



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 03:25 AM UTC

PDB ID : 9NLQ / pdb_00009nlq
EMDB ID : EMD-29408
Title : E. coli initiation complex with EQ2-YbiT in Hydrolytic 1/PtIM(a) conformation
Authors : Singh, S.; Hunt, J.F.
Deposited on : 2025-03-03
Resolution : 3.30 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

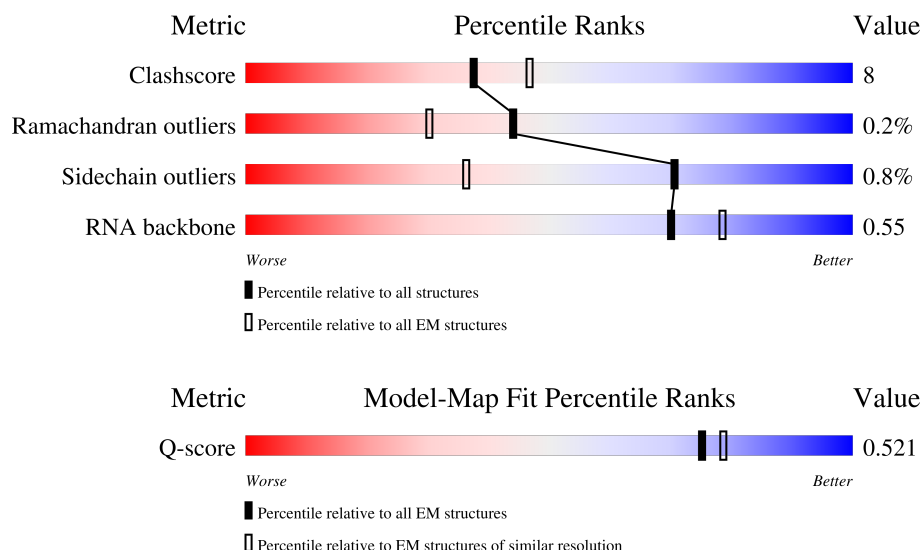
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



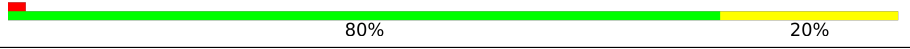
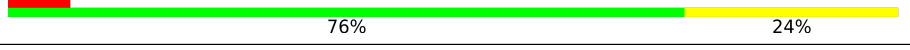
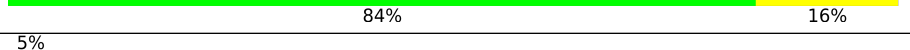
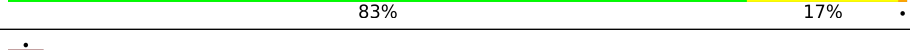
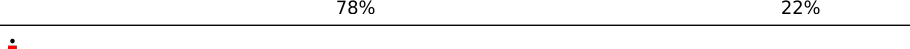
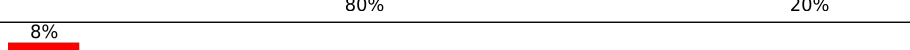
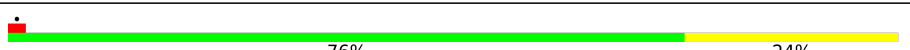
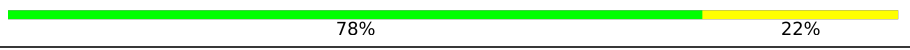
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	1	220	
2	13	142	
3	14	122	

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Mol	Chain	Length	Quality of chain
4	15	144	
5	16	136	
6	17	120	
7	18	116	
8	19	114	
9	2	271	
10	20	117	
11	21	103	
12	22	110	
13	23	93	
14	24	102	
15	25	94	
16	27	77	
17	28	77	
18	29	63	
19	3	209	
20	30	58	
21	31	66	
22	32	56	
23	33	50	
24	34	46	
25	35	64	
26	36	38	
27	4	201	
28	5	177	

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Mol	Chain	Length	Quality of chain
29	6	176	
30	9	149	
31	M	9	
32	R1	2903	
33	R2	119	
34	R3	1539	
35	T	77	
36	Y	530	
37	sb	218	
38	sc	206	
39	sd	205	
40	se	157	
41	sf	100	
42	sg	151	
43	sh	129	
44	si	127	
45	sj	98	
46	sk	116	
47	sl	123	
48	sm	114	
49	sn	100	
50	so	88	
51	sp	82	
52	sq	80	
53	sr	65	

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Mol	Chain	Length	Quality of chain
54	ss	79	
55	st	85	
56	su	65	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	H2U	T	20	X	-	-	-
35	4OC	T	32	X	-	-	-
35	5MU	T	54	X	-	-	-
35	PSU	T	55	X	-	-	-
35	4SU	T	8	X	-	-	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 149989 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 2 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 3 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 4 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	15	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 5 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 6 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	18	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 8 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	2	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	20	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 11 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 14 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	24	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 15 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	25	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 16 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	27	77	Total	C	N	O	S	0	0
			588	363	118	106	1		

- Molecule 17 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	28	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 18 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	29	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 19 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	3	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	30	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 21 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	31	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 23 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	33	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 26 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 29 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 30 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	9	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 31 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	9	Total	C	N	O	P	0	0
			195	88	40	58	9		

- Molecule 32 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R1	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R1	1847	G	A	conflict	GB 2019144442

- Molecule 33 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	R2	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	R3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 35 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	T	77	Total	C	N	O	P	S	0	0
			1639	734	294	534	76	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	8	4SU	G	conflict	GB 932857508

- Molecule 36 is a protein called Probable ATP-binding protein YbiT.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	527	Total	C	N	O	S	0	0
			4170	2636	715	800	19		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	181	GLN	GLU	conflict	UNP P0A9U3
Y	464	GLN	GLU	conflict	UNP P0A9U3

- Molecule 37 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 38 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 41 is a protein called 30S ribosomal protein S6, non-modified isoform.

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

- Molecule 42 is a protein called 30S ribosomal protein S7.

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

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

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

- Molecule 46 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 51 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 53 is a protein called 30S ribosomal protein S18.

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

- Molecule 54 is a protein called 30S ribosomal protein S19.

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

- Molecule 55 is a protein called 30S ribosomal protein S20.

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

- Molecule 56 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

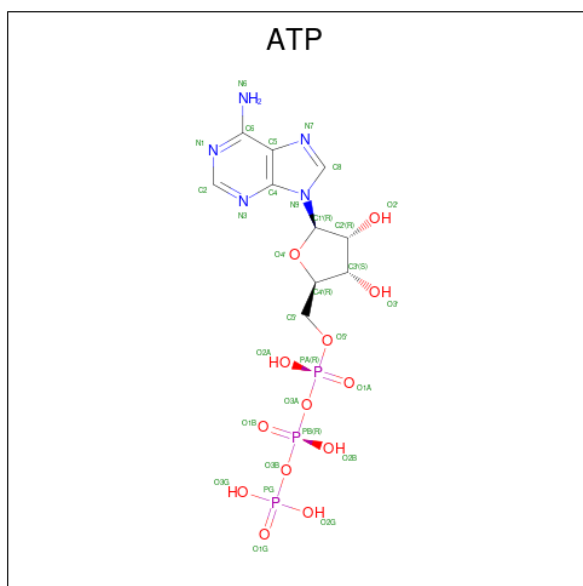
Mol	Chain	Residues	Atoms		AltConf
57	15	1	Total	Mg	0
			1	1	
57	17	1	Total	Mg	0
			1	1	
57	32	1	Total	Mg	0
			1	1	
57	M	1	Total	Mg	0
			1	1	
57	R1	184	Total	Mg	0
			184	184	
57	R3	53	Total	Mg	0
			53	53	

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
58	T	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 59 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
59	Y	1	Total	C	N	O	P	0
			31	10	5	13	3	
59	Y	1	Total	C	N	O	P	0
			31	10	5	13	3	

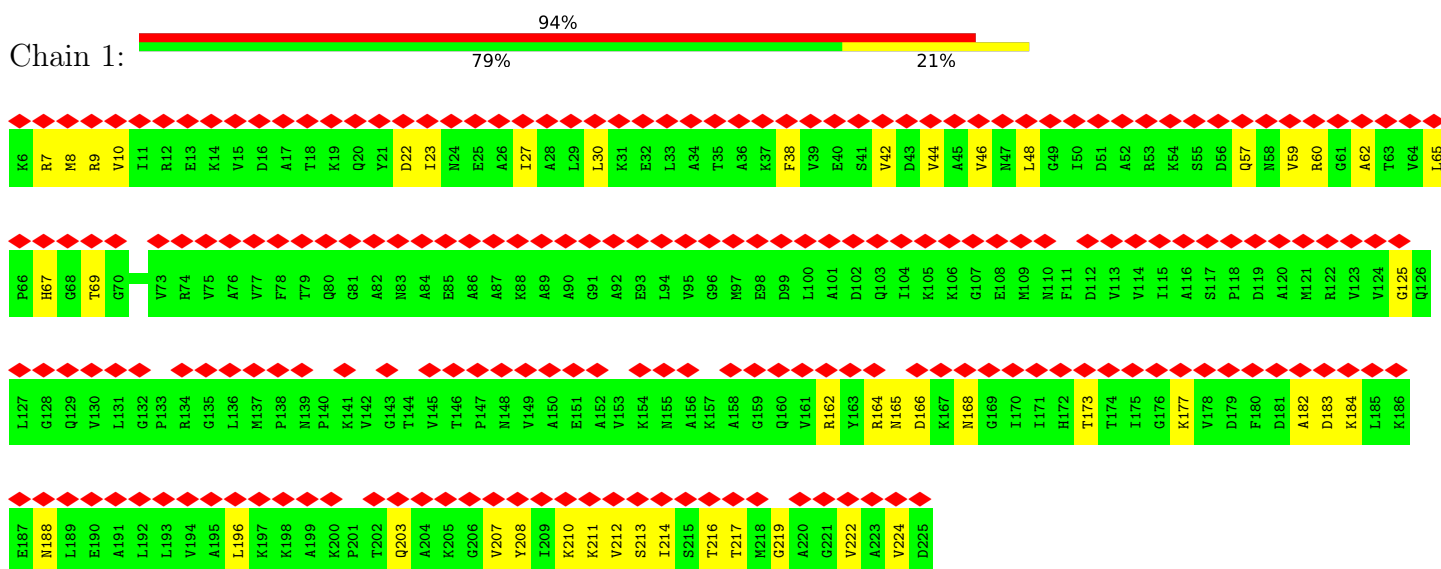
- Molecule 60 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
60	Y	2	Total	Na	0
			2	2	

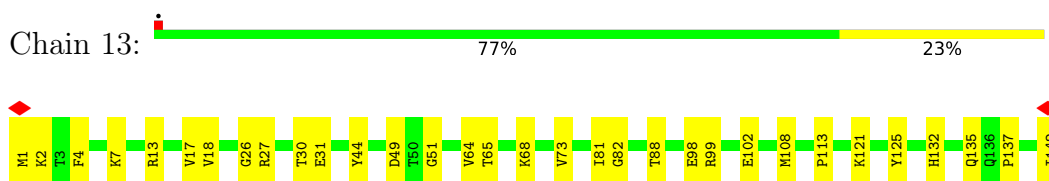
3 Residue-property plots

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.

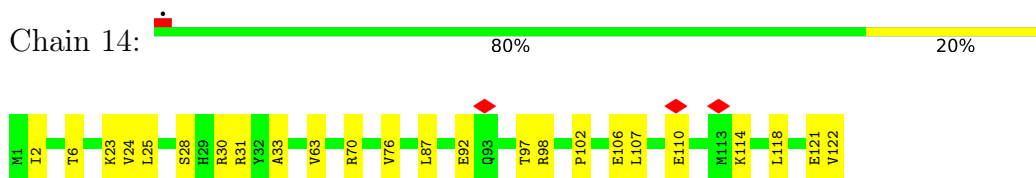
- Molecule 1: Large ribosomal subunit protein uL1



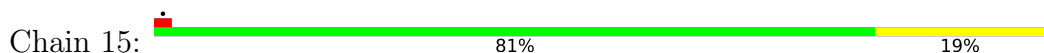
- Molecule 2: Large ribosomal subunit protein uL13

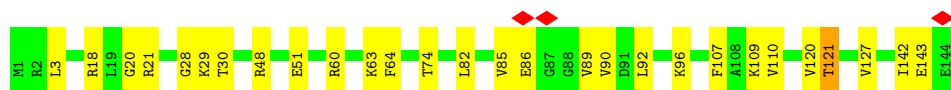


- Molecule 3: 50S ribosomal protein L14

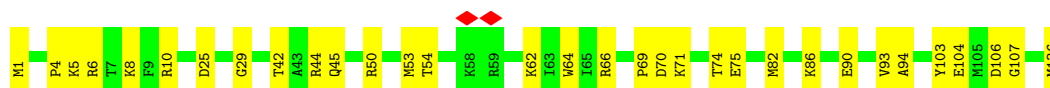
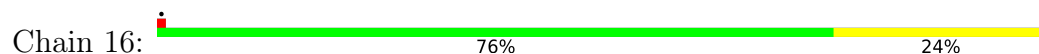


- Molecule 4: Large ribosomal subunit protein uL15

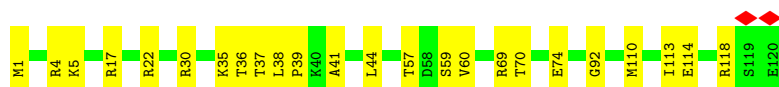




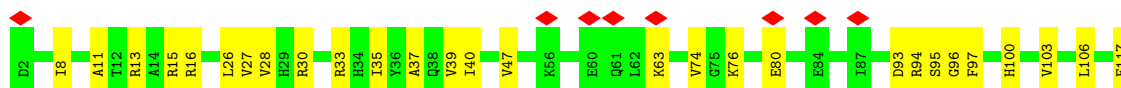
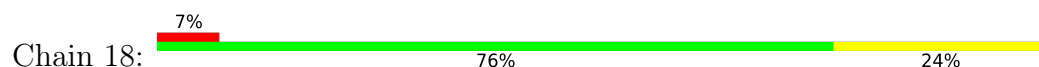
- Molecule 5: 50S ribosomal protein L16



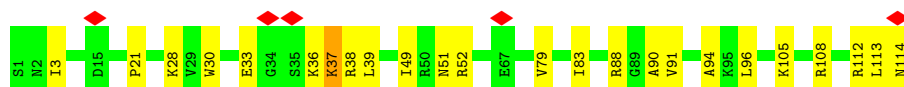
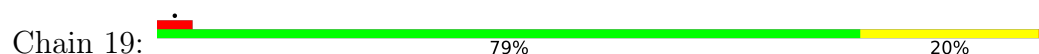
- Molecule 6: Large ribosomal subunit protein bL17



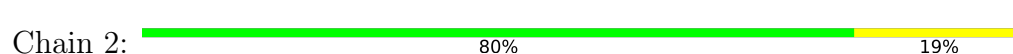
- Molecule 7: Large ribosomal subunit protein uL18



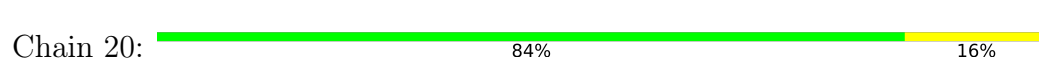
- Molecule 8: 50S ribosomal protein L19



- Molecule 9: 50S ribosomal protein L2

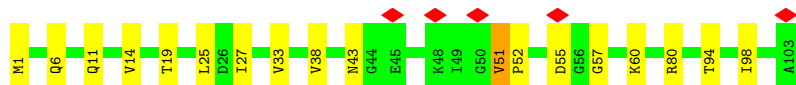
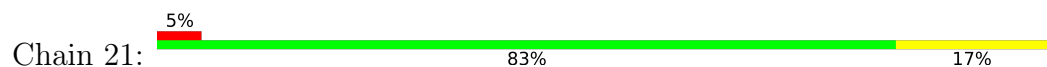


- Molecule 10: Large ribosomal subunit protein bL20

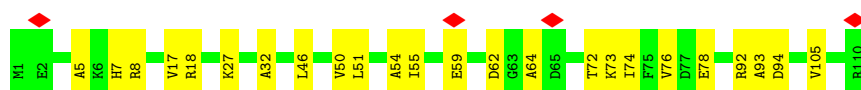
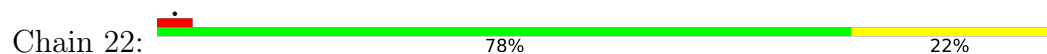




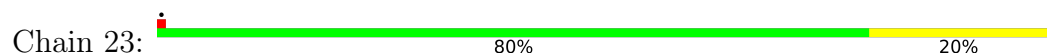
- Molecule 11: Large ribosomal subunit protein bL21



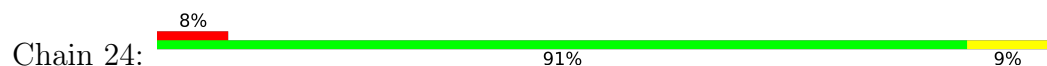
- Molecule 12: Large ribosomal subunit protein uL22



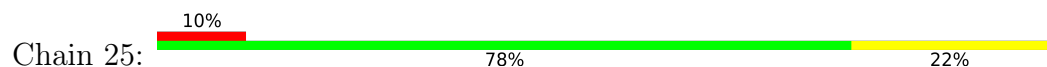
- Molecule 13: Large ribosomal subunit protein uL23



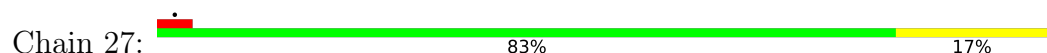
- Molecule 14: Large ribosomal subunit protein uL24



- Molecule 15: Large ribosomal subunit protein bL25

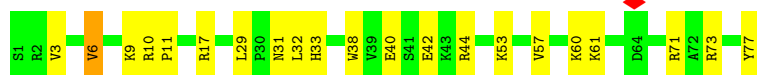


- Molecule 16: Large ribosomal subunit protein bL27



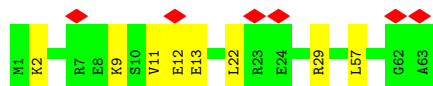
- Molecule 17: 50S ribosomal protein L28

Chain 28:  73% 26%



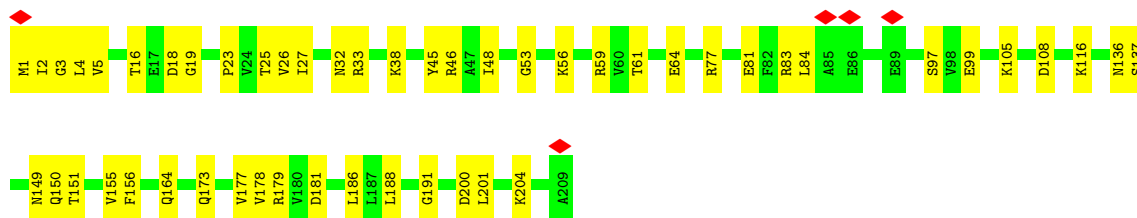
- Molecule 18: Large ribosomal subunit protein uL29

Chain 29:  10% 87% 13%



- Molecule 19: 50S ribosomal protein L3

Chain 3:  76% 24%



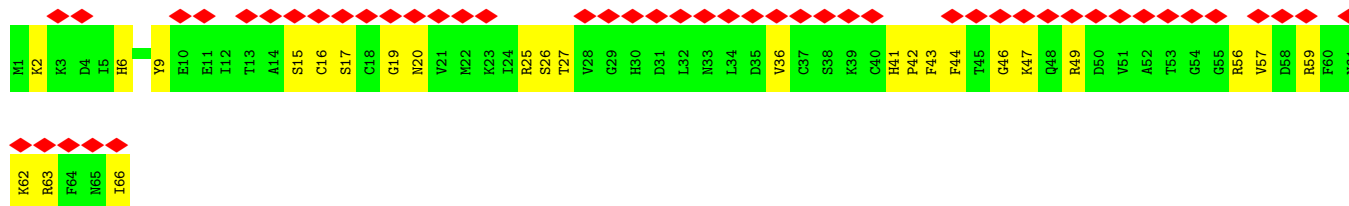
- Molecule 20: 50S ribosomal protein L30

Chain 30:  78% 22%



- Molecule 21: Large ribosomal subunit protein bL31

Chain 31:  74% 62% 38%

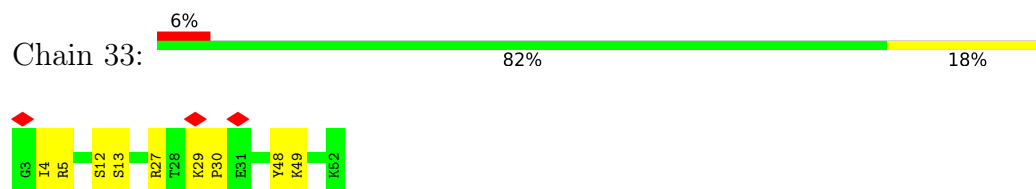


- Molecule 22: 50S ribosomal protein L32

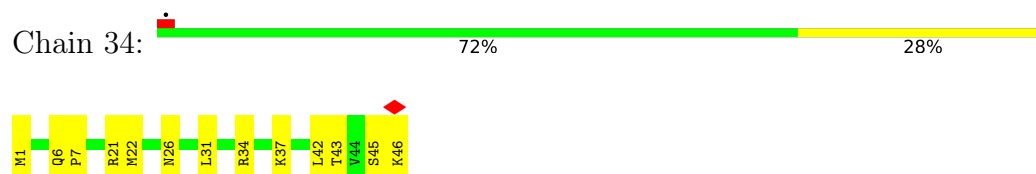
Chain 32:  55% 45%



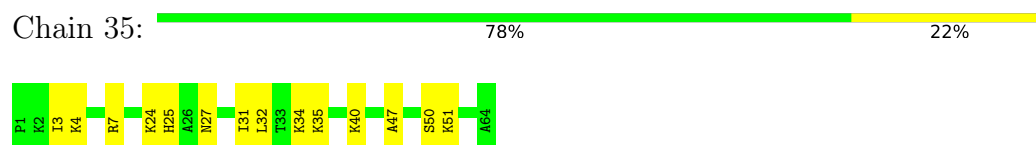
- Molecule 23: Large ribosomal subunit protein bL33



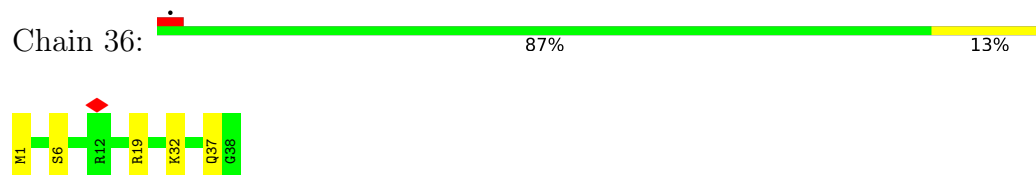
- Molecule 24: 50S ribosomal protein L34



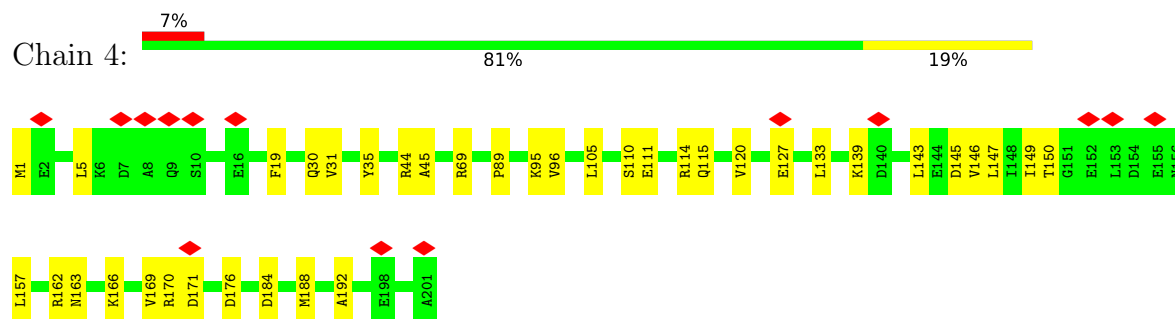
- Molecule 25: Large ribosomal subunit protein bL35



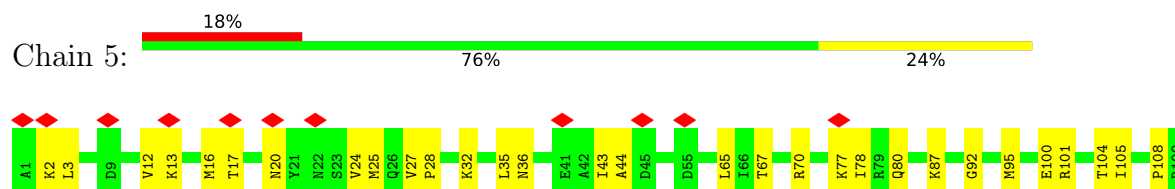
- Molecule 26: 50S ribosomal protein L36

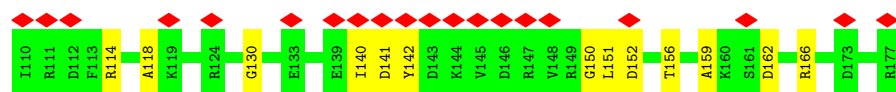


- Molecule 27: Large ribosomal subunit protein uL4

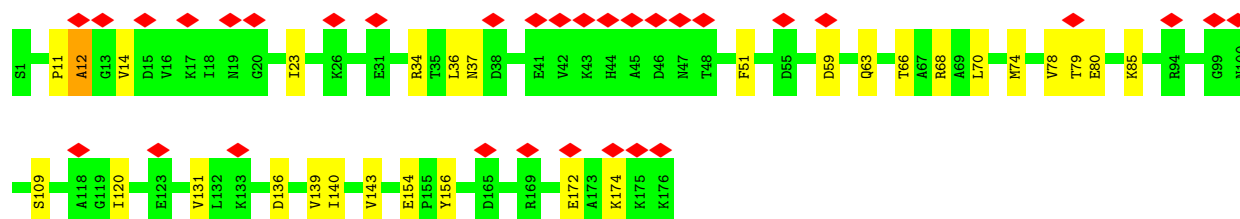
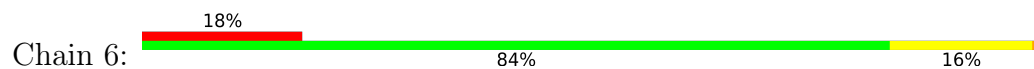


- Molecule 28: 50S ribosomal protein L5

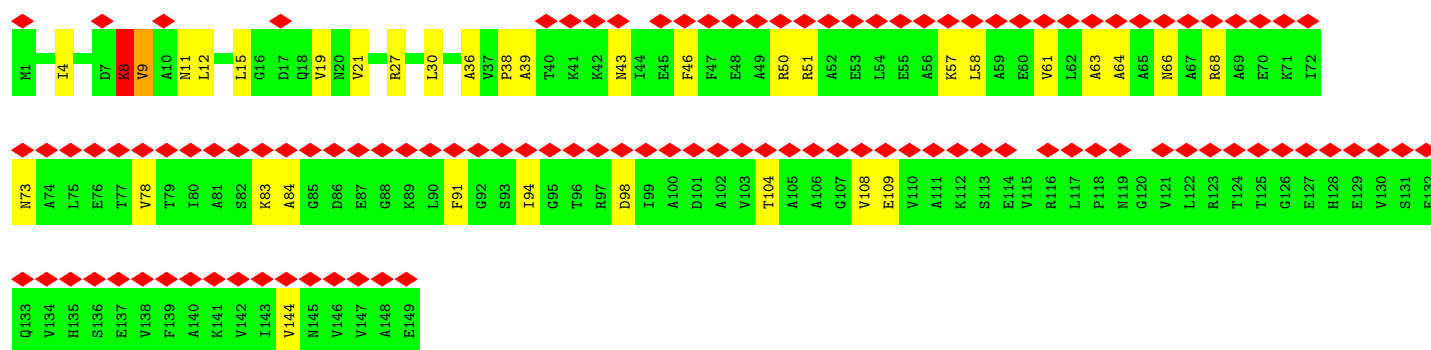
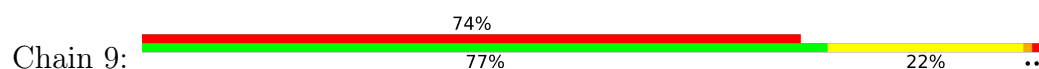




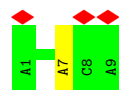
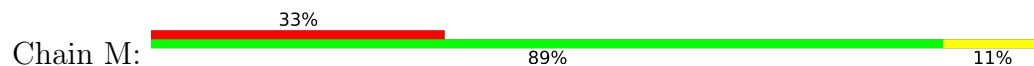
- Molecule 29: Large ribosomal subunit protein uL6



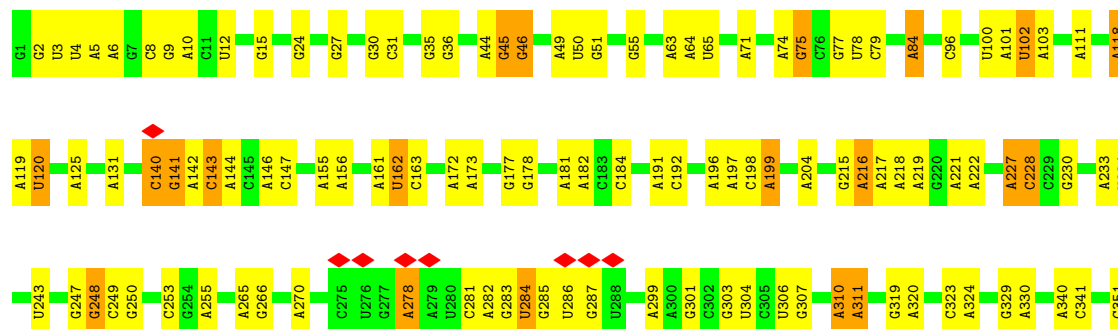
- Molecule 30: Large ribosomal subunit protein bL9



- Molecule 31: mRNA

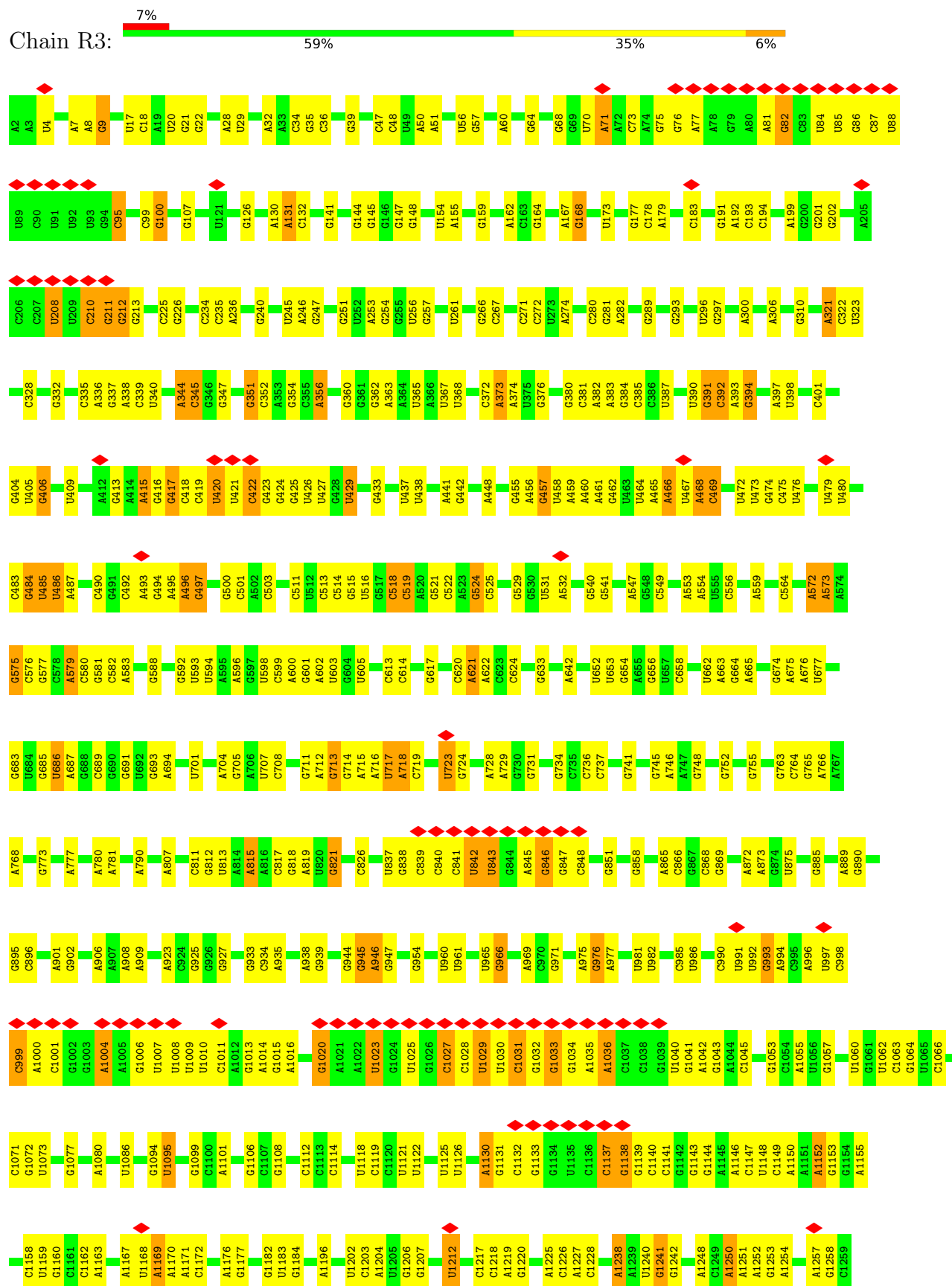


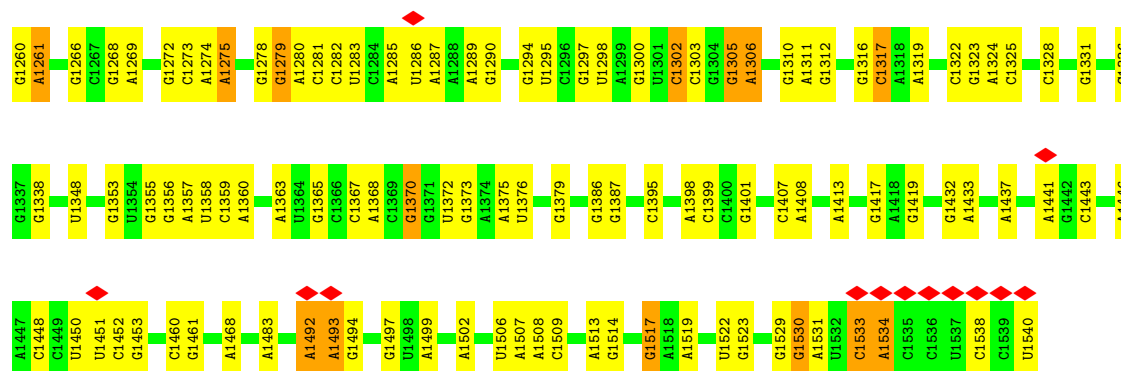
- Molecule 32: 23S ribosomal RNA



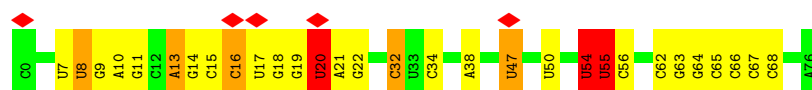


• Molecule 34: 16S ribosomal RNA

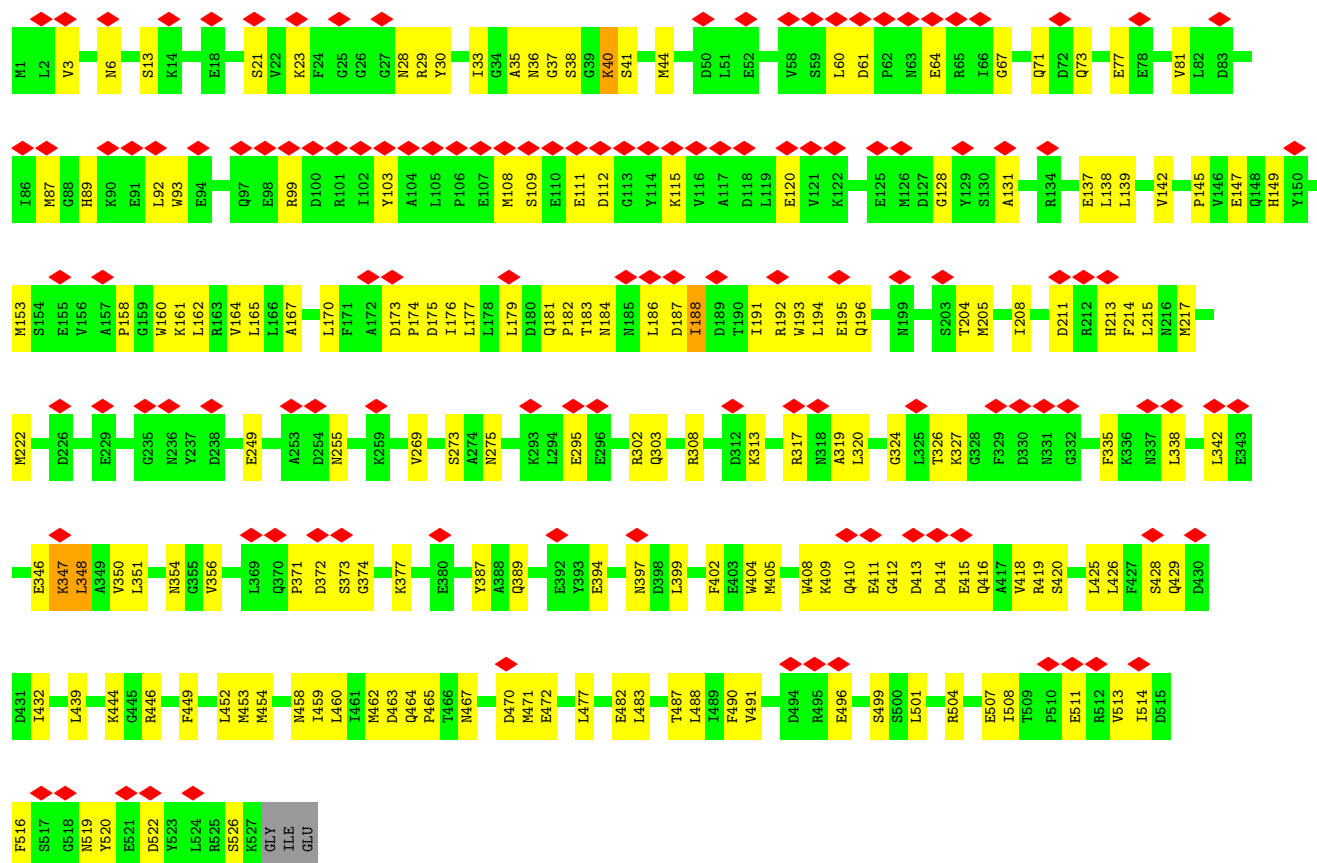




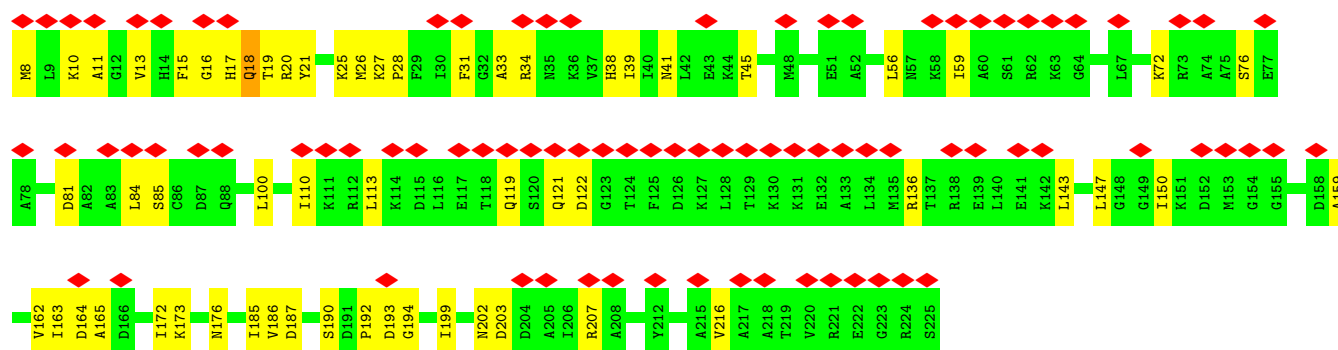
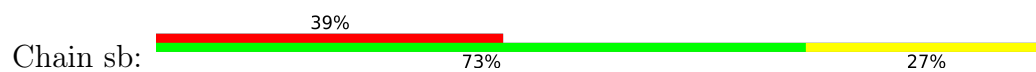
• Molecule 35: tRNA



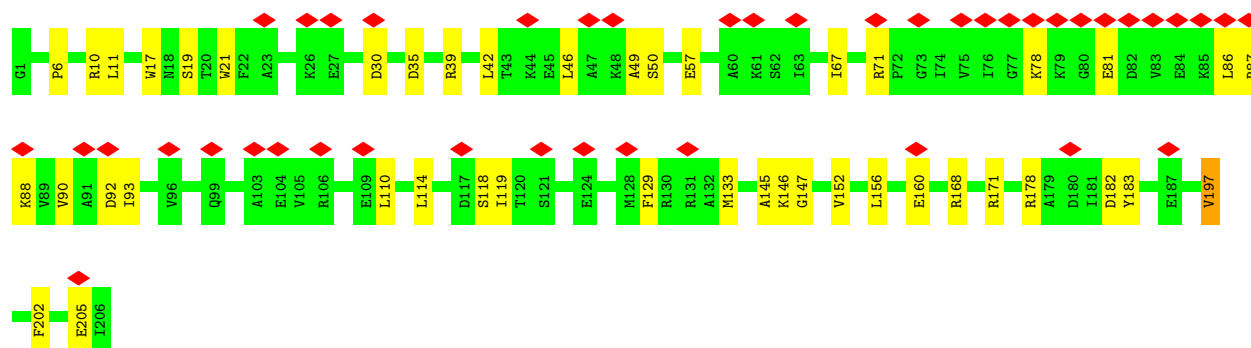
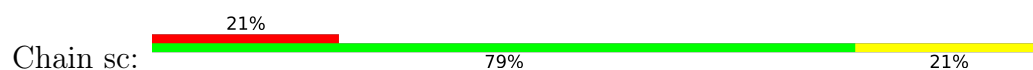
• Molecule 36: Probable ATP-binding protein YbiT



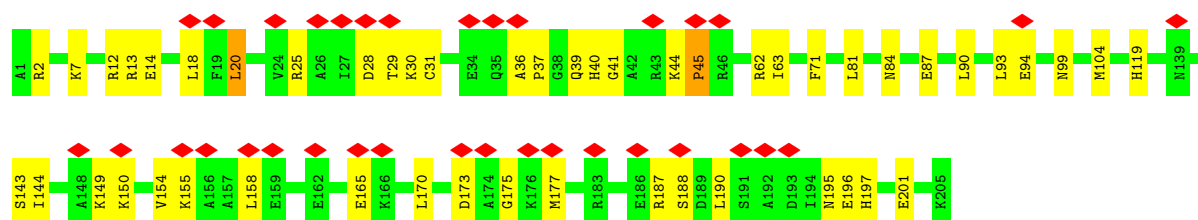
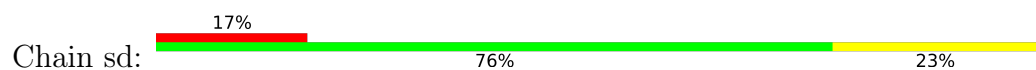
• Molecule 37: Small ribosomal subunit protein uS2



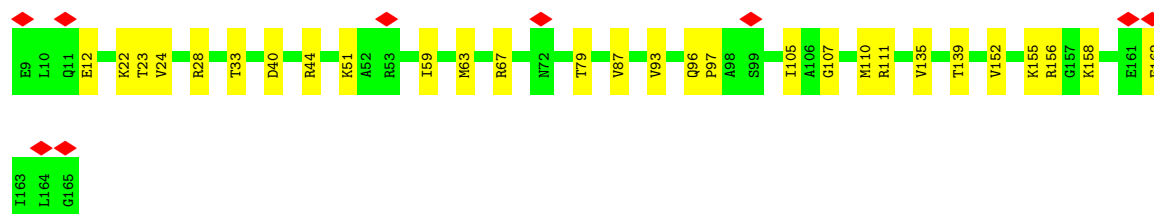
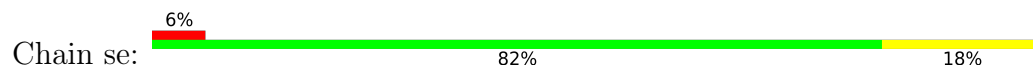
• Molecule 38: Small ribosomal subunit protein uS3



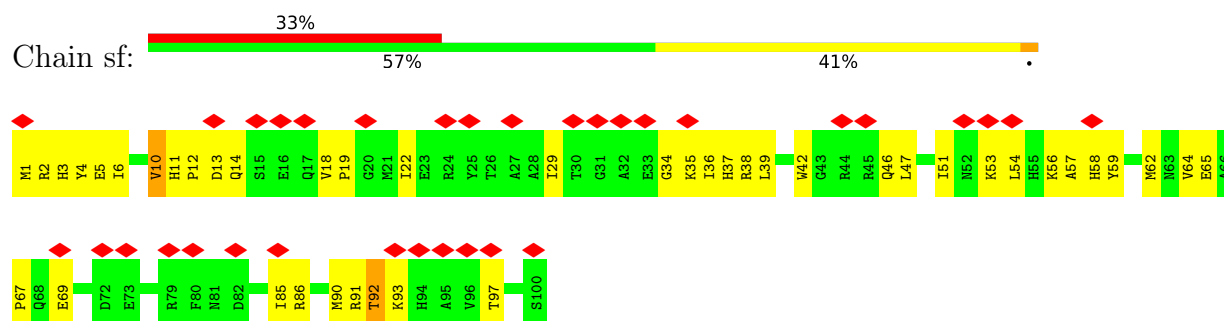
• Molecule 39: 30S ribosomal protein S4



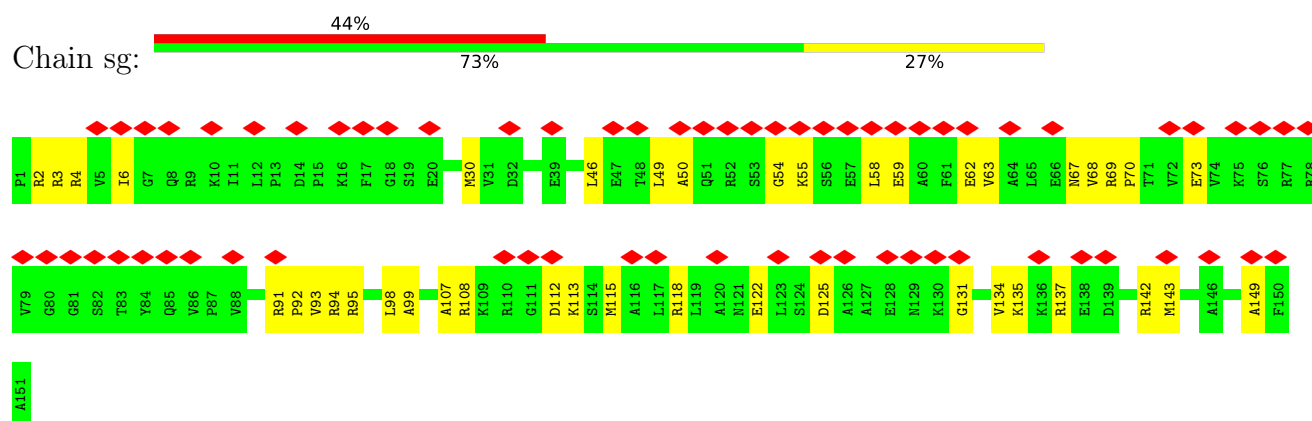
• Molecule 40: Small ribosomal subunit protein uS5



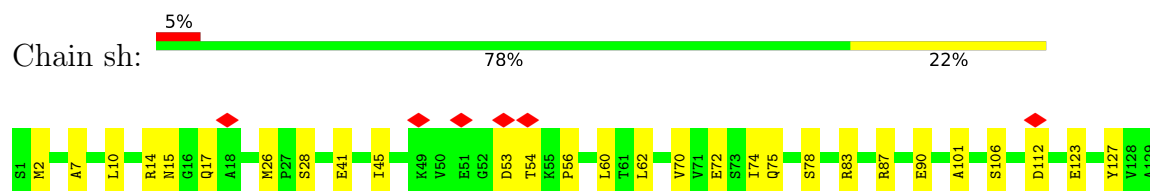
- Molecule 41: 30S ribosomal protein S6, non-modified isoform



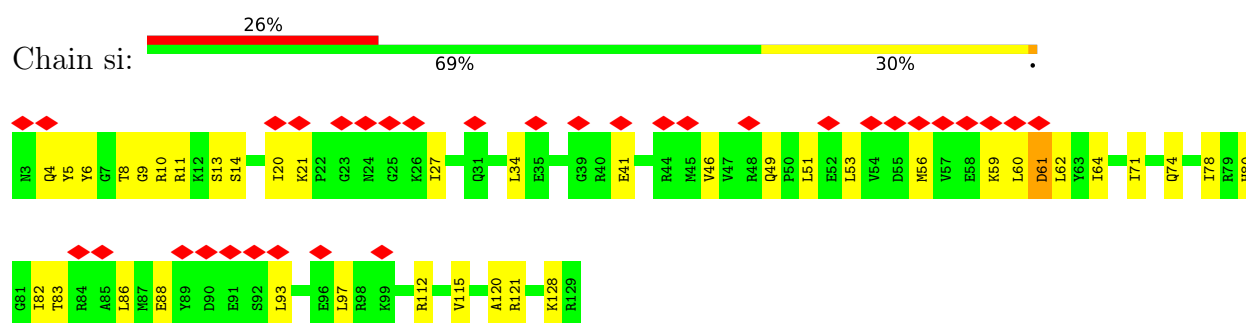
- Molecule 42: 30S ribosomal protein S7



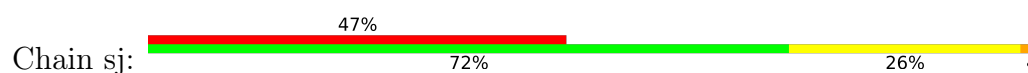
- Molecule 43: 30S ribosomal protein S8

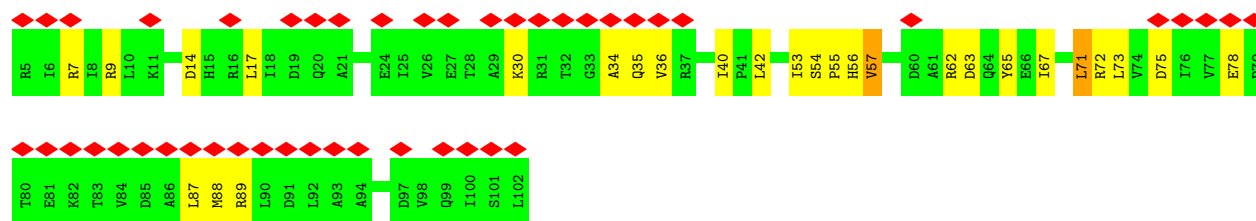


- Molecule 44: Small ribosomal subunit protein uS9

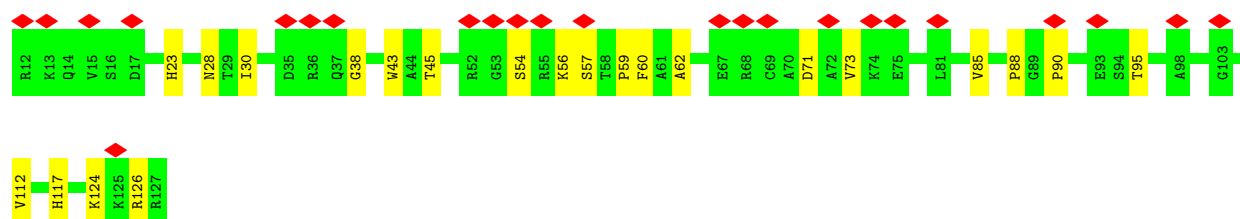
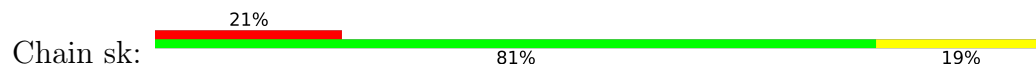


- Molecule 45: 30S ribosomal protein S10

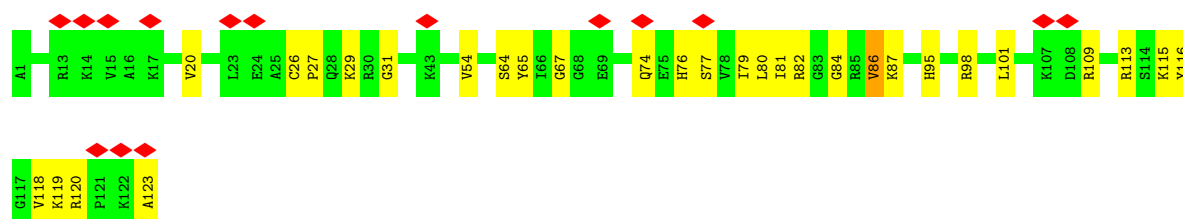
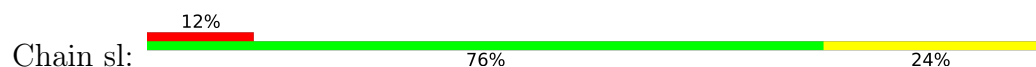




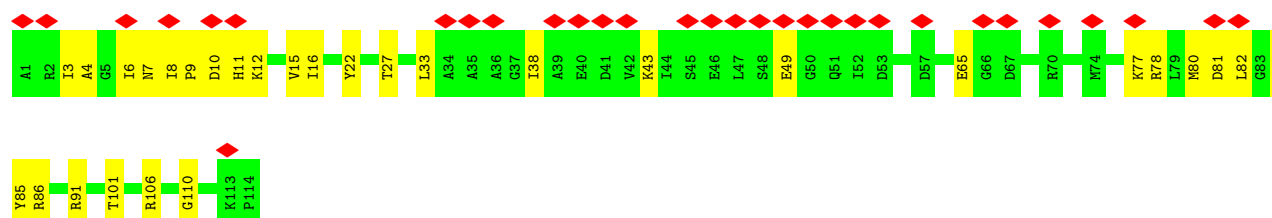
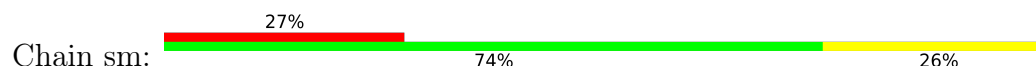
- Molecule 46: Small ribosomal subunit protein uS11



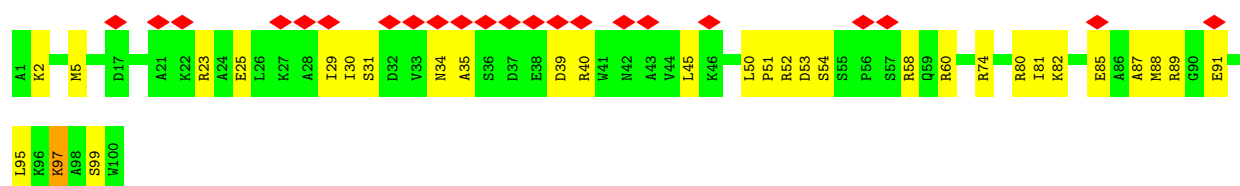
- Molecule 47: Small ribosomal subunit protein uS12



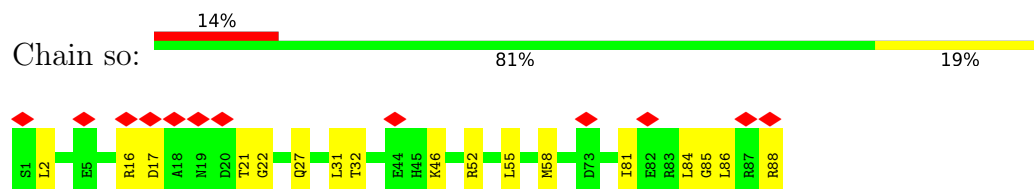
- Molecule 48: 30S ribosomal protein S13



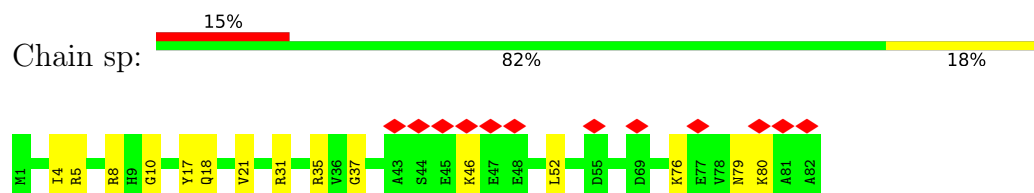
- Molecule 49: Small ribosomal subunit protein uS14



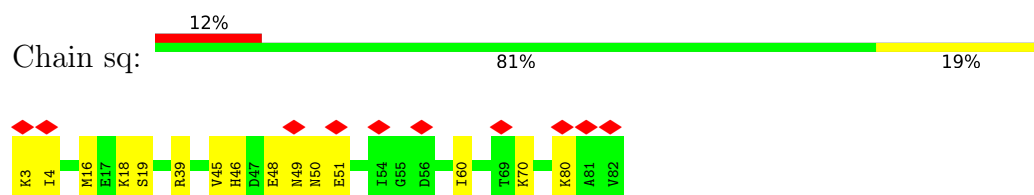
- Molecule 50: Small ribosomal subunit protein uS15



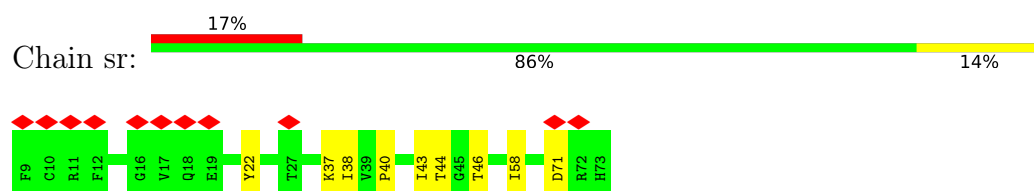
- Molecule 51: Small ribosomal subunit protein bS16



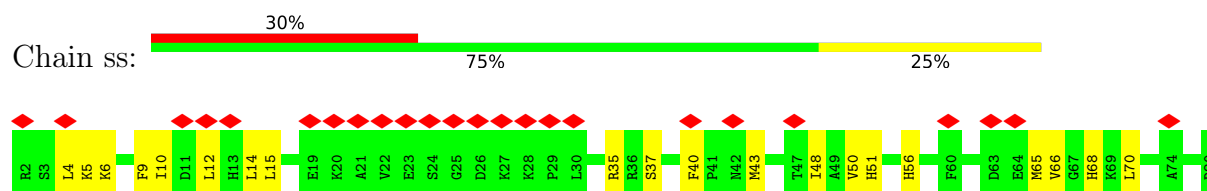
- Molecule 52: Small ribosomal subunit protein uS17



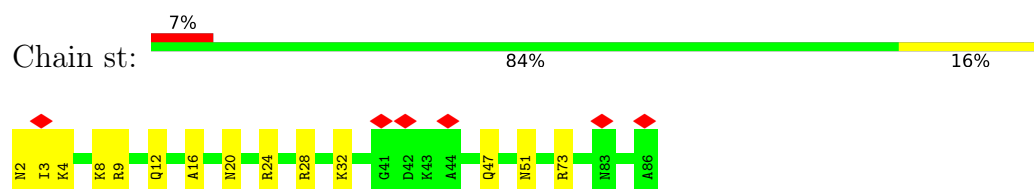
- Molecule 53: 30S ribosomal protein S18



- Molecule 54: 30S ribosomal protein S19



- Molecule 55: 30S ribosomal protein S20



- Molecule 56: Small ribosomal subunit protein bS21





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40604	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.8	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.138	Depositor
Minimum map value	-3.742	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.237	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ATP, 4SU, 4OC, PSU, NA, FME, H2U, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.11	0/1361	0.30	0/1796
2	13	0.20	0/1152	0.28	0/1551
3	14	0.21	0/947	0.37	0/1268
4	15	0.21	0/1062	0.31	0/1413
5	16	0.20	0/1093	0.34	0/1460
6	17	0.22	0/973	0.36	0/1301
7	18	0.15	0/902	0.29	0/1209
8	19	0.20	0/929	0.35	0/1242
9	2	0.20	0/2121	0.35	0/2852
10	20	0.23	0/960	0.31	0/1278
11	21	0.20	0/829	0.40	0/1107
12	22	0.20	0/864	0.32	0/1156
13	23	0.18	0/744	0.34	0/994
14	24	0.16	0/787	0.29	0/1051
15	25	0.16	0/766	0.28	0/1025
16	27	0.22	0/595	0.31	0/787
17	28	0.19	0/635	0.28	0/848
18	29	0.14	0/510	0.24	0/677
19	3	0.22	0/1586	0.35	0/2134
20	30	0.20	0/453	0.28	0/605
21	31	0.12	0/531	0.35	0/709
22	32	0.20	0/450	0.38	0/599
23	33	0.18	0/416	0.40	0/554
24	34	0.23	0/380	0.38	0/498
25	35	0.21	0/513	0.32	0/676
26	36	0.18	0/303	0.25	0/397
27	4	0.19	0/1571	0.30	0/2113
28	5	0.14	0/1434	0.32	0/1926
29	6	0.21	0/1343	0.53	3/1816 (0.2%)
30	9	0.14	0/1122	0.42	0/1515
31	M	0.11	0/219	0.21	0/339
32	R1	0.21	0/69797	0.28	0/108890

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	R2	0.17	0/2847	0.28	0/4440
34	R3	0.16	0/36963	0.26	0/57662
35	T	0.19	1/1716 (0.1%)	0.26	0/2672
36	Y	0.16	0/4245	0.44	1/5723 (0.0%)
37	sb	0.13	0/1735	0.36	0/2338
38	sc	0.13	0/1651	0.27	0/2225
39	sd	0.20	1/1665 (0.1%)	0.44	3/2227 (0.1%)
40	se	0.16	0/1169	0.40	0/1573
41	sf	0.14	0/835	0.49	0/1128
42	sg	0.11	0/1195	0.31	0/1602
43	sh	0.14	0/989	0.27	0/1326
44	si	0.13	0/1034	0.37	0/1375
45	sj	0.14	0/796	0.36	0/1077
46	sk	0.13	0/885	0.29	0/1195
47	sl	0.19	0/969	0.43	0/1300
48	sm	0.14	0/892	0.40	0/1193
49	sn	0.15	0/817	0.40	0/1088
50	so	0.13	0/722	0.23	0/964
51	sp	0.14	0/659	0.26	0/884
52	sq	0.16	0/657	0.32	0/881
53	sr	0.11	0/544	0.22	0/731
54	ss	0.14	0/652	0.29	0/877
55	st	0.14	0/671	0.26	0/888
56	su	0.16	0/550	0.53	0/728
All	All	0.19	2/162206 (0.0%)	0.30	7/241883 (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
29	6	0	1
30	9	0	1
35	T	7	0
41	sf	0	2
47	sl	0	1
49	sn	0	1
56	su	0	1
All	All	7	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	sd	45	PRO	CG-CD	-6.13	1.29	1.50
35	T	8	4SU	O3'-P	5.11	1.61	1.56

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	sd	45	PRO	N-CD-CG	-11.10	86.55	103.20
29	6	11	PRO	N-CD-CG	-10.04	88.14	103.20
29	6	11	PRO	CA-CB-CG	-7.83	89.62	104.50
29	6	11	PRO	CA-N-CD	-6.91	102.33	112.00
39	sd	45	PRO	CA-CB-CG	-6.56	92.03	104.50

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	T	8	4SU	C1',C2'
35	T	20	H2U	C2'
35	T	32	4OC	C2'
35	T	54	5MU	C3',C4'
35	T	55	PSU	C4'

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	6	12	ALA	Peptide
30	9	8	LYS	Peptide
41	sf	11	HIS	Peptide
41	sf	92	THR	Peptide
47	sl	86	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1353	0	1159	31	0
2	13	1129	0	1162	27	0
3	14	938	0	1012	21	0
4	15	1053	0	1129	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	16	1074	0	1157	21	0
6	17	960	0	1000	17	0
7	18	892	0	923	21	0
8	19	917	0	965	18	0
9	2	2082	0	2157	35	0
10	20	947	0	1022	17	0
11	21	816	0	839	14	0
12	22	857	0	922	16	0
13	23	738	0	807	12	0
14	24	779	0	834	5	0
15	25	753	0	780	12	0
16	27	588	0	604	12	0
17	28	625	0	655	13	0
18	29	509	0	543	6	0
19	3	1565	0	1616	38	0
20	30	449	0	491	7	0
21	31	522	0	524	20	0
22	32	444	0	461	20	0
23	33	409	0	440	6	0
24	34	377	0	418	11	0
25	35	504	0	574	10	0
26	36	302	0	343	5	0
27	4	1552	0	1619	26	0
28	5	1410	0	1447	36	0
29	6	1323	0	1374	19	0
30	9	1111	0	1148	22	0
31	M	195	0	99	0	0
32	R1	62318	0	31344	580	0
33	R2	2546	0	1292	34	0
34	R3	33012	0	16617	352	0
35	T	1639	0	843	18	0
36	Y	4170	0	4132	136	0
37	sb	1704	0	1732	42	0
38	sc	1624	0	1699	29	0
39	sd	1643	0	1710	36	0
40	se	1156	0	1199	20	0
41	sf	817	0	808	28	0
42	sg	1181	0	1240	34	0
43	sh	979	0	1034	19	0
44	si	1022	0	1070	29	0
45	sj	786	0	828	21	0
46	sk	869	0	878	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	sl	955	0	1019	23	0
48	sm	883	0	944	25	0
49	sn	805	0	847	29	0
50	so	714	0	737	13	0
51	sp	649	0	666	10	0
52	sq	648	0	691	12	0
53	sr	535	0	552	8	0
54	ss	637	0	665	16	0
55	st	665	0	714	14	0
56	su	544	0	579	30	0
57	15	1	0	0	0	0
57	17	1	0	0	0	0
57	32	1	0	0	0	0
57	M	1	0	0	0	0
57	R1	184	0	0	0	0
57	R3	53	0	0	0	0
58	T	10	0	10	1	0
59	Y	62	0	24	3	0
60	Y	2	0	0	0	0
All	All	149989	0	102098	1852	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 8.

The worst 5 of 1852 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)
36:Y:347:LYS:HZ2	36:Y:501:LEU:HB2	1.15	1.07
32:R1:1847:G:HO2'	32:R1:1848:A:H8	1.04	0.97
11:21:51:VAL:HG12	11:21:52:PRO:HD2	1.48	0.96
8:19:113:LEU:HD12	8:19:114:ASN:H	1.37	0.90
34:R3:705:G:H21	46:sk:30:ILE:HD11	1.39	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	218/220 (99%)	202 (93%)	16 (7%)	0	100	100
2	13	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
3	14	120/122 (98%)	108 (90%)	12 (10%)	0	100	100
4	15	142/144 (99%)	131 (92%)	11 (8%)	0	100	100
5	16	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
6	17	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
7	18	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
8	19	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
9	2	269/271 (99%)	245 (91%)	24 (9%)	0	100	100
10	20	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
11	21	101/103 (98%)	93 (92%)	7 (7%)	1 (1%)	12	40
12	22	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
13	23	91/93 (98%)	79 (87%)	12 (13%)	0	100	100
14	24	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
15	25	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
16	27	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
17	28	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
18	29	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
19	3	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
20	30	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
21	31	64/66 (97%)	55 (86%)	9 (14%)	0	100	100
22	32	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
23	33	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
24	34	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
25	35	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	36	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
27	4	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
28	5	175/177 (99%)	166 (95%)	9 (5%)	0	100	100
29	6	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
30	9	147/149 (99%)	129 (88%)	16 (11%)	2 (1%)	9	33
36	Y	525/530 (99%)	445 (85%)	75 (14%)	5 (1%)	12	40
37	sb	216/218 (99%)	196 (91%)	19 (9%)	1 (0%)	24	55
38	sc	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
39	sd	203/205 (99%)	187 (92%)	16 (8%)	0	100	100
40	se	155/157 (99%)	130 (84%)	25 (16%)	0	100	100
41	sf	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
42	sg	149/151 (99%)	135 (91%)	14 (9%)	0	100	100
43	sh	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
44	si	125/127 (98%)	104 (83%)	20 (16%)	1 (1%)	16	45
45	sj	96/98 (98%)	88 (92%)	7 (7%)	1 (1%)	12	40
46	sk	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
47	sl	121/123 (98%)	94 (78%)	27 (22%)	0	100	100
48	sm	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
49	sn	98/100 (98%)	78 (80%)	19 (19%)	1 (1%)	12	40
50	so	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
51	sp	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
52	sq	78/80 (98%)	65 (83%)	13 (17%)	0	100	100
53	sr	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
54	ss	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
55	st	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
56	su	63/65 (97%)	42 (67%)	21 (33%)	0	100	100
All	All	6324/6429 (98%)	5720 (90%)	591 (9%)	13 (0%)	44	71

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	21	51	VAL
36	Y	188	ILE

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Mol	Chain	Res	Type
30	9	9	VAL
36	Y	420	SER
36	Y	377	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	106/171 (62%)	105 (99%)	1 (1%)	70	78
2	13	116/116 (100%)	116 (100%)	0	100	100
3	14	103/103 (100%)	103 (100%)	0	100	100
4	15	103/103 (100%)	101 (98%)	2 (2%)	50	68
5	16	109/109 (100%)	109 (100%)	0	100	100
6	17	100/100 (100%)	100 (100%)	0	100	100
7	18	86/86 (100%)	85 (99%)	1 (1%)	63	75
8	19	99/99 (100%)	98 (99%)	1 (1%)	68	76
9	2	216/216 (100%)	212 (98%)	4 (2%)	50	68
10	20	89/89 (100%)	88 (99%)	1 (1%)	65	76
11	21	84/84 (100%)	82 (98%)	2 (2%)	43	65
12	22	93/93 (100%)	93 (100%)	0	100	100
13	23	80/80 (100%)	79 (99%)	1 (1%)	61	74
14	24	83/83 (100%)	82 (99%)	1 (1%)	63	75
15	25	78/78 (100%)	77 (99%)	1 (1%)	61	74
16	27	59/59 (100%)	59 (100%)	0	100	100
17	28	67/67 (100%)	65 (97%)	2 (3%)	36	61
18	29	55/55 (100%)	54 (98%)	1 (2%)	51	70
19	3	164/164 (100%)	161 (98%)	3 (2%)	51	70
20	30	48/48 (100%)	46 (96%)	2 (4%)	26	55
21	31	59/59 (100%)	58 (98%)	1 (2%)	53	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	32	47/47 (100%)	47 (100%)	0	100	100
23	33	45/45 (100%)	45 (100%)	0	100	100
24	34	38/38 (100%)	37 (97%)	1 (3%)	40	64
25	35	51/51 (100%)	51 (100%)	0	100	100
26	36	34/34 (100%)	34 (100%)	0	100	100
27	4	165/165 (100%)	165 (100%)	0	100	100
28	5	148/148 (100%)	148 (100%)	0	100	100
29	6	137/137 (100%)	137 (100%)	0	100	100
30	9	114/114 (100%)	114 (100%)	0	100	100
36	Y	449/456 (98%)	448 (100%)	1 (0%)	87	88
37	sb	180/180 (100%)	179 (99%)	1 (1%)	78	81
38	sc	170/170 (100%)	168 (99%)	2 (1%)	63	75
39	sd	172/172 (100%)	170 (99%)	2 (1%)	63	75
40	se	119/119 (100%)	118 (99%)	1 (1%)	73	79
41	sf	87/87 (100%)	85 (98%)	2 (2%)	44	66
42	sg	124/124 (100%)	124 (100%)	0	100	100
43	sh	104/104 (100%)	103 (99%)	1 (1%)	68	76
44	si	105/105 (100%)	104 (99%)	1 (1%)	68	76
45	sj	86/86 (100%)	84 (98%)	2 (2%)	44	66
46	sk	89/89 (100%)	88 (99%)	1 (1%)	65	76
47	sl	103/103 (100%)	103 (100%)	0	100	100
48	sm	92/92 (100%)	92 (100%)	0	100	100
49	sn	83/83 (100%)	83 (100%)	0	100	100
50	so	76/76 (100%)	76 (100%)	0	100	100
51	sp	65/65 (100%)	65 (100%)	0	100	100
52	sq	74/74 (100%)	74 (100%)	0	100	100
53	sr	56/56 (100%)	56 (100%)	0	100	100
54	ss	70/70 (100%)	70 (100%)	0	100	100
55	st	65/65 (100%)	65 (100%)	0	100	100
56	su	55/55 (100%)	54 (98%)	1 (2%)	51	70
All	All	5200/5272 (99%)	5160 (99%)	40 (1%)	70	79

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	sc	197	VAL
44	si	61	ASP
39	sd	20	LEU
41	sf	10	VAL
45	sj	87	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
36	Y	337	ASN
39	sd	125	ASN
36	Y	391	HIS
37	sb	17	HIS
39	sd	163	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	M	8/9 (88%)	1 (12%)	0
32	R1	2902/2903 (99%)	471 (16%)	8 (0%)
33	R2	118/119 (99%)	13 (11%)	1 (0%)
34	R3	1538/1539 (99%)	278 (18%)	5 (0%)
35	T	76/77 (98%)	12 (15%)	3 (3%)
All	All	4642/4647 (99%)	775 (16%)	17 (0%)

5 of 775 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	M	7	A
32	R1	10	A
32	R1	15	G
32	R1	35	G
32	R1	36	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	T	17	U
35	T	55	PSU

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Mol	Chain	Res	Type
32	R1	2326	C
33	R2	66	A
34	R3	391	G

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

5 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	$\# Z > 2$
35	H2U	T	20	35	18,21,22	4.39	5 (27%)	19,30,33	3.81	6 (31%)
35	PSU	T	55	35	18,21,22	2.19	9 (50%)	21,30,33	2.31	4 (19%)
35	4OC	T	32	35	20,23,24	3.21	3 (15%)	25,32,35	1.10	3 (12%)
35	5MU	T	54	35	19,22,23	2.17	6 (31%)	27,32,35	2.25	8 (29%)
35	4SU	T	8	35	18,21,22	3.84	8 (44%)	25,30,33	2.33	6 (24%)

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
35	H2U	T	20	35	1/1/8/9	5/7/38/39	0/2/2/2
35	PSU	T	55	35	1/1/5/5	1/7/25/26	0/2/2/2
35	4OC	T	32	35	1/1/5/6	0/9/29/30	0/2/2/2
35	5MU	T	54	35	2/2/5/5	4/7/25/26	0/2/2/2
35	4SU	T	8	35	2/2/5/5	0/7/25/26	0/2/2/2

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	T	8	4SU	O2-C2	12.07	1.44	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	T	32	4OC	O2-C2	11.42	1.45	1.23
35	T	20	H2U	O4-C4	10.38	1.43	1.23
35	T	20	H2U	C2-N1	9.34	1.48	1.35
35	T	20	H2U	O2-C2	8.49	1.38	1.23

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	T	20	H2U	O2-C2-N1	-10.07	111.00	123.10
35	T	8	4SU	C4-N3-C2	-7.16	120.45	127.31
35	T	20	H2U	O4-C4-N3	-7.07	109.41	120.30
35	T	55	PSU	N1-C2-N3	7.04	122.59	115.17
35	T	20	H2U	O4-C4-C5	-6.38	109.14	122.20

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	T	20	H2U	C2'
35	T	32	4OC	C2'
35	T	54	5MU	C3'
35	T	54	5MU	C4'
35	T	55	PSU	C4'

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	T	20	H2U	O4'-C4'-C5'-O5'
35	T	20	H2U	C3'-C4'-C5'-O5'
35	T	20	H2U	O4'-C1'-N1-C2
35	T	20	H2U	O4'-C1'-N1-C6
35	T	54	5MU	C4'-C5'-O5'-P

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	T	20	H2U	2	0
35	T	55	PSU	1	0
35	T	32	4OC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 246 ligands modelled in this entry, 243 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	ATP	Y	602	60	32,33,33	0.30	0	48,52,52	0.29	0
58	FME	T	101	35	8,9,10	0.95	0	8,9,11	0.97	0
59	ATP	Y	601	60	32,33,33	0.39	0	48,52,52	0.34	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	ATP	Y	602	60	-	3/22/38/38	0/3/3/3
58	FME	T	101	35	-	5/7/9/11	-
59	ATP	Y	601	60	-	6/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

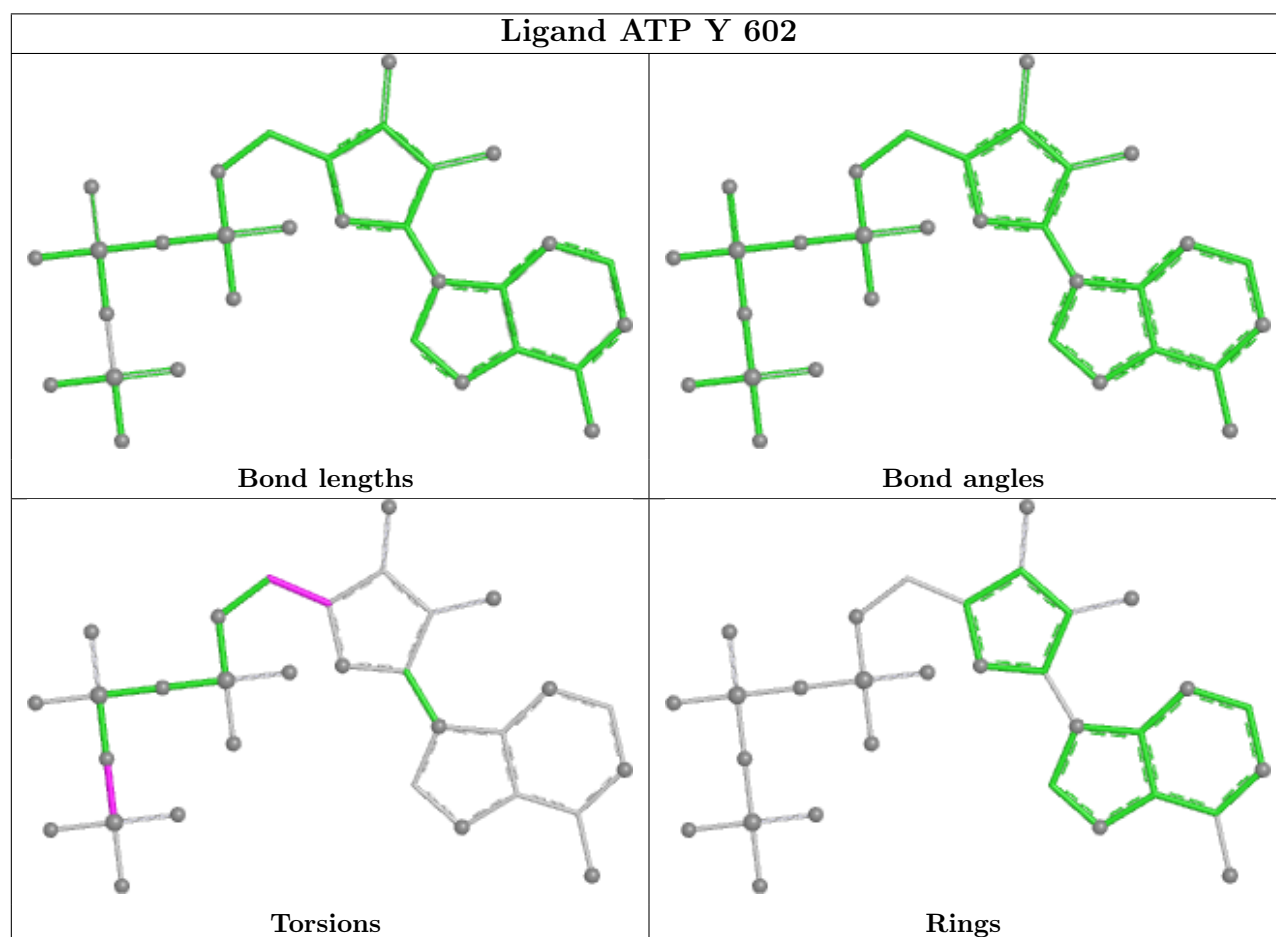
Mol	Chain	Res	Type	Atoms
58	T	101	FME	O1-CN-N-CA
58	T	101	FME	O-C-CA-CB
59	Y	601	ATP	C5'-O5'-PA-O1A
59	Y	601	ATP	C5'-O5'-PA-O2A
59	Y	601	ATP	C5'-O5'-PA-O3A

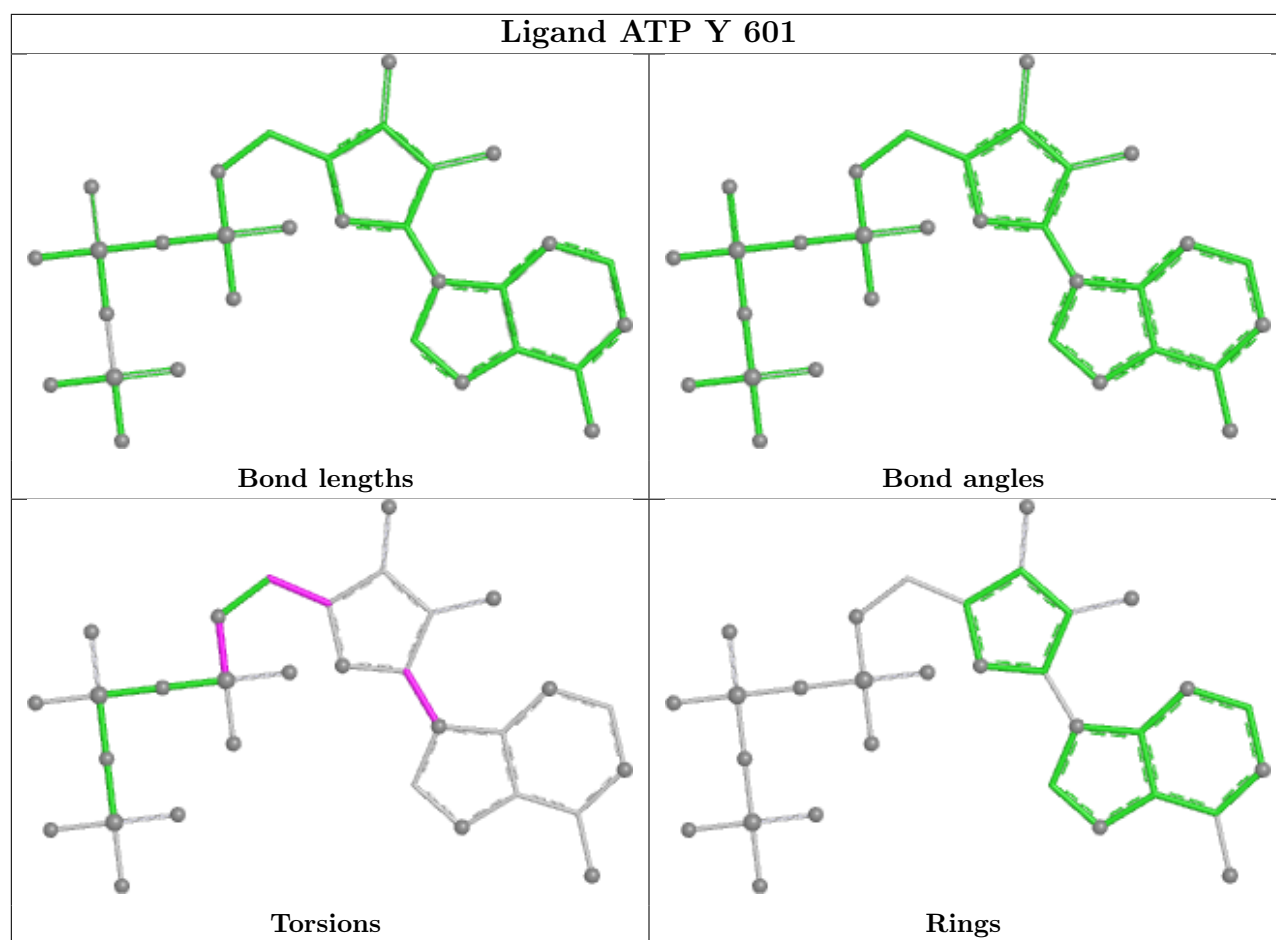
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	Y	602	ATP	1	0
58	T	101	FME	1	0
59	Y	601	ATP	2	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.

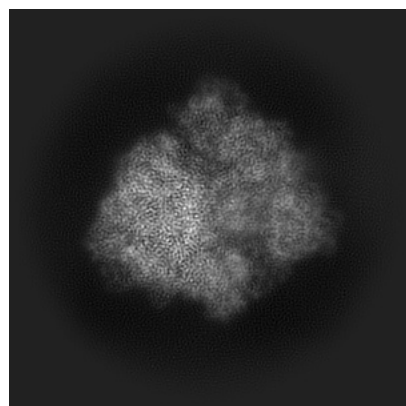
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29408. These allow visual inspection of the internal detail of the map and identification of artifacts.

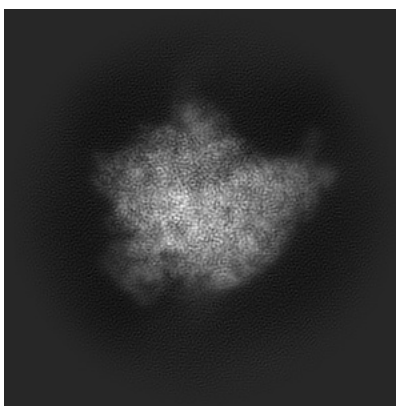
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

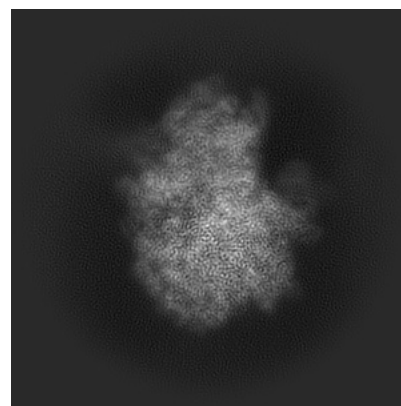
6.1.1 Primary map



X

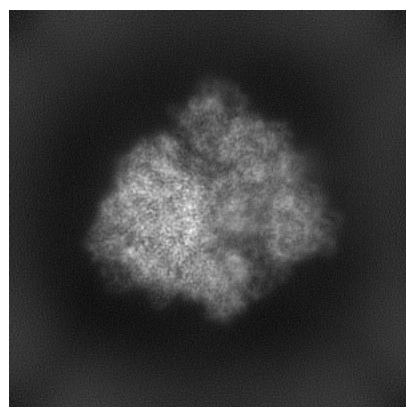


Y

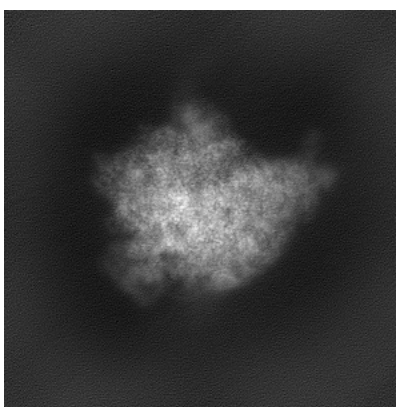


Z

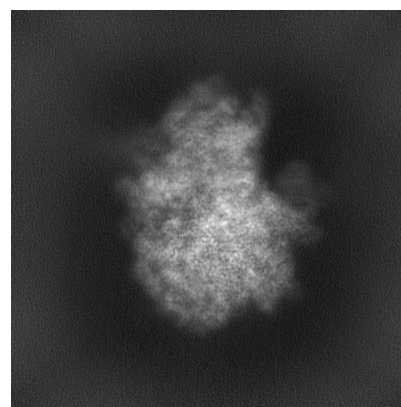
6.1.2 Raw map



X



Y

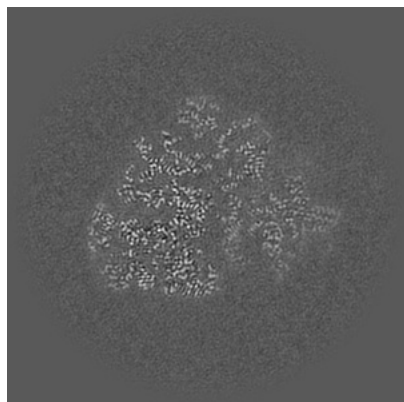


Z

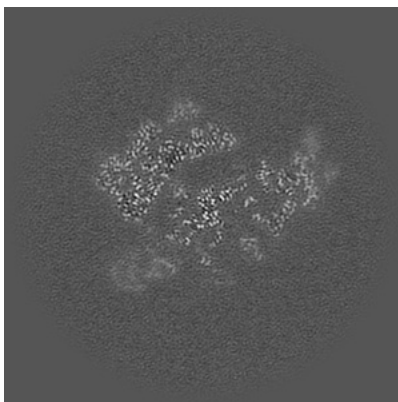
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

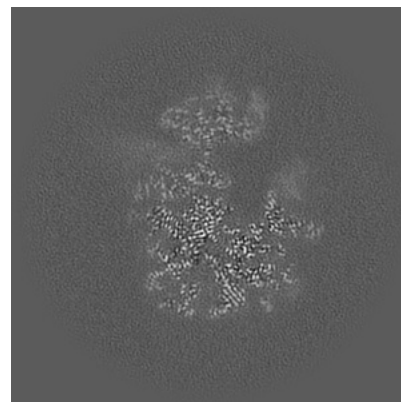
6.2.1 Primary map



X Index: 200

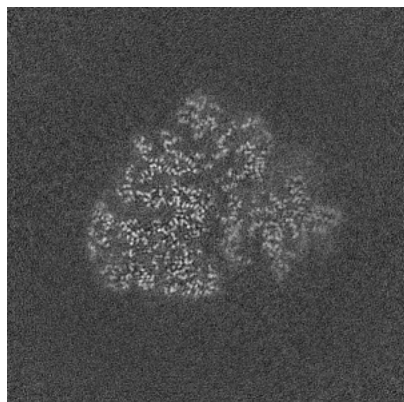


Y Index: 200

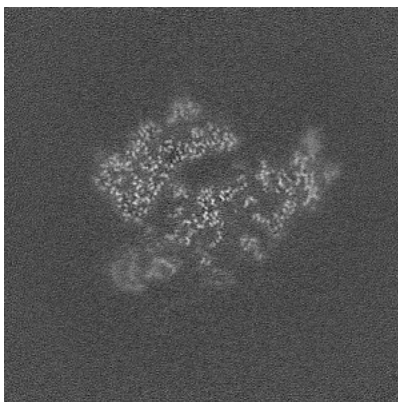


Z Index: 200

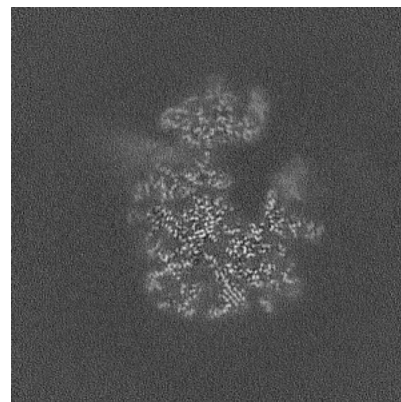
6.2.2 Raw map



X Index: 200



Y Index: 200

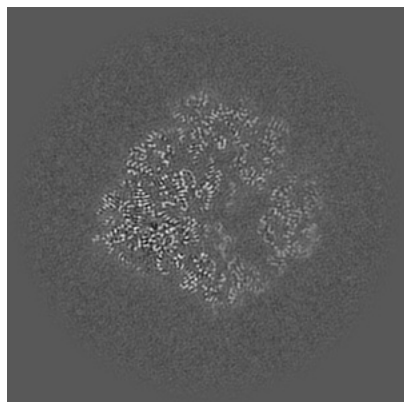


Z Index: 200

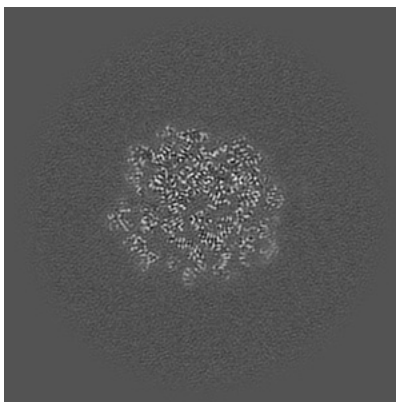
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

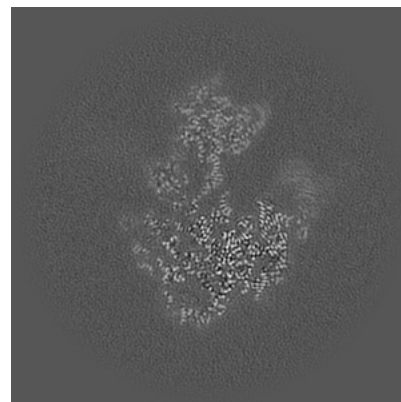
6.3.1 Primary map



X Index: 215

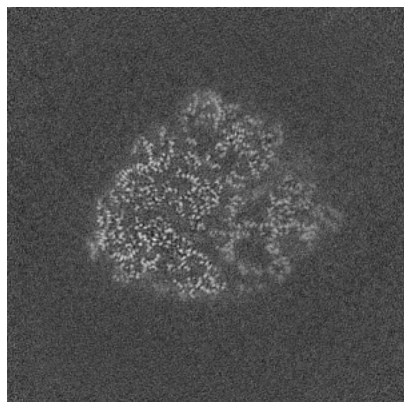


Y Index: 156

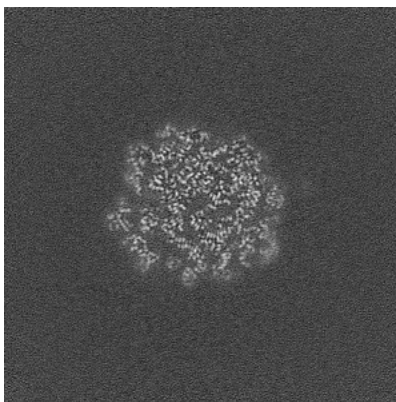


Z Index: 181

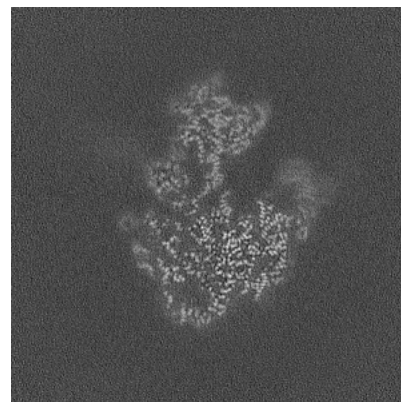
6.3.2 Raw map



X Index: 207



Y Index: 156

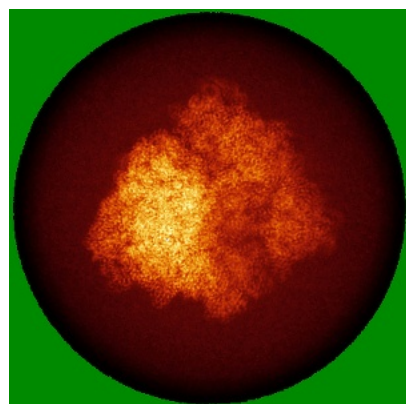


Z Index: 181

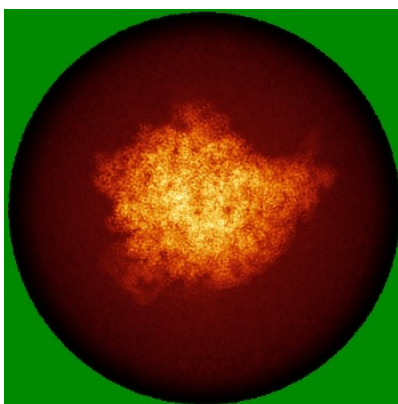
The images above show the largest variance slices of the map in three orthogonal directions.

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

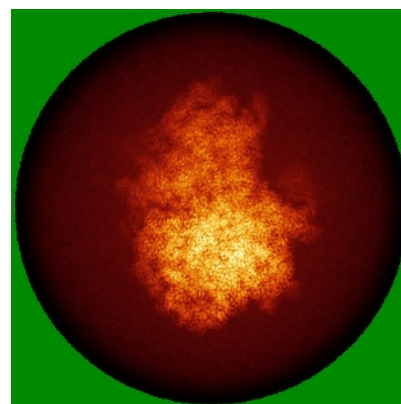
6.4.1 Primary map



X

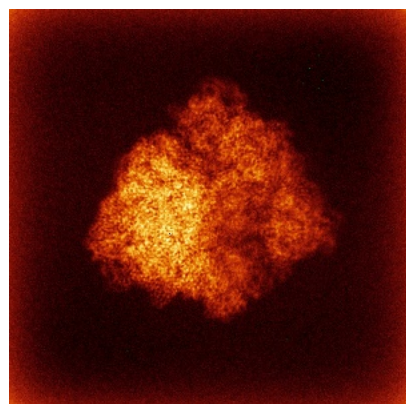


Y

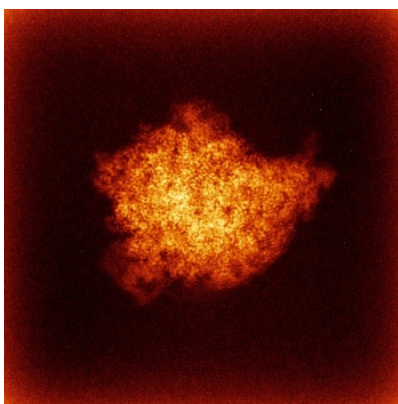


Z

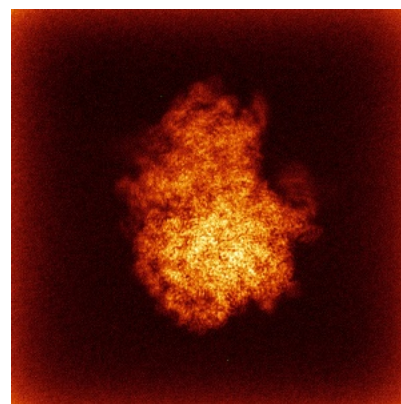
6.4.2 Raw map



X



Y

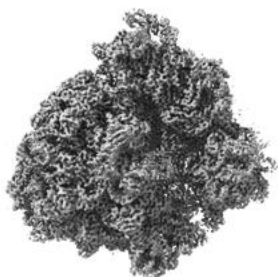


Z

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](#)

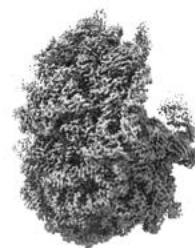
6.5.1 Primary map



X



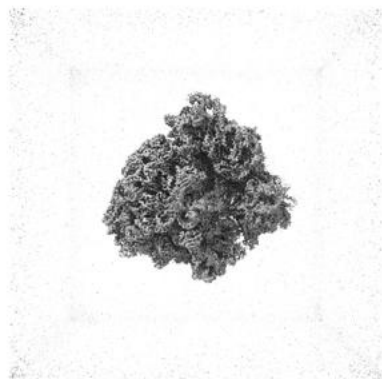
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

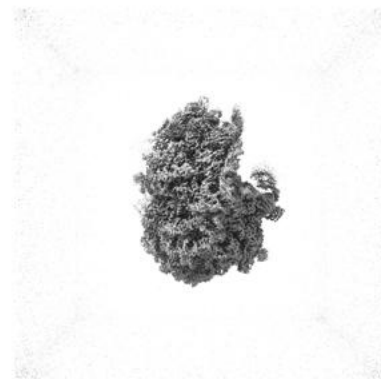
6.5.2 Raw map



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.

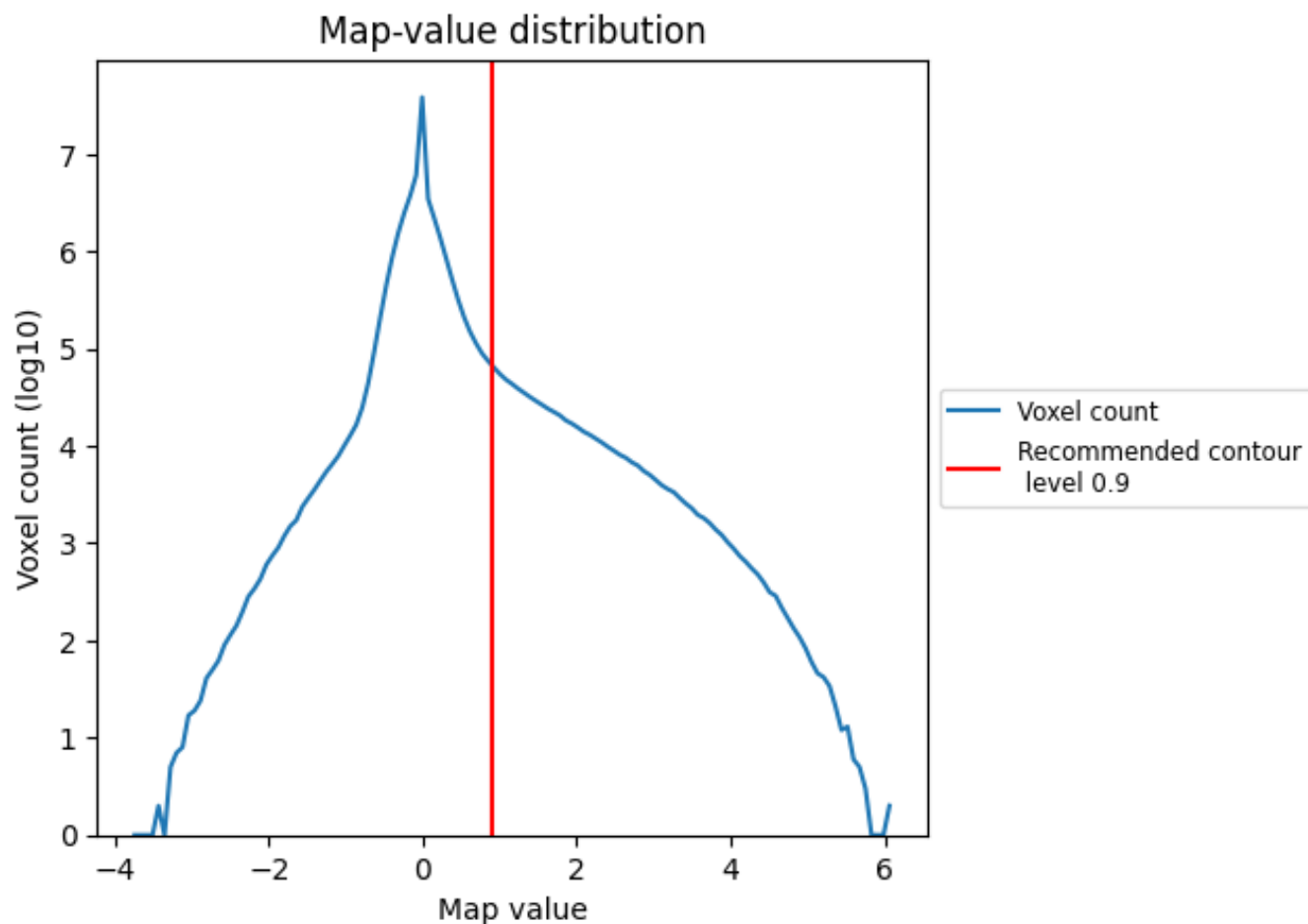
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

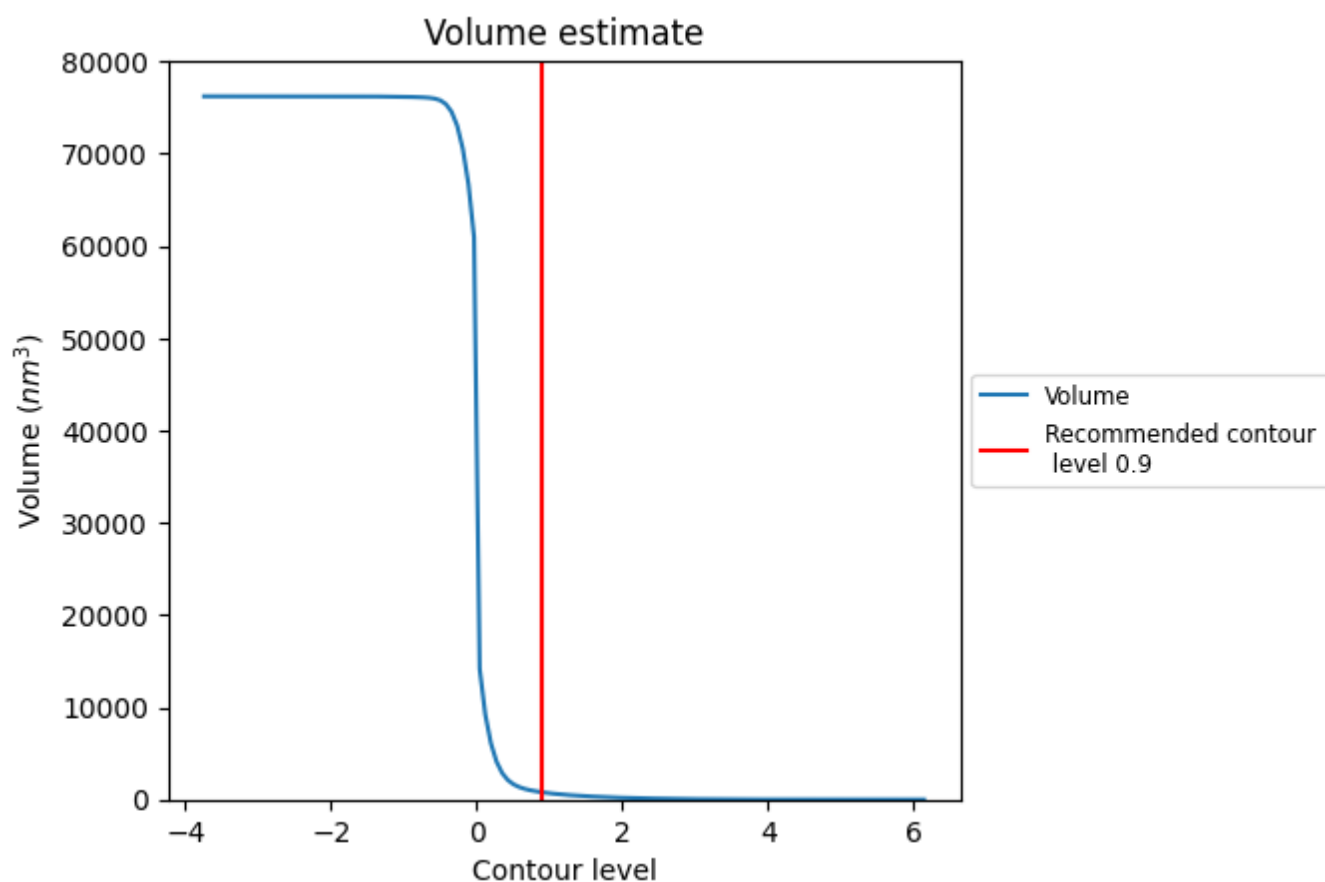
This section contains the results of statistical analysis of the map.

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.

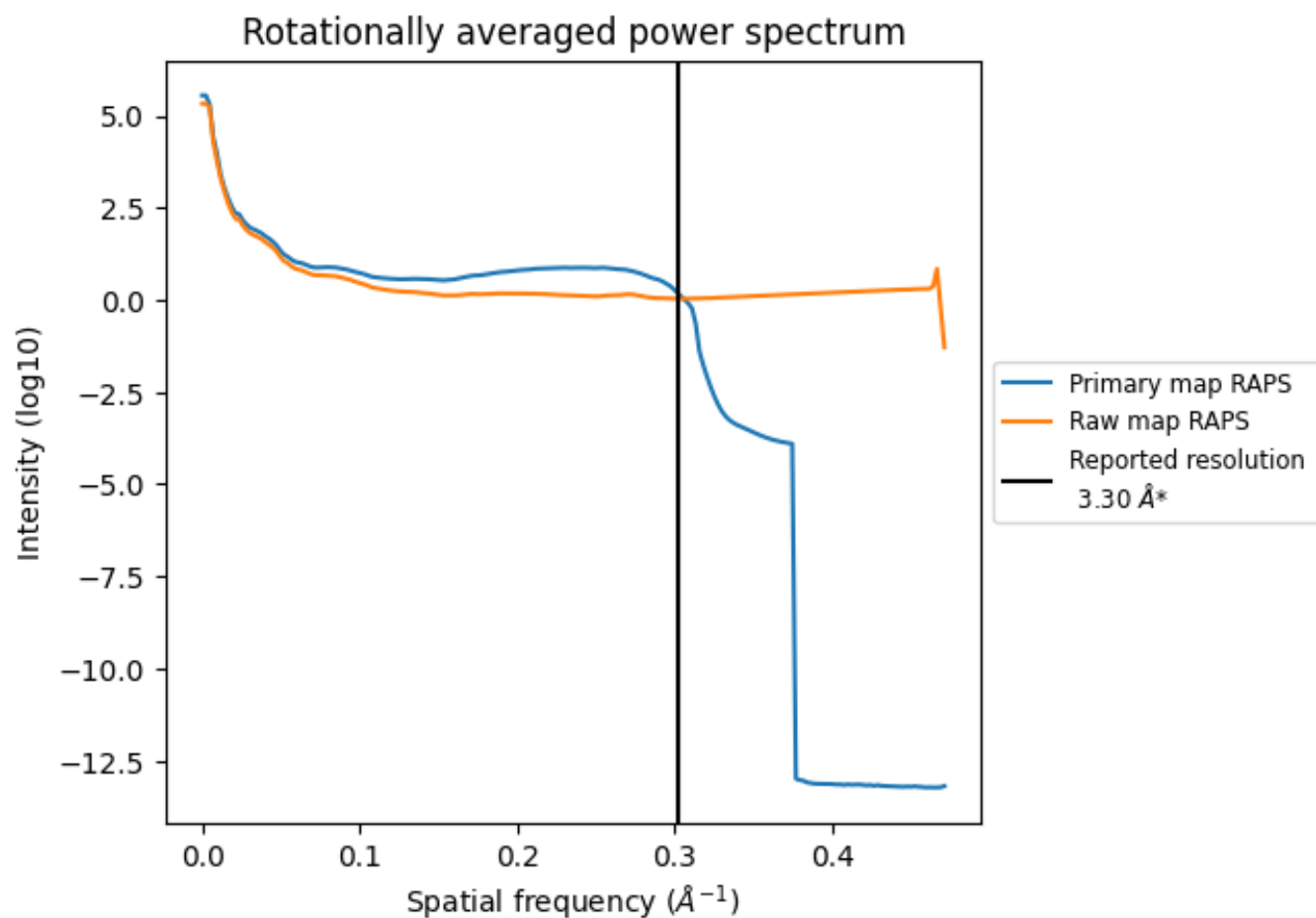
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 784 nm³; this corresponds to an approximate mass of 708 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 ⓘ

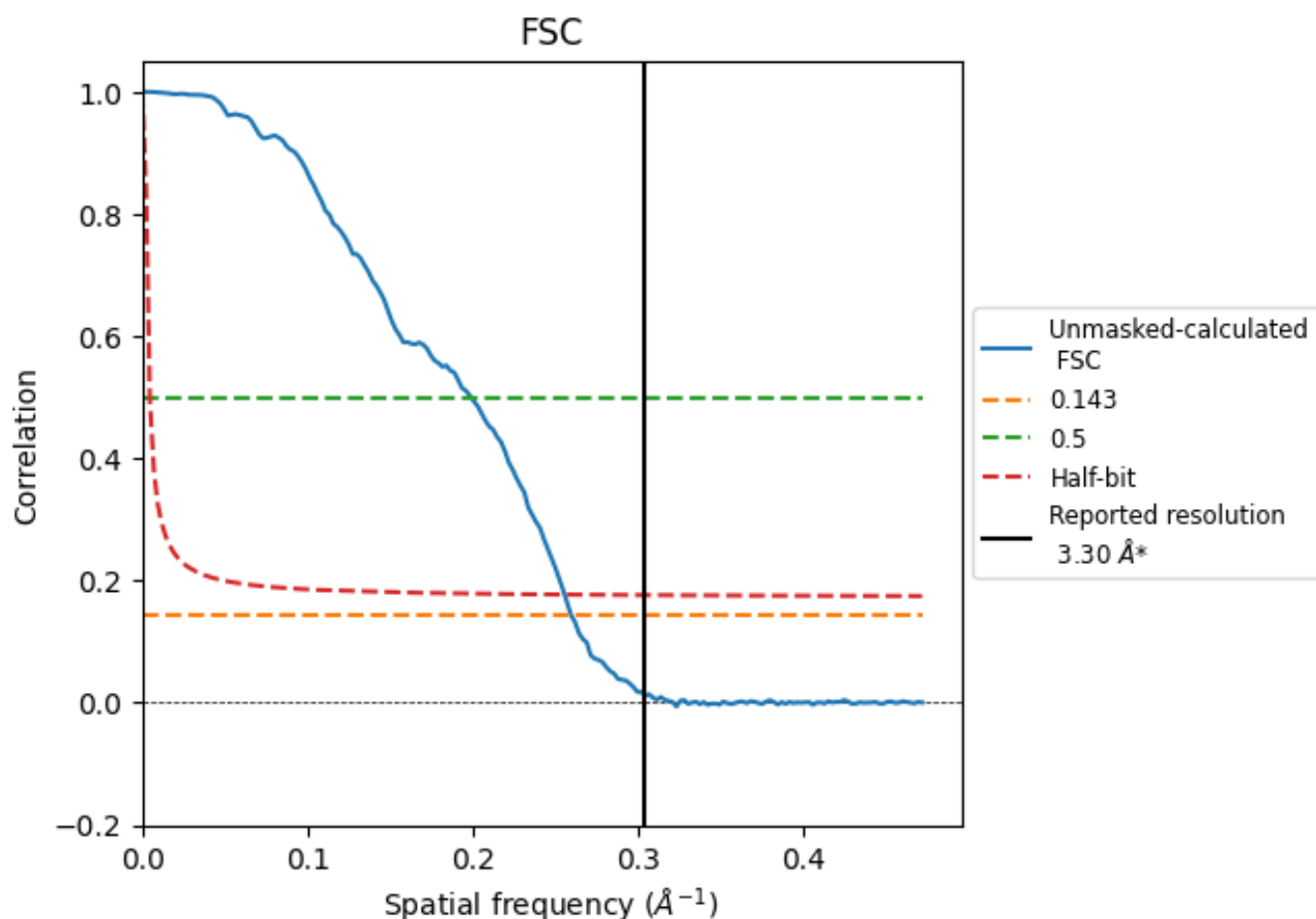


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

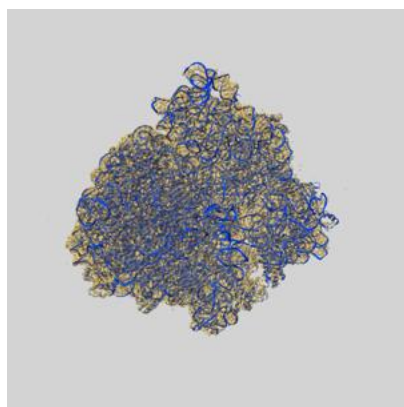
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.86	5.03	3.92

*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 3.86 differs from the reported value 3.3 by more than 10 %

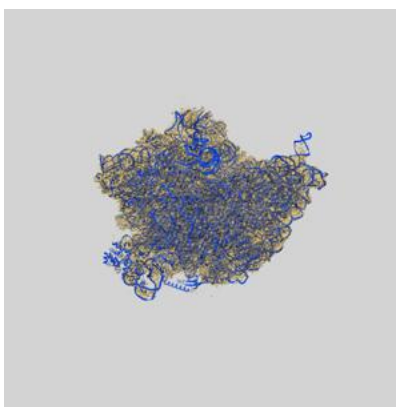
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29408 and PDB model 9NLQ. Per-residue inclusion information can be found in section 3 on page 17.

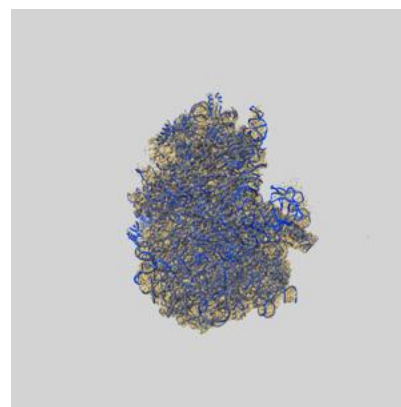
9.1 Map-model overlay [i](#)



X



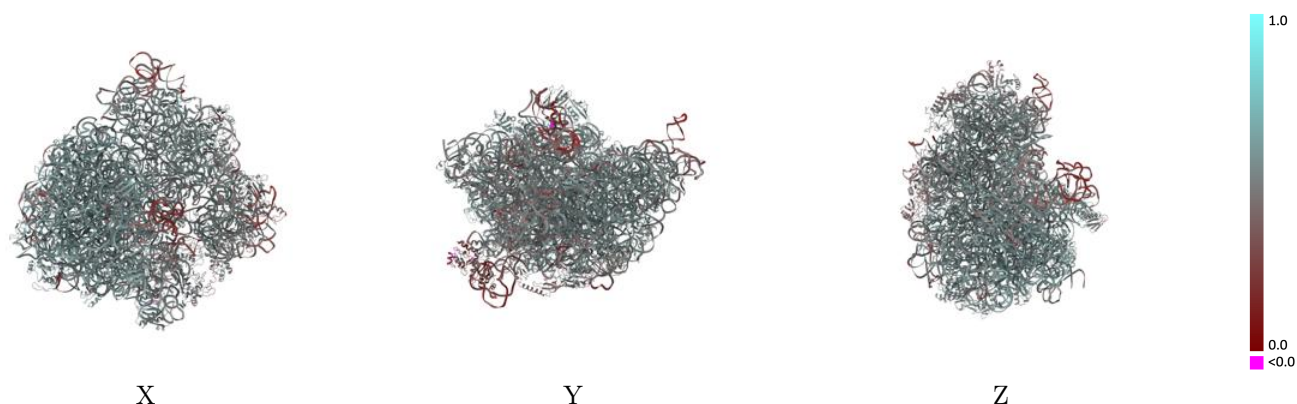
Y



Z

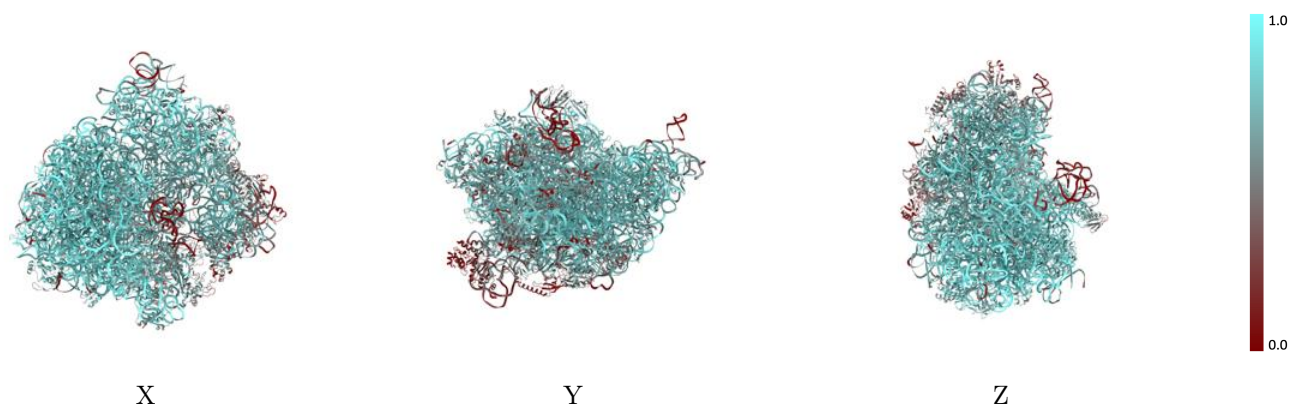
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



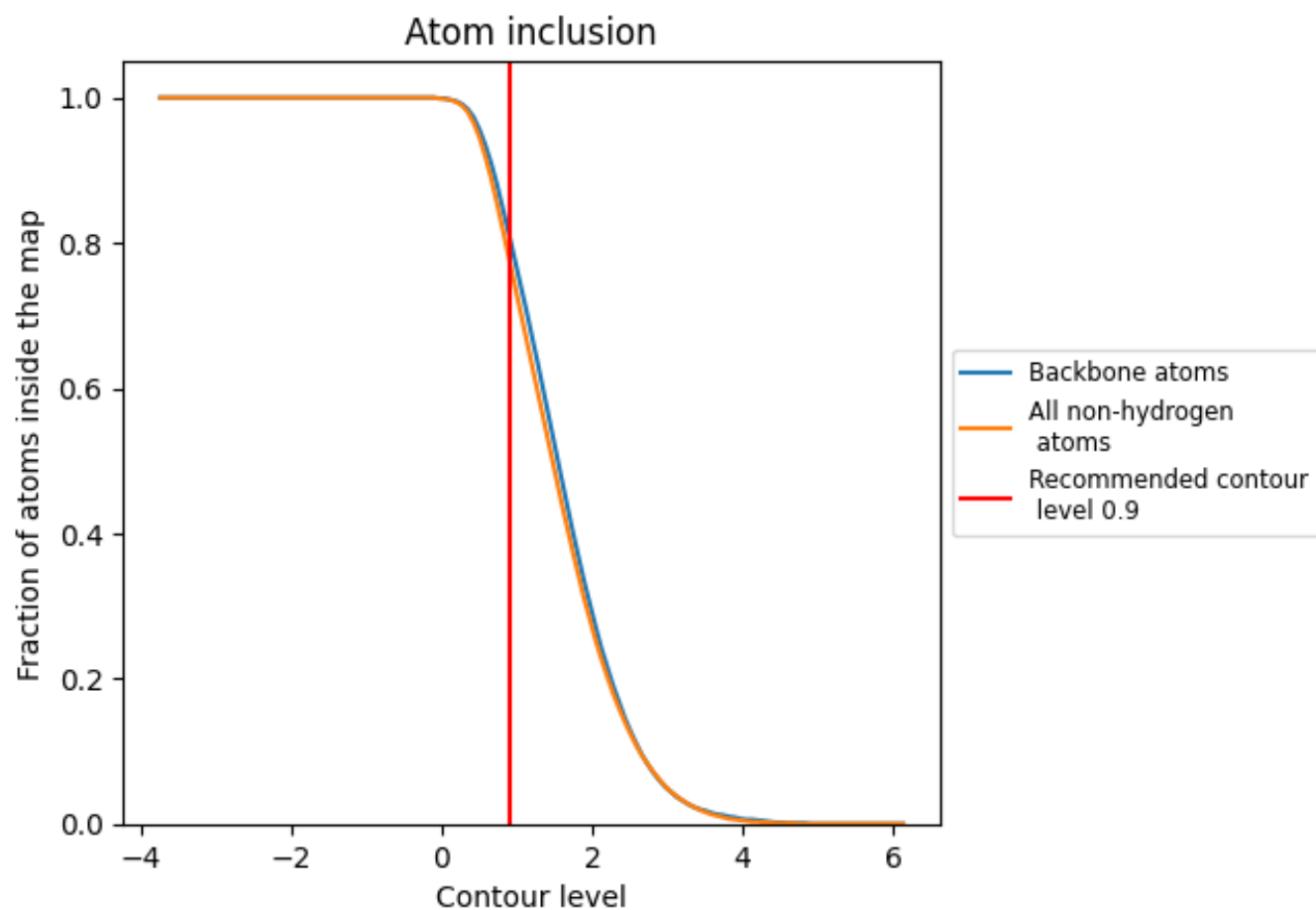
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 78% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7770	 0.5210
1	 0.0900	 0.3160
13	 0.8550	 0.5820
14	 0.8180	 0.5790
15	 0.8180	 0.5730
16	 0.8220	 0.5780
17	 0.8610	 0.5760
18	 0.7390	 0.5520
19	 0.8100	 0.5800
2	 0.8460	 0.5810
20	 0.8810	 0.5860
21	 0.7930	 0.5690
22	 0.8400	 0.5780
23	 0.7880	 0.5590
24	 0.7170	 0.5400
25	 0.7150	 0.5480
27	 0.8320	 0.5780
28	 0.8170	 0.5810
29	 0.7040	 0.5420
3	 0.8380	 0.5760
30	 0.8100	 0.5730
31	 0.3070	 0.3970
32	 0.8370	 0.5760
33	 0.7530	 0.5610
34	 0.8730	 0.5920
35	 0.8900	 0.6000
36	 0.8220	 0.5870
4	 0.7690	 0.5590
5	 0.5950	 0.5040
6	 0.6150	 0.5160
9	 0.2350	 0.4180
M	 0.5460	 0.4790
R1	 0.8570	 0.5320
R2	 0.8410	 0.5160
R3	 0.8000	 0.4980



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
T	 0.7290	 0.4890
Y	 0.5700	 0.4930
sb	 0.4820	 0.4610
sc	 0.5920	 0.5240
sd	 0.6240	 0.5160
se	 0.7240	 0.5430
sf	 0.4890	 0.4660
sg	 0.4530	 0.4650
sh	 0.7150	 0.5420
si	 0.5910	 0.4990
sj	 0.4350	 0.4330
sk	 0.5910	 0.5100
sl	 0.7080	 0.5380
sm	 0.5660	 0.5070
sn	 0.6060	 0.4940
so	 0.6430	 0.5380
sp	 0.7290	 0.5430
sq	 0.6600	 0.5300
sr	 0.6210	 0.5130
ss	 0.5220	 0.4800
st	 0.7280	 0.5420
su	 0.3870	 0.4010