



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:21 AM UTC

PDB ID : 8V9L / pdb_00008v9l
EMDB ID : EMD-43076
Title : Cryo-EM structure of the Mycobacterium smegmatis 70S ribosome in complex with hibernation factor Msmeg1130 (Balon) and MsmegEF-Tu(GDP) (Composite structure 6)
Authors : Rybak, M.Y.; Helena-Bueno, K.; Hill, C.H.; Melnikov, S.V.; Gagnon, M.G.
Deposited on : 2023-12-08
Resolution : 3.00 Å (reported)
Based on initial model : 5o61

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

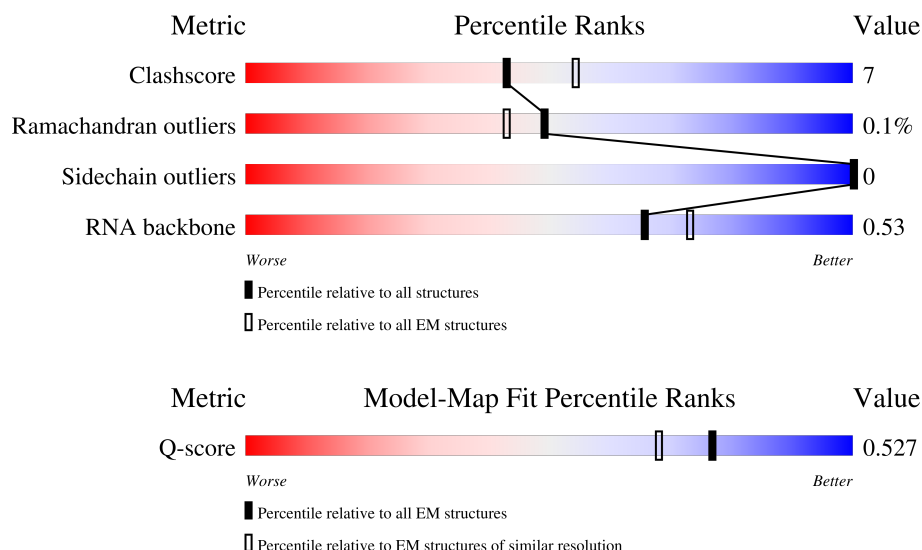
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	a	1528	
2	b	277	

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Mol	Chain	Length	Quality of chain
3	c	275	
4	d	201	
5	e	214	
6	f	96	
7	g	156	
8	h	132	
9	i	150	
10	j	101	
11	k	138	
12	l	124	
13	m	124	
14	n	61	
15	o	89	
16	p	156	
17	q	98	
18	r	84	
19	s	93	
20	t	86	
21	u	33	
22	v	4	
23	x	396	
24	y	76	
25	z	375	
26	A	3164	
27	B	118	

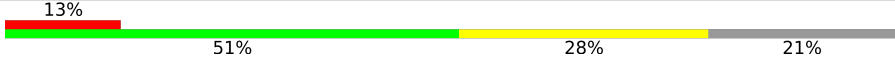
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Mol	Chain	Length	Quality of chain
28	C	278	 90% 9% .
29	D	217	 85% 14% .
30	E	215	 90% 7% .
31	F	187	 75% 22% .
32	G	179	 88% 10% .
33	H	151	 73% 79% 21%
34	I	175	 21% 56% 16% 28%
35	J	142	 78% 15% 6%
36	L	147	 91% 8% .
37	M	122	 92% 8%
38	N	147	 84% 15% .
39	O	137	 80% 19% ..
40	P	199	 51% 8% 41%
41	Q	127	 84% 15% .
42	R	113	 89% 11%
43	S	129	 84% 12% .
44	T	103	 93% . .
45	U	153	 69% 5% 25%
46	V	100	 86% 11% .
47	W	105	 8% 76% 16% 8%
48	X	215	 82% 7% 11%
49	Y	88	 85% 5% 10%
50	Z	64	 89% 9% .
51	1	77	 68% 16% 17%
52	2	61	 84% 13% .

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Mol	Chain	Length	Quality of chain
53	3	75	
54	4	57	
55	5	55	
56	6	47	
57	7	64	
58	8	37	
59	9	24	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 155647 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	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	126	Total	C	N	O	S	0	0
			994	630	194	170			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 21 is a protein called 30S Ribosomal Protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called poly-U mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	4	Total	C	N	O	P	0	0
			80	36	8	32	4		

- Molecule 23 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	387	Total	C	N	O	S	0	0
			2997	1877	525	585	10		

- Molecule 24 is a RNA chain called pe/E deacylated phenylalanine-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	y	74	Total	C	N	O	P	S	0	0
			1581	707	285	515	73	1		

- Molecule 25 is a protein called Ribosome hibernation factor Balon (MSMEG_1130).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	375	Total	C	N	O	S	0	0
			2909	1800	550	550	9		

- Molecule 26 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	3073	Total	C	N	O	P	0	0
			65997	29416	12137	21371	3073		

- Molecule 27 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 30 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 31 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	F	182	Total	C	N	O	S	0	0
			1439	904	268	261	6		

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 34 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 35 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	97	Total	C	N	O		0	0
			756	479	138	139			

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	192	Total	C	N	O		0	0
			1428	881	255	292			

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	Y	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 53 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	59	Total	C	N	O	S	0	0
			413	253	73	82	5		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 55 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	63	Total	C	N	O		0	0
			502	302	115	85			

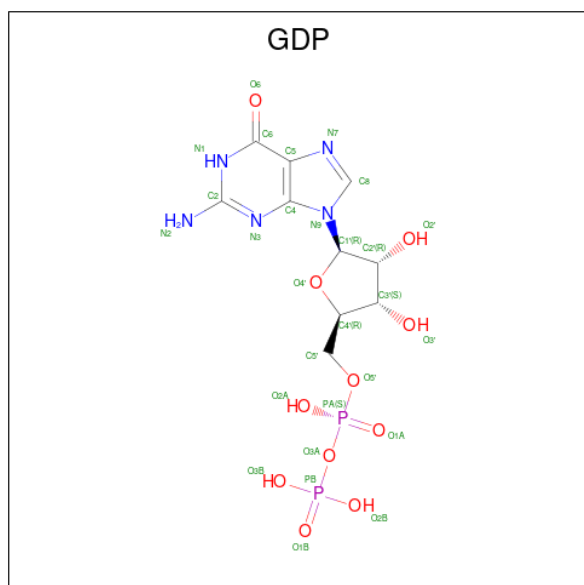
- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 59 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	9	23	Total	C	N	O		0	0
			189	111	50	28			

- Molecule 60 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

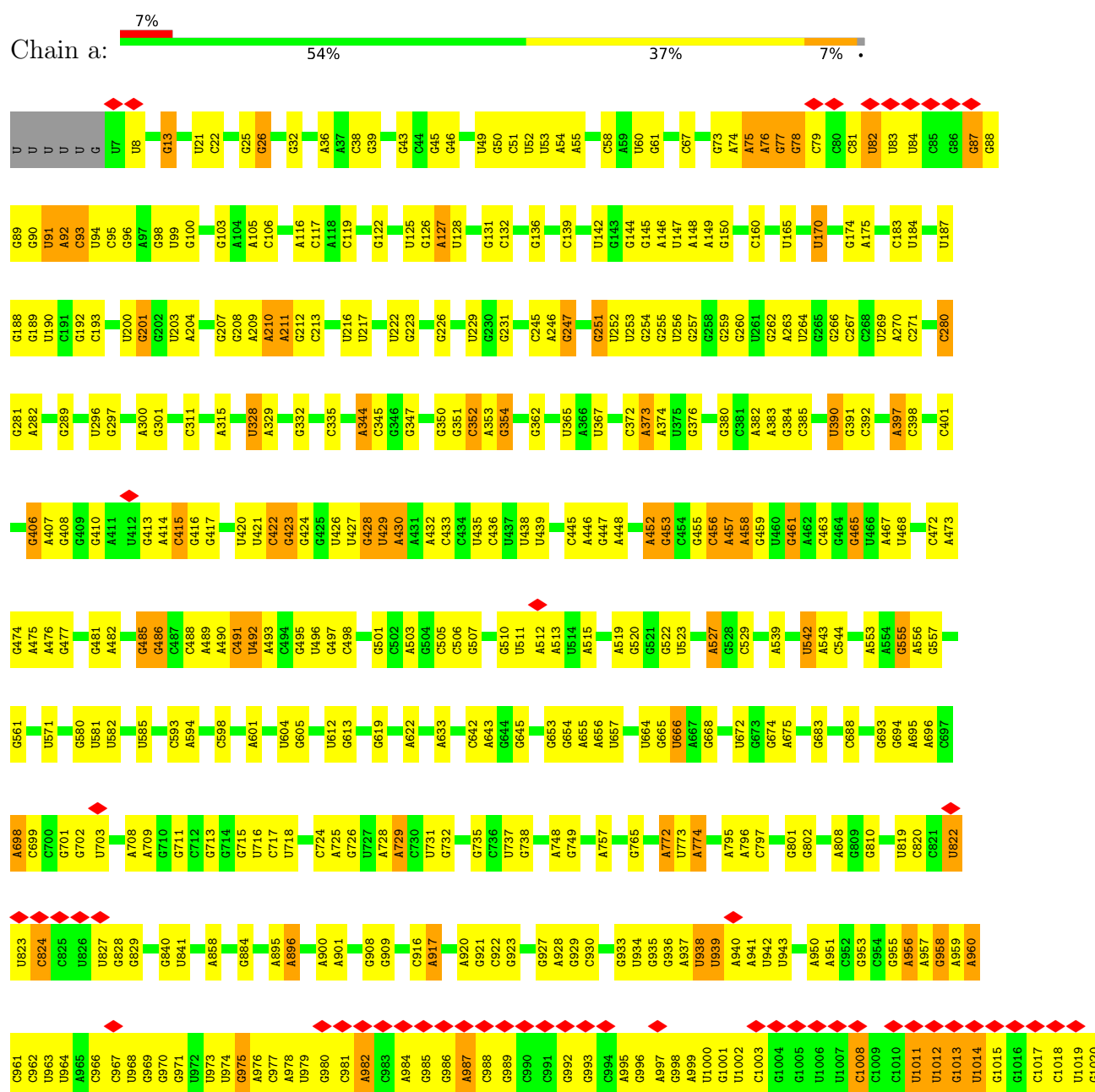
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

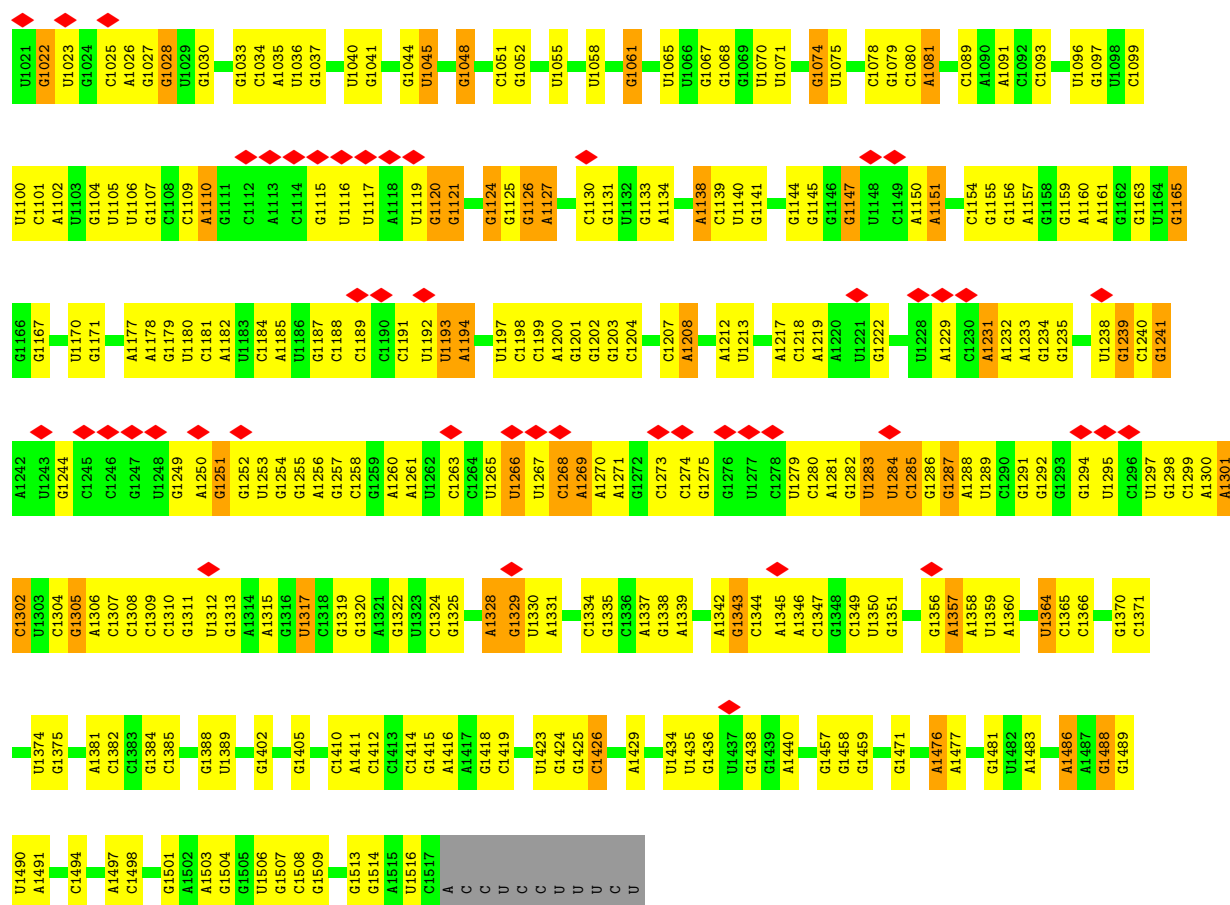
Mol	Chain	Residues	Atoms		AltConf
61	Z	1	Total 1	Zn 1	0
61	5	1	Total 1	Zn 1	0

3 Residue-property plots

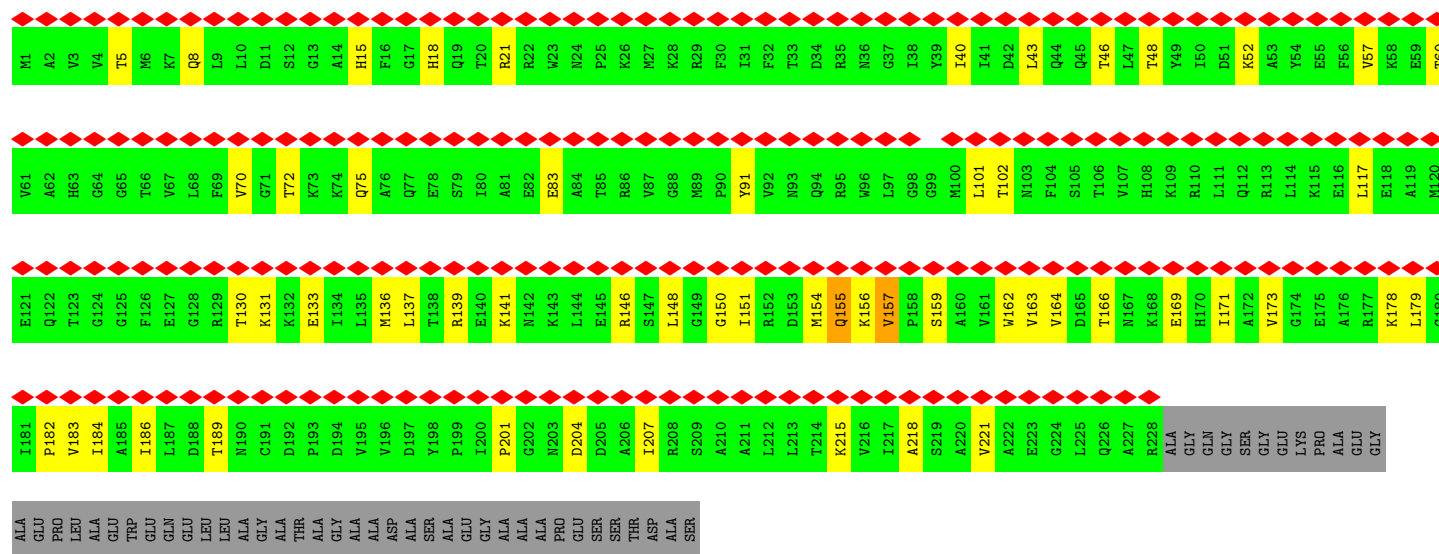
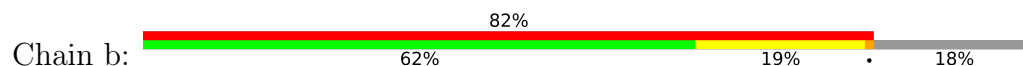
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



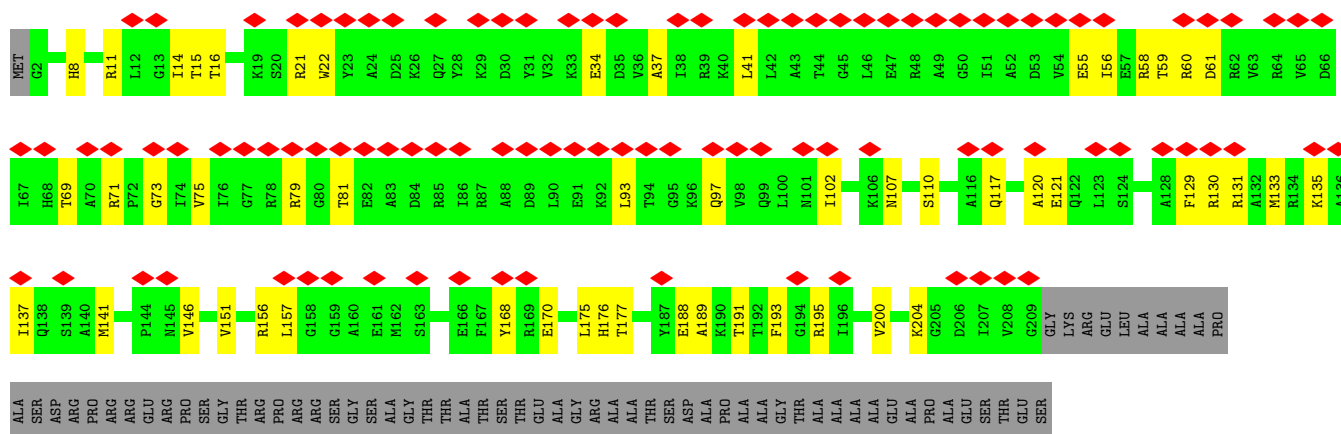


• Molecule 2: 30S Ribosomal Protein S2

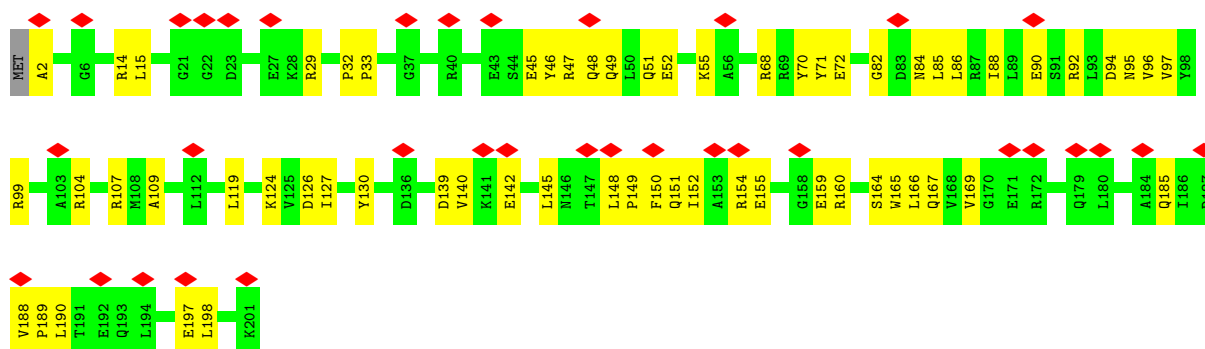


• Molecule 3: 30S ribosomal protein S3

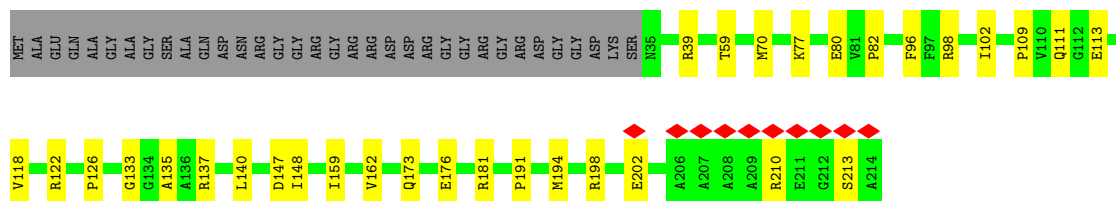




- Molecule 4: 30S ribosomal protein S4



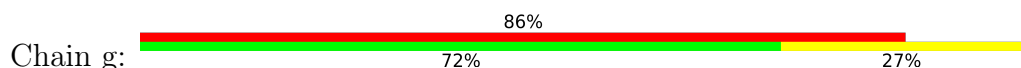
- Molecule 5: Small ribosomal subunit protein uS5

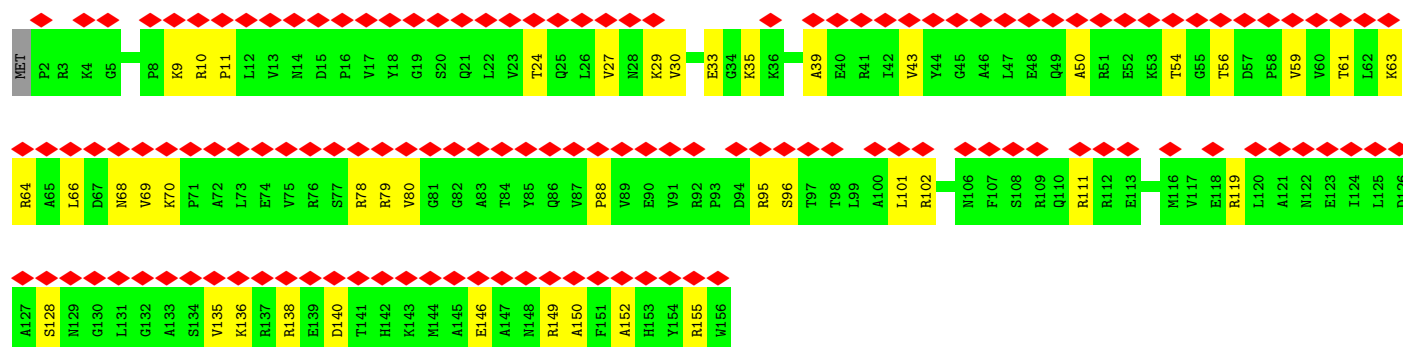


- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7





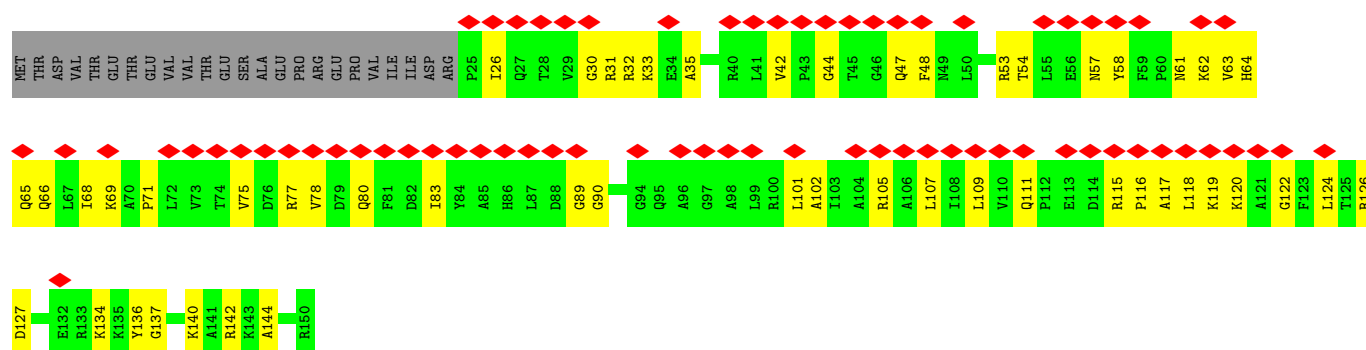
• Molecule 8: Small ribosomal subunit protein uS8

Chain h: 83% 16% .



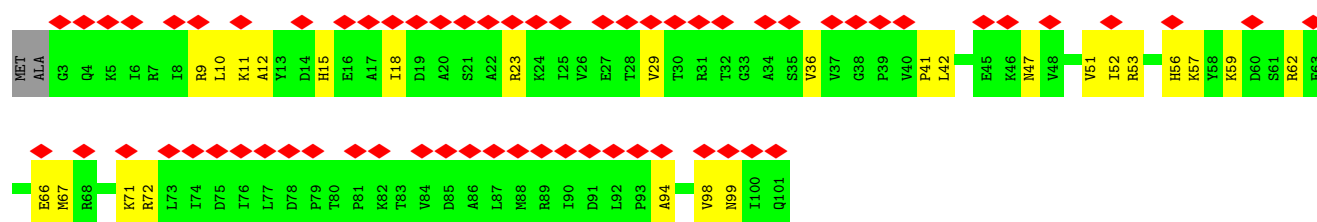
• Molecule 9: 30S ribosomal protein S9

Chain i: 49% 35% 16% .



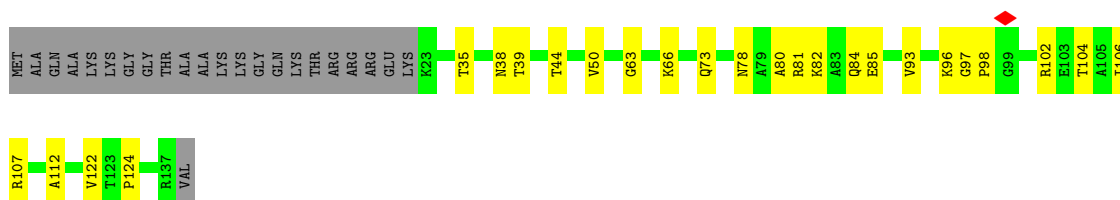
• Molecule 10: 30S ribosomal protein S10

Chain j: 63% 72% 26% .

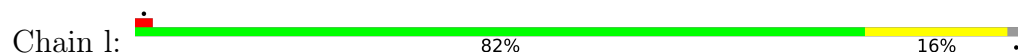


• Molecule 11: 30S ribosomal protein S11

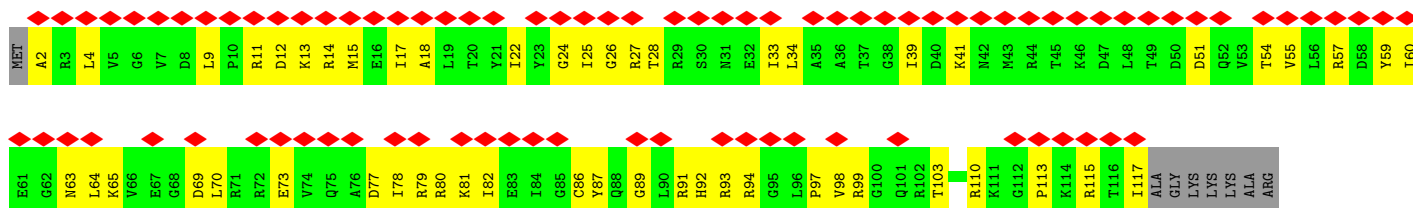
Chain k: 65% 18% 17% .



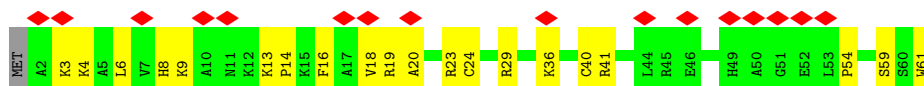
- Molecule 12: 30S ribosomal protein S12



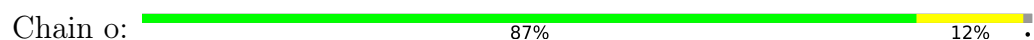
- Molecule 13: 30S ribosomal protein S13



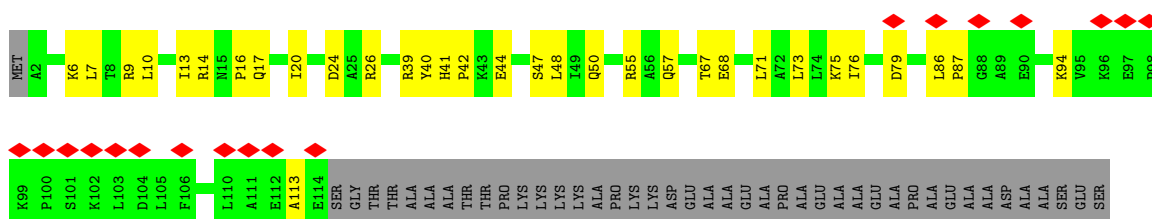
- Molecule 14: Small ribosomal subunit protein uS14B



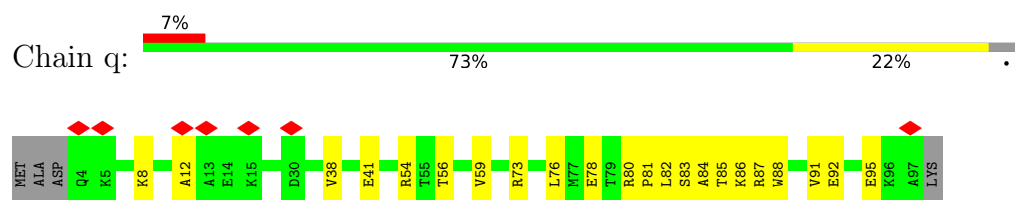
- Molecule 15: Small ribosomal subunit protein uS15



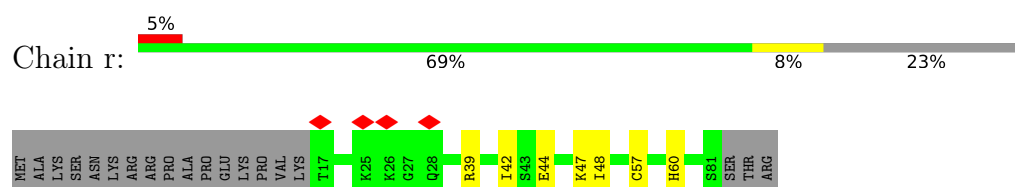
- Molecule 16: 30S ribosomal protein S16



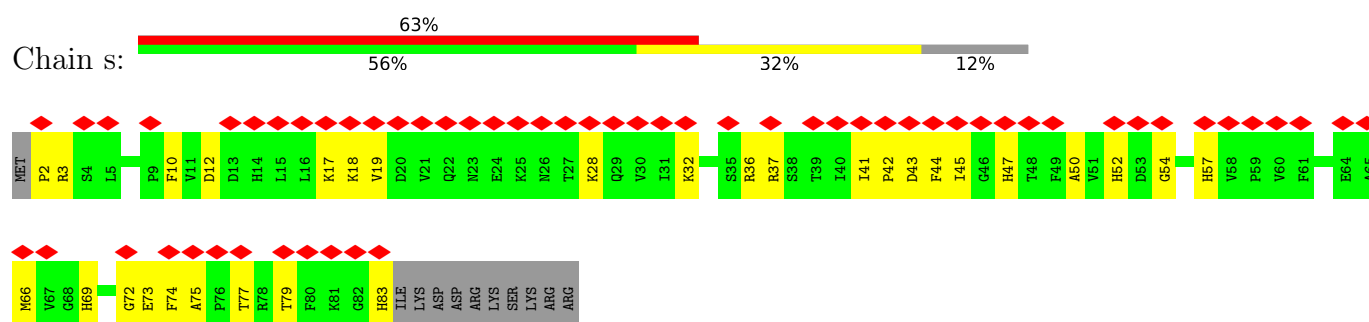
- Molecule 17: 30S ribosomal protein S17



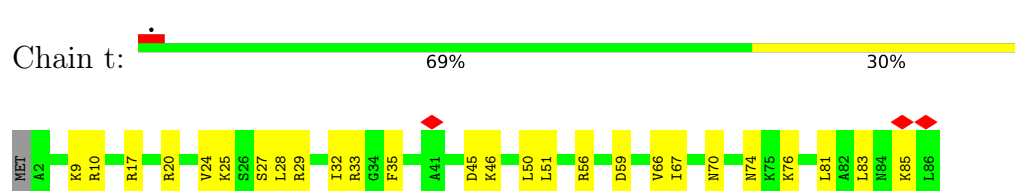
- Molecule 18: Small ribosomal subunit protein bS18B



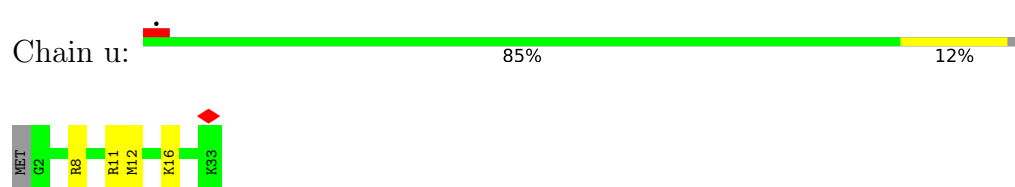
- Molecule 19: 30S ribosomal protein S19



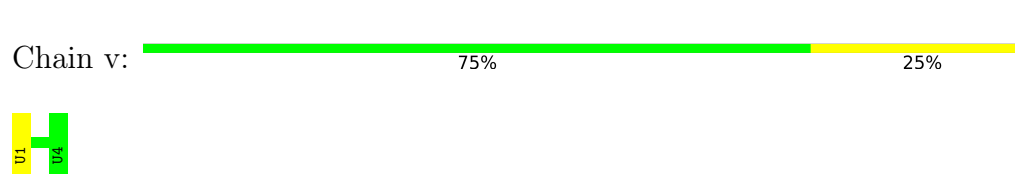
- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S Ribosomal Protein S22



- Molecule 22: poly-U mRNA



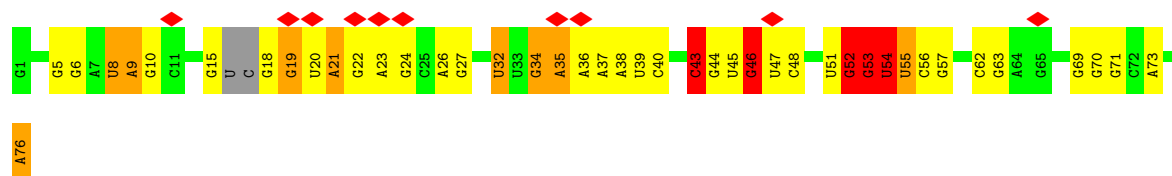
- Molecule 23: Elongation factor Tu

Chain x: 



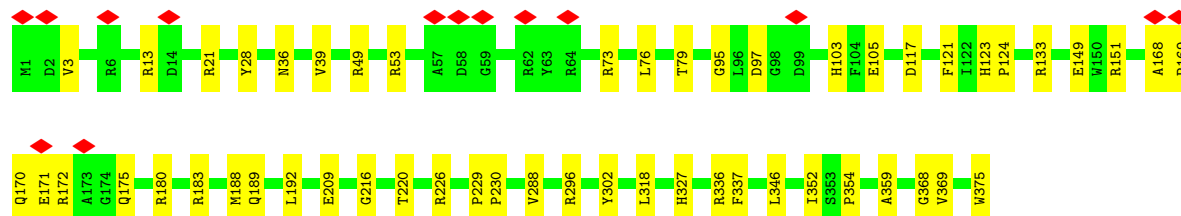
• Molecule 24: pe/E deacylated phenylalanine-tRNA

Chain y: 



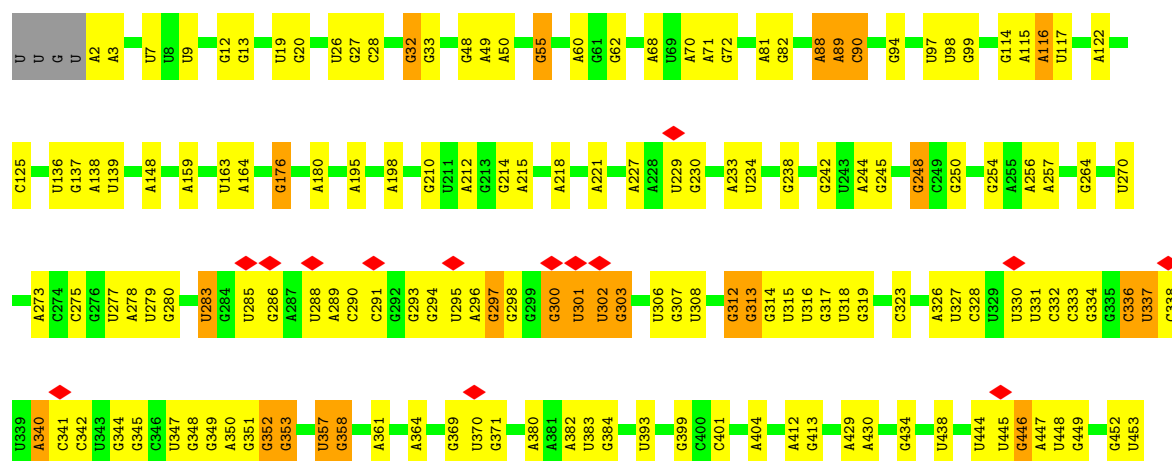
• Molecule 25: Ribosome hibernation factor Balon (MSMEG_1130)

Chain z: 

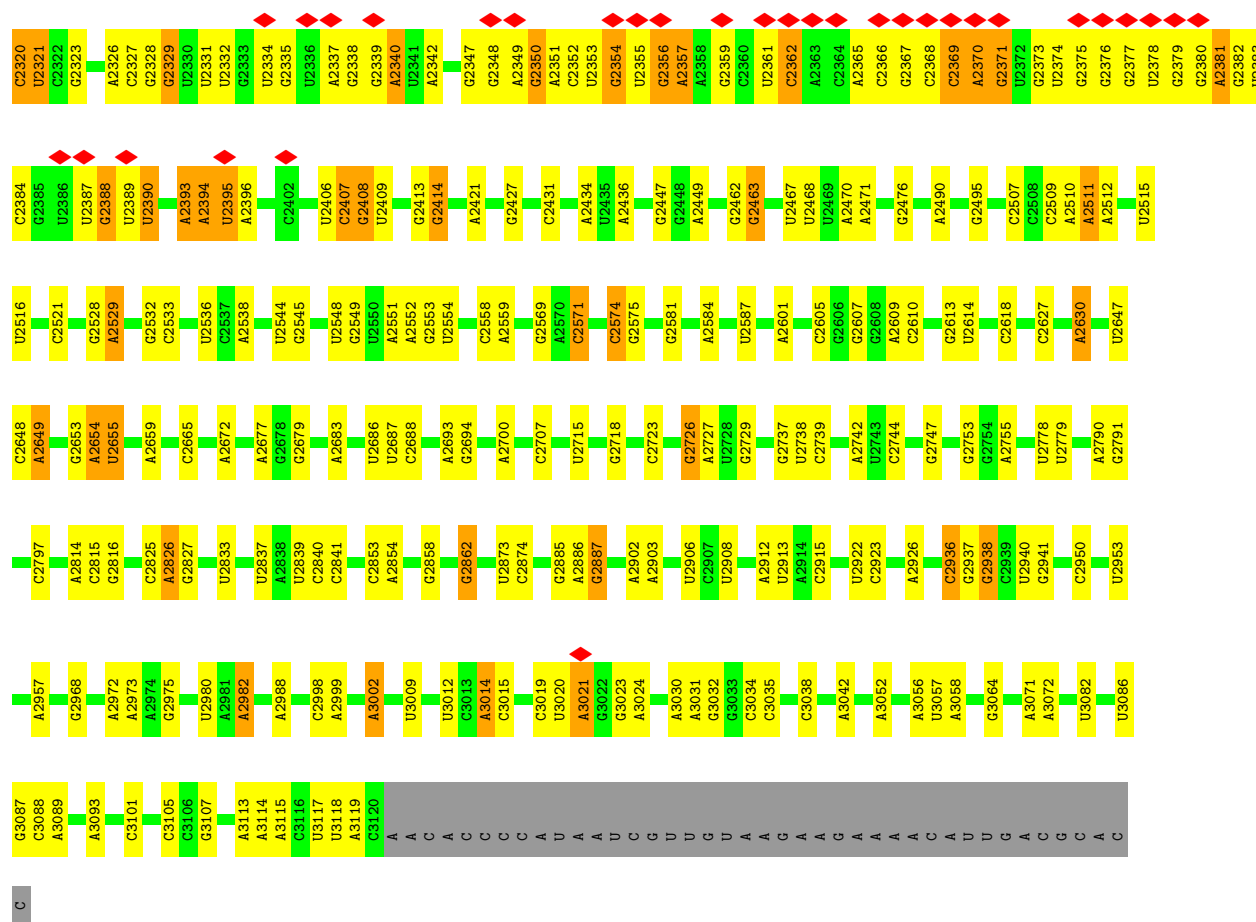


• Molecule 26: 23S Ribosomal RNA

Chain A: 



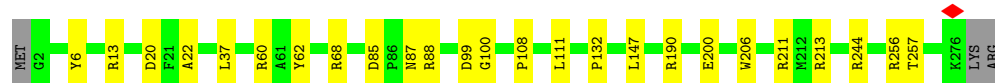




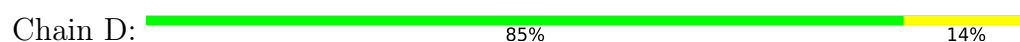
• Molecule 27: 5S Ribosomal RNA



• Molecule 28: 50S ribosomal protein L2



• Molecule 29: 50S ribosomal protein L3



• Molecule 30: Large ribosomal subunit protein uL4

Chain E:  90% 7% .



- Molecule 31: Large ribosomal subunit protein uL5

Chain F:  75% 22% .



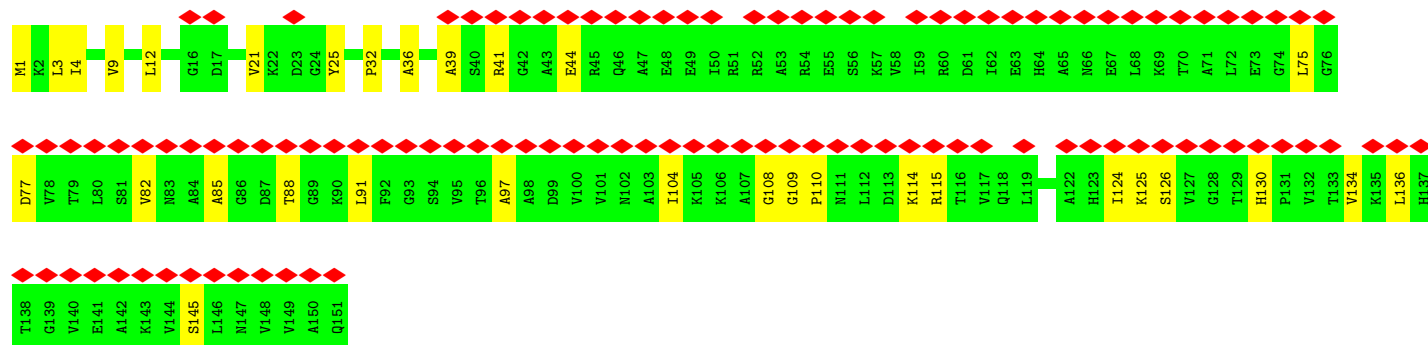
- Molecule 32: 50S ribosomal protein L6

Chain G:  88% 10% .



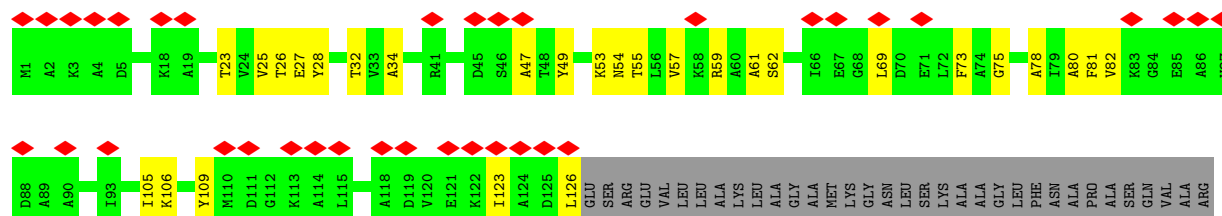
- Molecule 33: 50S ribosomal protein L9

Chain H:  73% 79% 21%



- Molecule 34: 50S ribosomal protein L10

Chain I:  21% 56% 16% 28%



LEU
ALA
ALA
ALA
LEU
GLN
GLU
LYS
LYS
ALA
GLY
GLU
ALA
ALA

- Molecule 35: 50S ribosomal protein L11

Chain J:  78% 15% 6%

MET
ALA
PRO
LYS
LYS
VAL
ALA
GLY
L10
Q14
P22
A23
V26
G27
N36
E39
E49
R52
P67
T74
P75
P76
A77
L81
L82
S91
H95
K96
W104
R108
E109
I110
K114
M137
E142

- Molecule 36: Large ribosomal subunit protein uL13

Chain L:  91% 8%

MET
P2
T34
R37
G38
K39
P42
D49
H96
P97
E102
I106
P110
L114
K121
Q147

- Molecule 37: 50S ribosomal protein L14

Chain M:  92% 8%

H1
T2
Q3
R7
L20
Y32
K44
H51
E68
Y76
P93
I114
L122

- Molecule 38: 50S ribosomal protein L15

Chain N:  84% 15%

MET
SER
V3
L6
E15
V22
K29
G30
K31
T37
K44
N45
M49
G53
H58
M59
K63
K68
G81
N84
R105
G116
K117
L118
G131
E135
L147

- Molecule 39: Large ribosomal subunit protein uL16

Chain O:  80% 19%

H1
S22
G30
A36
Y41
I42
T43
N44
R45
K59
R60
W65
P70
L74
T75
P90
E91
W92
W93
V94
V97
R101
V102
L103
F104
E105
Y108
P109
K124
T133
R134
E135
GLN

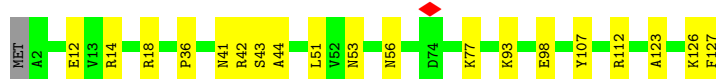
- Molecule 40: 50S ribosomal protein L17

Chain P:  51% 8% 41%

MET
P2
G7
P8
R9
L10
G11
H16
T37
E38
P39
R42
R45
P46
R63
M67
I70
V76
D106
K119
THR
VAL
THR
ASP
GLU
GLU
SER
ASN
ARG
ALA
ARG
ALA
ALA
SER
GLU
ALA
SER
LYS
ASP
ASP
GLU
ARG
ALA
ALA
ASP
GLU
LYS
ALA
ASP
GLU

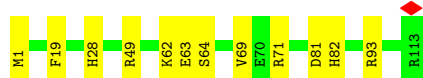
- Molecule 41: Large ribosomal subunit protein uL18

Chain Q:  84% 15%



- Molecule 42: 50S ribosomal protein L19

Chain R:  89% 11%



- Molecule 43: Large ribosomal subunit protein bL20

Chain S:  84% 12%



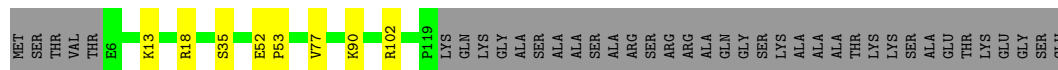
- Molecule 44: Large ribosomal subunit protein bL21

Chain T:  93%



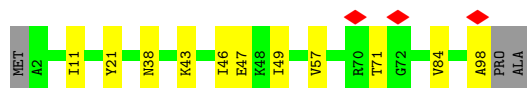
- Molecule 45: Large ribosomal subunit protein uL22

Chain U:  69% 5% 25%



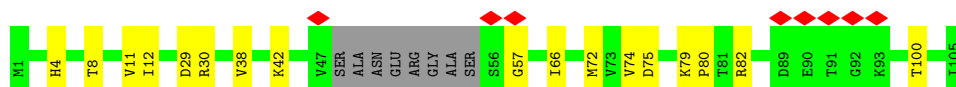
- Molecule 46: Large ribosomal subunit protein uL23

Chain V:  86% 11%

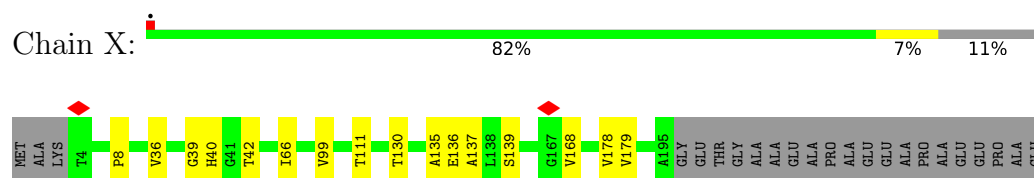


- Molecule 47: 50S ribosomal protein L24

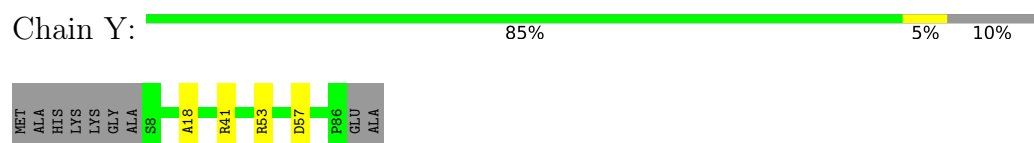
Chain W:  8% 76% 16% 8%



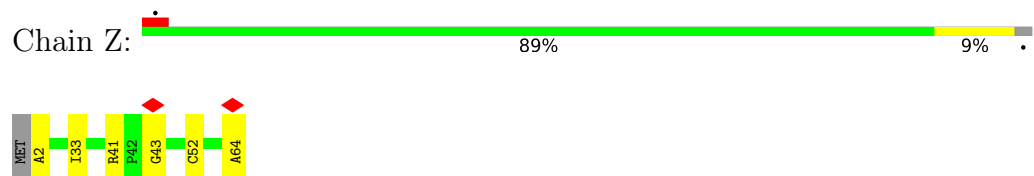
- Molecule 48: 50S ribosomal protein L25



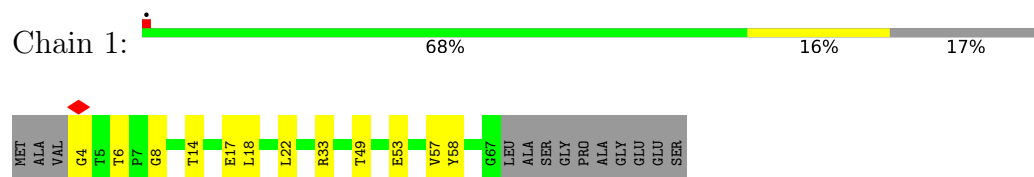
- Molecule 49: 50S ribosomal protein L27



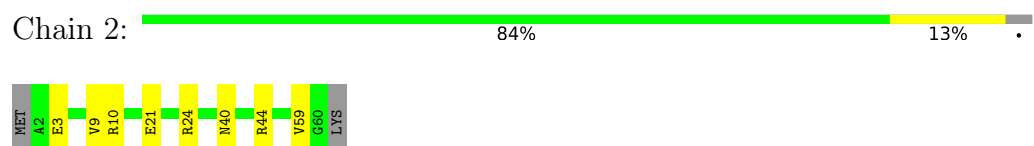
- Molecule 50: Large ribosomal subunit protein bL28



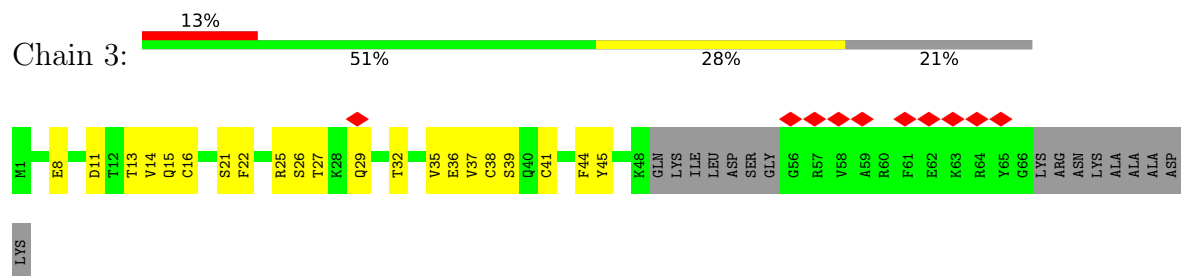
- Molecule 51: 50S ribosomal protein L29



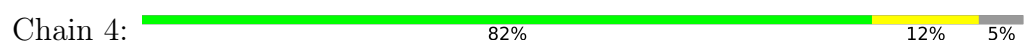
- Molecule 52: 50S ribosomal protein L30



- Molecule 53: Large ribosomal subunit protein bL31

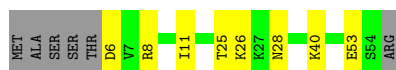


- Molecule 54: 50S ribosomal protein L32

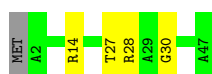
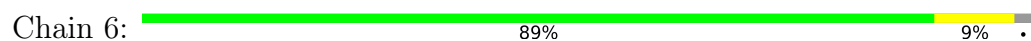




- Molecule 55: Large ribosomal subunit protein bL33A



- Molecule 56: 50S ribosomal protein L34



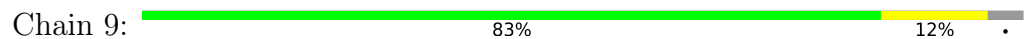
- Molecule 57: 50S ribosomal protein L35



- Molecule 58: 50S ribosomal protein L36



- Molecule 59: 50S Ribosomal Protein L27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	101909	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.12	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	31.354	Depositor
Minimum map value	-19.105	Depositor
Average map value	0.002	Depositor
Map value standard deviation	1.016	Depositor
Recommended contour level	2.8	Depositor
Map size ($\text{\AA}$)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, ZN, 5MU, 7MG, PSU, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.19	0/36309	0.28	0/56657
2	b	0.12	0/1822	0.33	0/2457
3	c	0.14	0/1684	0.35	0/2261
4	d	0.17	0/1672	0.44	1/2251 (0.0%)
5	e	0.18	0/1312	0.35	0/1772
6	f	0.17	0/782	0.34	0/1059
7	g	0.12	0/1252	0.33	0/1690
8	h	0.20	0/1025	0.32	0/1385
9	i	0.12	0/1012	0.32	0/1362
10	j	0.13	0/802	0.34	0/1086
11	k	0.19	0/873	0.39	0/1180
12	l	0.19	0/969	0.34	0/1294
13	m	0.16	0/942	0.40	0/1260
14	n	0.12	0/488	0.31	0/650
15	o	0.20	0/729	0.30	0/977
16	p	0.18	0/908	0.43	0/1226
17	q	0.17	0/759	0.31	0/1016
18	r	0.16	0/518	0.24	0/693
19	s	0.11	0/680	0.28	0/915
20	t	0.22	0/663	0.40	0/882
21	u	0.21	0/280	0.36	0/359
22	v	0.15	0/87	0.18	0/132
23	x	0.29	0/3049	0.37	0/4140
24	y	0.32	0/1628	0.54	4/2536 (0.2%)
25	z	0.20	0/2955	0.32	0/4003
26	A	0.29	0/73900	0.32	0/115307
27	B	0.23	0/2821	0.30	0/4396
28	C	0.30	0/2153	0.35	0/2895
29	D	0.28	0/1609	0.42	0/2165
30	E	0.27	0/1592	0.37	0/2153
31	F	0.17	0/1461	0.29	0/1966
32	G	0.22	0/1369	0.36	2/1848 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	0.12	0/1027	0.30	0/1398
34	I	0.12	0/925	0.27	0/1246
35	J	0.19	0/1006	0.35	0/1364
36	L	0.27	0/1157	0.34	0/1567
37	M	0.27	0/946	0.34	0/1268
38	N	0.29	0/1091	0.45	0/1457
39	O	0.26	0/1118	0.34	0/1506
40	P	0.29	0/945	0.34	0/1267
41	Q	0.20	0/966	0.28	0/1298
42	R	0.26	0/921	0.41	0/1236
43	S	0.31	0/1000	0.30	0/1341
44	T	0.27	0/764	0.29	0/1030
45	U	0.26	0/887	0.33	0/1204
46	V	0.26	0/766	0.29	0/1030
47	W	0.22	0/738	0.34	0/987
48	X	0.20	0/1443	0.30	0/1970
49	Y	0.26	0/595	0.33	0/798
50	Z	0.28	0/478	0.37	0/641
51	1	0.25	0/534	0.29	0/713
52	2	0.29	0/477	0.27	0/640
53	3	0.13	0/420	0.32	0/569
54	4	0.30	0/427	0.33	0/572
55	5	0.23	0/413	0.32	0/553
56	6	0.32	0/380	0.36	0/500
57	7	0.28	0/507	0.36	0/672
58	8	0.27	0/303	0.34	0/401
59	9	0.31	0/191	0.30	0/247
All	All	0.25	0/168530	0.32	7/251448 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	y	43	C	C1'-C2'-O2'	-11.30	91.45	108.40
24	y	53	G	C4'-C3'-C2'	-6.32	96.28	102.60
24	y	52	G	C2'-C3'-O3'	-5.98	104.74	113.70
24	y	52	G	C1'-C2'-O2'	5.80	117.09	108.40
4	d	33	PRO	CA-N-CD	-5.47	104.34	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32439	0	16321	476	0
2	b	1793	0	1839	38	0
3	c	1660	0	1707	44	0
4	d	1641	0	1668	47	0
5	e	1296	0	1360	21	0
6	f	771	0	797	15	0
7	g	1232	0	1282	30	0
8	h	1010	0	1046	14	0
9	i	994	0	1050	42	0
10	j	788	0	819	24	0
11	k	855	0	863	17	0
12	l	958	0	1045	14	0
13	m	935	0	986	47	0
14	n	477	0	503	22	0
15	o	720	0	760	8	0
16	p	891	0	935	28	0
17	q	748	0	795	17	0
18	r	513	0	540	5	0
19	s	662	0	677	34	0
20	t	660	0	712	17	0
21	u	280	0	342	4	0
22	v	80	0	41	1	0
23	x	2997	0	2987	73	0
24	y	1581	0	808	33	0
25	z	2909	0	2895	36	0
26	A	65997	0	33205	447	0
27	B	2522	0	1285	15	0
28	C	2110	0	2165	20	0
29	D	1587	0	1630	23	0
30	E	1569	0	1607	13	0
31	F	1439	0	1465	31	0
32	G	1348	0	1399	11	0
33	H	1018	0	988	20	0
34	I	918	0	959	16	0
35	J	990	0	1021	16	0
36	L	1130	0	1167	7	0
37	M	938	0	1000	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1078	0	1151	20	0
39	O	1092	0	1128	15	0
40	P	928	0	972	10	0
41	Q	956	0	991	13	0
42	R	907	0	938	9	0
43	S	988	0	1038	13	0
44	T	754	0	802	2	0
45	U	873	0	909	6	0
46	V	756	0	802	9	0
47	W	732	0	782	15	0
48	X	1428	0	1443	10	0
49	Y	586	0	601	3	0
50	Z	470	0	480	6	0
51	1	531	0	541	9	0
52	2	474	0	500	4	0
53	3	413	0	367	13	0
54	4	423	0	463	9	0
55	5	405	0	407	6	0
56	6	377	0	411	3	0
57	7	502	0	541	12	0
58	8	299	0	324	5	0
59	9	189	0	205	3	0
60	x	28	0	12	0	0
61	5	1	0	0	0	0
61	Z	1	0	0	0	0
All	All	155647	0	106477	1701	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 1701 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)
26:A:273:A:H62	26:A:313:G:N2	1.49	1.09
26:A:273:A:N6	26:A:313:G:H21	1.55	1.04
26:A:283:U:H3	26:A:303:G:H1	1.04	0.95
26:A:1540:U:H3	26:A:1632:G:H1	1.07	0.95
26:A:1547:G:H1	26:A:1623:U:H3	0.93	0.92

There are no symmetry-related clashes.

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	
2	b	226/277 (82%)	213 (94%)	11 (5%)	2 (1%)	14	48
3	c	206/275 (75%)	190 (92%)	16 (8%)	0	100	100
4	d	198/201 (98%)	187 (94%)	11 (6%)	0	100	100
5	e	178/214 (83%)	171 (96%)	7 (4%)	0	100	100
6	f	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
7	g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
8	h	129/132 (98%)	125 (97%)	4 (3%)	0	100	100
9	i	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
10	j	97/101 (96%)	89 (92%)	7 (7%)	1 (1%)	12	45
11	k	113/138 (82%)	105 (93%)	8 (7%)	0	100	100
12	l	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
13	m	114/124 (92%)	105 (92%)	9 (8%)	0	100	100
14	n	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	111/156 (71%)	103 (93%)	8 (7%)	0	100	100
17	q	92/98 (94%)	88 (96%)	4 (4%)	0	100	100
18	r	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
19	s	80/93 (86%)	76 (95%)	4 (5%)	0	100	100
20	t	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
21	u	30/33 (91%)	29 (97%)	1 (3%)	0	100	100
23	x	385/396 (97%)	361 (94%)	23 (6%)	1 (0%)	36	70
25	z	373/375 (100%)	363 (97%)	10 (3%)	0	100	100
28	C	273/278 (98%)	261 (96%)	12 (4%)	0	100	100
29	D	212/217 (98%)	201 (95%)	11 (5%)	0	100	100
30	E	207/215 (96%)	199 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	F	180/187 (96%)	172 (96%)	8 (4%)	0	100	100
32	G	174/179 (97%)	168 (97%)	6 (3%)	0	100	100
33	H	149/151 (99%)	143 (96%)	6 (4%)	0	100	100
34	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
35	J	131/142 (92%)	125 (95%)	6 (5%)	0	100	100
36	L	144/147 (98%)	136 (94%)	8 (6%)	0	100	100
37	M	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
38	N	143/147 (97%)	129 (90%)	14 (10%)	0	100	100
39	O	134/137 (98%)	126 (94%)	7 (5%)	1 (1%)	18	53
40	P	116/199 (58%)	112 (97%)	4 (3%)	0	100	100
41	Q	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
42	R	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
43	S	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
44	T	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
45	U	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
46	V	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
47	W	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
48	X	190/215 (88%)	183 (96%)	7 (4%)	0	100	100
49	Y	77/88 (88%)	75 (97%)	2 (3%)	0	100	100
50	Z	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
51	1	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
52	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
53	3	55/75 (73%)	53 (96%)	2 (4%)	0	100	100
54	4	52/57 (91%)	52 (100%)	0	0	100	100
55	5	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
56	6	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
57	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
58	8	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
59	9	21/24 (88%)	21 (100%)	0	0	100	100
All	All	6737/7449 (90%)	6423 (95%)	309 (5%)	5 (0%)	49	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	j	57	LYS
39	O	59	LYS
2	b	155	GLN
23	x	336	ARG
2	b	157	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	191/218 (88%)	191 (100%)	0	100	100
3	c	170/212 (80%)	170 (100%)	0	100	100
4	d	175/176 (99%)	175 (100%)	0	100	100
5	e	127/147 (86%)	127 (100%)	0	100	100
6	f	85/85 (100%)	85 (100%)	0	100	100
7	g	131/132 (99%)	131 (100%)	0	100	100
8	h	107/108 (99%)	107 (100%)	0	100	100
9	i	102/125 (82%)	102 (100%)	0	100	100
10	j	89/90 (99%)	89 (100%)	0	100	100
11	k	89/105 (85%)	89 (100%)	0	100	100
12	l	103/105 (98%)	103 (100%)	0	100	100
13	m	99/104 (95%)	99 (100%)	0	100	100
14	n	49/50 (98%)	49 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	92/118 (78%)	92 (100%)	0	100	100
17	q	80/83 (96%)	80 (100%)	0	100	100
18	r	55/72 (76%)	55 (100%)	0	100	100
19	s	73/84 (87%)	73 (100%)	0	100	100
20	t	69/70 (99%)	69 (100%)	0	100	100
21	u	30/31 (97%)	30 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	x	327/335 (98%)	327 (100%)	0	100	100
25	z	297/297 (100%)	297 (100%)	0	100	100
28	C	215/218 (99%)	215 (100%)	0	100	100
29	D	160/163 (98%)	160 (100%)	0	100	100
30	E	169/173 (98%)	169 (100%)	0	100	100
31	F	150/156 (96%)	150 (100%)	0	100	100
32	G	148/150 (99%)	148 (100%)	0	100	100
33	H	90/116 (78%)	90 (100%)	0	100	100
34	I	89/120 (74%)	89 (100%)	0	100	100
35	J	102/108 (94%)	102 (100%)	0	100	100
36	L	119/120 (99%)	119 (100%)	0	100	100
37	M	100/100 (100%)	100 (100%)	0	100	100
38	N	112/114 (98%)	112 (100%)	0	100	100
39	O	114/115 (99%)	114 (100%)	0	100	100
40	P	97/158 (61%)	97 (100%)	0	100	100
41	Q	93/94 (99%)	93 (100%)	0	100	100
42	R	100/100 (100%)	100 (100%)	0	100	100
43	S	97/99 (98%)	97 (100%)	0	100	100
44	T	81/83 (98%)	81 (100%)	0	100	100
45	U	90/117 (77%)	90 (100%)	0	100	100
46	V	83/85 (98%)	83 (100%)	0	100	100
47	W	81/86 (94%)	81 (100%)	0	100	100
48	X	155/168 (92%)	155 (100%)	0	100	100
49	Y	58/63 (92%)	58 (100%)	0	100	100
50	Z	50/51 (98%)	50 (100%)	0	100	100
51	1	58/66 (88%)	58 (100%)	0	100	100
52	2	52/54 (96%)	52 (100%)	0	100	100
53	3	42/63 (67%)	42 (100%)	0	100	100
54	4	43/46 (94%)	43 (100%)	0	100	100
55	5	47/52 (90%)	47 (100%)	0	100	100
56	6	35/36 (97%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	7	53/54 (98%)	53 (100%)	0	100	100
58	8	35/35 (100%)	35 (100%)	0	100	100
59	9	18/19 (95%)	18 (100%)	0	100	100
All	All	5552/6006 (92%)	5552 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
29	D	178	GLN
39	O	17	GLN
31	F	13	GLN
32	G	23	ASN
41	Q	8	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1510/1528 (98%)	270 (17%)	0
22	v	3/4 (75%)	0	0
24	y	72/76 (94%)	18 (25%)	0
26	A	3071/3164 (97%)	491 (15%)	13 (0%)
27	B	117/118 (99%)	15 (12%)	1 (0%)
All	All	4773/4890 (97%)	794 (16%)	14 (0%)

5 of 794 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	U
1	a	13	G
1	a	26	G
1	a	36	A
1	a	43	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	A	981	U

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Mol	Chain	Res	Type
26	A	986	G
27	B	10	G
26	A	2094	G
26	A	2381	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
24	4SU	y	8	24	18,21,22	1.83	4 (22%)	25,30,33	2.30	5 (20%)
24	7MG	y	46	24	23,26,27	1.78	4 (17%)	27,39,42	3.30	9 (33%)
24	PSU	y	39	24	18,21,22	1.41	3 (16%)	21,30,33	1.93	3 (14%)
24	5MU	y	54	24	19,22,23	1.98	3 (15%)	27,32,35	4.09	13 (48%)
24	PSU	y	55	24	18,21,22	2.56	8 (44%)	21,30,33	3.67	12 (57%)
24	PSU	y	32	24	18,21,22	1.37	2 (11%)	21,30,33	2.03	4 (19%)

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
24	4SU	y	8	24	-	0/7/25/26	0/2/2/2
24	7MG	y	46	24	-	2/7/37/38	0/3/3/3
24	PSU	y	39	24	-	2/7/25/26	0/2/2/2
24	5MU	y	54	24	-	2/7/25/26	0/2/2/2
24	PSU	y	55	24	-	2/7/25/26	0/2/2/2
24	PSU	y	32	24	-	0/7/25/26	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	y	55	PSU	C4-N3	-5.22	1.29	1.38
24	y	46	7MG	C6-N1	-5.05	1.29	1.38
24	y	54	5MU	C2-N3	-4.99	1.29	1.38
24	y	8	4SU	C4-S4	-4.99	1.59	1.68
24	y	54	5MU	C4-N3	-4.78	1.29	1.38

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	y	54	5MU	O4-C4-C5	-9.73	113.78	124.92
24	y	54	5MU	C5-C4-N3	9.70	123.75	115.32
24	y	46	7MG	N9-C4-N3	9.47	139.33	125.46
24	y	55	PSU	O2'-C2'-C1'	-9.07	89.68	111.21
24	y	54	5MU	C4-N3-C2	-8.63	116.03	127.34

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	y	55	PSU	C3'-C4'-C5'-O5'
24	y	55	PSU	O4'-C4'-C5'-O5'
24	y	39	PSU	C3'-C4'-C5'-O5'
24	y	39	PSU	O4'-C4'-C5'-O5'
24	y	46	7MG	C2'-C1'-N9-C8

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	y	8	4SU	1	0
24	y	46	7MG	2	0
24	y	54	5MU	2	0
24	y	32	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 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	$\# Z > 2$
60	GDP	x	401	-	29,30,30	1.16	3 (10%)	45,47,47	1.82	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
60	GDP	x	401	-	-	0/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	x	401	GDP	C5-C4	3.03	1.47	1.38
60	x	401	GDP	C6-N1	-2.54	1.34	1.38
60	x	401	GDP	C5-N7	-2.30	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	x	401	GDP	C5-C4-N3	-6.12	118.65	128.39
60	x	401	GDP	C2-N3-C4	5.00	120.91	112.30
60	x	401	GDP	N9-C4-N3	4.47	134.89	125.95
60	x	401	GDP	C6-C5-N7	3.23	136.16	130.29
60	x	401	GDP	C4-C5-N7	-2.62	106.52	110.67

There are no chirality outliers.

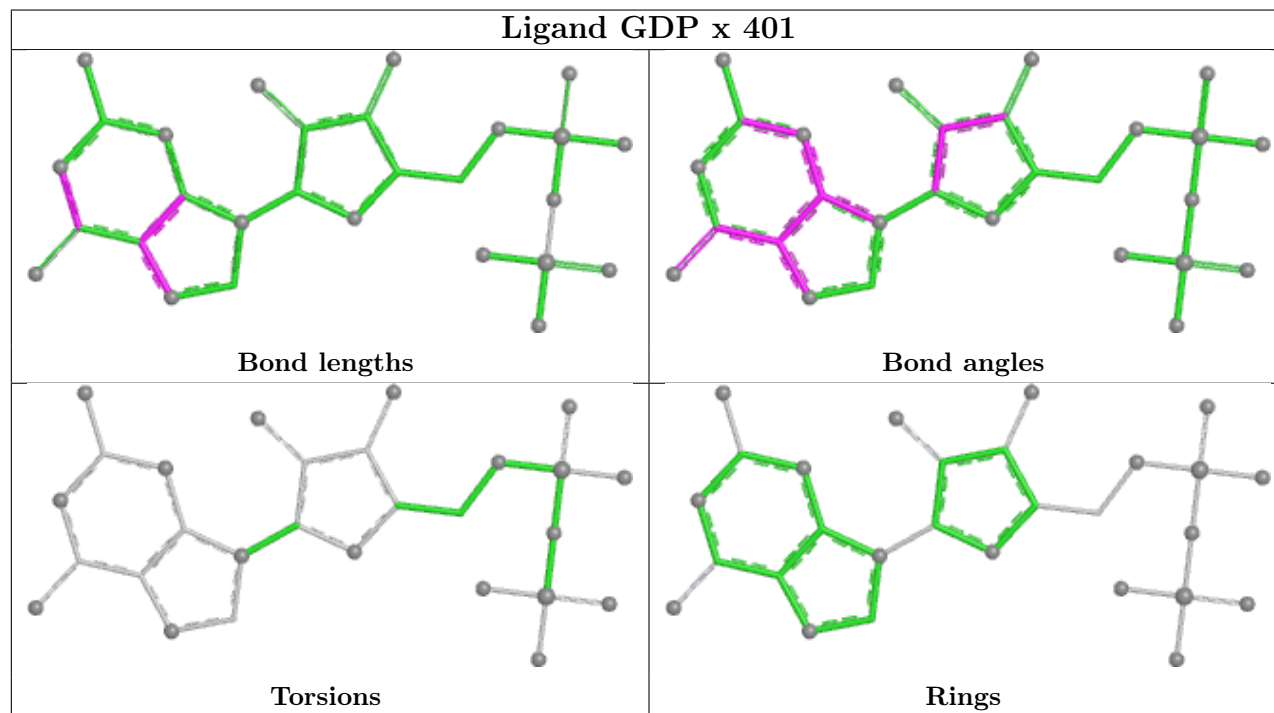
There are no torsion outliers.

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.

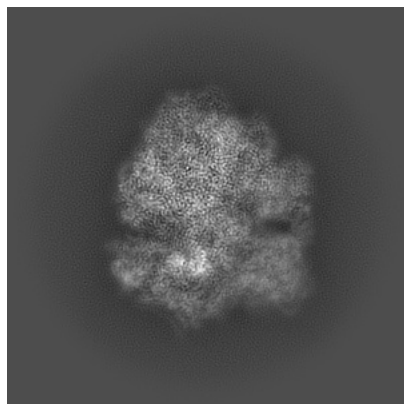
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43076. These allow visual inspection of the internal detail of the map and identification of artifacts.

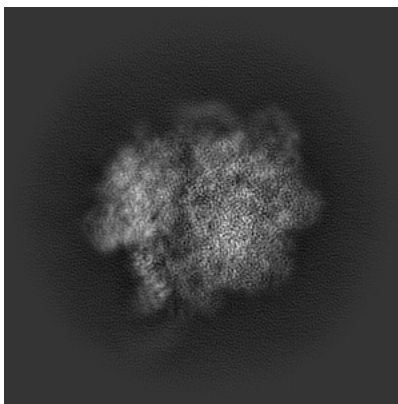
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

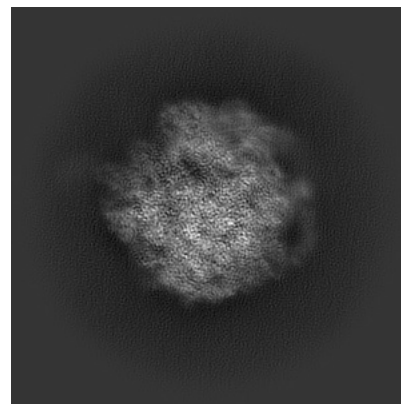
6.1.1 Primary map



X

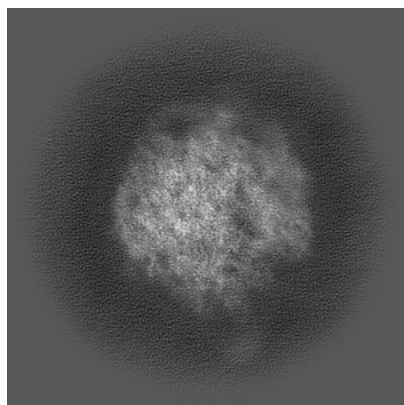


Y

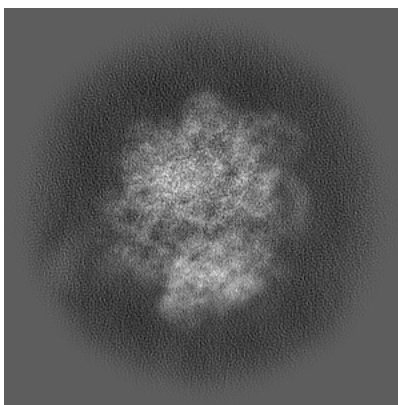


Z

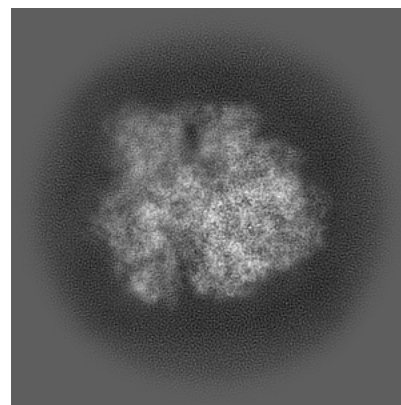
6.1.2 Raw map



X



Y

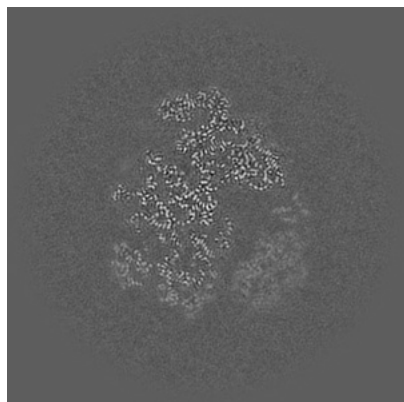


Z

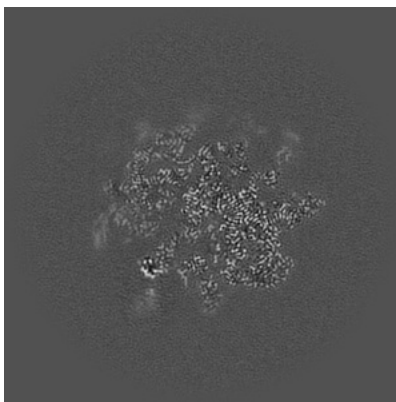
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

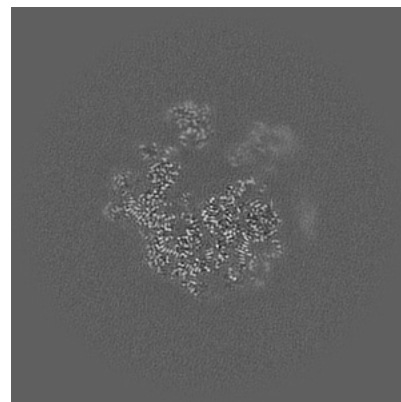
6.2.1 Primary map



X Index: 256

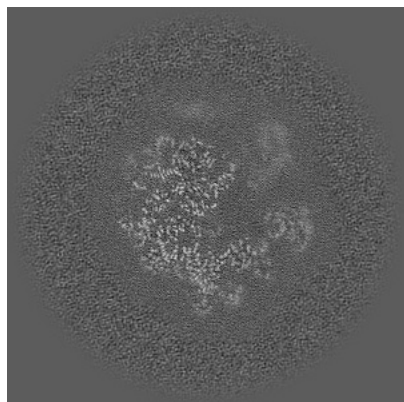


Y Index: 256

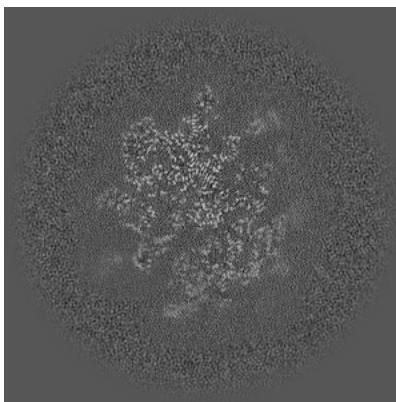


Z Index: 256

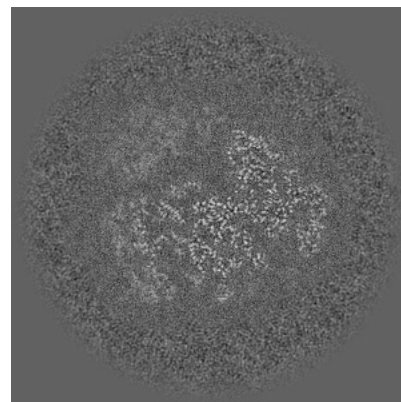
6.2.2 Raw map



X Index: 256



Y Index: 256

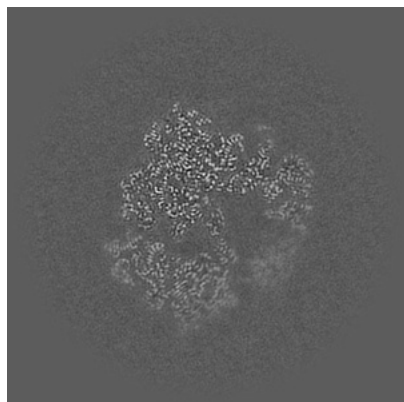


Z Index: 256

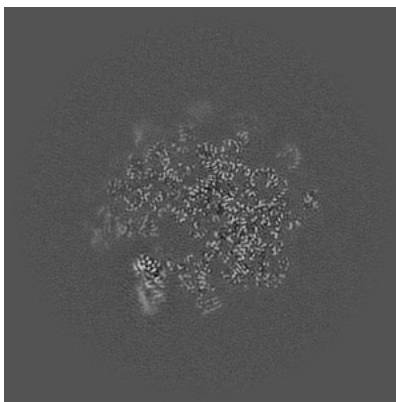
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

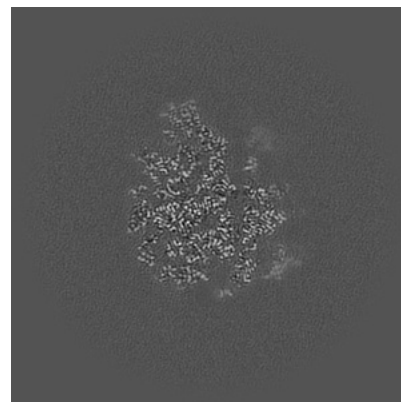
6.3.1 Primary map



X Index: 229

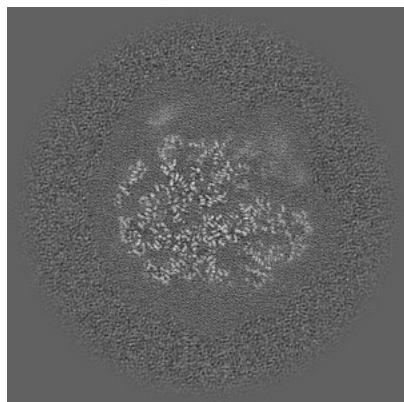


Y Index: 248

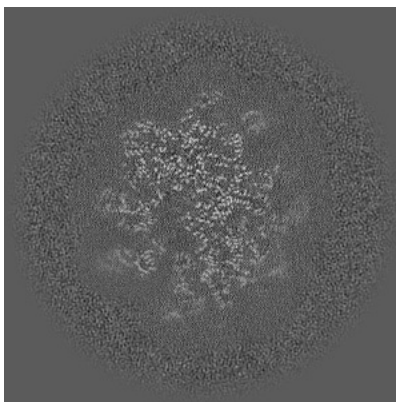


Z Index: 298

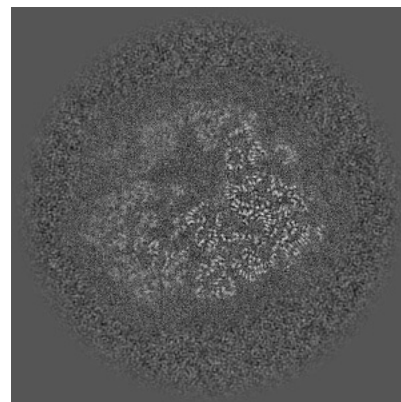
6.3.2 Raw map



X Index: 284



Y Index: 250

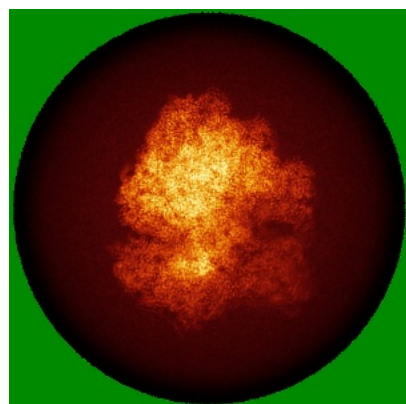


Z Index: 240

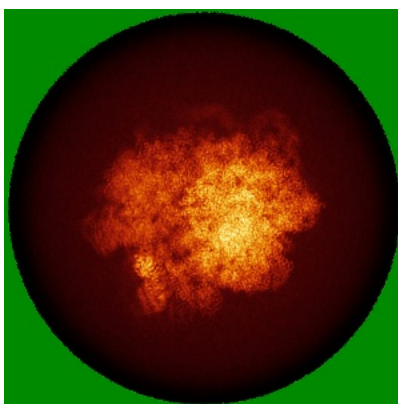
The images above show the largest variance slices of the map in three orthogonal directions.

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

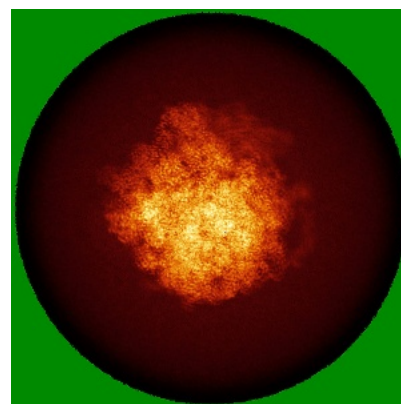
6.4.1 Primary map



X

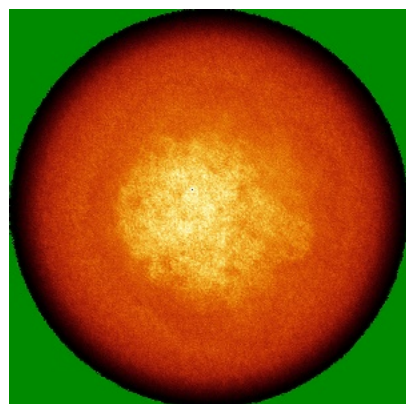


Y

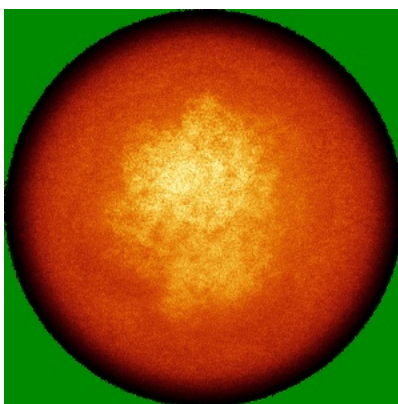


Z

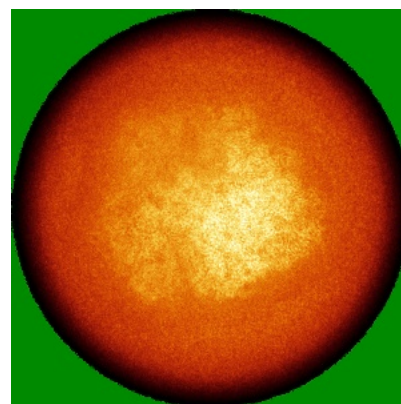
6.4.2 Raw map



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.

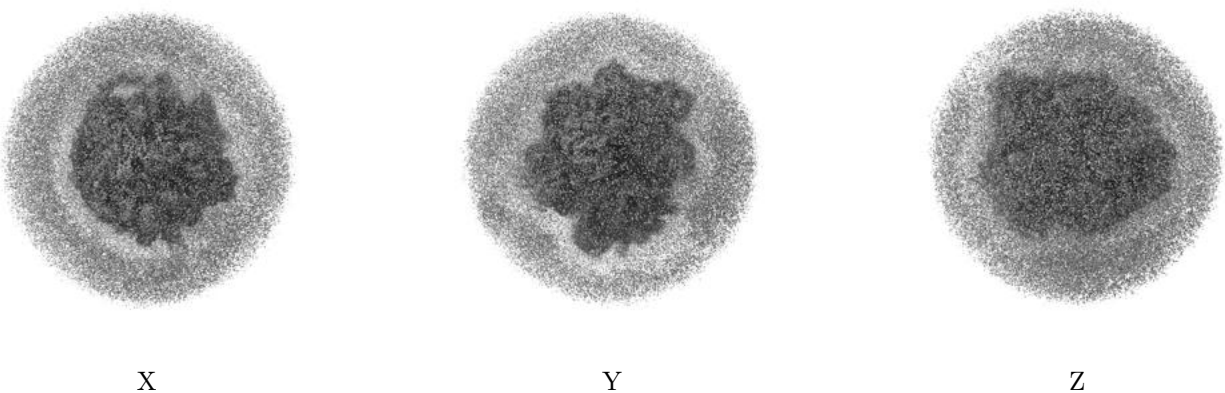
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.8. 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.

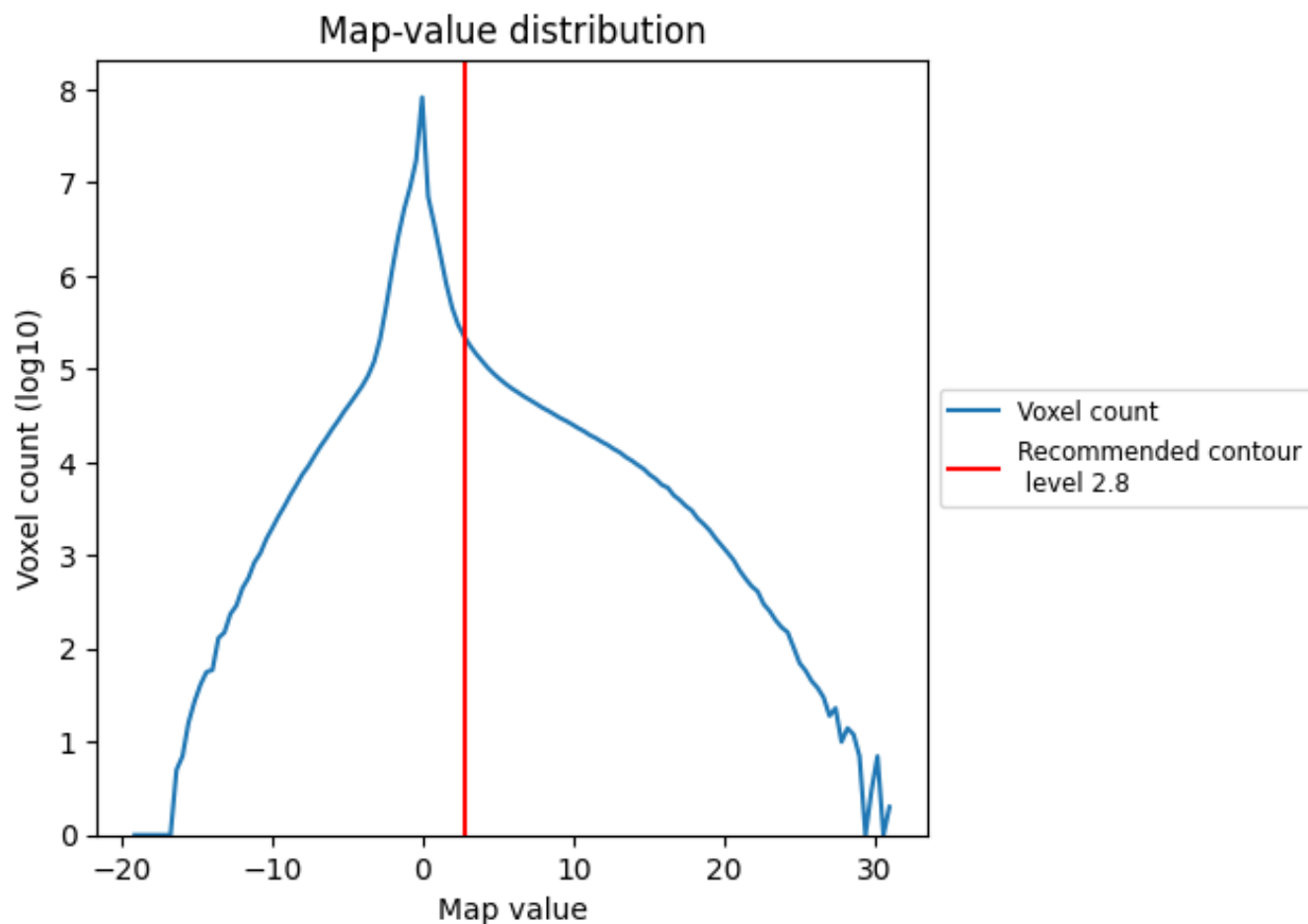
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

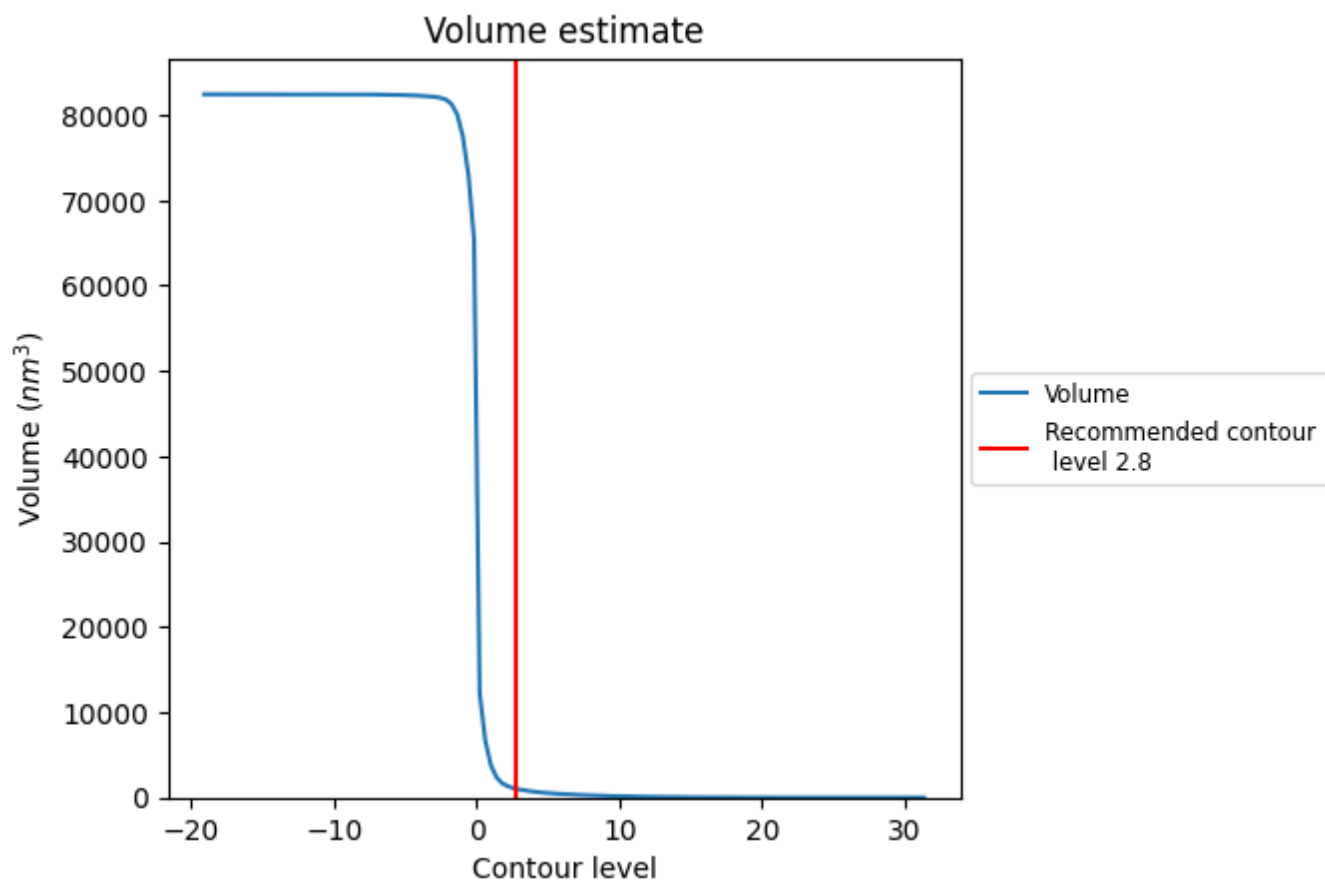
This section contains the results of statistical analysis of the map.

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.

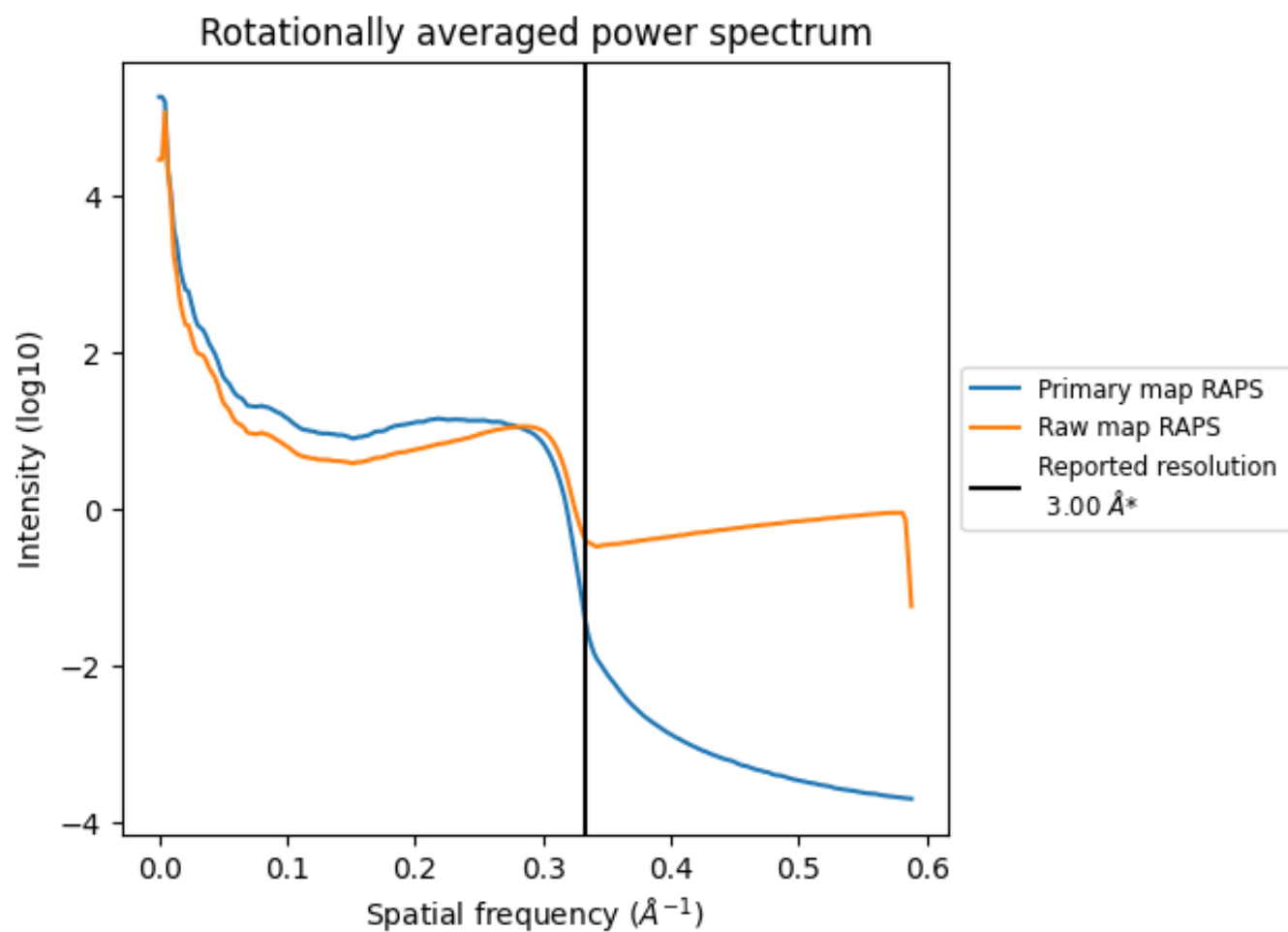
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1022 nm^3 ; this corresponds to an approximate mass of 923 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 ⓘ

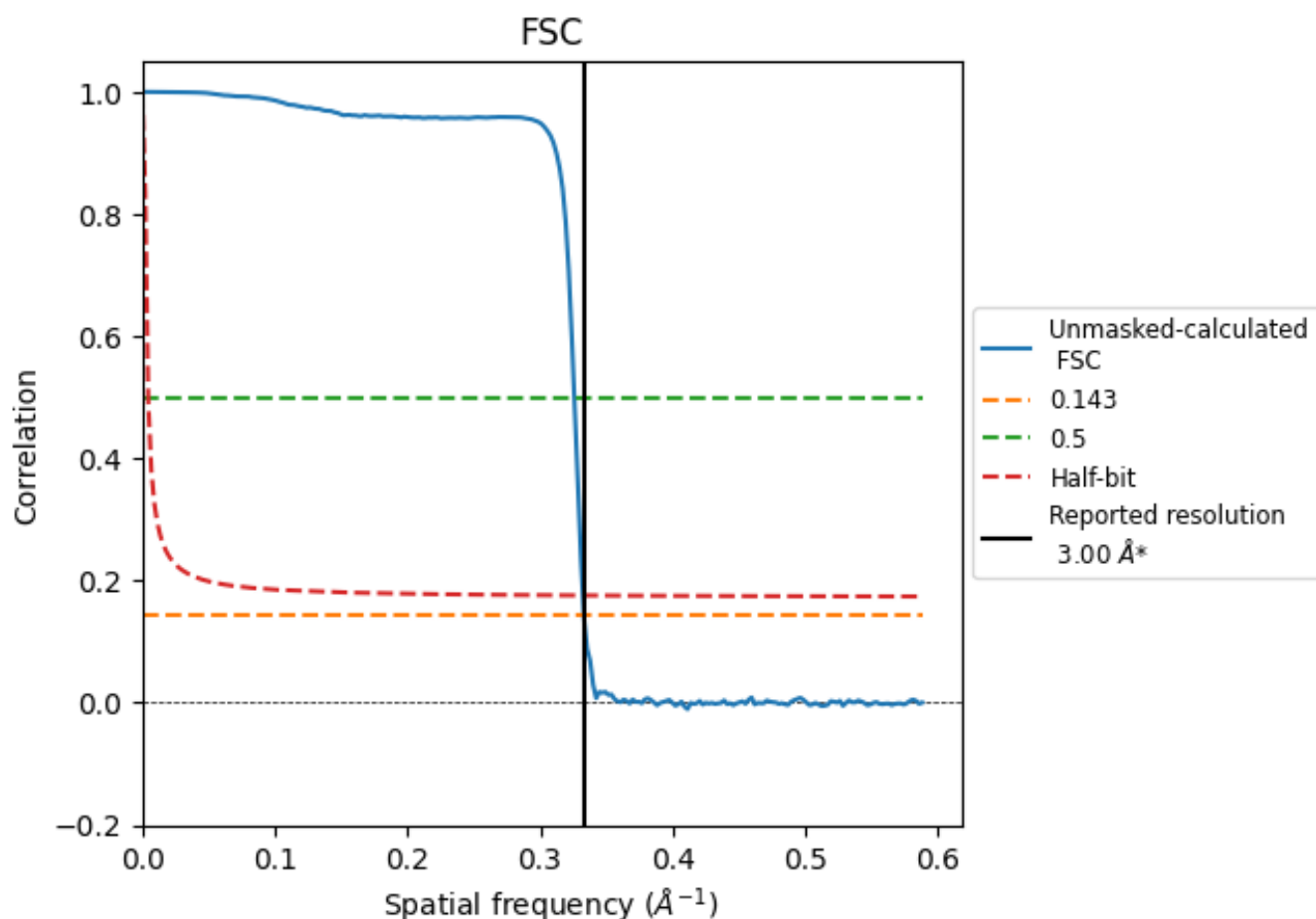


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 $0.333 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.07	3.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

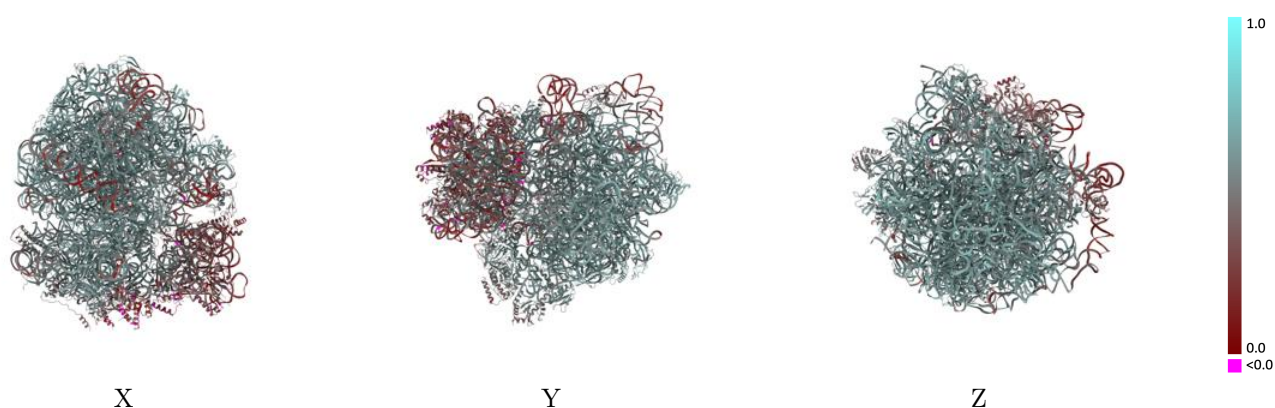
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43076 and PDB model 8V9L. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

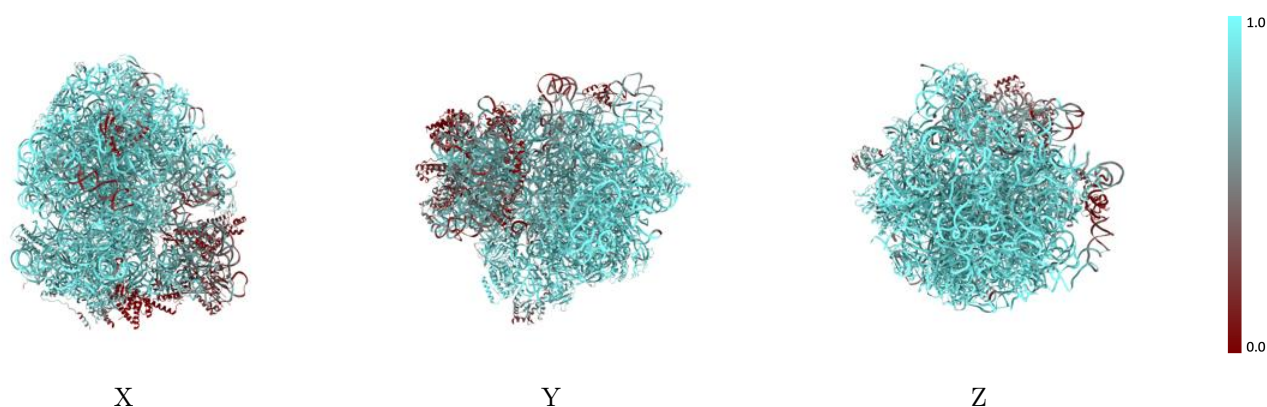
This section was not generated.

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



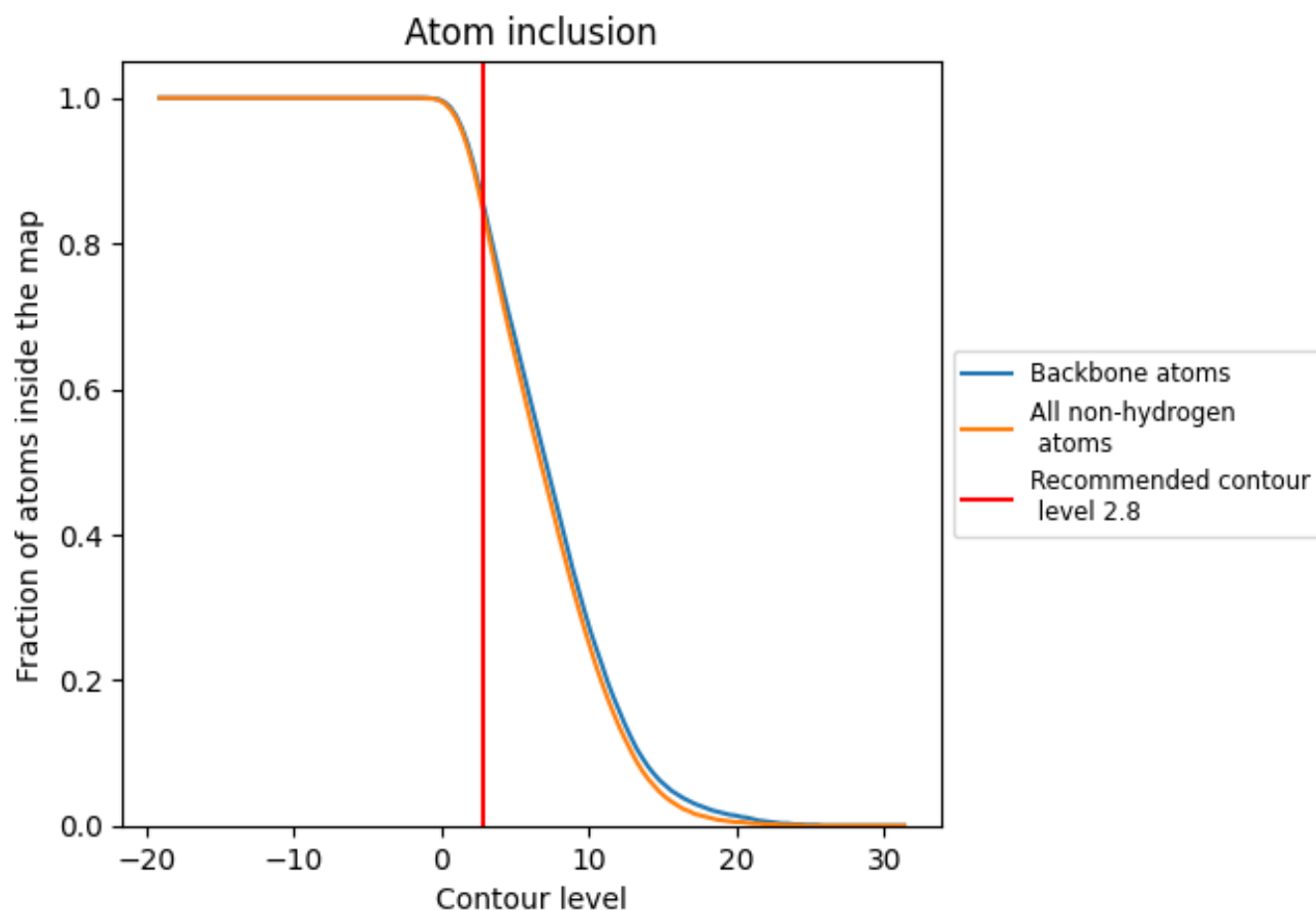
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 85% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8470	 0.5270
1	 0.8880	 0.5950
2	 0.9410	 0.6130
3	 0.6750	 0.4400
4	 0.9180	 0.5980
5	 0.9370	 0.5980
6	 0.9600	 0.6190
7	 0.9420	 0.6110
8	 0.9510	 0.6060
9	 0.9330	 0.6180
A	 0.9280	 0.5630
B	 0.9490	 0.5710
C	 0.9400	 0.6110
D	 0.9370	 0.6060
E	 0.9160	 0.6000
F	 0.7650	 0.5110
G	 0.8770	 0.5690
H	 0.2650	 0.4330
I	 0.5400	 0.4540
J	 0.8560	 0.5300
L	 0.9370	 0.6080
M	 0.9100	 0.6050
N	 0.9300	 0.6010
O	 0.9360	 0.6050
P	 0.9480	 0.6060
Q	 0.8940	 0.5830
R	 0.8910	 0.5920
S	 0.9440	 0.6160
T	 0.9380	 0.6140
U	 0.9510	 0.6130
V	 0.8880	 0.5850
W	 0.8310	 0.5670
X	 0.8240	 0.5670
Y	 0.9330	 0.6070
Z	 0.9140	 0.6000



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Chain	Atom inclusion	Q-score
a	 0.8330	 0.4780
b	 0.0030	 0.2310
c	 0.4120	 0.3470
d	 0.6030	 0.4070
e	 0.8090	 0.5330
f	 0.8020	 0.5320
g	 0.1920	 0.2900
h	 0.8560	 0.5660
i	 0.3860	 0.3370
j	 0.3220	 0.3090
k	 0.8200	 0.5530
l	 0.7850	 0.5550
m	 0.2240	 0.2750
n	 0.5240	 0.3560
o	 0.8640	 0.5680
p	 0.7170	 0.4700
q	 0.7600	 0.5160
r	 0.8080	 0.5370
s	 0.2860	 0.2750
t	 0.8220	 0.5070
u	 0.8130	 0.5680
v	 0.7130	 0.5120
x	 0.9690	 0.4720
y	 0.6270	 0.4560
z	 0.8120	 0.5480