



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 10:47 AM 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:

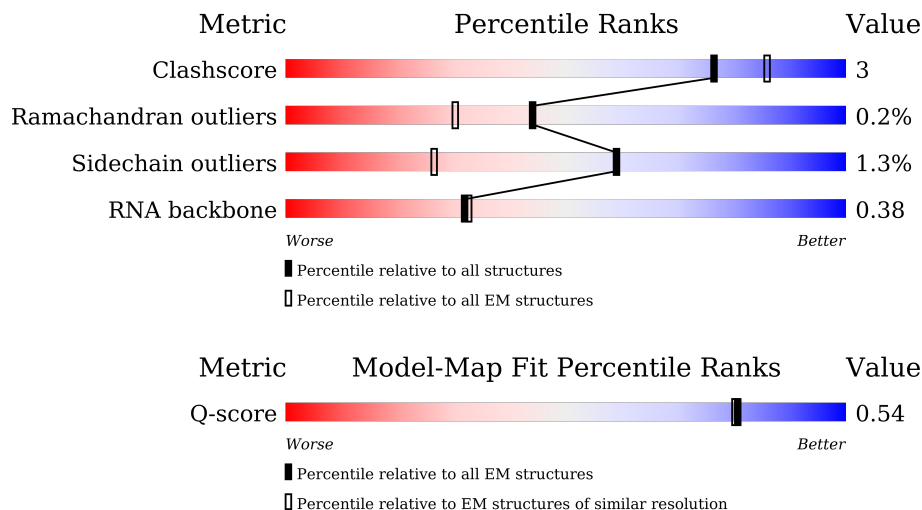
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 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.



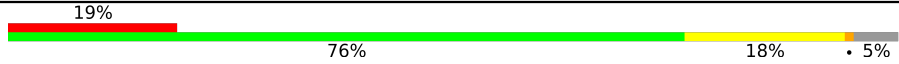







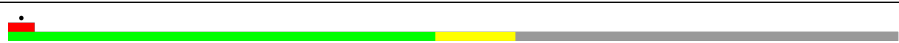

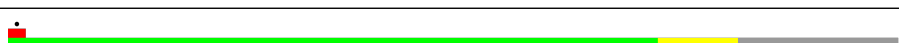


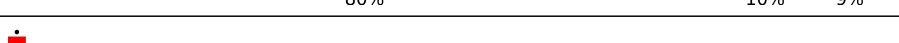
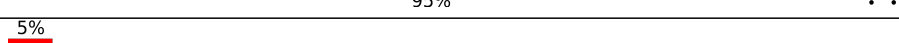
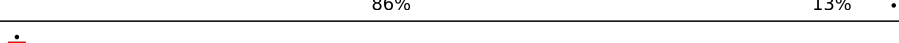
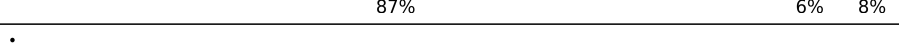
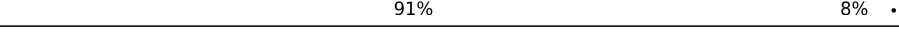
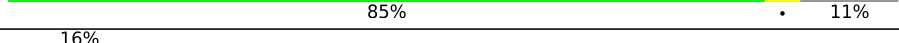

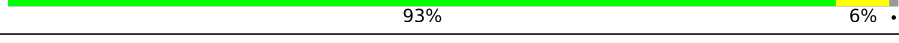




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14478 (2.63 - 3.63)

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	
2	2	5070	
3	3	503	

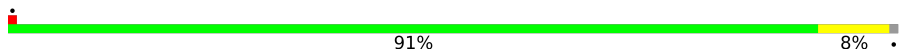


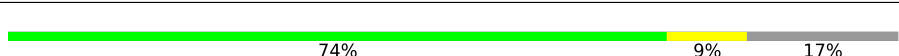
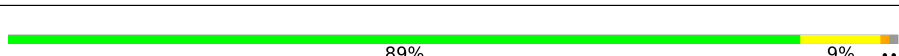
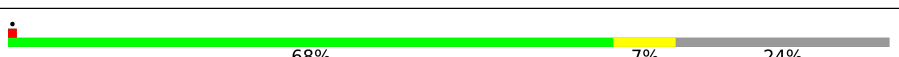
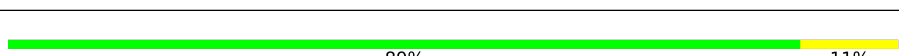
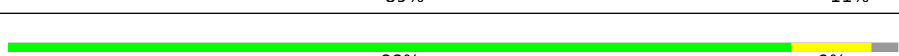
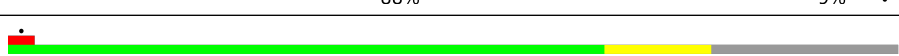

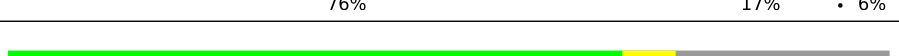
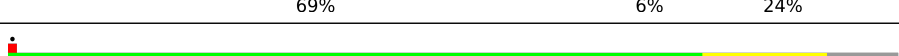

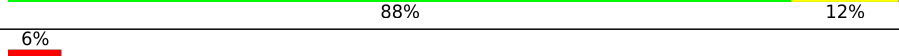





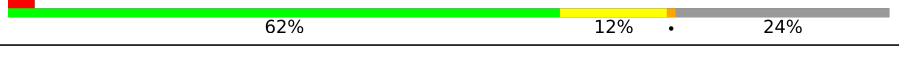

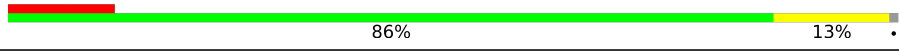
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Mol	Chain	Length	Quality of chain
4	4	634	
5	5	120	
6	6	245	
7	7	163	
8	8	156	
9	9	134	
10	A	217	
11	B	403	
12	C	159	
13	D	427	
14	E	115	
15	F	117	
16	G	266	
17	H	123	
18	I	192	
19	K	105	
20	L	148	
21	M	97	
22	N	178	
23	O	70	
24	P	51	
25	Q	211	
26	R	203	
27	S	215	
28	U	204	

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Mol	Chain	Length	Quality of chain
29	V	203	 91% 8%
30	W	106	 7% 87% 10%
31	X	92	 90% 7%
32	Y	184	 74% 9% 17%
33	Z	188	 89% 9%
34	a	196	 68% 7% 24%
35	b	176	 89% 11%
36	c	160	 88% 9%
37	d	128	 67% 12% 21%
38	e	140	 76% 17% 6%
39	g	156	 69% 6% 24%
40	h	145	 78% 14% 8%
41	i	136	 88% 12%
42	j	125	 6% 73% 13% 14%
43	k	135	 86% 9% 5%
44	l	137	 80% 11% 9%
45	m	257	 87% 8%
46	n	110	 87% 12%
47	o	288	 62% 12% 24%
48	p	248	 81% 9% 9%
49	r	297	 12% 86% 13%
50	z	129	 19% 7% 74%

2 Entry composition [i](#)

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
			Total	C	N	O	S		
1	1	19	148	88	23	35	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
28	U	203	1701	1072	359	266	4	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
49	r	293	2386	1510	435	427	14	0	0

- Molecule 50 is a protein called Protein LLP homolog.

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

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

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

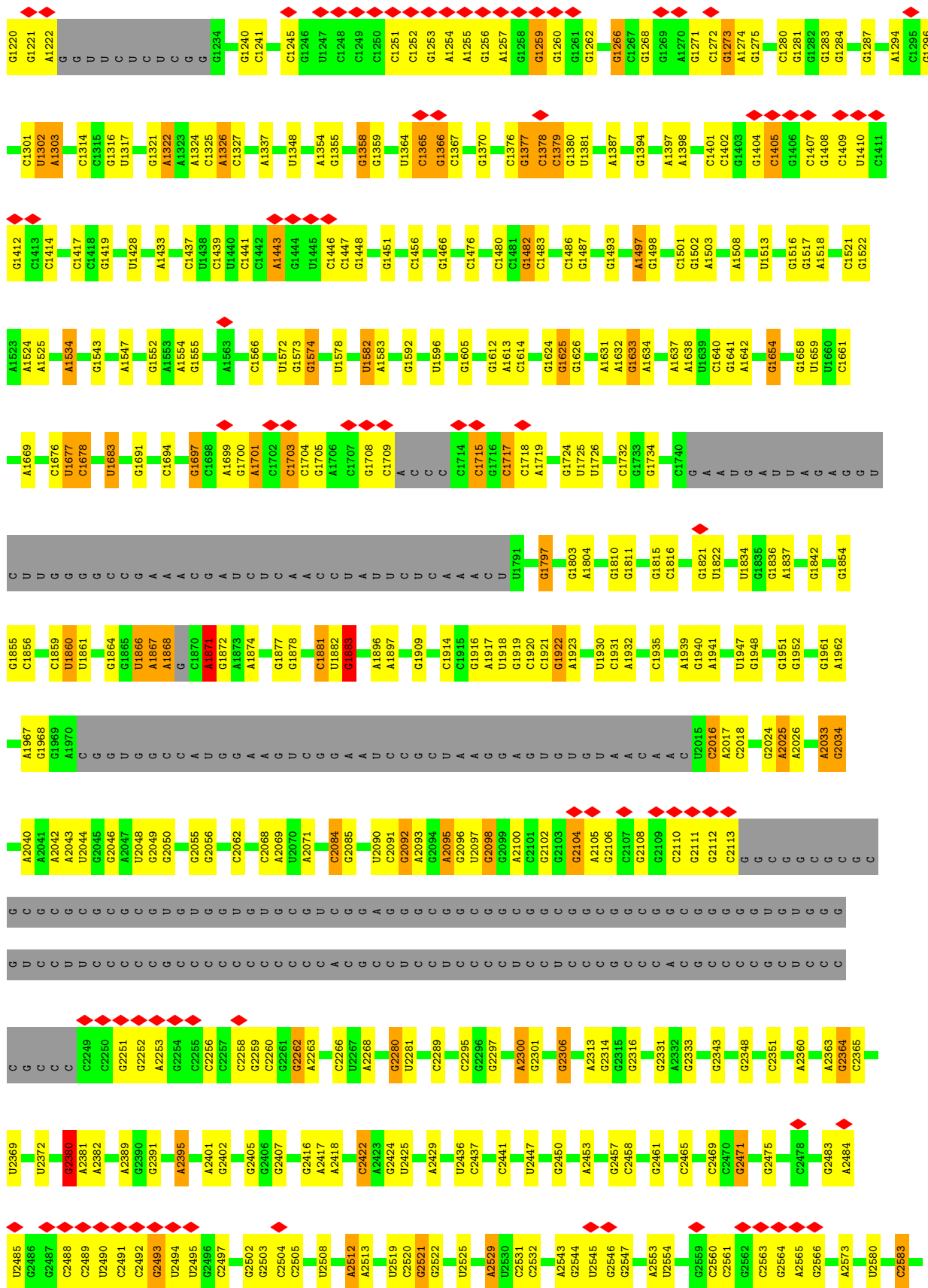
- Molecule 52 is water.

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

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

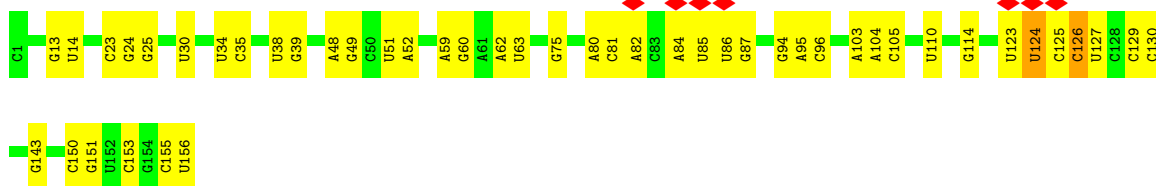




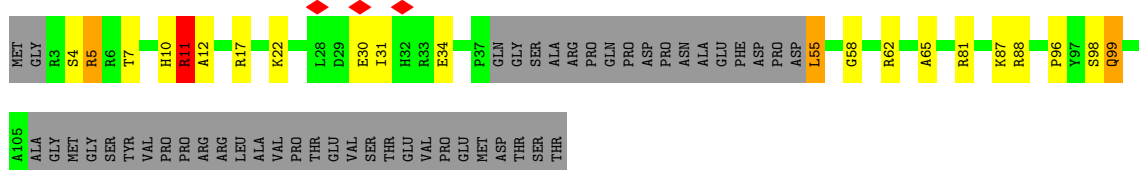
• Molecule 7: Probable ribosome biogenesis protein RLP24



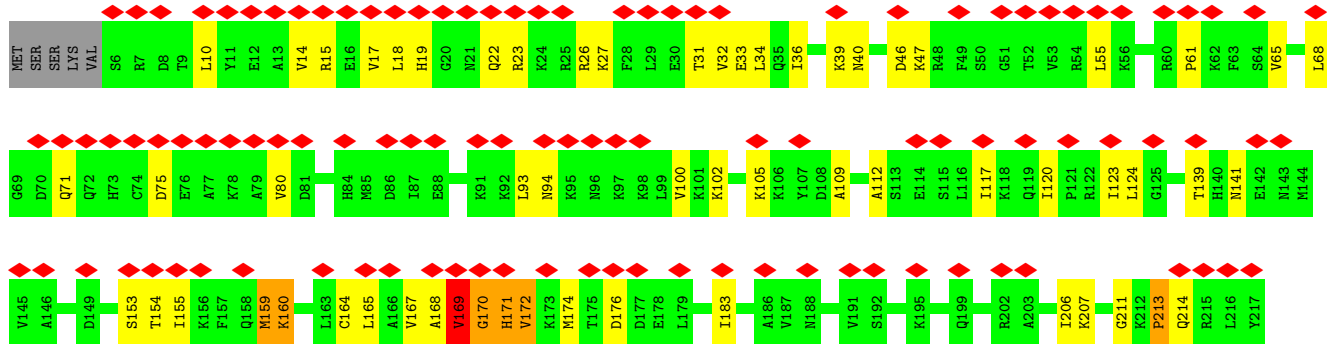
• Molecule 8: 5.8S rRNA



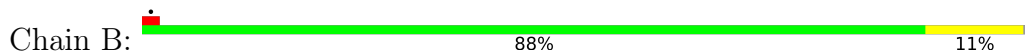
• Molecule 9: Zinc finger protein 593

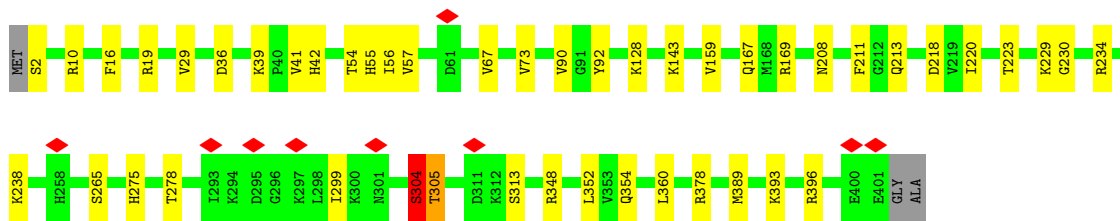


• Molecule 10: 60S ribosomal protein L10a

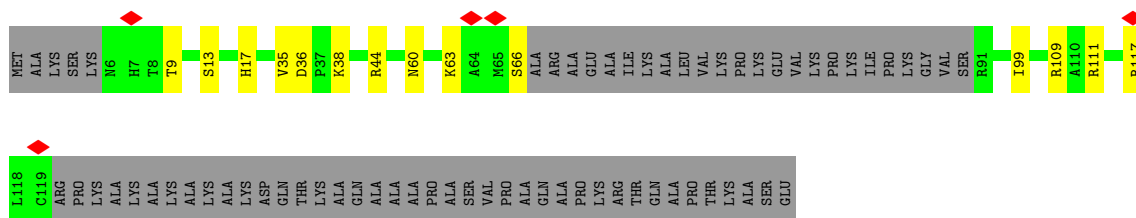


• Molecule 11: 60S ribosomal protein L3

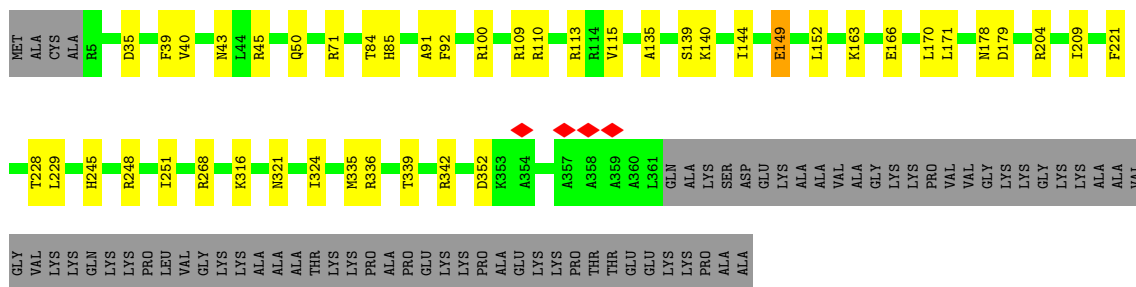




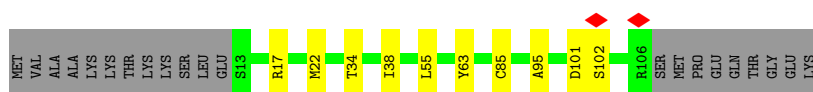
• Molecule 12: 60S ribosomal protein L29



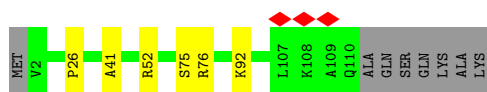
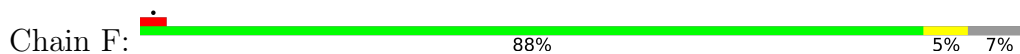
• Molecule 13: 60S ribosomal protein L4



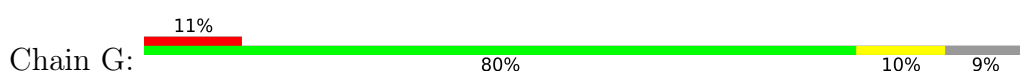
• Molecule 14: 60S ribosomal protein L30

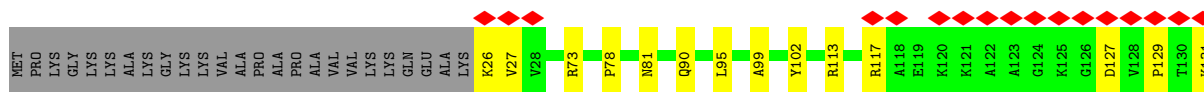


• Molecule 15: 60S ribosomal protein L34

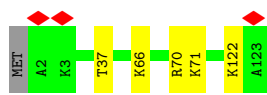


• Molecule 16: 60S ribosomal protein L7a

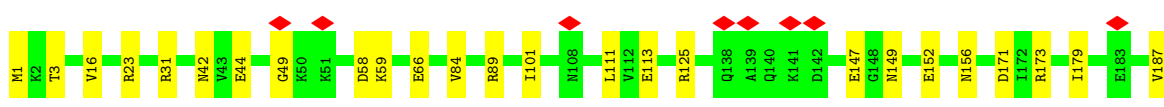
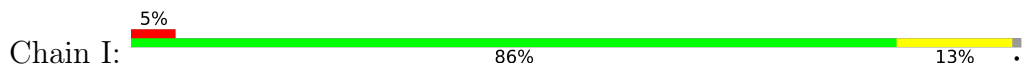




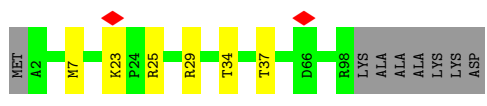
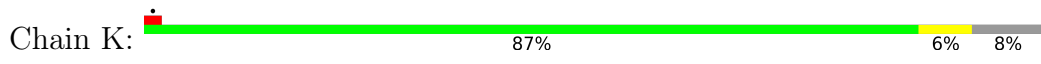
- Molecule 17: 60S ribosomal protein L35



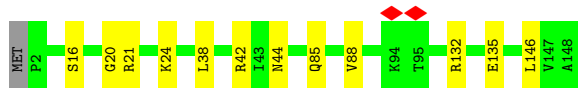
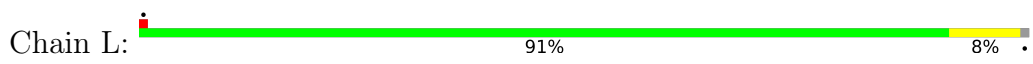
- Molecule 18: 60S ribosomal protein L9



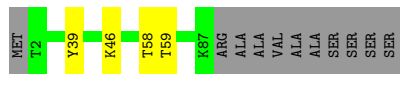
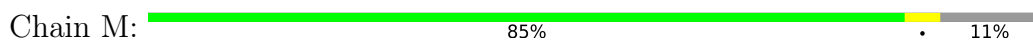
- Molecule 19: 60S ribosomal protein L36



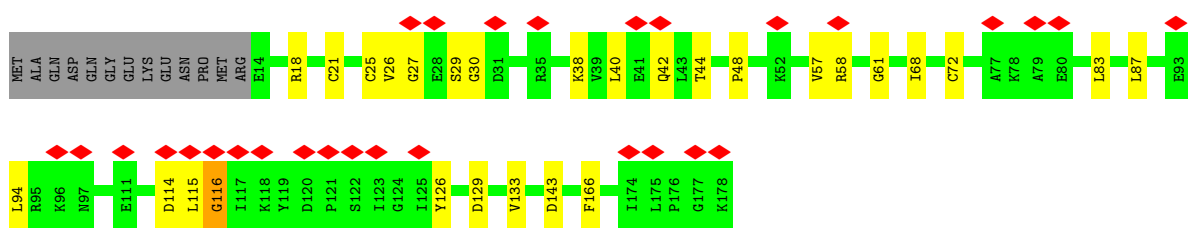
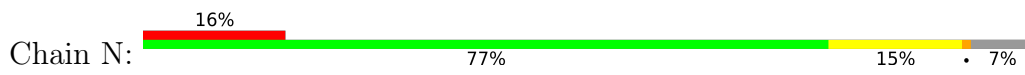
- Molecule 20: 60S ribosomal protein L27a



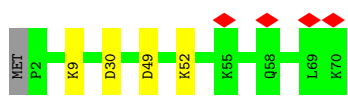
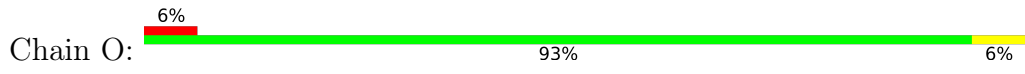
- Molecule 21: 60S ribosomal protein L37



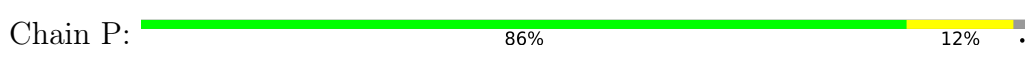
- Molecule 22: 60S ribosomal protein L11



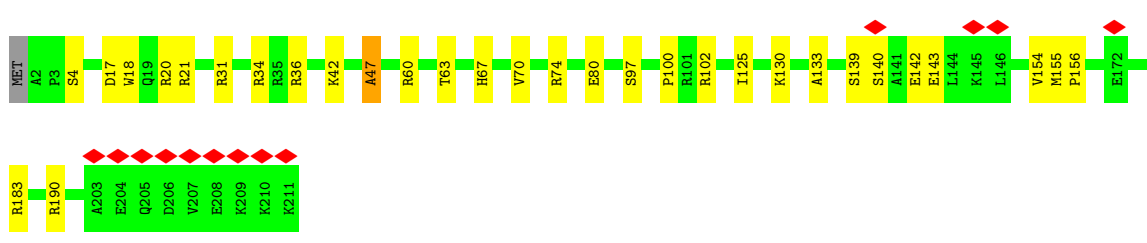
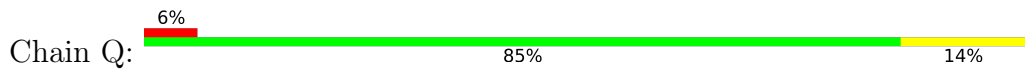
- Molecule 23: 60S ribosomal protein L38



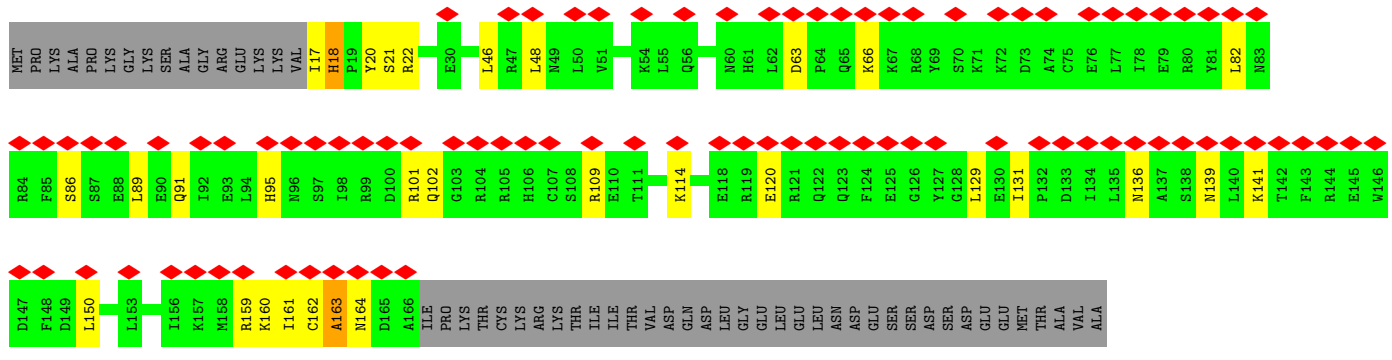
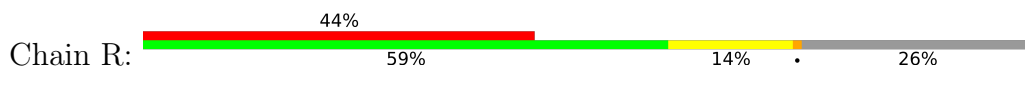
- Molecule 24: 60S ribosomal protein L39



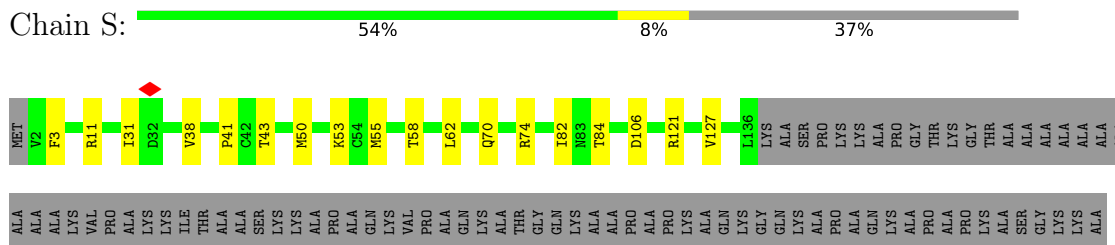
- Molecule 25: 60S ribosomal protein L13



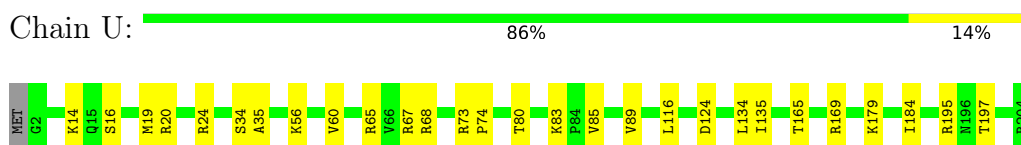
- Molecule 26: Translation machinery-associated protein 16



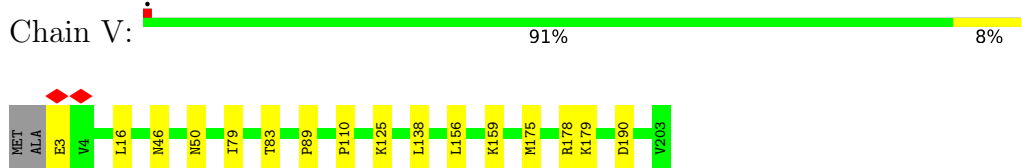
- Molecule 27: 60S ribosomal protein L14



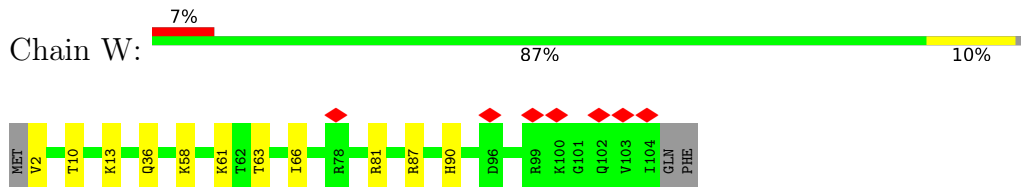
- Molecule 28: 60S ribosomal protein L15



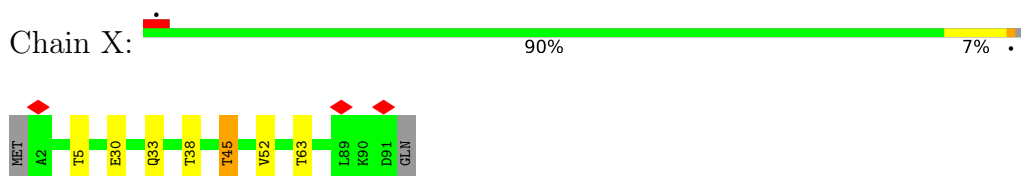
- Molecule 29: 60S ribosomal protein L13a



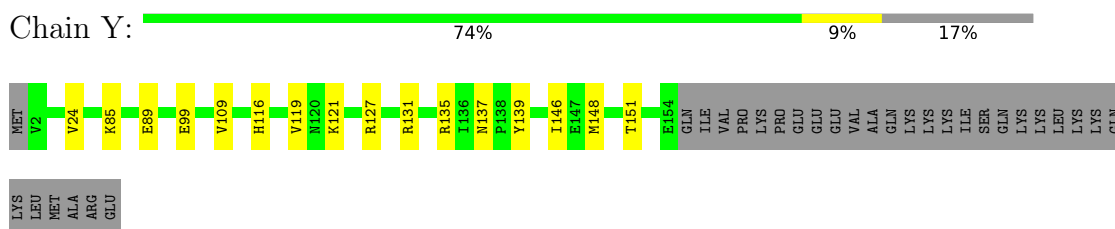
- Molecule 30: 60S ribosomal protein L36a




- Molecule 31: 60S ribosomal protein L37a



- Molecule 32: 60S ribosomal protein L17



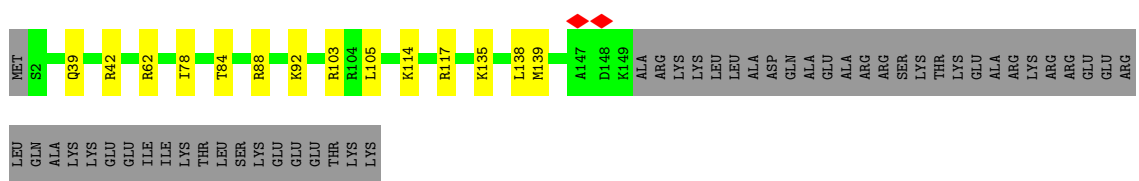
- Molecule 33: 60S ribosomal protein L18

Chain Z:  89% 9% ..




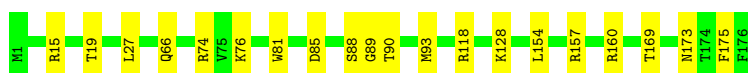
• Molecule 34: 60S ribosomal protein L19

Chain a:  68% 7% 24%




• Molecule 35: 60S ribosomal protein L18a

Chain b:  89% 11%



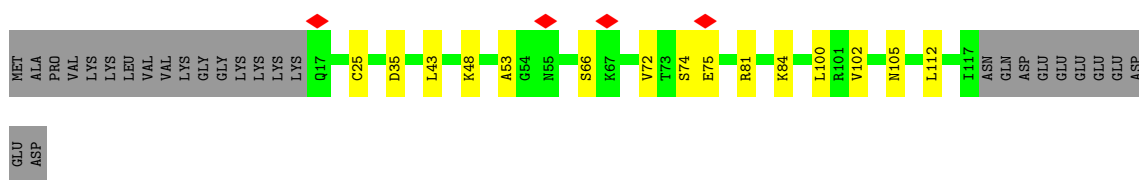
• Molecule 36: 60S ribosomal protein L21

Chain c:  88% 9% .



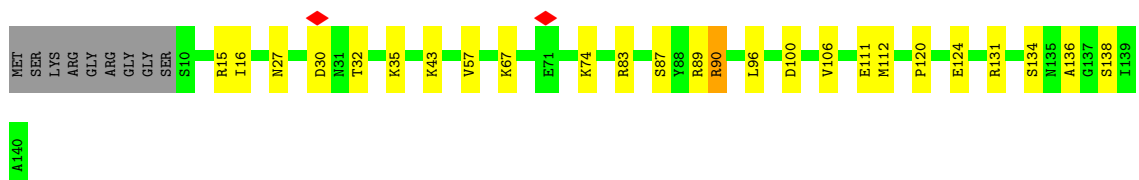
• Molecule 37: 60S ribosomal protein L22

Chain d:  67% 12% 21%



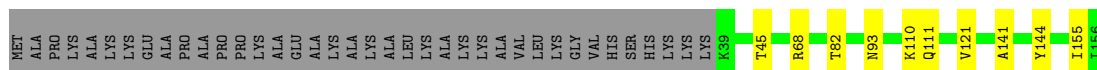
• Molecule 38: 60S ribosomal protein L23

Chain e:  76% 17% 6%




• Molecule 39: 60S ribosomal protein L23a

Chain g:  69% 6% 24%



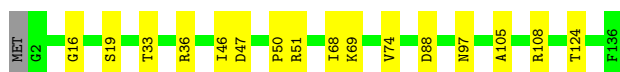
- Molecule 40: 60S ribosomal protein L26

Chain h:  78% 14% 8%




- Molecule 41: 60S ribosomal protein L27

Chain i:  88% 12%




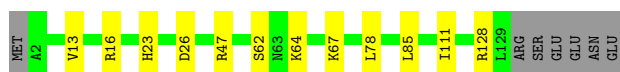
- Molecule 42: 60S ribosomal protein L31

Chain j:  6% 73% 13% 14%




- Molecule 43: 60S ribosomal protein L32

Chain k:  86% 9% 5%




- Molecule 44: 60S ribosomal protein L28

Chain l:  80% 11% 9%



- Molecule 45: 60S ribosomal protein L8

Chain m:  87% 8%



ILE
LYS
ARG
ASN
LYS
LYS
THR
LEU
LEU
ASP
GLN
HIS
GLY
GLN
TYR
PRO
TRP
ILE
TRP
MET
ASN
GLN
ARG
GLN
GLN
ARG
LYS
ARG
LEU
LYS
ALA
LYS
ARG
GLU
LYS
ARG
LYS
GLY
LYS
SER
LYS
ALA
LYS
ALA
VAL
LYS
VAL
ALA
LYS
GLY
LEU
ALA
TRP

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: 5MC, E7G, B8W, I4U, B8H, P4U, P7G, 5MU, 7MG, 6MZ, 2MG, B9H, B8Q, B8T, A2M, OMC, MHG, B9B, MG, E6G, PSU, M7A, 1MA, B8K, OMU, BGH, OMG, UR3

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	0.36	0/148	0.76	0/196
2	2	0.46	2/81168 (0.0%)	0.60	19/126540 (0.0%)
3	3	0.40	0/1990	0.86	7/2685 (0.3%)
4	4	0.42	0/5048	0.88	12/6774 (0.2%)
5	5	0.41	0/2858	0.57	0/4455
6	6	0.43	0/1877	0.81	3/2554 (0.1%)
7	7	0.43	0/1181	0.87	6/1563 (0.4%)
8	8	0.49	0/3679	0.58	0/5732
9	9	0.42	0/723	0.98	6/961 (0.6%)
10	A	0.44	1/1736 (0.1%)	1.12	6/2328 (0.3%)
11	B	0.49	0/3306	0.87	11/4423 (0.2%)
12	C	0.37	0/755	0.70	0/996
13	D	0.52	0/2902	0.86	8/3898 (0.2%)
14	E	0.40	0/742	0.70	0/996
15	F	0.48	0/878	0.73	0/1170
16	G	0.45	0/1976	0.89	8/2658 (0.3%)
17	H	0.41	0/1023	0.72	0/1351
18	I	0.40	0/1537	0.76	0/2066
19	K	0.36	0/810	0.84	2/1072 (0.2%)
20	L	0.50	0/1191	0.72	0/1591
21	M	0.61	1/720 (0.1%)	0.82	0/952
22	N	0.40	0/1341	0.94	6/1793 (0.3%)
23	O	0.37	0/575	0.64	0/761
24	P	0.53	0/454	0.77	0/599
25	Q	0.47	0/1732	0.76	1/2315 (0.0%)
26	R	0.38	0/1293	0.89	3/1725 (0.2%)
27	S	0.43	0/1133	0.76	0/1516
28	U	0.49	0/1746	0.76	0/2338
29	V	0.48	0/1682	0.76	1/2250 (0.0%)
30	W	0.46	0/855	0.76	0/1128
31	X	0.44	0/708	0.70	0/941

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.48	0/1268	0.75	0/1701
33	Z	0.50	0/1537	0.79	1/2052 (0.0%)
34	a	0.44	0/1255	0.76	1/1662 (0.1%)
35	b	0.45	0/1501	0.70	1/2013 (0.0%)
36	c	0.44	0/1291	0.78	2/1725 (0.1%)
37	d	0.43	0/839	0.95	3/1126 (0.3%)
38	e	0.45	0/993	0.78	2/1332 (0.2%)
39	g	0.44	0/984	0.69	0/1323
40	h	0.45	0/1132	0.79	2/1504 (0.1%)
41	i	0.43	0/1130	0.76	4/1507 (0.3%)
42	j	0.51	1/903 (0.1%)	0.78	1/1216 (0.1%)
43	k	0.52	0/1071	0.80	2/1429 (0.1%)
44	l	0.45	0/1017	0.79	0/1364
45	m	0.51	0/1936	0.85	7/2596 (0.3%)
46	n	0.50	0/895	0.73	0/1198
47	o	0.41	0/1784	0.84	6/2393 (0.3%)
48	p	0.49	0/1916	0.82	5/2553 (0.2%)
49	r	0.40	0/2432	0.79	5/3256 (0.2%)
50	z	0.38	0/286	0.76	0/372
All	All	0.46	5/151937 (0.0%)	0.69	141/222649 (0.1%)

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	j	58	GLY	C-N	-6.85	1.21	1.33
21	M	39	TYR	C-N	6.22	1.39	1.33
10	A	170	GLY	N-CA	5.85	1.53	1.45
2	2	1326	A2M	O3'-P	5.51	1.61	1.56
2	2	1534	A2M	O3'-P	5.12	1.61	1.56

The worst 5 of 141 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	169	VAL	O-C-N	-21.20	96.07	122.57
10	A	211	GLY	CA-C-N	13.25	139.31	120.49
10	A	211	GLY	C-N-CA	13.25	139.31	120.49
9	9	11	ARG	N-CA-C	10.15	125.96	113.17
10	A	172	VAL	N-CA-C	8.92	122.20	111.05

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](#)

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	148	0	135	1	0
2	2	74680	0	37505	240	0
3	3	1951	0	1970	13	0
4	4	4965	0	5099	81	0
5	5	2558	0	1296	5	0
6	6	1852	0	1828	33	0
7	7	1159	0	1224	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	8	3315	0	1685	11	0
9	9	711	0	724	20	0
10	A	1708	0	1815	32	0
11	B	3235	0	3381	42	0
12	C	743	0	800	11	0
13	D	2848	0	3023	26	0
14	E	732	0	769	6	0
15	F	868	0	963	5	0
16	G	1940	0	2096	14	0
17	H	1015	0	1148	4	0
18	I	1518	0	1601	11	0
19	K	799	0	876	4	0
20	L	1162	0	1213	10	0
21	M	705	0	741	2	0
22	N	1319	0	1358	15	0
23	O	569	0	637	3	0
24	P	444	0	483	4	0
25	Q	1701	0	1818	19	0
26	R	1272	0	1291	18	0
27	S	1111	0	1174	11	0
28	U	1701	0	1749	18	0
29	V	1650	0	1794	10	0
30	W	842	0	915	6	0
31	X	698	0	752	3	0
32	Y	1242	0	1268	8	0
33	Z	1513	0	1628	11	0
34	a	1239	0	1362	13	0
35	b	1461	0	1502	12	0
36	c	1264	0	1337	6	0
37	d	825	0	850	8	0
38	e	979	0	1039	17	0
39	g	967	0	1040	6	0
40	h	1115	0	1205	11	0
41	i	1107	0	1182	10	0
42	j	888	0	930	8	0
43	k	1053	0	1147	8	0
44	l	1002	0	1068	10	0
45	m	1898	0	1993	13	0
46	n	876	0	912	8	0
47	o	1750	0	1895	24	0
48	p	1878	0	2009	14	0
49	r	2386	0	2421	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	z	284	0	333	22	0
51	2	229	0	0	0	0
51	5	3	0	0	0	0
51	8	6	0	0	0	0
51	B	1	0	0	0	0
51	D	1	0	0	0	0
51	F	1	0	0	0	0
51	L	1	0	0	0	0
51	M	1	0	0	0	0
51	k	1	0	0	0	0
51	m	1	0	0	0	0
51	n	1	0	0	0	0
51	p	1	0	0	0	0
52	2	13	0	0	0	0
52	k	1	0	0	0	0
52	o	1	0	0	0	0
52	p	1	0	0	0	0
All	All	143909	0	106984	719	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 719 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)
2:2:1860:B8H:C5	2:2:1860:B8H:C4	1.81	1.56
2:2:4296:B8H:C5	2:2:4296:B8H:C4	1.80	1.56
11:B:42:HIS:HB3	50:z:34:LYS:NZ	1.34	1.40
2:2:4129:B8W:O4'	2:2:4129:B8W:C1'	1.65	1.26
2:2:4472:B8W:O4'	2:2:4472:B8W:C1'	1.66	1.24

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	17/731 (2%)	17 (100%)	0	0	100	100
3	3	237/503 (47%)	211 (89%)	25 (10%)	1 (0%)	30	59
4	4	601/634 (95%)	539 (90%)	59 (10%)	3 (0%)	24	54
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%)	4	19
10	A	210/217 (97%)	176 (84%)	32 (15%)	2 (1%)	12	38
11	B	399/403 (99%)	373 (94%)	24 (6%)	2 (0%)	24	54
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%)	24	54
26	R	148/203 (73%)	137 (93%)	9 (6%)	2 (1%)	9	31
27	S	133/215 (62%)	124 (93%)	9 (7%)	0	100	100
28	U	201/204 (98%)	190 (94%)	10 (5%)	1 (0%)	24	54
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	a	146/196 (74%)	139 (95%)	7 (5%)	0	100	100
35	b	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
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	59
46	n	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
47	o	212/288 (74%)	189 (89%)	21 (10%)	2 (1%)	14	41
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%)	44	70

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 [i](#)

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
3	3	223/457 (49%)	217 (97%)	6 (3%)	39	63
4	4	548/574 (96%)	539 (98%)	9 (2%)	55	71
6	6	212/213 (100%)	206 (97%)	6 (3%)	38	62
7	7	126/149 (85%)	125 (99%)	1 (1%)	73	78
9	9	74/114 (65%)	72 (97%)	2 (3%)	39	63
10	A	191/196 (97%)	187 (98%)	4 (2%)	47	67
11	B	349/349 (100%)	348 (100%)	1 (0%)	86	85
12	C	76/126 (60%)	75 (99%)	1 (1%)	61	73
13	D	298/348 (86%)	294 (99%)	4 (1%)	61	73
14	E	79/97 (81%)	79 (100%)	0	100	100
15	F	94/100 (94%)	94 (100%)	0	100	100
16	G	206/223 (92%)	206 (100%)	0	100	100
17	H	109/110 (99%)	108 (99%)	1 (1%)	70	77
18	I	169/171 (99%)	166 (98%)	3 (2%)	51	69
19	K	84/89 (94%)	84 (100%)	0	100	100
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%)	76	79
23	O	64/65 (98%)	64 (100%)	0	100	100
24	P	47/48 (98%)	46 (98%)	1 (2%)	47	67
25	Q	176/177 (99%)	173 (98%)	3 (2%)	53	70
26	R	138/184 (75%)	136 (99%)	2 (1%)	59	72
27	S	115/161 (71%)	112 (97%)	3 (3%)	40	64
28	U	171/172 (99%)	168 (98%)	3 (2%)	51	69
29	V	173/174 (99%)	173 (100%)	0	100	100
30	W	91/94 (97%)	89 (98%)	2 (2%)	45	67
31	X	73/75 (97%)	70 (96%)	3 (4%)	27	55
32	Y	134/163 (82%)	132 (98%)	2 (2%)	57	71
33	Z	164/165 (99%)	160 (98%)	4 (2%)	43	65
34	a	133/175 (76%)	132 (99%)	1 (1%)	73	78
35	b	157/157 (100%)	156 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	c	136/140 (97%)	131 (96%)	5 (4%)	30	57
37	d	91/115 (79%)	90 (99%)	1 (1%)	65	75
38	e	101/107 (94%)	101 (100%)	0	100	100
39	g	106/133 (80%)	105 (99%)	1 (1%)	70	77
40	h	124/135 (92%)	121 (98%)	3 (2%)	43	65
41	i	117/118 (99%)	117 (100%)	0	100	100
42	j	98/110 (89%)	97 (99%)	1 (1%)	68	76
43	k	114/121 (94%)	113 (99%)	1 (1%)	70	77
44	l	109/121 (90%)	109 (100%)	0	100	100
45	m	190/199 (96%)	189 (100%)	1 (0%)	81	82
46	n	88/89 (99%)	88 (100%)	0	100	100
47	o	192/252 (76%)	187 (97%)	5 (3%)	40	64
48	p	195/215 (91%)	195 (100%)	0	100	100
49	r	247/250 (99%)	244 (99%)	3 (1%)	63	74
50	z	30/115 (26%)	30 (100%)	0	100	100
All	All	6760/8350 (81%)	6675 (99%)	85 (1%)	59	73

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	Y	151	THR
40	h	55	VAL
33	Z	5	ILE
36	c	48	VAL
43	k	13	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
44	l	36	ASN
45	m	132	ASN
49	r	195	HIS
16	G	43	GLN
14	E	33	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	3458/5070 (68%)	912 (26%)	25 (0%)
5	5	119/120 (99%)	24 (20%)	0
8	8	155/156 (99%)	39 (25%)	0
All	All	3732/5346 (69%)	975 (26%)	25 (0%)

5 of 975 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 [i](#)

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	OMC	2	3887	2	19,22,23	2.95	7 (36%)	26,31,34	1.31	4 (15%)
2	B8W	2	2380	2	23,26,27	3.65	11 (47%)	33,38,41	2.58	15 (45%)
2	OMG	2	373	2	23,26,27	2.20	7 (30%)	33,38,41	2.02	9 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	2	2364	2	23,26,27	2.23	7 (30%)	33,38,41	1.88	8 (24%)
2	A2M	2	2401	2	22,25,26	3.40	9 (40%)	31,36,39	2.72	9 (29%)
2	OMG	2	1316	2,51	23,26,27	2.30	8 (34%)	33,38,41	1.95	11 (33%)
2	MHG	2	4371	2	29,32,33	3.94	12 (41%)	34,46,49	2.61	10 (29%)
2	1MA	2	4415	2	21,25,26	2.84	5 (23%)	31,37,40	1.82	7 (22%)
2	OMG	2	4370	2	23,26,27	2.34	9 (39%)	33,38,41	1.86	9 (27%)
2	1MA	2	1322	2,51	21,25,26	2.82	5 (23%)	31,37,40	1.77	6 (19%)
2	OMG	2	2773	2	23,26,27	2.25	9 (39%)	33,38,41	1.89	9 (27%)
2	OMG	2	2050	2	23,26,27	2.22	7 (30%)	33,38,41	1.94	8 (24%)
2	UR3	2	4530	2	19,22,23	2.66	6 (31%)	26,32,35	1.37	3 (11%)
2	P7G	2	1909	2	24,28,29	4.57	11 (45%)	27,41,44	1.82	5 (18%)
2	OMG	2	4870	2	23,26,27	2.31	9 (39%)	33,38,41	1.87	9 (27%)
2	I4U	2	1659	2,51	21,24,25	4.63	15 (71%)	27,34,37	1.65	4 (14%)
2	A2M	2	3723	2	22,25,26	3.44	8 (36%)	31,36,39	2.51	8 (25%)
2	I4U	2	4194	2	21,24,25	4.72	15 (71%)	27,34,37	1.33	2 (7%)
2	PSU	2	1582	2	18,21,22	1.07	1 (5%)	22,30,33	1.76	5 (22%)
2	OMC	2	4536	2	19,22,23	2.78	7 (36%)	26,31,34	1.03	2 (7%)
2	B8Q	2	1456	2	17,22,23	2.90	4 (23%)	22,32,35	2.63	6 (27%)
2	OMG	2	4623	2	23,26,27	2.24	8 (34%)	33,38,41	1.80	9 (27%)
2	A2M	2	2363	2,51	22,25,26	3.57	10 (45%)	31,36,39	2.71	9 (29%)
2	OMU	2	4620	2	19,22,23	2.63	7 (36%)	26,31,34	1.75	5 (19%)
2	B9B	2	2754	2	25,28,29	3.41	11 (44%)	35,40,43	2.35	15 (42%)
2	7MG	2	4550	2	22,26,27	3.50	10 (45%)	29,39,42	2.08	10 (34%)
2	PSU	2	4403	2	18,21,22	1.00	1 (5%)	22,30,33	1.70	5 (22%)
2	P4U	2	1348	2	21,24,25	3.51	7 (33%)	27,33,36	1.38	4 (14%)
2	B9B	2	237	2	25,28,29	3.50	12 (48%)	35,40,43	2.58	14 (40%)
2	E6G	2	4355	2	24,27,28	3.52	12 (50%)	34,39,42	2.69	13 (38%)
2	7MG	2	1605	2	22,26,27	3.19	10 (45%)	29,39,42	2.18	10 (34%)
2	OMC	2	2804	2	19,22,23	2.63	7 (36%)	26,31,34	1.26	3 (11%)
2	E7G	2	1797	2	24,27,28	3.81	11 (45%)	30,40,43	2.26	10 (33%)
2	7MG	2	2522	2	22,26,27	3.44	10 (45%)	29,39,42	2.11	10 (34%)
2	OMG	2	2424	2	23,26,27	2.31	7 (30%)	33,38,41	1.75	6 (18%)
2	OMG	2	4196	2,51	23,26,27	2.44	8 (34%)	33,38,41	2.05	9 (27%)
2	OMC	2	2422	2,51	19,22,23	2.76	7 (36%)	26,31,34	1.39	3 (11%)
2	A2M	2	1524	2	22,25,26	3.45	10 (45%)	31,36,39	2.82	12 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMU	2	4306	2	19,22,23	2.68	7 (36%)	26,31,34	1.78	5 (19%)
2	PSU	2	2508	2	18,21,22	1.01	1 (5%)	22,30,33	1.66	4 (18%)
2	A2M	2	4571	2	22,25,26	3.56	9 (40%)	31,36,39	2.66	8 (25%)
2	P7G	2	3880	2	24,28,29	4.67	11 (45%)	27,41,44	1.58	3 (11%)
2	A2M	2	1871	2	22,25,26	3.40	9 (40%)	31,36,39	2.70	8 (25%)
2	BGH	2	3899	2	25,29,30	4.24	17 (68%)	31,43,46	2.46	11 (35%)
2	A2M	2	3867	2	22,25,26	3.49	9 (40%)	31,36,39	2.70	9 (29%)
2	B8H	2	1860	2	19,22,23	6.76	6 (31%)	22,32,35	2.21	5 (22%)
2	PSU	2	4636	2	18,21,22	1.12	1 (5%)	22,30,33	1.79	3 (13%)
2	PSU	2	1677	2	18,21,22	1.31	3 (16%)	22,30,33	1.82	5 (22%)
2	OMC	2	3869	2	19,22,23	2.80	7 (36%)	26,31,34	2.17	6 (23%)
2	2MG	2	4872	2	23,26,27	2.64	8 (34%)	32,38,41	2.23	8 (25%)
2	A2M	2	3825	2	22,25,26	3.46	10 (45%)	31,36,39	2.60	8 (25%)
2	OMG	2	4494	2	23,26,27	2.31	8 (34%)	33,38,41	1.98	7 (21%)
2	6MZ	2	4220	2	22,25,26	2.60	5 (22%)	30,36,39	3.39	12 (40%)
2	OMC	2	2861	2	19,22,23	2.85	8 (42%)	26,31,34	1.06	2 (7%)
2	A2M	2	398	2	22,25,26	3.43	9 (40%)	31,36,39	2.59	9 (29%)
2	5MU	2	4083	2	19,22,23	4.66	7 (36%)	28,32,35	3.87	10 (35%)
2	A2M	2	1326	2,51	22,25,26	3.43	9 (40%)	31,36,39	2.60	10 (32%)
2	UR3	2	4597	2	19,22,23	2.69	7 (36%)	26,32,35	2.45	6 (23%)
2	A2M	2	1534	2,51	22,25,26	3.51	9 (40%)	31,36,39	2.74	10 (32%)
2	E7G	2	2297	2	24,27,28	3.74	11 (45%)	30,40,43	2.27	10 (33%)
2	B8W	2	4129	2	23,26,27	3.76	8 (34%)	33,38,41	3.35	14 (42%)
2	B8H	2	4296	2	19,22,23	6.87	6 (31%)	22,32,35	2.47	5 (22%)
2	OMC	2	3909	2	19,22,23	2.98	8 (42%)	26,31,34	2.61	6 (23%)
2	PSU	2	4293	2	18,21,22	0.97	1 (5%)	22,30,33	1.78	5 (22%)
2	B8T	2	4483	2	19,22,23	3.49	8 (42%)	26,31,34	1.06	3 (11%)
2	PSU	2	4628	2	18,21,22	1.06	1 (5%)	22,30,33	1.76	4 (18%)
2	OMG	2	1522	2	23,26,27	2.25	6 (26%)	33,38,41	1.75	7 (21%)
2	A2M	2	4523	2	22,25,26	3.42	9 (40%)	31,36,39	2.74	9 (29%)
2	B8W	2	4185	2	23,26,27	3.71	9 (39%)	33,38,41	2.69	12 (36%)
2	B9H	2	2786	2	20,25,26	2.95	5 (25%)	22,35,38	3.29	7 (31%)
2	B8W	2	4472	2	23,26,27	3.71	9 (39%)	33,38,41	2.66	13 (39%)
2	PSU	2	3729	2	18,21,22	0.99	1 (5%)	22,30,33	1.68	4 (18%)
8	OMU	8	14	8,2	19,22,23	2.58	6 (31%)	26,31,34	1.97	5 (19%)

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	OMG	2	1625	2	23,26,27	2.24	7 (30%)	33,38,41	1.96	9 (27%)
2	2MG	2	729	2	23,26,27	2.65	7 (30%)	32,38,41	2.35	8 (25%)
2	2MG	2	978	2	23,26,27	2.78	9 (39%)	32,38,41	2.32	12 (37%)
2	M7A	2	4564	2	20,25,26	1.94	3 (15%)	28,37,40	3.99	6 (21%)
2	OMC	2	2365	2,51	19,22,23	2.76	7 (36%)	26,31,34	0.97	1 (3%)
2	OMC	2	3701	2,51	19,22,23	2.78	8 (42%)	26,31,34	0.93	0
2	B8K	2	3897	2	24,28,29	4.33	16 (66%)	30,42,45	2.60	13 (43%)
2	OMG	2	4637	2	23,26,27	2.34	6 (26%)	33,38,41	2.06	9 (27%)
2	B9B	2	1574	2	25,28,29	3.55	12 (48%)	35,40,43	2.35	15 (42%)
2	B8W	2	4529	2,51	23,26,27	3.78	10 (43%)	33,38,41	2.98	19 (57%)
2	UR3	2	1866	2	19,22,23	1.04	2 (10%)	26,32,35	1.62	2 (7%)
2	2MG	2	1517	2	23,26,27	2.65	6 (26%)	32,38,41	2.99	9 (28%)
2	PSU	2	3715	2	18,21,22	1.10	1 (5%)	22,30,33	1.68	4 (18%)
2	PSU	2	1683	2	18,21,22	1.15	1 (5%)	22,30,33	1.90	5 (22%)
2	OMG	2	1883	2	23,26,27	2.31	7 (30%)	33,38,41	2.06	9 (27%)
2	5MC	2	4335	2	18,22,23	3.34	7 (38%)	26,32,35	1.14	2 (7%)
2	A2M	2	3718	2	22,25,26	3.50	11 (50%)	31,36,39	2.37	7 (22%)
2	B8K	2	4690	2	24,28,29	4.45	16 (66%)	30,42,45	2.72	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
2	OMC	2	3887	2	-	1/9/27/28	0/2/2/2
2	B8W	2	2380	2	-	4/9/27/28	0/3/3/3
2	OMG	2	373	2	-	1/9/27/28	0/3/3/3
2	OMG	2	2364	2	-	2/9/27/28	0/3/3/3
2	A2M	2	2401	2	-	1/9/27/28	0/3/3/3
2	OMG	2	1316	2,51	-	0/9/27/28	0/3/3/3
2	MHG	2	4371	2	-	7/16/46/47	0/3/3/3
2	1MA	2	4415	2	-	2/7/25/26	0/3/3/3
2	OMG	2	4370	2	-	0/9/27/28	0/3/3/3
2	1MA	2	1322	2,51	-	0/7/25/26	0/3/3/3
2	OMG	2	2773	2	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	2	2050	2	-	0/9/27/28	0/3/3/3
2	UR3	2	4530	2	-	0/7/25/26	0/2/2/2
2	P7G	2	1909	2	-	1/10/40/41	0/3/3/3
2	OMG	2	4870	2	-	3/9/27/28	0/3/3/3
2	I4U	2	1659	2,51	-	2/9/29/30	0/2/2/2
2	A2M	2	3723	2	-	0/9/27/28	0/3/3/3
2	I4U	2	4194	2	-	4/9/29/30	0/2/2/2
2	PSU	2	1582	2	-	2/7/25/26	0/2/2/2
2	OMC	2	4536	2	-	0/9/27/28	0/2/2/2
2	B8Q	2	1456	2	-	0/7/42/43	0/2/2/2
2	OMG	2	4623	2	-	0/9/27/28	0/3/3/3
2	A2M	2	2363	2,51	-	1/9/27/28	0/3/3/3
2	OMU	2	4620	2	-	0/9/27/28	0/2/2/2
2	B9B	2	2754	2	-	2/11/29/30	0/3/3/3
2	7MG	2	4550	2	-	0/7/37/38	0/3/3/3
2	PSU	2	4403	2	-	2/7/25/26	0/2/2/2
2	P4U	2	1348	2	-	1/10/29/30	0/2/2/2
2	B9B	2	237	2	-	6/11/29/30	0/3/3/3
2	E6G	2	4355	2	-	3/10/28/29	0/3/3/3
2	7MG	2	1605	2	-	1/7/37/38	0/3/3/3
2	OMC	2	2804	2	-	0/9/27/28	0/2/2/2
2	E7G	2	1797	2	-	2/9/39/40	0/3/3/3
2	7MG	2	2522	2	-	0/7/37/38	0/3/3/3
2	OMG	2	2424	2	-	2/9/27/28	0/3/3/3
2	OMG	2	4196	2,51	-	3/9/27/28	0/3/3/3
2	OMC	2	2422	2,51	-	1/9/27/28	0/2/2/2
2	A2M	2	1524	2	-	1/9/27/28	0/3/3/3
2	OMU	2	4306	2	-	0/9/27/28	0/2/2/2
2	PSU	2	2508	2	-	0/7/25/26	0/2/2/2
2	A2M	2	4571	2	-	0/9/27/28	0/3/3/3
2	P7G	2	3880	2	-	1/10/40/41	0/3/3/3
2	A2M	2	1871	2	-	3/9/27/28	0/3/3/3
2	BGH	2	3899	2	-	0/13/43/44	0/3/3/3
2	A2M	2	3867	2	-	2/9/27/28	0/3/3/3
2	B8H	2	1860	2	-	0/7/25/26	0/2/2/2
2	PSU	2	4636	2	-	3/7/25/26	0/2/2/2
2	PSU	2	1677	2	-	3/7/25/26	0/2/2/2
2	OMC	2	3869	2	-	3/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	2	4872	2	-	2/9/27/28	0/3/3/3
2	A2M	2	3825	2	-	0/9/27/28	0/3/3/3
2	OMG	2	4494	2	-	0/9/27/28	0/3/3/3
2	6MZ	2	4220	2	-	2/9/27/28	0/3/3/3
2	OMC	2	2861	2	-	0/9/27/28	0/2/2/2
2	A2M	2	398	2	-	2/9/27/28	0/3/3/3
2	5MU	2	4083	2	-	0/7/25/26	0/2/2/2
2	A2M	2	1326	2,51	-	1/9/27/28	0/3/3/3
2	UR3	2	4597	2	-	2/7/25/26	0/2/2/2
2	A2M	2	1534	2,51	-	2/9/27/28	0/3/3/3
2	E7G	2	2297	2	-	1/9/39/40	0/3/3/3
2	B8W	2	4129	2	-	2/9/27/28	0/3/3/3
2	B8H	2	4296	2	-	2/7/25/26	0/2/2/2
2	OMC	2	3909	2	-	0/9/27/28	0/2/2/2
2	PSU	2	4293	2	-	2/7/25/26	0/2/2/2
2	B8T	2	4483	2	-	0/7/27/28	0/2/2/2
2	PSU	2	4628	2	-	0/7/25/26	0/2/2/2
2	OMG	2	1522	2	-	0/9/27/28	0/3/3/3
2	A2M	2	4523	2	-	4/9/27/28	0/3/3/3
2	B8W	2	4185	2	-	3/9/27/28	0/3/3/3
2	B9H	2	2786	2	-	0/12/47/48	0/2/2/2
2	B8W	2	4472	2	-	2/9/27/28	0/3/3/3
2	PSU	2	3729	2	-	2/7/25/26	0/2/2/2
8	OMU	8	14	8,2	-	1/9/27/28	0/2/2/2
2	B8T	2	4671	2	-	0/7/27/28	0/2/2/2
2	OMG	2	1625	2	-	2/9/27/28	0/3/3/3
2	2MG	2	729	2	-	1/9/27/28	0/3/3/3
2	2MG	2	978	2	-	0/9/27/28	0/3/3/3
2	M7A	2	4564	2	-	0/7/37/38	0/3/3/3
2	OMC	2	2365	2,51	-	0/9/27/28	0/2/2/2
2	OMC	2	3701	2,51	-	4/9/27/28	0/2/2/2
2	B8K	2	3897	2	-	3/11/41/42	0/3/3/3
2	OMG	2	4637	2	-	2/9/27/28	0/3/3/3
2	B9B	2	1574	2	-	3/11/29/30	0/3/3/3
2	B8W	2	4529	2,51	-	4/9/27/28	0/3/3/3
2	UR3	2	1866	2	-	3/7/25/26	0/2/2/2
2	2MG	2	1517	2	-	0/9/27/28	0/3/3/3
2	PSU	2	3715	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	2	1683	2	-	0/7/25/26	0/2/2/2
2	OMG	2	1883	2	-	2/9/27/28	0/3/3/3
2	5MC	2	4335	2	-	0/7/25/26	0/2/2/2
2	A2M	2	3718	2	-	1/9/27/28	0/3/3/3
2	B8K	2	4690	2	-	0/11/41/42	0/3/3/3

The worst 5 of 712 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4296	B8H	C6-C5	-17.22	1.10	1.34
2	2	1860	B8H	C6-C5	-16.35	1.12	1.34
2	2	4296	B8H	C4-N3	-16.35	1.08	1.38
2	2	1860	B8H	C4-N3	-15.83	1.09	1.38
2	2	3880	P7G	C8-N9	14.23	1.53	1.46

The worst 5 of 692 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	4129	B8W	C61-O6-C6	12.20	129.31	117.21
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 125 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.

21 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	2380	B8W	1	0
2	2	3723	A2M	1	0
2	2	4623	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	4403	PSU	1	0
2	2	4306	OMU	1	0
2	2	1871	A2M	1	0
2	2	3899	BGH	2	0
2	2	1860	B8H	1	0
2	2	4129	B8W	1	0
2	2	4296	B8H	1	0
2	2	4293	PSU	1	0
2	2	4483	B8T	1	0
2	2	4185	B8W	1	0
2	2	4472	B8W	2	0
2	2	729	2MG	1	0
2	2	3897	B8K	1	0
2	2	1574	B9B	1	0
2	2	4529	B8W	1	0
2	2	1683	PSU	1	0
2	2	1883	OMG	1	0
2	2	4690	B8K	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

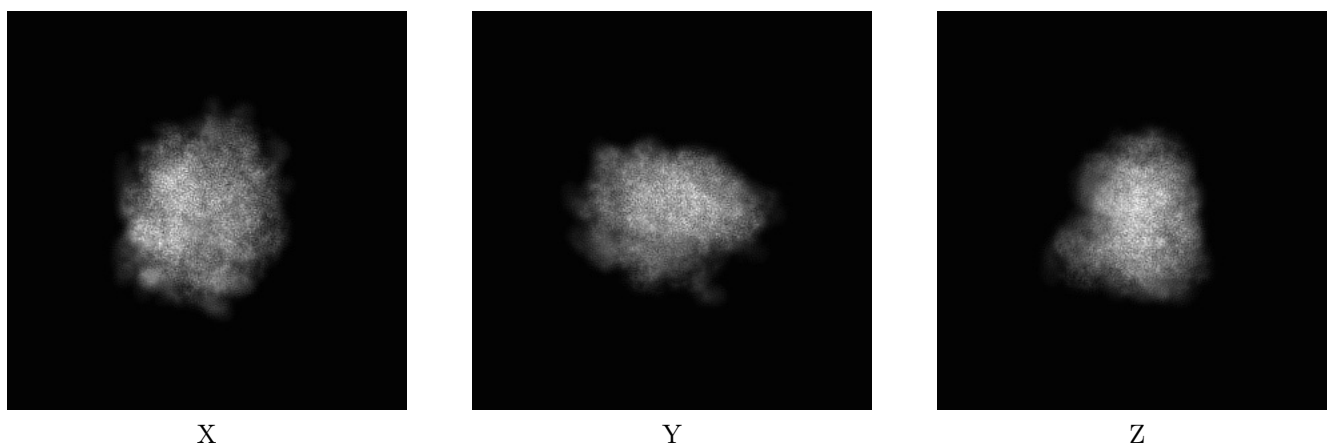
6 Map visualisation [i](#)

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](#)

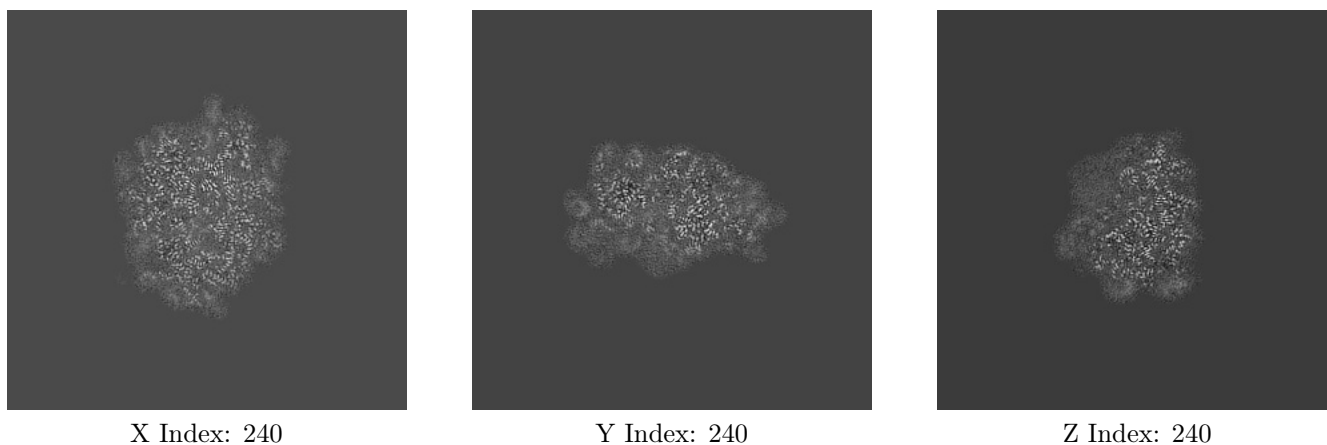
6.1.1 Primary map



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

6.2 Central slices [i](#)

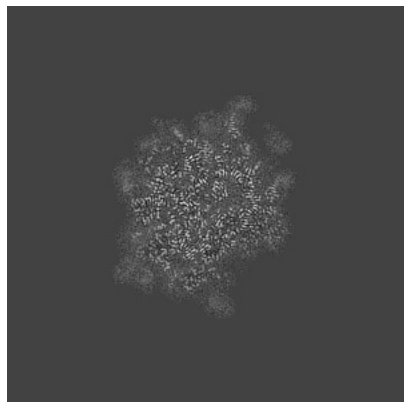
6.2.1 Primary map



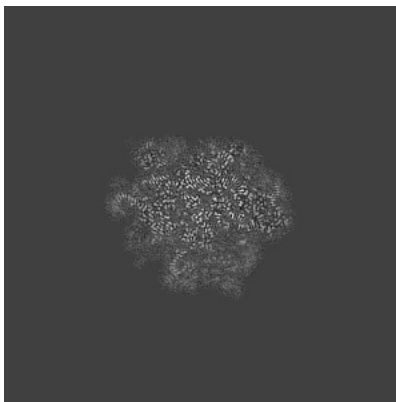
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

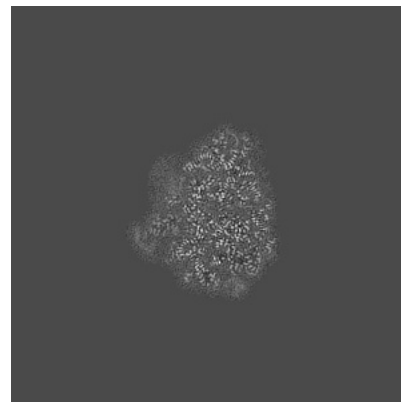
6.3.1 Primary map



X Index: 256



Y Index: 203

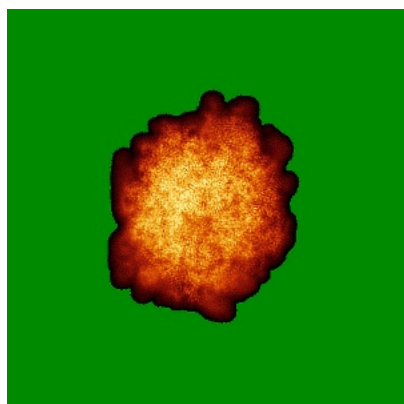


Z Index: 255

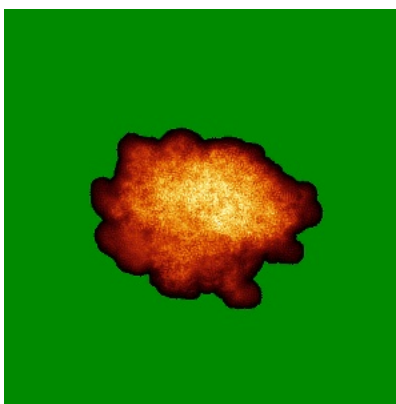
The images above show the largest variance slices of the map in three orthogonal directions.

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

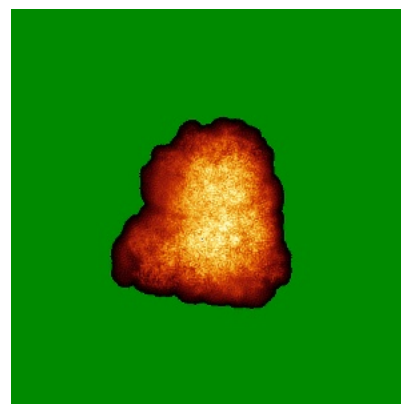
6.4.1 Primary map



X



Y

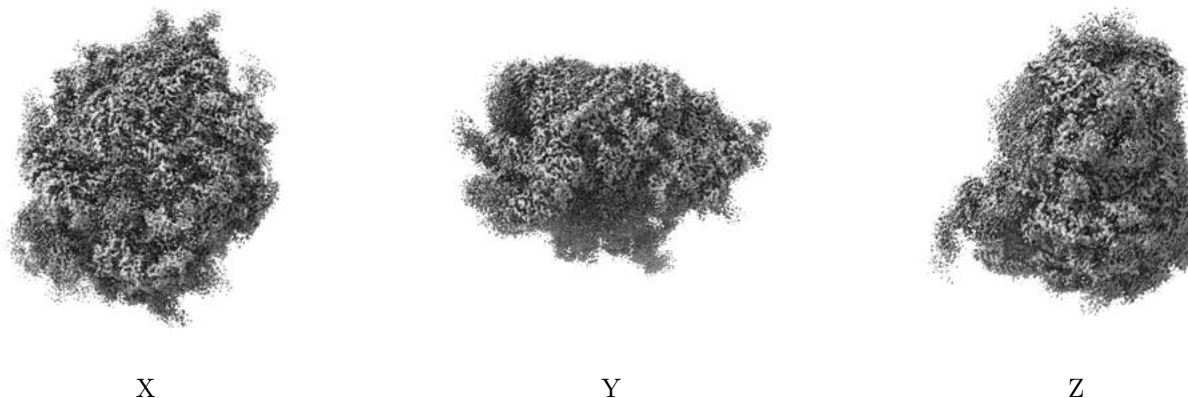


Z

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.

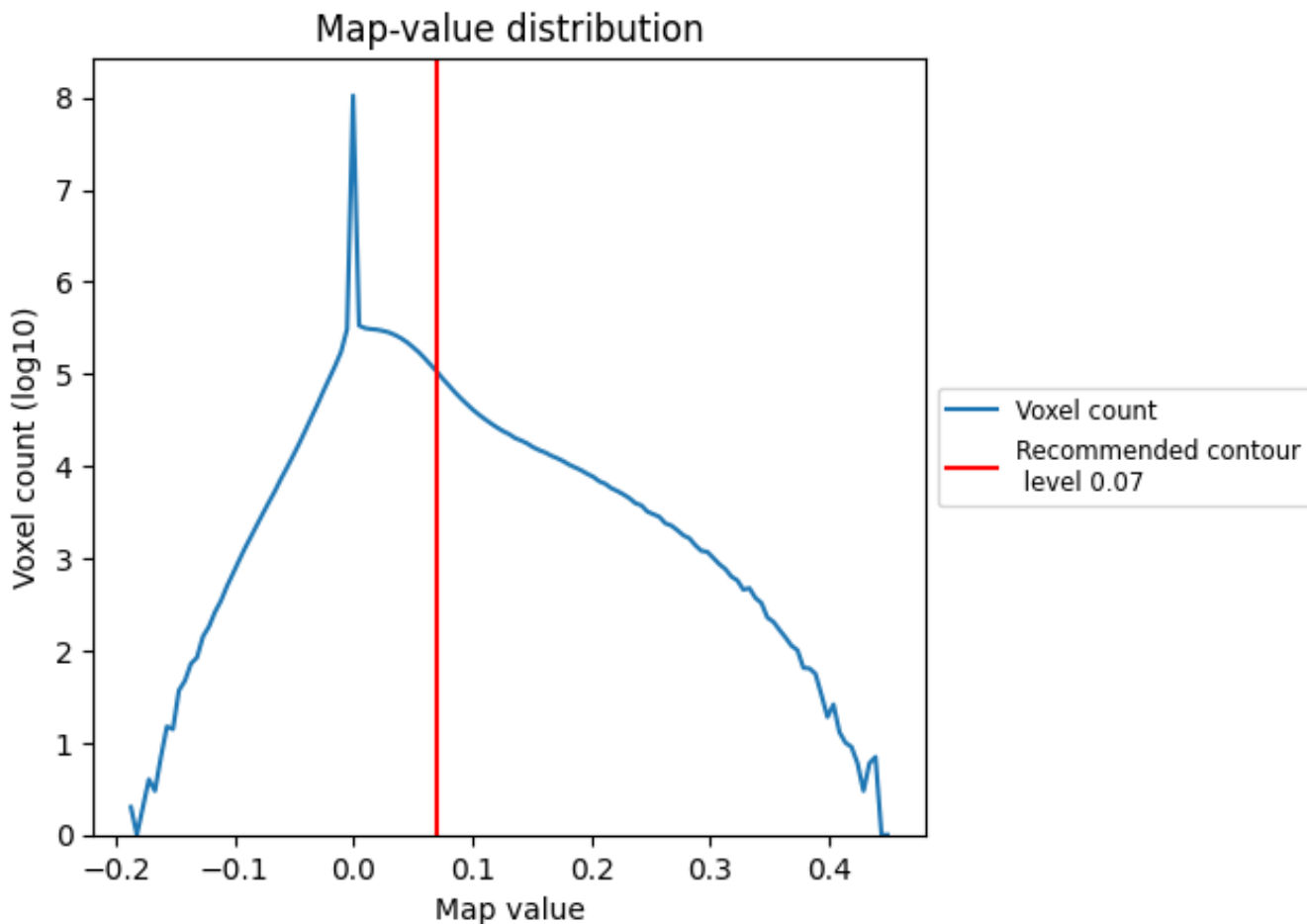
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

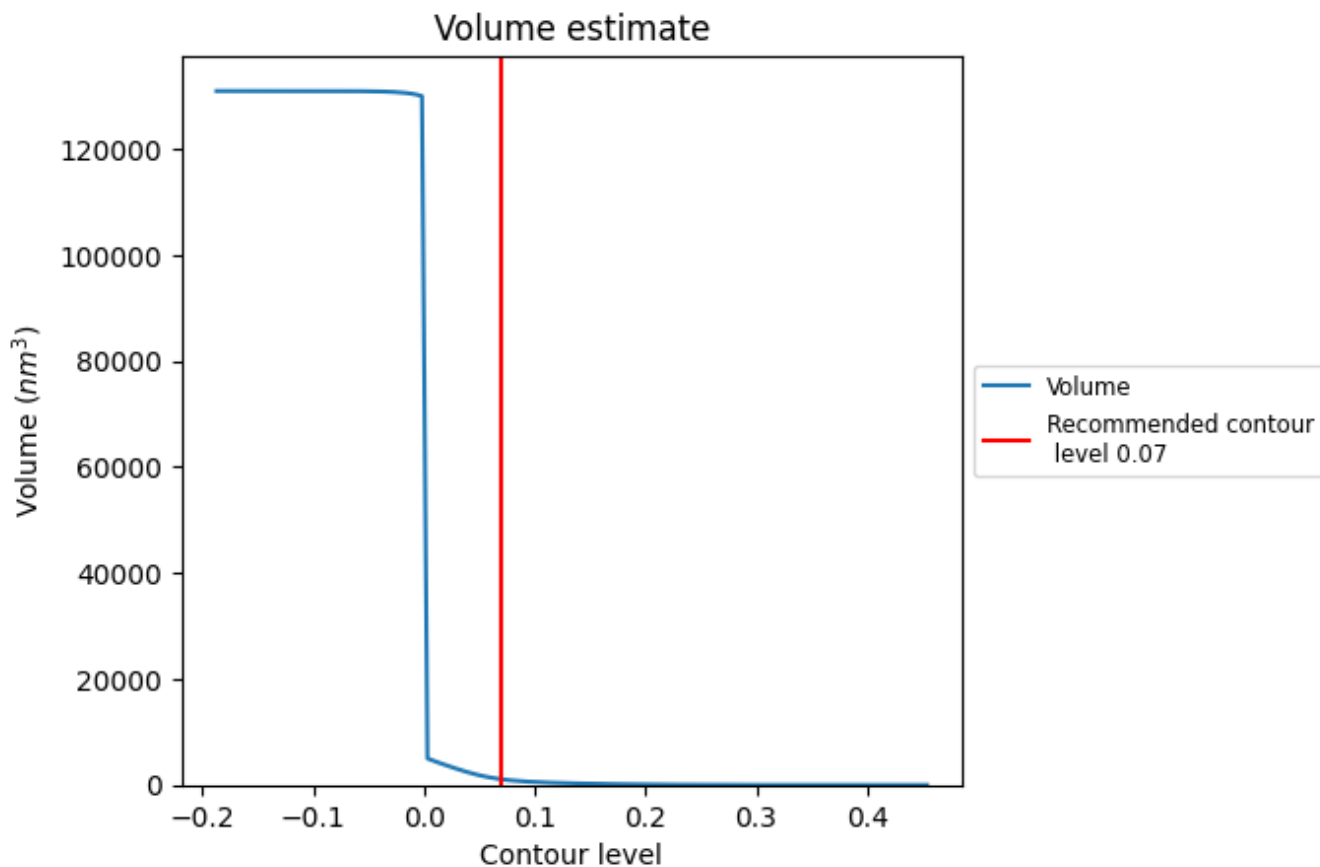
This section contains the results of statistical analysis of the map.

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.

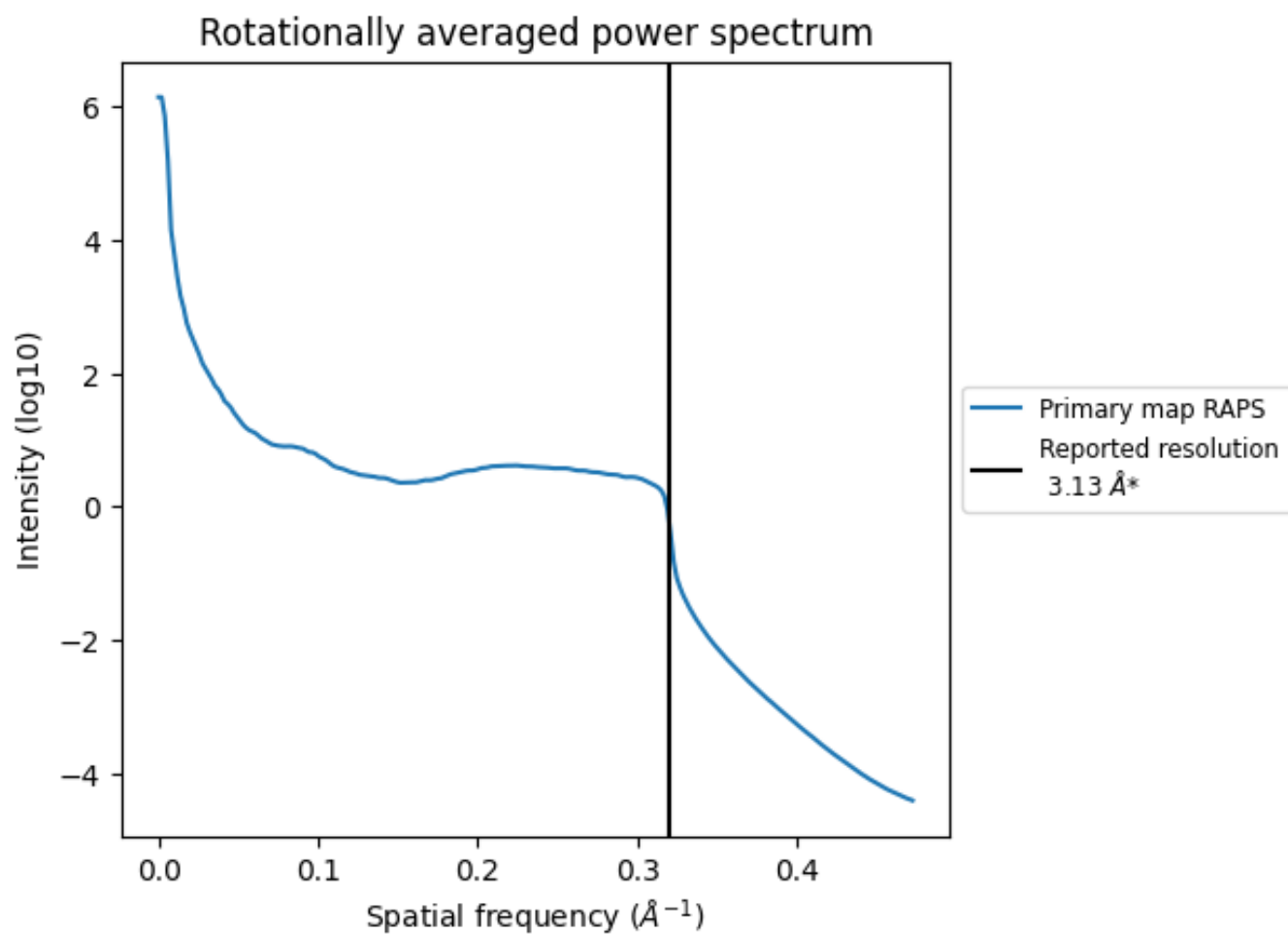
7.2 Volume estimate [\(i\)](#)



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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.319\AA^{-1}

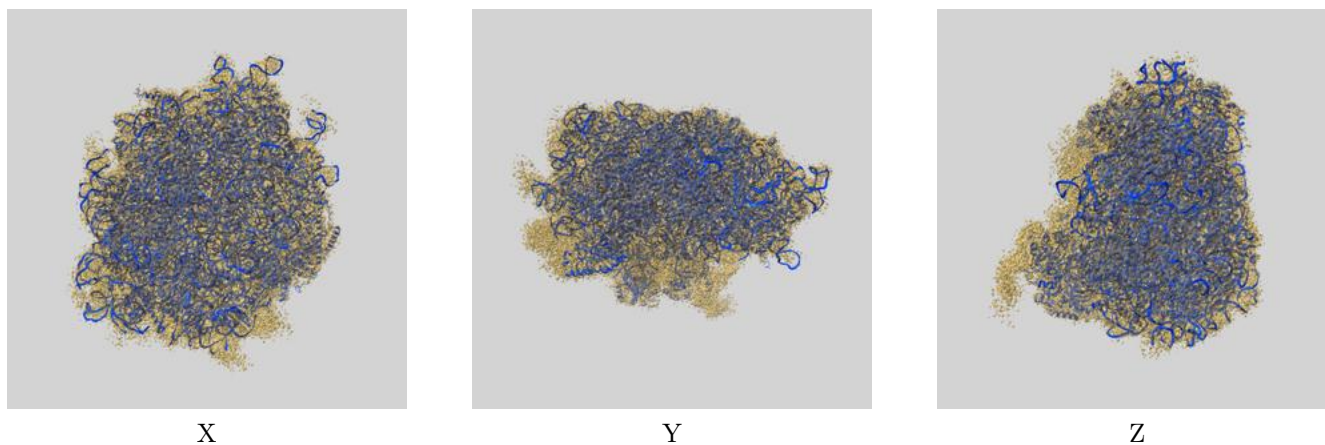
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

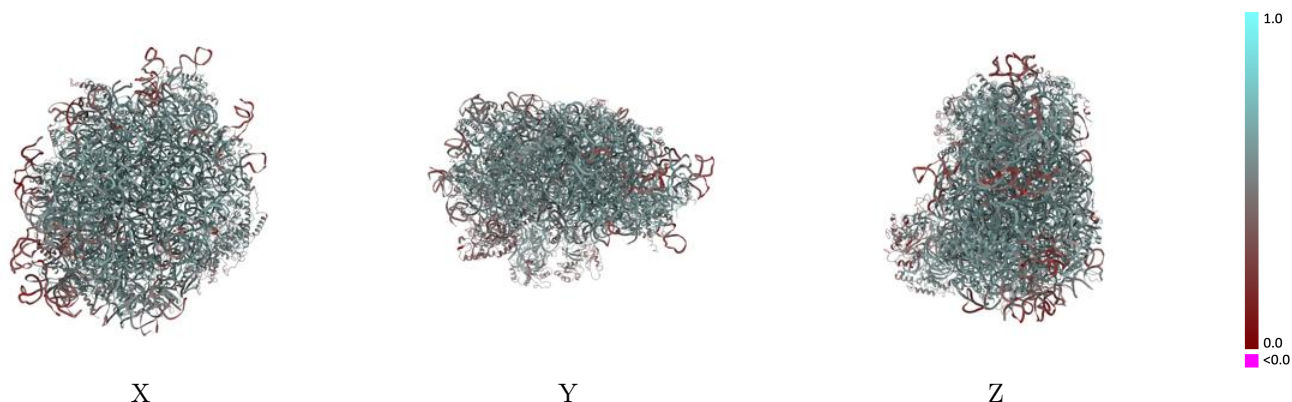
This section contains information regarding the fit between EMDB map EMD-0978 and PDB model 6LU8. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



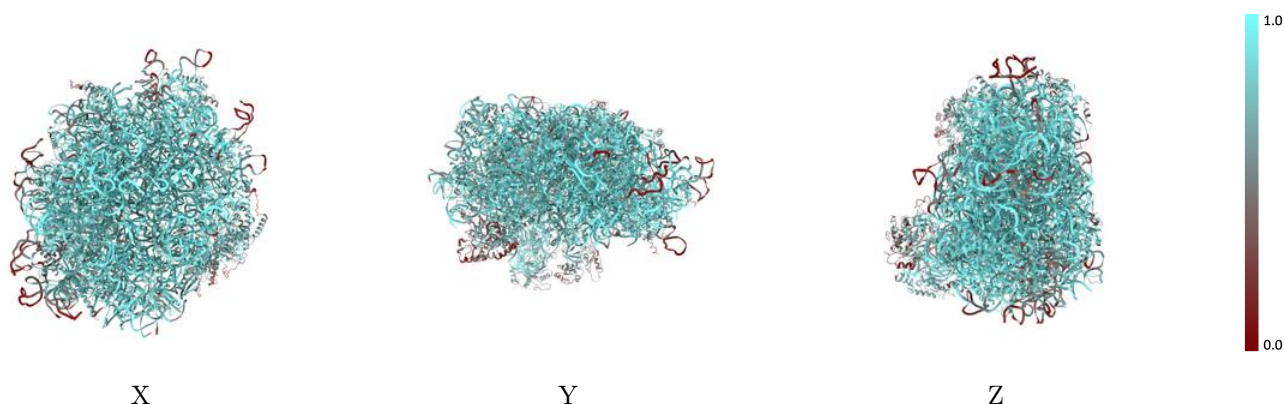
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



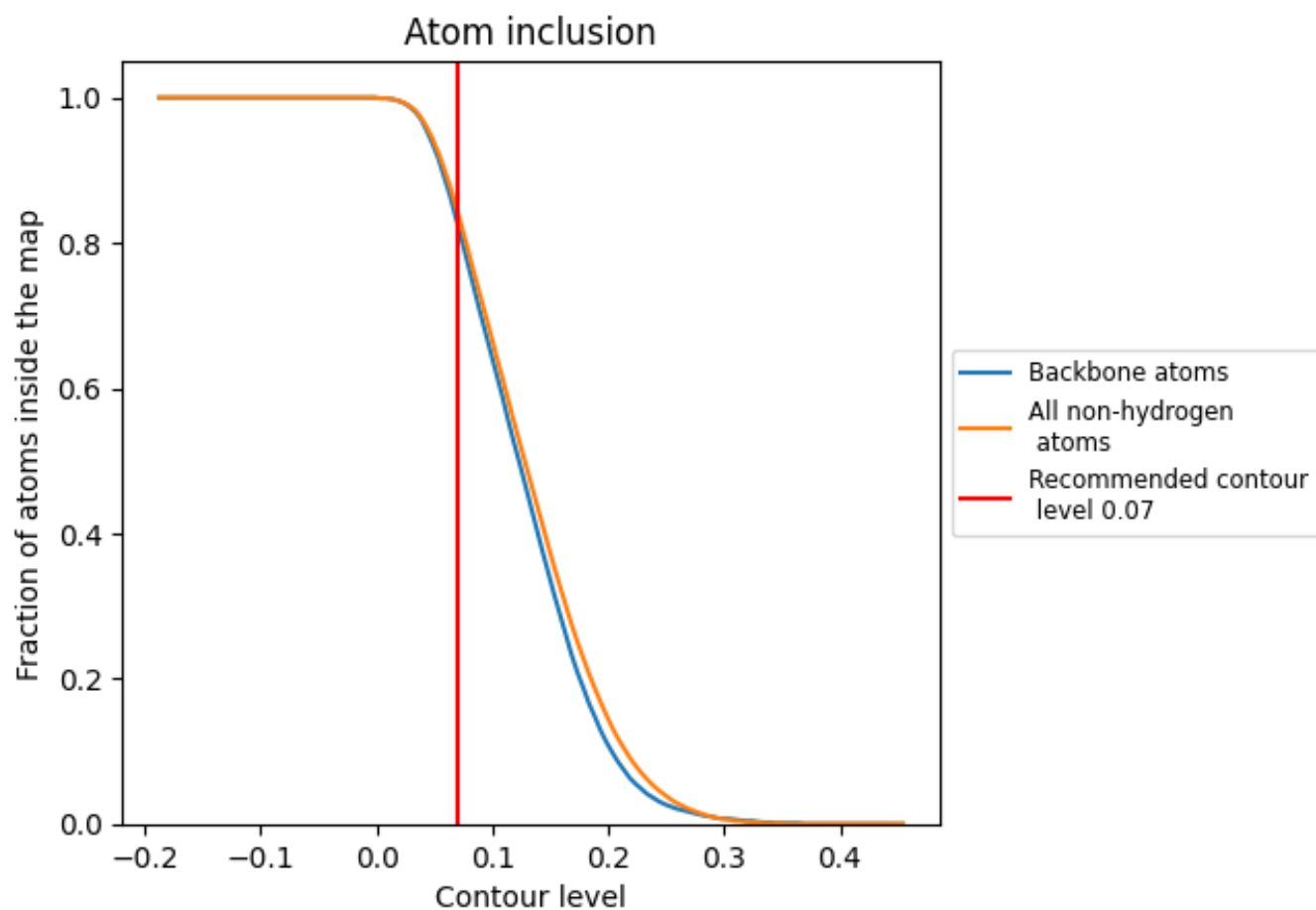
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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