



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 02:18 AM UTC

PDB ID : 5OT7 / pdb_00005ot7
EMDB ID : EMD-3852
Title : Elongation factor G-ribosome complex captures in the absence of inhibitors.
Authors : Mace, K.; Giudice, E.; Chat, S.; Gillet, R.
Deposited on : 2017-08-21
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

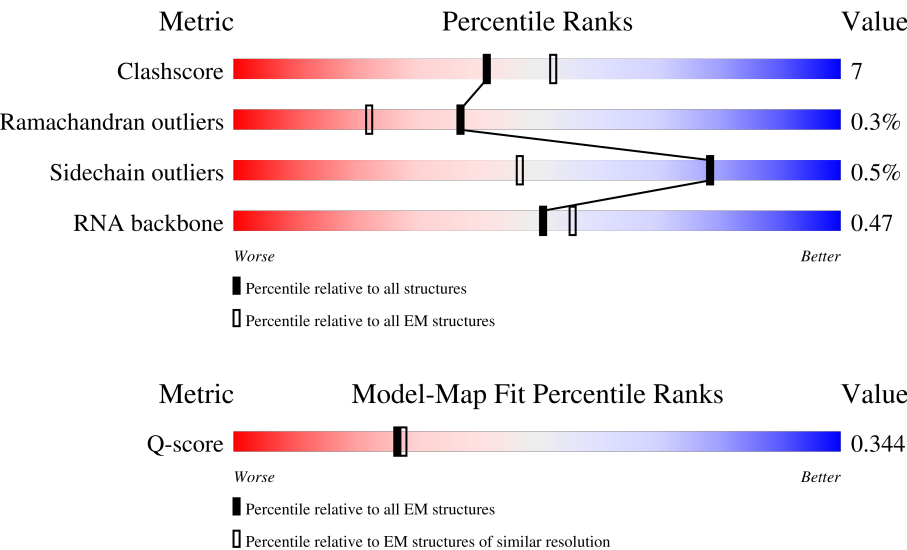
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



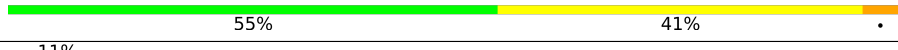
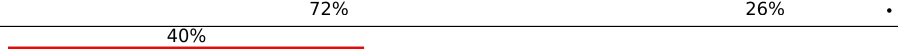
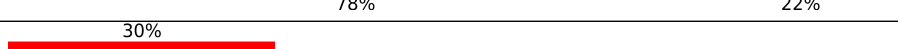
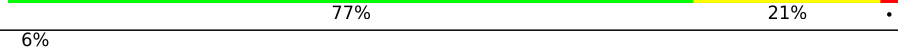
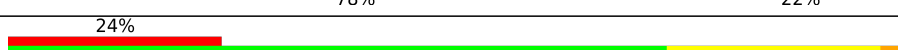
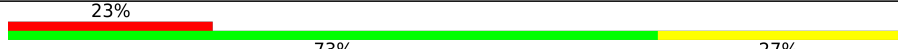
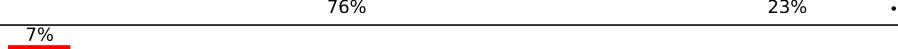
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	1	1507	
2	2	76	
3	3	15	

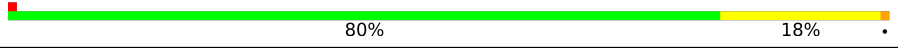
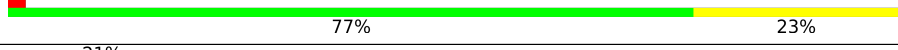
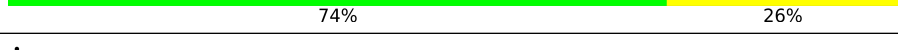
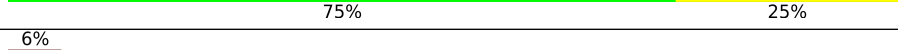
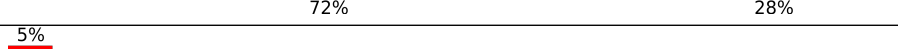
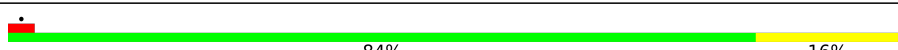
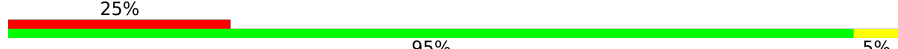
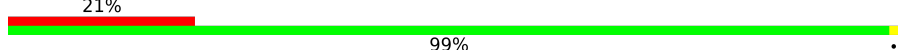
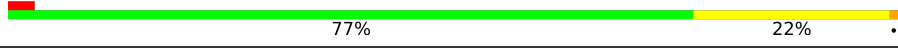
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Mol	Chain	Length	Quality of chain
4	4	2901	
5	5	119	
6	6	178	
7	7	146	
8	A	235	
9	B	207	
10	C	208	
11	D	151	
12	E	101	
13	F	155	
14	G	138	
15	H	127	
16	I	99	
17	J	119	
18	K	125	
19	L	119	
20	M	60	
21	N	88	
22	O	84	
23	P	100	
24	Q	70	
25	R	88	
26	S	99	
27	T	25	
28	U	687	

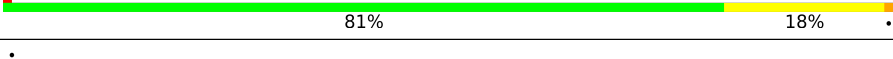
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Mol	Chain	Length	Quality of chain
29	V	78	
30	W	94	
31	X	71	
32	Y	60	
33	Z	71	
34	a	59	
35	b	50	
36	c	48	
37	d	64	
38	e	37	
39	f	227	
40	g	275	
41	h	205	
42	i	208	
43	j	179	
44	k	176	
45	l	130	
46	m	140	
47	n	71	
48	o	139	
49	p	122	
50	q	150	
51	r	141	
52	s	118	
53	t	99	

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Mol	Chain	Length	Quality of chain
54	u	138	 7% 69% 31%
55	v	117	 83% 17%
56	w	101	 82% 18%
57	x	113	 86% 12%
58	y	93	 81% 18%
59	z	101	 66% 27% 7%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 154665 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1507	Total	C	N	O	P	0	0
			32391	14418	6002	10465	1506		

- Molecule 2 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	10	Total	C	N	O	P	0	0
			214	95	35	74	10		

- Molecule 4 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	2901	Total	C	N	O	P	0	0
			62476	27807	11683	20086	2900		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	1041	G	C	conflict	GB 55771382
4	2133	A	G	conflict	GB 55771382

- Molecule 5 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 6 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	178	Total	C	N	O	S	0	0
			1418	906	254	256	2		

- Molecule 7 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	146	Total	C	N	O	S	0	0
			1136	726	201	208	1		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	235	Total	C	N	O	S	0	1
			1901	1213	342	341	5		

- Molecule 9 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	207	Total	C	N	O	S	0	1
			1613	1016	315	281	1		

- Molecule 10 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	151	Total	C	N	O	S	0	1
			1147	724	218	201	4		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 14 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 15 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	99	Total	C	N	O	S	0	1
			795	499	157	138	1		

- Molecule 17 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 18 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	125	Total	C	N	O	S	0	1
			971	611	196	163	1		

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	119	Total	C	N	O	S	0	1
			938	579	194	163	2		

- Molecule 20 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 21 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	84	Total	C	N	O	S	0	1
			701	443	140	117	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	100	Total	C	N	O	S	0	1
			824	528	152	142	2		

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Q	70	Total	C	N	O	0	0
			574	367	112	95		

- Molecule 25 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	88	Total	C	N	O	S	0	1
			692	440	128	122	2		

- Molecule 26 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 27 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	T	25	Total	C	N	O	0	1
			209	128	51	30		

- Molecule 28 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	661	Total	C	N	O	S	0	0
			5173	3288	884	983	18		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	78	Total	C	N	O	S	0	0
			617	381	130	105	1		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	94	Total	C	N	O	S	0	1
			732	460	146	125	1		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	71	Total	C	N	O	S	0	0
			598	370	121	106	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	60	Total	C	N	O	S	0	1
			468	298	91	78	1		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	71	Total	C	N	O	S	0	0
			581	364	108	104	5		

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	50	Total	C	N	O	S	0	0
			433	270	88	71	4		

- Molecule 36 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	48	Total	C	N	O	S	0	0
			419	257	104	56	2		

- Molecule 37 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	64	Total	C	N	O	S	0	1
			508	326	102	78	2		

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 39 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	227	Total	C	N	O	S	0	0
			1735	1096	318	318	3		

- Molecule 40 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	275	Total	C	N	O	S	0	0
			2145	1353	428	361	3		

- Molecule 41 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	205	Total	C	N	O	S	0	1
			1564	988	300	270	6		

- Molecule 42 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	208	Total	C	N	O	S	0	1
			1624	1035	304	282	3		

- Molecule 43 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	179	Total	C	N	O	S	0	0
			1459	931	266	258	4		

- Molecule 44 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	176	Total	C	N	O	S	0	1
			1345	853	253	237	2		

- Molecule 45 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	l	130	Total	C	N	O	0	0
			654	393	130	131		

- Molecule 46 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	m	140	Total	C	N	O	0	0
			701	420	140	141		

- Molecule 47 is a protein called Ribosomal protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	n	71	Total	C	N	O	0	0
			356	213	71	72		

- Molecule 48 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	139	Total	C	N	O	S	0	1
			1105	712	207	182	4		

- Molecule 49 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		

- Molecule 51 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 52 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	118	Total	C	N	O	S	0	0
			968	604	203	160	1		

- Molecule 53 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	t	99	Total	C	N	O	0	1
			771	486	155	130		

- Molecule 54 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	138	Total	C	N	O	S	0	1
			1142	710	235	196	1		

- Molecule 55 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 56 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 57 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 58 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	93	Total	C	N	O		0	1
			726	471	132	123			

- Molecule 59 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	101	Total	C	N	O	S	0	1
			776	500	149	123	4		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	1	125	Total	Mg	0
			125	125	
60	4	320	Total	Mg	0
			320	320	
60	D	1	Total	Mg	0
			1	1	
60	K	1	Total	Mg	0
			1	1	
60	O	2	Total	Mg	0
			2	2	
60	S	1	Total	Mg	0
			1	1	

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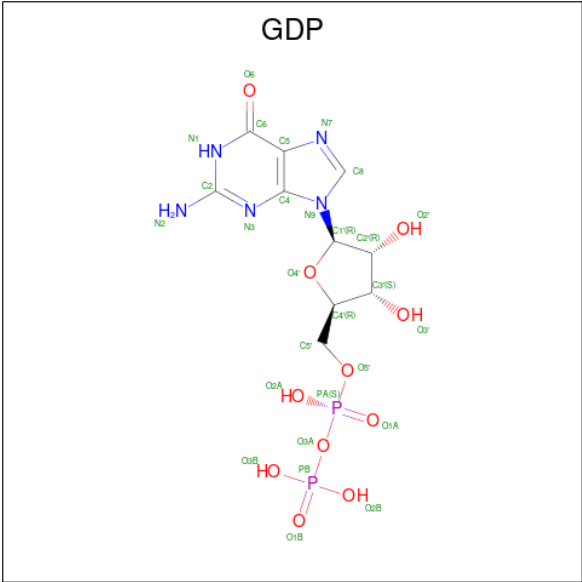
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Mol	Chain	Residues	Atoms		AltConf
60	U	1	Total 1	Mg 1	0
60	a	1	Total 1	Mg 1	0
60	c	1	Total 1	Mg 1	0
60	e	1	Total 1	Mg 1	0
60	h	1	Total 1	Mg 1	0
60	i	1	Total 1	Mg 1	0
60	q	1	Total 1	Mg 1	0
60	t	3	Total 3	Mg 3	0
60	u	1	Total 1	Mg 1	0
60	x	1	Total 1	Mg 1	0

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	C	1	Total 1	Zn 1	0
61	M	1	Total 1	Zn 1	0
61	e	1	Total 1	Zn 1	0

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

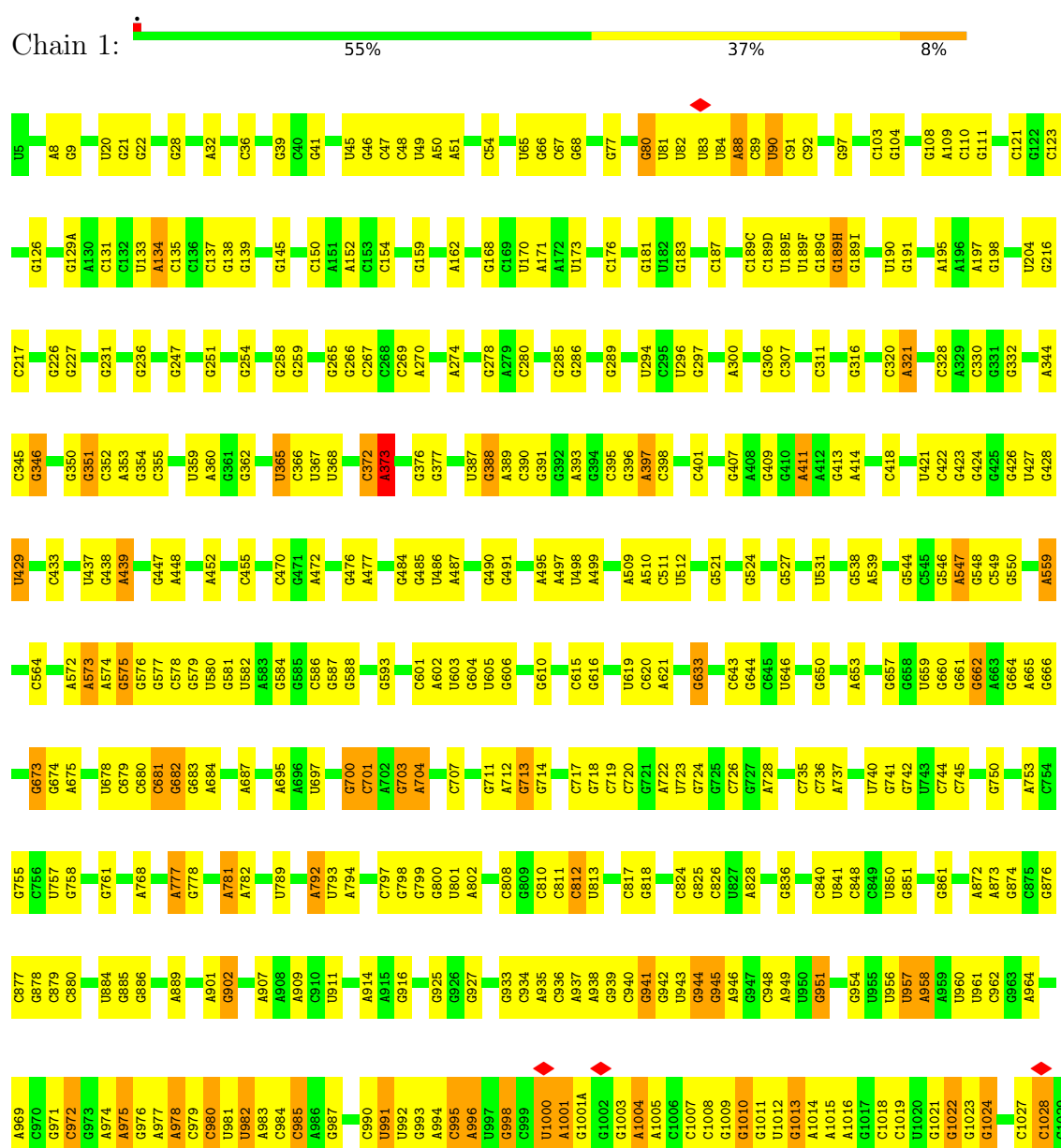


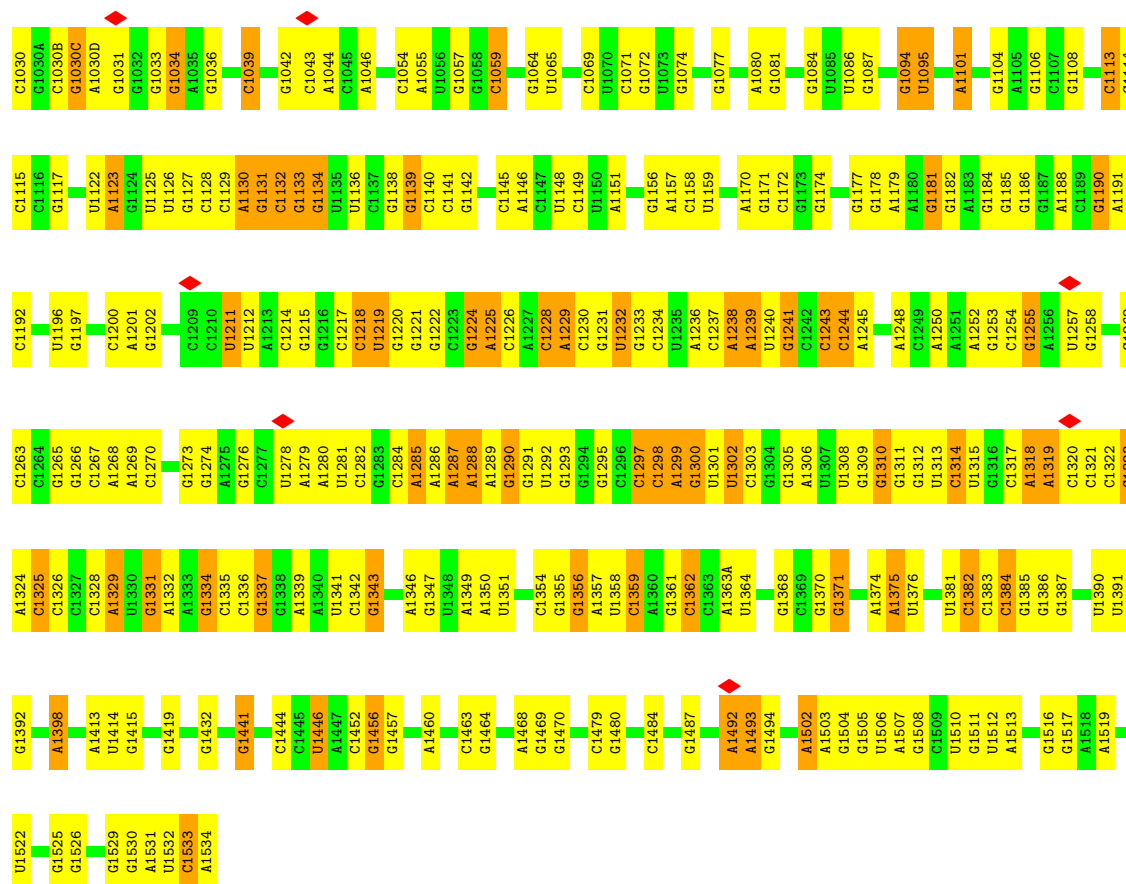
Mol	Chain	Residues	Atoms					AltConf
62	U	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

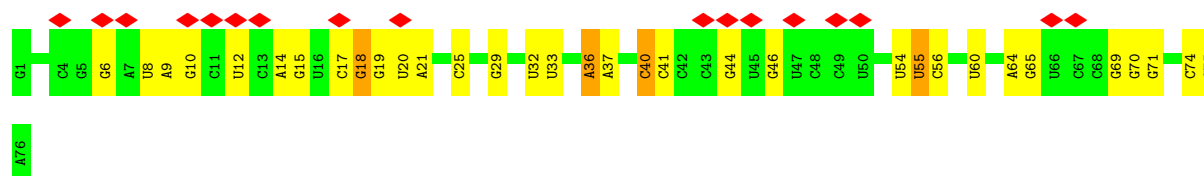
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S Ribosomal RNA





• Molecule 2: tRNA-Phe



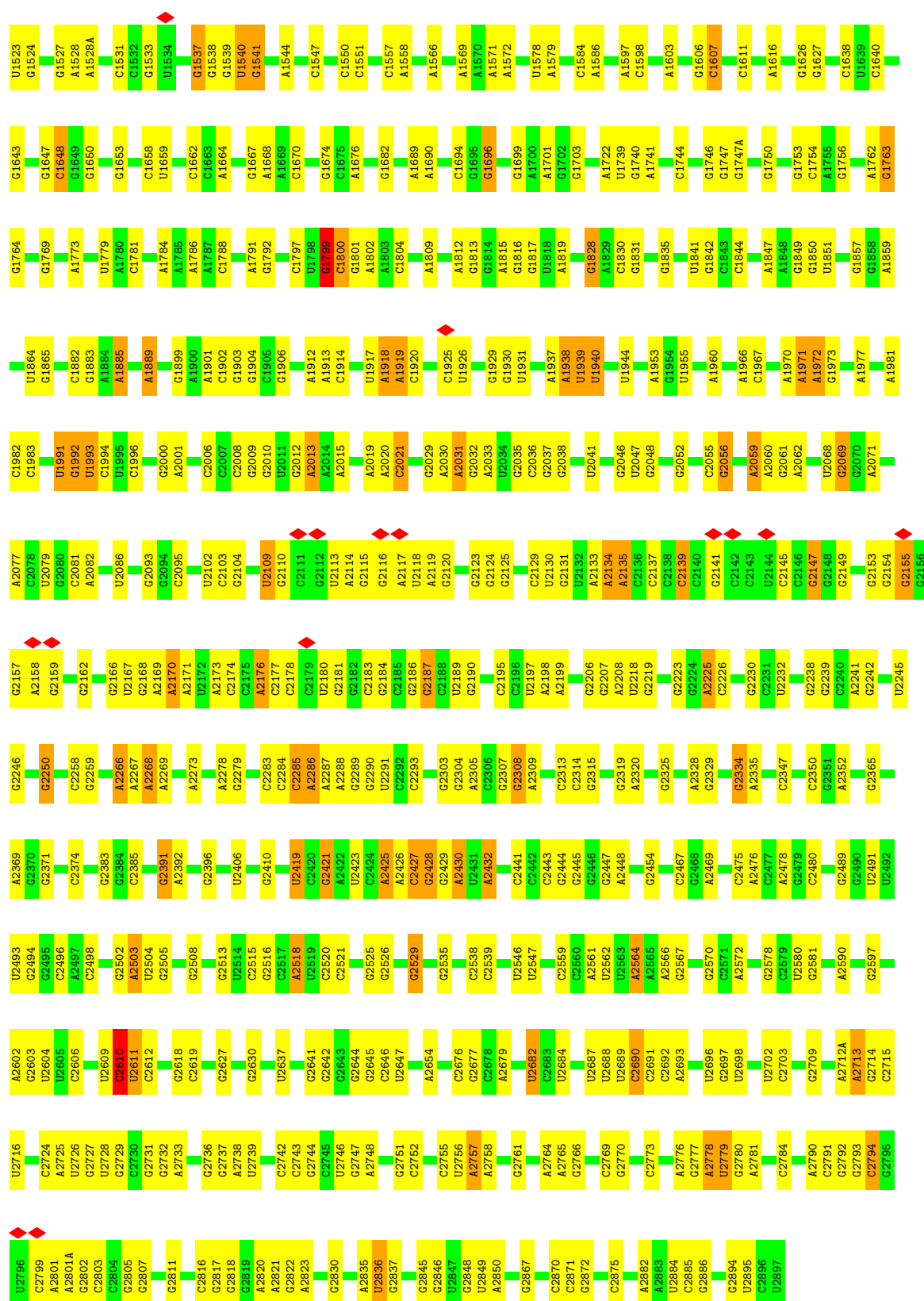
• Molecule 3: mRNA



• Molecule 4: 23S Ribosomal RNA

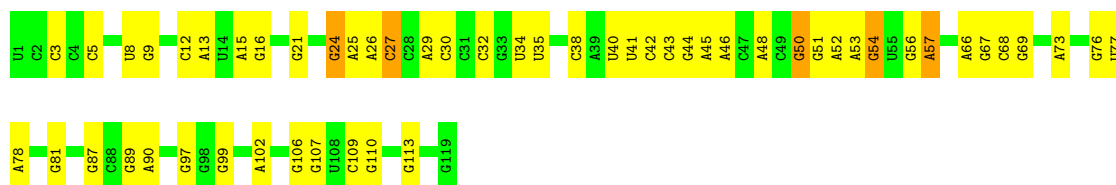


C1411	G1296	G1186	C1092	C395	A887	C790	A670	A609	A526	G438	G327	C264	G125
A1412	U1300	A1189	G1093	A996	C888	C791	A675	U614	C527	G442	G328	A265	C128
G1416	A1301	G1190	U1094	A1009	C889	A792	A676	U614A	A528	G443	G329	C266	G131
C1417	C1306	G1193	U1097	A1010	C892	A793	G679	G614B	A529	G446	G330	C267	A330
U1420	G1309	C1196	C1102	U1012	C893	A800	G680	A614C	C531	A449	A331	U269	G139A
G1423	G1310	G1197	A1103	U1013	U895	G805	G681	G615	G532	G450	C334	A270	G140
G1424	G1311	G1203	G1106	G1015	A896	C806	G686	G620	U534	C271B	U339	C271B	G141
A1427	C1314	A1204	G1116	G1022	C897	U807	G686	G622	A536	C271C	A340	C271C	G143
C1428	C1315	U1205	C1116	G1025	G906	U811	G690	A627	G552	C271G	A345	C271G	U156
U1431	G1325	A1210	G1122	U1026	A909	C812	G690	G628	G553	G271H	A346	G271H	U157
G1435	U1329	U1211	C1123	A1027	A910	C814	C698	G629	U554	U271L	G352	U271L	U159
U1438	C1330	G1212	G1124	A1028	C915	G818	A699	G630	U555	U271N	G353	U271N	G177
A1439	U1329	A1212	G1125	U1033	G919	G819	G704	A631	G556	G463	G358	G271R	G178
G1445	C1330	A1220	A1126	U1038	G922	U826	G721	G636	U557	A466	U358	G271R	C184
U1445	U1331	A1222	A1127	C1038	A941	U827	A722	A637	G558	C467	A359	G271R	U185
A1452	C1332	G1225	G1130	G1039	A945	U828	G726	G638	G559	G468	U362	G271U	A196
U1453	G1334	C1230	U1130	A1045	G946	A829	G727	U639	C560	G469	G363	G271U	A197
G1458	U1341	G1231	C1135	A1046	C947	U829	G728	G642	U568	A471	U366	G271X	C198
A1459	C1346	U1231	G1141	G1051	G948	U830	G733	A643	A572	A472	C370	G271X	A199
A1460	U1235	U1235	U1142	A1054	G948	C831	A734	G648	A573	U475	G372	G272C	U200
C1467	G1236	G1236	A1143	G1055	G948	U832	U740	C650	C574	G476	U373	G272C	G205
U1477	A1247	A1247	G1144	G1059	A953	C838	U743	G651	A575	G477	A374	A276	C210
A1478	G1252	G1252	A1148	U1060	G954	U839	G744	A654	A576	G480	U380	C277	C211
G1482	A1253	A1253	C1152	U1061	A957	C840	G744	G654A	A577	G481	G381	A278	G212
G1484	A1254	U1255	C1153	U1065	U958	A841	G748	C654B	G579	A482	U387	A283	G215
G1485	U1255	G1256	G1154	U1066	A959	G852	G748	G654C	G580	G494	U387	A288	A216
A1486	G1263	U1263	A1155	A1067	A960	C855	A752	G654D	C581	G496	A394	A289	G217
G1487	U1264	A1265	G1156	G1068	C961	C856	C753	G654E	G582	A501	U395	A294	A222
A1490	G1266	G1266	G1157	A1069	G962	C857	G765	G654F	G585	A505	G396	G295	A223
C1493	U1267	U1267	C1158	U1070	C964	U858	G766	G654G	U588	A508	G397	A300	A227
A1494	A1268	U1268	G1161	G1071	U869	U860	C766	G654H	C589	G301	G398	G301	A228
C1499	C1270	C1270	U1165	G1074	G972	A861	G768	G654I	A590	C302	C404	C302	A229
G1500	G1271	G1271	G1173	A1075	A973	C864	A774	G654J	C591	U305	U405	U305	C237
C1504	U1272	U1272	A1174	A1077	C975	C865	G775	G654K	G592	G411	G411	G309	A244
U1509	U1273	U1273	U1175	C1079	G975A	A866	G776	G654L	G593	G512	A412	A310	G245
C1505	A1274	A1274	G1176	C1080	A980	G873	A777	G654M	U594	A513	A414	A311	C246
U1509	C1177	C1177	A1084	A1084	G980	G874	A781	G654N	U597	A514	A415	G312	G247
A1509A	A1275	A1275	A1085	A1085	A983	C875	A782	G654O	G598	C516	C420	A314	C249
U1516	U1279	U1279	A1086	A1086	A984	G875	A783	G654P	C601	C517	U421	G317	G250
G1517	G1279	G1279	C1181	A1087	C985	G881	A784	A655	G602	G518	A422	G318	A251
C1516	U1289	U1289	A1182	A1088	C985	G882	G785	G656	A603	U519	A428	C318	G252
G1517	C1398	C1398	G1183	A1089	G989	C883	G788	U657	G605	G520	A429	G321	C253
	U1184	U1184	C1184	U1090	C985	C884	A788	G658	U606	G521	A322	A322	G254
	G1091	G1091	C1185	G1091	C994	C886	A789	G660	A608	G522	G437	G323	C263

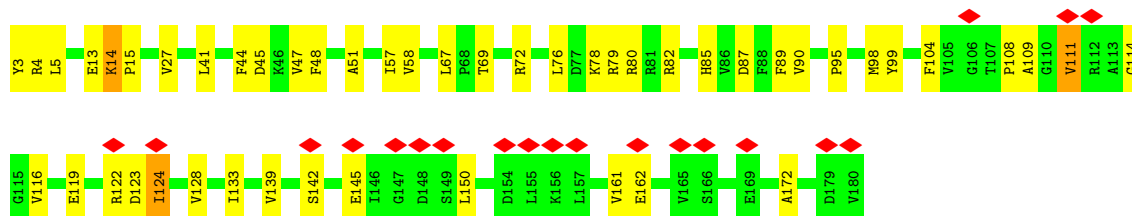


• Molecule 5: 5S Ribosomal RNA

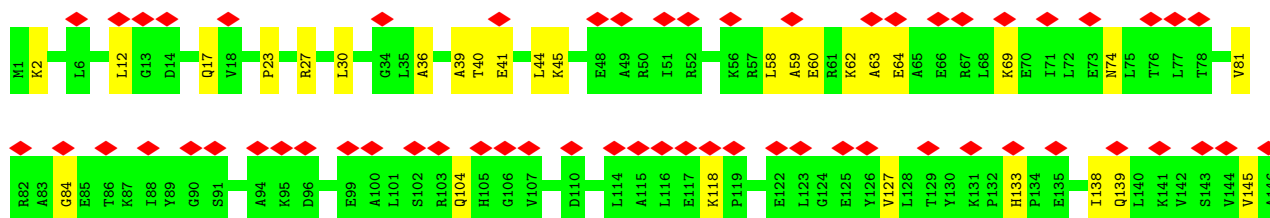
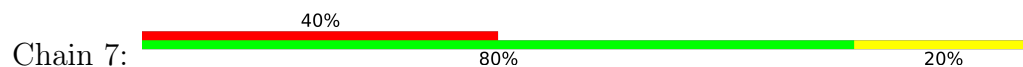
Chain 5: 55% 41%



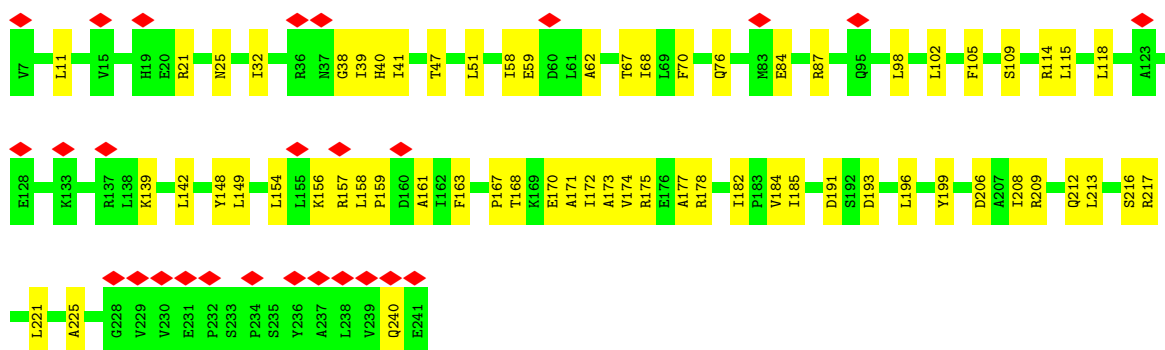
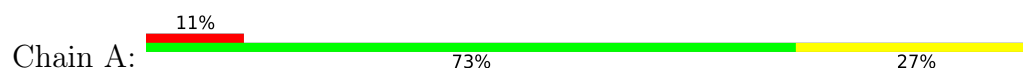
• Molecule 6: 50S ribosomal protein L25



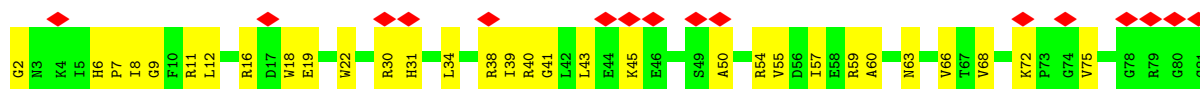
• Molecule 7: 50S ribosomal protein L9

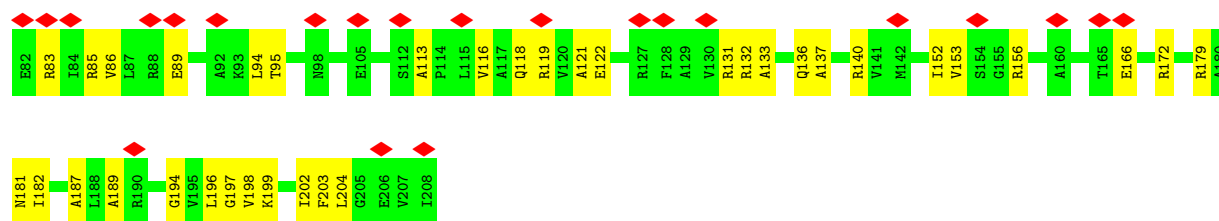


• Molecule 8: 30S ribosomal protein S2

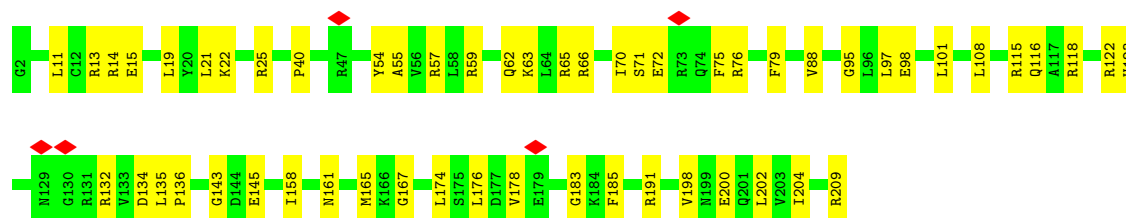


• Molecule 9: 30S ribosomal protein S3

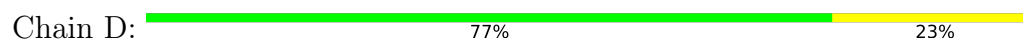




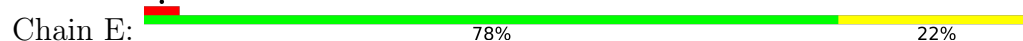
- Molecule 10: 30S ribosomal protein S4



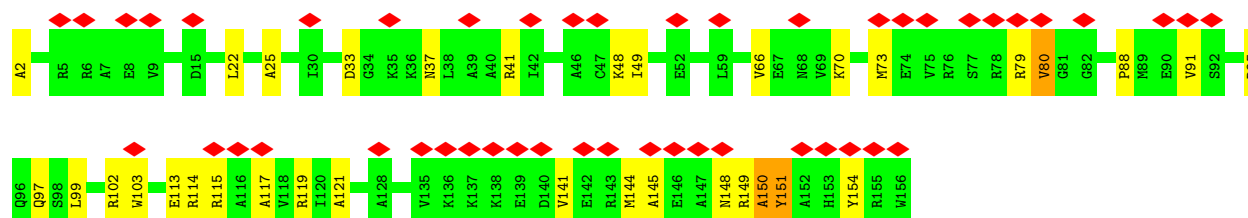
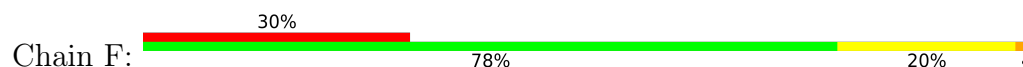
- Molecule 11: 30S ribosomal protein S5



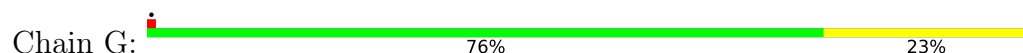
- Molecule 12: 30S ribosomal protein S6

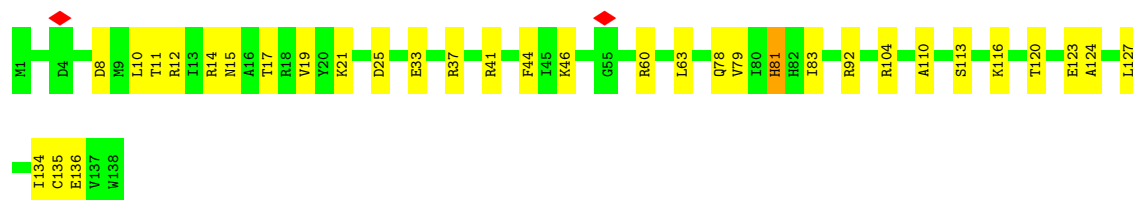


- Molecule 13: 30S ribosomal protein S7

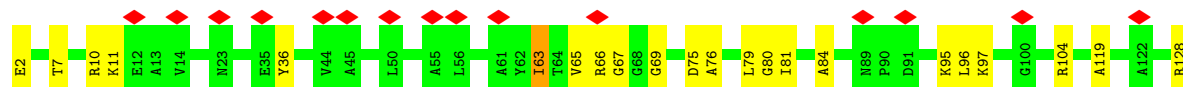
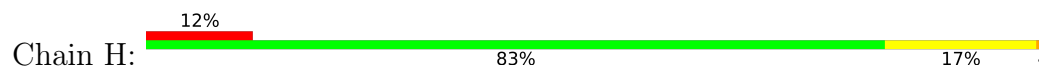


- Molecule 14: 30S ribosomal protein S8

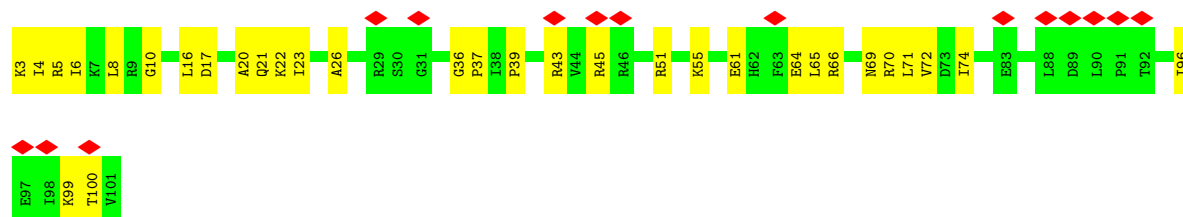




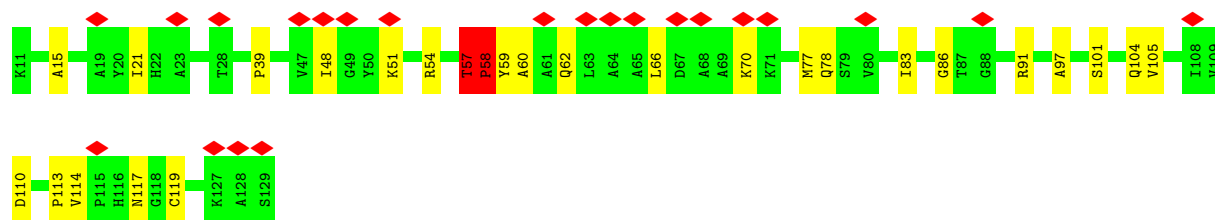
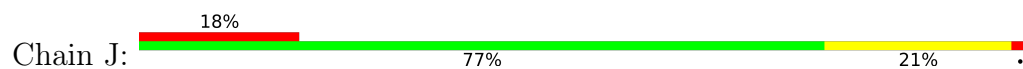
- Molecule 15: 30S ribosomal protein S9



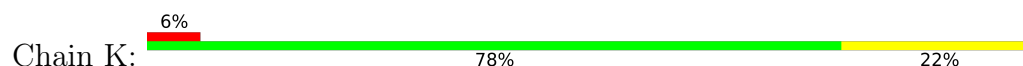
- Molecule 16: 30S ribosomal protein S10



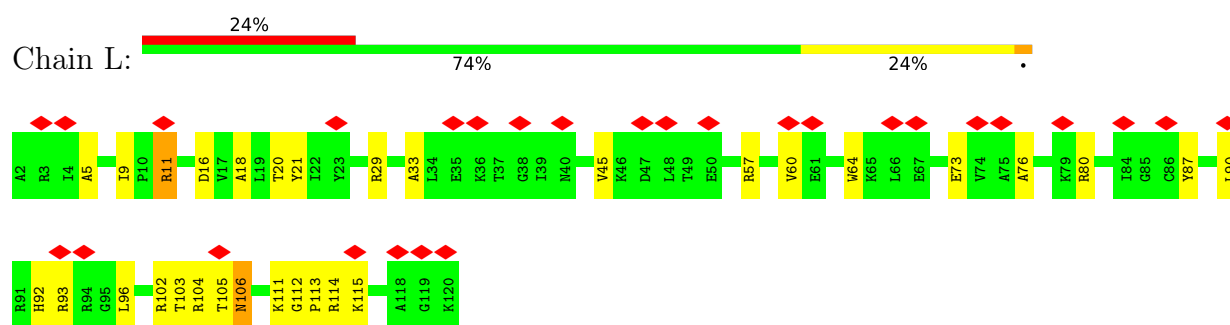
- Molecule 17: 30S ribosomal protein S11



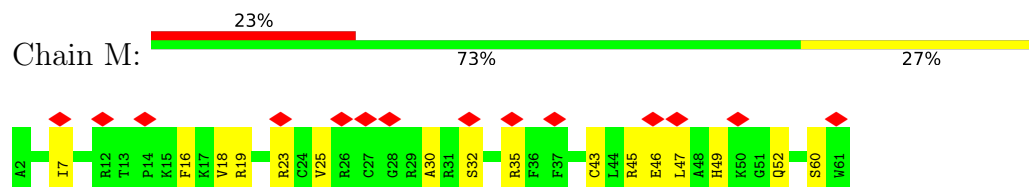
- Molecule 18: 30S ribosomal protein S12



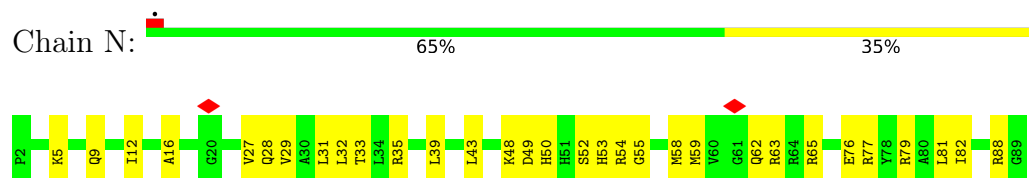
- Molecule 19: 30S ribosomal protein S13



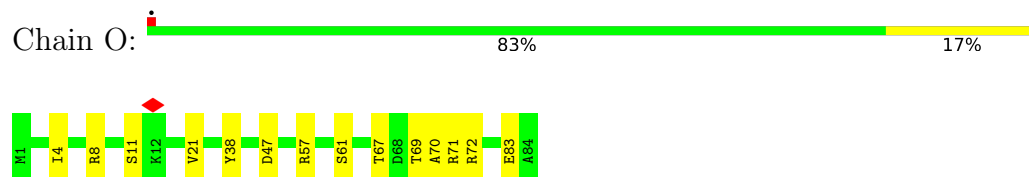
- Molecule 20: 30S ribosomal protein S14 type Z



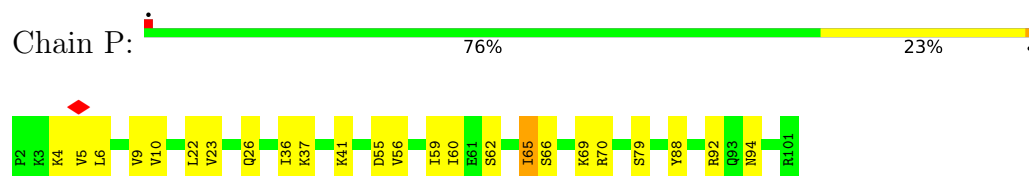
- Molecule 21: 30S ribosomal protein S15



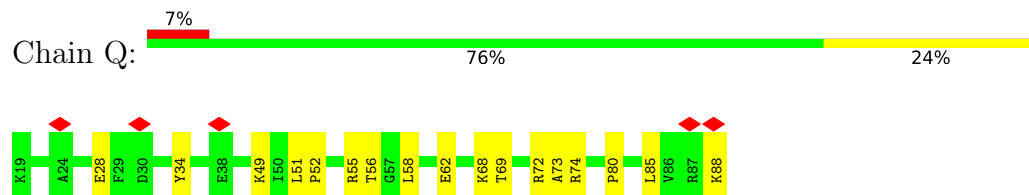
- Molecule 22: 30S ribosomal protein S16



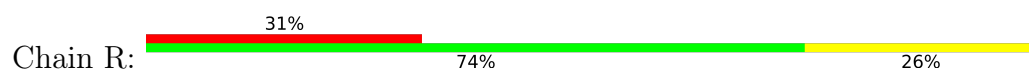
- Molecule 23: 30S ribosomal protein S17

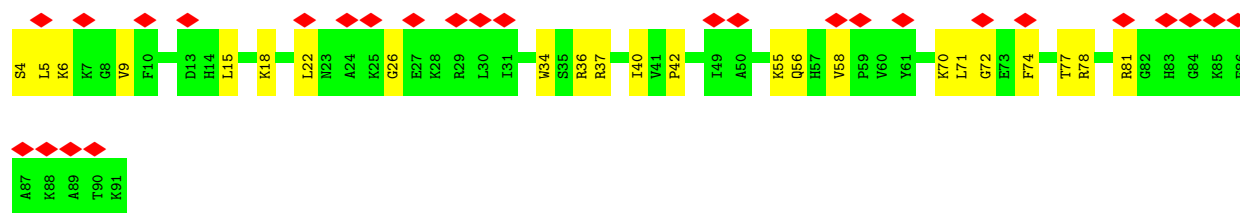


- Molecule 24: 30S ribosomal protein S18

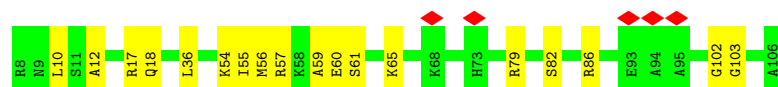
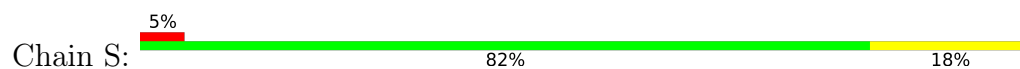


- Molecule 25: 30S ribosomal protein S19

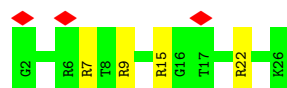
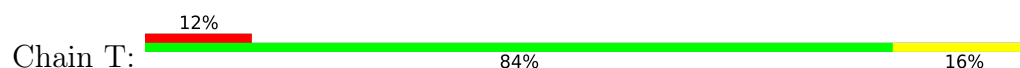




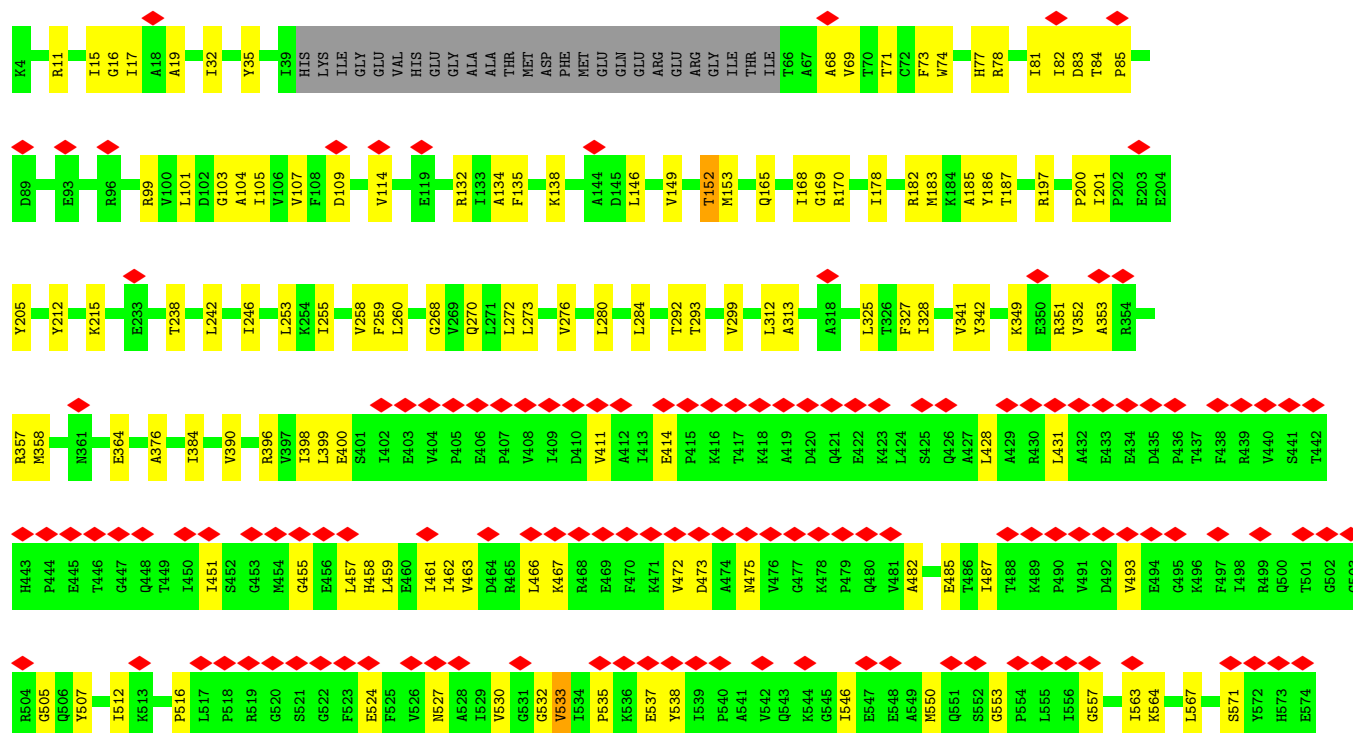
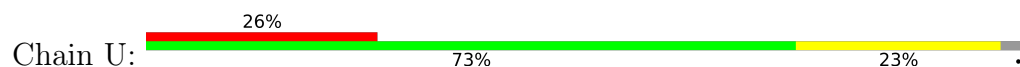
- Molecule 26: 30S ribosomal protein S20

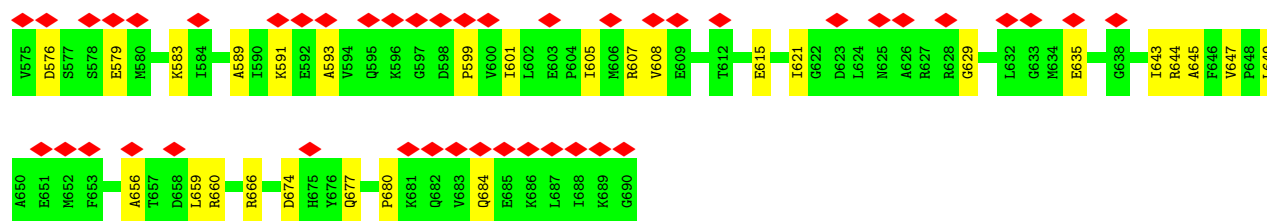


- Molecule 27: 30S ribosomal protein Thx

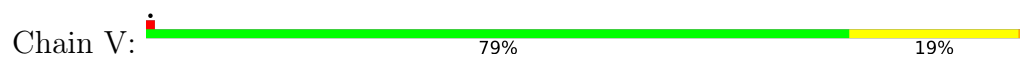


- Molecule 28: Elongation factor G

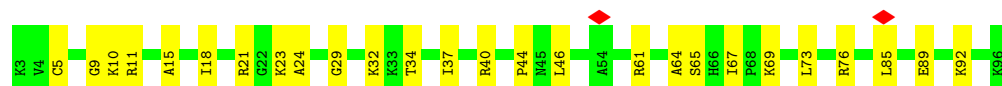




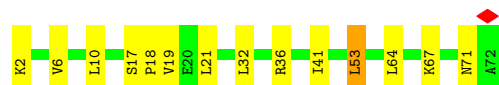
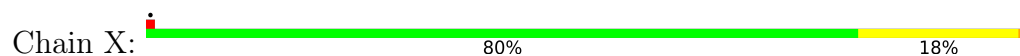
- Molecule 29: 50S ribosomal protein L27



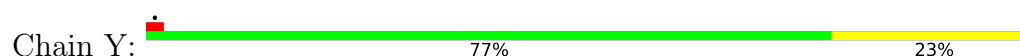
- Molecule 30: 50S ribosomal protein L28



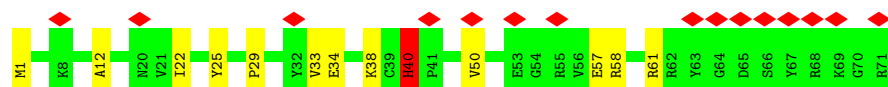
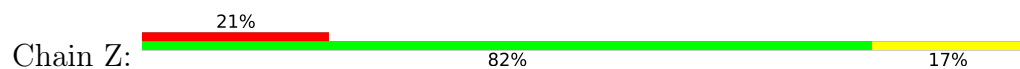
- Molecule 31: 50S ribosomal protein L29



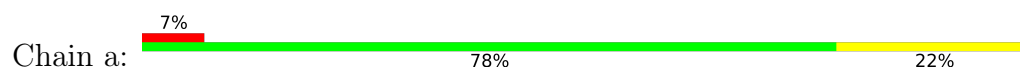
- Molecule 32: 50S ribosomal protein L30



- Molecule 33: 50S ribosomal protein L31

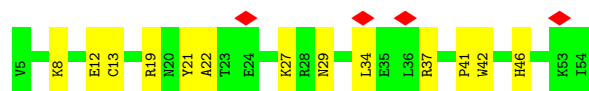
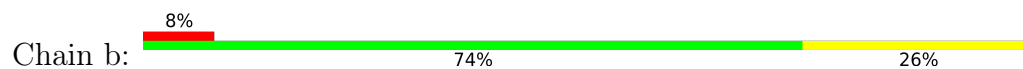


- Molecule 34: 50S ribosomal protein L32

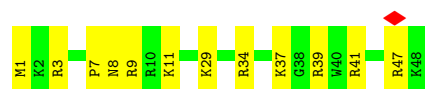
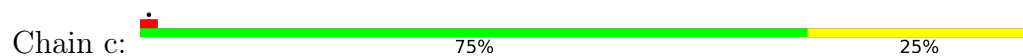




- Molecule 35: 50S ribosomal protein L33



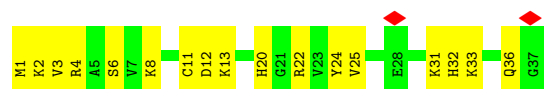
- Molecule 36: 50S ribosomal protein L34



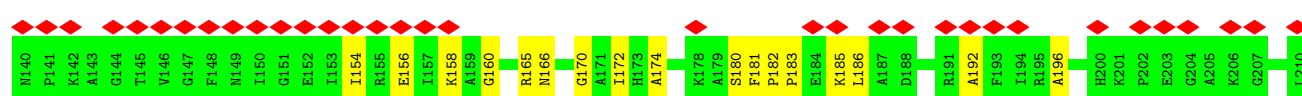
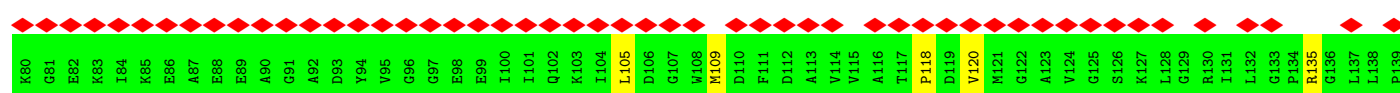
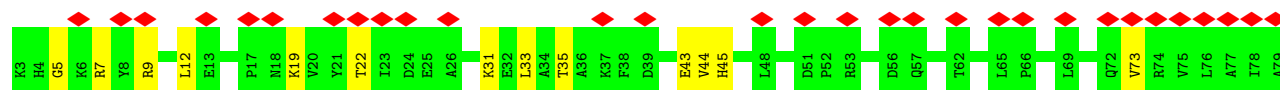
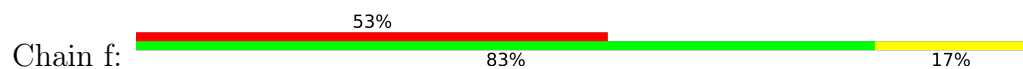
- Molecule 37: 50S ribosomal protein L35

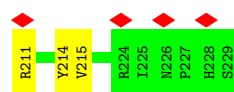


- Molecule 38: 50S ribosomal protein L36



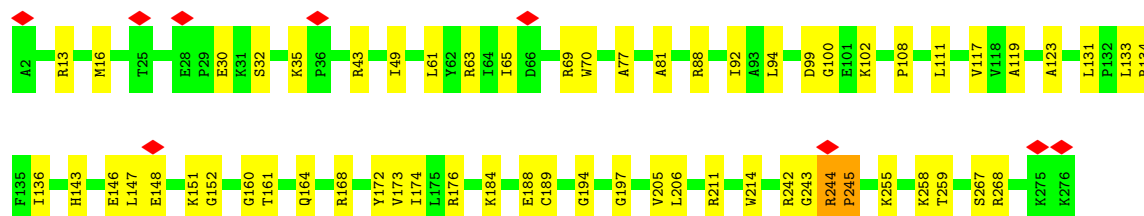
- Molecule 39: 50S ribosomal protein L1





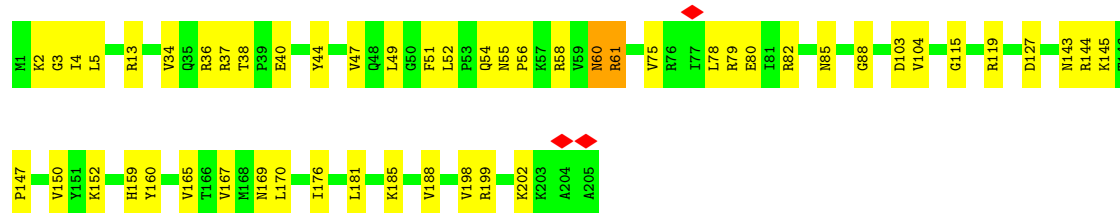
- Molecule 40: 50S ribosomal protein L2

Chain g: 78% 21%



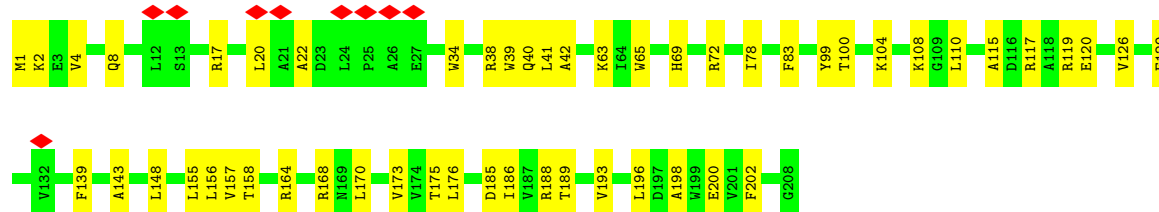
- Molecule 41: 50S ribosomal protein L3

Chain h: 75% 24%



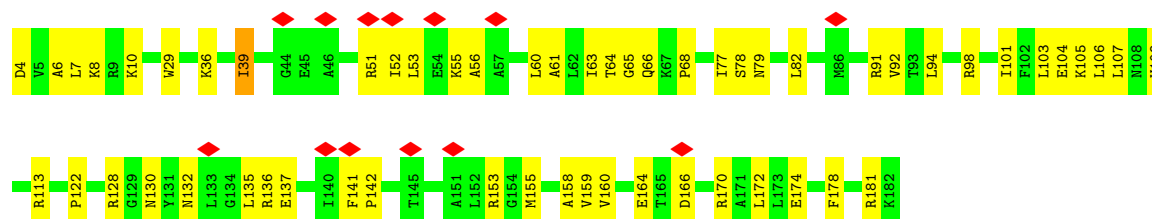
- Molecule 42: 50S ribosomal protein L4

Chain i: 75% 25%



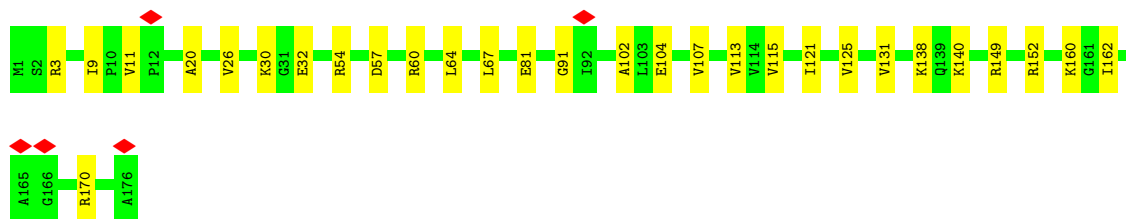
- Molecule 43: 50S ribosomal protein L5

Chain j: 7% 68% 31%



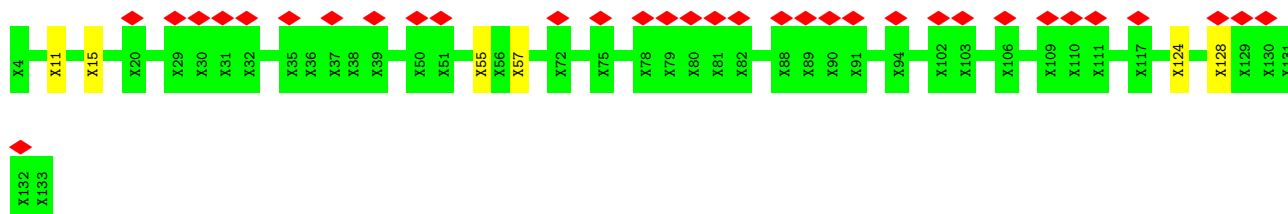
- Molecule 44: 50S ribosomal protein L6

Chain k:  84% 16%



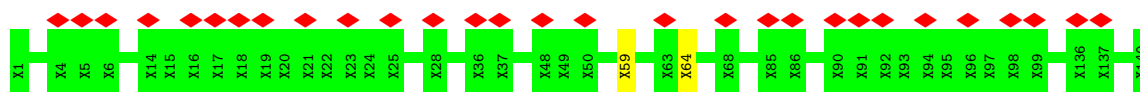
- Molecule 45: Ribosomal protein uL10

Chain l:  25% 95% 5%



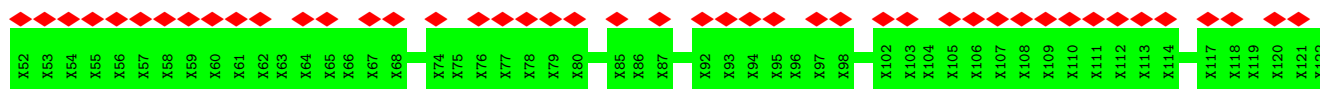
- Molecule 46: Ribosomal protein uL11

Chain m:  21% 99%



- Molecule 47: Ribosomal protein bL12

Chain n:  63% 100%



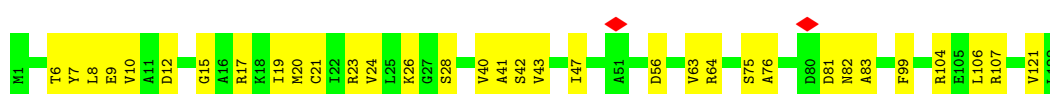
- Molecule 48: 50S ribosomal protein L13

Chain o:  86% 14%

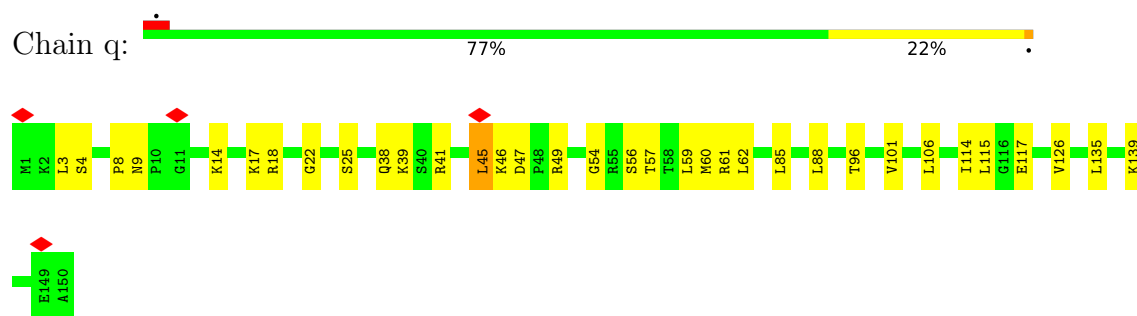


- Molecule 49: 50S ribosomal protein L14

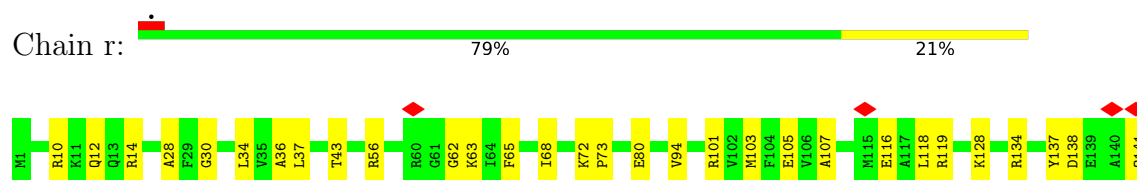
Chain p:  73% 27%



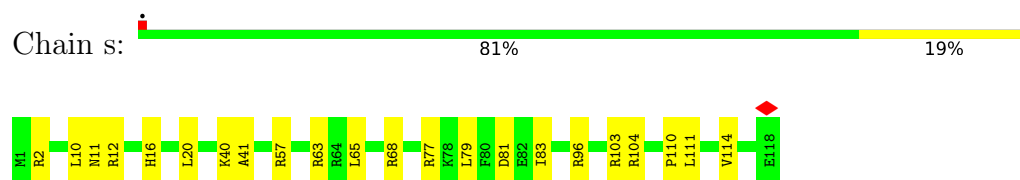
- Molecule 50: 50S ribosomal protein L15



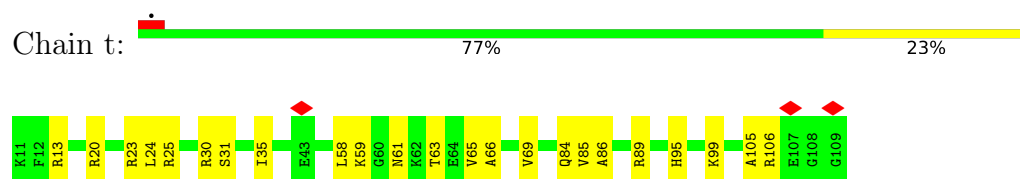
- Molecule 51: 50S ribosomal protein L16



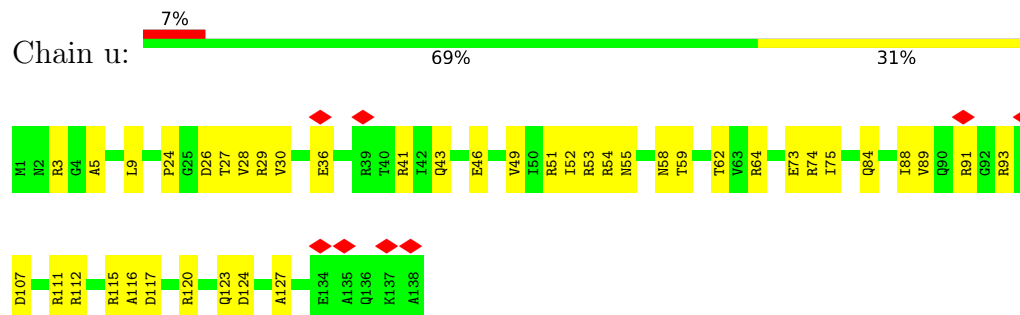
- Molecule 52: 50S ribosomal protein L17



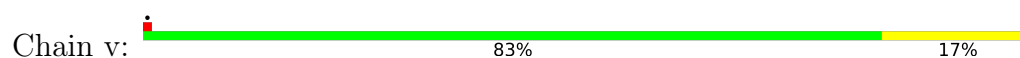
- Molecule 53: 50S ribosomal protein L18



- Molecule 54: 50S ribosomal protein L19

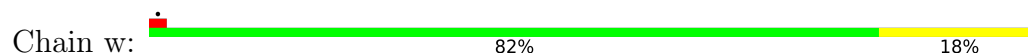


- Molecule 55: 50S ribosomal protein L20

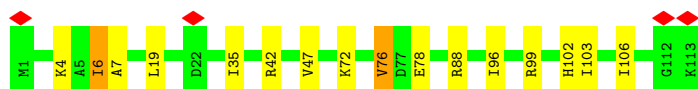
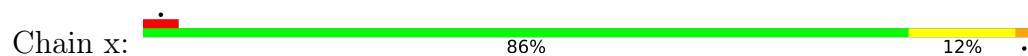




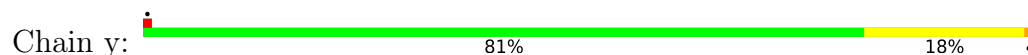
- Molecule 56: 50S ribosomal protein L21



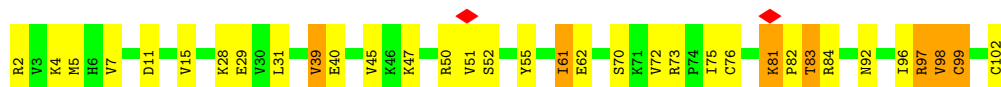
- Molecule 57: 50S ribosomal protein L22



- Molecule 58: 50S ribosomal protein L23



- Molecule 59: 50S ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32383	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	120443	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.453	Depositor
Minimum map value	-0.272	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	463.05, 463.05, 463.05	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1025, 1.1025, 1.1025	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, ZN, MG

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	1	0.14	0/36259	0.33	5/56593 (0.0%)
2	2	0.13	0/1809	0.30	0/2819
3	3	0.22	0/238	0.54	0/369
4	4	0.15	0/69975	0.32	3/109242 (0.0%)
5	5	0.17	0/2853	0.38	0/4451
6	6	0.27	0/1450	0.77	7/1970 (0.4%)
7	7	0.25	0/1151	0.69	4/1558 (0.3%)
8	A	0.21	0/1936	0.59	0/2611
9	B	0.24	0/1637	0.66	0/2207
10	C	0.20	0/1733	0.55	0/2318
11	D	0.20	0/1163	0.53	0/1566
12	E	0.21	0/856	0.56	0/1154
13	F	0.28	0/1276	0.72	1/1709 (0.1%)
14	G	0.21	0/1136	0.55	0/1527
15	H	0.27	0/1029	0.72	2/1379 (0.1%)
16	I	0.21	0/808	0.55	0/1087
17	J	0.29	0/900	0.75	3/1213 (0.2%)
18	K	0.23	0/987	0.52	0/1322
19	L	0.24	0/948	0.73	1/1272 (0.1%)
20	M	0.22	0/501	0.60	0/664
21	N	0.20	0/745	0.57	0/992
22	O	0.18	0/717	0.53	0/965
23	P	0.19	0/837	0.57	0/1119
24	Q	0.19	0/579	0.51	0/768
25	R	0.19	0/706	0.56	0/950
26	S	0.17	0/765	0.51	0/1007
27	T	0.19	0/213	0.59	0/279
28	U	0.22	0/5270	0.61	3/7135 (0.0%)
29	V	0.24	0/625	0.63	0/832
30	W	0.23	0/739	0.57	0/983
31	X	0.20	0/600	0.54	0/793
32	Y	0.16	0/473	0.52	0/636

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.28	0/594	0.93	2/795 (0.3%)
34	a	0.24	0/473	0.62	0/639
35	b	0.29	0/440	0.89	1/586 (0.2%)
36	c	0.16	0/427	0.48	0/561
37	d	0.31	0/516	0.65	0/681
38	e	0.26	0/310	0.78	0/407
39	f	0.24	0/1766	0.66	2/2380 (0.1%)
40	g	0.23	0/2195	0.65	3/2955 (0.1%)
41	h	0.24	0/1597	0.75	6/2155 (0.3%)
42	i	0.20	0/1659	0.55	0/2246
43	j	0.28	0/1483	0.84	0/1994
44	k	0.23	0/1371	0.66	0/1853
45	l	0.05	0/7	0.09	0/8
48	o	0.21	0/1132	0.58	0/1527
49	p	0.19	0/943	0.50	0/1269
50	q	0.28	0/1162	0.83	4/1544 (0.3%)
51	r	0.18	0/1143	0.48	0/1527
52	s	0.25	0/982	0.62	0/1312
53	t	0.25	0/779	0.77	0/1038
54	u	0.25	0/1156	0.63	0/1544
55	v	0.17	0/975	0.52	0/1297
56	w	0.19	0/790	0.53	0/1057
57	x	0.22	0/907	0.64	0/1216
58	y	0.24	0/740	0.68	0/995
59	z	0.43	1/789 (0.1%)	1.09	10/1053 (0.9%)
All	All	0.18	1/165250 (0.0%)	0.44	57/246129 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	6	0	3
7	7	0	1
8	A	0	2
9	B	0	1
13	F	0	2
14	G	0	1
23	P	0	1
28	U	0	3
29	V	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	Z	0	1
40	g	0	2
41	h	0	3
43	j	0	2
44	k	0	2
45	l	0	1
50	q	0	1
57	x	0	1
58	y	0	2
59	z	0	5
All	All	0	35

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	z	98	VAL	CA-C	5.11	1.59	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	373	A	OP1-P-O3'	-9.35	79.96	108.00
1	1	231	G	OP1-P-O3'	-9.25	80.24	108.00
41	h	61	ARG	CA-C-N	-8.44	109.29	119.84
41	h	61	ARG	C-N-CA	-8.44	109.29	119.84
6	6	78	LYS	CA-C-N	7.74	136.33	121.54

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	6	123	ASP	Peptide
6	6	14	LYS	Peptide
6	6	142	SER	Peptide
7	7	133	HIS	Peptide
8	A	156	LYS	Peptide

5.2 Too-close contacts [i](#)

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	32391	0	16347	342	0
2	2	1619	0	822	6	0
3	3	214	0	106	3	0
4	4	62476	0	31492	503	0
5	5	2551	0	1295	15	0
6	6	1418	0	1445	28	0
7	7	1136	0	1223	17	0
8	A	1901	0	1951	40	0
9	B	1613	0	1677	47	0
10	C	1703	0	1765	38	0
11	D	1147	0	1207	23	0
12	E	843	0	857	13	0
13	F	1257	0	1296	27	0
14	G	1116	0	1177	21	0
15	H	1010	0	1037	17	0
16	I	795	0	840	24	0
17	J	885	0	904	25	0
18	K	971	0	1057	15	0
19	L	938	0	995	22	0
20	M	492	0	529	15	0
21	N	734	0	771	22	0
22	O	701	0	720	8	0
23	P	824	0	891	15	0
24	Q	574	0	644	14	0
25	R	692	0	714	20	0
26	S	763	0	861	15	0
27	T	209	0	221	9	0
28	U	5173	0	5238	95	0
29	V	617	0	636	10	0
30	W	732	0	808	17	0
31	X	598	0	653	10	0
32	Y	468	0	523	9	0
33	Z	581	0	577	13	0
34	a	459	0	476	12	0
35	b	433	0	461	10	0
36	c	419	0	467	9	0
37	d	508	0	576	17	0
38	e	307	0	337	11	0
39	f	1735	0	1790	26	0
40	g	2145	0	2234	45	0
41	h	1564	0	1629	35	0
42	i	1624	0	1677	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	j	1459	0	1516	37	0
44	k	1345	0	1430	14	0
45	l	654	0	160	3	0
46	m	701	0	168	1	0
47	n	356	0	89	0	0
48	o	1105	0	1180	13	0
49	p	933	0	996	22	0
50	q	1145	0	1228	26	0
51	r	1122	0	1179	24	0
52	s	968	0	1033	16	0
53	t	771	0	832	18	0
54	u	1142	0	1202	32	0
55	v	958	0	1015	15	0
56	w	779	0	852	13	0
57	x	896	0	953	11	0
58	y	726	0	778	11	0
59	z	776	0	867	16	0
60	1	125	0	0	0	0
60	4	320	0	0	0	0
60	D	1	0	0	0	0
60	K	1	0	0	0	0
60	O	2	0	0	0	0
60	S	1	0	0	0	0
60	U	1	0	0	0	0
60	a	1	0	0	0	0
60	c	1	0	0	0	0
60	e	1	0	0	0	0
60	h	1	0	0	0	0
60	i	1	0	0	0	0
60	q	1	0	0	0	0
60	t	3	0	0	0	0
60	u	1	0	0	0	0
60	x	1	0	0	0	0
61	C	1	0	0	0	0
61	M	1	0	0	0	0
61	e	1	0	0	0	0
62	U	28	0	12	0	0
All	All	154665	0	106416	1684	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1684 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1243:C:O2'	27:T:7:ARG:NH2	1.73	1.19
4:4:827:U:O2	4:4:2426:A:C2	2.02	1.12
1:1:1238:A:N6	1:1:1299:A:N6	2.00	1.10
1:1:941:G:O2'	1:1:942:G:C5'	2.01	1.07
4:4:827:U:C2	4:4:2426:A:H2	1.70	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	6	176/178 (99%)	134 (76%)	38 (22%)	4 (2%)	5	30
7	7	144/146 (99%)	124 (86%)	20 (14%)	0	100	100
8	A	233/235 (99%)	203 (87%)	29 (12%)	1 (0%)	30	62
9	B	205/207 (99%)	170 (83%)	35 (17%)	0	100	100
10	C	206/208 (99%)	190 (92%)	16 (8%)	0	100	100
11	D	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
12	E	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
13	F	153/155 (99%)	118 (77%)	34 (22%)	1 (1%)	18	51
14	G	136/138 (99%)	122 (90%)	14 (10%)	0	100	100
15	H	125/127 (98%)	109 (87%)	16 (13%)	0	100	100
16	I	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
17	J	117/119 (98%)	100 (86%)	16 (14%)	1 (1%)	14	45
18	K	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
19	L	117/119 (98%)	101 (86%)	15 (13%)	1 (1%)	14	45
20	M	58/60 (97%)	47 (81%)	11 (19%)	0	100	100
21	N	86/88 (98%)	79 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	O	82/84 (98%)	73 (89%)	8 (10%)	1 (1%)	10	40
23	P	98/100 (98%)	93 (95%)	4 (4%)	1 (1%)	12	43
24	Q	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
25	R	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
26	S	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
27	T	23/25 (92%)	20 (87%)	3 (13%)	0	100	100
28	U	657/687 (96%)	555 (84%)	100 (15%)	2 (0%)	36	67
29	V	76/78 (97%)	68 (90%)	8 (10%)	0	100	100
30	W	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
31	X	69/71 (97%)	65 (94%)	4 (6%)	0	100	100
32	Y	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
33	Z	69/71 (97%)	40 (58%)	29 (42%)	0	100	100
34	a	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
35	b	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
36	c	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
37	d	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
38	e	35/37 (95%)	30 (86%)	4 (11%)	1 (3%)	3	25
39	f	225/227 (99%)	189 (84%)	36 (16%)	0	100	100
40	g	273/275 (99%)	244 (89%)	28 (10%)	1 (0%)	30	62
41	h	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
42	i	206/208 (99%)	187 (91%)	19 (9%)	0	100	100
43	j	177/179 (99%)	145 (82%)	31 (18%)	1 (1%)	21	54
44	k	174/176 (99%)	148 (85%)	25 (14%)	1 (1%)	21	54
45	l	1/130 (1%)	1 (100%)	0	0	100	100
48	o	137/139 (99%)	126 (92%)	11 (8%)	0	100	100
49	p	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
50	q	148/150 (99%)	120 (81%)	28 (19%)	0	100	100
51	r	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
52	s	116/118 (98%)	104 (90%)	12 (10%)	0	100	100
53	t	97/99 (98%)	86 (89%)	11 (11%)	0	100	100
54	u	136/138 (99%)	121 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	v	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
56	w	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
57	x	111/113 (98%)	102 (92%)	8 (7%)	1 (1%)	14	45
58	y	91/93 (98%)	83 (91%)	7 (8%)	1 (1%)	11	41
59	z	99/101 (98%)	72 (73%)	25 (25%)	2 (2%)	6	32
All	All	6614/6873 (96%)	5765 (87%)	829 (12%)	20 (0%)	37	67

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
59	z	98	VAL
19	L	106	ASN
22	O	83	GLU
28	U	146	LEU
38	e	12	ASP

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	
6	6	157/157 (100%)	157 (100%)	0	100	100
7	7	122/122 (100%)	122 (100%)	0	100	100
8	A	202/203 (100%)	200 (99%)	2 (1%)	68	74
9	B	160/161 (99%)	159 (99%)	1 (1%)	78	79
10	C	180/180 (100%)	180 (100%)	0	100	100
11	D	115/116 (99%)	115 (100%)	0	100	100
12	E	90/90 (100%)	90 (100%)	0	100	100
13	F	126/126 (100%)	126 (100%)	0	100	100
14	G	119/119 (100%)	119 (100%)	0	100	100
15	H	98/98 (100%)	97 (99%)	1 (1%)	68	74
16	I	88/89 (99%)	87 (99%)	1 (1%)	65	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	J	90/90 (100%)	89 (99%)	1 (1%)	65	73
18	K	104/104 (100%)	103 (99%)	1 (1%)	68	74
19	L	94/95 (99%)	94 (100%)	0	100	100
20	M	49/49 (100%)	49 (100%)	0	100	100
21	N	79/79 (100%)	79 (100%)	0	100	100
22	O	72/72 (100%)	72 (100%)	0	100	100
23	P	94/95 (99%)	93 (99%)	1 (1%)	65	73
24	Q	61/61 (100%)	61 (100%)	0	100	100
25	R	74/75 (99%)	74 (100%)	0	100	100
26	S	76/76 (100%)	76 (100%)	0	100	100
27	T	19/20 (95%)	19 (100%)	0	100	100
28	U	558/579 (96%)	556 (100%)	2 (0%)	84	83
29	V	62/62 (100%)	62 (100%)	0	100	100
30	W	78/79 (99%)	77 (99%)	1 (1%)	61	71
31	X	66/66 (100%)	64 (97%)	2 (3%)	36	57
32	Y	51/52 (98%)	51 (100%)	0	100	100
33	Z	63/63 (100%)	63 (100%)	0	100	100
34	a	51/51 (100%)	51 (100%)	0	100	100
35	b	49/49 (100%)	48 (98%)	1 (2%)	48	65
36	c	41/41 (100%)	41 (100%)	0	100	100
37	d	53/54 (98%)	53 (100%)	0	100	100
38	e	34/34 (100%)	34 (100%)	0	100	100
39	f	179/179 (100%)	179 (100%)	0	100	100
40	g	217/217 (100%)	216 (100%)	1 (0%)	81	81
41	h	165/165 (100%)	165 (100%)	0	100	100
42	i	165/165 (100%)	164 (99%)	1 (1%)	78	79
43	j	153/153 (100%)	150 (98%)	3 (2%)	48	65
44	k	146/146 (100%)	145 (99%)	1 (1%)	76	77
45	l	1/1 (100%)	1 (100%)	0	100	100
48	o	117/118 (99%)	117 (100%)	0	100	100
49	p	100/100 (100%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	q	116/116 (100%)	115 (99%)	1 (1%)	70	74
51	r	111/111 (100%)	111 (100%)	0	100	100
52	s	101/101 (100%)	101 (100%)	0	100	100
53	t	77/77 (100%)	77 (100%)	0	100	100
54	u	120/120 (100%)	118 (98%)	2 (2%)	53	67
55	v	92/93 (99%)	91 (99%)	1 (1%)	65	73
56	w	82/82 (100%)	82 (100%)	0	100	100
57	x	91/92 (99%)	90 (99%)	1 (1%)	65	73
58	y	74/75 (99%)	74 (100%)	0	100	100
59	z	84/85 (99%)	82 (98%)	2 (2%)	43	62
All	All	5566/5603 (99%)	5539 (100%)	27 (0%)	78	81

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	g	65	ILE
43	j	94	LEU
57	x	76	VAL
43	j	39	ILE
43	j	159	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
28	U	641	GLN
55	v	72	HIS
40	g	227	ASN
54	u	58	ASN
56	w	80	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1506/1507 (99%)	396 (26%)	11 (0%)
2	2	75/76 (98%)	27 (36%)	0
3	3	9/15 (60%)	7 (77%)	1 (11%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	4	2900/2901 (99%)	544 (18%)	10 (0%)
5	5	118/119 (99%)	36 (30%)	4 (3%)
All	All	4608/4618 (99%)	1010 (21%)	26 (0%)

5 of 1010 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	8	A
1	1	9	G
1	1	32	A
1	1	39	G
1	1	41	G

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	4	1077	A
4	4	1799	G
5	5	44	G
4	4	1647	G
4	4	1919	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 466 ligands modelled in this entry, 465 are monoatomic - leaving 1 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	U	702	60	29,30,30	1.19	4 (13%)	45,47,47	1.77	7 (15%)

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	U	702	60	-	7/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	U	702	GDP	C5-C4	3.12	1.47	1.38
62	U	702	GDP	C6-N1	-2.45	1.34	1.38
62	U	702	GDP	C5-N7	-2.09	1.34	1.39
62	U	702	GDP	PA-O3A	2.05	1.61	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	U	702	GDP	C5-C4-N3	-6.17	118.57	128.39
62	U	702	GDP	C2-N3-C4	5.05	120.99	112.30
62	U	702	GDP	N9-C4-N3	4.60	135.14	125.95
62	U	702	GDP	C6-C5-N7	3.21	136.12	130.29
62	U	702	GDP	C4-C5-N7	-2.54	106.64	110.67

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

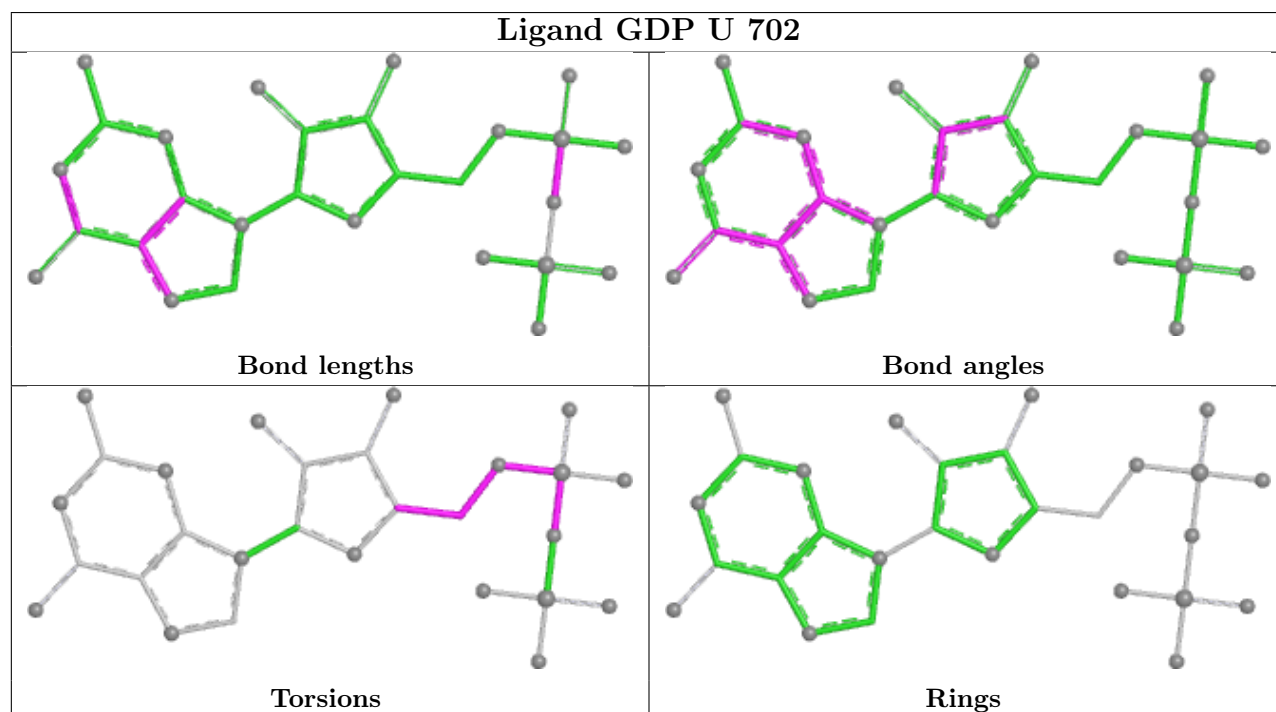
Mol	Chain	Res	Type	Atoms
62	U	702	GDP	C5'-O5'-PA-O3A
62	U	702	GDP	C5'-O5'-PA-O2A
62	U	702	GDP	C3'-C4'-C5'-O5'
62	U	702	GDP	O4'-C4'-C5'-O5'
62	U	702	GDP	PB-O3A-PA-O5'

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 [i](#)

There are no chain breaks in this entry.

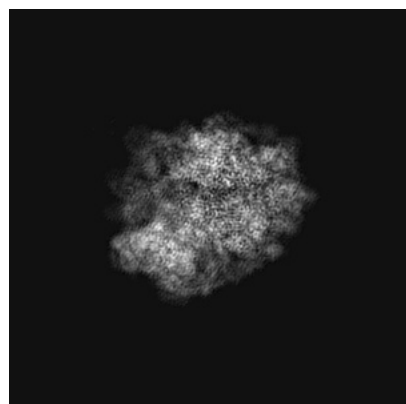
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3852. These allow visual inspection of the internal detail of the map and identification of artifacts.

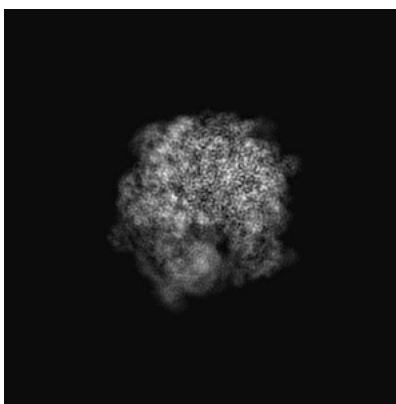
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

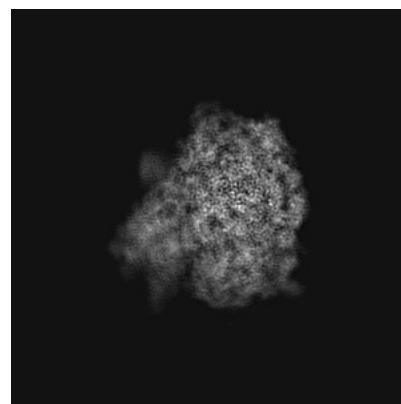
6.1.1 Primary map



X

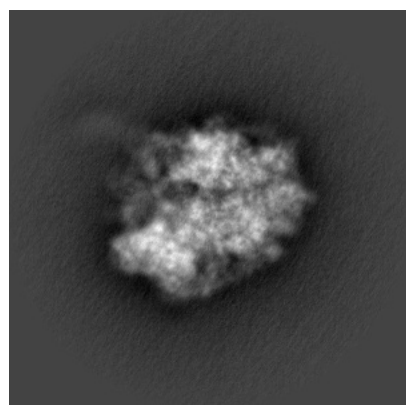


Y

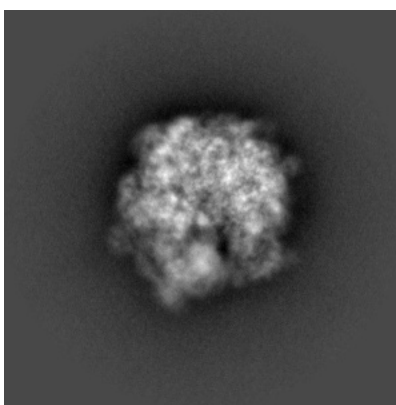


Z

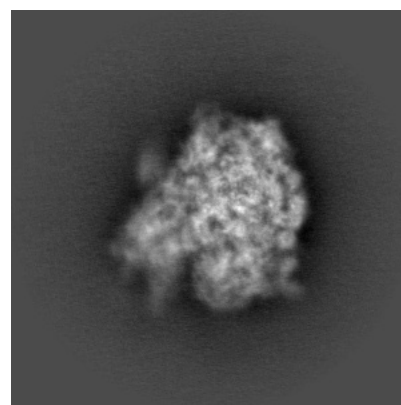
6.1.2 Raw map



X



Y

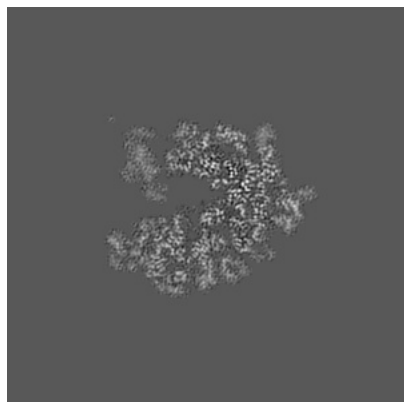


Z

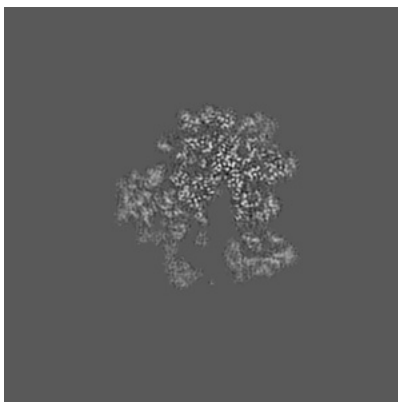
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

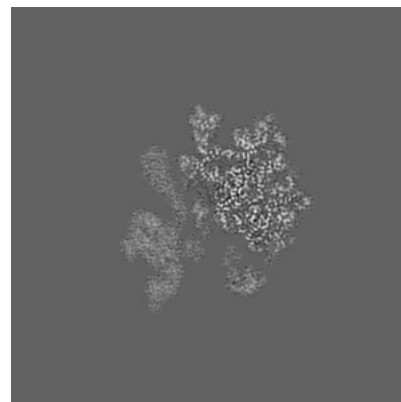
6.2.1 Primary map



X Index: 210

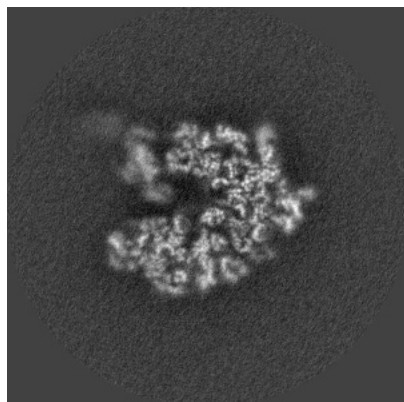


Y Index: 210

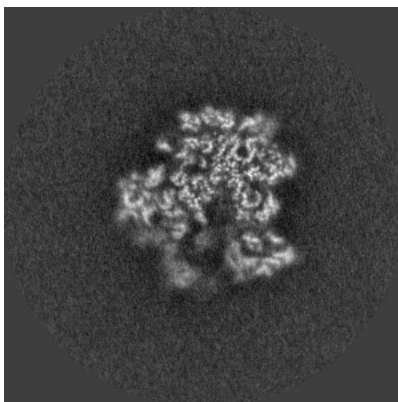


Z Index: 210

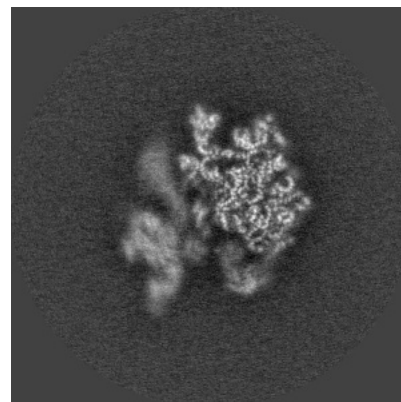
6.2.2 Raw map



X Index: 210



Y Index: 210

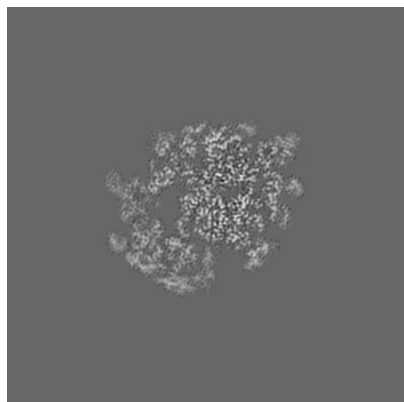


Z Index: 210

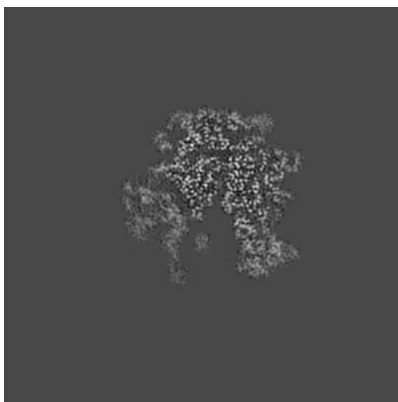
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

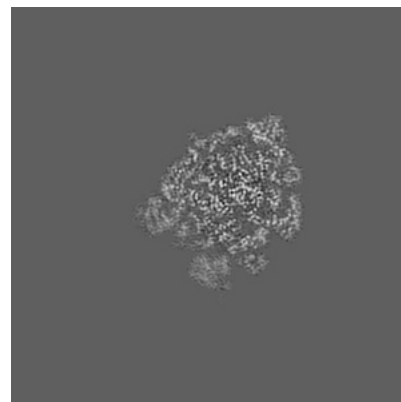
6.3.1 Primary map



X Index: 239

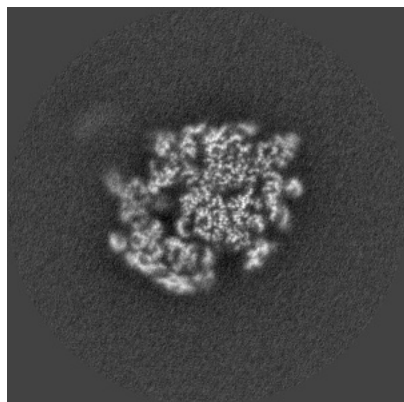


Y Index: 218

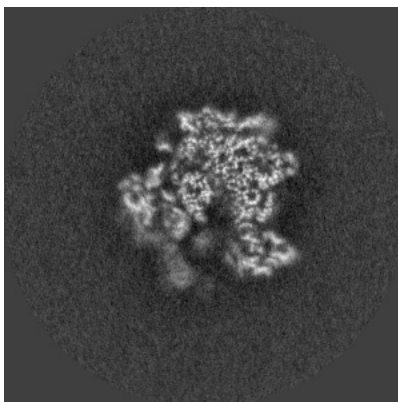


Z Index: 254

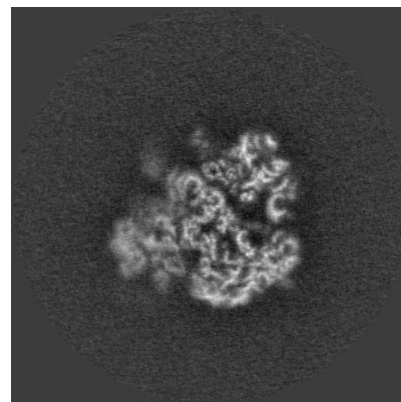
6.3.2 Raw map



X Index: 239



Y Index: 213

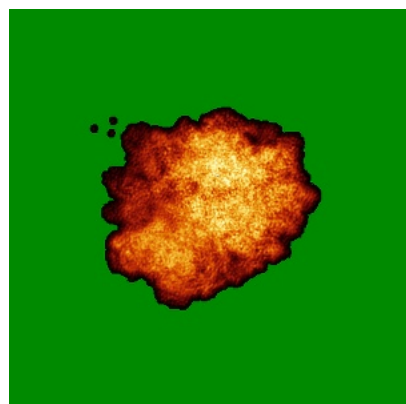


Z Index: 171

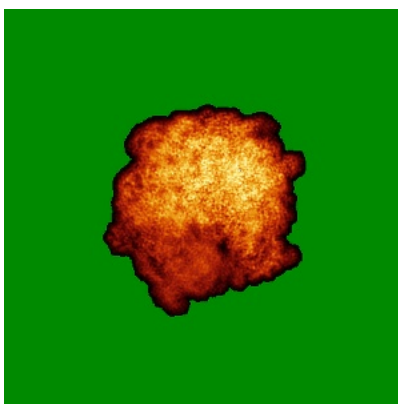
The images above show the largest variance slices of the map in three orthogonal directions.

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

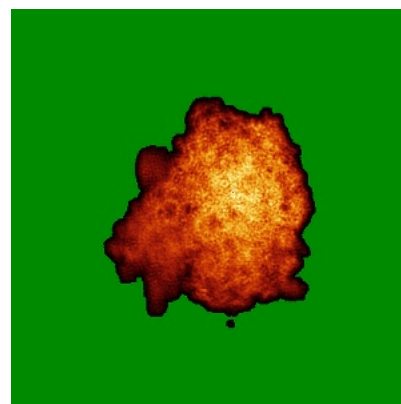
6.4.1 Primary map



X

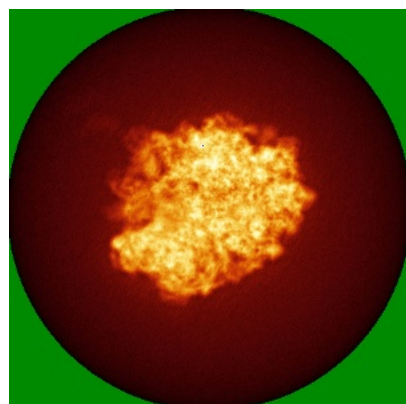


Y

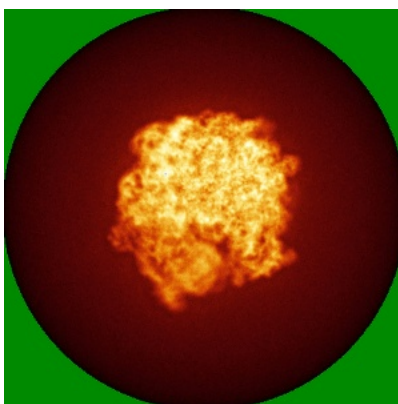


Z

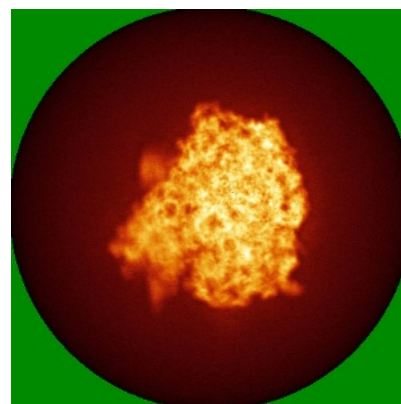
6.4.2 Raw map



X



Y

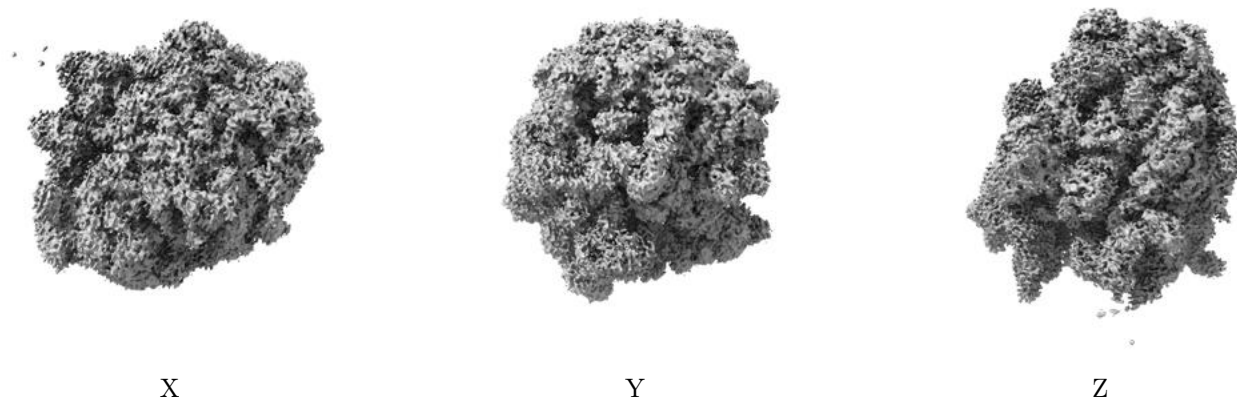


Z

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.

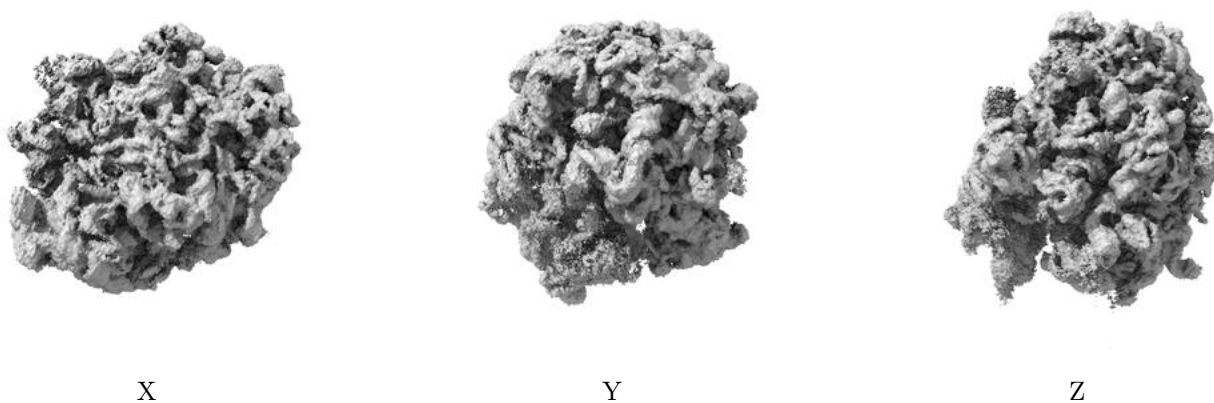
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

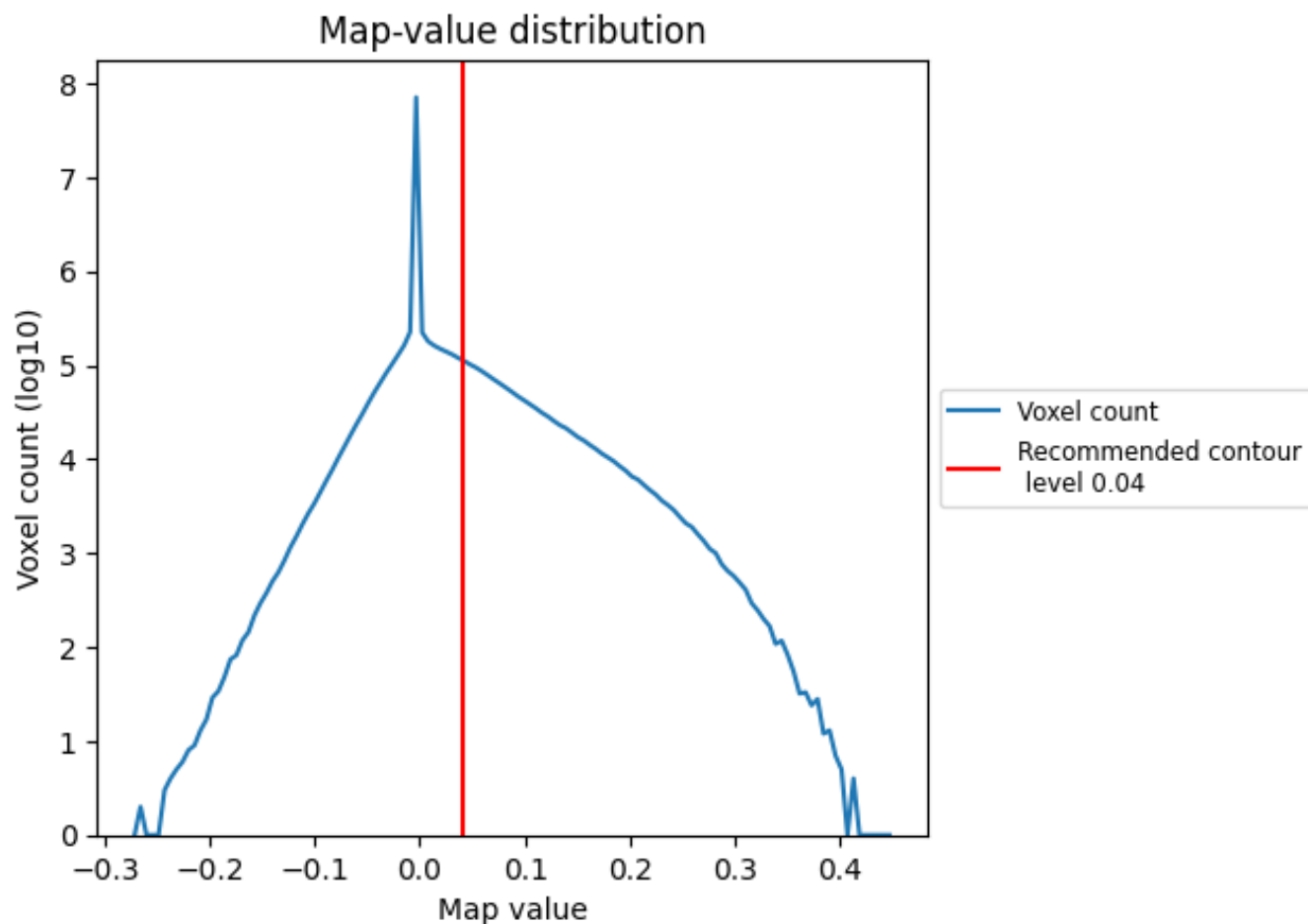
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

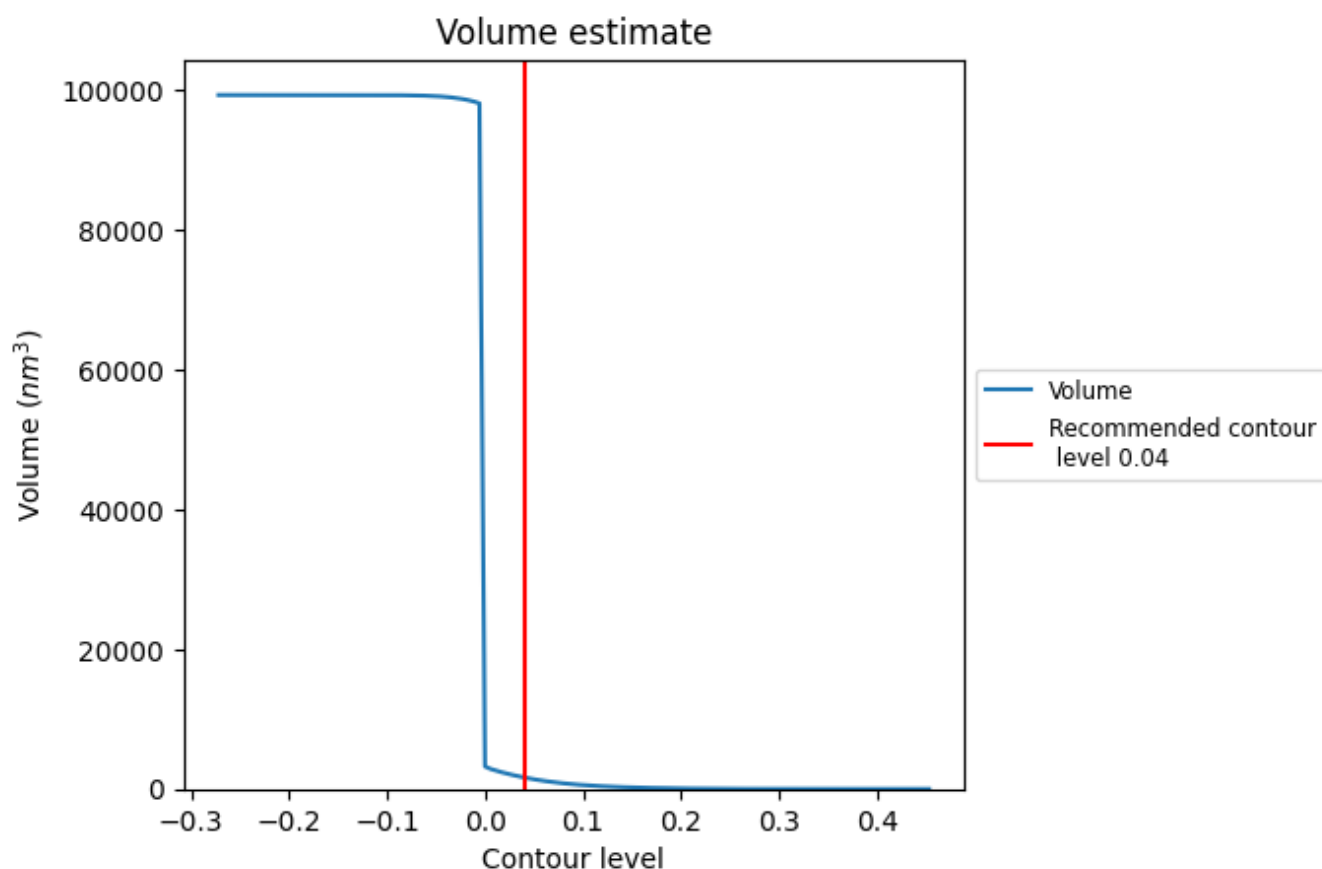
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

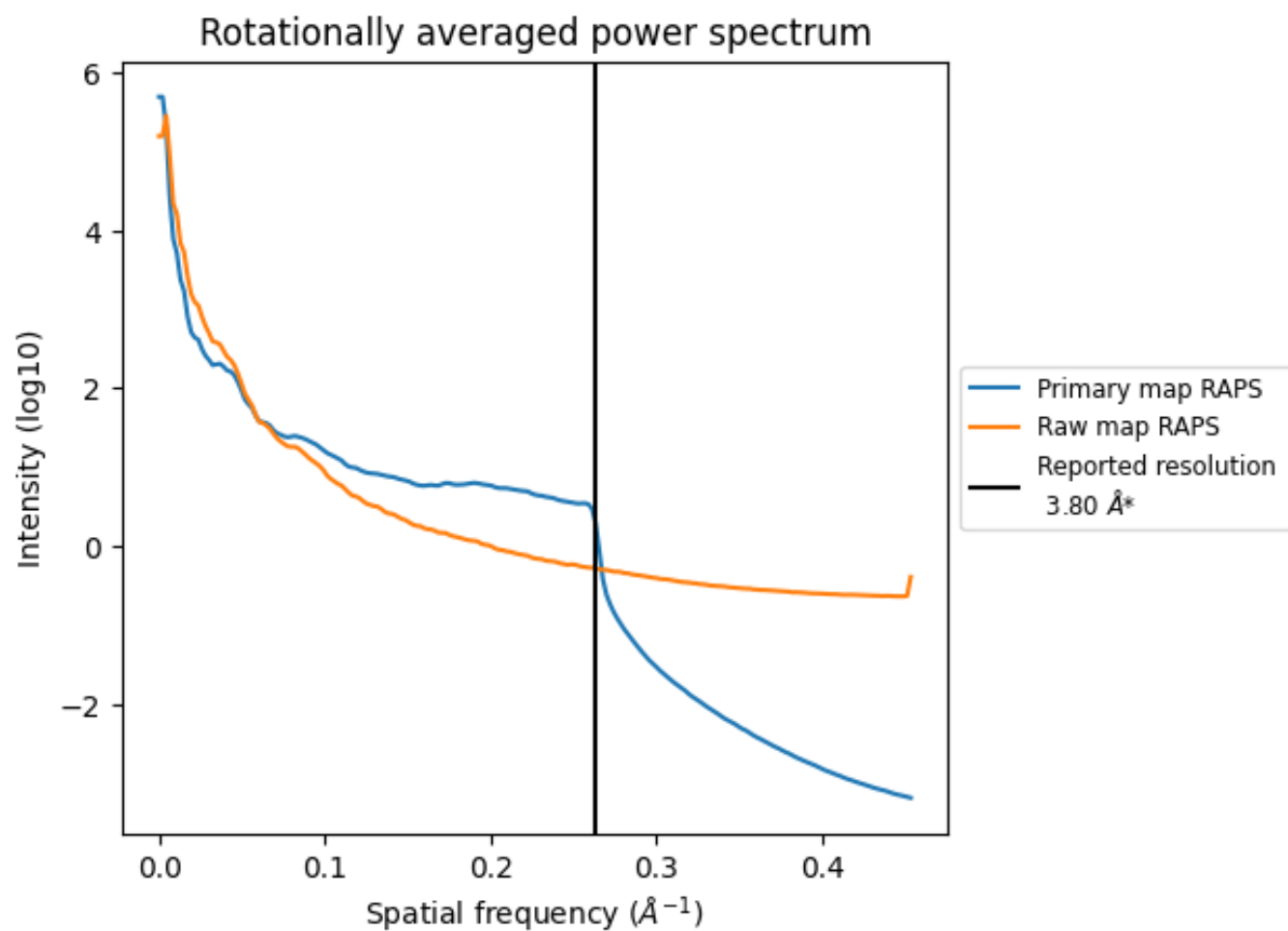
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1646 nm^3 ; this corresponds to an approximate mass of 1487 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 ⓘ

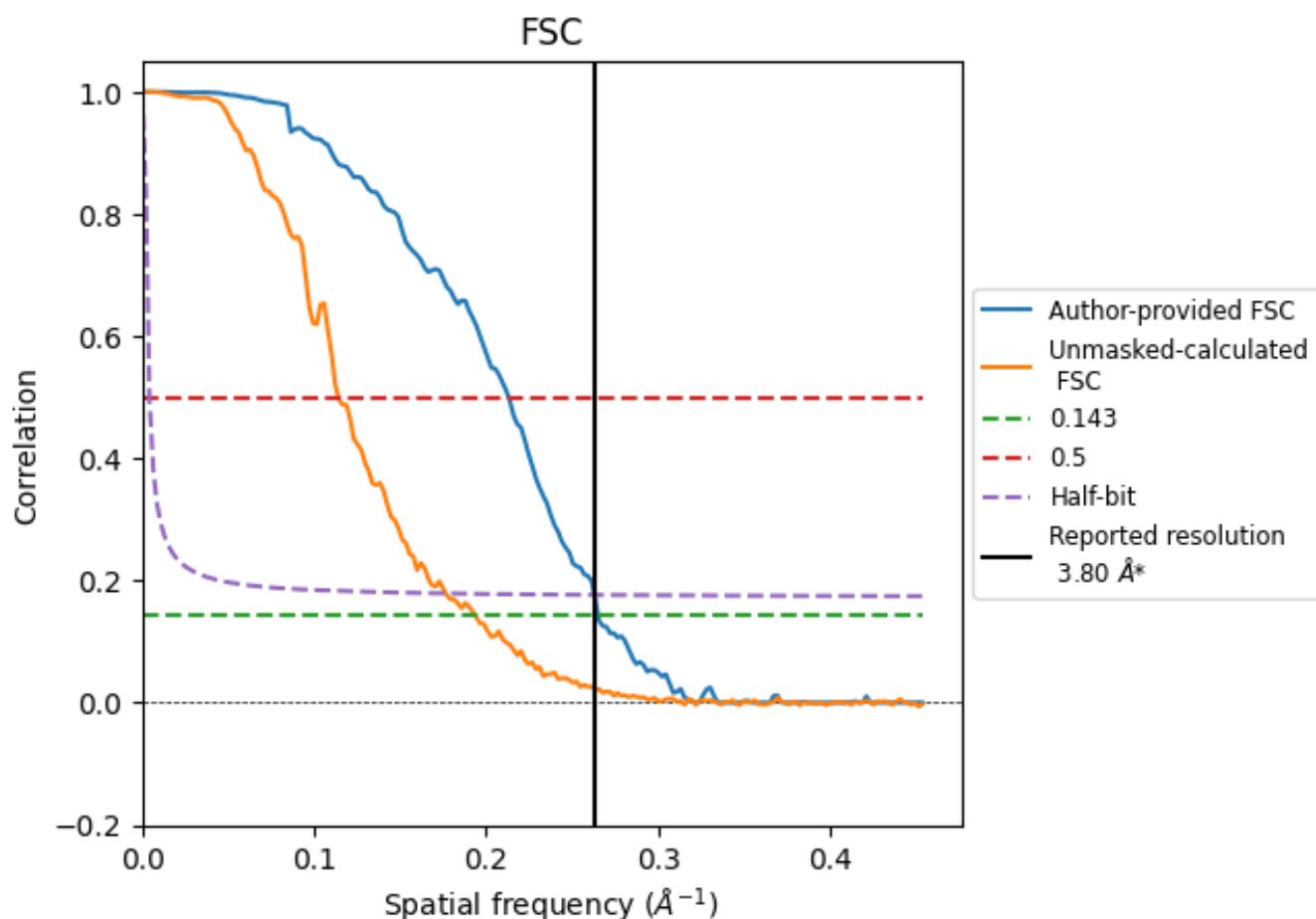


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

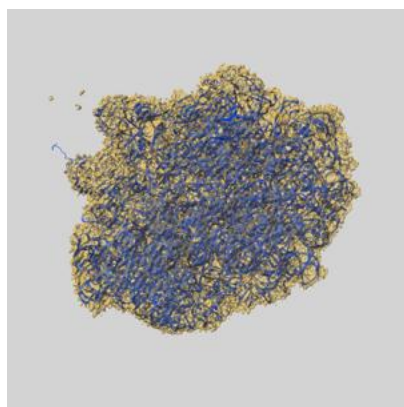
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.77	4.69	3.80
Unmasked-calculated*	5.17	8.76	5.67

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.17 differs from the reported value 3.8 by more than 10 %

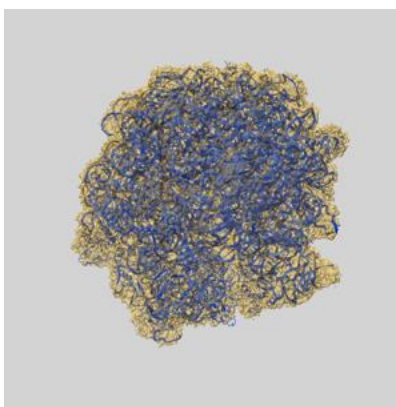
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3852 and PDB model 5OT7. Per-residue inclusion information can be found in section [3](#) on page [17](#).

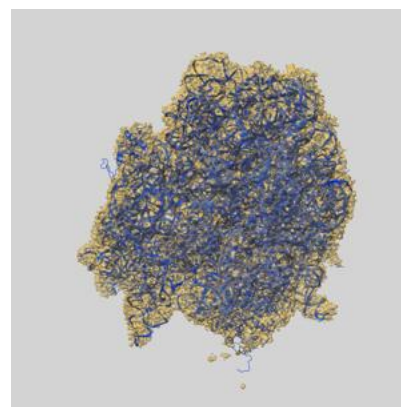
9.1 Map-model overlay [i](#)



X



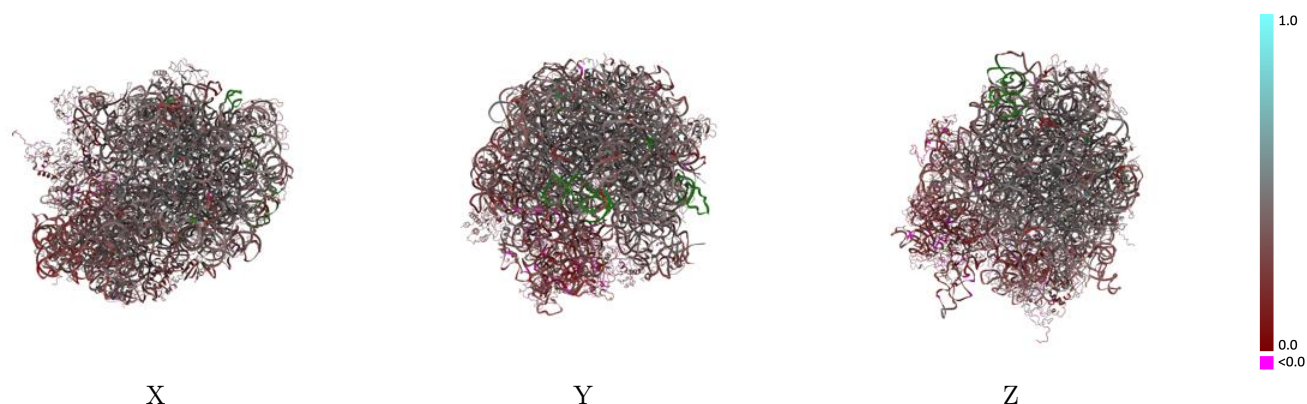
Y



Z

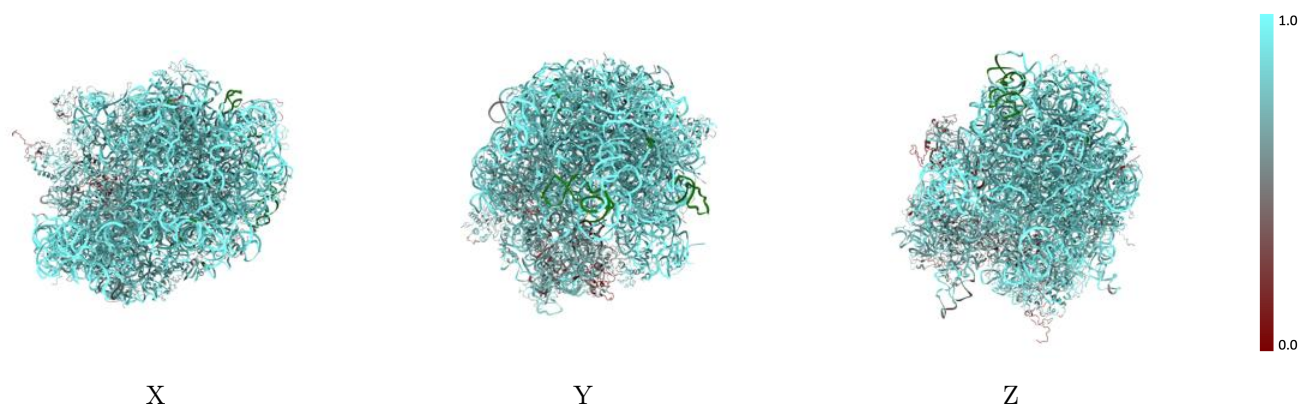
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



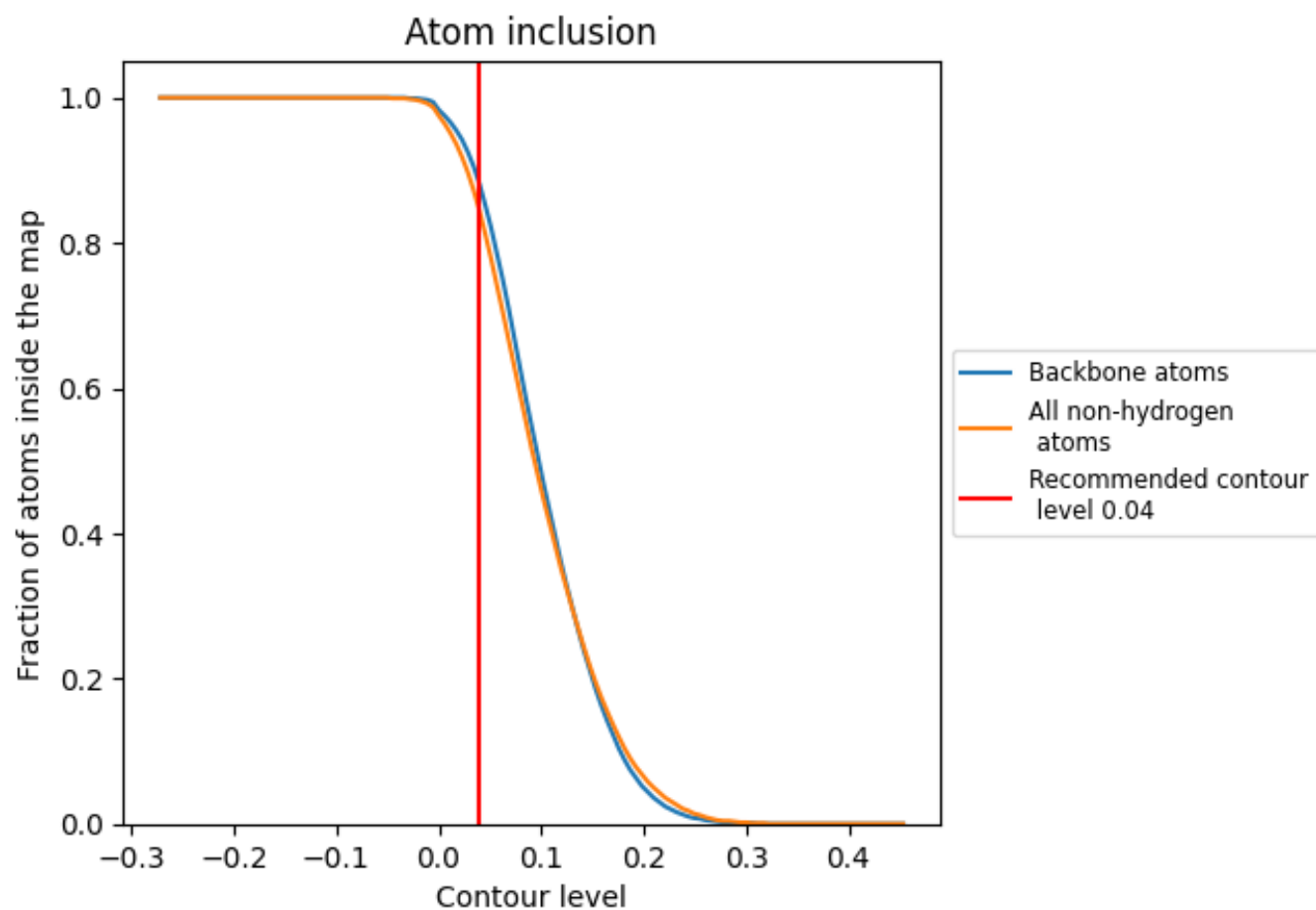
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.3440
1	 0.8890	 0.3010
2	 0.5590	 0.2480
3	 0.6780	 0.2650
4	 0.9240	 0.3940
5	 0.9650	 0.3580
6	 0.7330	 0.3180
7	 0.4860	 0.2480
A	 0.6840	 0.2650
B	 0.6540	 0.2580
C	 0.8090	 0.3130
D	 0.8150	 0.3780
E	 0.7700	 0.2750
F	 0.5820	 0.1940
G	 0.8140	 0.3510
H	 0.7010	 0.1920
I	 0.6580	 0.2290
J	 0.6410	 0.2150
K	 0.7260	 0.3820
L	 0.5810	 0.1840
M	 0.5980	 0.2100
N	 0.7770	 0.2670
O	 0.8240	 0.3540
P	 0.7680	 0.3500
Q	 0.7220	 0.2550
R	 0.5870	 0.1950
S	 0.7810	 0.3210
T	 0.7760	 0.1910
U	 0.5980	 0.2490
V	 0.8320	 0.4170
W	 0.7910	 0.3990
X	 0.8270	 0.3490
Y	 0.8150	 0.4020
Z	 0.6210	 0.1960
a	 0.7970	 0.3880



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Chain	Atom inclusion	Q-score
b	 0.7400	 0.2870
c	 0.8360	 0.4320
d	 0.7700	 0.3950
e	 0.8110	 0.4110
f	 0.3720	 0.1640
g	 0.8040	 0.4150
h	 0.8260	 0.4170
i	 0.8170	 0.3790
j	 0.7360	 0.2460
k	 0.8160	 0.3440
l	 0.6640	 0.3220
m	 0.7230	 0.3070
n	 0.3790	 0.2920
o	 0.8370	 0.4000
p	 0.7610	 0.4150
q	 0.8120	 0.3700
r	 0.8120	 0.4220
s	 0.8320	 0.4080
t	 0.8430	 0.3330
u	 0.7780	 0.3570
v	 0.8580	 0.4180
w	 0.7910	 0.3700
x	 0.8280	 0.4310
y	 0.8470	 0.4000
z	 0.7930	 0.2990