



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 04:27 PM EDT

PDB ID : 6OM6 / pdb_00006om6
EMDB ID : EMD-20121
Title : Structure of trans-translation inhibitor bound to E. coli 70S ribosome with P site tRNA
Authors : Hoffer, E.D.; Mehrani, A.; Keiler, K.C.; Stagg, S.M.; Dunham, C.M.
Deposited on : 2019-04-18
Resolution : 3.10 Å(reported)
Based on initial model : 5MDV

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:

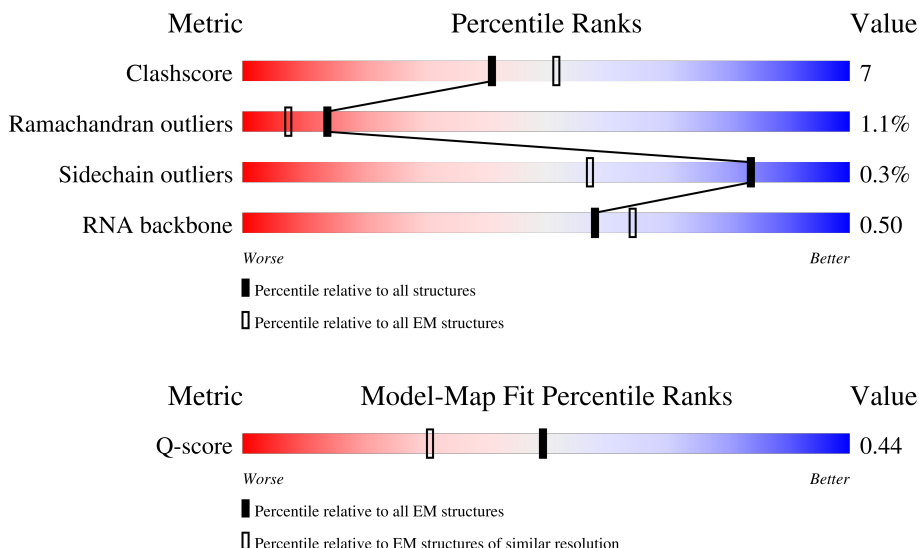
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	1	2904	
2	2	1534	
3	3	120	

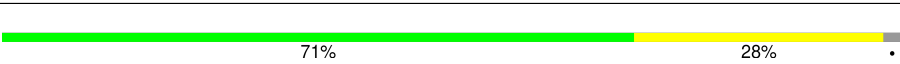
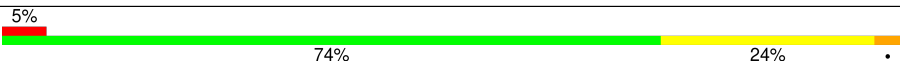
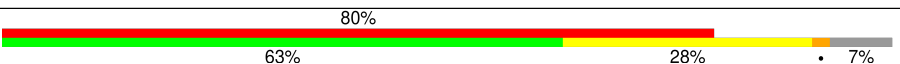
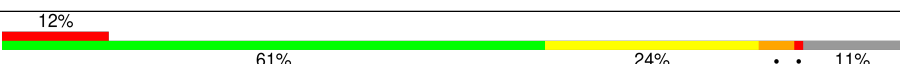
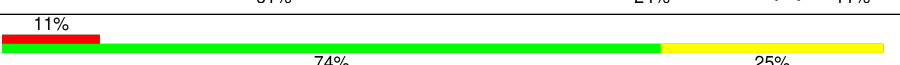
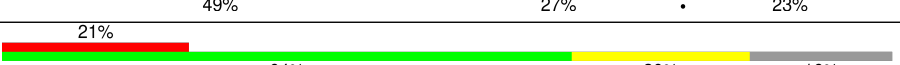
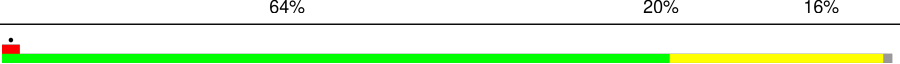
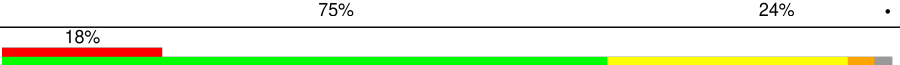
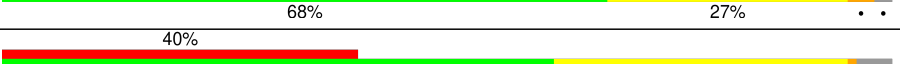
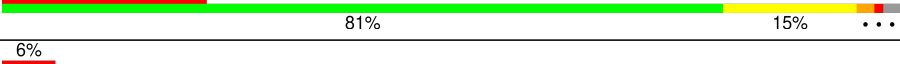
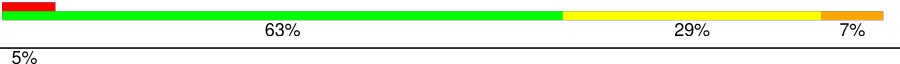
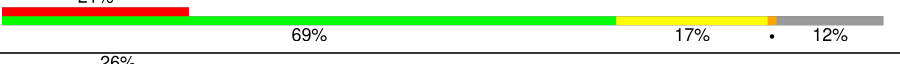
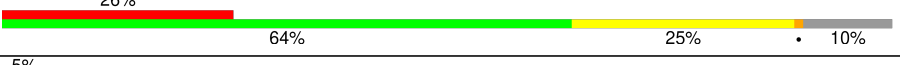
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Mol	Chain	Length	Quality of chain
4	4	5	100%
5	5	76	86% 51% 41% 8%
6	B	273	73% 25% ..
7	C	209	78% 21% .
8	D	201	5% 71% 28% .
9	E	179	13% 70% 25% ..
10	F	177	7% 78% 19% ..
11	G	149	87% 71% 26% .
12	J	142	76% 24%
13	K	123	78% 21% .
14	L	144	76% 24%
15	M	136	83% 17%
16	N	127	82% 12% 6%
17	O	117	65% 32% ..
18	P	115	76% 23% .
19	Q	118	79% 18% ..
20	R	103	71% 28% .
21	S	110	76% 23% .
22	T	100	73% 21% 6%
23	U	104	5% 74% 21% ..
24	V	94	76% 24%
25	X	78	68% 28% ..
26	Y	63	79% 19% .
27	Z	59	76% 22% .
28	a	70	94% 61% 30% 6%

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Mol	Chain	Length	Quality of chain
29	b	57	
30	c	55	
31	d	46	
32	e	65	
33	f	38	
34	g	241	
35	h	233	
36	i	206	
37	j	167	
38	k	135	
39	l	179	
40	m	130	
41	n	130	
42	o	103	
43	p	129	
44	q	124	
45	r	118	
46	s	101	
47	t	89	
48	u	82	
49	v	84	
50	w	75	
51	x	92	
52	y	87	
53	z	71	

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Mol	Chain	Length	Quality of chain
54	W	85	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
55	KKL	1	3301	-	X	-	-

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 144295 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62334	27814	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	5	Total	C	N	O	P	0	0
			110	49	23	33	5		

- Molecule 5 is a RNA chain called tRNA(gly).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	76	Total	C	N	O	P	0	0
			1619	722	284	537	76		

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

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

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

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

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

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

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

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

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

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

- Molecule 44 is a protein called 30S ribosomal protein S12.

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

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

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

- Molecule 49 is a protein called 30S ribosomal protein S17.

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

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

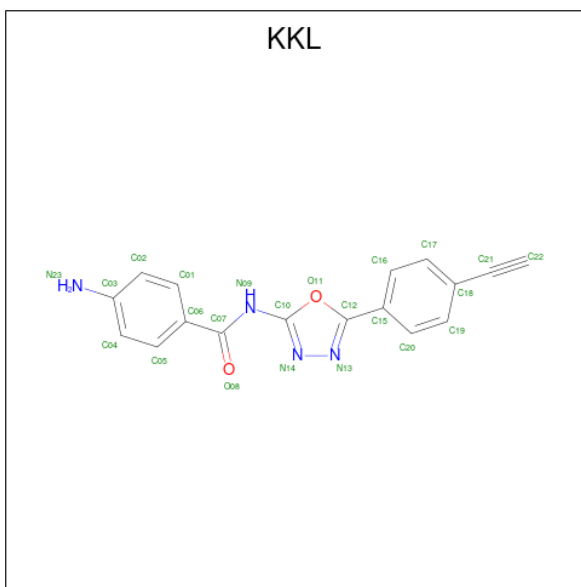
- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	W	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 55 is 4-amino-N-[5-(4-ethynylphenyl)-1,3,4-oxadiazol-2-yl]benzamide (CCD ID: KKL) (formula: C₁₇H₁₂N₄O₂) (labeled as "Ligand of Interest" by depositor).

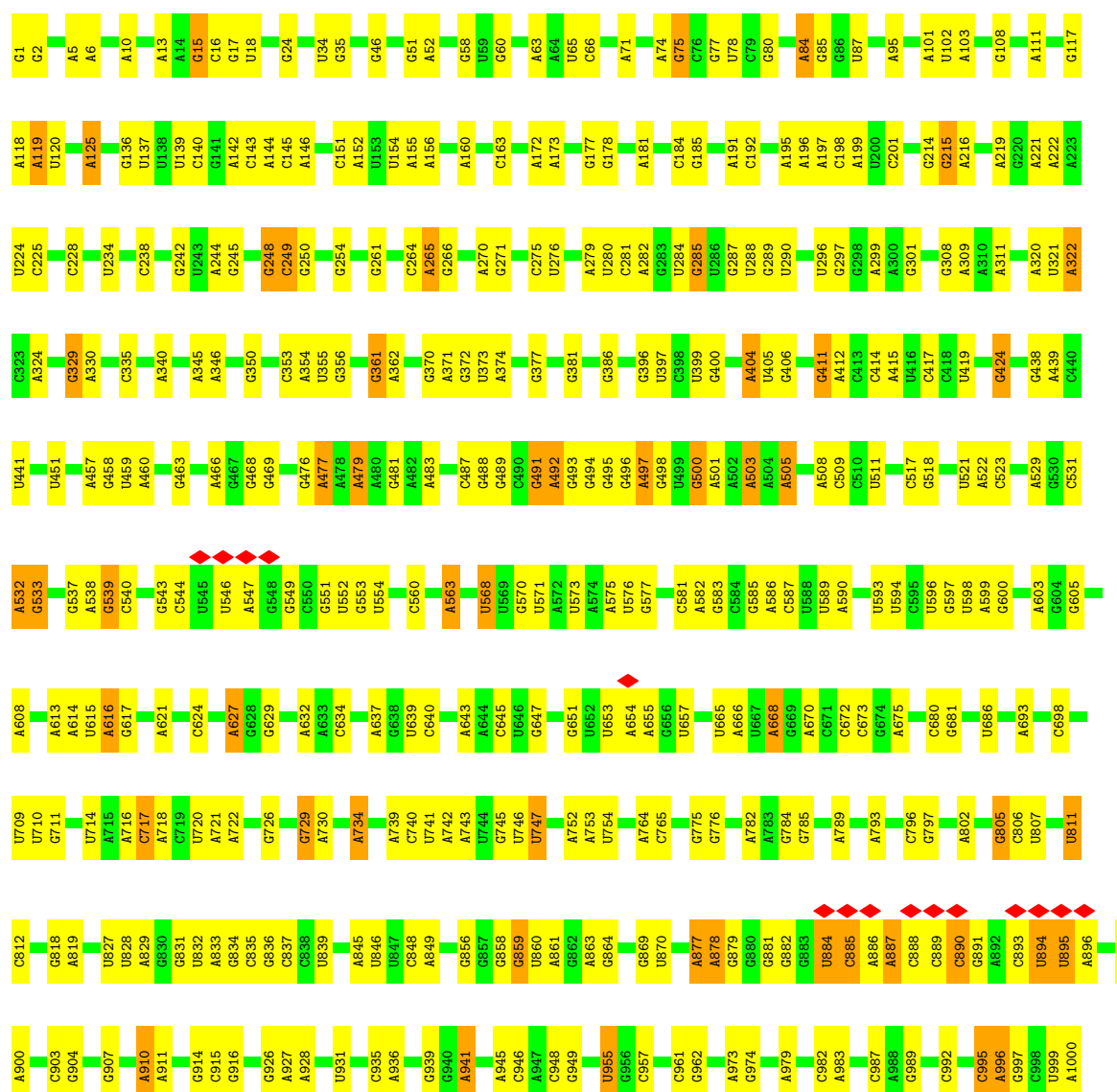


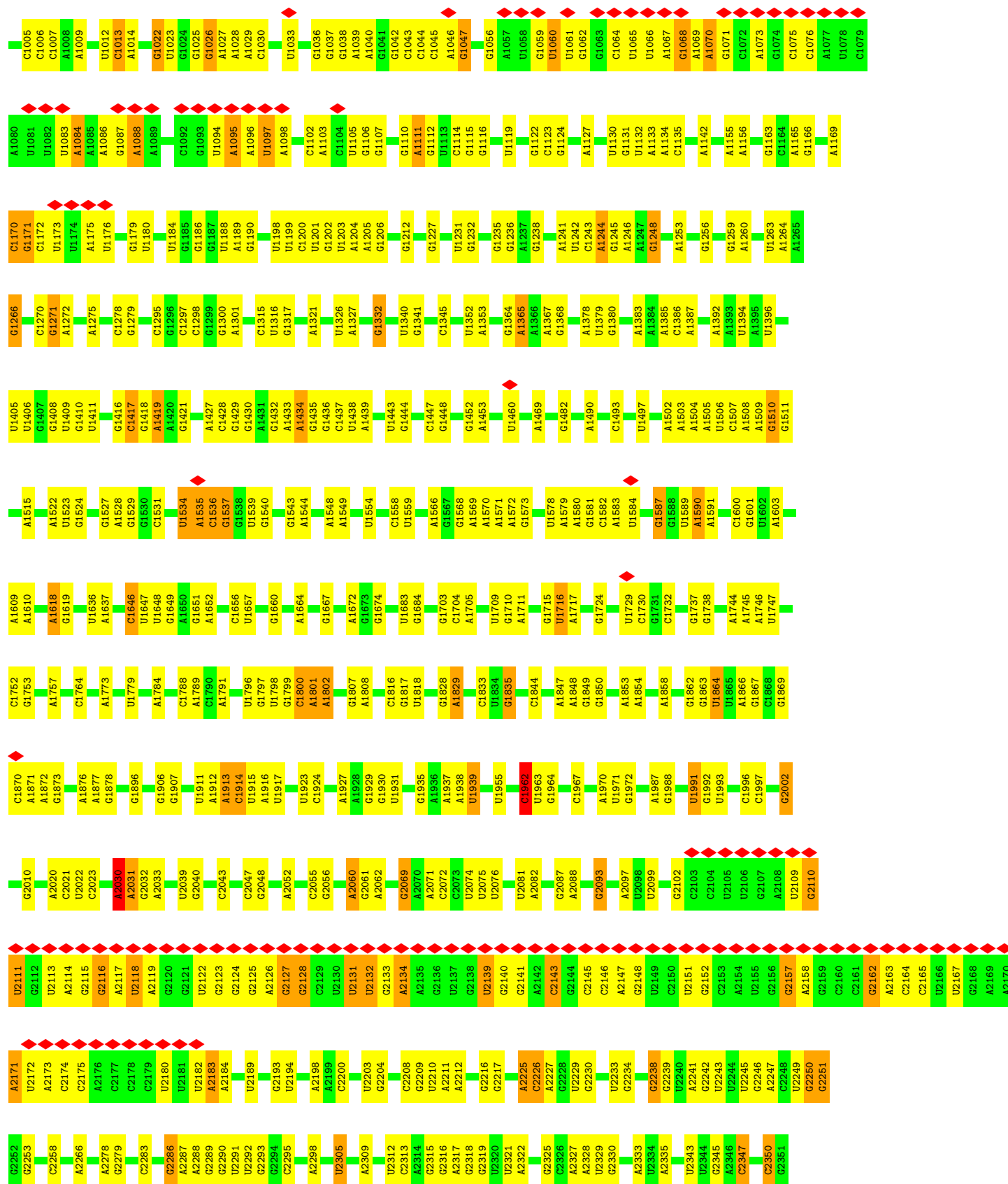
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
55	1	1	23	17	4	2	0

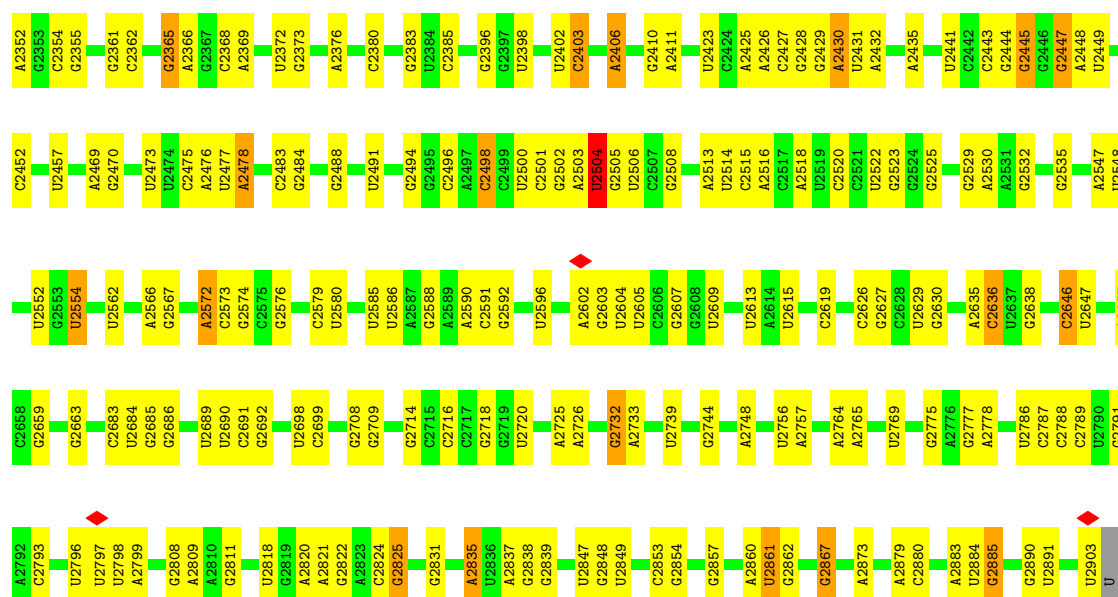
3 Residue-property plots

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

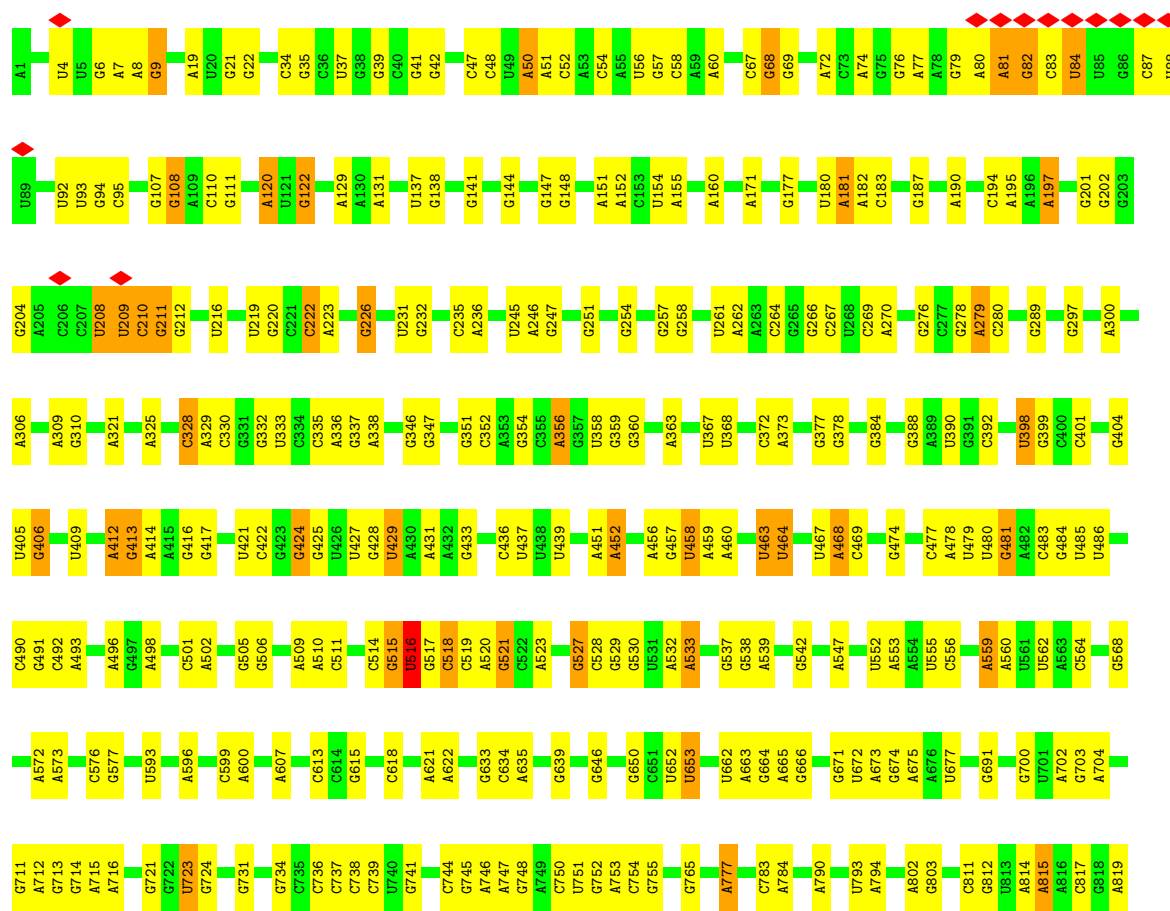
• Molecule 1: 23S ribosomal RNA

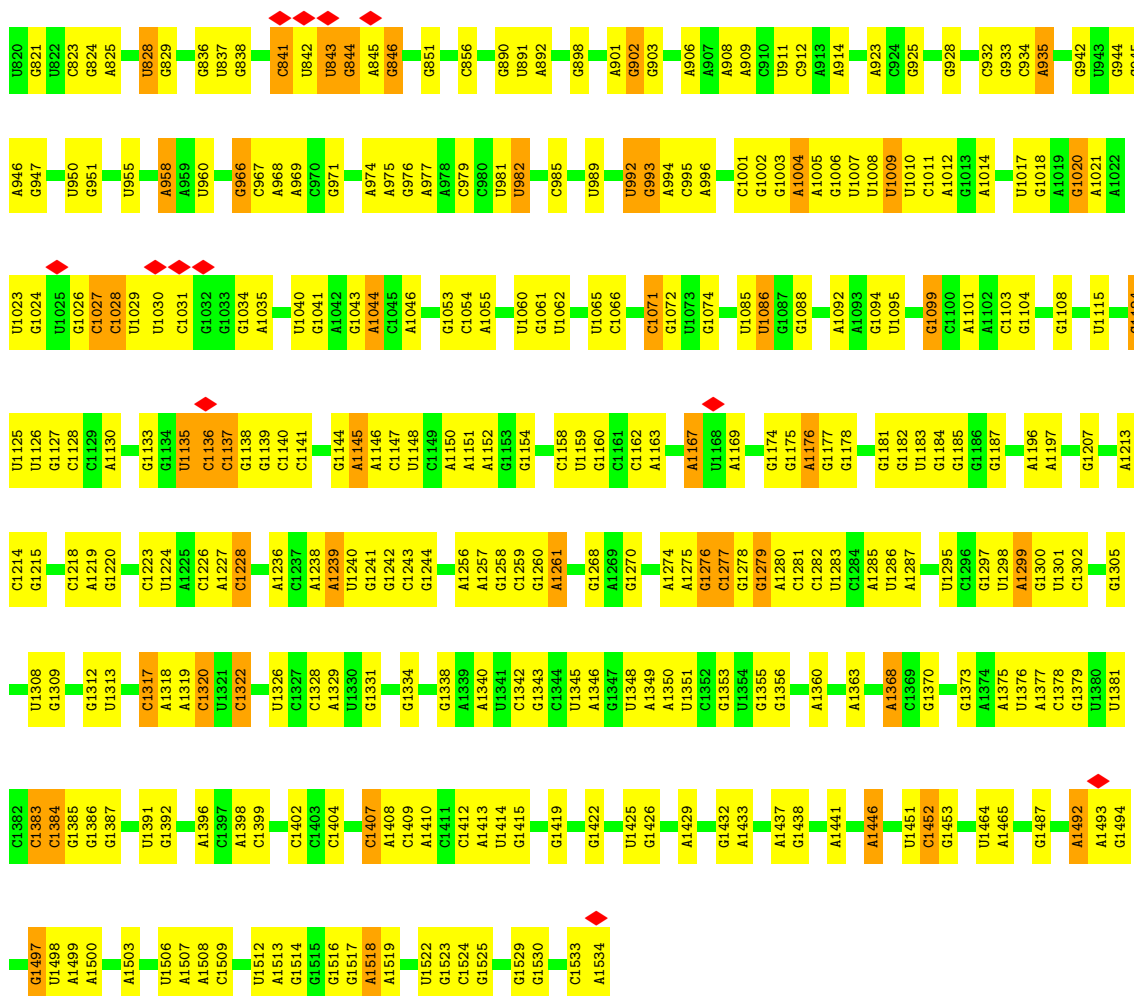






• Molecule 2: 16S ribosomal RNA





- Molecule 3: 5S ribosomal RNA

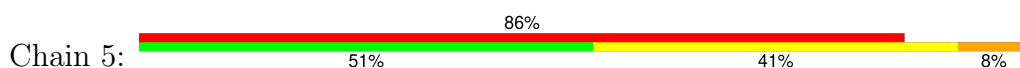


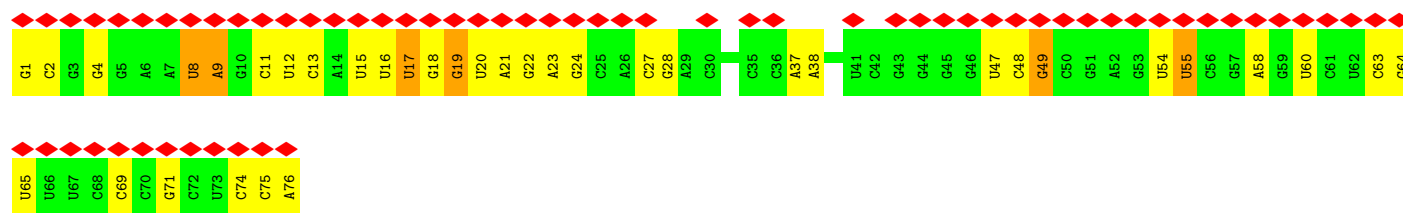
- Molecule 4: mRNA



There are no outlier residues recorded for this chain.

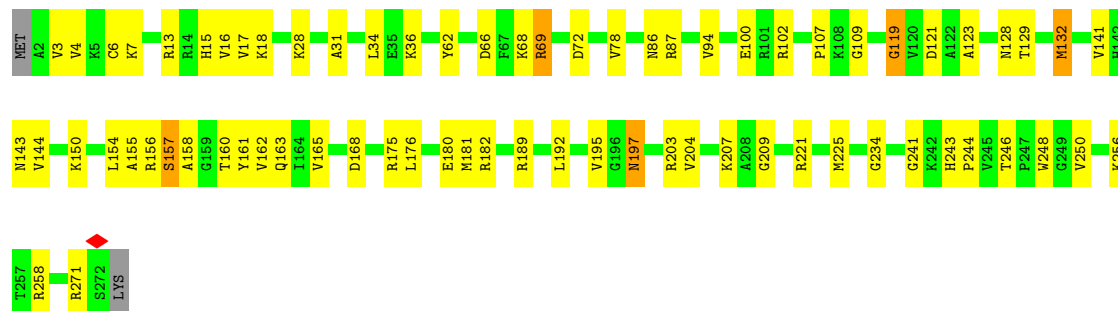
- Molecule 5: tRNA(gly)





• Molecule 6: 50S ribosomal protein L2

Chain B: 73% 25%



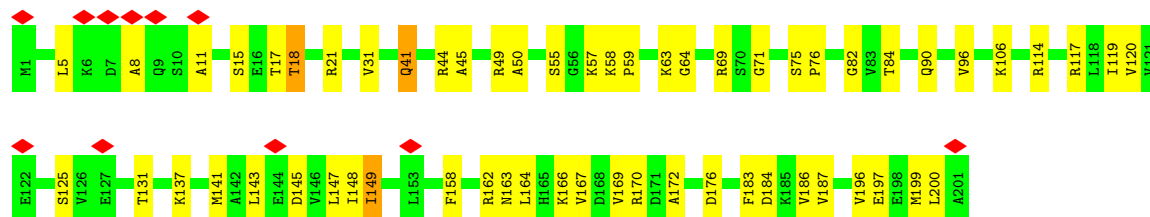
• Molecule 7: 50S ribosomal protein L3

Chain C: 78% 21%



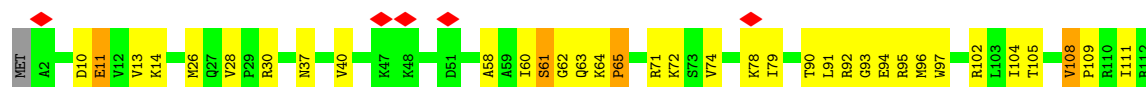
• Molecule 8: 50S ribosomal protein L4

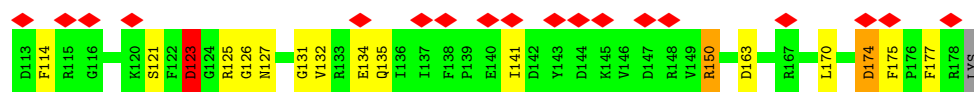
Chain D: 5% 71% 28%



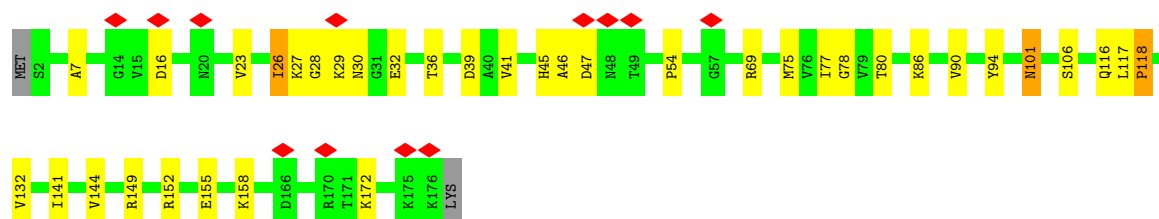
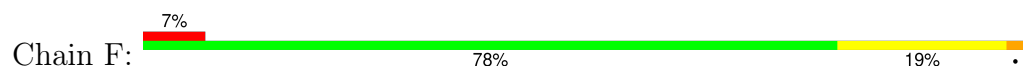
• Molecule 9: 50S ribosomal protein L5

Chain E: 13% 70% 25%

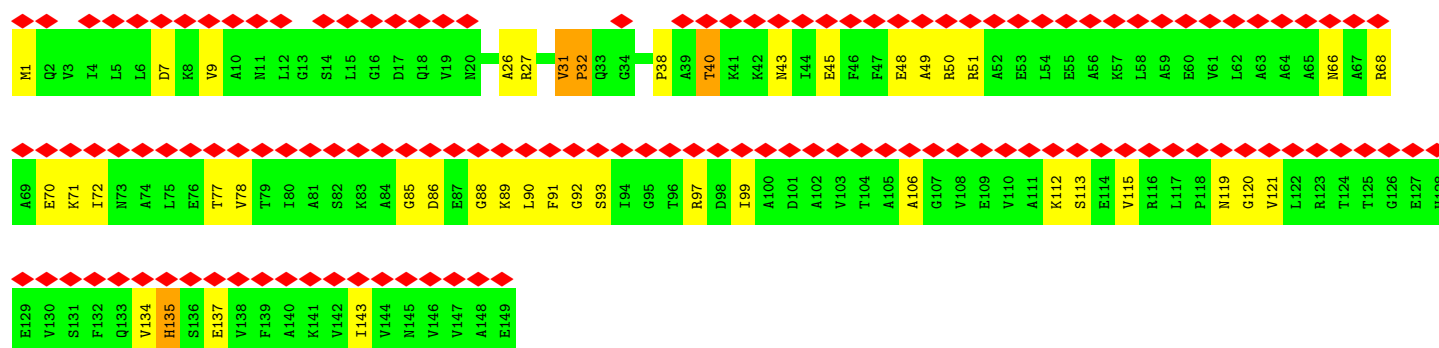
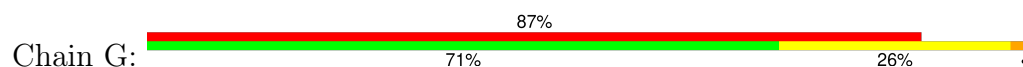




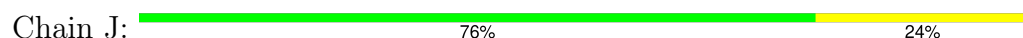
- Molecule 10: 50S ribosomal protein L6



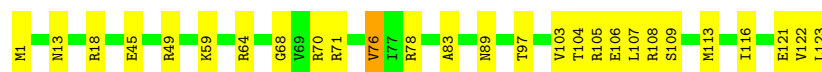
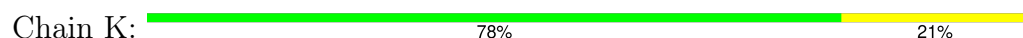
- Molecule 11: 50S ribosomal protein L9



- Molecule 12: 50S ribosomal protein L13

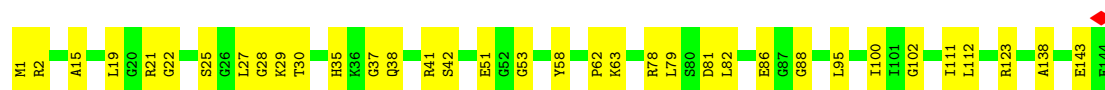


- Molecule 13: 50S ribosomal protein L14

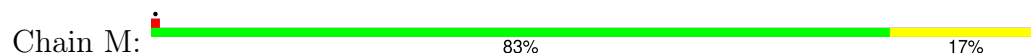


- Molecule 14: 50S ribosomal protein L15

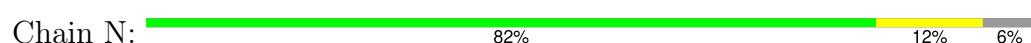




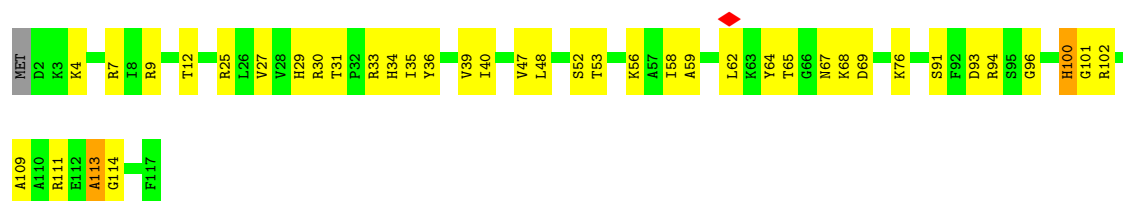
- Molecule 15: 50S ribosomal protein L16



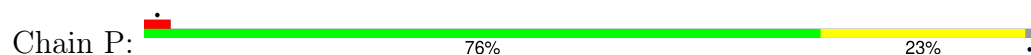
- Molecule 16: 50S ribosomal protein L17



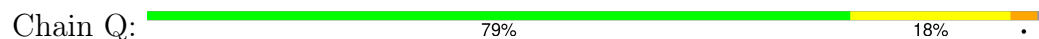
- Molecule 17: 50S ribosomal protein L18



- Molecule 18: 50S ribosomal protein L19

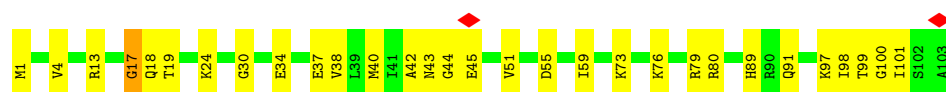


- Molecule 19: 50S ribosomal protein L20

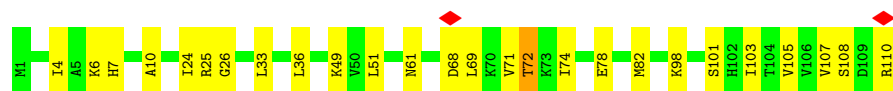
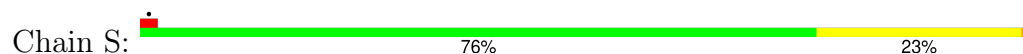


- Molecule 20: 50S ribosomal protein L21





- Molecule 21: 50S ribosomal protein L22



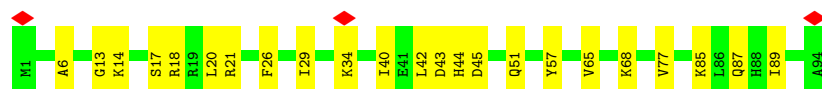
- Molecule 22: 50S ribosomal protein L23



- Molecule 23: 50S ribosomal protein L24



- Molecule 24: 50S ribosomal protein L25



- Molecule 25: 50S ribosomal protein L28

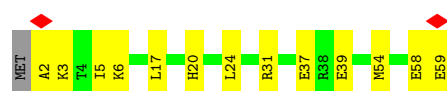


- Molecule 26: 50S ribosomal protein L29

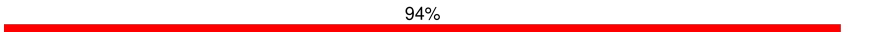


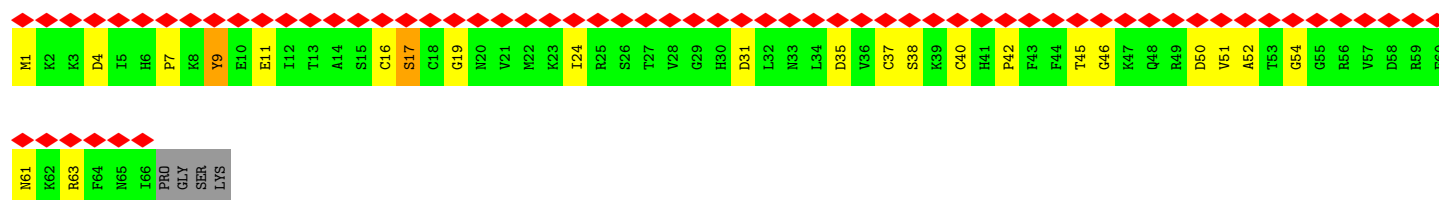
- Molecule 27: 50S ribosomal protein L30

Chain Z:  76% 22%



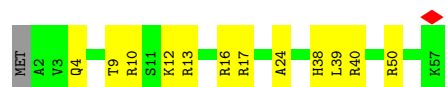
- Molecule 28: 50S ribosomal protein L31

Chain a:  94% 61% 30% 6%



- Molecule 29: 50S ribosomal protein L32

Chain b:  77% 21%



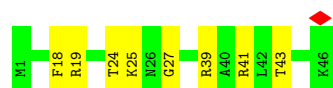
- Molecule 30: 50S ribosomal protein L33

Chain c:  11% 71% 22% 5%



- Molecule 31: 50S ribosomal protein L34

Chain d:  83% 17%



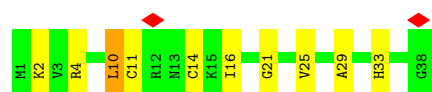
- Molecule 32: 50S ribosomal protein L35

Chain e:  71% 28%

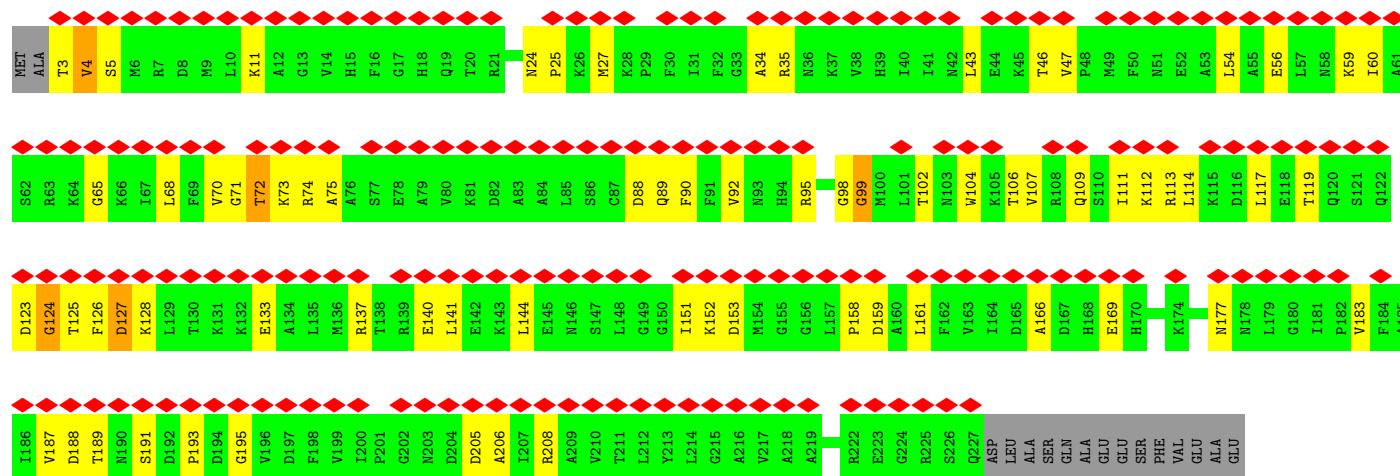
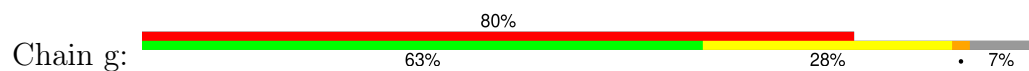


- Molecule 33: 50S ribosomal protein L36

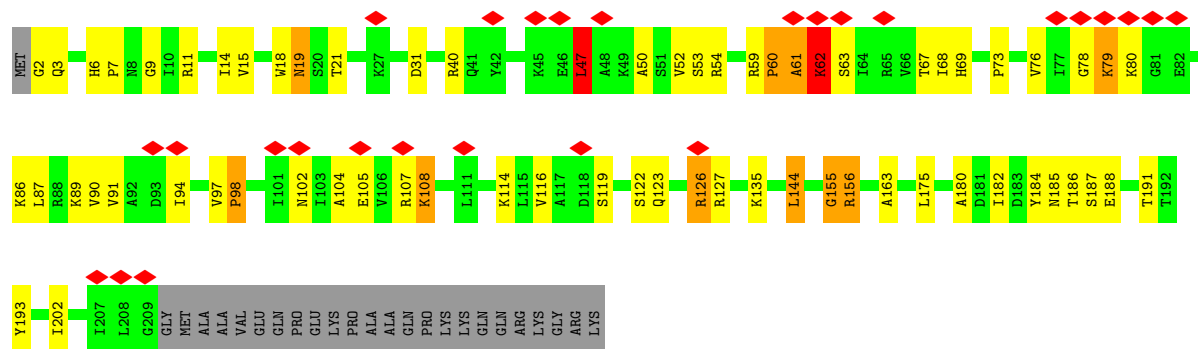
Chain f:  5% 74% 24%



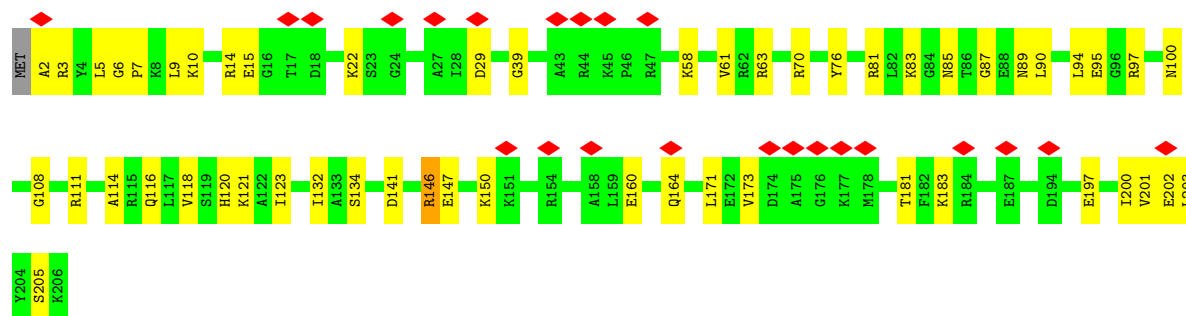
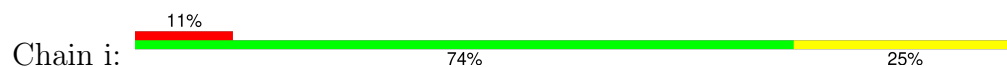
• Molecule 34: 30S ribosomal protein S2



• Molecule 35: 30S ribosomal protein S3

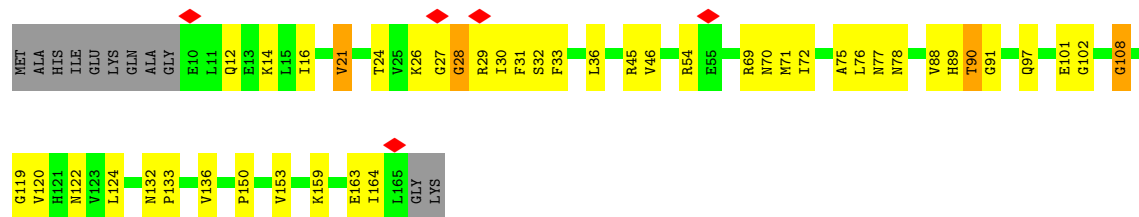


• Molecule 36: 30S ribosomal protein S4



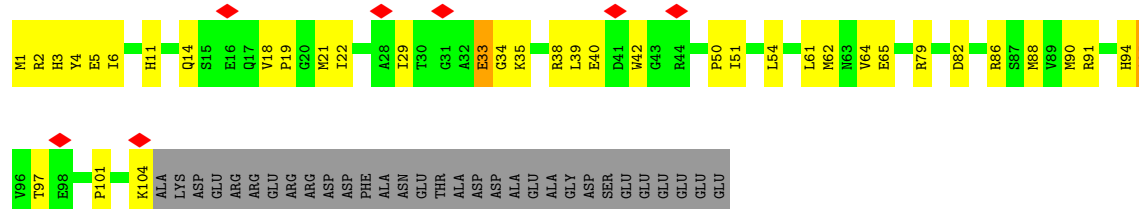
- Molecule 37: 30S ribosomal protein S5

Chain j: 



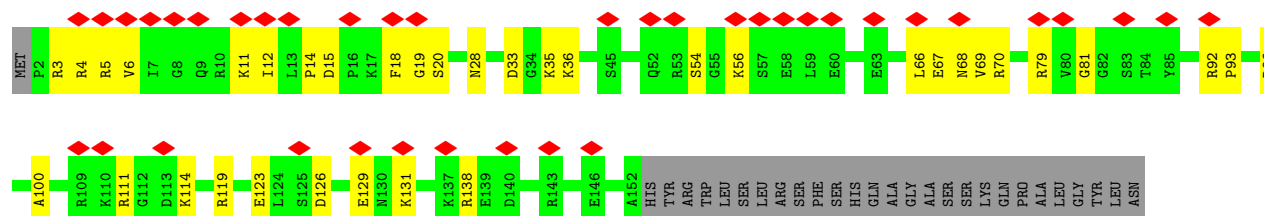
- Molecule 38: 30S ribosomal protein S6

Chain k: 



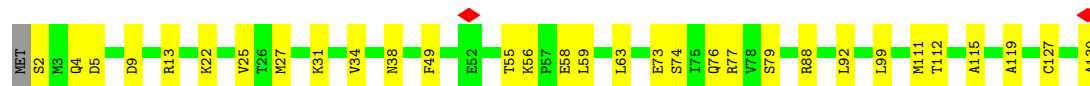
- Molecule 39: 30S ribosomal protein S7

Chain l: 



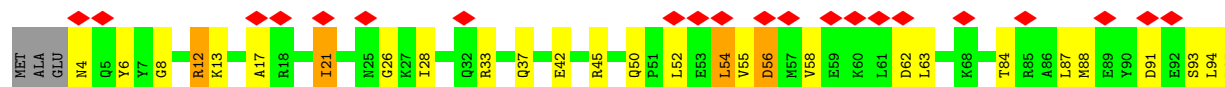
- Molecule 40: 30S ribosomal protein S8

Chain m: 



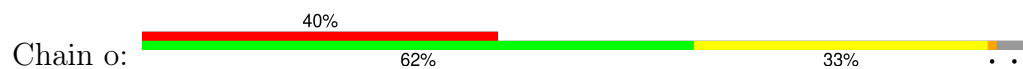
- Molecule 41: 30S ribosomal protein S9

Chain n: 

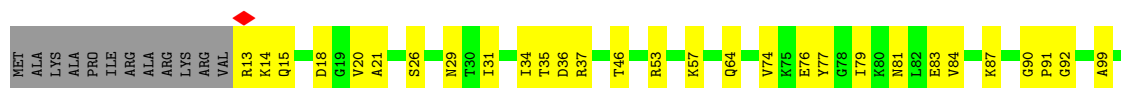




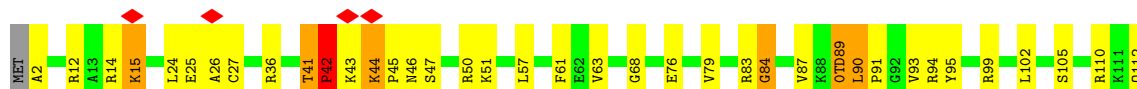
- Molecule 42: 30S ribosomal protein S10



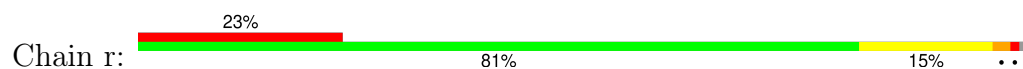
- Molecule 43: 30S ribosomal protein S11



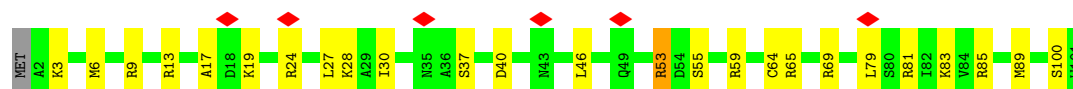
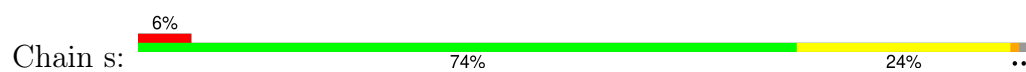
- Molecule 44: 30S ribosomal protein S12



- Molecule 45: 30S ribosomal protein S13



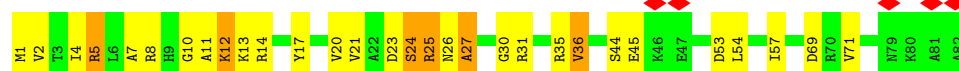
- Molecule 46: 30S ribosomal protein S14



- Molecule 47: 30S ribosomal protein S15



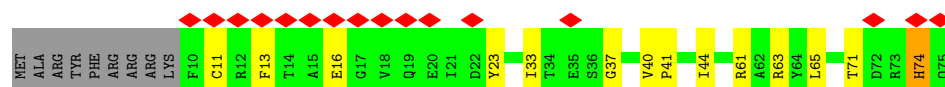
- Molecule 48: 30S ribosomal protein S16



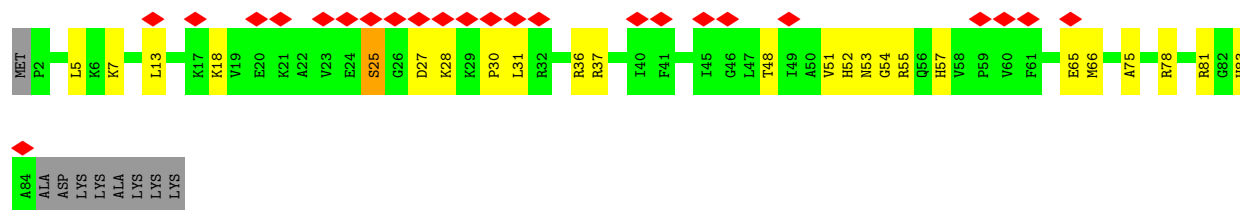
- Molecule 49: 30S ribosomal protein S17



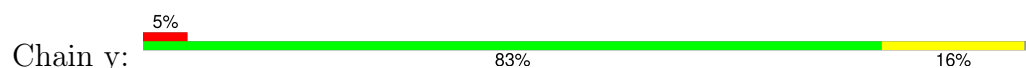
- Molecule 50: 30S ribosomal protein S18

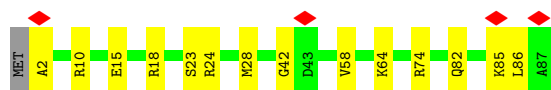


- Molecule 51: 30S ribosomal protein S19

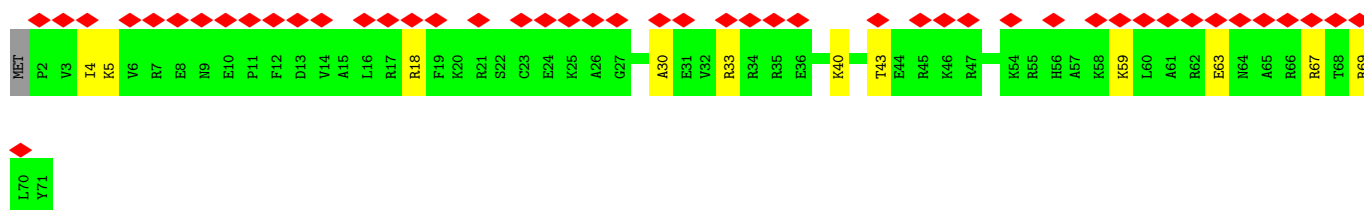
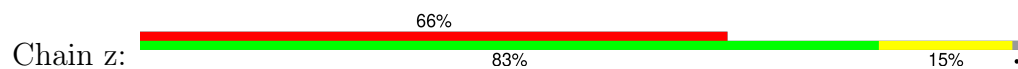


- Molecule 52: 30S ribosomal protein S20

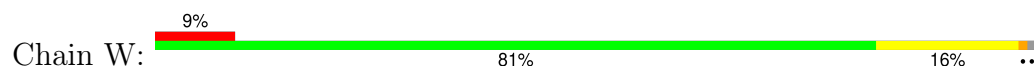




- Molecule 53: 30S ribosomal protein S21



- Molecule 54: 50S ribosomal protein L27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28121	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58.00	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	59000	Depositor
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	457.344, 457.344, 457.344	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.191, 1.191, 1.191	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 1MG, 6MZ, OMC, 7MG, OMU, 2MG, 2MA, PSU, 4OC, UR3, 5MU, 0TD, KKL, OMG, G7M, MA6

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.41	1/69335 (0.0%)	0.41	1/108168 (0.0%)
2	2	0.34	2/36590 (0.0%)	0.40	4/57074 (0.0%)
3	3	0.36	0/2872	0.48	0/4478
4	4	0.18	0/123	0.31	0/190
5	5	0.21	0/1762	0.42	1/2745 (0.0%)
6	B	0.40	0/2121	0.63	0/2852
7	C	0.40	0/1586	0.65	0/2134
8	D	0.35	0/1571	0.66	0/2113
9	E	0.26	0/1434	0.70	0/1926
10	F	0.27	0/1333	0.59	0/1805
11	G	0.26	0/1122	0.71	0/1515
12	J	0.37	0/1152	0.59	0/1551
13	K	0.37	0/955	0.66	1/1279 (0.1%)
14	L	0.36	0/1062	0.62	1/1413 (0.1%)
15	M	0.36	0/1093	0.59	0/1460
16	N	0.38	0/964	0.69	0/1289
17	O	0.32	0/902	0.71	1/1209 (0.1%)
18	P	0.36	0/929	0.59	0/1242
19	Q	0.37	0/960	0.62	0/1278
20	R	0.36	0/829	0.60	0/1107
21	S	0.35	0/864	0.57	0/1156
22	T	0.34	0/752	0.60	0/1005
23	U	0.34	0/796	0.66	0/1062
24	V	0.32	0/766	0.58	0/1025
25	X	0.37	0/635	0.55	0/848
26	Y	0.27	0/502	0.52	0/667
27	Z	0.35	0/452	0.59	0/605
28	a	0.22	0/531	0.65	0/709
29	b	0.35	0/450	0.60	0/599
30	c	0.26	0/433	0.62	0/576
31	d	0.39	0/380	0.56	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.42	0/513	0.74	0/676
33	f	0.36	0/303	0.57	0/397
34	g	0.34	1/1791 (0.1%)	0.79	1/2413 (0.0%)
35	h	0.29	0/1663	0.67	0/2241
36	i	0.27	0/1665	0.62	0/2227
37	j	0.36	0/1165	0.71	0/1568
38	k	0.32	0/867	0.73	2/1171 (0.2%)
39	l	0.25	0/1195	0.65	0/1602
40	m	0.32	0/989	0.61	0/1326
41	n	0.26	0/1034	0.71	1/1375 (0.1%)
42	o	0.30	0/800	0.68	0/1082
43	p	0.31	0/893	0.64	0/1205
44	q	0.71	1/960 (0.1%)	0.93	3/1286 (0.2%)
45	r	0.23	0/909	0.62	0/1215
46	s	0.26	0/817	0.62	0/1088
47	t	0.31	0/722	0.63	0/964
48	u	0.30	0/659	0.64	0/884
49	v	0.28	0/657	0.64	0/881
50	w	0.28	0/553	0.62	0/743
51	x	0.24	0/680	0.65	0/915
52	y	0.29	0/675	0.59	0/895
53	z	0.22	0/597	0.63	0/792
54	W	0.37	0/642	0.67	1/848 (0.1%)
All	All	0.37	5/156005 (0.0%)	0.48	17/233372 (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
6	B	0	17
7	C	0	9
8	D	0	11
9	E	0	11
10	F	0	10
11	G	0	18
12	J	0	4
13	K	0	3
14	L	0	11
15	M	0	2
16	N	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	O	0	8
18	P	0	6
19	Q	0	5
20	R	0	6
21	S	0	2
22	T	0	2
23	U	0	8
24	V	0	5
25	X	0	6
26	Y	0	2
27	Z	0	2
28	a	0	10
29	b	0	1
30	c	0	2
32	e	0	5
33	f	0	3
34	g	0	17
35	h	0	18
36	i	0	7
37	j	0	15
38	k	0	9
39	l	0	3
40	m	0	3
41	n	0	7
42	o	0	3
43	p	0	6
44	q	0	9
45	r	0	5
46	s	0	1
47	t	0	2
48	u	0	10
49	v	0	5
50	w	0	3
51	x	0	6
53	z	0	2
54	W	0	2
All	All	0	306

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	q	42	PRO	N-CA	17.76	1.70	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2030	A	O3'-P	-13.43	1.41	1.61
2	2	1383	C	O3'-P	-9.17	1.47	1.61
2	2	1276	G	O3'-P	-6.47	1.51	1.61
34	g	47	VAL	C-N	5.26	1.40	1.34

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1383	C	C2'-C3'-O3'	18.72	141.78	113.70
44	q	41	THR	CA-C-N	15.84	139.64	119.84
44	q	41	THR	C-N-CA	15.84	139.64	119.84
2	2	1276	G	C4'-C3'-O3'	-12.97	93.55	113.00
2	2	1383	C	P-O3'-C3'	9.57	134.55	120.20

There are no chirality outliers.

5 of 306 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B	18	LYS	Peptide
6	B	3	VAL	Peptide
6	B	31	ALA	Peptide
6	B	34	LEU	Peptide
6	B	4	VAL	Peptide

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	1	62334	0	31368	516	0
2	2	32929	0	16588	352	0
3	3	2569	0	1301	33	0
4	4	110	0	56	0	0
5	5	1619	0	821	11	0
6	B	2082	0	2154	42	0
7	C	1565	0	1616	28	0
8	D	1552	0	1619	35	0
9	E	1410	0	1444	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	F	1313	0	1358	19	0
11	G	1111	0	1148	14	0
12	J	1129	0	1162	18	0
13	K	946	0	1023	17	0
14	L	1053	0	1129	20	0
15	M	1074	0	1157	15	0
16	N	951	0	994	8	0
17	O	892	0	923	25	0
18	P	917	0	962	15	0
19	Q	947	0	1019	18	0
20	R	816	0	839	15	0
21	S	857	0	922	15	0
22	T	746	0	811	12	0
23	U	788	0	844	12	0
24	V	753	0	780	13	0
25	X	625	0	652	15	0
26	Y	501	0	531	7	0
27	Z	448	0	488	7	0
28	a	522	0	524	11	0
29	b	444	0	458	9	0
30	c	426	0	464	9	0
31	d	377	0	418	6	0
32	e	504	0	572	13	0
33	f	302	0	343	5	0
34	g	1760	0	1787	31	0
35	h	1636	0	1710	39	0
36	i	1643	0	1707	33	0
37	j	1152	0	1196	20	0
38	k	848	0	846	20	0
39	l	1181	0	1238	23	0
40	m	979	0	1031	20	0
41	n	1022	0	1070	22	0
42	o	790	0	831	19	0
43	p	877	0	887	21	0
44	q	957	0	1017	45	0
45	r	900	0	965	12	0
46	s	805	0	844	21	0
47	t	714	0	734	14	0
48	u	649	0	666	17	0
49	v	648	0	691	13	0
50	w	544	0	560	9	0
51	x	663	0	688	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	y	669	0	719	10	0
53	z	589	0	629	7	0
54	W	634	0	653	9	0
55	1	23	0	0	3	0
All	All	144295	0	96957	1520	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1520 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)
44:q:42:PRO:CA	44:q:42:PRO:N	1.70	1.41
55:1:3301:KKL:N14	55:1:3301:KKL:N13	1.73	1.19
44:q:50:ARG:NE	44:q:89:0TD:OD1	1.78	1.16
44:q:87:VAL:HG23	44:q:90:LEU:HB2	1.36	1.04
44:q:87:VAL:HG23	44:q:90:LEU:CB	1.93	0.98

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	
6	B	269/273 (98%)	256 (95%)	10 (4%)	3 (1%)	11	39
7	C	207/209 (99%)	200 (97%)	6 (3%)	1 (0%)	24	57
8	D	199/201 (99%)	192 (96%)	5 (2%)	2 (1%)	12	41
9	E	175/179 (98%)	158 (90%)	12 (7%)	5 (3%)	3	19
10	F	173/177 (98%)	162 (94%)	9 (5%)	2 (1%)	10	37
11	G	147/149 (99%)	131 (89%)	11 (8%)	5 (3%)	3	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	J	140/142 (99%)	136 (97%)	3 (2%)	1 (1%)	18	49
13	K	121/123 (98%)	117 (97%)	3 (2%)	1 (1%)	16	47
14	L	142/144 (99%)	135 (95%)	6 (4%)	1 (1%)	18	49
15	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
16	N	117/127 (92%)	111 (95%)	5 (4%)	1 (1%)	14	44
17	O	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
18	P	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	14	44
19	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
20	R	101/103 (98%)	93 (92%)	5 (5%)	3 (3%)	3	19
21	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
22	T	92/100 (92%)	88 (96%)	4 (4%)	0	100	100
23	U	101/104 (97%)	95 (94%)	5 (5%)	1 (1%)	12	41
24	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
25	X	75/78 (96%)	73 (97%)	1 (1%)	1 (1%)	9	35
26	Y	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
27	Z	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	6	28
28	a	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
29	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
30	c	50/55 (91%)	49 (98%)	1 (2%)	0	100	100
31	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
32	e	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	7	30
33	f	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	20
34	g	223/241 (92%)	207 (93%)	11 (5%)	5 (2%)	5	24
35	h	206/233 (88%)	190 (92%)	13 (6%)	3 (2%)	8	32
36	i	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
37	j	154/167 (92%)	143 (93%)	8 (5%)	3 (2%)	6	27
38	k	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	41
39	l	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	49
40	m	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
41	n	125/130 (96%)	116 (93%)	6 (5%)	3 (2%)	4	22
42	o	97/103 (94%)	89 (92%)	6 (6%)	2 (2%)	5	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	p	115/129 (89%)	109 (95%)	5 (4%)	1 (1%)	14	44
44	q	120/124 (97%)	109 (91%)	7 (6%)	4 (3%)	3	17
45	r	114/118 (97%)	108 (95%)	3 (3%)	3 (3%)	4	21
46	s	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
47	t	86/89 (97%)	83 (96%)	2 (2%)	1 (1%)	10	37
48	u	80/82 (98%)	75 (94%)	3 (4%)	2 (2%)	4	21
49	v	78/84 (93%)	71 (91%)	5 (6%)	2 (3%)	4	21
50	w	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
51	x	81/92 (88%)	76 (94%)	5 (6%)	0	100	100
52	y	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
53	z	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
54	W	82/85 (96%)	76 (93%)	5 (6%)	1 (1%)	10	37
All	All	5616/5913 (95%)	5316 (95%)	237 (4%)	63 (1%)	14	39

5 of 63 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	D	18	THR
9	E	123	ASP
11	G	91	PHE
13	K	109	SER
20	R	80	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	B	216/218 (99%)	216 (100%)	0	100	100
7	C	164/164 (100%)	164 (100%)	0	100	100
8	D	165/165 (100%)	165 (100%)	0	100	100
9	E	148/150 (99%)	146 (99%)	2 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	F	136/138 (99%)	136 (100%)	0	100	100
11	G	114/114 (100%)	113 (99%)	1 (1%)	70	80
12	J	116/116 (100%)	116 (100%)	0	100	100
13	K	104/104 (100%)	103 (99%)	1 (1%)	68	79
14	L	103/103 (100%)	103 (100%)	0	100	100
15	M	109/109 (100%)	108 (99%)	1 (1%)	70	80
16	N	99/103 (96%)	99 (100%)	0	100	100
17	O	86/87 (99%)	86 (100%)	0	100	100
18	P	99/100 (99%)	98 (99%)	1 (1%)	68	79
19	Q	89/90 (99%)	89 (100%)	0	100	100
20	R	84/84 (100%)	84 (100%)	0	100	100
21	S	93/93 (100%)	93 (100%)	0	100	100
22	T	81/84 (96%)	81 (100%)	0	100	100
23	U	84/85 (99%)	84 (100%)	0	100	100
24	V	78/78 (100%)	78 (100%)	0	100	100
25	X	67/68 (98%)	67 (100%)	0	100	100
26	Y	54/55 (98%)	54 (100%)	0	100	100
27	Z	48/49 (98%)	48 (100%)	0	100	100
28	a	59/62 (95%)	59 (100%)	0	100	100
29	b	47/48 (98%)	47 (100%)	0	100	100
30	c	47/49 (96%)	47 (100%)	0	100	100
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/52 (98%)	51 (100%)	0	100	100
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/199 (94%)	187 (100%)	0	100	100
35	h	171/190 (90%)	169 (99%)	2 (1%)	63	78
36	i	172/173 (99%)	172 (100%)	0	100	100
37	j	119/126 (94%)	118 (99%)	1 (1%)	73	81
38	k	91/116 (78%)	91 (100%)	0	100	100
39	l	124/147 (84%)	124 (100%)	0	100	100
40	m	104/105 (99%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	n	105/107 (98%)	105 (100%)	0	100	100
42	o	86/90 (96%)	85 (99%)	1 (1%)	63	78
43	p	90/99 (91%)	90 (100%)	0	100	100
44	q	102/103 (99%)	99 (97%)	3 (3%)	37	66
45	r	94/96 (98%)	93 (99%)	1 (1%)	65	78
46	s	83/84 (99%)	83 (100%)	0	100	100
47	t	76/77 (99%)	76 (100%)	0	100	100
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/78 (95%)	74 (100%)	0	100	100
50	w	57/65 (88%)	57 (100%)	0	100	100
51	x	72/79 (91%)	72 (100%)	0	100	100
52	y	65/66 (98%)	65 (100%)	0	100	100
53	z	60/61 (98%)	60 (100%)	0	100	100
54	W	62/63 (98%)	62 (100%)	0	100	100
All	All	4672/4829 (97%)	4658 (100%)	14 (0%)	84	87

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	h	52	VAL
37	j	21	VAL
45	r	9	ILE
44	q	63	VAL
44	q	90	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
39	l	148	ASN
42	o	99	GLN
47	t	35	GLN
18	P	15	GLN
18	P	12	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	552 (19%)	12 (0%)
2	2	1531/1534 (99%)	279 (18%)	4 (0%)
3	3	119/120 (99%)	33 (27%)	0
4	4	4/5 (80%)	0	0
5	5	75/76 (98%)	25 (33%)	2 (2%)
All	All	4631/4639 (99%)	889 (19%)	18 (0%)

5 of 889 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	46	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	516	PSU
5	5	47	U
5	5	17	U
1	1	2225	A
2	2	496	A

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

34 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	$\# Z > 2$
1	PSU	1	1911	1	18,21,22	4.32	7 (38%)	21,30,33	1.97	5 (23%)
1	G7M	1	2069	1	23,26,27	2.57	9 (39%)	34,39,42	2.27	11 (32%)
1	PSU	1	2580	1	18,21,22	4.15	8 (44%)	21,30,33	2.18	6 (28%)
1	PSU	1	746	1	18,21,22	4.26	8 (44%)	21,30,33	1.90	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	1MG	1	745	1	23,26,27	3.12	8 (34%)	33,39,42	2.36	8 (24%)
2	PSU	2	516	2	18,21,22	4.24	7 (38%)	21,30,33	1.90	5 (23%)
1	5MU	1	1939	1	19,22,23	4.72	7 (36%)	27,32,35	3.90	10 (37%)
1	2MG	1	1835	1	23,26,27	2.78	8 (34%)	33,38,41	2.10	8 (24%)
2	MA6	2	1519	2	23,26,27	1.52	4 (17%)	33,38,41	3.17	12 (36%)
2	2MG	2	1207	2	23,26,27	2.83	8 (34%)	33,38,41	2.25	9 (27%)
2	5MC	2	1407	2	19,22,23	3.58	8 (42%)	26,32,35	0.99	2 (7%)
1	5MU	1	747	1	19,22,23	4.77	7 (36%)	27,32,35	3.77	10 (37%)
1	PSU	1	1917	1	18,21,22	4.16	7 (38%)	21,30,33	1.96	4 (19%)
1	6MZ	1	1618	1	22,25,26	2.44	5 (22%)	29,36,39	3.24	11 (37%)
1	5MC	1	1962	1	19,22,23	3.55	8 (42%)	26,32,35	1.15	1 (3%)
1	PSU	1	2605	1	18,21,22	4.12	7 (38%)	21,30,33	2.07	5 (23%)
2	2MG	2	1516	2	23,26,27	2.77	9 (39%)	33,38,41	2.35	12 (36%)
5	5MU	5	54	5	19,22,23	5.06	7 (36%)	27,32,35	3.62	9 (33%)
2	MA6	2	1518	2	23,26,27	1.50	4 (17%)	33,38,41	3.14	12 (36%)
1	PSU	1	2504	1	18,21,22	4.19	7 (38%)	21,30,33	1.99	5 (23%)
2	2MG	2	966	2	23,26,27	2.85	8 (34%)	33,38,41	2.37	8 (24%)
2	7MG	2	527	2	23,26,27	1.35	3 (13%)	27,39,42	2.71	8 (29%)
1	2MA	1	2503	1	22,25,26	3.63	10 (45%)	32,37,40	2.15	6 (18%)
2	UR3	2	1498	2	19,22,23	2.73	6 (31%)	26,32,35	1.59	4 (15%)
1	PSU	1	955	1	18,21,22	4.11	7 (38%)	21,30,33	2.15	5 (23%)
1	PSU	1	2457	1	18,21,22	4.09	8 (44%)	21,30,33	2.39	6 (28%)
1	OMG	1	2251	5,1	23,26,27	2.28	8 (34%)	32,38,41	1.91	9 (28%)
44	0TD	q	89	44	8,9,10	3.58	2 (25%)	6,11,13	2.23	3 (50%)
5	PSU	5	55	5	18,21,22	4.44	7 (38%)	21,30,33	1.91	5 (23%)
1	OMU	1	2552	1	19,22,23	2.83	8 (42%)	25,31,34	2.01	5 (20%)
1	2MG	1	2445	1	23,26,27	2.71	8 (34%)	33,38,41	2.48	11 (33%)
2	5MC	2	967	2	19,22,23	3.70	8 (42%)	26,32,35	1.04	1 (3%)
1	OMC	1	2498	1	19,22,23	0.82	0	25,31,34	1.02	1 (4%)
2	4OC	2	1402	2	20,23,24	3.03	8 (40%)	25,32,35	1.03	3 (12%)

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
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	0/7/25/26	0/3/3/3
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	746	1	-	4/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
2	PSU	2	516	2	-	3/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	4/11/29/30	0/3/3/3
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
5	5MU	5	54	5	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	2/9/27/28	0/3/3/3
2	7MG	2	527	2	-	3/7/37/38	0/3/3/3
1	2MA	1	2503	1	-	1/7/25/26	0/3/3/3
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	5,1	-	0/9/27/28	0/3/3/3
44	0TD	q	89	44	-	1/7/12/14	-
5	PSU	5	55	5	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
2	4OC	2	1402	2	-	1/9/29/30	0/2/2/2

The worst 5 of 234 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	5	54	5MU	C2-N1	11.97	1.57	1.38
5	5	55	PSU	C6-C5	11.77	1.48	1.35
1	1	1911	PSU	C6-C5	11.71	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	516	PSU	C6-C5	11.22	1.47	1.35
1	1	2504	PSU	C6-C5	11.16	1.47	1.35

The worst 5 of 225 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	C5-C4-N3	12.59	126.27	115.32
5	5	54	5MU	C5-C4-N3	12.08	125.82	115.32
1	1	747	5MU	C5-C4-N3	11.83	125.61	115.32
2	2	1519	MA6	N1-C6-N6	-11.13	103.29	116.86
2	2	1518	MA6	N1-C6-N6	-10.99	103.47	116.86

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	746	PSU	C2'-C1'-C5-C4
1	1	746	PSU	C2'-C1'-C5-C6
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	2504	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	1	0
1	1	1939	5MU	1	0
2	2	1407	5MC	1	0
1	1	1962	5MC	1	0
2	2	1518	MA6	1	0
1	1	2504	PSU	1	0
1	1	955	PSU	1	0
1	1	2251	OMG	1	0
44	q	89	0TD	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	$\# Z > 2$
55	KKL	1	3301	-	25,25,25	7.48	21 (84%)	32,34,34	2.42	10 (31%)

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
55	KKL	1	3301	-	-	2/14/14/14	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1	3301	KKL	C07-N09	15.96	1.65	1.37
55	1	3301	KKL	N14-N13	15.73	1.73	1.39
55	1	3301	KKL	C16-C15	14.12	1.60	1.39
55	1	3301	KKL	C05-C04	12.61	1.59	1.38
55	1	3301	KKL	O11-C10	10.33	1.50	1.36

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1	3301	KKL	O11-C10-N14	-7.35	108.96	113.12
55	1	3301	KKL	C10-N14-N13	5.47	108.57	105.37
55	1	3301	KKL	O11-C12-N13	-5.10	107.73	112.34
55	1	3301	KKL	O11-C12-C15	4.15	125.97	118.73
55	1	3301	KKL	C17-C18-C21	-3.40	115.68	120.66

There are no chirality outliers.

All (2) torsion outliers are listed below:

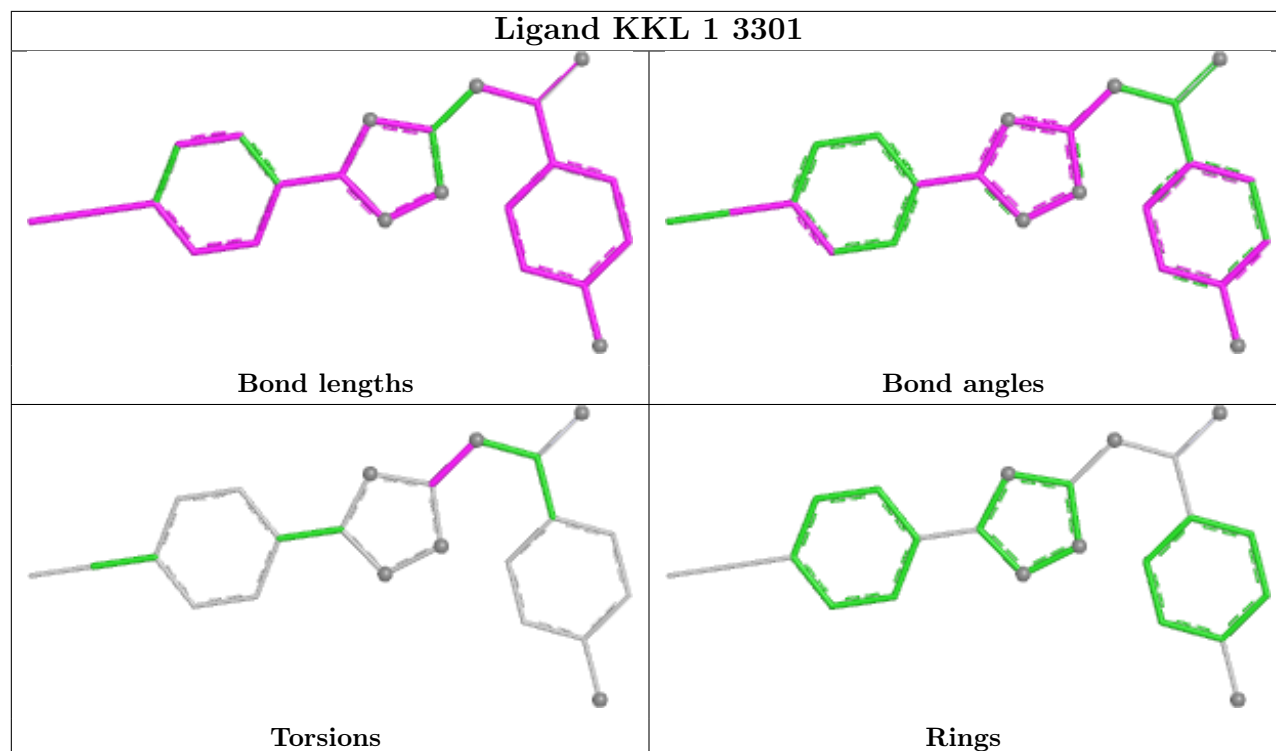
Mol	Chain	Res	Type	Atoms
55	1	3301	KKL	N14-C10-N09-C07
55	1	3301	KKL	O11-C10-N09-C07

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	1	3301	KKL	3	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.

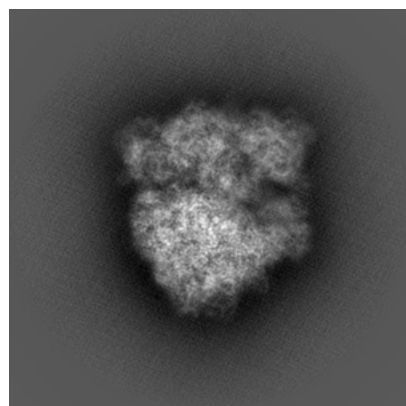
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20121. These allow visual inspection of the internal detail of the map and identification of artifacts.

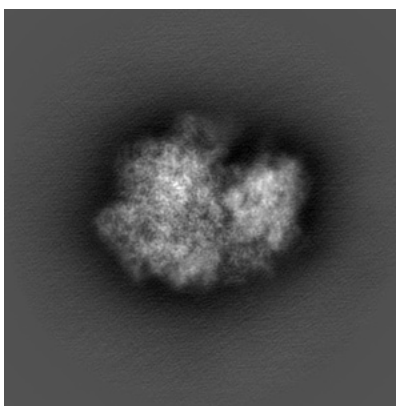
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

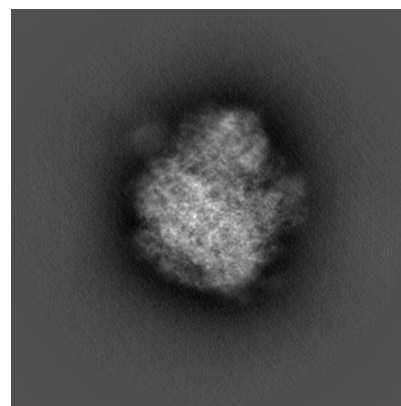
6.1.1 Primary map



X

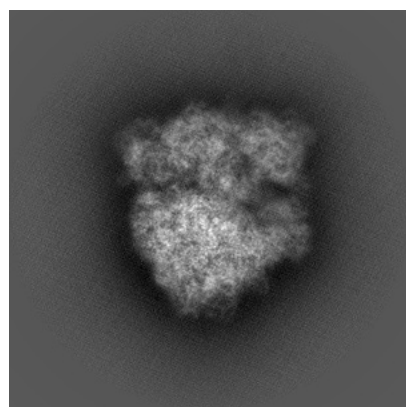


Y

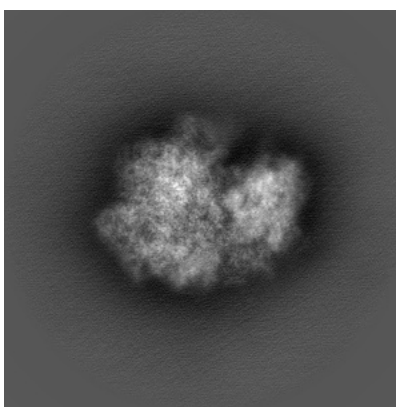


Z

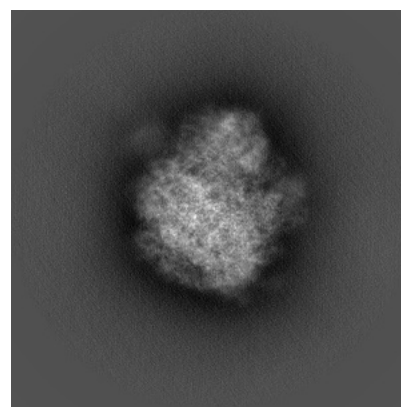
6.1.2 Raw map



X



Y

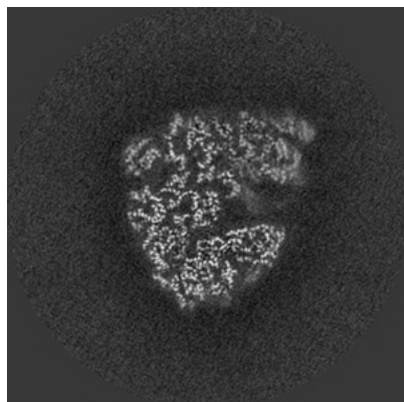


Z

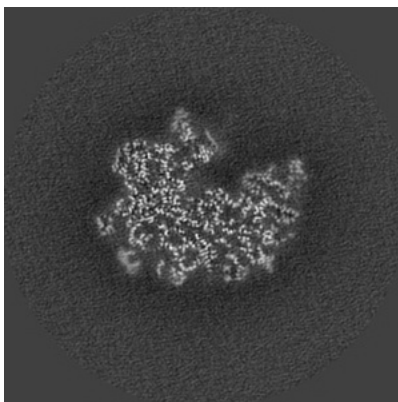
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

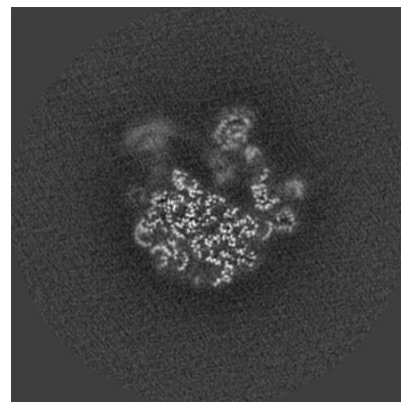
6.2.1 Primary map



X Index: 192

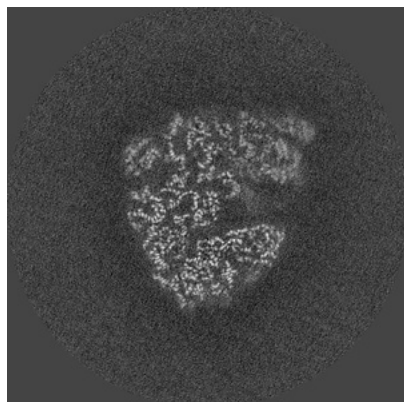


Y Index: 192

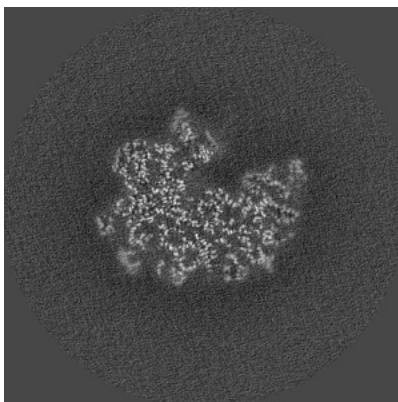


Z Index: 192

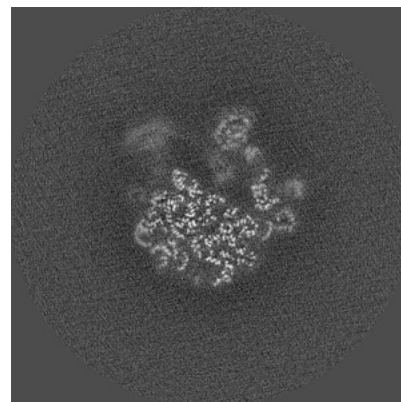
6.2.2 Raw map



X Index: 192



Y Index: 192

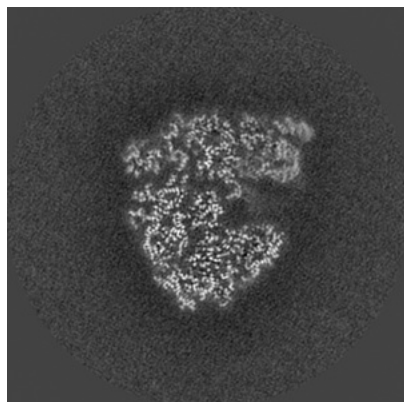


Z Index: 192

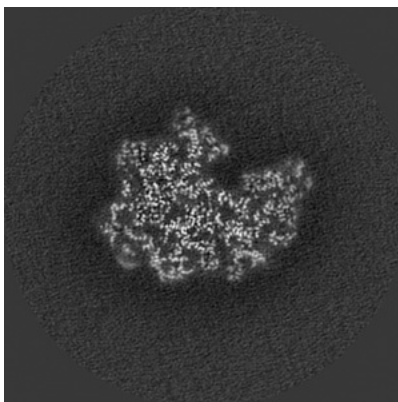
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

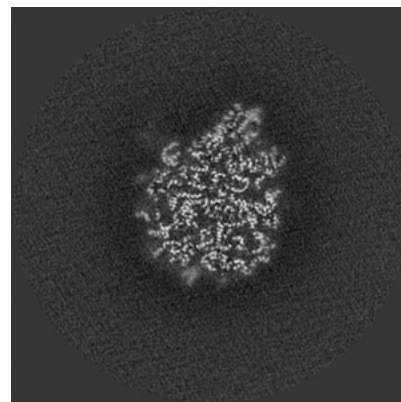
6.3.1 Primary map



X Index: 190

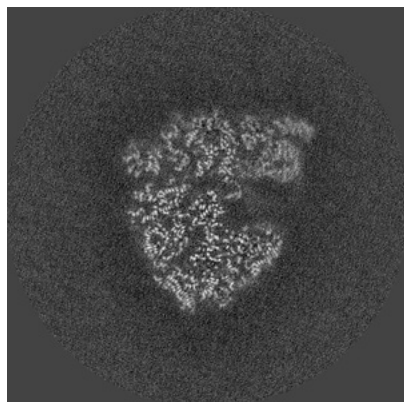


Y Index: 187

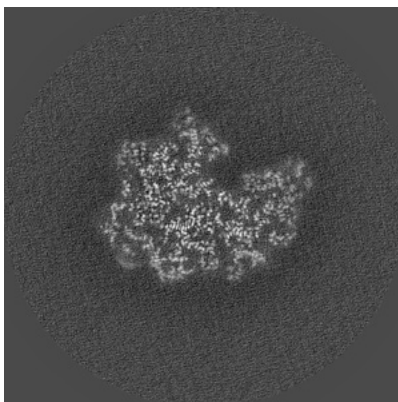


Z Index: 156

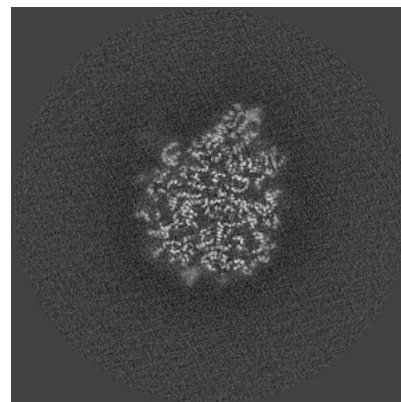
6.3.2 Raw map



X Index: 189



Y Index: 187

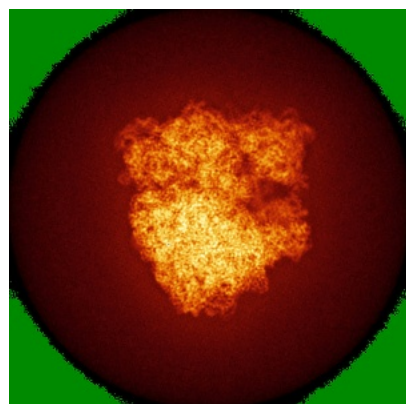


Z Index: 156

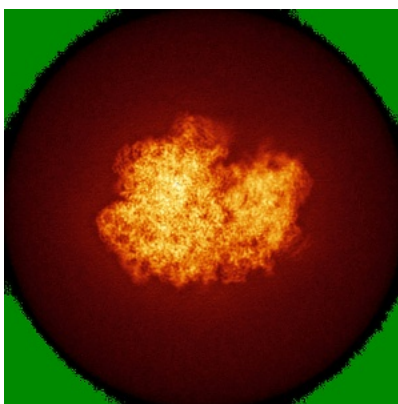
The images above show the largest variance slices of the map in three orthogonal directions.

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

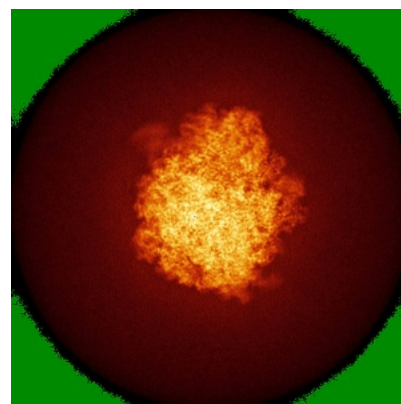
6.4.1 Primary map



X

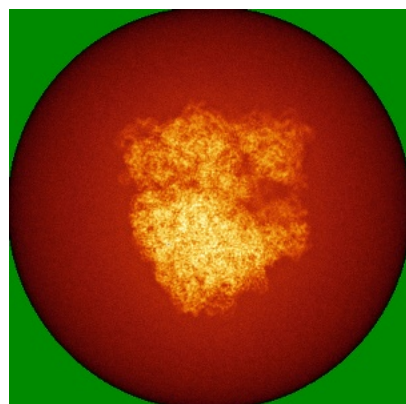


Y

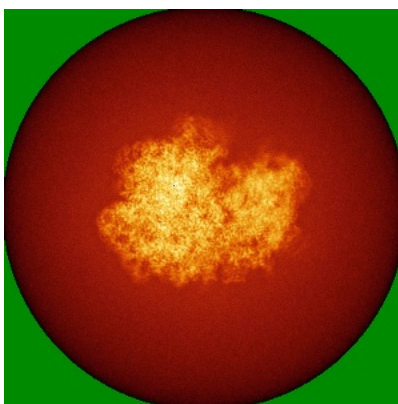


Z

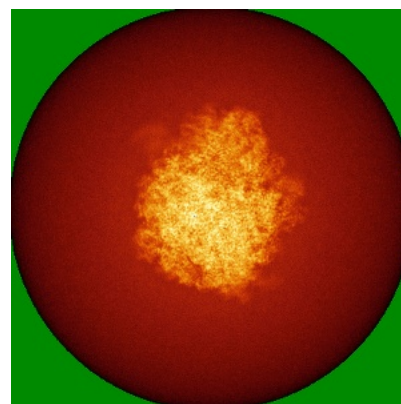
6.4.2 Raw map



X



Y

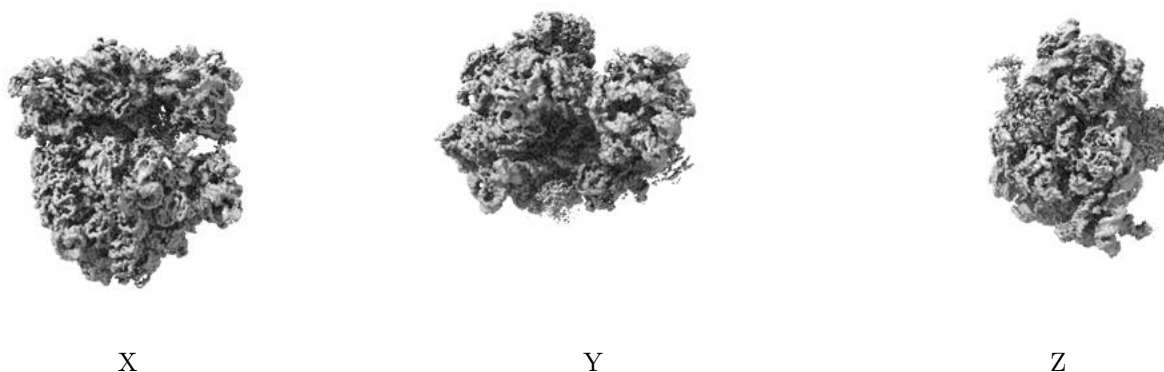


Z

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.

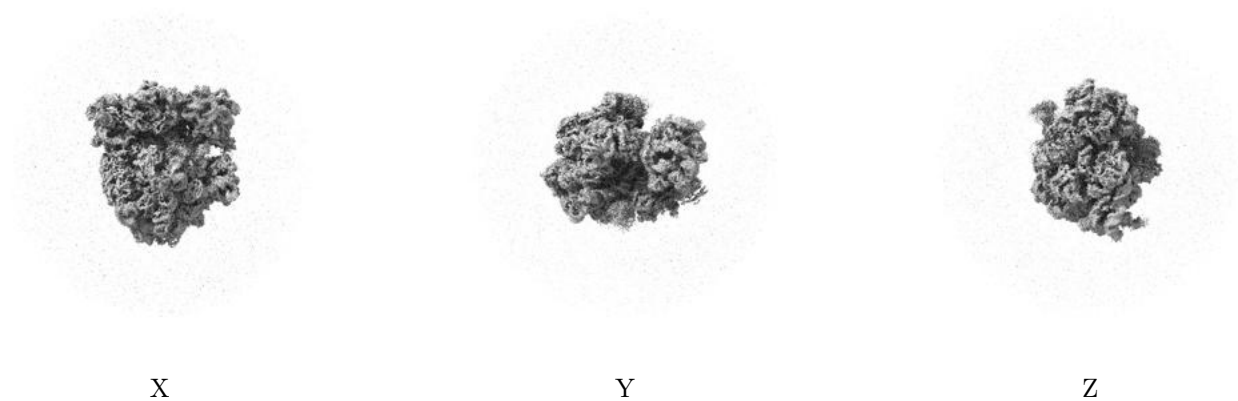
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

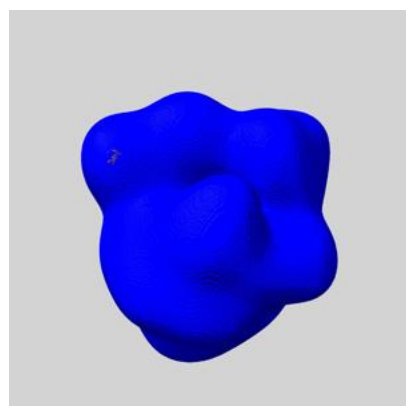
6.6 Mask visualisation [i](#)

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

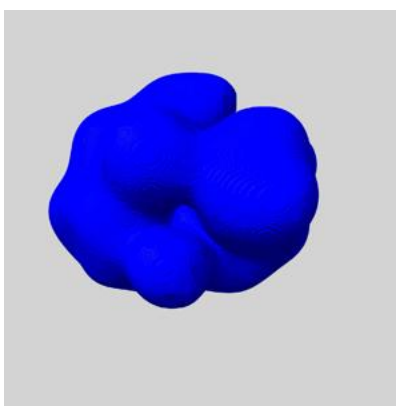
A mask typically either:

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

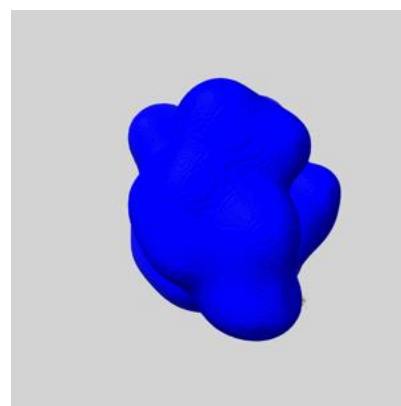
6.6.1 emd_20121_msk_1.map [i](#)



X



Y

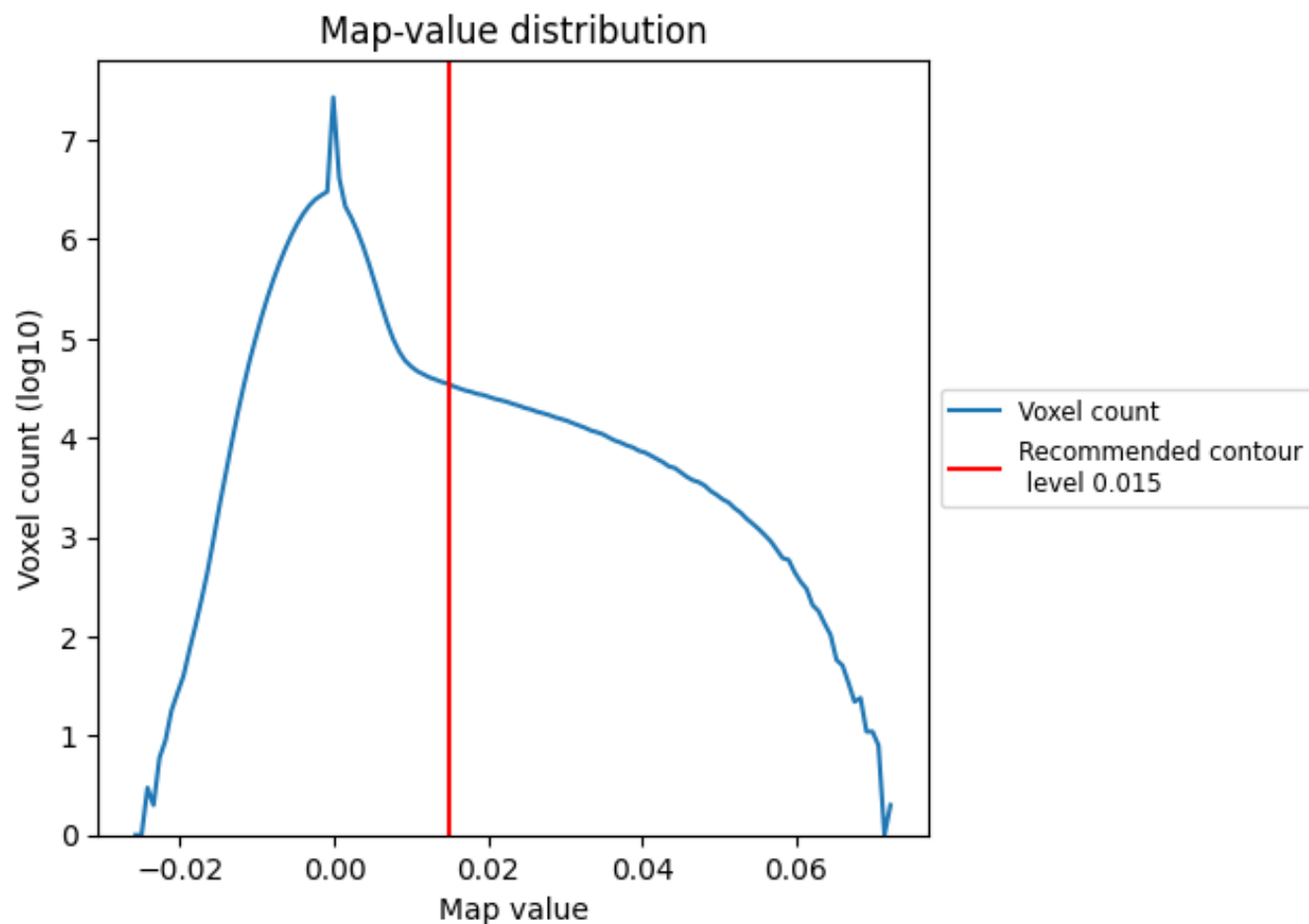


Z

7 Map analysis [i](#)

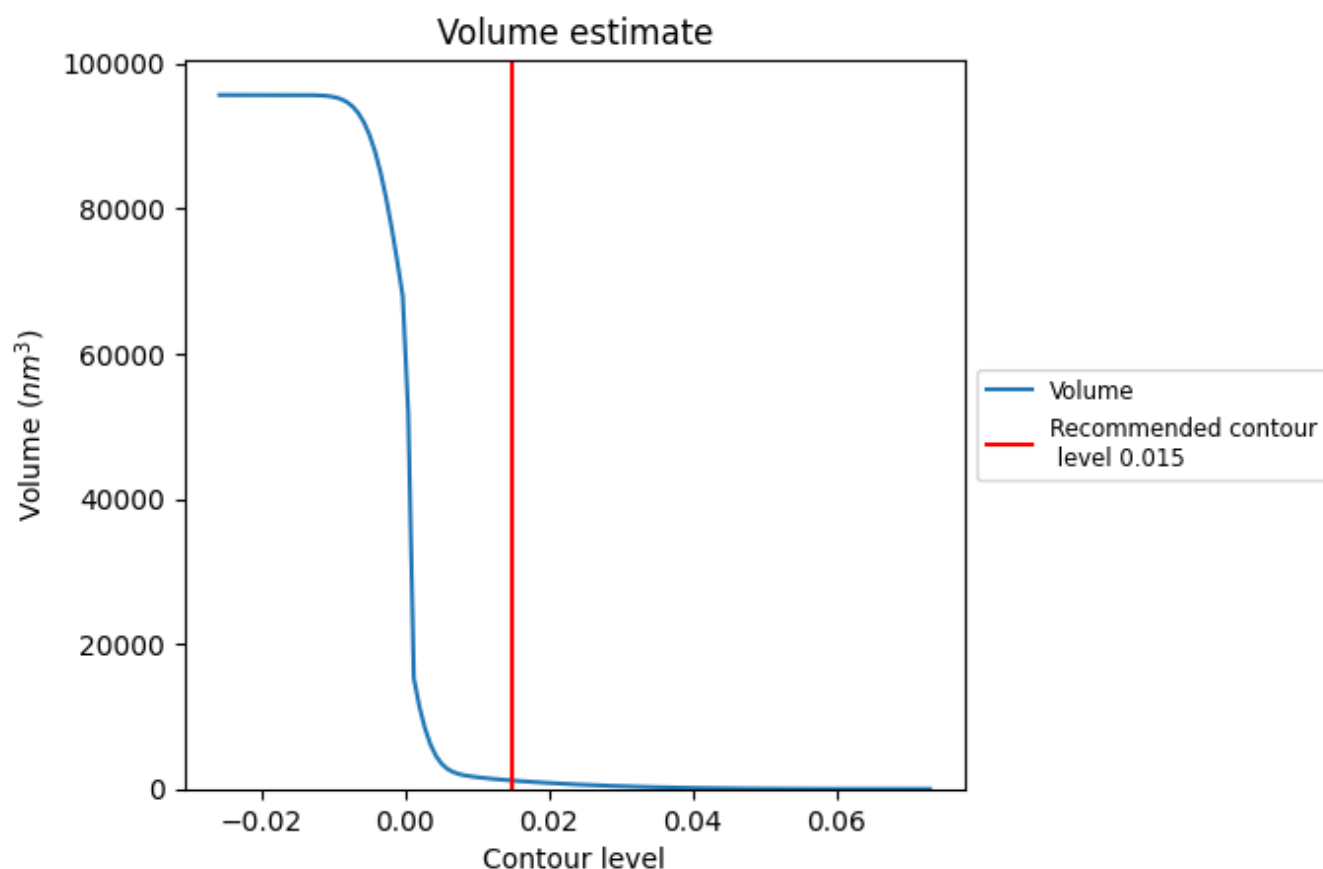
This section contains the results of statistical analysis of the map.

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.

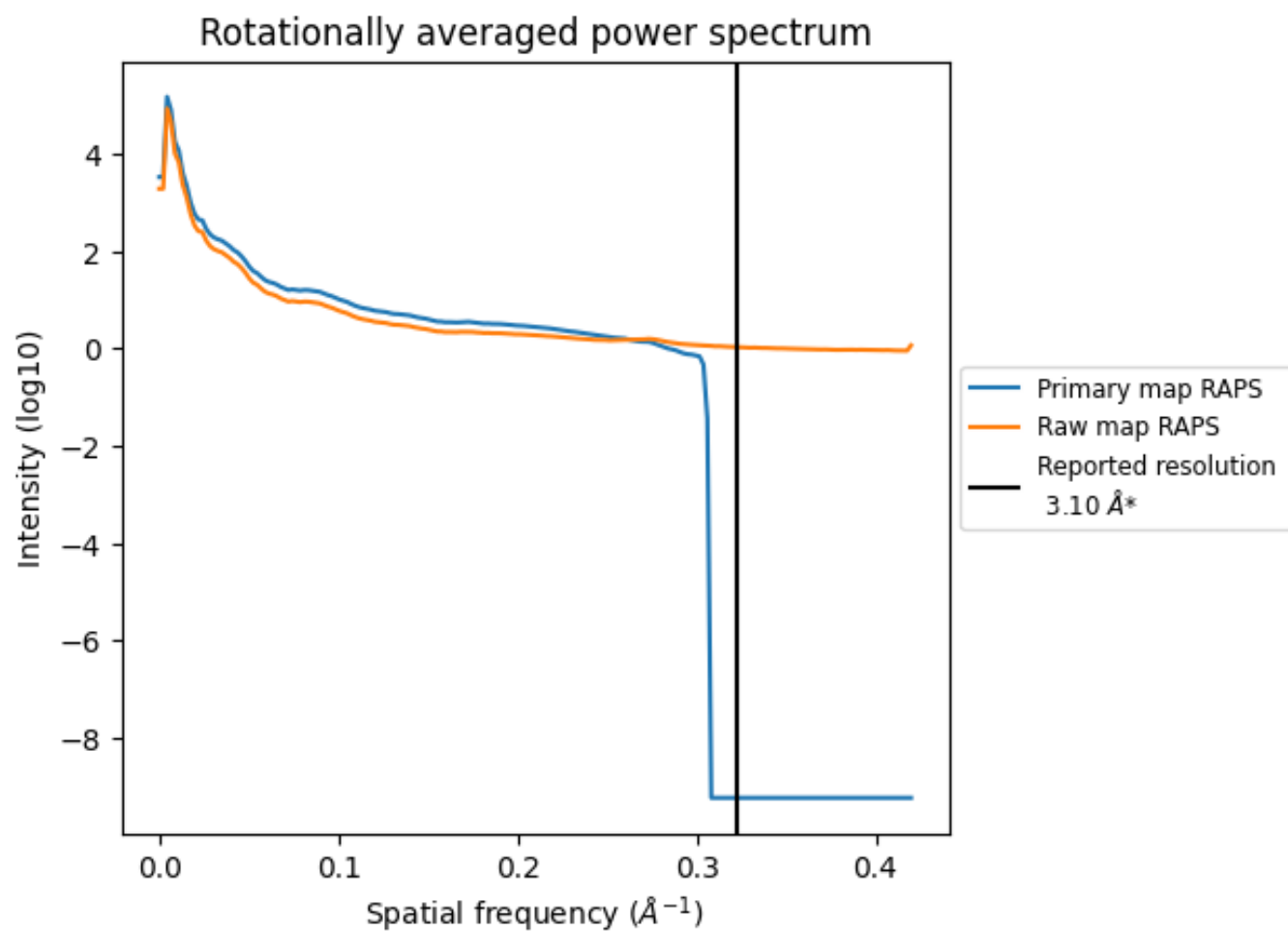
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1158 nm³; this corresponds to an approximate mass of 1046 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 ⓘ

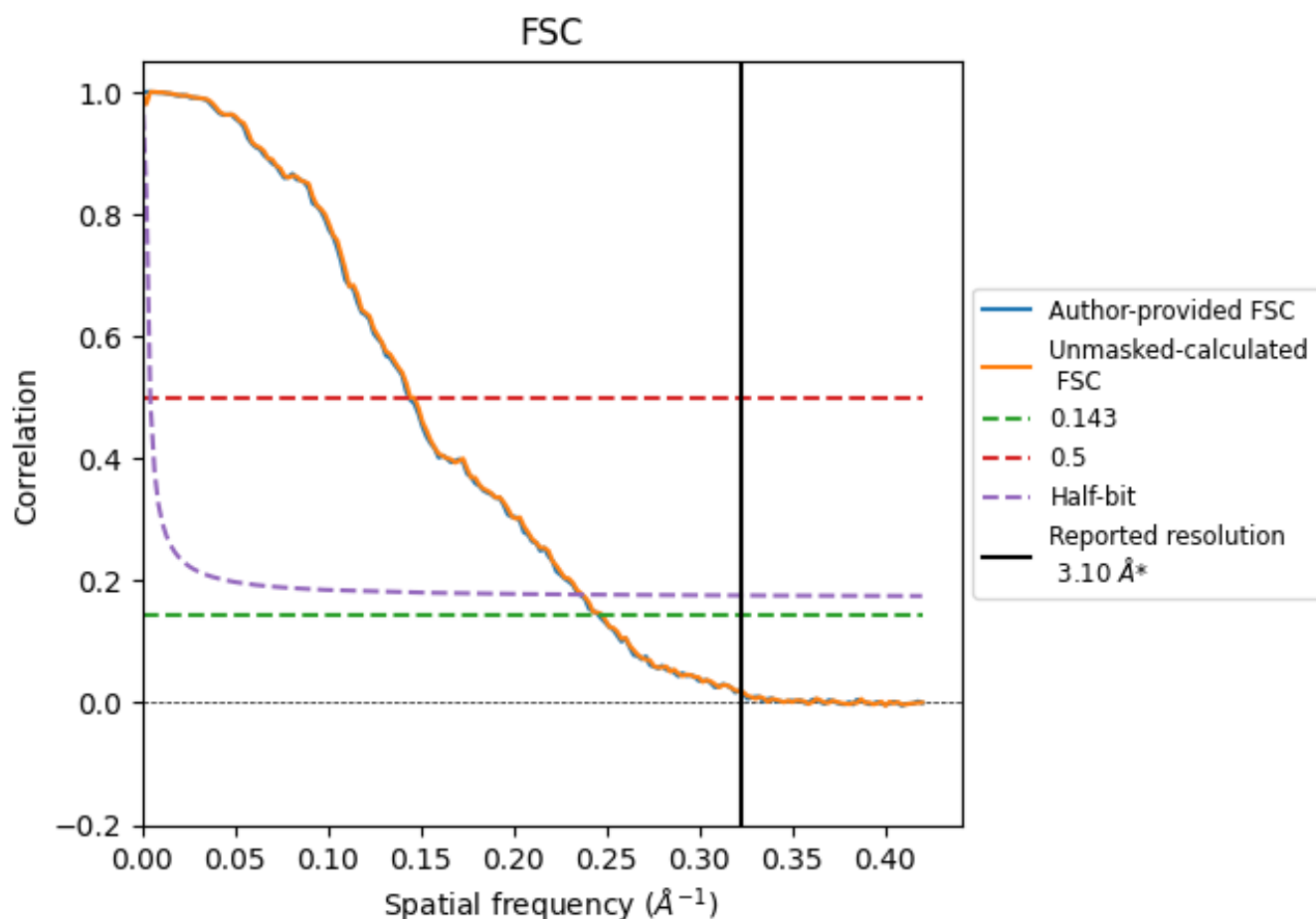


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	4.07	6.96	4.25
Unmasked-calculated*	4.04	6.93	4.22

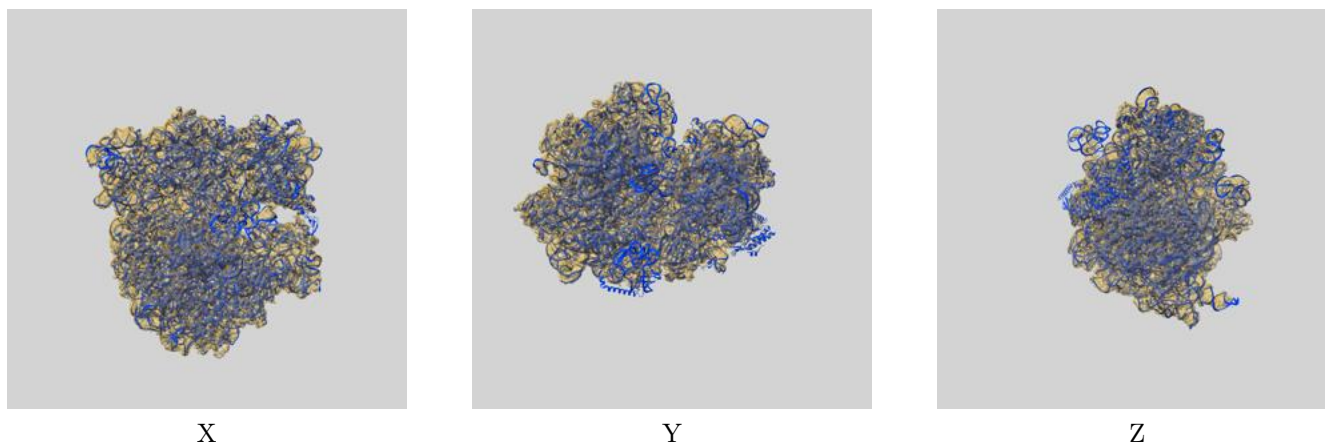
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.07 differs from the reported value 3.1 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.04 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

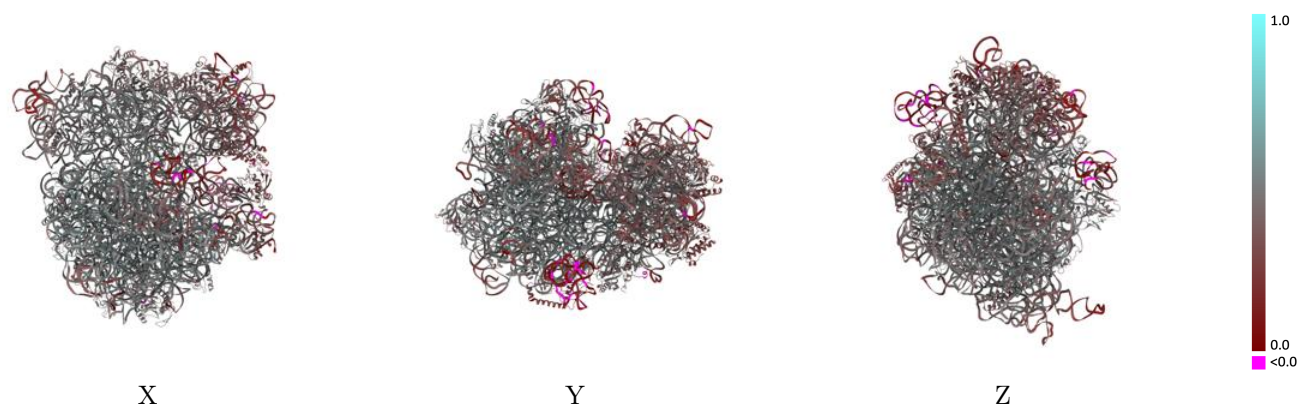
This section contains information regarding the fit between EMDB map EMD-20121 and PDB model 6OM6. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



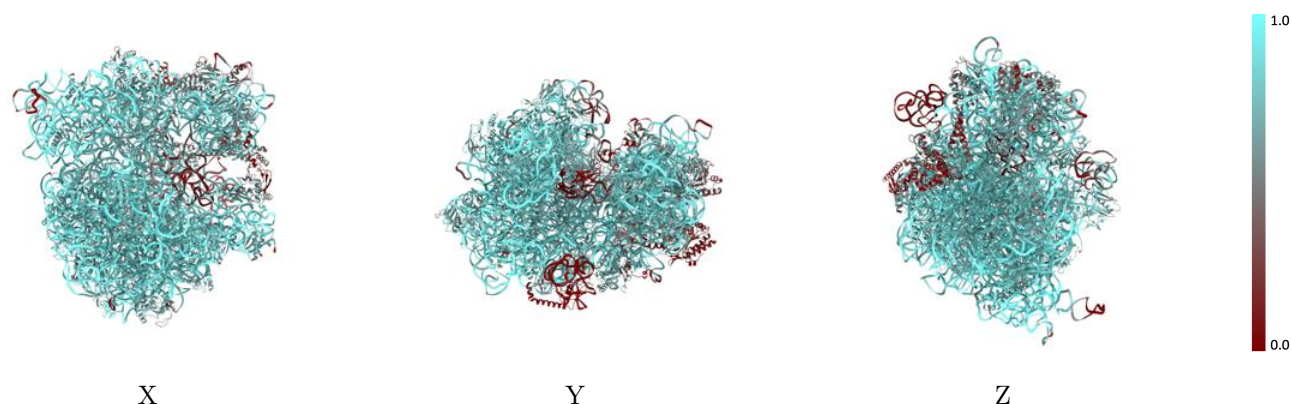
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



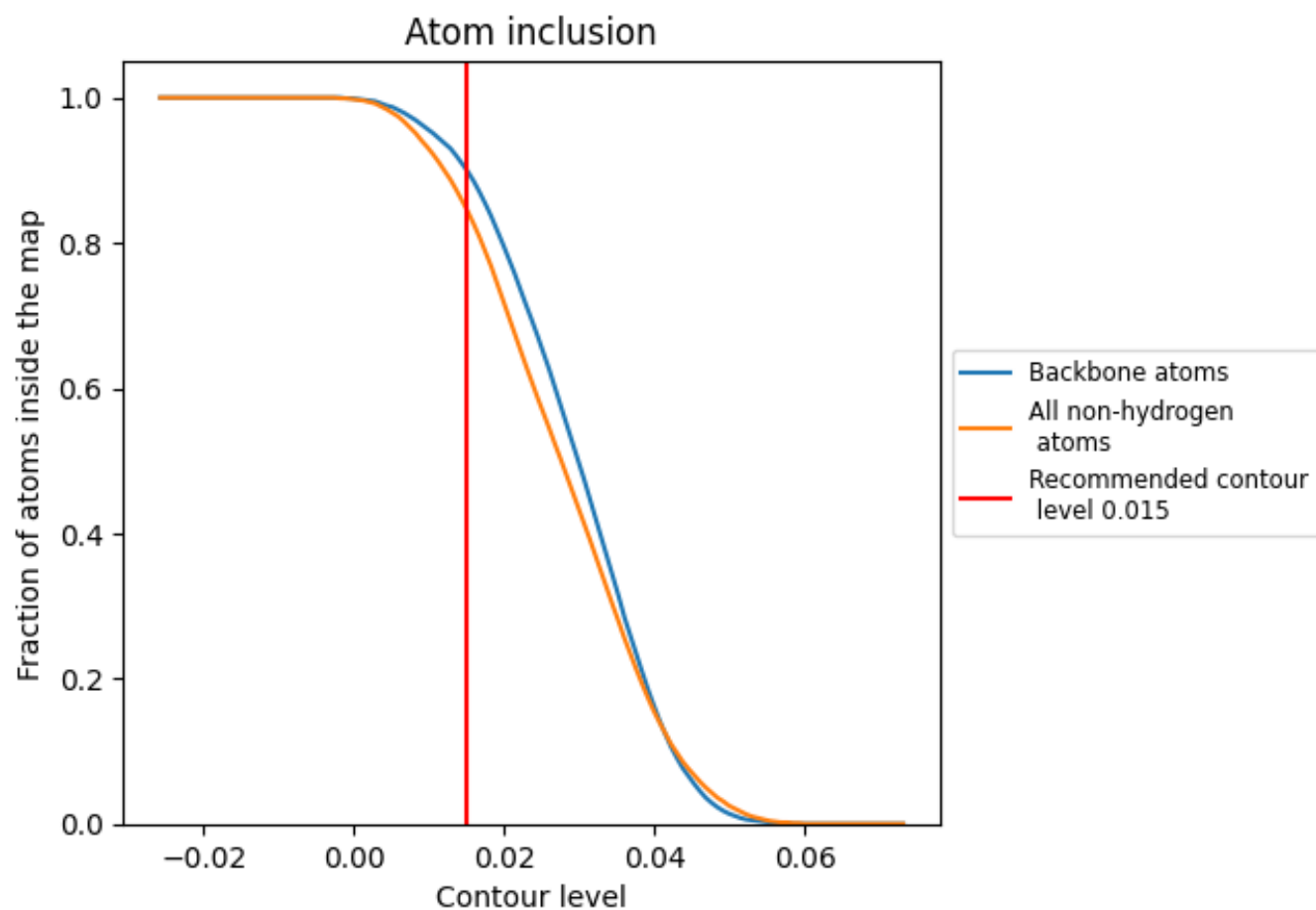
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4400
1	 0.9250	 0.4580
2	 0.9340	 0.4320
3	 0.8930	 0.3130
4	 0.6360	 0.4200
5	 0.1700	 0.2800
B	 0.8590	 0.5210
C	 0.8440	 0.5120
D	 0.7550	 0.4720
E	 0.6070	 0.3490
F	 0.7090	 0.4190
G	 0.1130	 0.2760
J	 0.8320	 0.5060
K	 0.8020	 0.5000
L	 0.8160	 0.4880
M	 0.8410	 0.5030
N	 0.8810	 0.5150
O	 0.7680	 0.4150
P	 0.8010	 0.4920
Q	 0.8590	 0.4950
R	 0.7990	 0.4870
S	 0.8190	 0.5050
T	 0.7700	 0.4810
U	 0.7600	 0.4500
V	 0.7750	 0.4620
W	 0.7780	 0.4810
X	 0.8520	 0.4900
Y	 0.7420	 0.4340
Z	 0.8030	 0.4990
a	 0.0040	 0.2160
b	 0.8270	 0.5040
c	 0.6630	 0.4600
d	 0.8700	 0.5210
e	 0.8640	 0.5180
f	 0.8080	 0.4910



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.1780	 0.3300
h	 0.6130	 0.3990
i	 0.6670	 0.4080
j	 0.7640	 0.4470
k	 0.6540	 0.4050
l	 0.5700	 0.3460
m	 0.7630	 0.4520
n	 0.6080	 0.3470
o	 0.5020	 0.3450
p	 0.7570	 0.4410
q	 0.7420	 0.4560
r	 0.5910	 0.3380
s	 0.6460	 0.3620
t	 0.7740	 0.4330
u	 0.7540	 0.4600
v	 0.7310	 0.4330
w	 0.5850	 0.3720
x	 0.5750	 0.3220
y	 0.7480	 0.3990
z	 0.3000	 0.3490