



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 12:04 pm BST

PDB ID : 6HRM / pdb_00006hrm
EMDB ID : EMD-0261
Title : E. coli 70S d2d8 stapled ribosome
Authors : Schmied, W.H.; Tnimov, Z.; Uttamapinant, C.; Rae, C.D.; Fried, S.D.; Chin, J.W.
Deposited on : 2018-09-27
Resolution : 2.96 Å(reported)
Based on initial model : 5MDZ

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 : 1.8.4, 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

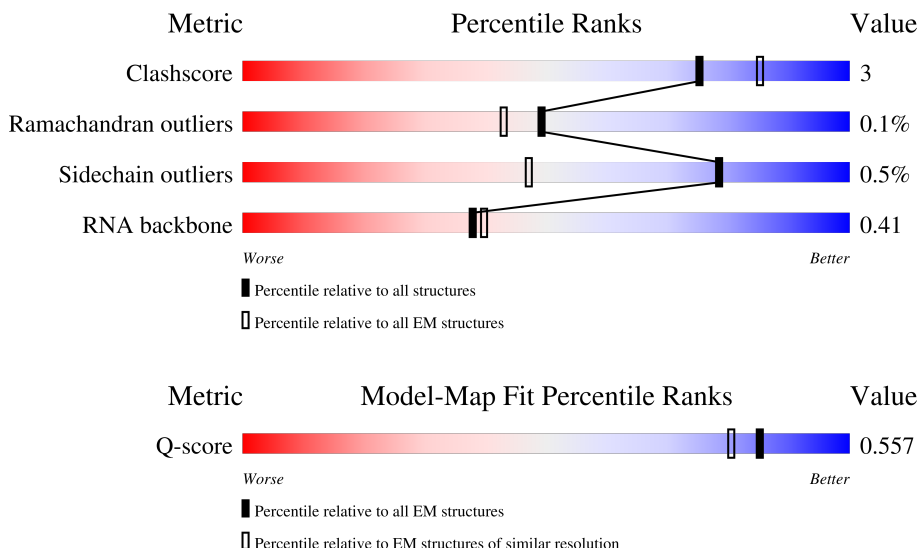
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	4458	
2	3	120	
3	B	271	

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Mol	Chain	Length	Quality of chain
4	C	209	
5	D	201	
6	E	177	
7	F	175	
8	G	149	
9	H	130	
10	I	135	
11	J	142	
12	K	123	
13	L	144	
14	M	136	
15	N	119	
16	O	116	
17	P	114	
18	Q	117	
19	R	103	
20	S	110	
21	T	94	
22	U	103	
23	V	94	
24	W	76	
25	X	77	
26	Y	62	
27	Z	58	
28	a	66	

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Mol	Chain	Length	Quality of chain
29	b	56	
30	c	52	
31	d	46	
32	e	64	
33	f	38	
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	123	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	

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
1	4OC	1	1402	X	-	-	-
1	1MG	1	2251	X	-	-	-
1	PSU	1	2252	X	-	-	-
1	5MU	1	2253	X	-	-	-
1	PSU	1	2461	X	-	-	-
1	6MZ	1	3124	X	-	-	-
1	PSU	1	3417	X	-	-	-
1	3TD	1	3421	X	-	-	-
1	PSU	1	3423	X	-	-	-
1	5MU	1	3445	X	-	-	-
1	6MZ	1	3536	X	-	-	-
1	G7M	1	3575	X	-	-	-
1	OMG	1	3757	X	-	-	-
1	PSU	1	3963	X	-	-	-
1	OMC	1	4004	X	-	-	-
1	2MA	1	4009	X	-	-	-
1	PSU	1	4010	X	-	-	-
1	OMU	1	4058	X	-	-	-
1	PSU	1	4086	X	-	-	-
1	PSU	1	4111	X	-	-	-
1	PSU	1	516	X	-	-	-
1	7MG	1	527	X	-	-	-

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 145179 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 stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA,stapled 16S-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	4450	Total	C	N	O	P	0	0
			95544	42634	17562	30898	4450		

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1450	G	-	linker	GB 1370526422
1	1451	G	-	linker	GB 1370526422
1	1452	U	-	linker	GB 1370526422
1	1453	C	-	linker	GB 1370526422
1	1454	A	-	linker	GB 1370526422
1	1455	A	-	linker	GB 1370526422
1	1456	C	-	linker	GB 1370526422
1	1457	A	-	linker	GB 1370526422
1	1458	G	-	linker	GB 1370526422
1	1459	C	-	linker	GB 1370526422
1	1460	C	-	linker	GB 1370526422
1	1461	G	-	linker	GB 1370526422
1	1462	U	-	linker	GB 1370526422
1	1463	U	-	linker	GB 1370526422
1	1464	U	-	linker	GB 1370526422
1	1465	G	-	linker	GB 1370526422
1	1466	A	-	linker	GB 1370526422
1	1467	G	-	linker	GB 1370526422
1	1468	C	-	linker	GB 1370526422
1	1469	U	-	linker	GB 1370526422
1	1470	A	-	linker	GB 1370526422
1	1471	A	-	linker	GB 1370526422
1	1472	C	-	linker	GB 1370526422
1	1473	C	-	linker	GB 1370526422
1	1474	G	-	linker	GB 1370526422
1	1475	G	-	linker	GB 1370526422
1	1476	U	-	linker	GB 1370526422

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Chain	Residue	Modelled	Actual	Comment	Reference
1	1477	A	-	linker	GB 1370526422
1	1478	C	-	linker	GB 1370526422
1	1479	U	-	linker	GB 1370526422
1	1480	A	-	linker	GB 1370526422
1	1481	A	-	linker	GB 1370526422
1	1482	U	-	linker	GB 1370526422
1	1483	G	-	linker	GB 1370526422
1	1484	A	-	linker	GB 1370526422
1	1485	A	-	linker	GB 1370526422
1	1486	C	-	linker	GB 1370526422
1	1487	C	-	linker	GB 1370526422
1	1488	G	-	linker	GB 1370526422
1	1489	U	-	linker	GB 1370526422
1	1490	G	-	linker	GB 1370526422
1	1491	A	-	linker	GB 1370526422
1	1492	G	-	linker	GB 1370526422
1	1493	G	-	linker	GB 1370526422
1	1494	C	-	linker	GB 1370526422
1	1495	U	-	linker	GB 1370526422
1	1496	U	-	linker	GB 1370526422
1	1497	A	-	linker	GB 1370526422
1	1498	A	-	linker	GB 1370526422
1	1499	C	-	linker	GB 1370526422
1	1500	C	-	linker	GB 1370526422
1	1504	A	U	conflict	GB 1063812051
1	4358	A	-	expression tag	GB 1063812051
1	4359	C	-	expression tag	GB 1063812051
1	4360	G	-	expression tag	GB 1063812051
1	4361	G	-	expression tag	GB 1063812051
1	4362	A	-	expression tag	GB 1063812051
1	4363	C	-	expression tag	GB 1063812051
1	4364	A	-	expression tag	GB 1063812051
1	4365	U	-	expression tag	GB 1063812051
1	4366	G	-	expression tag	GB 1063812051
1	4367	G	-	expression tag	GB 1063812051
1	4368	U	-	expression tag	GB 1063812051
1	4369	U	-	expression tag	GB 1063812051
1	4370	G	-	expression tag	GB 1063812051
1	4371	G	-	expression tag	GB 1063812051
1	4372	A	-	expression tag	GB 1063812051
1	4373	G	-	expression tag	GB 1063812051
1	4374	G	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4375	G	-	expression tag	GB 1063812051
1	4376	C	-	expression tag	GB 1063812051
1	4377	G	-	expression tag	GB 1063812051
1	4378	C	-	expression tag	GB 1063812051
1	4379	U	-	expression tag	GB 1063812051
1	4380	U	-	expression tag	GB 1063812051
1	4381	A	-	expression tag	GB 1063812051
1	4382	C	-	expression tag	GB 1063812051
1	4383	C	-	expression tag	GB 1063812051
1	4384	A	-	expression tag	GB 1063812051
1	4385	C	-	expression tag	GB 1063812051
1	4386	U	-	expression tag	GB 1063812051
1	4387	U	-	expression tag	GB 1063812051
1	4388	U	-	expression tag	GB 1063812051
1	4389	G	-	expression tag	GB 1063812051
1	4390	U	-	expression tag	GB 1063812051
1	4391	G	-	expression tag	GB 1063812051
1	4392	A	-	expression tag	GB 1063812051
1	4393	U	-	expression tag	GB 1063812051
1	4394	U	-	expression tag	GB 1063812051
1	4395	C	-	expression tag	GB 1063812051
1	4396	A	-	expression tag	GB 1063812051
1	4397	U	-	expression tag	GB 1063812051
1	4398	G	-	expression tag	GB 1063812051
1	4399	A	-	expression tag	GB 1063812051
1	4400	C	-	expression tag	GB 1063812051
1	4401	U	-	expression tag	GB 1063812051
1	4402	G	-	expression tag	GB 1063812051
1	4403	G	-	expression tag	GB 1063812051
1	4404	G	-	expression tag	GB 1063812051
1	4405	G	-	expression tag	GB 1063812051
1	4406	U	-	expression tag	GB 1063812051
1	4407	G	-	expression tag	GB 1063812051
1	4408	A	-	expression tag	GB 1063812051
1	4409	A	-	expression tag	GB 1063812051
1	4410	G	-	expression tag	GB 1063812051
1	4411	U	-	expression tag	GB 1063812051
1	4412	C	-	expression tag	GB 1063812051
1	4413	G	-	expression tag	GB 1063812051
1	4414	UR3	-	expression tag	GB 1063812051
1	4415	A	-	expression tag	GB 1063812051
1	4416	A	-	expression tag	GB 1063812051

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Chain	Residue	Modelled	Actual	Comment	Reference
1	4417	C	-	expression tag	GB 1063812051
1	4418	A	-	expression tag	GB 1063812051
1	4419	A	-	expression tag	GB 1063812051
1	4420	G	-	expression tag	GB 1063812051
1	4421	G	-	expression tag	GB 1063812051
1	4422	U	-	expression tag	GB 1063812051
1	4423	A	-	expression tag	GB 1063812051
1	4424	A	-	expression tag	GB 1063812051
1	4425	C	-	expression tag	GB 1063812051
1	4426	C	-	expression tag	GB 1063812051
1	4427	G	-	expression tag	GB 1063812051
1	4428	U	-	expression tag	GB 1063812051
1	4429	A	-	expression tag	GB 1063812051
1	4430	G	-	expression tag	GB 1063812051
1	4431	G	-	expression tag	GB 1063812051
1	4432	2MG	-	expression tag	GB 1063812051
1	4433	G	-	expression tag	GB 1063812051
1	4434	MA6	-	expression tag	GB 1063812051
1	4435	MA6	-	expression tag	GB 1063812051
1	4436	C	-	expression tag	GB 1063812051
1	4437	C	-	expression tag	GB 1063812051
1	4438	U	-	expression tag	GB 1063812051
1	4439	G	-	expression tag	GB 1063812051
1	4440	C	-	expression tag	GB 1063812051
1	4441	G	-	expression tag	GB 1063812051
1	4442	G	-	expression tag	GB 1063812051
1	4443	U	-	expression tag	GB 1063812051
1	4444	U	-	expression tag	GB 1063812051
1	4445	G	-	expression tag	GB 1063812051
1	4446	G	-	expression tag	GB 1063812051
1	4447	A	-	expression tag	GB 1063812051
1	4448	U	-	expression tag	GB 1063812051
1	4449	C	-	expression tag	GB 1063812051
1	4450	A	-	expression tag	GB 1063812051
1	4451	C	-	expression tag	GB 1063812051
1	4452	C	-	expression tag	GB 1063812051
1	4453	U	-	expression tag	GB 1063812051
1	4454	C	-	expression tag	GB 1063812051
1	4455	C	-	expression tag	GB 1063812051
1	4456	U	-	expression tag	GB 1063812051
1	4457	U	-	expression tag	GB 1063812051
1	4458	A	-	expression tag	GB 1063812051

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

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

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

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

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

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	135	Total	C	N	O	S	0	0
			984	622	171	185	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

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

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

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

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

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

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

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

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

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1	422	Total	Mg	0
			422	422	
54	3	8	Total	Mg	0
			8	8	
54	N	1	Total	Mg	0
			1	1	
54	P	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	U	1	Total	Mg	0
			1	1	
54	b	1	Total	Mg	0
			1	1	
54	i	1	Total	Mg	0
			1	1	

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	a	1	Total	Zn	0
			1	1	
55	f	1	Total	Zn	0
			1	1	

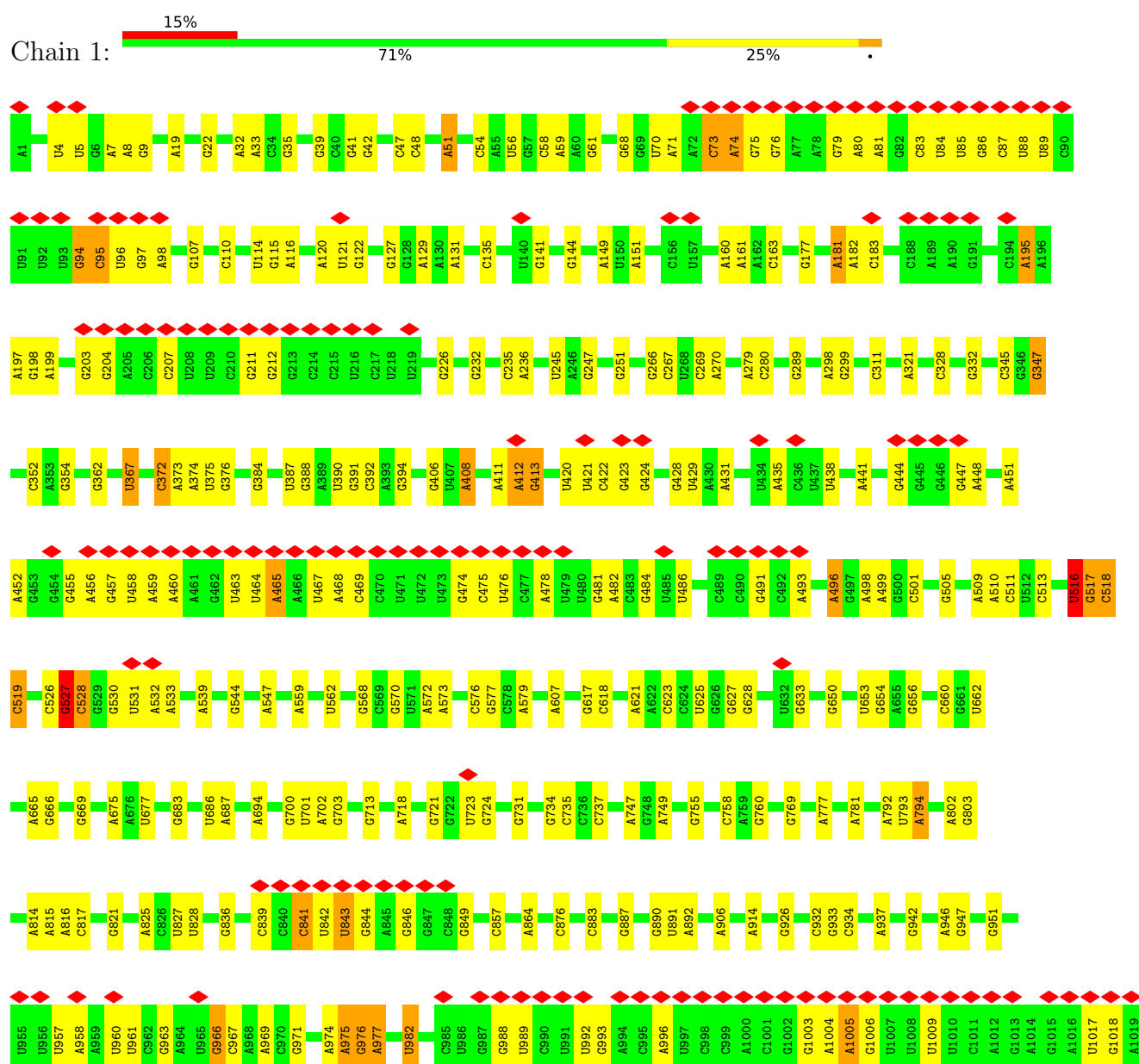
- Molecule 56 is water.

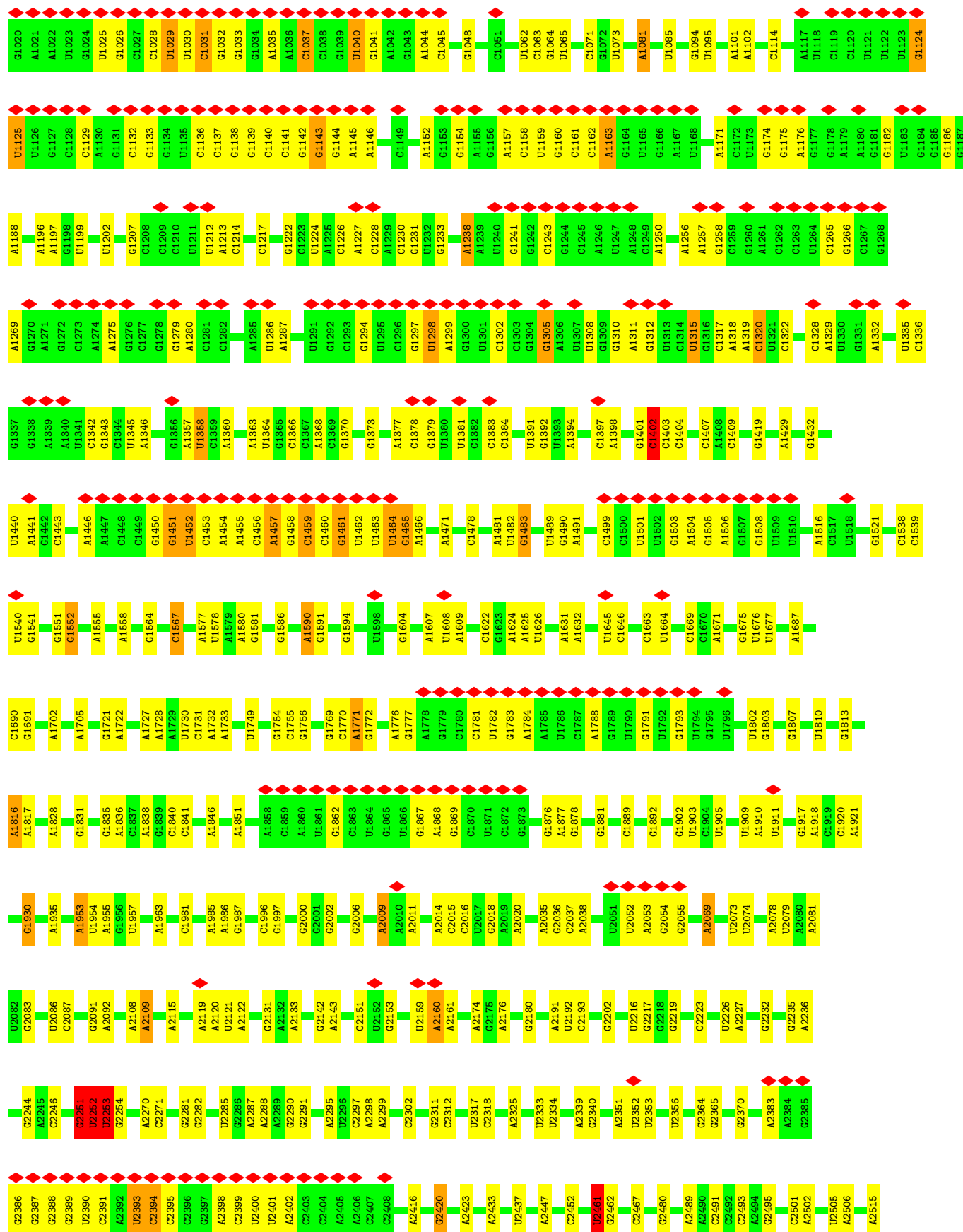
Mol	Chain	Residues	Atoms		AltConf
56	B	2	Total	O	0
			2	2	

3 Residue-property plots [i](#)

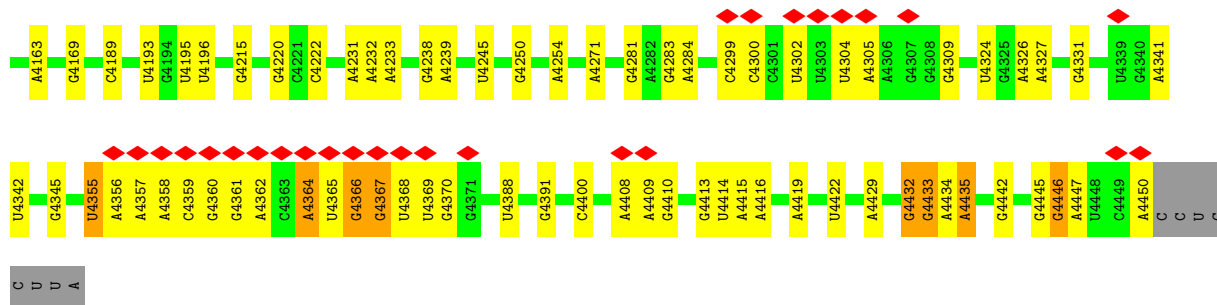
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA, stapled 16S-23S rRNA

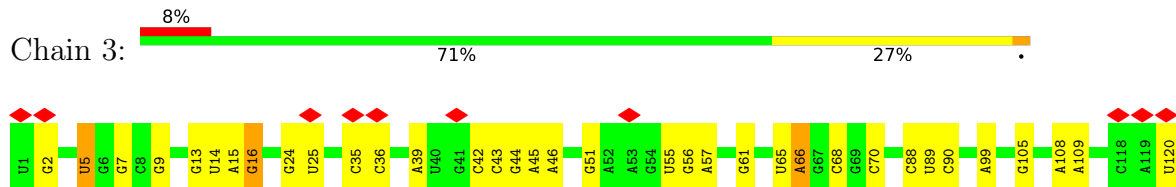




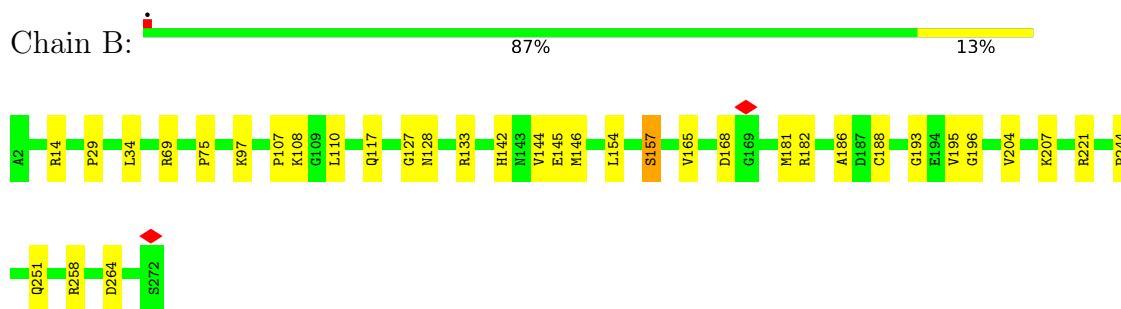
G4031	U3910	C3789	C3670	A3472	A3314	A3136	U3003	G2847	G2883	G2593	U2518
G4035	G3911	G3792	C3671	C3473	G3317	A3140	C3004	U2850	C2884	A2594	C2519
C4038	A3916	A3793	U3672	A3475	C3322	G3151	A3009	C2851	G2885	A2595	G2528
C4042	G3917	A3803	U3673	U3476	C3323	G3152	A3010	U2858	U2886	A2596	G2532
U4043	G3929	A3804	G3674	G3478	U3324	U3153	U3012	A2871	U2887	G2597	G2539
C4045	C3930	U3808	A3675	G3486	A3335	U3154	C3013	G2874	G2692	G2598	U2543
C4053	A3931	U3811	A3676	U3497	C3339	U3155	A3014	G2874	A2710	U2600	G2543
U4058	A3932	C3812	U3677	G3498	U3340	A3156	A3015	G2880	G2718	A2602	G2544
G4059	G3936	G3813	U3678	U3499	G3341	A3157	G3016	U2885	G2742	A2603	A2546
U4060	A3937	A3814	A3679	U3499	A3353	A3158	G3016	G2886	G2743	A2604	G2547
U4061	G3941	C3816	C3680	C3503	A3354	G3159	A3021	U2889	G2744	G2605	G2548
C4062	G3946	U3817	C3681	G3508	U3370	A3175	A3028	A2889	G2745	G2606	C2549
A4066	U3947	U3818	C3682	A3519	U3371	G3180	U3029	C2892	U2746	U2607	C2550
A4070	G3951	C3819	A3625	G3527	G3375	U3199	G3030	A2893	U2748	C2608	C2551
A4071	G3822	G3822	G3626	C3527	C3375	U3220	C3037	U2900	G2751	A2609	A2552
A4072	A3823	A3823	U3627	C3528	C3376	G3221	A3038	A2901	G2756	C2610	C2553
C4073	G3824	G3824	U3628	C3529	A3377	G3230	C3039	U2902	A2759	U2611	A2554
U4074	G3825	G3825	G3629	G3533	G3378	G3231	U3040	C2903	A2760	G2612	A2555
G4075	A3828	A3828	G3630	A3536	A3406	G3232	G3041	C2904	U2761	G2613	G2557
C3973	G3831	G3831	G3631	A3537	A3406	U3230	A3041	C2905	G2762	U2614	C2558
G3976	A3832	A3832	A3632	G3538	G3412	U3231	C3042	U2917	C2615	G2615	A2560
C3977	C3833	C3833	G3633	A3539	G3413	C3232	G3043	G2921	A2617	G2616	C2561
U3979	A3833	A3833	G3634	U3540	G3416	C3233	G3044	C2922	G2772	C2620	A2562
U4086	A3839	A3839	G3635	G3541	U3417	C3234	U3045	A2925	U2773	G2621	U2564
C4087	U3840	U3840	U3637	C3542	A3418	U3235	G3046	G2924	G2778	G2622	G2565
C4088	G3851	G3851	U3638	G3545	A3419	C3236	C3047	A2926	U2779	C2623	U2566
A3984	A3852	A3852	G3639	G3546	C3420	G3237	C3047	A2926	A2780	C2624	U2567
U4090	C3853	C3853	G3639	C3549	3TD3421	G3238	G3066	C2934	A2781	U2625	G2568
U4091	G3856	G3856	A3640	G3559	U3422	G3239	A3072	C2934	G2789	G2626	C2569
A4108	G3857	G3857	A3641	A3560	A3424	G3240	A3075	A2940	A2790	G2627	C2570
U4111	A3858	A3858	G3642	C3561	A3425	U3242	U3084	G2941	A2791	G2628	G2571
C4003	C3865	C3865	U3643	G3562	A3425	G3243	A3085	G2958	A2792	A2632	U2572
C4005	G3867	G3867	G3644	A3566	U3429	G3244	A3086	A2959	G2795	U2636	A2573
G4008	A3883	A3883	U3645	A3568	G3435	A3250	A3089	A2966	G2802	G2637	G2574
A4009	G3889	G3889	G3646	G3575	G3436	A3263	U3090	C2967	G2806	A2639	A2575
U4010	U3726	U3726	A3648	C3578	A3442	C3270	A3092	G2984	G2807	A2640	A2576
U4012	A3731	A3731	G3649	A3578	A3443	A3279	U3095	G2988	U2819	G2641	G2577
C4018	C3732	C3732	C3650	G3599	U3446	A3295	A3096	U2992	C2820	G2642	C2578
U4024	G3744	G3744	G3652	U3604	A3458	A3306	A3109	A2996	C2821	A2648	A2579
U4025	U3749	U3749	A3653	U3605	A3459	U3302	C3113	C2995	A2675	A2682	G2580
C4026	G3756	G3756	G3654	G3606	U3461	G3303	A3114	A2996	G2677	G2676	C2581
C4027	C3757	C3757	U3657	G3608	C3468	A3307	A3115	C2999	C2678	A2681	C2582
U4028	A3774	A3774	G3658	C3609	G3468	A3308	A3116	G2999	U2679	U2680	A2583
U4153	A3780	A3780	A3659	G3663	G3663	A3308	A3124	G2999	G2677	G2676	U2584
	A3784	A3784	U3661	G3662	G3662	A3308	G3125	G2999	C2678	U2680	C2585
			G3663	A3664	A3664	A3308	G3125	G2999	U2680	A2681	U2587
			A3664	G3665	G3665	A3308	G3125	G2999	U2680	U2681	U2588
			G3665	C3666	C3666	A3308	G3125	G2999	U2680	U2681	U2589
			C3666	G3667	G3667	A3308	G3125	G2999	U2680	U2681	A2590
			G3667	A3669	A3669	A3308	G3125	G2999	U2680	U2681	A2591
			A3669			A3308	G3125	G2999	U2680	U2681	A2592



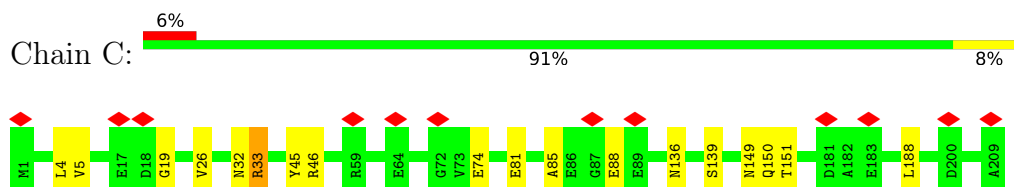
• Molecule 2: 5S ribosomal RNA



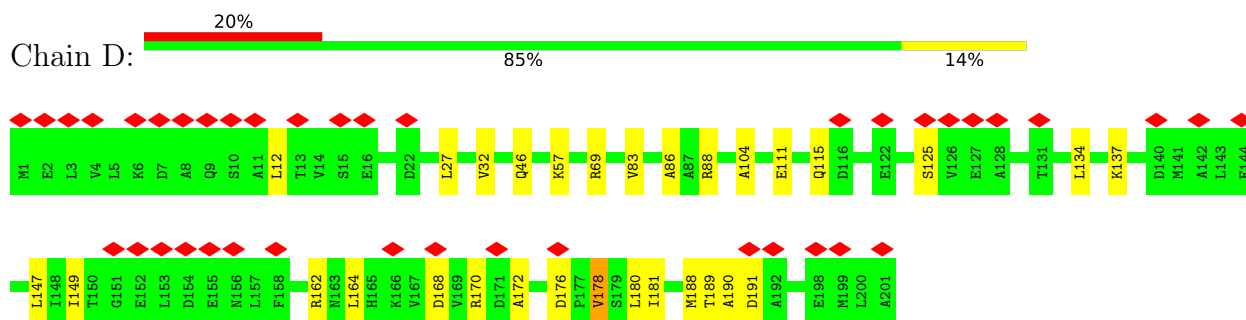
• Molecule 3: 50S ribosomal protein L2



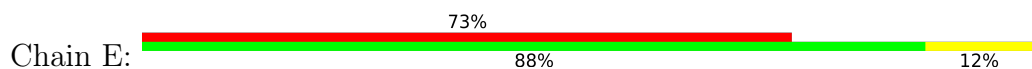
• Molecule 4: 50S ribosomal protein L3

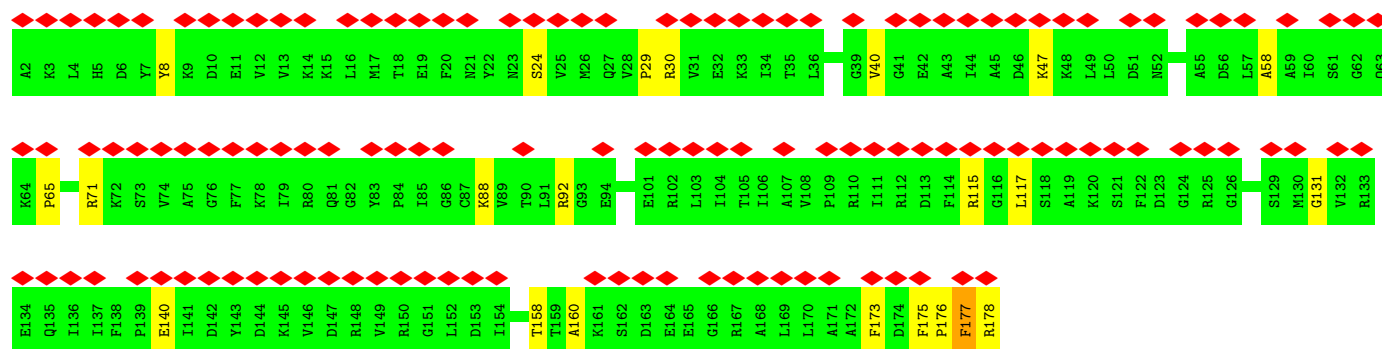


• Molecule 5: 50S ribosomal protein L4

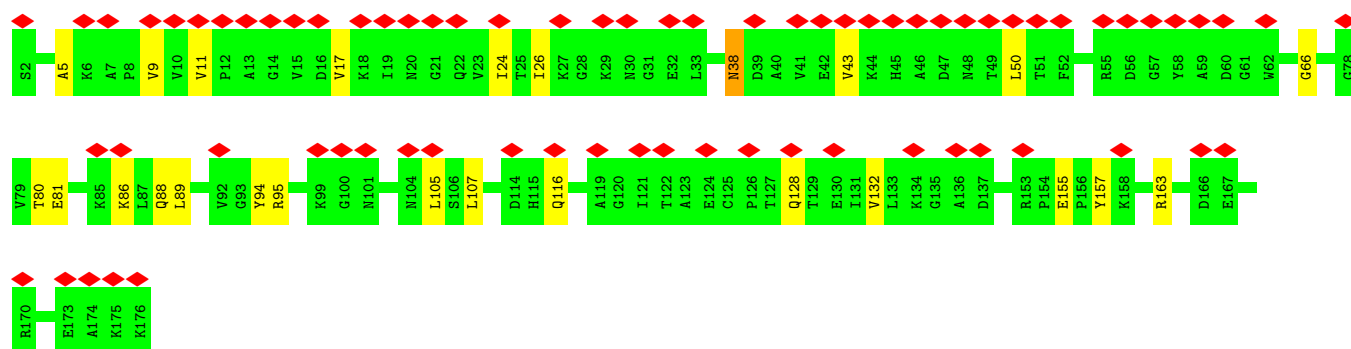
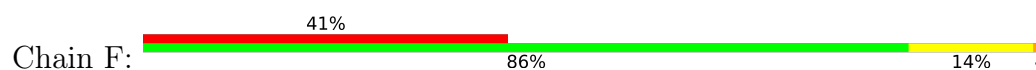


• Molecule 6: 50S ribosomal protein L5

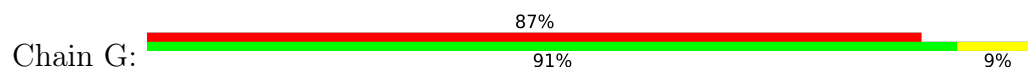




• Molecule 7: 50S ribosomal protein L6



• Molecule 8: 50S ribosomal protein L9

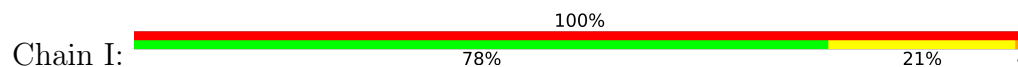


• Molecule 9: 50S ribosomal protein L10

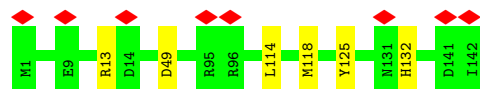




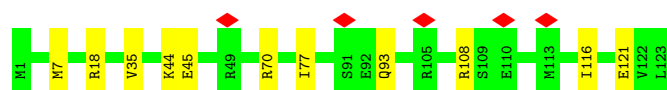
• Molecule 10: 50S ribosomal protein L11



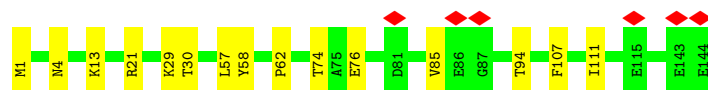
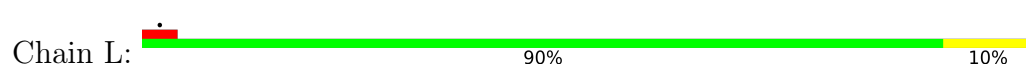
• Molecule 11: 50S ribosomal protein L13



• Molecule 12: 50S ribosomal protein L14

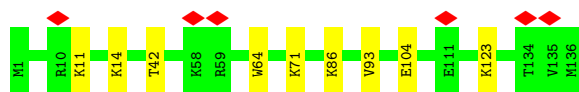


• Molecule 13: 50S ribosomal protein L15



• Molecule 14: 50S ribosomal protein L16

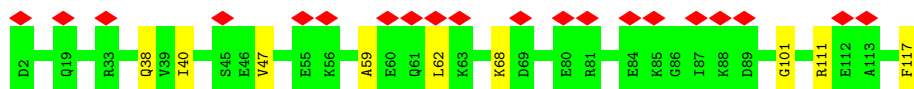
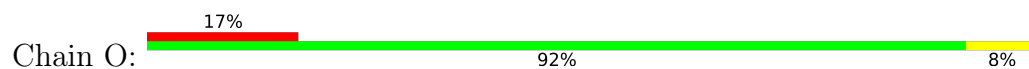




- Molecule 15: 50S ribosomal protein L17



- Molecule 16: 50S ribosomal protein L18



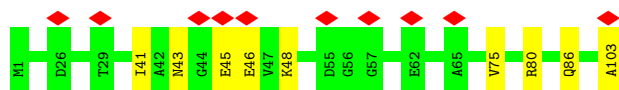
- Molecule 17: 50S ribosomal protein L19



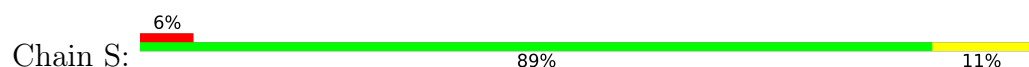
- Molecule 18: 50S ribosomal protein L20



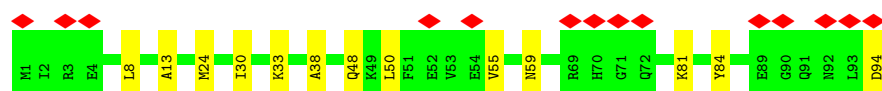
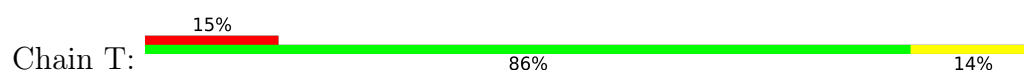
- Molecule 19: 50S ribosomal protein L21



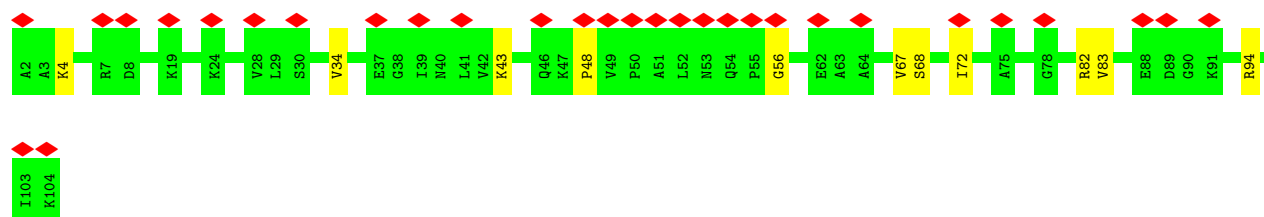
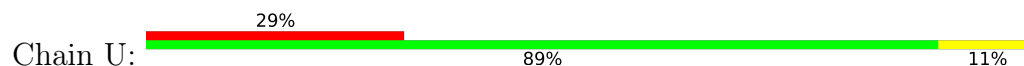
- Molecule 20: 50S ribosomal protein L22



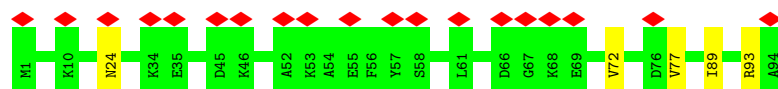
- Molecule 21: 50S ribosomal protein L23



- Molecule 22: 50S ribosomal protein L24



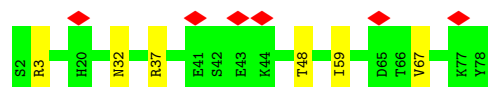
- Molecule 23: 50S ribosomal protein L25



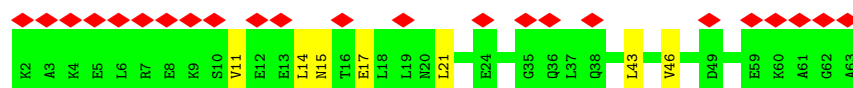
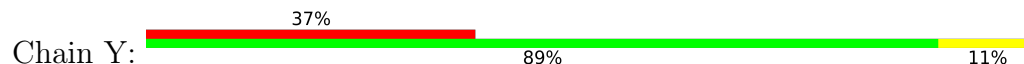
- Molecule 24: 50S ribosomal protein L27



- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29

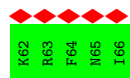
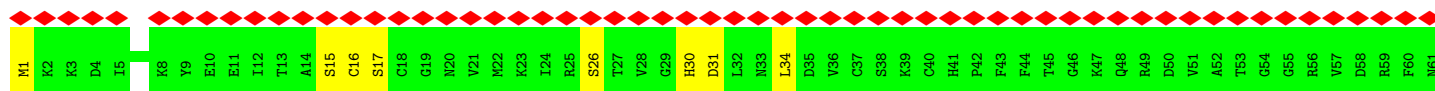
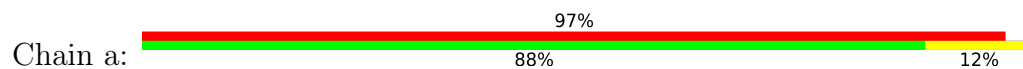


- Molecule 27: 50S ribosomal protein L30

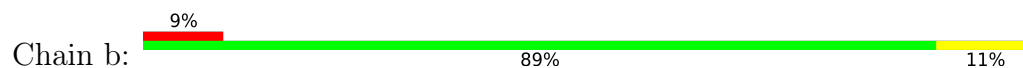




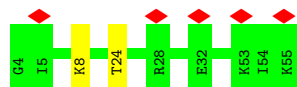
- Molecule 28: 50S ribosomal protein L31



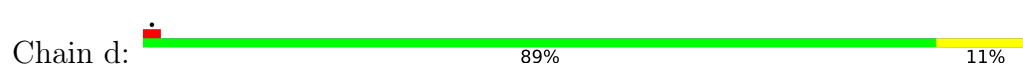
- Molecule 29: 50S ribosomal protein L32



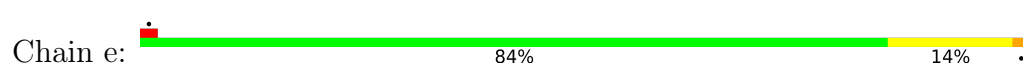
- Molecule 30: 50S ribosomal protein L33



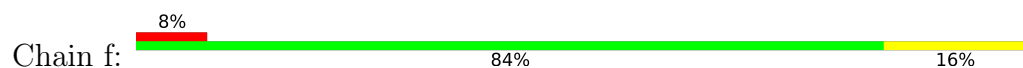
- Molecule 31: 50S ribosomal protein L34

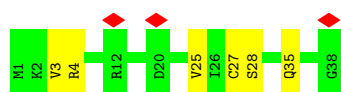


- Molecule 32: 50S ribosomal protein L35

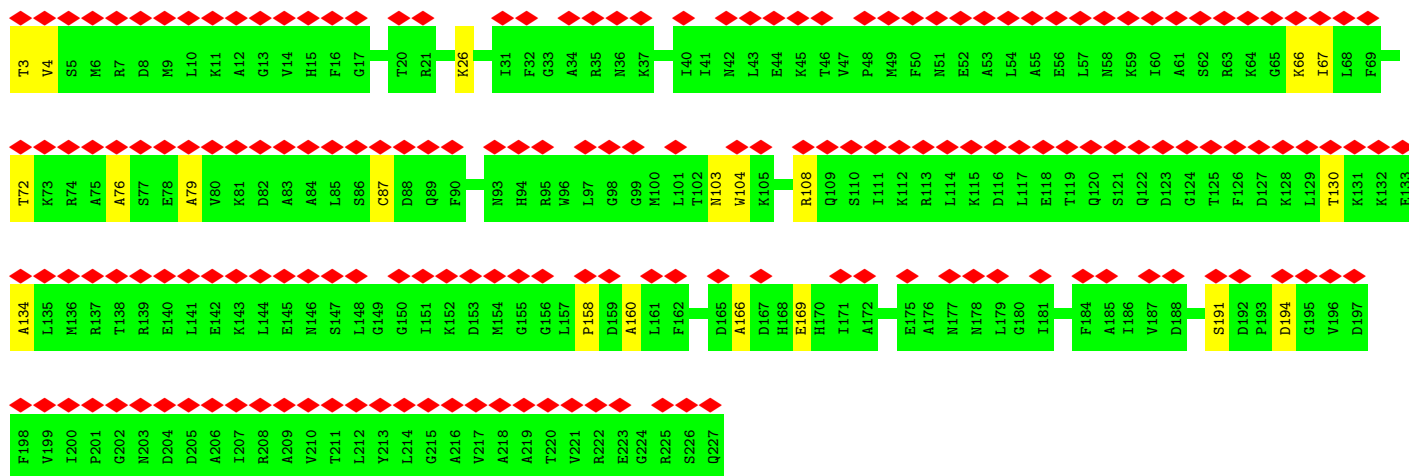
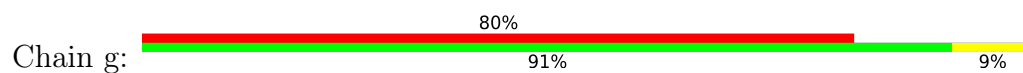


- Molecule 33: 50S ribosomal protein L36

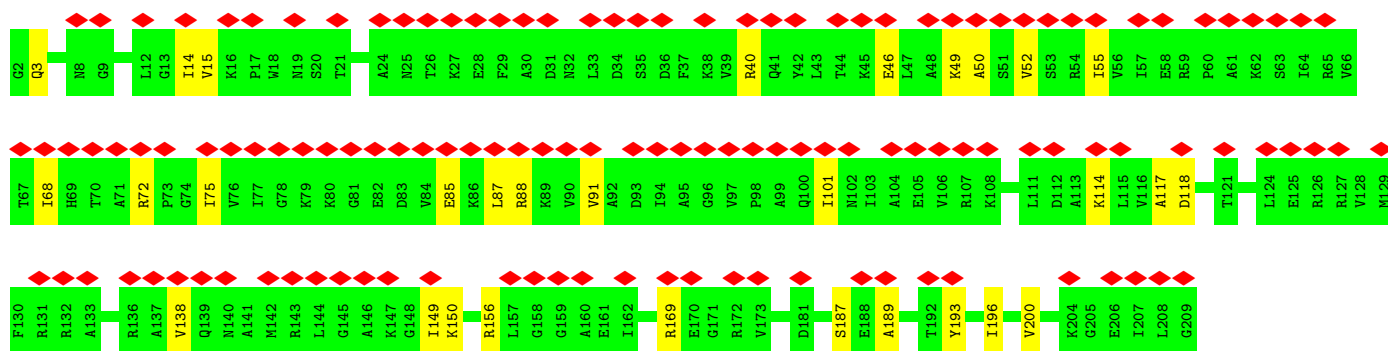
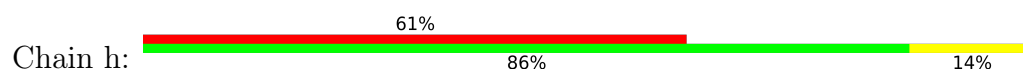




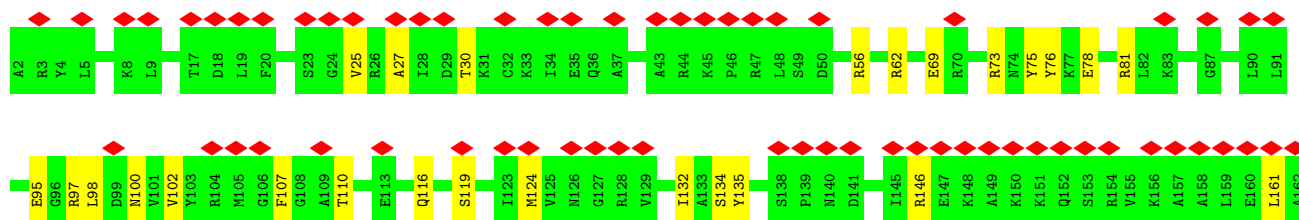
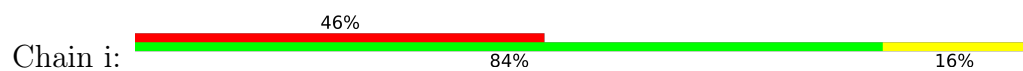
• Molecule 34: 30S ribosomal protein S2

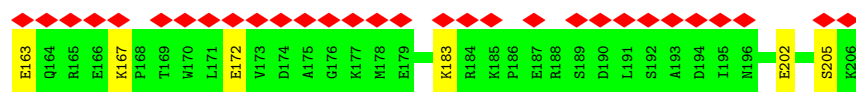


• Molecule 35: 30S ribosomal protein S3

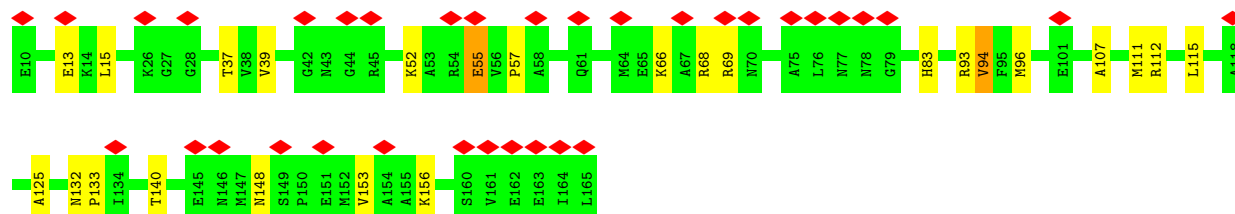
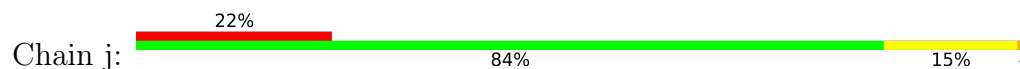


• Molecule 36: 30S ribosomal protein S4

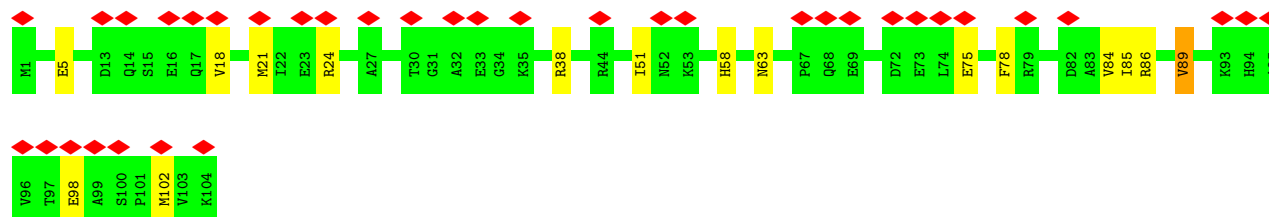
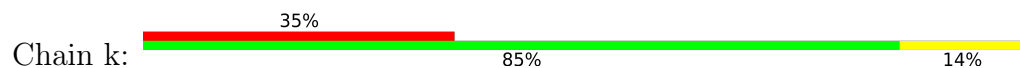




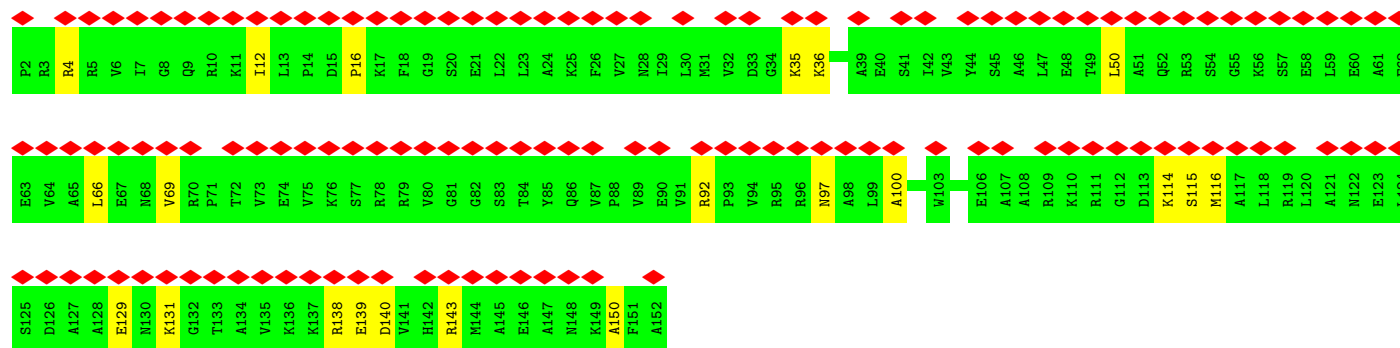
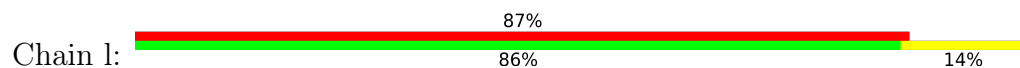
- Molecule 37: 30S ribosomal protein S5



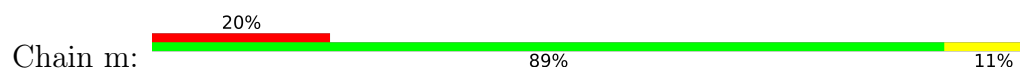
- Molecule 38: 30S ribosomal protein S6

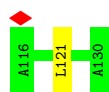


- Molecule 39: 30S ribosomal protein S7

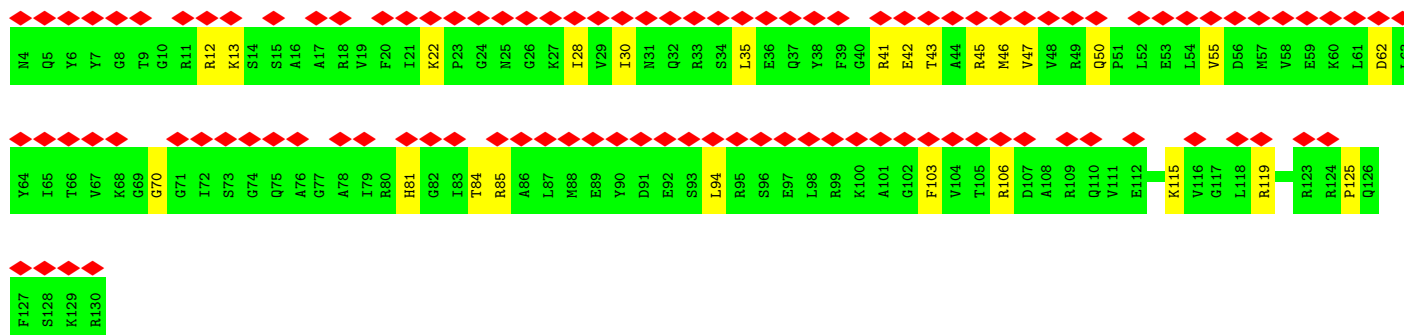
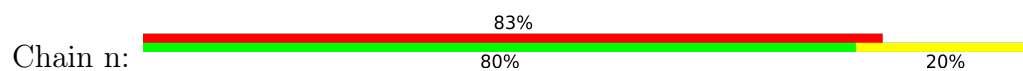


- Molecule 40: 30S ribosomal protein S8

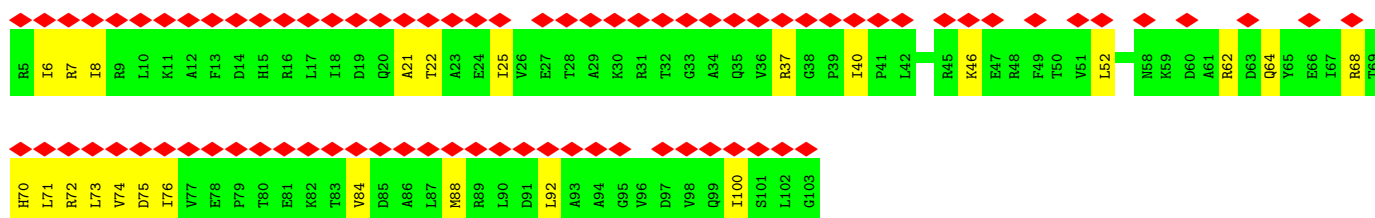
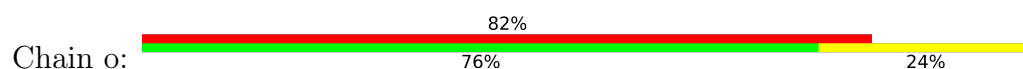




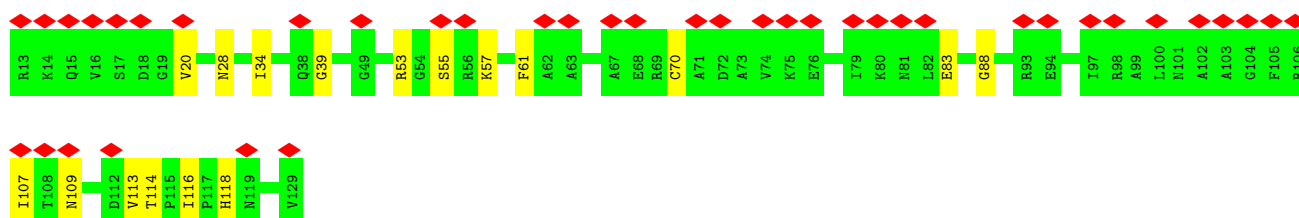
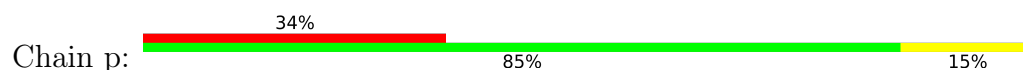
- Molecule 41: 30S ribosomal protein S9



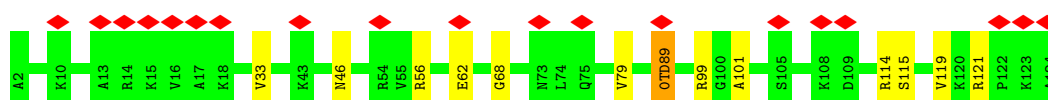
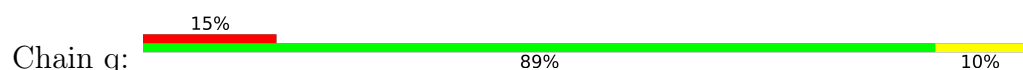
- Molecule 42: 30S ribosomal protein S10



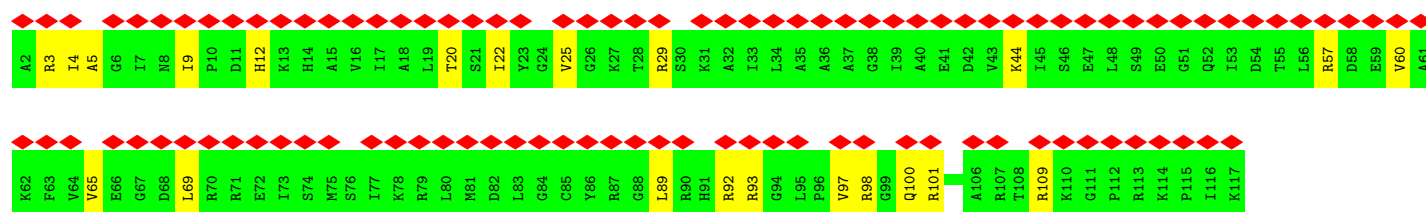
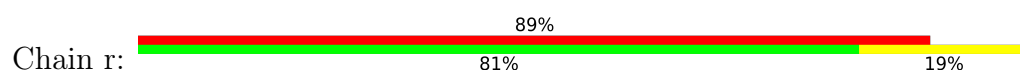
- Molecule 43: 30S ribosomal protein S11



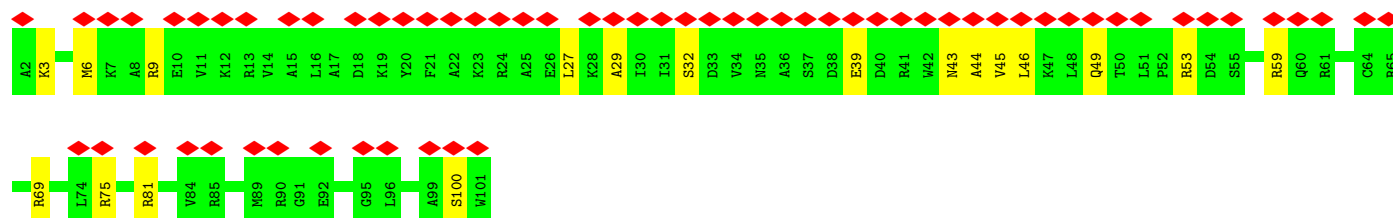
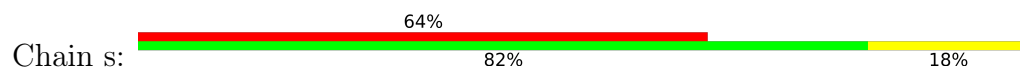
- Molecule 44: 30S ribosomal protein S12



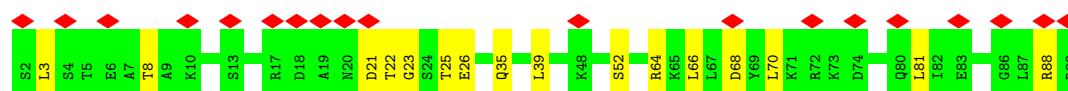
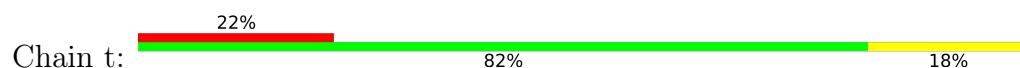
- Molecule 45: 30S ribosomal protein S13



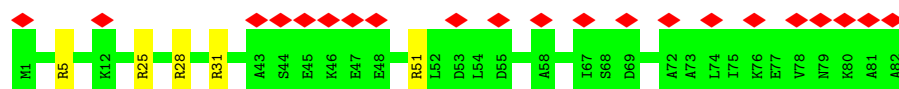
• Molecule 46: 30S ribosomal protein S14



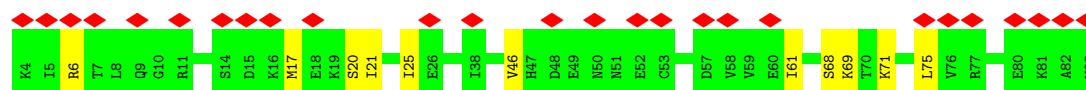
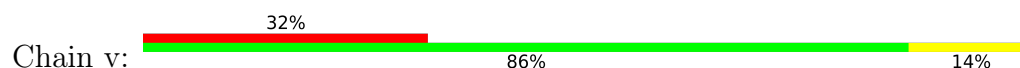
• Molecule 47: 30S ribosomal protein S15



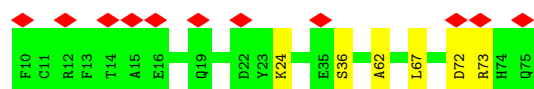
• Molecule 48: 30S ribosomal protein S16



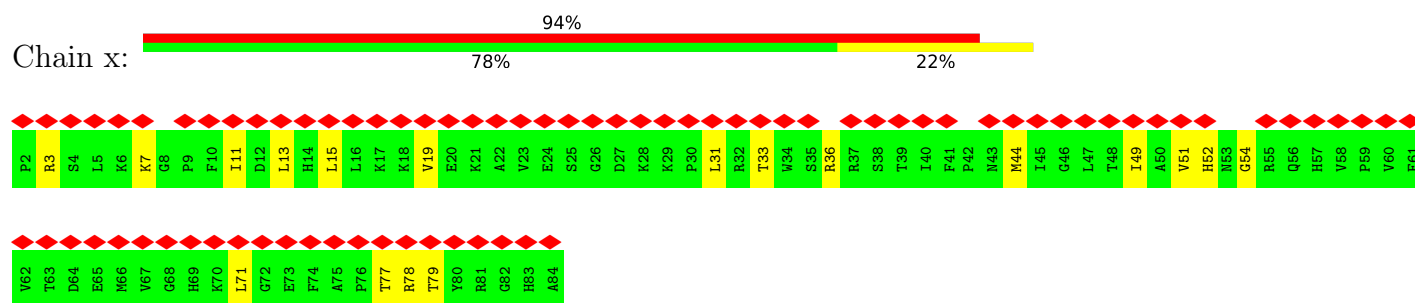
• Molecule 49: 30S ribosomal protein S17



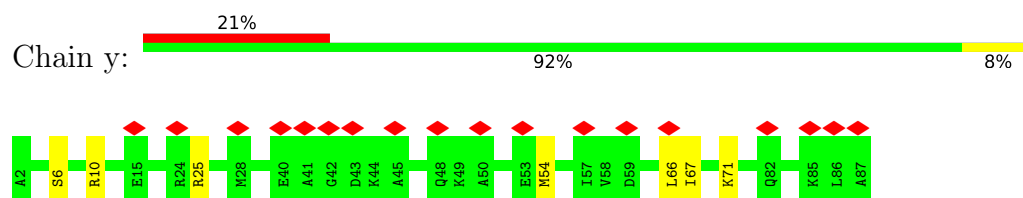
• Molecule 50: 30S ribosomal protein S18



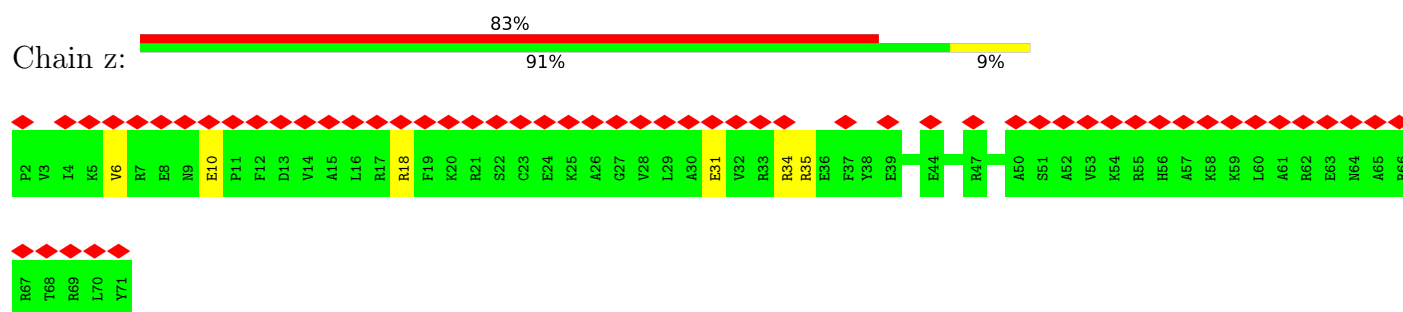
- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94371	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 ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.875	Depositor
Minimum map value	-0.602	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	392.19998, 392.19998, 392.19998	wwPDB
Map dimensions	370, 370, 370	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: MA6, G7M, 2MA, UR3, MG, OMG, 5MU, OMU, 7MG, 3TD, 4OC, 5MC, 0TD, 1MG, OMC, 6MZ, 2MG, ZN, PSU

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	0.44	2/106185 (0.0%)	0.45	3/165633 (0.0%)
2	3	0.35	0/2872	0.40	0/4478
3	B	0.49	0/2122	0.68	0/2852
4	C	0.47	0/1586	0.67	0/2134
5	D	0.41	0/1571	0.63	0/2113
6	E	0.29	0/1435	0.66	2/1926 (0.1%)
7	F	0.29	0/1333	0.60	2/1805 (0.1%)
8	G	0.25	0/1122	0.58	0/1515
9	H	0.32	0/993	0.79	2/1340 (0.1%)
10	I	0.30	0/998	0.71	0/1348
11	J	0.44	0/1152	0.58	0/1551
12	K	0.46	0/955	0.68	0/1279
13	L	0.43	0/1062	0.63	0/1413
14	M	0.42	0/1093	0.60	0/1460
15	N	0.48	0/964	0.68	0/1289
16	O	0.33	0/902	0.63	0/1209
17	P	0.42	0/929	0.61	0/1242
18	Q	0.49	0/960	0.73	1/1278 (0.1%)
19	R	0.42	0/829	0.65	0/1107
20	S	0.46	0/864	0.61	0/1156
21	T	0.36	0/752	0.62	0/1005
22	U	0.34	0/796	0.67	0/1062
23	V	0.37	0/766	0.58	0/1025
24	W	0.43	0/589	0.59	0/779
25	X	0.43	0/635	0.61	0/848
26	Y	0.32	0/502	0.56	0/667
27	Z	0.39	0/452	0.61	0/605
28	a	0.25	0/531	0.61	0/709
29	b	0.46	0/450	0.74	0/599
30	c	0.39	0/433	0.65	0/576
31	d	0.54	0/380	0.78	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.48	0/513	0.78	0/676
33	f	0.45	0/303	0.65	0/397
34	g	0.29	0/1791	0.66	2/2413 (0.1%)
35	h	0.28	0/1663	0.60	1/2241 (0.0%)
36	i	0.30	0/1665	0.58	0/2227
37	j	0.39	0/1165	0.74	2/1568 (0.1%)
38	k	0.33	0/867	0.64	0/1171
39	l	0.27	0/1195	0.71	2/1602 (0.1%)
40	m	0.36	0/989	0.61	0/1326
41	n	0.29	0/1034	0.69	0/1375
42	o	0.29	0/800	0.65	0/1082
43	p	0.33	0/893	0.57	0/1205
44	q	0.38	0/960	0.68	2/1286 (0.2%)
45	r	0.28	0/909	0.69	0/1215
46	s	0.28	0/817	0.52	0/1088
47	t	0.38	0/722	0.60	0/964
48	u	0.32	0/659	0.62	0/884
49	v	0.32	0/658	0.67	0/881
50	w	0.35	0/553	0.59	0/743
51	x	0.25	0/680	0.56	0/915
52	y	0.33	0/675	0.54	0/895
53	z	0.27	0/597	0.57	0/792
All	All	0.42	2/156321 (0.0%)	0.51	19/233447 (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
1	1	39	0
3	B	0	2
10	I	0	1
12	K	0	1
32	e	0	1
38	k	0	1
All	All	39	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2393	U	C1'-N1	6.77	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	4058	OMU	O3'-P	5.32	1.61	1.56

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	1	12	ILE	CA-C-N	8.44	132.90	120.83
39	1	12	ILE	C-N-CA	8.44	132.90	120.83
7	F	116	GLN	CA-C-N	7.44	130.77	120.65
7	F	116	GLN	C-N-CA	7.44	130.77	120.65
1	1	4058	OMU	P-O3'-C3'	6.64	127.67	119.70

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4',C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C1',C3'
1	1	2251	1MG	C2',C1'
1	1	2252	PSU	C4',C3'

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	157	SER	Peptide
3	B	195	VAL	Peptide
10	I	116	MET	Peptide
12	K	93	GLN	Peptide
32	e	31	HIS	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	95544	0	48102	281	0
2	3	2569	0	1301	9	0
3	B	2083	0	2154	20	0
4	C	1565	0	1616	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1552	0	1619	19	0
6	E	1411	0	1444	13	0
7	F	1313	0	1358	12	0
8	G	1111	0	1148	7	0
9	H	980	0	1013	26	0
10	I	984	0	1035	19	0
11	J	1129	0	1162	3	0
12	K	946	0	1023	7	0
13	L	1053	0	1129	12	0
14	M	1074	0	1157	5	0
15	N	951	0	994	5	0
16	O	892	0	923	6	0
17	P	917	0	962	7	0
18	Q	947	0	1019	7	0
19	R	816	0	839	6	0
20	S	857	0	922	8	0
21	T	746	0	811	8	0
22	U	788	0	844	8	0
23	V	753	0	780	2	0
24	W	582	0	599	3	0
25	X	625	0	652	4	0
26	Y	501	0	531	4	0
27	Z	448	0	488	2	0
28	a	522	0	521	5	0
29	b	444	0	458	4	0
30	c	426	0	464	2	0
31	d	377	0	418	2	0
32	e	504	0	572	9	0
33	f	302	0	340	4	0
34	g	1760	0	1787	10	0
35	h	1636	0	1710	16	0
36	i	1643	0	1707	18	0
37	j	1152	0	1196	17	0
38	k	848	0	846	9	0
39	l	1181	0	1238	15	0
40	m	979	0	1031	9	0
41	n	1022	0	1070	17	0
42	o	790	0	831	16	0
43	p	877	0	887	13	0
44	q	957	0	1017	9	0
45	r	900	0	965	16	0
46	s	805	0	844	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	t	714	0	734	8	0
48	u	649	0	666	5	0
49	v	649	0	691	7	0
50	w	544	0	560	4	0
51	x	663	0	688	14	0
52	y	669	0	719	4	0
53	z	589	0	629	5	0
54	1	422	0	0	0	0
54	3	8	0	0	0	0
54	N	1	0	0	0	0
54	P	1	0	0	0	0
54	Q	1	0	0	0	0
54	U	1	0	0	0	0
54	b	1	0	0	0	0
54	i	1	0	0	0	0
55	a	1	0	0	0	0
55	f	1	0	0	0	0
56	B	2	0	0	0	0
All	All	145179	0	98214	637	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 3.

The worst 5 of 637 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)
43:p:88:GLY:H	43:p:114:THR:HG22	1.54	0.71
4:C:33:ARG:HH22	4:C:74:GLU:HB3	1.56	0.70
45:r:4:ILE:HB	45:r:9:ILE:HD12	1.76	0.68
20:S:11:ARG:HH12	20:S:98:LYS:HG2	1.59	0.68
1:1:4302:U:H3	1:1:4305:A:H61	1.40	0.68

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	
3	B	269/271 (99%)	259 (96%)	10 (4%)	0	100	100
4	C	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
5	D	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
6	E	175/177 (99%)	159 (91%)	15 (9%)	1 (1%)	21	45
7	F	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
8	G	147/149 (99%)	134 (91%)	13 (9%)	0	100	100
9	H	128/130 (98%)	105 (82%)	23 (18%)	0	100	100
10	I	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
11	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
12	K	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
13	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
14	M	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
15	N	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
19	R	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
20	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
21	T	92/94 (98%)	92 (100%)	0	0	100	100
22	U	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
23	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
24	W	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
25	X	75/77 (97%)	75 (100%)	0	0	100	100
26	Y	60/62 (97%)	60 (100%)	0	0	100	100
27	Z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
28	a	64/66 (97%)	58 (91%)	6 (9%)	0	100	100
29	b	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	c	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
31	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
32	e	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	7	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	212 (95%)	11 (5%)	0	100	100
35	h	206/208 (99%)	190 (92%)	16 (8%)	0	100	100
36	i	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	j	154/156 (99%)	136 (88%)	18 (12%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
40	m	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
41	n	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
44	q	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
45	r	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
46	s	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
47	t	86/88 (98%)	82 (95%)	3 (4%)	1 (1%)	10	28
48	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
49	v	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
50	w	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
51	x	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
52	y	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	z	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
All	All	5869/5972 (98%)	5563 (95%)	303 (5%)	3 (0%)	49	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	e	32	ILE
6	E	177	PHE
47	t	22	THR

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	B	216/216 (100%)	215 (100%)	1 (0%)	81	90
4	C	164/164 (100%)	162 (99%)	2 (1%)	63	79
5	D	165/165 (100%)	164 (99%)	1 (1%)	78	89
6	E	148/148 (100%)	146 (99%)	2 (1%)	59	77
7	F	136/136 (100%)	134 (98%)	2 (2%)	57	76
8	G	114/114 (100%)	113 (99%)	1 (1%)	70	83
9	H	99/99 (100%)	99 (100%)	0	100	100
10	I	104/104 (100%)	103 (99%)	1 (1%)	68	82
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	104/104 (100%)	103 (99%)	1 (1%)	68	82
13	L	103/103 (100%)	103 (100%)	0	100	100
14	M	109/109 (100%)	109 (100%)	0	100	100
15	N	99/99 (100%)	99 (100%)	0	100	100
16	O	86/86 (100%)	86 (100%)	0	100	100
17	P	99/99 (100%)	99 (100%)	0	100	100
18	Q	89/89 (100%)	89 (100%)	0	100	100
19	R	84/84 (100%)	84 (100%)	0	100	100
20	S	93/93 (100%)	93 (100%)	0	100	100
21	T	81/81 (100%)	81 (100%)	0	100	100
22	U	84/84 (100%)	84 (100%)	0	100	100
23	V	78/78 (100%)	77 (99%)	1 (1%)	61	78
24	W	58/58 (100%)	58 (100%)	0	100	100
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	54/54 (100%)	54 (100%)	0	100	100
27	Z	48/48 (100%)	48 (100%)	0	100	100
28	a	59/59 (100%)	59 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	38/38 (100%)	36 (95%)	2 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	e	51/51 (100%)	50 (98%)	1 (2%)	48	71
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	187 (100%)	0	100	100
35	h	171/171 (100%)	170 (99%)	1 (1%)	78	89
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	117 (98%)	2 (2%)	53	73
38	k	91/91 (100%)	90 (99%)	1 (1%)	65	80
39	l	124/124 (100%)	123 (99%)	1 (1%)	73	85
40	m	104/104 (100%)	102 (98%)	2 (2%)	50	71
41	n	105/105 (100%)	105 (100%)	0	100	100
42	o	86/86 (100%)	86 (100%)	0	100	100
43	p	90/90 (100%)	90 (100%)	0	100	100
44	q	102/102 (100%)	102 (100%)	0	100	100
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	75 (99%)	1 (1%)	61	78
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	72 (100%)	0	100	100
52	y	65/65 (100%)	64 (98%)	1 (2%)	57	76
53	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4871/4871 (100%)	4847 (100%)	24 (0%)	78	90

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	e	55	LEU
37	j	94	VAL
37	j	93	ARG
38	k	89	VAL
7	F	11	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
21	T	48	GLN
47	t	50	HIS
28	a	20	ASN
47	t	40	GLN
52	y	3	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	4444/4458 (99%)	960 (21%)	24 (0%)
2	3	119/120 (99%)	25 (21%)	0
All	All	4563/4578 (99%)	985 (21%)	24 (0%)

5 of 985 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	9	G
1	1	19	A
1	1	22	G
1	1	32	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	3445	5MU
1	1	3814	G
1	1	3668	G
1	1	3931	A
1	1	2192	U

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

34 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	1	4434	1	23,26,27	1.37	3 (13%)	34,38,41	2.21	10 (29%)
1	PSU	1	4010	1	18,21,22	2.35	5 (27%)	22,30,33	2.37	5 (22%)
1	UR3	1	4414	1	19,22,23	2.82	6 (31%)	26,32,35	1.45	3 (11%)
1	2MG	1	966	1	23,26,27	2.63	6 (26%)	32,38,41	2.42	8 (25%)
1	G7M	1	3575	1	23,26,27	2.76	6 (26%)	35,39,42	1.99	7 (20%)
1	1MG	1	2251	1	22,26,27	2.58	6 (27%)	33,39,42	2.88	16 (48%)
1	5MC	1	3468	1	18,22,23	2.14	3 (16%)	26,32,35	1.41	4 (15%)
1	2MA	1	4009	1,54	22,25,26	1.59	3 (13%)	33,37,40	2.36	11 (33%)
1	4OC	1	1402	1	20,23,24	2.44	5 (25%)	26,32,35	2.32	9 (34%)
1	5MU	1	3445	1	19,22,23	2.52	7 (36%)	28,32,35	3.54	9 (32%)
1	PSU	1	3417	1	18,21,22	1.97	5 (27%)	22,30,33	2.12	4 (18%)
1	2MG	1	3951	1	23,26,27	2.65	6 (26%)	32,38,41	2.28	9 (28%)
1	5MC	1	1407	1	18,22,23	2.05	3 (16%)	26,32,35	1.38	3 (11%)
1	PSU	1	3423	1	18,21,22	2.11	5 (27%)	22,30,33	2.07	5 (22%)
1	5MU	1	2253	1	19,22,23	2.32	7 (36%)	28,32,35	4.01	13 (46%)
1	2MG	1	4432	1	23,26,27	2.62	6 (26%)	32,38,41	2.47	11 (34%)
1	OMC	1	4004	1,54	19,22,23	1.77	6 (31%)	26,31,34	2.10	9 (34%)
1	3TD	1	3421	1	18,22,23	2.84	8 (44%)	22,32,35	1.72	2 (9%)
1	PSU	1	2461	1	18,21,22	2.25	5 (27%)	22,30,33	2.22	5 (22%)
1	OMG	1	3757	1	23,26,27	2.64	7 (30%)	33,38,41	2.35	10 (30%)
1	6MZ	1	3536	1	22,25,26	2.91	4 (18%)	30,36,39	3.18	19 (63%)
1	PSU	1	4111	1	18,21,22	2.18	5 (27%)	22,30,33	2.09	4 (18%)
1	PSU	1	516	1	18,21,22	2.10	6 (33%)	22,30,33	2.20	5 (22%)
1	OMU	1	4058	1	19,22,23	2.76	7 (36%)	26,31,34	2.38	12 (46%)
1	PSU	1	4086	1	18,21,22	2.17	5 (27%)	22,30,33	2.14	7 (31%)
1	MA6	1	4435	1	23,26,27	1.27	3 (13%)	34,38,41	2.27	9 (26%)
1	5MC	1	967	1,54	18,22,23	2.01	3 (16%)	26,32,35	1.44	4 (15%)
1	PSU	1	2252	1,54	18,21,22	2.25	6 (33%)	22,30,33	2.30	5 (22%)
1	2MG	1	3341	1	23,26,27	2.56	6 (26%)	32,38,41	2.45	9 (28%)
44	0TD	q	89	44	7,9,10	1.40	0	6,11,13	2.82	3 (50%)
1	PSU	1	3963	1	18,21,22	2.29	5 (27%)	22,30,33	2.29	5 (22%)
1	2MG	1	1207	1	23,26,27	2.58	6 (26%)	32,38,41	2.37	10 (31%)
1	7MG	1	527	1	22,26,27	6.31	6 (27%)	29,39,42	2.43	10 (34%)
1	6MZ	1	3124	1	22,25,26	2.82	4 (18%)	30,36,39	2.43	12 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	1	4434	1	-	1/11/29/30	0/3/3/3
1	PSU	1	4010	1	2/2/5/5	3/7/25/26	0/2/2/2
1	UR3	1	4414	1	-	0/7/25/26	0/2/2/2
1	2MG	1	966	1	-	4/9/27/28	0/3/3/3
1	G7M	1	3575	1	1/1/5/5	2/7/25/26	0/3/3/3
1	1MG	1	2251	1	2/2/5/5	2/7/25/26	0/3/3/3
1	5MC	1	3468	1	-	0/7/25/26	0/2/2/2
1	2MA	1	4009	1,54	2/2/5/5	4/7/25/26	0/3/3/3
1	4OC	1	1402	1	2/2/5/6	4/9/29/30	0/2/2/2
1	5MU	1	3445	1	2/2/5/5	1/7/25/26	0/2/2/2
1	PSU	1	3417	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	3951	1	-	0/9/27/28	0/3/3/3
1	PSU	1	3423	1	2/2/5/5	3/7/25/26	0/2/2/2
1	5MC	1	1407	1	-	0/7/25/26	0/2/2/2
1	5MU	1	2253	1	2/2/5/5	5/7/25/26	0/2/2/2
1	2MG	1	4432	1	-	0/9/27/28	0/3/3/3
1	OMC	1	4004	1,54	1/1/5/5	4/9/27/28	0/2/2/2
1	3TD	1	3421	1	1/1/5/5	4/7/25/26	0/2/2/2
1	PSU	1	2461	1	2/2/5/5	3/7/25/26	0/2/2/2
1	OMG	1	3757	1	1/1/5/5	2/9/27/28	0/3/3/3
1	6MZ	1	3536	1	2/2/5/6	2/9/27/28	0/3/3/3
1	PSU	1	4111	1	2/2/5/5	3/7/25/26	0/2/2/2
1	PSU	1	516	1	2/2/5/5	5/7/25/26	0/2/2/2
1	OMU	1	4058	1	2/2/5/5	3/9/27/28	0/2/2/2
1	PSU	1	4086	1	2/2/5/5	3/7/25/26	0/2/2/2
1	MA6	1	4435	1	-	3/11/29/30	0/3/3/3
1	5MC	1	967	1,54	-	0/7/25/26	0/2/2/2
1	PSU	1	2252	1,54	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	3341	1	-	0/9/27/28	0/3/3/3
44	0TD	q	89	44	-	1/7/12/14	-
1	PSU	1	3963	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	1	1207	1	-	0/9/27/28	0/3/3/3
1	7MG	1	527	1	1/1/7/7	3/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	6MZ	1	3124	1	2/2/5/6	7/9/27/28	0/3/3/3

The worst 5 of 174 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	527	7MG	C8-N9	-27.11	1.30	1.46
1	1	3124	6MZ	C6-N6	11.86	1.47	1.34
1	1	3536	6MZ	C6-N6	11.66	1.46	1.34
1	1	3575	G7M	O6-C6	10.22	1.43	1.23
1	1	966	2MG	O6-C6	9.34	1.41	1.23

The worst 5 of 267 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2253	5MU	N3-C2-N1	9.66	127.72	114.89
1	1	2253	5MU	C5M-C5-C4	9.47	129.19	118.77
1	1	3445	5MU	C5M-C5-C4	8.86	128.52	118.77
1	1	3536	6MZ	C9-N6-C6	-8.64	115.43	122.87
1	1	3445	5MU	N3-C2-N1	8.41	126.06	114.89

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	516	PSU	C4'
1	1	516	PSU	C3'
1	1	527	7MG	C3'
1	1	1402	4OC	C1'
1	1	1402	4OC	C3'

5 of 81 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	516	PSU	O4'-C1'-C5-C4
1	1	516	PSU	O4'-C1'-C5-C6
1	1	516	PSU	C3'-C4'-C5'-O5'
1	1	516	PSU	O4'-C4'-C5'-O5'
1	1	527	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	1402	4OC	1	0
1	1	3445	5MU	1	0
1	1	4432	2MG	1	0
1	1	3536	6MZ	1	0
1	1	4435	MA6	2	0
44	q	89	0TD	1	0
1	1	527	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 438 ligands modelled in this entry, 438 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
1	1	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1501:U	O3'	1502:U	P	3.88
1	1	1276:G	O3'	1277:C	P	3.82

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	3820:A	O3'	3821:G	P	3.74
1	1	1383:C	O3'	1384:C	P	3.50
1	1	147:G	O3'	148:G	P	3.31

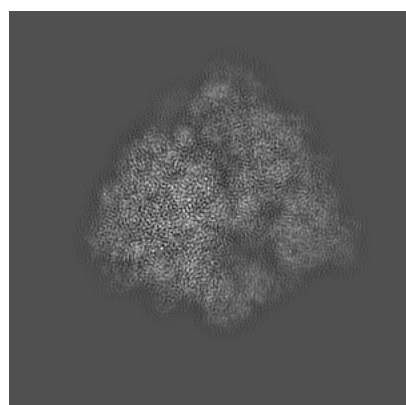
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0261. These allow visual inspection of the internal detail of the map and identification of artifacts.

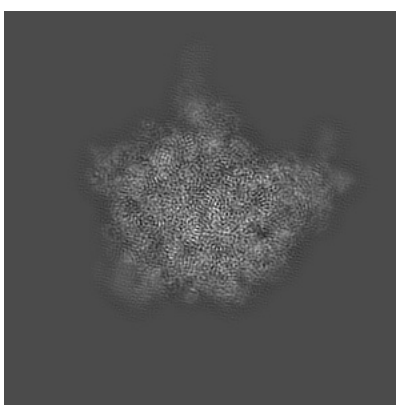
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

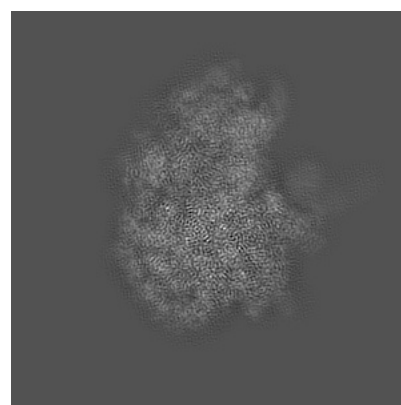
6.1.1 Primary map



X



Y

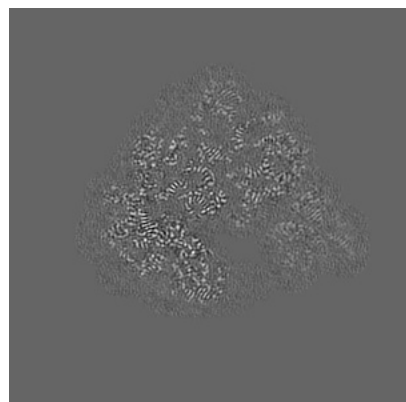


Z

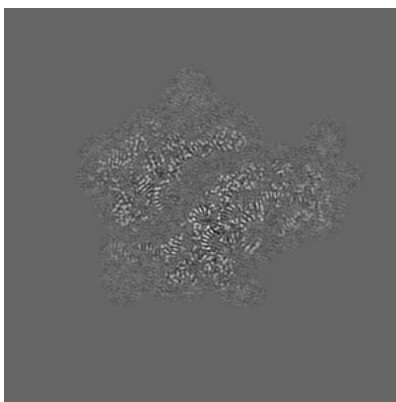
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

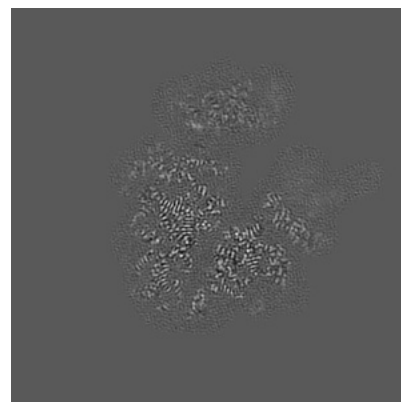
6.2.1 Primary map



X Index: 185



Y Index: 185

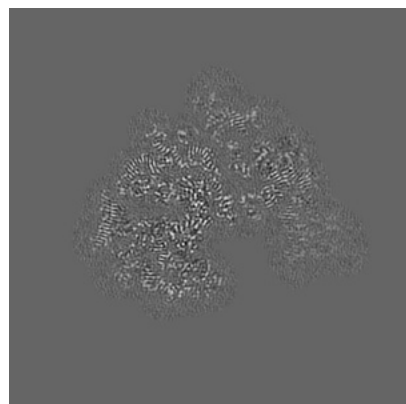


Z Index: 185

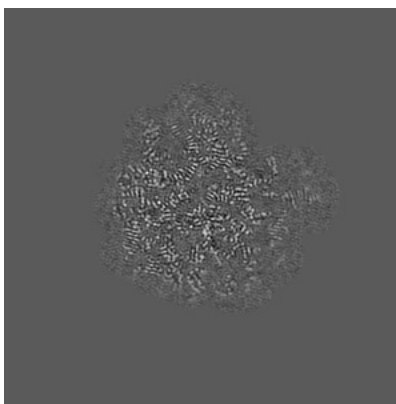
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

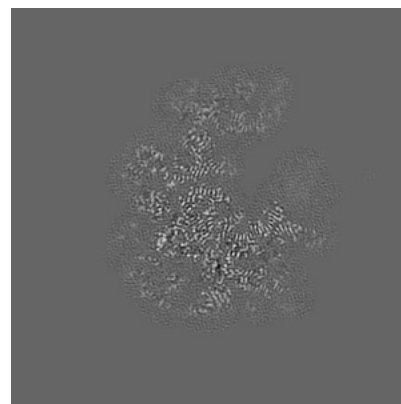
6.3.1 Primary map



X Index: 175



Y Index: 168

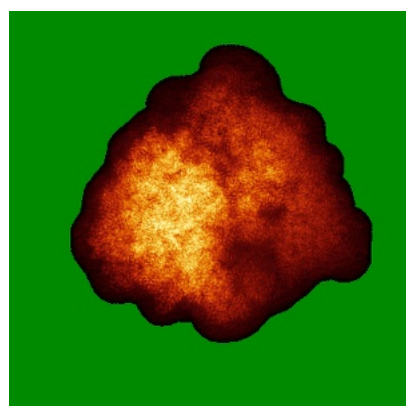


Z Index: 194

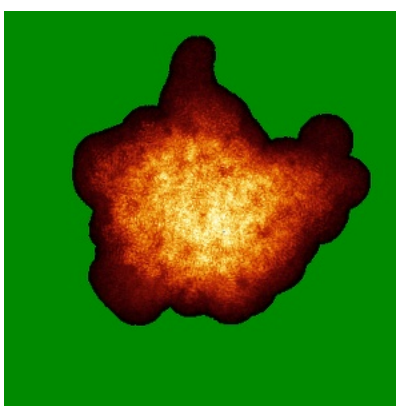
The images above show the largest variance slices of the map in three orthogonal directions.

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

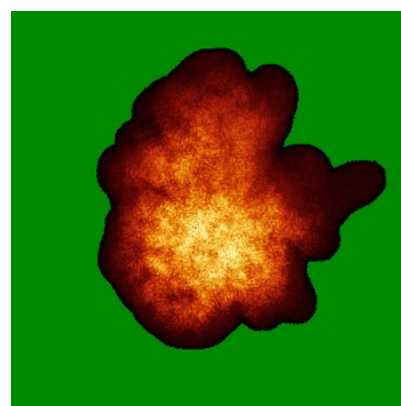
6.4.1 Primary map



X



Y

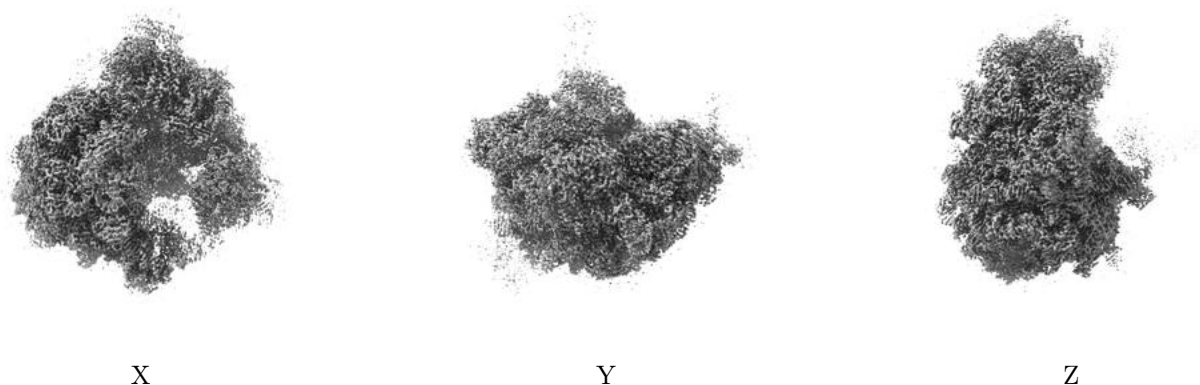


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

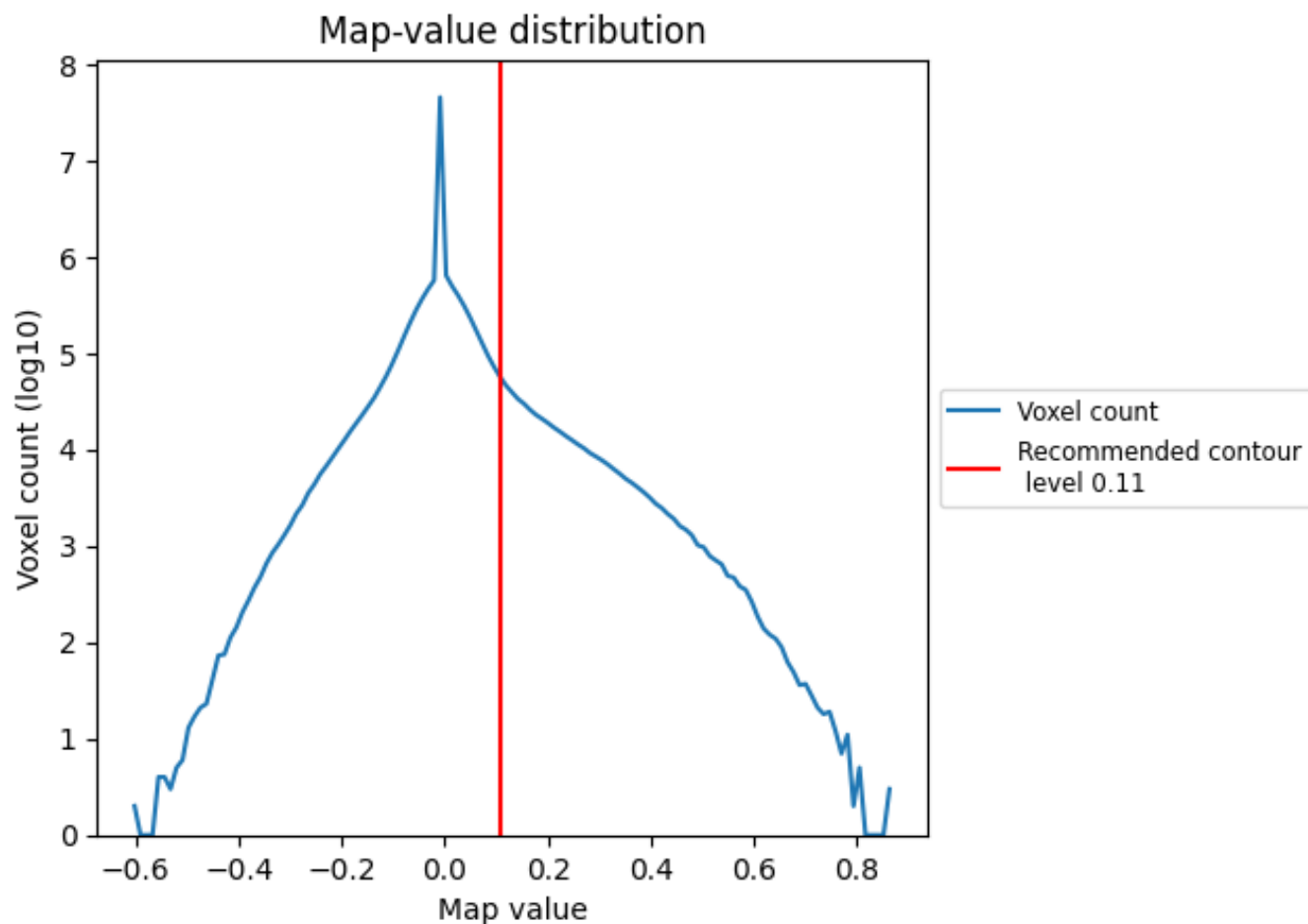
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

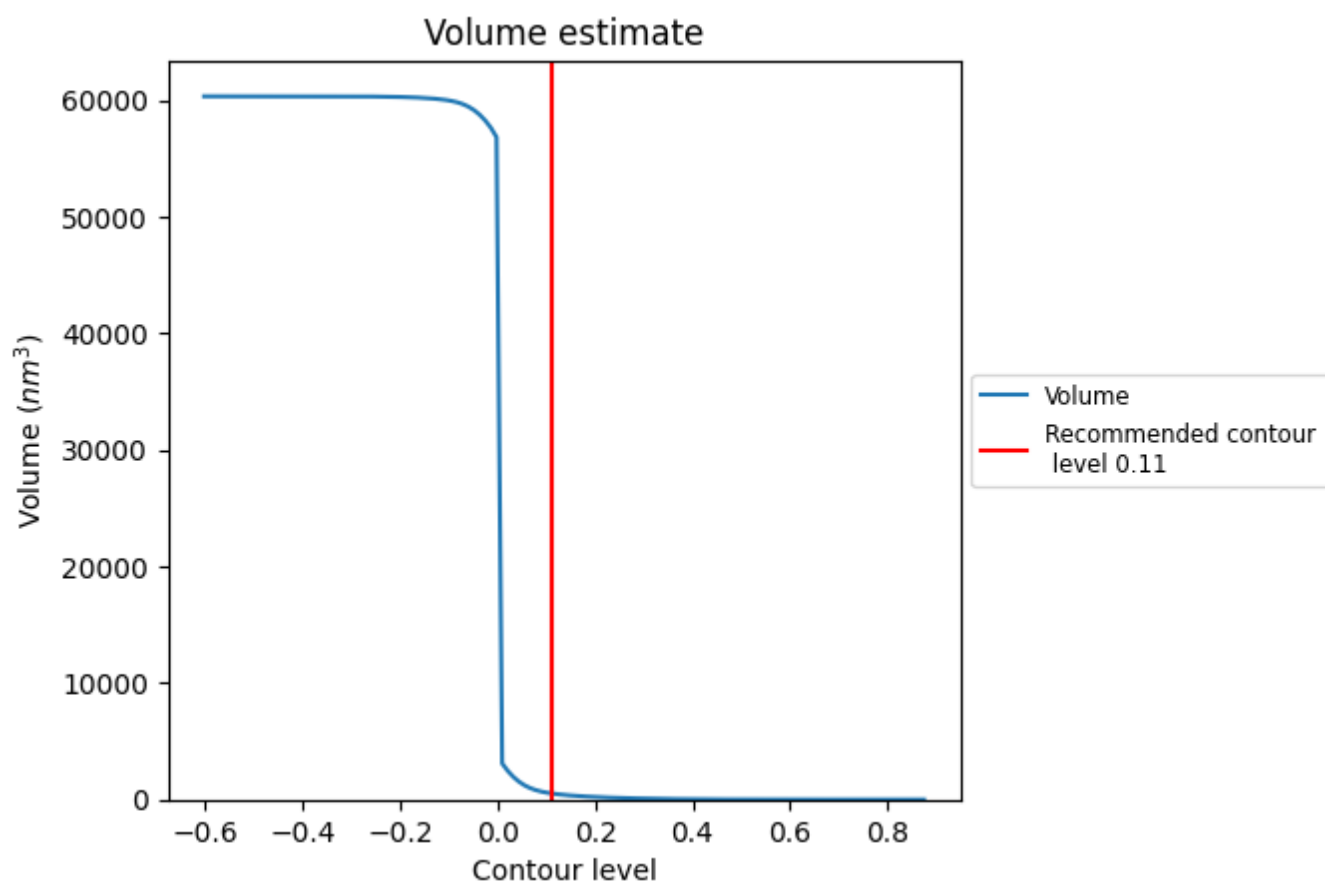
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

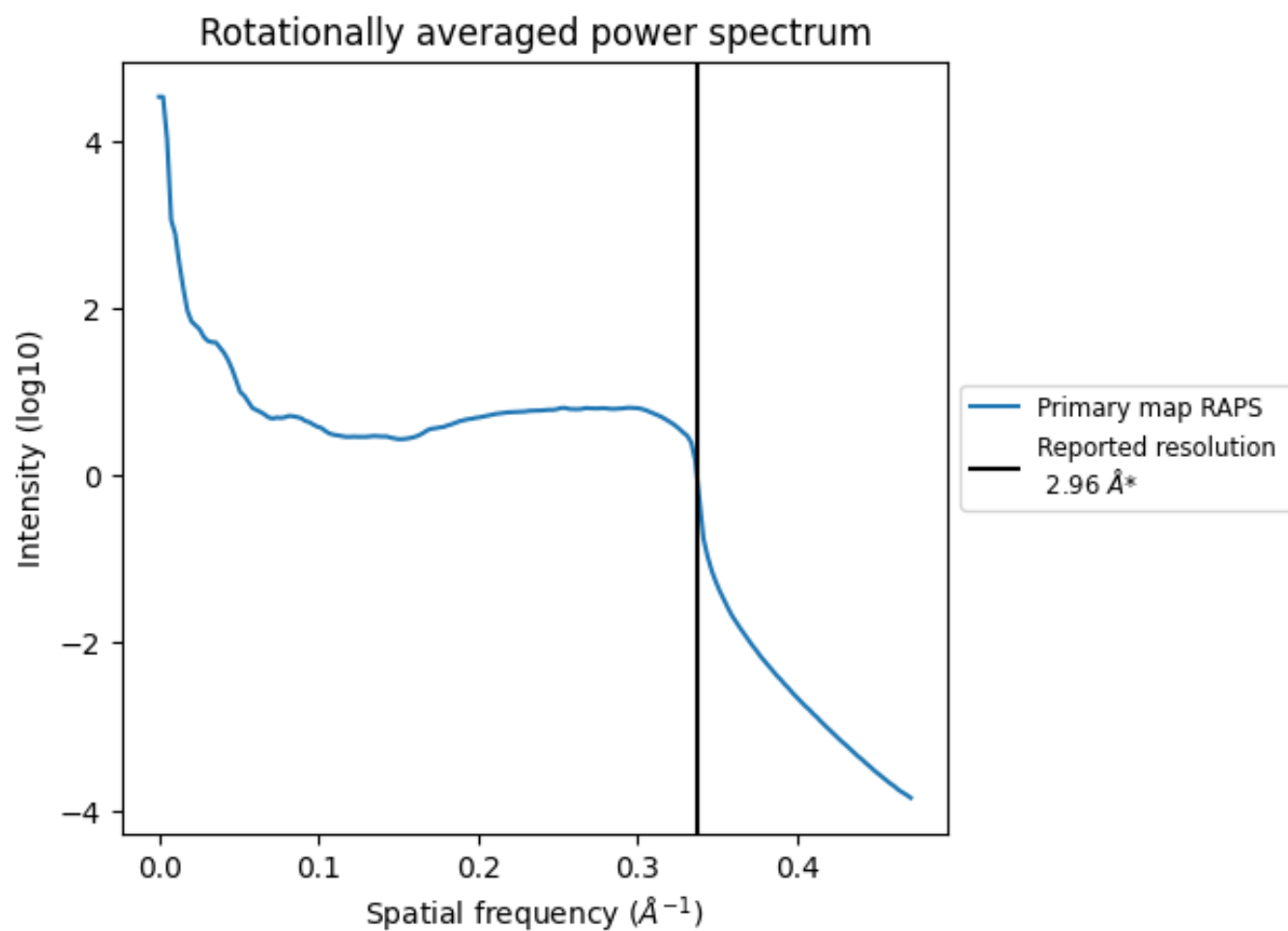
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 532 nm³; this corresponds to an approximate mass of 480 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 ⓘ

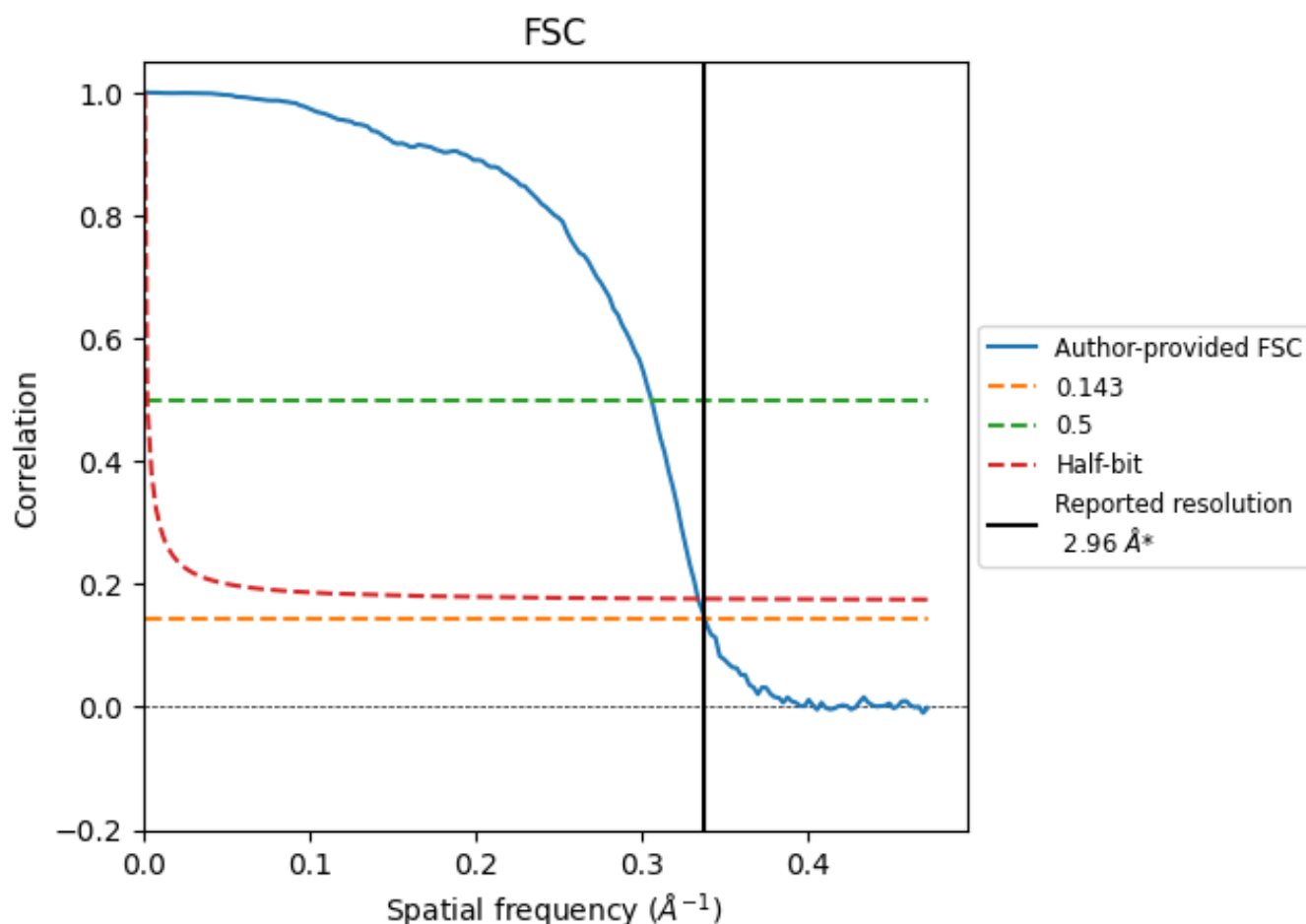


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

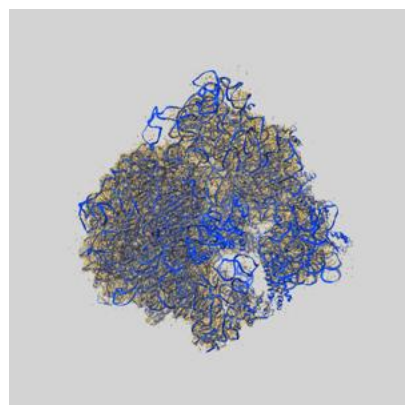
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.27	3.00
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

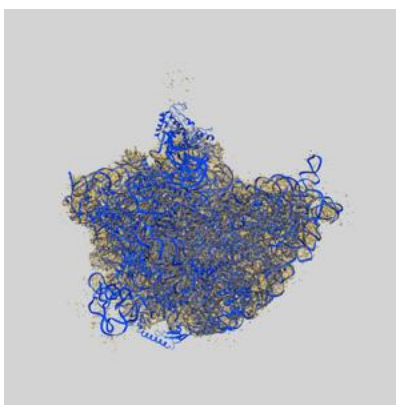
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0261 and PDB model 6HRM. Per-residue inclusion information can be found in section [3](#) on page [19](#).

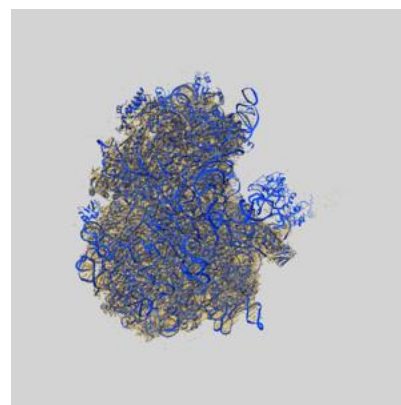
9.1 Map-model overlay [i](#)



X



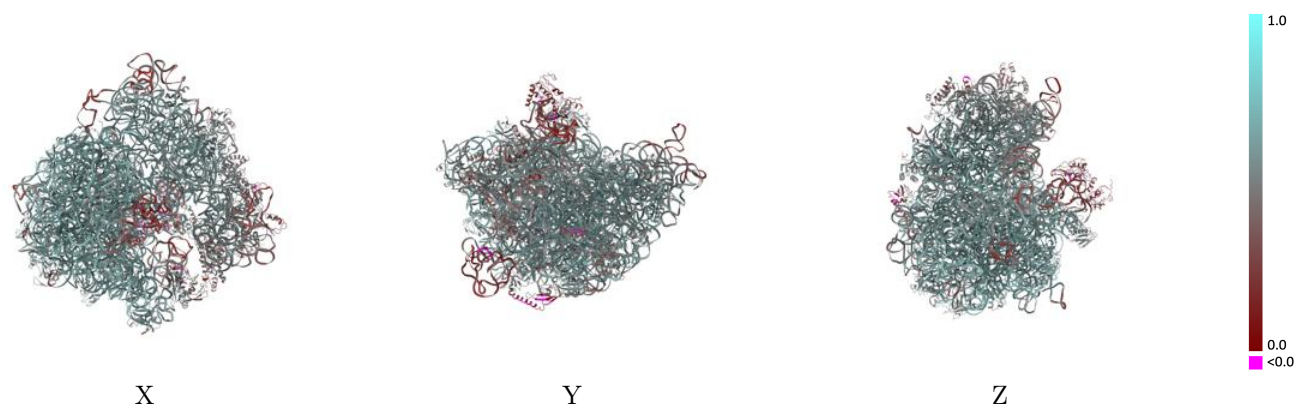
Y



Z

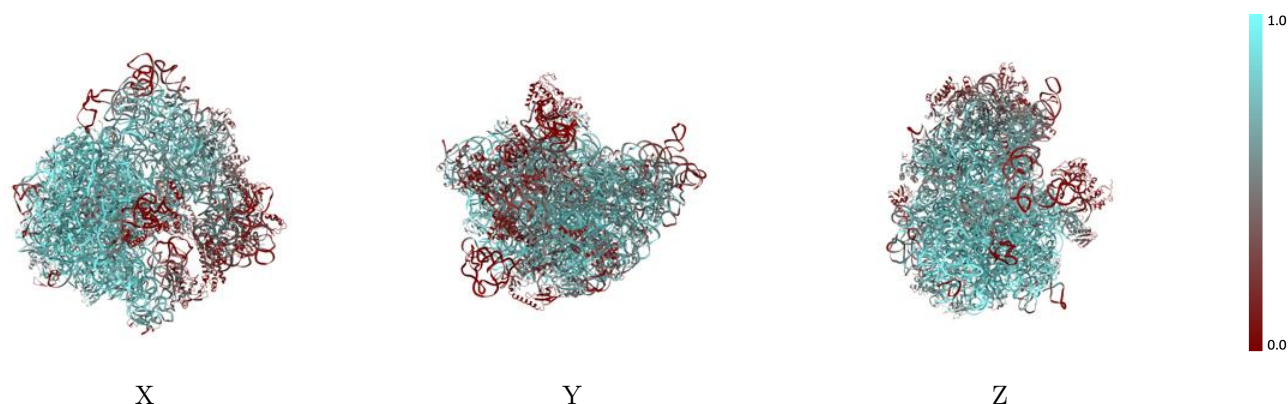
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



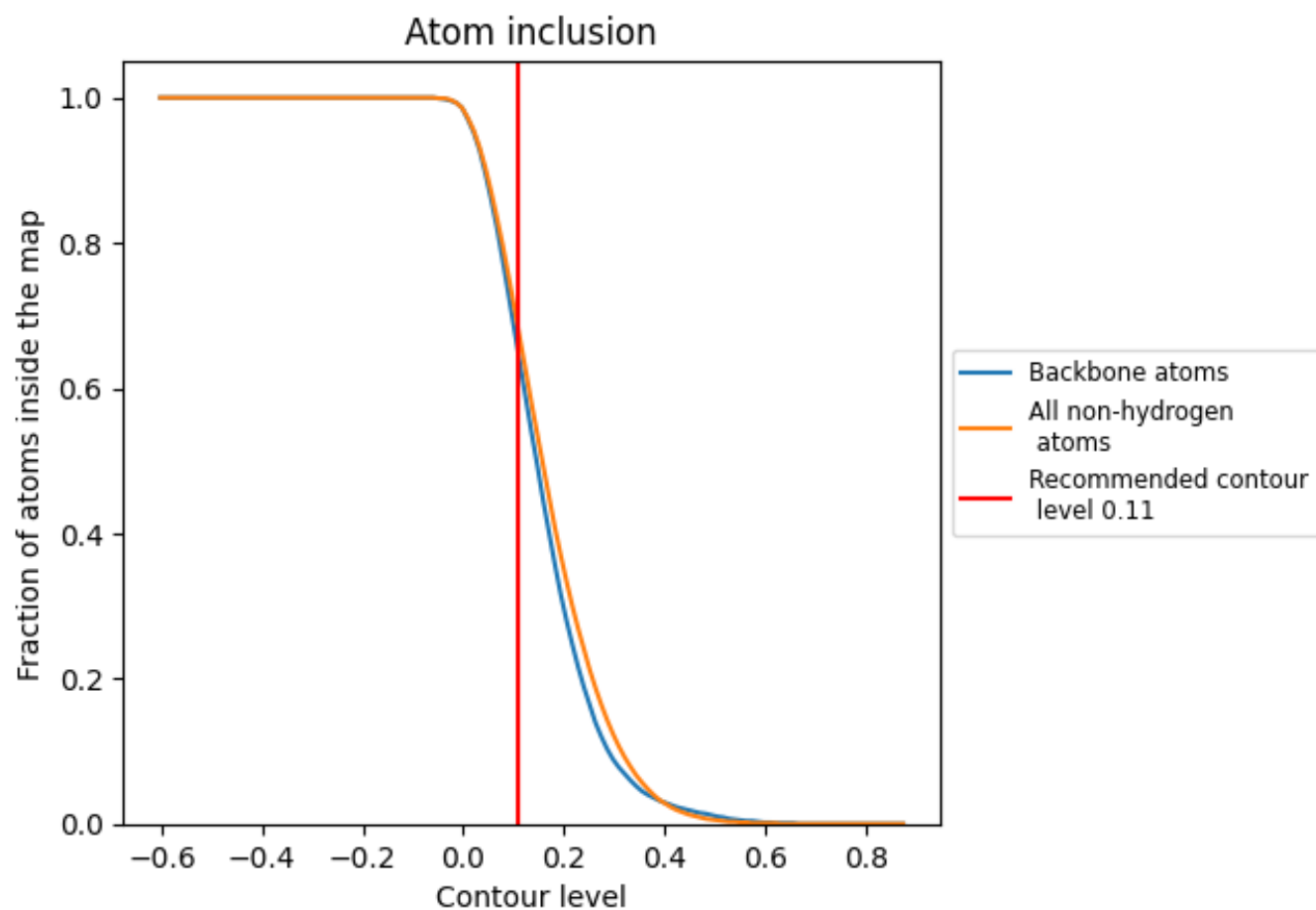
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 68% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.5570
1	 0.7540	 0.5750
3	 0.7280	 0.5840
B	 0.8470	 0.6190
C	 0.7980	 0.6040
D	 0.6460	 0.5600
E	 0.2810	 0.4640
F	 0.4600	 0.5240
G	 0.1190	 0.2870
H	 0.0070	 0.2210
I	 0.0030	 0.2590
J	 0.7960	 0.6100
K	 0.7950	 0.6010
L	 0.7540	 0.5920
M	 0.7700	 0.5990
N	 0.8370	 0.6130
O	 0.6140	 0.5590
P	 0.7450	 0.5980
Q	 0.8240	 0.6160
R	 0.7240	 0.5830
S	 0.7670	 0.6060
T	 0.6750	 0.5670
U	 0.5510	 0.5240
V	 0.6480	 0.5690
W	 0.7970	 0.6160
X	 0.7640	 0.6030
Y	 0.4970	 0.5300
Z	 0.7480	 0.5870
a	 0.1230	 0.3660
b	 0.7580	 0.6050
c	 0.6910	 0.5810
d	 0.8620	 0.6100
e	 0.8350	 0.6260
f	 0.7820	 0.5930
g	 0.2600	 0.4290



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Chain	Atom inclusion	Q-score
h	 0.3520	 0.4760
i	 0.4220	 0.4960
j	 0.5740	 0.5210
k	 0.5080	 0.5170
l	 0.1840	 0.4350
m	 0.6050	 0.5470
n	 0.1950	 0.4340
o	 0.2340	 0.3990
p	 0.5250	 0.5310
q	 0.6450	 0.5530
r	 0.1840	 0.4320
s	 0.3330	 0.4810
t	 0.6320	 0.5630
u	 0.5330	 0.5260
v	 0.5130	 0.5240
w	 0.6180	 0.5470
x	 0.1510	 0.4140
y	 0.5810	 0.5540
z	 0.2330	 0.4530