



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:26 AM UTC

PDB ID : 8Y5P / pdb_00008y5p
EMDB ID : EMD-38945
Title : E.coli transcription translation coupling complex in TTC-B state 4 (subclass 1) containing mRNA with 24-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 6.50 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:

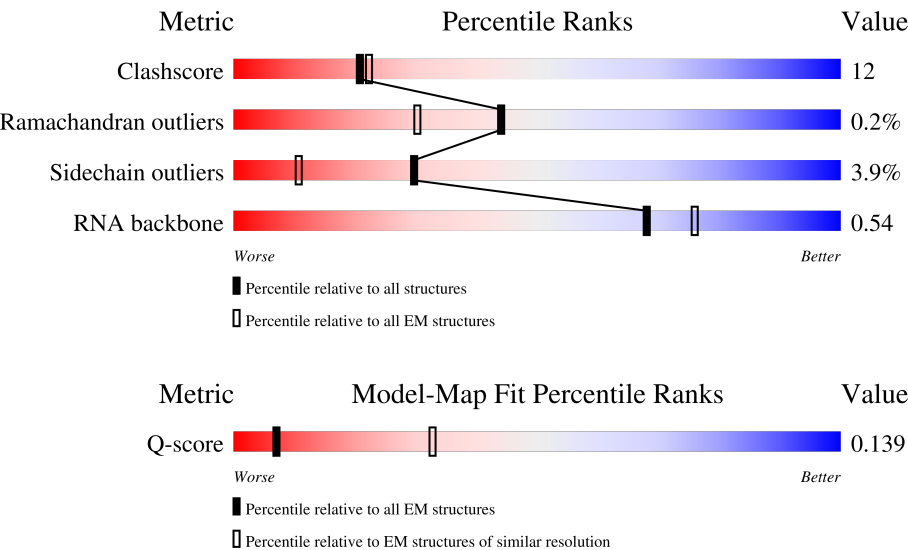
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 6.50 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.



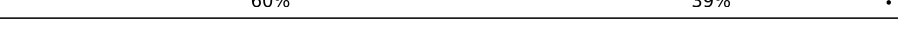
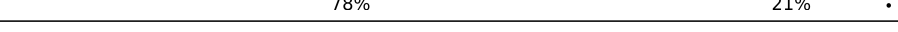
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	556 (6.00 - 7.00)

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	
2	B	57	
3	C	55	

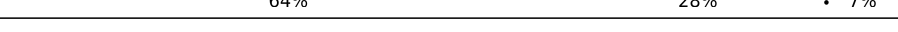
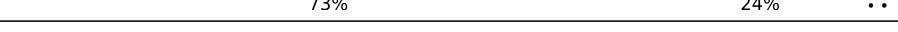
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	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

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Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	

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Mol	Chain	Length	Quality of chain
54	4	41	
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	6	77	
64	a	234	
65	0	716	
66	h	6	

2 Entry composition

There are 69 unique types of molecules in this entry. The entry contains 181755 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	46	Total	C	N	O	S	0	0
			355	221	62	66	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	149	Total	C	N	O	S	0	0
			1111	699	197	214	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	30	Total	C	N	O	P	0	0
			627	280	92	225	30		

- 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(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 64 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	a	132	Total	C	N	O	S	0	0
			1013	638	183	190	2		

- Molecule 65 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

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

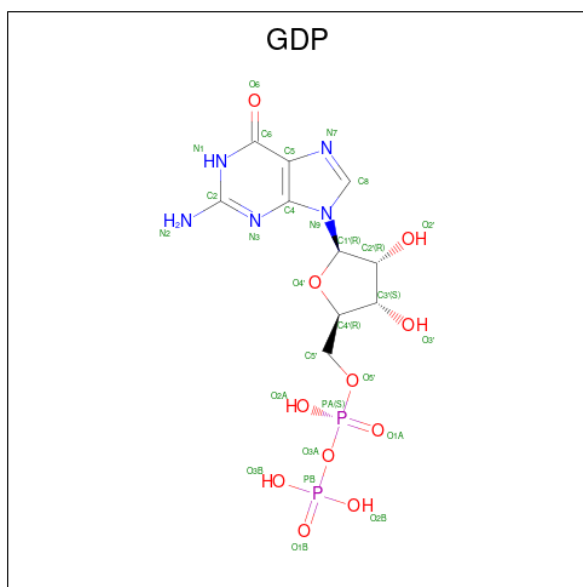
- Molecule 66 is a protein (with D amino acids) called Viomycin.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

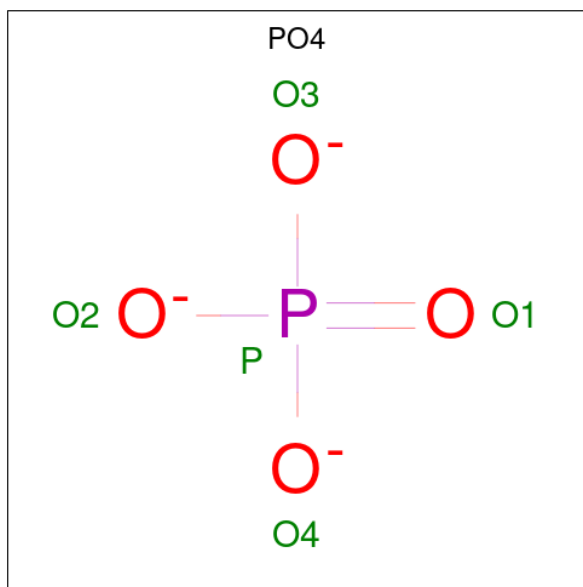
Mol	Chain	Residues	Atoms		AltConf
67	B1	1	Total	Mg	0
			1	1	

- Molecule 68 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
68	0	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 69 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

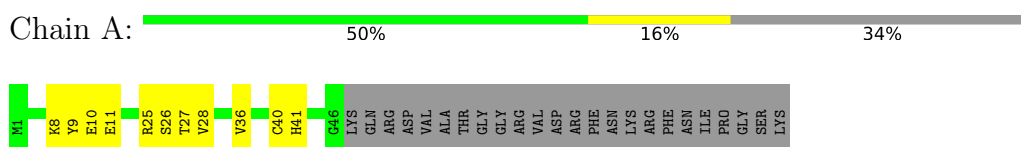


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
69	0	1	5	4	1	0

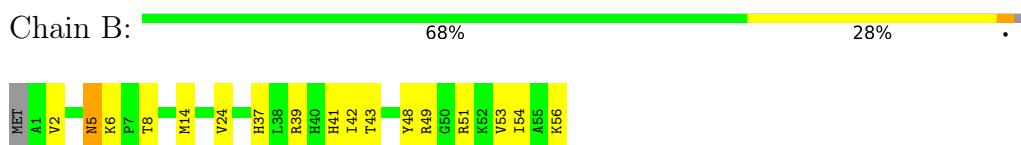
3 Residue-property plots [i](#)

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.

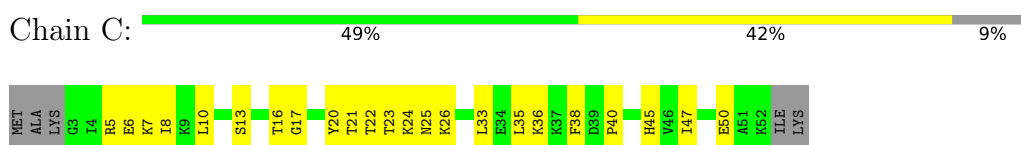
- Molecule 1: 50S ribosomal protein L31



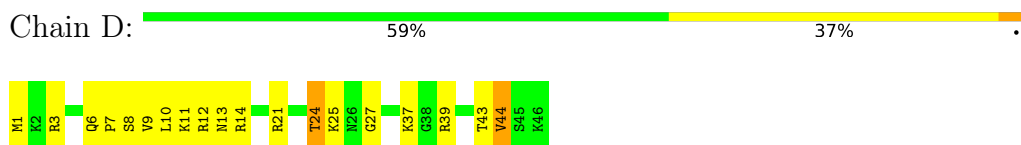
- Molecule 2: 50S ribosomal protein L32



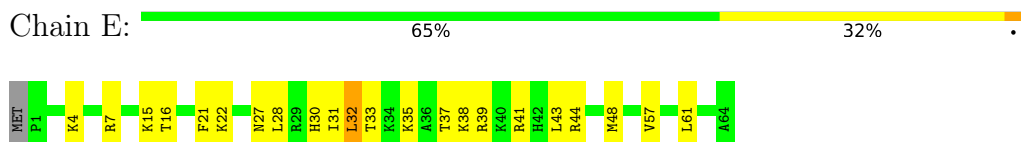
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34

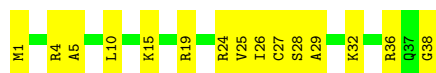


- Molecule 5: 50S ribosomal protein L35



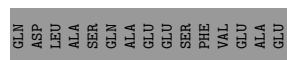
- Molecule 6: 50S ribosomal protein L36

Chain F:  61% 39%



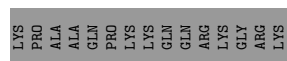
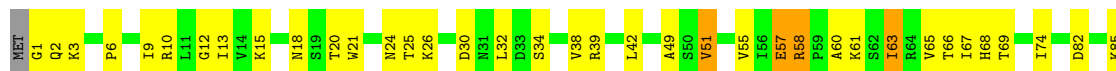
• Molecule 7: 30S ribosomal protein S2

Chain G:  64% 26% 10%



• Molecule 8: 30S ribosomal protein S3

Chain H:  61% 25% 12%



• Molecule 9: 30S ribosomal protein S4

Chain I:  71% 28%



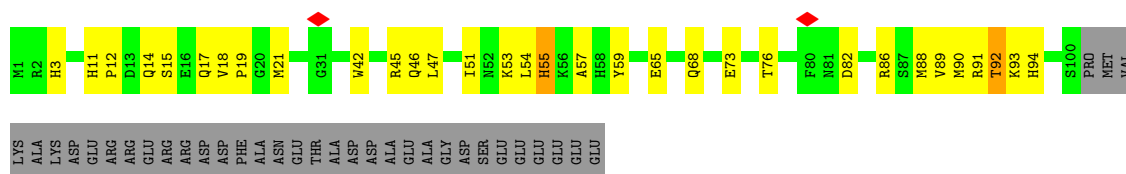
• Molecule 10: 30S ribosomal protein S5

Chain J:  66% 28% 6%

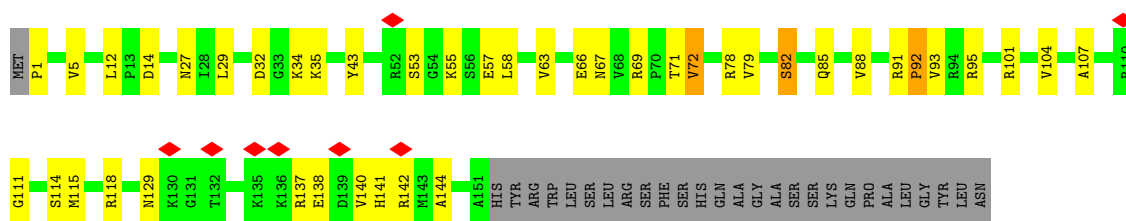




- Molecule 11: 30S ribosomal protein S6, fully modified isoform



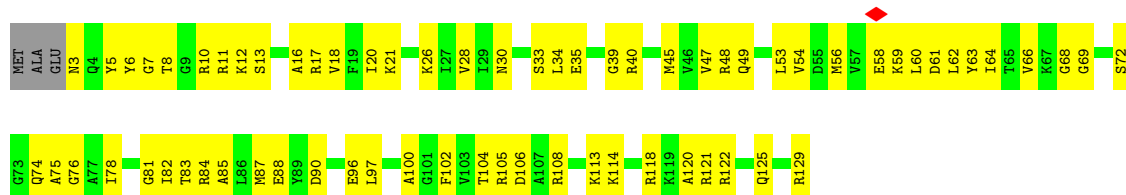
- Molecule 12: 30S ribosomal protein S7



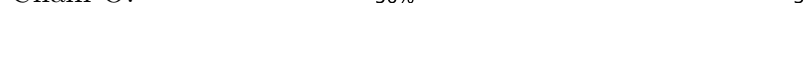
- Molecule 13: 30S ribosomal protein S8

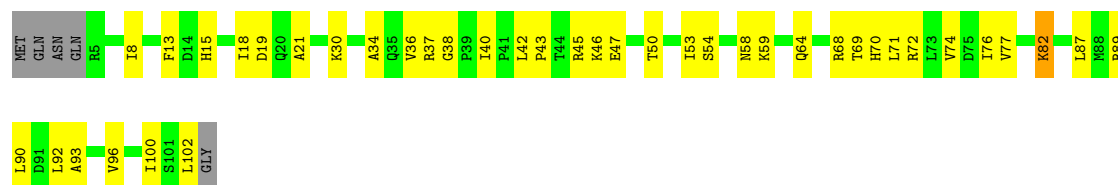


- Molecule 14: 30S ribosomal protein S9



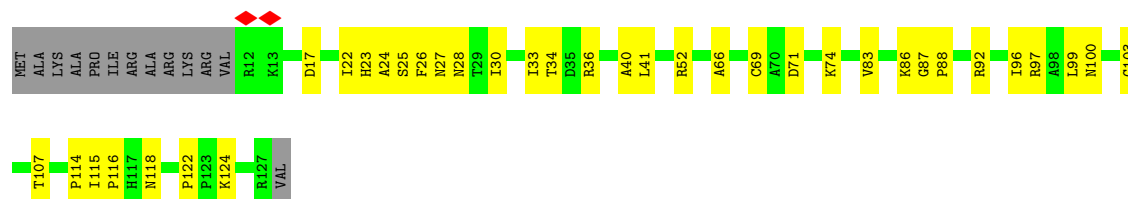
- Molecule 15: 30S ribosomal protein S10





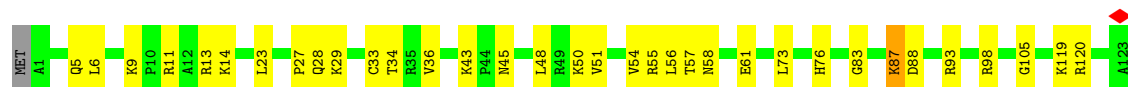
- Molecule 16: 30S ribosomal protein S11

Chain P: 62% 28% 10%



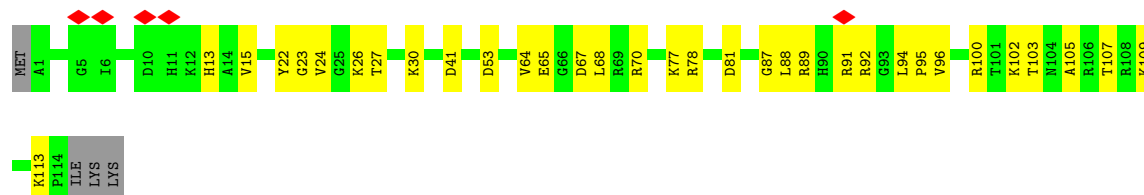
- Molecule 17: 30S ribosomal protein S12

Chain Q: 72% 27% ..



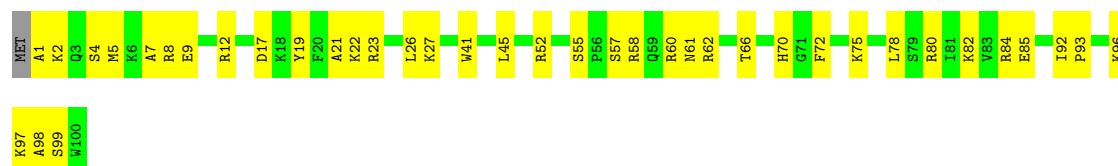
- Molecule 18: 30S ribosomal protein S13

Chain R: 69% 28% .



- Molecule 19: 30S ribosomal protein S14

Chain S: 60% 39% .



- Molecule 20: 30S ribosomal protein S15

Chain T: 78% 21% .



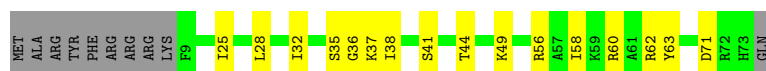
- Molecule 21: 30S ribosomal protein S16



- Molecule 22: 30S ribosomal protein S17



- Molecule 23: 30S ribosomal protein S18



- Molecule 24: 30S ribosomal protein S19



- Molecule 25: 30S ribosomal protein S20

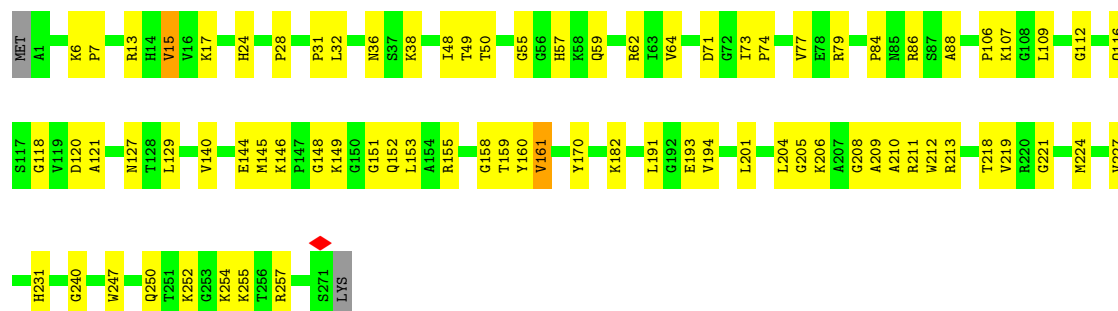


- Molecule 26: 30S ribosomal protein S21

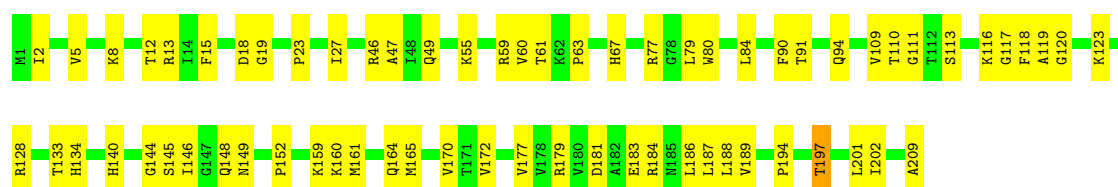


- Molecule 27: 50S ribosomal protein L2

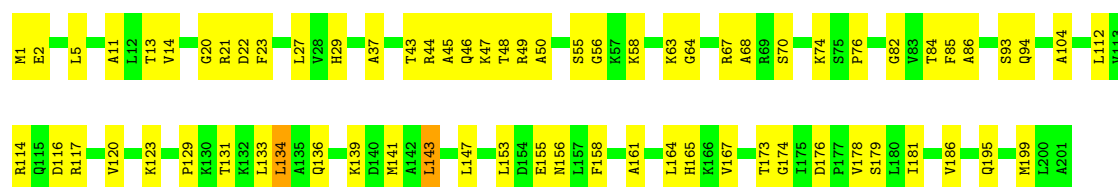




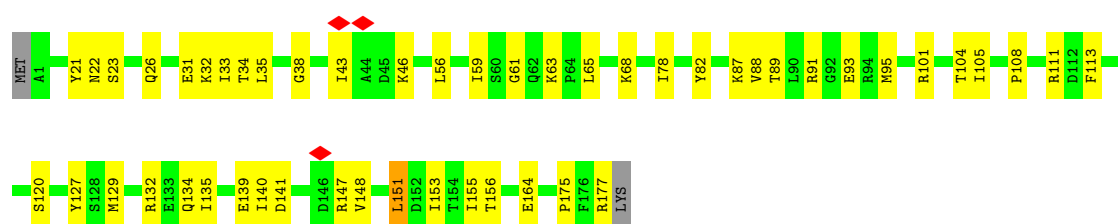
• Molecule 28: 50S ribosomal protein L3



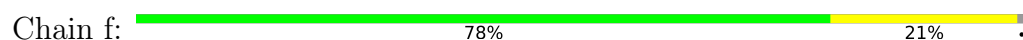
• Molecule 29: 50S ribosomal protein L4



• Molecule 30: 50S ribosomal protein L5

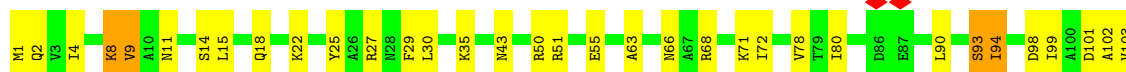
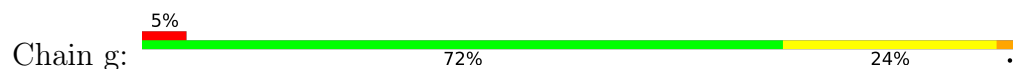


• Molecule 31: 50S ribosomal protein L6

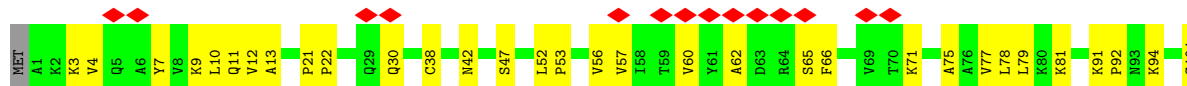




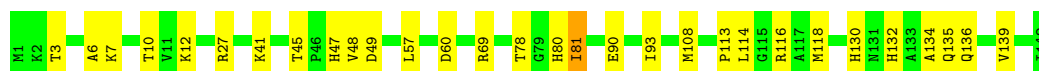
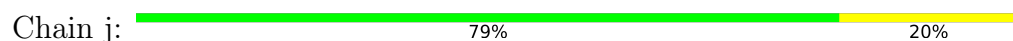
- Molecule 32: 50S ribosomal protein L9



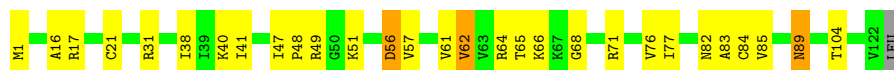
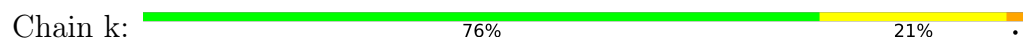
- Molecule 33: 50S ribosomal protein L11



- Molecule 34: 50S ribosomal protein L13



- Molecule 35: 50S ribosomal protein L14

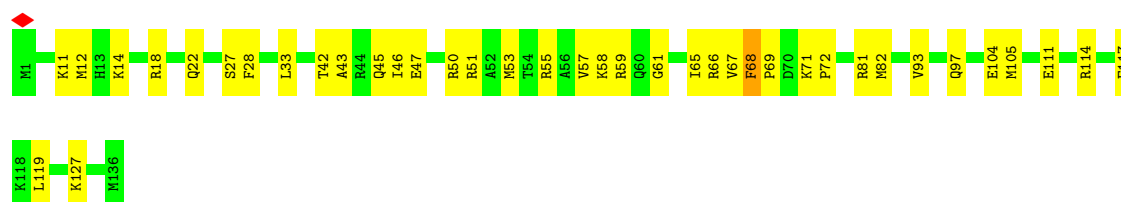


- Molecule 36: 50S ribosomal protein L15



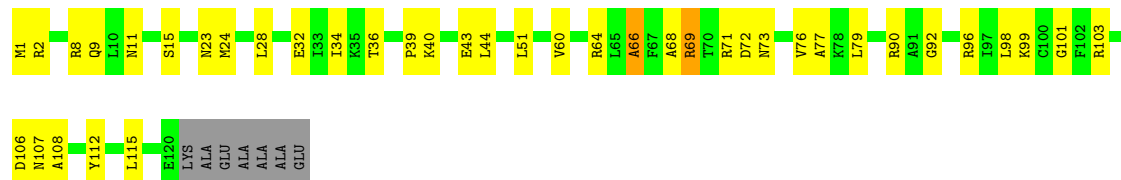
- Molecule 37: 50S ribosomal protein L16





- Molecule 38: 50S ribosomal protein L17

Chain n: 63% 30% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o: 71% 28%



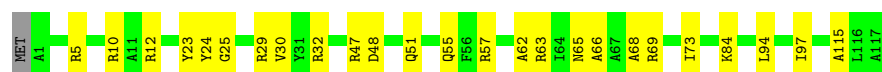
- Molecule 40: 50S ribosomal protein L19

Chain p: 76% 23%



- Molecule 41: 50S ribosomal protein L20

Chain q: 78% 21%



- Molecule 42: 50S ribosomal protein L21

Chain r: 71% 29%



- Molecule 43: 50S ribosomal protein L22

Chain s: 72% 28%



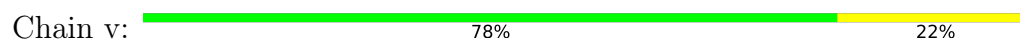
- Molecule 44: 50S ribosomal protein L23



- Molecule 45: 50S ribosomal protein L24



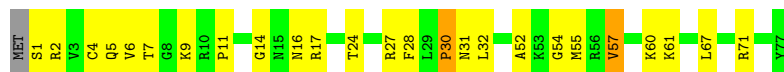
- Molecule 46: 50S ribosomal protein L25



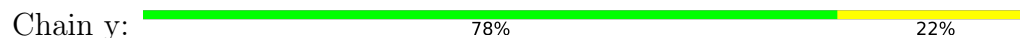
- Molecule 47: 50S ribosomal protein L27



- Molecule 48: 50S ribosomal protein L28



- Molecule 49: 50S ribosomal protein L29



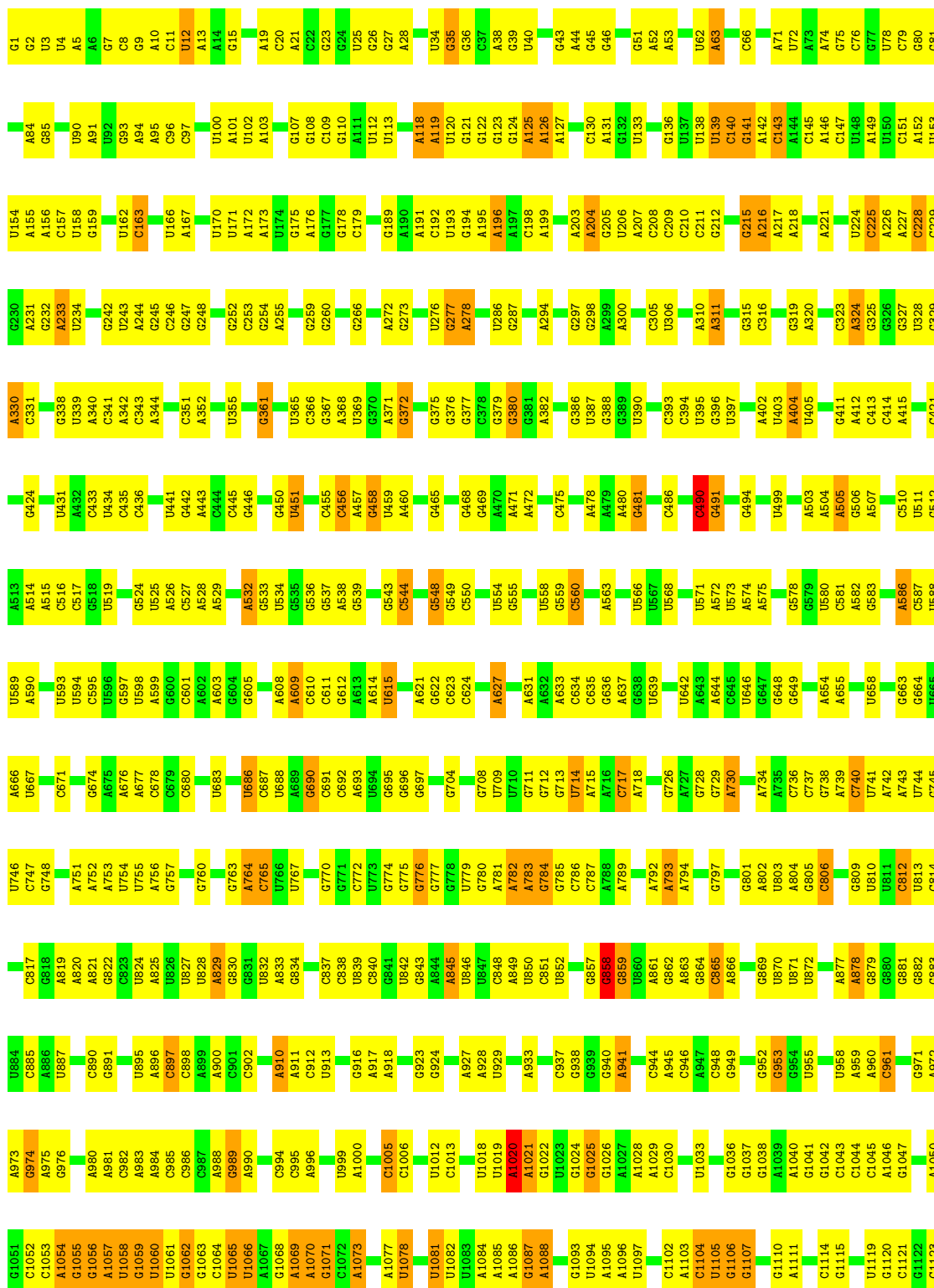
- Molecule 50: 50S ribosomal protein L30



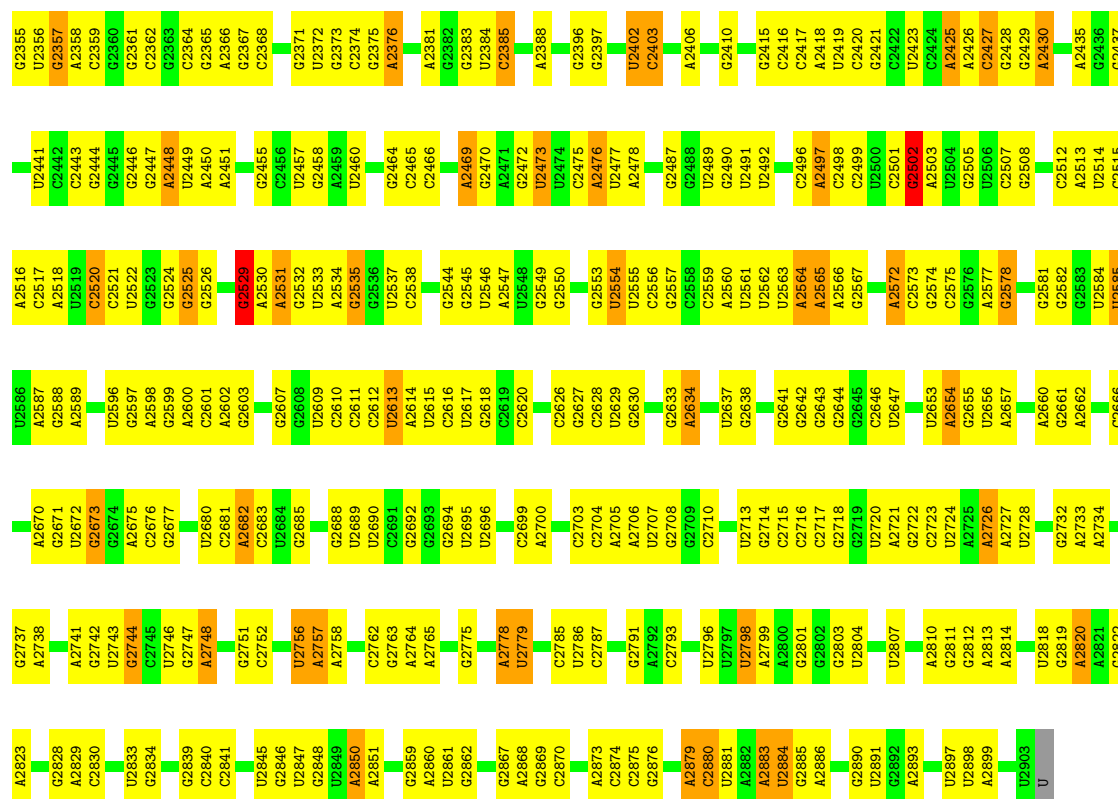


• Molecule 51: 23S rRNA

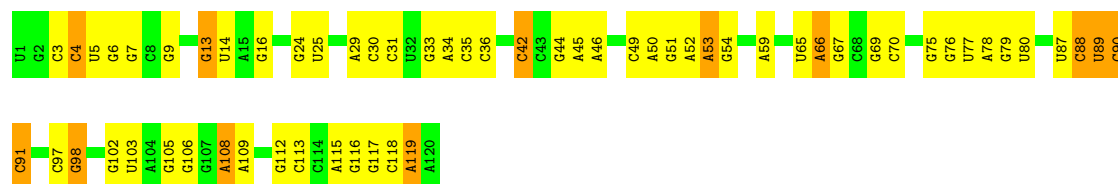
Chain 1: 44% 48% 8%



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A2284	A2126	C2050	G1973	G1884	G1797	G1718	C1550	C1461	G1369	C1289	G1197	G1125
C2285	G2127	A2051	C1974	G1975	U1798	G1719	A1551	C1462	G1370	U1294	U1198	A1126
G2286	G2128	A2052	G1976	A1989	C1800	C1730	G1555	G1463	G1371	U1297	U1203	A1127
A2287	U2132	C2055	A1977	A1890	A1801	G1736	C1558	G1464	U1372	G1300	A1204	G1128
A2288	G2133	G2056	A1978	A1891	A1802	U1737	U1589	U1468	G1373	G1301	U1330	A1205
G2289	A2134	A2135	U1979	C1893	A1803	G1738	G1642	A1469	G1374	A1301	G1206	G1131
A2297	G2136	A2059	G1980	C1894	C1804	G1739	G1643	A1470	A1378	U1302	A1207	U1300
A2298	G2137	A2060	U1981	A1900	C1806	A1730	C1564	G1471	G1379	A1303	U1209	A1132
G2299	G2138	G2061	G1982	A1901	G1807	G1741	C1565	G1472	G1380	G1302	G1210	A1133
C2300	U2139	A2062	G1983	A1902	A1808	U1742	C1566	U1473	A1383	C1305	G1211	A1134
C2301	G2140	C2064	C1985	G1903	A1809	G1743	C1567	G1474	U1373	C1306	G1212	G1135
U2302	G2141	G2065	C1986	G1904	A1810	A1744	C1568	G1475	A1387	G1307	G1137	G1136
G2303	A2142	C2066	G1990	C1905	A1811	A1745	A1569	U1476	A1388	A1308	G1216	G1138
G2304	G2143	G2067	U1991	A1912	A1815	A1746	G1651	G1478	G1389	A1309	U1219	C1139
U2305	C2144	U2068	G1992	A1913	C1816	U1747	A1572	U1481	U1140	G1310	G1220	U1141
C2306	C2145	G2069	U1993	C1914	G1817	C1748	C1573	G1482	U1391	G1311	A1142	A1143
G2307	C2146	A2071	C1994	C1914	G1818	C1752	C1574	G1483	U1394	U1312	G1225	A1144
G2308	G2071	A2070	C1995	U1917	U1819	G1753	C1580	U1484	A1395	U1313	A1226	C1145
G2309	C2072	C2073	U1996	A1918	A1820	A1754	G1581	U1485	U1396	C1319	C1229	C1146
A2311	G2073	U2074	C1997	U1919	A1821	G1755	C1582	U1486	U1397	C1320	A1230	A1147
C2312	A2075	A2076	C1998	C1914	C1822	G1756	G1587	A1490	A1403	A1321	G1236	U1148
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G2315	G2082	G2083	U1995	U1931	U1825	A1759	C1591	U1506	U1409	U1326	A1247	A1155
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G2182	G2087	G2087	C2000	G1933	G1828	C1761	C1593	A1509	U1412	C1330	G1250	C1158
C2185	U2092	G2087	U2007	C1934	A1829	C1764	U1594	G1510	U1413	G1331	C1251	C1161
U2187	G2093	A2094	A2013	G1935	C1830	G1767	C1595	G1511	G1332	G1332	C1252	G1162
U2187	U2094	A2094	A2020	G1935	C1831	G1767	C1596	G1512	U1415	G1333	A1253	C1161
U2187	G2095	A2094	C2021	A1937	C1832	G1770	C1597	G1512	G1416	G1334	U1255	A1169
U2187	U2096	A2094	C2022	A1938	C1833	C1771	C1598	G1515	C1417	G1337	G1256	C1170
U2187	G2100	U2099	C2023	U1939	C1836	A1772	C1600	G1518	A1419	G1338	C1257	G1171
U2187	C2174	G2100	G2024	U1940	C1837	A1773	G1601	G1518	A1420	G1339	U1258	C1172
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U2187	C2177	G2103	C2026	U1943	C1843	U1777	C1607	U1523	G1425	A1342	A1262	U1175
U2187	U2106	U2106	G2029	U1951	C1844	U1777	C1608	G1524	C1428	G1343	U1176	U1176
U2187	G2107	G2107	A2030	A1952	A1853	A1780	A1609	G1528	G1429	U1352	A1265	G1177
U2187	A2108	A2108	A2031	A1953	A1854	U1781	A1614	G1529	G1429	A1353	G1266	C1178
U2187	U2111	U2111	G2032	G1954	U1854	U1782	C1615	G1529	G1432	A1354	U1267	G1179
U2187	U2112	U2112	A2033	U1955	U1855	A1783	A1616	U1534	A1433	G1355	A1268	U1180
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U2187	U2115	U2115	A2037	G1964	U1864	A1788	U1620	G1541	U1440	G1360	G1185	G1185
U2187	U2116	U2116	G2040	C1965	U1864	A1789	U1621	U1542	G1444	G1361	A1275	G1186
U2187	U2117	U2117	U2041	A1966	G1867	C1790	U1621	U1542	G1445	C1362	A1276	G1187
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U2187	G2120	G2120	C2043	G1968	C1869	G1792	A1626	G1546	G1447	G1364	C1278	G1192
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U2187	U2122	U2122	C2047	A1970	C1870	C1795	G1631	A1548	G1448	A1366	A1287	G1193
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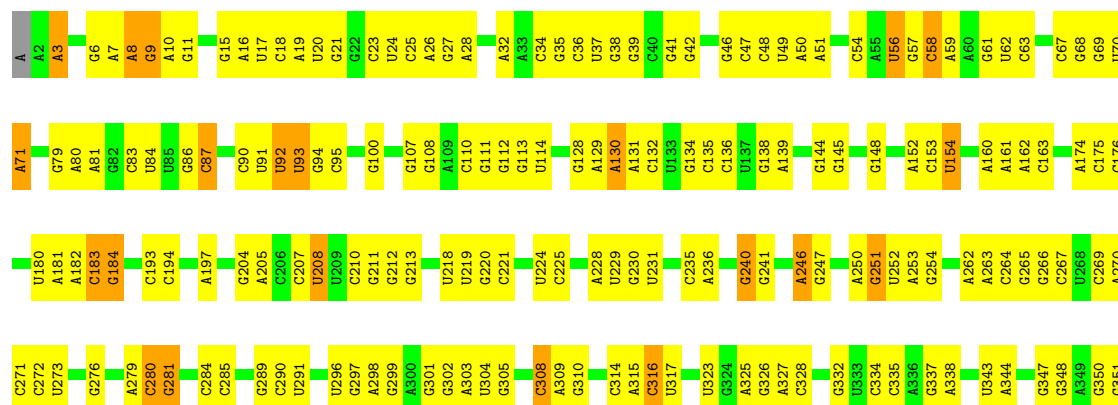


Chain 2: 50% 40% 10%

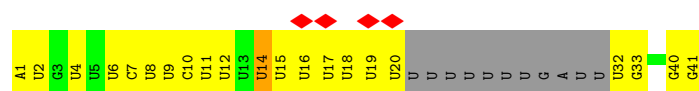
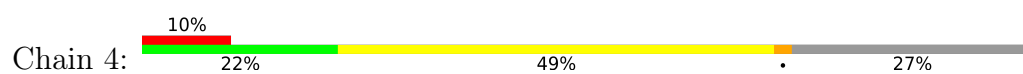


• Molecule 53: 16S rRNA

Chain 3: 45% 48% 6%



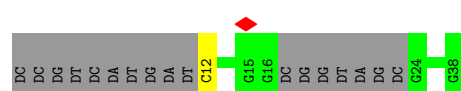
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G1491	C1399	C1325	A1250	U1095	A1016	G945	C858	C679	G597	C513	G425	A353
A1492	C1400	C1326	A1251	C1096	U1017	G946	C859	U684	U598	C514	U426	G354
A1493	C1401	C1327	A1252	C1097	U1018	A946	A860	G685	C599	G515	U427	C355
C1496	C1402	C1328	G1253	G1098	A1019	G947	C861	U677	A600	U516	G428	A356
G1497	C1403	A1329	A1254	G1099	A1022	U950	U863	G690	A602	G517	U429	G357
	G1404	U1330	G1255	C1100	U1023	G951	A864	G691		C518	A430	U358
A1502	U1406	A1256	A1257	A1101	G1024	U952	A865	U701	A607	A520	A431	G399
A1503	C1407	A1332	A1257	C1102	U1025	G953	C866	A702	A608	G528	A432	G362
G1504		A1333		G1103	G1026	G954	C867	G703		G529	U434	A363
G1505	C1412	A1339	G1260	A1105	G1027	U955	A872	A706	C613	G530	U437	A366
U1506	A1413	A1261	A1261	C1106	C1028	U956	A873	U707	C620	U531	U438	U867
A1507	U1414	C1282	C1282	C1107	U1029	U957	G874		A621	A532	U439	G368
A1508	G1415	U1284	U1284	G1108	U1030	A958	U875	A715	A622	A533	C440	G369
		C1283	C1283	C1109	G1031	A959	C876	G710	C623	U534	G445	C372
U1512	U1420	C1267	C1267	A1110	G1032	U960	C877	G713	U625	A535		
A1513	G1421	U1274	A1274	A1111	G1033	U961	G878	A718	G626	A539	A448	G376
G1514	G1422	G1268	A1275	A1112	G1034	G962	A878	C719	G627	G540	G452	G377
G1515	G1423	A1349	A1271	A1117	A1035	G963	G881	C720	G631	C545	G453	G378
G1516	U1424	A1350	A1274	U1118		A964	C882	G721	U632	A546	G454	G380
G1517	U1425	U1351	A1275	C1119	G1042	G965	C883	G722	U634	A547	G455	G384
A1518	U1425	U1351	A1275	C1120	G1043	G966	C884	G723	C634	U552	U458	C385
	G1432	U1354	A1275	U1121	G1047	G967	U884	G724	U636	U553	A459	G386
G1435		G1355	A1275	U1122	G1047	G968	C885	G725	C637	A554	A460	U387
U1436	G1435	G1356	A1275	U1123	G1048	G969	C886	G726	U638	U555	G461	G388
A1437		A1357	A1275	G1124	G1049	G970	G887	G727	C639	C556	G462	U389
A1441		G1361	A1275	U1125	U1050	G971	A889	G728	U640	G557	U467	G391
U1446		G1362	A1275	U1126	G1053	G972	G894	G729	U641	G558	A468	C392
A1447		G1363	A1275	C1127	G1054	G973	G895	G730	U642	A560	U478	A393
C1448		G1364	A1275	C1128	C1054	G974	G896	G731	U644	U561	A479	A397
C1452		G1365	A1275	C1129	G1057	G975	A900	G732	G650	U562	U480	C400
U1458		G1366	A1275	G1134	G1058	G976	A901	G733	C651	C564	C483	C401
U1464		G1367	A1275	C1136	G1059	A977	G902	G734	U652	U565	G484	G402
A1465		G1368	A1275	C1137	U1060	C978	G903	G735	U653	G566	U486	U405
C1466		G1369	A1275	C1138	G1061	C980	U904	G736	G657	C569	G406	G406
		G1370	A1275	G1139	U1062	U981	U905	G737	C658	G570	U467	U407
		G1371	A1275	C1140	G1063	U986	A906	G738	U659	U571	A408	U409
		G1372	A1275	G1147	U1064	G987	A907	G739	G661	A572	G410	G410
		G1373	A1275	U1148	U1065	G987	A908			A573	G413	G413
		G1374	A1275	C1149	C1069	C990	C910	G742	U657	C575	A414	A414
		G1375	A1275	C1150	G1070	U991	A913	G743	C660	G576	A415	A415
		G1376	A1275	A1150	C1071	U992	G917	G744	C661	A574	G416	G416
		G1377	A1275	A1151	G1072	A994	G923	G745	G665	A575	C501	C501
		G1378	A1275	A1152	G1073	A994	G924	G746	G666	C578	A502	G417
		G1379	A1275	G1153	G1074	A1000	G925	G747	G667	C579	G505	C418
		G1380	A1275	G1154	G1075	C1001	G926	G748	G668	C580	G506	C419
		G1381	A1275	A1155	G1076	A1004	G927	G749	G669	G581	U420	U420
		G1382	A1275	G1156	G1077	A1005	G928	G750	A665	G582	A509	U421
		G1383	A1275	A1157	G1078	A1006	G929	G751	G666	C583	A510	C422
		G1384	A1275	C1158	G1079	U1007	G934	G752	G667	C584	G507	G423
		G1385	A1275	U1159	G1084	U1008	G935	G753	G668	C585		
		G1386	A1275	G1160	G1088	A1012	A937	G754	G669	C586		
		G1387	A1275	C1161	G1089	A1013	A938	G755	A673	U593		
		G1388	A1275	C1162	U1091	A1014	G939	G756	G674	U594		
		G1389	A1275	U1091	A1092			G757	A675	C422		
		G1390	A1275	U1091	A1093			G758	U676	G423		
		G1391	A1275	U1091	A1094			G759	U677			
		G1392	A1275	U1091	A1095			G760	U678			
		G1393	A1275	U1091	A1096			G761	U679			
		G1394	A1275	U1091	A1097			G762	U680			
		G1395	A1275	U1091	A1098			G763	U681			
		G1396	A1275	U1091	A1099			G764	U682			
		G1397	A1275	U1091	A1100			G765	U683			
		G1398	A1275	U1091	A1101			G766	U684			
		G1399	A1275	U1091	A1102			G767	U685			
		G1400	A1275	U1091	A1103			G768	U686			
		G1401	A1275	U1091	A1104			G769	U687			
		G1402	A1275	U1091	A1105			G770	U688			
		G1403	A1275	U1091	A1106			G771	U689			
		G1404	A1275	U1091	A1107			G772	U690			
		G1405	A1275	U1091	A1108			G773	U691			
		G1406	A1275	U1091	A1109			G774	U692			
		G1407	A1275	U1091	A1110			G775	U693			
		G1408	A1275	U1091	A1111			G776	U694			
		G1409	A1275	U1091	A1112			G777	U695			
		G1410	A1275	U1091	A1113			G778	U696			
		G1411	A1275	U1091	A1114			G779	U697			
		G1412	A1275	U1091	A1115			G780	U698			
		G1413	A1275	U1091	A1116			G781	U699			
		G1414	A1275	U1091	A1117			G782	U700			
		G1415	A1275	U1091	A1118			G783	U701			
		G1416	A1275	U1091	A1119			G784	U702			
		G1417	A1275	U1091	A1120			G785	U703			
		G1418	A1275	U1091	A1121			G786	U704			
		G1419	A1275	U1091	A1122			G787	U705			
		G1420	A1275	U1091	A1123			G788	U706			
		G1421	A1275	U1091	A1124			G789	U707			
		G1422	A1275	U1091	A1125			G790	U708			
		G1423	A1275	U1091	A1126			G791	U709			
		G1424	A1275	U1091	A1127			G792	U710			
		G1425	A1275	U1091	A1128			G793	U711			
		G1426	A1275	U1091	A1129			G794	U712			
		G1427	A1275	U1091	A1130			G795	U713			
		G1428	A1275	U1091	A1131			G796	U714			
		G1429	A1275	U1091	A1132			G797	U715			
		G1430	A1275	U1091	A1133			G798	U716			
		G1431	A1275	U1091	A1134			G799	U717			
		G1432	A1275	U1091	A1135			G800	U718			
		G1433	A1275	U1091	A1136			G801	U719			
		G1434	A1275	U1091	A1137			G802	U720			
		G1435	A1275	U1091	A1138			G803	U721			
		G1436	A1275	U1091	A1139			G804	U722			
		G1437	A1275	U1091	A1140			G805	U723			
		G1438	A1275	U1091	A1141			G806	U724			
		G1439	A1275	U1091	A1142			G807	U725			
		G1440	A1275	U1091	A1143			G808	U726			
		G1441	A1275	U1091	A1144			G809	U727			
		G1442	A1275	U1091	A1145			G810	U728			
		G1443	A1275	U1091	A1146			G811	U729			
		G1444	A1275	U1091	A1147			G812	U730			
		G1445	A1275	U1091	A1148			G813	U731			
		G1446	A1275	U1091	A1149			G814	U732			
		G1447	A1275	U1091	A1150			G815	U733			
		G1448	A1275	U1091	A1151			G816	U734			
		G1449	A1275	U1091	A1152			G817	U735			
		G1450	A1275	U1091	A1153			G818	U736			
		G1451	A1275	U1091	A1154			G819	U737			
		G1452	A1275	U1091	A1155			G820	U738			
		G1453	A1275	U1091	A1156			G821	U739			
		G1454	A1275	U1091	A1157			G822	U740			
		G1455	A1275	U1091	A1158			G823	U741			
		G1456	A1275	U1091	A1159			G824	U742			
		G1457	A1275	U1091	A1160			G825	U743			
		G1458	A1275	U1091	A1161			G826	U744			
		G1459	A1275</									



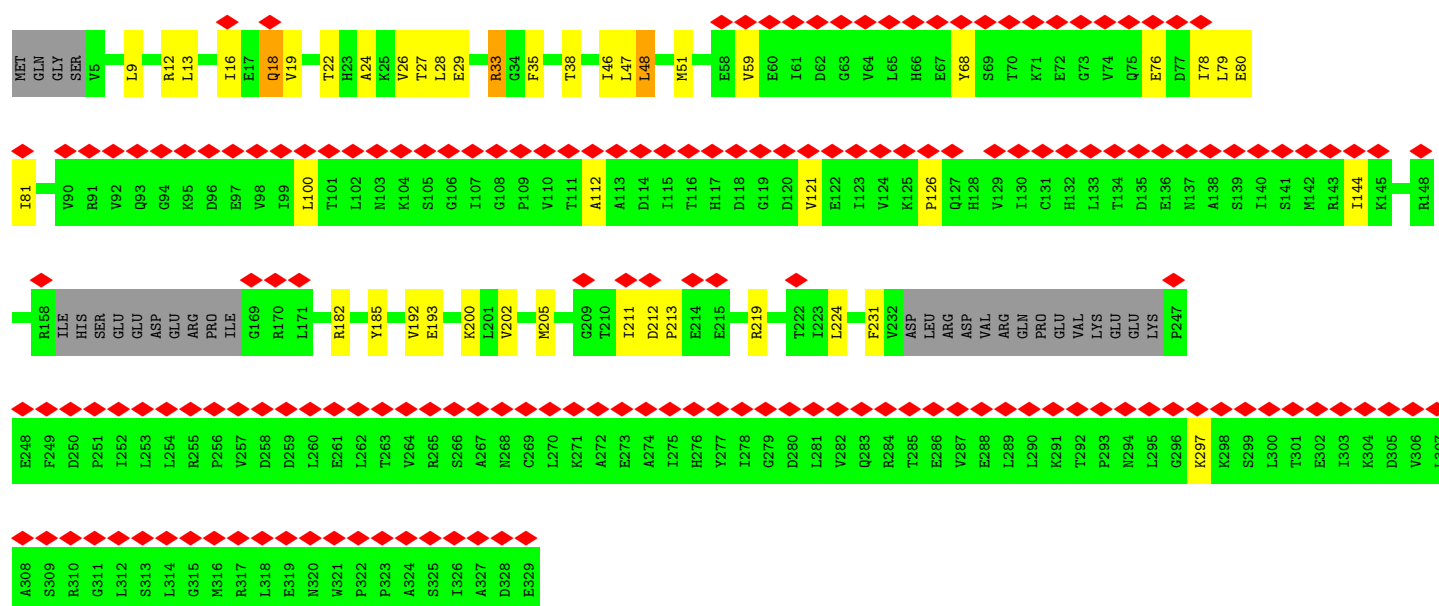
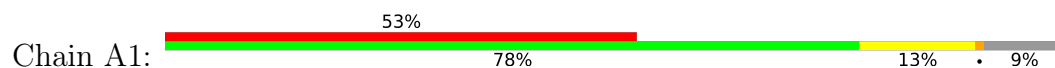
- Molecule 55: template DNA strand



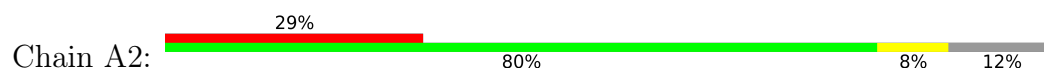
- Molecule 56: non-template DNA strand

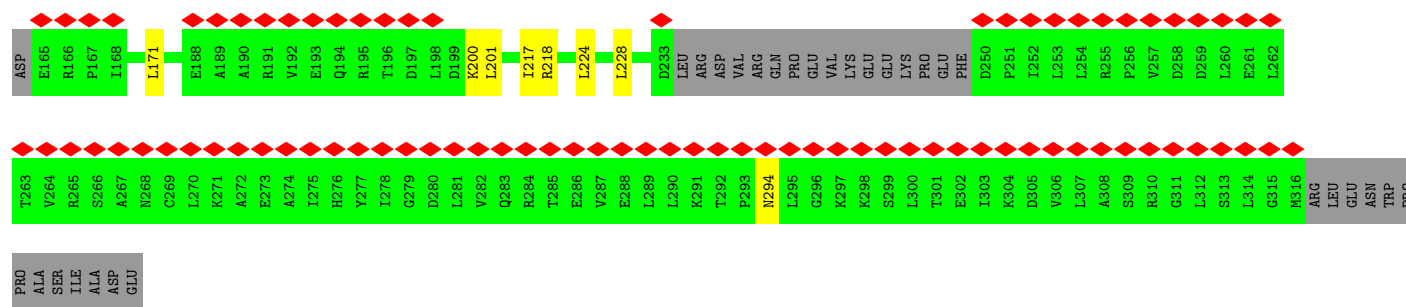


- Molecule 57: DNA-directed RNA polymerase subunit alpha



- Molecule 57: DNA-directed RNA polymerase subunit alpha

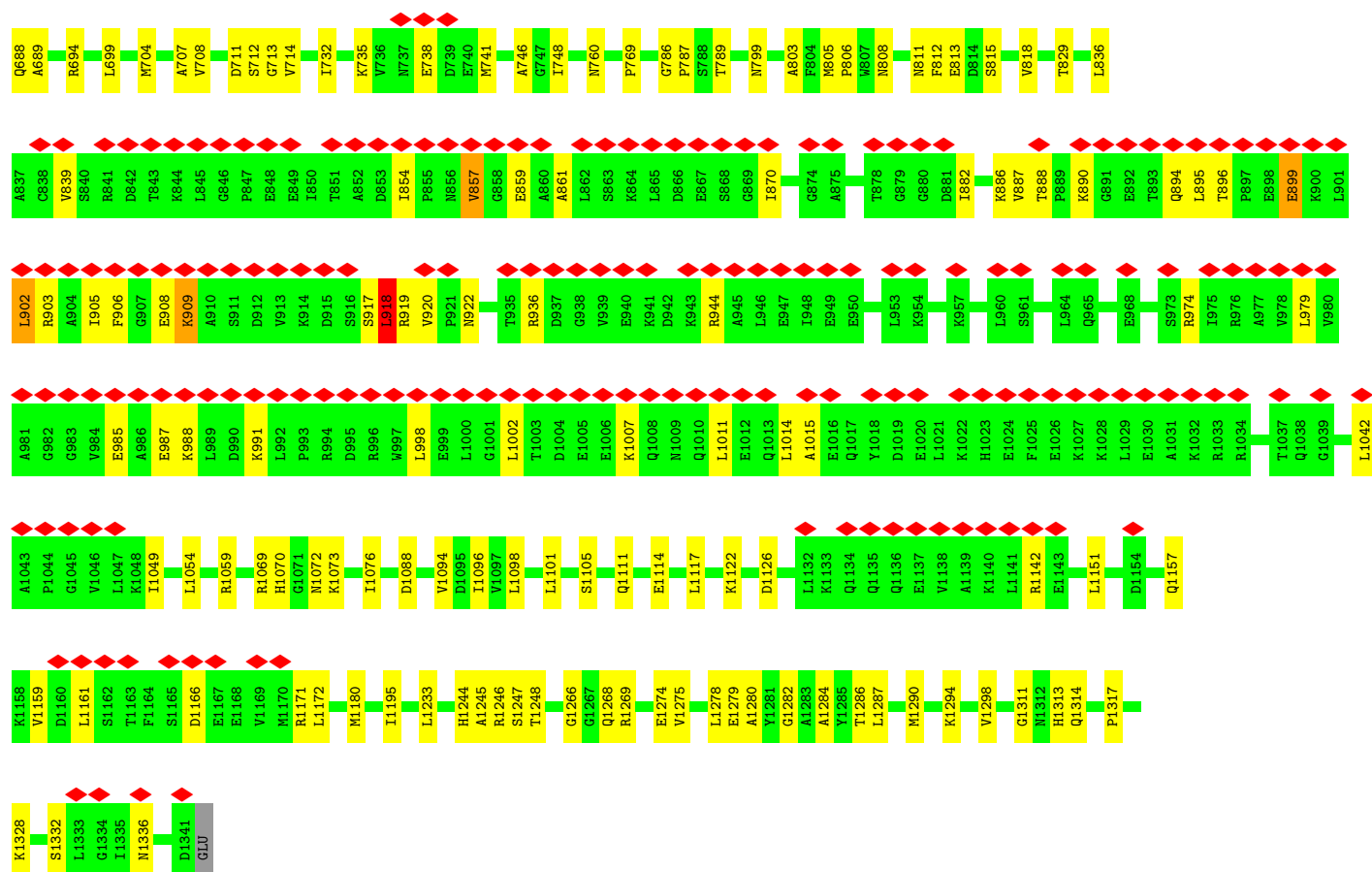




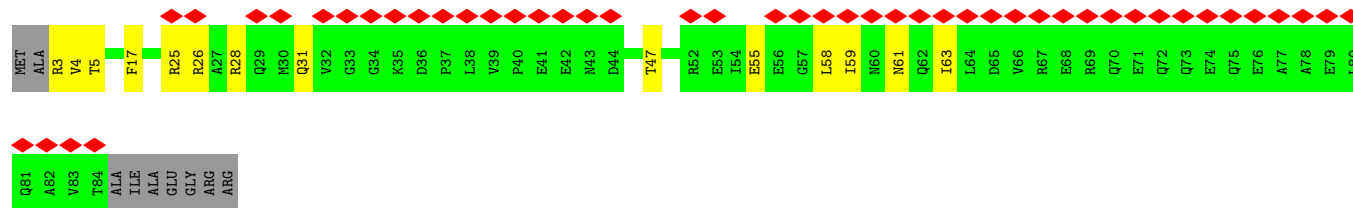
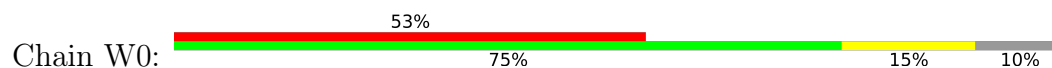
- Molecule 58: DNA-directed RNA polymerase subunit beta'

Chain B1:

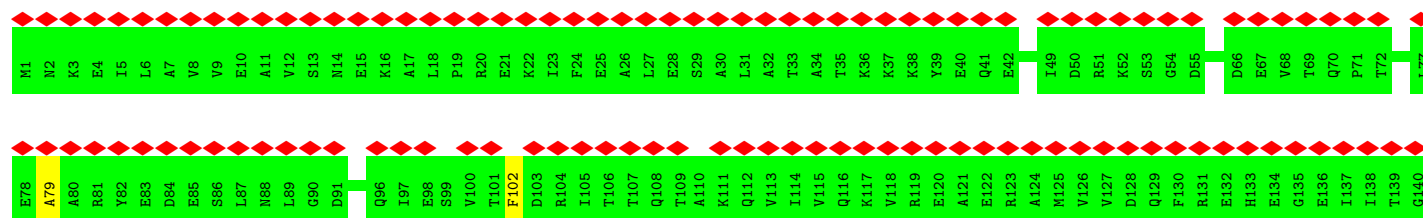
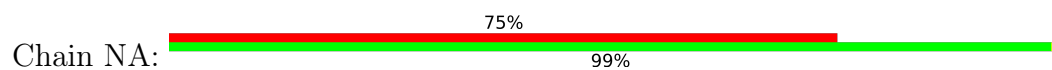


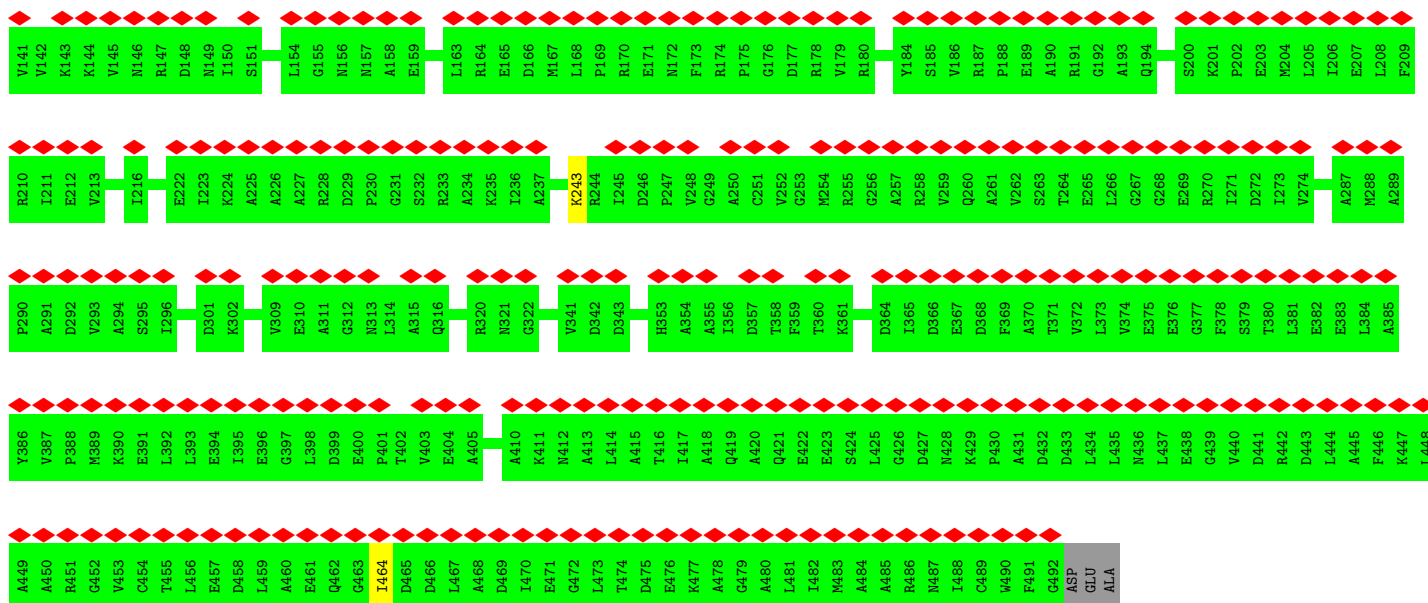


- Molecule 60: DNA-directed RNA polymerase subunit omega

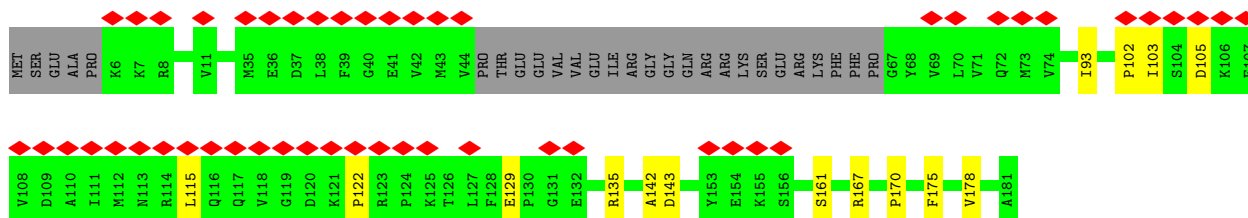
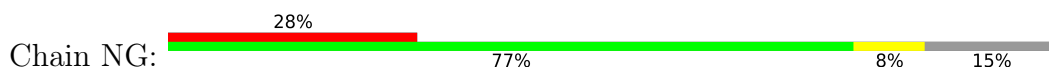


- Molecule 61: Transcription termination/antitermination protein NusA





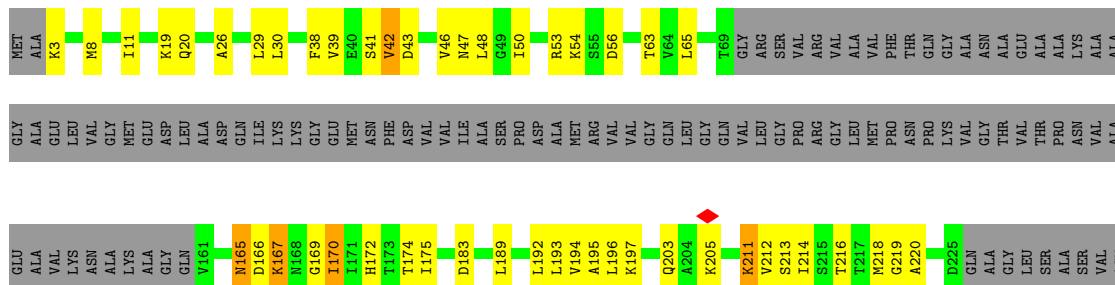
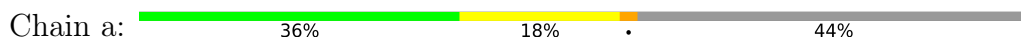
- Molecule 62: Transcription termination/antitermination protein NusG



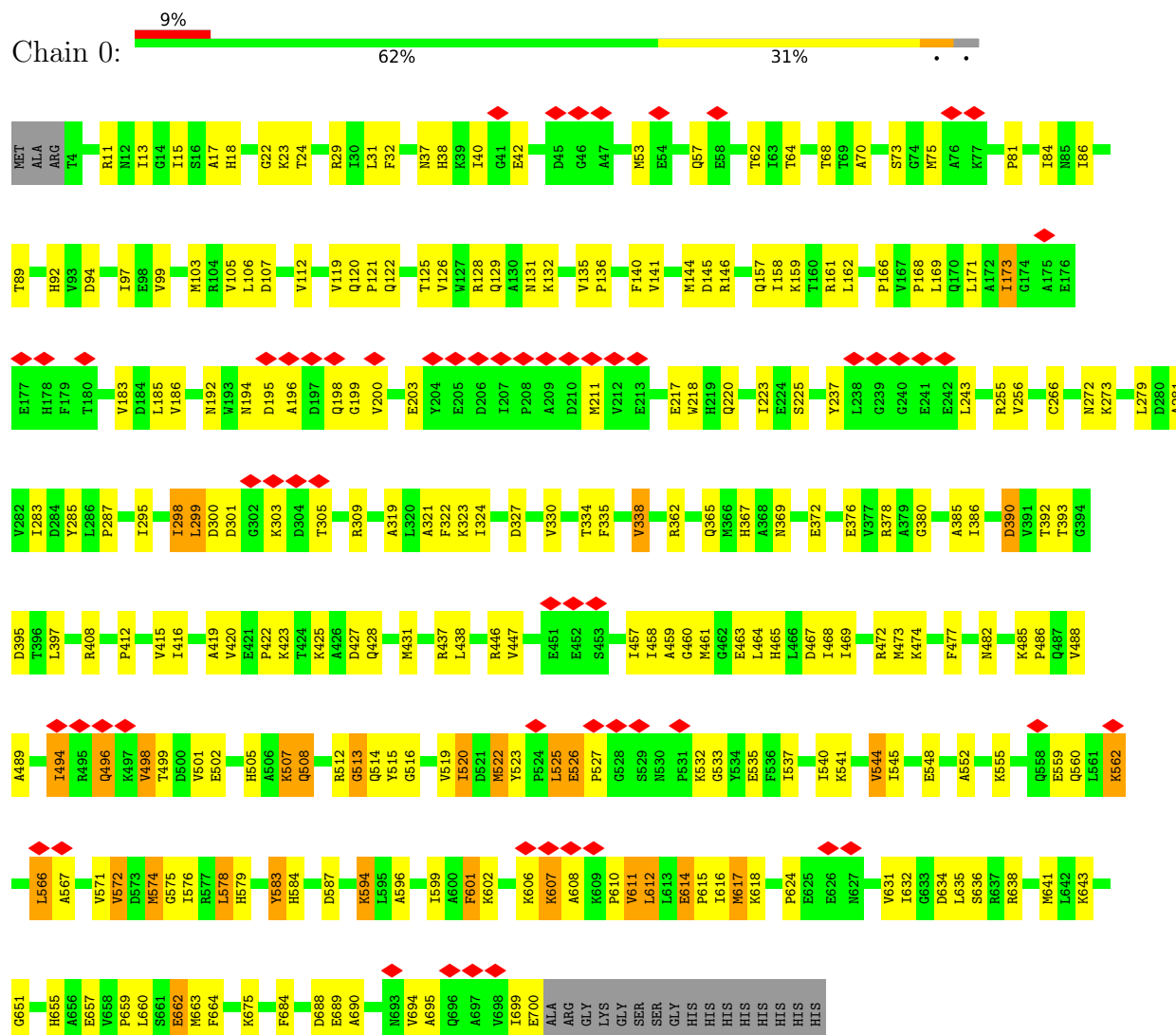
- Molecule 63: tRNA(fMet)



- Molecule 64: Large ribosomal subunit protein uL1



Chain 0:



Chain h:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23500	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	0.085	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	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: MG, KBE, PO4, DPP, UAL, GDP, 5OH

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	0.25	0/362	0.72	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.48	0/380	0.95	0/498
5	E	0.46	0/513	0.80	0/676
6	F	0.40	0/303	0.79	0/397
7	G	0.39	0/1735	0.82	0/2338
8	H	0.42	0/1651	0.80	0/2225
9	I	0.28	0/1665	0.76	1/2227 (0.0%)
10	J	0.47	0/1169	0.81	0/1573
11	K	0.44	0/835	0.86	0/1128
12	L	0.41	0/1195	0.82	2/1602 (0.1%)
13	M	0.31	0/989	0.75	0/1326
14	N	0.29	0/1034	0.74	0/1375
15	O	0.56	0/796	0.81	0/1077
16	P	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.80	0/1300
18	R	0.29	0/892	0.68	0/1193
19	S	0.28	0/817	0.68	1/1088 (0.1%)
20	T	0.37	0/722	0.74	0/964
21	U	0.29	0/659	0.63	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.28	0/544	0.69	0/731
24	X	0.28	0/652	0.65	0/877
25	Y	0.26	0/671	0.64	2/888 (0.2%)
26	Z	0.56	0/550	1.09	1/728 (0.1%)
27	b	0.49	0/2121	0.82	0/2852
28	c	0.45	0/1586	0.77	0/2134
29	d	0.40	0/1571	0.80	3/2113 (0.1%)
30	e	0.30	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.34	0/1122	0.77	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.39	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.91	1/1268 (0.1%)
36	l	0.41	1/1054 (0.1%)	0.81	4/1403 (0.3%)
37	m	0.40	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.87	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	0/1242
41	q	0.43	0/960	0.71	0/1278
42	r	0.38	0/829	0.78	1/1107 (0.1%)
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.33	0/787	0.74	2/1051 (0.2%)
46	v	0.36	0/766	0.66	0/1025
47	w	0.40	0/582	0.78	0/769
48	x	0.62	0/635	1.16	5/848 (0.6%)
49	y	0.28	0/510	0.71	0/677
50	z	0.36	0/453	0.76	1/605 (0.2%)
51	1	0.59	0/69796	0.60	16/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	5/57662 (0.0%)
54	4	0.64	0/695	0.79	0/1076
55	8	0.56	0/599	0.70	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	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.46	1/10714 (0.0%)	0.67	0/14459
60	W0	0.30	0/652	0.61	0/879
61	NA	0.76	0/2431	1.22	0/3385
62	NG	1.16	0/756	1.04	0/1048
63	6	0.60	0/1832	0.59	0/2855
64	a	0.49	0/1020	0.80	0/1370
65	0	0.55	0/5501	0.82	3/7446 (0.0%)
66	h	3.22	2/11 (18.2%)	0.75	0/13
All	All	0.55	9/194888 (0.0%)	0.67	67/286567 (0.0%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	3	SER	CA-C	-6.75	1.38	1.52
66	h	4	SER	CA-C	-6.34	1.39	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	n	66	ALA	CA-C	-5.96	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.24	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.15	1.33	1.23

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.51	98.44	113.47
51	1	1020	A	C2'-C3'-O3'	7.36	120.55	109.50
48	x	11	PRO	N-CA-C	-7.36	99.48	111.77
51	1	2425	A	O3'-P-O5'	-6.95	93.57	104.00
12	L	82	SER	N-CA-C	6.90	116.43	108.49

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	355	0	353	10	0
2	B	444	0	461	14	0
3	C	409	0	440	20	0
4	D	377	0	418	17	0
5	E	504	0	574	16	0
6	F	302	0	341	14	0
7	G	1704	0	1732	44	0
8	H	1624	0	1699	45	0
9	I	1643	0	1710	44	0
10	J	1156	0	1199	39	0
11	K	817	0	808	23	0
12	L	1181	0	1240	44	0
13	M	979	0	1034	31	0
14	N	1022	0	1070	55	0
15	O	786	0	828	32	0
16	P	869	0	878	27	0
17	Q	955	0	1019	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	883	0	944	25	0
19	S	805	0	847	35	0
20	T	714	0	737	17	0
21	U	649	0	666	21	0
22	V	648	0	691	18	0
23	W	535	0	552	16	0
24	X	637	0	665	17	0
25	Y	665	0	714	22	0
26	Z	544	0	579	15	0
27	b	2082	0	2157	70	0
28	c	1565	0	1616	57	0
29	d	1552	0	1619	51	0
30	e	1410	0	1447	43	0
31	f	1323	0	1374	31	0
32	g	1111	0	1148	31	0
33	i	1032	0	1088	35	0
34	j	1129	0	1162	31	0
35	k	938	0	1012	22	0
36	l	1045	0	1117	30	0
37	m	1074	0	1157	28	0
38	n	960	0	1000	34	0
39	o	892	0	923	20	0
40	p	917	0	965	24	0
41	q	947	0	1022	22	0
42	r	816	0	839	22	0
43	s	857	0	922	18	0
44	t	738	0	807	15	0
45	u	779	0	834	21	0
46	v	753	0	780	14	0
47	w	575	0	592	20	0
48	x	625	0	655	22	0
49	y	509	0	543	9	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1373	0
52	2	2568	0	1303	58	0
53	3	33012	0	16618	724	0
54	4	627	0	313	8	0
55	8	539	0	305	27	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	24	0
57	A2	2029	0	1864	18	0
58	B1	10353	0	10548	323	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	B2	10546	0	10550	171	0
60	W0	650	0	658	11	0
61	NA	2432	0	1171	5	0
62	NG	758	0	334	10	0
63	6	1640	0	837	27	0
64	a	1013	0	1081	41	0
65	0	5399	0	5363	140	0
66	h	48	0	40	6	0
67	B1	1	0	0	0	0
68	0	28	0	12	1	0
69	0	5	0	0	0	0
All	All	181755	0	131931	3749	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 12.

The worst 5 of 3749 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)
12:L:92:PRO:HA	12:L:95:ARG:HE	1.12	1.13
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.10
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.10
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.06

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	44/70 (63%)	38 (86%)	6 (14%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
3	C	48/55 (87%)	37 (77%)	11 (23%)	0	100	100
4	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
5	E	62/65 (95%)	48 (77%)	13 (21%)	1 (2%)	7	38
6	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100
8	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
9	I	203/206 (98%)	171 (84%)	31 (15%)	1 (0%)	24	63
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	79 (81%)	19 (19%)	0	100	100
12	L	149/179 (83%)	129 (87%)	20 (13%)	0	100	100
13	M	127/130 (98%)	110 (87%)	17 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
15	O	96/103 (93%)	82 (85%)	14 (15%)	0	100	100
16	P	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
17	Q	121/124 (98%)	97 (80%)	23 (19%)	1 (1%)	16	54
18	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
19	S	98/101 (97%)	86 (88%)	12 (12%)	0	100	100
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
25	Y	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
26	Z	63/71 (89%)	47 (75%)	16 (25%)	0	100	100
27	b	269/273 (98%)	227 (84%)	42 (16%)	0	100	100
28	c	207/209 (99%)	177 (86%)	30 (14%)	0	100	100
29	d	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
30	e	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	124 (84%)	23 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
34	j	140/142 (99%)	120 (86%)	20 (14%)	0	100	100
35	k	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
36	l	141/144 (98%)	117 (83%)	24 (17%)	0	100	100
37	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
39	o	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
40	p	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	q	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	t	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
45	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
46	v	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
47	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
48	x	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
49	y	61/63 (97%)	61 (100%)	0	0	100	100
50	z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
57	A1	295/329 (90%)	274 (93%)	21 (7%)	0	100	100
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1206 (91%)	119 (9%)	4 (0%)	36	72
59	B2	1338/1342 (100%)	1208 (90%)	126 (9%)	4 (0%)	36	72
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	476 (97%)	14 (3%)	0	100	100
62	NG	150/181 (83%)	133 (89%)	12 (8%)	5 (3%)	3	21
64	a	128/234 (55%)	105 (82%)	23 (18%)	0	100	100
65	0	695/716 (97%)	598 (86%)	87 (12%)	10 (1%)	9	40
66	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	10486/11185 (94%)	9306 (89%)	1154 (11%)	26 (0%)	44	78

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	121	PRO
62	NG	103	ILE
62	NG	122	PRO
59	B2	43	PRO
59	B2	918	LEU

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	42/62 (68%)	42 (100%)	0	100	100
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%)	35 (92%)	3 (8%)	11	32
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	24
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	47
8	H	170/190 (90%)	162 (95%)	8 (5%)	23	45
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	75
10	J	119/126 (94%)	113 (95%)	6 (5%)	22	43
11	K	87/116 (75%)	83 (95%)	4 (5%)	24	45
12	L	124/147 (84%)	121 (98%)	3 (2%)	43	64
13	M	104/105 (99%)	102 (98%)	2 (2%)	50	67
14	N	105/107 (98%)	105 (100%)	0	100	100
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	26
16	P	89/99 (90%)	88 (99%)	1 (1%)	65	76
17	Q	103/104 (99%)	101 (98%)	2 (2%)	50	67
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	76
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	75
20	T	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	U	65/65 (100%)	65 (100%)	0	100	100
22	V	74/78 (95%)	74 (100%)	0	100	100
23	W	56/65 (86%)	56 (100%)	0	100	100
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	46 (84%)	9 (16%)	2	10
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	67
28	c	164/164 (100%)	163 (99%)	1 (1%)	78	83
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	57
30	e	148/150 (99%)	146 (99%)	2 (1%)	59	72
31	f	137/138 (99%)	136 (99%)	1 (1%)	76	81
32	g	114/114 (100%)	111 (97%)	3 (3%)	40	62
33	i	109/110 (99%)	109 (100%)	0	100	100
34	j	116/116 (100%)	113 (97%)	3 (3%)	40	62
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	48	66
37	m	109/109 (100%)	108 (99%)	1 (1%)	70	79
38	n	100/103 (97%)	98 (98%)	2 (2%)	48	66
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	89 (100%)	0	100	100
42	r	84/84 (100%)	84 (100%)	0	100	100
43	s	93/93 (100%)	86 (92%)	7 (8%)	12	33
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	50
45	u	83/85 (98%)	82 (99%)	1 (1%)	63	75
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	74
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	65 (97%)	2 (3%)	36	57
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	47 (98%)	1 (2%)	47	65
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	A2	186/286 (65%)	184 (99%)	2 (1%)	65	76
58	B1	1110/1168 (95%)	1021 (92%)	89 (8%)	11	31
59	B2	1150/1157 (99%)	1121 (98%)	29 (2%)	42	63
60	W0	70/75 (93%)	68 (97%)	2 (3%)	37	58
64	a	109/181 (60%)	98 (90%)	11 (10%)	7	23
65	0	574/588 (98%)	512 (89%)	62 (11%)	6	21
66	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8120/8683 (94%)	7807 (96%)	313 (4%)	30	49

5 of 313 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	B2	908	GLU
65	0	562	LYS
60	W0	4	VAL
65	0	390	ASP
65	0	607	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 149 such sidechains are listed below:

Mol	Chain	Res	Type
58	B1	364	HIS
65	0	170	GLN
58	B1	865	HIS
59	B2	808	ASN
22	V	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	439 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)
54	4	29/41 (70%)	15 (51%)	4 (13%)
63	6	76/77 (98%)	14 (18%)	0
All	All	4664/4684 (99%)	679 (14%)	11 (0%)

5 of 679 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	23	G
51	1	34	U
51	1	35	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	4	10	C
54	4	18	U
54	4	32	U
54	4	19	U
51	1	2326	C

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

4 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	$\# Z > 2$
66	5OH	h	6	66	7,12,13	0.77	0	4,16,18	1.32	1 (25%)
66	UAL	h	5	66	6,8,9	2.34	2 (33%)	4,9,11	1.88	1 (25%)
66	KBE	h	1	66	8,8,9	0.60	0	6,8,10	1.19	0
66	DPP	h	2	66	4,5,6	0.51	0	1,5,7	0.06	0

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
66	5OH	h	6	66	-	0/2/18/20	0/1/1/1
66	UAL	h	5	66	-	0/3/7/9	-
66	KBE	h	1	66	-	0/7/7/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
66	DPP	h	2	66	-	0/2/4/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	5	UAL	C1-N1	-4.88	1.32	1.40
66	h	5	UAL	C-CA	-2.83	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	h	5	UAL	O-C-CA	-3.29	121.26	125.39
66	h	6	5OH	CR-CB-CA	-2.37	110.09	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	h	6	5OH	4	0
66	h	5	UAL	2	0
66	h	2	DPP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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
68	GDP	0	801	-	29,30,30	1.17	3 (10%)	45,47,47	1.88	8 (17%)
69	PO4	0	802	-	4,4,4	1.00	0	6,6,6	0.51	0

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
68	GDP	0	801	-	-	2/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
68	0	801	GDP	C5-C4	2.75	1.46	1.38
68	0	801	GDP	C6-N1	-2.60	1.34	1.38
68	0	801	GDP	C4-N9	-2.01	1.33	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	0	801	GDP	C5-C4-N3	-5.97	118.89	128.39
68	0	801	GDP	C2-N3-C4	5.04	120.98	112.30
68	0	801	GDP	N9-C4-N3	4.45	134.86	125.95
68	0	801	GDP	C6-C5-N7	3.60	136.84	130.29
68	0	801	GDP	C4-C5-N7	-2.75	106.31	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

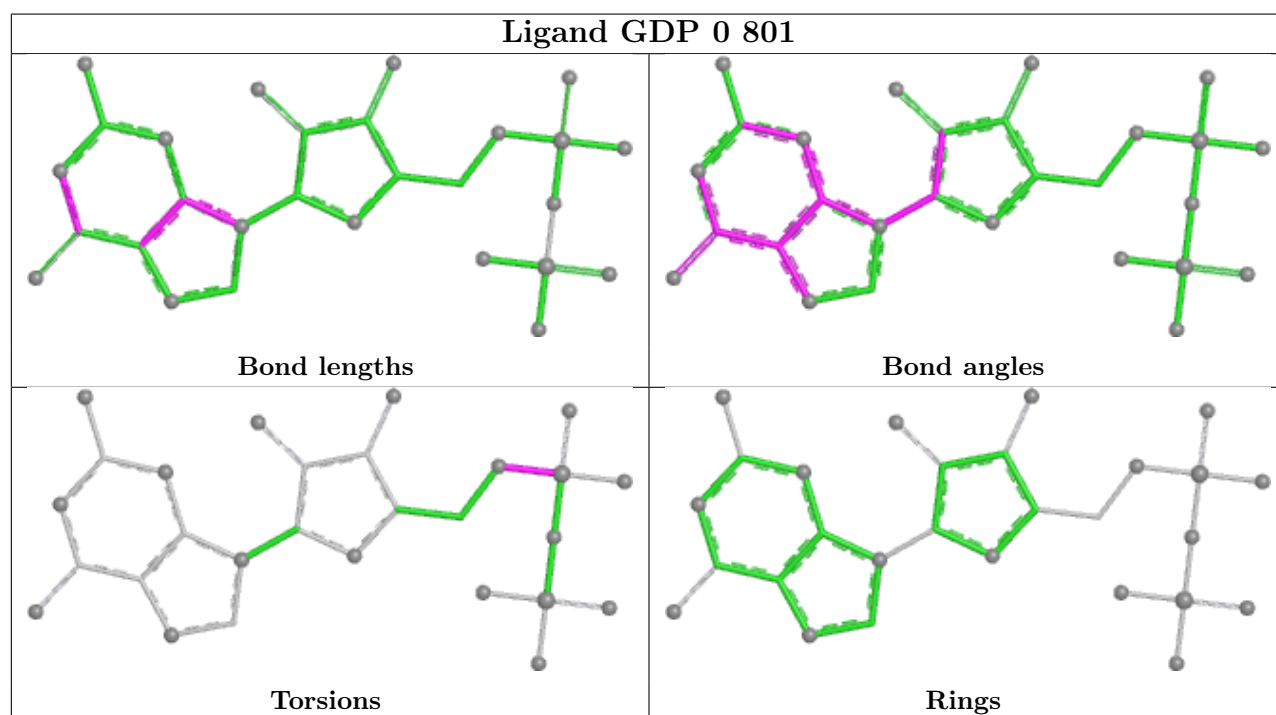
Mol	Chain	Res	Type	Atoms
68	0	801	GDP	C5'-O5'-PA-O3A
68	0	801	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	0	801	GDP	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

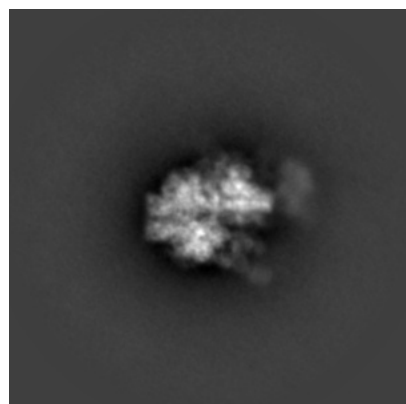
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38945. These allow visual inspection of the internal detail of the map and identification of artifacts.

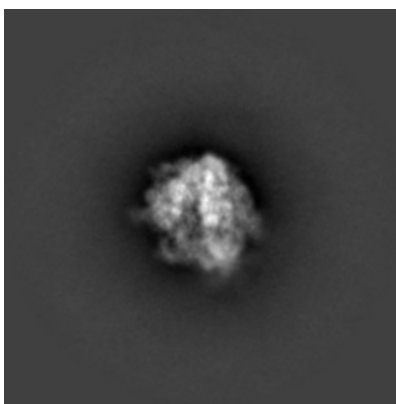
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

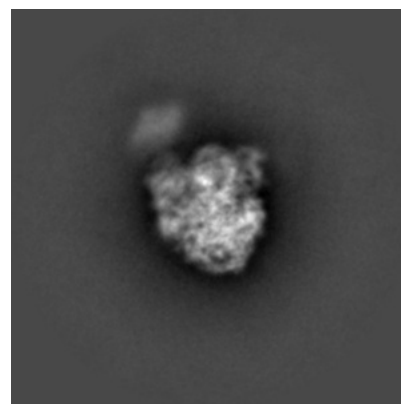
6.1.1 Primary map



X

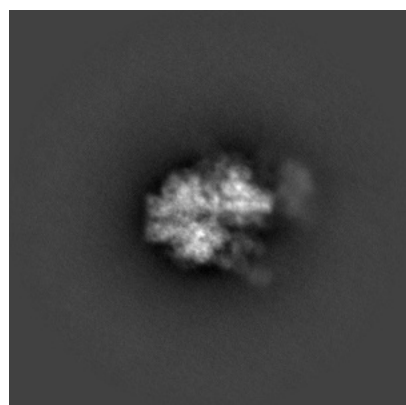


Y

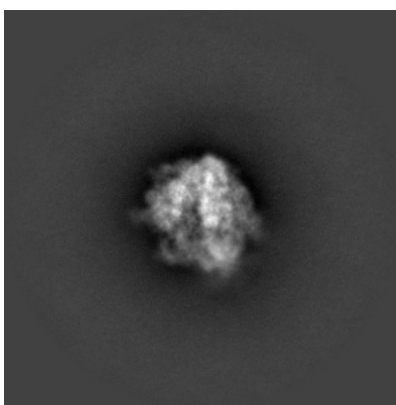


Z

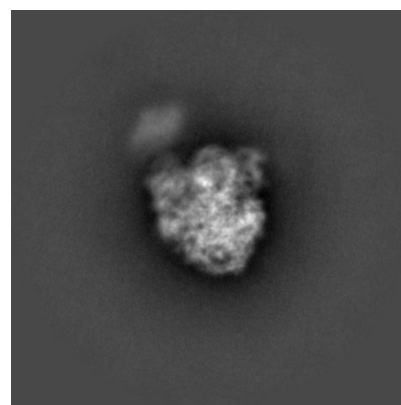
6.1.2 Raw map



X



Y

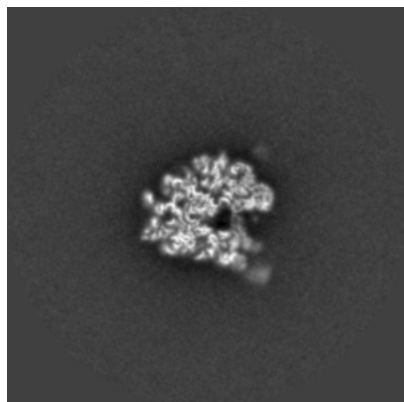


Z

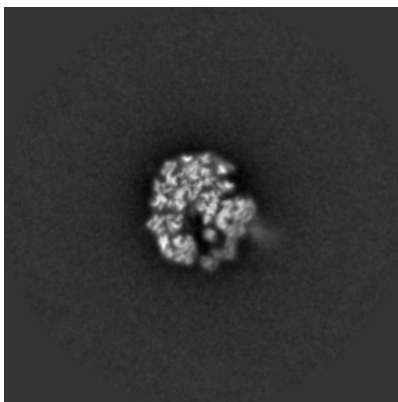
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

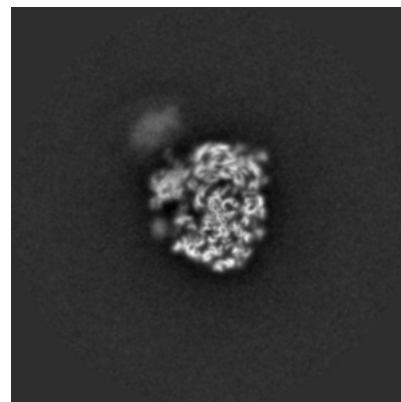
6.2.1 Primary map



X Index: 240

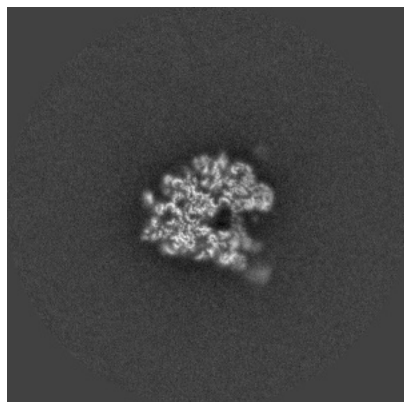


Y Index: 240

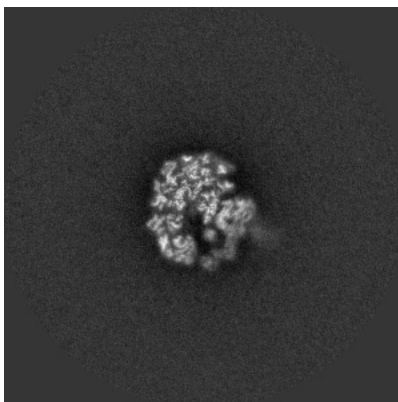


Z Index: 240

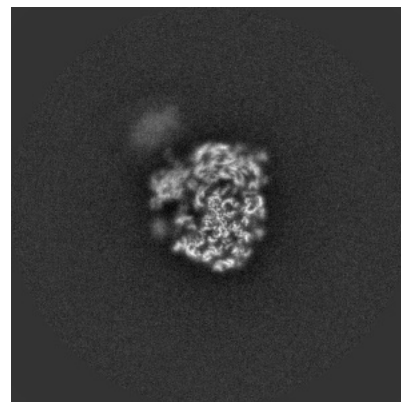
6.2.2 Raw map



X Index: 240



Y Index: 240

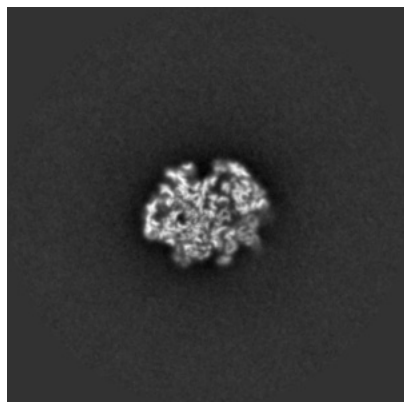


Z Index: 240

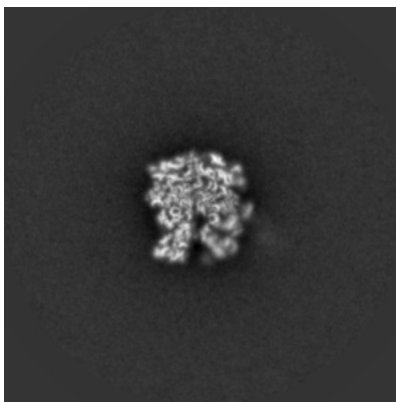
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

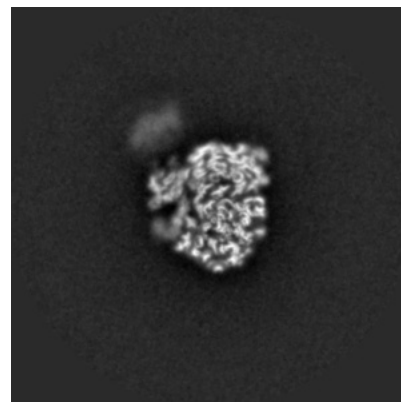
6.3.1 Primary map



X Index: 263

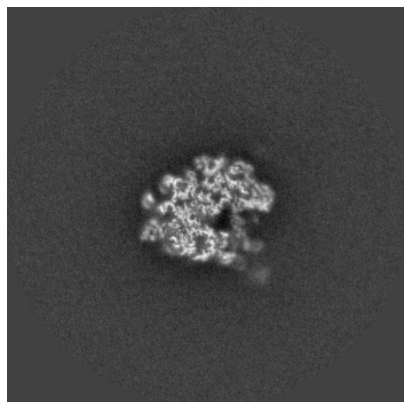


Y Index: 225

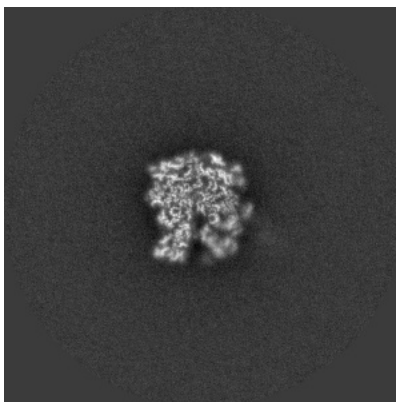


Z Index: 244

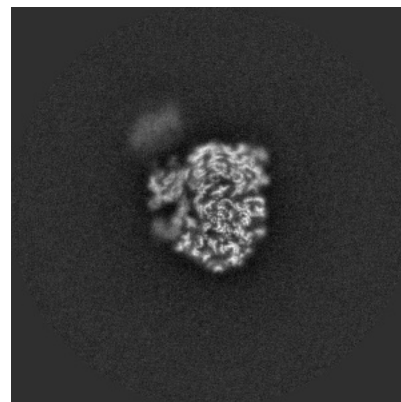
6.3.2 Raw map



X Index: 243



Y Index: 225

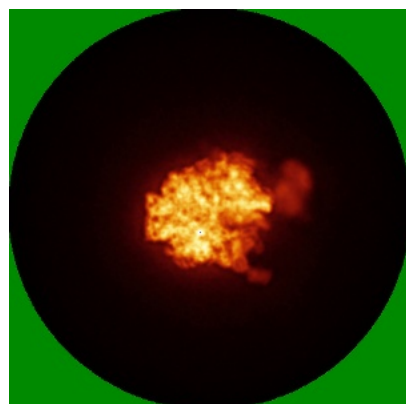


Z Index: 244

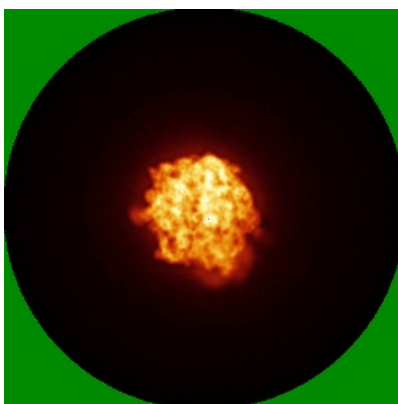
The images above show the largest variance slices of the map in three orthogonal directions.

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

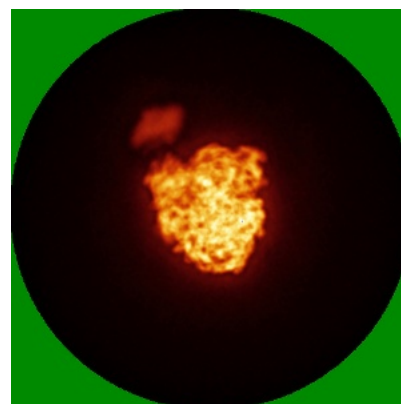
6.4.1 Primary map



X

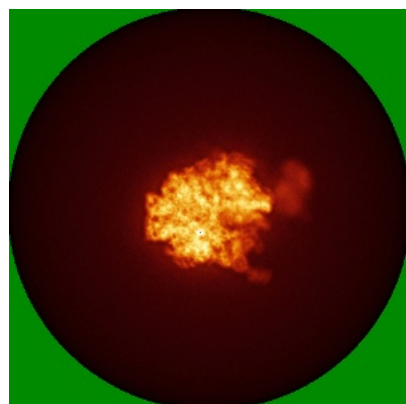


Y

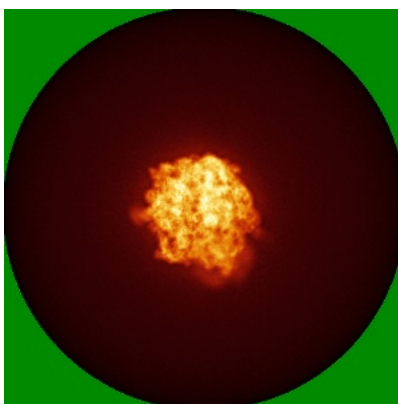


Z

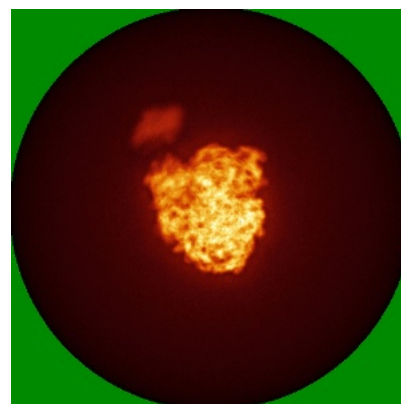
6.4.2 Raw map



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.

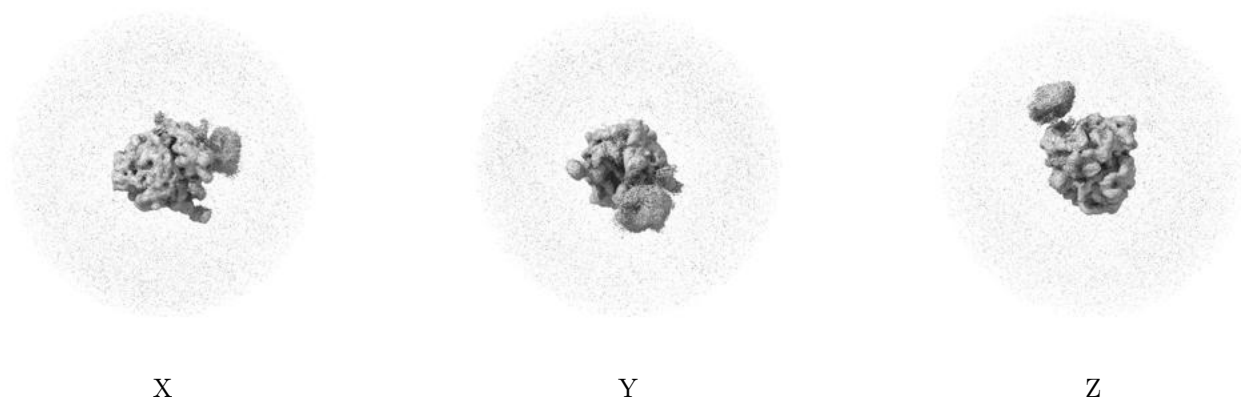
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

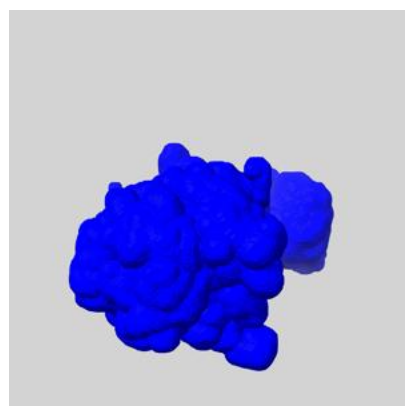
6.6 Mask visualisation [i](#)

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

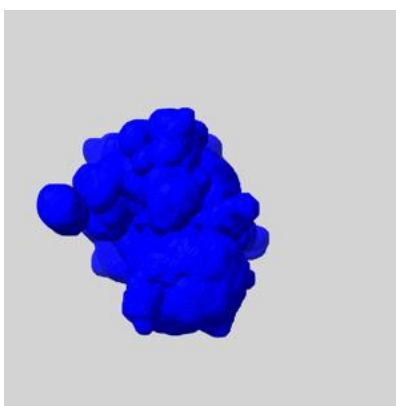
A mask typically either:

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

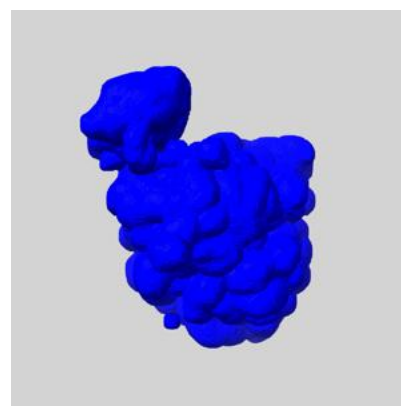
6.6.1 emd_38945_msk_1.map [i](#)



X



Y

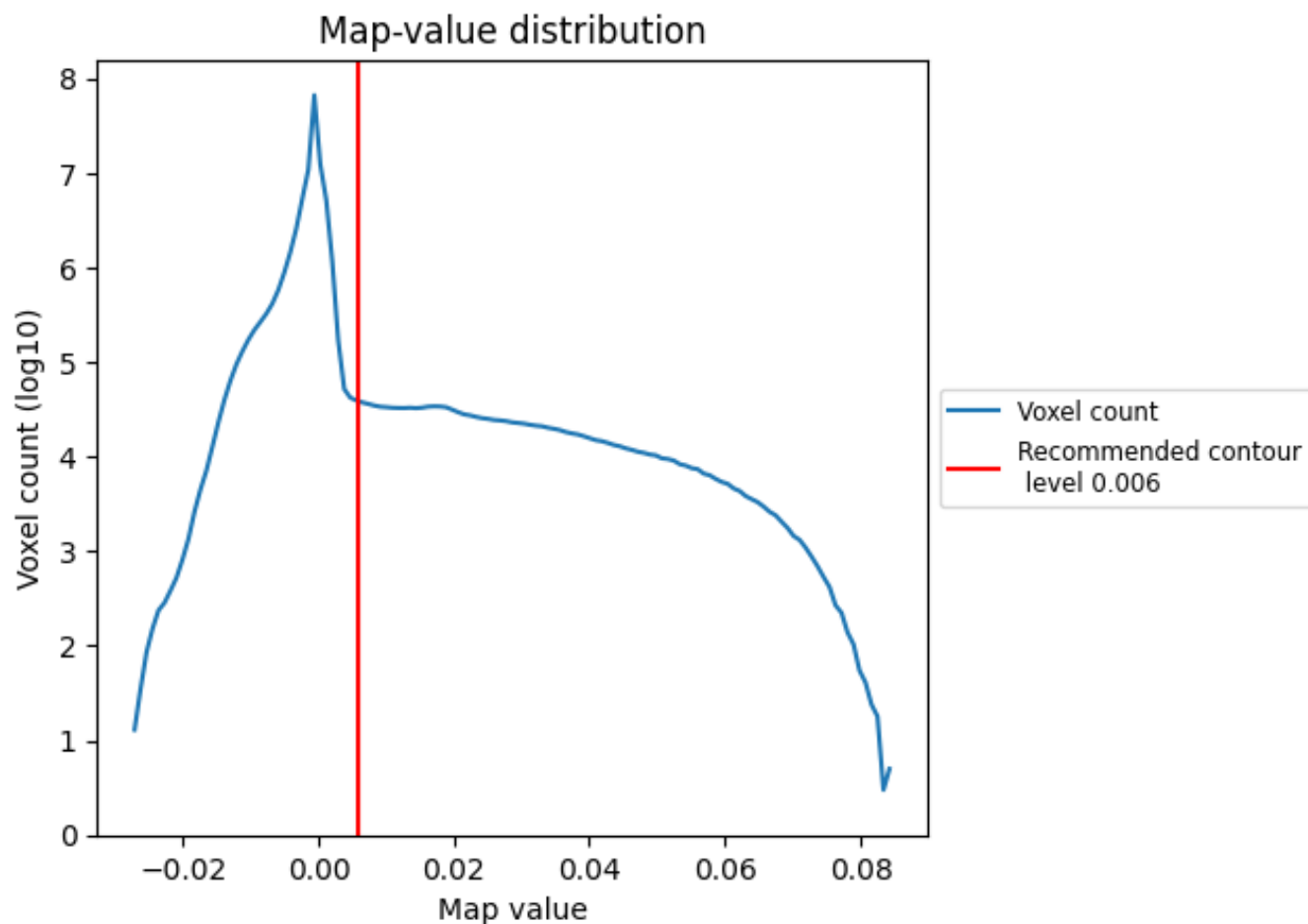


Z

7 Map analysis [i](#)

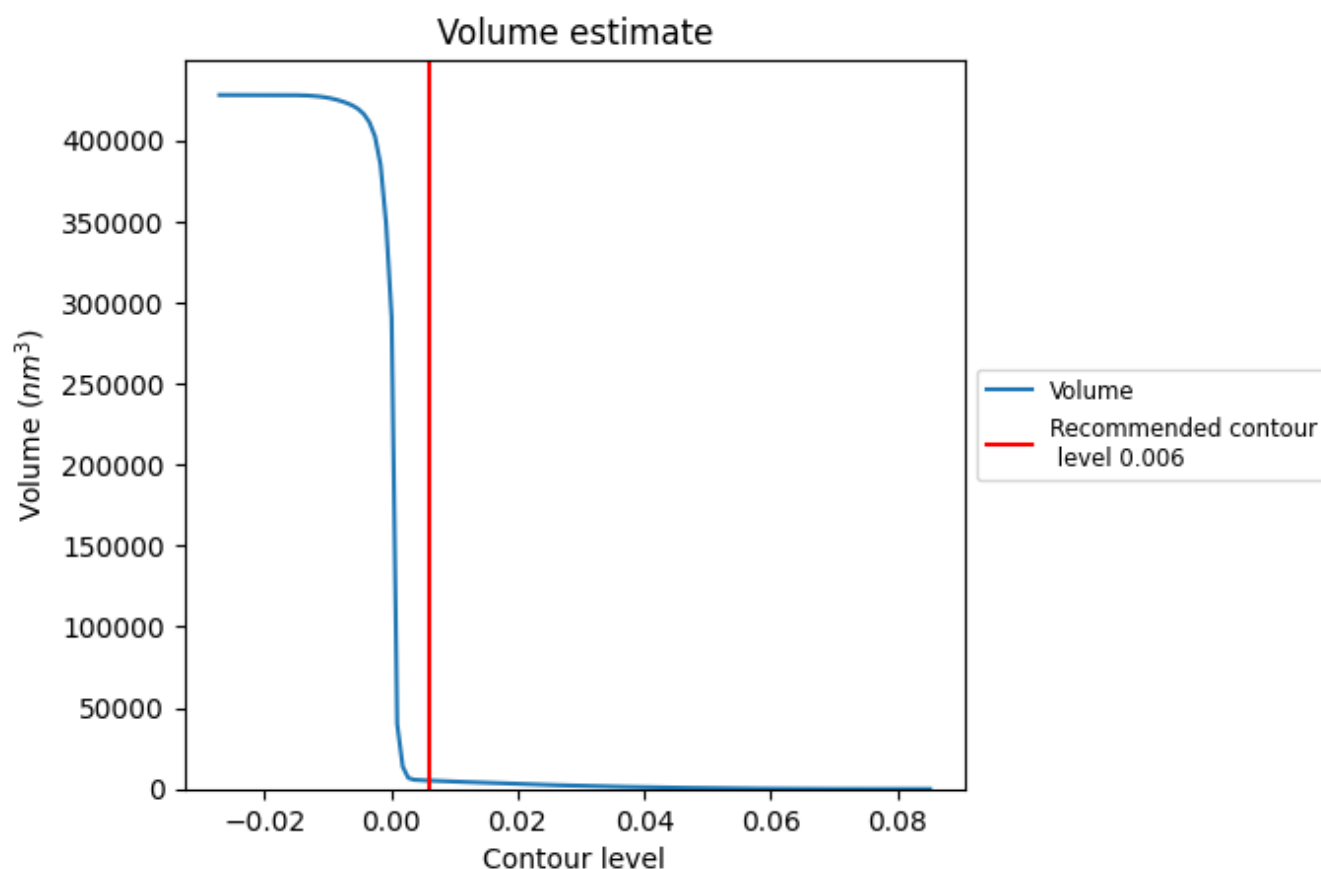
This section contains the results of statistical analysis of the map.

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.

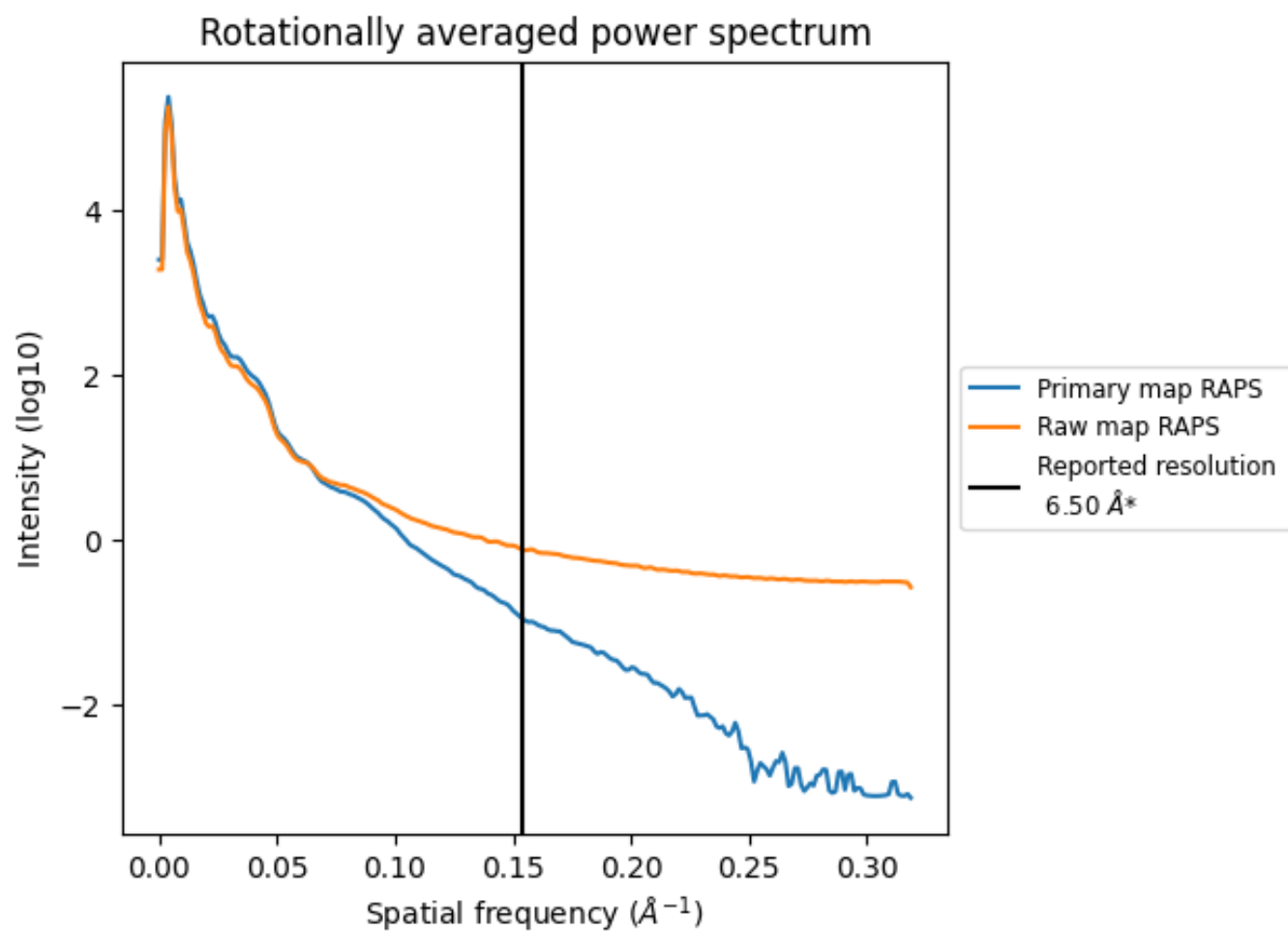
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5183 nm^3 ; this corresponds to an approximate mass of 4682 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 ⓘ

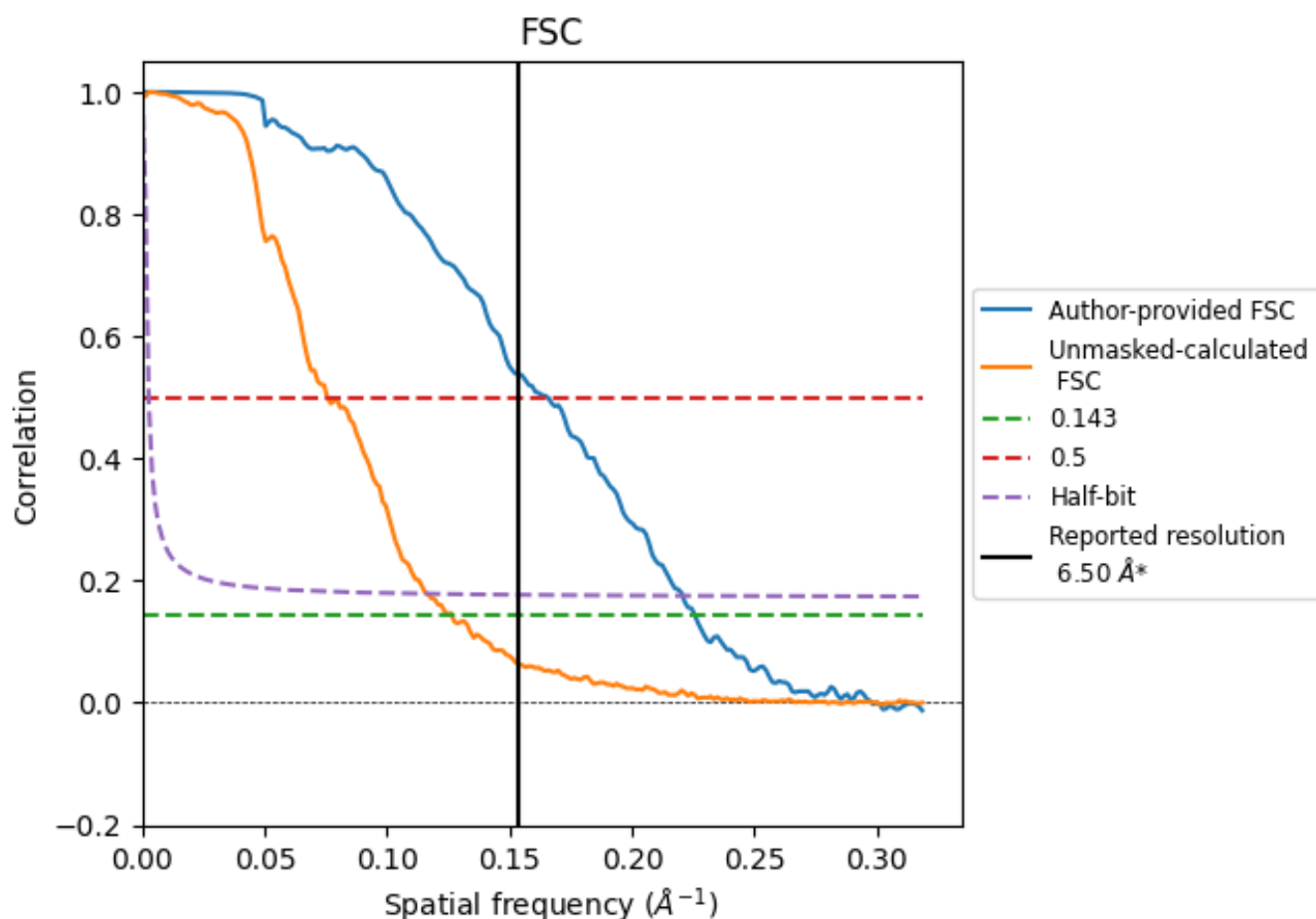


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

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 $0.154 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	4.43	6.04	4.53
Unmasked-calculated*	7.91	13.23	8.58

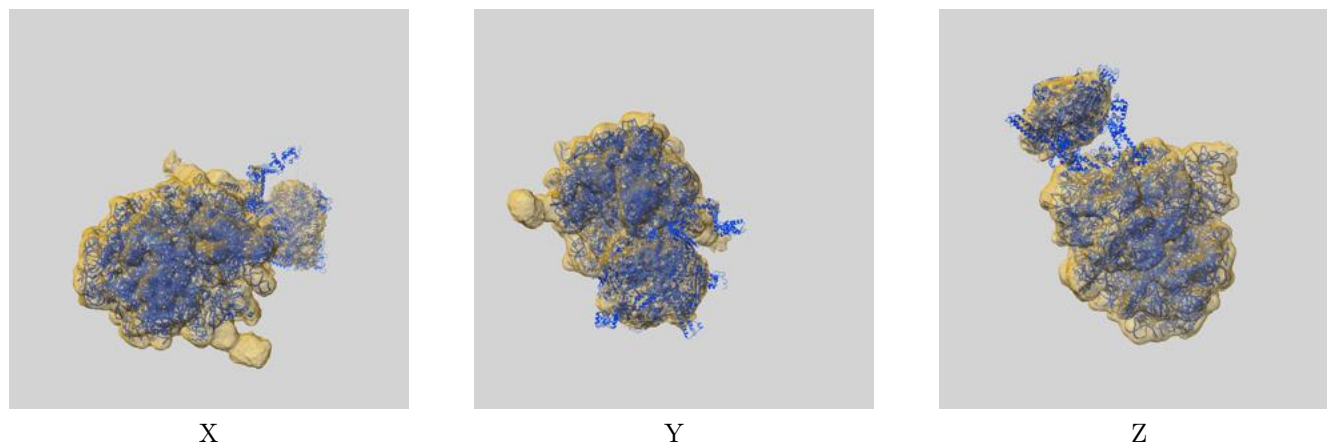
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.43 differs from the reported value 6.5 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.91 differs from the reported value 6.5 by more than 10 %

9 Map-model fit [i](#)

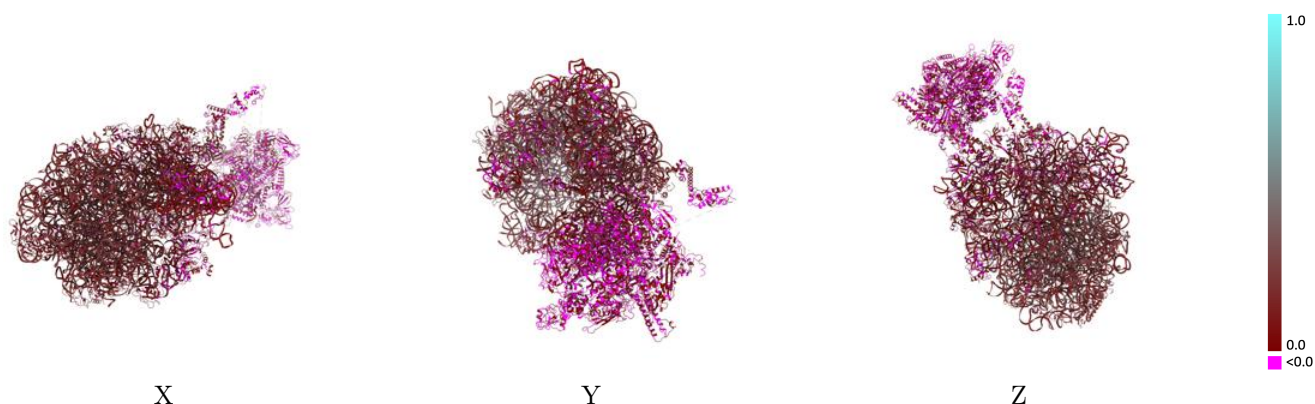
This section contains information regarding the fit between EMDB map EMD-38945 and PDB model 8Y5P. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



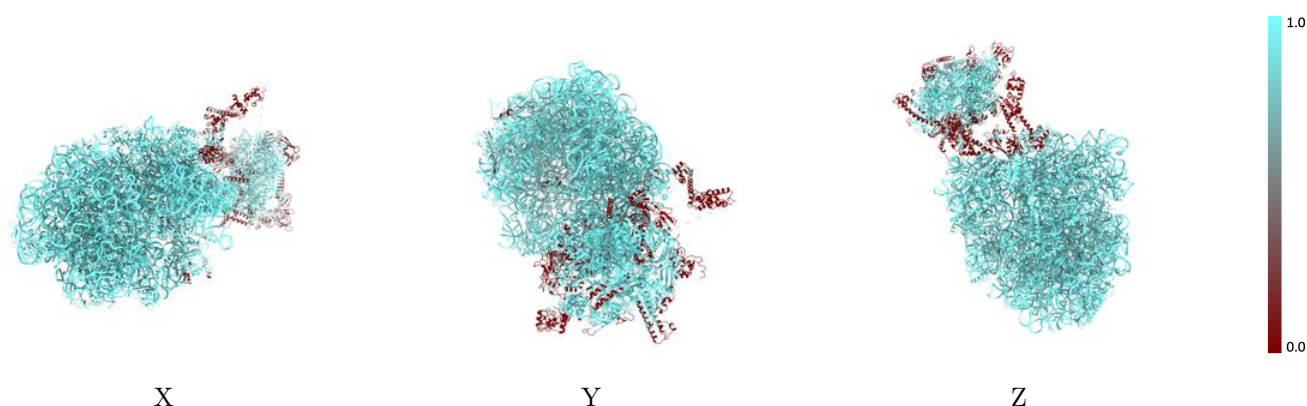
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



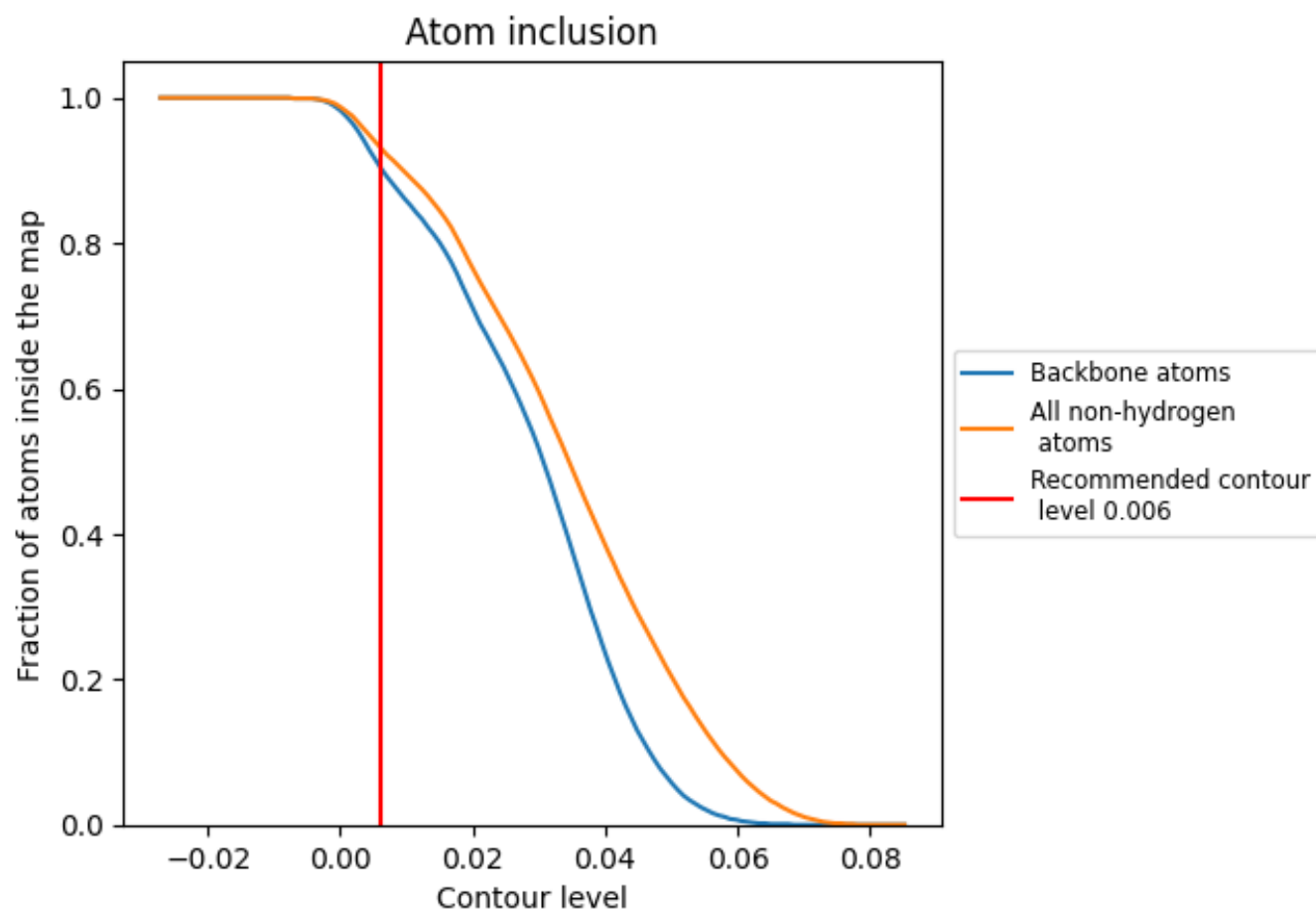
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 93% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.1390
0	 0.8770	 0.0760
1	 0.9990	 0.2080
2	 1.0000	 0.1520
3	 0.9970	 0.1390
4	 0.8760	 0.0290
6	 0.9510	 0.1390
8	 0.9670	 0.0360
9	 0.9300	 0.0510
A	 1.0000	 0.0870
A1	 0.4560	 0.0160
A2	 0.7130	 0.0400
B	 1.0000	 0.1670
B1	 0.6540	 0.0120
B2	 0.7320	 0.0340
C	 0.9730	 0.1540
D	 0.9940	 0.1610
E	 1.0000	 0.1390
F	 1.0000	 0.1210
G	 0.9930	 0.1290
H	 0.9860	 0.1040
I	 0.9930	 0.0840
J	 0.9990	 0.1090
K	 0.9550	 0.1190
L	 0.9370	 0.0950
M	 0.9820	 0.1010
N	 0.9710	 0.0680
NA	 0.2450	 0.1180
NG	 0.6730	 0.0300
O	 0.9960	 0.0660
P	 0.9700	 0.0930
Q	 0.9650	 0.1240
R	 0.9360	 0.1010
S	 1.0000	 0.0860
T	 0.9970	 0.1080



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Chain	Atom inclusion	Q-score
U	 0.9950	 0.0520
V	 0.9980	 0.0940
W	 1.0000	 0.1040
W0	 0.4040	 -0.0020
X	 0.9860	 0.0820
Y	 0.9850	 0.1080
Z	 0.9630	 0.1060
a	 0.9890	 0.0730
b	 0.9940	 0.1870
c	 0.9970	 0.1620
d	 0.9960	 0.1610
e	 0.9570	 0.0890
f	 0.9850	 0.1310
g	 0.9140	 0.1290
h	 1.0000	 0.1790
i	 0.8740	 0.0240
j	 1.0000	 0.1700
k	 0.9840	 0.1860
l	 0.9990	 0.1430
m	 0.9780	 0.1480
n	 0.9970	 0.1640
o	 1.0000	 0.0910
p	 0.9960	 0.1660
q	 0.9990	 0.1430
r	 1.0000	 0.1600
s	 0.9980	 0.1810
t	 0.9990	 0.1660
u	 0.9950	 0.1500
v	 0.9990	 0.1440
w	 0.9980	 0.1150
x	 1.0000	 0.1710
y	 0.9980	 0.1460
z	 0.9930	 0.1560