



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 10:46 AM JST

PDB ID : 6LSS / pdb_00006lss
EMDB ID : EMD-0964
Title : Cryo-EM structure of a pre-60S ribosomal subunit - state preA
Authors : Liang, X.; Zuo, M.; Zhang, Y.; Li, N.; Ma, C.; Dong, M.; Gao, N.
Deposited on : 2020-01-20
Resolution : 3.23 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

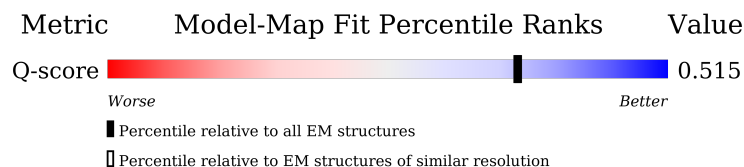
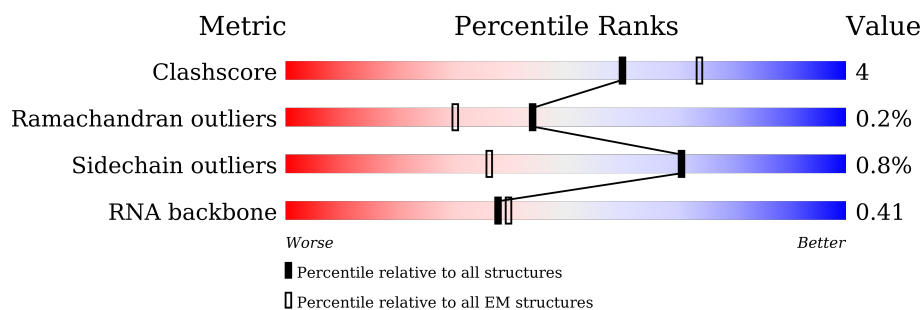
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 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.



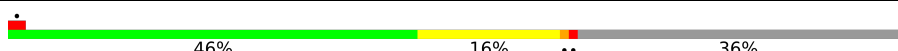
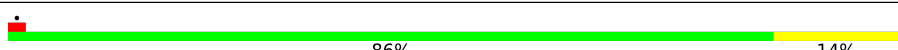
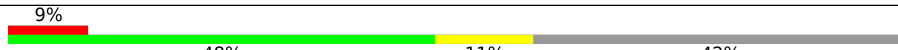
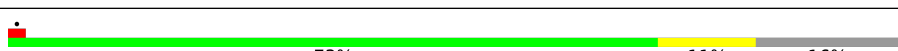
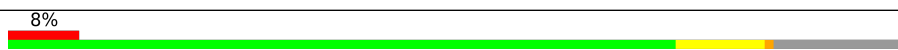
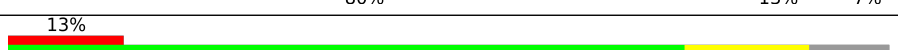
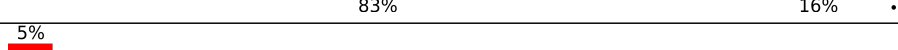
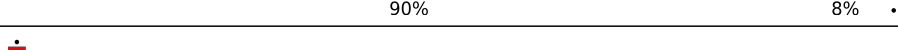
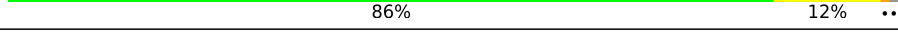
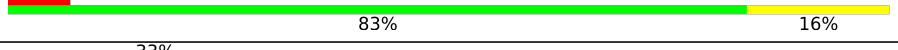
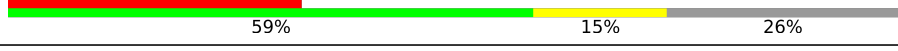
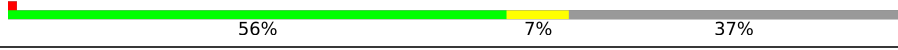
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14612 (2.73 - 3.73)

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% 43% 21% 31%
3	4	634	 20% 82% 16%

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Mol	Chain	Length	Quality of chain
4	5	120	
5	6	245	
6	7	163	
7	8	156	
8	9	134	
9	B	403	
10	C	159	
11	D	427	
12	E	115	
13	F	117	
14	G	266	
15	H	123	
16	I	192	
17	K	105	
18	L	148	
19	M	97	
20	N	178	
21	O	70	
22	P	51	
23	Q	211	
24	R	203	
25	S	215	
26	U	204	
27	V	203	
28	W	106	

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Mol	Chain	Length	Quality of chain
29	X	92	
30	Y	184	
31	Z	188	
32	a	196	
33	b	176	
34	c	160	
35	d	128	
36	e	140	
37	g	156	
38	h	145	
39	i	136	
40	j	125	
41	k	135	
42	l	137	
43	m	257	
44	n	110	
45	o	288	
46	p	248	
47	r	297	
48	z	129	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140545 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	3474	Total	C	N	O	P	0	0
			74611	33280	13653	24205	3473		

- Molecule 3 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	620	Total	C	N	O	S	0	0
			5093	3198	935	933	27		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 5 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	244	Total	C	N	O	S	0	0
			1852	1149	318	372	13		

- Molecule 6 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	135	Total	C	N	O	S	0	0
			1159	737	225	187	10		

- Molecule 7 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 8 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	86	Total	C	N	O	S	0	0
			711	433	154	121	3		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	402	Total	C	N	O	S	1	0
			3244	2065	609	556	14		

- Molecule 10 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	93	Total	C	N	O	S	0	0
			764	476	167	117	4		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 12 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 13 is a protein called 60S ribosomal protein L34.

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

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	241	Total	C	N	O	S	1	0
			1935	1233	374	324	4		

- Molecule 15 is a protein called 60S ribosomal protein L35.

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

- Molecule 16 is a protein called 60S ribosomal protein L9.

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

- Molecule 17 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 18 is a protein called 60S ribosomal protein L27a.

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

- Molecule 19 is a protein called 60S ribosomal protein L37.

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

- Molecule 20 is a protein called 60S ribosomal protein L11.

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

- Molecule 21 is a protein called 60S ribosomal protein L38.

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

- Molecule 22 is a protein called 60S ribosomal protein L39.

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

- Molecule 23 is a protein called 60S ribosomal protein L13.

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

- Molecule 24 is a protein called Translation machinery-associated protein 16.

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

- Molecule 25 is a protein called 60S ribosomal protein L14.

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

- Molecule 26 is a protein called 60S ribosomal protein L15.

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

- Molecule 27 is a protein called 60S ribosomal protein L13a.

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

- Molecule 28 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	101	Total	C	N	O	S	0	0
			827	517	170	134	6		

- Molecule 29 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 30 is a protein called 60S ribosomal protein L17.

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

- Molecule 31 is a protein called 60S ribosomal protein L18.

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

- Molecule 32 is a protein called 60S ribosomal protein L19.

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

- Molecule 33 is a protein called 60S ribosomal protein L18a.

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

- Molecule 34 is a protein called 60S ribosomal protein L21.

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

- Molecule 35 is a protein called 60S ribosomal protein L22.

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

- Molecule 36 is a protein called 60S ribosomal protein L23.

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

- Molecule 37 is a protein called 60S ribosomal protein L23a.

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

- Molecule 38 is a protein called 60S ribosomal protein L26.

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

- Molecule 39 is a protein called 60S ribosomal protein L27.

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

- Molecule 40 is a protein called 60S ribosomal protein L31.

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

- Molecule 41 is a protein called 60S ribosomal protein L32.

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

- Molecule 42 is a protein called 60S ribosomal protein L28.

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

- Molecule 43 is a protein called 60S ribosomal protein L8.

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

- Molecule 44 is a protein called 60S ribosomal protein L35a.

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

- Molecule 45 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	235	Total	C	N	O	S	0	0
			1897	1217	360	316	4		

- Molecule 46 is a protein called 60S ribosomal protein L7.

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

- Molecule 47 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 48 is a protein called Protein LLP homolog.

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

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	2	229	Total 229	Mg 229	0
49	4	1	Total 1	Mg 1	0
49	5	3	Total 3	Mg 3	0
49	8	5	Total 5	Mg 5	0
49	9	1	Total 1	Mg 1	0
49	B	2	Total 2	Mg 2	0
49	D	1	Total 1	Mg 1	0
49	F	1	Total 1	Mg 1	0
49	L	1	Total 1	Mg 1	0
49	M	1	Total 1	Mg 1	0
49	R	1	Total 1	Mg 1	0
49	k	1	Total 1	Mg 1	0
49	m	1	Total 1	Mg 1	0
49	n	1	Total 1	Mg 1	0
49	p	1	Total 1	Mg 1	0

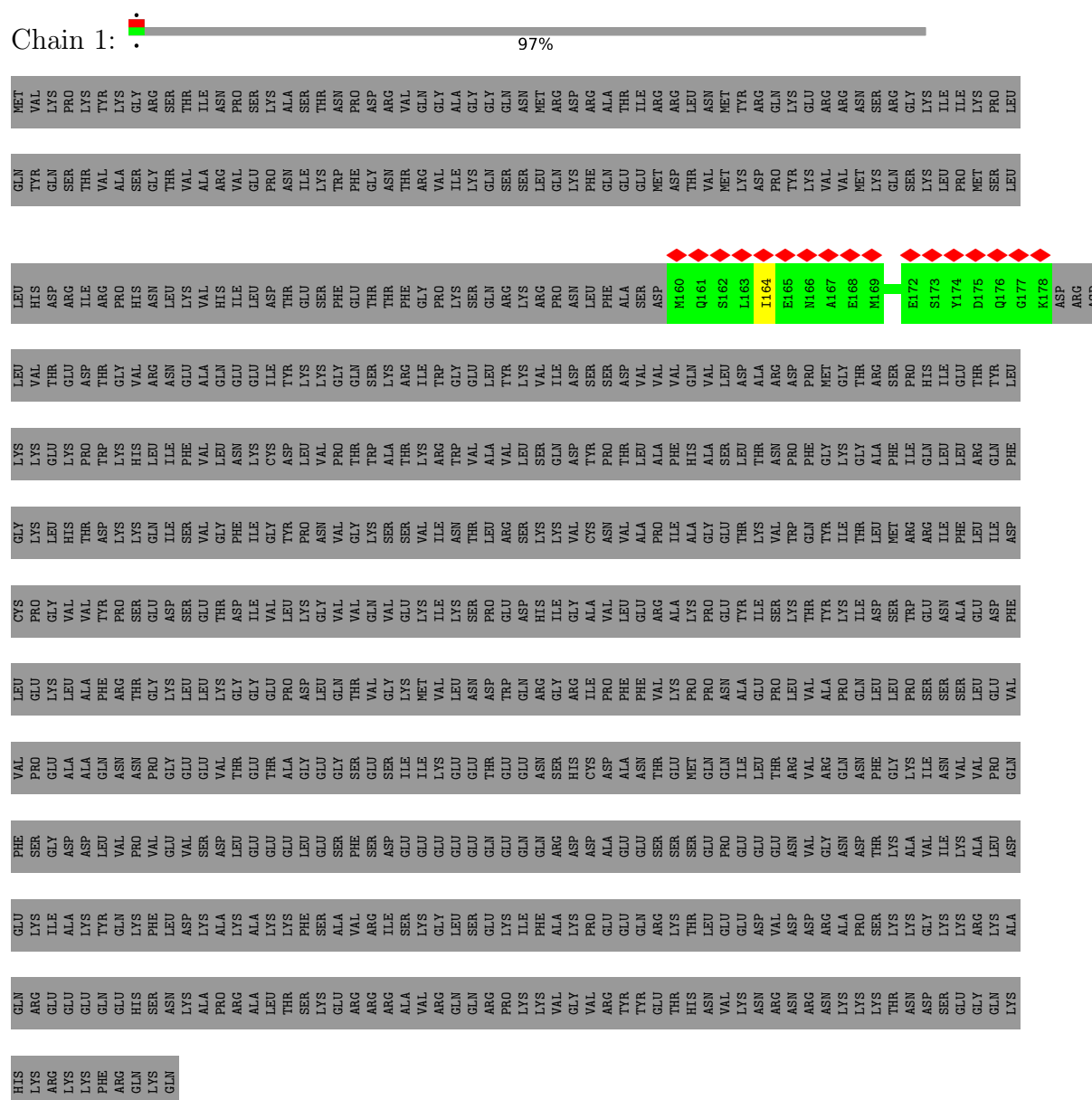
- Molecule 50 is water.

Mol	Chain	Residues	Atoms		AltConf
50	2	13	Total 13	O 13	0
50	k	1	Total 1	O 1	0
50	o	1	Total 1	O 1	0
50	p	1	Total 1	O 1	0

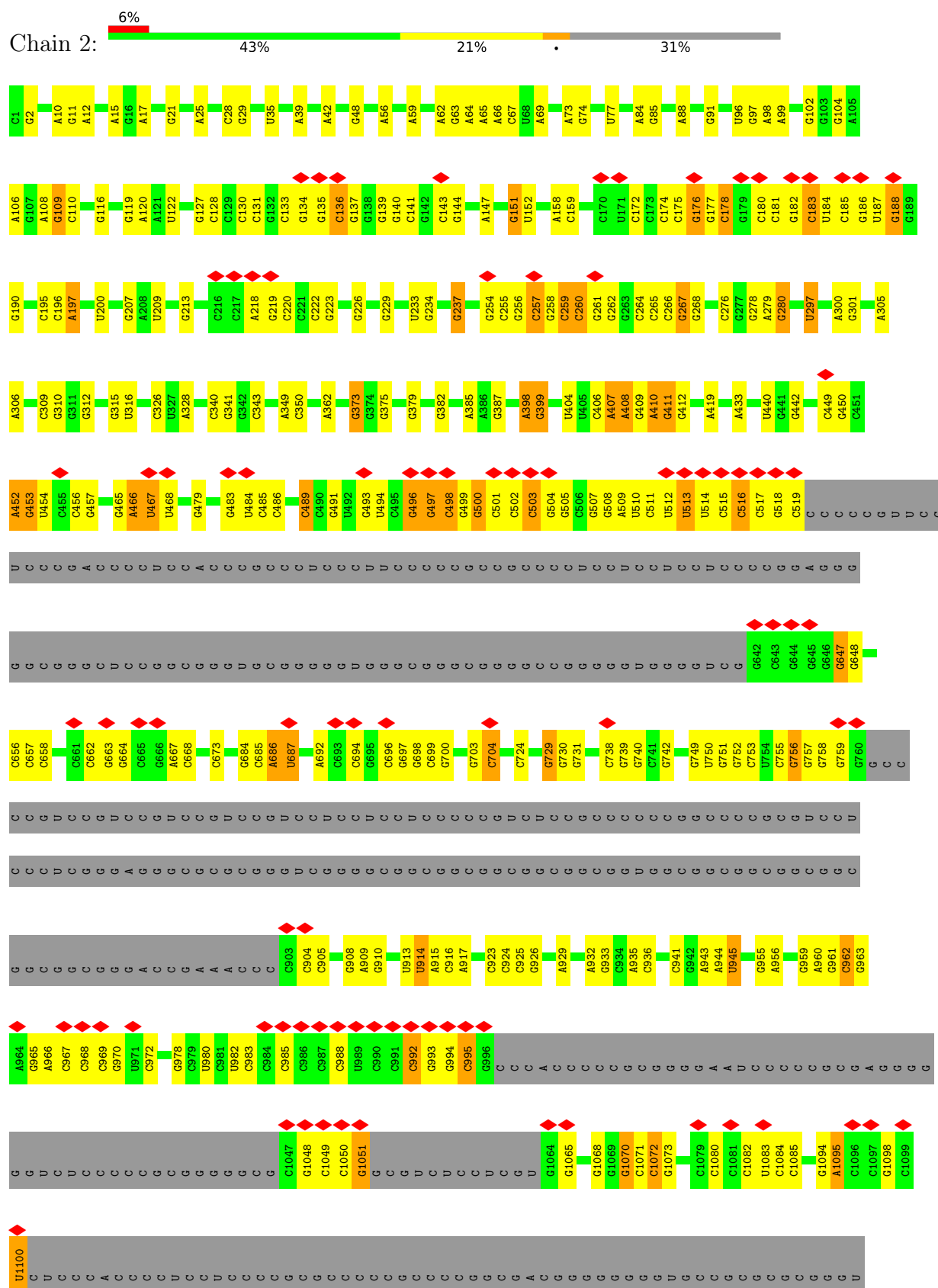
3 Residue-property plots

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

• Molecule 1: Nucleolar GTP-binding protein 2



• Molecule 2: 28S rRNA

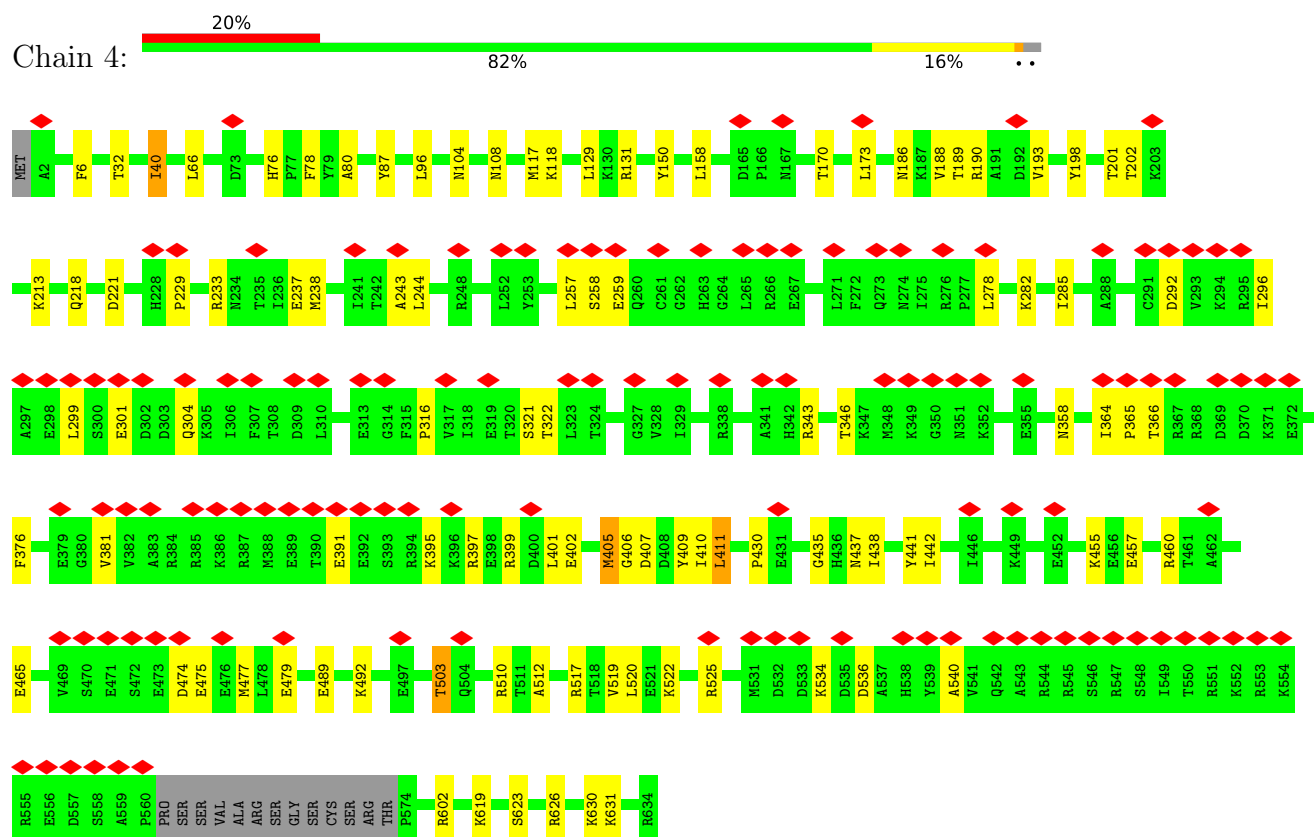




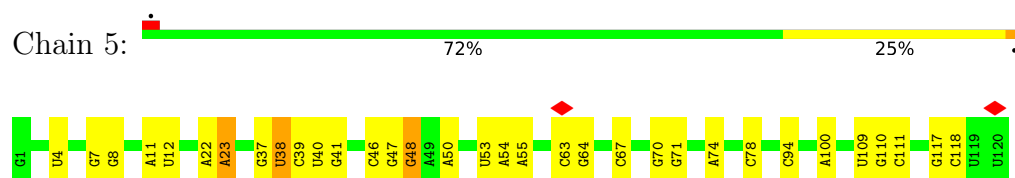




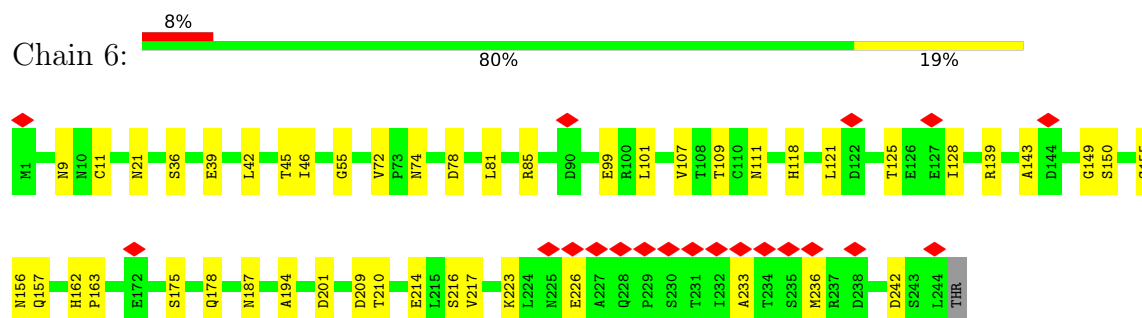
- Molecule 3: Nucleolar GTP-binding protein 1



- Molecule 4: 5S rRNA



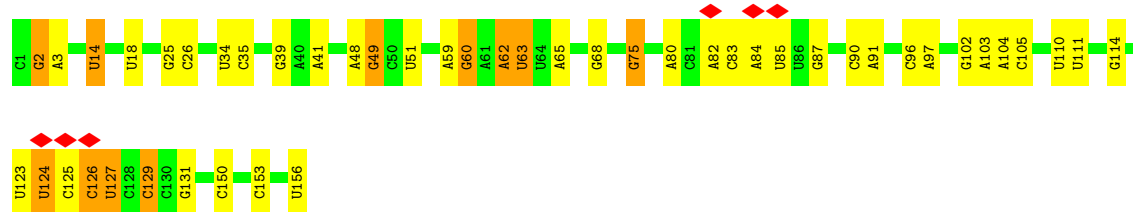
- Molecule 5: Eukaryotic translation initiation factor 6



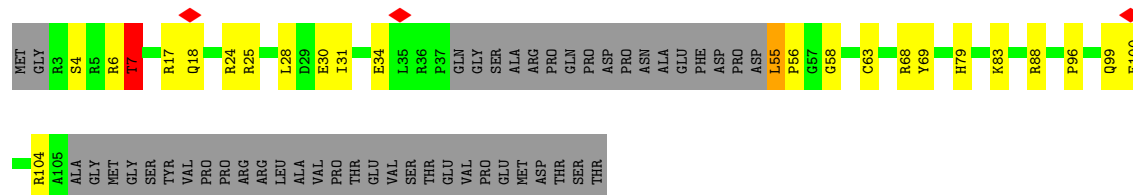
- Molecule 6: Probable ribosome biogenesis protein RLP24



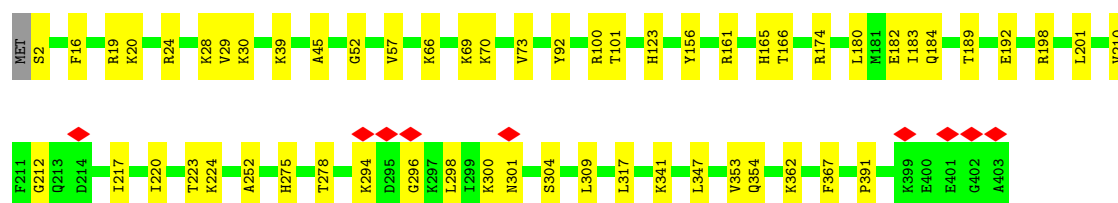
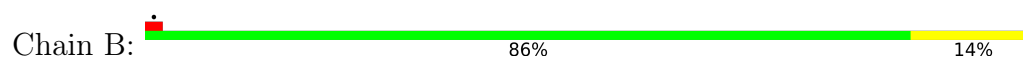
- Molecule 7: 28S rRNA



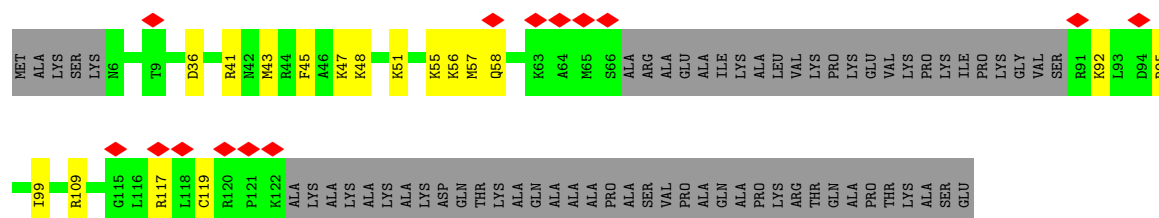
- Molecule 8: Zinc finger protein 593



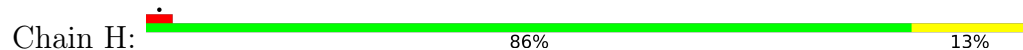
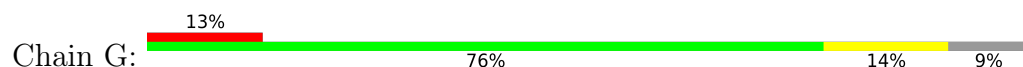
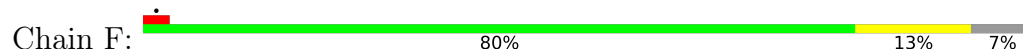
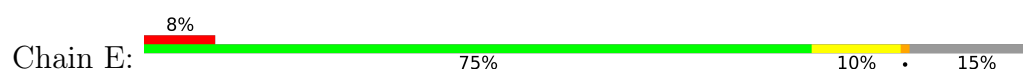
- Molecule 9: 60S ribosomal protein L3



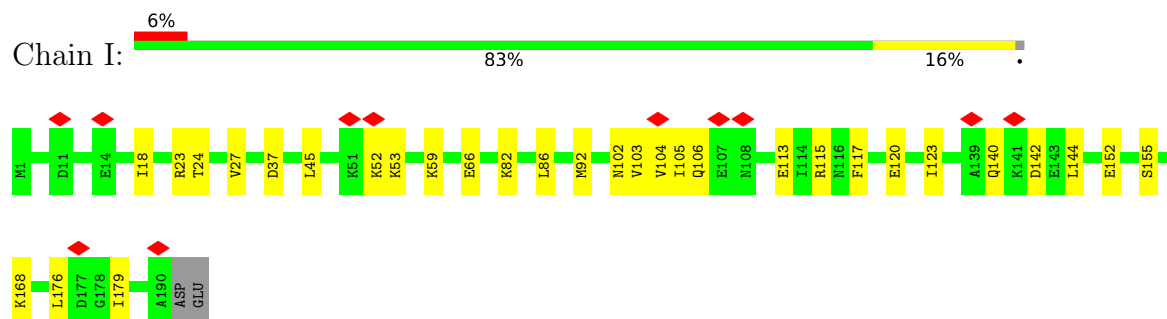
- Molecule 10: 60S ribosomal protein L29



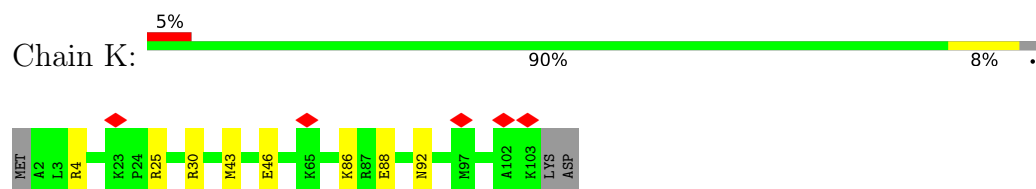
Chain D: 73% 11% 16%



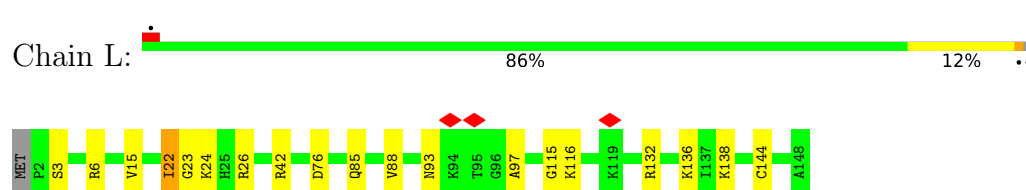
- Molecule 16: 60S ribosomal protein L9



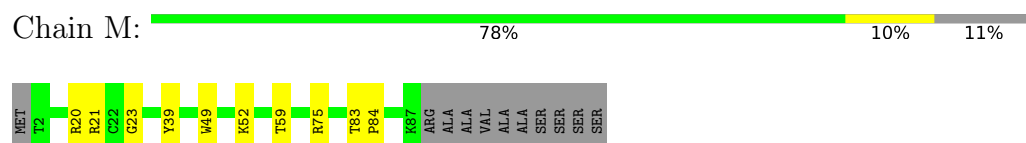
- Molecule 17: 60S ribosomal protein L36



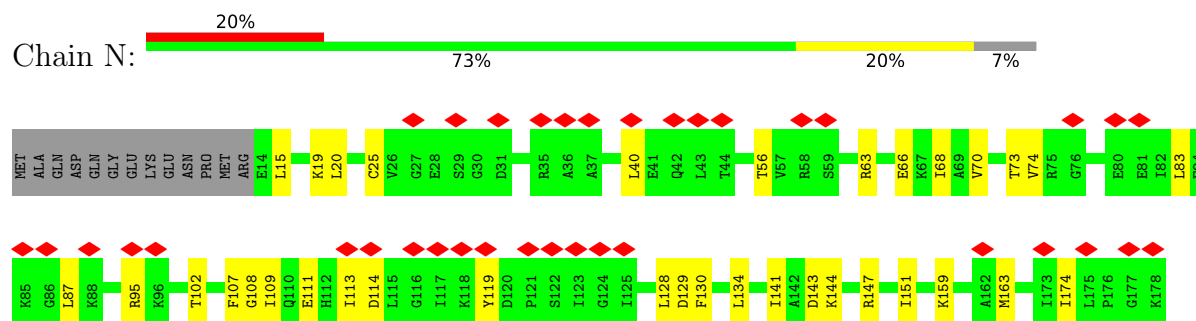
- Molecule 18: 60S ribosomal protein L27a



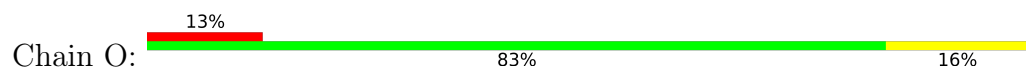
- Molecule 19: 60S ribosomal protein L37

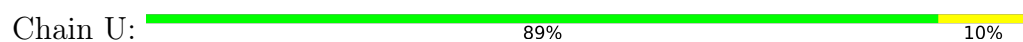


- Molecule 20: 60S ribosomal protein L11



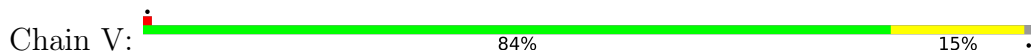
- Molecule 21: 60S ribosomal protein L38



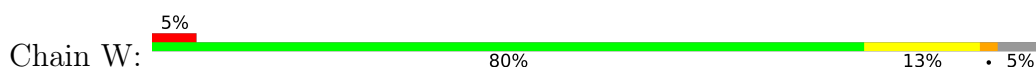




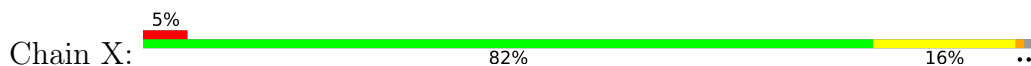
- Molecule 27: 60S ribosomal protein L13a



- Molecule 28: 60S ribosomal protein L36a



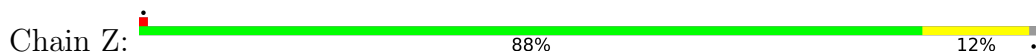
- Molecule 29: 60S ribosomal protein L37a



- Molecule 30: 60S ribosomal protein L17

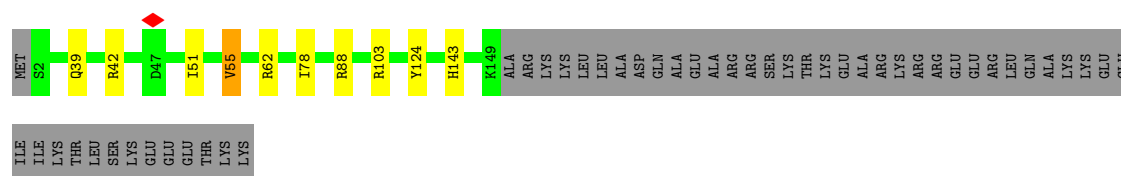


- Molecule 31: 60S ribosomal protein L18

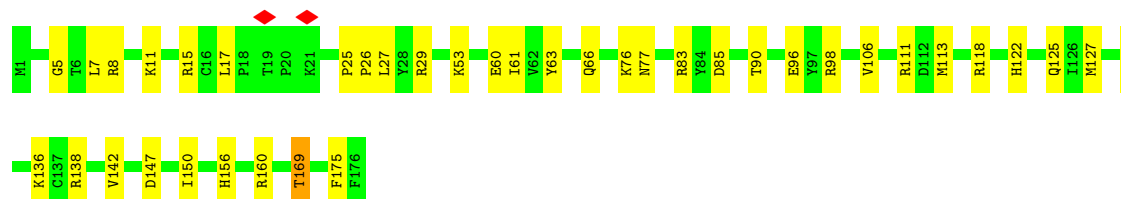
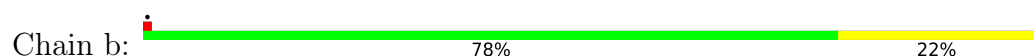


- Molecule 32: 60S ribosomal protein L19

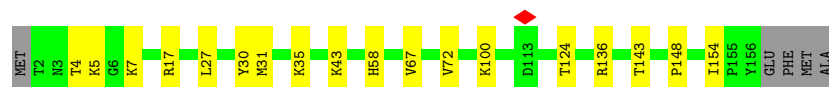
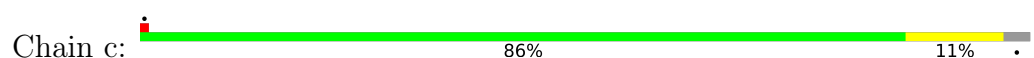




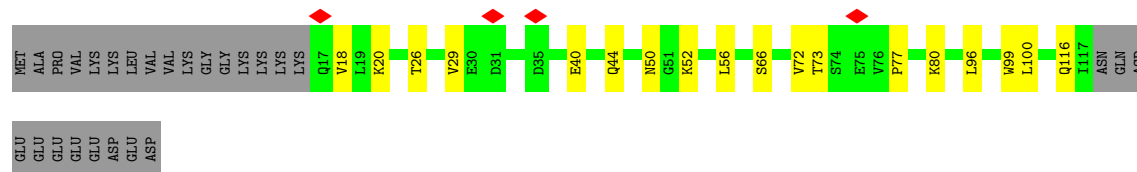
- Molecule 33: 60S ribosomal protein L18a



- Molecule 34: 60S ribosomal protein L21



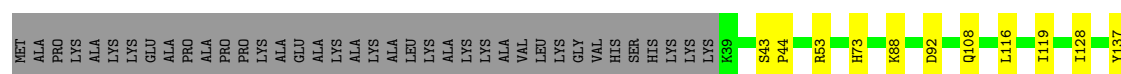
- Molecule 35: 60S ribosomal protein L22



- Molecule 36: 60S ribosomal protein L23

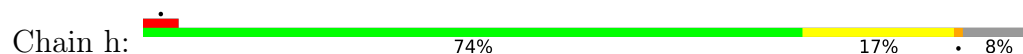


- Molecule 37: 60S ribosomal protein L23a

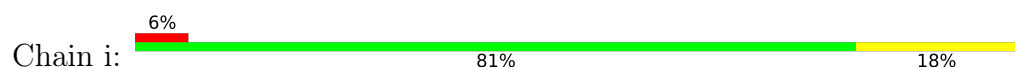




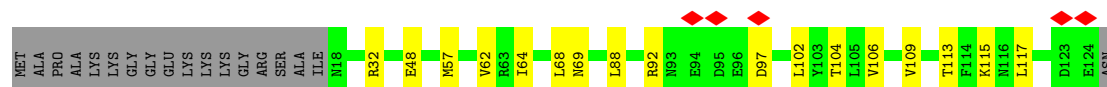
- Molecule 38: 60S ribosomal protein L26



- Molecule 39: 60S ribosomal protein L27



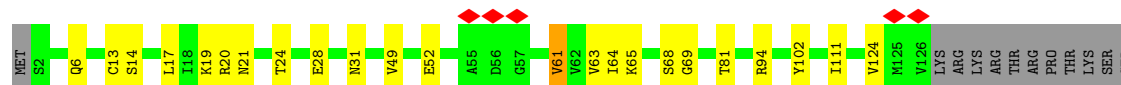
- Molecule 40: 60S ribosomal protein L31



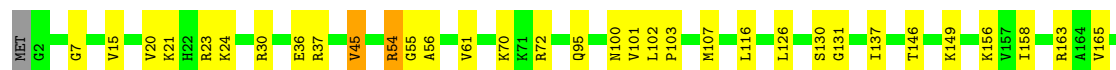
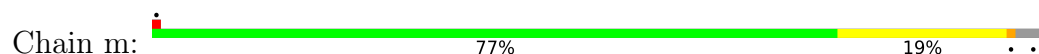
- Molecule 41: 60S ribosomal protein L32



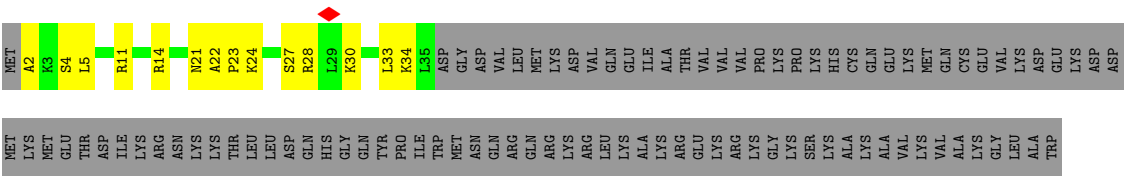
- Molecule 42: 60S ribosomal protein L28



- Molecule 43: 60S ribosomal protein L8



● Molecule 48: Protein LLP homolog



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10277	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	0.377	Depositor
Minimum map value	-0.158	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.065	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: 2MG, MHG, B8H, UR3, B9B, 7MG, OMU, BGH, B8K, E6G, P7G, E7G, 6MZ, A2M, B8T, 5MU, 5MC, OMG, I4U, OMC, PSU, M7A, MG, 1MA, B9H, P4U, B8Q, B8W

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	0.21	0/148	0.36	0/196
2	2	0.39	1/81090 (0.0%)	0.47	2/126417 (0.0%)
3	4	0.33	0/5177	0.75	8/6942 (0.1%)
4	5	0.35	0/2858	0.44	0/4455
5	6	0.36	0/1877	0.65	1/2554 (0.0%)
6	7	0.52	0/1181	0.88	5/1563 (0.3%)
7	8	0.42	0/3679	0.42	0/5732
8	9	0.38	0/723	0.79	3/961 (0.3%)
9	B	0.42	0/3315	0.65	0/4435
10	C	0.31	0/777	0.62	0/1026
11	D	0.44	0/2907	0.68	1/3905 (0.0%)
12	E	0.31	0/774	0.52	0/1038
13	F	0.41	0/878	0.63	0/1170
14	G	0.36	0/1971	0.64	0/2651
15	H	0.36	0/1023	0.55	0/1351
16	I	0.35	0/1537	0.64	0/2066
17	K	0.30	0/843	0.56	0/1115
18	L	0.44	0/1191	0.57	0/1591
19	M	0.45	0/720	0.65	0/952
20	N	0.31	0/1341	0.69	2/1793 (0.1%)
21	O	0.34	0/575	0.57	0/761
22	P	0.45	0/454	0.64	0/599
23	Q	0.39	0/1732	0.67	0/2315
24	R	0.28	0/1293	0.70	0/1725
25	S	0.36	0/1133	0.58	0/1516
26	U	0.44	0/1746	0.60	0/2338
27	V	0.41	0/1682	0.61	1/2250 (0.0%)
28	W	0.35	0/840	0.63	0/1107
29	X	0.39	0/718	0.58	0/953
30	Y	0.42	0/1268	0.62	1/1701 (0.1%)
31	Z	0.40	0/1537	0.61	0/2052

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	a	0.39	0/1255	0.60	1/1662 (0.1%)
33	b	0.39	0/1501	0.54	0/2013
34	c	0.37	0/1291	0.58	0/1725
35	d	0.36	0/839	0.72	0/1126
36	e	0.40	0/993	0.64	0/1332
37	g	0.36	0/984	0.52	0/1323
38	h	0.40	0/1132	0.65	0/1504
39	i	0.35	0/1130	0.60	0/1507
40	j	0.40	0/903	0.64	0/1216
41	k	0.46	0/1071	0.60	0/1429
42	l	0.40	0/1017	0.63	0/1364
43	m	0.43	0/1936	0.70	1/2596 (0.0%)
44	n	0.46	0/895	0.71	3/1198 (0.3%)
45	o	0.36	0/1935	0.66	1/2596 (0.0%)
46	p	0.41	0/1916	0.61	0/2553
47	r	0.32	0/2428	0.60	0/3252
48	z	0.41	0/286	0.59	0/372
All	All	0.39	1/148500 (0.0%)	0.54	30/217998 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	4	0	4
9	B	0	2
23	Q	0	1
24	R	0	1
43	m	0	1
44	n	0	1
45	o	0	1
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1534	A2M	O3'-P	5.38	1.61	1.56

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	n	106	TYR	N-CA-C	7.25	125.83	109.81
20	N	119	TYR	CA-C-N	7.16	139.68	122.36
20	N	119	TYR	C-N-CA	7.16	139.68	122.36
44	n	105	LEU	CA-C-N	7.00	138.89	121.80
44	n	105	LEU	C-N-CA	7.00	138.89	121.80

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	4	198	TYR	Peptide
3	4	365	PRO	Peptide
3	4	40	ILE	Peptide
3	4	503	THR	Peptide
9	B	16	PHE	Peptide

5.2 Too-close contacts

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	74611	0	37473	390	0
3	4	5093	0	5239	77	0
4	5	2558	0	1296	12	0
5	6	1852	0	1828	34	0
6	7	1159	0	1224	39	0
7	8	3315	0	1685	22	0
8	9	711	0	724	26	0
9	B	3244	0	3389	54	0
10	C	764	0	822	12	0
11	D	2853	0	3028	36	0
12	E	764	0	804	6	0
13	F	868	0	963	13	0
14	G	1935	0	2087	24	0
15	H	1015	0	1148	16	0
16	I	1518	0	1601	21	0
17	K	832	0	917	7	0
18	L	1162	0	1213	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	M	705	0	741	8	0
20	N	1319	0	1358	23	0
21	O	569	0	637	6	0
22	P	444	0	483	11	0
23	Q	1701	0	1818	23	0
24	R	1272	0	1291	21	0
25	S	1111	0	1174	10	0
26	U	1701	0	1749	19	0
27	V	1650	0	1794	21	0
28	W	827	0	895	13	0
29	X	708	0	760	11	0
30	Y	1242	0	1268	16	0
31	Z	1513	0	1628	13	0
32	a	1239	0	1362	8	0
33	b	1461	0	1502	32	0
34	c	1264	0	1337	17	0
35	d	825	0	850	12	0
36	e	979	0	1039	17	0
37	g	967	0	1040	11	0
38	h	1115	0	1205	17	0
39	i	1107	0	1182	16	0
40	j	888	0	930	8	0
41	k	1053	0	1147	7	0
42	l	1002	0	1068	14	0
43	m	1898	0	1993	33	0
44	n	876	0	912	7	0
45	o	1897	0	2046	39	0
46	p	1878	0	2009	18	0
47	r	2382	0	2410	32	0
48	z	284	0	333	30	0
49	2	229	0	0	0	0
49	4	1	0	0	0	0
49	5	3	0	0	0	0
49	8	5	0	0	0	0
49	9	1	0	0	0	0
49	B	2	0	0	0	0
49	D	1	0	0	0	0
49	F	1	0	0	0	0
49	L	1	0	0	0	0
49	M	1	0	0	0	0
49	R	1	0	0	0	0
49	k	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	m	1	0	0	0	0
49	n	1	0	0	0	0
49	p	1	0	0	0	0
50	2	13	0	0	0	0
50	k	1	0	0	0	0
50	o	1	0	0	0	0
50	p	1	0	0	0	0
All	All	140545	0	103537	1029	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 4.

The worst 5 of 1029 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	1.59
2:2:4296:B8H:C5	2:2:4296:B8H:C4	1.80	1.55
9:B:39:LYS:HE2	48:z:30:LYS:NZ	1.50	1.24
2:2:2380:B8W:O4'	2:2:2380:B8W:C1'	1.65	1.23
2:2:4690:B8K:O4'	2:2:4690:B8K:C4'	1.67	1.20

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	4	616/634 (97%)	535 (87%)	78 (13%)	3 (0%)	24	56
5	6	242/245 (99%)	224 (93%)	18 (7%)	0	100	100
6	7	133/163 (82%)	124 (93%)	7 (5%)	2 (2%)	8	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	9	82/134 (61%)	71 (87%)	10 (12%)	1 (1%)	10	38
9	B	401/403 (100%)	368 (92%)	33 (8%)	0	100	100
10	C	89/159 (56%)	85 (96%)	4 (4%)	0	100	100
11	D	356/427 (83%)	330 (93%)	26 (7%)	0	100	100
12	E	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
13	F	107/117 (92%)	105 (98%)	2 (2%)	0	100	100
14	G	240/266 (90%)	221 (92%)	19 (8%)	0	100	100
15	H	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
16	I	188/192 (98%)	167 (89%)	21 (11%)	0	100	100
17	K	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
18	L	145/148 (98%)	134 (92%)	10 (7%)	1 (1%)	18	50
19	M	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
20	N	163/178 (92%)	144 (88%)	19 (12%)	0	100	100
21	O	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
22	P	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
23	Q	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
24	R	148/203 (73%)	137 (93%)	11 (7%)	0	100	100
25	S	133/215 (62%)	122 (92%)	11 (8%)	0	100	100
26	U	201/204 (98%)	189 (94%)	11 (6%)	1 (0%)	24	56
27	V	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
28	W	99/106 (93%)	89 (90%)	10 (10%)	0	100	100
29	X	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
30	Y	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
31	Z	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
32	a	146/196 (74%)	138 (94%)	8 (6%)	0	100	100
33	b	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
34	c	153/160 (96%)	144 (94%)	9 (6%)	0	100	100
35	d	99/128 (77%)	88 (89%)	11 (11%)	0	100	100
36	e	129/140 (92%)	118 (92%)	11 (8%)	0	100	100
37	g	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
38	h	132/145 (91%)	130 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	i	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
40	j	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
41	k	126/135 (93%)	115 (91%)	11 (9%)	0	100	100
42	l	123/137 (90%)	111 (90%)	12 (10%)	0	100	100
43	m	246/257 (96%)	216 (88%)	29 (12%)	1 (0%)	30	60
44	n	107/110 (97%)	97 (91%)	8 (8%)	2 (2%)	6	30
45	o	231/288 (80%)	210 (91%)	21 (9%)	0	100	100
46	p	224/248 (90%)	210 (94%)	14 (6%)	0	100	100
47	r	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
48	z	32/129 (25%)	30 (94%)	2 (6%)	0	100	100
All	All	7274/8927 (82%)	6701 (92%)	562 (8%)	11 (0%)	44	72

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	7	66	ASP
6	7	70	GLU
44	n	106	TYR
3	4	301	GLU
8	9	99	GLN

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
3	4	562/574 (98%)	557 (99%)	5 (1%)	70	79
5	6	212/213 (100%)	212 (100%)	0	100	100
6	7	126/149 (85%)	122 (97%)	4 (3%)	34	62
8	9	74/114 (65%)	72 (97%)	2 (3%)	39	65
9	B	349/349 (100%)	348 (100%)	1 (0%)	86	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	C	78/126 (62%)	78 (100%)	0	100	100
11	D	298/348 (86%)	295 (99%)	3 (1%)	68	78
12	E	83/97 (86%)	81 (98%)	2 (2%)	43	67
13	F	94/100 (94%)	94 (100%)	0	100	100
14	G	204/223 (92%)	204 (100%)	0	100	100
15	H	109/110 (99%)	108 (99%)	1 (1%)	70	79
16	I	169/171 (99%)	167 (99%)	2 (1%)	63	76
17	K	86/89 (97%)	86 (100%)	0	100	100
18	L	120/121 (99%)	119 (99%)	1 (1%)	73	80
19	M	73/80 (91%)	73 (100%)	0	100	100
20	N	138/149 (93%)	137 (99%)	1 (1%)	76	81
21	O	64/65 (98%)	64 (100%)	0	100	100
22	P	47/48 (98%)	47 (100%)	0	100	100
23	Q	176/177 (99%)	174 (99%)	2 (1%)	65	77
24	R	138/184 (75%)	138 (100%)	0	100	100
25	S	115/161 (71%)	114 (99%)	1 (1%)	70	79
26	U	171/172 (99%)	170 (99%)	1 (1%)	78	83
27	V	173/174 (99%)	172 (99%)	1 (1%)	78	83
28	W	89/94 (95%)	87 (98%)	2 (2%)	45	68
29	X	74/75 (99%)	72 (97%)	2 (3%)	39	65
30	Y	134/163 (82%)	133 (99%)	1 (1%)	76	81
31	Z	164/165 (99%)	164 (100%)	0	100	100
32	a	133/175 (76%)	132 (99%)	1 (1%)	73	80
33	b	157/157 (100%)	156 (99%)	1 (1%)	78	83
34	c	136/140 (97%)	135 (99%)	1 (1%)	76	81
35	d	91/115 (79%)	90 (99%)	1 (1%)	65	77
36	e	101/107 (94%)	100 (99%)	1 (1%)	68	78
37	g	106/133 (80%)	105 (99%)	1 (1%)	70	79
38	h	124/135 (92%)	121 (98%)	3 (2%)	43	67
39	i	117/118 (99%)	116 (99%)	1 (1%)	70	79
40	j	98/110 (89%)	94 (96%)	4 (4%)	27	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	k	114/121 (94%)	114 (100%)	0	100	100
42	l	109/121 (90%)	106 (97%)	3 (3%)	38	64
43	m	190/199 (96%)	189 (100%)	1 (0%)	81	84
44	n	88/89 (99%)	87 (99%)	1 (1%)	65	77
45	o	208/252 (82%)	207 (100%)	1 (0%)	81	84
46	p	195/215 (91%)	195 (100%)	0	100	100
47	r	246/250 (98%)	245 (100%)	1 (0%)	84	85
48	z	30/115 (26%)	30 (100%)	0	100	100
All	All	6380/7697 (83%)	6327 (99%)	53 (1%)	70	80

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	W	23	VAL
35	d	72	VAL
43	m	45	VAL
29	X	59	SER
32	a	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
24	R	91	GLN
43	m	187	HIS
30	Y	21	ASN
43	m	132	ASN
47	r	244	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	2	3455/5070 (68%)	899 (26%)	18 (0%)
4	5	119/120 (99%)	20 (16%)	0
7	8	155/156 (99%)	32 (20%)	0
All	All	3729/5346 (69%)	951 (25%)	18 (0%)

5 of 951 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	2	2	G
2	2	15	A
2	2	17	A
2	2	21	G
2	2	25	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	4529	B8W
2	2	4913	G
2	2	4694	G
2	2	3596	A
2	2	4498	U

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	PSU	2	1683	2	18,21,22	1.13	2 (11%)	22,30,33	1.80	4 (18%)
2	OMC	2	2804	2	19,22,23	2.74	7 (36%)	26,31,34	0.99	1 (3%)
2	B9B	2	1574	2	25,28,29	3.49	12 (48%)	35,40,43	2.22	15 (42%)
2	B8W	2	2380	2	23,26,27	3.72	11 (47%)	33,38,41	2.46	15 (45%)
2	PSU	2	1677	2	18,21,22	1.13	2 (11%)	22,30,33	1.95	5 (22%)
2	OMG	2	2773	2	23,26,27	2.27	9 (39%)	33,38,41	1.88	9 (27%)
2	B9H	2	2786	2,49	20,25,26	2.73	5 (25%)	22,35,38	2.13	6 (27%)
2	OMG	2	2050	2	23,26,27	2.28	7 (30%)	33,38,41	1.89	7 (21%)
2	1MA	2	1322	2,49	21,25,26	2.79	5 (23%)	31,37,40	1.76	7 (22%)
7	OMU	8	14	2,7	19,22,23	2.73	7 (36%)	26,31,34	1.75	6 (23%)
2	UR3	2	4530	2	19,22,23	2.77	5 (26%)	26,32,35	1.31	2 (7%)
2	P7G	2	3880	2	24,28,29	4.73	11 (45%)	27,41,44	1.80	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	E7G	2	1797	2	24,27,28	3.78	11 (45%)	30,40,43	2.18	9 (30%)
2	B8H	2	4296	2	19,22,23	6.78	7 (36%)	22,32,35	2.29	5 (22%)
2	OMG	2	4637	2	23,26,27	2.30	8 (34%)	33,38,41	1.94	9 (27%)
2	OMG	2	4623	2	23,26,27	2.27	7 (30%)	33,38,41	1.75	8 (24%)
2	OMC	2	2861	2	19,22,23	2.84	7 (36%)	26,31,34	0.95	1 (3%)
2	OMG	2	1522	2	23,26,27	2.28	9 (39%)	33,38,41	1.79	7 (21%)
2	2MG	2	978	2	23,26,27	2.74	8 (34%)	32,38,41	2.25	10 (31%)
2	OMU	2	4306	2	19,22,23	2.78	8 (42%)	26,31,34	1.89	5 (19%)
2	B8T	2	4483	2	19,22,23	3.52	8 (42%)	26,31,34	1.26	4 (15%)
2	PSU	2	4628	2	18,21,22	1.04	1 (5%)	22,30,33	1.75	4 (18%)
2	7MG	2	4550	2	22,26,27	3.57	10 (45%)	29,39,42	1.97	9 (31%)
2	A2M	2	3867	2	22,25,26	3.52	9 (40%)	31,36,39	2.68	12 (38%)
2	PSU	2	4636	2	18,21,22	1.14	3 (16%)	22,30,33	1.88	4 (18%)
2	OMG	2	4370	2	23,26,27	2.30	9 (39%)	33,38,41	1.80	9 (27%)
2	MHG	2	4371	2	29,32,33	3.92	12 (41%)	34,46,49	2.25	11 (32%)
2	B8W	2	4472	2	23,26,27	3.67	9 (39%)	33,38,41	2.53	10 (30%)
2	7MG	2	2522	2	22,26,27	3.38	10 (45%)	29,39,42	1.98	9 (31%)
2	1MA	2	4415	2	21,25,26	2.86	5 (23%)	31,37,40	1.81	6 (19%)
2	PSU	2	4403	2	18,21,22	1.02	1 (5%)	22,30,33	1.84	5 (22%)
2	B8W	2	4529	2	23,26,27	3.79	8 (34%)	33,38,41	2.70	13 (39%)
2	OMG	2	373	2	23,26,27	2.26	8 (34%)	33,38,41	1.98	9 (27%)
2	P7G	2	1909	2	24,28,29	4.57	11 (45%)	27,41,44	1.68	4 (14%)
2	B9B	2	237	2	25,28,29	3.49	12 (48%)	35,40,43	2.46	11 (31%)
2	I4U	2	1659	2,49	21,24,25	4.70	14 (66%)	27,34,37	1.56	6 (22%)
2	A2M	2	1871	2	22,25,26	3.41	10 (45%)	31,36,39	2.58	10 (32%)
2	OMG	2	2364	2	23,26,27	2.29	7 (30%)	33,38,41	1.91	9 (27%)
2	BGH	2	3899	2	25,29,30	4.40	17 (68%)	31,43,46	2.56	12 (38%)
2	A2M	2	398	2	22,25,26	3.44	9 (40%)	31,36,39	2.43	8 (25%)
2	5MU	2	4083	2	19,22,23	4.69	7 (36%)	28,32,35	3.63	10 (35%)
2	B8K	2	4690	2	24,28,29	4.45	16 (66%)	30,42,45	2.65	11 (36%)
2	A2M	2	2363	2,49	22,25,26	3.56	10 (45%)	31,36,39	2.64	9 (29%)
2	5MC	2	4335	2	18,22,23	3.40	7 (38%)	26,32,35	1.24	2 (7%)
2	2MG	2	729	2	23,26,27	2.66	7 (30%)	32,38,41	2.24	8 (25%)
2	OMG	2	4494	2	23,26,27	2.31	9 (39%)	33,38,41	1.86	7 (21%)
2	UR3	2	4597	2	19,22,23	2.69	7 (36%)	26,32,35	1.87	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	B8Q	2	1456	2	17,22,23	2.91	4 (23%)	22,32,35	2.23	6 (27%)
2	B9B	2	2754	2	25,28,29	3.44	11 (44%)	35,40,43	2.23	12 (34%)
2	OMG	2	4870	2	23,26,27	2.34	9 (39%)	33,38,41	1.83	9 (27%)
2	A2M	2	1524	2	22,25,26	3.44	9 (40%)	31,36,39	2.71	12 (38%)
2	B8K	2	3897	2	24,28,29	4.36	15 (62%)	30,42,45	2.49	13 (43%)
2	PSU	2	1582	2	18,21,22	1.04	1 (5%)	22,30,33	1.65	3 (13%)
2	B8W	2	4129	2	23,26,27	3.77	7 (30%)	33,38,41	2.67	14 (42%)
2	M7A	2	4564	2	20,25,26	1.96	3 (15%)	28,37,40	3.82	7 (25%)
2	PSU	2	4293	2	18,21,22	1.01	1 (5%)	22,30,33	1.96	4 (18%)
2	A2M	2	4523	2	22,25,26	3.47	10 (45%)	31,36,39	2.58	12 (38%)
2	A2M	2	1534	2,49	22,25,26	3.42	9 (40%)	31,36,39	2.74	12 (38%)
2	6MZ	2	4220	2	22,25,26	2.62	4 (18%)	30,36,39	3.34	10 (33%)
2	OMC	2	3887	2	19,22,23	2.91	8 (42%)	26,31,34	0.96	0
2	OMC	2	2365	2,49	19,22,23	2.75	8 (42%)	26,31,34	0.77	0
2	A2M	2	3723	2	22,25,26	3.49	9 (40%)	31,36,39	2.52	9 (29%)
2	OMC	2	3701	2,49	19,22,23	2.82	8 (42%)	26,31,34	0.64	0
2	B8H	2	1860	2	19,22,23	6.76	6 (31%)	22,32,35	2.29	5 (22%)
2	B8W	2	4185	2	23,26,27	3.71	9 (39%)	33,38,41	2.51	14 (42%)
2	PSU	2	2508	2	18,21,22	1.00	1 (5%)	22,30,33	1.69	3 (13%)
2	OMC	2	2422	2,49	19,22,23	2.89	8 (42%)	26,31,34	1.06	2 (7%)
2	7MG	2	1605	2	22,26,27	3.38	10 (45%)	29,39,42	1.94	9 (31%)
2	OMG	2	1883	2	23,26,27	2.28	7 (30%)	33,38,41	1.93	7 (21%)
2	UR3	2	1866	2	19,22,23	2.88	6 (31%)	26,32,35	1.30	2 (7%)
2	2MG	2	4872	2	23,26,27	2.75	7 (30%)	32,38,41	2.25	8 (25%)
2	E7G	2	2297	2	24,27,28	3.65	11 (45%)	30,40,43	2.19	10 (33%)
2	A2M	2	1326	2,49	22,25,26	3.52	9 (40%)	31,36,39	2.57	10 (32%)
2	OMG	2	4196	2	23,26,27	2.37	8 (34%)	33,38,41	1.90	9 (27%)
2	P4U	2	1348	2	21,24,25	3.74	8 (38%)	27,33,36	1.17	2 (7%)
2	B8T	2	4671	2	19,22,23	3.43	8 (42%)	26,31,34	0.90	1 (3%)
2	OMG	2	2424	2	23,26,27	2.36	9 (39%)	33,38,41	1.86	8 (24%)
2	OMC	2	3869	2	19,22,23	2.84	8 (42%)	26,31,34	1.39	3 (11%)
2	OMG	2	1316	2,49	23,26,27	2.37	9 (39%)	33,38,41	2.06	10 (30%)
2	PSU	2	3715	2	18,21,22	1.08	1 (5%)	22,30,33	1.67	4 (18%)
2	A2M	2	2401	2	22,25,26	3.52	10 (45%)	31,36,39	2.66	9 (29%)
2	A2M	2	3718	2	22,25,26	3.51	9 (40%)	31,36,39	2.43	10 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMC	2	4536	2	19,22,23	2.75	7 (36%)	26,31,34	0.92	1 (3%)
2	PSU	2	3729	2	18,21,22	1.07	1 (5%)	22,30,33	1.69	4 (18%)
2	A2M	2	3825	2	22,25,26	3.51	10 (45%)	31,36,39	2.47	10 (32%)
2	A2M	2	4571	2	22,25,26	3.54	10 (45%)	31,36,39	2.49	8 (25%)
2	OMG	2	1625	2	23,26,27	2.27	8 (34%)	33,38,41	1.99	10 (30%)
2	2MG	2	1517	2	23,26,27	2.65	8 (34%)	32,38,41	2.46	8 (25%)
2	OMC	2	3909	2	19,22,23	2.91	8 (42%)	26,31,34	1.10	2 (7%)
2	OMU	2	4620	2	19,22,23	2.72	7 (36%)	26,31,34	1.72	5 (19%)
2	E6G	2	4355	2	24,27,28	3.56	12 (50%)	34,39,42	2.52	13 (38%)
2	I4U	2	4194	2,49	21,24,25	4.89	15 (71%)	27,34,37	1.07	1 (3%)

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	PSU	2	1683	2	-	0/7/25/26	0/2/2/2
2	OMC	2	2804	2	-	0/9/27/28	0/2/2/2
2	B9B	2	1574	2	-	3/11/29/30	0/3/3/3
2	B8W	2	2380	2	-	0/9/27/28	0/3/3/3
2	PSU	2	1677	2	-	1/7/25/26	0/2/2/2
2	OMG	2	2773	2	-	2/9/27/28	0/3/3/3
2	B9H	2	2786	2,49	-	1/12/47/48	0/2/2/2
2	OMG	2	2050	2	-	0/9/27/28	0/3/3/3
2	1MA	2	1322	2,49	-	2/7/25/26	0/3/3/3
7	OMU	8	14	2,7	-	1/9/27/28	0/2/2/2
2	UR3	2	4530	2	-	0/7/25/26	0/2/2/2
2	P7G	2	3880	2	-	4/10/40/41	0/3/3/3
2	E7G	2	1797	2	-	4/9/39/40	0/3/3/3
2	B8H	2	4296	2	-	0/7/25/26	0/2/2/2
2	OMG	2	4637	2	-	0/9/27/28	0/3/3/3
2	OMG	2	4623	2	-	0/9/27/28	0/3/3/3
2	OMC	2	2861	2	-	2/9/27/28	0/2/2/2
2	OMG	2	1522	2	-	0/9/27/28	0/3/3/3
2	2MG	2	978	2	-	0/9/27/28	0/3/3/3
2	OMU	2	4306	2	-	0/9/27/28	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7MG	2	4550	2	-	2/7/37/38	0/3/3/3
2	A2M	2	3867	2	-	4/9/27/28	0/3/3/3
2	PSU	2	4636	2	-	4/7/25/26	0/2/2/2
2	OMG	2	4370	2	-	0/9/27/28	0/3/3/3
2	MHG	2	4371	2	-	9/16/46/47	0/3/3/3
2	B8W	2	4472	2	-	2/9/27/28	0/3/3/3
2	7MG	2	2522	2	-	0/7/37/38	0/3/3/3
2	1MA	2	4415	2	-	3/7/25/26	0/3/3/3
2	PSU	2	4403	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4529	2	-	3/9/27/28	0/3/3/3
2	OMG	2	373	2	-	1/9/27/28	0/3/3/3
2	P7G	2	1909	2	-	2/10/40/41	0/3/3/3
2	B9B	2	237	2	-	5/11/29/30	0/3/3/3
2	I4U	2	1659	2,49	-	2/9/29/30	0/2/2/2
2	A2M	2	1871	2	-	2/9/27/28	0/3/3/3
2	OMG	2	2364	2	-	2/9/27/28	0/3/3/3
2	BGH	2	3899	2	-	1/13/43/44	0/3/3/3
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	B8K	2	4690	2	-	0/11/41/42	0/3/3/3
2	A2M	2	2363	2,49	-	0/9/27/28	0/3/3/3
2	5MC	2	4335	2	-	0/7/25/26	0/2/2/2
2	2MG	2	729	2	-	1/9/27/28	0/3/3/3
2	OMG	2	4494	2	-	0/9/27/28	0/3/3/3
2	UR3	2	4597	2	-	0/7/25/26	0/2/2/2
2	B8Q	2	1456	2	-	1/7/42/43	0/2/2/2
2	B9B	2	2754	2	-	2/11/29/30	0/3/3/3
2	OMG	2	4870	2	-	3/9/27/28	0/3/3/3
2	A2M	2	1524	2	-	1/9/27/28	0/3/3/3
2	B8K	2	3897	2	-	3/11/41/42	0/3/3/3
2	PSU	2	1582	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4129	2	-	2/9/27/28	0/3/3/3
2	M7A	2	4564	2	-	0/7/37/38	0/3/3/3
2	PSU	2	4293	2	-	2/7/25/26	0/2/2/2
2	A2M	2	4523	2	-	2/9/27/28	0/3/3/3
2	A2M	2	1534	2,49	-	3/9/27/28	0/3/3/3
2	6MZ	2	4220	2	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	2	3887	2	-	1/9/27/28	0/2/2/2
2	OMC	2	2365	2,49	-	0/9/27/28	0/2/2/2
2	A2M	2	3723	2	-	0/9/27/28	0/3/3/3
2	OMC	2	3701	2,49	-	4/9/27/28	0/2/2/2
2	B8H	2	1860	2	-	2/7/25/26	0/2/2/2
2	B8W	2	4185	2	-	2/9/27/28	0/3/3/3
2	PSU	2	2508	2	-	1/7/25/26	0/2/2/2
2	OMC	2	2422	2,49	-	1/9/27/28	0/2/2/2
2	7MG	2	1605	2	-	0/7/37/38	0/3/3/3
2	OMG	2	1883	2	-	2/9/27/28	0/3/3/3
2	UR3	2	1866	2	-	1/7/25/26	0/2/2/2
2	2MG	2	4872	2	-	2/9/27/28	0/3/3/3
2	E7G	2	2297	2	-	2/9/39/40	0/3/3/3
2	A2M	2	1326	2,49	-	1/9/27/28	0/3/3/3
2	OMG	2	4196	2	-	0/9/27/28	0/3/3/3
2	P4U	2	1348	2	-	1/10/29/30	0/2/2/2
2	B8T	2	4671	2	-	2/7/27/28	0/2/2/2
2	OMG	2	2424	2	-	2/9/27/28	0/3/3/3
2	OMC	2	3869	2	-	4/9/27/28	0/2/2/2
2	OMG	2	1316	2,49	-	0/9/27/28	0/3/3/3
2	PSU	2	3715	2	-	0/7/25/26	0/2/2/2
2	A2M	2	2401	2	-	0/9/27/28	0/3/3/3
2	A2M	2	3718	2	-	0/9/27/28	0/3/3/3
2	OMC	2	4536	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	3825	2	-	0/9/27/28	0/3/3/3
2	A2M	2	4571	2	-	0/9/27/28	0/3/3/3
2	OMG	2	1625	2	-	2/9/27/28	0/3/3/3
2	2MG	2	1517	2	-	0/9/27/28	0/3/3/3
2	OMC	2	3909	2	-	2/9/27/28	0/2/2/2
2	OMU	2	4620	2	-	0/9/27/28	0/2/2/2
2	E6G	2	4355	2	-	2/10/28/29	0/3/3/3
2	I4U	2	4194	2,49	-	5/9/29/30	0/2/2/2

The worst 5 of 730 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4296	B8H	C6-C5	-16.73	1.11	1.34
2	2	1860	B8H	C6-C5	-16.52	1.11	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	4296	B8H	C4-N3	-16.04	1.09	1.38
2	2	1860	B8H	C4-N3	-15.68	1.09	1.38
2	2	3880	P7G	C8-N9	14.43	1.54	1.46

The worst 5 of 661 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	4564	M7A	C5-C6-N6	13.64	147.03	123.74
2	2	4083	5MU	C5-C4-N3	11.90	125.47	115.31
2	2	4564	M7A	N6-C6-N1	-11.41	93.35	118.35
2	2	4220	6MZ	C4-N9-C1'	-9.41	104.18	126.59
2	2	4083	5MU	C5-C6-N1	-9.34	113.73	123.34

There are no chirality outliers.

5 of 131 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	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	O4'-C4'-C5'-O5'

There are no ring outliers.

26 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1574	B9B	1	0
2	2	2380	B8W	2	0
7	8	14	OMU	1	0
2	2	1797	E7G	1	0
2	2	4296	B8H	1	0
2	2	4637	OMG	1	0
2	2	4623	OMG	1	0
2	2	3867	A2M	1	0
2	2	4636	PSU	1	0
2	2	4472	B8W	1	0
2	2	2522	7MG	1	0
2	2	4529	B8W	2	0
2	2	373	OMG	1	0
2	2	2364	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	3899	BGH	2	0
2	2	4690	B8K	1	0
2	2	729	2MG	2	0
2	2	3897	B8K	1	0
2	2	4129	B8W	1	0
2	2	4220	6MZ	1	0
2	2	3887	OMC	1	0
2	2	1860	B8H	1	0
2	2	4185	B8W	1	0
2	2	1883	OMG	1	0
2	2	3718	A2M	2	0
2	2	1517	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 250 ligands modelled in this entry, 250 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

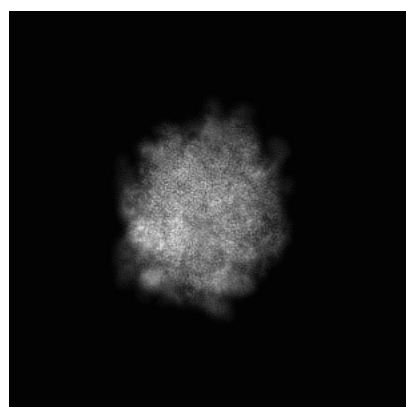
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0964. These allow visual inspection of the internal detail of the map and identification of artifacts.

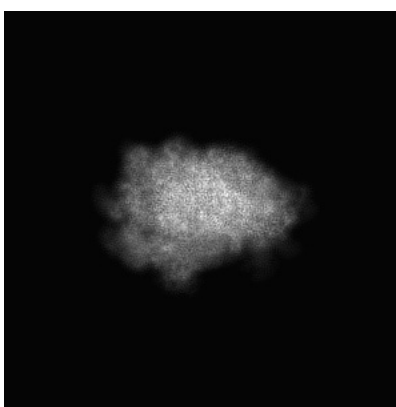
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

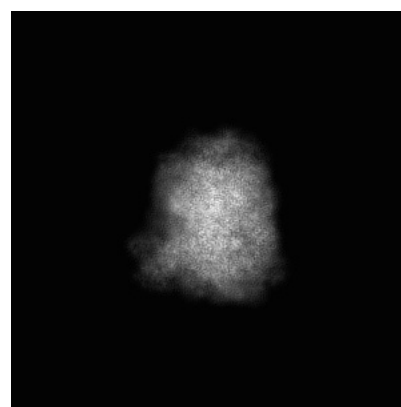
6.1.1 Primary map



X



Y

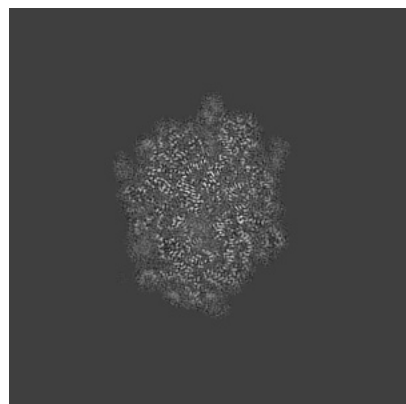


Z

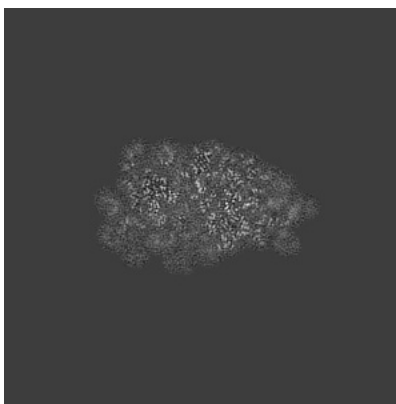
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

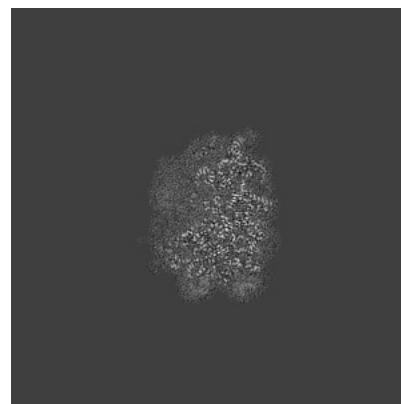
6.2.1 Primary map



X Index: 240



Y Index: 240

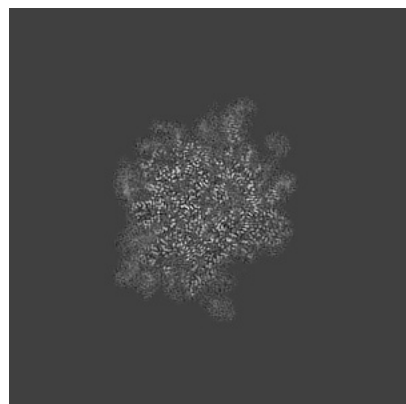


Z Index: 240

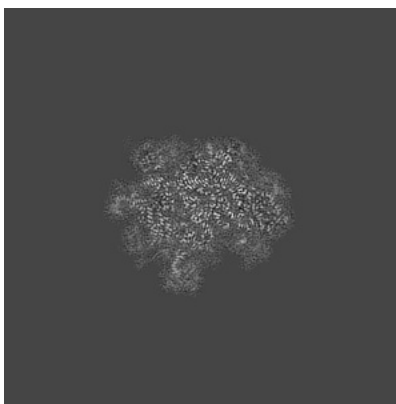
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

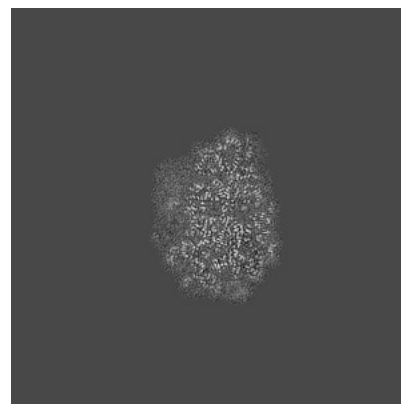
6.3.1 Primary map



X Index: 258



Y Index: 201

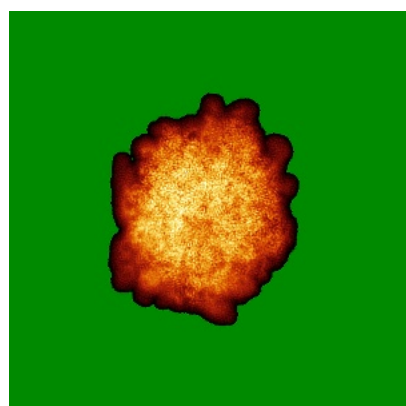


Z Index: 252

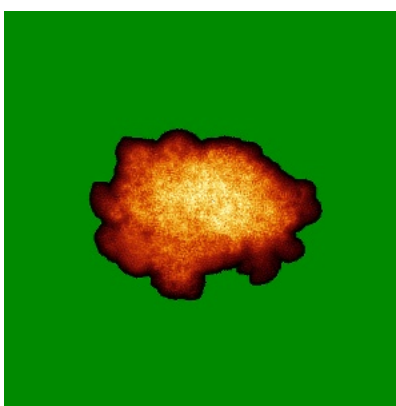
The images above show the largest variance slices of the map in three orthogonal directions.

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

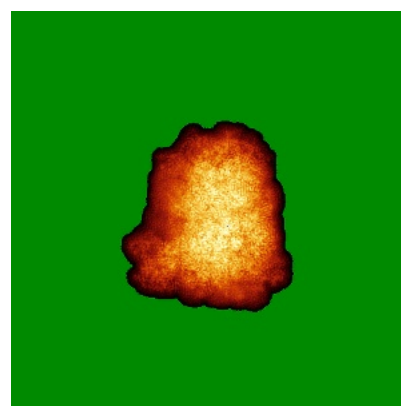
6.4.1 Primary map



X



Y

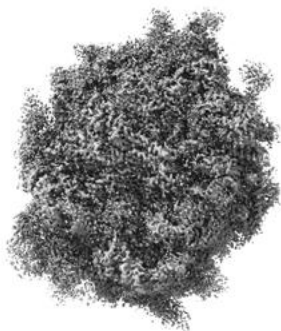


Z

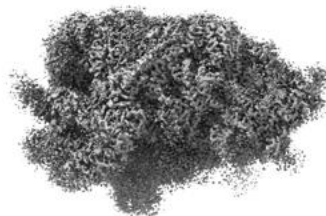
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

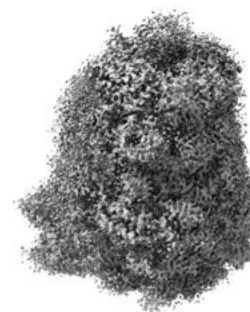
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

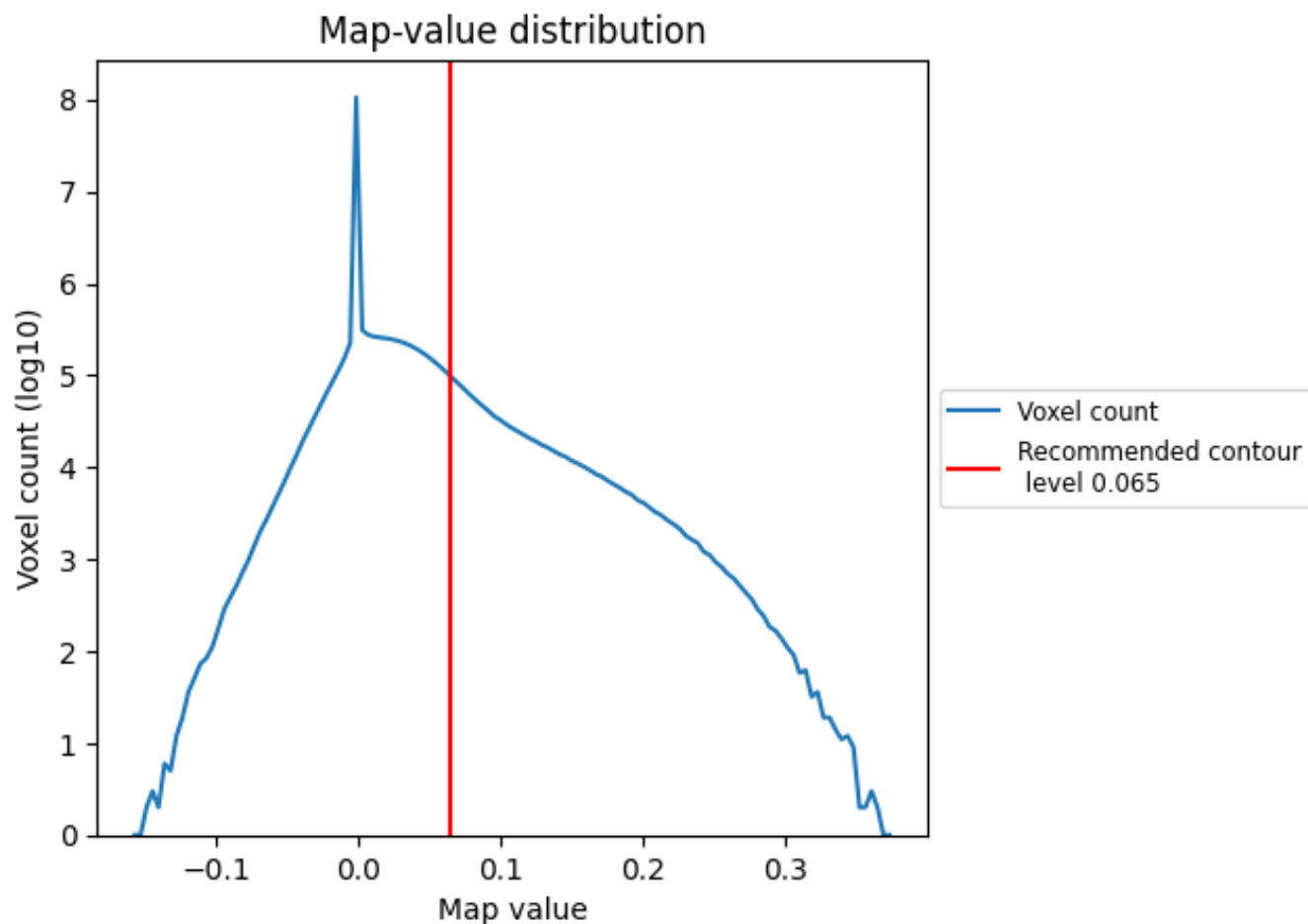
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

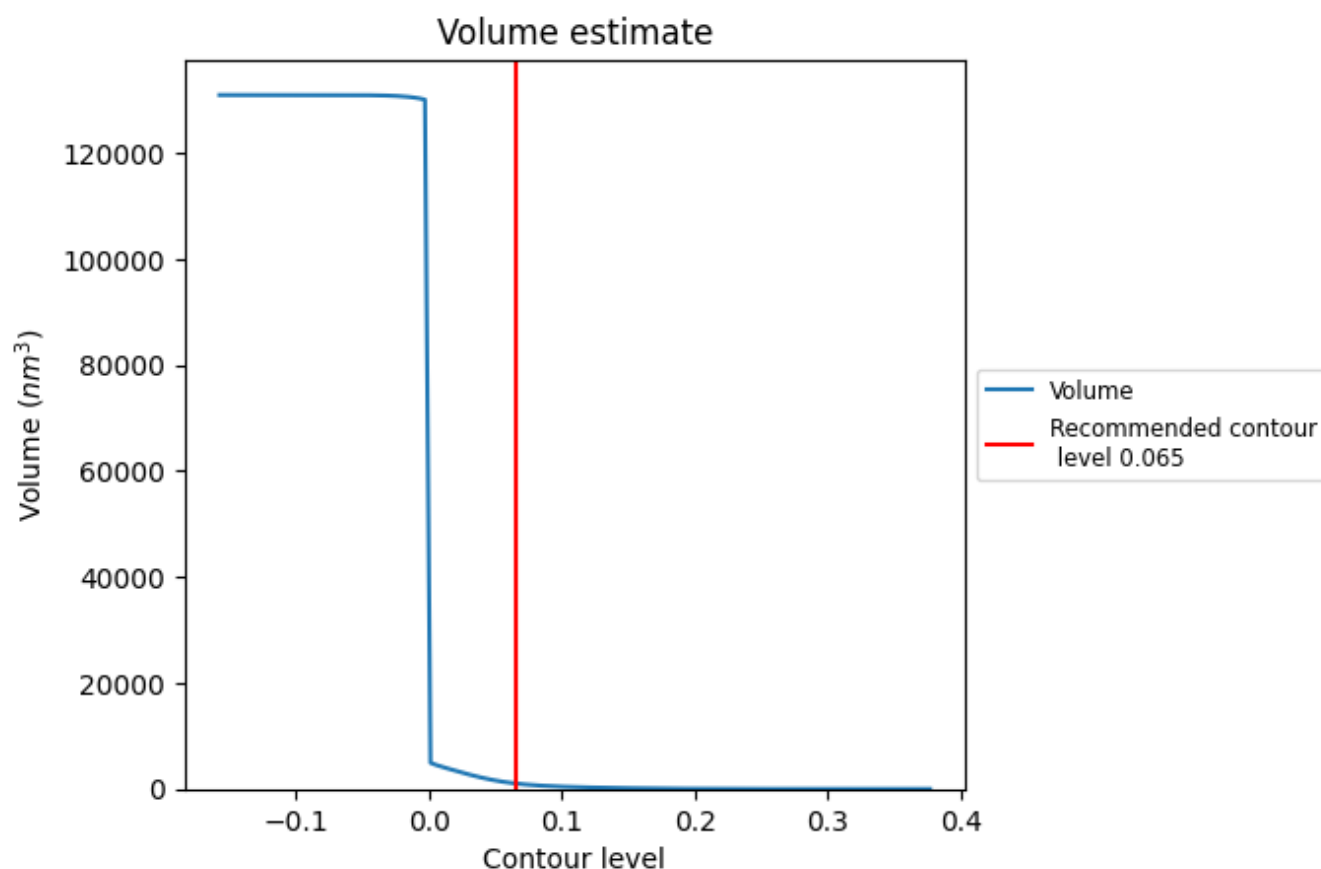
This section contains the results of statistical analysis of the map.

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.

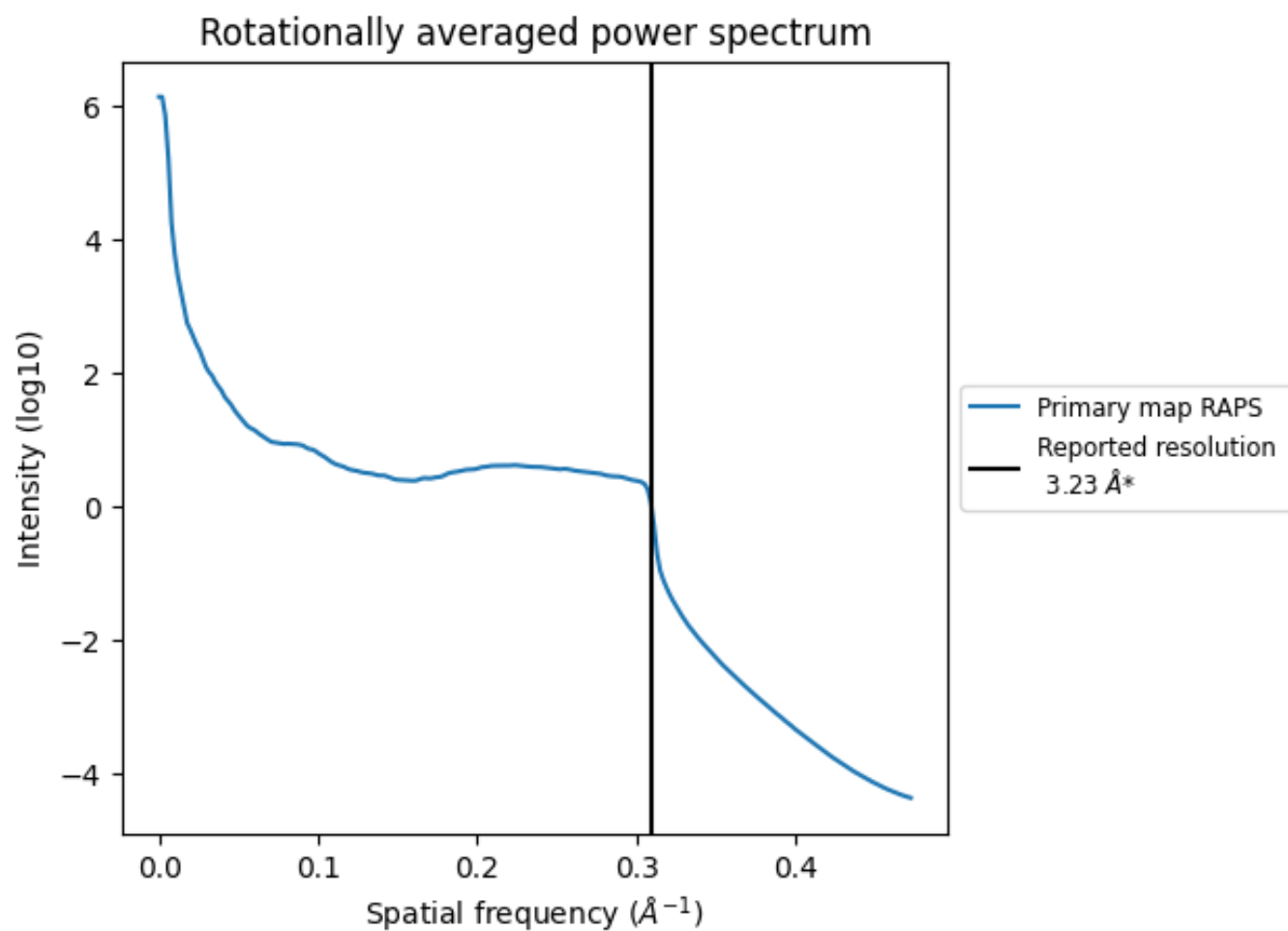
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1045 nm^3 ; this corresponds to an approximate mass of 944 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 0.310 Å⁻¹

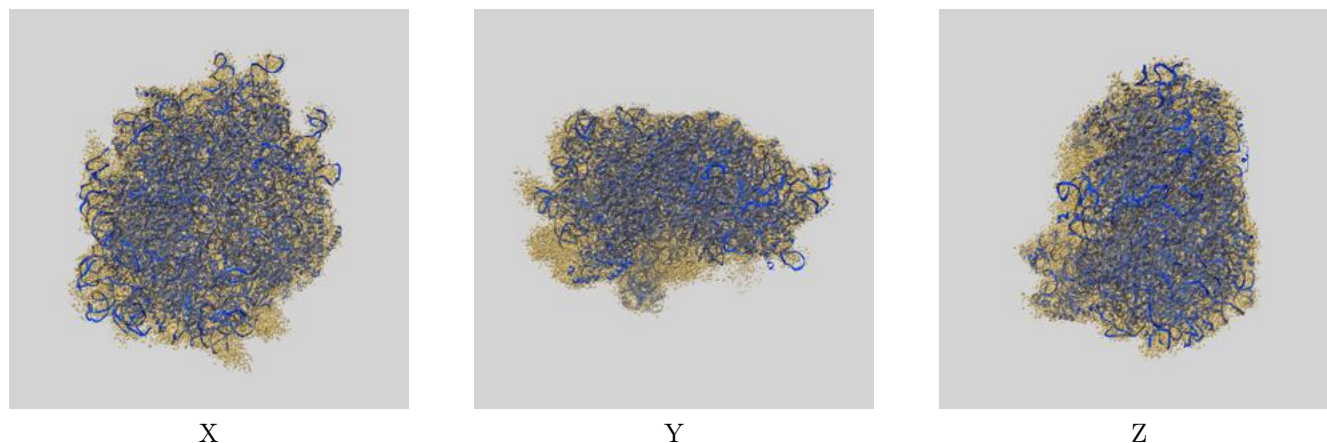
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

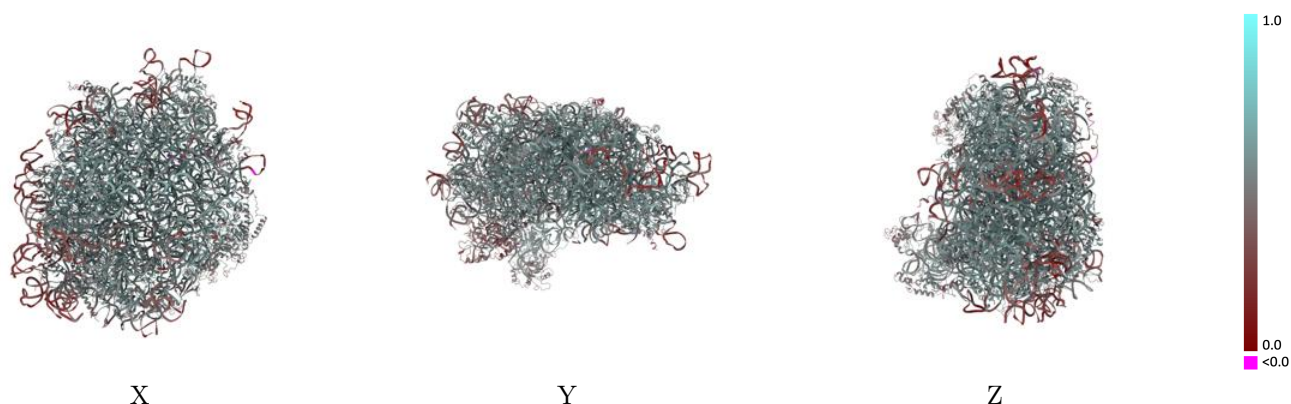
This section contains information regarding the fit between EMDB map EMD-0964 and PDB model 6LSS. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



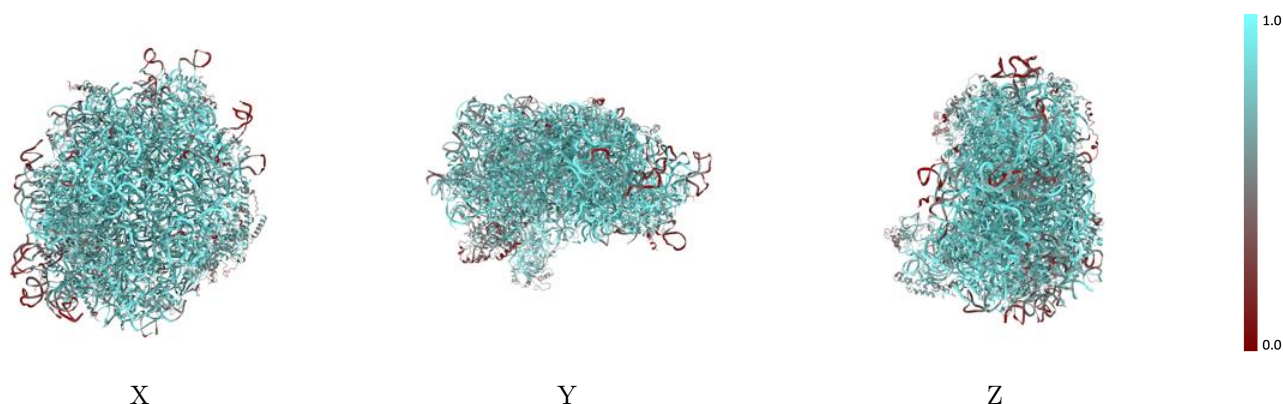
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



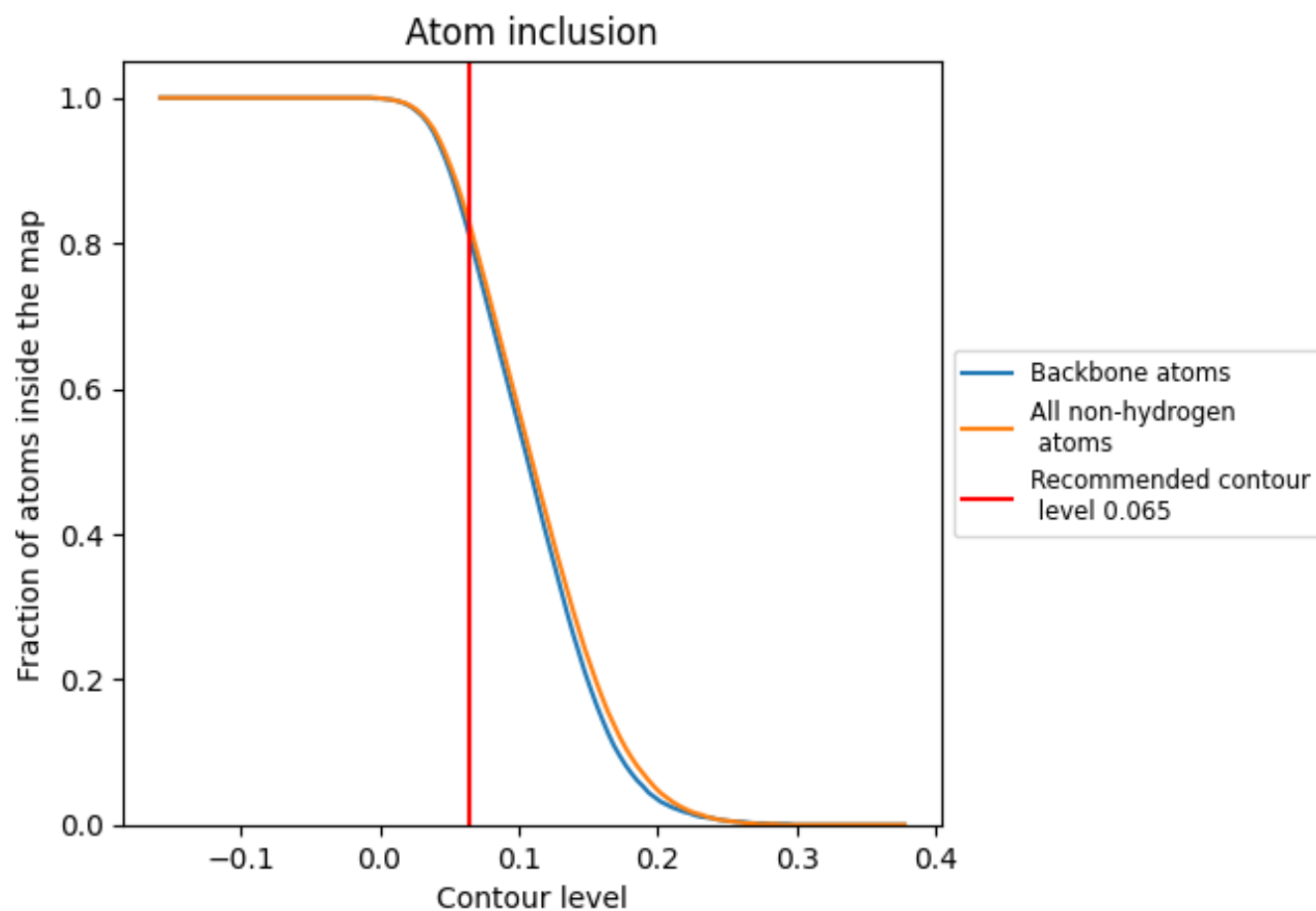
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 82% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.5150
1	 0.2250	 0.3490
2	 0.8480	 0.5010
4	 0.6350	 0.4600
5	 0.9100	 0.5160
6	 0.7040	 0.5070
7	 0.7970	 0.5370
8	 0.9110	 0.5400
9	 0.7750	 0.5180
B	 0.8620	 0.5620
C	 0.7330	 0.4790
D	 0.8830	 0.5660
E	 0.7150	 0.5260
F	 0.8560	 0.5530
G	 0.7140	 0.5090
H	 0.8140	 0.5490
I	 0.7600	 0.5200
K	 0.7830	 0.5200
L	 0.8970	 0.5790
M	 0.9440	 0.5800
N	 0.5780	 0.4230
O	 0.6800	 0.5060
P	 0.9170	 0.5750
Q	 0.7950	 0.5280
R	 0.4480	 0.3980
S	 0.8330	 0.5430
U	 0.9310	 0.5890
V	 0.8710	 0.5640
W	 0.8190	 0.5370
X	 0.8240	 0.5460
Y	 0.8960	 0.5710
Z	 0.8960	 0.5800
a	 0.8370	 0.5550
b	 0.8760	 0.5710
c	 0.8610	 0.5510



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Chain	Atom inclusion	Q-score
d	 0.7340	 0.5120
e	 0.8380	 0.5350
g	 0.8310	 0.5480
h	 0.8250	 0.5530
i	 0.7730	 0.5370
j	 0.8160	 0.5480
k	 0.8930	 0.5780
l	 0.8540	 0.5610
m	 0.8810	 0.5670
n	 0.9040	 0.5820
o	 0.7010	 0.4950
p	 0.8580	 0.5540
r	 0.6740	 0.4820
z	 0.7400	 0.5190