



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:35 AM UTC

PDB ID : 7NSO / pdb_00007nso
EMDB ID : EMD-12573
Title : Structure of ErmDL-Erythromycin-stalled 70S E. coli ribosomal complex with P-tRNA
Authors : Beckert, B.; Wilson, D.N.
Deposited on : 2021-03-08
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

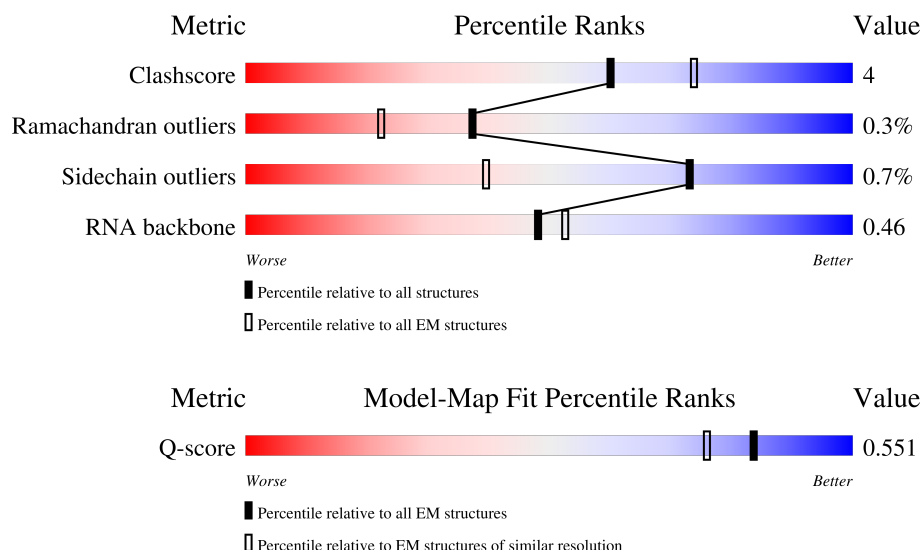
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	2903	
2	B	120	
3	C	271	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	201	
6	F	177	
7	G	174	
8	H	149	
9	J	142	
10	K	122	
11	L	144	
12	M	136	
13	N	118	
14	O	116	
15	P	114	
16	Q	117	
17	R	103	
18	S	110	
19	T	89	
20	U	102	
21	V	94	
22	W	75	
23	X	77	
24	Y	63	
25	Z	58	
26	0	55	
27	1	50	
28	2	46	

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Mol	Chain	Length	Quality of chain
29	3	64	
30	4	38	
31	5	65	
32	6	3	
33	7	7	
34	8	87	
35	a	1540	
36	b	224	
37	c	206	
38	d	205	
39	e	157	
40	f	99	
41	g	151	
42	h	129	
43	i	127	
44	j	98	
45	k	117	
46	l	123	
47	m	114	
48	n	100	
49	o	88	
50	p	82	
51	q	80	
52	r	66	
53	s	83	

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Mol	Chain	Length	Quality of chain
54	t	86	14% 85% 15%
55	u	70	83% 86% 14%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 144454 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 rRNA (2903-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 3 is a protein called 50S ribosomal protein L2.

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

- Molecule 4 is a protein called 50S ribosomal protein L3.

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

- Molecule 5 is a protein called 50S ribosomal protein L4.

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

- Molecule 6 is a protein called 50S ribosomal protein L5.

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

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	174	Total	C	N	O	S	0	0
			1304	820	239	243	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	T	89	Total	C	N	O	S	0
			709	449	133	125	2	0

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	0	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	65	Total	C	N	O	S	0	0
			514	317	98	93	6		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

- Molecule 33 is a protein called ermDL.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	7	Total	C	N	O	S	1	0
			69	41	16	10	2		

- Molecule 34 is a RNA chain called PtRNA-Leu.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	87	Total	C	N	O	P	0	0
			1861	829	333	612	87		

- Molecule 35 is a RNA chain called 16S rRNA (1540-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	1540	Total	C	N	O	P	0	0
			33037	14735	6057	10705	1540		

- Molecule 36 is a protein called 30S ribosomal protein S2.

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

- Molecule 37 is a protein called 30S ribosomal protein S3.

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

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

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

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	99	Total	C	N	O	S	0	0
			811	512	147	146	6		

- Molecule 41 is a protein called 30S ribosomal protein S7.

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

- Molecule 42 is a protein called 30S ribosomal protein S8.

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

- Molecule 43 is a protein called 30S ribosomal protein S9.

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

- Molecule 44 is a protein called 30S ribosomal protein S10.

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

- Molecule 45 is a protein called 30S ribosomal protein S11.

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

- Molecule 46 is a protein called 30S ribosomal protein S12.

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

- Molecule 47 is a protein called 30S ribosomal protein S13.

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

- Molecule 48 is a protein called 30S ribosomal protein S14.

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

- Molecule 49 is a protein called 30S ribosomal protein S15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called 30S ribosomal protein S17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	66	Total	C	N	O	S	0	0
			545	344	102	98	1		

- Molecule 53 is a protein called 30S ribosomal protein S19.

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

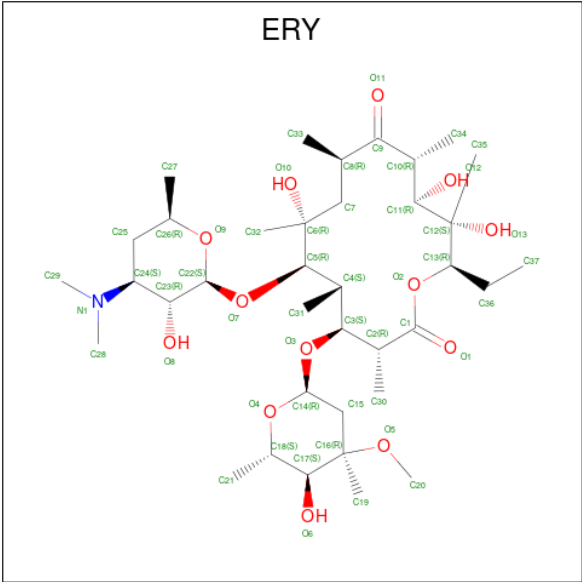
- Molecule 54 is a protein called 30S ribosomal protein S20.

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

- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 56 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$) (labeled as "Ligand of Interest" by depositor).

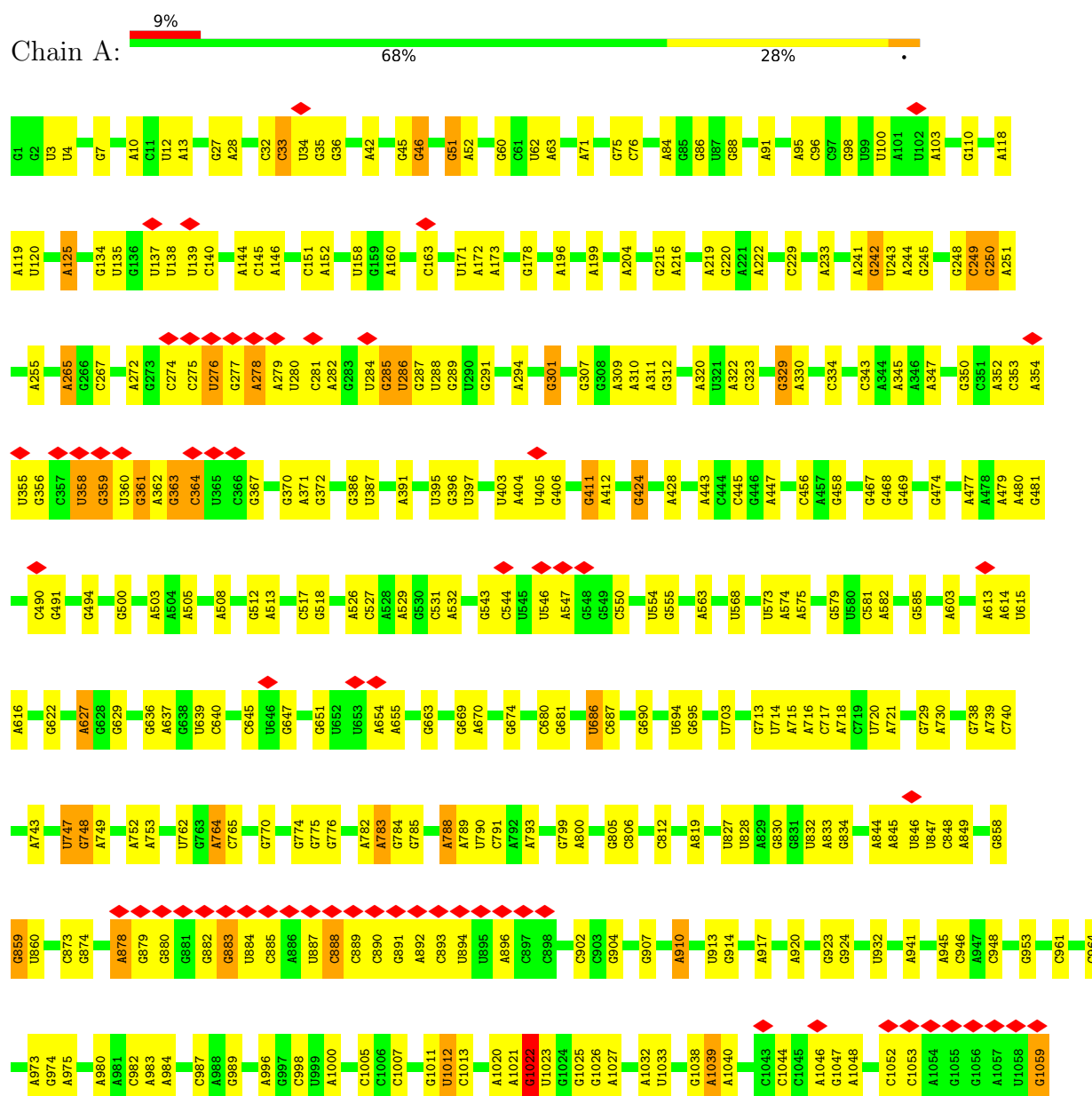


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
56	7	1	51	37	1	13	0

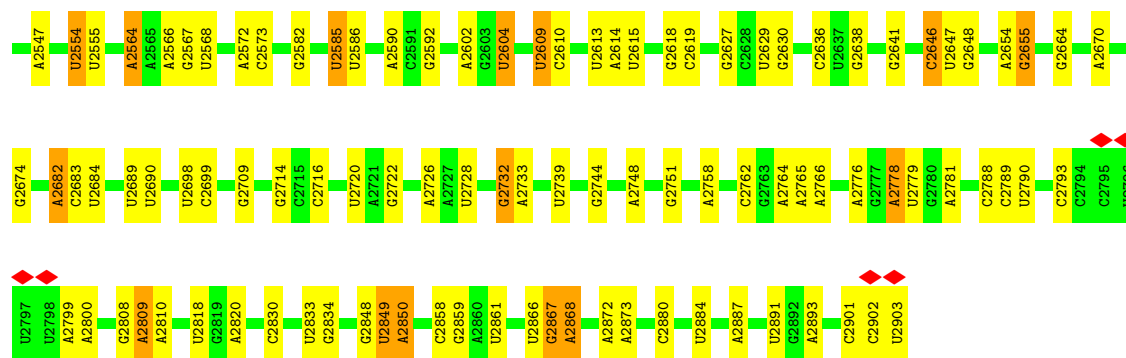
3 Residue-property plots

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.

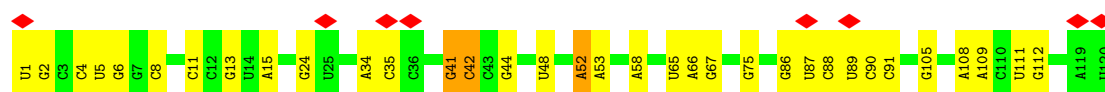
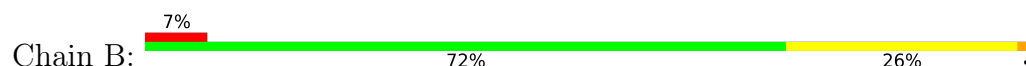
• Molecule 1: 23S rRNA (2903-MER)



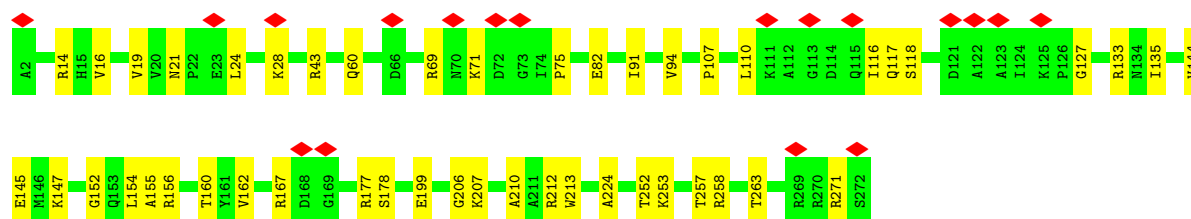
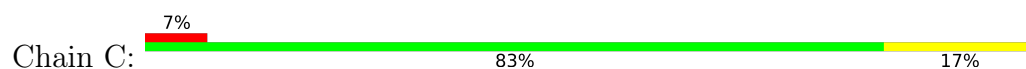
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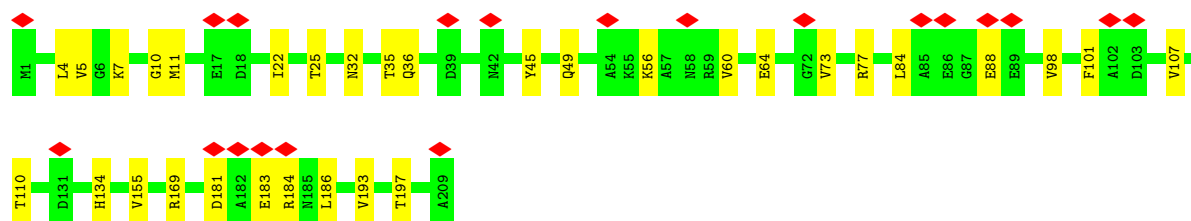
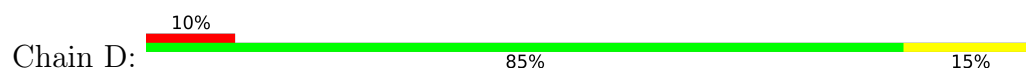
- Molecule 2: 5S rRNA



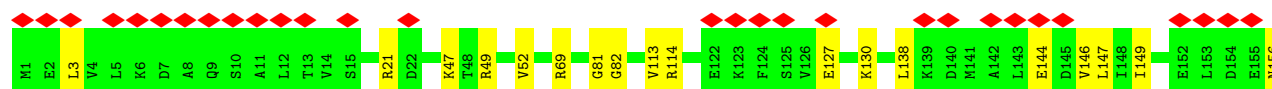
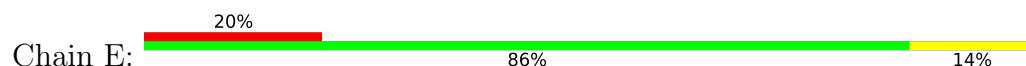
- Molecule 3: 50S ribosomal protein L2

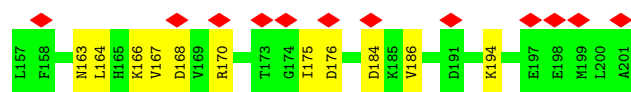


- Molecule 4: 50S ribosomal protein L3

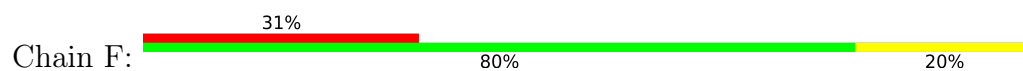


- Molecule 5: 50S ribosomal protein L4

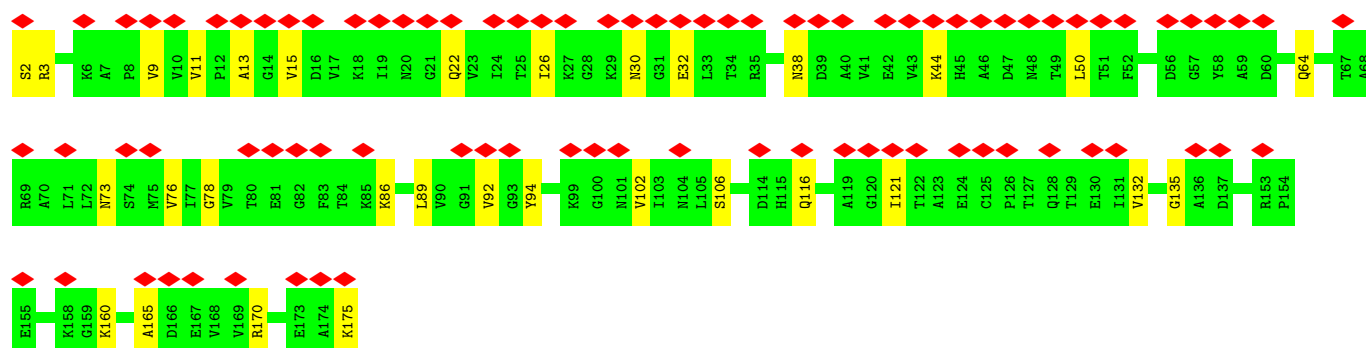
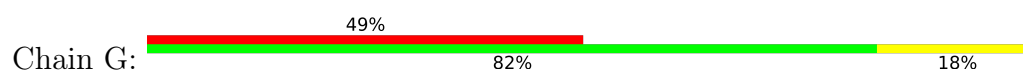




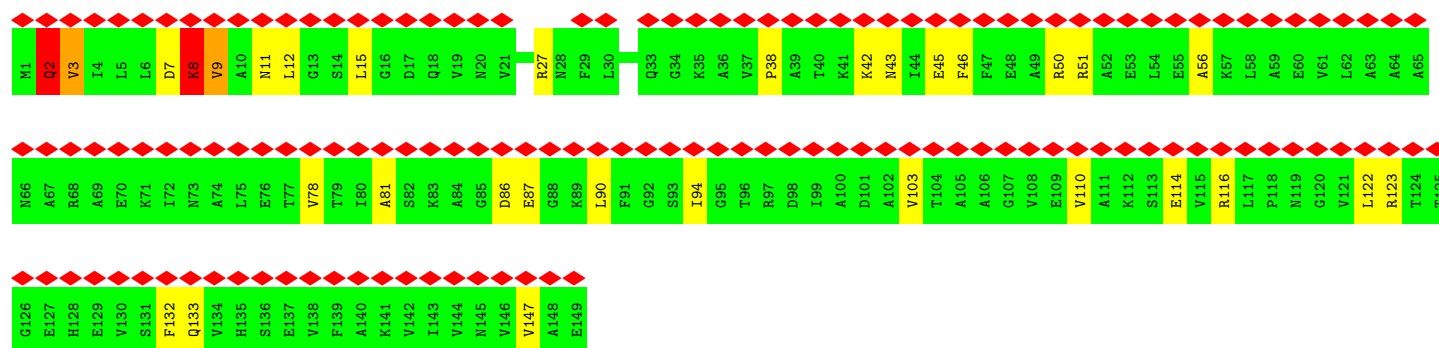
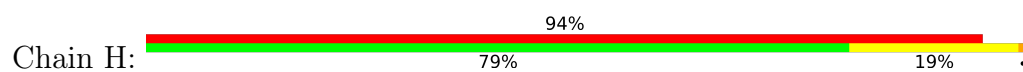
- Molecule 6: 50S ribosomal protein L5



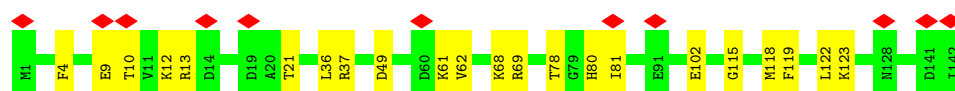
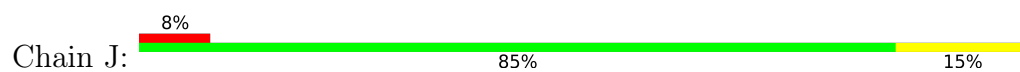
- Molecule 7: 50S ribosomal protein L6



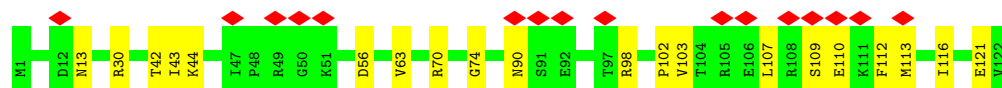
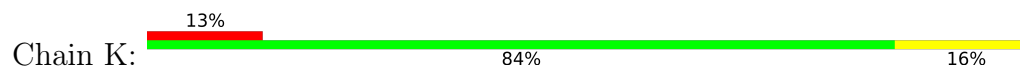
- Molecule 8: 50S ribosomal protein L9



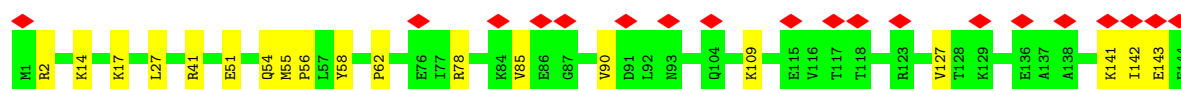
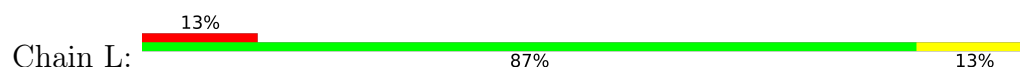
- Molecule 9: 50S ribosomal protein L13



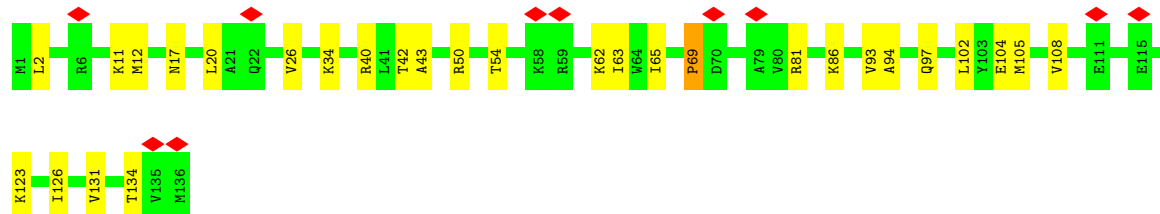
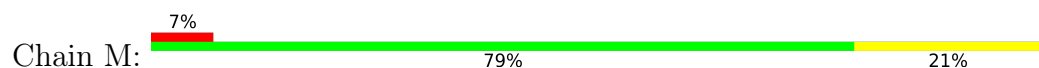
- Molecule 10: 50S ribosomal protein L14



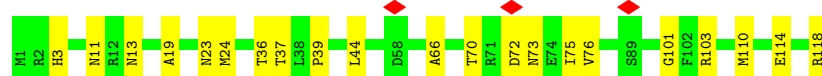
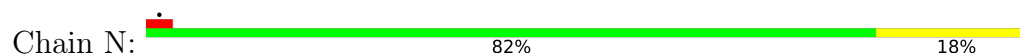
- Molecule 11: 50S ribosomal protein L15



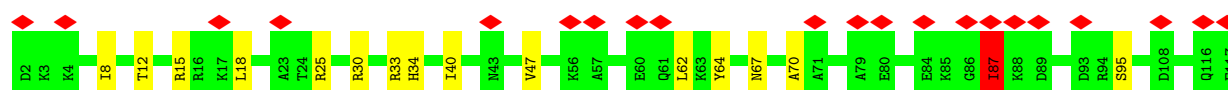
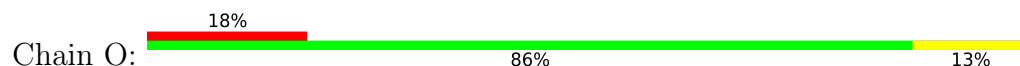
- Molecule 12: 50S ribosomal protein L16



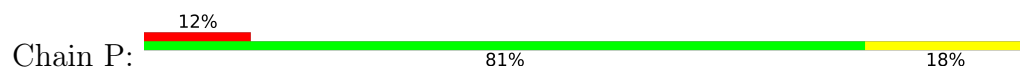
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

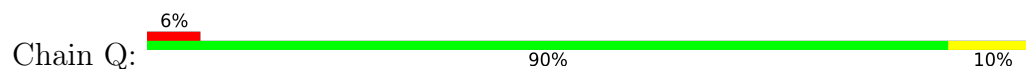


- Molecule 15: 50S ribosomal protein L19

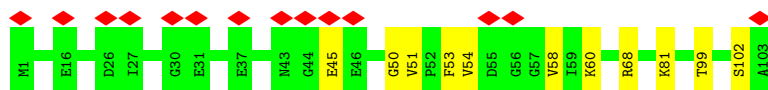
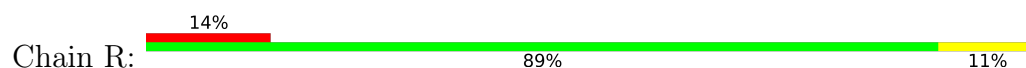




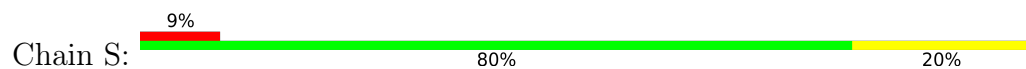
- Molecule 16: 50S ribosomal protein L20



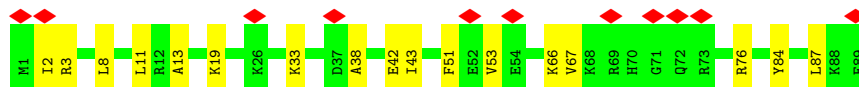
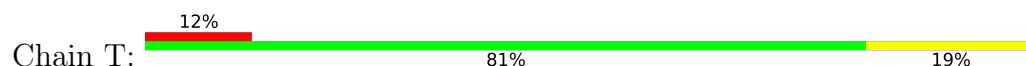
- Molecule 17: 50S ribosomal protein L21



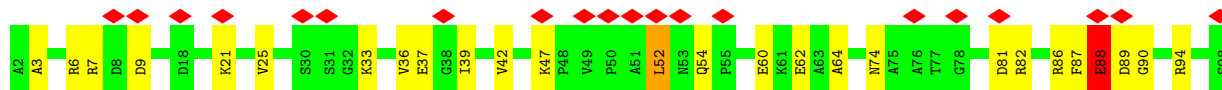
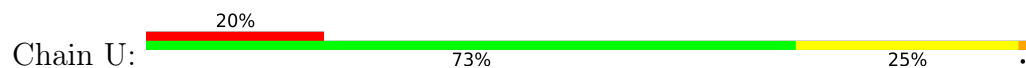
- Molecule 18: 50S ribosomal protein L22



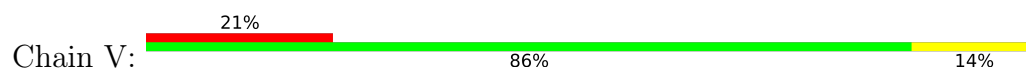
- Molecule 19: 50S ribosomal protein L23

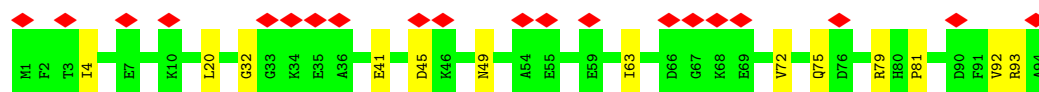


- Molecule 20: 50S ribosomal protein L24

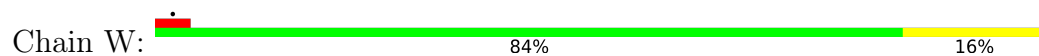


- Molecule 21: 50S ribosomal protein L25

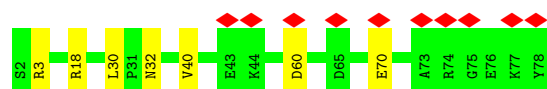




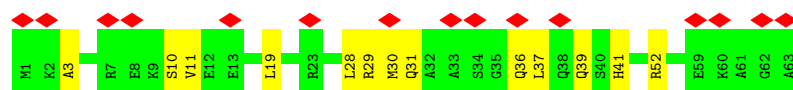
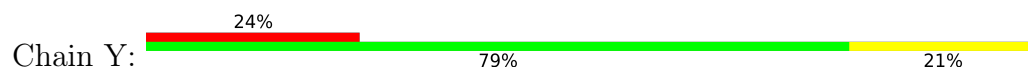
- Molecule 22: 50S ribosomal protein L27



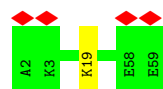
- Molecule 23: 50S ribosomal protein L28



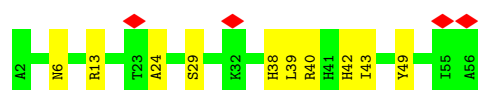
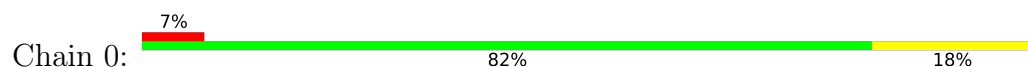
- Molecule 24: 50S ribosomal protein L29



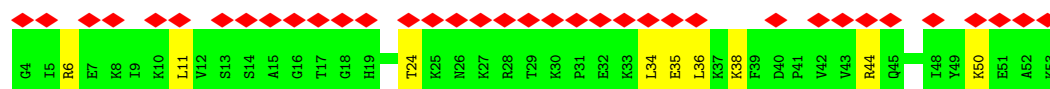
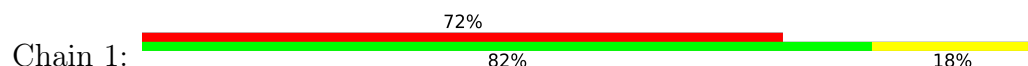
- Molecule 25: 50S ribosomal protein L30



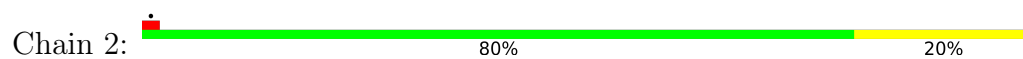
- Molecule 26: 50S ribosomal protein L32



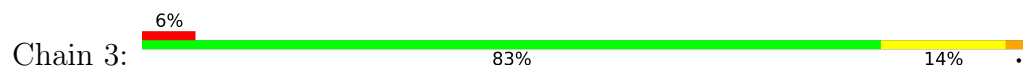
- Molecule 27: 50S ribosomal protein L33



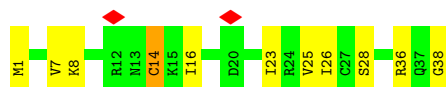
- Molecule 28: 50S ribosomal protein L34



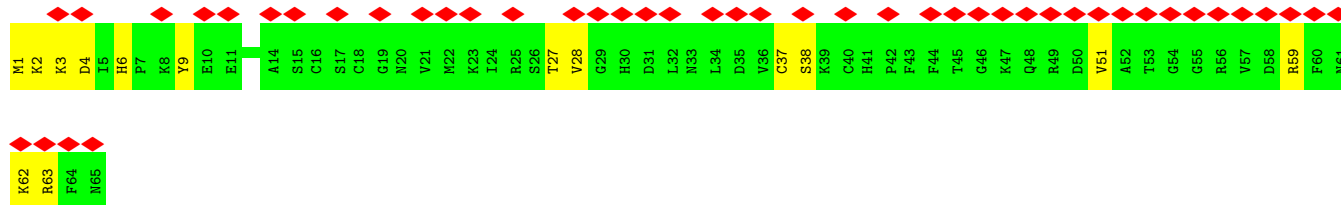
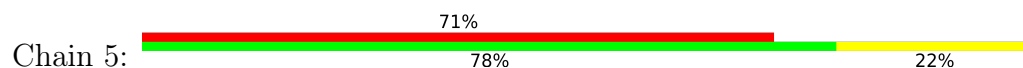
- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 50S ribosomal protein L31



- Molecule 32: mRNA



- Molecule 33: ermDL

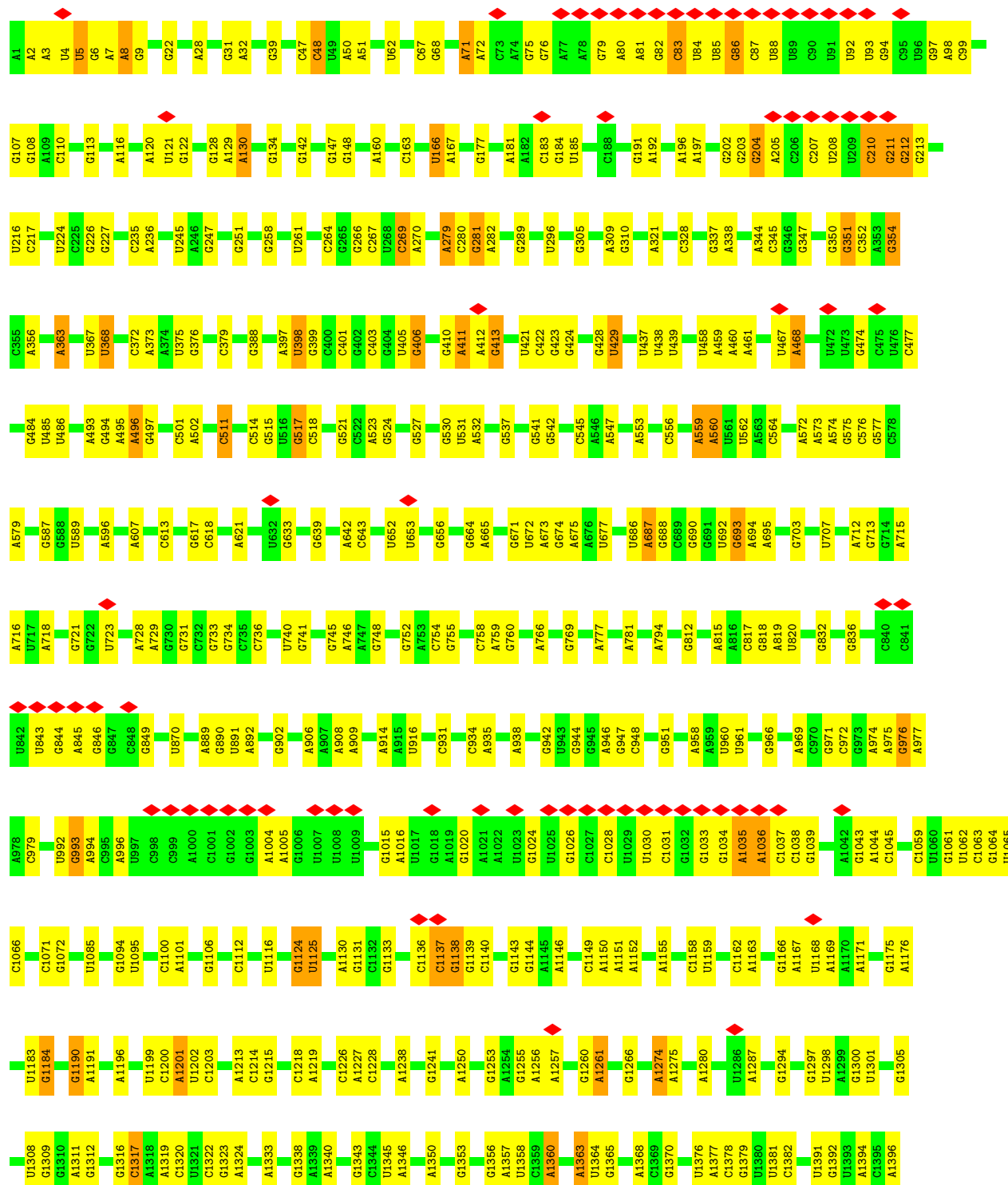


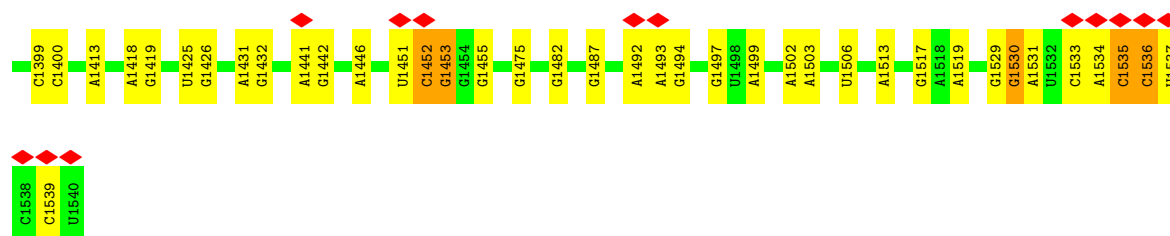
- Molecule 34: PtRNA-Leu



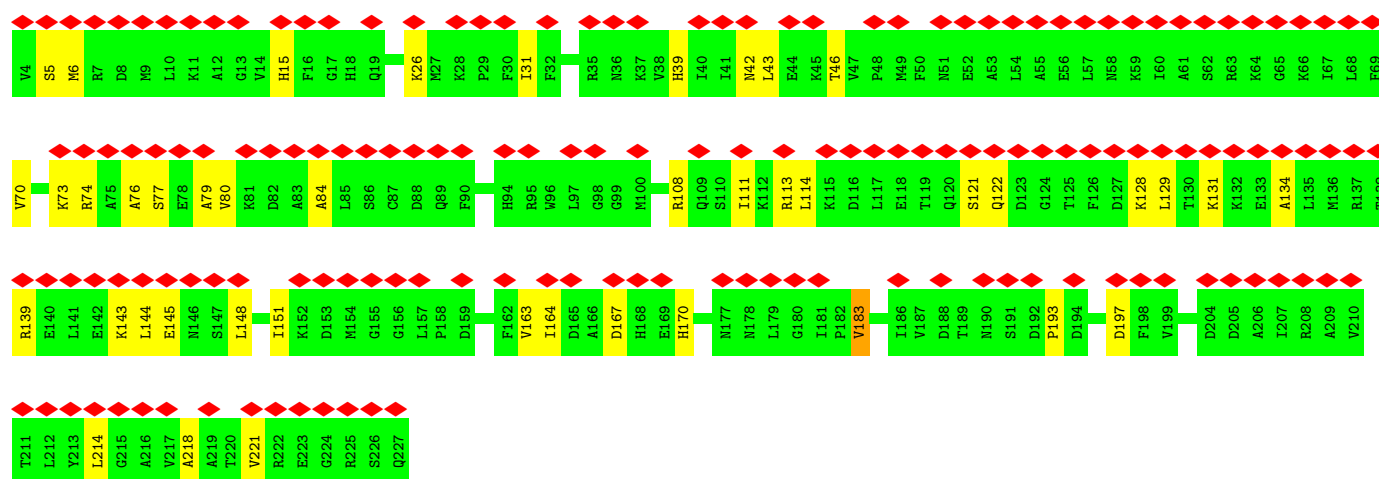
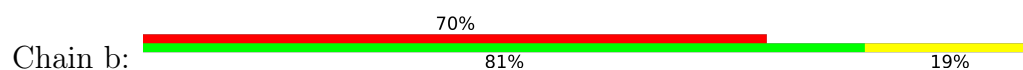


• Molecule 35: 16S rRNA (1540-MER)

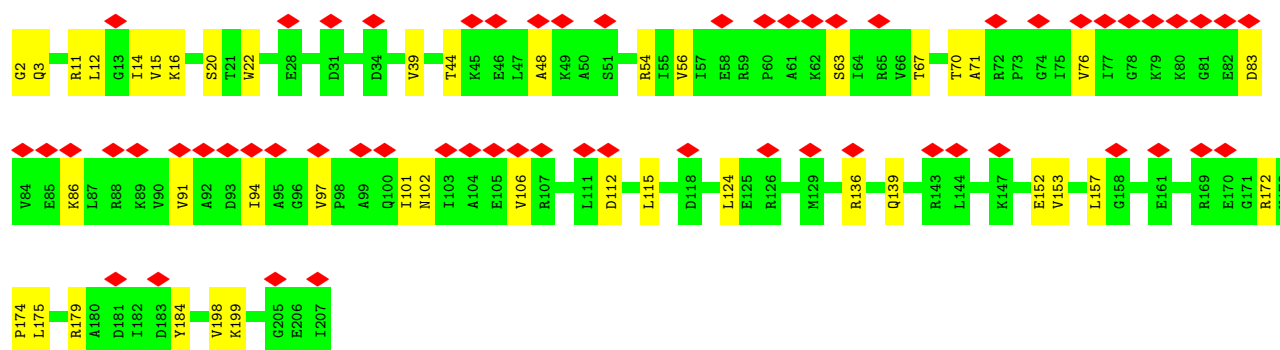
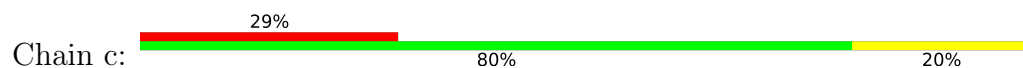




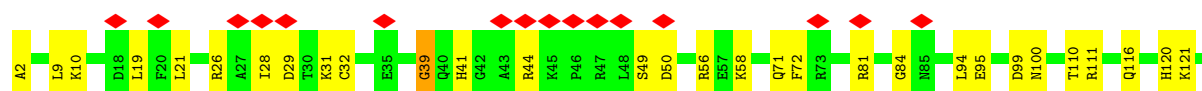
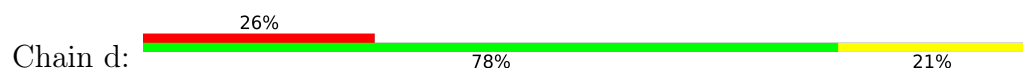
• Molecule 36: 30S ribosomal protein S2

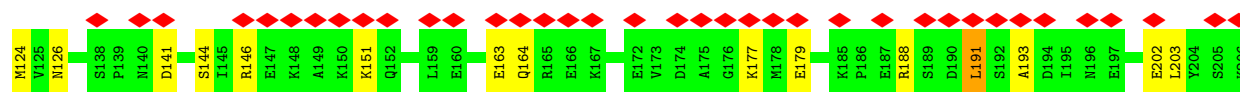


• Molecule 37: 30S ribosomal protein S3

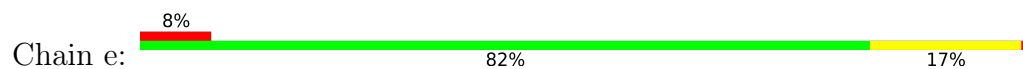


• Molecule 38: 30S ribosomal protein S4

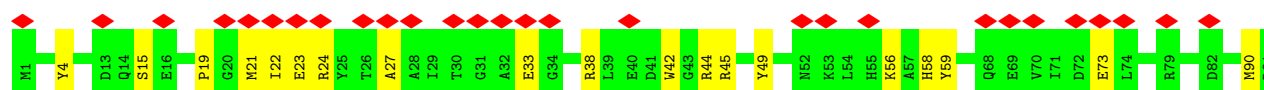
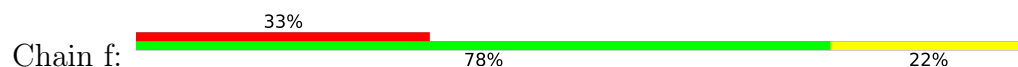




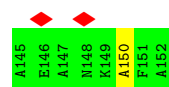
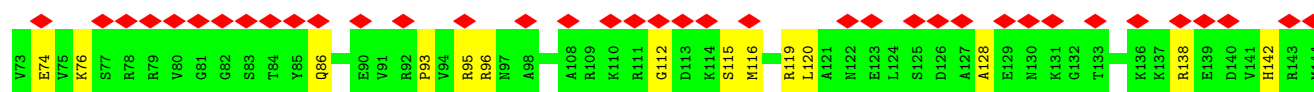
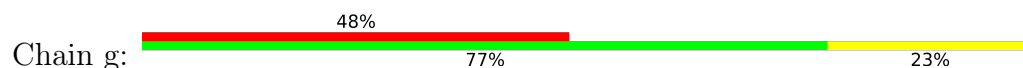
- Molecule 39: 30S ribosomal protein S5



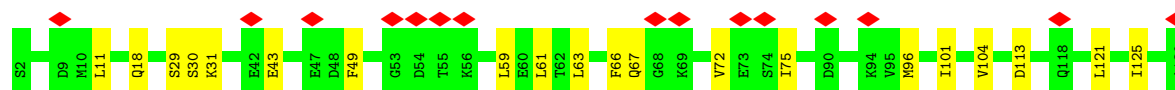
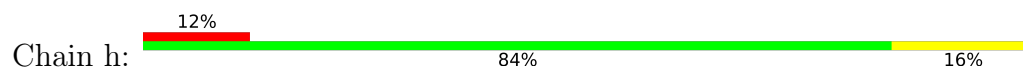
- Molecule 40: 30S ribosomal protein S6



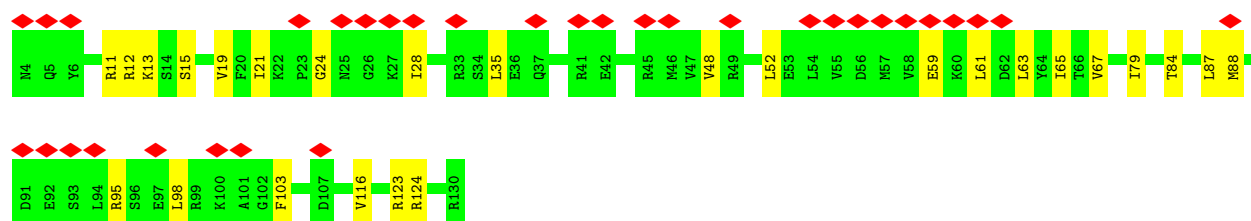
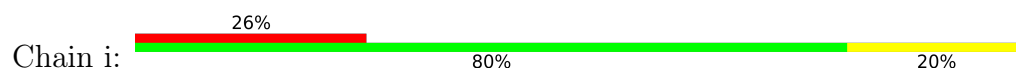
- Molecule 41: 30S ribosomal protein S7



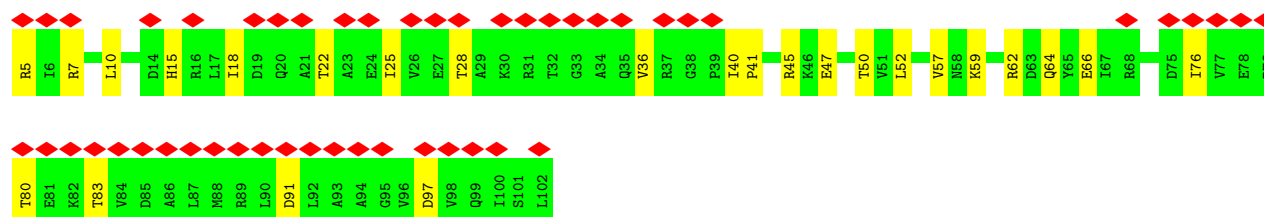
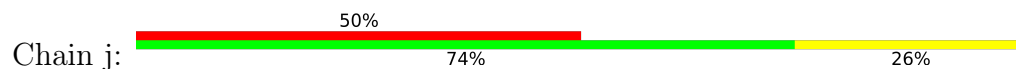
- Molecule 42: 30S ribosomal protein S8



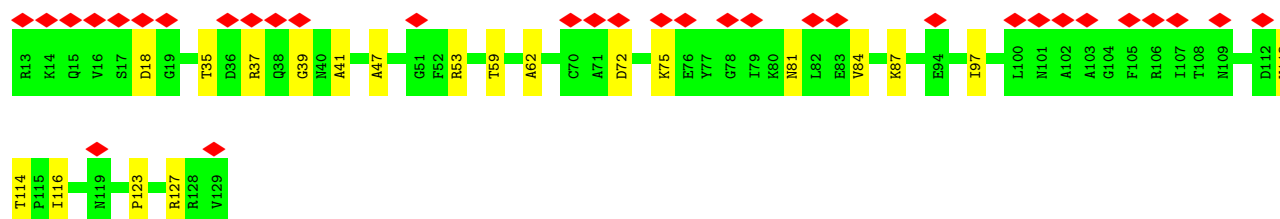
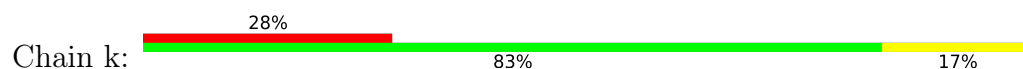
- Molecule 43: 30S ribosomal protein S9



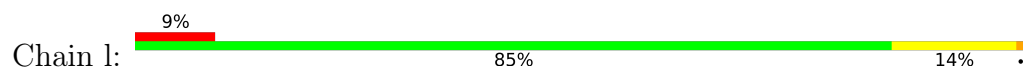
• Molecule 44: 30S ribosomal protein S10



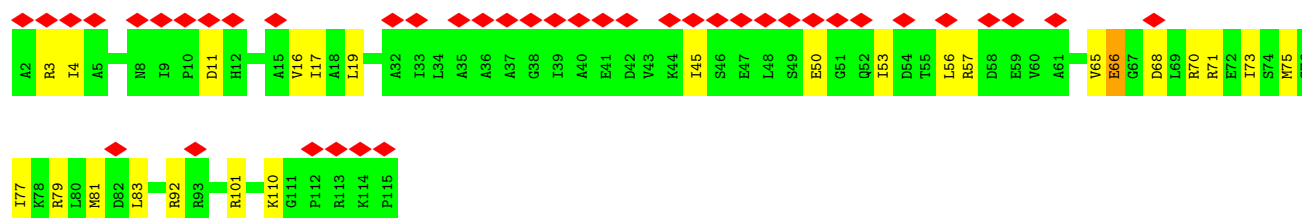
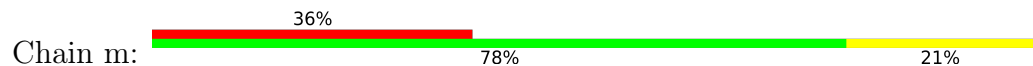
• Molecule 45: 30S ribosomal protein S11



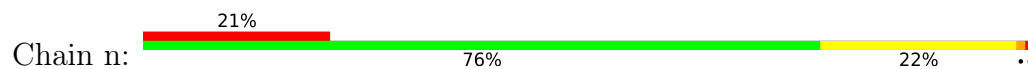
• Molecule 46: 30S ribosomal protein S12



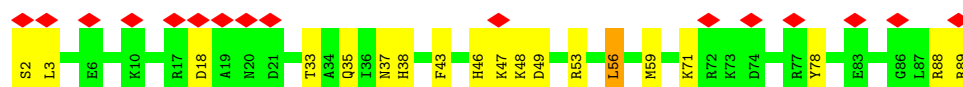
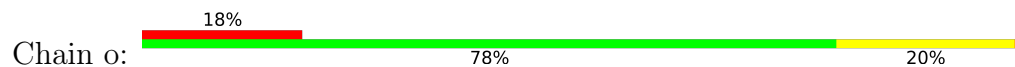
• Molecule 47: 30S ribosomal protein S13



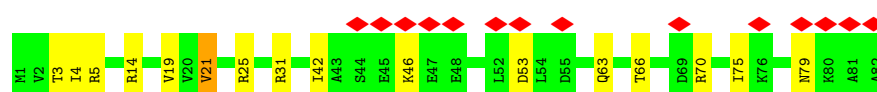
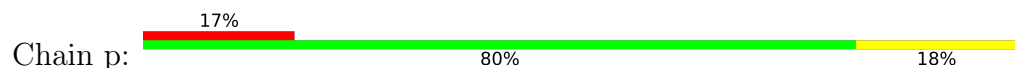
- Molecule 48: 30S ribosomal protein S14



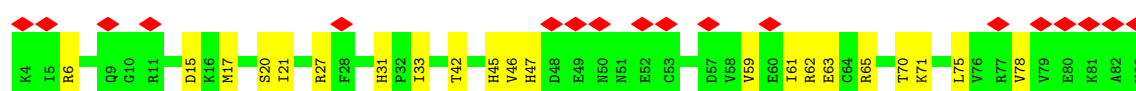
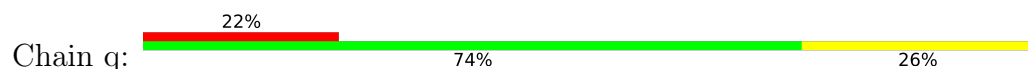
- Molecule 49: 30S ribosomal protein S15



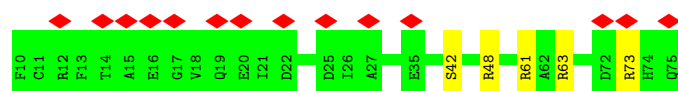
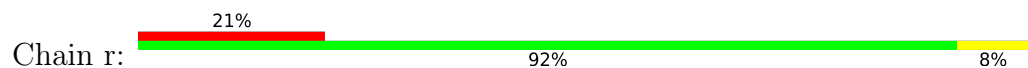
- Molecule 50: 30S ribosomal protein S16



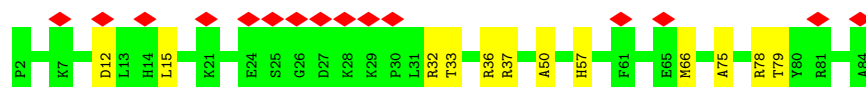
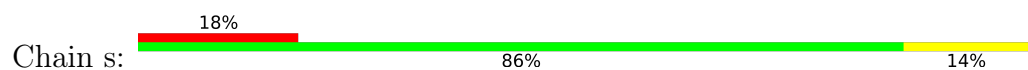
- Molecule 51: 30S ribosomal protein S17



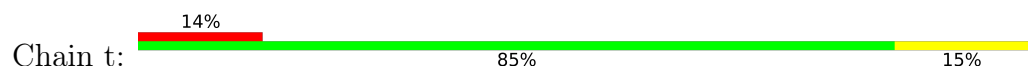
- Molecule 52: 30S ribosomal protein S18

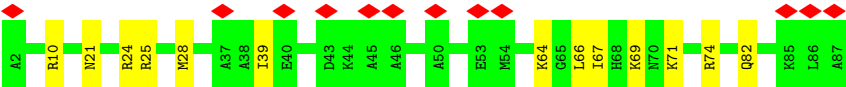


- Molecule 53: 30S ribosomal protein S19

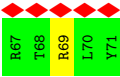
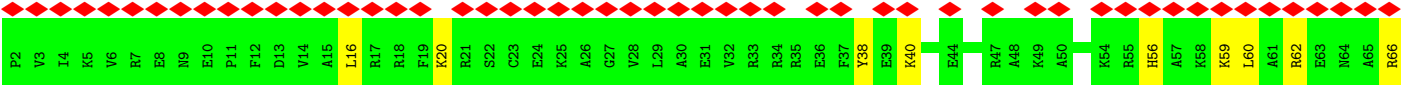
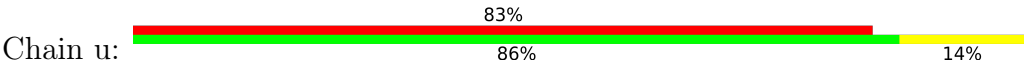


- Molecule 54: 30S ribosomal protein S20





• Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	172175	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 ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.748	Depositor
Minimum map value	-0.390	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	398.88, 398.88, 398.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.108, 1.108, 1.108	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.41	1/69800 (0.0%)	0.46	8/108892 (0.0%)
2	B	0.28	0/2873	0.43	0/4478
3	C	0.41	0/2121	0.70	2/2852 (0.1%)
4	D	0.38	0/1586	0.64	0/2134
5	E	0.31	0/1571	0.61	0/2113
6	F	0.29	0/1434	0.69	0/1926
7	G	0.27	0/1324	0.70	1/1794 (0.1%)
8	H	0.30	0/1122	0.85	4/1515 (0.3%)
9	J	0.34	0/1152	0.55	0/1551
10	K	0.37	0/947	0.71	0/1268
11	L	0.35	0/1062	0.73	0/1413
12	M	0.34	0/1093	0.62	0/1460
13	N	0.38	0/958	0.65	0/1281
14	O	0.28	0/902	0.67	2/1209 (0.2%)
15	P	0.35	0/929	0.61	0/1242
16	Q	0.40	0/960	0.55	0/1278
17	R	0.35	0/829	0.71	0/1107
18	S	0.35	0/864	0.63	0/1156
19	T	0.29	0/715	0.63	1/955 (0.1%)
20	U	0.33	0/787	0.76	3/1051 (0.3%)
21	V	0.29	0/766	0.58	0/1025
22	W	0.34	0/582	0.57	0/769
23	X	0.34	0/635	0.60	0/848
24	Y	0.29	0/510	0.61	0/677
25	Z	0.30	0/453	0.51	0/605
26	0	0.38	0/440	0.61	0/588
27	1	0.31	0/416	0.76	0/554
28	2	0.39	0/380	0.64	0/498
29	3	0.37	0/513	0.78	3/676 (0.4%)
30	4	0.39	0/303	0.73	0/397
31	5	0.27	0/523	0.80	1/698 (0.1%)
32	6	0.38	0/65	0.46	0/98

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.30	0/69	0.94	0/89
34	8	0.25	0/2080	0.40	0/3242
35	a	0.44	0/36991	0.46	1/57705 (0.0%)
36	b	0.33	0/1784	0.77	0/2403
37	c	0.36	0/1651	0.74	1/2225 (0.0%)
38	d	0.34	0/1665	0.73	0/2227
39	e	0.41	0/1169	0.75	0/1573
40	f	0.35	0/829	0.73	0/1120
41	g	0.32	0/1195	0.79	1/1602 (0.1%)
42	h	0.41	0/989	0.66	0/1326
43	i	0.38	0/1034	0.79	0/1375
44	j	0.36	0/796	0.77	0/1077
45	k	0.34	0/893	0.66	0/1205
46	l	0.43	0/969	0.79	3/1300 (0.2%)
47	m	0.35	0/892	0.79	3/1193 (0.3%)
48	n	0.40	0/817	0.70	0/1088
49	o	0.36	0/722	0.67	0/964
50	p	0.39	0/659	0.76	0/884
51	q	0.37	0/657	0.79	1/881 (0.1%)
52	r	0.32	0/554	0.61	0/743
53	s	0.31	0/680	0.61	0/915
54	t	0.34	0/676	0.57	0/895
55	u	0.28	0/598	0.66	0/792
All	All	0.40	1/156984 (0.0%)	0.53	35/234932 (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
5	E	0	1
8	H	0	2
14	O	0	1
17	R	0	3
18	S	0	2
20	U	0	2
27	1	0	1
29	3	0	1
33	7	0	1
36	b	0	1
38	d	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
39	e	0	1
40	f	0	1
41	g	0	1
42	h	0	1
43	i	0	1
44	j	0	1
47	m	0	1
48	n	0	3
50	p	0	1
51	q	0	1
52	r	0	2
All	All	0	32

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2604	U	N3-C4	-5.73	1.26	1.38

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	g	65	ALA	N-CA-C	-8.15	104.21	114.56
47	m	4	ILE	CA-C-N	6.63	130.77	120.82
47	m	4	ILE	C-N-CA	6.63	130.77	120.82
19	T	2	ILE	N-CA-C	-6.20	105.32	111.77
8	H	8	LYS	CA-C-N	6.20	133.12	121.97

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	82	GLY	Peptide
8	H	2	GLN	Peptide
8	H	8	LYS	Peptide
14	O	87	ILE	Peptide
17	R	50	GLY	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	A	62321	0	31343	296	0
2	B	2570	0	1301	10	0
3	C	2082	0	2154	31	0
4	D	1565	0	1616	17	0
5	E	1552	0	1619	18	0
6	F	1410	0	1444	21	0
7	G	1304	0	1345	18	0
8	H	1111	0	1148	20	0
9	J	1129	0	1162	14	0
10	K	938	0	1012	13	0
11	L	1053	0	1129	13	0
12	M	1074	0	1157	18	0
13	N	945	0	989	14	0
14	O	892	0	923	10	0
15	P	917	0	962	14	0
16	Q	947	0	1019	11	0
17	R	816	0	839	5	0
18	S	857	0	922	15	0
19	T	709	0	779	11	0
20	U	779	0	831	16	0
21	V	753	0	780	8	0
22	W	575	0	592	9	0
23	X	625	0	652	5	0
24	Y	509	0	543	10	0
25	Z	449	0	488	1	0
26	0	434	0	445	7	0
27	1	409	0	440	5	0
28	2	377	0	418	7	0
29	3	504	0	572	8	0
30	4	302	0	340	7	0
31	5	514	0	509	10	0
32	6	60	0	32	0	0
33	7	69	0	75	17	0
34	8	1861	0	937	12	0
35	a	33037	0	16628	169	0
36	b	1753	0	1780	22	0
37	c	1624	0	1696	28	0
38	d	1643	0	1707	32	0
39	e	1156	0	1199	16	0
40	f	811	0	803	15	0
41	g	1181	0	1238	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	h	979	0	1031	12	0
43	i	1022	0	1070	15	0
44	j	786	0	828	16	0
45	k	877	0	887	19	0
46	l	955	0	1016	11	0
47	m	883	0	941	14	0
48	n	805	0	844	21	0
49	o	714	0	734	12	0
50	p	649	0	666	13	0
51	q	648	0	691	13	0
52	r	545	0	560	3	0
53	s	663	0	688	11	0
54	t	670	0	719	10	0
55	u	590	0	629	7	0
56	7	51	0	67	11	0
All	All	144454	0	96939	973	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 4.

The worst 5 of 973 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)
33:7:5:MET:SD	56:7:101:ERY:H273	1.58	1.42
33:7:5:MET:SD	56:7:101:ERY:C27	2.16	1.32
33:7:6[B]:ARG:NH1	33:7:6[B]:ARG:HB3	1.55	1.21
33:7:6[B]:ARG:HB3	33:7:6[B]:ARG:HH11	1.06	1.05
33:7:5:MET:SD	56:7:101:ERY:H271	2.01	1.00

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	
3	C	269/271 (99%)	251 (93%)	18 (7%)	0	100	100
4	D	207/209 (99%)	191 (92%)	16 (8%)	0	100	100
5	E	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
6	F	175/177 (99%)	162 (93%)	13 (7%)	0	100	100
7	G	172/174 (99%)	157 (91%)	15 (9%)	0	100	100
8	H	147/149 (99%)	126 (86%)	18 (12%)	3 (2%)	6	22
9	J	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
10	K	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
11	L	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
12	M	134/136 (98%)	131 (98%)	2 (2%)	1 (1%)	18	48
13	N	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
14	O	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
15	P	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
16	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
17	R	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12	39
18	S	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
19	T	87/89 (98%)	81 (93%)	6 (7%)	0	100	100
20	U	100/102 (98%)	88 (88%)	10 (10%)	2 (2%)	6	22
21	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
22	W	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
23	X	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
24	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
26	0	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
27	1	48/50 (96%)	44 (92%)	3 (6%)	1 (2%)	5	21
28	2	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
29	3	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	13
30	4	36/38 (95%)	36 (100%)	0	0	100	100
31	5	63/65 (97%)	56 (89%)	7 (11%)	0	100	100
33	7	6/7 (86%)	6 (100%)	0	0	100	100
36	b	222/224 (99%)	204 (92%)	18 (8%)	0	100	100
37	c	204/206 (99%)	193 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	d	203/205 (99%)	178 (88%)	25 (12%)	0	100	100
39	e	155/157 (99%)	140 (90%)	13 (8%)	2 (1%)	9	32
40	f	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
41	g	149/151 (99%)	138 (93%)	11 (7%)	0	100	100
42	h	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
43	i	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
44	j	96/98 (98%)	86 (90%)	9 (9%)	1 (1%)	12	39
45	k	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
46	l	121/123 (98%)	108 (89%)	12 (10%)	1 (1%)	16	44
47	m	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
48	n	98/100 (98%)	88 (90%)	9 (9%)	1 (1%)	12	39
49	o	86/88 (98%)	80 (93%)	5 (6%)	1 (1%)	10	34
50	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
51	q	78/80 (98%)	68 (87%)	10 (13%)	0	100	100
52	r	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
53	s	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
54	t	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
55	u	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
All	All	5592/5691 (98%)	5179 (93%)	397 (7%)	16 (0%)	37	65

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	U	89	ASP
29	3	32	ILE
8	H	9	VAL
27	1	35	GLU
39	e	99	ALA

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	
3	C	216/216 (100%)	216 (100%)	0	100	100
4	D	164/164 (100%)	161 (98%)	3 (2%)	51	80
5	E	165/165 (100%)	165 (100%)	0	100	100
6	F	148/148 (100%)	145 (98%)	3 (2%)	48	78
7	G	135/135 (100%)	135 (100%)	0	100	100
8	H	114/114 (100%)	112 (98%)	2 (2%)	51	80
9	J	116/116 (100%)	116 (100%)	0	100	100
10	K	103/103 (100%)	103 (100%)	0	100	100
11	L	103/103 (100%)	102 (99%)	1 (1%)	68	89
12	M	109/109 (100%)	109 (100%)	0	100	100
13	N	98/98 (100%)	98 (100%)	0	100	100
14	O	86/86 (100%)	85 (99%)	1 (1%)	63	86
15	P	99/99 (100%)	98 (99%)	1 (1%)	68	89
16	Q	89/89 (100%)	89 (100%)	0	100	100
17	R	84/84 (100%)	84 (100%)	0	100	100
18	S	93/93 (100%)	93 (100%)	0	100	100
19	T	77/77 (100%)	77 (100%)	0	100	100
20	U	83/83 (100%)	82 (99%)	1 (1%)	63	86
21	V	78/78 (100%)	78 (100%)	0	100	100
22	W	57/57 (100%)	57 (100%)	0	100	100
23	X	67/67 (100%)	65 (97%)	2 (3%)	36	70
24	Y	55/55 (100%)	55 (100%)	0	100	100
25	Z	48/48 (100%)	48 (100%)	0	100	100
26	0	46/46 (100%)	46 (100%)	0	100	100
27	1	45/45 (100%)	45 (100%)	0	100	100
28	2	38/38 (100%)	38 (100%)	0	100	100
29	3	51/51 (100%)	51 (100%)	0	100	100
30	4	34/34 (100%)	33 (97%)	1 (3%)	37	71
31	5	58/58 (100%)	56 (97%)	2 (3%)	32	66
33	7	8/7 (114%)	8 (100%)	0	100	100
36	b	186/186 (100%)	185 (100%)	1 (0%)	81	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	c	170/170 (100%)	170 (100%)	0	100	100
38	d	172/172 (100%)	171 (99%)	1 (1%)	78	93
39	e	119/119 (100%)	118 (99%)	1 (1%)	73	90
40	f	86/86 (100%)	85 (99%)	1 (1%)	63	86
41	g	124/124 (100%)	124 (100%)	0	100	100
42	h	104/104 (100%)	103 (99%)	1 (1%)	68	89
43	i	105/105 (100%)	103 (98%)	2 (2%)	50	79
44	j	86/86 (100%)	86 (100%)	0	100	100
45	k	90/90 (100%)	90 (100%)	0	100	100
46	l	103/103 (100%)	102 (99%)	1 (1%)	68	89
47	m	92/92 (100%)	91 (99%)	1 (1%)	65	88
48	n	83/83 (100%)	83 (100%)	0	100	100
49	o	76/76 (100%)	75 (99%)	1 (1%)	61	86
50	p	65/65 (100%)	63 (97%)	2 (3%)	35	69
51	q	74/74 (100%)	74 (100%)	0	100	100
52	r	57/57 (100%)	57 (100%)	0	100	100
53	s	72/72 (100%)	71 (99%)	1 (1%)	59	85
54	t	65/65 (100%)	65 (100%)	0	100	100
55	u	60/60 (100%)	59 (98%)	1 (2%)	53	82
All	All	4656/4655 (100%)	4625 (99%)	31 (1%)	73	92

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	4	14	CYS
50	p	19	VAL
36	b	183	VAL
53	s	79	THR
46	l	16	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
45	k	15	GLN

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Mol	Chain	Res	Type
48	n	49	GLN
50	p	63	GLN
17	R	11	GLN
16	Q	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2902/2903 (99%)	640 (22%)	47 (1%)
2	B	119/120 (99%)	23 (19%)	3 (2%)
32	6	2/3 (66%)	1 (50%)	0
34	8	86/87 (98%)	25 (29%)	1 (1%)
35	a	1539/1540 (99%)	310 (20%)	0
All	All	4648/4653 (99%)	999 (21%)	51 (1%)

5 of 999 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	U
1	A	10	A
1	A	12	U
1	A	13	A
1	A	33	C

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1173	U
1	A	1508	A
2	B	88	C
1	A	1179	G
1	A	1300	G

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

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

5.5 Carbohydrates ⓘ

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
56	ERY	7	101	-	53,53,53	1.70	6 (11%)	82,82,82	1.62	16 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	ERY	7	101	-	-	5/72/107/107	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	7	101	ERY	C10-C9	-7.36	1.40	1.52
56	7	101	ERY	C2-C1	-6.65	1.37	1.51
56	7	101	ERY	C8-C9	-3.17	1.42	1.52
56	7	101	ERY	C10-C11	2.61	1.57	1.54
56	7	101	ERY	O7-C22	2.19	1.47	1.41

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	7	101	ERY	O5-C16-C17	4.59	110.52	103.86
56	7	101	ERY	C27-C26-C25	-3.97	107.26	113.27
56	7	101	ERY	C6-C5-C4	-3.49	108.83	113.89
56	7	101	ERY	C29-N1-C28	-3.42	100.45	110.49
56	7	101	ERY	O8-C23-C24	3.36	116.02	109.87

There are no chirality outliers.

All (5) torsion outliers are listed below:

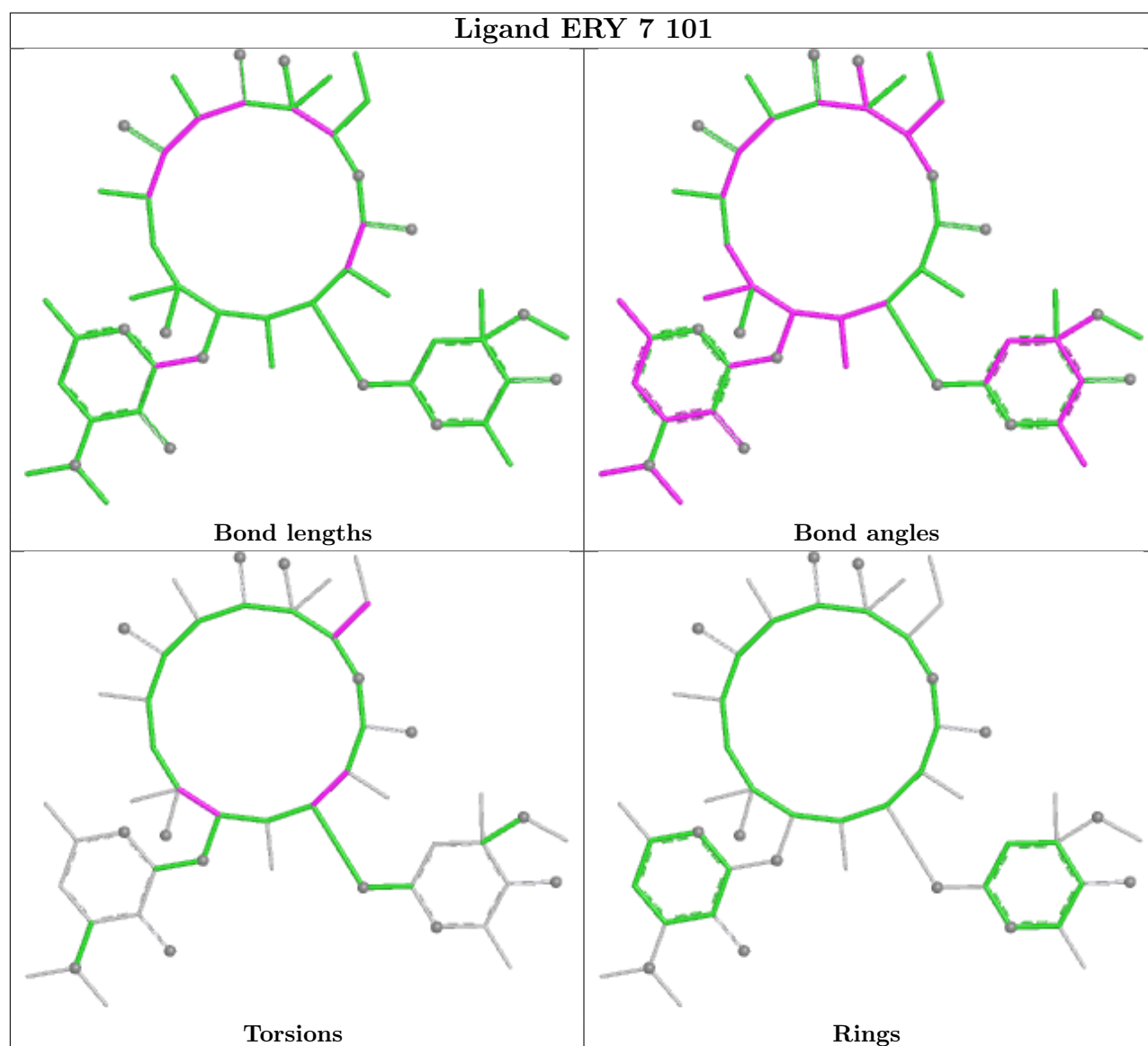
Mol	Chain	Res	Type	Atoms
56	7	101	ERY	C4-C5-C6-O10
56	7	101	ERY	O2-C13-C36-C37
56	7	101	ERY	C12-C13-C36-C37
56	7	101	ERY	C4-C5-C6-C32
56	7	101	ERY	C30-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	7	101	ERY	11	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.

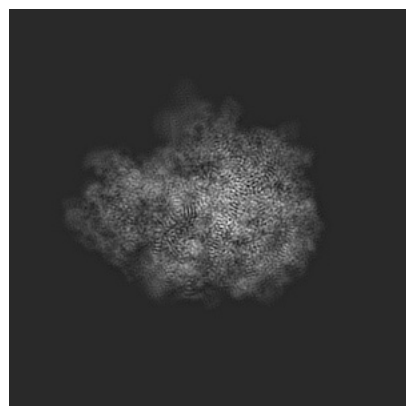
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12573. These allow visual inspection of the internal detail of the map and identification of artifacts.

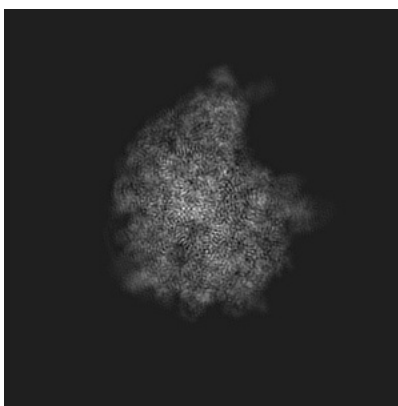
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

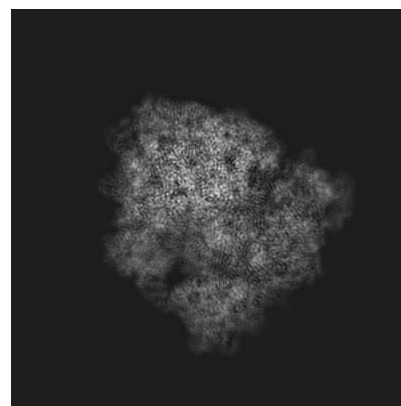
6.1.1 Primary map



X

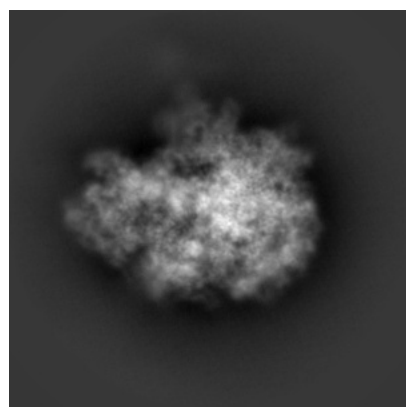


Y

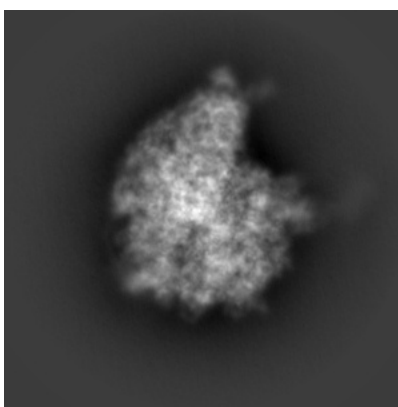


Z

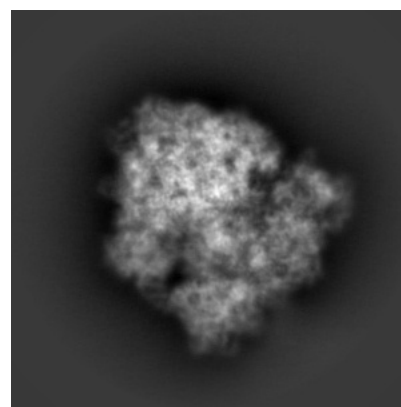
6.1.2 Raw map



X



Y

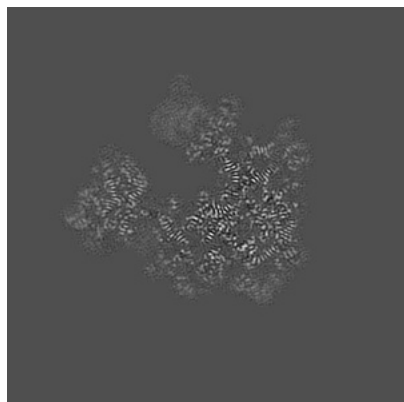


Z

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

6.2 Central slices [i](#)

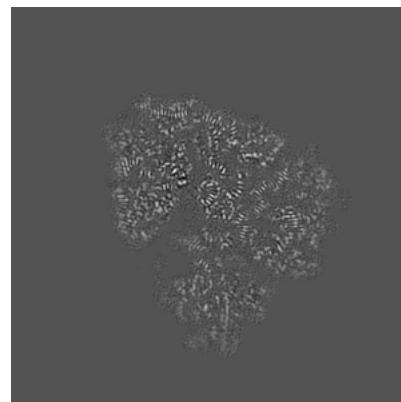
6.2.1 Primary map



X Index: 180

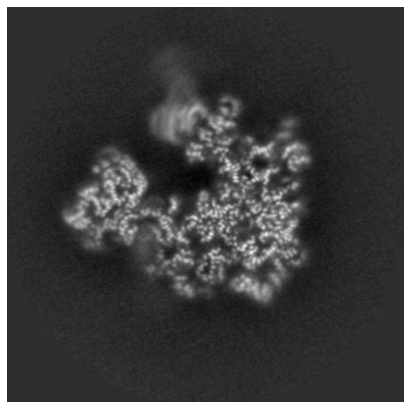


Y Index: 180

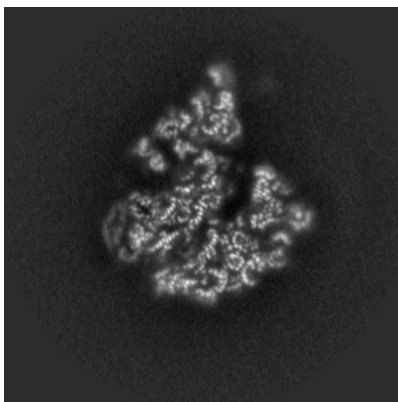


Z Index: 180

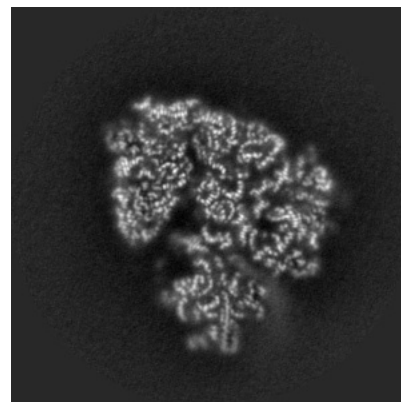
6.2.2 Raw map



X Index: 180



Y Index: 180

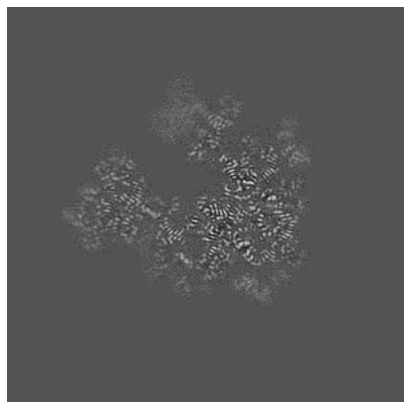


Z Index: 180

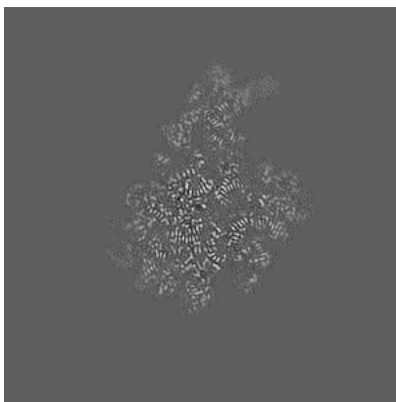
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

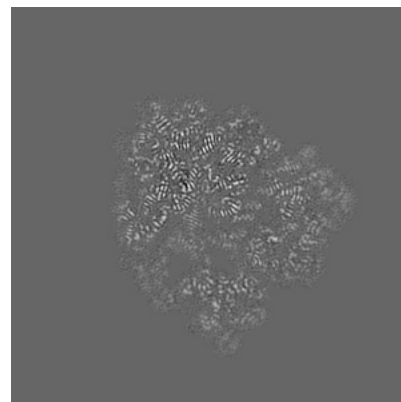
6.3.1 Primary map



X Index: 178

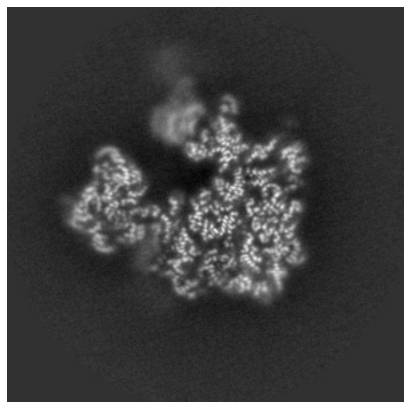


Y Index: 190

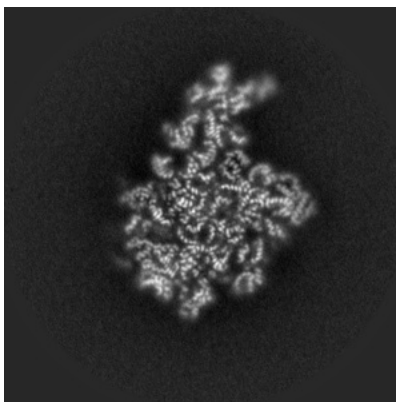


Z Index: 188

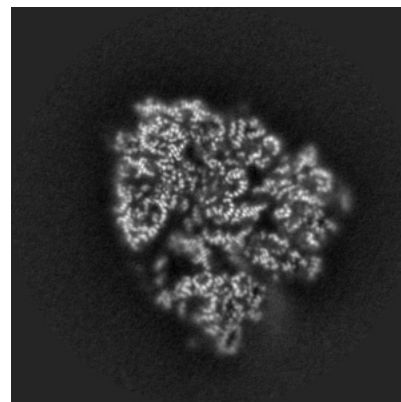
6.3.2 Raw map



X Index: 184



Y Index: 194

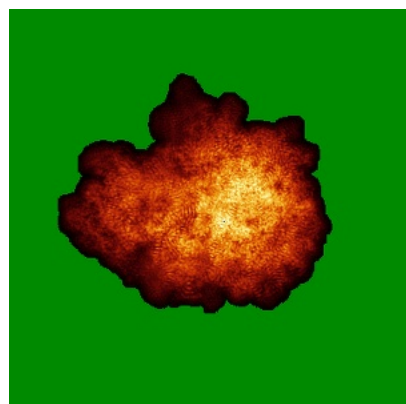


Z Index: 184

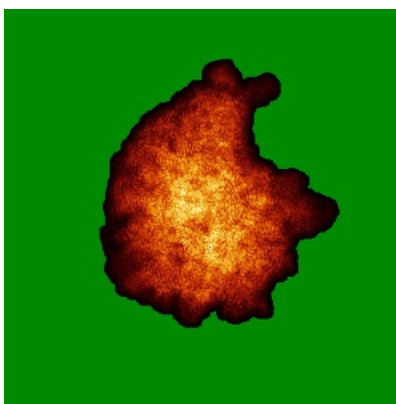
The images above show the largest variance slices of the map in three orthogonal directions.

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

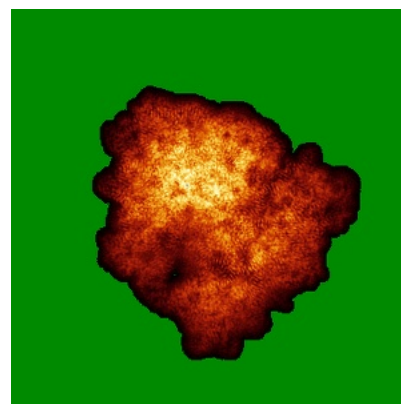
6.4.1 Primary map



X

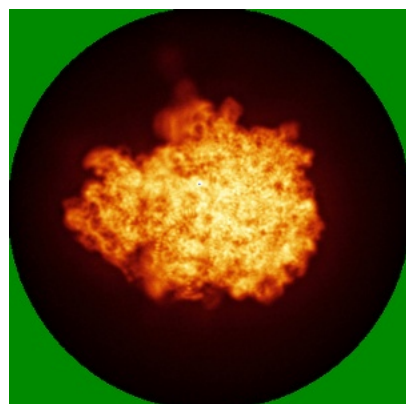


Y

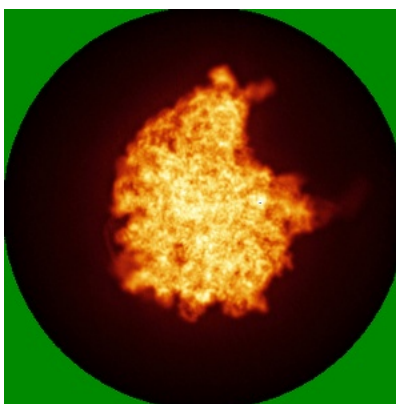


Z

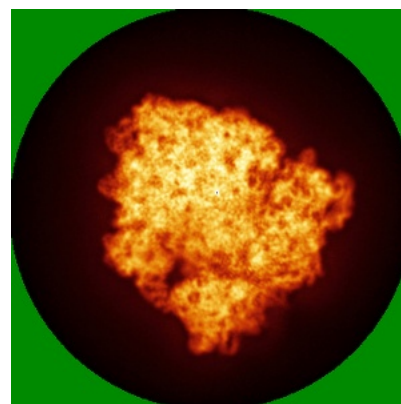
6.4.2 Raw map



X



Y

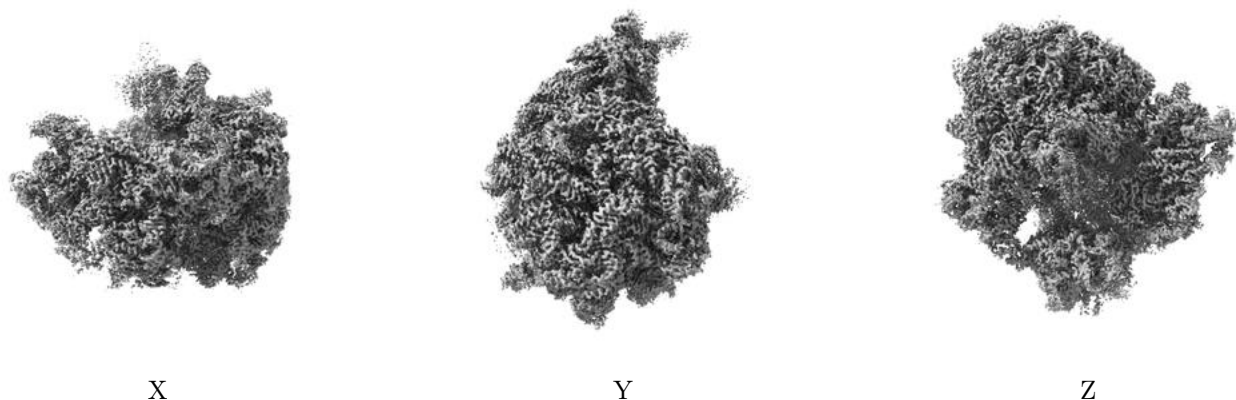


Z

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

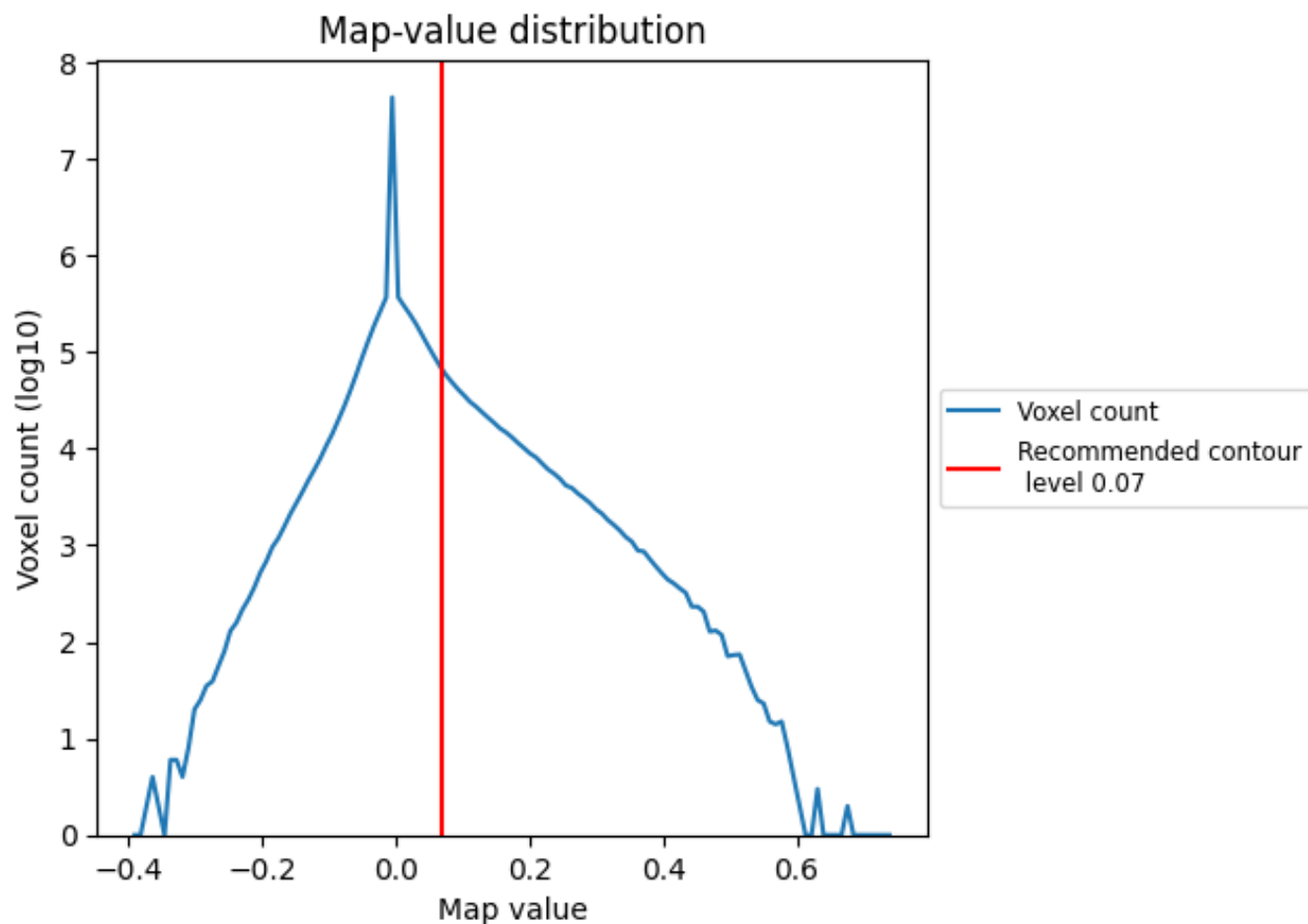
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

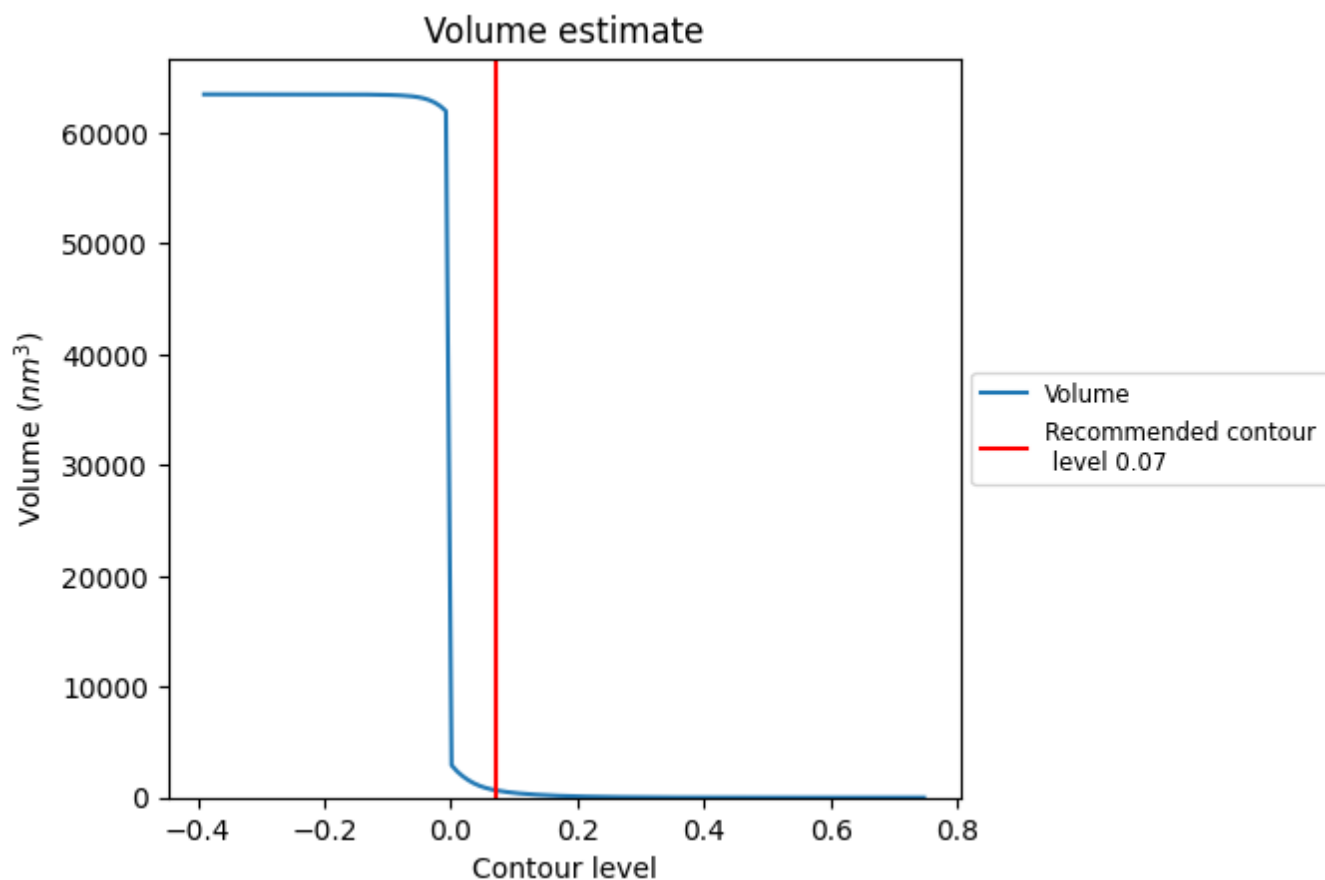
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

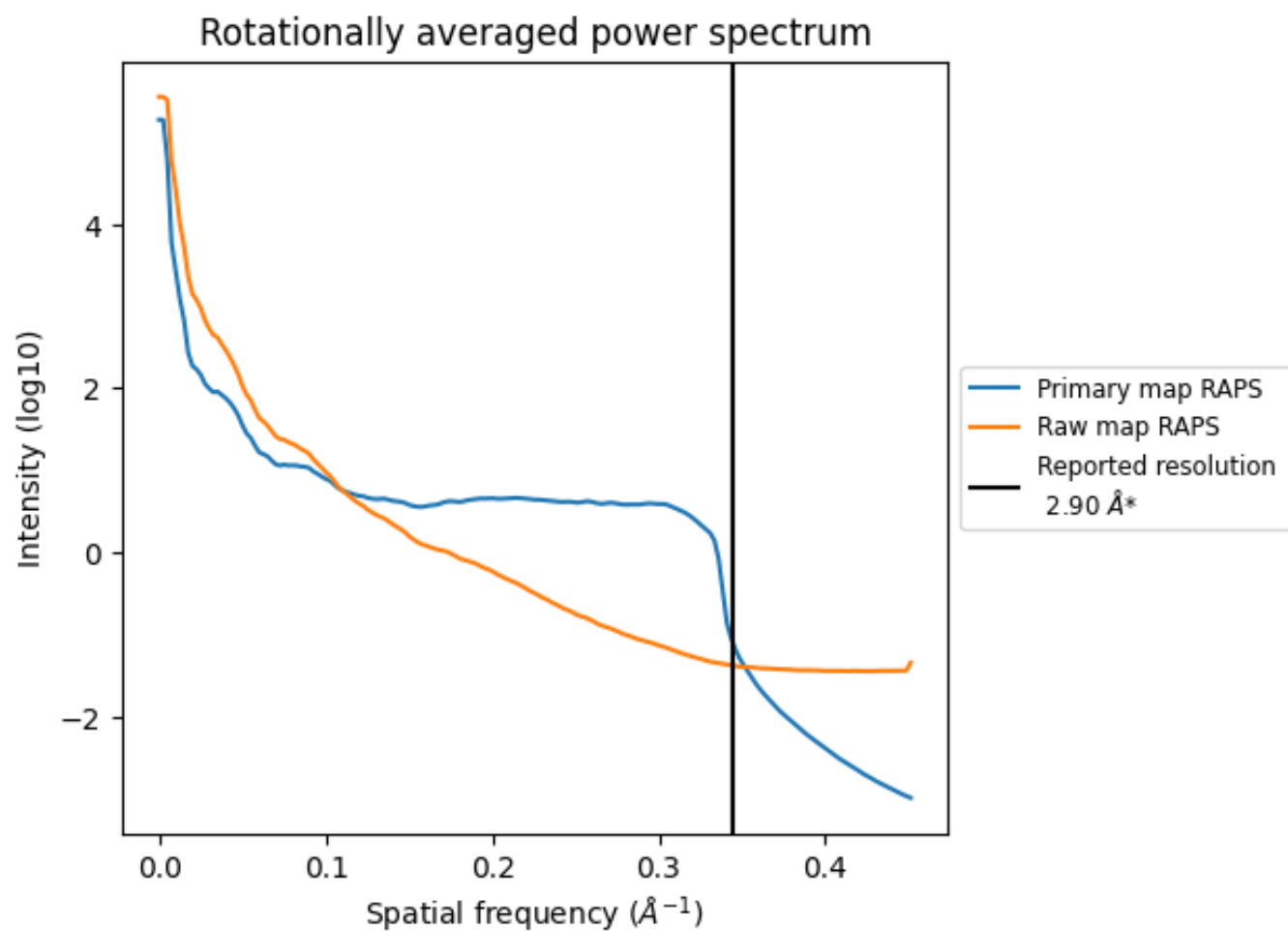
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 670 nm^3 ; this corresponds to an approximate mass of 605 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 ⓘ

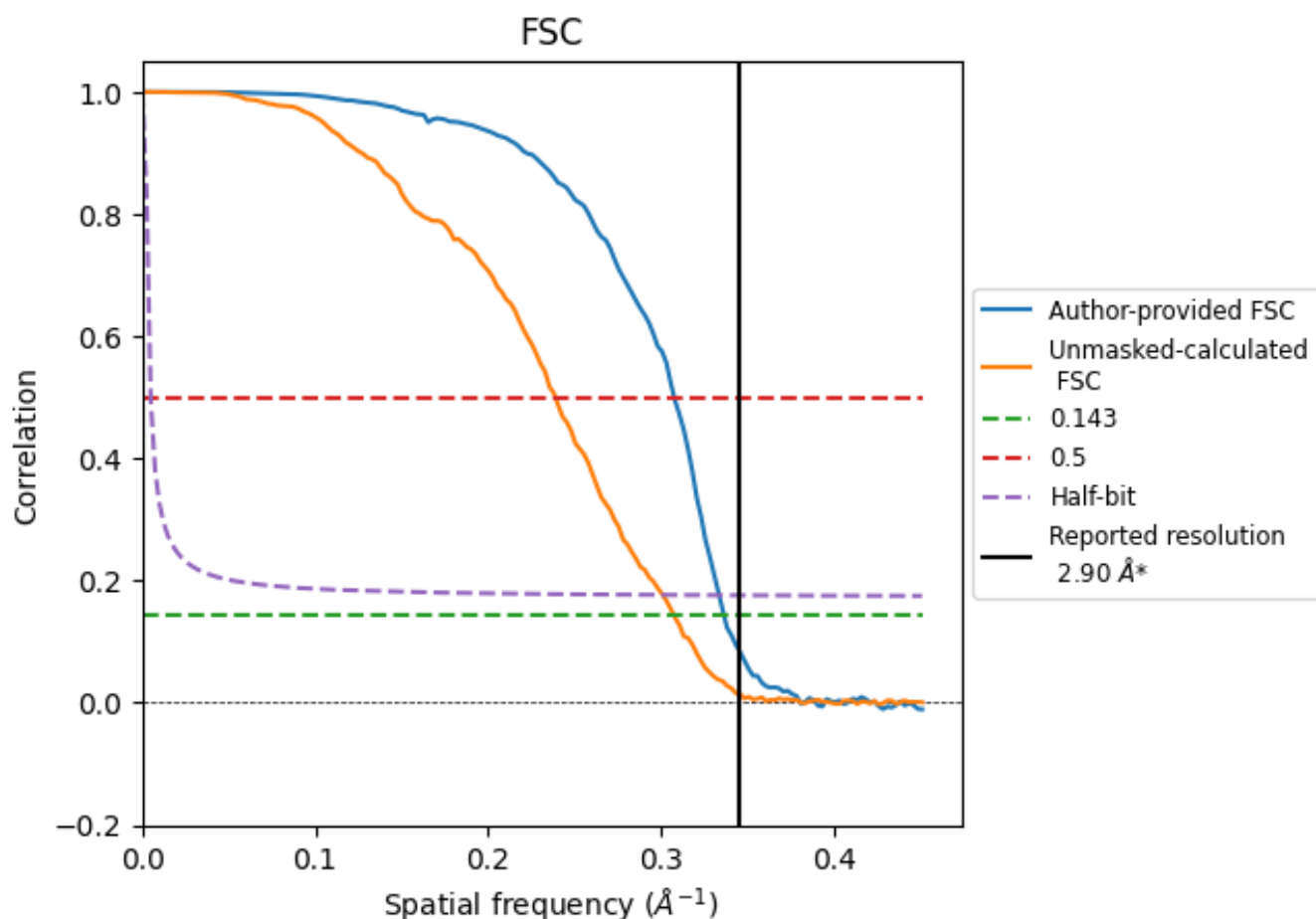


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

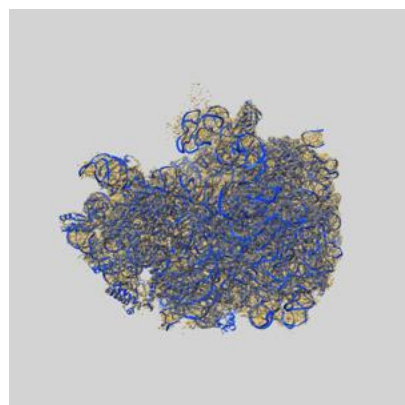
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.97	3.25	2.99
Unmasked-calculated*	3.25	4.18	3.32

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.25 differs from the reported value 2.9 by more than 10 %

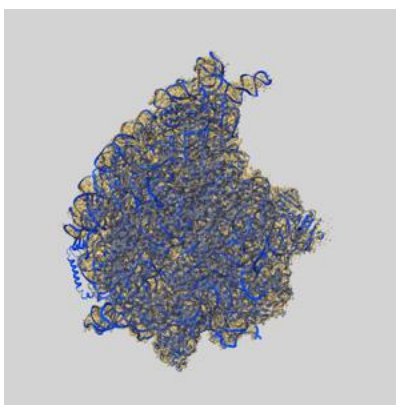
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12573 and PDB model 7NSO. Per-residue inclusion information can be found in section [3](#) on page [15](#).

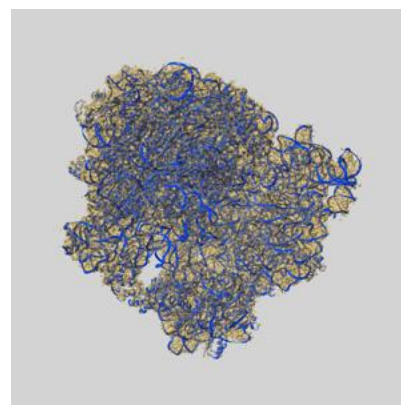
9.1 Map-model overlay [i](#)



X



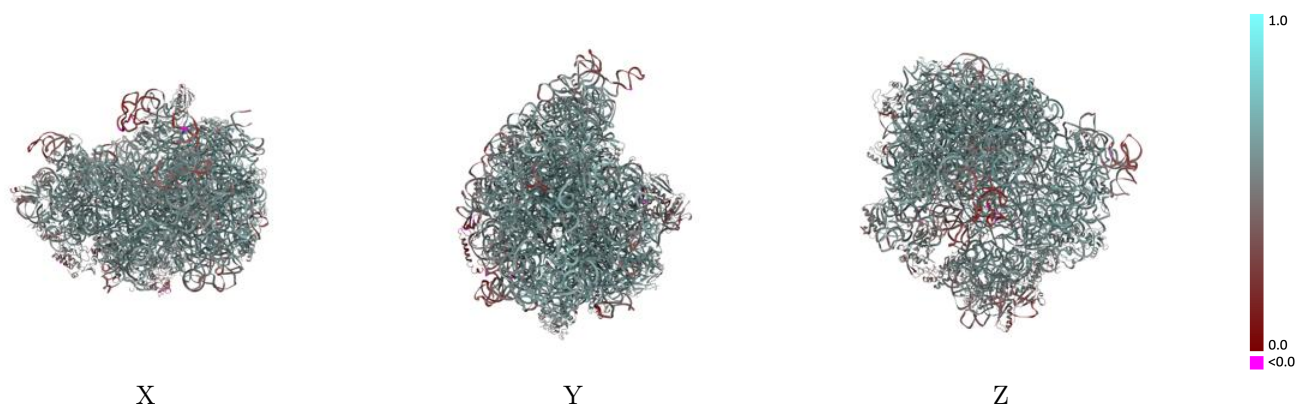
Y



Z

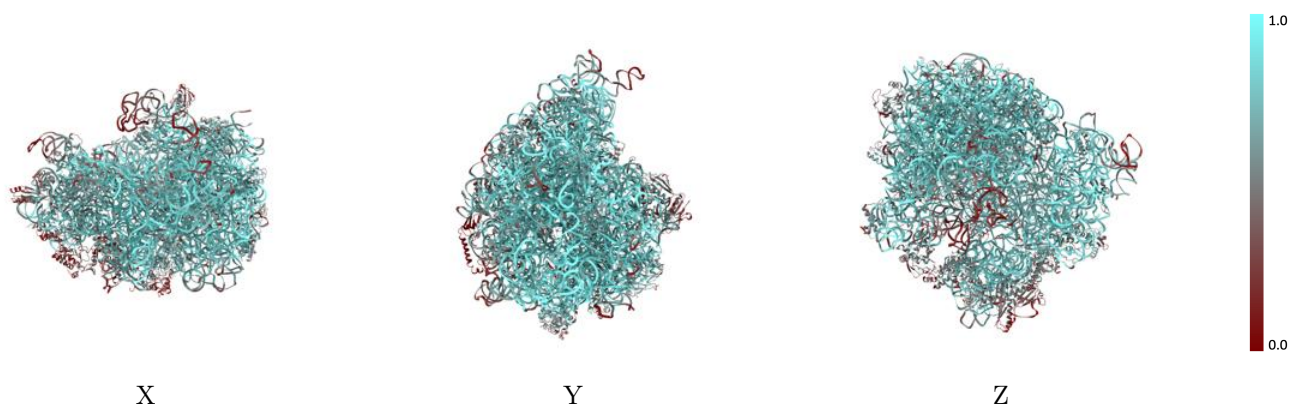
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



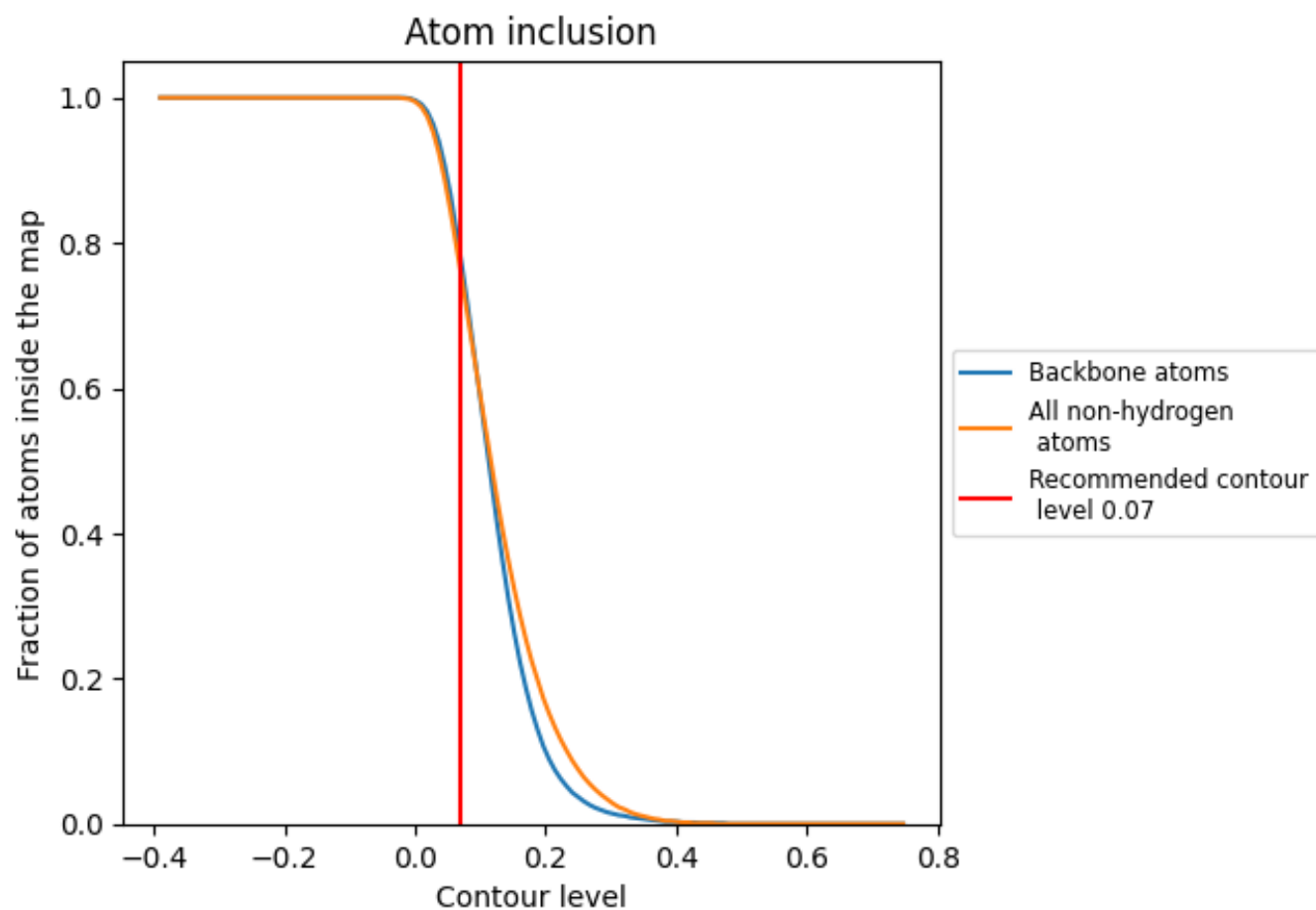
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 76% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7600	 0.5510
0	 0.7560	 0.5810
1	 0.2740	 0.4920
2	 0.8390	 0.6160
3	 0.7900	 0.6010
4	 0.7430	 0.5660
5	 0.2840	 0.4000
6	 0.9330	 0.5950
7	 0.6730	 0.5630
8	 0.5780	 0.4730
A	 0.8420	 0.5670
B	 0.7840	 0.5230
C	 0.7720	 0.5890
D	 0.7280	 0.5760
E	 0.6370	 0.5410
F	 0.5110	 0.4870
G	 0.4350	 0.4710
H	 0.0740	 0.2870
J	 0.7330	 0.5690
K	 0.6990	 0.5710
L	 0.6880	 0.5570
M	 0.7260	 0.5770
N	 0.7830	 0.5830
O	 0.5940	 0.5080
P	 0.6820	 0.5580
Q	 0.7900	 0.5880
R	 0.6600	 0.5510
S	 0.7240	 0.5720
T	 0.6310	 0.5470
U	 0.6000	 0.5270
V	 0.6150	 0.5380
W	 0.7690	 0.5980
X	 0.6970	 0.5720
Y	 0.5590	 0.5070
Z	 0.7050	 0.5680



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Chain	Atom inclusion	Q-score
a	 0.8330	 0.5610
b	 0.2850	 0.4430
c	 0.5600	 0.5190
d	 0.5790	 0.5300
e	 0.6750	 0.5540
f	 0.4850	 0.4870
g	 0.4140	 0.4680
h	 0.6490	 0.5530
i	 0.5430	 0.4930
j	 0.4520	 0.4860
k	 0.5720	 0.5220
l	 0.6940	 0.5740
m	 0.5100	 0.4930
n	 0.6090	 0.5150
o	 0.6230	 0.5310
p	 0.6430	 0.5350
q	 0.6000	 0.5390
r	 0.5920	 0.5330
s	 0.5750	 0.5200
t	 0.6380	 0.5260
u	 0.1800	 0.4310