



wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 07:00 PM JST

PDB ID : 6LU8 / pdb_00006lu8
EMDB ID : EMD-0978
Title : Cryo-EM structure of a human pre-60S ribosomal subunit - state A
Authors : Liang, X.; Zuo, M.; Zhang, Y.; Li, N.; Ma, C.; Dong, M.; Gao, N.
Deposited on : 2020-01-26
Resolution : 3.13 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:

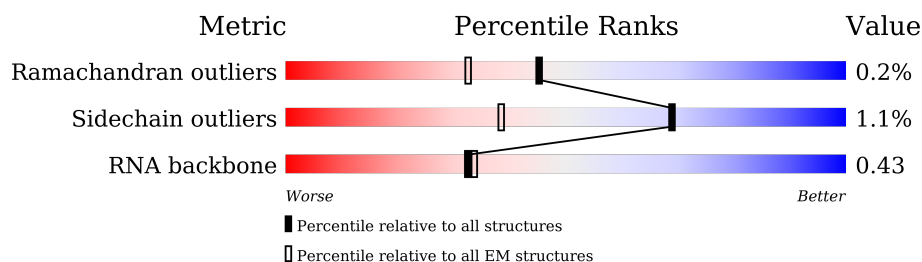
EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

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 3.13 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.





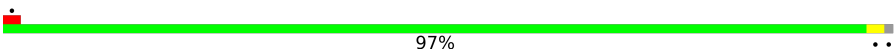


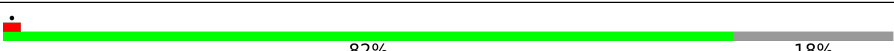
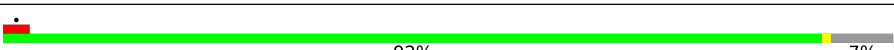

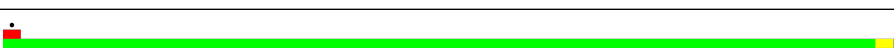
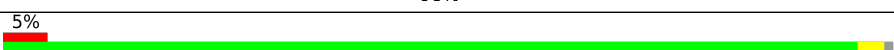
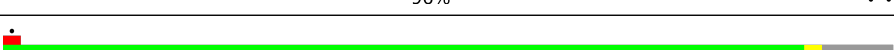
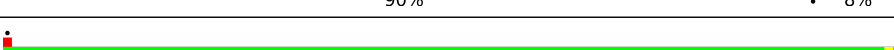
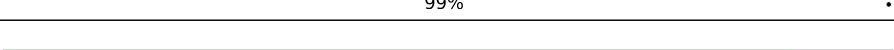
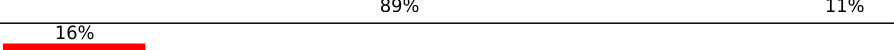
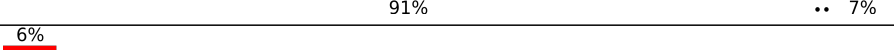
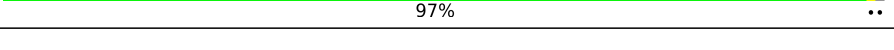
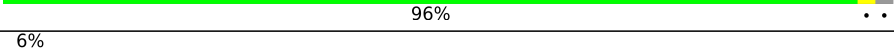
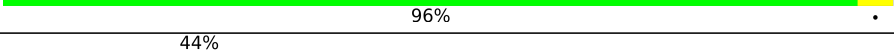


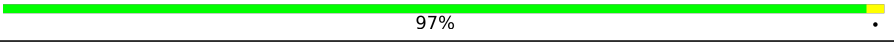
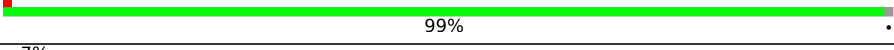
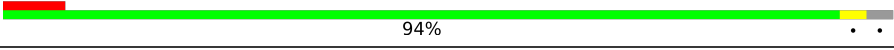
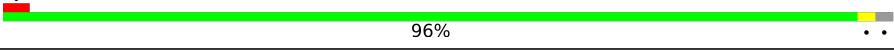

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	731	 97%
2	2	5070	 6% 24% 36% 9% 31%
3	3	503	 19% 47% 52%
4	4	634	 7% 19% 91% 5%
5	5	120	 42% 47% 11%
6	6	245	 7% 97%
7	7	163	 82% 17%
8	8	156	 37% 53% 10%


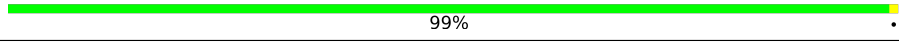
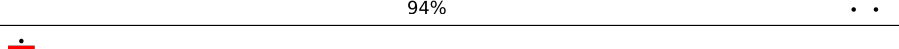
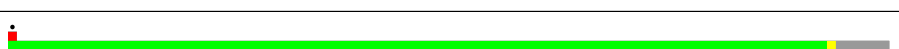

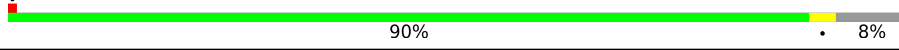
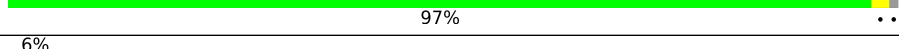
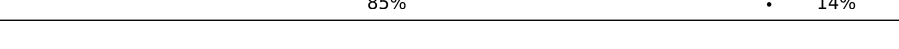

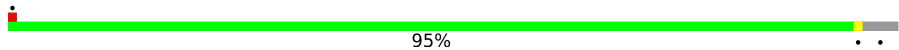
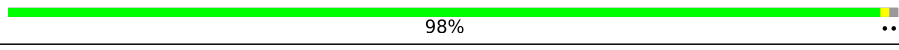
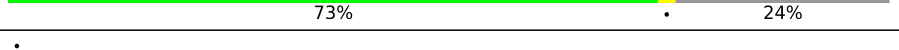
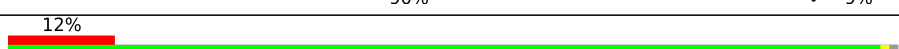




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Mol	Chain	Length	Quality of chain
9	9	134	
10	A	217	
11	B	403	
12	C	159	
13	D	427	
14	E	115	
15	F	117	
16	G	266	
17	H	123	
18	I	192	
19	K	105	
20	L	148	
21	M	97	
22	N	178	
23	O	70	
24	P	51	
25	Q	211	
26	R	203	
27	S	215	
28	U	204	
29	V	203	
30	W	106	
31	X	92	
32	Y	184	
33	Z	188	

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Mol	Chain	Length	Quality of chain
34	a	196	
35	b	176	
36	c	160	
37	d	128	
38	e	140	
39	g	156	
40	h	145	
41	i	136	
42	j	125	
43	k	135	
44	l	137	
45	m	257	
46	n	110	
47	o	288	
48	p	248	
49	r	297	
50	z	129	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 143909 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 Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	19	Total	C	N	O	S	0	0
			148	88	23	35	2		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3477	Total	C	N	O	P	0	0
			74680	33310	13669	24225	3476		

- Molecule 3 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	243	Total	C	N	O	S	0	0
			1951	1242	341	351	17		

- Molecule 4 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	605	Total	C	N	O	S	0	0
			4965	3124	903	911	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	244	Total	C	N	O	S	0	0
			1852	1149	318	372	13		

- Molecule 7 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	135	Total	C	N	O	S	0	0
			1159	737	225	187	10		

- Molecule 8 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 9 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	86	Total	C	N	O	S	0	0
			711	433	154	121	3		

- Molecule 10 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	212	Total	C	N	O	S	0	0
			1708	1092	308	300	8		

- Molecule 11 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	400	Total	C	N	O	S	1	0
			3235	2060	607	554	14		

- Molecule 12 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	90	Total	C	N	O	S	0	0
			743	462	163	114	4		

- Molecule 13 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	357	Total	C	N	O	S	0	0
			2848	1794	569	472	13		

- Molecule 14 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 15 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	109	Total	C	N	O	S	0	0
			868	544	179	139	6		

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	241	Total	C	N	O	S	1	0
			1940	1236	374	326	4		

- Molecule 17 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 18 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	97	Total	C	N	O	S	0	0
			799	500	170	124	5		

- Molecule 20 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 21 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 22 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	165	Total	C	N	O	S	0	0
			1319	836	245	233	5		

- Molecule 23 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 24 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 25 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 26 is a protein called Translation machinery-associated protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	150	Total	C	N	O	S	0	0
			1272	793	244	230	5		

- Molecule 27 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 28 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 29 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 30 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 31 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	90	Total	C	N	O	S	0	0
			698	440	134	117	7		

- Molecule 32 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 33 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 34 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	148	Total	C	N	O	S	0	0
			1239	772	266	192	9		

- Molecule 35 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 36 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	155	Total	C	N	O	S	0	0
			1264	801	248	210	5		

- Molecule 37 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 38 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 39 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 41 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 42 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 43 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 44 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 45 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 46 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 47 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	218	Total	C	N	O	S	0	0
			1750	1125	332	289	4		

- Molecule 48 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	225	Total	C	N	O	S	1	0
			1878	1207	361	301	9		

- Molecule 49 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	293	Total	C	N	O	S	0	0
			2386	1510	435	427	14		

- Molecule 50 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	34	Total	C	N	O	S	0	0
			284	179	61	43	1		

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	2	229	Total	Mg	0
			229	229	
51	5	3	Total	Mg	0
			3	3	
51	8	6	Total	Mg	0
			6	6	
51	B	1	Total	Mg	0
			1	1	
51	D	1	Total	Mg	0
			1	1	
51	F	1	Total	Mg	0
			1	1	
51	L	1	Total	Mg	0
			1	1	
51	M	1	Total	Mg	0
			1	1	
51	k	1	Total	Mg	0
			1	1	
51	m	1	Total	Mg	0
			1	1	
51	n	1	Total	Mg	0
			1	1	
51	p	1	Total	Mg	0
			1	1	

- Molecule 52 is water.

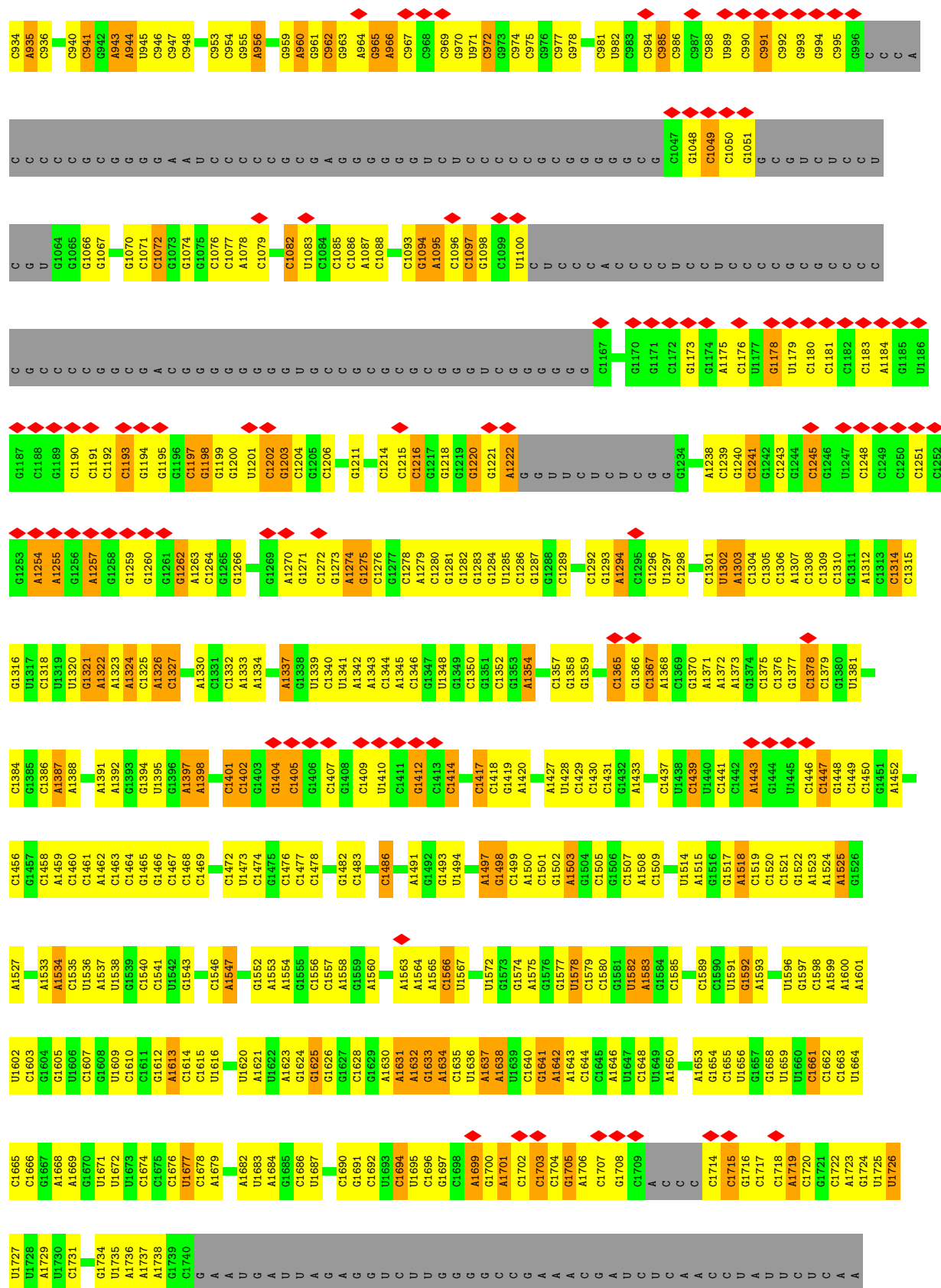
Mol	Chain	Residues	Atoms		AltConf
52	2	13	Total	O	0
			13	13	

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Mol	Chain	Residues	Atoms		AltConf
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52	o	1	Total 1	O 1	0
52	p	1	Total 1	O 1	0

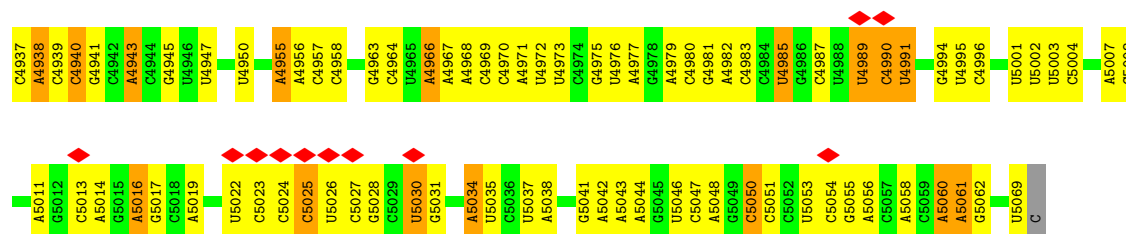




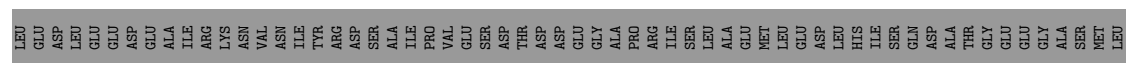
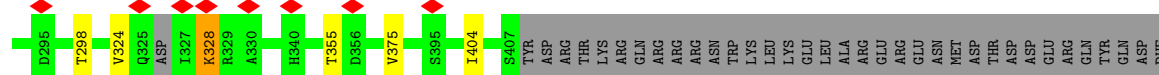
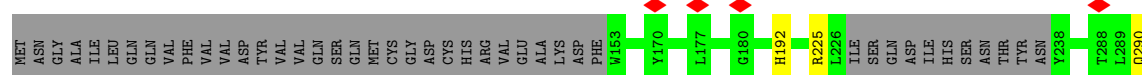
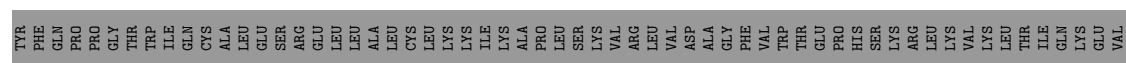
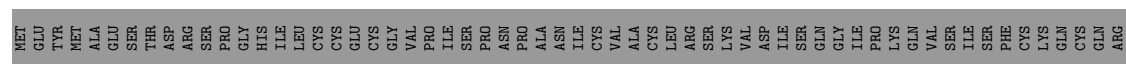




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C4871	G4745	U4685	A4616	G4549	A4484	U4420	U4352	U4290	A4220	G4139	U	G
G4872	G4886	C4886	U4619	U4551	C4486	C4421	U4353	G4291	C4223	C4140	U4068	C
G4873	A4687	A4687	U4620	U4552	C4487	A4422	G4355	A4292	C4224	C4141	U4071	C
A4874	U4748	C4688	A4621	A4553	A4488	U4423	U4358	C4294	G4225	C4142	C4072	C
G4875	G4749	U4689	A4622	C4554	G4489	A4424	U4359	U4295	C4226	C4143	A4073	C
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G4877	G4751	A4691	A4624	U4556	U4493	G4425	U4361	U4297	G4228	C4145	U4075	G
C4878	U4752	A4692	C4625	U4557	A4494	C4426	U4362	A4298	C4229	C4146	A4076	C
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	C	A4716	C4652	C4653	A4517	U4450	A4386	A4324	C4258	C4172		C
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	C	C4719	A4655	A4590	G4520	U4453	C4389	C4327	C4262	C4175		G
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	C	G4722	C4658	U4594	A4523	C4456	G4393	G4330	G4265	C4178		G
	C	A4723	C4662	G4595	C4524	U4460	A4394	C4331	G4266	C4179		G
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	C	C4730	U4668	U4601	U4532	C4466	G	C4337	U4194	G4115		C
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	C	C4732	C4670	C4603	A4534	U4468	C	A4339	G4196	U4117		A
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	C	G4734	A4672	A4605	C4536	G4470	U4404	C4341	C4120	C4119		U
	C	C4735	U4673	G4606	U4537	U4471	G4405	C4342	A4203	U4120		A
	C	A4674	A4607	C4537	C4538	C4472	U4406	U4343	G4121	C4121		C
	C	U4675	U4675	G4538	U4539	A4473		C4344	A4205	C4122		U
	C	C4676	C4609	G4539	U4540	U4474	C4413	C4345	C4206	C4123		C
	C	G4677	A4610	U4541	A4544	C4475	A4414	U4346	C4207	C4124		U
	C	U4678	A4611	A4545	G4546	C4476	A4415	A4347	A4212	A4127		A
	C	A4681	C4612	U4546	A4547	U4477	A4416	C4348	A4213	G4128		U
	C	U4682	C4613	G4547	A4548	G4478	C4417	A4349	C4287	G4129		C
	C	U4683	C4614	A4549	A4550	U4479		C4350	C4130	C4130		G
	C	G4743				U4480		C4131	C4131	C4131		G
	C					U4481		C4132	C4132	C4132		G
	C					U4482		C4133	C4133	C4133		G
	C							C4134	C4134	C4134		G
	C							C4135	C4135	C4135		G
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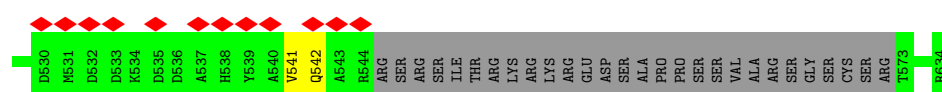
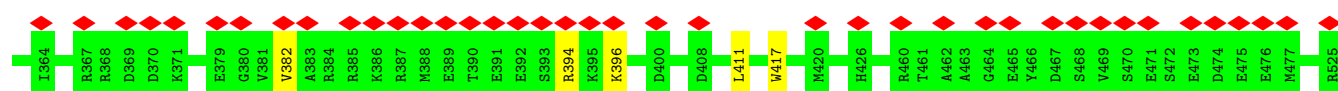
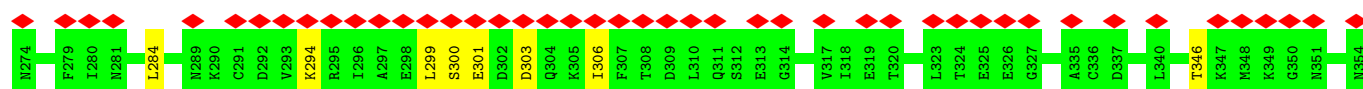
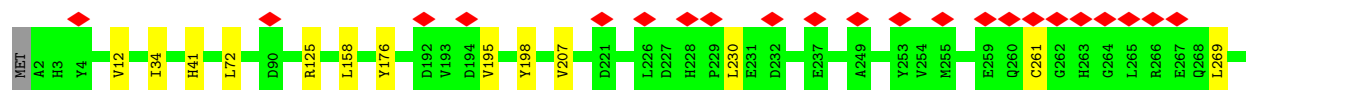


• Molecule 3: 60S ribosomal export protein NMD3



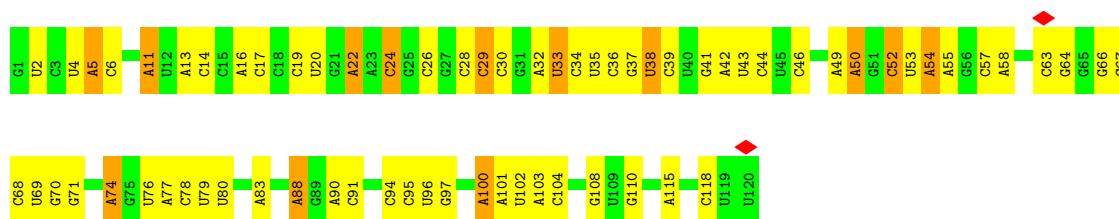
THR

• Molecule 4: Nucleolar GTP-binding protein 1



• Molecule 5: 5S rRNA

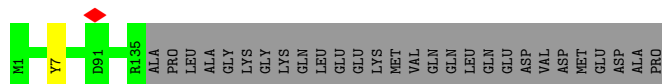
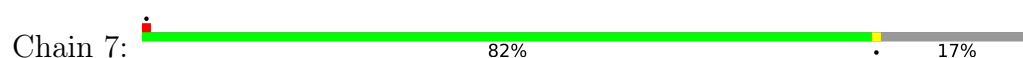




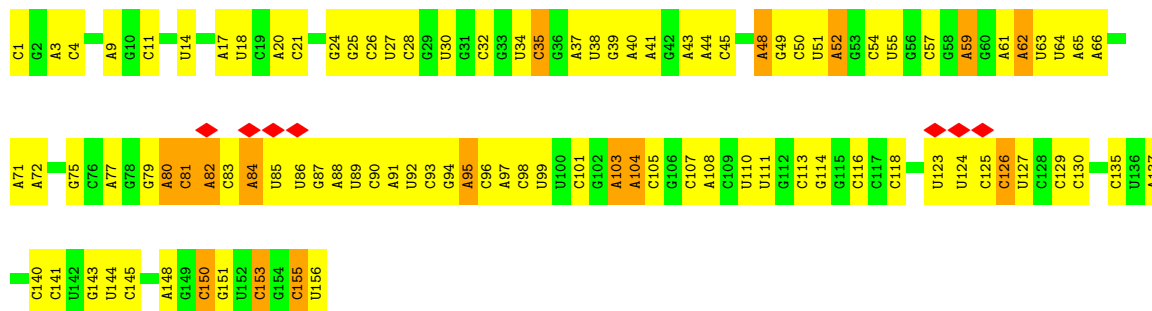
- Molecule 6: Eukaryotic translation initiation factor 6



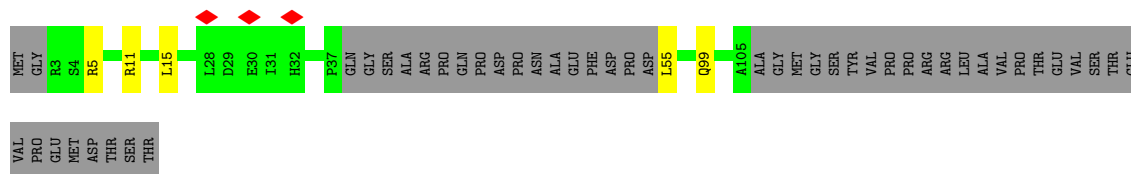
- Molecule 7: Probable ribosome biogenesis protein RLP24



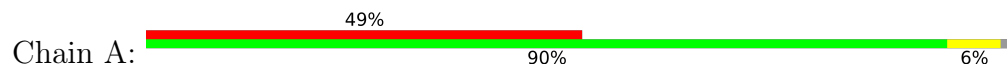
- Molecule 8: 5.8S rRNA

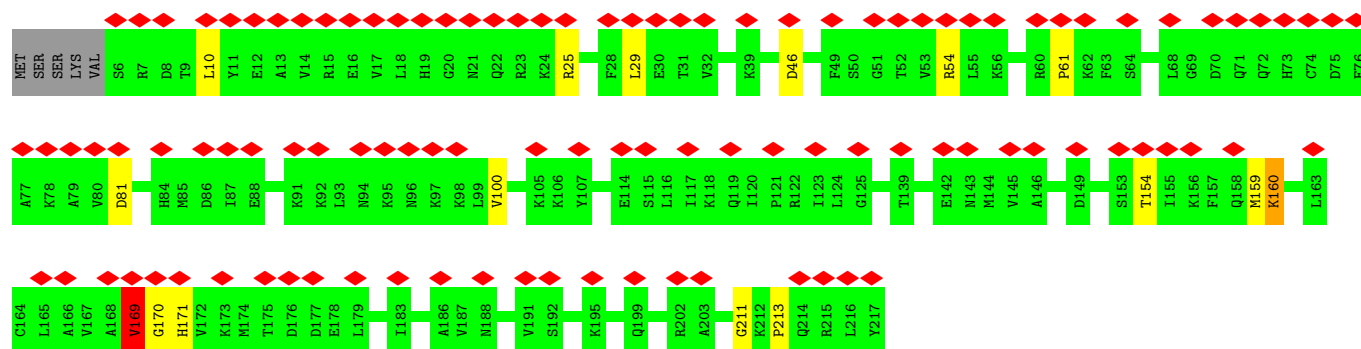


- Molecule 9: Zinc finger protein 593

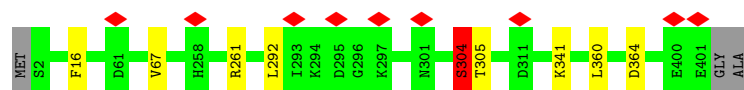


- Molecule 10: 60S ribosomal protein L10a

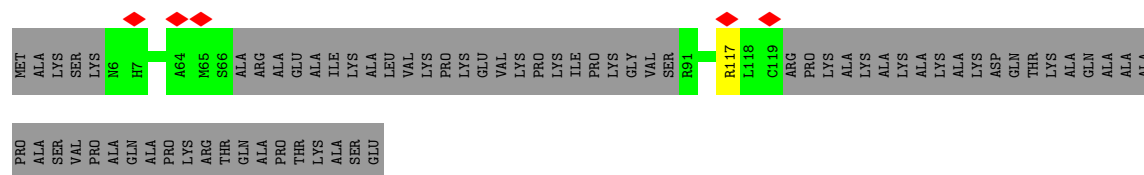




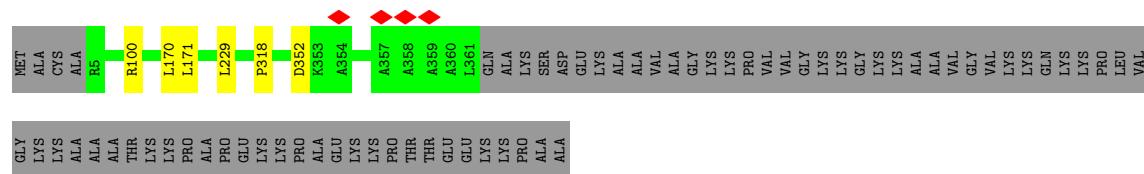
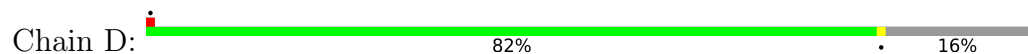
- Molecule 11: 60S ribosomal protein L3



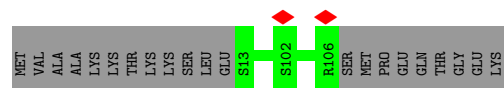
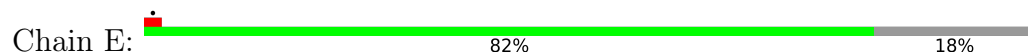
- Molecule 12: 60S ribosomal protein L29



- Molecule 13: 60S ribosomal protein L4

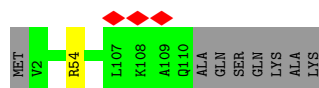


- Molecule 14: 60S ribosomal protein L30

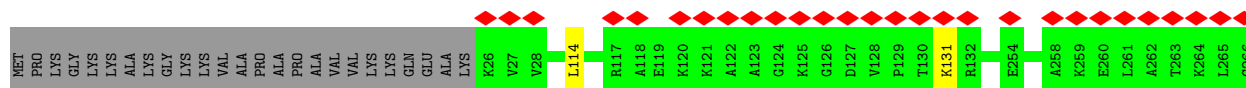
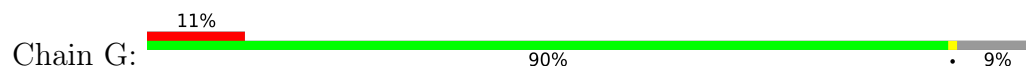


- Molecule 15: 60S ribosomal protein L34

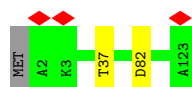




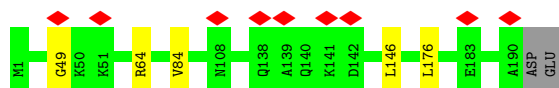
- Molecule 16: 60S ribosomal protein L7a



- Molecule 17: 60S ribosomal protein L35



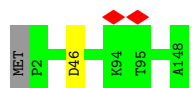
- Molecule 18: 60S ribosomal protein L9



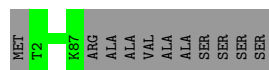
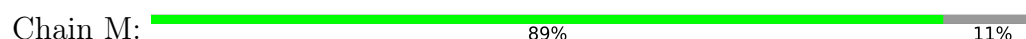
- Molecule 19: 60S ribosomal protein L36



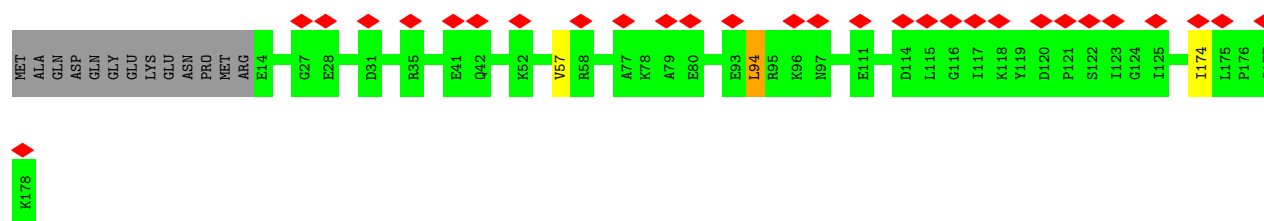
- Molecule 20: 60S ribosomal protein L27a



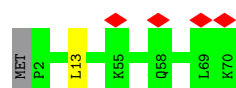
- Molecule 21: 60S ribosomal protein L37



- Molecule 22: 60S ribosomal protein L11



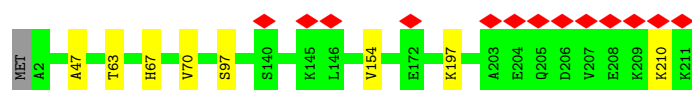
- Molecule 23: 60S ribosomal protein L38



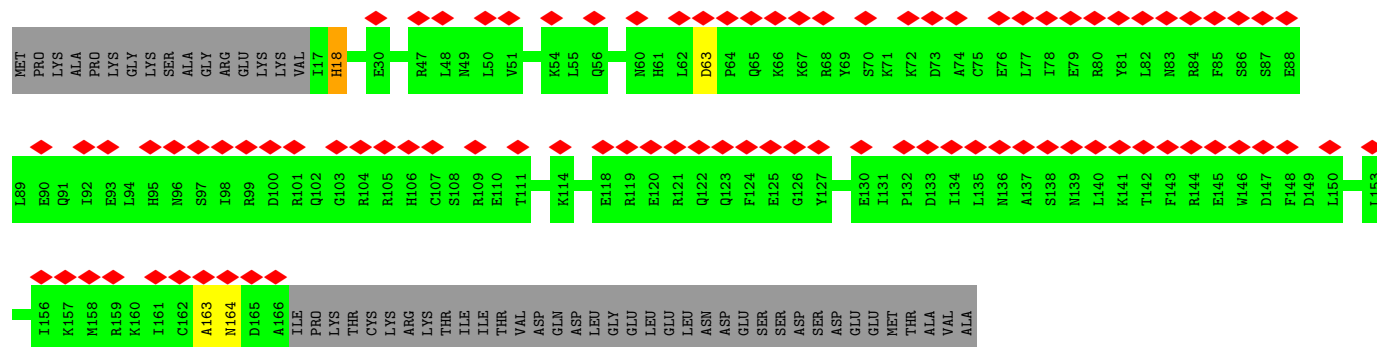
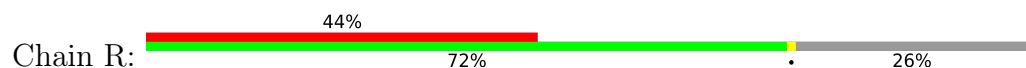
- Molecule 24: 60S ribosomal protein L39



- Molecule 25: 60S ribosomal protein L13

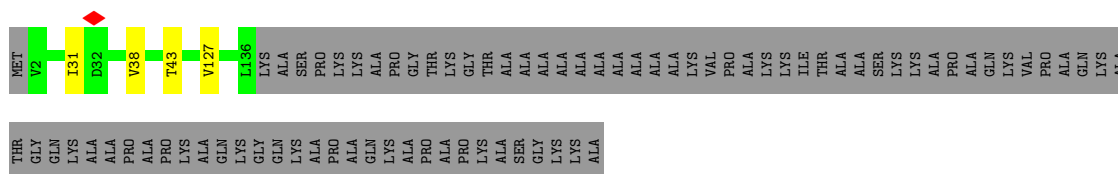


- Molecule 26: Translation machinery-associated protein 16



- Molecule 27: 60S ribosomal protein L14





- Molecule 28: 60S ribosomal protein L15

Chain U: 97%



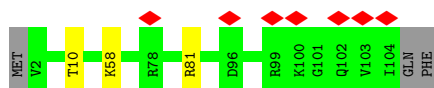
- Molecule 29: 60S ribosomal protein L13a

Chain V: 99%



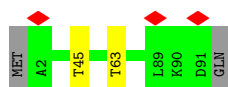
- Molecule 30: 60S ribosomal protein L36a

Chain W: 7% 94%



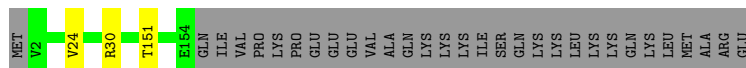
- Molecule 31: 60S ribosomal protein L37a

Chain X: 96%



- Molecule 32: 60S ribosomal protein L17

Chain Y: 82% 17%

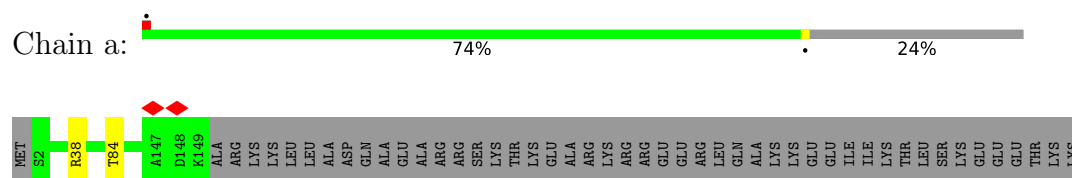


- Molecule 33: 60S ribosomal protein L18

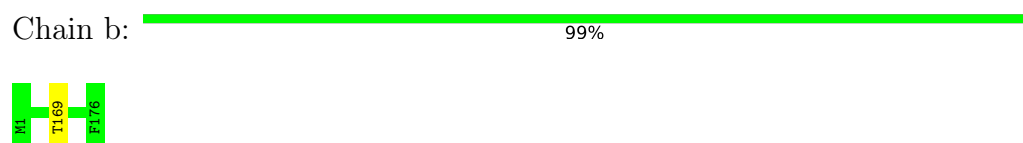
Chain Z: 98%



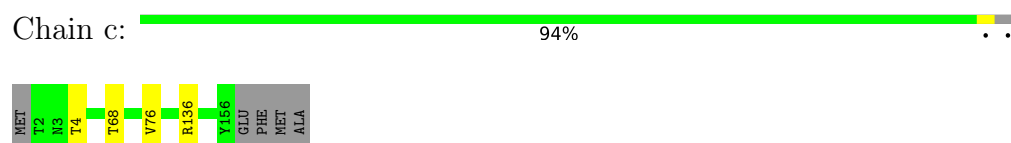
- Molecule 34: 60S ribosomal protein L19



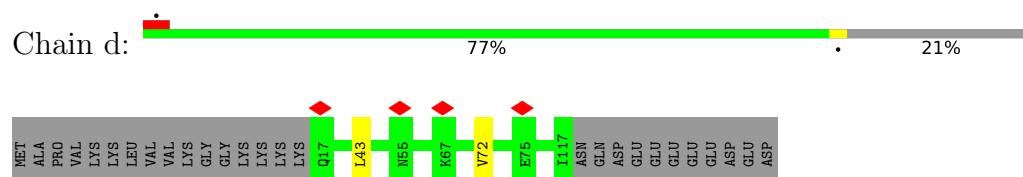
- Molecule 35: 60S ribosomal protein L18a



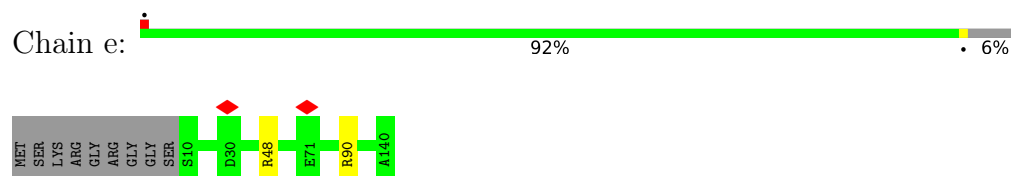
- Molecule 36: 60S ribosomal protein L21



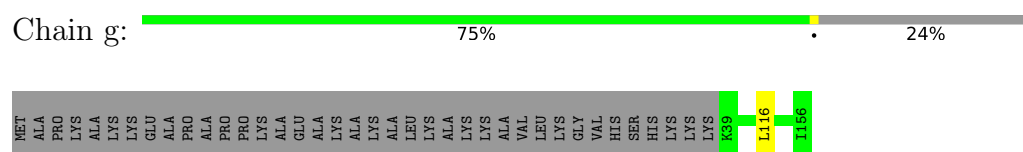
- Molecule 37: 60S ribosomal protein L22



- Molecule 38: 60S ribosomal protein L23

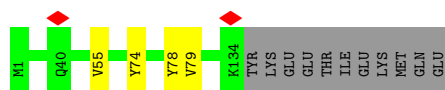


- Molecule 39: 60S ribosomal protein L23a



- Molecule 40: 60S ribosomal protein L26





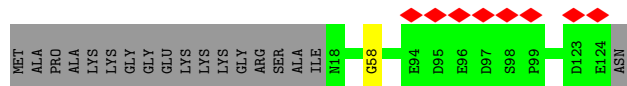
- Molecule 41: 60S ribosomal protein L27

Chain i: 97%



- Molecule 42: 60S ribosomal protein L31

Chain j: 6% 85% 14%



- Molecule 43: 60S ribosomal protein L32

Chain k: 95% 5%



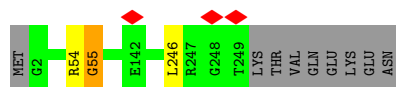
- Molecule 44: 60S ribosomal protein L28

Chain l: 91% 9%



- Molecule 45: 60S ribosomal protein L8

Chain m: 95%

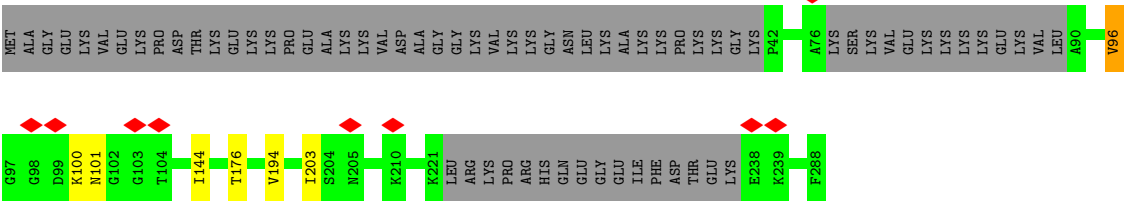


- Molecule 46: 60S ribosomal protein L35a

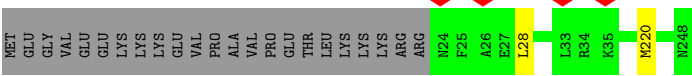
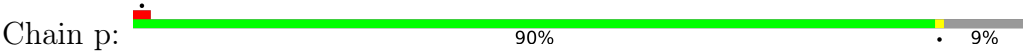
Chain n: 98%



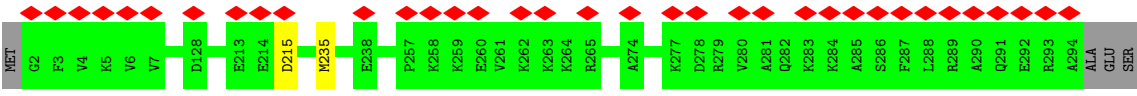
- Molecule 47: 60S ribosomal protein L6



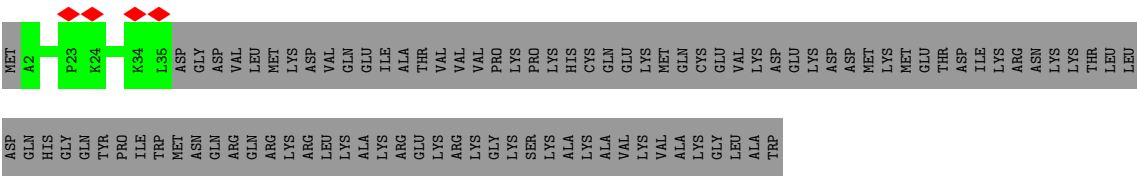
• Molecule 48: 60S ribosomal protein L7



• Molecule 49: 60S ribosomal protein L5



• Molecule 50: Protein LLP homolog



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21489	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.454	Depositor
Minimum map value	-0.187	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	507.84, 507.84, 507.84	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, OMC, B8W, OMG, I4U, B9B, BGH, PSU, OMU, 5MU, E7G, B8H, UR3, B8T, P7G, B9H, 5MC, M7A, 6MZ, B8K, 2MG, MHG, MG, E6G, P4U, A2M, 1MA, B8Q

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	0.37	0/148	0.72	0/196
2	2	0.92	13/81168 (0.0%)	1.80	3749/126540 (3.0%)
3	3	0.42	0/1990	0.71	2/2685 (0.1%)
4	4	0.42	0/5048	0.76	12/6774 (0.2%)
5	5	0.81	0/2858	1.77	129/4455 (2.9%)
6	6	0.45	0/1877	0.74	1/2554 (0.0%)
7	7	0.45	0/1181	0.71	1/1563 (0.1%)
8	8	0.98	0/3679	1.78	161/5732 (2.8%)
9	9	0.39	0/723	0.77	2/961 (0.2%)
10	A	0.43	1/1736 (0.1%)	0.92	6/2328 (0.3%)
11	B	0.53	0/3306	0.79	7/4423 (0.2%)
12	C	0.37	0/755	0.63	0/996
13	D	0.51	0/2902	0.73	2/3898 (0.1%)
14	E	0.42	0/742	0.69	0/996
15	F	0.49	0/878	0.72	0/1170
16	G	0.47	0/1976	0.77	2/2658 (0.1%)
17	H	0.42	0/1023	0.63	0/1351
18	I	0.44	0/1537	0.69	2/2066 (0.1%)
19	K	0.39	0/810	0.65	1/1072 (0.1%)
20	L	0.51	0/1191	0.72	1/1591 (0.1%)
21	M	0.56	0/720	0.72	0/952
22	N	0.42	0/1341	0.78	2/1793 (0.1%)
23	O	0.42	0/575	0.65	1/761 (0.1%)
24	P	0.50	0/454	0.70	0/599
25	Q	0.48	0/1732	0.66	0/2315
26	R	0.38	0/1293	0.71	0/1725
27	S	0.48	0/1133	0.70	1/1516 (0.1%)
28	U	0.51	0/1746	0.71	1/2338 (0.0%)
29	V	0.49	0/1682	0.69	0/2250
30	W	0.48	0/855	0.75	2/1128 (0.2%)
31	X	0.49	0/708	0.65	0/941

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.48	0/1268	0.67	0/1701
33	Z	0.50	0/1537	0.74	1/2052 (0.0%)
34	a	0.46	0/1255	0.66	1/1662 (0.1%)
35	b	0.48	0/1501	0.65	0/2013
36	c	0.47	0/1291	0.69	0/1725
37	d	0.45	0/839	0.83	1/1126 (0.1%)
38	e	0.49	0/993	0.72	1/1332 (0.1%)
39	g	0.45	0/984	0.63	1/1323 (0.1%)
40	h	0.49	0/1132	0.68	0/1504
41	i	0.47	0/1130	0.68	0/1507
42	j	0.51	1/903 (0.1%)	0.70	0/1216
43	k	0.53	0/1071	0.69	0/1429
44	l	0.46	0/1017	0.72	1/1364 (0.1%)
45	m	0.53	0/1936	0.77	2/2596 (0.1%)
46	n	0.52	0/895	0.72	0/1198
47	o	0.42	0/1784	0.73	1/2393 (0.0%)
48	p	0.49	0/1916	0.72	2/2553 (0.1%)
49	r	0.43	0/2432	0.71	1/3256 (0.0%)
50	z	0.37	0/286	0.54	0/372
All	All	0.76	15/151937 (0.0%)	1.48	4097/222649 (1.8%)

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
3	3	0	2
4	4	0	6
6	6	0	1
10	A	0	7
11	B	0	2
18	I	0	1
22	N	0	1
25	Q	0	1
26	R	0	1
27	S	0	1
30	W	0	1
41	i	0	1
45	m	0	1
46	n	0	1
47	o	0	2
All	All	0	29

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	256	G	N7-C5	-7.57	1.34	1.39
2	2	2465	C	N1-C6	-7.32	1.32	1.37
2	2	1577	G	C2-N3	-7.08	1.27	1.32
2	2	4764	A	N9-C4	-6.65	1.33	1.37
2	2	1254	A	N9-C4	6.39	1.41	1.37

The worst 5 of 4097 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	516	C	N1-C2-O2	16.84	129.00	118.90
2	2	485	C	C2-N1-C1'	16.20	136.62	118.80
10	A	169	VAL	O-C-N	-15.96	96.07	123.20
2	2	4119	C	N1-C2-O2	15.50	128.20	118.90
2	2	449	C	C2-N1-C1'	15.49	135.84	118.80

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	225	ARG	Peptide
3	3	328	LYS	Peptide
4	4	176	TYR	Peptide
4	4	198	TYR	Peptide
4	4	294	LYS	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	17/731 (2%)	17 (100%)	0	0	100	100
3	3	237/503 (47%)	211 (89%)	25 (10%)	1 (0%)	30	60
4	4	601/634 (95%)	539 (90%)	59 (10%)	3 (0%)	25	55
6	6	242/245 (99%)	225 (93%)	17 (7%)	0	100	100
7	7	133/163 (82%)	126 (95%)	7 (5%)	0	100	100
9	9	82/134 (61%)	71 (87%)	9 (11%)	2 (2%)	5	20
10	A	210/217 (97%)	176 (84%)	32 (15%)	2 (1%)	13	40
11	B	399/403 (99%)	373 (94%)	24 (6%)	2 (0%)	25	55
12	C	86/159 (54%)	82 (95%)	4 (5%)	0	100	100
13	D	355/427 (83%)	333 (94%)	22 (6%)	0	100	100
14	E	92/115 (80%)	88 (96%)	4 (4%)	0	100	100
15	F	107/117 (92%)	104 (97%)	3 (3%)	0	100	100
16	G	240/266 (90%)	224 (93%)	16 (7%)	0	100	100
17	H	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
18	I	188/192 (98%)	175 (93%)	13 (7%)	0	100	100
19	K	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
20	L	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
21	M	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
22	N	163/178 (92%)	145 (89%)	18 (11%)	0	100	100
23	O	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
24	P	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
25	Q	208/211 (99%)	189 (91%)	18 (9%)	1 (0%)	25	55
26	R	148/203 (73%)	137 (93%)	9 (6%)	2 (1%)	9	32
27	S	133/215 (62%)	124 (93%)	9 (7%)	0	100	100
28	U	201/204 (98%)	190 (94%)	10 (5%)	1 (0%)	25	55
29	V	199/203 (98%)	192 (96%)	7 (4%)	0	100	100
30	W	101/106 (95%)	93 (92%)	8 (8%)	0	100	100
31	X	88/92 (96%)	84 (96%)	4 (4%)	0	100	100
32	Y	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
33	Z	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
34	a	146/196 (74%)	139 (95%)	7 (5%)	0	100	100
35	b	174/176 (99%)	165 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	c	153/160 (96%)	148 (97%)	5 (3%)	0	100	100
37	d	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
38	e	129/140 (92%)	117 (91%)	12 (9%)	0	100	100
39	g	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
40	h	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
41	i	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
42	j	105/125 (84%)	93 (89%)	12 (11%)	0	100	100
43	k	126/135 (93%)	114 (90%)	12 (10%)	0	100	100
44	l	123/137 (90%)	112 (91%)	11 (9%)	0	100	100
45	m	246/257 (96%)	221 (90%)	24 (10%)	1 (0%)	30	60
46	n	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
47	o	212/288 (74%)	189 (89%)	21 (10%)	2 (1%)	14	43
48	p	224/248 (90%)	211 (94%)	13 (6%)	0	100	100
49	r	291/297 (98%)	268 (92%)	23 (8%)	0	100	100
50	z	32/129 (25%)	30 (94%)	2 (6%)	0	100	100
All	All	7673/9647 (80%)	7100 (92%)	556 (7%)	17 (0%)	45	72

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	5	ARG
9	9	99	GLN
47	o	96	VAL
11	B	304	SER
11	B	305	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	
1	1	17/654 (3%)	17 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	223/457 (49%)	218 (98%)	5 (2%)	47	69
4	4	548/574 (96%)	541 (99%)	7 (1%)	65	80
6	6	212/213 (100%)	207 (98%)	5 (2%)	44	67
7	7	126/149 (85%)	126 (100%)	0	100	100
9	9	74/114 (65%)	73 (99%)	1 (1%)	62	79
10	A	191/196 (97%)	187 (98%)	4 (2%)	48	70
11	B	349/349 (100%)	347 (99%)	2 (1%)	84	91
12	C	76/126 (60%)	75 (99%)	1 (1%)	65	80
13	D	298/348 (86%)	294 (99%)	4 (1%)	65	80
14	E	79/97 (81%)	79 (100%)	0	100	100
15	F	94/100 (94%)	93 (99%)	1 (1%)	70	83
16	G	206/223 (92%)	206 (100%)	0	100	100
17	H	109/110 (99%)	107 (98%)	2 (2%)	54	74
18	I	169/171 (99%)	167 (99%)	2 (1%)	67	81
19	K	84/89 (94%)	83 (99%)	1 (1%)	67	81
20	L	120/121 (99%)	120 (100%)	0	100	100
21	M	73/80 (91%)	73 (100%)	0	100	100
22	N	138/149 (93%)	137 (99%)	1 (1%)	81	89
23	O	64/65 (98%)	64 (100%)	0	100	100
24	P	47/48 (98%)	46 (98%)	1 (2%)	48	70
25	Q	176/177 (99%)	170 (97%)	6 (3%)	32	59
26	R	138/184 (75%)	136 (99%)	2 (1%)	62	79
27	S	115/161 (71%)	113 (98%)	2 (2%)	56	75
28	U	171/172 (99%)	168 (98%)	3 (2%)	54	74
29	V	173/174 (99%)	172 (99%)	1 (1%)	84	91
30	W	91/94 (97%)	90 (99%)	1 (1%)	70	83
31	X	73/75 (97%)	71 (97%)	2 (3%)	40	64
32	Y	134/163 (82%)	131 (98%)	3 (2%)	47	69
33	Z	164/165 (99%)	162 (99%)	2 (1%)	67	81
34	a	133/175 (76%)	132 (99%)	1 (1%)	79	88
35	b	157/157 (100%)	156 (99%)	1 (1%)	84	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	c	136/140 (97%)	132 (97%)	4 (3%)	37	62
37	d	91/115 (79%)	90 (99%)	1 (1%)	70	83
38	e	101/107 (94%)	100 (99%)	1 (1%)	73	85
39	g	106/133 (80%)	106 (100%)	0	100	100
40	h	124/135 (92%)	120 (97%)	4 (3%)	34	60
41	i	117/118 (99%)	115 (98%)	2 (2%)	56	75
42	j	98/110 (89%)	98 (100%)	0	100	100
43	k	114/121 (94%)	114 (100%)	0	100	100
44	l	109/121 (90%)	109 (100%)	0	100	100
45	m	190/199 (96%)	190 (100%)	0	100	100
46	n	88/89 (99%)	88 (100%)	0	100	100
47	o	192/252 (76%)	189 (98%)	3 (2%)	58	77
48	p	195/215 (91%)	195 (100%)	0	100	100
49	r	247/250 (99%)	246 (100%)	1 (0%)	89	94
50	z	30/115 (26%)	30 (100%)	0	100	100
All	All	6760/8350 (81%)	6683 (99%)	77 (1%)	69	83

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	Z	28	LEU
41	i	52	LYS
34	a	84	THR
37	d	72	VAL
47	o	194	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
13	D	178	ASN
43	k	117	GLN
20	L	85	GLN
42	j	69	ASN
48	p	39	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	3431/5070 (67%)	904 (26%)	25 (0%)
5	5	119/120 (99%)	24 (20%)	0
8	8	155/156 (99%)	39 (25%)	0
All	All	3705/5346 (69%)	967 (26%)	25 (0%)

5 of 967 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	2	17	A
2	2	20	U
2	2	25	A
2	2	36	U
2	2	39	A

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	3596	A
2	2	4136	G
2	2	4913	G
2	2	3905	A
2	2	4196	OMG

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

92 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	$\# Z > 2$
2	7MG	2	4550	2	22,26,27	3.50	10 (45%)	29,39,42	2.08	10 (34%)
2	I4U	2	4194	2	21,24,25	4.72	15 (71%)	27,34,37	1.33	2 (7%)
2	UR3	2	4597	2	19,22,23	2.69	7 (36%)	26,32,35	2.45	6 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	B8T	2	4671	2	19,22,23	3.30	8 (42%)	26,31,34	1.04	1 (3%)
2	A2M	2	3825	2	18,25,26	4.21	7 (38%)	18,36,39	3.34	3 (16%)
2	B8W	2	4529	2,51	18,26,27	6.27	7 (38%)	21,38,41	2.85	10 (47%)
2	MHG	2	4371	2	29,32,33	3.94	12 (41%)	34,46,49	2.61	10 (29%)
2	A2M	2	3718	2	18,25,26	4.20	7 (38%)	18,36,39	3.12	3 (16%)
2	PSU	2	4293	2,30	18,21,22	0.97	1 (5%)	22,30,33	1.78	5 (22%)
2	BGH	2	3899	2	25,29,30	4.24	17 (68%)	31,43,46	2.46	11 (35%)
2	B8H	2	1860	2	19,22,23	6.76	6 (31%)	22,32,35	2.21	5 (22%)
2	2MG	2	1517	2	18,26,27	2.33	7 (38%)	16,38,41	1.98	5 (31%)
2	OMG	2	1883	2	18,26,27	2.34	6 (33%)	19,38,41	1.92	4 (21%)
2	A2M	2	4571	2	18,25,26	4.26	7 (38%)	18,36,39	3.17	3 (16%)
2	2MG	2	4872	2	18,26,27	2.25	7 (38%)	16,38,41	1.58	4 (25%)
2	B9B	2	237	2	21,28,29	5.70	9 (42%)	23,40,43	2.62	6 (26%)
2	OMC	2	3701	2,51	19,22,23	2.78	8 (42%)	26,31,34	0.93	0
2	PSU	2	4628	2	18,21,22	1.06	1 (5%)	22,30,33	1.76	4 (18%)
2	OMG	2	1522	2	18,26,27	2.30	7 (38%)	19,38,41	1.51	4 (21%)
2	2MG	2	729	2	18,26,27	2.30	7 (38%)	16,38,41	1.43	4 (25%)
2	B8T	2	4483	2	19,22,23	3.49	8 (42%)	26,31,34	1.06	3 (11%)
2	OMG	2	2050	2	18,26,27	2.26	7 (38%)	19,38,41	1.61	4 (21%)
2	OMG	2	4870	2	18,26,27	2.40	8 (44%)	19,38,41	1.58	4 (21%)
2	PSU	2	4403	2	18,21,22	1.00	1 (5%)	22,30,33	1.70	5 (22%)
2	M7A	2	4564	2	20,25,26	1.94	3 (15%)	28,37,40	3.99	6 (21%)
2	B8W	2	2380	2	18,26,27	6.12	7 (38%)	21,38,41	2.43	6 (28%)
2	OMG	2	4623	2	18,26,27	2.28	8 (44%)	19,38,41	1.57	5 (26%)
2	PSU	2	1683	2	18,21,22	1.15	1 (5%)	22,30,33	1.90	5 (22%)
2	B9B	2	2754	2	21,28,29	5.50	8 (38%)	23,40,43	2.39	7 (30%)
2	A2M	2	1534	2,51	18,25,26	4.17	7 (38%)	18,36,39	3.43	4 (22%)
2	I4U	2	1659	2,51	21,24,25	4.63	15 (71%)	27,34,37	1.65	4 (14%)
2	OMG	2	2424	2	18,26,27	2.33	7 (38%)	19,38,41	1.56	3 (15%)
2	7MG	2	2522	2	22,26,27	3.44	10 (45%)	29,39,42	2.11	10 (34%)
2	OMU	2	4620	2	19,22,23	2.63	7 (36%)	26,31,34	1.75	5 (19%)
2	UR3	2	1866	2	19,22,23	1.04	2 (10%)	26,32,35	1.62	2 (7%)
2	P7G	2	1909	2	24,28,29	4.57	11 (45%)	27,41,44	1.82	5 (18%)
2	OMG	2	373	2	18,26,27	2.27	7 (38%)	19,38,41	1.70	5 (26%)
2	A2M	2	4523	2	18,25,26	4.24	7 (38%)	18,36,39	3.23	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	2	2508	2	18,21,22	1.01	1 (5%)	22,30,33	1.66	4 (18%)
2	B8W	2	4129	2	18,26,27	6.08	6 (33%)	21,38,41	2.83	8 (38%)
2	A2M	2	3867	2	18,25,26	4.13	7 (38%)	18,36,39	3.16	4 (22%)
2	PSU	2	4636	2	18,21,22	1.12	1 (5%)	22,30,33	1.79	3 (13%)
2	B8K	2	3897	2	24,28,29	4.33	16 (66%)	30,42,45	2.60	13 (43%)
2	2MG	2	978	2	18,26,27	2.41	7 (38%)	16,38,41	1.60	4 (25%)
2	5MU	2	4083	2	19,22,23	4.66	7 (36%)	28,32,35	3.87	10 (35%)
2	OMC	2	2365	2,51	19,22,23	2.76	7 (36%)	26,31,34	0.97	1 (3%)
2	OMC	2	3869	2	19,22,23	2.80	7 (36%)	26,31,34	2.17	6 (23%)
2	OMG	2	4637	2	18,26,27	2.38	6 (33%)	19,38,41	1.66	4 (21%)
2	A2M	2	1326	2,51	18,25,26	4.00	6 (33%)	18,36,39	3.29	4 (22%)
2	OMC	2	2804	2	19,22,23	2.63	7 (36%)	26,31,34	1.26	3 (11%)
2	OMC	2	3887	2	19,22,23	2.95	7 (36%)	26,31,34	1.31	4 (15%)
2	OMU	2	4306	2	19,22,23	2.68	7 (36%)	26,31,34	1.78	5 (19%)
2	PSU	2	3729	2	18,21,22	0.99	1 (5%)	22,30,33	1.68	4 (18%)
2	A2M	2	1871	2	18,25,26	4.31	7 (38%)	18,36,39	3.09	3 (16%)
2	E7G	2	2297	2	24,27,28	3.74	11 (45%)	30,40,43	2.27	10 (33%)
2	OMG	2	2364	2	18,26,27	2.27	7 (38%)	19,38,41	1.61	4 (21%)
2	OMG	2	1625	2	18,26,27	2.32	7 (38%)	19,38,41	1.58	4 (21%)
2	B8K	2	4690	2	24,28,29	4.45	16 (66%)	30,42,45	2.72	12 (40%)
2	6MZ	2	4220	2	18,25,26	1.88	3 (16%)	16,36,39	3.77	4 (25%)
2	B8Q	2	1456	2	17,22,23	2.90	4 (23%)	22,32,35	2.63	6 (27%)
2	PSU	2	1677	2	18,21,22	1.31	3 (16%)	22,30,33	1.82	5 (22%)
8	OMU	8	14	8,2	19,22,23	2.58	6 (31%)	26,31,34	1.97	5 (19%)
2	P7G	2	3880	2	24,28,29	4.67	11 (45%)	27,41,44	1.58	3 (11%)
2	B9H	2	2786	2	20,25,26	2.95	5 (25%)	22,35,38	3.29	7 (31%)
2	A2M	2	2363	2,51	18,25,26	4.14	7 (38%)	18,36,39	3.27	3 (16%)
2	7MG	2	1605	2	22,26,27	3.19	10 (45%)	29,39,42	2.18	10 (34%)
2	B9B	2	1574	2	21,28,29	5.64	8 (38%)	23,40,43	2.45	6 (26%)
2	1MA	2	1322	2,51	16,25,26	3.95	4 (25%)	18,37,40	1.63	3 (16%)
2	PSU	2	1582	2	18,21,22	1.07	1 (5%)	22,30,33	1.76	5 (22%)
2	OMG	2	4370	2	18,26,27	2.40	8 (44%)	19,38,41	1.56	4 (21%)
2	A2M	2	398	2	18,25,26	4.23	6 (33%)	18,36,39	3.13	3 (16%)
2	OMC	2	2861	2	19,22,23	2.85	8 (42%)	26,31,34	1.06	2 (7%)
2	A2M	2	3723	2	18,25,26	4.29	7 (38%)	18,36,39	3.06	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	UR3	2	4530	2	19,22,23	2.66	6 (31%)	26,32,35	1.37	3 (11%)
2	OMC	2	2422	32,2,51	19,22,23	2.76	7 (36%)	26,31,34	1.39	3 (11%)
2	P4U	2	1348	2	21,24,25	3.51	7 (33%)	27,33,36	1.38	4 (14%)
2	A2M	2	1524	2	18,25,26	4.07	7 (38%)	18,36,39	3.20	4 (22%)
2	B8W	2	4472	2	18,26,27	6.09	7 (38%)	21,38,41	2.62	7 (33%)
2	E6G	2	4355	2	20,27,28	5.74	9 (45%)	22,39,42	3.05	8 (36%)
2	E7G	2	1797	2	24,27,28	3.81	11 (45%)	30,40,43	2.26	10 (33%)
2	OMG	2	4196	2,3,51	18,26,27	2.57	8 (44%)	19,38,41	1.93	6 (31%)
2	B8W	2	4185	2	18,26,27	6.16	7 (38%)	21,38,41	2.63	6 (28%)
2	PSU	2	3715	2	18,21,22	1.10	1 (5%)	22,30,33	1.68	4 (18%)
2	OMC	2	4536	2	19,22,23	2.78	7 (36%)	26,31,34	1.03	2 (7%)
2	B8H	2	4296	2	19,22,23	6.87	6 (31%)	22,32,35	2.47	5 (22%)
2	A2M	2	2401	2	18,25,26	4.12	6 (33%)	18,36,39	3.28	3 (16%)
2	OMG	2	1316	2,51	18,26,27	2.35	8 (44%)	19,38,41	1.77	5 (26%)
2	OMG	2	4494	2	18,26,27	2.39	8 (44%)	19,38,41	1.62	4 (21%)
2	OMG	2	2773	2	18,26,27	2.37	8 (44%)	19,38,41	1.61	5 (26%)
2	OMC	2	3909	2	19,22,23	2.98	8 (42%)	26,31,34	2.61	6 (23%)
2	5MC	2	4335	2	18,22,23	3.34	7 (38%)	26,32,35	1.14	2 (7%)
2	1MA	2	4415	2	16,25,26	3.95	4 (25%)	18,37,40	1.64	3 (16%)

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
2	7MG	2	4550	2	-	0/7/37/38	0/3/3/3
2	I4U	2	4194	2	-	4/9/29/30	0/2/2/2
2	UR3	2	4597	2	-	2/7/25/26	0/2/2/2
2	B8T	2	4671	2	-	0/7/27/28	0/2/2/2
2	A2M	2	3825	2	-	0/5/27/28	0/3/3/3
2	B8W	2	4529	2,51	-	4/5/27/28	0/3/3/3
2	MHG	2	4371	2	-	7/16/46/47	0/3/3/3
2	A2M	2	3718	2	-	1/5/27/28	0/3/3/3
2	PSU	2	4293	2,30	-	2/7/25/26	0/2/2/2
2	BGH	2	3899	2	-	0/13/43/44	0/3/3/3
2	B8H	2	1860	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	2	1517	2	-	0/5/27/28	0/3/3/3
2	OMG	2	1883	2	-	2/5/27/28	0/3/3/3
2	A2M	2	4571	2	-	0/5/27/28	0/3/3/3
2	2MG	2	4872	2	-	2/5/27/28	0/3/3/3
2	B9B	2	237	2	-	6/7/29/30	0/3/3/3
2	OMC	2	3701	2,51	-	4/9/27/28	0/2/2/2
2	PSU	2	4628	2	-	0/7/25/26	0/2/2/2
2	OMG	2	1522	2	-	0/5/27/28	0/3/3/3
2	2MG	2	729	2	-	1/5/27/28	0/3/3/3
2	B8T	2	4483	2	-	0/7/27/28	0/2/2/2
2	OMG	2	2050	2	-	0/5/27/28	0/3/3/3
2	OMG	2	4870	2	-	3/5/27/28	0/3/3/3
2	PSU	2	4403	2	-	2/7/25/26	0/2/2/2
2	M7A	2	4564	2	-	0/7/37/38	0/3/3/3
2	B8W	2	2380	2	-	4/5/27/28	0/3/3/3
2	OMG	2	4623	2	-	0/5/27/28	0/3/3/3
2	PSU	2	1683	2	-	0/7/25/26	0/2/2/2
2	B9B	2	2754	2	-	2/7/29/30	0/3/3/3
2	A2M	2	1534	2,51	-	2/5/27/28	0/3/3/3
2	I4U	2	1659	2,51	-	2/9/29/30	0/2/2/2
2	OMG	2	2424	2	-	2/5/27/28	0/3/3/3
2	7MG	2	2522	2	-	0/7/37/38	0/3/3/3
2	OMU	2	4620	2	-	0/9/27/28	0/2/2/2
2	UR3	2	1866	2	-	3/7/25/26	0/2/2/2
2	P7G	2	1909	2	-	1/10/40/41	0/3/3/3
2	OMG	2	373	2	-	1/5/27/28	0/3/3/3
2	A2M	2	4523	2	-	4/5/27/28	0/3/3/3
2	PSU	2	2508	2	-	0/7/25/26	0/2/2/2
2	B8W	2	4129	2	-	2/5/27/28	0/3/3/3
2	A2M	2	3867	2	-	2/5/27/28	0/3/3/3
2	PSU	2	4636	2	-	3/7/25/26	0/2/2/2
2	B8K	2	3897	2	-	3/11/41/42	0/3/3/3
2	2MG	2	978	2	-	0/5/27/28	0/3/3/3
2	5MU	2	4083	2	-	0/7/25/26	0/2/2/2
2	OMC	2	2365	2,51	-	0/9/27/28	0/2/2/2
2	OMC	2	3869	2	-	3/9/27/28	0/2/2/2
2	OMG	2	4637	2	-	2/5/27/28	0/3/3/3
2	A2M	2	1326	2,51	-	1/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	2	2804	2	-	0/9/27/28	0/2/2/2
2	OMC	2	3887	2	-	1/9/27/28	0/2/2/2
2	OMU	2	4306	2	-	0/9/27/28	0/2/2/2
2	PSU	2	3729	2	-	2/7/25/26	0/2/2/2
2	A2M	2	1871	2	-	3/5/27/28	0/3/3/3
2	E7G	2	2297	2	-	1/9/39/40	0/3/3/3
2	OMG	2	2364	2	-	2/5/27/28	0/3/3/3
2	OMG	2	1625	2	-	2/5/27/28	0/3/3/3
2	B8K	2	4690	2	-	0/11/41/42	0/3/3/3
2	6MZ	2	4220	2	-	2/5/27/28	0/3/3/3
2	B8Q	2	1456	2	-	0/7/42/43	0/2/2/2
2	PSU	2	1677	2	-	3/7/25/26	0/2/2/2
8	OMU	8	14	8,2	-	1/9/27/28	0/2/2/2
2	P7G	2	3880	2	-	1/10/40/41	0/3/3/3
2	B9H	2	2786	2	-	0/12/47/48	0/2/2/2
2	A2M	2	2363	2,51	-	1/5/27/28	0/3/3/3
2	7MG	2	1605	2	-	1/7/37/38	0/3/3/3
2	B9B	2	1574	2	-	3/7/29/30	0/3/3/3
2	1MA	2	1322	2,51	-	0/3/25/26	0/3/3/3
2	PSU	2	1582	2	-	2/7/25/26	0/2/2/2
2	OMG	2	4370	2	-	0/5/27/28	0/3/3/3
2	A2M	2	398	2	-	2/5/27/28	0/3/3/3
2	OMC	2	2861	2	-	0/9/27/28	0/2/2/2
2	A2M	2	3723	2	-	0/5/27/28	0/3/3/3
2	UR3	2	4530	2	-	0/7/25/26	0/2/2/2
2	OMC	2	2422	32,2,51	-	1/9/27/28	0/2/2/2
2	P4U	2	1348	2	-	1/10/29/30	0/2/2/2
2	A2M	2	1524	2	-	0/5/27/28	0/3/3/3
2	B8W	2	4472	2	-	2/5/27/28	0/3/3/3
2	E6G	2	4355	2	-	3/6/28/29	0/3/3/3
2	E7G	2	1797	2	-	2/9/39/40	0/3/3/3
2	OMG	2	4196	2,3,51	-	3/5/27/28	0/3/3/3
2	B8W	2	4185	2	-	3/5/27/28	0/3/3/3
2	PSU	2	3715	2	-	0/7/25/26	0/2/2/2
2	OMC	2	4536	2	-	0/9/27/28	0/2/2/2
2	B8H	2	4296	2	-	2/7/25/26	0/2/2/2
2	A2M	2	2401	2	-	1/5/27/28	0/3/3/3
2	OMG	2	1316	2,51	-	0/5/27/28	0/3/3/3
2	OMG	2	4494	2	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	2	2773	2	-	0/5/27/28	0/3/3/3
2	OMC	2	3909	2	-	0/9/27/28	0/2/2/2
2	5MC	2	4335	2	-	0/7/25/26	0/2/2/2
2	1MA	2	4415	2	-	2/3/25/26	0/3/3/3

The worst 5 of 644 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4529	B8W	O4'-C1'	18.29	1.66	1.41
2	2	4472	B8W	O4'-C1'	17.88	1.66	1.41
2	2	2380	B8W	O4'-C1'	17.65	1.65	1.41
2	2	4185	B8W	O4'-C1'	17.55	1.65	1.41
2	2	4129	B8W	O4'-C1'	17.42	1.65	1.41

The worst 5 of 455 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4564	M7A	C5-C6-N6	13.77	147.26	123.74
2	2	4083	5MU	C5-C4-N3	13.36	126.71	115.31
2	2	4220	6MZ	C1'-N9-C4	-12.25	105.12	126.64
2	2	4564	M7A	N6-C6-N1	-11.95	92.17	118.35
2	2	2786	B9H	C6-N1-C2	-10.19	112.66	121.79

There are no chirality outliers.

5 of 124 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	8	14	OMU	C1'-C2'-O2'-CM2
2	2	237	B9B	C5-C6-O6-C61
2	2	237	B9B	N1-C6-O6-C61
2	2	237	B9B	C3'-C4'-C5'-O5'
2	2	237	B9B	C62-C61-O6-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 247 ligands modelled in this entry, 247 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

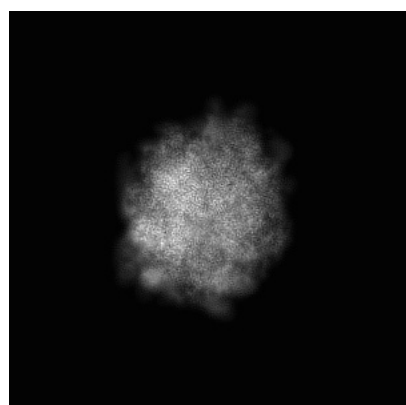
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0978. These allow visual inspection of the internal detail of the map and identification of artifacts.

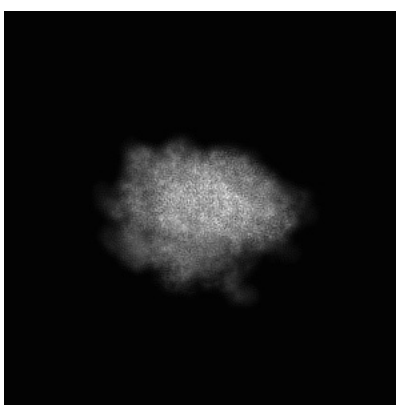
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

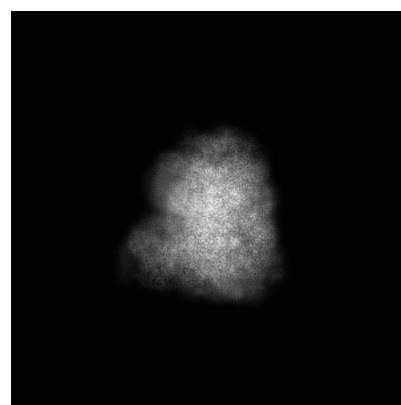
6.1.1 Primary map



X



Y

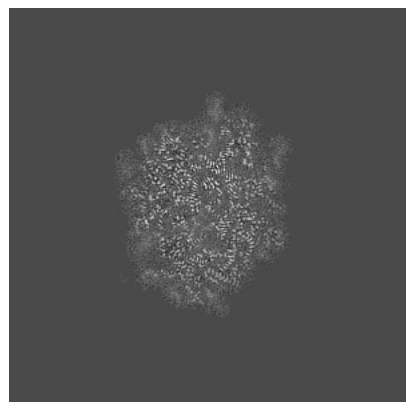


Z

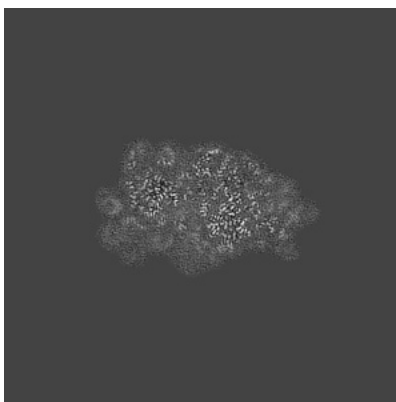
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

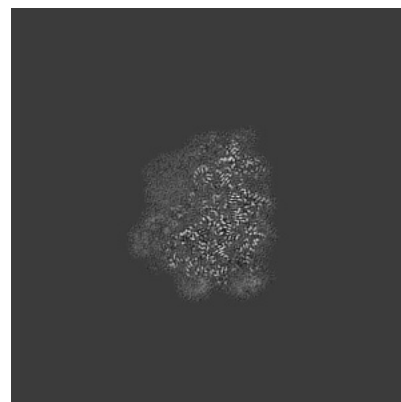
6.2.1 Primary map



X Index: 240



Y Index: 240

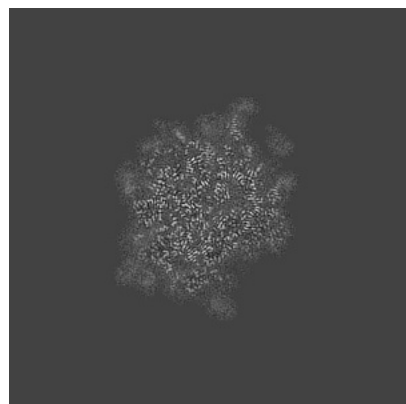


Z Index: 240

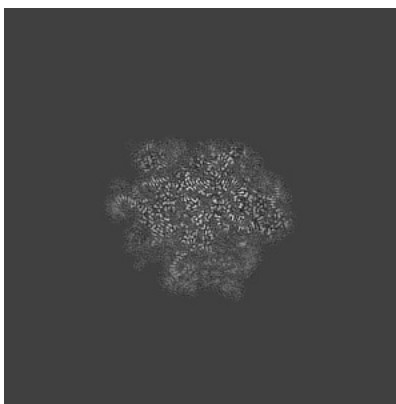
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

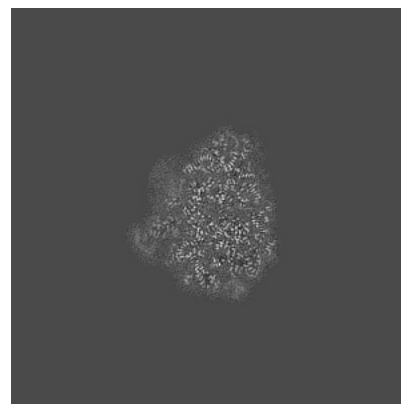
6.3.1 Primary map



X Index: 256



Y Index: 203

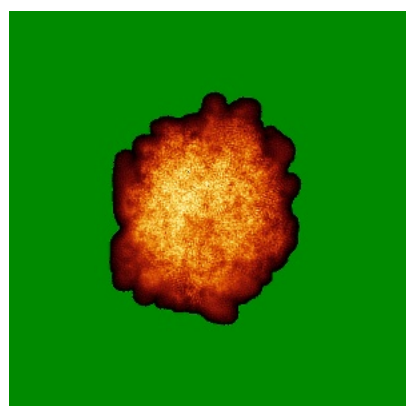


Z Index: 255

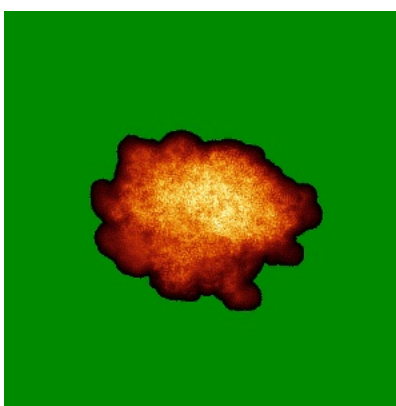
The images above show the largest variance slices of the map in three orthogonal directions.

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

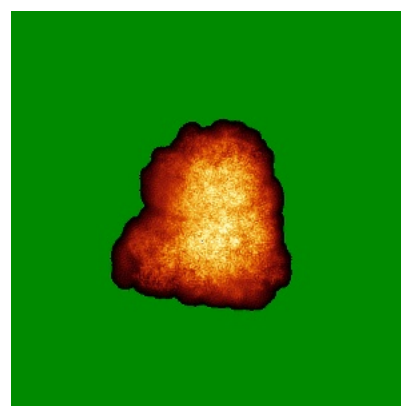
6.4.1 Primary map



X



Y

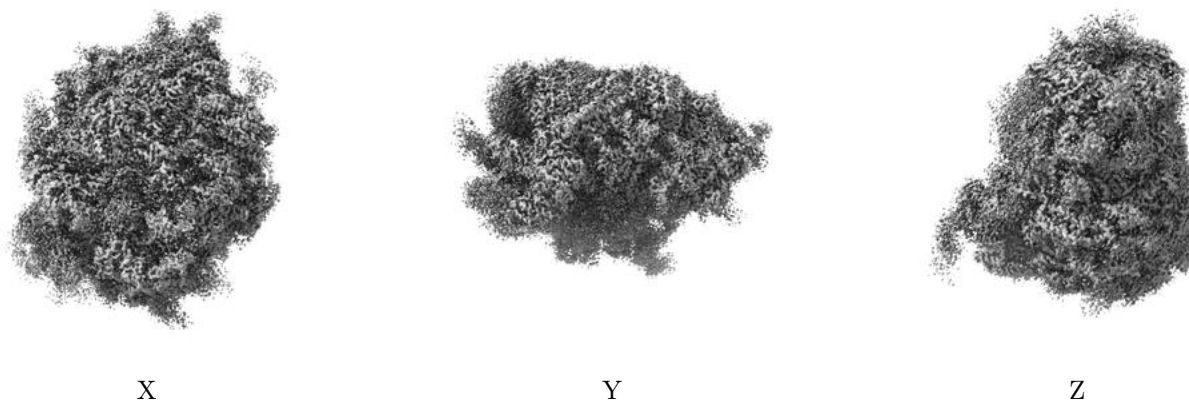


Z

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

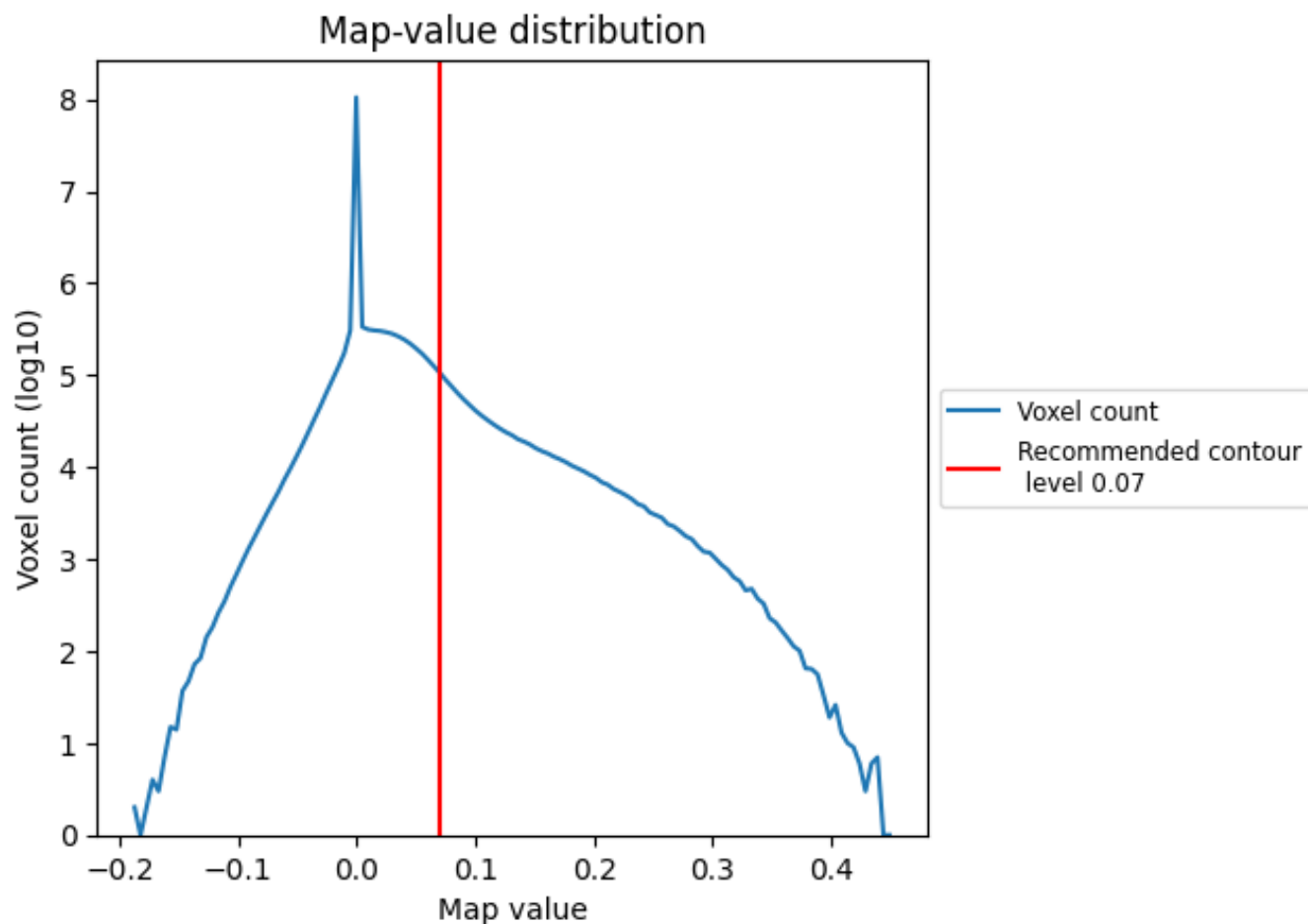
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

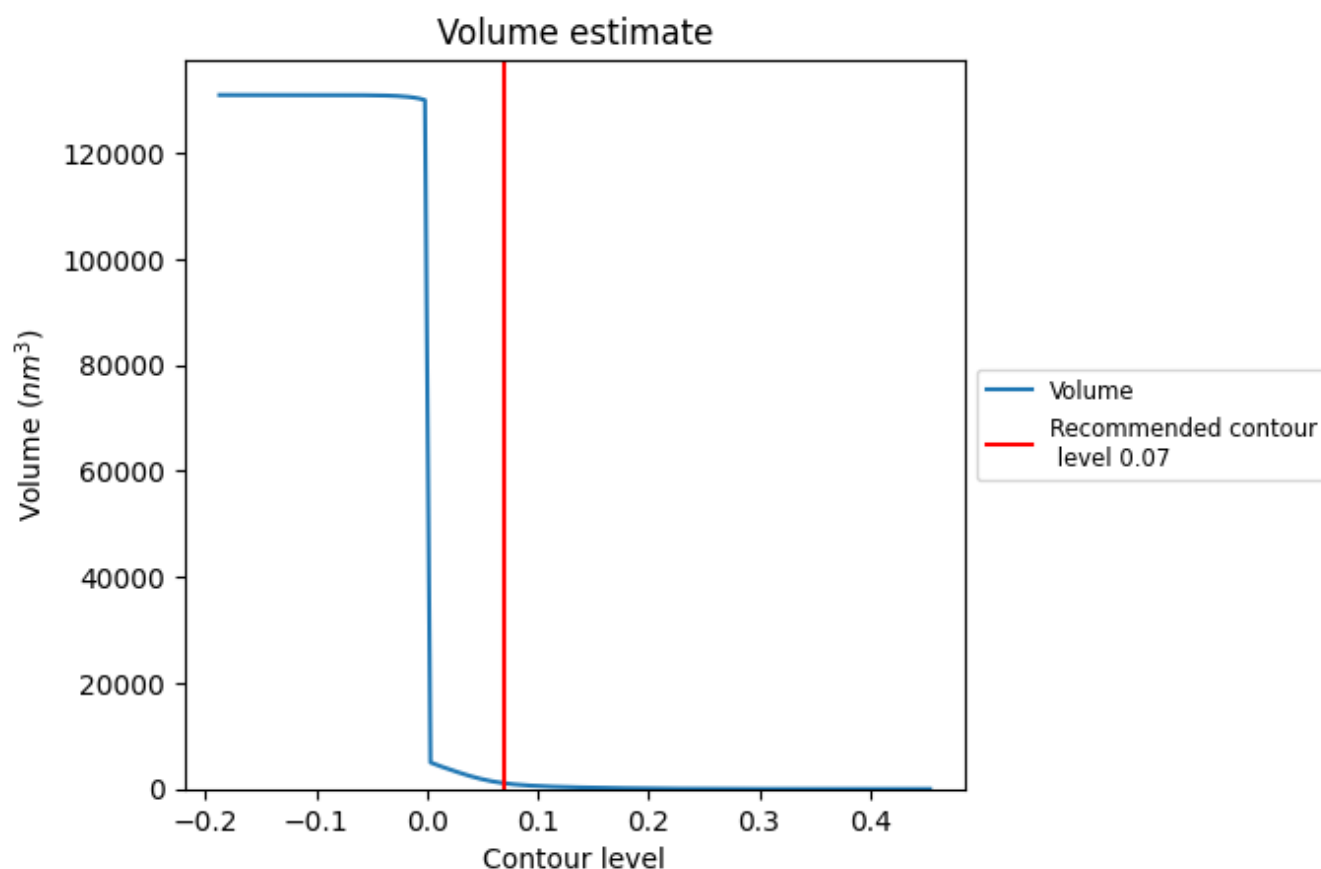
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

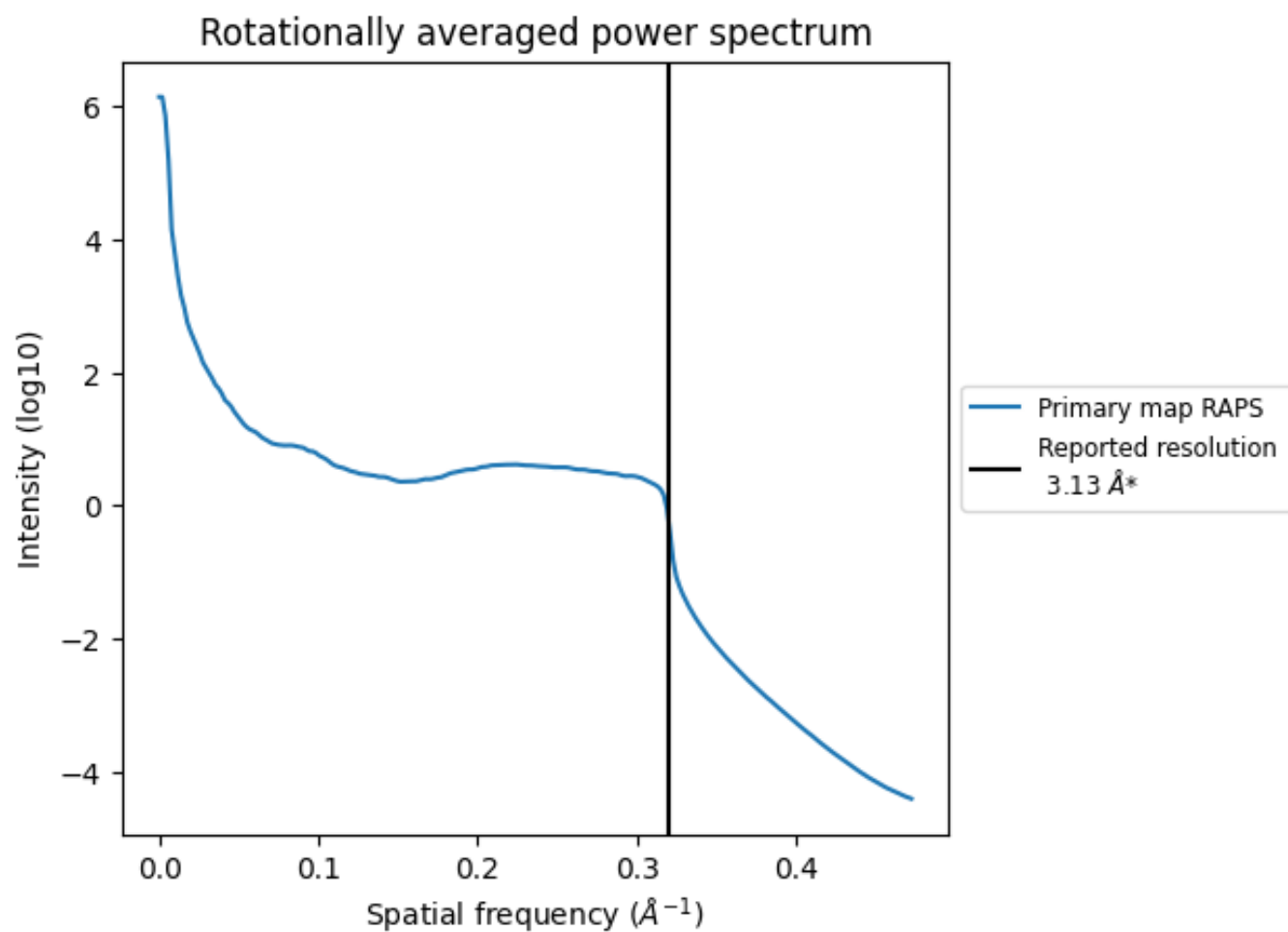
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1075 nm³; this corresponds to an approximate mass of 971 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 0.319 Å⁻¹

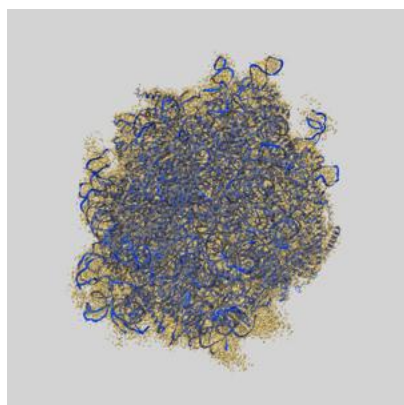
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

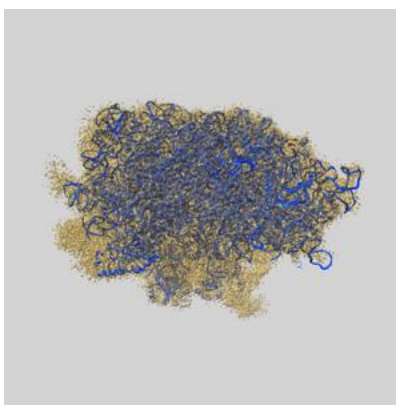
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0978 and PDB model 6LU8. Per-residue inclusion information can be found in section [3](#) on page [14](#).

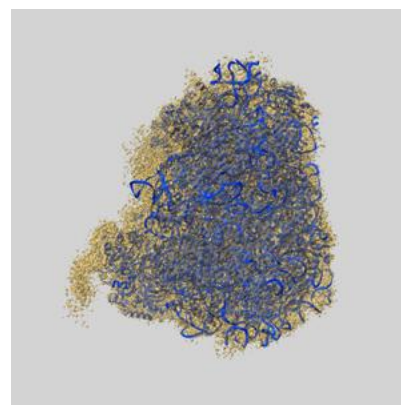
9.1 Map-model overlay [i](#)



X



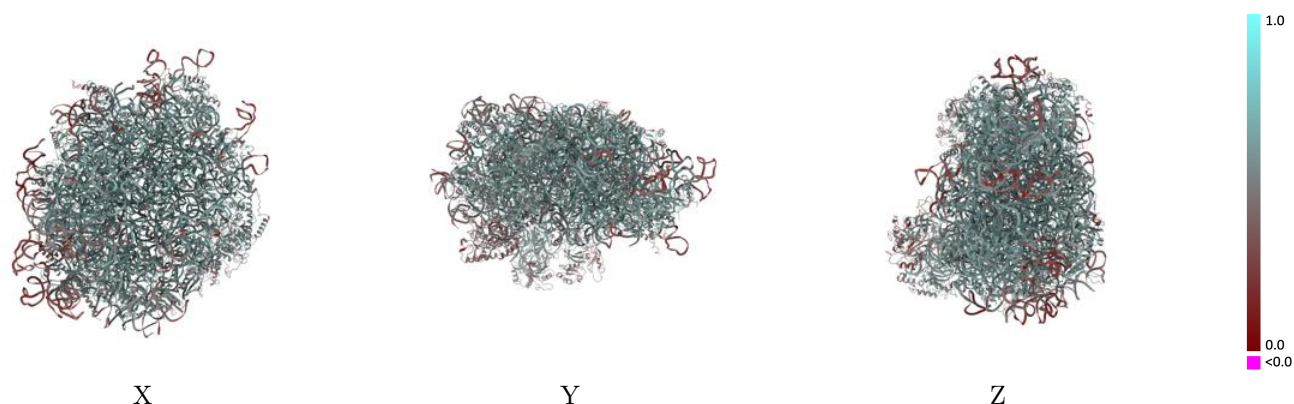
Y



Z

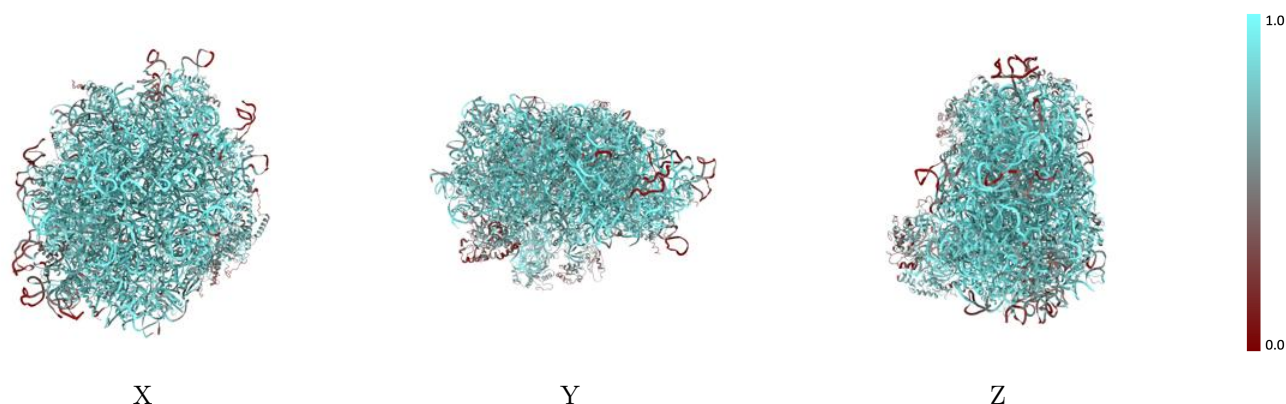
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



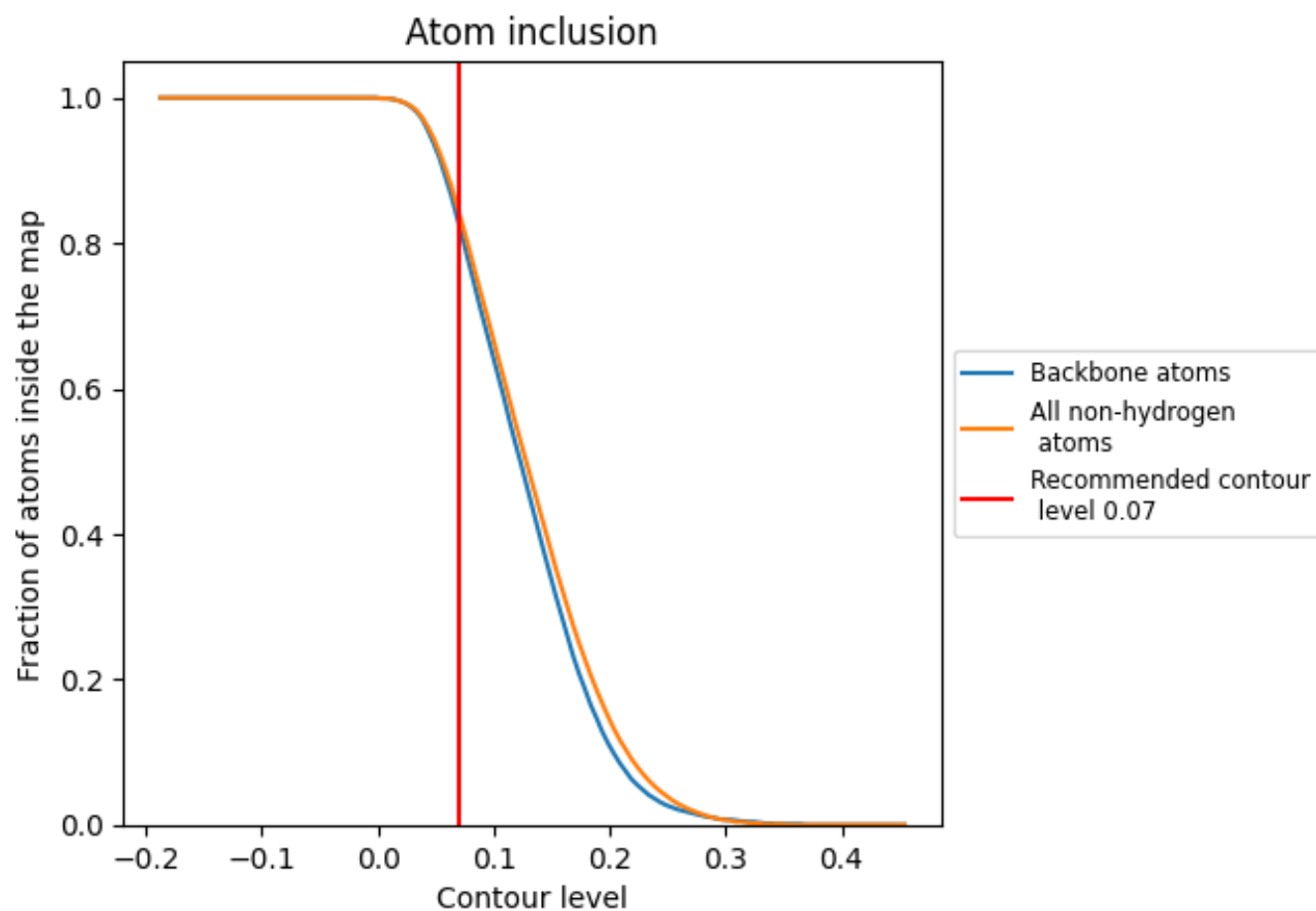
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

































The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.5400
1	 0.2520	 0.3670
2	 0.8670	 0.5310
3	 0.7710	 0.5010
4	 0.6460	 0.4800
5	 0.9340	 0.5570
6	 0.7360	 0.5280
7	 0.8130	 0.5550
8	 0.9230	 0.5670
9	 0.7570	 0.5340
A	 0.4020	 0.3520
B	 0.8820	 0.5790
C	 0.8070	 0.5320
D	 0.8990	 0.5870
E	 0.7900	 0.5490
F	 0.9010	 0.5820
G	 0.7430	 0.5350
H	 0.8620	 0.5730
I	 0.7760	 0.5400
K	 0.8340	 0.5530
L	 0.9280	 0.6040
M	 0.9420	 0.5900
N	 0.6440	 0.4660
O	 0.7380	 0.5460
P	 0.9340	 0.5880
Q	 0.8320	 0.5600
R	 0.3800	 0.4050
S	 0.8720	 0.5680
U	 0.9610	 0.6110
V	 0.8900	 0.5840
W	 0.8520	 0.5700
X	 0.8610	 0.5670
Y	 0.9040	 0.5890
Z	 0.9370	 0.6030
a	 0.8860	 0.5840



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Chain	Atom inclusion	Q-score
b	 0.9300	 0.5950
c	 0.9030	 0.5780
d	 0.7690	 0.5410
e	 0.8670	 0.5670
g	 0.8700	 0.5750
h	 0.8650	 0.5780
i	 0.8280	 0.5600
j	 0.8390	 0.5660
k	 0.9270	 0.5940
l	 0.8780	 0.5830
m	 0.9160	 0.5920
n	 0.9420	 0.6070
o	 0.8140	 0.5460
p	 0.8930	 0.5790
r	 0.7250	 0.5170
z	 0.7330	 0.5280