



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 11:36 am BST

PDB ID : 5IQR / pdb_00005iqr
EMDB ID : EMD-8107
Title : Structure of RelA bound to the 70S ribosome
Authors : Brown, A.; Fernandez, I.S.; Gordiyenko, Y.; Ramakrishnan, V.
Deposited on : 2016-03-11
Resolution : 3.00 Å(reported)
Based on initial model : 4YBB

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:

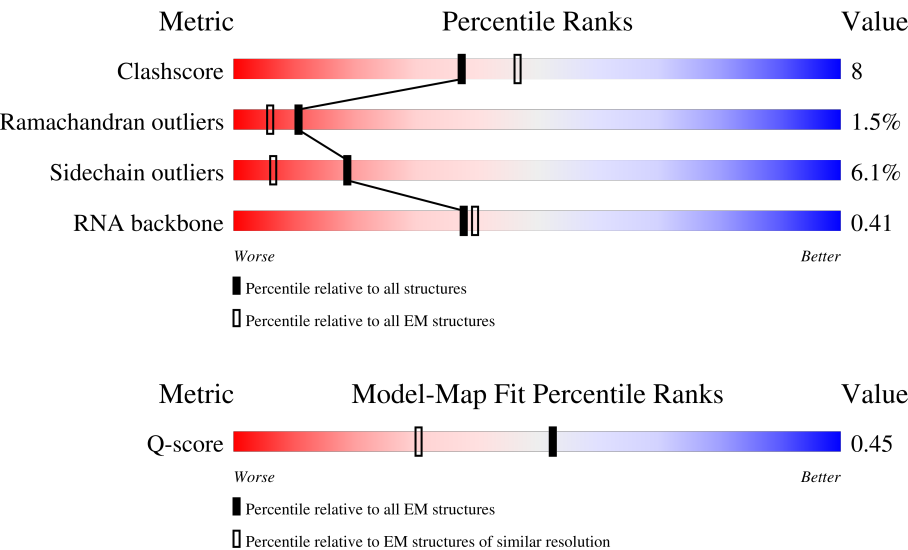
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 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.



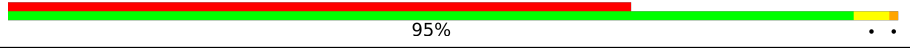
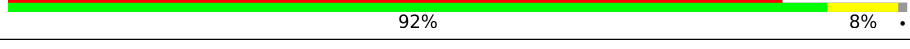
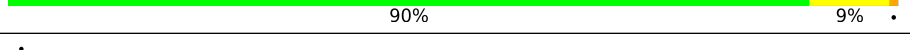
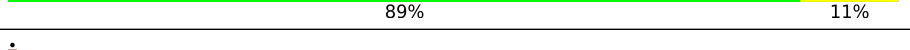
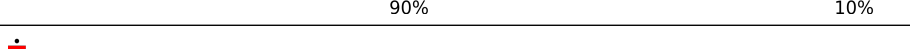
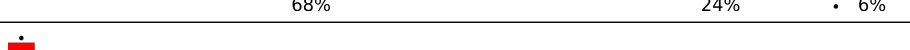
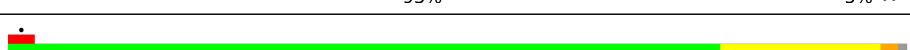
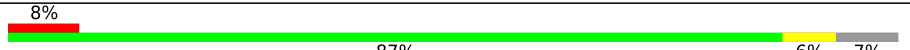
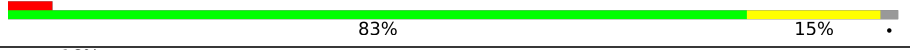
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	B	273	85% 13% ..
2	C	209	86% 13%
3	D	201	9% 87% 12%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	E	179	
5	F	177	
6	G	149	
7	H	165	
8	I	142	
9	J	142	
10	K	123	
11	L	144	
12	M	136	
13	N	127	
14	O	117	
15	P	115	
16	Q	118	
17	R	103	
18	S	110	
19	T	100	
20	U	104	
21	V	94	
22	W	85	
23	X	78	
24	Y	63	
25	Z	59	
26	a	70	
27	b	57	
28	c	55	

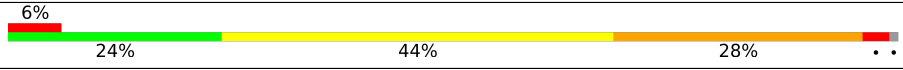
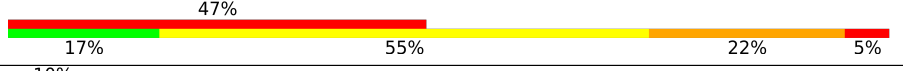
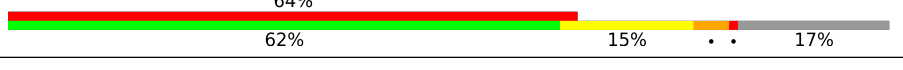
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	46	
30	e	65	
31	f	38	
32	g	241	
33	h	233	
34	i	206	
35	j	167	
36	k	135	
37	l	179	
38	m	130	
39	n	130	
40	o	103	
41	p	129	
42	q	124	
43	r	118	
44	s	101	
45	t	89	
46	u	82	
47	v	84	
48	w	75	
49	x	92	
50	y	87	
51	z	71	
52	1	2904	
53	2	1533	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	3	118	
55	4	76	
56	5	78	
57	6	76	
58	7	10	
59	8	744	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	H2U	6	16	X	-	-	-
57	H2U	6	20	X	-	-	-
57	PSU	6	32	X	-	-	-
57	6IA	6	37	X	-	-	-
57	PSU	6	55	X	-	-	-

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 154519 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

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

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

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

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	77	Total	C	N	O	S	0	0
			588	363	118	106	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L31.

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

- Molecule 27 is a protein called 50S ribosomal protein L32.

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

- Molecule 28 is a protein called 50S ribosomal protein L33.

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

- Molecule 29 is a protein called 50S ribosomal protein L34.

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

- Molecule 30 is a protein called 50S ribosomal protein L35.

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

- Molecule 31 is a protein called 50S ribosomal protein L36.

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

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	207	Total	C	N	O	S	0	0
			1628	1030	306	289	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	207	LEU	ILE	conflict	UNP P0A7V3
h	208	GLY	LEU	conflict	UNP P0A7V3

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

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

- Molecule 37 is a protein called 30S ribosomal protein S7.

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

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

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

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

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

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

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

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	65	Total	C	N	O	S	0	0
			539	341	100	97	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	15	GLU	ALA	conflict	UNP P0A7T7

- Molecule 49 is a protein called 30S ribosomal protein S19.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	56	Total	C	N	O	S	0	0
			465	290	96	78	1		

- Molecule 52 is a RNA chain called LSU rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	2904	Total	C	N	O	P	0	0
			62356	27825	11472	20155	2904		

- Molecule 53 is a RNA chain called SSU rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	1533	Total	C	N	O	P	0	0
			32907	14683	6036	10655	1533		

- Molecule 54 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 55 is a RNA chain called E-site tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
56	5	77	Total	C	N	O	P	S	0	0
			1639	734	294	534	76	1		

- Molecule 57 is a RNA chain called A/T tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
57	6	76	Total	C	N	O	P	S	0	0
			1637	734	290	536	76	1		

- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	7	10	Total	C	N	O	P	0	0
			211	95	36	70	10		

- Molecule 59 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	8	615	Total	C	N	O	S	0	0
			4792	3010	875	885	22		

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

Mol	Chain	Residues	Atoms		AltConf
60	B	1	Total	Mg	0
			1	1	
60	C	1	Total	Mg	0
			1	1	
60	L	2	Total	Mg	0
			2	2	

Continued on next page...

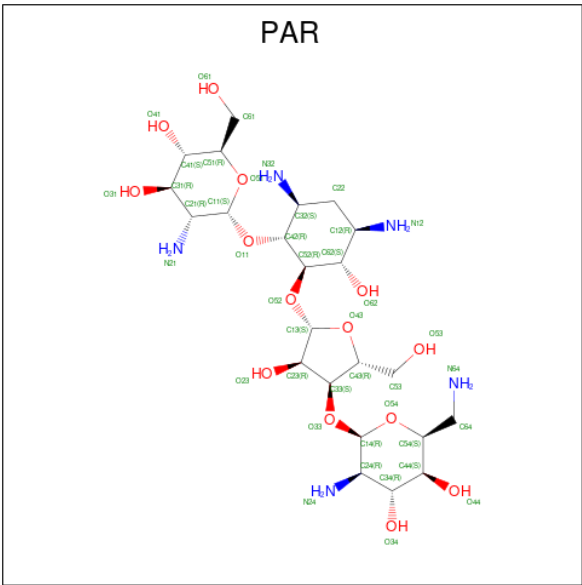
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
60	N	1	Total 1	Mg 1	0
60	U	1	Total 1	Mg 1	0
60	r	1	Total 1	Mg 1	0
60	s	1	Total 1	Mg 1	0
60	1	220	Total 220	Mg 220	0
60	2	64	Total 64	Mg 64	0
60	3	6	Total 6	Mg 6	0
60	8	1	Total 1	Mg 1	0

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

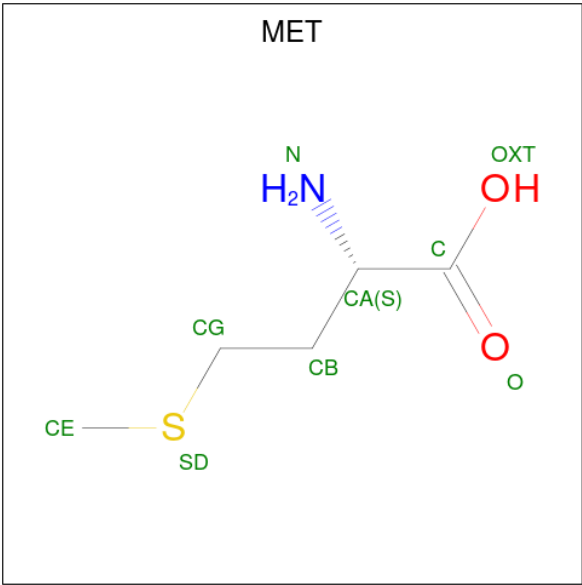
Mol	Chain	Residues	Atoms		AltConf
61	a	1	Total 1	Zn 1	0
61	f	1	Total 1	Zn 1	0
61	8	1	Total 1	Zn 1	0

- Molecule 62 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
62	2	1	42	23	5	14	0

- Molecule 63 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
63	5	1	8	5	1	1	1	0

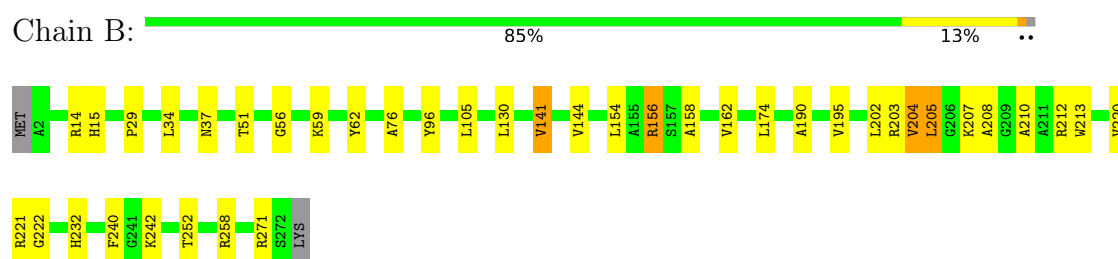
- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	B	2	Total	O	0
			2	2	

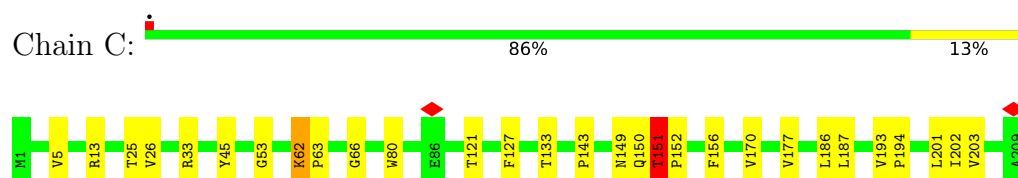
3 Residue-property plots [i](#)

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

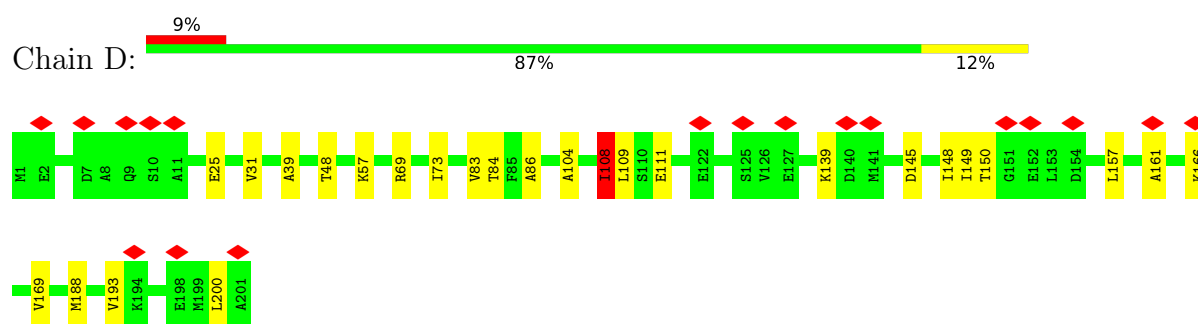
- Molecule 1: 50S ribosomal protein L2



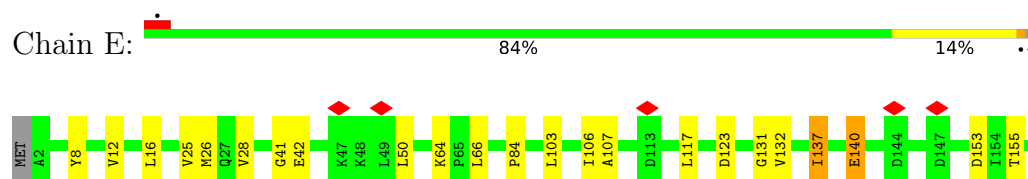
- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4

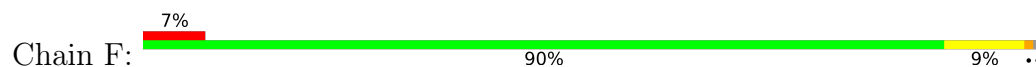


- Molecule 4: 50S ribosomal protein L5

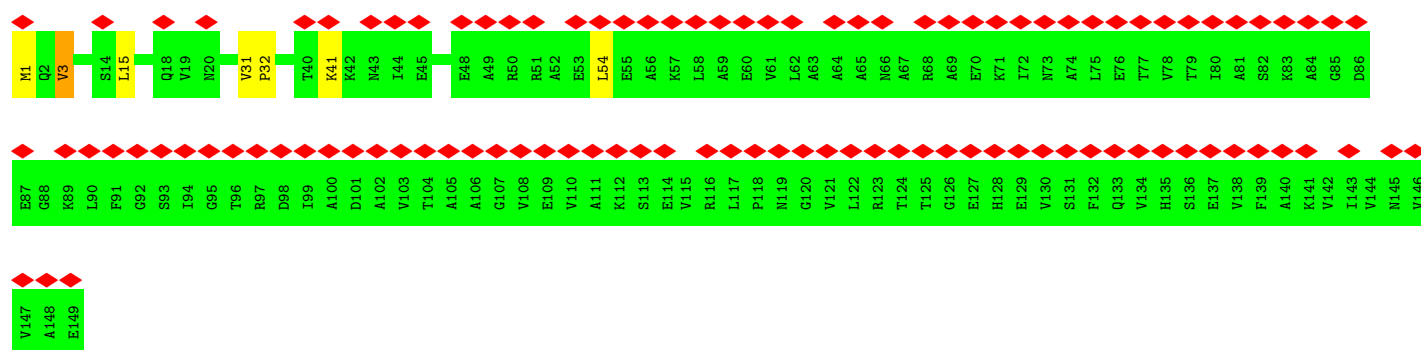




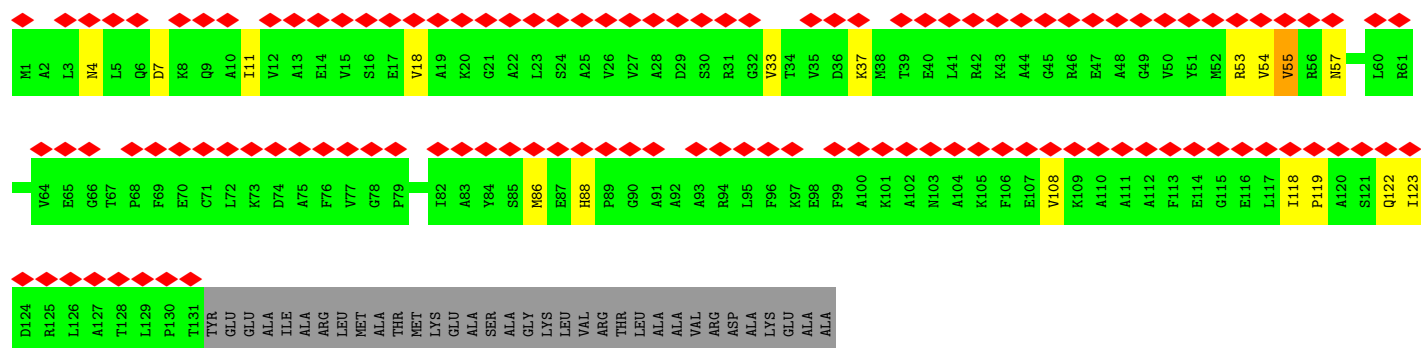
- Molecule 5: 50S ribosomal protein L6



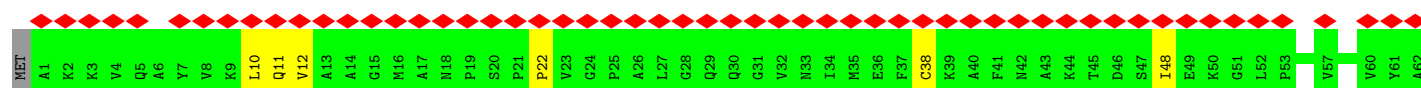
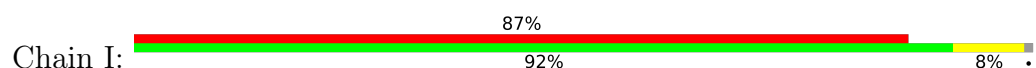
- Molecule 6: 50S ribosomal protein L9

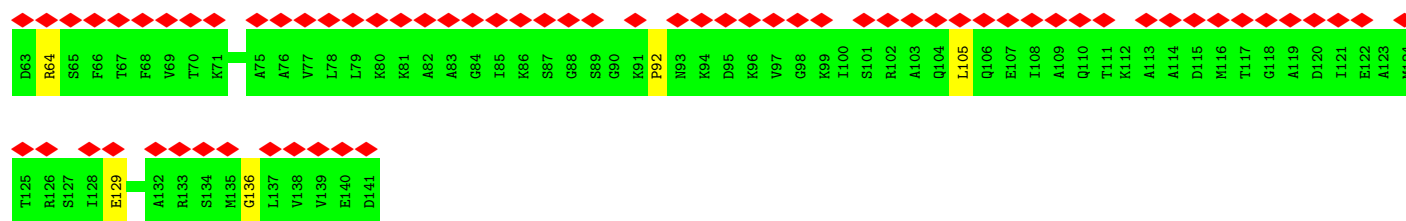


- Molecule 7: 50S ribosomal protein L10

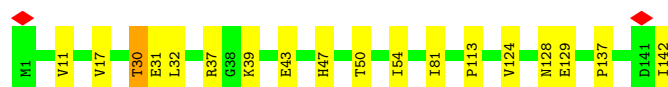
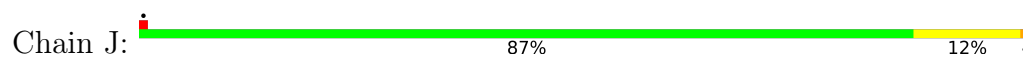


- Molecule 8: 50S ribosomal protein L11

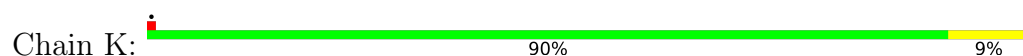




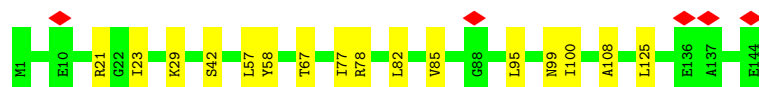
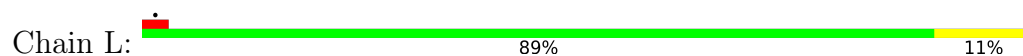
- Molecule 9: 50S ribosomal protein L13



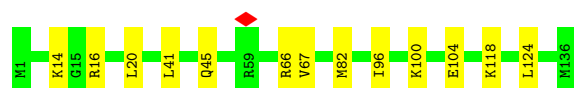
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16



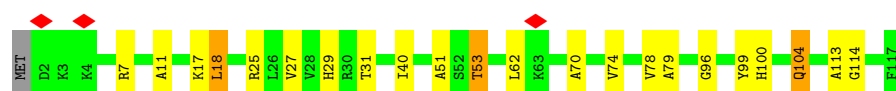
- Molecule 13: 50S ribosomal protein L17



ALA
ALA
GLU

- Molecule 14: 50S ribosomal protein L18

Chain O:  80% 16% ..



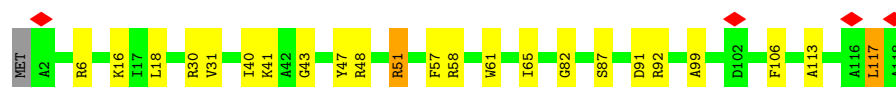
- Molecule 15: 50S ribosomal protein L19

Chain P:  93% 5% ..



- Molecule 16: 50S ribosomal protein L20

Chain Q:  80% 18% ..



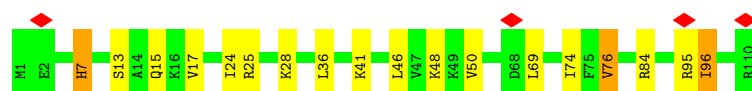
- Molecule 17: 50S ribosomal protein L21

Chain R:  7% 87% 12% ..



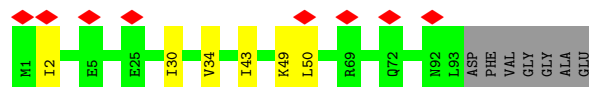
- Molecule 18: 50S ribosomal protein L22

Chain S:  84% 14% ..



- Molecule 19: 50S ribosomal protein L23

Chain T:  8% 87% 6% 7%

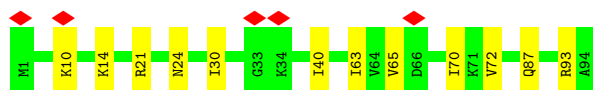
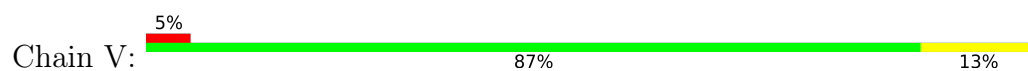


- Molecule 20: 50S ribosomal protein L24

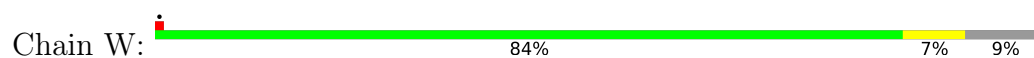
Chain U:  90% 7% ..



• Molecule 21: 50S ribosomal protein L25



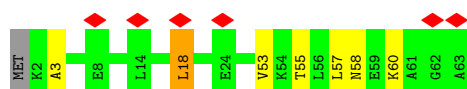
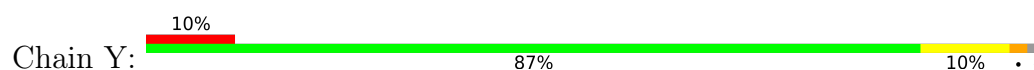
• Molecule 22: 50S ribosomal protein L27



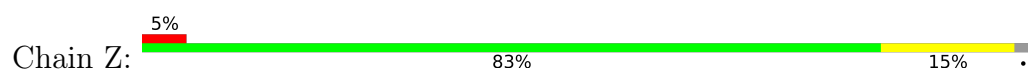
• Molecule 23: 50S ribosomal protein L28



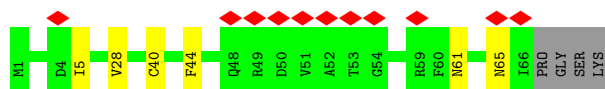
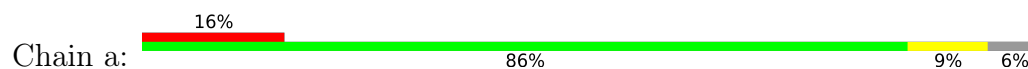
• Molecule 24: 50S ribosomal protein L29



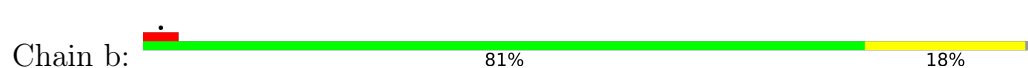
• Molecule 25: 50S ribosomal protein L30



• Molecule 26: 50S ribosomal protein L31

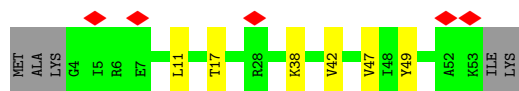
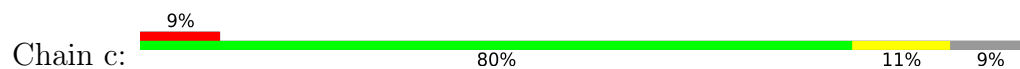


• Molecule 27: 50S ribosomal protein L32

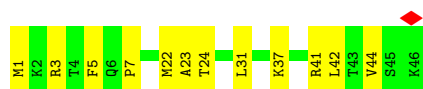




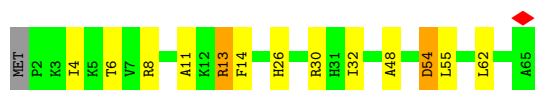
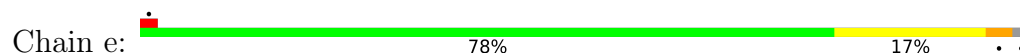
- Molecule 28: 50S ribosomal protein L33



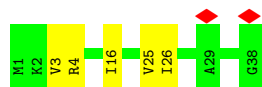
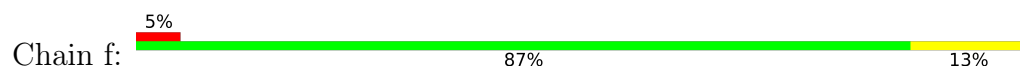
- Molecule 29: 50S ribosomal protein L34



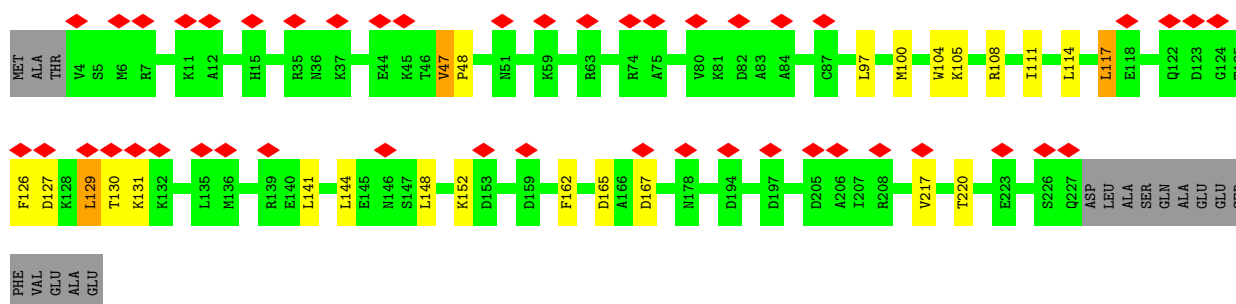
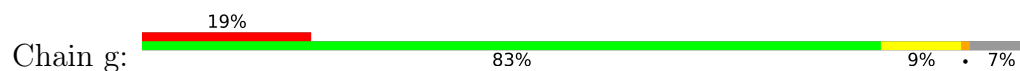
- Molecule 30: 50S ribosomal protein L35



- Molecule 31: 50S ribosomal protein L36

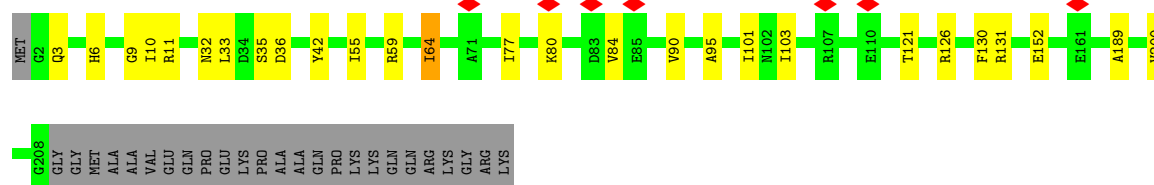


- Molecule 32: 30S ribosomal protein S2



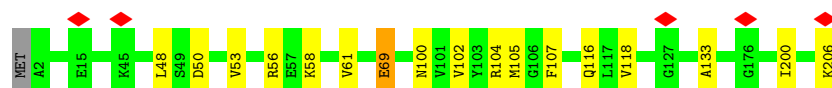
- Molecule 33: 30S ribosomal protein S3

Chain h: 



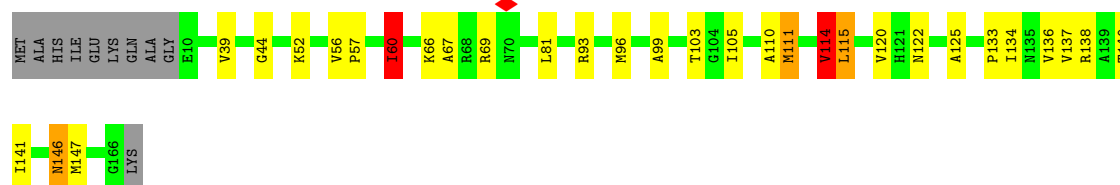
- Molecule 34: 30S ribosomal protein S4

Chain i: 



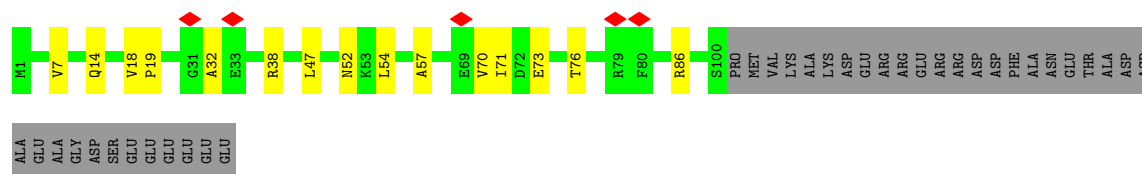
- Molecule 35: 30S ribosomal protein S5

Chain j: 



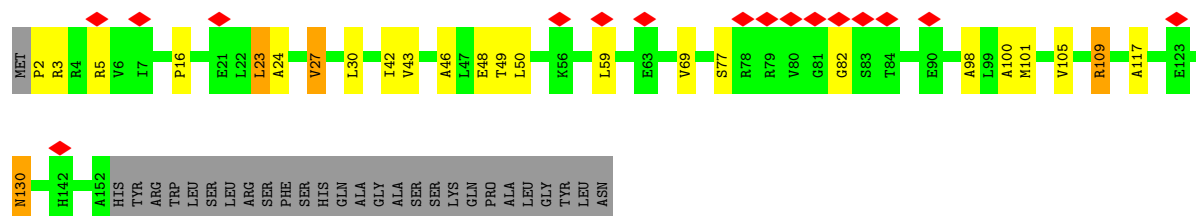
- Molecule 36: 30S ribosomal protein S6

Chain k: 



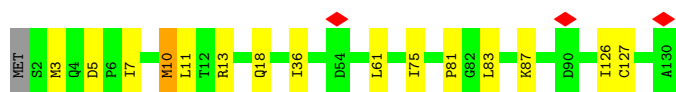
- Molecule 37: 30S ribosomal protein S7

Chain l: 



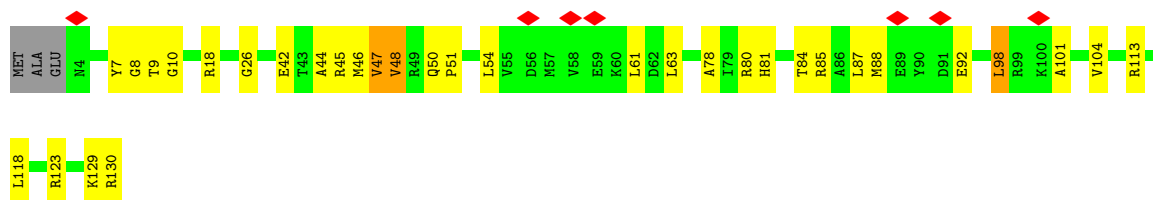
- Molecule 38: 30S ribosomal protein S8

Chain m:  88% 11% ..



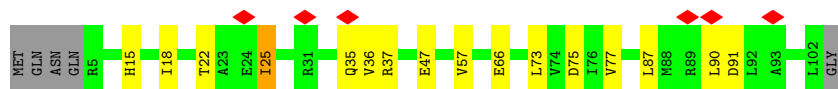
- Molecule 39: 30S ribosomal protein S9

Chain n:  5% 72% 23% ..



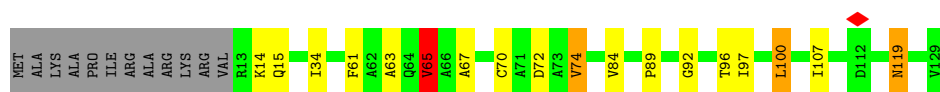
- Molecule 40: 30S ribosomal protein S10

Chain o:  6% 80% 15% 5%



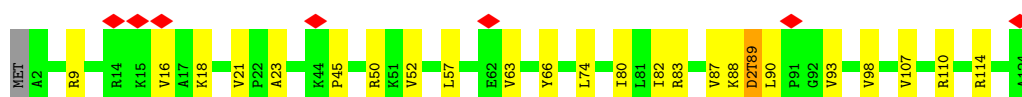
- Molecule 41: 30S ribosomal protein S11

Chain p:  77% 11% 9% ..



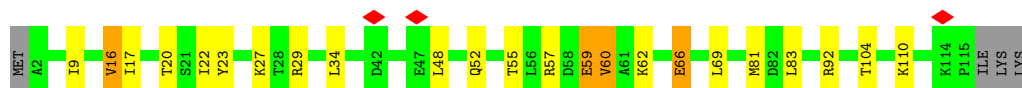
- Molecule 42: 30S ribosomal protein S12

Chain q:  6% 80% 19% ..



- Molecule 43: 30S ribosomal protein S13

Chain r:  77% 16% ..

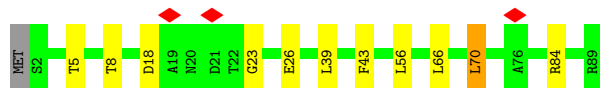
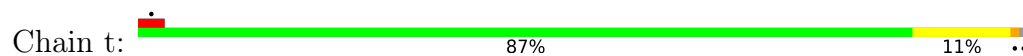


- Molecule 44: 30S ribosomal protein S14

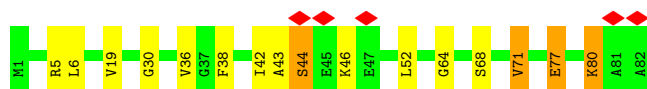
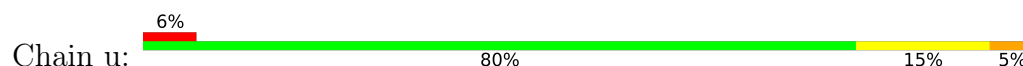
Chain s:  87% 9% ..



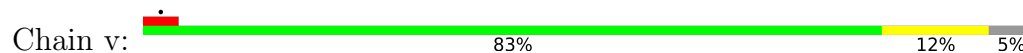
- Molecule 45: 30S ribosomal protein S15



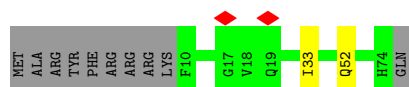
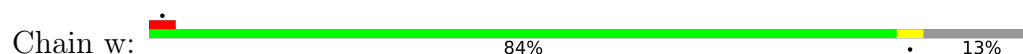
- Molecule 46: 30S ribosomal protein S16



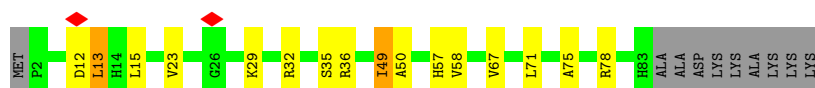
- Molecule 47: 30S ribosomal protein S17



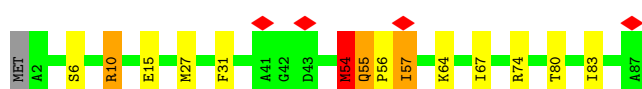
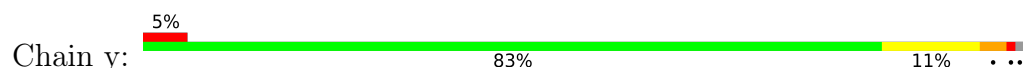
- Molecule 48: 30S ribosomal protein S18



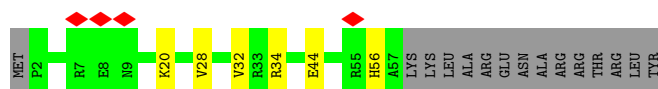
- Molecule 49: 30S ribosomal protein S19



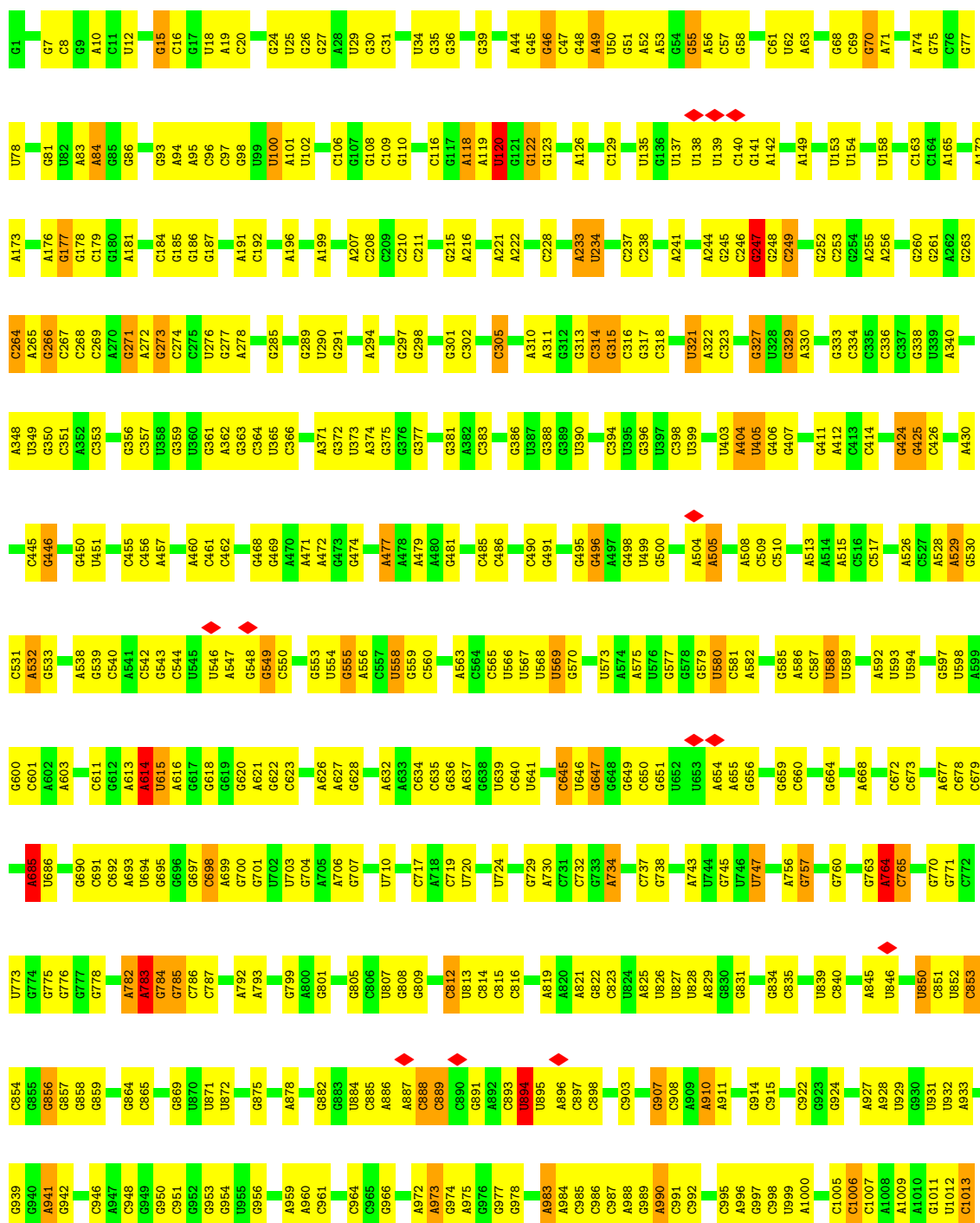
- Molecule 50: 30S ribosomal protein S20

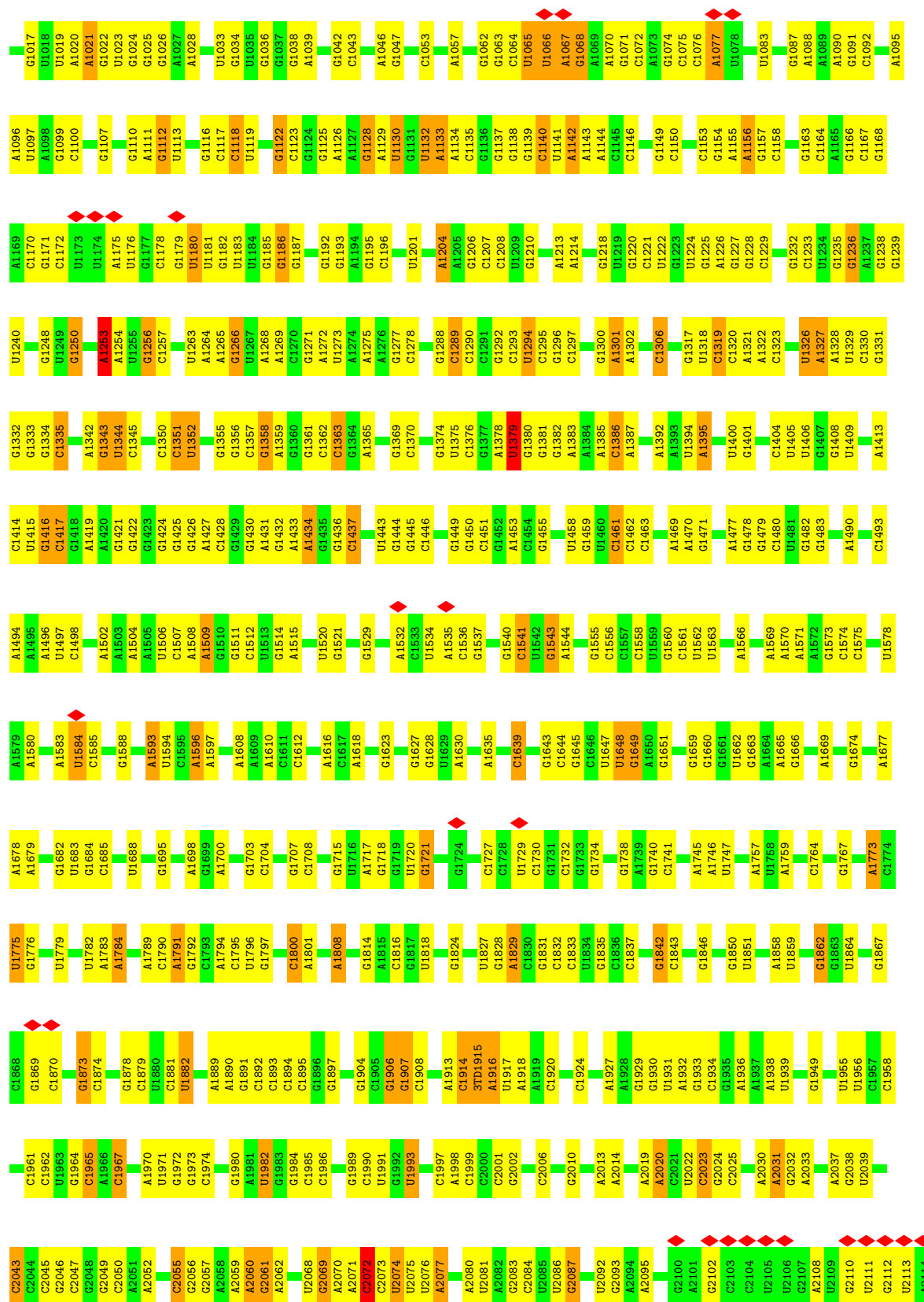


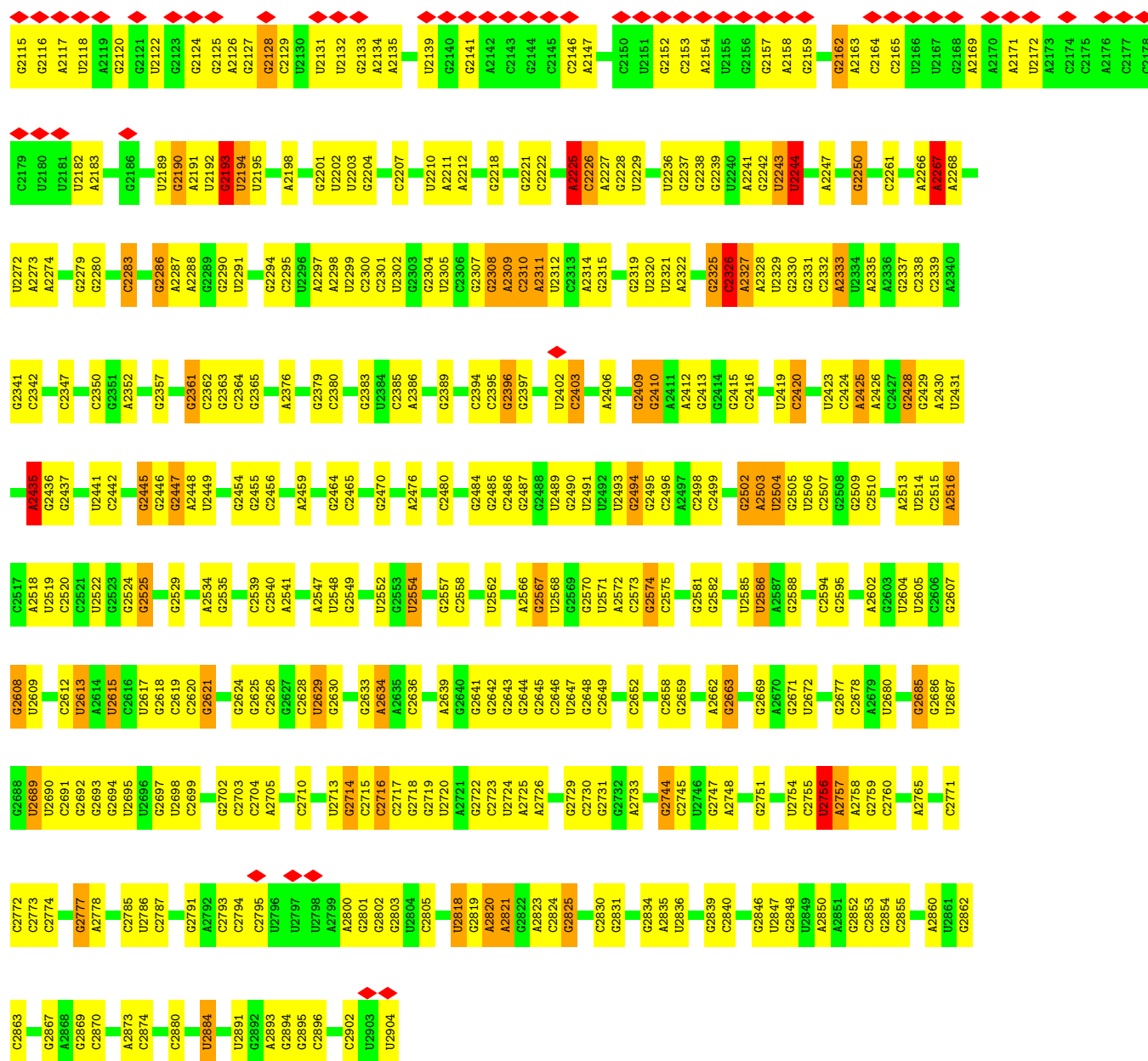
- Molecule 51: 30S ribosomal protein S21



• Molecule 52: LSU rRNA

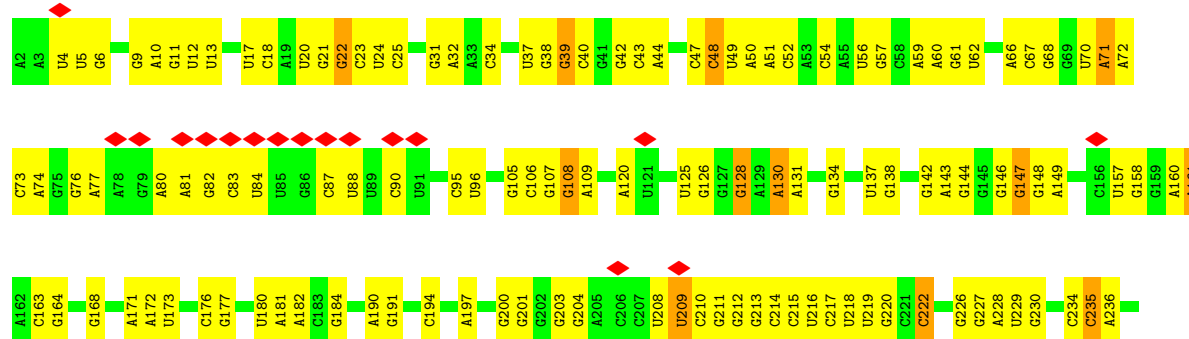






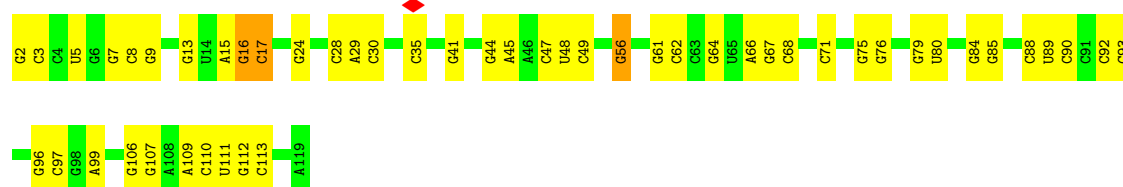
• Molecule 53: SSU rRNA

Chain 2: 51% 43% 6%

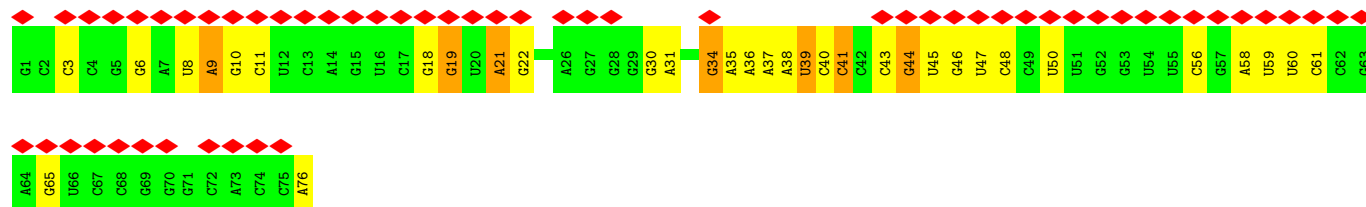
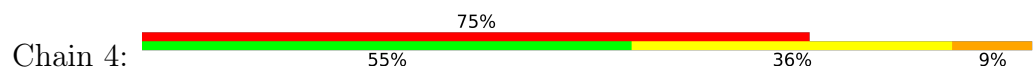




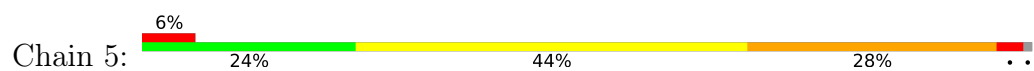
- Molecule 54: 5S rRNA



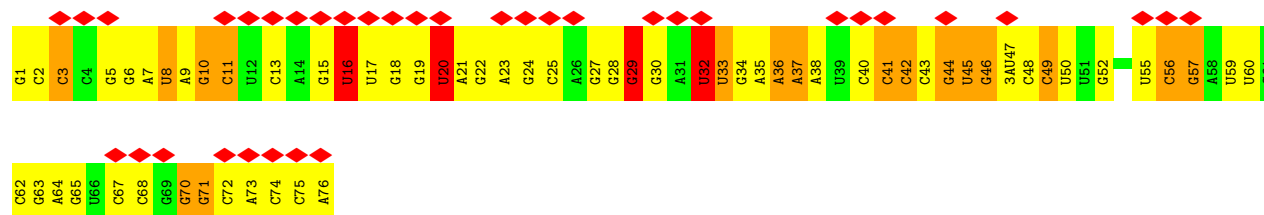
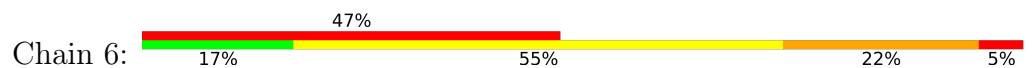
- Molecule 55: E-site tRNA(Phe)



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

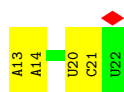


- Molecule 57: A/T tRNA(Phe)

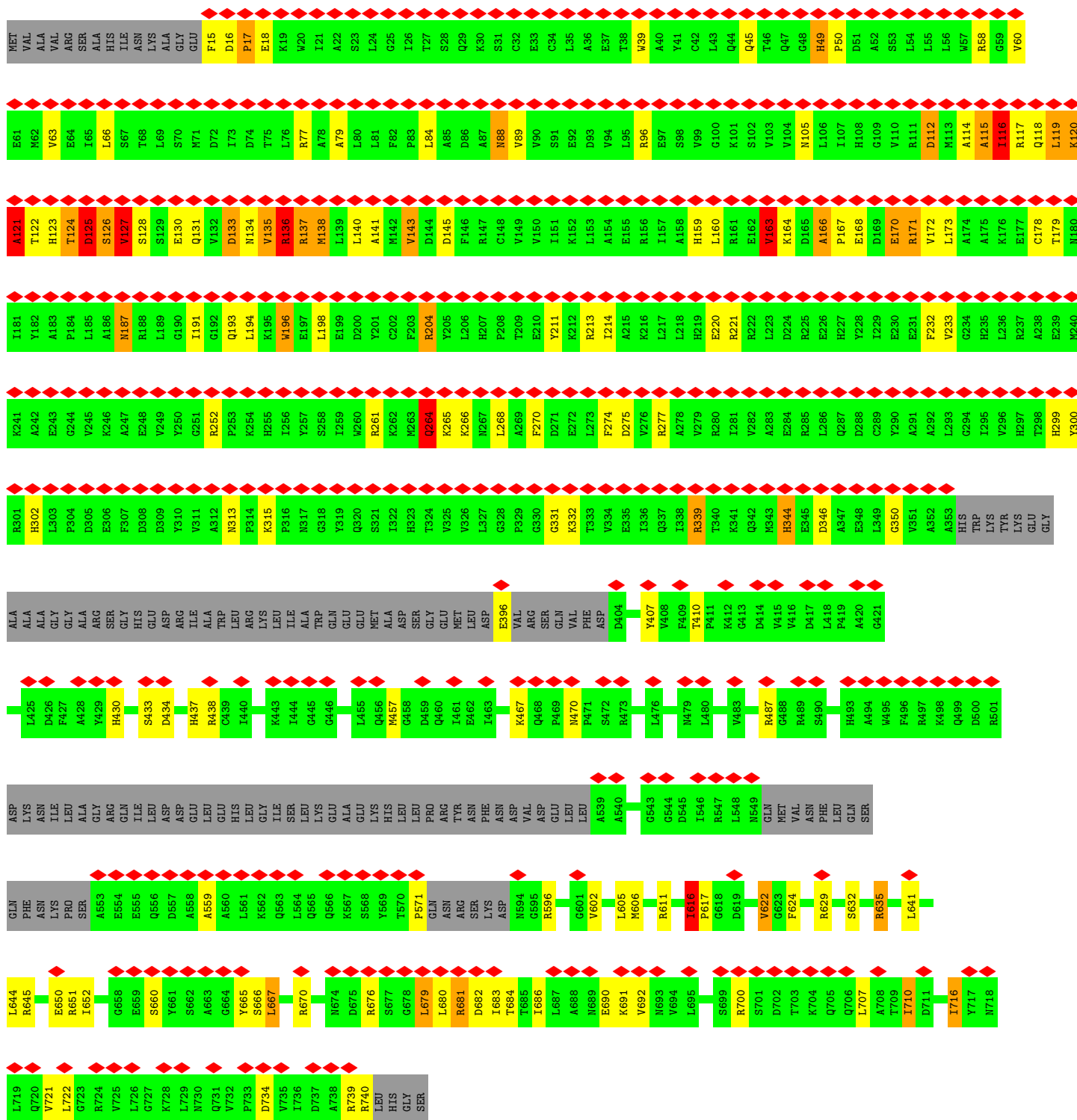


- Molecule 58: mRNA





• Molecule 59: GTP pyrophosphokinase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98498	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	104478	Depositor
Image detector	OTHER	Depositor
Maximum map value	1.341	Depositor
Minimum map value	-0.666	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	536.0, 536.0, 536.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, 1MG, 4OC, G7M, 6MZ, MA6, 5MU, 5MC, OMC, OMU, MG, 2MG, PAR, 4SU, 3AU, 3TD, UR3, 7MG, H2U, 6IA, OMG, D2T, 2MA, 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	B	0.49	0/2121	0.81	0/2852
2	C	0.49	0/1586	0.83	3/2134 (0.1%)
3	D	0.58	0/1571	1.02	1/2113 (0.0%)
4	E	0.61	0/1434	0.99	0/1926
5	F	0.57	0/1343	0.86	0/1816
6	G	0.63	0/1122	0.96	0/1515
7	H	0.66	0/1001	0.94	0/1350
8	I	0.65	0/1046	0.94	0/1410
9	J	0.61	0/1152	0.95	0/1551
10	K	0.49	0/955	0.85	0/1279
11	L	0.54	0/1062	0.93	1/1413 (0.1%)
12	M	0.52	0/1093	0.92	0/1460
13	N	0.65	0/973	1.10	1/1301 (0.1%)
14	O	0.62	0/902	1.08	0/1209
15	P	0.48	0/929	0.79	0/1242
16	Q	0.74	0/960	1.28	0/1278
17	R	0.45	0/829	0.77	0/1107
18	S	0.57	0/864	1.03	0/1156
19	T	0.56	0/744	0.91	0/994
20	U	0.49	0/787	0.76	0/1051
21	V	0.52	0/766	0.85	0/1025
22	W	0.44	0/595	0.70	0/787
23	X	0.54	0/635	0.95	0/848
24	Y	0.67	0/502	1.25	0/667
25	Z	0.64	0/453	1.01	0/605
26	a	0.58	0/531	0.94	0/709
27	b	0.55	0/450	0.86	0/599
28	c	0.45	0/416	0.71	0/554
29	d	0.65	0/380	1.21	1/498 (0.2%)
30	e	0.56	0/513	1.06	0/676
31	f	0.45	0/303	0.84	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	g	0.64	0/1784	1.07	1/2403 (0.0%)
33	h	0.58	0/1655	0.97	0/2230
34	i	0.61	0/1665	1.05	1/2227 (0.0%)
35	j	0.59	0/1169	1.07	2/1573 (0.1%)
36	k	0.58	0/835	0.95	0/1128
37	l	0.67	0/1195	1.13	1/1602 (0.1%)
38	m	0.57	0/989	0.95	0/1326
39	n	0.58	0/1034	1.01	2/1375 (0.1%)
40	o	0.59	0/796	0.90	1/1077 (0.1%)
41	p	0.57	0/893	0.92	1/1205 (0.1%)
42	q	0.50	0/960	0.79	0/1286
43	r	0.64	0/892	1.19	0/1193
44	s	0.61	0/817	1.07	1/1088 (0.1%)
45	t	0.69	0/722	1.24	0/964
46	u	0.58	0/659	0.97	1/884 (0.1%)
47	v	0.53	0/657	0.73	0/881
48	w	0.62	0/548	1.02	1/736 (0.1%)
49	x	0.56	0/675	0.85	0/908
50	y	0.77	0/676	1.35	3/895 (0.3%)
51	z	0.65	0/472	1.14	0/627
52	1	0.38	4/69300 (0.0%)	0.75	48/108089 (0.0%)
53	2	0.37	0/36561	0.72	12/57019 (0.0%)
54	3	0.36	0/2828	0.70	0/4410
55	4	0.38	0/1808	0.69	0/2815
56	5	0.44	1/1716 (0.1%)	0.85	4/2672 (0.1%)
57	6	0.42	0/1606	0.83	1/2497 (0.0%)
58	7	0.40	0/235	0.75	0/363
59	8	0.78	0/4878	1.45	50/6606 (0.8%)
All	All	0.46	5/166043 (0.0%)	0.84	137/247601 (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
52	1	0	9
53	2	0	2
57	6	8	3
59	8	0	19
All	All	8	33

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	1	2244	U	N3-C4	7.84	1.54	1.38
52	1	2244	U	C2-N3	6.73	1.51	1.37
52	1	2244	U	N1-C2	6.14	1.50	1.38
56	5	8	4SU	O3'-P	6.06	1.62	1.56
52	1	2435	A	C6-N1	-5.52	1.24	1.35

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	8	274	PHE	CA-CB-CG	8.46	122.26	113.80
52	1	100	U	C4'-C3'-O3'	8.40	122.00	109.40
59	8	130	GLU	CB-CA-C	8.03	124.80	111.31
52	1	614	A	C2'-C3'-O3'	7.60	120.90	109.50
52	1	2447	G	C2'-C3'-O3'	-7.55	98.18	109.50

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
57	6	16	H2U	C3',C1',C2'
57	6	20	H2U	C1',C2'
57	6	32	PSU	C1'
57	6	37	6IA	C3'
57	6	55	PSU	C1'

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	1	1319	C	Sidechain
52	1	1335	C	Sidechain
52	1	305	C	Sidechain
52	1	314	C	Sidechain
52	1	764	A	Sidechain

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	B	2082	0	2154	27	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1565	0	1616	26	0
3	D	1552	0	1619	10	0
4	E	1410	0	1444	12	0
5	F	1323	0	1371	7	0
6	G	1111	0	1148	2	0
7	H	988	0	1025	3	0
8	I	1032	0	1088	1	0
9	J	1129	0	1162	9	0
10	K	946	0	1023	4	0
11	L	1053	0	1129	9	0
12	M	1074	0	1157	8	0
13	N	960	0	1000	22	0
14	O	892	0	923	11	0
15	P	917	0	962	4	0
16	Q	947	0	1019	13	0
17	R	816	0	839	6	0
18	S	857	0	922	9	0
19	T	738	0	807	1	0
20	U	779	0	831	3	0
21	V	753	0	780	5	0
22	W	588	0	604	4	0
23	X	625	0	652	4	0
24	Y	501	0	531	2	0
25	Z	449	0	488	6	0
26	a	522	0	521	2	0
27	b	444	0	458	7	0
28	c	409	0	440	3	0
29	d	377	0	418	3	0
30	e	504	0	572	10	0
31	f	302	0	342	1	0
32	g	1753	0	1780	7	0
33	h	1628	0	1699	13	0
34	i	1643	0	1707	9	0
35	j	1156	0	1199	14	0
36	k	817	0	808	4	0
37	l	1181	0	1238	11	0
38	m	979	0	1031	6	0
39	n	1022	0	1070	16	0
40	o	786	0	828	3	0
41	p	877	0	887	9	0
42	q	957	0	1017	13	0
43	r	883	0	941	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	s	805	0	844	7	0
45	t	714	0	734	5	0
46	u	649	0	666	7	0
47	v	648	0	691	1	0
48	w	539	0	553	0	0
49	x	658	0	683	9	0
50	y	670	0	719	7	0
51	z	465	0	491	2	0
52	1	62356	0	31391	967	0
53	2	32907	0	16580	489	0
54	3	2529	0	1281	37	0
55	4	1619	0	823	32	0
56	5	1639	0	843	41	0
57	6	1637	0	840	41	0
58	7	211	0	107	14	0
59	8	4792	0	4726	43	0
60	1	220	0	0	0	0
60	2	64	0	0	0	0
60	3	6	0	0	0	0
60	8	1	0	0	0	0
60	B	1	0	0	0	0
60	C	1	0	0	0	0
60	L	2	0	0	0	0
60	N	1	0	0	0	0
60	U	1	0	0	0	0
60	r	1	0	0	0	0
60	s	1	0	0	0	0
61	8	1	0	0	0	0
61	a	1	0	0	0	0
61	f	1	0	0	0	0
62	2	42	0	45	1	0
63	5	8	0	8	1	0
64	B	2	0	0	0	0
All	All	154519	0	105275	1927	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 8.

The worst 5 of 1927 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)
52:1:2244:U:N3	52:1:2435:A:C6	1.94	1.32
53:2:13:U:N3	53:2:915:A:N6	1.76	1.31
52:1:2244:U:N3	52:1:2435:A:N6	1.79	1.29
52:1:1067:A:N3	57:6:56:C:N3	1.85	1.23
55:4:31:A:N1	55:4:39:U:O4	1.75	1.19

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	269/273 (98%)	249 (93%)	18 (7%)	2 (1%)	18	53
2	C	207/209 (99%)	190 (92%)	16 (8%)	1 (0%)	24	60
3	D	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	60
4	E	175/179 (98%)	158 (90%)	13 (7%)	4 (2%)	5	25
5	F	174/177 (98%)	156 (90%)	17 (10%)	1 (1%)	21	56
6	G	147/149 (99%)	126 (86%)	17 (12%)	4 (3%)	4	22
7	H	129/165 (78%)	103 (80%)	18 (14%)	8 (6%)	1	6
8	I	139/142 (98%)	113 (81%)	20 (14%)	6 (4%)	2	12
9	J	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
10	K	121/123 (98%)	110 (91%)	11 (9%)	0	100	100
11	L	142/144 (99%)	131 (92%)	9 (6%)	2 (1%)	9	36
12	M	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
13	N	118/127 (93%)	107 (91%)	10 (8%)	1 (1%)	16	50
14	O	114/117 (97%)	103 (90%)	9 (8%)	2 (2%)	6	31
15	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
16	Q	115/118 (98%)	111 (96%)	3 (3%)	1 (1%)	14	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	101/103 (98%)	90 (89%)	9 (9%)	2 (2%)	6	28
18	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
19	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
20	U	100/104 (96%)	91 (91%)	7 (7%)	2 (2%)	6	28
21	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
22	W	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
23	X	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
24	Y	60/63 (95%)	56 (93%)	3 (5%)	1 (2%)	7	32
25	Z	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
26	a	64/70 (91%)	51 (80%)	12 (19%)	1 (2%)	7	34
27	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
28	c	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
29	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
30	e	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	7	34
31	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
32	g	222/241 (92%)	200 (90%)	15 (7%)	7 (3%)	3	18
33	h	205/233 (88%)	185 (90%)	18 (9%)	2 (1%)	12	45
34	i	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
35	j	155/167 (93%)	142 (92%)	10 (6%)	3 (2%)	6	30
36	k	98/135 (73%)	88 (90%)	9 (9%)	1 (1%)	12	45
37	l	149/179 (83%)	140 (94%)	7 (5%)	2 (1%)	9	38
38	m	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	50
39	n	125/130 (96%)	113 (90%)	10 (8%)	2 (2%)	7	34
40	o	96/103 (93%)	82 (85%)	11 (12%)	3 (3%)	3	19
41	p	115/129 (89%)	98 (85%)	15 (13%)	2 (2%)	7	32
42	q	120/124 (97%)	109 (91%)	10 (8%)	1 (1%)	16	50
43	r	112/118 (95%)	106 (95%)	6 (5%)	0	100	100
44	s	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
45	t	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
46	u	80/82 (98%)	69 (86%)	7 (9%)	4 (5%)	1	10
47	v	78/84 (93%)	72 (92%)	4 (5%)	2 (3%)	4	23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	w	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
49	x	80/92 (87%)	73 (91%)	5 (6%)	2 (2%)	4	23
50	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
51	z	54/71 (76%)	52 (96%)	1 (2%)	1 (2%)	6	30
59	8	604/744 (81%)	528 (87%)	55 (9%)	21 (4%)	3	16
All	All	6455/6964 (93%)	5874 (91%)	487 (8%)	94 (2%)	11	35

5 of 94 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	175	PHE
7	H	4	ASN
7	H	123	ILE
11	L	99	ASN
17	R	51	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	
1	B	216/218 (99%)	203 (94%)	13 (6%)	17	50
2	C	164/164 (100%)	160 (98%)	4 (2%)	43	73
3	D	165/165 (100%)	155 (94%)	10 (6%)	17	49
4	E	148/150 (99%)	138 (93%)	10 (7%)	14	45
5	F	137/138 (99%)	131 (96%)	6 (4%)	25	60
6	G	114/114 (100%)	114 (100%)	0	100	100
7	H	100/123 (81%)	96 (96%)	4 (4%)	28	62
8	I	109/110 (99%)	106 (97%)	3 (3%)	38	70
9	J	116/116 (100%)	109 (94%)	7 (6%)	17	50
10	K	104/104 (100%)	98 (94%)	6 (6%)	18	51
11	L	103/103 (100%)	100 (97%)	3 (3%)	37	70

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	M	109/109 (100%)	105 (96%)	4 (4%)	30	64
13	N	100/103 (97%)	98 (98%)	2 (2%)	48	76
14	O	86/87 (99%)	80 (93%)	6 (7%)	14	44
15	P	99/100 (99%)	95 (96%)	4 (4%)	28	62
16	Q	89/90 (99%)	82 (92%)	7 (8%)	11	39
17	R	84/84 (100%)	80 (95%)	4 (5%)	23	57
18	S	93/93 (100%)	85 (91%)	8 (9%)	10	36
19	T	80/84 (95%)	76 (95%)	4 (5%)	22	56
20	U	83/85 (98%)	81 (98%)	2 (2%)	43	73
21	V	78/78 (100%)	73 (94%)	5 (6%)	16	48
22	W	59/63 (94%)	58 (98%)	1 (2%)	53	78
23	X	67/68 (98%)	65 (97%)	2 (3%)	36	69
24	Y	54/55 (98%)	50 (93%)	4 (7%)	13	42
25	Z	48/49 (98%)	47 (98%)	1 (2%)	47	75
26	a	59/62 (95%)	57 (97%)	2 (3%)	32	66
27	b	47/48 (98%)	44 (94%)	3 (6%)	16	48
28	c	45/49 (92%)	44 (98%)	1 (2%)	45	74
29	d	38/38 (100%)	30 (79%)	8 (21%)	1	6
30	e	51/52 (98%)	47 (92%)	4 (8%)	11	39
31	f	34/34 (100%)	31 (91%)	3 (9%)	9	35
32	g	186/199 (94%)	180 (97%)	6 (3%)	34	67
33	h	170/189 (90%)	162 (95%)	8 (5%)	23	58
34	i	172/173 (99%)	169 (98%)	3 (2%)	53	78
35	j	119/126 (94%)	107 (90%)	12 (10%)	7	29
36	k	87/116 (75%)	81 (93%)	6 (7%)	14	45
37	l	124/147 (84%)	114 (92%)	10 (8%)	11	38
38	m	104/105 (99%)	99 (95%)	5 (5%)	23	57
39	n	105/107 (98%)	96 (91%)	9 (9%)	10	36
40	o	86/90 (96%)	79 (92%)	7 (8%)	11	38
41	p	90/99 (91%)	84 (93%)	6 (7%)	15	46
42	q	102/103 (99%)	97 (95%)	5 (5%)	22	56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	r	92/96 (96%)	81 (88%)	11 (12%)	5	22
44	s	83/84 (99%)	79 (95%)	4 (5%)	23	57
45	t	76/77 (99%)	71 (93%)	5 (7%)	15	46
46	u	65/65 (100%)	61 (94%)	4 (6%)	16	49
47	v	74/78 (95%)	68 (92%)	6 (8%)	11	38
48	w	57/66 (86%)	56 (98%)	1 (2%)	51	77
49	x	72/79 (91%)	68 (94%)	4 (6%)	19	52
50	y	65/66 (98%)	58 (89%)	7 (11%)	6	26
51	z	48/61 (79%)	45 (94%)	3 (6%)	16	48
59	8	500/629 (80%)	439 (88%)	61 (12%)	5	21
All	All	5356/5691 (94%)	5032 (94%)	324 (6%)	19	50

5 of 324 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	s	55	SER
59	8	220	GLU
46	u	36	VAL
51	z	20	LYS
59	8	487	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
50	y	21	ASN
50	y	68	HIS
14	O	116	GLN
13	N	73	ASN
59	8	108	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	1	2901/2904 (99%)	621 (21%)	61 (2%)
53	2	1531/1533 (99%)	326 (21%)	24 (1%)
54	3	117/118 (99%)	19 (16%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
55	4	74/76 (97%)	22 (29%)	0
56	5	76/78 (97%)	37 (48%)	14 (18%)
57	6	75/76 (98%)	44 (58%)	11 (14%)
58	7	9/10 (90%)	0	0
All	All	4783/4795 (99%)	1069 (22%)	110 (2%)

5 of 1069 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	1	10	A
52	1	15	G
52	1	34	U
52	1	35	G
52	1	39	G

5 of 110 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	1	2751	G
53	2	518	C
57	6	75	C
57	6	10	G
52	1	2830	C

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

48 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	$\# Z > 2$
57	4SU	6	8	57	18,21,22	0.47	0	26,30,33	1.66	2 (7%)
52	OMU	1	2552	52,60	19,22,23	0.23	0	26,31,34	0.60	0
57	3AU	6	47	57	25,28,29	0.54	0	32,40,43	0.77	1 (3%)
57	PSU	6	32	57	18,21,22	0.56	0	22,30,33	1.37	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	PSU	5	55	56	18,21,22	0.49	0	22,30,33	0.81	0
52	3TD	1	1915	52	18,22,23	0.38	0	22,32,35	1.07	1 (4%)
52	PSU	1	2580	52	18,21,22	0.53	0	22,30,33	0.79	0
53	5MC	2	967	53	18,22,23	0.41	0	26,32,35	0.70	0
57	5MU	6	54	57	19,22,23	0.26	0	28,32,35	0.56	0
56	4OC	5	32	56	20,23,24	0.22	0	26,32,35	0.51	0
53	4OC	2	1402	53	20,23,24	0.22	0	26,32,35	0.68	0
56	4SU	5	8	56	18,21,22	0.50	0	26,30,33	1.77	5 (19%)
53	UR3	2	1498	53	19,22,23	0.35	0	26,32,35	0.73	1 (3%)
57	6IA	6	37	58,57	26,29,30	0.29	0	37,41,44	1.42	5 (13%)
53	2MG	2	1207	53	23,26,27	0.37	0	32,38,41	0.86	1 (3%)
56	H2U	5	20	56	18,21,22	0.50	0	21,30,33	0.71	0
53	MA6	2	1519	53	23,26,27	0.26	0	34,38,41	1.02	2 (5%)
52	PSU	1	1911	52	18,21,22	0.47	0	22,30,33	0.81	0
56	5MU	5	54	56	19,22,23	0.26	0	28,32,35	0.60	0
57	PSU	6	55	57	18,21,22	0.58	0	22,30,33	1.27	2 (9%)
52	2MA	1	2503	52,60	22,25,26	1.16	3 (13%)	33,37,40	1.33	4 (12%)
52	2MG	1	2445	52	23,26,27	0.41	0	32,38,41	0.81	1 (3%)
52	PSU	1	955	52	18,21,22	0.51	0	22,30,33	0.74	0
52	PSU	1	2457	52	18,21,22	0.50	0	22,30,33	0.78	0
52	PSU	1	746	52,60	18,21,22	0.47	0	22,30,33	0.82	0
53	G7M	2	527	53	23,26,27	0.32	0	35,39,42	0.71	1 (2%)
53	5MC	2	1407	53	18,22,23	0.32	0	26,32,35	0.84	0
52	2MG	1	1835	52	23,26,27	0.36	0	32,38,41	0.75	1 (3%)
42	D2T	q	89	42	7,9,10	1.10	0	6,11,13	2.12	3 (50%)
52	5MU	1	1939	52	19,22,23	0.26	0	28,32,35	0.62	0
53	2MG	2	966	53	23,26,27	0.38	0	32,38,41	0.81	1 (3%)
52	6MZ	1	2030	52	22,25,26	0.31	0	30,36,39	0.83	0
52	5MU	1	747	52	19,22,23	0.26	0	28,32,35	0.67	0
52	PSU	1	1917	52	18,21,22	0.49	0	22,30,33	0.68	0
52	OMC	1	2498	52,60	19,22,23	0.26	0	26,31,34	0.57	0
52	PSU	1	2605	52	18,21,22	0.54	0	22,30,33	0.88	1 (4%)
53	PSU	2	516	53	18,21,22	0.50	0	22,30,33	1.16	1 (4%)
52	PSU	1	2504	52	18,21,22	0.51	0	22,30,33	0.89	1 (4%)
52	5MC	1	1962	52	18,22,23	0.40	0	26,32,35	0.64	0
57	H2U	6	20	57	18,21,22	0.59	0	21,30,33	1.77	4 (19%)
52	G7M	1	2069	52	23,26,27	0.42	0	35,39,42	0.73	1 (2%)
53	2MG	2	1516	53	23,26,27	0.38	0	32,38,41	0.76	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	MA6	2	1518	53	23,26,27	0.26	0	34,38,41	0.99	1 (2%)
57	H2U	6	16	57	18,21,22	0.53	0	21,30,33	2.68	7 (33%)
52	OMG	1	2251	52,56	23,26,27	0.34	0	33,38,41	0.52	0
52	6MZ	1	1618	52	22,25,26	0.26	0	30,36,39	0.80	0
57	7MG	6	46	57	22,26,27	0.89	1 (4%)	29,39,42	0.94	3 (10%)
52	1MG	1	745	52	22,26,27	0.43	0	33,39,42	0.73	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	4SU	6	8	57	-	4/7/25/26	0/2/2/2
52	OMU	1	2552	52,60	-	0/9/27/28	0/2/2/2
57	3AU	6	47	57	-	3/16/34/35	0/2/2/2
57	PSU	6	32	57	1/1/5/5	1/7/25/26	0/2/2/2
56	PSU	5	55	56	-	3/7/25/26	0/2/2/2
52	3TD	1	1915	52	-	1/7/25/26	0/2/2/2
52	PSU	1	2580	52	-	0/7/25/26	0/2/2/2
53	5MC	2	967	53	-	0/7/25/26	0/2/2/2
57	5MU	6	54	57	-	0/7/25/26	0/2/2/2
56	4OC	5	32	56	-	0/9/29/30	0/2/2/2
53	4OC	2	1402	53	-	0/9/29/30	0/2/2/2
56	4SU	5	8	56	-	4/7/25/26	0/2/2/2
53	UR3	2	1498	53	-	0/7/25/26	0/2/2/2
57	6IA	6	37	58,57	1/1/6/7	6/13/31/32	0/3/3/3
53	2MG	2	1207	53	-	2/9/27/28	0/3/3/3
56	H2U	5	20	56	-	3/7/38/39	0/2/2/2
53	MA6	2	1519	53	-	6/11/29/30	0/3/3/3
52	PSU	1	1911	52	-	0/7/25/26	0/2/2/2
56	5MU	5	54	56	-	0/7/25/26	0/2/2/2
57	PSU	6	55	57	1/1/5/5	2/7/25/26	0/2/2/2
52	2MA	1	2503	52,60	-	1/7/25/26	0/3/3/3
52	2MG	1	2445	52	-	1/9/27/28	0/3/3/3
52	PSU	1	955	52	-	0/7/25/26	0/2/2/2
52	PSU	1	2457	52	-	0/7/25/26	0/2/2/2
52	PSU	1	746	52,60	-	1/7/25/26	0/2/2/2
53	G7M	2	527	53	-	2/7/25/26	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	5MC	2	1407	53	-	0/7/25/26	0/2/2/2
52	2MG	1	1835	52	-	2/9/27/28	0/3/3/3
42	D2T	q	89	42	-	2/7/12/14	-
52	5MU	1	1939	52	-	0/7/25/26	0/2/2/2
53	2MG	2	966	53	-	0/9/27/28	0/3/3/3
52	6MZ	1	2030	52	-	1/9/27/28	0/3/3/3
52	5MU	1	747	52	-	0/7/25/26	0/2/2/2
52	PSU	1	1917	52	-	2/7/25/26	0/2/2/2
52	OMC	1	2498	52,60	-	1/9/27/28	0/2/2/2
52	PSU	1	2605	52	-	0/7/25/26	0/2/2/2
53	PSU	2	516	53	-	2/7/25/26	0/2/2/2
52	PSU	1	2504	52	-	2/7/25/26	0/2/2/2
52	5MC	1	1962	52	-	0/7/25/26	0/2/2/2
57	H2U	6	20	57	2/2/8/9	6/7/38/39	0/2/2/2
57	H2U	6	16	57	3/3/8/9	5/7/38/39	0/2/2/2
52	G7M	1	2069	52	-	2/7/25/26	0/3/3/3
53	2MG	2	1516	53	-	0/9/27/28	0/3/3/3
53	MA6	2	1518	53	-	0/11/29/30	0/3/3/3
52	OMG	1	2251	52,56	-	0/9/27/28	0/3/3/3
52	6MZ	1	1618	52	-	3/9/27/28	0/3/3/3
57	7MG	6	46	57	-	1/7/37/38	0/3/3/3
52	1MG	1	745	52	-	0/7/25/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	6	46	7MG	C5-N7	3.57	1.39	1.35
52	1	2503	2MA	C6-N1	3.14	1.39	1.35
52	1	2503	2MA	C6-N6	-2.62	1.27	1.34
52	1	2503	2MA	C2-N1	2.56	1.38	1.34

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	6	16	H2U	O3'-C3'-C4'	6.75	130.56	111.05
57	6	8	4SU	C4-N3-C2	-6.66	120.87	127.34
57	6	16	H2U	O2'-C2'-C1'	5.37	127.99	110.02
56	5	8	4SU	C4-N3-C2	-5.20	122.29	127.34
57	6	16	H2U	O4'-C1'-N1	5.07	116.20	109.30

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
57	6	16	H2U	C3'
57	6	16	H2U	C1'
57	6	16	H2U	C2'
57	6	20	H2U	C1'
57	6	20	H2U	C2'

5 of 69 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	q	89	D2T	SB-CB-CG-OD2
52	1	1618	6MZ	N1-C6-N6-C9
52	1	1618	6MZ	O4'-C4'-C5'-O5'
52	1	1618	6MZ	C3'-C4'-C5'-O5'
52	1	1835	2MG	N1-C2-N2-CM2

There are no ring outliers.

21 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	1	2552	OMU	1	0
57	6	32	PSU	2	0
52	1	1915	3TD	1	0
53	2	967	5MC	2	0
56	5	32	4OC	1	0
53	2	1402	4OC	1	0
56	5	8	4SU	1	0
53	2	1207	2MG	1	0
56	5	20	H2U	3	0
53	2	1519	MA6	1	0
56	5	54	5MU	2	0
52	1	2503	2MA	2	0
52	1	2445	2MG	2	0
42	q	89	D2T	1	0
52	1	1939	5MU	1	0
53	2	966	2MG	2	0
52	1	2030	6MZ	3	0
52	1	747	5MU	1	0
52	1	2498	OMC	1	0
53	2	516	PSU	1	0
53	2	1518	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 304 ligands modelled in this entry, 302 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
63	MET	5	101	-	6,7,8	0.53	0	2,7,9	0.43	0
62	PAR	2	1665	-	45,45,45	0.81	2 (4%)	64,67,67	0.67	1 (1%)

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
63	MET	5	101	-	-	2/5/6/8	-
62	PAR	2	1665	-	-	3/18/94/94	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	2	1665	PAR	O51-C11	-3.78	1.32	1.41
62	2	1665	PAR	C14-C24	-2.17	1.48	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	2	1665	PAR	O51-C11-C21	2.36	115.36	110.06

There are no chirality outliers.

All (5) torsion outliers are listed below:

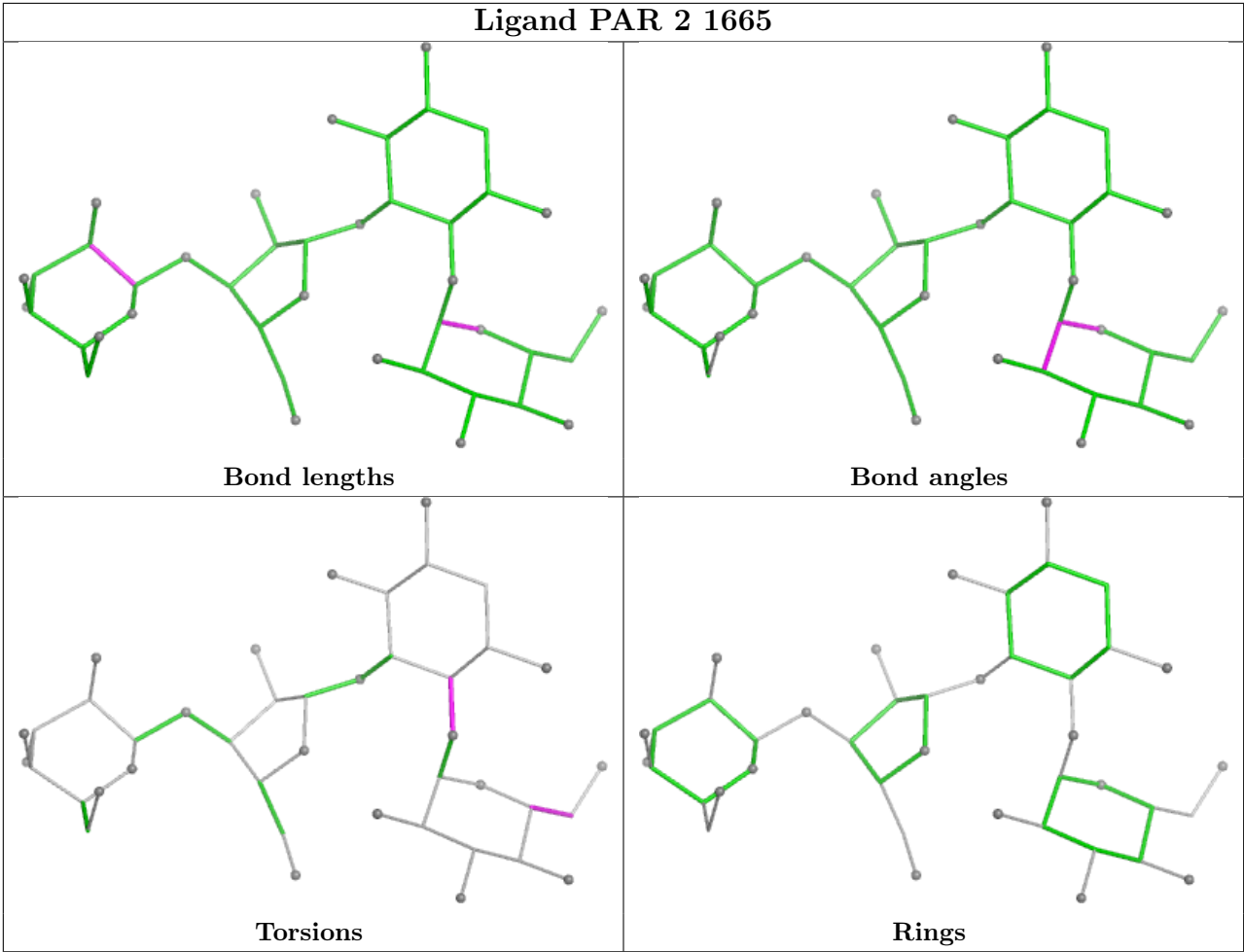
Mol	Chain	Res	Type	Atoms
62	2	1665	PAR	C41-C51-C61-O61
63	5	101	MET	CA-CB-CG-SD
63	5	101	MET	CB-CG-SD-CE
62	2	1665	PAR	O51-C51-C61-O61
62	2	1665	PAR	C52-C42-O11-C11

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	5	101	MET	1	0
62	2	1665	PAR	1	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
52	1	8
53	2	4
55	4	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1588:G	O3'	1589:U	P	4.95
1	4	1:G	O3'	2:C	P	4.28

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	2098:U	O3'	2099:U	P	3.58
1	2	480:U	O3'	481:G	P	3.44
1	1	1408:G	O3'	1409:U	P	3.41

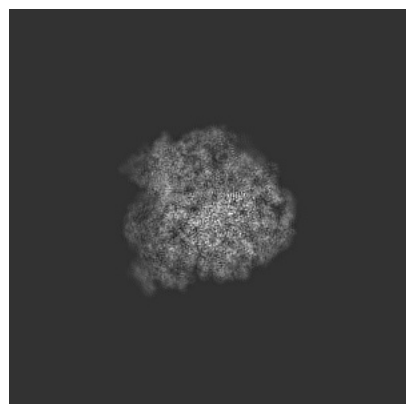
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8107. These allow visual inspection of the internal detail of the map and identification of artifacts.

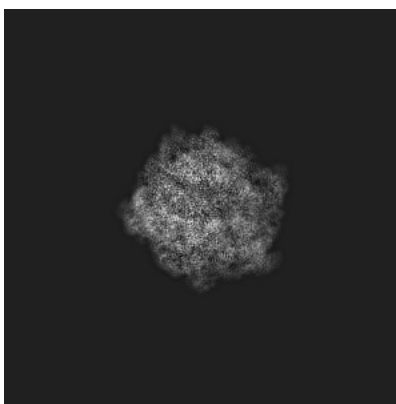
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

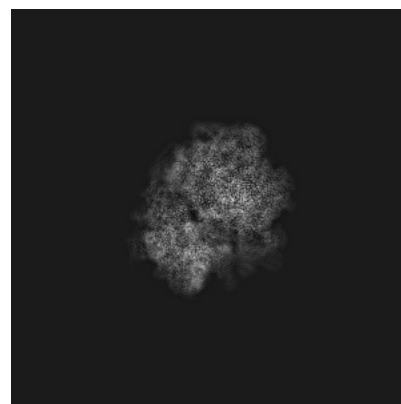
6.1.1 Primary map



X

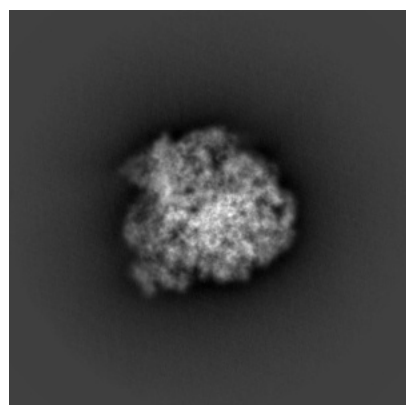


Y

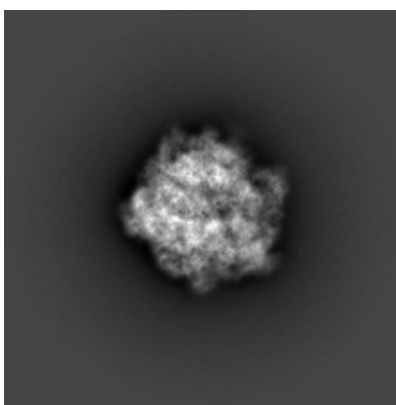


Z

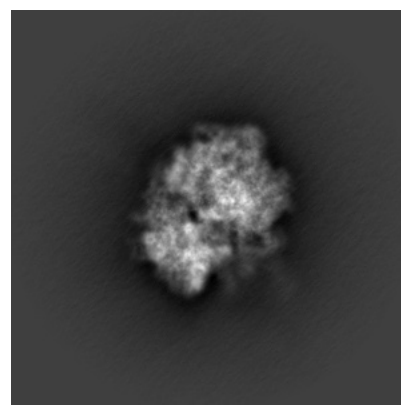
6.1.2 Raw map



X



Y

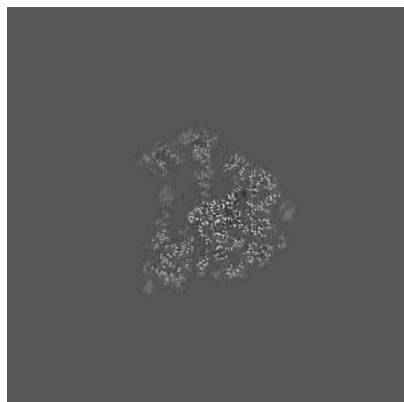


Z

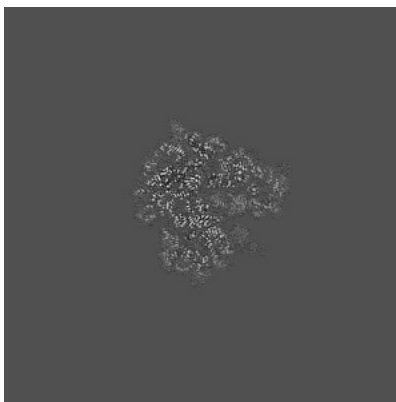
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

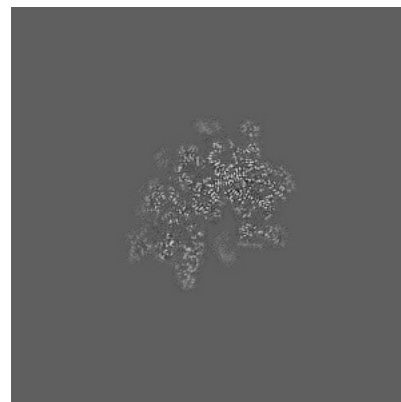
6.2.1 Primary map



X Index: 200

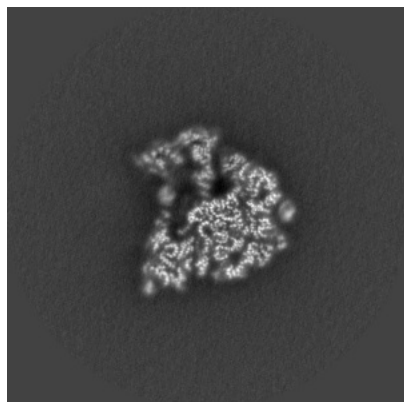


Y Index: 200

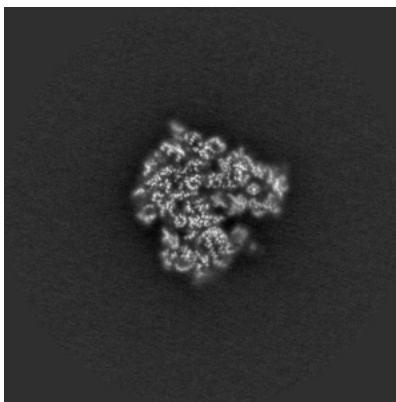


Z Index: 200

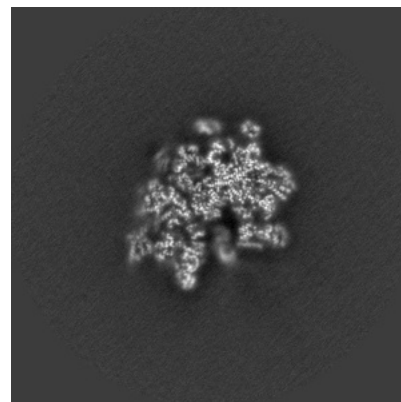
6.2.2 Raw map



X Index: 200



Y Index: 200

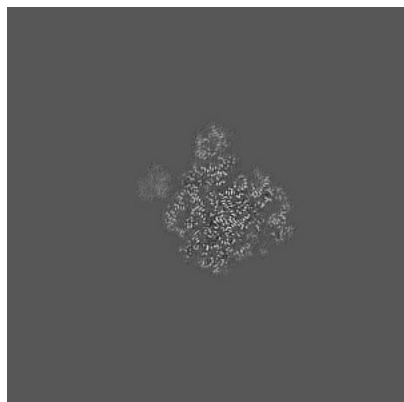


Z Index: 200

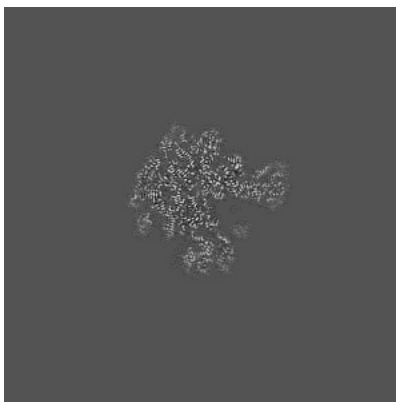
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

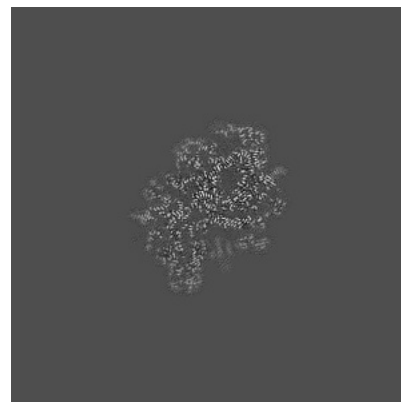
6.3.1 Primary map



X Index: 233

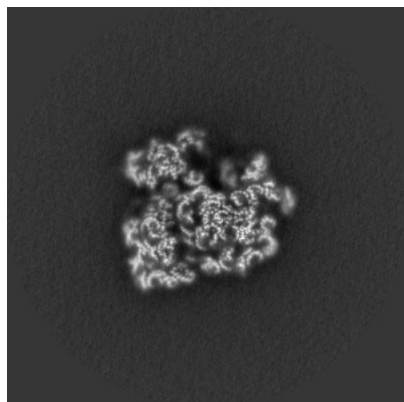


Y Index: 209

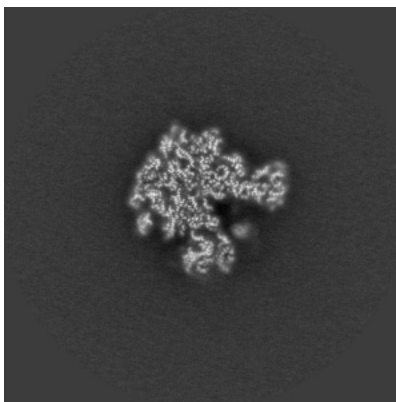


Z Index: 185

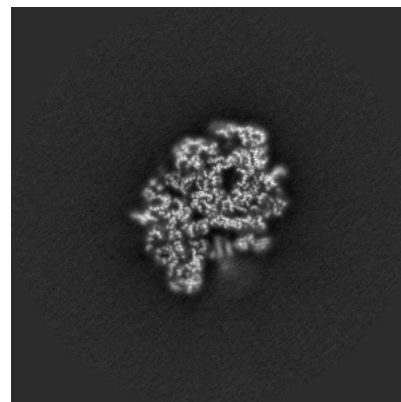
6.3.2 Raw map



X Index: 188



Y Index: 209

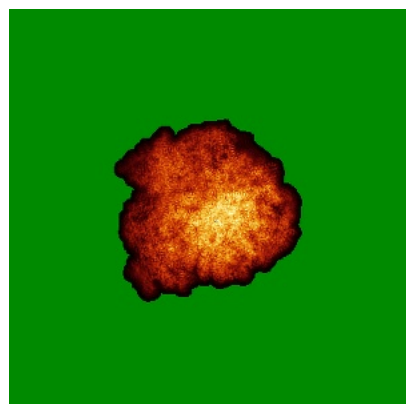


Z Index: 185

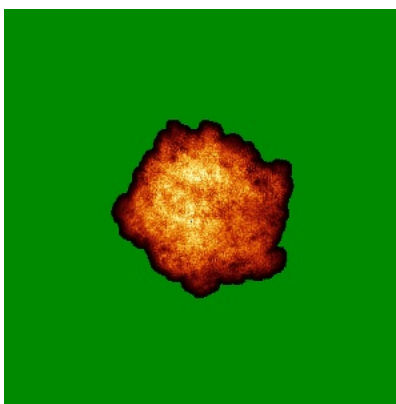
The images above show the largest variance slices of the map in three orthogonal directions.

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

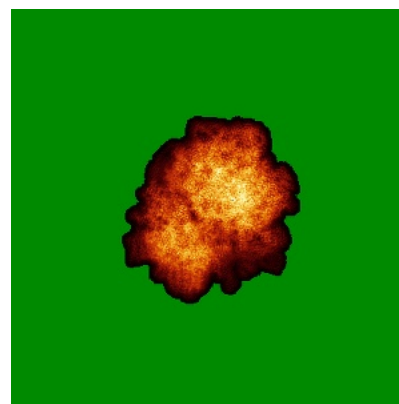
6.4.1 Primary map



X

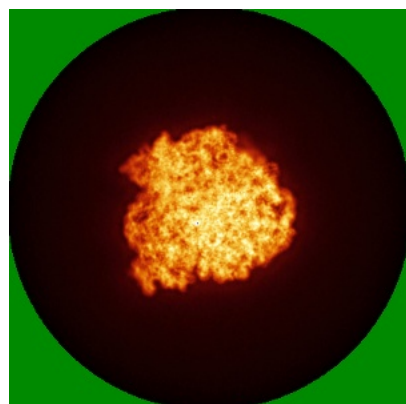


Y

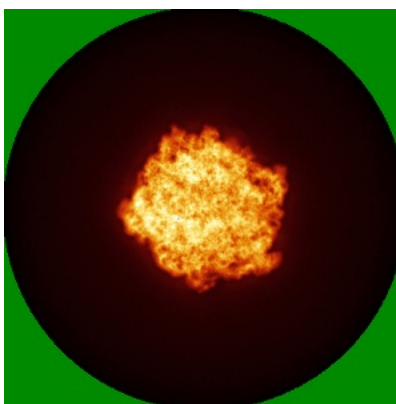


Z

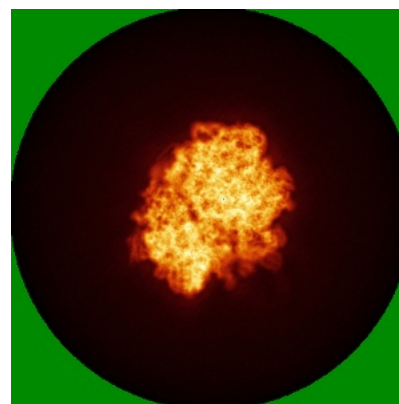
6.4.2 Raw map



X



Y

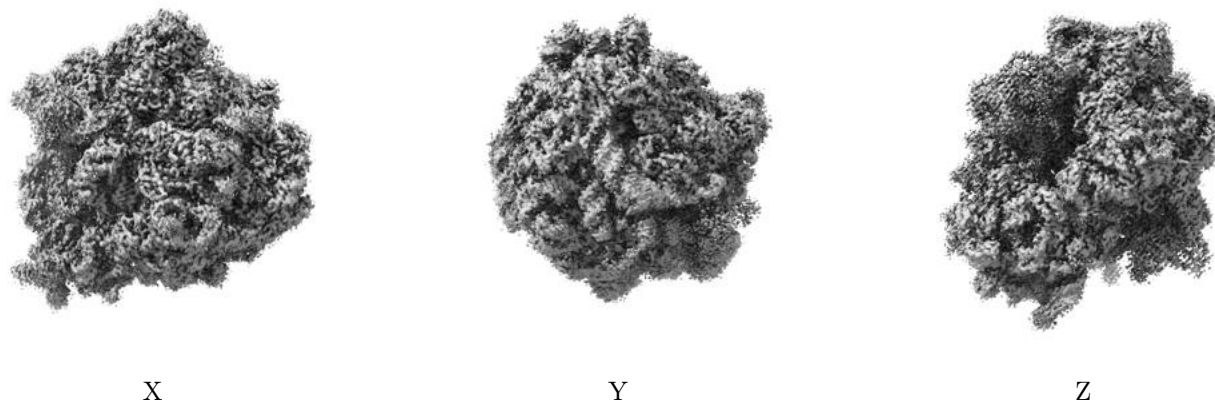


Z

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 0.1. 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.

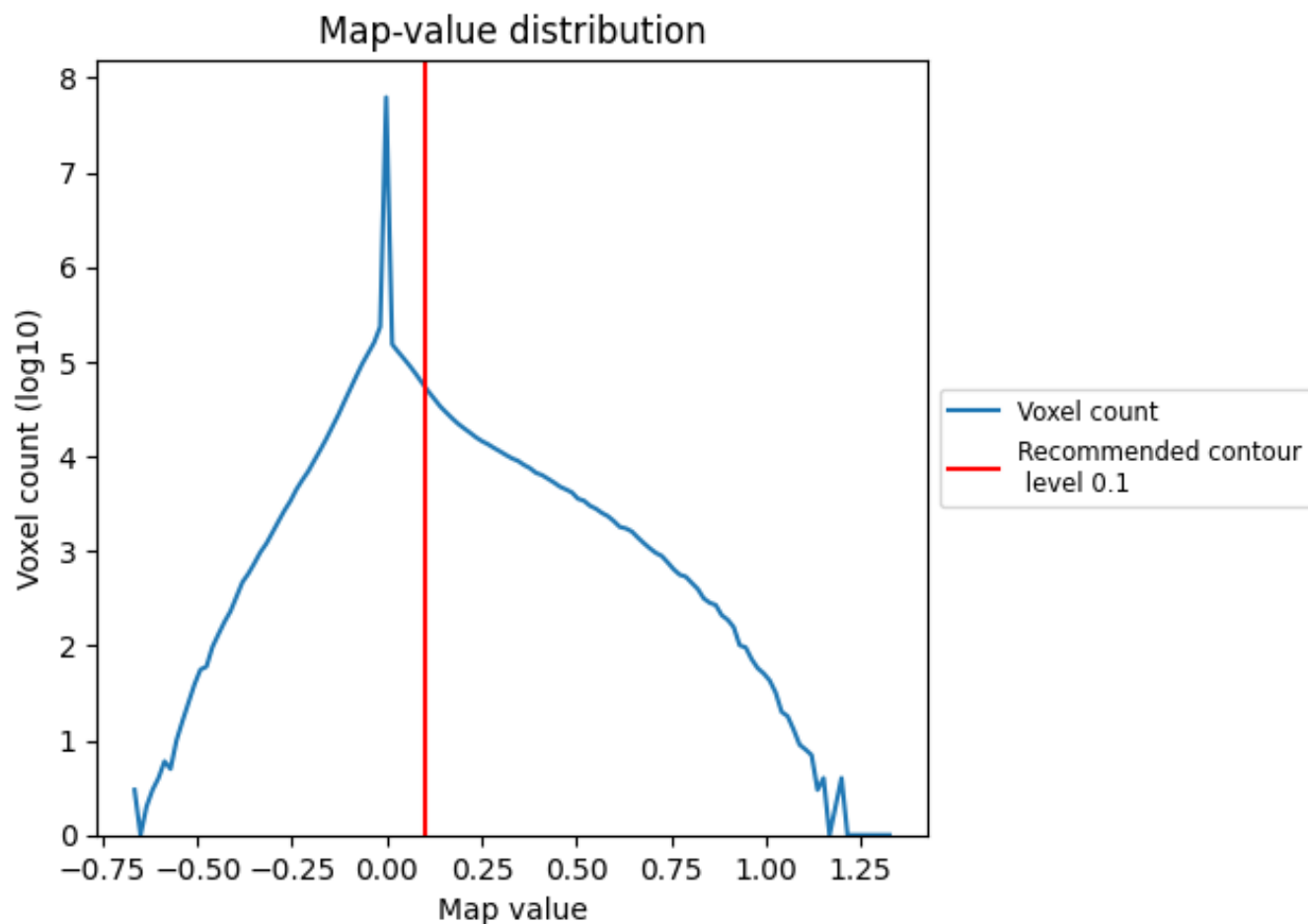
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

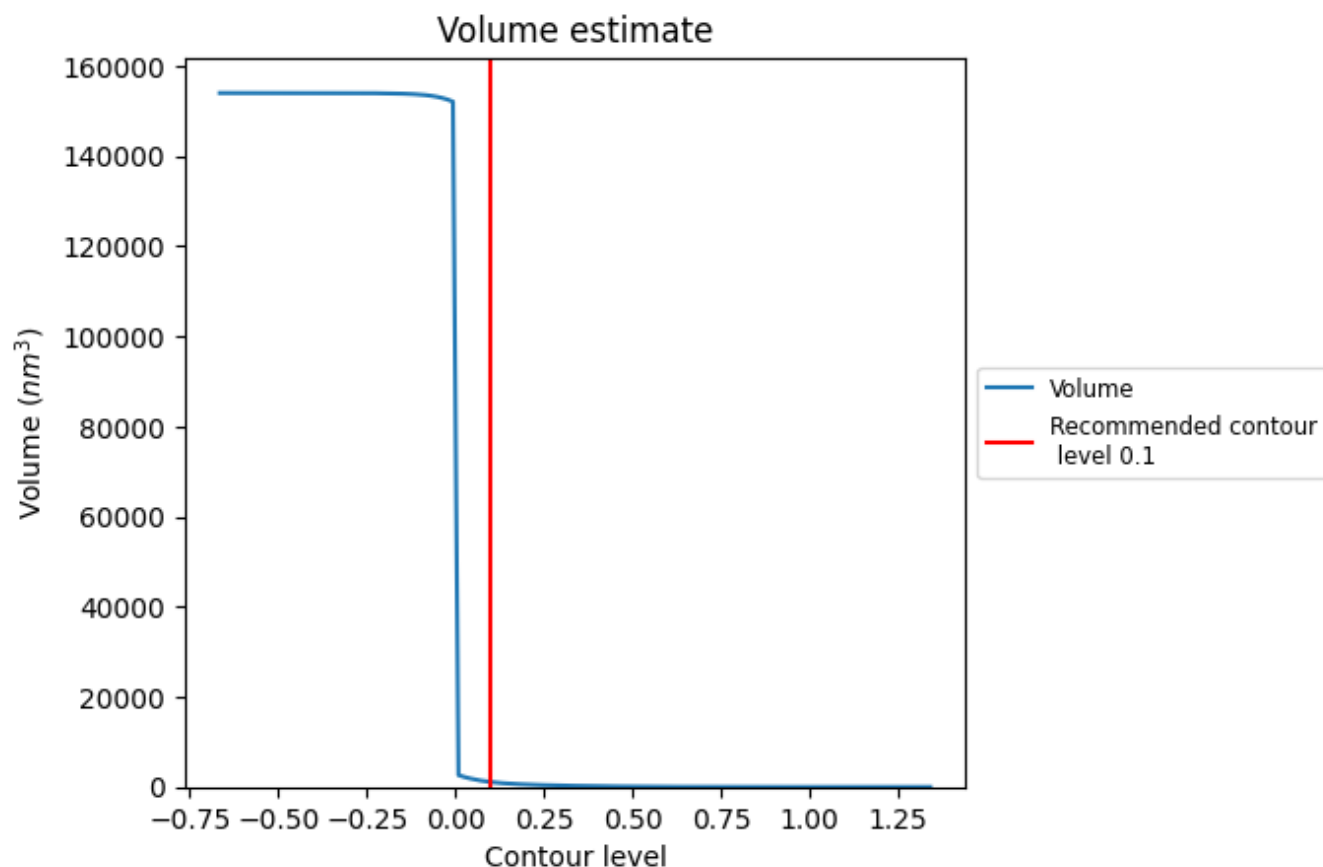
This section contains the results of statistical analysis of the map.

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.

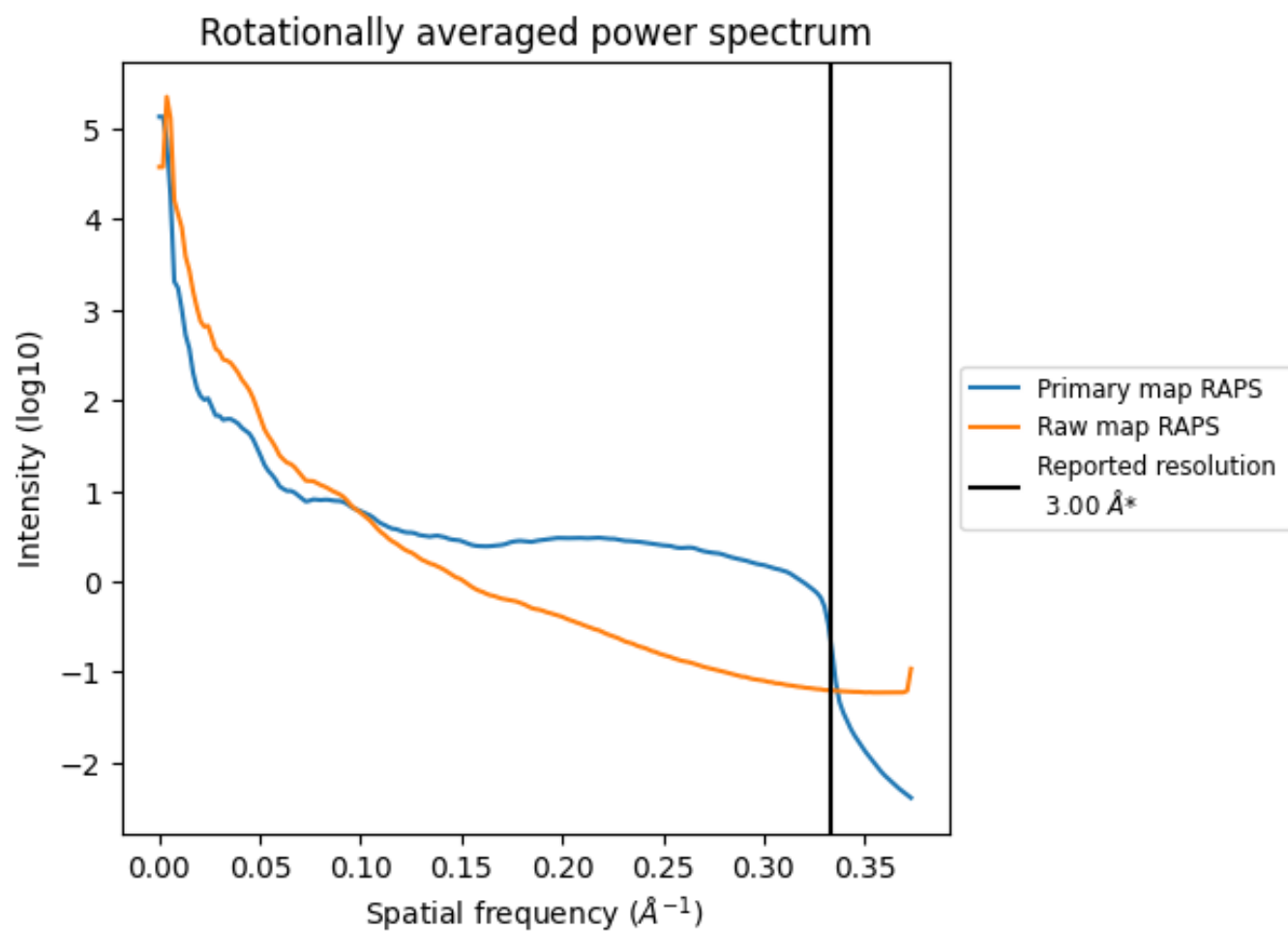
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1094 nm³; this corresponds to an approximate mass of 988 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

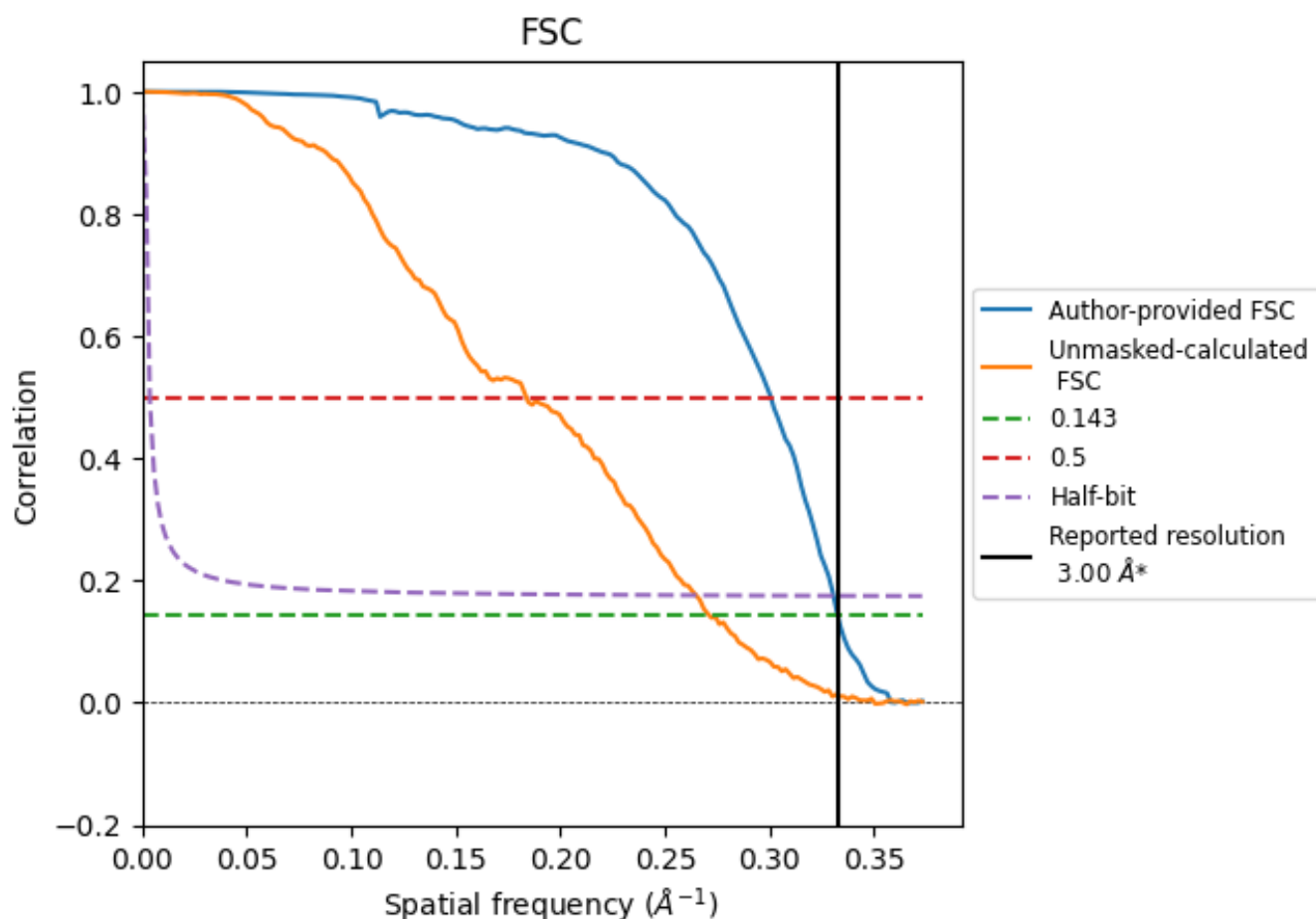


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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](#)

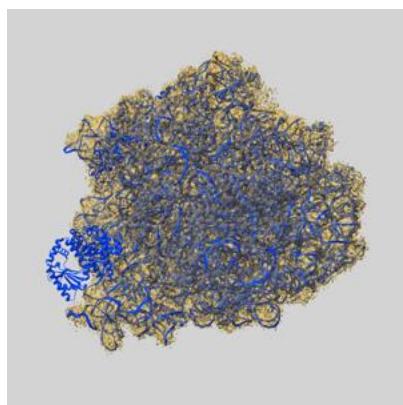
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.01	3.33	3.02
Unmasked-calculated*	3.69	5.44	3.77

*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 3.69 differs from the reported value 3.0 by more than 10 %

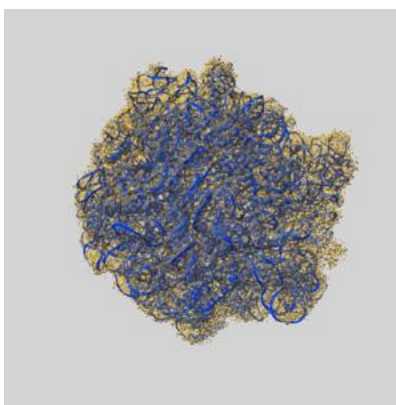
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8107 and PDB model 5IQR. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

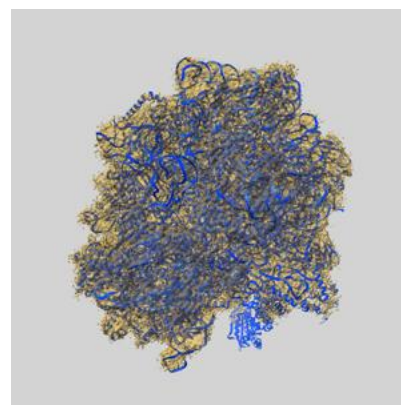
9.1 Map-model overlay [i](#)



X



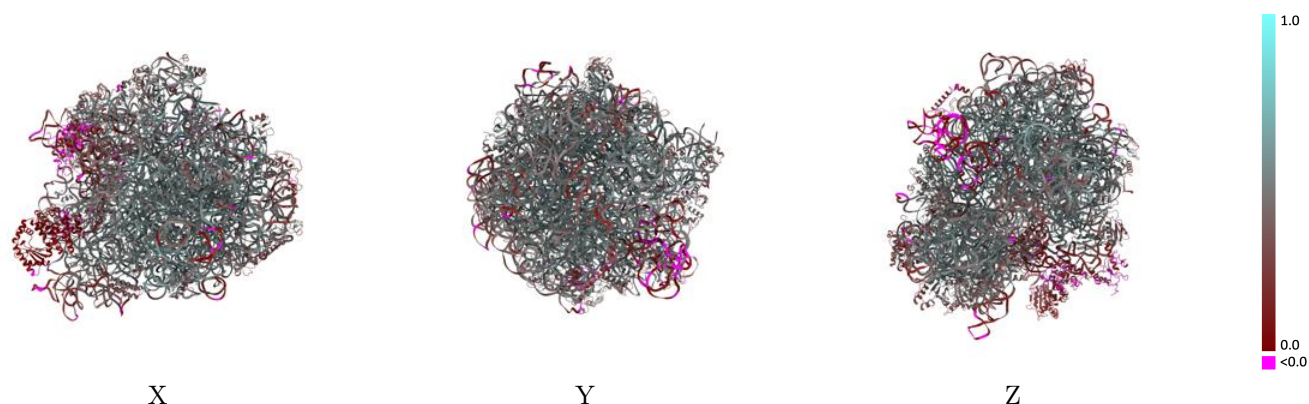
Y



Z

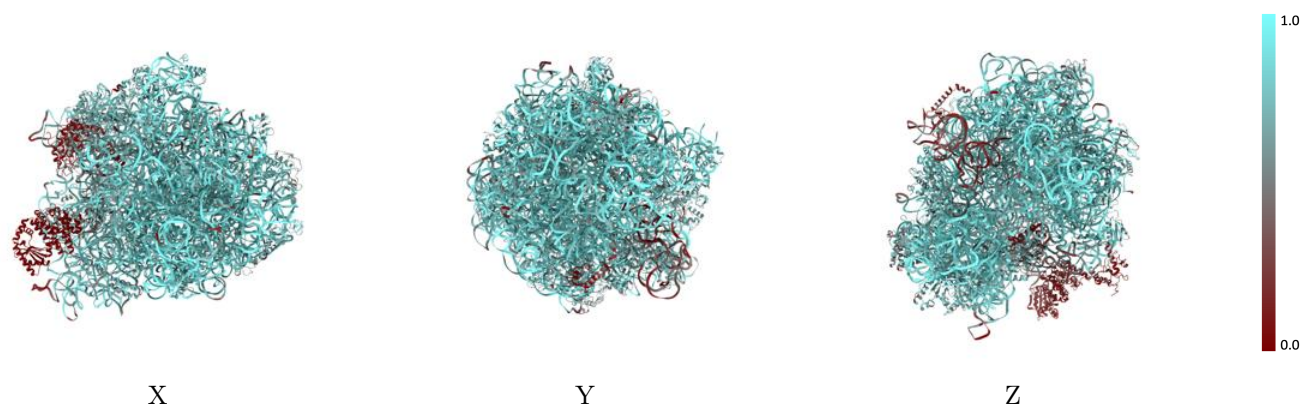
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



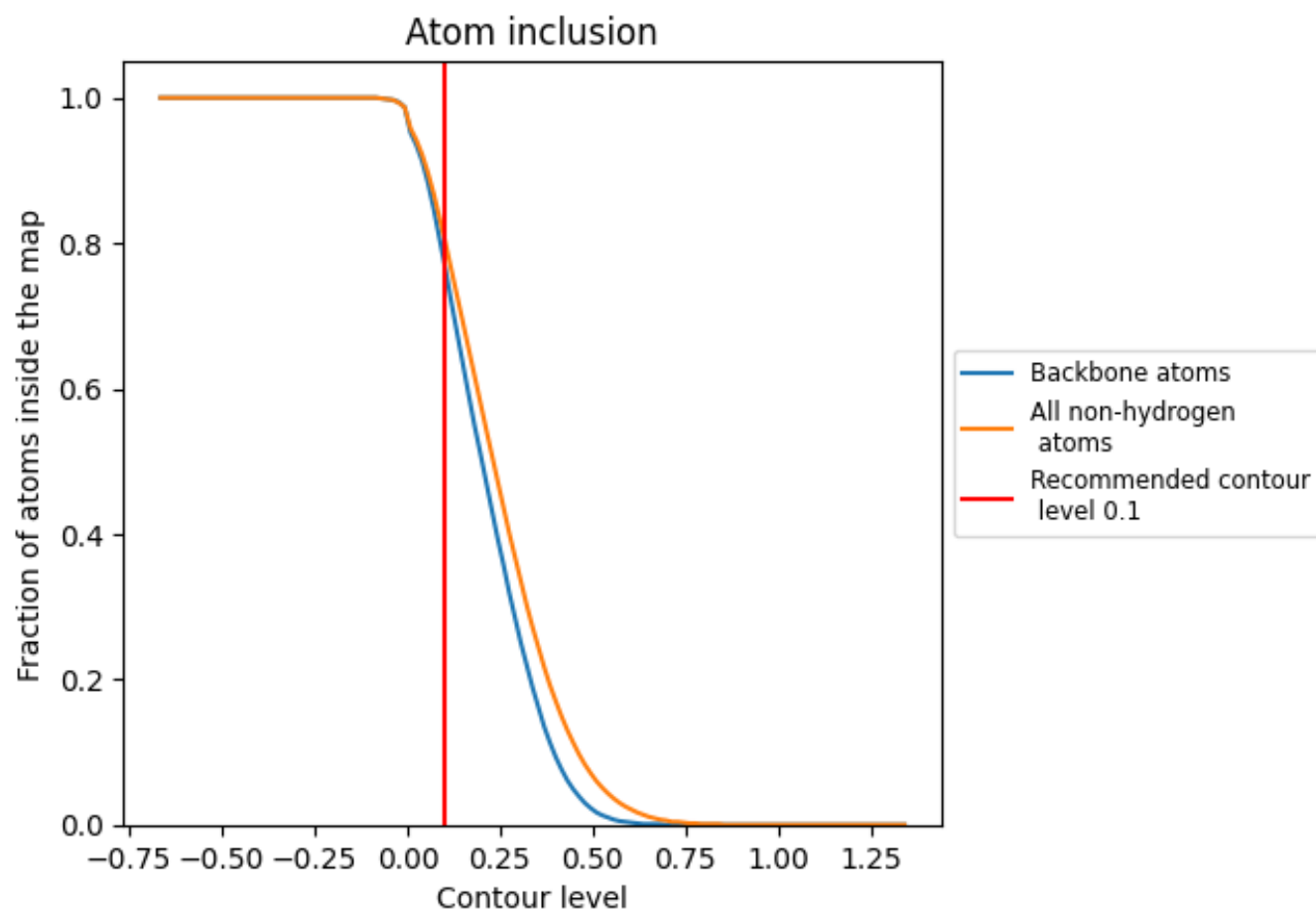
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 81% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8070	 0.4500
1	 0.8940	 0.4900
2	 0.8930	 0.4730
3	 0.9120	 0.4820
4	 0.2790	 0.1370
5	 0.8140	 0.4620
6	 0.4260	 0.1880
7	 0.7630	 0.4750
8	 0.1790	 0.1070
B	 0.8310	 0.5430
C	 0.8340	 0.5140
D	 0.7430	 0.4050
E	 0.7390	 0.4090
F	 0.7260	 0.4090
G	 0.2980	 0.1910
H	 0.1330	 0.0520
I	 0.1670	 0.0780
J	 0.8140	 0.5080
K	 0.8210	 0.5330
L	 0.7910	 0.4820
M	 0.8230	 0.5250
N	 0.8420	 0.4970
O	 0.7910	 0.4290
P	 0.8060	 0.4990
Q	 0.8160	 0.4890
R	 0.7940	 0.4680
S	 0.7870	 0.4790
T	 0.7300	 0.4260
U	 0.7330	 0.4160
V	 0.7760	 0.4630
W	 0.8440	 0.5360
X	 0.8200	 0.5060
Y	 0.6770	 0.3200
Z	 0.7960	 0.4800
a	 0.6310	 0.3090



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
b	 0.8290	 0.4960
c	 0.7380	 0.4780
d	 0.8170	 0.5370
e	 0.8600	 0.5470
f	 0.8400	 0.5240
g	 0.5940	 0.3550
h	 0.7500	 0.4520
i	 0.7350	 0.4100
j	 0.7940	 0.4840
k	 0.7520	 0.4300
l	 0.6870	 0.3920
m	 0.7910	 0.4900
n	 0.7600	 0.4160
o	 0.7280	 0.4060
p	 0.8100	 0.4930
q	 0.7430	 0.4770
r	 0.7650	 0.4440
s	 0.7810	 0.4650
t	 0.7560	 0.4430
u	 0.7660	 0.4420
v	 0.7420	 0.4420
w	 0.7840	 0.4710
x	 0.7850	 0.4690
y	 0.7500	 0.3950
z	 0.6620	 0.3940