



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 01:10 PM JST

PDB ID : 7Y7C / pdb_00007y7c
EMDB ID : EMD-33660
Title : Structure of the Bacterial Ribosome with human tRNA Asp(G34) and mRNA(GAU)
Authors : Ishiguro, K.; Yokoyama, T.; Shirouzu, M.; Suzuki, T.
Deposited on : 2022-06-22
Resolution : 2.51 Å(reported)
Based on initial model : 7K00

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
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

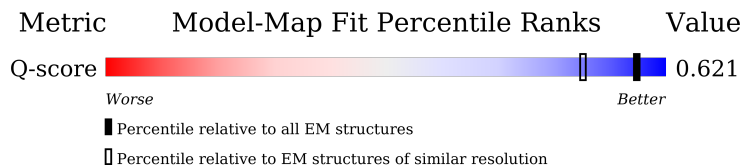
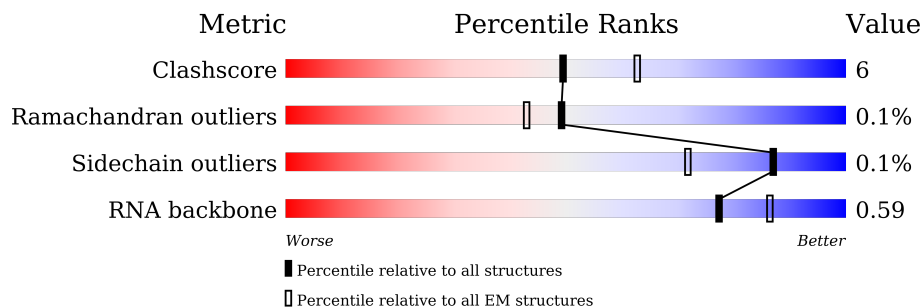
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.51 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	7159 (2.01 - 3.01)

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	1542	
2	B	241	
3	C	233	

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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	a	2904	
23	b	120	
24	c	273	
25	d	209	
26	e	201	
27	f	179	
28	g	177	

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Mol	Chain	Length	Quality of chain
29	h	149	
30	i	142	
31	j	123	
32	k	144	
33	l	136	
34	m	127	
35	n	117	
36	o	115	
37	p	118	
38	q	103	
39	r	110	
40	s	100	
41	t	104	
42	u	94	
43	v	85	
44	w	78	
45	x	63	
46	y	59	
47	z	57	
48	0	55	
49	1	46	
50	2	65	
51	3	38	
52	4	70	
53	X	35	

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Mol	Chain	Length	Quality of chain
54	Z	77	36% 71% 19% 8%
55	V	75	33% 59% 29% 9%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 141933 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1520	Total	C	N	O	P	0	0
			32634	14562	5991	10561	1520		

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

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

- Molecule 32 is a protein called 50S ribosomal protein L15.

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

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

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

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

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

- Molecule 41 is a protein called 50S ribosomal protein L24.

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

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	84	Total	C	N	O	S	0	0
			628	388	126	113	1		

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	X	13	Total	C	N	O	P	0	0
			279	125	52	89	13		

- Molecule 54 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Z	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

- Molecule 55 is a RNA chain called A-site tRNA-Asp.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	V	75	Total	C	N	O	P		0	0
			1603	719	283	527	74			

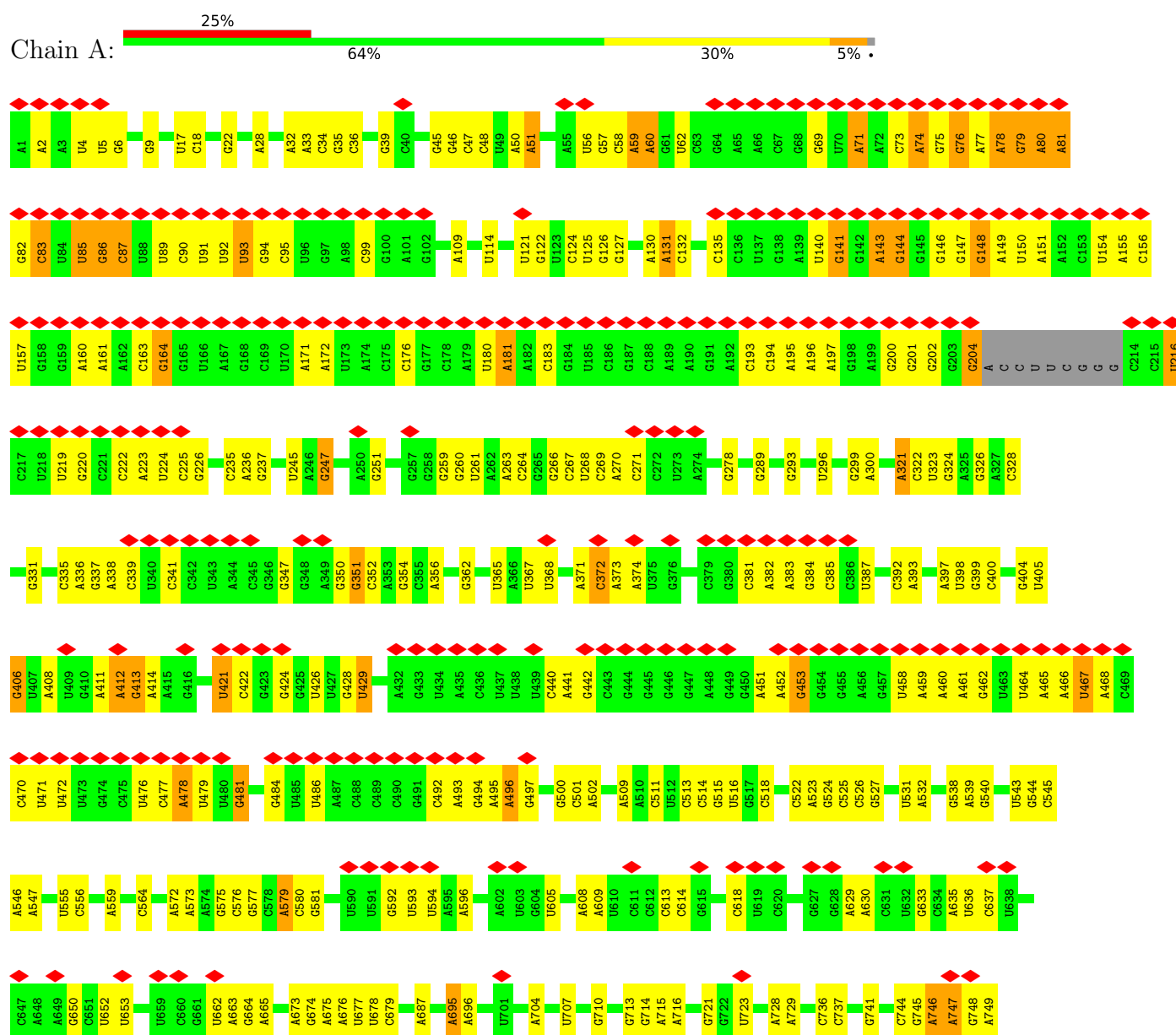
- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

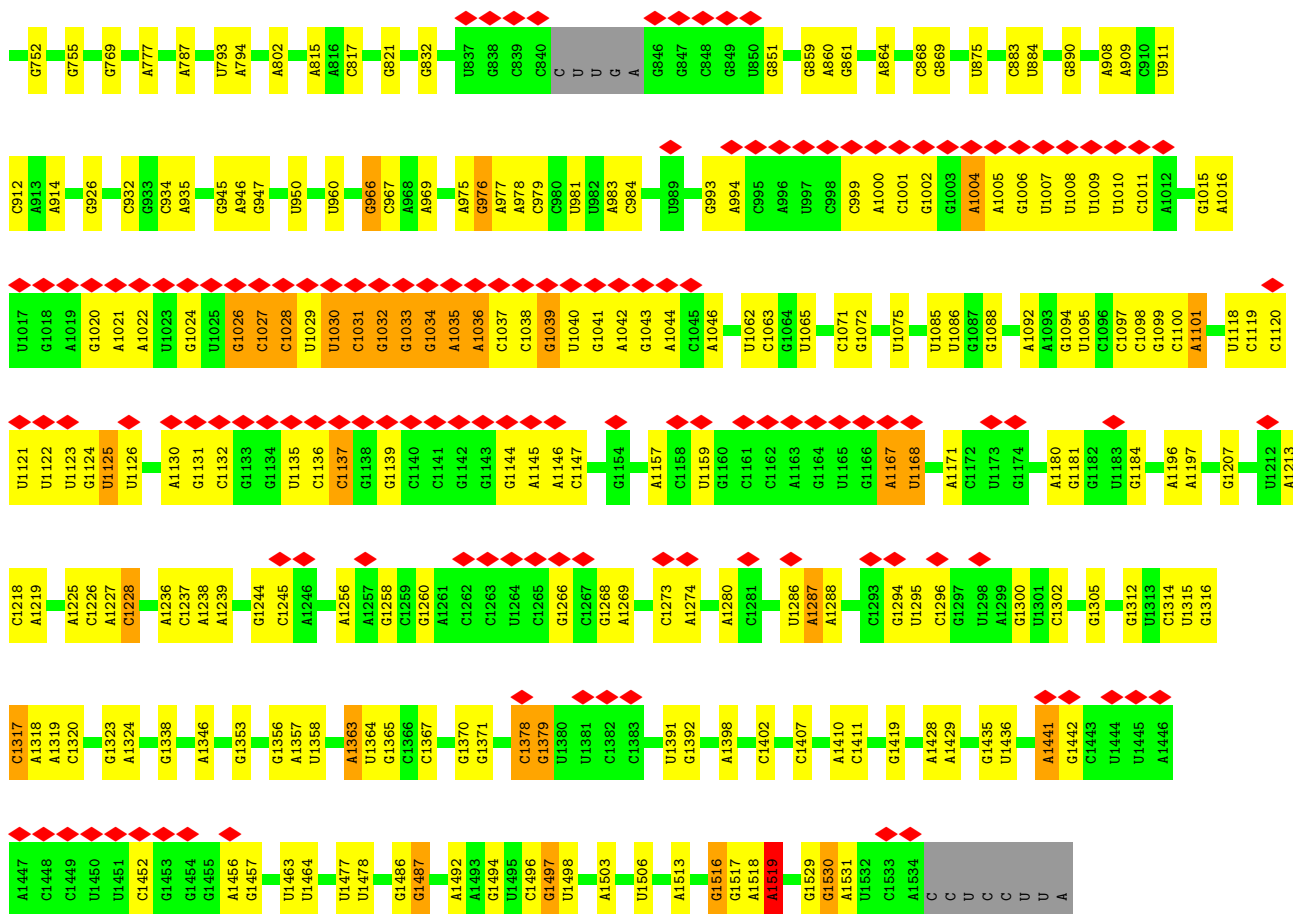
Mol	Chain	Residues	Atoms		AltConf
56	A	73	Total	Mg	0
			73	73	
56	a	200	Total	Mg	0
			200	200	
56	b	3	Total	Mg	0
			3	3	
56	d	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	
56	Z	3	Total	Mg	0
			3	3	
56	V	2	Total	Mg	0
			2	2	

3 Residue-property plots

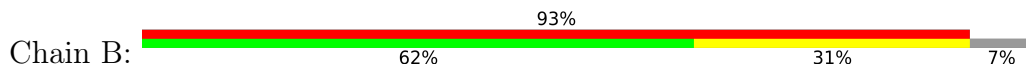
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

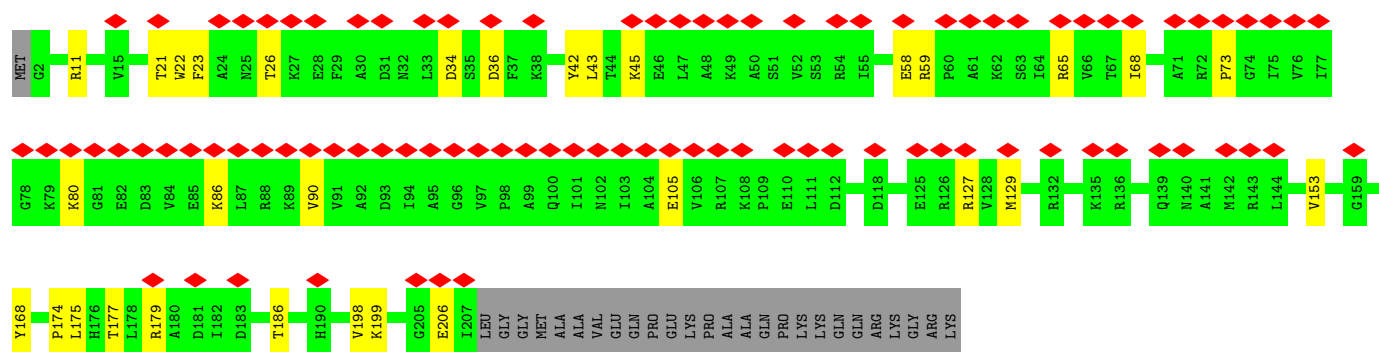
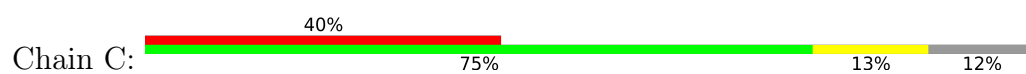




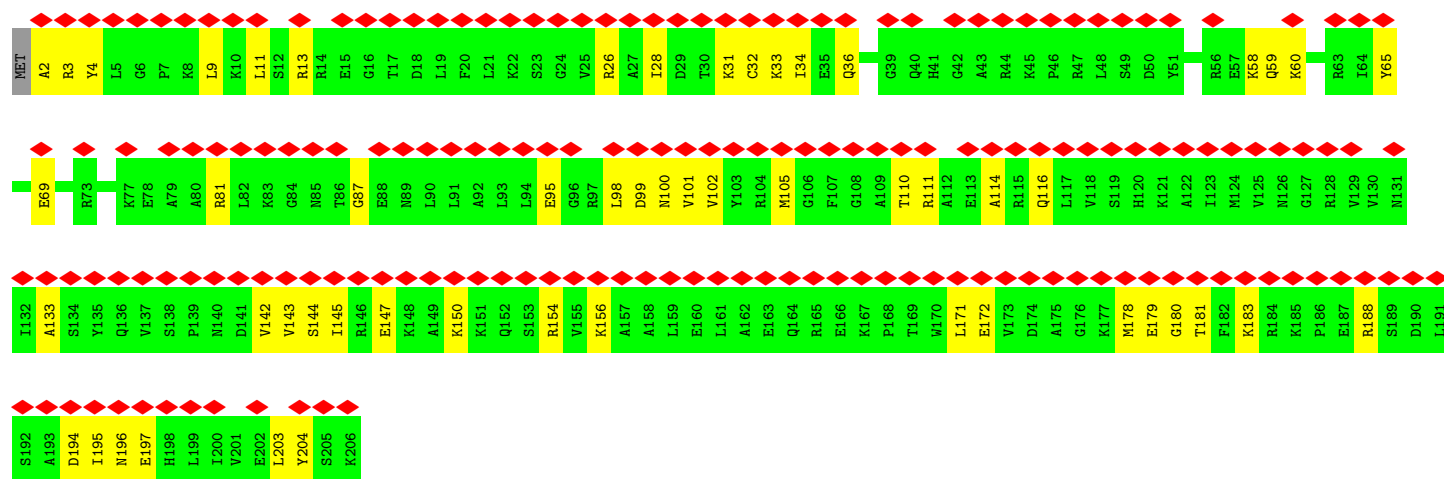
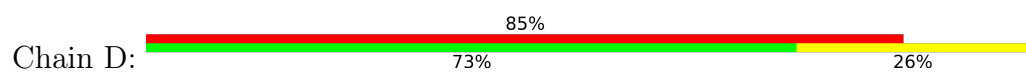
• Molecule 2: 30S ribosomal protein S2



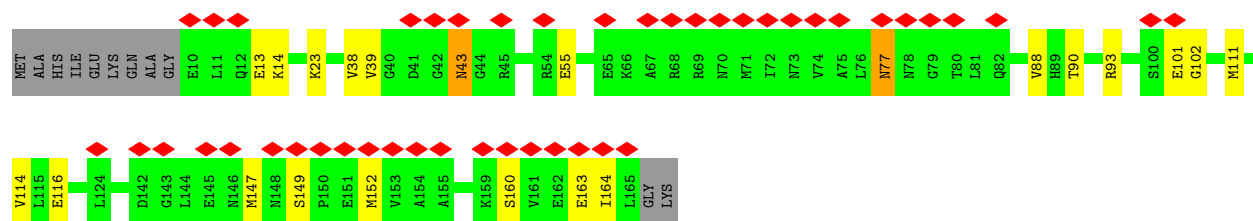
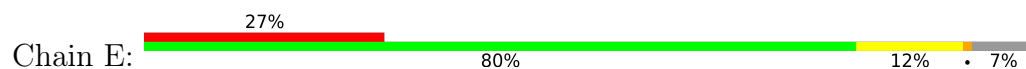
• Molecule 3: 30S ribosomal protein S3



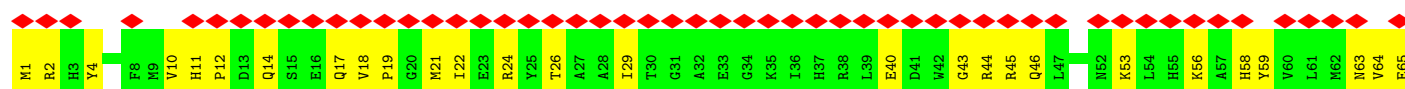
• Molecule 4: 30S ribosomal protein S4

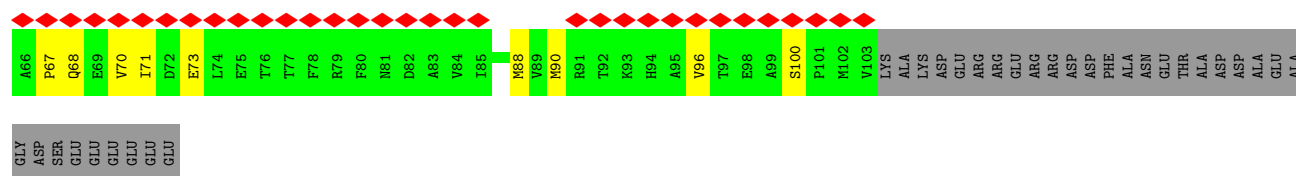


• Molecule 5: 30S ribosomal protein S5

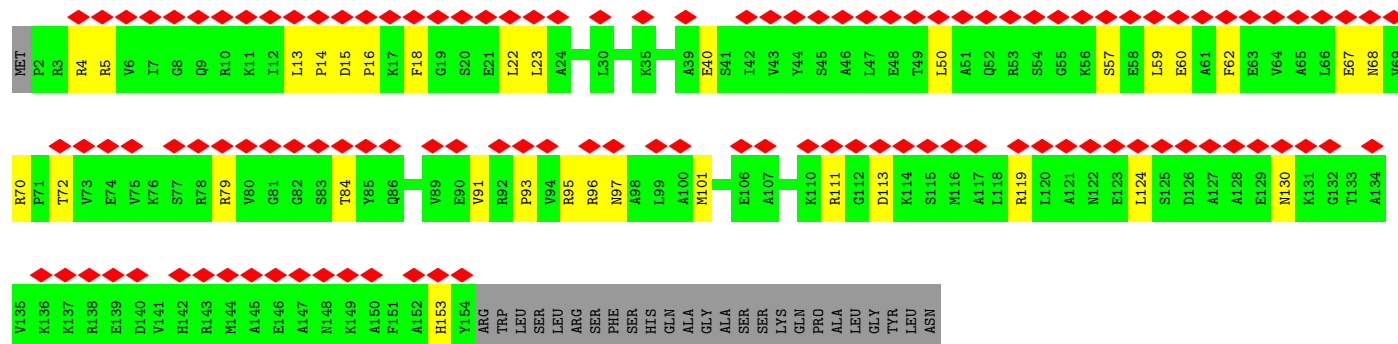


• Molecule 6: 30S ribosomal protein S6, fully modified isoform

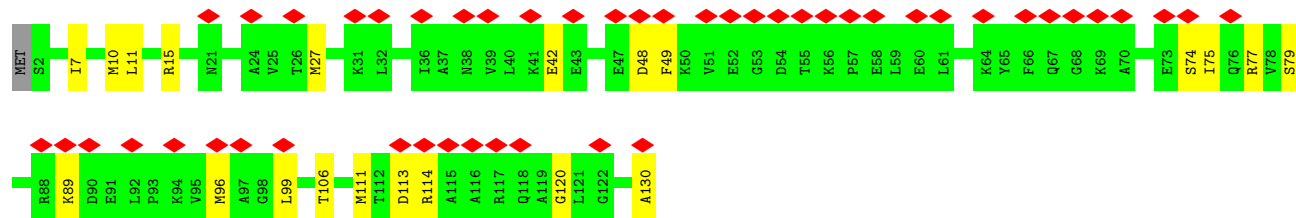
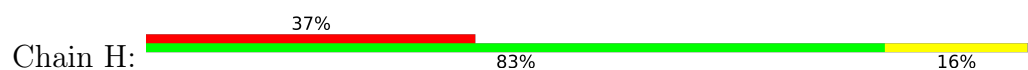




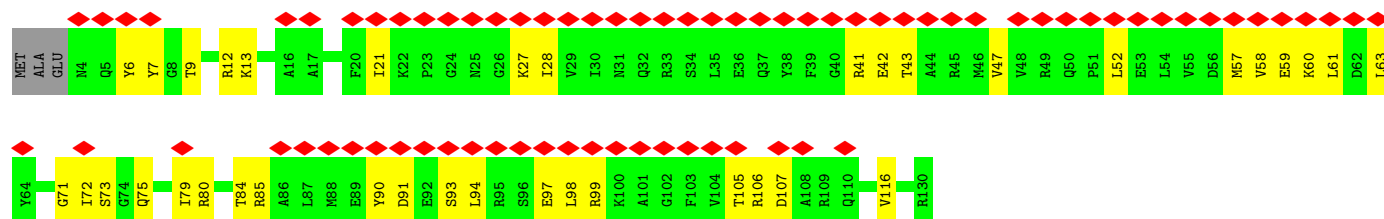
• Molecule 7: 30S ribosomal protein S7



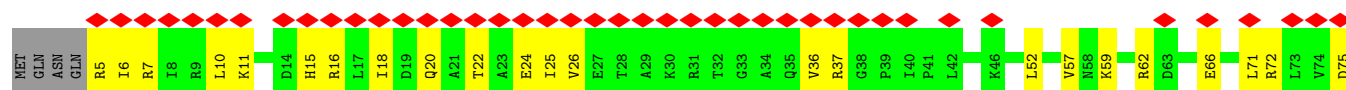
• Molecule 8: 30S ribosomal protein S8

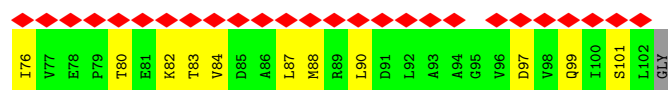


• Molecule 9: 30S ribosomal protein S9

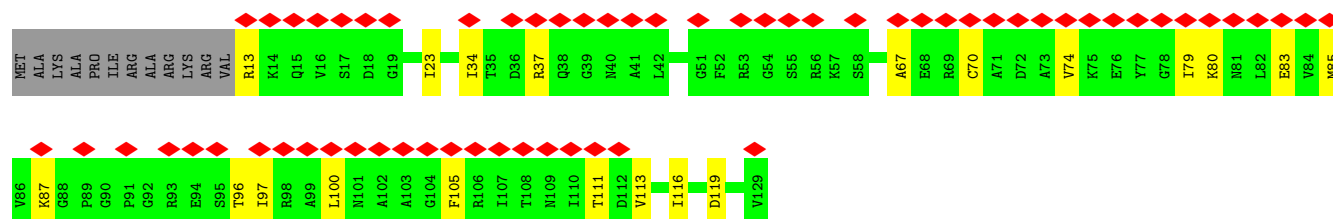
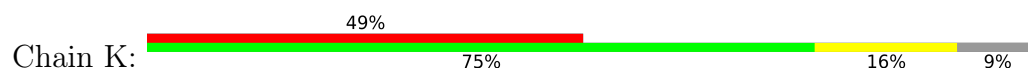


• Molecule 10: 30S ribosomal protein S10

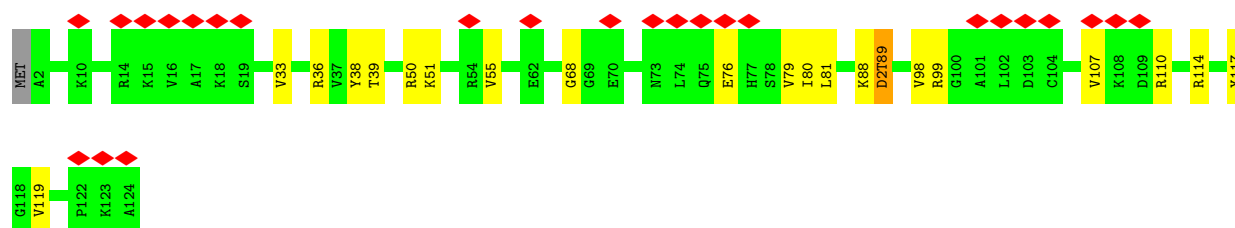
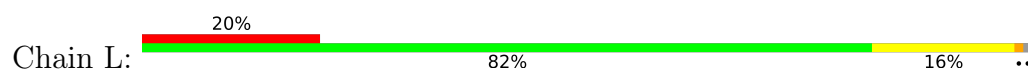




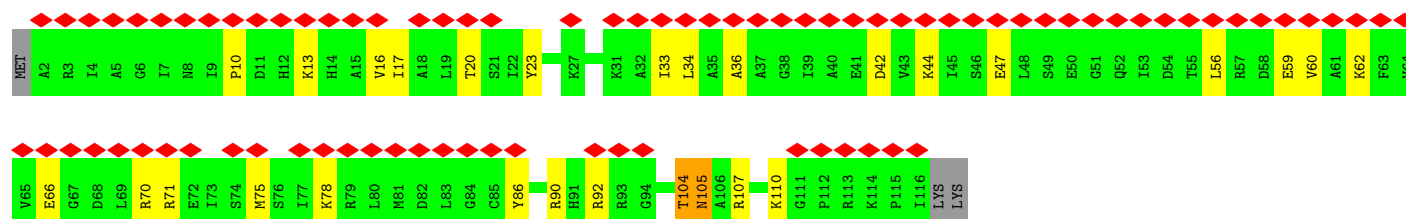
- Molecule 11: 30S ribosomal protein S11



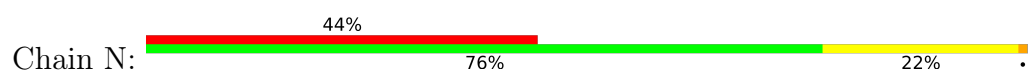
- Molecule 12: 30S ribosomal protein S12



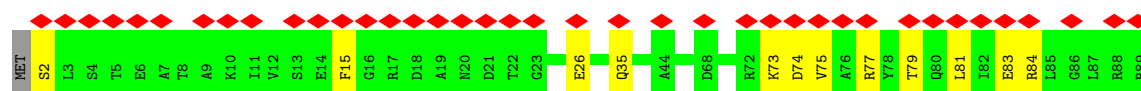
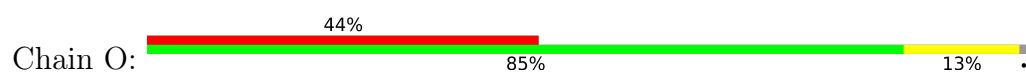
- Molecule 13: 30S ribosomal protein S13



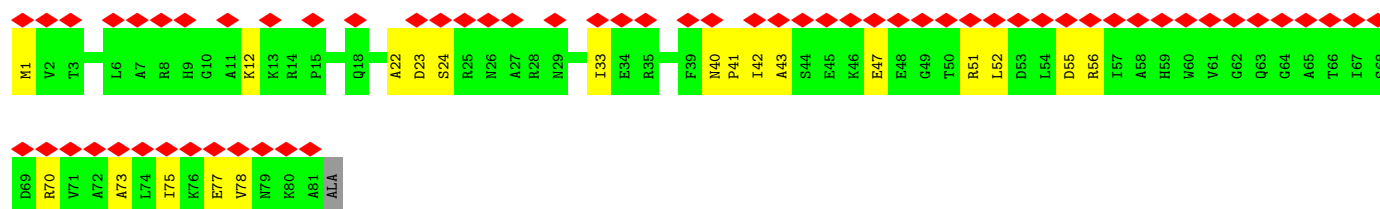
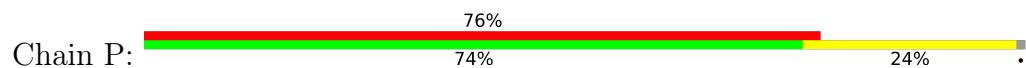
- Molecule 14: 30S ribosomal protein S14



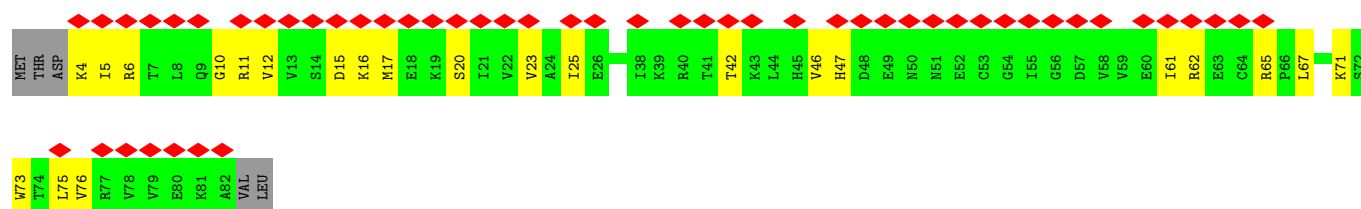
- Molecule 15: 30S ribosomal protein S15



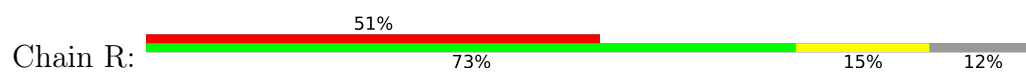
• Molecule 16: 30S ribosomal protein S16



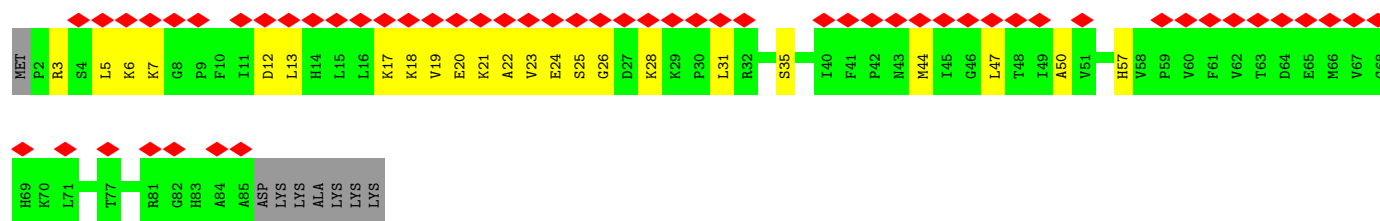
• Molecule 17: 30S ribosomal protein S17



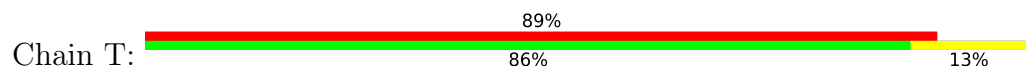
• Molecule 18: 30S ribosomal protein S18

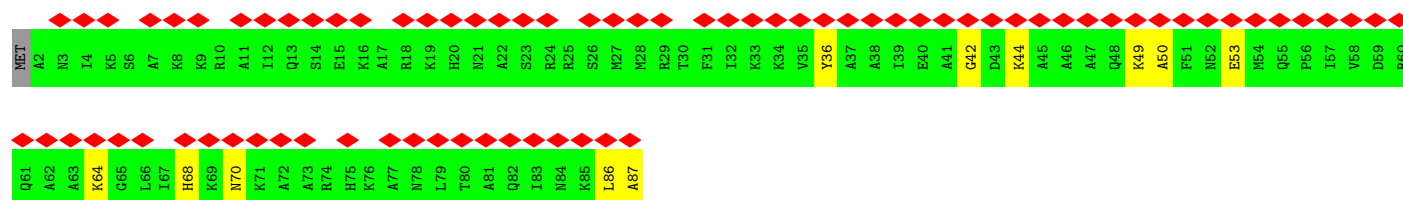


• Molecule 19: 30S ribosomal protein S19

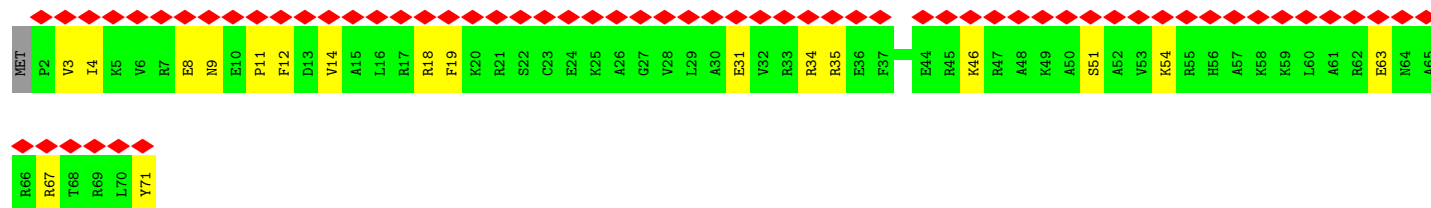
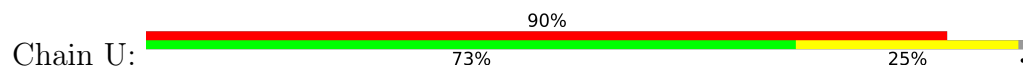


• Molecule 20: 30S ribosomal protein S20

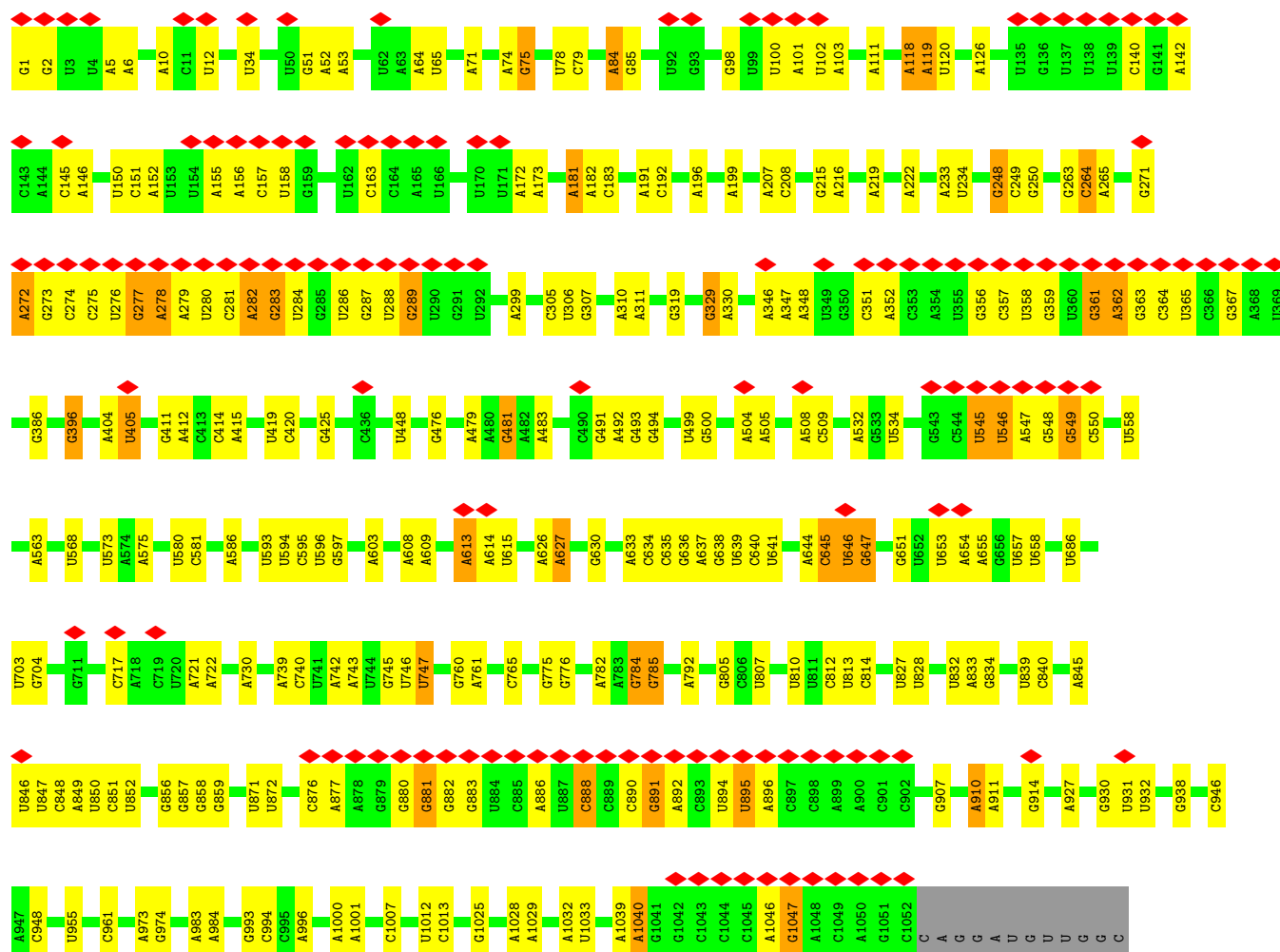




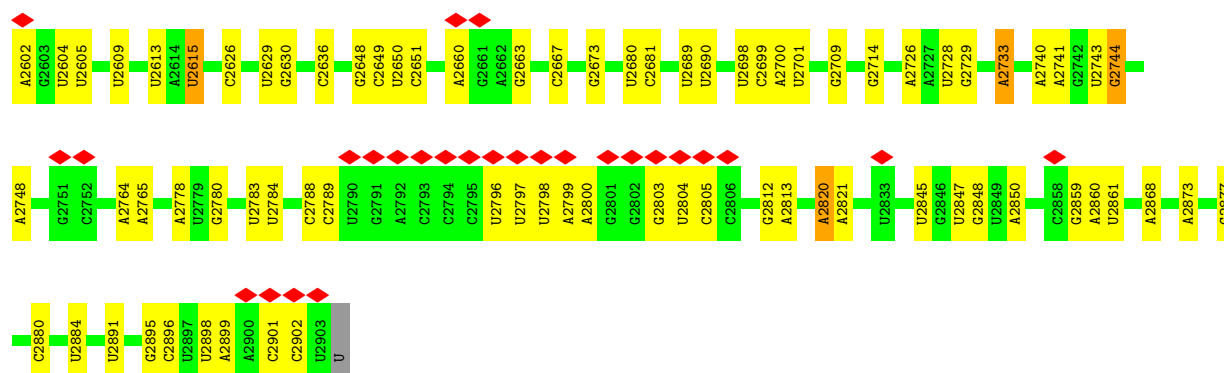
• Molecule 21: 30S ribosomal protein S21



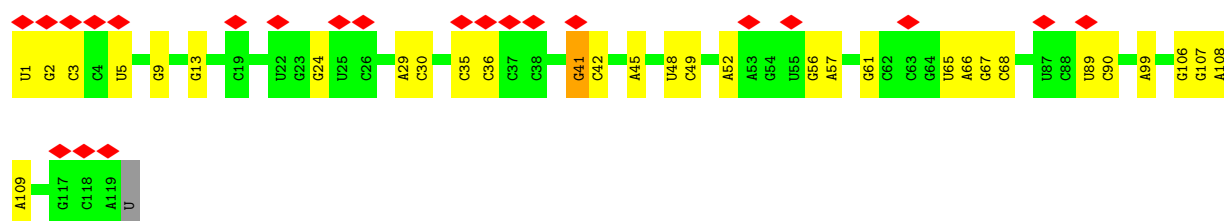
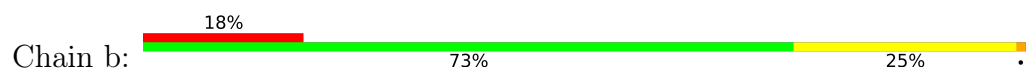
• Molecule 22: 23S rRNA



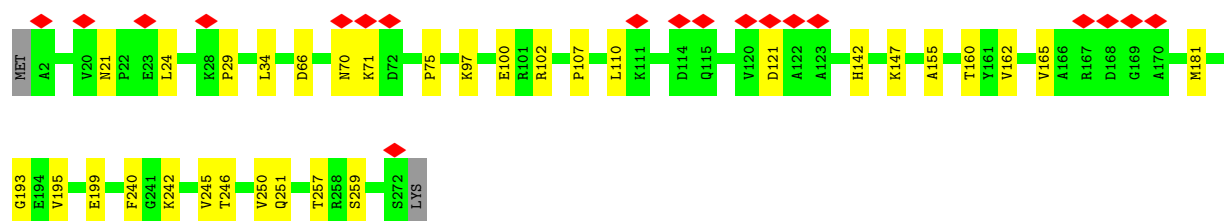
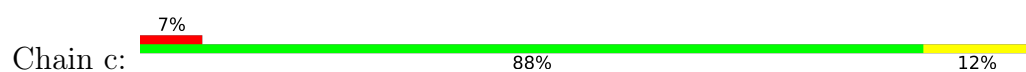




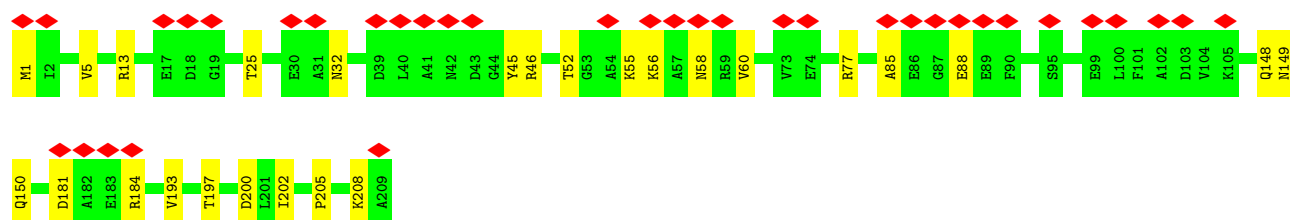
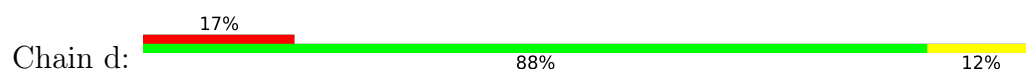
• Molecule 23: 5S rRNA



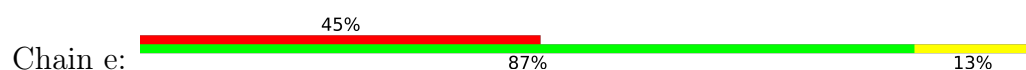
• Molecule 24: 50S ribosomal protein L2

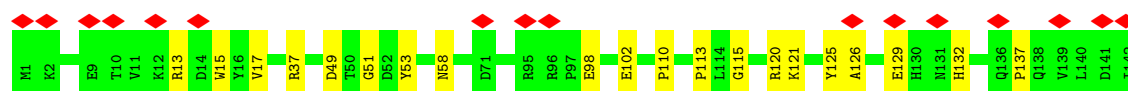
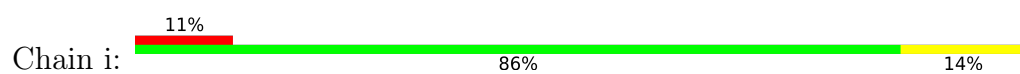


• Molecule 25: 50S ribosomal protein L3

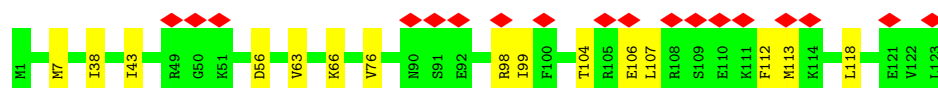
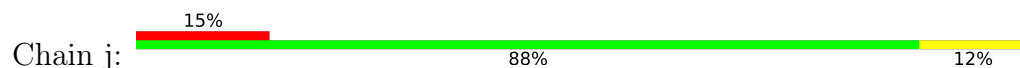


• Molecule 26: 50S ribosomal protein L4

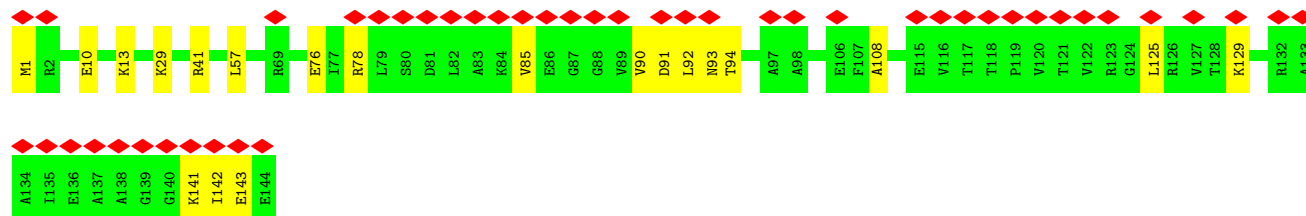
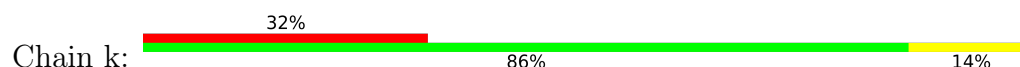




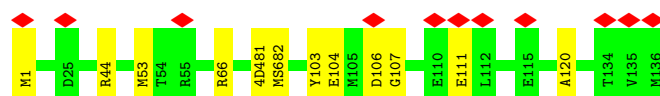
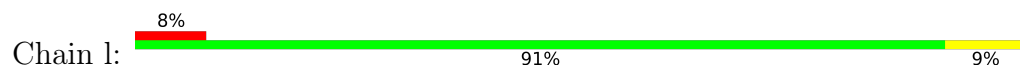
- Molecule 31: 50S ribosomal protein L14



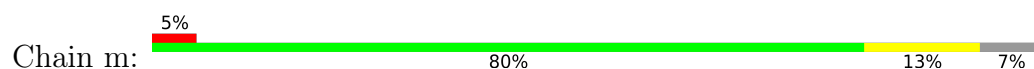
- Molecule 32: 50S ribosomal protein L15



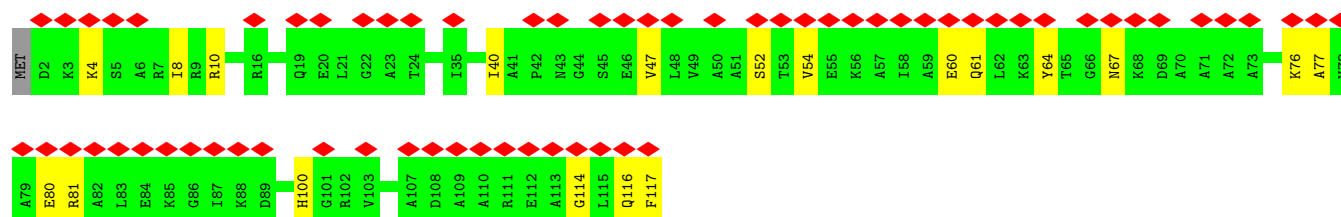
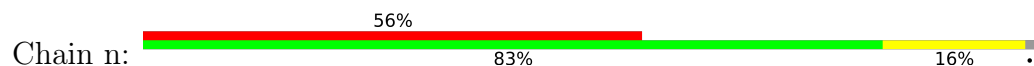
- Molecule 33: 50S ribosomal protein L16



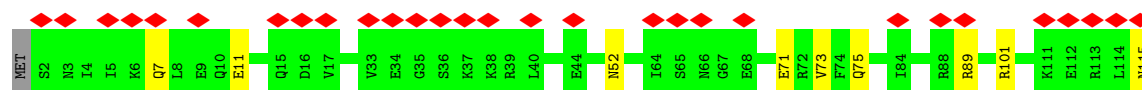
- Molecule 34: 50S ribosomal protein L17



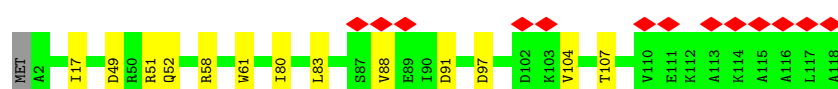
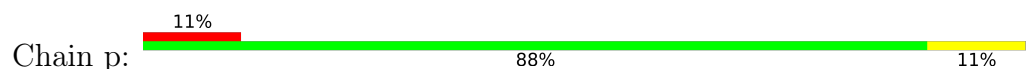
- Molecule 35: 50S ribosomal protein L18



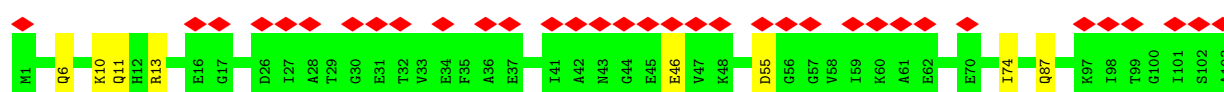
- Molecule 36: 50S ribosomal protein L19



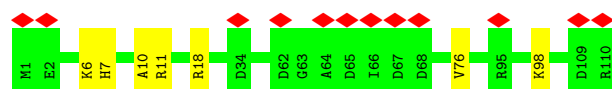
- Molecule 37: 50S ribosomal protein L20



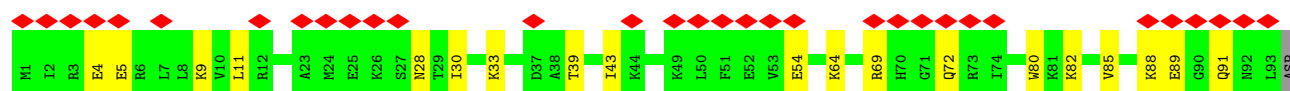
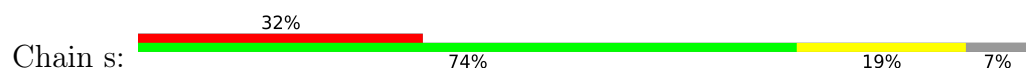
- Molecule 38: 50S ribosomal protein L21



- Molecule 39: 50S ribosomal protein L22

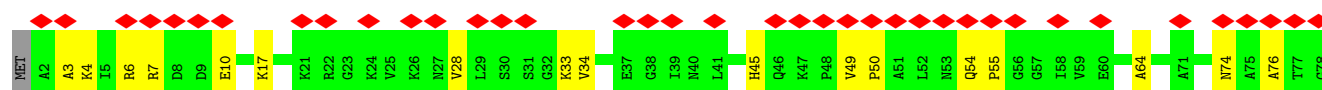


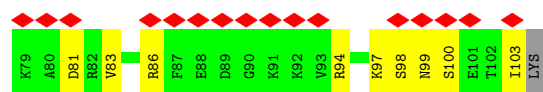
- Molecule 40: 50S ribosomal protein L23



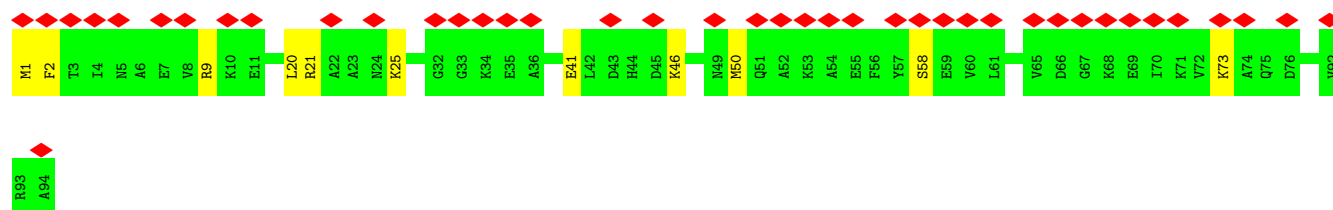
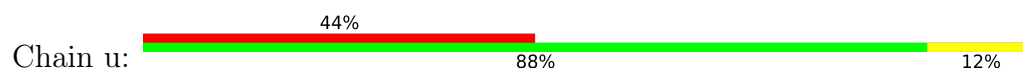
PHE
VAL
GLY
GLY
ALA
GLU

- Molecule 41: 50S ribosomal protein L24

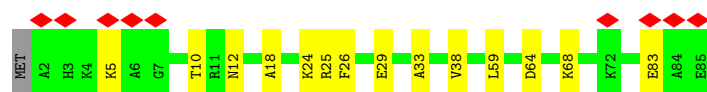
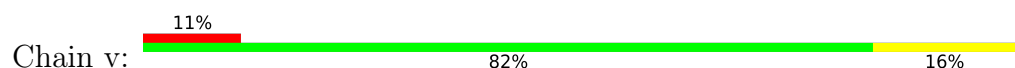




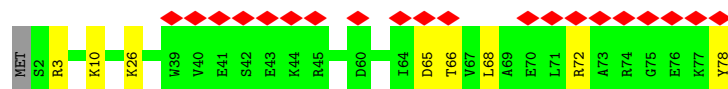
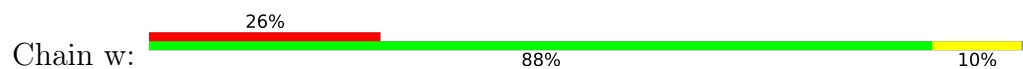
- Molecule 42: 50S ribosomal protein L25



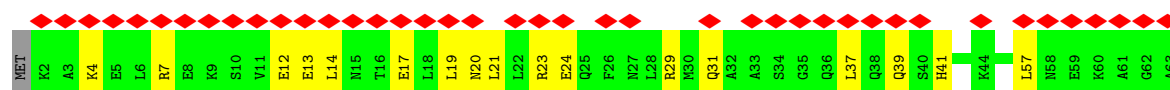
- Molecule 43: 50S ribosomal protein L27



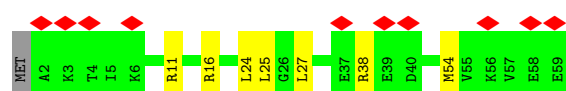
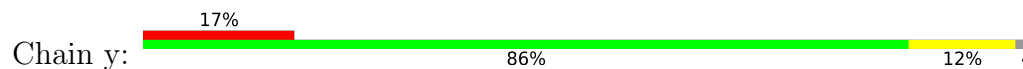
- Molecule 44: 50S ribosomal protein L28



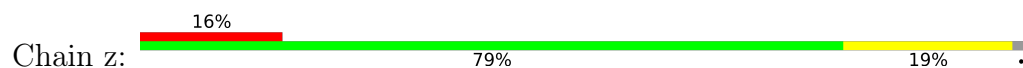
- Molecule 45: 50S ribosomal protein L29



- Molecule 46: 50S ribosomal protein L30

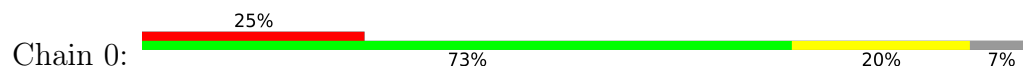


- Molecule 47: 50S ribosomal protein L32

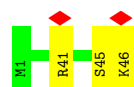




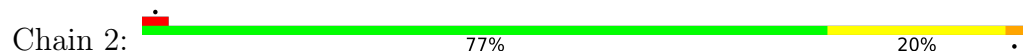
- Molecule 48: 50S ribosomal protein L33



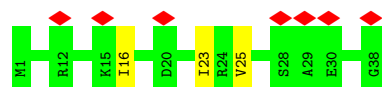
- Molecule 49: 50S ribosomal protein L34



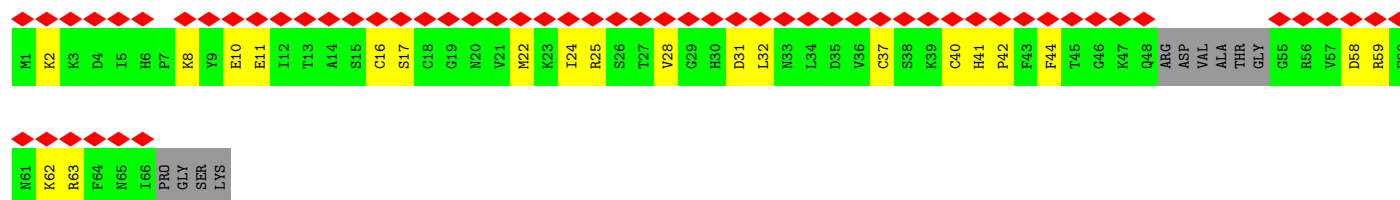
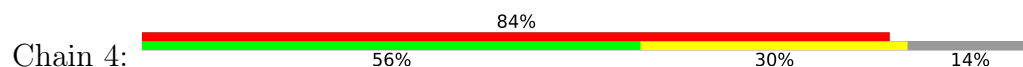
- Molecule 50: 50S ribosomal protein L35



- Molecule 51: 50S ribosomal protein L36

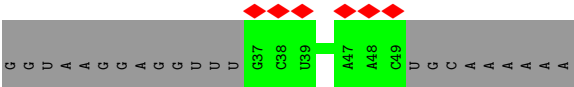


- Molecule 52: 50S ribosomal protein L31

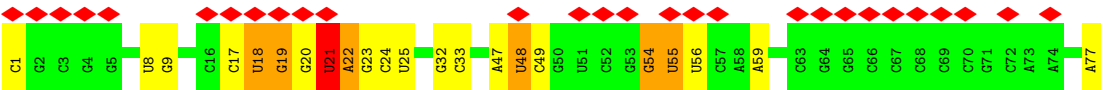


- Molecule 53: mRNA





• Molecule 54: P-site tRNA-fMet



• Molecule 55: A-site tRNA-Asp



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	400281	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.285	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	439.10498, 439.10498, 439.10498	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8285, 0.8285, 0.8285	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4OC, MA6, OMU, MG, H2U, UR3, 2MG, 6MZ, 1MG, PSU, 1MA, G7M, D2T, 4SU, OMG, 3TD, IAS, 5MU, 4D4, 2MA, MEQ, MS6, 5MC, OMC

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	0.52	0/36261	0.33	0/56559
2	B	0.18	0/1784	0.46	0/2403
3	C	0.43	0/1651	0.46	0/2225
4	D	0.33	0/1665	0.41	0/2227
5	E	0.46	0/1165	0.46	0/1568
6	F	0.37	0/858	0.43	0/1160
7	G	0.36	0/1219	0.47	0/1635
8	H	0.43	0/989	0.42	0/1326
9	I	0.41	0/1034	0.49	0/1375
10	J	0.41	0/796	0.49	0/1077
11	K	0.41	0/884	0.45	0/1191
12	L	0.48	0/960	0.47	0/1286
13	M	0.39	0/900	0.54	0/1204
14	N	0.43	0/817	0.54	0/1088
15	O	0.42	0/722	0.50	0/964
16	P	0.35	0/653	0.47	0/877
17	Q	0.41	0/650	0.47	0/871
18	R	0.43	0/553	0.42	0/742
19	S	0.38	0/685	0.46	0/922
20	T	0.37	0/676	0.49	0/895
21	U	0.28	0/597	0.46	0/792
22	a	0.64	0/65651	0.36	0/102413
23	b	0.48	0/2850	0.29	0/4444
24	c	0.57	0/2121	0.46	0/2852
25	d	0.55	0/1576	0.45	0/2119
26	e	0.46	0/1571	0.45	0/2113
27	f	0.40	0/1434	0.50	0/1926
28	g	0.35	0/1343	0.50	0/1816
29	h	0.24	0/306	0.54	0/413
30	i	0.53	0/1152	0.46	0/1551
31	j	0.54	0/955	0.47	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	k	0.53	0/1062	0.50	0/1413
33	l	0.54	0/1073	0.43	0/1433
34	m	0.56	0/958	0.55	0/1281
35	n	0.39	0/902	0.47	0/1209
36	o	0.49	0/929	0.43	0/1242
37	p	0.60	0/960	0.46	0/1278
38	q	0.53	0/829	0.49	0/1107
39	r	0.56	0/864	0.45	0/1156
40	s	0.46	0/744	0.53	0/994
41	t	0.45	0/787	0.57	0/1051
42	u	0.43	0/766	0.44	0/1025
43	v	0.52	0/636	0.44	0/841
44	w	0.52	0/635	0.46	0/848
45	x	0.40	0/502	0.53	0/667
46	y	0.50	0/453	0.47	0/605
47	z	0.54	0/450	0.46	0/599
48	0	0.50	0/424	0.46	0/565
49	1	0.62	0/380	0.49	0/498
50	2	0.57	0/513	0.50	0/676
51	3	0.53	0/303	0.49	0/397
52	4	0.29	0/488	0.47	0/649
53	X	0.50	0/312	0.30	0/484
54	Z	0.47	0/1725	0.33	0/2687
55	V	0.44	0/1552	0.36	0/2420
All	All	0.55	0/152725	0.38	0/228438

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
13	M	0	1
28	g	0	1
50	2	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	2	31	HIS	Peptide
13	M	104	THR	Peptide
28	g	47	ASP	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	32634	0	16443	318	0
2	B	1753	0	1780	49	0
3	C	1624	0	1696	23	0
4	D	1643	0	1707	42	0
5	E	1152	0	1196	18	0
6	F	839	0	833	29	0
7	G	1203	0	1254	24	0
8	H	979	0	1031	16	0
9	I	1022	0	1070	30	0
10	J	786	0	828	25	0
11	K	877	0	883	16	0
12	L	957	0	1017	17	0
13	M	891	0	952	23	0
14	N	805	0	844	21	0
15	O	714	0	734	8	0
16	P	643	0	661	13	0
17	Q	641	0	682	18	0
18	R	544	0	565	8	0
19	S	668	0	693	16	0
20	T	670	0	719	7	0
21	U	589	0	629	12	0
22	a	59130	0	29766	357	0
23	b	2549	0	1291	17	0
24	c	2082	0	2154	23	0
25	d	1566	0	1618	17	0
26	e	1552	0	1619	17	0
27	f	1410	0	1444	33	0
28	g	1323	0	1371	29	0
29	h	303	0	327	6	0
30	i	1129	0	1162	16	0
31	j	946	0	1023	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	k	1053	0	1129	19	0
33	l	1075	0	1144	7	0
34	m	945	0	989	10	0
35	n	892	0	923	12	0
36	o	917	0	962	7	0
37	p	947	0	1019	11	0
38	q	816	0	839	6	0
39	r	857	0	922	6	0
40	s	738	0	807	20	0
41	t	779	0	831	17	0
42	u	753	0	780	6	0
43	v	628	0	642	9	0
44	w	625	0	652	6	0
45	x	501	0	531	13	0
46	y	449	0	488	6	0
47	z	444	0	458	8	0
48	0	417	0	451	10	0
49	1	377	0	418	3	0
50	2	504	0	572	9	0
51	3	302	0	343	2	0
52	4	480	0	482	21	0
53	X	279	0	141	0	0
54	Z	1645	0	842	11	0
55	V	1603	0	824	15	0
56	A	73	0	0	0	0
56	V	2	0	0	0	0
56	Z	3	0	0	0	0
56	a	200	0	0	0	0
56	b	3	0	0	0	0
56	d	1	0	0	0	0
56	z	1	0	0	0	0
All	All	141933	0	95181	1342	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 6.

The worst 5 of 1342 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)
40:s:69:ARG:HH12	40:s:72:GLN:H	1.09	0.96
22:a:2304:G:H22	22:a:2312:U:H3	1.16	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:n:76:LYS:NZ	35:n:80:GLU:OE1	2.07	0.86
4:D:100:ASN:OD1	4:D:111:ARG:NH1	2.08	0.85
40:s:69:ARG:HH12	40:s:72:GLN:N	1.73	0.85

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	
2	B	222/241 (92%)	207 (93%)	15 (7%)	0	100	100
3	C	204/233 (88%)	192 (94%)	12 (6%)	0	100	100
4	D	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
5	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
6	F	101/135 (75%)	94 (93%)	7 (7%)	0	100	100
7	G	151/179 (84%)	145 (96%)	6 (4%)	0	100	100
8	H	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
9	I	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
10	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	24
11	K	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
12	L	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
13	M	113/118 (96%)	108 (96%)	4 (4%)	1 (1%)	14	27
14	N	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
15	O	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	P	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
17	Q	77/84 (92%)	76 (99%)	1 (1%)	0	100	100
18	R	64/75 (85%)	61 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	82/92 (89%)	80 (98%)	2 (2%)	0	100	100
20	T	84/87 (97%)	84 (100%)	0	0	100	100
21	U	68/71 (96%)	68 (100%)	0	0	100	100
24	c	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
25	d	206/209 (99%)	199 (97%)	6 (3%)	1 (0%)	24	43
26	e	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
27	f	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
28	g	174/177 (98%)	161 (92%)	11 (6%)	2 (1%)	11	22
29	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
30	i	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
31	j	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
32	k	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
33	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
34	m	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
35	n	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
36	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
37	p	115/118 (98%)	115 (100%)	0	0	100	100
38	q	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
39	r	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
40	s	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
41	t	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
42	u	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
43	v	82/85 (96%)	79 (96%)	3 (4%)	0	100	100
44	w	75/78 (96%)	75 (100%)	0	0	100	100
45	x	60/63 (95%)	54 (90%)	6 (10%)	0	100	100
46	y	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
47	z	54/57 (95%)	54 (100%)	0	0	100	100
48	0	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	14
51	3	36/38 (95%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	4	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
All	All	5487/5913 (93%)	5278 (96%)	203 (4%)	6 (0%)	49	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	57	VAL
25	d	149	ASN
50	2	32	ILE
13	M	105	ASN
28	g	47	ASP

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	
2	B	186/199 (94%)	186 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	171 (99%)	1 (1%)	78	91
5	E	119/126 (94%)	117 (98%)	2 (2%)	53	78
6	F	90/116 (78%)	90 (100%)	0	100	100
7	G	126/147 (86%)	126 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	102 (100%)	0	100	100
13	M	93/96 (97%)	93 (100%)	0	100	100
14	N	83/84 (99%)	82 (99%)	1 (1%)	63	83
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	73/78 (94%)	73 (100%)	0	100	100
18	R	57/65 (88%)	57 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	60 (100%)	0	100	100
24	c	216/218 (99%)	216 (100%)	0	100	100
25	d	163/163 (100%)	163 (100%)	0	100	100
26	e	165/165 (100%)	165 (100%)	0	100	100
27	f	148/150 (99%)	148 (100%)	0	100	100
28	g	137/138 (99%)	137 (100%)	0	100	100
29	h	32/114 (28%)	32 (100%)	0	100	100
30	i	116/116 (100%)	116 (100%)	0	100	100
31	j	104/104 (100%)	104 (100%)	0	100	100
32	k	103/103 (100%)	103 (100%)	0	100	100
33	l	107/107 (100%)	107 (100%)	0	100	100
34	m	98/103 (95%)	98 (100%)	0	100	100
35	n	86/87 (99%)	86 (100%)	0	100	100
36	o	99/100 (99%)	99 (100%)	0	100	100
37	p	89/90 (99%)	89 (100%)	0	100	100
38	q	84/84 (100%)	84 (100%)	0	100	100
39	r	93/93 (100%)	93 (100%)	0	100	100
40	s	80/84 (95%)	80 (100%)	0	100	100
41	t	83/85 (98%)	83 (100%)	0	100	100
42	u	78/78 (100%)	78 (100%)	0	100	100
43	v	61/63 (97%)	61 (100%)	0	100	100
44	w	67/68 (98%)	67 (100%)	0	100	100
45	x	54/55 (98%)	54 (100%)	0	100	100
46	y	48/49 (98%)	48 (100%)	0	100	100
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	46 (100%)	0	100	100
49	1	38/38 (100%)	38 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	2	51/52 (98%)	51 (100%)	0	100	100
51	3	34/34 (100%)	34 (100%)	0	100	100
52	4	55/62 (89%)	55 (100%)	0	100	100
All	All	4575/4825 (95%)	4571 (100%)	4 (0%)	87	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	196	ASN
5	E	43	ASN
5	E	77	ASN
14	N	35	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
37	p	81	ASN
41	t	46	GLN
38	q	87	GLN
42	u	87	GLN
13	M	105	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1517/1542 (98%)	201 (13%)	6 (0%)
22	a	2749/2904 (94%)	297 (10%)	0
23	b	118/120 (98%)	16 (13%)	0
53	X	12/35 (34%)	0	0
54	Z	76/77 (98%)	10 (13%)	1 (1%)
55	V	74/75 (98%)	13 (17%)	2 (2%)
All	All	4546/4753 (95%)	537 (11%)	9 (0%)

5 of 537 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	4	U
1	A	5	U

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Mol	Chain	Res	Type
1	A	6	G
1	A	9	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	V	5	C
55	V	10	G
1	A	1026	G
1	A	1033	G
1	A	1035	A

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

55 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
22	PSU	a	1911	22	18,21,22	1.08	3 (16%)	22,30,33	1.93	5 (22%)
22	PSU	a	2605	22	18,21,22	1.16	1 (5%)	22,30,33	1.92	4 (18%)
54	4SU	Z	8	54	18,21,22	3.97	8 (44%)	26,30,33	2.35	5 (19%)
22	G7M	a	2069	22	23,26,27	2.69	8 (34%)	35,39,42	1.82	9 (25%)
22	OMG	a	2251	54,22	23,26,27	2.50	8 (34%)	33,38,41	1.99	9 (27%)
1	PSU	A	516	56,1	18,21,22	1.05	3 (16%)	22,30,33	1.74	5 (22%)
22	PSU	a	955	22	18,21,22	1.19	1 (5%)	22,30,33	1.97	4 (18%)
55	H2U	V	19	55	18,21,22	1.24	3 (16%)	21,30,33	0.97	0
1	4OC	A	1402	56,1	20,23,24	2.75	8 (40%)	26,32,35	0.96	2 (7%)
1	MA6	A	1518	1	23,26,27	1.60	5 (21%)	34,38,41	2.26	12 (35%)
1	MA6	A	1519	1	23,26,27	1.62	5 (21%)	34,38,41	2.32	12 (35%)
22	PSU	a	746	56,22	18,21,22	1.11	3 (16%)	22,30,33	1.74	3 (13%)
22	2MG	a	1835	22	23,26,27	2.48	6 (26%)	32,38,41	2.31	10 (31%)
22	PSU	a	2457	22	18,21,22	1.20	2 (11%)	22,30,33	2.05	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	OMC	Z	33	54	19,22,23	2.72	7 (36%)	26,31,34	0.76	0
1	5MC	A	967	1	18,22,23	3.52	7 (38%)	26,32,35	1.05	1 (3%)
54	H2U	Z	21	54	18,21,22	1.09	2 (11%)	21,30,33	0.86	0
22	1MG	a	745	22	22,26,27	2.51	7 (31%)	33,39,42	1.73	8 (24%)
1	G7M	A	527	1	23,26,27	2.73	8 (34%)	35,39,42	1.74	9 (25%)
22	PSU	a	2604	22	18,21,22	1.11	1 (5%)	22,30,33	1.92	4 (18%)
55	PSU	V	13	55	18,21,22	1.06	1 (5%)	22,30,33	1.91	5 (22%)
22	H2U	a	2449	22	18,21,22	1.49	3 (16%)	21,30,33	0.96	2 (9%)
22	PSU	a	2504	22	18,21,22	1.07	2 (11%)	22,30,33	1.83	4 (18%)
55	PSU	V	54	55	18,21,22	1.06	2 (11%)	22,30,33	1.94	5 (22%)
1	2MG	A	966	1	23,26,27	2.51	7 (30%)	32,38,41	2.26	10 (31%)
33	MS6	l	82	33	5,7,8	0.65	0	2,7,9	1.98	1 (50%)
54	5MU	Z	55	54	19,22,23	4.56	7 (36%)	28,32,35	3.82	9 (32%)
1	5MC	A	1407	1	18,22,23	3.34	7 (38%)	26,32,35	1.10	2 (7%)
55	2MG	V	6	55	23,26,27	2.53	7 (30%)	32,38,41	2.16	9 (28%)
22	6MZ	a	2030	22	22,25,26	2.62	5 (22%)	30,36,39	2.52	12 (40%)
22	2MA	a	2503	56,22	22,25,26	3.70	10 (45%)	33,37,40	2.88	9 (27%)
33	4D4	l	81	33	9,11,12	1.81	3 (33%)	8,13,15	2.05	3 (37%)
22	OMU	a	2552	22	19,22,23	2.52	6 (31%)	26,31,34	1.90	5 (19%)
55	5MC	V	47	55	18,22,23	3.56	8 (44%)	26,32,35	1.07	2 (7%)
12	D2T	L	89	12	7,9,10	1.19	0	6,11,13	2.24	3 (50%)
54	PSU	Z	56	54	18,21,22	0.99	1 (5%)	22,30,33	1.82	4 (18%)
55	1MA	V	9	55	21,25,26	0.72	0	31,37,40	0.80	1 (3%)
22	2MG	a	2445	22	23,26,27	2.46	7 (30%)	32,38,41	2.25	10 (31%)
1	2MG	A	1516	1	23,26,27	2.46	7 (30%)	32,38,41	2.19	11 (34%)
55	5MC	V	38	55	18,22,23	3.46	8 (44%)	26,32,35	1.22	2 (7%)
22	3TD	a	1915	22	18,22,23	3.86	7 (38%)	22,32,35	1.83	3 (13%)
22	PSU	a	2580	22	18,21,22	1.27	2 (11%)	22,30,33	2.15	6 (27%)
25	MEQ	d	150	25	8,9,10	1.33	1 (12%)	5,10,12	1.42	1 (20%)
1	UR3	A	1498	1	19,22,23	2.43	6 (31%)	26,32,35	1.33	1 (3%)
55	1MA	V	57	55	21,25,26	0.74	0	31,37,40	0.79	1 (3%)
1	2MG	A	1207	1	23,26,27	2.48	7 (30%)	32,38,41	2.21	10 (31%)
22	5MU	a	747	22	19,22,23	4.41	7 (36%)	28,32,35	3.84	10 (35%)
55	5MC	V	48	55	18,22,23	3.56	8 (44%)	26,32,35	1.08	1 (3%)
11	IAS	K	119	11	6,7,8	1.02	0	6,8,10	1.28	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PSU	a	1917	22	18,21,22	1.09	3 (16%)	22,30,33	1.93	5 (22%)
22	OMC	a	2498	56,22	19,22,23	2.60	7 (36%)	26,31,34	0.89	1 (3%)
22	6MZ	a	1618	22	22,25,26	2.64	5 (22%)	30,36,39	2.49	11 (36%)
22	5MC	a	1962	22	18,22,23	3.31	7 (38%)	26,32,35	1.15	2 (7%)
55	5MU	V	53	55	19,22,23	4.41	7 (36%)	28,32,35	3.80	9 (32%)
22	5MU	a	1939	22	19,22,23	4.36	7 (36%)	28,32,35	3.92	10 (35%)

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
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
54	4SU	Z	8	54	-	0/7/25/26	0/2/2/2
22	G7M	a	2069	22	-	2/7/25/26	0/3/3/3
22	OMG	a	2251	54,22	-	0/9/27/28	0/3/3/3
1	PSU	A	516	56,1	-	0/7/25/26	0/2/2/2
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
55	H2U	V	19	55	-	3/7/38/39	0/2/2/2
1	4OC	A	1402	56,1	-	1/9/29/30	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
1	MA6	A	1519	1	-	3/11/29/30	0/3/3/3
22	PSU	a	746	56,22	-	1/7/25/26	0/2/2/2
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
54	OMC	Z	33	54	-	0/9/27/28	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
54	H2U	Z	21	54	-	5/7/38/39	0/2/2/2
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
1	G7M	A	527	1	-	3/7/25/26	0/3/3/3
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
55	PSU	V	13	55	-	0/7/25/26	0/2/2/2
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2
22	PSU	a	2504	22	-	2/7/25/26	0/2/2/2
55	PSU	V	54	55	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	1/9/27/28	0/3/3/3
33	MS6	l	82	33	-	1/4/6/8	-
54	5MU	Z	55	54	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
55	2MG	V	6	55	-	0/9/27/28	0/3/3/3
22	6MZ	a	2030	22	-	2/9/27/28	0/3/3/3
22	2MA	a	2503	56,22	-	1/7/25/26	0/3/3/3
33	4D4	l	81	33	-	2/11/12/14	-
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
55	5MC	V	47	55	-	3/7/25/26	0/2/2/2
12	D2T	L	89	12	-	1/7/12/14	-
54	PSU	Z	56	54	-	0/7/25/26	0/2/2/2
55	1MA	V	9	55	-	2/7/25/26	0/3/3/3
22	2MG	a	2445	22	-	2/9/27/28	0/3/3/3
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
55	5MC	V	38	55	-	1/7/25/26	0/2/2/2
22	3TD	a	1915	22	-	1/7/25/26	0/2/2/2
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
25	MEQ	d	150	25	-	2/8/9/11	-
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
55	1MA	V	57	55	-	0/7/25/26	0/3/3/3
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
22	5MU	a	747	22	-	0/7/25/26	0/2/2/2
55	5MC	V	48	55	-	2/7/25/26	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
22	OMC	a	2498	56,22	-	0/9/27/28	0/2/2/2
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
55	5MU	V	53	55	-	0/7/25/26	0/2/2/2
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2

The worst 5 of 261 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	11.56	1.48	1.35
22	a	2503	2MA	C4-N3	11.29	1.48	1.34
22	a	1618	6MZ	C6-N6	10.42	1.45	1.34
54	Z	55	5MU	C6-N1	10.39	1.55	1.38
54	Z	55	5MU	C2-N1	10.25	1.54	1.38

The worst 5 of 288 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	Z	55	5MU	C5-C4-N3	13.09	126.49	115.31
22	a	1939	5MU	C5-C4-N3	12.87	126.30	115.31
55	V	53	5MU	C5-C4-N3	12.81	126.25	115.31
22	a	747	5MU	C5-C4-N3	12.52	126.00	115.31
22	a	1939	5MU	C5-C6-N1	-11.20	111.81	123.34

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1519	MA6	O4'-C4'-C5'-O5'
54	Z	21	H2U	O4'-C1'-N1-C6
54	Z	21	H2U	C2'-C1'-N1-C6
22	a	2030	6MZ	O4'-C4'-C5'-O5'
55	V	47	5MC	C3'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	a	2251	OMG	1	0
1	A	1519	MA6	1	0
54	Z	21	H2U	2	0
54	Z	55	5MU	1	0
55	V	6	2MG	1	0
22	a	2030	6MZ	2	0
22	a	2503	2MA	1	0
12	L	89	D2T	2	0
1	A	1516	2MG	1	0
22	a	1915	3TD	1	0
22	a	2498	OMC	1	0
55	V	53	5MU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 283 ligands modelled in this entry, 283 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	J	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	53:ILE	C	54:SER	N	1.19

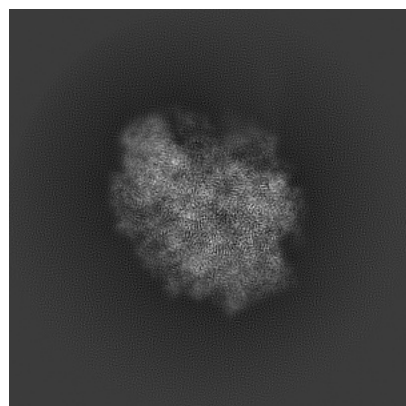
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33660. These allow visual inspection of the internal detail of the map and identification of artifacts.

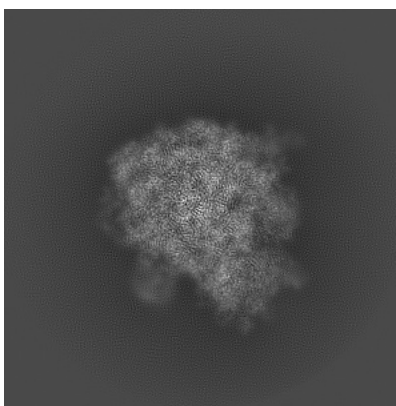
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

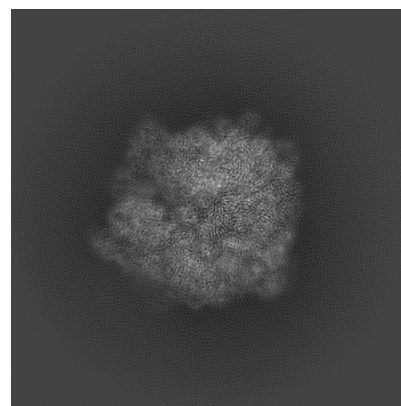
6.1.1 Primary map



X

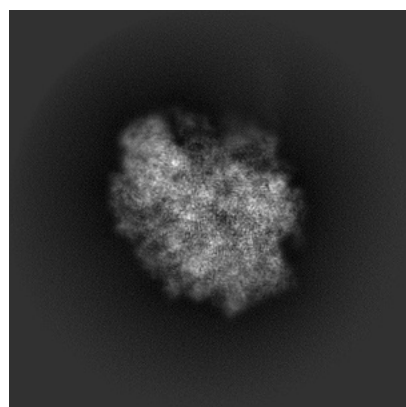


Y

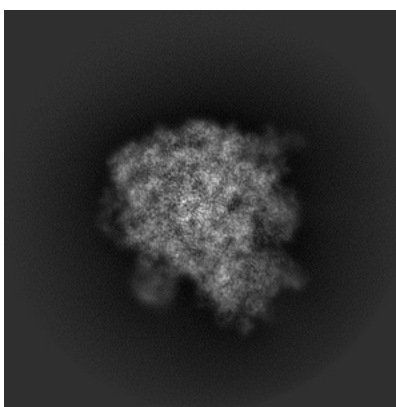


Z

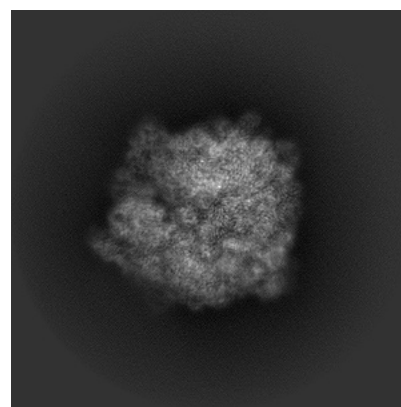
6.1.2 Raw map



X



Y

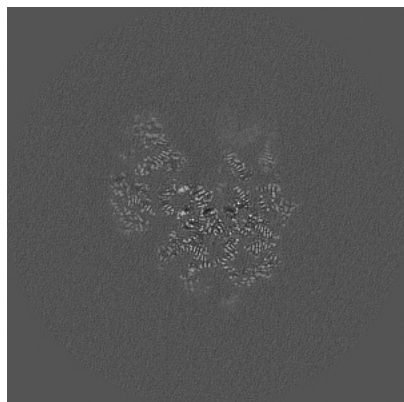


Z

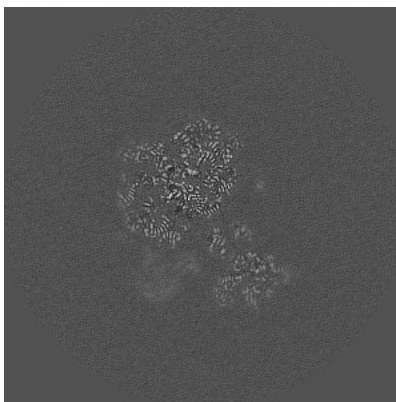
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

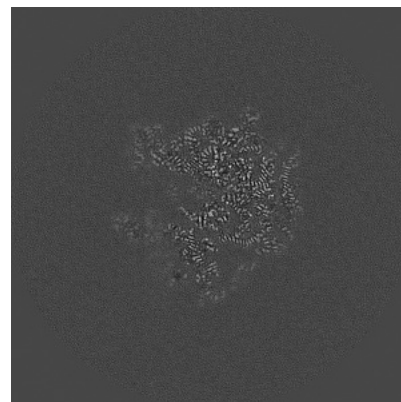
6.2.1 Primary map



X Index: 265

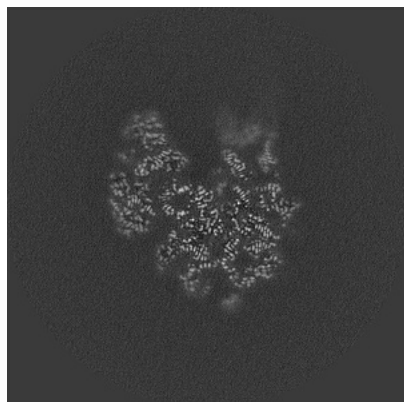


Y Index: 265

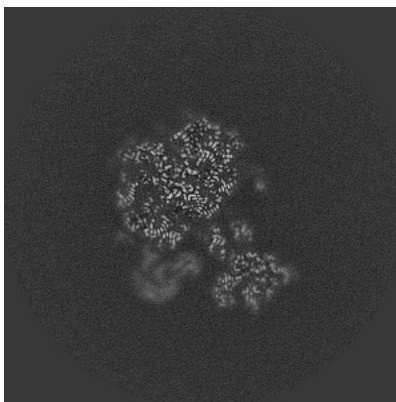


Z Index: 265

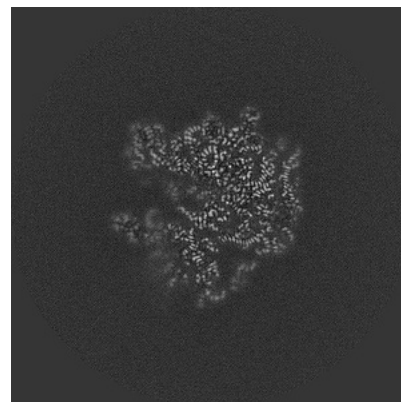
6.2.2 Raw map



X Index: 265



Y Index: 265

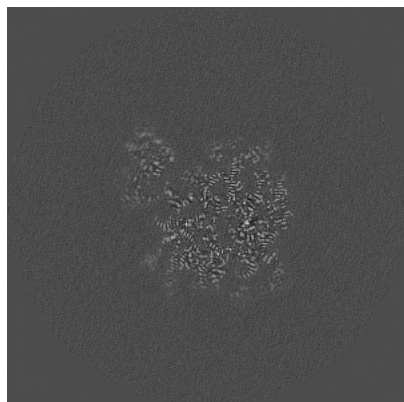


Z Index: 265

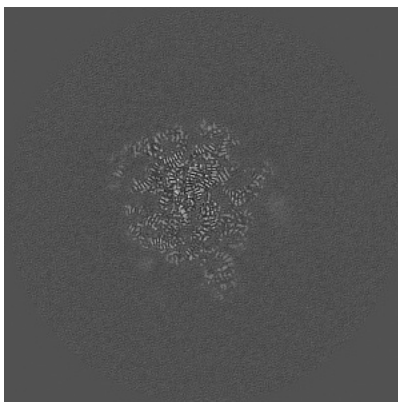
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

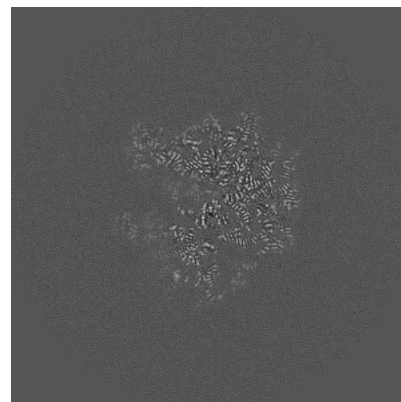
6.3.1 Primary map



X Index: 297

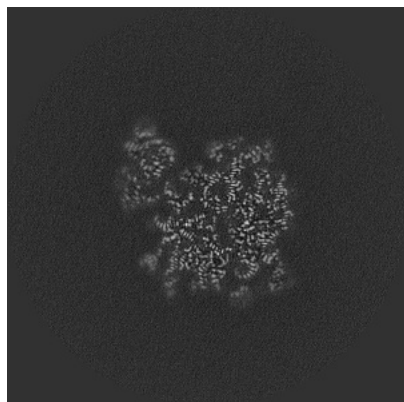


Y Index: 320

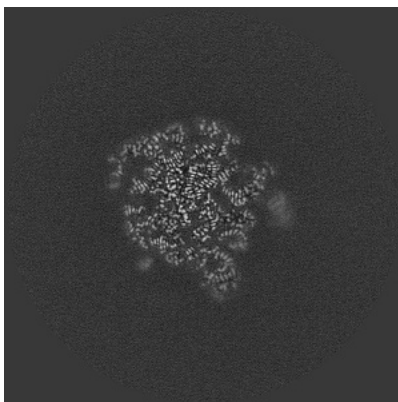


Z Index: 267

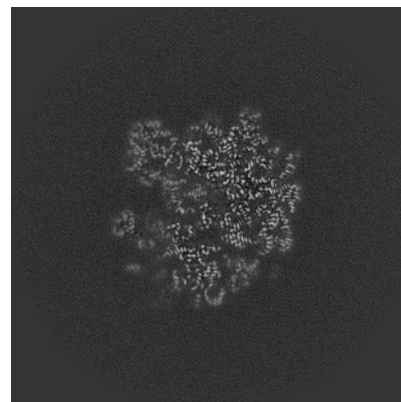
6.3.2 Raw map



X Index: 297



Y Index: 321

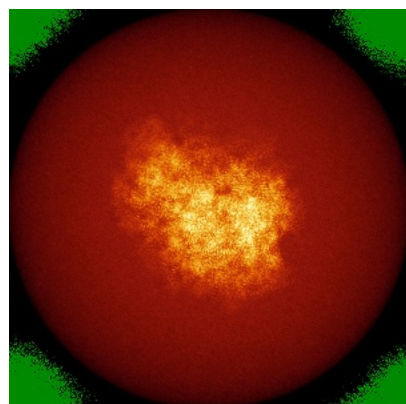


Z Index: 271

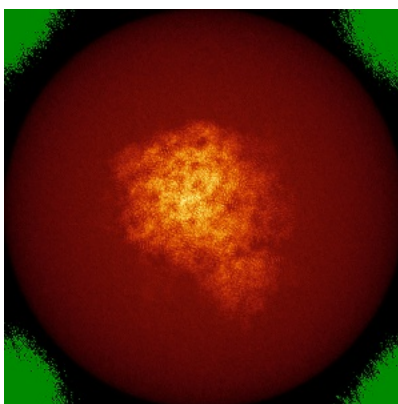
The images above show the largest variance slices of the map in three orthogonal directions.

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

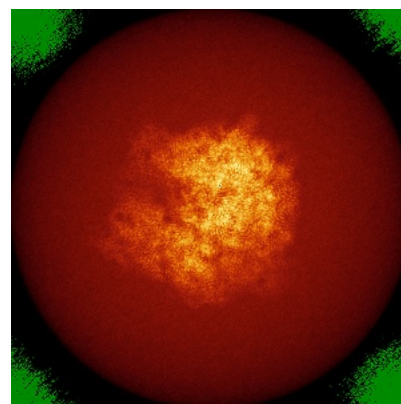
6.4.1 Primary map



X

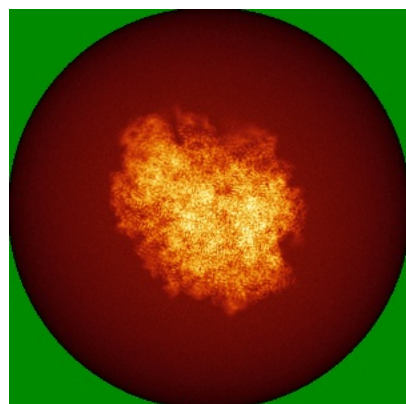


Y

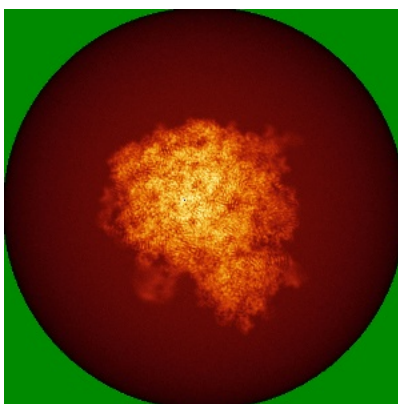


Z

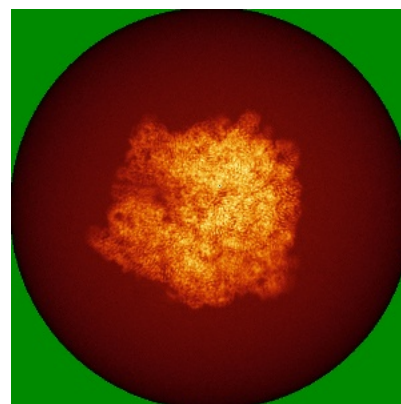
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

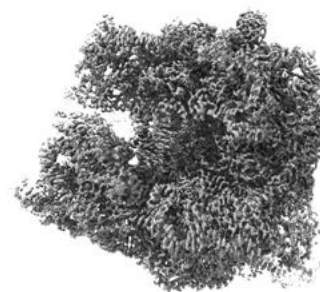
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

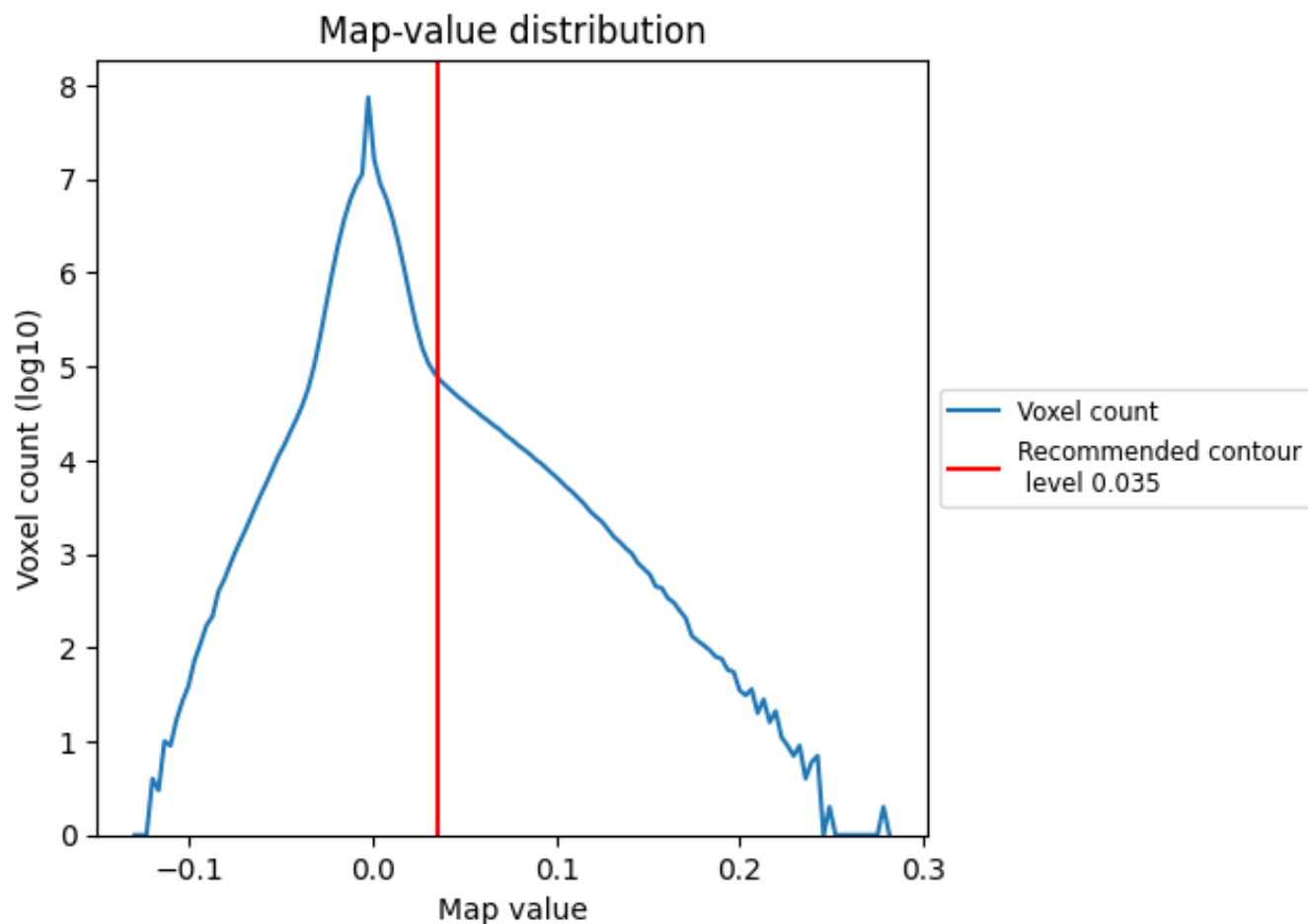
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

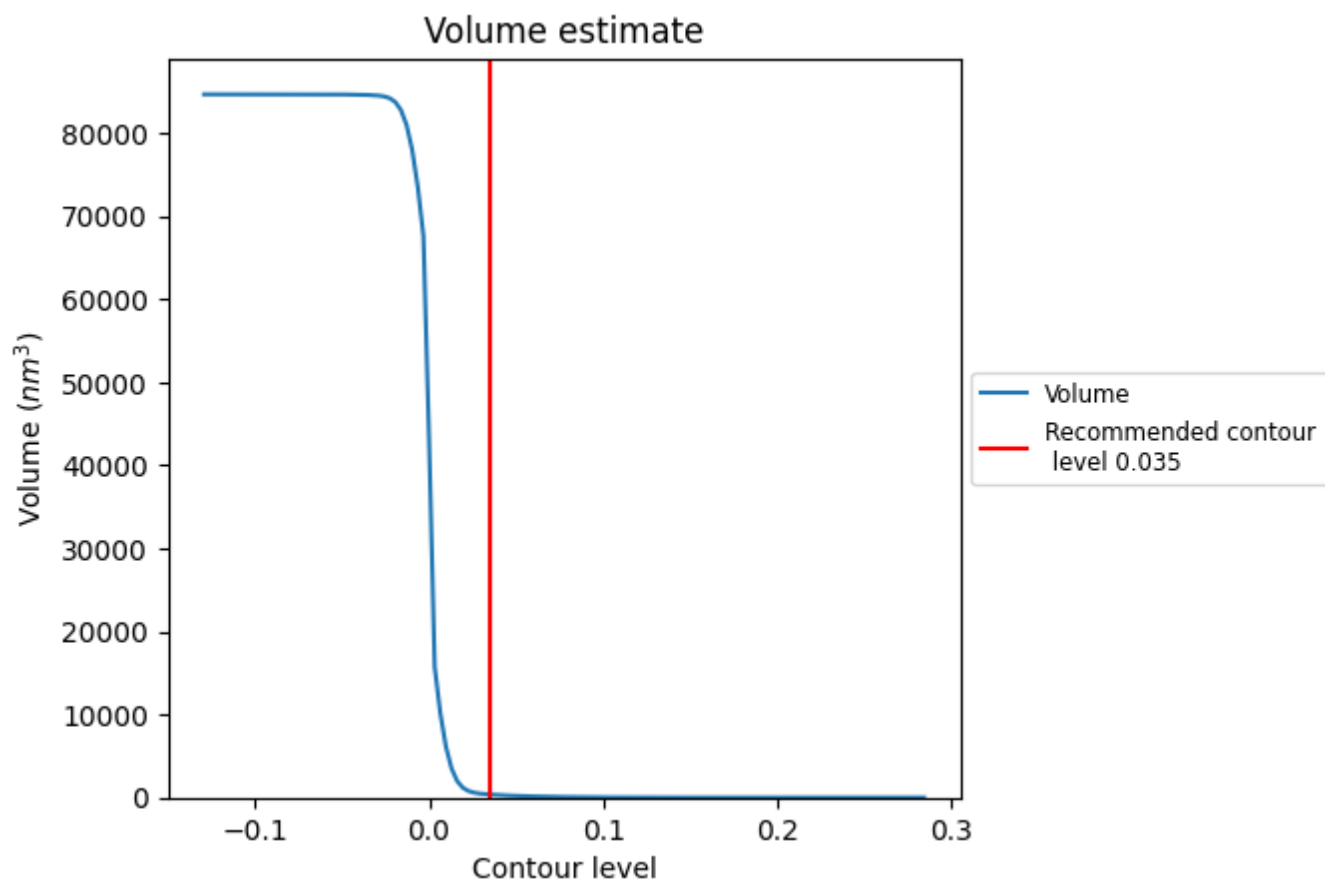
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

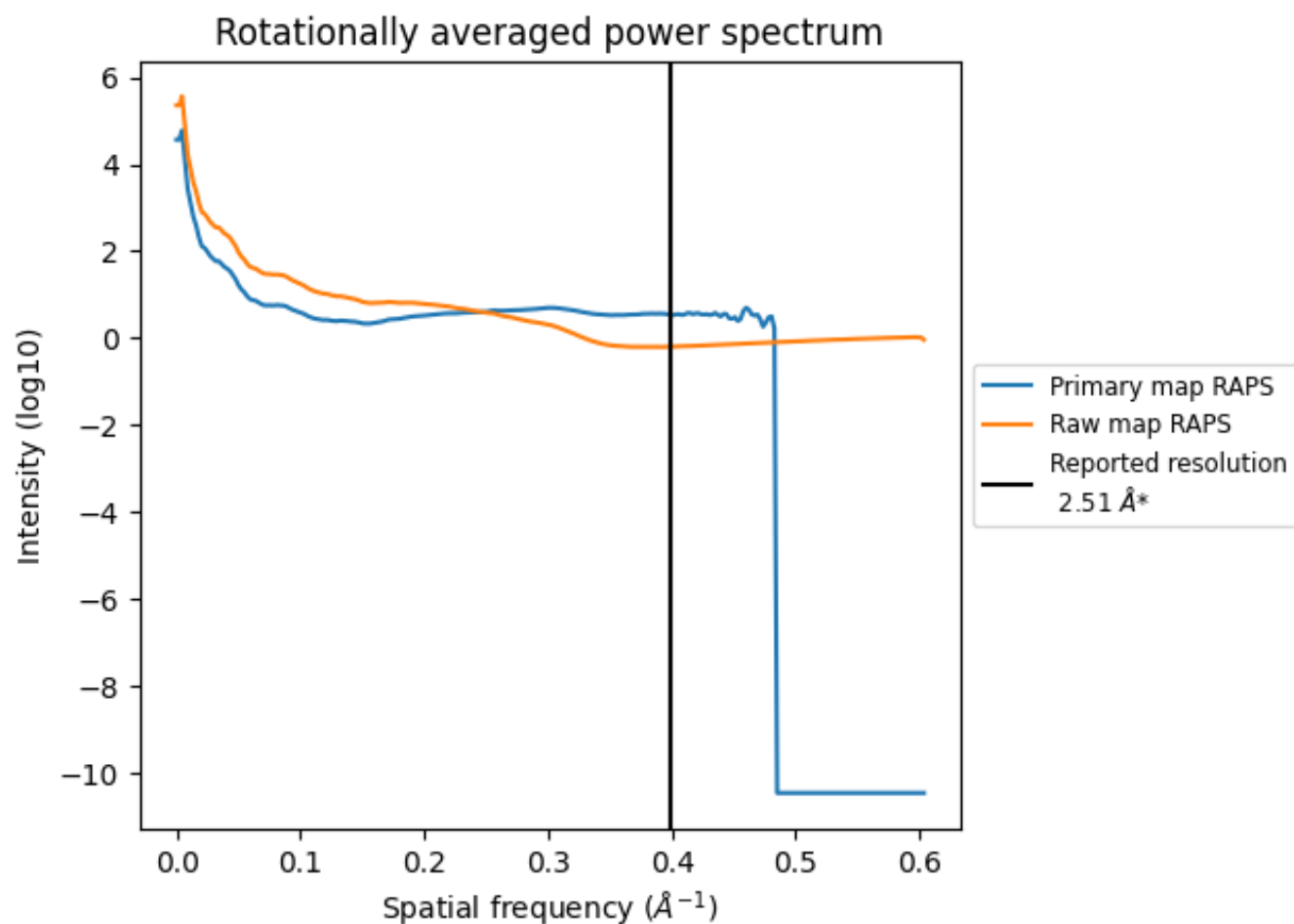
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 369 nm^3 ; this corresponds to an approximate mass of 333 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 ⓘ

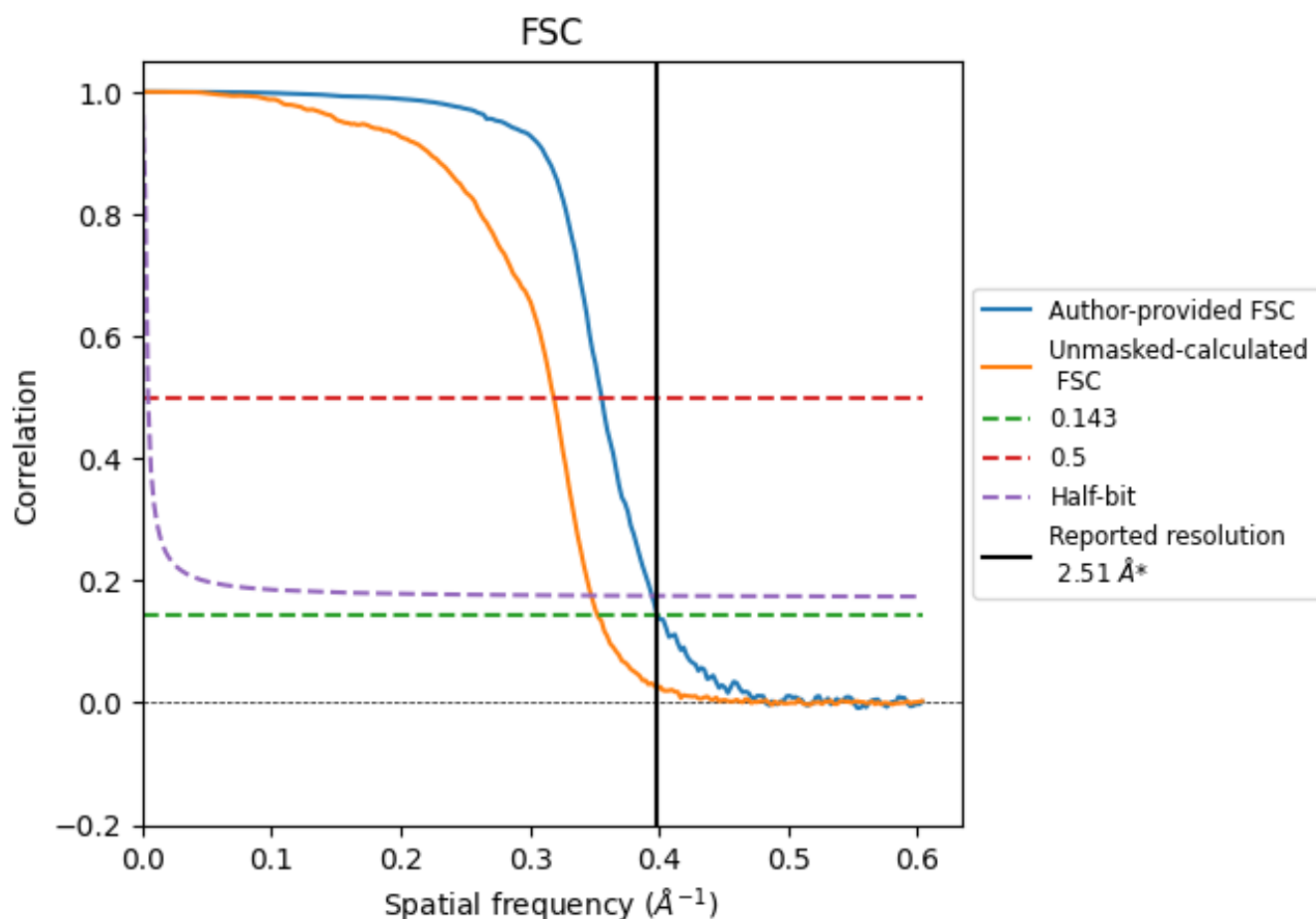


*Reported resolution corresponds to spatial frequency of 0.398 Å⁻¹

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 0.398 Å⁻¹

8.2 Resolution estimates [i](#)

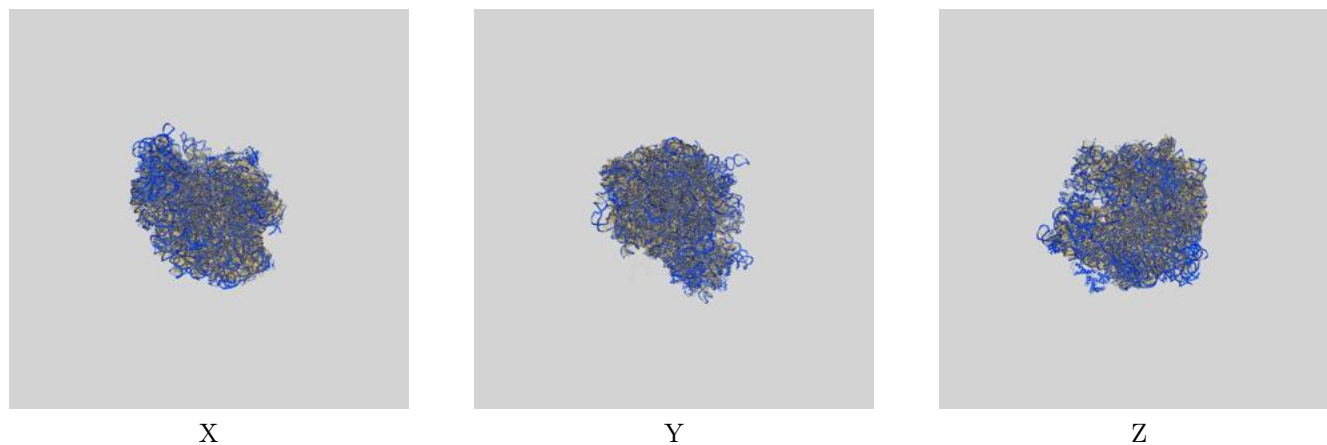
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.51	-	-
Author-provided FSC curve	2.51	2.81	2.53
Unmasked-calculated*	2.84	3.14	2.88

*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 2.84 differs from the reported value 2.51 by more than 10 %

9 Map-model fit [i](#)

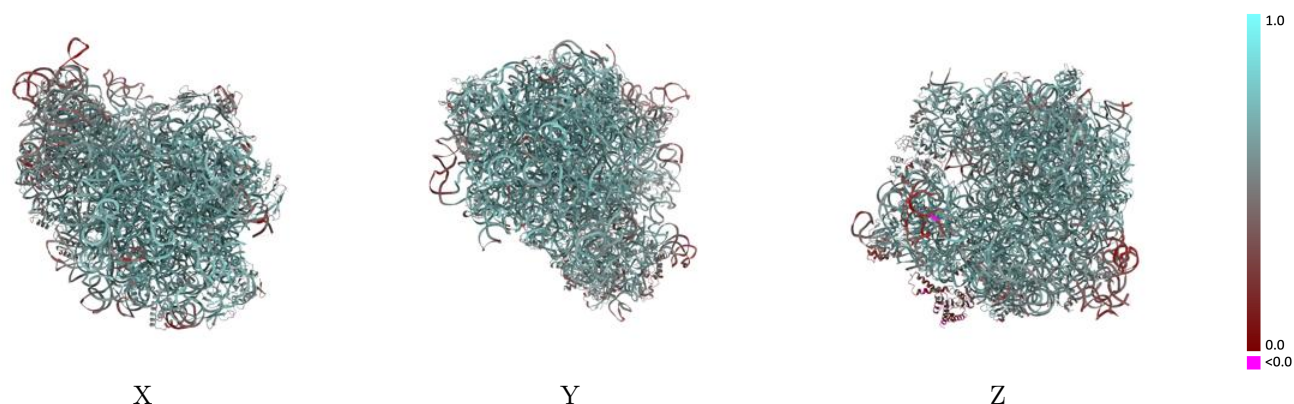
This section contains information regarding the fit between EMDB map EMD-33660 and PDB model 7Y7C. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



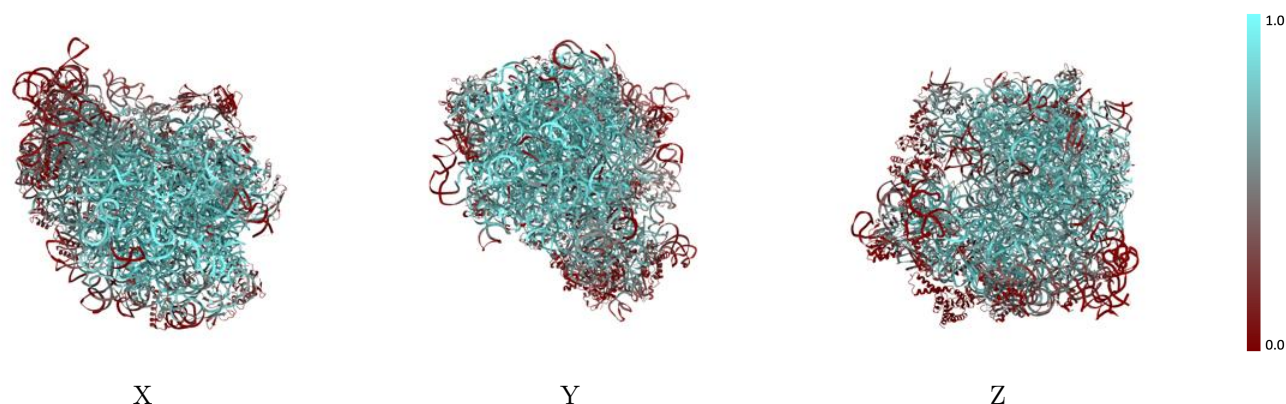
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



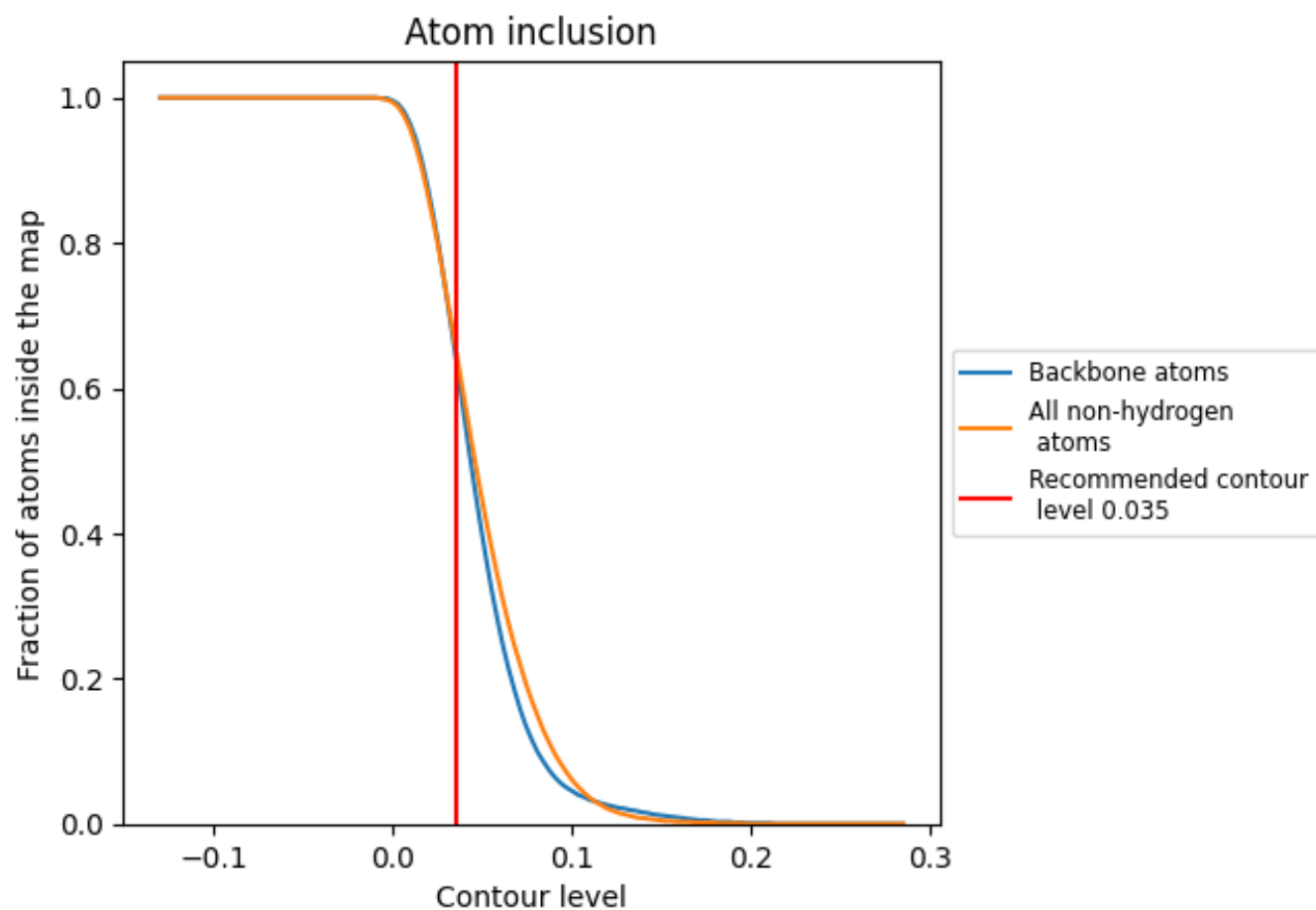
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 66% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6580	 0.6210
0	 0.5890	 0.6390
1	 0.9040	 0.7160
2	 0.8660	 0.7020
3	 0.7470	 0.6530
4	 0.0570	 0.4090
A	 0.6340	 0.5990
B	 0.0000	 0.2580
C	 0.4630	 0.6020
D	 0.1740	 0.5140
E	 0.5800	 0.6210
F	 0.2090	 0.5010
G	 0.2480	 0.5310
H	 0.4960	 0.6220
I	 0.3460	 0.5610
J	 0.2860	 0.4790
K	 0.4170	 0.5760
L	 0.6380	 0.6460
M	 0.3030	 0.5650
N	 0.4480	 0.5740
O	 0.4750	 0.5900
P	 0.2590	 0.5260
Q	 0.3360	 0.5580
R	 0.3590	 0.5460
S	 0.3220	 0.5530
T	 0.2170	 0.5140
U	 0.1180	 0.4510
V	 0.5240	 0.5850
X	 0.5630	 0.6040
Z	 0.5490	 0.5800
a	 0.8100	 0.6610
b	 0.5920	 0.6060
c	 0.8150	 0.6960
d	 0.7120	 0.6700
e	 0.5010	 0.6040



Continued on next page...

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Chain	Atom inclusion	Q-score
f	 0.2580	 0.5460
g	 0.1660	 0.4920
h	 0.0330	 0.4450
i	 0.7590	 0.6660
j	 0.7280	 0.6740
k	 0.6340	 0.6460
l	 0.7780	 0.6820
m	 0.8310	 0.6890
n	 0.3740	 0.5830
o	 0.6210	 0.6280
p	 0.8220	 0.6960
q	 0.6010	 0.6240
r	 0.7500	 0.6610
s	 0.5370	 0.6040
t	 0.3950	 0.5610
u	 0.4620	 0.5880
v	 0.7670	 0.6800
w	 0.6610	 0.6430
x	 0.3030	 0.5200
y	 0.6980	 0.6510
z	 0.7340	 0.6730