



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 03:28 AM UTC

PDB ID : 8Y5S / pdb_00008y5s
EMDB ID : EMD-38948
Title : E.coli Transcription translation coupling complex in TTC-B state 5 (subclass 2) containing mRNA with 27-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and GDPCP
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

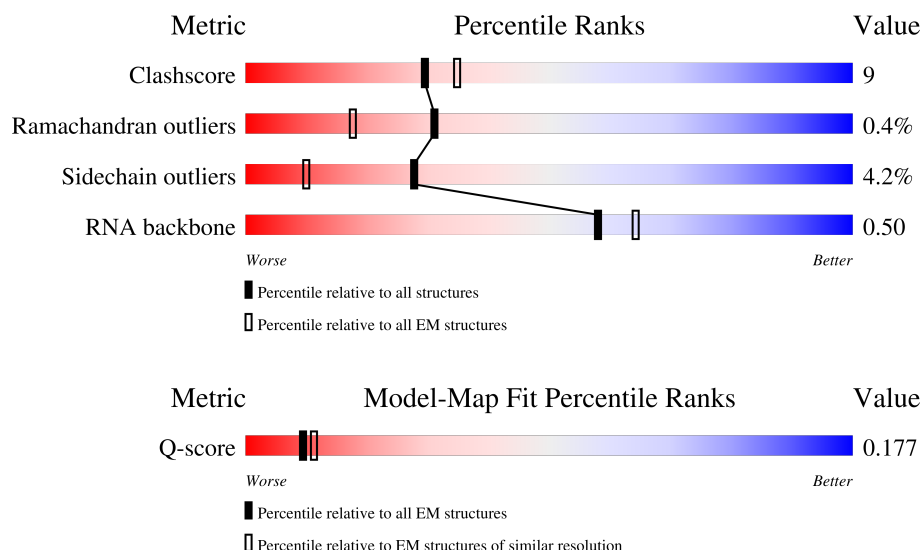
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 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.



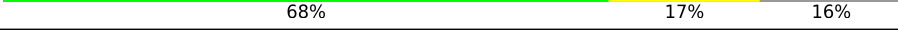
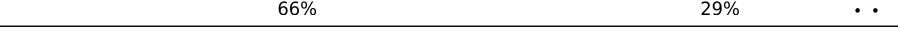
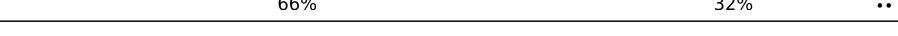
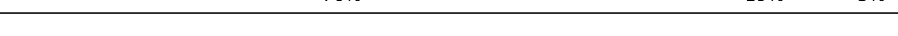
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	70	 81% 13% 6%
2	B	57	 79% 19% 2%
3	C	55	 84% 7% 9%

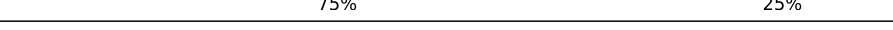
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	

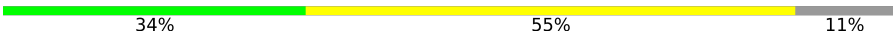
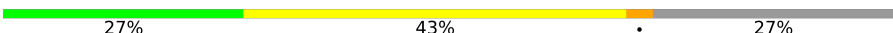
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	201	 81% 19%
30	e	179	 80% 18% ..
31	f	177	 72% 26% ..
32	g	149	 26% 9% 65%
33	i	142	 61% 35% ...
34	j	142	 81% 19%
35	k	123	 80% 20% .
36	l	144	 86% 13% .
37	m	136	 83% 17%
38	n	127	 75% 20% 6%
39	o	117	 81% 18% .
40	p	115	 83% 15% ..
41	q	118	 83% 15% ..
42	r	103	 75% 25%
43	s	110	 85% 15%
44	t	100	 74% 19% 7%
45	u	104	 72% 26% .
46	v	94	 85% 15%
47	w	85	 73% 15% 12%
48	x	78	 76% 22% ..
49	y	63	 73% 27%
50	z	59	 75% 24% .
51	1	2904	 43% 51% 6%
52	2	120	 74% 22% .
53	3	1542	 69% 29% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	4	44	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
65	0	716	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 181764 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 L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	66	Total	C	N	O	S	0	0
			521	323	98	94	6		

- Molecule 2 is a protein called 50S ribosomal protein L32.

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

- Molecule 3 is a protein called 50S ribosomal protein L33.

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

- Molecule 4 is a protein called 50S ribosomal protein L34.

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

- Molecule 5 is a protein called 50S ribosomal protein L35.

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

- Molecule 6 is a protein called 50S ribosomal protein L36.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

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

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

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

- Molecule 16 is a protein called 30S ribosomal protein S11.

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

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

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

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	52	Total	C	N	O	S	0	0
			400	256	73	70	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

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

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	39	Total	C	N	O	P	0	0
			809	362	113	295	39		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 63 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	0	673	Total	C	N	O	S	0	0
			5211	3289	900	999	23		

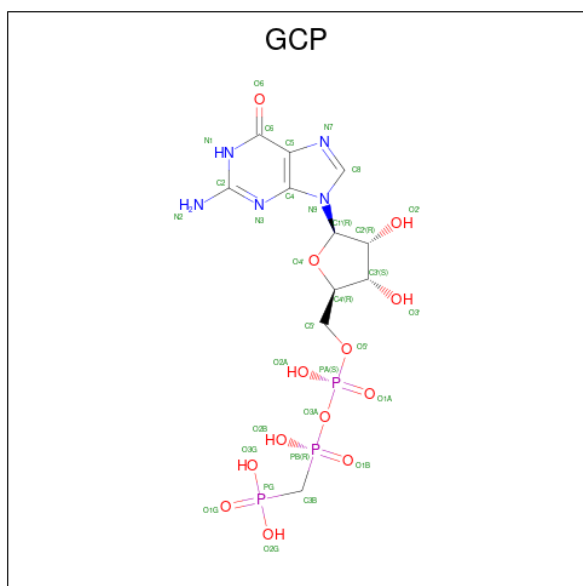
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	B1	1	Total	Mg	0
			1	1	

- Molecule 67 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $\text{C}_{11}\text{H}_{18}\text{N}_5\text{O}_{13}\text{P}_3$).



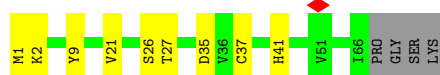
Mol	Chain	Residues	Atoms					AltConf
67	0	1	Total 32	C 11	N 5	O 13	P 3	0

3 Residue-property plots [i](#)

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

• Molecule 1: 50S ribosomal protein L31

Chain A: 



• Molecule 2: 50S ribosomal protein L32

Chain B: 



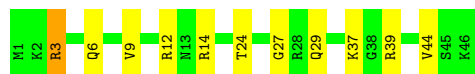
• Molecule 3: 50S ribosomal protein L33

Chain C: 



• Molecule 4: 50S ribosomal protein L34

Chain D: 



• Molecule 5: 50S ribosomal protein L35

Chain E: 



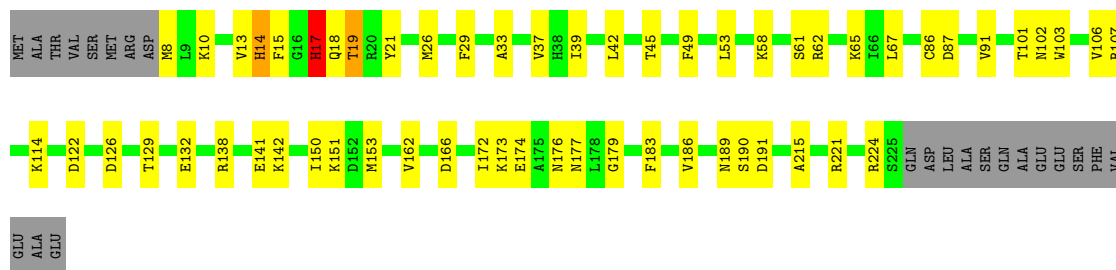
• Molecule 6: 50S ribosomal protein L36

Chain F:  82% 18%



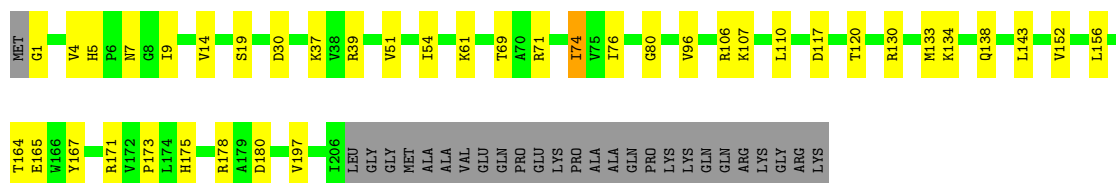
- Molecule 7: 30S ribosomal protein S2

Chain G:  66% 23% 10%



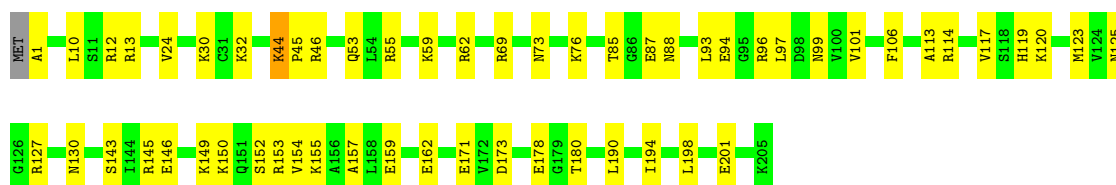
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% 12%



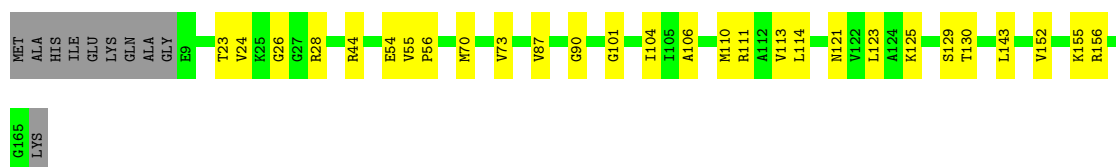
- Molecule 9: 30S ribosomal protein S4

Chain I:  72% 27%



- Molecule 10: 30S ribosomal protein S5

Chain J:  77% 17% 6%



- Molecule 11: 30S ribosomal protein S6, fully modified isoform



- Molecule 17: 30S ribosomal protein S12

Chain Q: 66% 32%



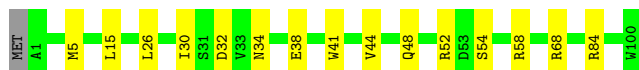
- Molecule 18: 30S ribosomal protein S13

Chain R: 68% 29%



- Molecule 19: 30S ribosomal protein S14

Chain S: 84% 15%



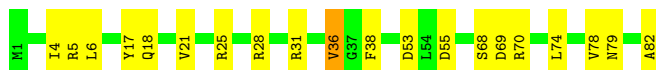
- Molecule 20: 30S ribosomal protein S15

Chain T: 85% 13%



- Molecule 21: 30S ribosomal protein S16

Chain U: 76% 23%



- Molecule 22: 30S ribosomal protein S17

Chain V: 76% 19% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W: 69% 16% 13%



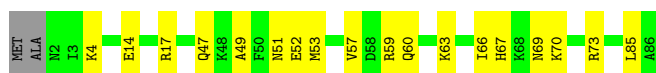
- Molecule 24: 30S ribosomal protein S19

Chain X: 73% 13% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y: 77% 21% 2%



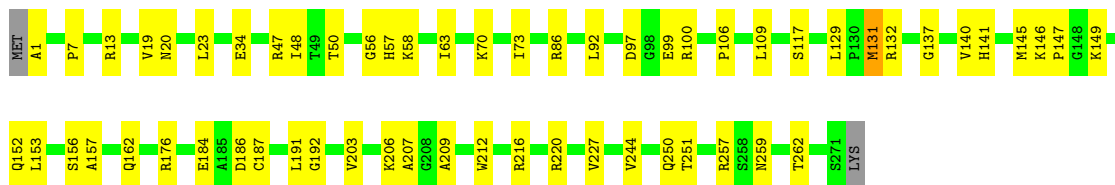
- Molecule 26: 30S ribosomal protein S21

Chain Z: 56% 31% 8%



- Molecule 27: 50S ribosomal protein L2

Chain b: 78% 21% 1%



- Molecule 28: 50S ribosomal protein L3

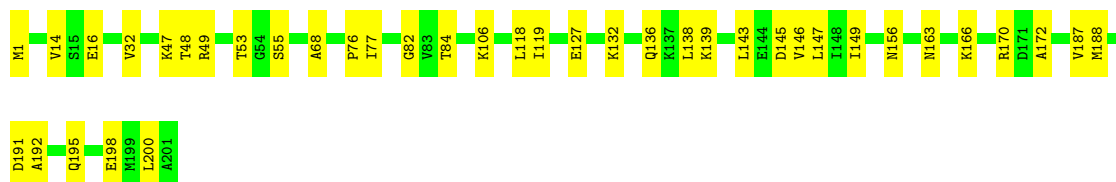
Chain c: 85% 15%





- Molecule 29: 50S ribosomal protein L4

Chain d: 81% 19%



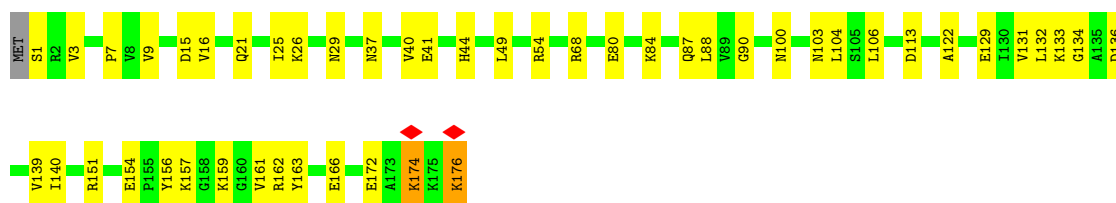
- Molecule 30: 50S ribosomal protein L5

Chain e: 80% 18% ..



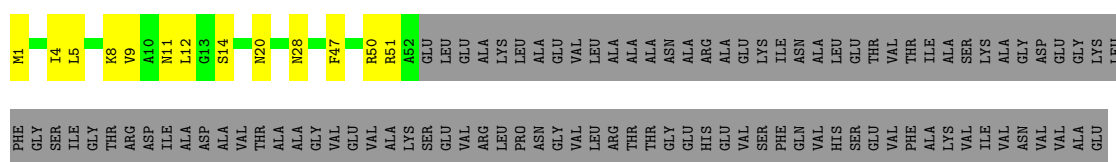
- Molecule 31: 50S ribosomal protein L6

Chain f: 72% 26% ..



- Molecule 32: 50S ribosomal protein L9

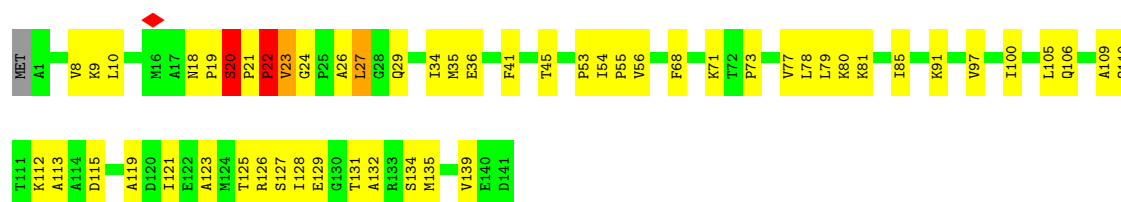
Chain g: 26% 9% 65%



- Molecule 33: 50S ribosomal protein L11

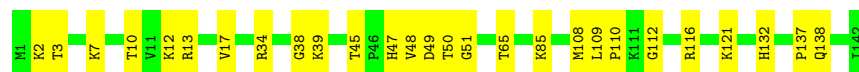
Chain i: 61% 35% ...





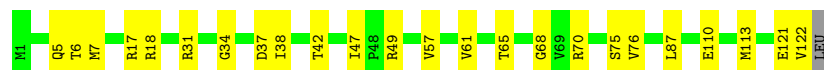
- Molecule 34: 50S ribosomal protein L13

Chain j: 81% 19%



- Molecule 35: 50S ribosomal protein L14

Chain k: 80% 20%



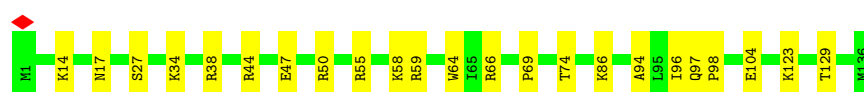
- Molecule 36: 50S ribosomal protein L15

Chain l: 86% 13%



- Molecule 37: 50S ribosomal protein L16

Chain m: 83% 17%



- Molecule 38: 50S ribosomal protein L17

Chain n: 75% 20% 6%



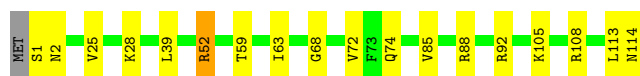
- Molecule 39: 50S ribosomal protein L18

Chain o: 81% 18%



- Molecule 40: 50S ribosomal protein L19

Chain p:  83% 15% ..



- Molecule 41: 50S ribosomal protein L20

Chain q:  83% 15% ..



- Molecule 42: 50S ribosomal protein L21

Chain r:  75% 25%



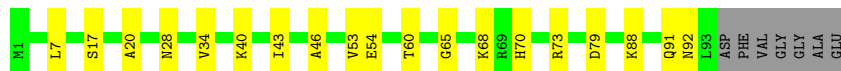
- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



- Molecule 44: 50S ribosomal protein L23

Chain t:  74% 19% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26% .



- Molecule 46: 50S ribosomal protein L25

Chain v:  85% 15%



- Molecule 47: 50S ribosomal protein L27

Chain w:  73% 15% 12%



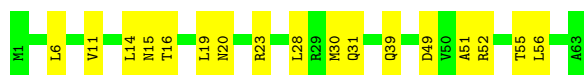
- Molecule 48: 50S ribosomal protein L28

Chain x:  76% 22% ..



- Molecule 49: 50S ribosomal protein L29

Chain y:  73% 27%



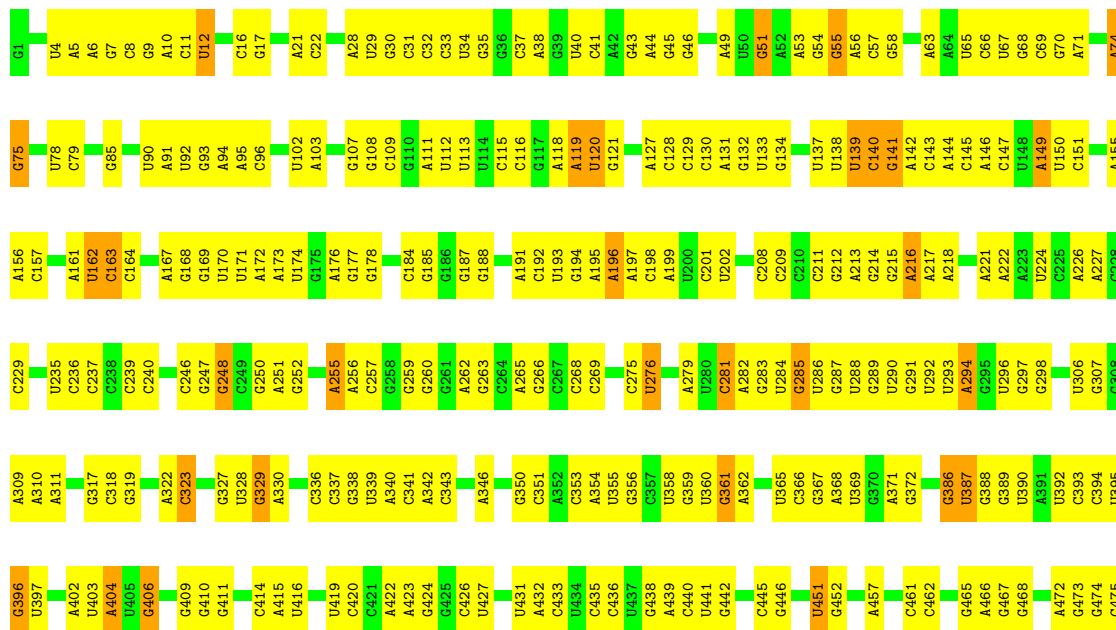
- Molecule 50: 50S ribosomal protein L30

Chain z:  75% 24% .



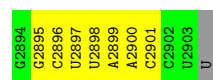
- Molecule 51: 23S rRNA

Chain 1:  43% 51% 6%



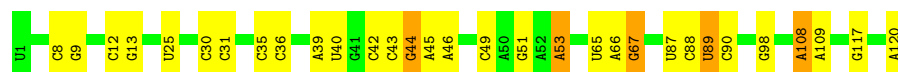
A1580	A1515	A1272	G1179	C1109	C961	C885	G809	G713	G630	G553	G476
G1581	G1516	U1273	U1180	G1110	C968	A886	U810	A718	A633	U554	A481
A1582	G1517	A1274	U1181	A1111	C968	U887	U811	C719	C634	G555	A482
	C1518	A1275	U1182	C1112	A972	C888	C812	U720	C635	C557	A488
G1588	G1519	C1278	U1184	C1114	A973	C889	U813	A721	C636	C558	C489
U1589	U1520	G1279	G1185	G1115	G974	C891	C814	A722	A637	C490	C490
G1590	G1521	G1280	G1186	G1116	A975	C892	C815	C723	C638	C491	A492
A1591	U1522	G1281	G1187	C1117	A979	C893	A819	U724	U639	A563	C493
A1592	U1523	U1282	U1188	C1118	A979	C894	A820	G725	C640	U562	C494
A1593	G1524	G1283	U1189	C1119	A981	C895	A821	U726	U641	U566	
A1594	A1525	U1284	G1193	G1120	C982	C896	A822	A727	A644	U567	
C1595	C1526	A1285	A1194	C1121	A983	C897	A823	G728	C645	U568	G498
A1596	G1527	A1286	G1195	U1130	A984	C898	U825	G729	C646	U569	U499
A1597	A1528	A1287	C1196	G1131	C985	A899	U826	A730	U647	G570	U499
A1598	G1529	G1288	U1197	G1132	C985	A900	U827	U731	G647	U571	G500
U1599	G1530	C1289	U1198	A1133	G989	C901	U828	C736	U648	A572	A501
C1600			U1199	A1134	G990	C902	A829		G649	U573	A502
G1601	C1533	G1292	C1200	C1135	G993	C903	G830	G745		A574	A503
U1602	U1534	C1293		C1136	C994	C904	G831	U746	U652	A575	A504
A1603	A1535	U1294	A1204	G1136	C994	A905	U832	C747	U653		A505
C1604	C1462	C1295	A1205	G1137	C995	A906	A833	A752	U654	U580	G506
G1605	G1536	G1296	U1201	G1138	A996	C907	G834		G655	C581	
C1606	G1537	C1297	U1209	A1139	G996	C908	C835	G757	G656	A582	C510
C1607	U1538	U1298	G1210	C1140	G1005	A909	G836	C758		A586	U511
A1608	G1540	G1299	G1211	U1141	G1009	A910	C837	G759	G662		G512
	C1541	G1300	U1212	A1142	A1009	A911		G760			
A1614	G1542	A1301	A1213	A1143	A1010		C840	G761	G669	A590	G518
C1615	G1543	C1306	U1219	C1144	U1011	G914	G841	U762	A670	U591	U519
A1616	A1544		C1220	A1145	U1012	C915	U842		C671	A592	G520
	A1545	G1309		C1146	U1013			G763	C672	U593	U521
G1625	G1546	G1310	G1225	A1147	A1014	A918	A845	A764	C673	U594	A522
A1626		G1311		U1148	U1015	U919	U846	C765	G674	C595	
A1634	C1550	G1312	U1230	A1149	U1016		U847	G774	A677	A526	A526
	A1551	C1314	U1231	C1150	U1017	G923	C848	G775	C678	A527	G527
G1642	A1552	G1315	G1232	A1151	A1084	G924	A849		C679	A528	A528
G1643	U1554	U1316	C1233	C1152	A1085	A925	U850		C680	A529	A529
C1644	G1555	G1317		C1153	A1086	G926	C851	U779	G681	G530	G530
G1645		U1318	A1237	G1154	G1087	A927	U852	G780	G682	C531	C531
C1646	U1559	C1319	G1238	A1155	A1088	A928	C853	A781	G682	A532	A532
U1647	U1560	C1320	G1239	G1157	A1089	U929	C854	A782	U683	G533	G533
U1648	C1561	A1321	U1240	G1158	A1090		G855	A783	G684	U534	U534
	U1562	C1322			G1091	U932	G858	G784	A685	G535	G535
G1651		C1323	A1246	G1160	C1092		G859	G785	U686	G536	G536
	C1565	G1324	A1247	C1161	G1093	C937	U889		C687	C610	C610
G1662	A1566	U1325		G1162	U1094	G938	U890	A788	U688	C611	G537
G1663	G1567	U1326	A1253	C1163	A1095	G939	U891	A789		G612	A538
	G1568	A1327	U1254	C1164	A1096	G940	G864	U790	G689	A613	G539
G1666	G1569	U1328	U1255	A1165	U1097	A941	C865	C791	G695	C540	C540
G1667	A1570	U1329	G1256	G1166	A1098	G942		A792	U615	A541	A541
A1668	U1571		C1257		G1099		U870	A793	G696	C542	C542
A1669	A1572	G1333	U1258	C1170	C1100	C946	U871	U703	G620	G543	G543
G1670	G1573	G1334	U1259	G1171	U1101	A947	U872	G704	A621	C544	C544
U1671	C1574	C1335	U1173	C1172	A1039		C873	A705	U546	U546	U546
A1672	G1575	A1336	U1174	A1103	A1040	U955		A706	C623	A547	A547
C1673		A1337	A1175	C1104	G1041	G956	C876	G707	G624	G548	G548
G1674	U1578	A1338	U1176	U1105	C1042	C957	A877	G708		G549	G549
C1675		G1339	U1177	G1106	C1043	U958	A878	U709	A627	C550	C550
A1676		G1339	G1271	G1107	C1044	U959	A879	G712	G628	G551	G551
				U1108	A1046	A960				U552	U552

A2810	G2732	C2649	U2571	A2476	U2390	A2309	G2230	G2162	C2096	U1834	C1761	A1677
G2811	A2733	U2650	A2572	A2482	G2591	C2310	U2233	A2163	A2097	A1916	C1761	A1678
A2812	G2734	C2651	C2573	A2483	U2392	U2311	G2234	C2164	U2098	A1917	C1762	A1679
G2813	G2735	C2652	G2574	C2483	U2393	U2312	G2235	C2165	U2099	A1918	G1763	U1690
A2814	A2736	C2653	C2575	G2488	C2394	A2313	U2236	U2166	G2101	C1920	G1764	G1681
G2815	G2737	C2659	G2576	U2489	C2395	A2314	U2237	U2167	A2101	G1921	U1765	G1696
G2816	G2738	A2660	A2577	G2490	G2396	G2315	G2238	A2170	G2102	U1922	G1766	G1697
A2820	G2742	A2661	G2578	G2491	U2402	G2316	G2239	A2171	C2103	U1923	G1767	A1698
G2827	U2743	A2662	U2492	U2492	C2403	U2321	U2240	U2172	C2104	C1924	G1768	G1699
C2827	G2744	G2663	U2493	C2496	U2404	G2325	G2241	A2173	A2015	A1927	A1772	G1702
G2828	G2747	C2667	C2496	C2497	A2405	G2326	G2242	A2174	U2016	G1928	A1773	C1774
A2829	A2748	C2668	C2497	C2498	A2406	A2327	U2243	C2174	G2107	G1929	A1774	G1703
G2830	U2749	U2585	U2499	C2499	A2407	A2328	U2244	U2180	G2108	U1931	G1776	A1710
G2834	G2751	C2671	G2502	G2502	A2411	U2329	A2247	U2181	G2110	A1935	A1780	A1711
A2835	U2752	U2672	U2593	U2593	A2412	G2330	G2248	U2182	U2111	G1936	U1781	G1715
G2837	C2676	C2676	G2595	U2505	G2420	A2333	U2257	U2183	G2112	A1937	U1782	U1716
G2839	A2679	U2596	U2506	U2506	G2421	U2334	C2258	G2186	G2113	A1938	A1783	U1717
C2840	U2756	U2680	C2507	C2507	C2422	A2335	U2259	U2187	U2118	U1939	A1784	G1718
G2843	A2757	C2681	C2510	C2510	U2423	A2336	C2260	U2188	A2119	C1942	A1785	G1719
G2844	G2758	A2682	U2511	U2511	C2424	G2337	G2261	U2189	G2122	U1943	A1786	U1720
U2845	C2683	C2683	U2512	A2516	A2425	C2338	A2267	G2190	U2123	U1944	A1787	G1721
G2846	U2684	U2684	A2517	C2517	C2427	A2339	A2268	U2191	G2124	G1945	A1788	A1722
G2847	U2687	U2687	U2518	U2518	G2428	A2340	G2271	U2192	G2125	G1948	C1790	G1723
G2848	G2688	C2681	U2519	A2519	A2429	G2341	G2272	G2193	G2126	A1952	A1794	U1725
U2849	A2764	U2689	C2612	U2520	A2430	A2346	C2275	U2194	G2127	A1953	A1795	C1726
A2850	A2765	U2690	U2613	G2525	U2431	C2347	C2276	C2196	G2128	G1954	U1796	C1727
A2851	U2768	C2692	G2614	G2526	A2432	U2348	A2278	U2197	U2129	A1955	U1797	U1729
G2852	C2773	U2697	U2615	C2527	A2433	G2349	A2279	A2198	U2130	U1956	G1798	C1730
C2853	U2776	U2698	U2616	U2528	A2434	C2350	G2280	A2199	U2131	U1882	G1799	G1731
G2858	A2777	C2699	U2617	G2529	A2435	A2351	A2281	C2200	G2132	U1883	C1800	C1732
A2860	A2778	U2701	G2618	U2530	A2436	A2352	G2282	G2201	U2133	G1884	A1801	G1733
U2861	U2779	G2702	C2619	U2533	G2437	G2353	C2283	U2202	A2134	A1885	A1802	G1734
G2867	G2782	U2707	G2625	A2534	C2440	G2361	A2284	G2204	U2137	U1886	A1807	A1735
A2868	U2783	C2708	C2626	C2539	U2441	C2362	G2285	A2205	G2138	C1887	A1808	U1736
G2869	G2784	U2710	G2627	G2545	G2445	C2363	G2286	C2208	G2141	G1967	A1809	G1737
C2870	A2711	G2630	U2628	U2546	G2446	G2364	A2287	G2209	U2142	G1968	G1738	A1739
U2871	C2712	G2631	G2629	A2547	G2447	A2365	G2288	U2210	G2143	A1969	U1812	G1740
A2872	U2713	A2632	C2630	U2554	A2448	G2366	U2290	A2211	C2145	U1970	G1813	C1741
G2876	G2714	U2633	G2631	C2555	G2455	C2367	U2291	A2212	G2146	U1971	C1816	U1742
A2879	C2715	A2634	U2632	U2556	U2456	G2368	U2292	U2213	A2147	G1975	G1817	G1743
C2880	U2718	U2637	G2633	G2557	U2457	U2372	G2293	C2214	G2148	U1976	G1818	A1745
G2885	G2719	G2638	G2634	U2561	G2458	G2379	U2294	C2215	U2149	A1977	A1819	A1746
C2888	A2726	U2643	A2565	A2566	C2467	C2380	U2295	G2216	U2151	G1978	U1820	U1747
G2889	U2804	G2644	A2567	G2567	C2468	A2381	U2296	G2217	G2152	A1901	A1821	C1748
G2890	C2805	U2647	U2568	U2569	A2469	G2382	A2297	G2218	U2074	G1906	G1822	G1749
A2893	U2806	C2730	G2569	G2570	A2471	C2383	U2298	G2219	U2075	G1907	G1823	U1750
		G2731	G2648			U2384	U2299	C2220	U2086	C1905	U1824	U1751
						A2385	U2300	G2221	C2073	G1906	U1825	G1752
						A2386	G2303	G2222	U2074	G1907	G1826	G1753
						U2387	G2304	G2223	U2075	G1908	U1827	G1754
						A2388	G2305	G2224	U2082	G1909	U1828	A1754
						G2389	U2306	A2225	G2093	G1910	A1829	A1755
							U2307	G2226	U2094	C1912	G1832	U1758
							G2308	A2227	C2160	A1913	A1832	
									C2161	U1915	A1833	



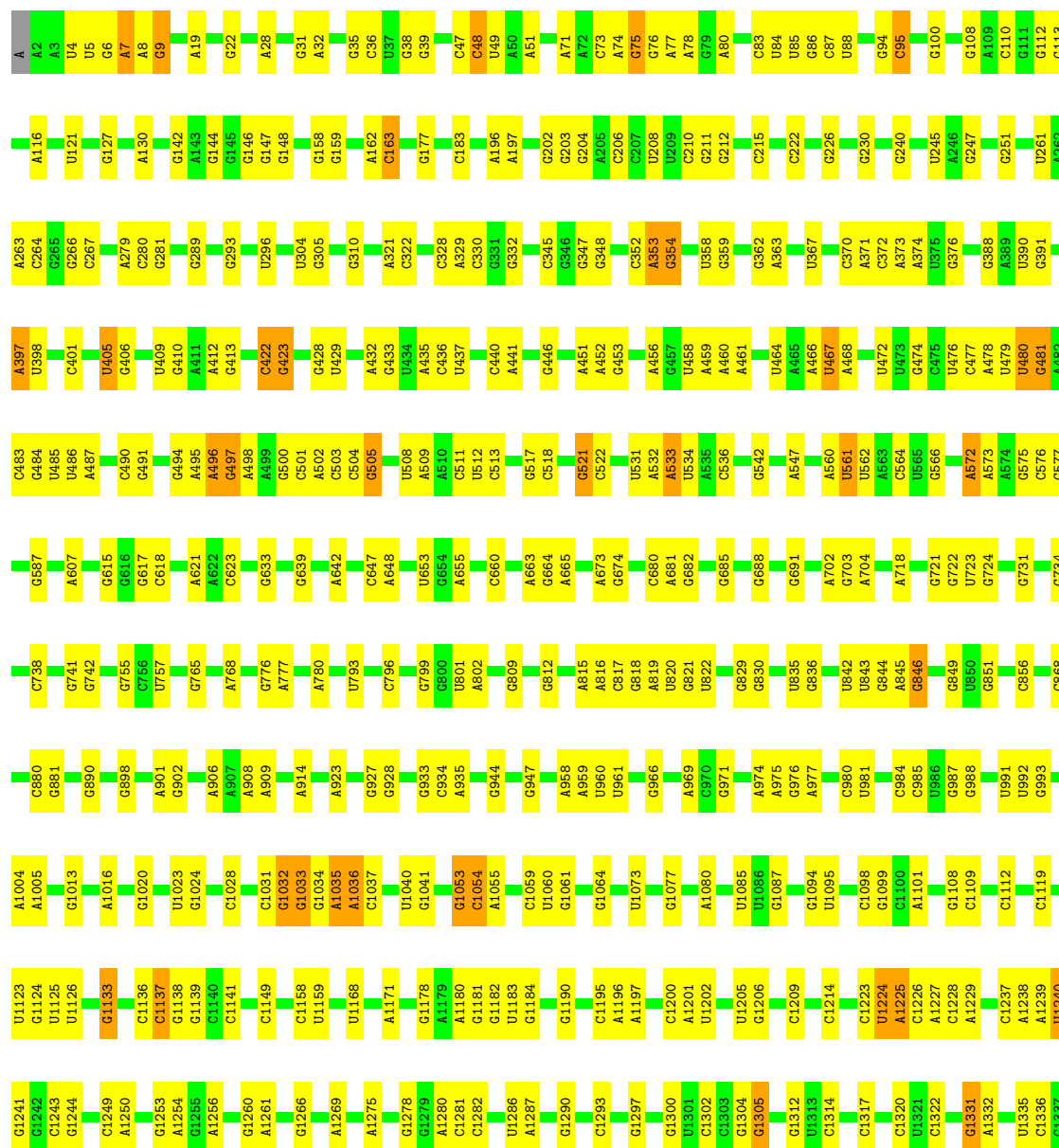
• Molecule 52: 5S rRNA

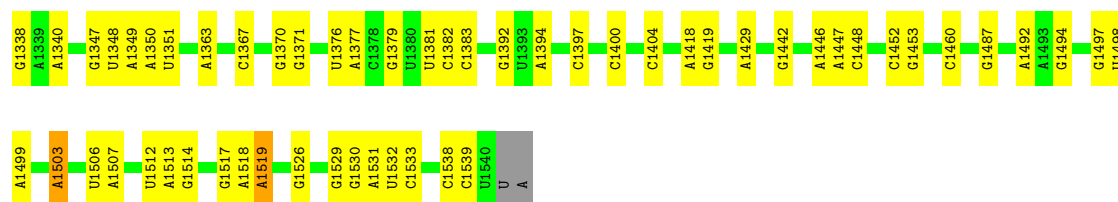
Chain 2: 74% 22% .



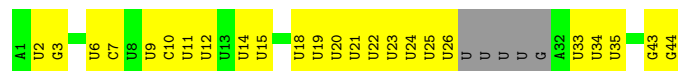
• Molecule 53: 16S rRNA

Chain 3: 69% 29% .

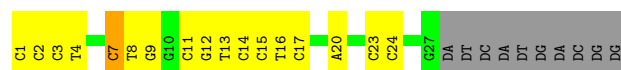




- Molecule 54: mRNA



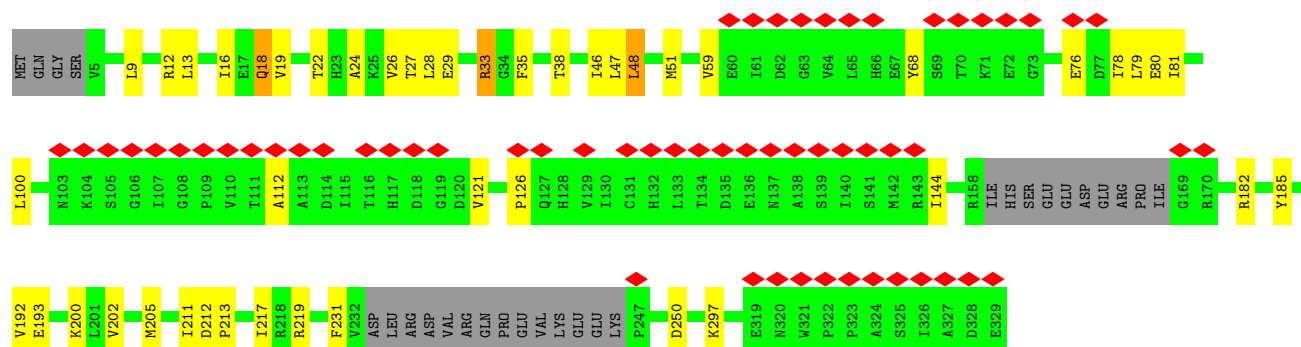
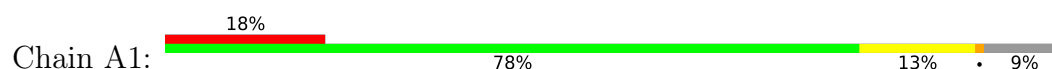
- Molecule 55: template DNA strand



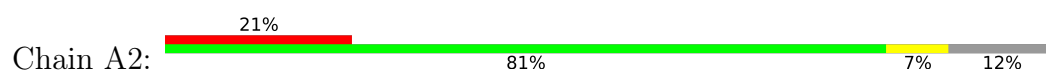
- Molecule 56: non-template DNA strand

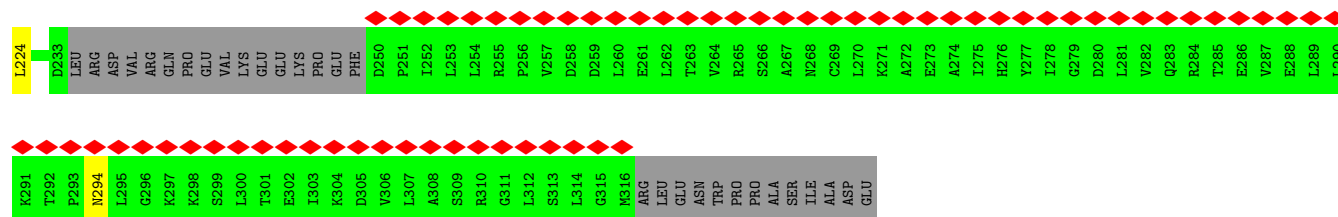


- Molecule 57: DNA-directed RNA polymerase subunit alpha

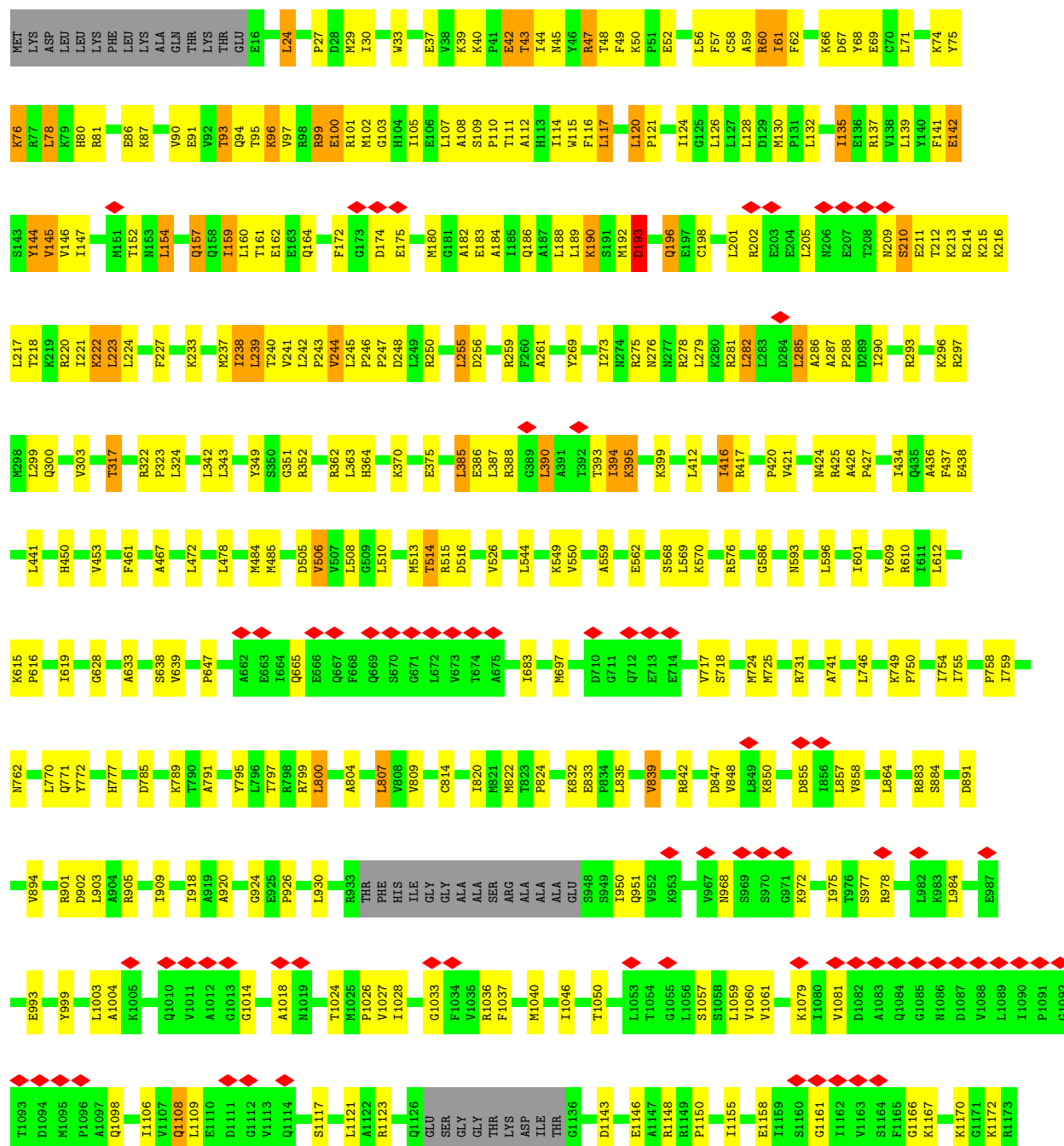


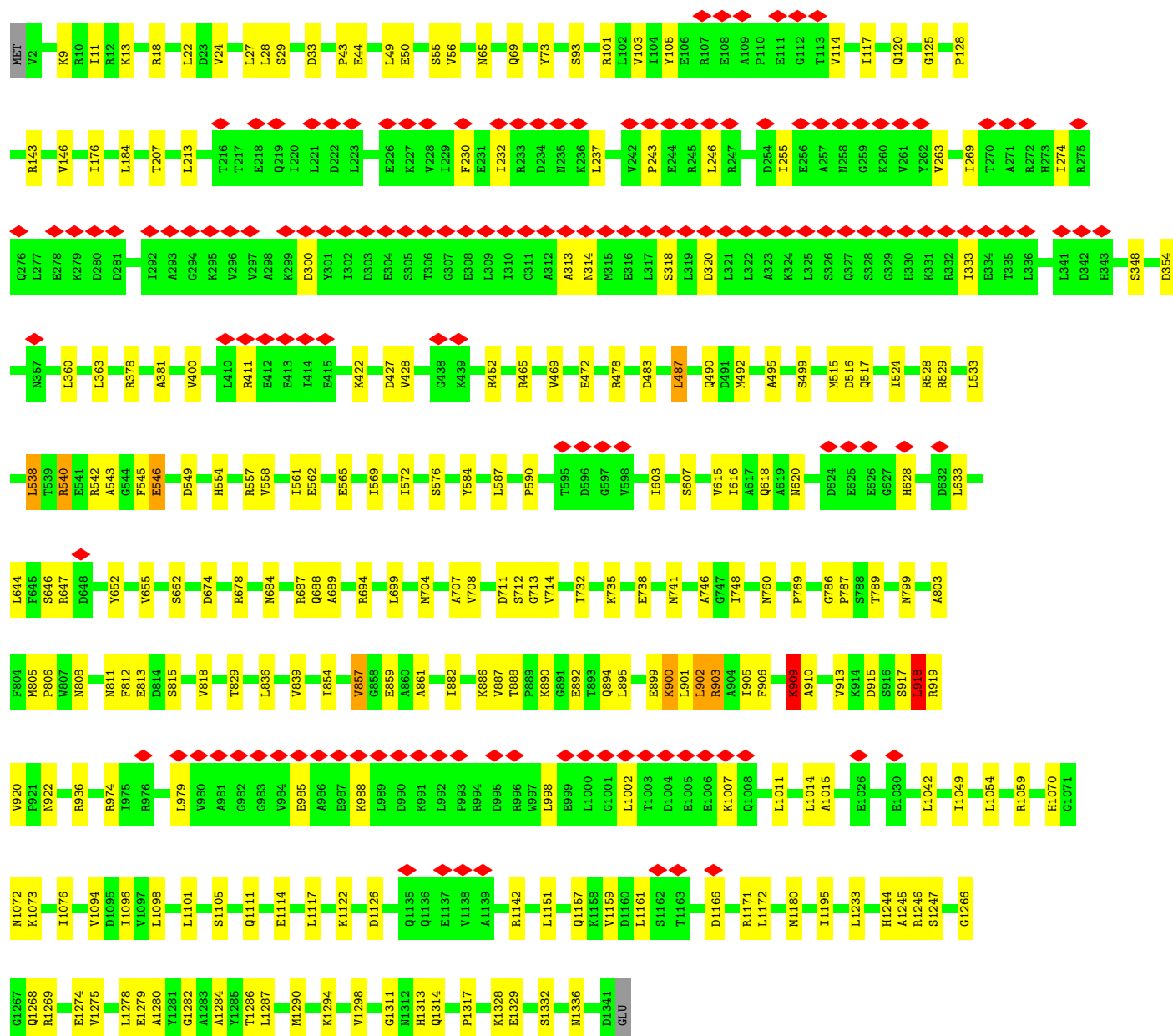
- Molecule 57: DNA-directed RNA polymerase subunit alpha



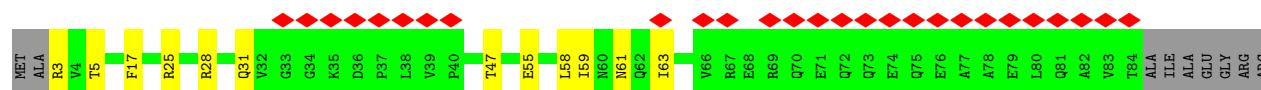
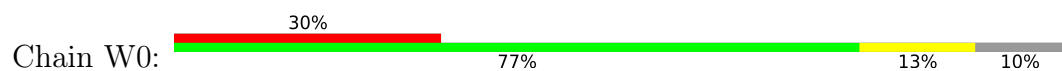


• Molecule 58: DNA-directed RNA polymerase subunit beta'

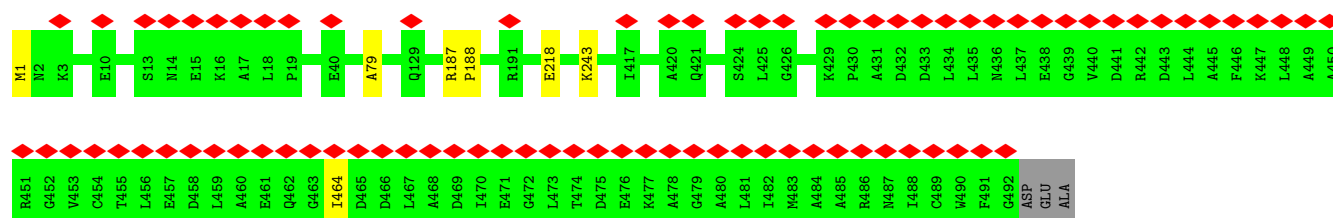




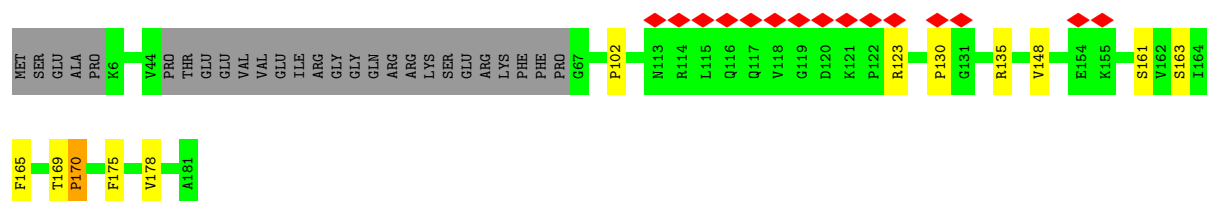
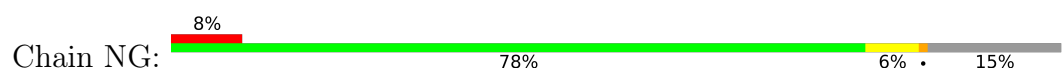
- Molecule 60: DNA-directed RNA polymerase subunit omega



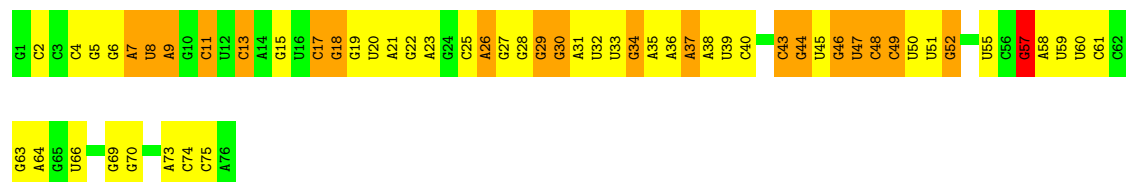
- Molecule 61: Transcription termination/antitermination protein NusA



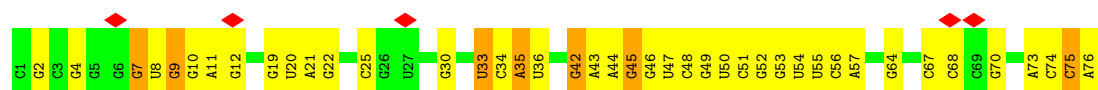
- Molecule 62: Transcription termination/antitermination protein NusG



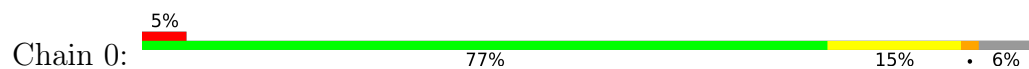
- Molecule 63: tRNA(Phe)



- Molecule 64: tRNA(fMet)



- Molecule 65: Elongation factor G





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	476340	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.090	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size ($\text{\AA}$)	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.57, 1.57, 1.57	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/530	0.54	0/707
2	B	0.40	0/450	0.60	0/599
3	C	0.28	0/416	0.52	0/554
4	D	0.47	0/380	0.76	2/498 (0.4%)
5	E	0.53	0/513	0.60	0/676
6	F	0.58	0/303	0.66	0/397
7	G	0.38	0/1735	0.64	0/2338
8	H	0.34	0/1651	0.55	0/2225
9	I	0.35	0/1665	0.71	0/2227
10	J	0.38	0/1169	0.68	2/1573 (0.1%)
11	K	0.46	0/835	0.77	0/1128
12	L	0.31	0/1195	0.66	3/1602 (0.2%)
13	M	0.35	0/989	0.52	0/1326
14	N	0.47	0/1034	0.77	0/1375
15	O	0.50	0/796	0.78	2/1077 (0.2%)
16	P	0.45	0/885	0.65	1/1195 (0.1%)
17	Q	0.50	0/969	0.86	2/1300 (0.2%)
18	R	0.33	0/892	0.73	4/1193 (0.3%)
19	S	0.33	0/817	0.61	0/1088
20	T	0.49	0/722	0.64	0/964
21	U	0.30	0/659	0.71	2/884 (0.2%)
22	V	0.44	0/657	0.71	0/881
23	W	0.55	0/544	0.74	1/731 (0.1%)
24	X	0.29	0/652	0.55	0/877
25	Y	0.29	0/671	0.52	0/888
26	Z	0.66	0/550	1.01	2/728 (0.3%)
27	b	0.49	0/2121	0.64	0/2852
28	c	0.42	0/1586	0.59	2/2134 (0.1%)
29	d	0.44	0/1571	0.62	0/2113
30	e	0.43	0/1434	0.65	2/1926 (0.1%)
31	f	0.35	0/1343	0.56	0/1816
32	g	0.32	0/405	0.75	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.51	0/1046	0.87	3/1410 (0.2%)
34	j	0.42	0/1152	0.55	1/1551 (0.1%)
35	k	0.45	0/947	0.66	0/1268
36	l	0.40	0/1054	0.63	0/1403
37	m	0.56	0/1093	0.74	0/1460
38	n	0.46	0/973	0.72	1/1301 (0.1%)
39	o	0.32	0/902	0.51	0/1209
40	p	0.42	0/929	0.63	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.46	0/829	0.70	0/1107
43	s	0.44	0/864	0.58	0/1156
44	t	0.33	0/744	0.52	0/994
45	u	0.46	0/787	0.75	0/1051
46	v	0.34	0/766	0.51	0/1025
47	w	0.40	0/582	0.52	0/769
48	x	0.43	0/635	0.63	1/848 (0.1%)
49	y	0.29	0/510	0.63	0/677
50	z	0.41	0/453	0.53	0/605
51	1	0.51	0/69796	0.62	21/108888 (0.0%)
52	2	0.44	0/2872	0.46	0/4479
53	3	0.42	0/36963	0.43	0/57662
54	4	0.52	0/896	0.68	0/1387
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.49	0/468	0.53	0/719
57	A1	0.56	0/2106	0.82	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.57	4/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	1/14459 (0.0%)
60	W0	0.31	0/652	0.60	0/879
61	NA	0.79	0/2431	1.22	0/3385
62	NG	1.11	0/756	1.05	0/1048
63	5	0.57	0/1812	0.85	1/2823 (0.0%)
64	6	0.40	0/1832	0.57	1/2855 (0.0%)
65	0	0.84	0/5308	1.17	8/7181 (0.1%)
All	All	0.50	4/195128 (0.0%)	0.64	73/287304 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
51	1	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.29	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.18	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.18	1.22	1.33
58	B1	665	GLN	CD-OE1	5.08	1.33	1.23

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	0	580	PHE	CA-CB-CG	9.59	123.39	113.80
16	P	73	VAL	N-CA-C	-9.02	104.54	113.20
41	q	33	VAL	N-CA-C	-8.75	104.77	112.12
12	L	64	ALA	N-CA-C	-7.68	105.07	114.75
51	1	1130	U	C2'-C3'-O3'	7.60	120.90	109.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	1	2446	G	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	A	521	0	520	7	0
2	B	444	0	461	9	0
3	C	409	0	440	3	0
4	D	377	0	418	9	0
5	E	504	0	574	4	0
6	F	302	0	343	2	0
7	G	1704	0	1732	36	0
8	H	1624	0	1699	25	0
9	I	1643	0	1710	36	0
10	J	1156	0	1199	18	0
11	K	817	0	808	17	0
12	L	1181	0	1240	19	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	979	0	1034	9	0
14	N	1022	0	1070	22	0
15	O	786	0	828	18	0
16	P	869	0	878	23	0
17	Q	955	0	1019	26	0
18	R	883	0	944	19	0
19	S	805	0	847	10	0
20	T	714	0	737	5	0
21	U	649	0	666	15	0
22	V	648	0	691	8	0
23	W	535	0	552	7	0
24	X	637	0	665	8	0
25	Y	665	0	714	11	0
26	Z	544	0	579	14	0
27	b	2082	0	2157	47	0
28	c	1565	0	1616	28	0
29	d	1552	0	1619	28	0
30	e	1410	0	1447	19	0
31	f	1323	0	1374	28	0
32	g	400	0	423	7	0
33	i	1032	0	1088	36	0
34	j	1129	0	1162	23	0
35	k	938	0	1012	18	0
36	l	1045	0	1117	17	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	18	0
39	o	892	0	923	15	0
40	p	917	0	965	14	0
41	q	947	0	1022	10	0
42	r	816	0	839	16	0
43	s	857	0	922	11	0
44	t	738	0	807	10	0
45	u	779	0	834	13	0
46	v	753	0	780	9	0
47	w	575	0	592	9	0
48	x	625	0	655	11	0
49	y	509	0	543	13	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1455	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	185	0
54	4	809	0	404	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	8	539	0	305	29	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	26	0
57	A2	2029	0	1864	16	0
58	B1	10353	0	10548	330	0
59	B2	10546	0	10550	166	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	8	0
62	NG	758	0	334	10	0
63	5	1622	0	821	27	0
64	6	1640	0	837	20	0
65	0	5211	0	5200	45	0
66	B1	1	0	0	0	0
67	0	32	0	13	0	0
All	All	181764	0	131004	2830	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 9.

The worst 5 of 2830 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)
51:1:275:C:H2'	51:1:276:U:H4'	1.37	1.06
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.03
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.03
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01

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	A	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
2	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	20
3	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
4	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
5	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
6	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	49
8	H	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
9	I	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	24	63
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
15	O	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	12	47
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	49
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	49
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	9	41
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	21
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	37
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
31	f	174/177 (98%)	160 (92%)	14 (8%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	31

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	110 (79%)	26 (19%)	3 (2%)	5	29
34	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
35	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
36	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
37	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	35
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
44	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
45	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	12	47
46	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
48	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	9	41
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	295/329 (90%)	273 (92%)	21 (7%)	1 (0%)	36	71
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1202 (90%)	123 (9%)	4 (0%)	36	71
59	B2	1338/1342 (100%)	1205 (90%)	128 (10%)	5 (0%)	30	67
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	471 (96%)	17 (4%)	2 (0%)	30	67
62	NG	150/181 (83%)	130 (87%)	15 (10%)	5 (3%)	3	21
65	0	669/716 (93%)	625 (93%)	43 (6%)	1 (0%)	48	83
All	All	10253/10945 (94%)	9280 (90%)	935 (9%)	38 (0%)	31	67

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	x	25	LYS
58	B1	121	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
61	NA	187	ARG
61	NA	188	PRO
62	NG	102	PRO

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	A	58/62 (94%)	57 (98%)	1 (2%)	53	67
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
4	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
5	E	51/52 (98%)	49 (96%)	2 (4%)	28	50
6	F	34/34 (100%)	30 (88%)	4 (12%)	5	19
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	55
8	H	170/190 (90%)	167 (98%)	3 (2%)	51	67
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	63
10	J	119/126 (94%)	117 (98%)	2 (2%)	53	67
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	41
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	68	76
14	N	105/107 (98%)	95 (90%)	10 (10%)	8	26
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	27
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	54
17	Q	103/104 (99%)	98 (95%)	5 (5%)	22	44
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	28	50
21	U	65/65 (100%)	64 (98%)	1 (2%)	57	70

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	V	74/78 (95%)	72 (97%)	2 (3%)	39	59
23	W	56/65 (86%)	52 (93%)	4 (7%)	13	35
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	57	70
26	Z	55/61 (90%)	47 (86%)	8 (14%)	3	14
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	51	67
30	e	148/150 (99%)	142 (96%)	6 (4%)	27	49
31	f	137/138 (99%)	132 (96%)	5 (4%)	31	52
32	g	41/114 (36%)	38 (93%)	3 (7%)	13	34
33	i	109/110 (99%)	100 (92%)	9 (8%)	10	31
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	68	76
37	m	109/109 (100%)	103 (94%)	6 (6%)	19	42
38	n	100/103 (97%)	99 (99%)	1 (1%)	68	76
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	98 (99%)	1 (1%)	68	76
41	q	89/90 (99%)	86 (97%)	3 (3%)	32	54
42	r	84/84 (100%)	82 (98%)	2 (2%)	43	63
43	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
44	t	80/84 (95%)	80 (100%)	0	100	100
45	u	83/85 (98%)	79 (95%)	4 (5%)	23	45
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	67 (100%)	0	100	100
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	46 (96%)	2 (4%)	26	48
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	40
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	B1	1110/1168 (95%)	1017 (92%)	93 (8%)	10	30
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	59
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	71
65	0	553/588 (94%)	482 (87%)	71 (13%)	4	17
All	All	7931/8500 (93%)	7594 (96%)	337 (4%)	28	48

5 of 337 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	B1	1331	VAL
65	0	370	LYS
59	B2	487	LEU
59	B2	918	LEU
65	0	472	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
59	B2	330	HIS
59	B2	688	GLN
65	0	496	GLN
27	b	89	ASN
27	b	69	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	398 (13%)	15 (0%)
52	2	119/120 (99%)	17 (14%)	2 (1%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	37/44 (84%)	21 (56%)	2 (5%)
63	5	75/76 (98%)	39 (52%)	6 (8%)
64	6	76/77 (98%)	27 (35%)	2 (2%)
All	All	4747/4763 (99%)	755 (15%)	31 (0%)

5 of 755 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	34	U
51	1	35	G
51	1	46	G

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	2326	C
63	5	57	G
53	3	4	U
64	6	33	U
63	5	32	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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	$\# Z > 2$
67	GCP	0	800	-	32,34,34	3.22	12 (37%)	49,54,54	1.60	8 (16%)

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
67	GCP	0	800	-	-	6/19/38/38	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	800	GCP	O4'-C1'	8.93	1.62	1.42
67	0	800	GCP	C2'-C1'	-7.12	1.31	1.53
67	0	800	GCP	PB-O3A	6.42	1.65	1.58
67	0	800	GCP	O4'-C4'	-6.21	1.31	1.45
67	0	800	GCP	PA-O3A	5.69	1.65	1.59

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	0	800	GCP	C5-C4-N3	-5.06	120.33	128.39
67	0	800	GCP	C2-N3-C4	4.62	120.26	112.30
67	0	800	GCP	C2-N1-C6	-3.08	119.52	125.11
67	0	800	GCP	N9-C8-N7	-2.98	107.88	113.40
67	0	800	GCP	C5-C6-N1	2.76	120.29	113.25

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

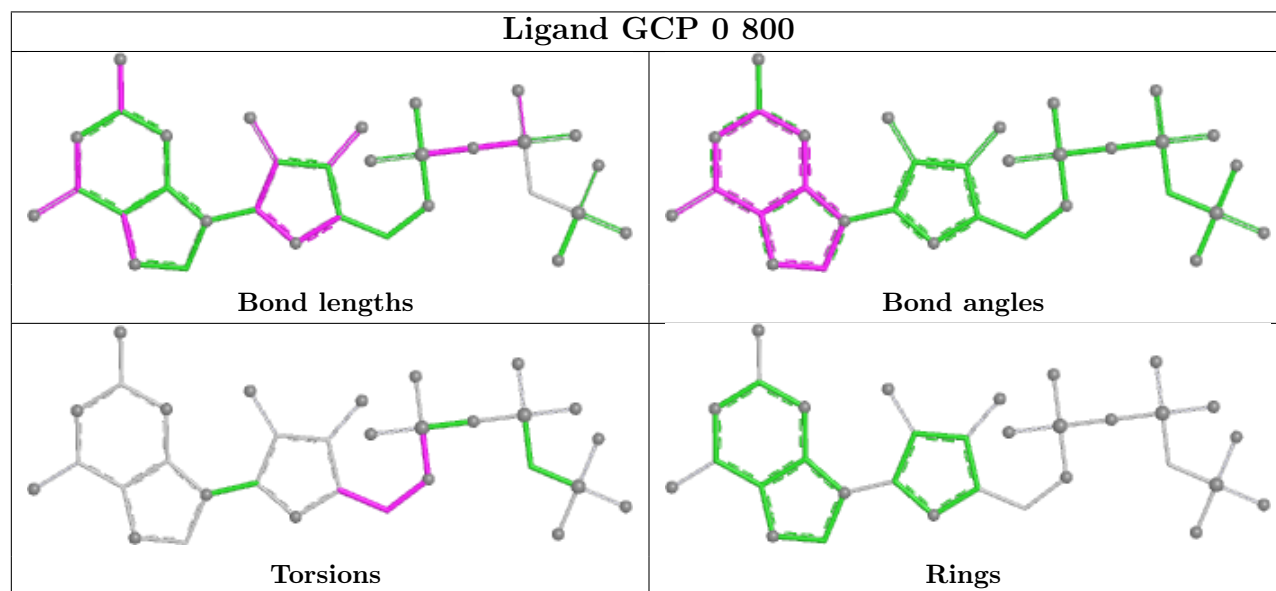
Mol	Chain	Res	Type	Atoms
67	0	800	GCP	C5'-O5'-PA-O3A
67	0	800	GCP	C5'-O5'-PA-O1A
67	0	800	GCP	C5'-O5'-PA-O2A
67	0	800	GCP	O4'-C4'-C5'-O5'
67	0	800	GCP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

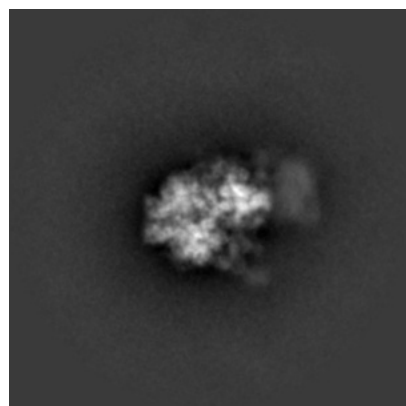
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38948. These allow visual inspection of the internal detail of the map and identification of artifacts.

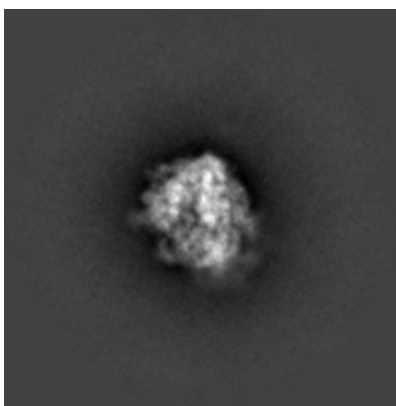
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

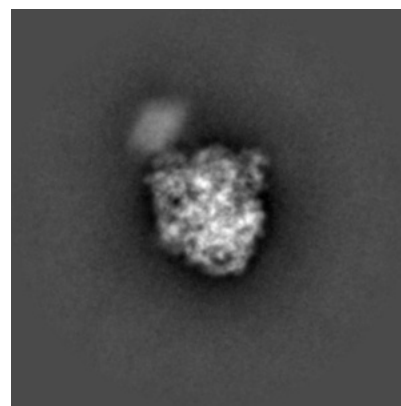
6.1.1 Primary map



X

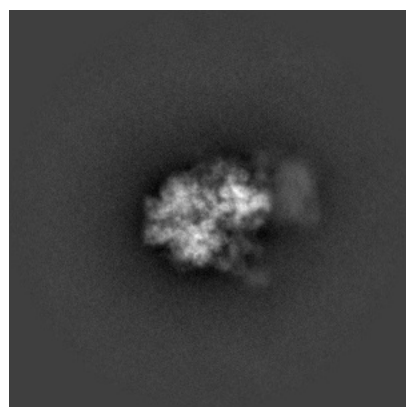


Y

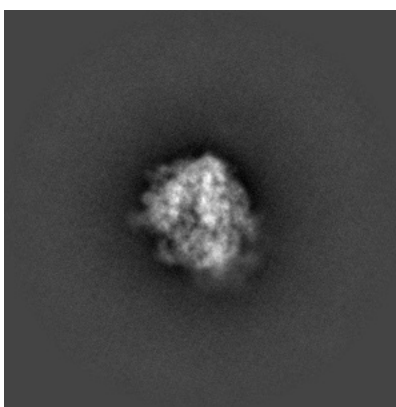


Z

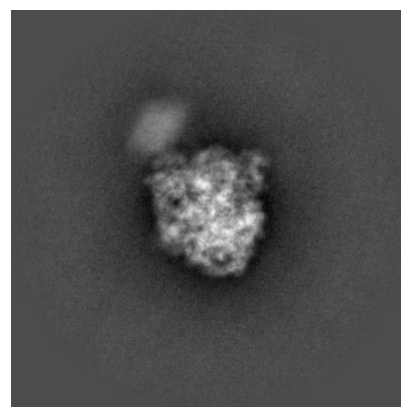
6.1.2 Raw map



X



Y

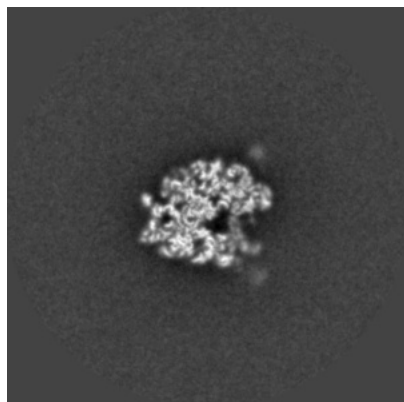


Z

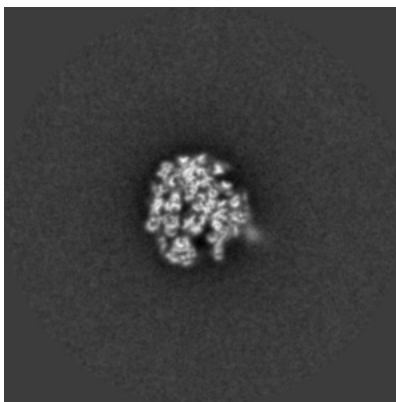
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

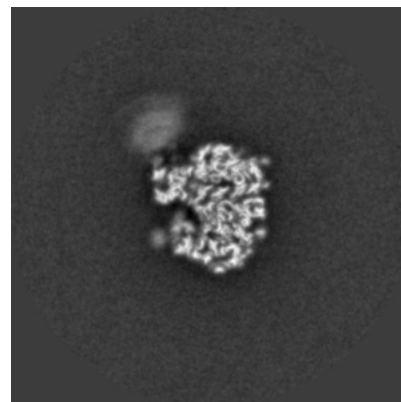
6.2.1 Primary map



X Index: 240

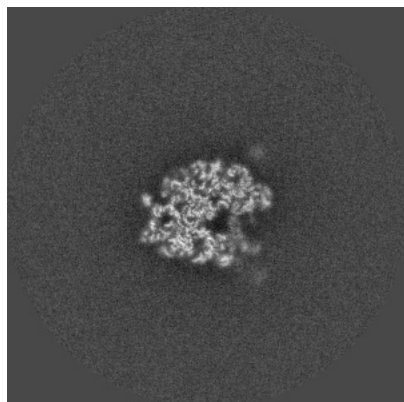


Y Index: 240

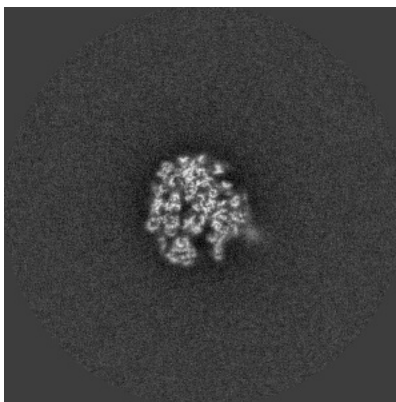


Z Index: 240

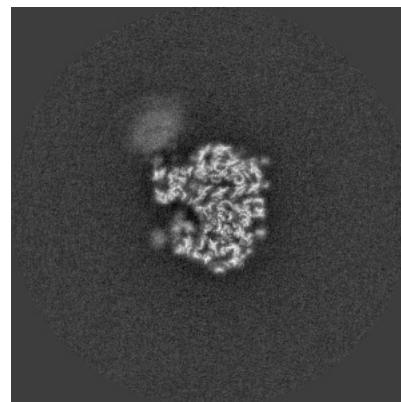
6.2.2 Raw map



X Index: 240



Y Index: 240

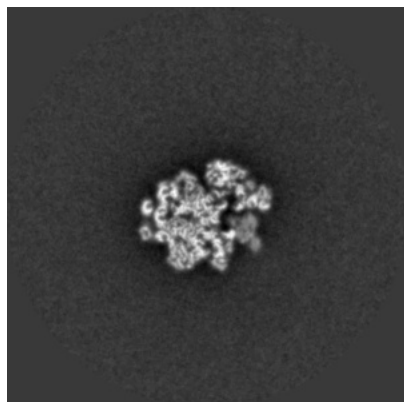


Z Index: 240

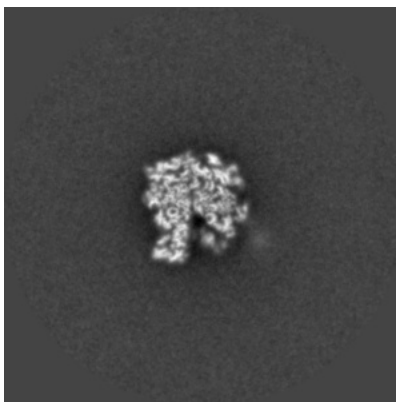
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

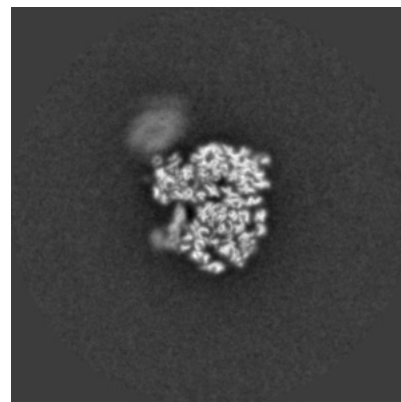
6.3.1 Primary map



X Index: 252

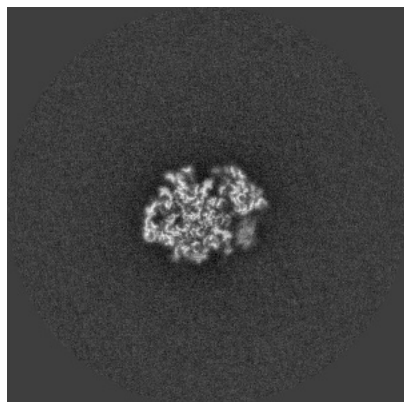


Y Index: 223

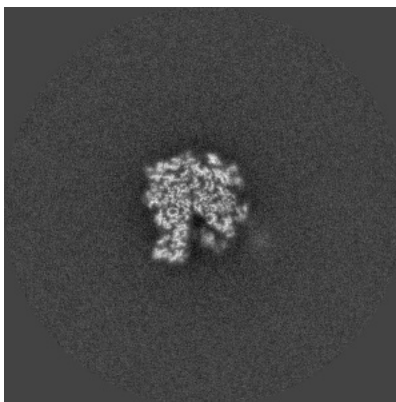


Z Index: 245

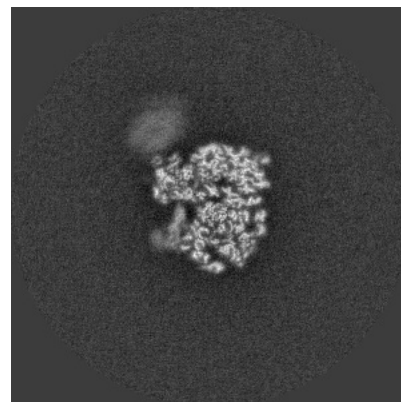
6.3.2 Raw map



X Index: 265



Y Index: 223

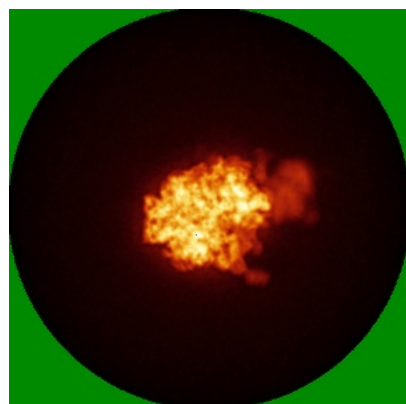


Z Index: 245

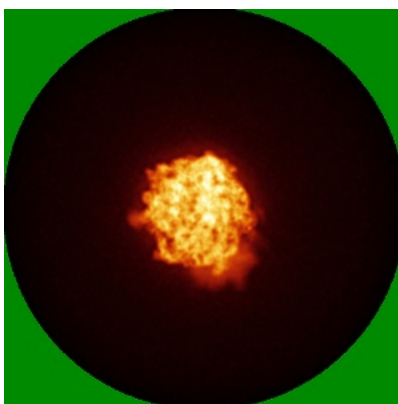
The images above show the largest variance slices of the map in three orthogonal directions.

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

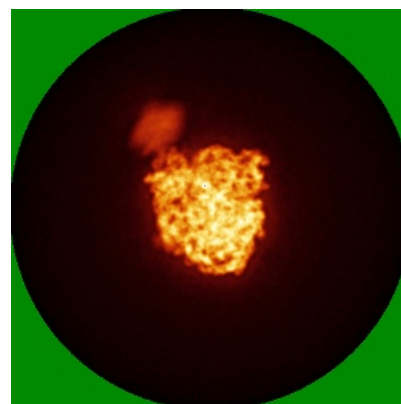
6.4.1 Primary map



X

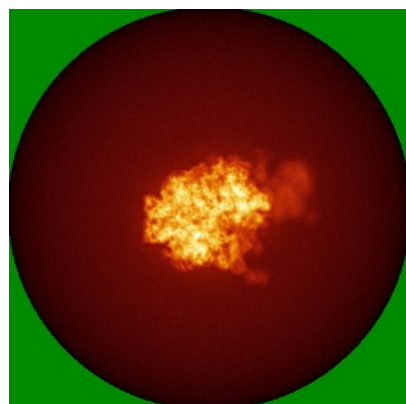


Y

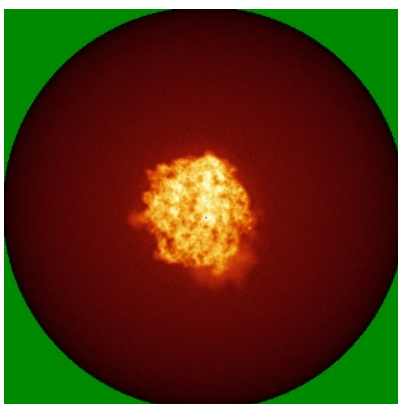


Z

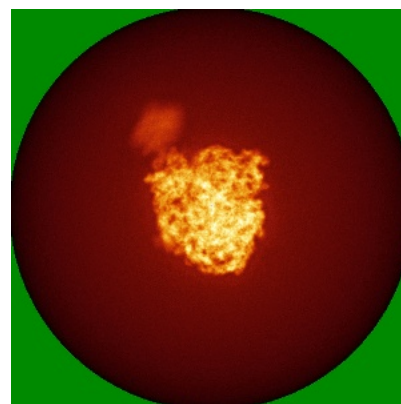
6.4.2 Raw map



X



Y

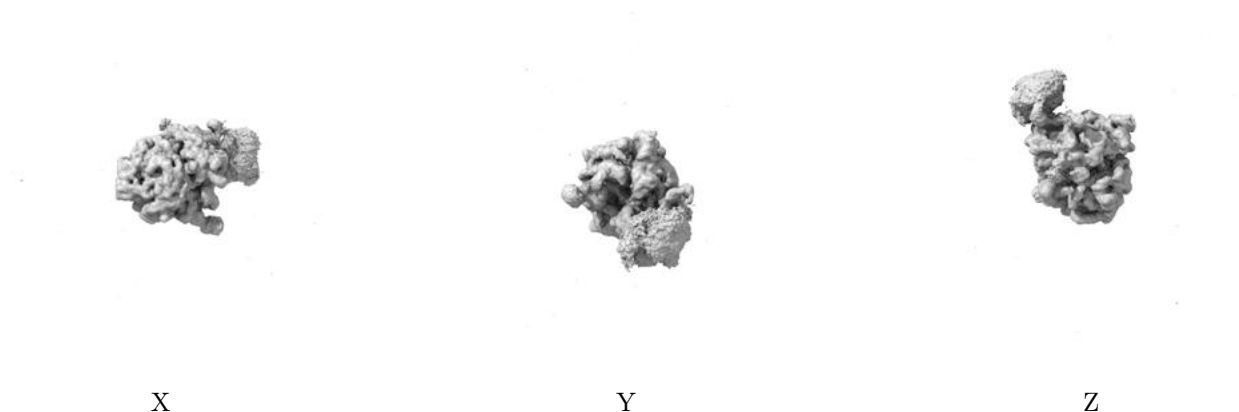


Z

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.

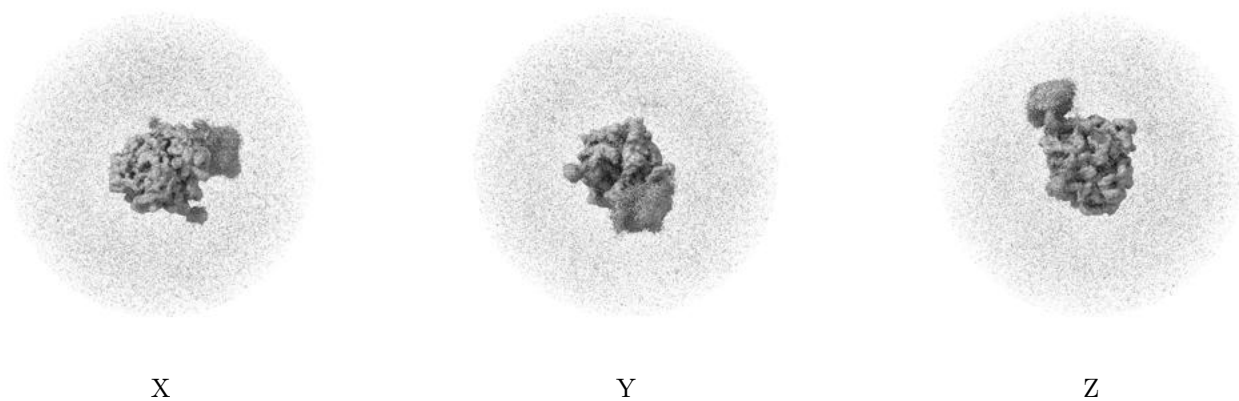
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. 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.

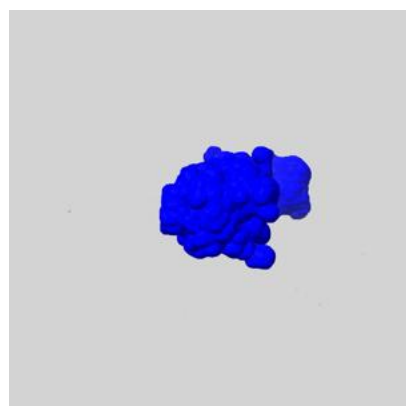
6.6 Mask visualisation [i](#)

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

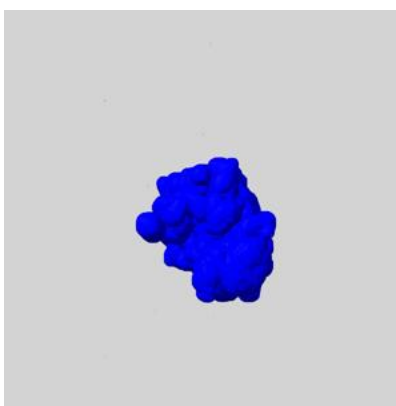
A mask typically either:

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

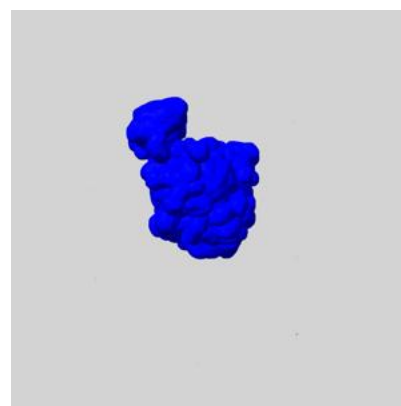
6.6.1 emd_38948_msk_1.map [i](#)



X



Y

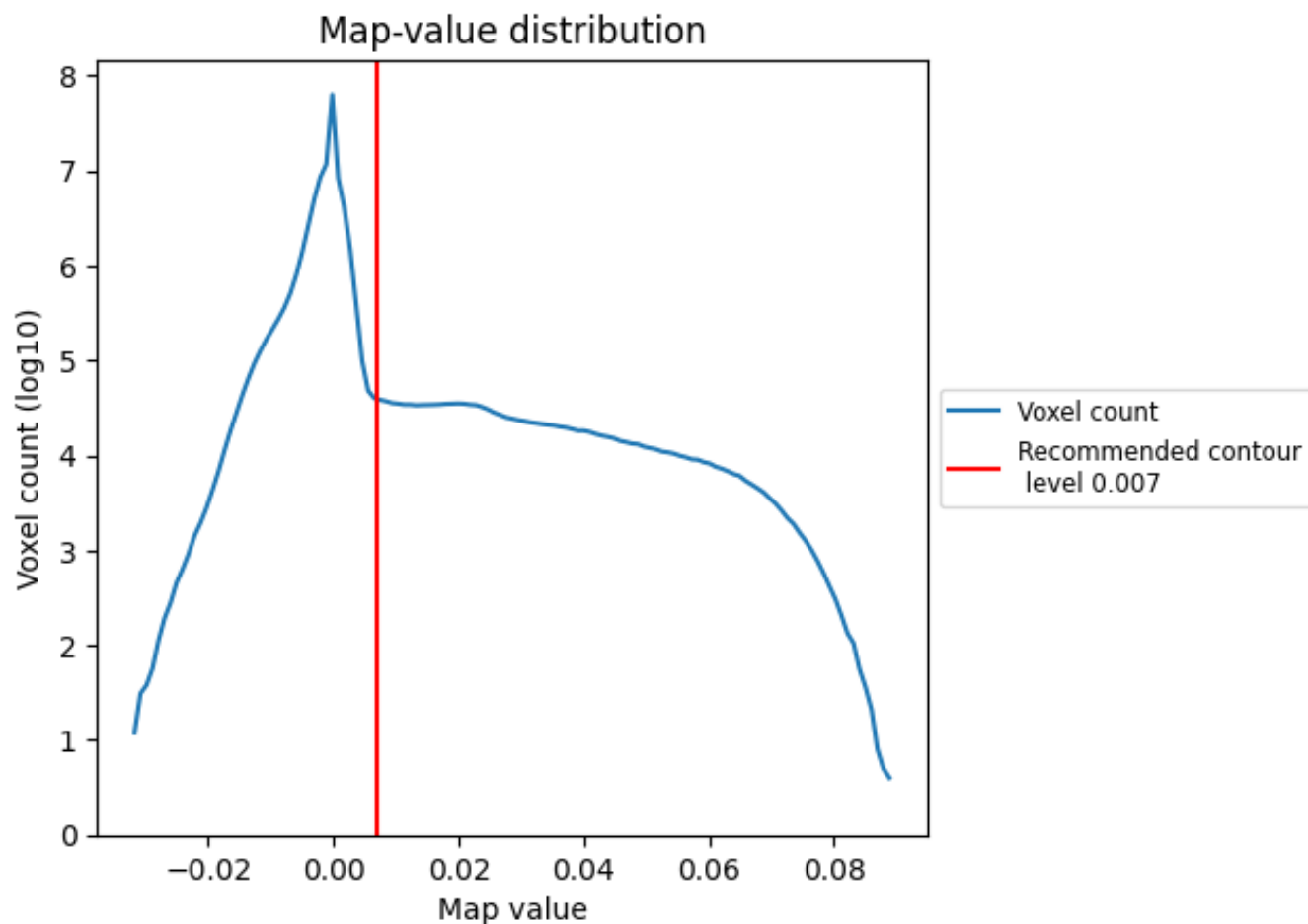


Z

7 Map analysis [i](#)

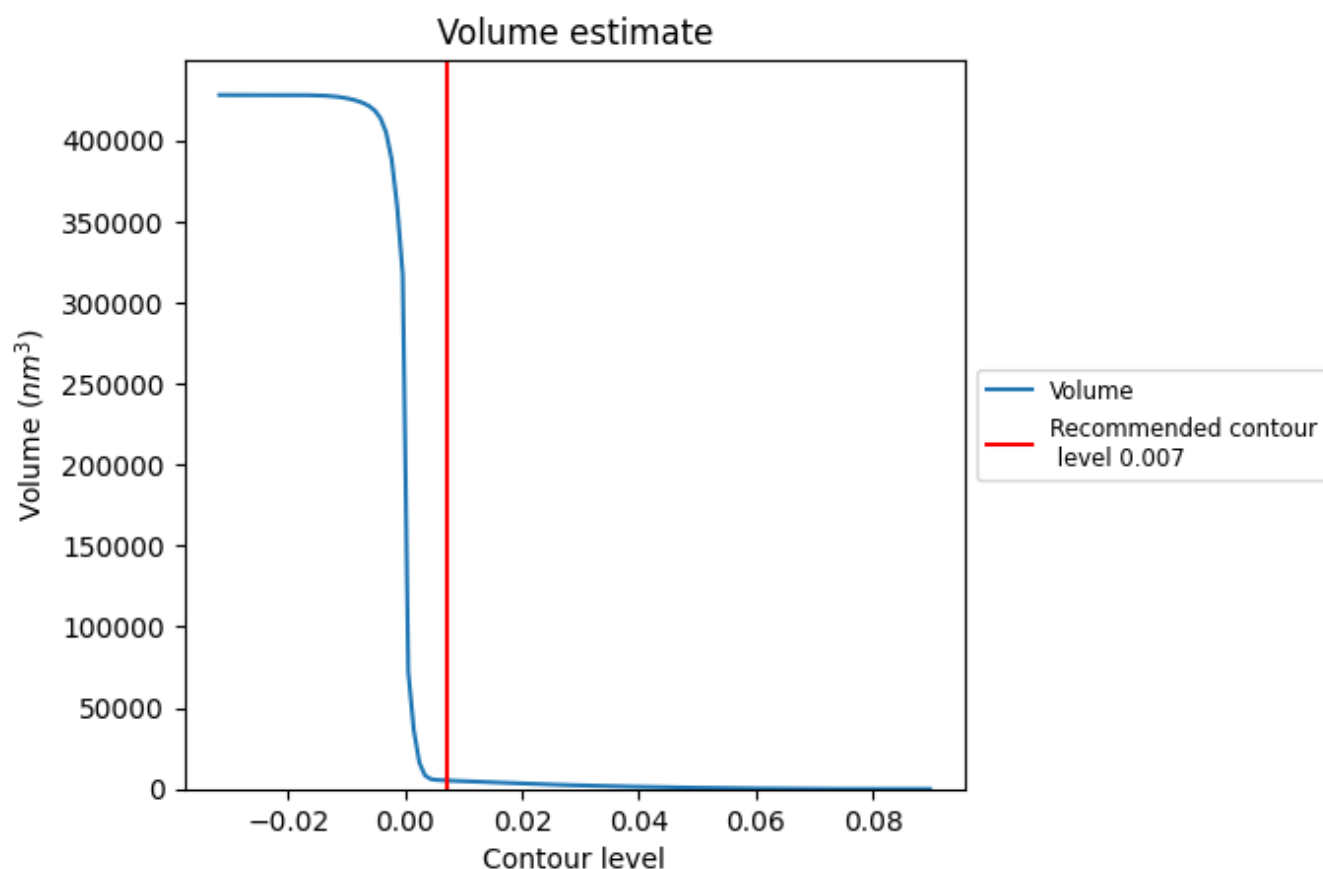
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

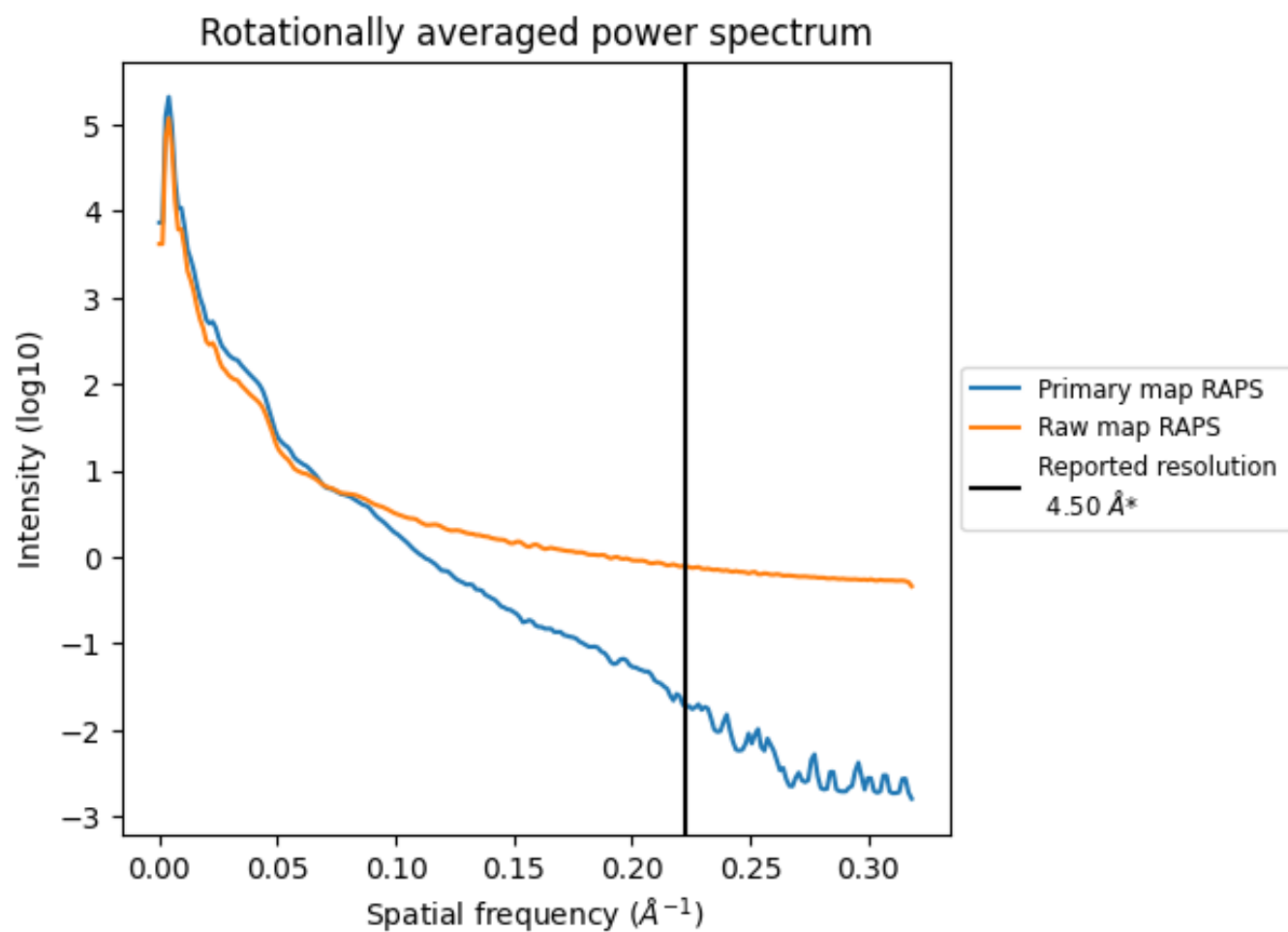
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5249 nm^3 ; this corresponds to an approximate mass of 4741 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 ⓘ

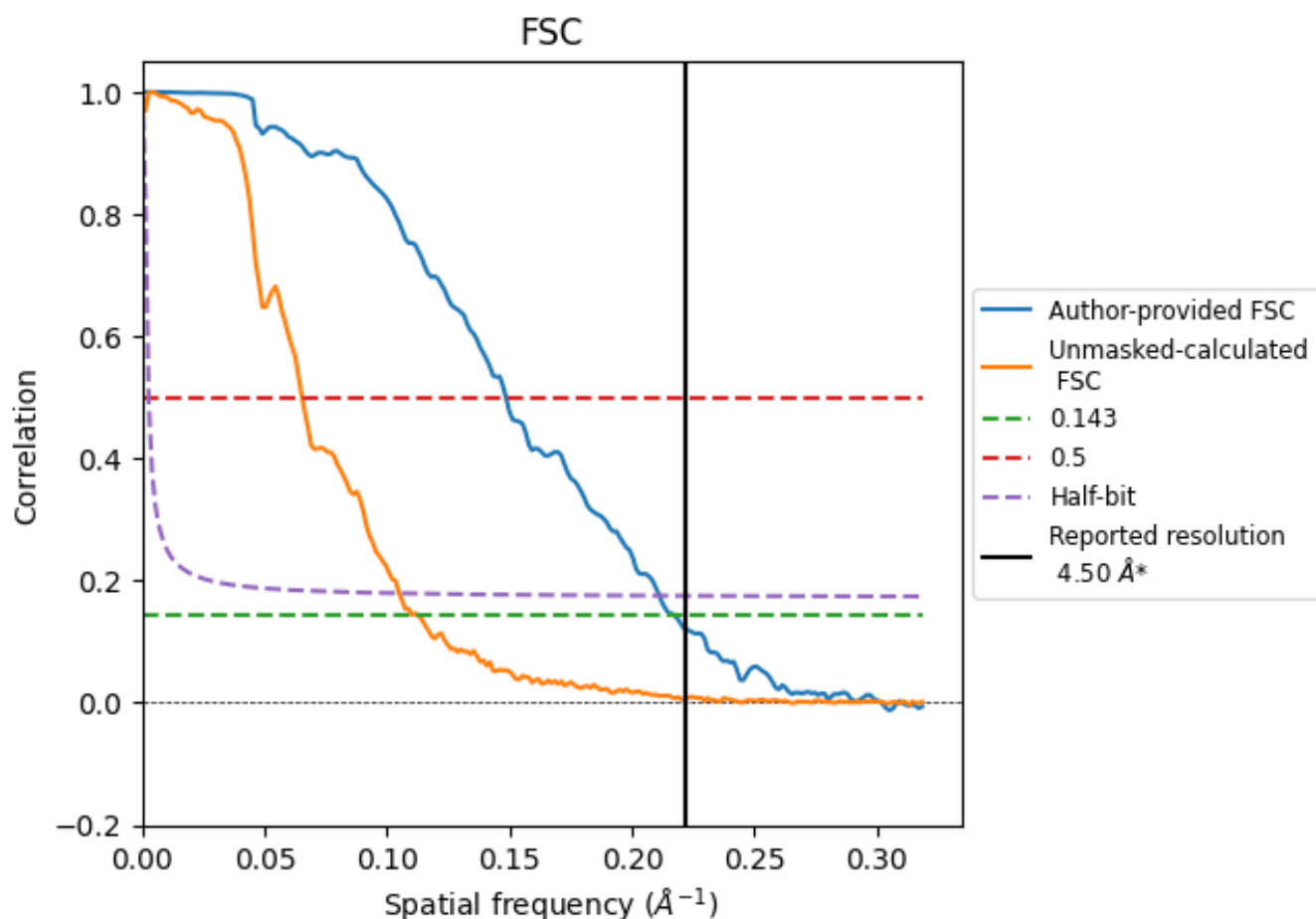


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 $0.222 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

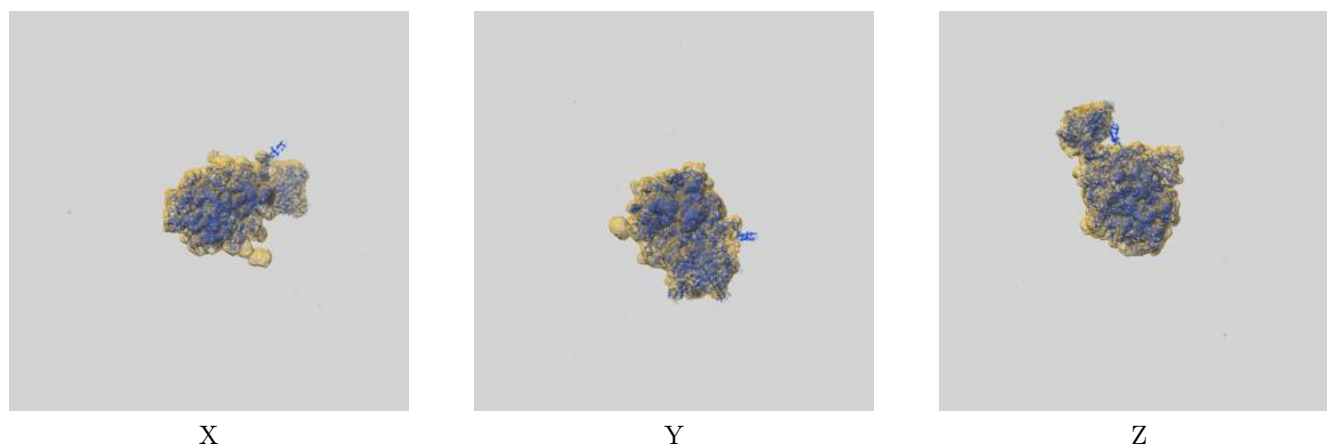
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.60	6.73	4.73
Unmasked-calculated*	8.87	15.31	9.52

*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 8.87 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

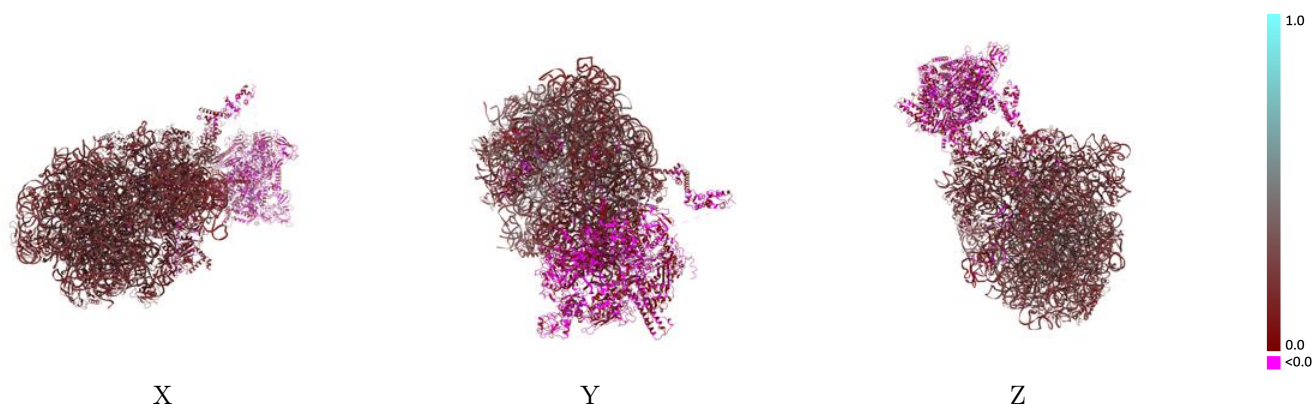
This section contains information regarding the fit between EMDB map EMD-38948 and PDB model 8Y5S. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



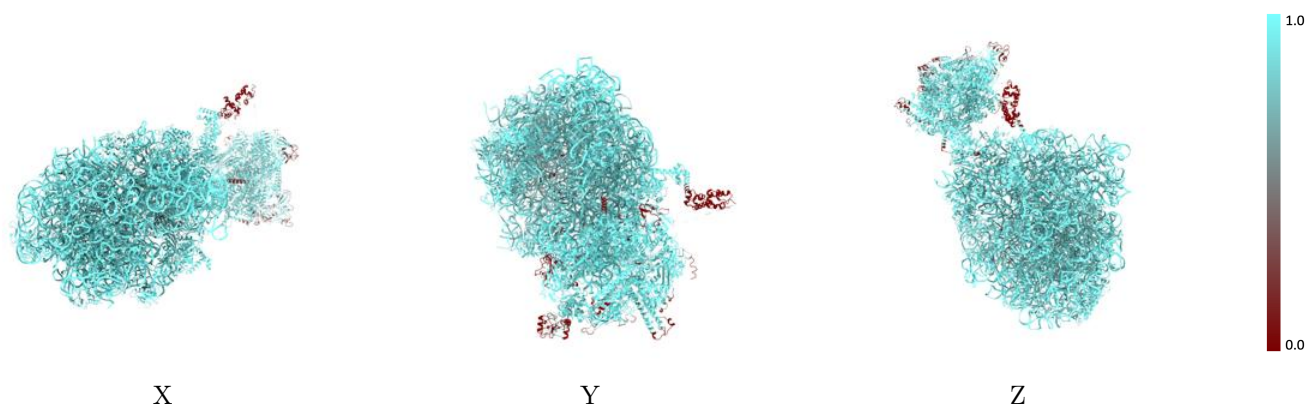
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



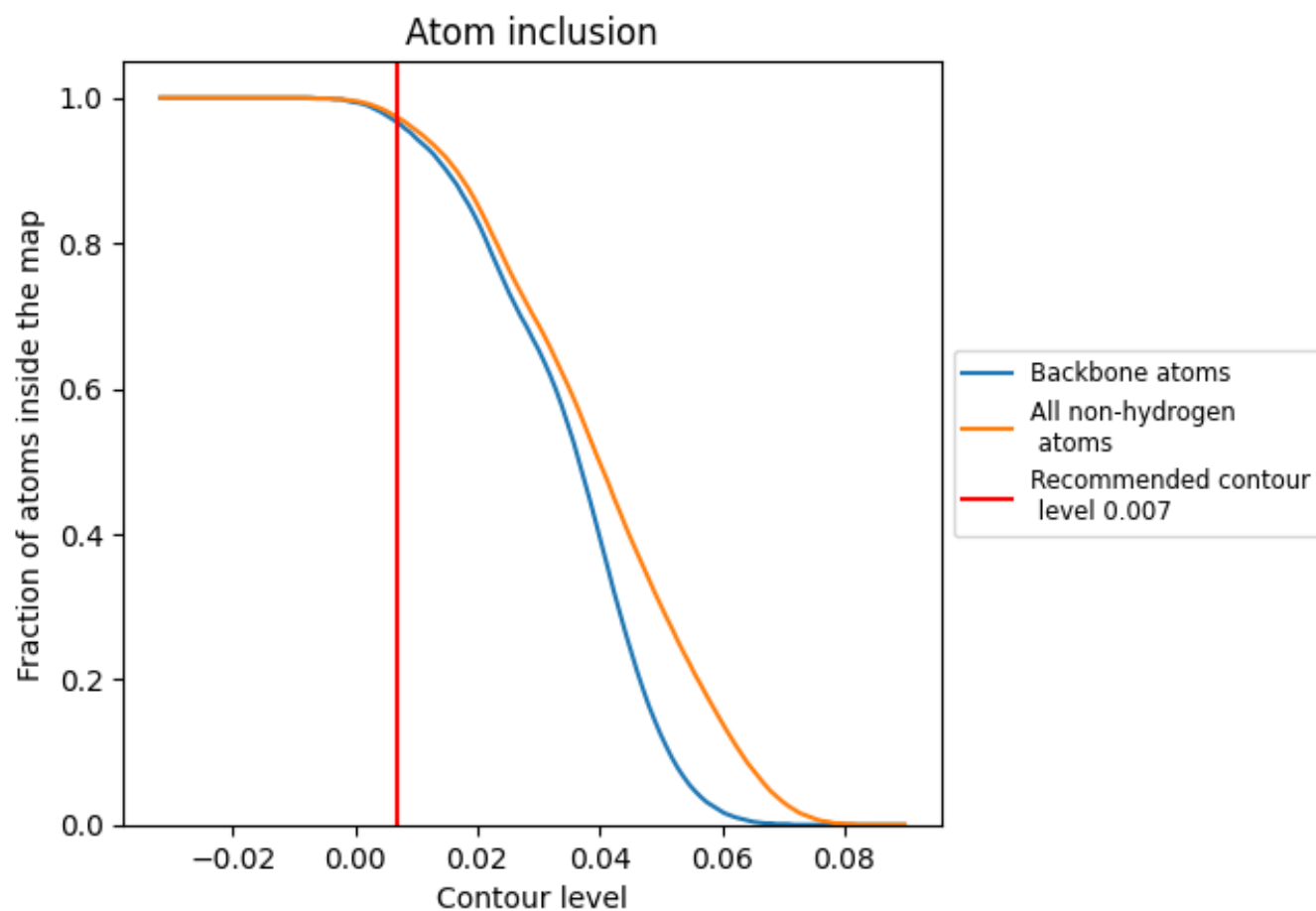
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.1770
0	 0.9140	 0.1160
1	 1.0000	 0.2320
2	 1.0000	 0.2050
3	 1.0000	 0.2190
4	 0.9520	 0.0440
5	 0.9830	 0.1360
6	 0.8450	 0.0790
8	 1.0000	 0.0170
9	 1.0000	 0.0250
A	 0.9780	 0.1310
A1	 0.7870	 0.0260
A2	 0.8240	 0.0550
B	 0.9950	 0.1850
B1	 0.9140	 0.0240
B2	 0.8720	 0.0340
C	 0.9850	 0.1700
D	 0.9800	 0.1680
E	 1.0000	 0.1560
F	 1.0000	 0.1470
G	 0.9920	 0.1820
H	 0.9860	 0.1730
I	 0.9980	 0.1540
J	 0.9970	 0.1910
K	 0.9950	 0.1910
L	 0.9950	 0.1830
M	 0.9900	 0.1790
N	 0.9990	 0.1590
NA	 0.8340	 0.1390
NG	 0.8920	 0.0610
O	 1.0000	 0.1500
P	 0.9990	 0.2050
Q	 0.9480	 0.1520
R	 0.9990	 0.1660
S	 0.9990	 0.1460



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T	 0.9930	 0.1680
U	 1.0000	 0.1620
V	 0.9910	 0.1830
W	 1.0000	 0.1670
W0	 0.6360	 0.0210
X	 0.9920	 0.1310
Y	 0.9970	 0.1690
Z	 0.9770	 0.1510
b	 0.9950	 0.2210
c	 0.9940	 0.1900
d	 0.9950	 0.1860
e	 0.9910	 0.1620
f	 0.9800	 0.1760
g	 1.0000	 0.1800
i	 0.9630	 0.0880
j	 0.9960	 0.1900
k	 0.9920	 0.2150
l	 1.0000	 0.1770
m	 0.9890	 0.1940
n	 1.0000	 0.1890
o	 1.0000	 0.1550
p	 0.9870	 0.2160
q	 0.9990	 0.1640
r	 1.0000	 0.1860
s	 0.9960	 0.1950
t	 0.9920	 0.1920
u	 0.9970	 0.1700
v	 0.9970	 0.1760
w	 1.0000	 0.1630
x	 1.0000	 0.1960
y	 1.0000	 0.1730
z	 0.9930	 0.1880