



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 10:46 pm BST

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.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

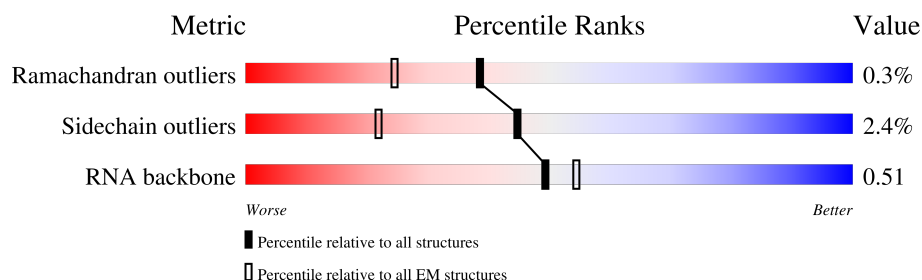
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	1507	
2	2	76	
3	3	15	
4	4	2901	
5	5	119	
6	6	178	
7	7	146	
8	A	235	

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Mol	Chain	Length	Quality of chain
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	
29	V	78	
30	W	94	
31	X	71	
32	Y	60	
33	Z	71	


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Mol	Chain	Length	Quality of chain
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	
54	u	138	
55	v	117	
56	w	101	
57	x	113	
58	y	93	

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Mol	Chain	Length	Quality of chain
59	z	101	 A horizontal bar chart showing the quality of the chain. The bar is 90% green and 10% yellow. A small red square is at the beginning of the bar. The text '90%' is centered below the green portion, and '10%' is centered below the yellow portion.

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	126	Total	Mg	0
			126	126	
60	4	322	Total	Mg	0
			322	322	
60	D	1	Total	Mg	0
			1	1	
60	O	2	Total	Mg	0
			2	2	
60	S	1	Total	Mg	0
			1	1	
60	U	1	Total	Mg	0
			1	1	

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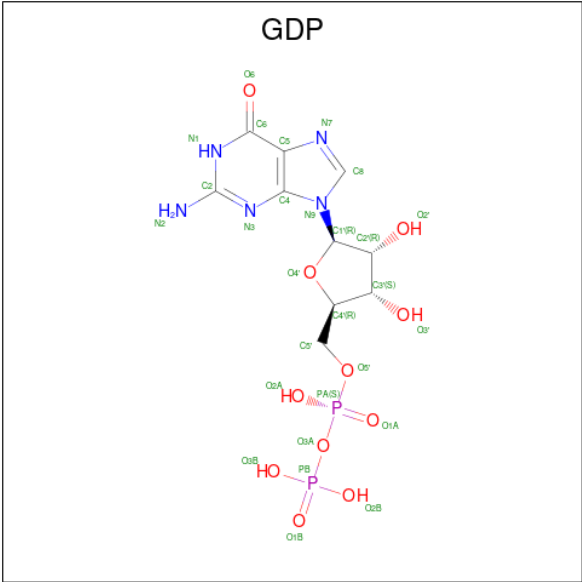
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Mol	Chain	Residues	Atoms		AltConf
60	c	1	Total 1	Mg 1	0
60	e	1	Total 1	Mg 1	0
60	h	1	Total 1	Mg 1	0
60	i	1	Total 1	Mg 1	0
60	q	1	Total 1	Mg 1	0
60	t	2	Total 2	Mg 2	0
60	u	1	Total 1	Mg 1	0
60	x	1	Total 1	Mg 1	0

- 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).

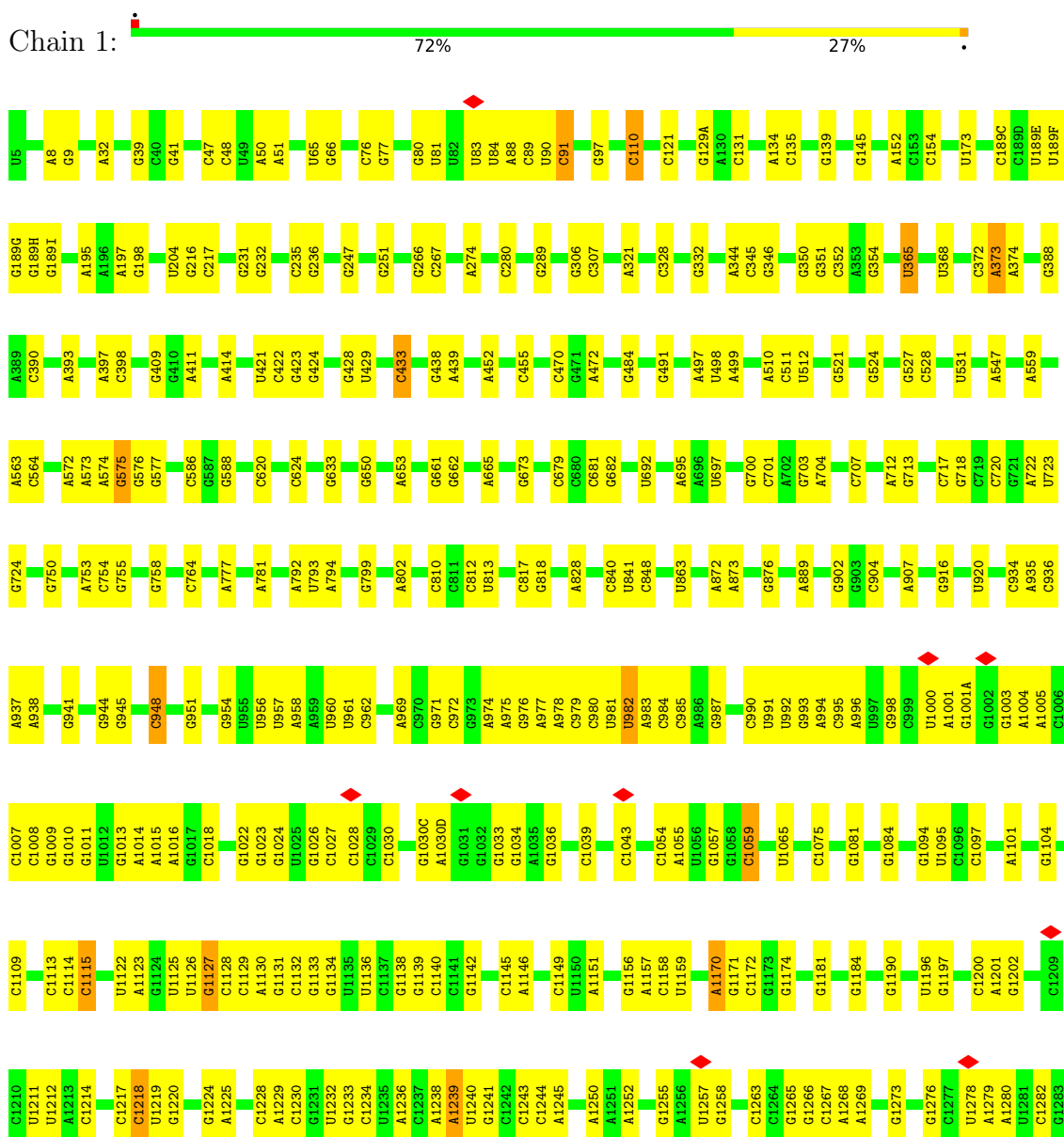


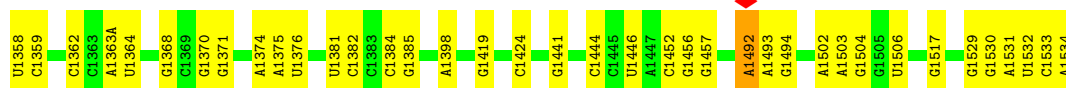
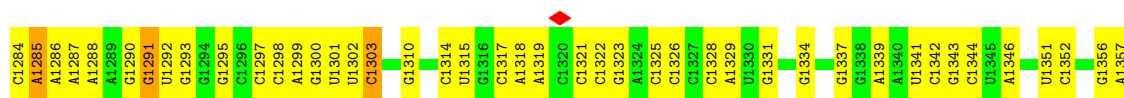
Mol	Chain	Residues	Atoms					AltConf
62	U	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

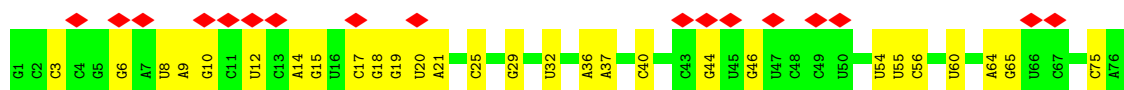
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

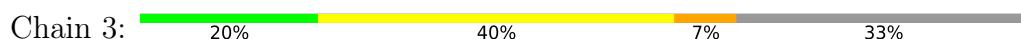




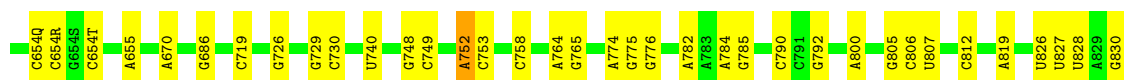
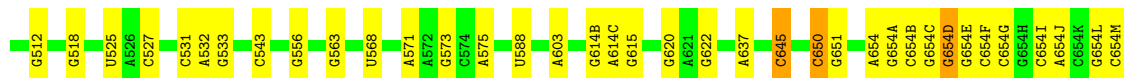
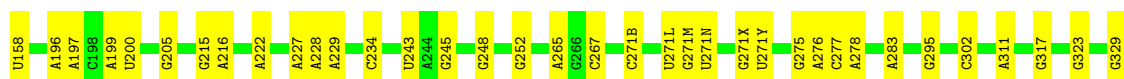
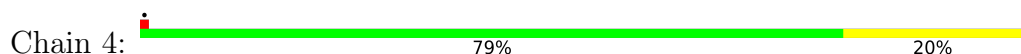
• Molecule 2: tRNA-Phe

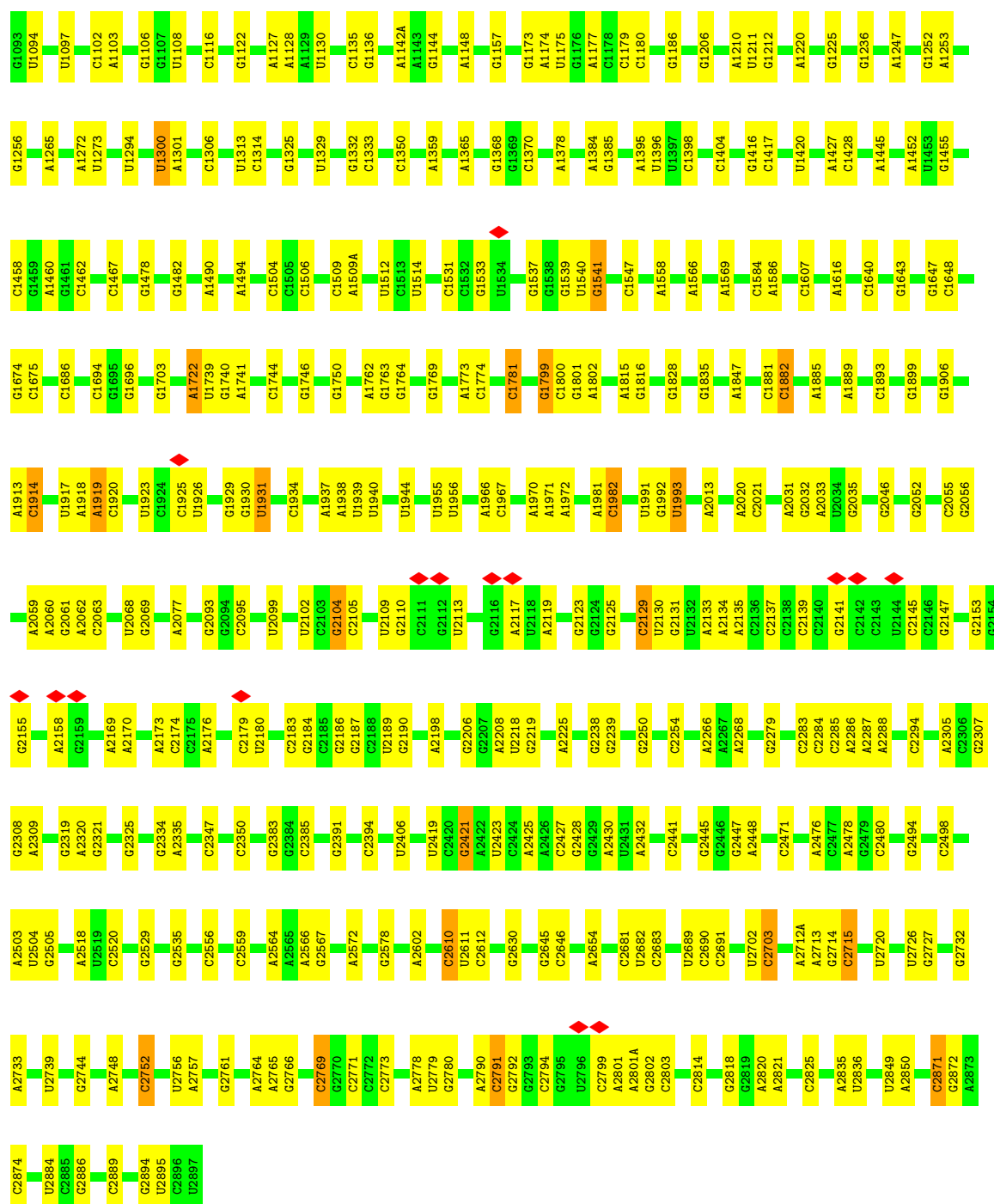


• Molecule 3: mRNA

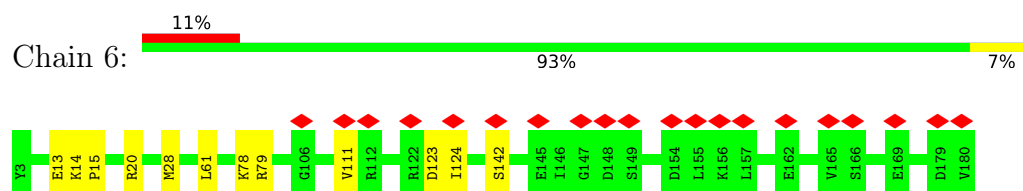


• Molecule 4: 23S Ribosomal RNA

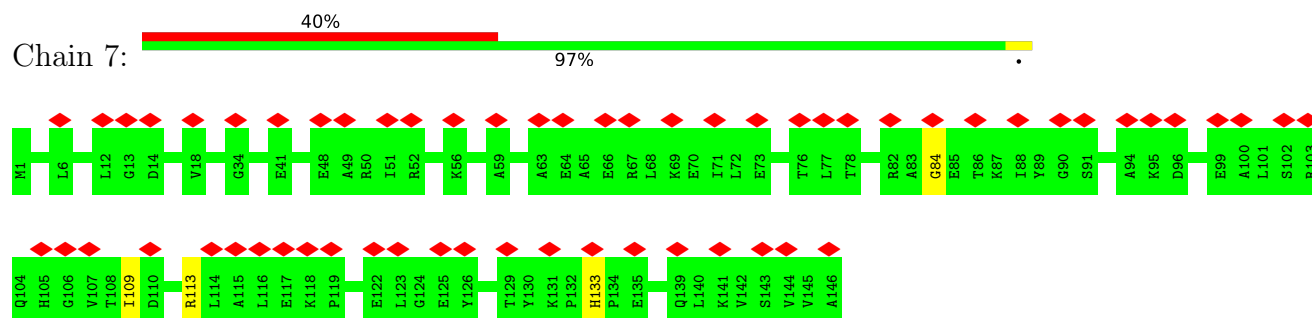




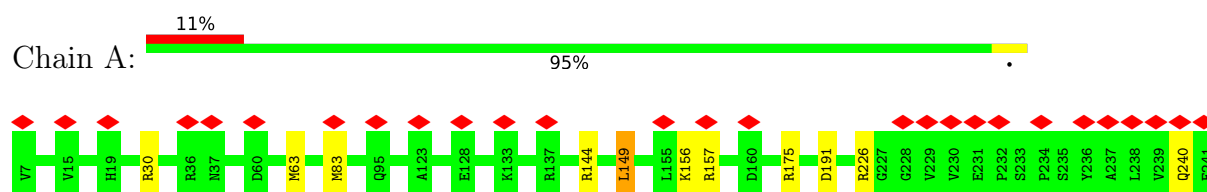
- Molecule 6: 50S ribosomal protein L25



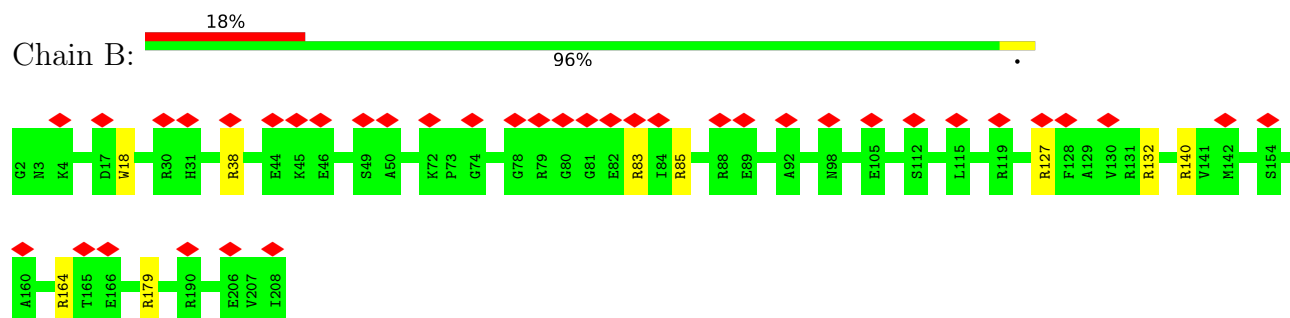
- Molecule 7: 50S ribosomal protein L9



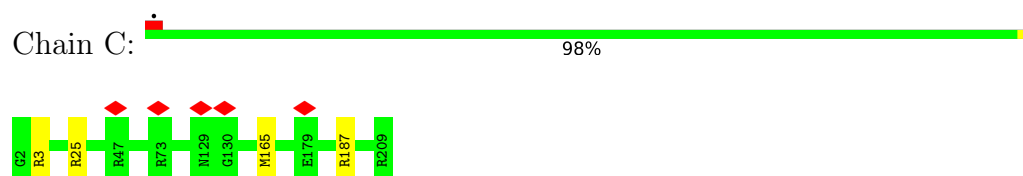
- Molecule 8: 30S ribosomal protein S2



- Molecule 9: 30S ribosomal protein S3

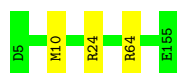


- Molecule 10: 30S ribosomal protein S4

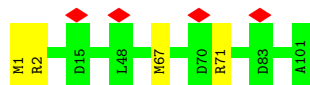


- Molecule 11: 30S ribosomal protein S5

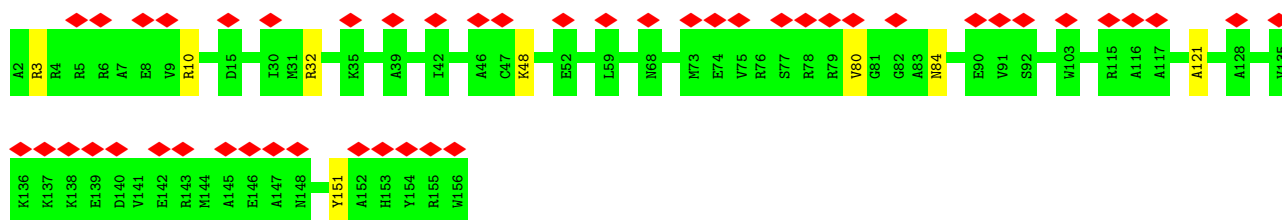




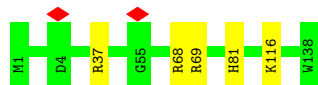
- Molecule 12: 30S ribosomal protein S6



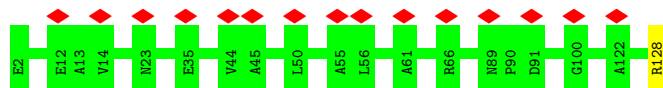
- Molecule 13: 30S ribosomal protein S7



- Molecule 14: 30S ribosomal protein S8



- Molecule 15: 30S ribosomal protein S9

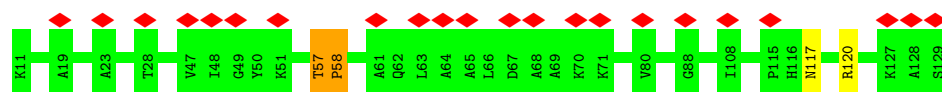


- Molecule 16: 30S ribosomal protein S10

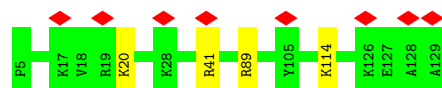


- Molecule 17: 30S ribosomal protein S11

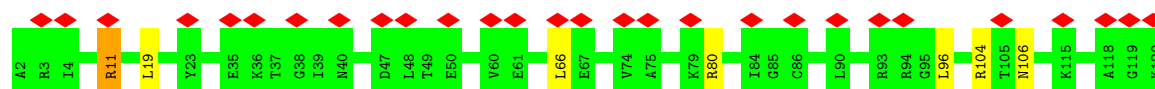




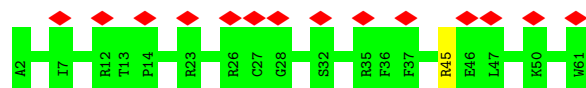
- Molecule 18: 30S ribosomal protein S12



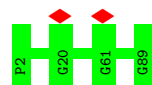
- Molecule 19: 30S ribosomal protein S13



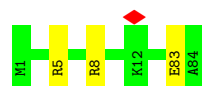
- Molecule 20: 30S ribosomal protein S14 type Z



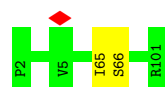
- Molecule 21: 30S ribosomal protein S15



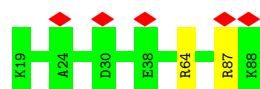
- Molecule 22: 30S ribosomal protein S16



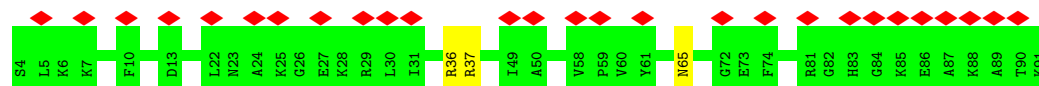
- Molecule 23: 30S ribosomal protein S17



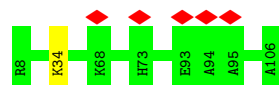
- Molecule 24: 30S ribosomal protein S18



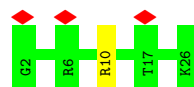
- Molecule 25: 30S ribosomal protein S19



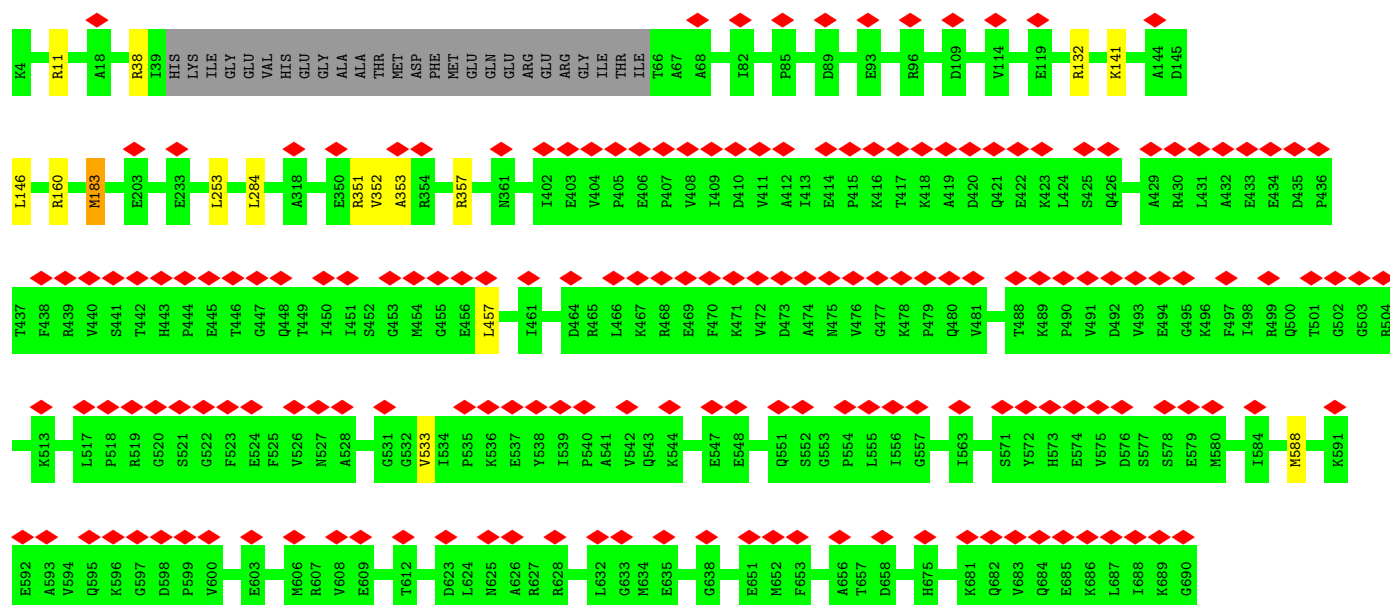
- Molecule 26: 30S ribosomal protein S20



- Molecule 27: 30S ribosomal protein Thx



- Molecule 28: Elongation factor G



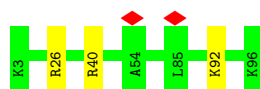
- Molecule 29: 50S ribosomal protein L27

Chain V:  96%



- Molecule 30: 50S ribosomal protein L28

Chain W:  97%



- Molecule 31: 50S ribosomal protein L29

Chain X:  94% 6%



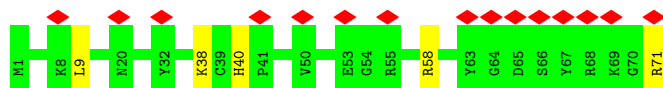
- Molecule 32: 50S ribosomal protein L30

Chain Y:  100%



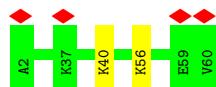
- Molecule 33: 50S ribosomal protein L31

Chain Z:  21% 93% 7%



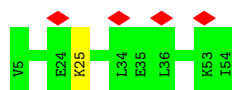
- Molecule 34: 50S ribosomal protein L32

Chain a:  7% 97%

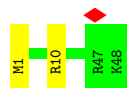


- Molecule 35: 50S ribosomal protein L33

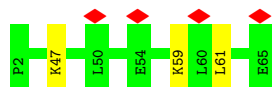
Chain b:  8% 98%



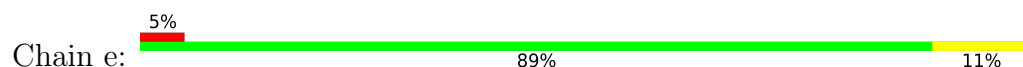
- Molecule 36: 50S ribosomal protein L34



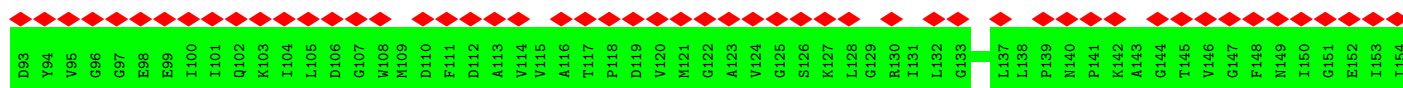
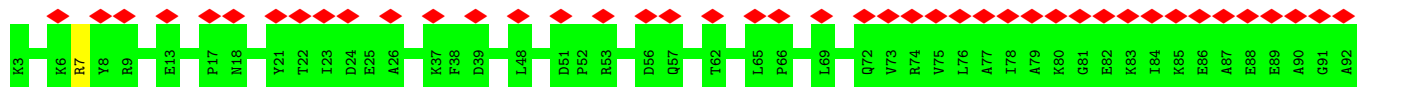
- Molecule 37: 50S ribosomal protein L35



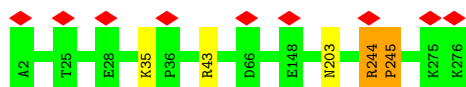
- Molecule 38: 50S ribosomal protein L36



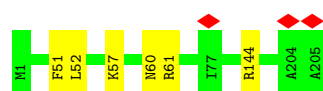
- Molecule 39: 50S ribosomal protein L1



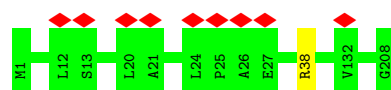
- Molecule 40: 50S ribosomal protein L2



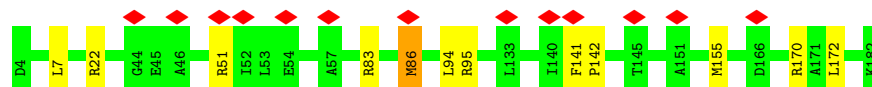
- Molecule 41: 50S ribosomal protein L3



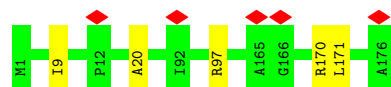
- Molecule 42: 50S ribosomal protein L4



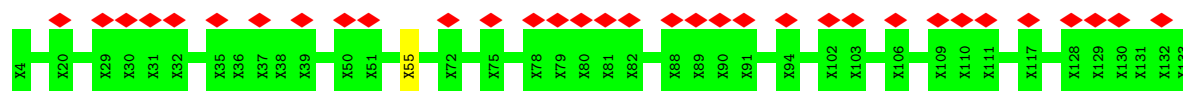
- Molecule 43: 50S ribosomal protein L5



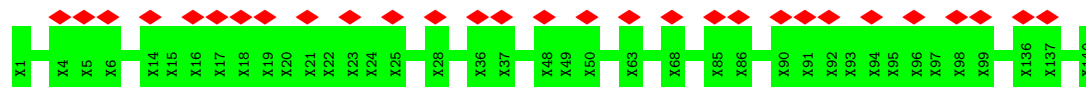
- Molecule 44: 50S ribosomal protein L6



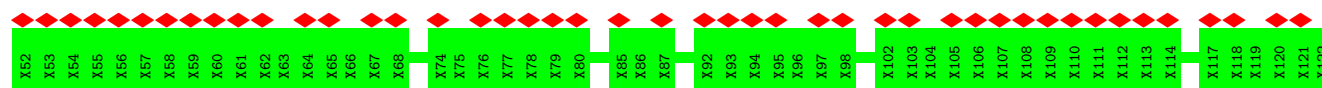
- Molecule 45: Ribosomal protein uL10



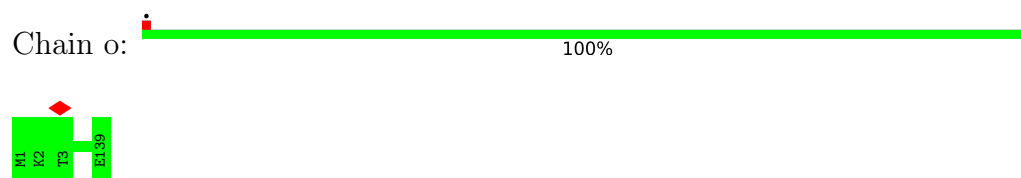
- Molecule 46: Ribosomal protein uL11



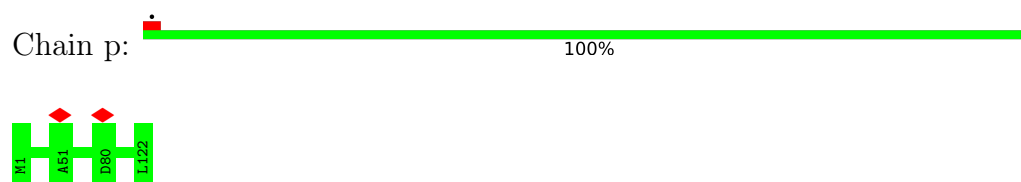
- Molecule 47: Ribosomal protein bL12



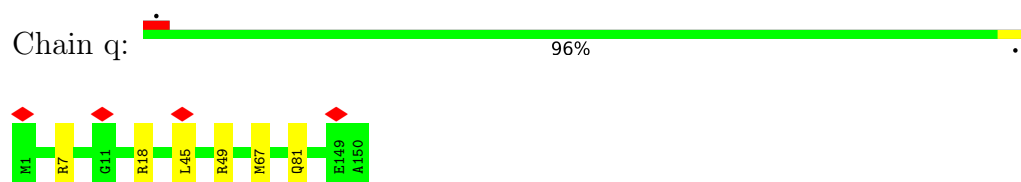
- Molecule 48: 50S ribosomal protein L13



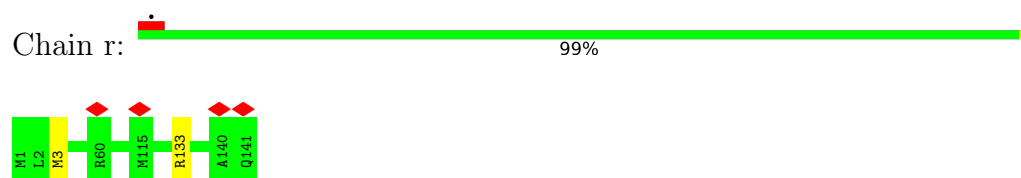
- Molecule 49: 50S ribosomal protein L14



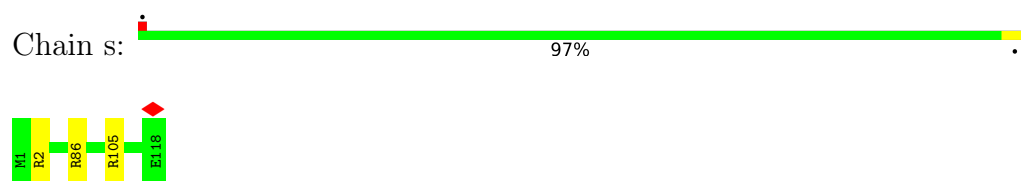
- Molecule 50: 50S ribosomal protein L15



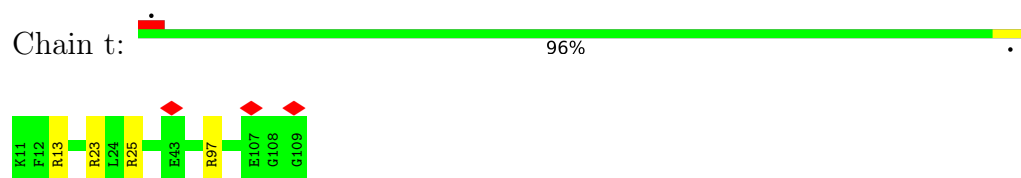
- Molecule 51: 50S ribosomal protein L16



- Molecule 52: 50S ribosomal protein L17



- Molecule 53: 50S ribosomal protein L18

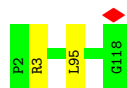


- Molecule 54: 50S ribosomal protein L19

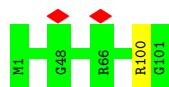




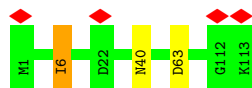
- Molecule 55: 50S ribosomal protein L20



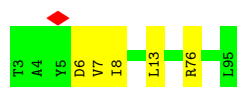
- Molecule 56: 50S ribosomal protein L21



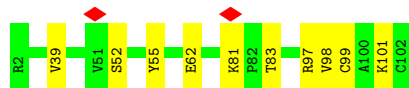
- Molecule 57: 50S ribosomal protein L22



- 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 (\AA)	463.05, 463.05, 463.05	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: MG, GDP, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.28	0/36259	0.99	100/56593 (0.2%)
2	2	0.25	0/1809	0.96	3/2819 (0.1%)
3	3	0.32	0/238	1.04	1/369 (0.3%)
4	4	0.29	0/69975	1.00	185/109242 (0.2%)
5	5	0.33	0/2853	1.07	12/4451 (0.3%)
6	6	0.28	0/1450	0.69	3/1970 (0.2%)
7	7	0.28	0/1151	0.66	2/1558 (0.1%)
8	A	0.27	0/1936	0.61	2/2611 (0.1%)
9	B	0.28	0/1637	0.63	0/2207
10	C	0.27	0/1733	0.55	0/2318
11	D	0.27	0/1163	0.58	0/1566
12	E	0.26	0/856	0.55	0/1154
13	F	0.31	0/1276	0.63	0/1709
14	G	0.26	0/1136	0.56	0/1527
15	H	0.29	0/1029	0.62	0/1379
16	I	0.27	0/808	0.58	0/1087
17	J	0.32	0/900	0.67	2/1213 (0.2%)
18	K	0.27	0/987	0.54	0/1322
19	L	0.27	0/948	0.65	3/1272 (0.2%)
20	M	0.29	0/501	0.60	0/664
21	N	0.26	0/745	0.57	0/992
22	O	0.24	0/717	0.52	0/965
23	P	0.26	0/837	0.62	0/1119
24	Q	0.27	0/579	0.53	0/768
25	R	0.26	0/706	0.58	0/950
26	S	0.25	0/765	0.56	0/1007
27	T	0.24	0/213	0.50	0/279
28	U	0.27	0/5270	0.60	2/7135 (0.0%)
29	V	0.28	0/625	0.60	0/832
30	W	0.27	0/739	0.58	0/983
31	X	0.26	0/600	0.55	0/793
32	Y	0.24	0/473	0.55	0/636

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.29	0/594	0.76	1/795 (0.1%)
34	a	0.29	0/473	0.60	0/639
35	b	0.29	0/440	0.76	0/586
36	c	0.24	0/427	0.47	0/561
37	d	0.30	0/516	0.66	1/681 (0.1%)
38	e	0.32	0/310	0.71	1/407 (0.2%)
39	f	0.28	0/1766	0.63	0/2380
40	g	0.28	0/2195	0.59	1/2955 (0.0%)
41	h	0.29	0/1597	0.64	2/2155 (0.1%)
42	i	0.27	0/1659	0.57	0/2246
43	j	0.30	0/1483	0.76	3/1994 (0.2%)
44	k	0.27	0/1371	0.60	1/1853 (0.1%)
45	l	0.17	0/7	0.20	0/8
48	o	0.26	0/1132	0.58	0/1527
49	p	0.28	0/943	0.53	0/1269
50	q	0.28	0/1162	0.72	1/1544 (0.1%)
51	r	0.25	0/1143	0.49	0/1527
52	s	0.27	0/982	0.63	0/1312
53	t	0.28	0/779	0.70	0/1038
54	u	0.29	0/1156	0.63	0/1544
55	v	0.26	0/975	0.53	0/1297
56	w	0.26	0/790	0.60	0/1057
57	x	0.28	0/907	0.61	1/1216 (0.1%)
58	y	0.27	0/740	0.59	1/995 (0.1%)
59	z	0.36	0/789	0.86	2/1053 (0.2%)
All	All	0.28	0/165250	0.90	330/246129 (0.1%)

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

There are no bond length outliers.

The worst 5 of 330 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	76	C	N1-C2-O2	13.27	126.86	118.90
1	1	76	C	N3-C2-O2	-12.51	113.14	121.90
1	1	754	C	C2-N1-C1'	11.57	131.53	118.80
1	1	373	A	OP1-P-O3'	-11.47	79.96	105.20
1	1	231	G	OP1-P-O3'	-11.35	80.24	105.20

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](#)

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	
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	63
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%)	19	52
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
22	O	82/84 (98%)	73 (89%)	8 (10%)	1 (1%)	11	40
23	P	98/100 (98%)	93 (95%)	4 (4%)	1 (1%)	13	44
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%)	37	69
29	V	76/78 (97%)	68 (90%)	8 (10%)	0	100	100
30	W	92/94 (98%)	88 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	26
39	f	225/227 (99%)	189 (84%)	36 (16%)	0	100	100
40	g	273/275 (99%)	244 (89%)	28 (10%)	1 (0%)	30	63
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%)	22	55
44	k	174/176 (99%)	148 (85%)	25 (14%)	1 (1%)	22	55
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
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%)	12	42
59	z	99/101 (98%)	72 (73%)	25 (25%)	2 (2%)	6	32
All	All	6614/6873 (96%)	5765 (87%)	829 (12%)	20 (0%)	38	69

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
59	z	98	VAL

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Mol	Chain	Res	Type
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%)	155 (99%)	2 (1%)	65	76
7	7	122/122 (100%)	121 (99%)	1 (1%)	79	84
8	A	202/203 (100%)	195 (96%)	7 (4%)	31	54
9	B	160/161 (99%)	152 (95%)	8 (5%)	20	45
10	C	180/180 (100%)	176 (98%)	4 (2%)	47	64
11	D	115/116 (99%)	112 (97%)	3 (3%)	41	61
12	E	90/90 (100%)	86 (96%)	4 (4%)	24	48
13	F	126/126 (100%)	121 (96%)	5 (4%)	27	50
14	G	119/119 (100%)	115 (97%)	4 (3%)	32	55
15	H	98/98 (100%)	97 (99%)	1 (1%)	73	80
16	I	88/89 (99%)	87 (99%)	1 (1%)	70	79
17	J	90/90 (100%)	87 (97%)	3 (3%)	33	56
18	K	104/104 (100%)	100 (96%)	4 (4%)	28	52
19	L	94/95 (99%)	90 (96%)	4 (4%)	25	49
20	M	49/49 (100%)	48 (98%)	1 (2%)	50	68
21	N	79/79 (100%)	79 (100%)	0	100	100
22	O	72/72 (100%)	70 (97%)	2 (3%)	38	59
23	P	94/95 (99%)	94 (100%)	0	100	100
24	Q	61/61 (100%)	59 (97%)	2 (3%)	33	56
25	R	74/75 (99%)	71 (96%)	3 (4%)	26	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	S	76/76 (100%)	75 (99%)	1 (1%)	65	76
27	T	19/20 (95%)	18 (95%)	1 (5%)	19	44
28	U	558/579 (96%)	548 (98%)	10 (2%)	54	71
29	V	62/62 (100%)	60 (97%)	2 (3%)	34	56
30	W	78/79 (99%)	75 (96%)	3 (4%)	28	52
31	X	66/66 (100%)	62 (94%)	4 (6%)	15	41
32	Y	51/52 (98%)	51 (100%)	0	100	100
33	Z	63/63 (100%)	60 (95%)	3 (5%)	21	46
34	a	51/51 (100%)	49 (96%)	2 (4%)	27	51
35	b	49/49 (100%)	48 (98%)	1 (2%)	50	68
36	c	41/41 (100%)	39 (95%)	2 (5%)	21	45
37	d	53/54 (98%)	51 (96%)	2 (4%)	28	52
38	e	34/34 (100%)	32 (94%)	2 (6%)	16	41
39	f	179/179 (100%)	178 (99%)	1 (1%)	84	88
40	g	217/217 (100%)	214 (99%)	3 (1%)	62	75
41	h	165/165 (100%)	164 (99%)	1 (1%)	84	88
42	i	165/165 (100%)	164 (99%)	1 (1%)	84	88
43	j	153/153 (100%)	146 (95%)	7 (5%)	23	47
44	k	146/146 (100%)	145 (99%)	1 (1%)	81	86
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
50	q	116/116 (100%)	112 (97%)	4 (3%)	32	55
51	r	111/111 (100%)	109 (98%)	2 (2%)	54	71
52	s	101/101 (100%)	98 (97%)	3 (3%)	36	58
53	t	77/77 (100%)	73 (95%)	4 (5%)	19	44
54	u	120/120 (100%)	114 (95%)	6 (5%)	20	45
55	v	92/93 (99%)	90 (98%)	2 (2%)	47	64
56	w	82/82 (100%)	81 (99%)	1 (1%)	67	77
57	x	91/92 (99%)	90 (99%)	1 (1%)	70	79
58	y	74/75 (99%)	73 (99%)	1 (1%)	62	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
59	z	84/85 (99%)	83 (99%)	1 (1%)	67 77
All	All	5566/5603 (99%)	5435 (98%)	131 (2%)	45 62

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	t	13	ARG
54	u	39	ARG
59	z	101	LYS
19	L	80	ARG
19	L	11	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
41	h	129	HIS
43	j	132	ASN
51	r	141	GLN
41	h	143	ASN
48	o	56	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1506/1507 (99%)	395 (26%)	11 (0%)
2	2	75/76 (98%)	27 (36%)	0
3	3	9/15 (60%)	7 (77%)	1 (11%)
4	4	2900/2901 (99%)	544 (18%)	10 (0%)
5	5	118/119 (99%)	36 (30%)	4 (3%)
All	All	4608/4618 (99%)	1009 (21%)	26 (0%)

5 of 1009 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	60,28	24,30,30	0.95	1 (4%)	30,47,47	1.26	4 (13%)

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	60,28	-	7/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	U	702	GDP	C6-N1	-2.42	1.34	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	U	702	GDP	C3'-C2'-C1'	3.46	106.18	100.98
62	U	702	GDP	PA-O3A-PB	-2.78	123.29	132.83
62	U	702	GDP	C5-C6-N1	2.34	118.08	113.95
62	U	702	GDP	C8-N7-C5	2.33	107.43	102.99

There are no chirality outliers.

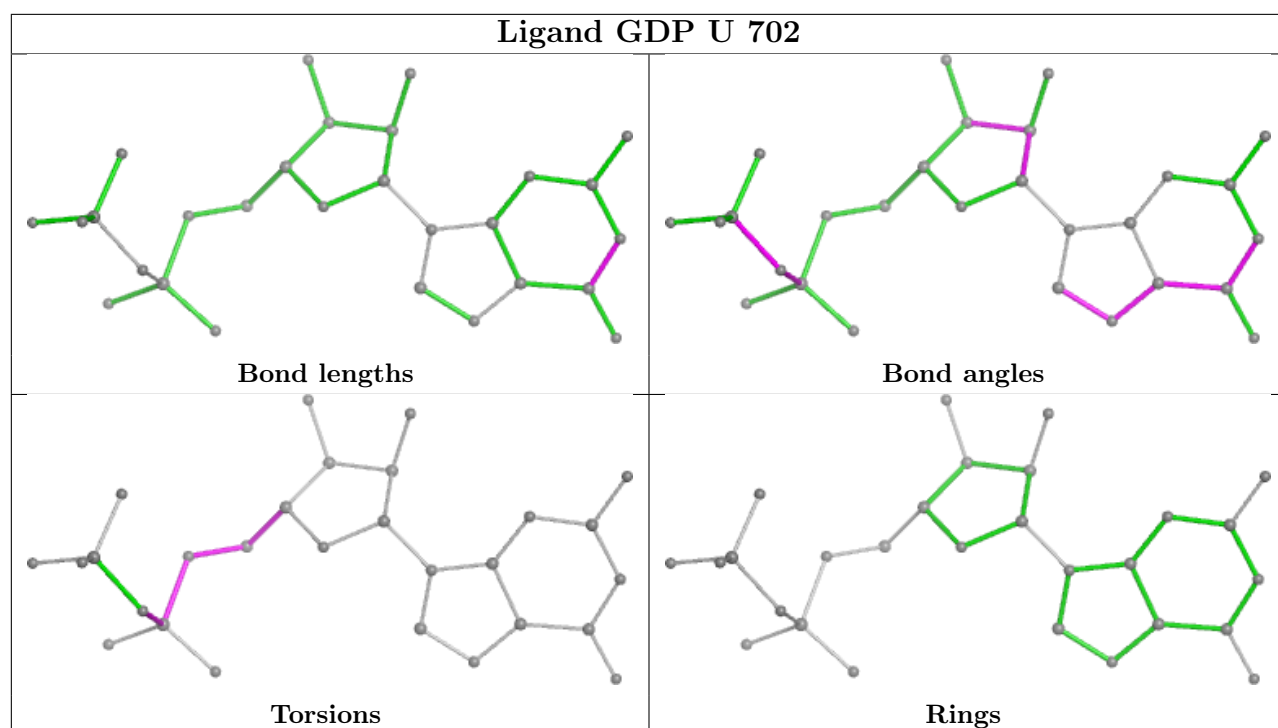
5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	U	702	GDP	C5'-O5'-PA-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'
62	U	702	GDP	C5'-O5'-PA-O1A

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.

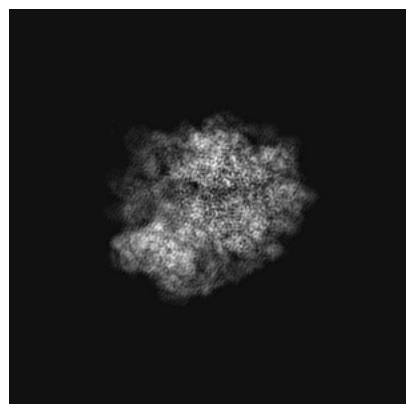
6 Map visualisation [i](#)

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.

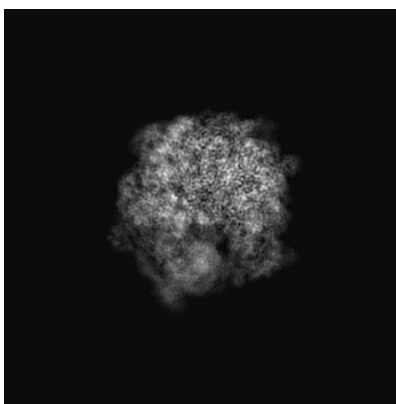
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

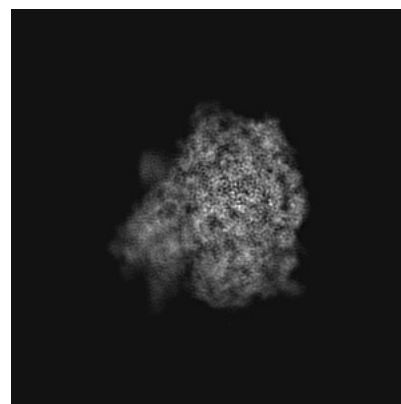
6.1.1 Primary map



X

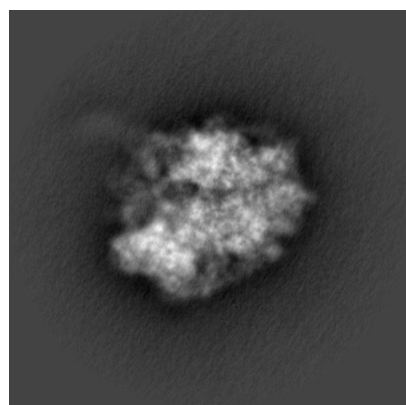


Y

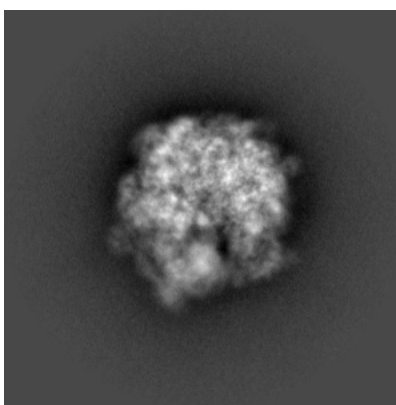


Z

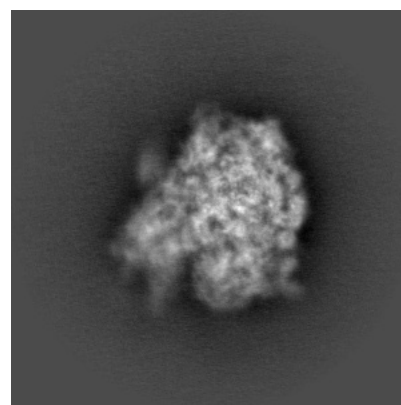
6.1.2 Raw map



X



Y

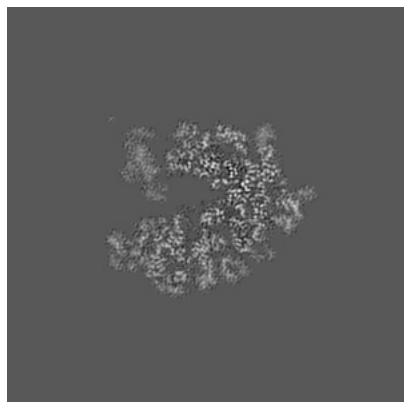


Z

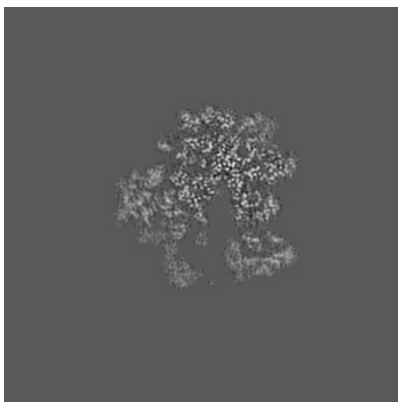
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

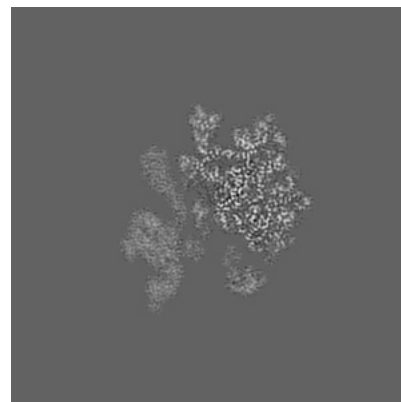
6.2.1 Primary map



X Index: 210

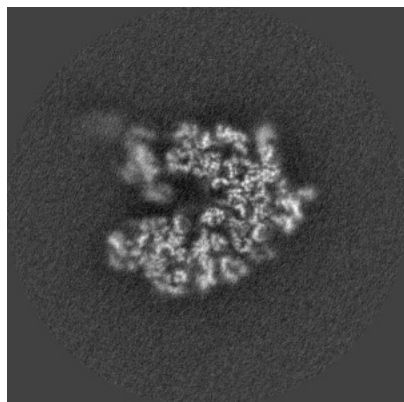


Y Index: 210

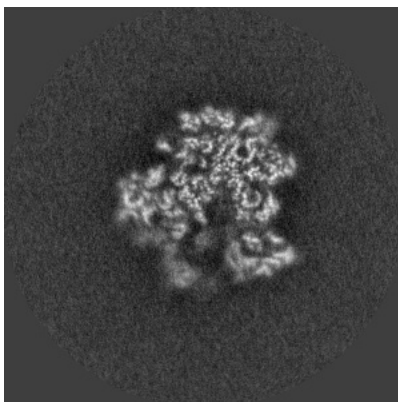


Z Index: 210

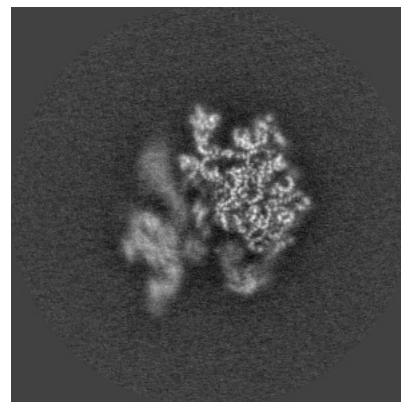
6.2.2 Raw map



X Index: 210



Y Index: 210

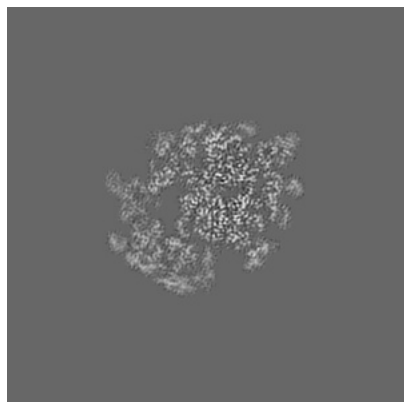


Z Index: 210

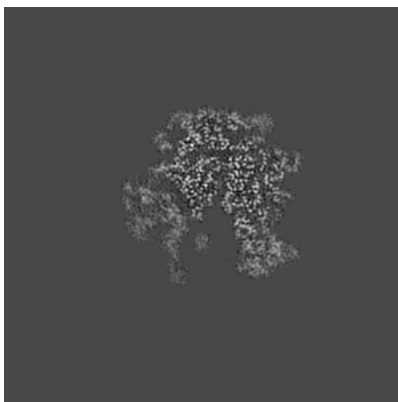
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

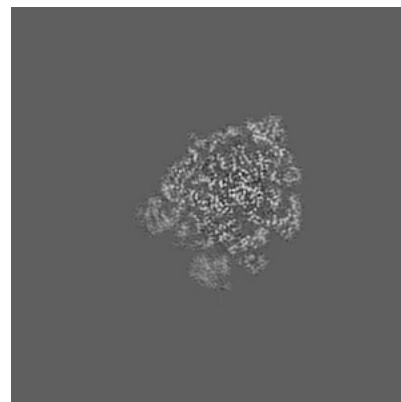
6.3.1 Primary map



X Index: 239

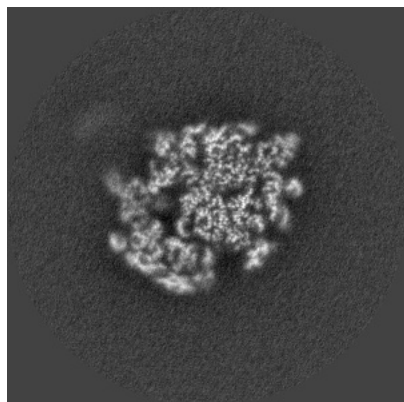


Y Index: 218

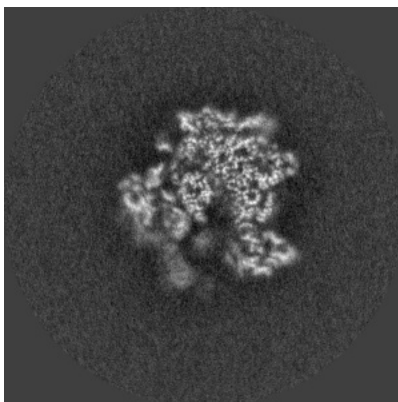


Z Index: 254

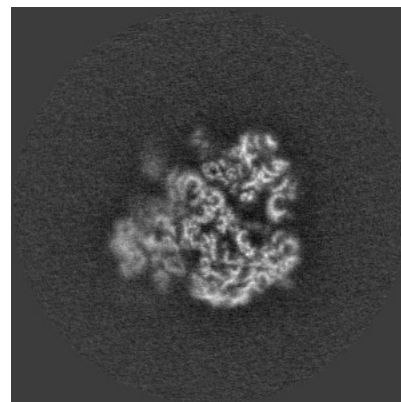
6.3.2 Raw map



X Index: 239



Y Index: 213

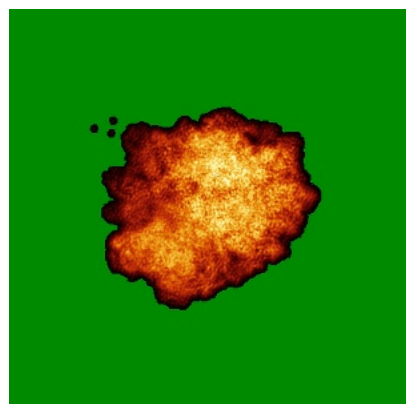


Z Index: 171

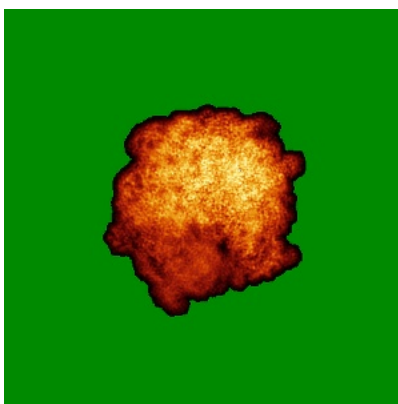
The images above show the largest variance slices of the map in three orthogonal directions.

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

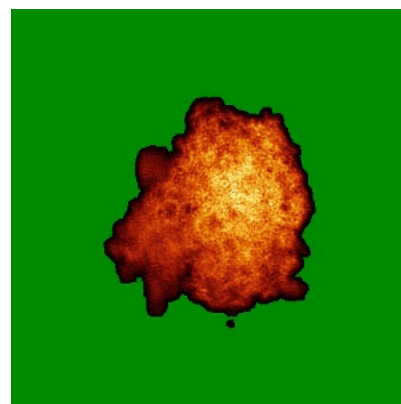
6.4.1 Primary map



X

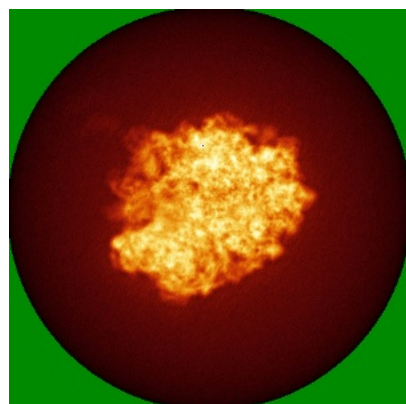


Y

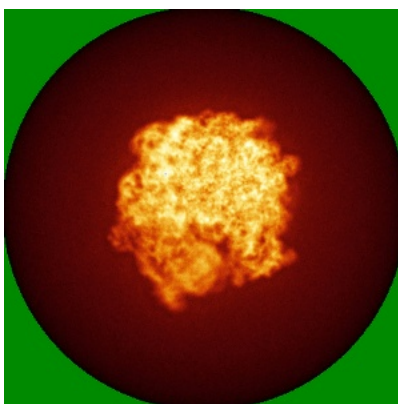


Z

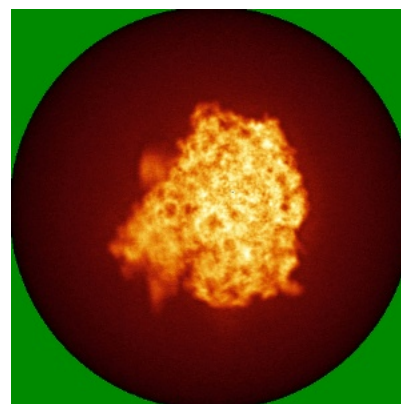
6.4.2 Raw map



X



Y

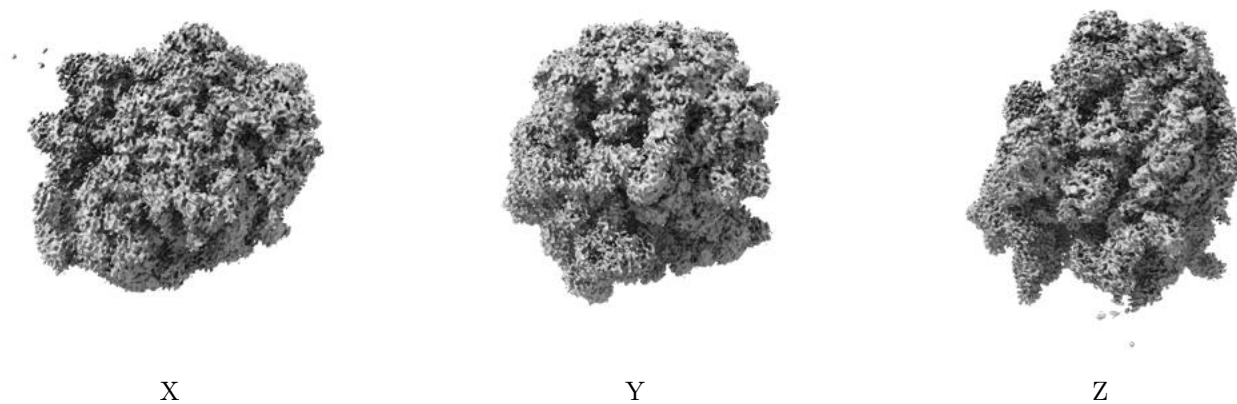


Z

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.

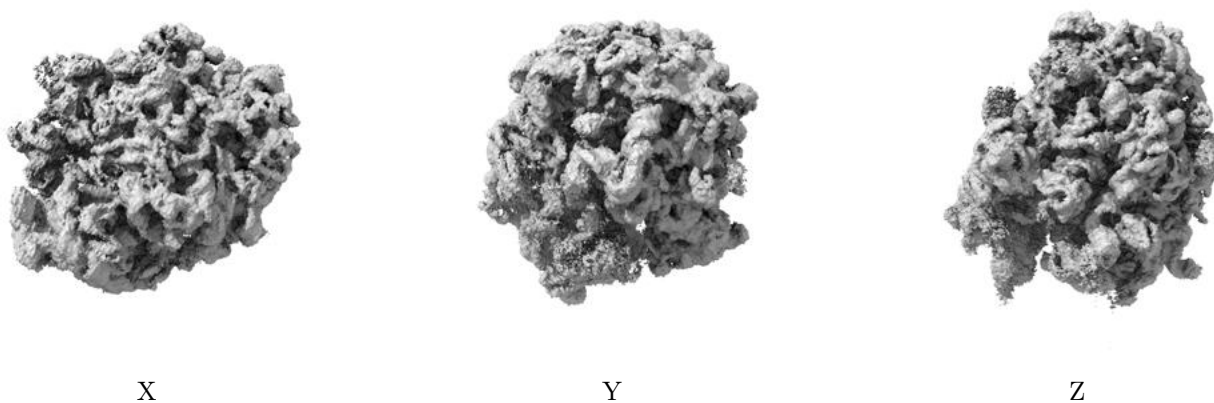
6.5 Orthogonal surface views [i](#)

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.

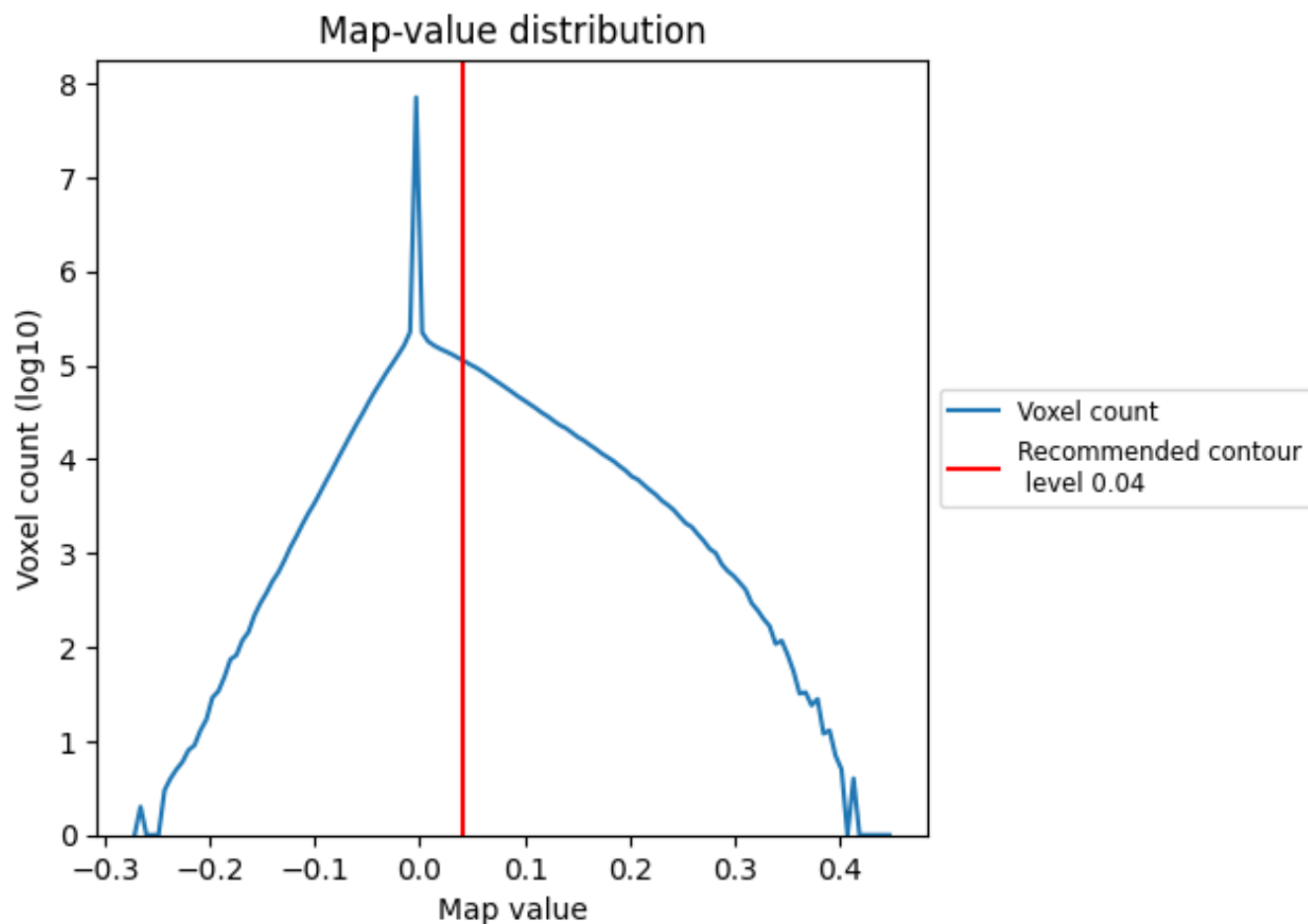
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

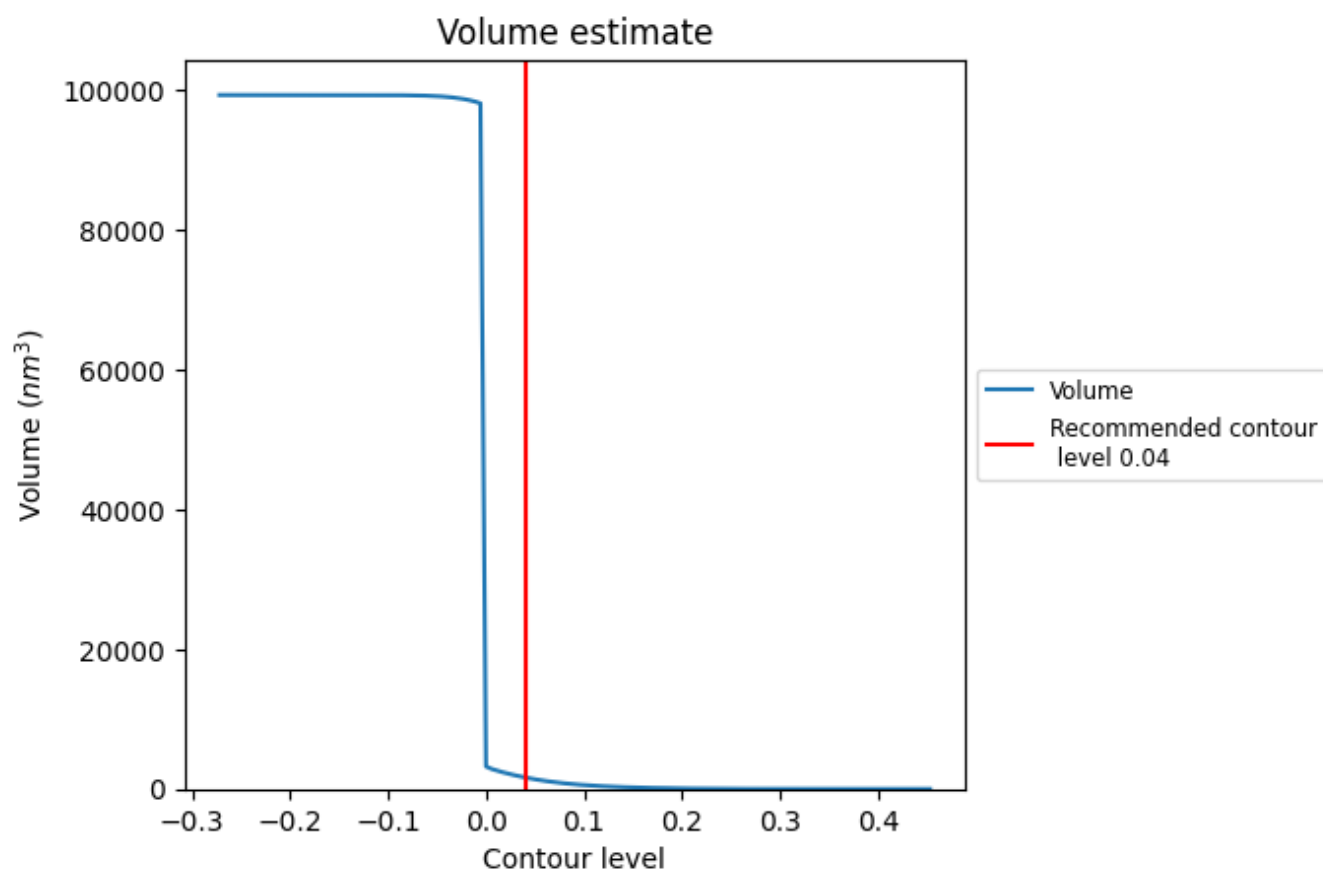
This section contains the results of statistical analysis of the map.

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.

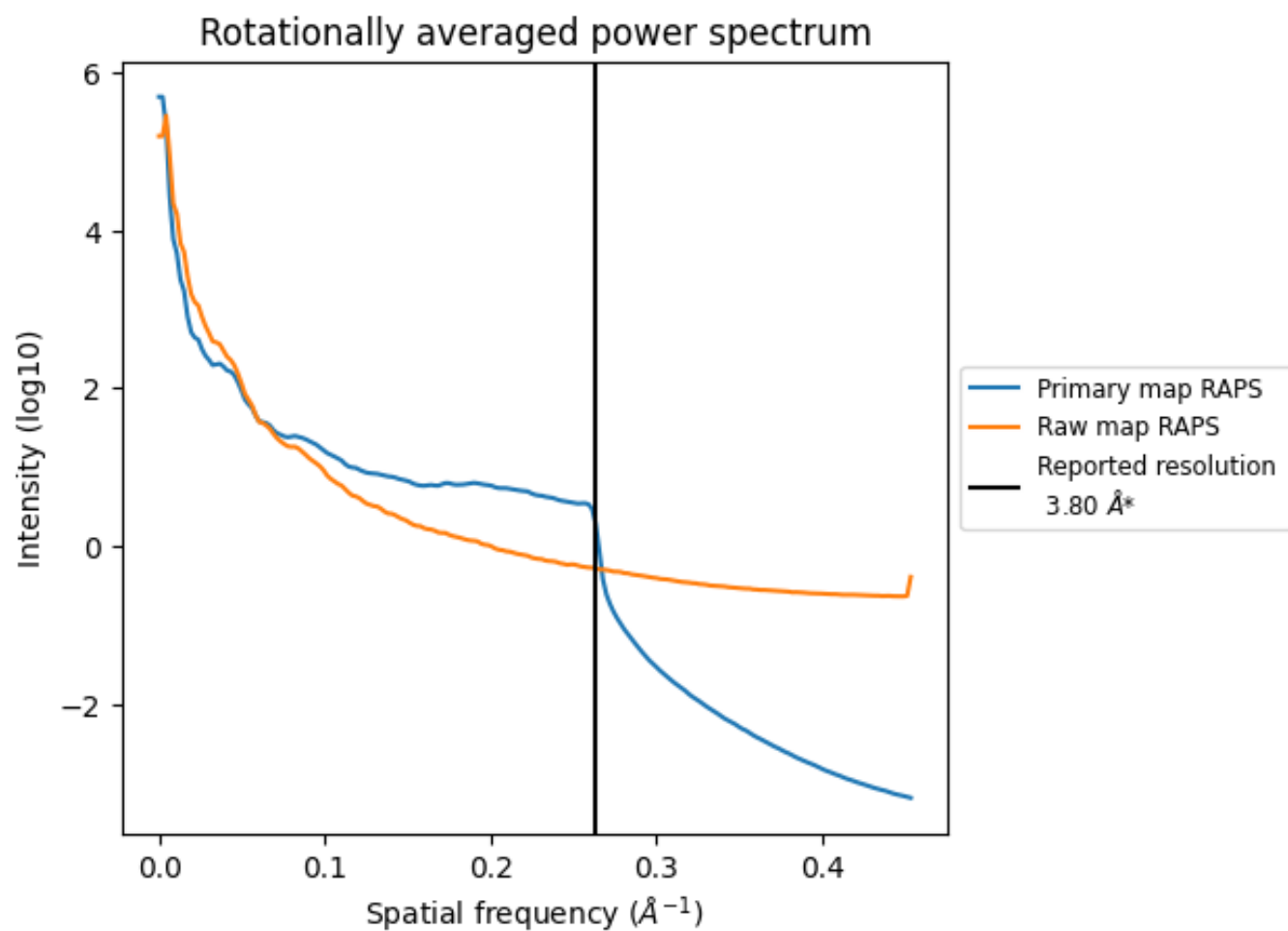
7.2 Volume estimate [i](#)



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 ⓘ

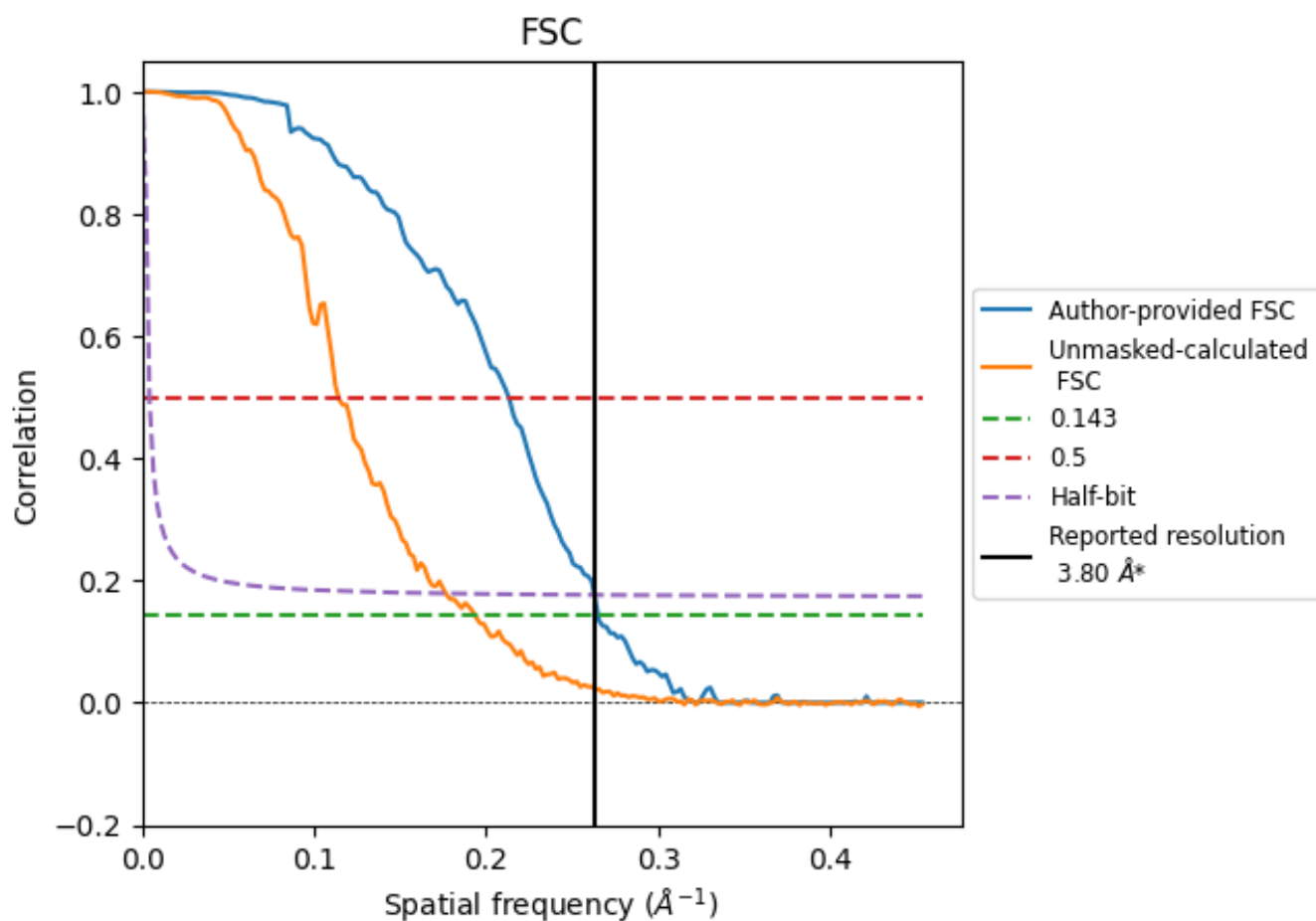


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 \AA^{-1}

8.2 Resolution estimates [i](#)

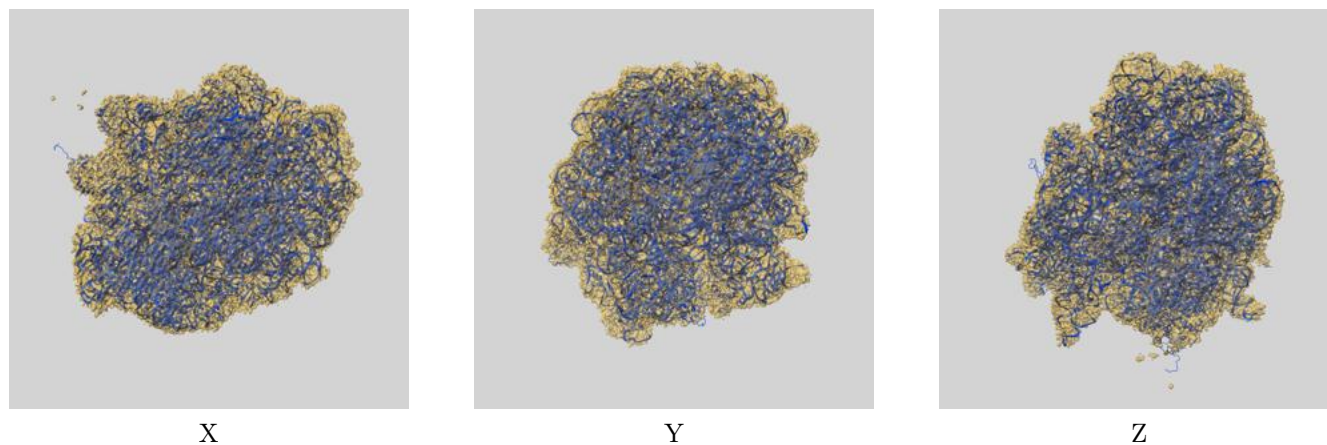
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.77	4.69	3.80
Unmasked-calculated*	5.17	8.76	5.67

*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](#)

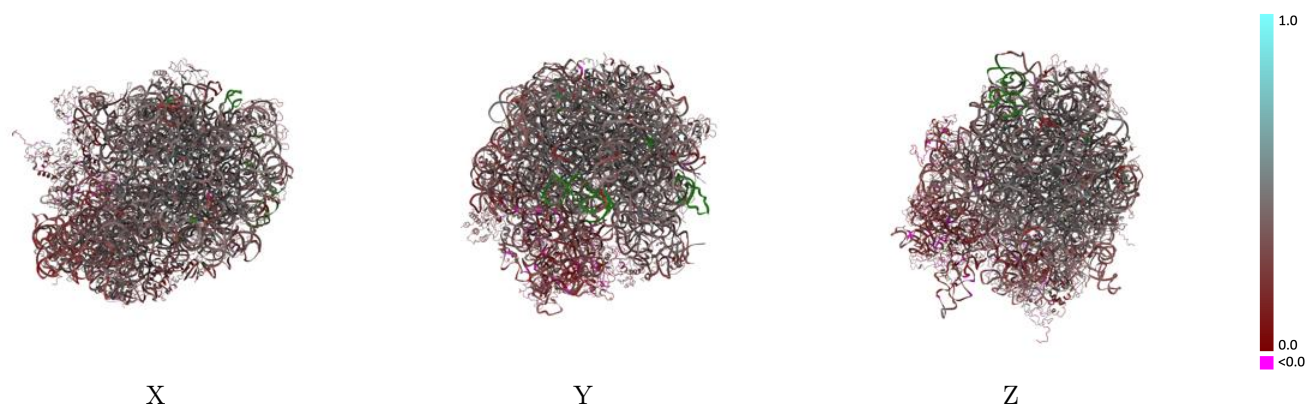
This section contains information regarding the fit between EMDB map EMD-3852 and PDB model 5OT7. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



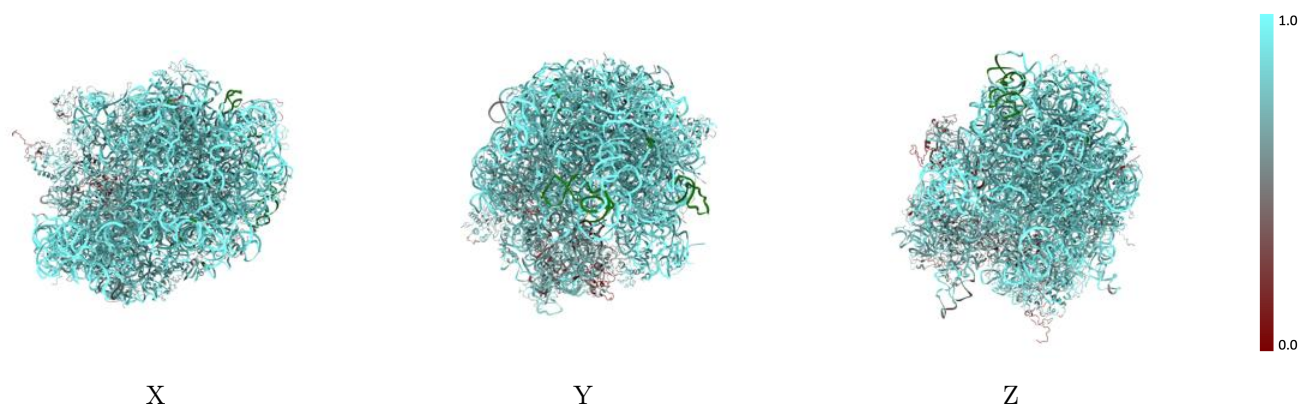
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



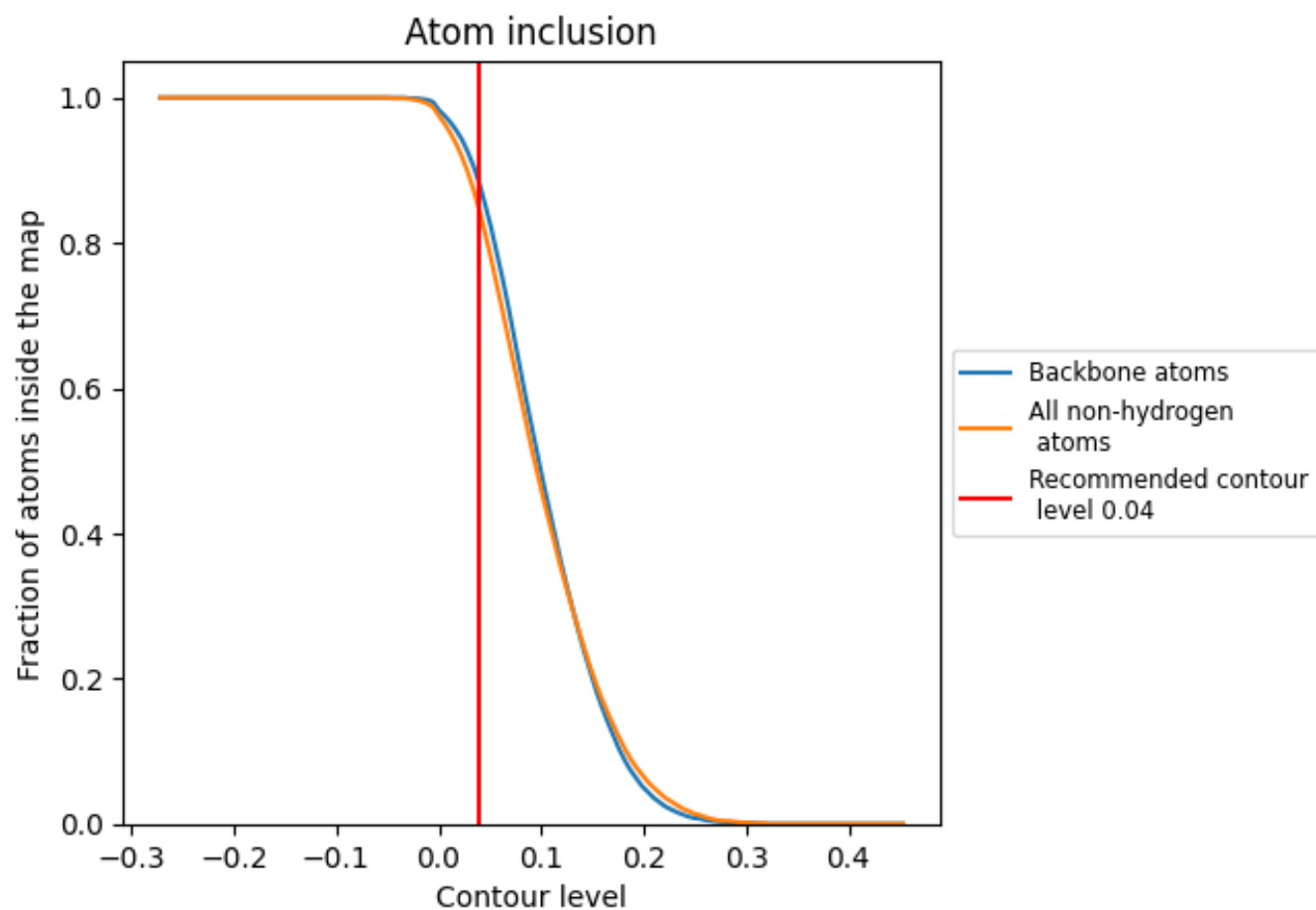
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7960	 0.3870



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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