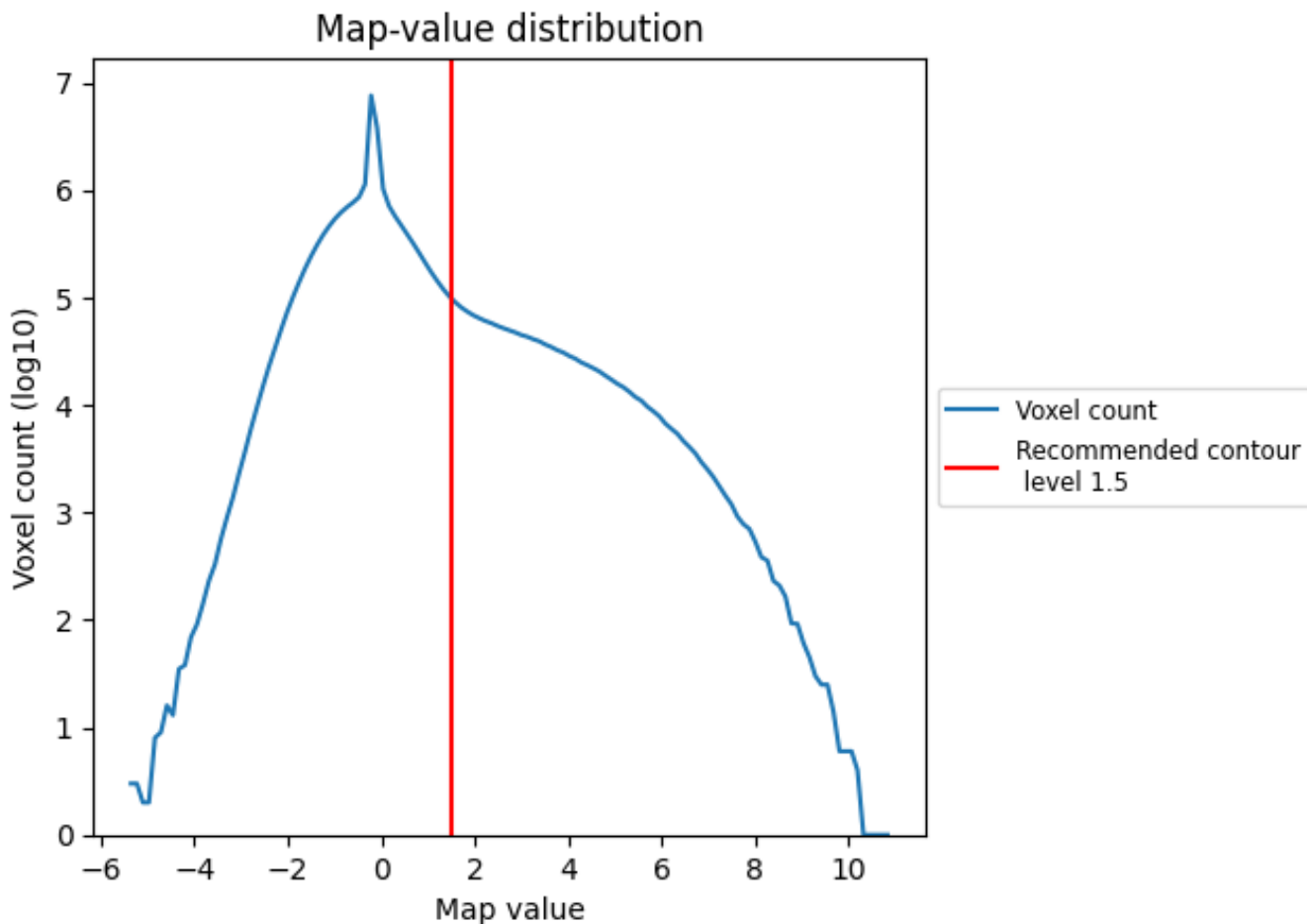


Z

7 Map analysis [i](#)

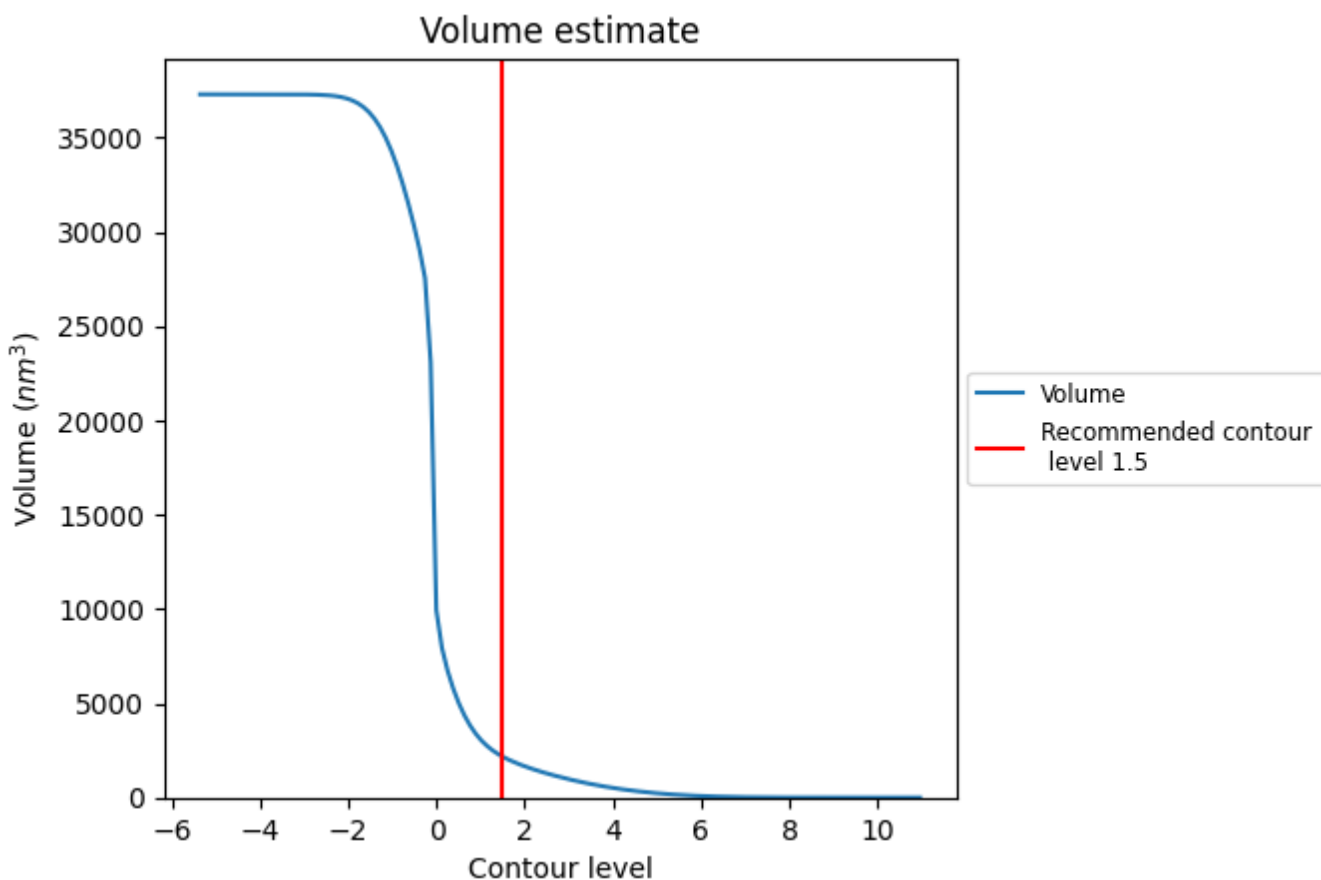
This section contains the results of statistical analysis of the map.

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.

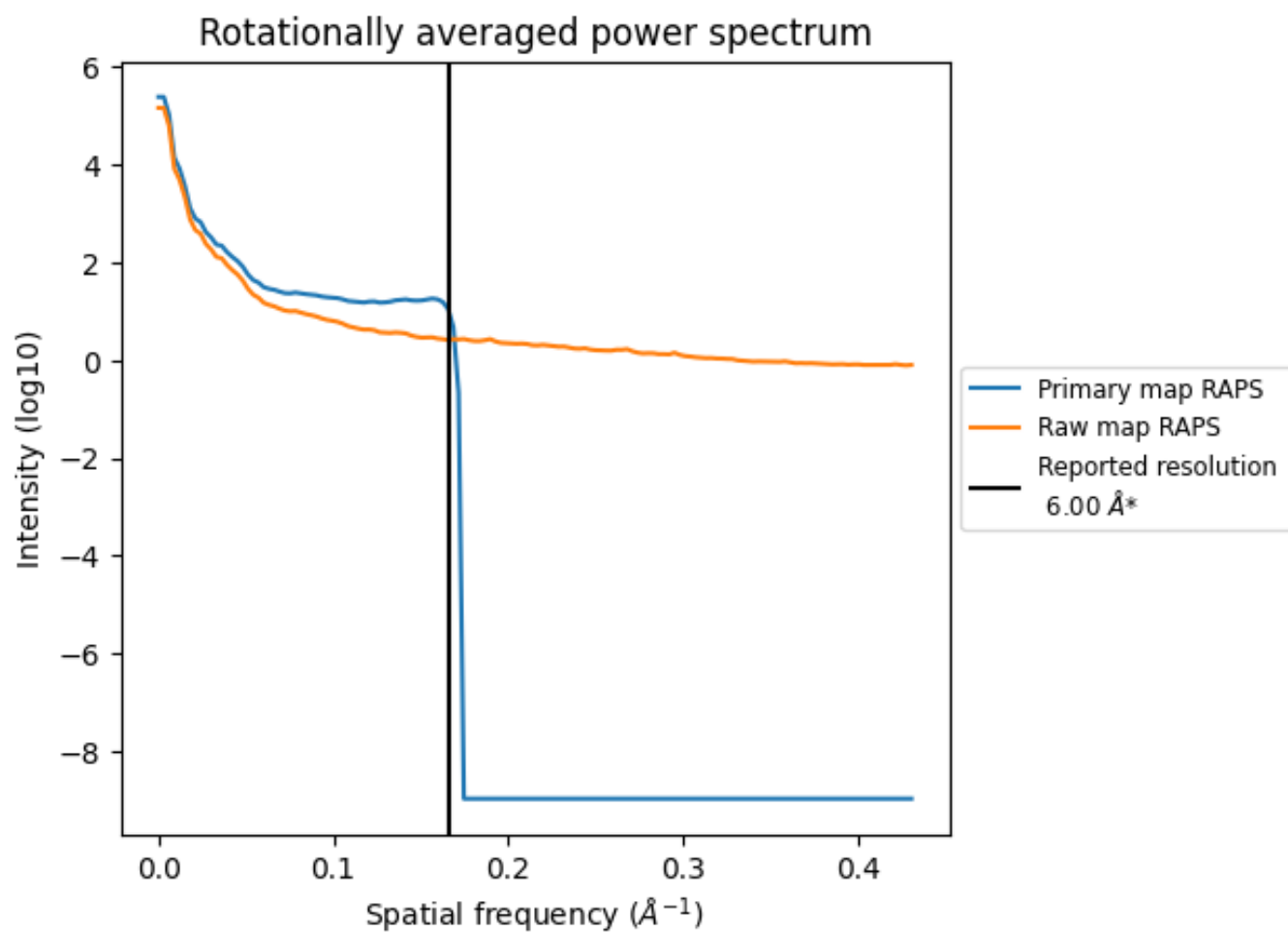
7.2 Volume estimate [i](#)



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 i

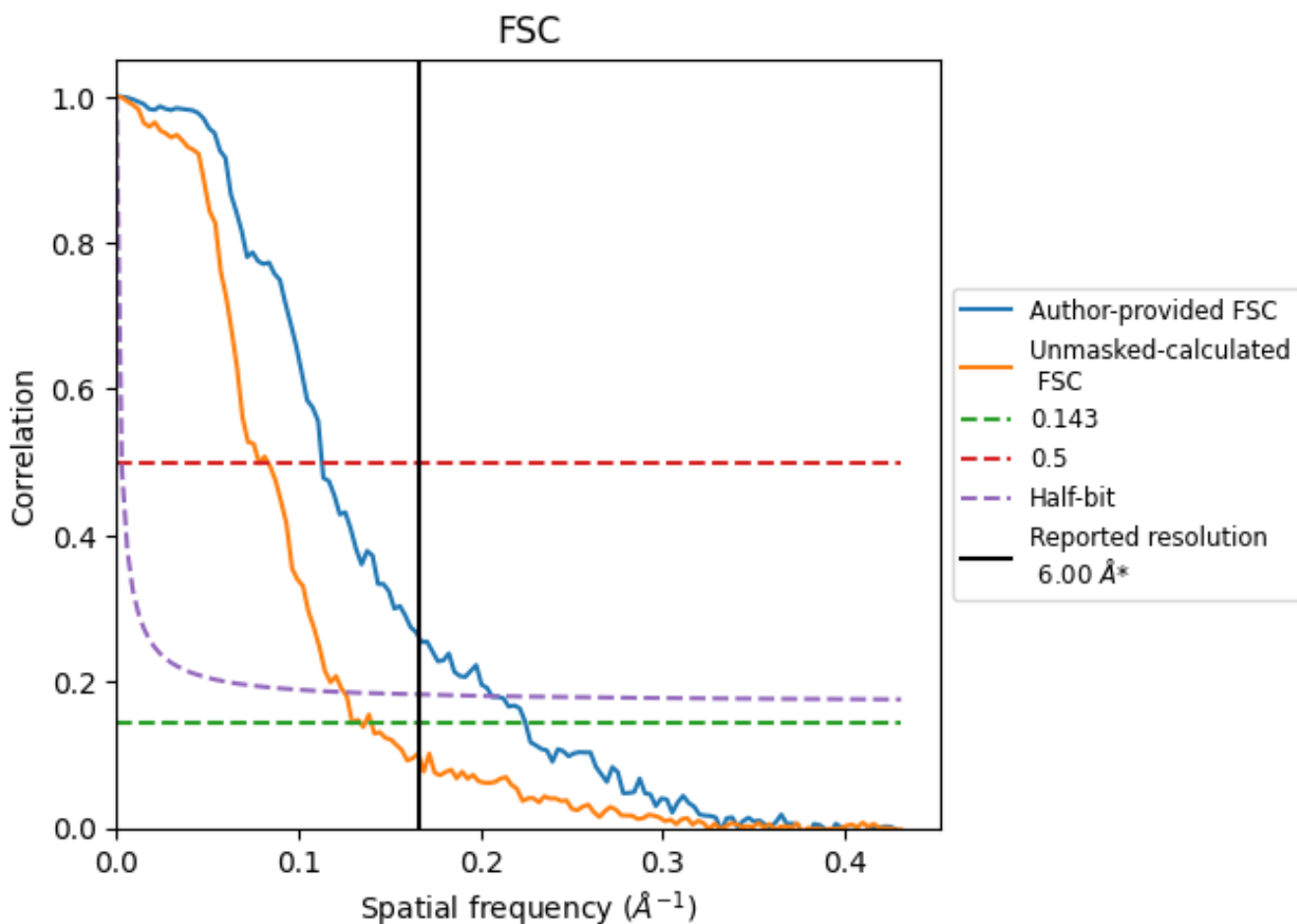


*Reported resolution corresponds to spatial frequency of 0.167 Å⁻¹

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 [i](#)

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*	7.72	12.79	8.00

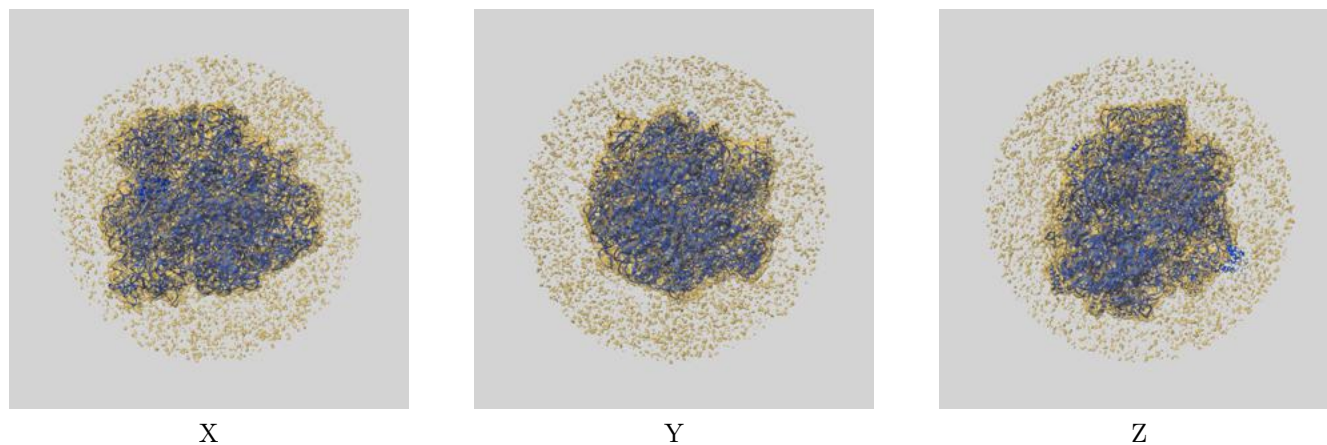
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.45 differs from the reported value 6.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.72 differs from the reported value 6.0 by more than 10 %

9 Map-model fit [i](#)

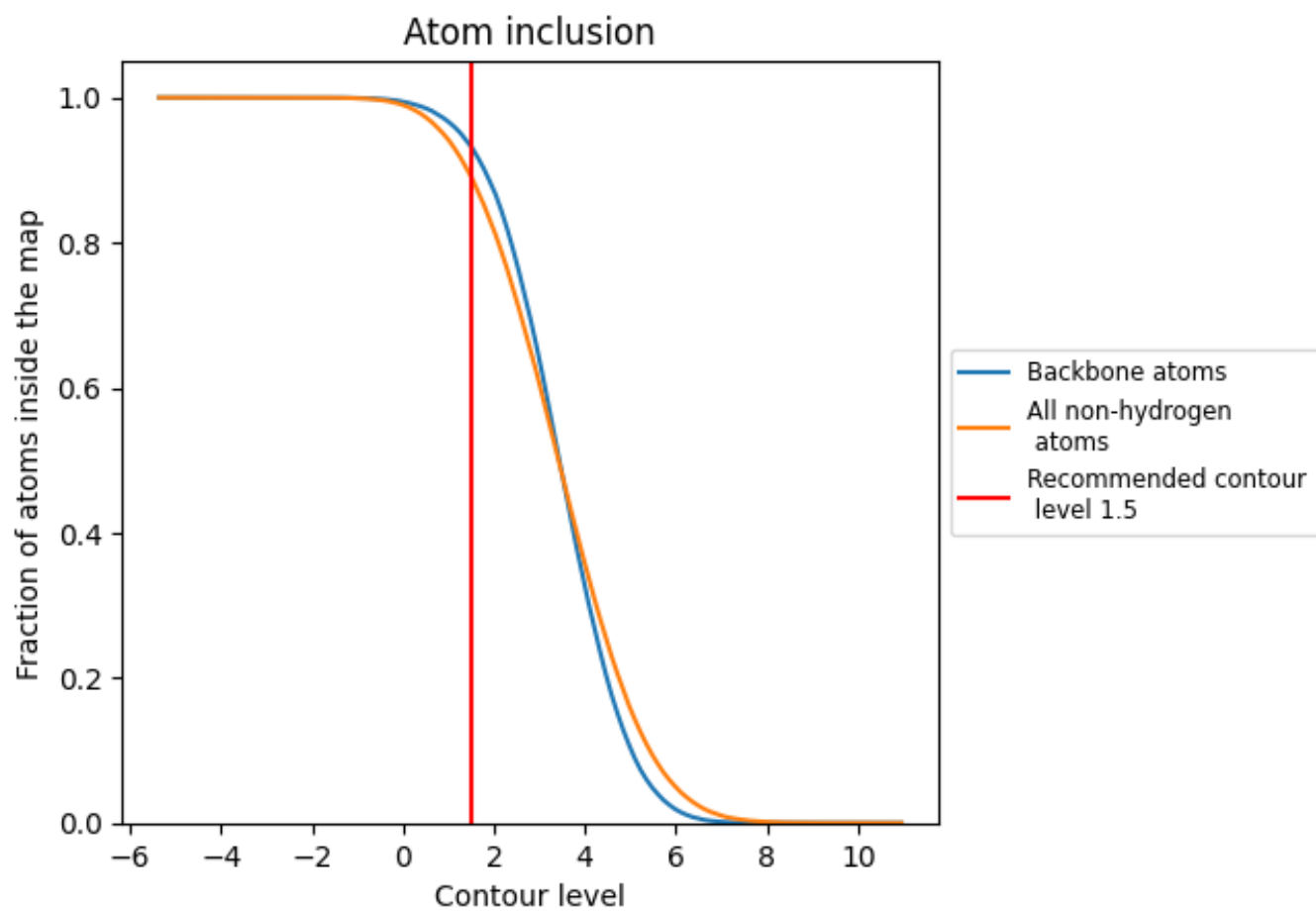
This section contains information regarding the fit between EMDB map EMD-13465 and PDB model 7PJZ. Per-residue inclusion information can be found in section 3 on page 16.

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 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.