



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 02:16 AM UTC

PDB ID : 6QTZ / pdb_00006qtz
EMDB ID : EMD-4636
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-02-26
Resolution : 3.50 Å(reported)
Based on initial model : 4V88

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:

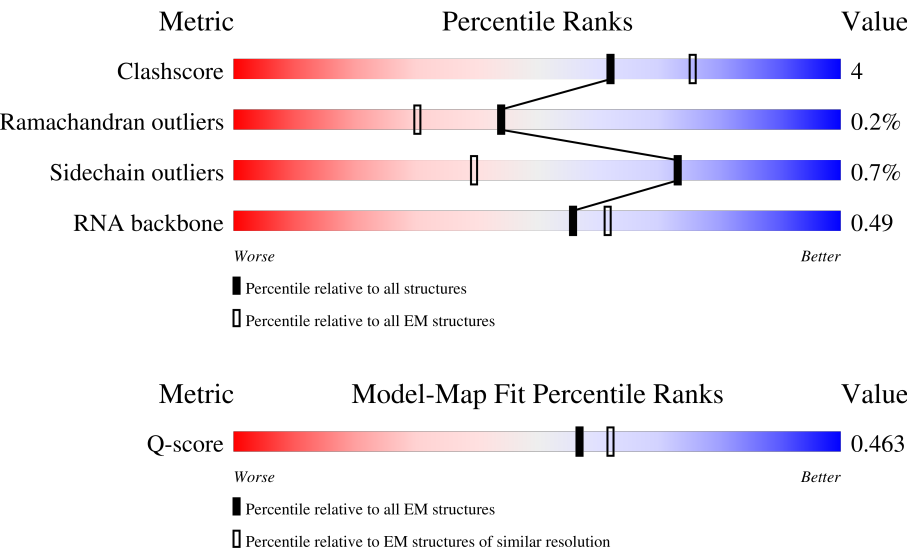
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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.



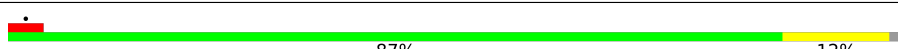
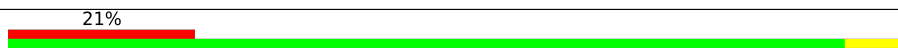
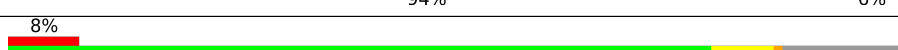
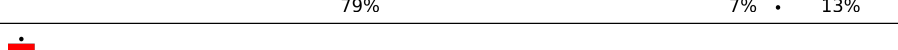
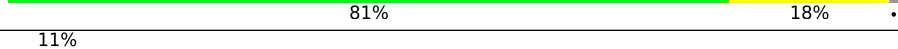
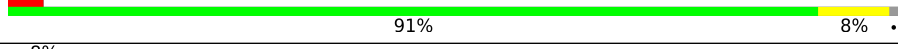
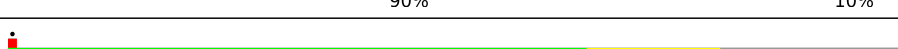
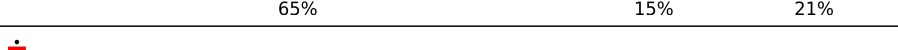
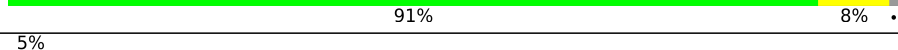
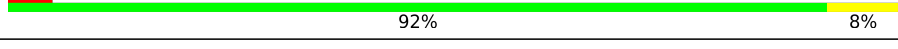
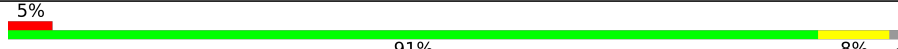
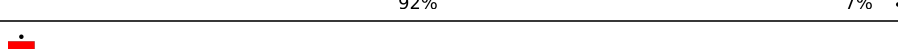
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	A	3396	63%24%6%7%
2	B	254	85%11%. .
3	C	387	83%15%. .

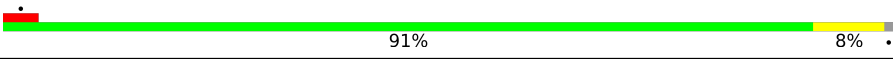
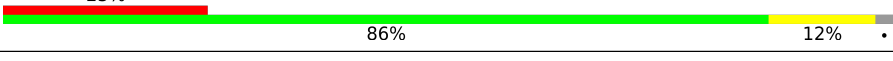
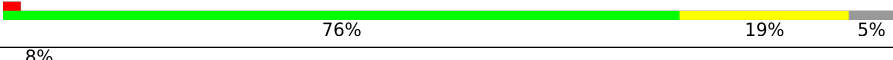
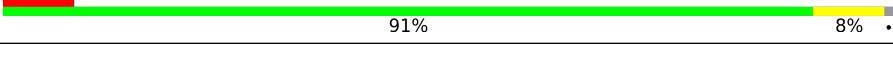
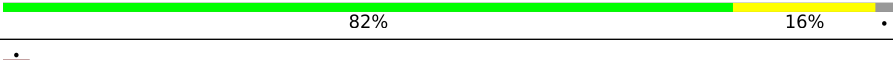
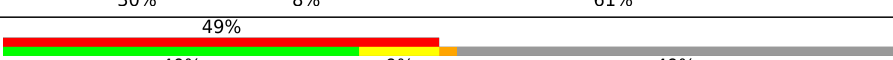
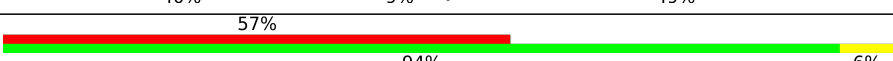
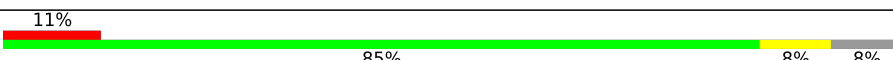
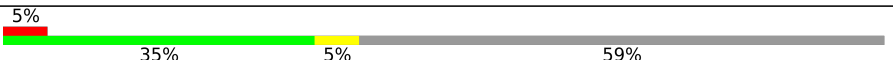
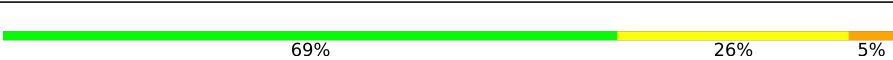
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Mol	Chain	Length	Quality of chain
4	D	362	
5	E	174	
6	F	191	
7	G	176	
8	H	256	
9	J	198	
10	K	199	
11	L	137	
12	M	138	
13	N	149	
14	O	204	
15	P	297	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	184	
21	V	121	
22	W	142	
23	X	127	
24	Y	136	
25	Z	120	
26	a	59	
27	b	244	
28	c	105	

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Mol	Chain	Length	Quality of chain
29	d	113	
30	e	130	
31	f	107	
32	g	121	
33	h	100	
34	i	88	
35	j	78	
36	k	51	
37	l	106	
38	m	92	
39	n	245	
40	z	432	
41	w	518	
42	v	155	
43	o	640	
44	p	210	
45	q	221	
46	t	128	
47	x	121	
48	y	158	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 130259 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3146	Total	C	N	O	P	0	0
			67289	30062	12142	21942	3143		

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	381	Total	C	N	O	S	0	0
			3039	1928	577	526	8		

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	361	Total	C	N	O	S	0	0
			2748	1730	522	493	3		

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	169	Total	C	N	O	S	0	0
			1352	847	253	248	4		

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	189	Total	C	N	O	S	0	0
			1502	953	272	273	4		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1399	902	251	245	1		

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	223	Total	C	N	O	S	0	0
			1742	1117	309	313	3		

- Molecule 9 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	197	Total	C	N	O	S	0	0
			1563	1005	292	265	1		

- Molecule 10 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	186	Total	C	N	O	S	0	0
			1486	929	304	253			

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	136	Total	C	N	O	S	0	0
			1002	628	189	178	7		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	135	Total	C	N	O	S	0	0
			1045	669	197	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	148	Total	C	N	O	S	0	0
			1172	749	231	189	3		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	203	Total	C	N	O	S	0	0
			1719	1077	361	280	1		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	269	Total	C	N	O	S	0	0
			2176	1378	375	421	2		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1440	908	290	240	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	150	Total	C	N	O		0	0
			1209	752	257	200			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	171	Total	C	N	O	S	0	0
			1436	925	266	242	3		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1275	805	246	220	4		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	154	Total	C	N	O		0	0
			1222	761	237	224			

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	99	Total	C	N	O	0	0
			786	510	129	147		

- Molecule 22 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	120	Total	C	N	O	S	0	0
			958	617	168	171	2		

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	135	Total	C	N	O	0	0
			1091	710	202	179		

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	118	Total	C	N	O	S	0	0
			963	612	185	165	1		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	52	Total	C	N	O	0	0
			415	259	90	66		

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	219	Total	C	N	O	S	0	0
			1760	1138	320	301	1		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	97	Total	C	N	O	S	0	0
			741	479	124	137	1		

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			872	553	165	153	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	127	Total	C	N	O	S	0	0
			1020	646	205	167	2		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	106	Total	C	N	O	S	0	0
			849	540	165	143	1		

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	103	Total	C	N	O	S	0	0
			812	504	167	137	4		

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	98	Total	C	N	O	S	0	0
			763	477	155	129	2		

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	j	77	Total	C	N	O	0	0
			611	391	115	105		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	50	Total	C	N	O	S	0	0
			435	272	97	64	2		

- Molecule 37 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	94	Total	C	N	O	S	0	0
			756	476	153	122	5		

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	224	Total	C	N	O	S	0	0
			1691	1051	293	340	7		

- Molecule 40 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	z	58	Total	C	N	O	S	0	0
			491	301	100	87	3		

- Molecule 41 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	389	Total	C	N	O	S	0	0
			3076	1955	530	571	20		

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	v	60	Total	C	N	O	S	0	0
			500	322	98	79	1		

- Molecule 43 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	325	Total	C	N	O	S	0	0
			2615	1672	454	482	7		

- Molecule 44 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	210	Total	C	N	O		0	0
			1050	630	210	210			

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	204	Total	C	N	O	S	0	0
			1671	1063	315	287	6		

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 47 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 48 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	156	Total	C	N	O	P	0	0
			3310	1482	582	1091	155		

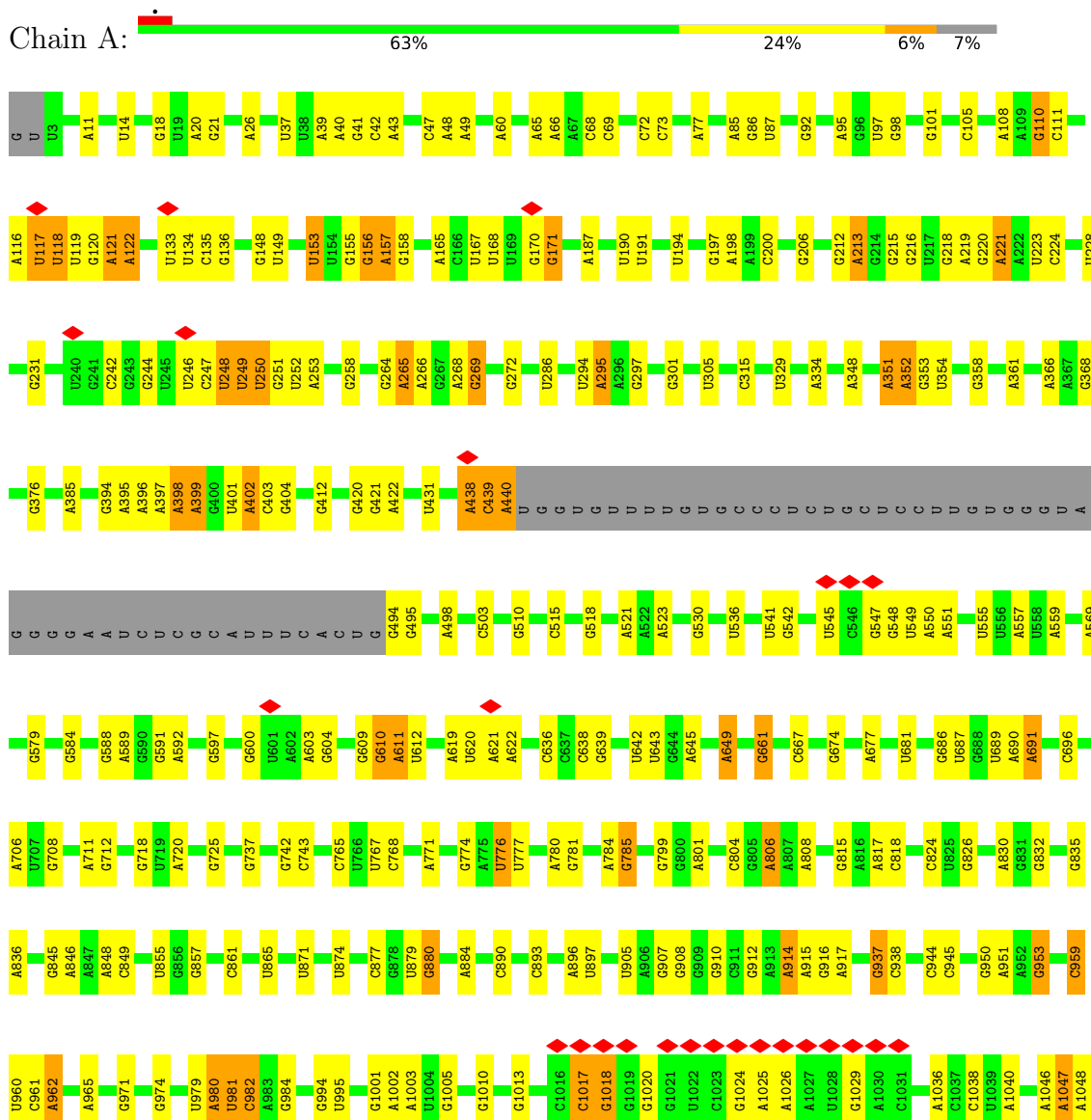
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	g	1	Total 1	Zn 1	0
49	i	1	Total 1	Zn 1	0
49	l	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	w	2	Total 2	Zn 2	0
49	t	1	Total 1	Zn 1	0

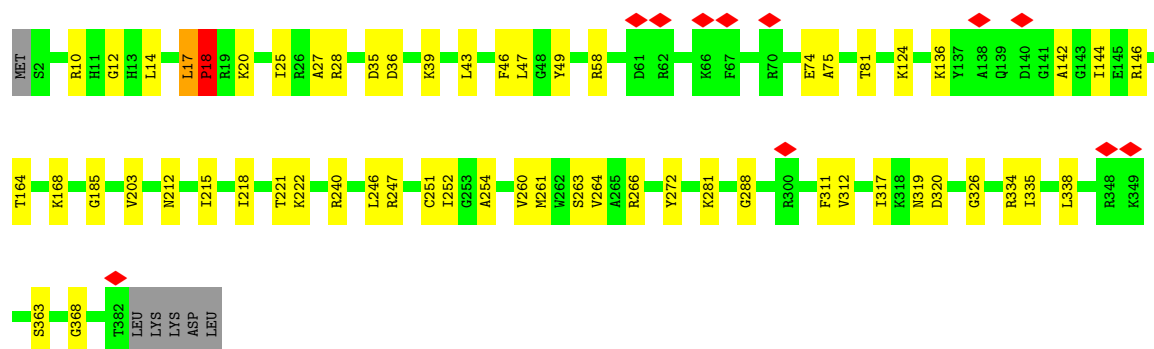
3 Residue-property plots

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.

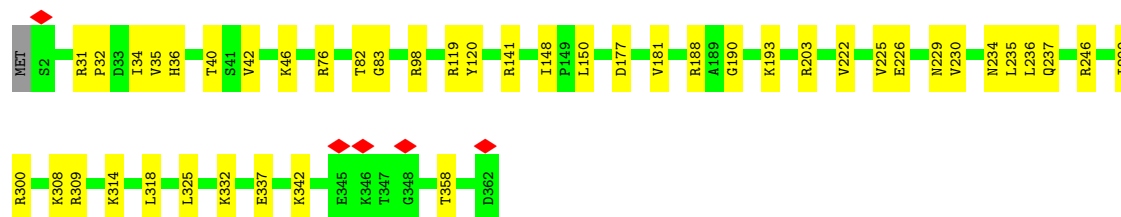
• Molecule 1: 25S rRNA



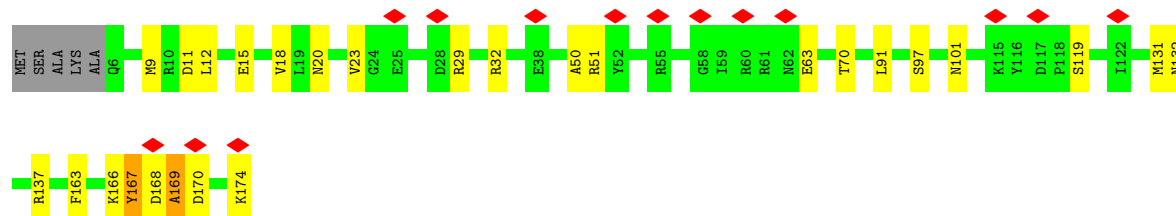
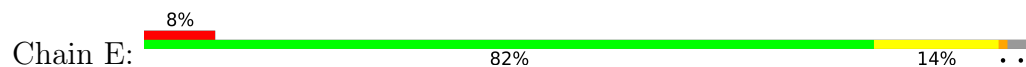




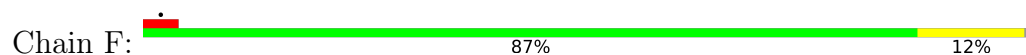
- Molecule 4: 60S ribosomal protein L4-A



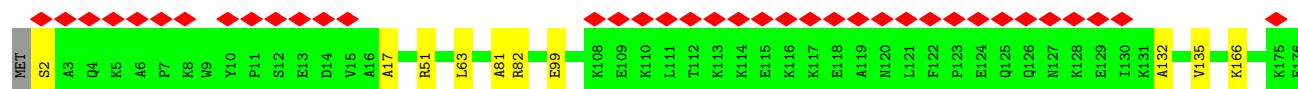
- Molecule 5: 60S ribosomal protein L11-A



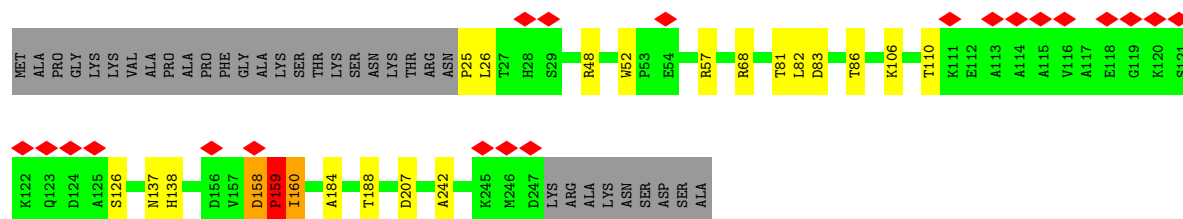
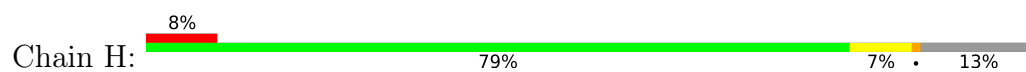
- Molecule 6: 60S ribosomal protein L9-A



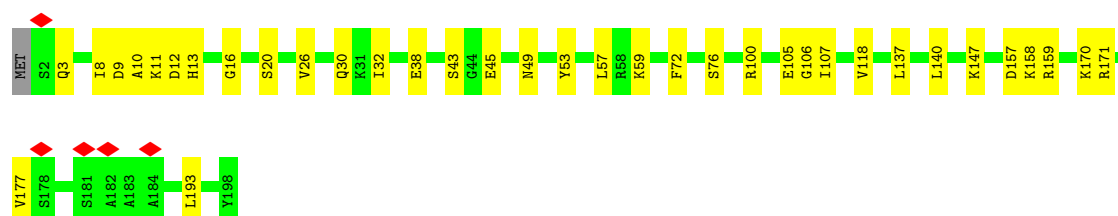
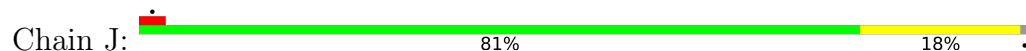
- Molecule 7: 60S ribosomal protein L6-A



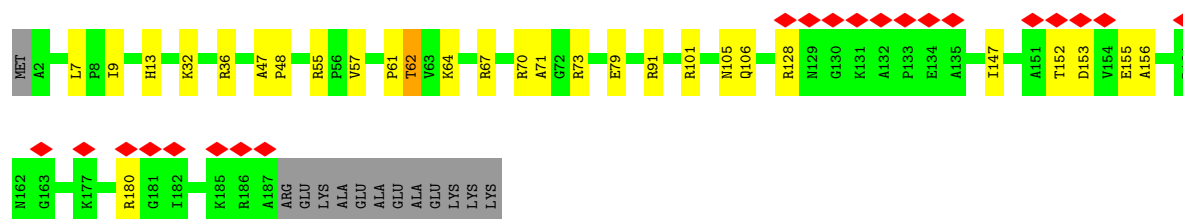
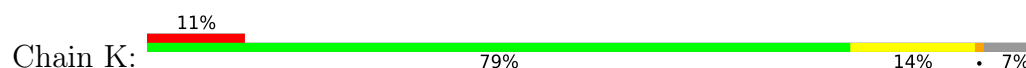
- Molecule 8: 60S ribosomal protein L8-A



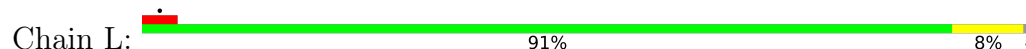
• Molecule 9: 60S ribosomal protein L16-B



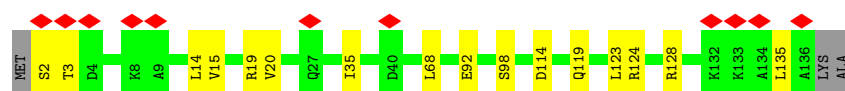
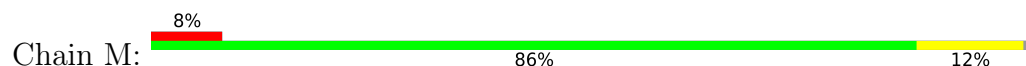
• Molecule 10: 60S ribosomal protein L13-A



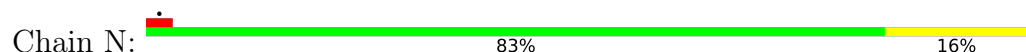
• Molecule 11: 60S ribosomal protein L23-A



• Molecule 12: 60S ribosomal protein L14-A

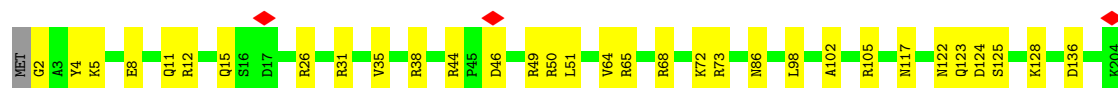
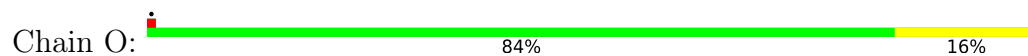


• Molecule 13: 60S ribosomal protein L28

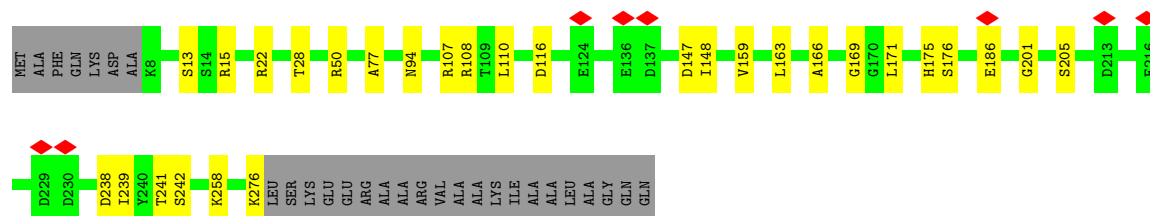
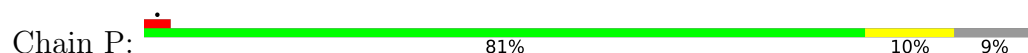




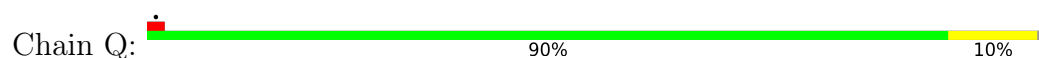
- Molecule 14: 60S ribosomal protein L15-A



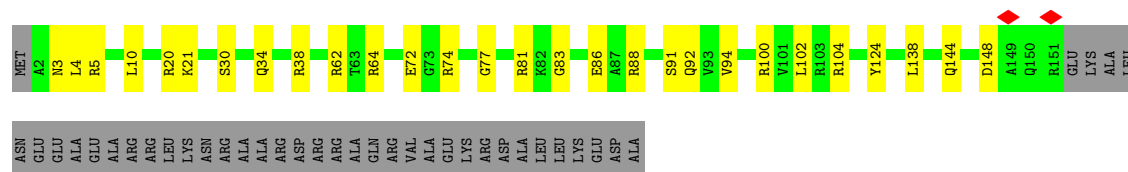
- Molecule 15: 60S ribosomal protein L5



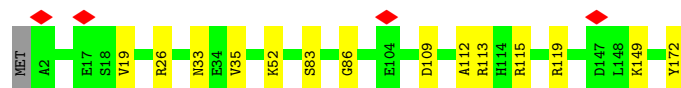
- Molecule 16: 60S ribosomal protein L18-A



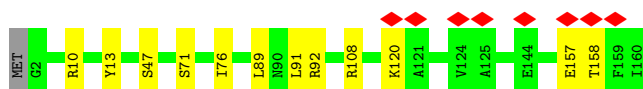
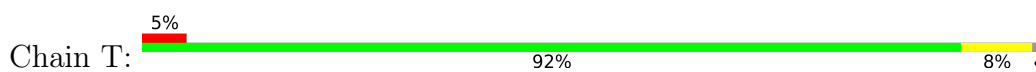
- Molecule 17: 60S ribosomal protein L19-A



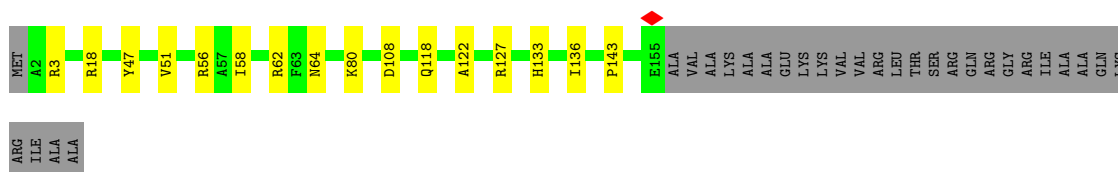
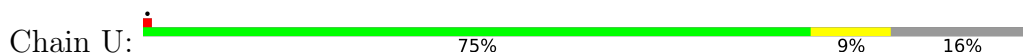
- Molecule 18: 60S ribosomal protein L20-A



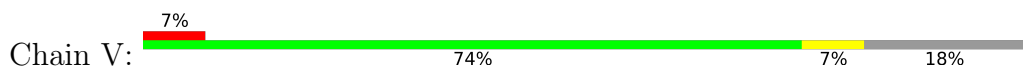
- Molecule 19: 60S ribosomal protein L21-A



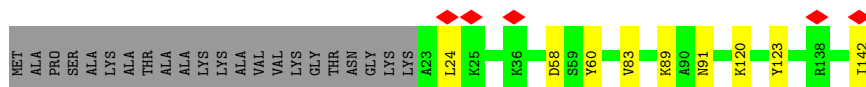
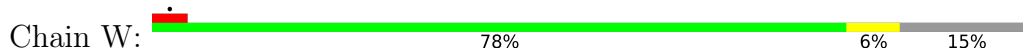
- Molecule 20: 60S ribosomal protein L17-A



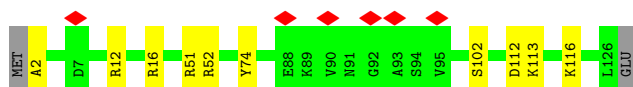
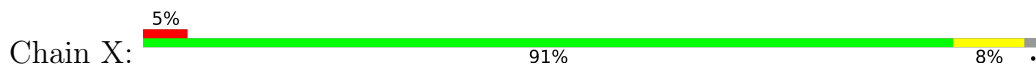
- Molecule 21: 60S ribosomal protein L22-A



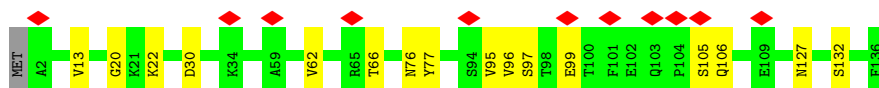
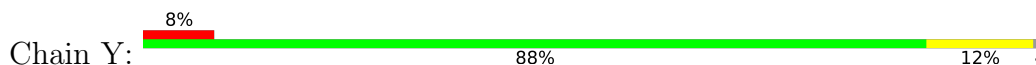
- Molecule 22: 60S ribosomal protein L25



- Molecule 23: 60S ribosomal protein L26-A

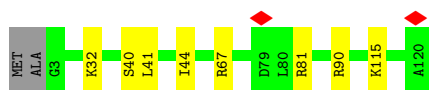


- Molecule 24: 60S ribosomal protein L27-A

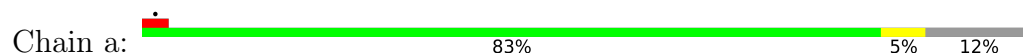


- Molecule 25: 60S ribosomal protein L35-A

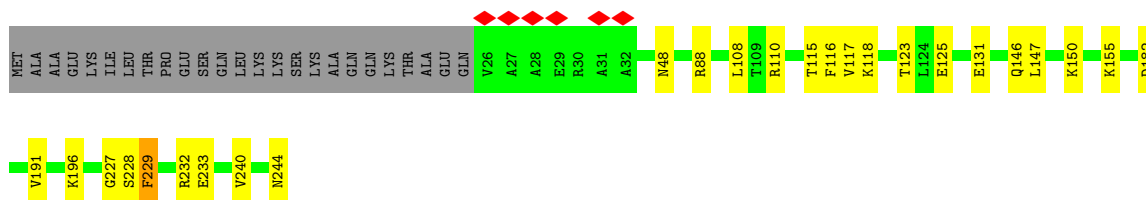
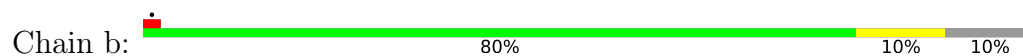




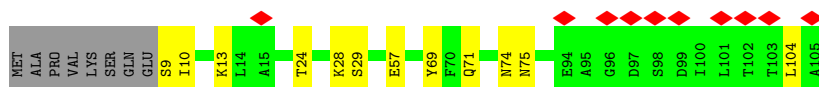
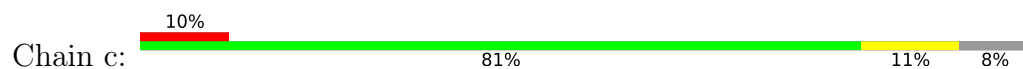
- Molecule 26: 60S ribosomal protein L29



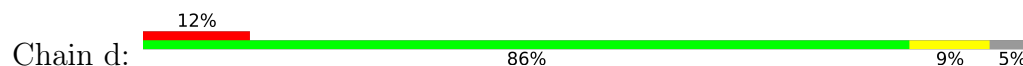
- Molecule 27: 60S ribosomal protein L7-A



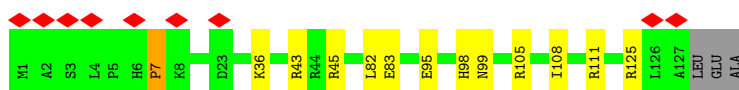
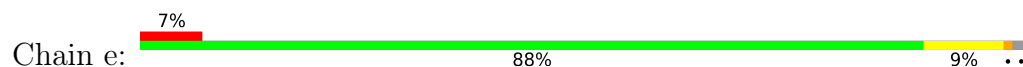
- Molecule 28: 60S ribosomal protein L30



- Molecule 29: 60S ribosomal protein L31-A

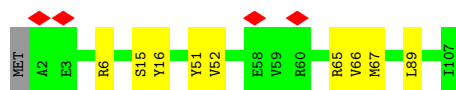


- Molecule 30: 60S ribosomal protein L32

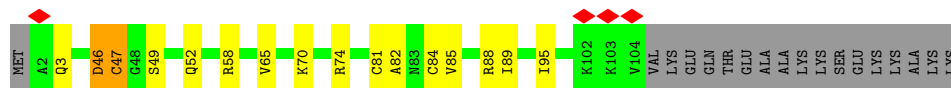


- Molecule 31: 60S ribosomal protein L33-A

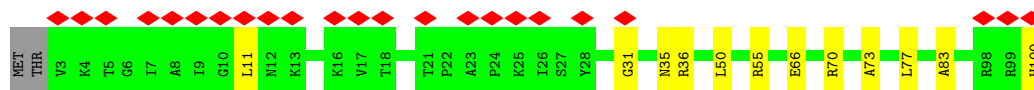
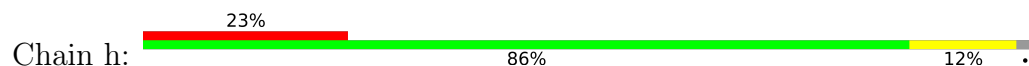




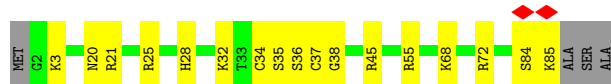
- Molecule 32: 60S ribosomal protein L34-A



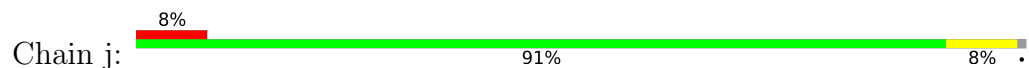
- Molecule 33: 60S ribosomal protein L36-A



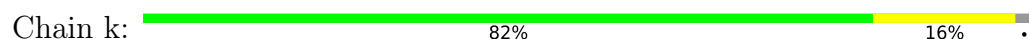
- Molecule 34: 60S ribosomal protein L37-A



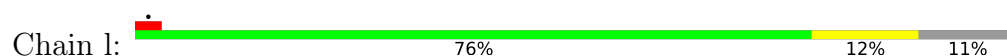
- Molecule 35: 60S ribosomal protein L38



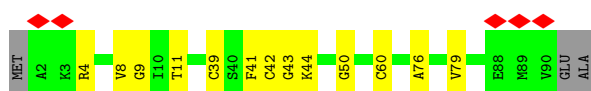
- Molecule 36: 60S ribosomal protein L39



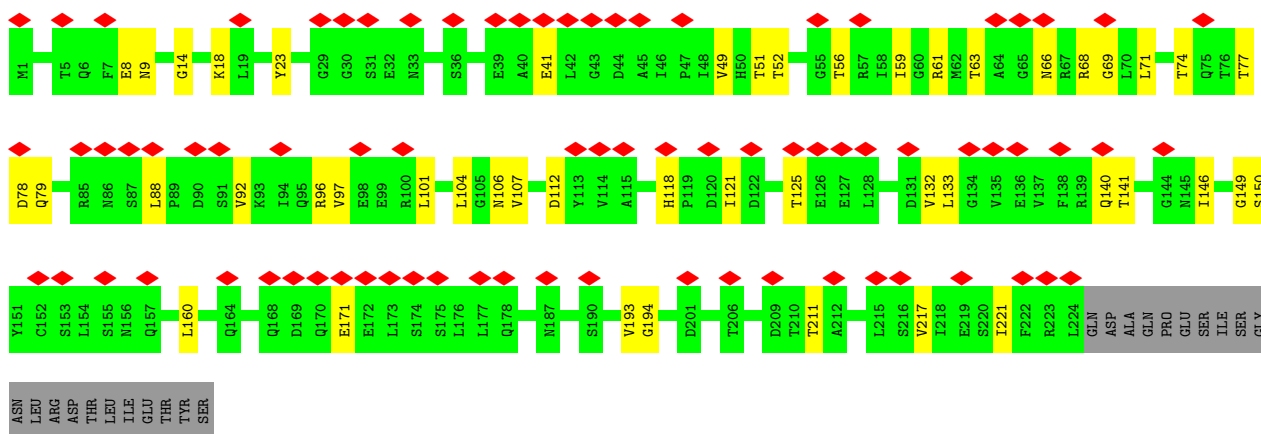
- Molecule 37: 60S ribosomal protein L42-A



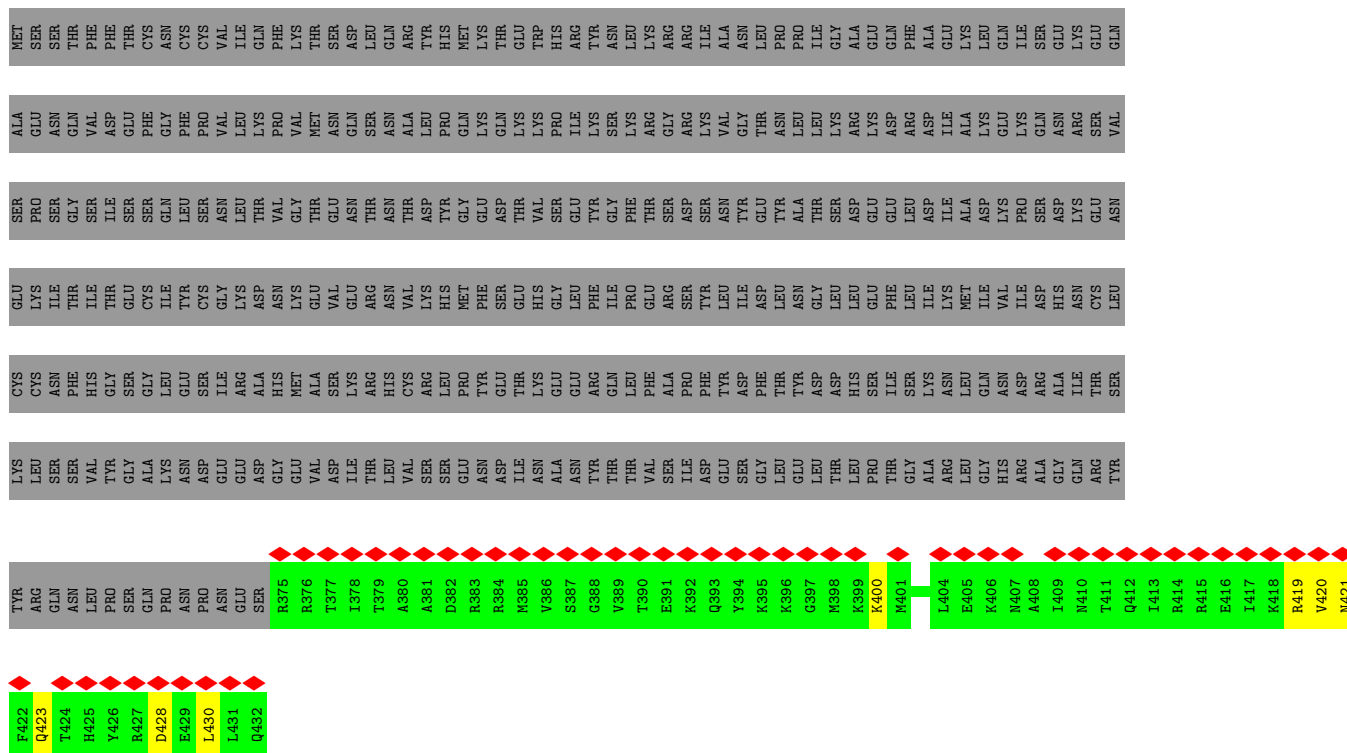
- Molecule 38: 60S ribosomal protein L43-A

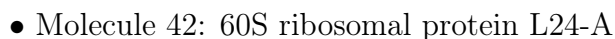


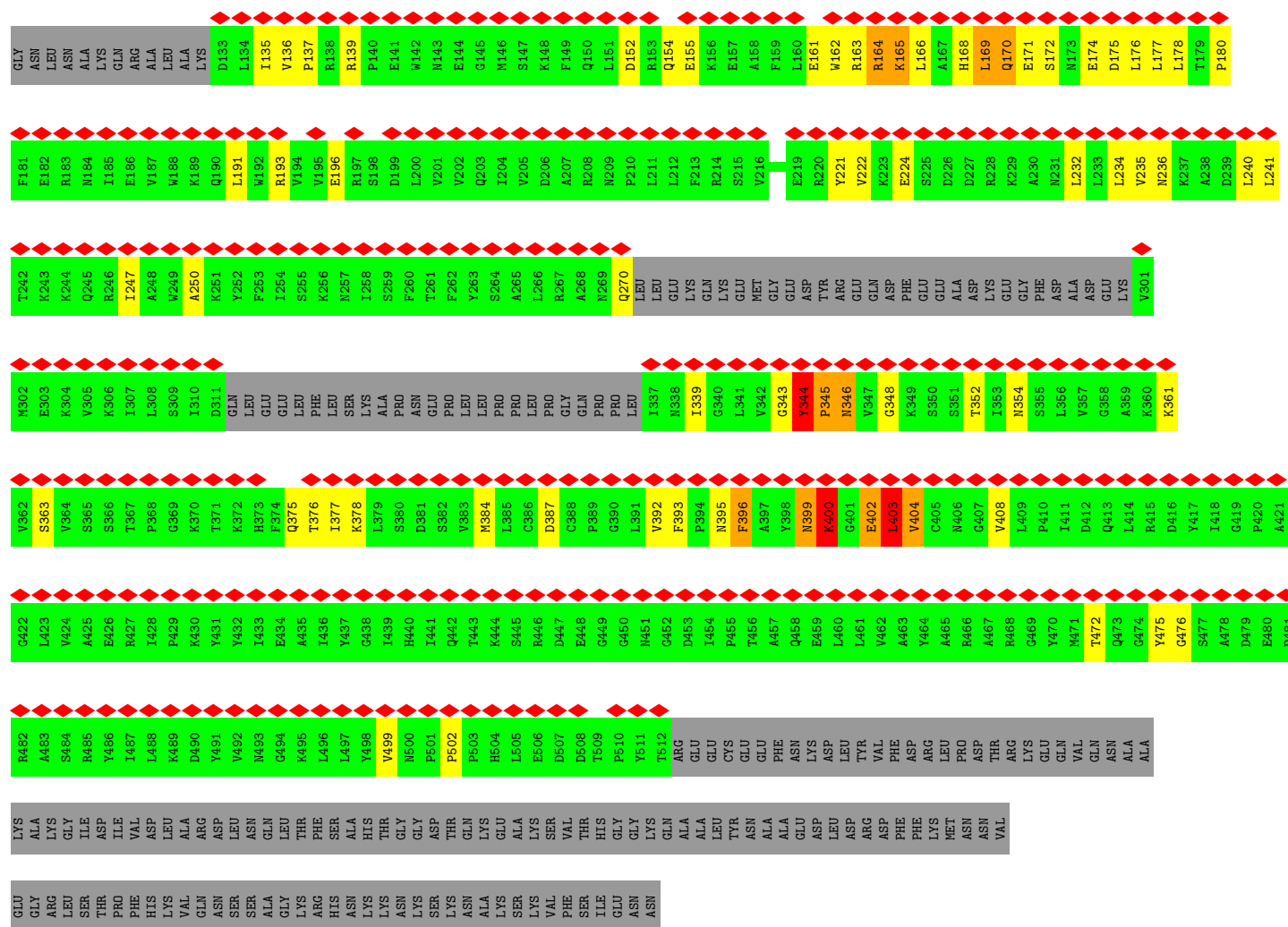
Chain n: 32% 72% 19% 9%



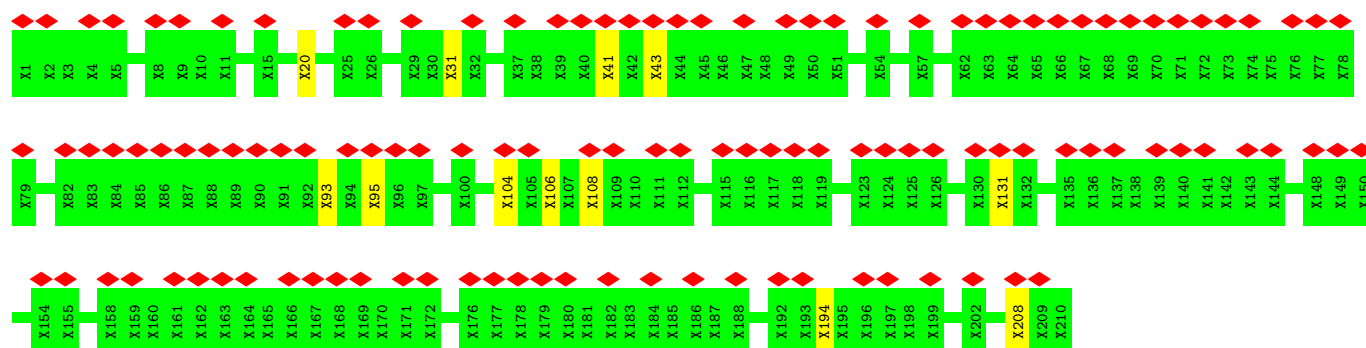
Chain z: 12% 12% 87%



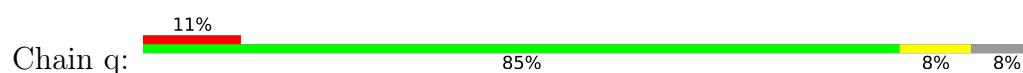


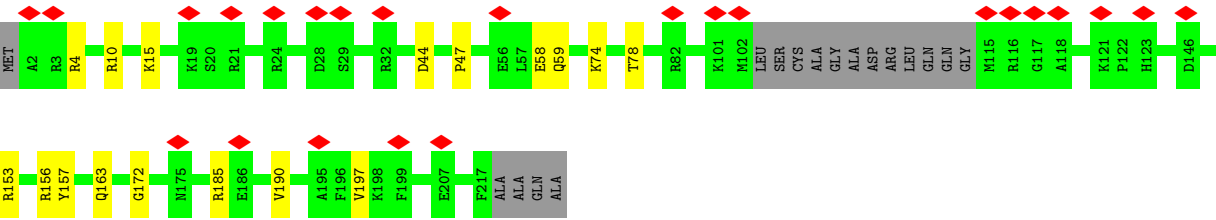


• Molecule 44: uL1

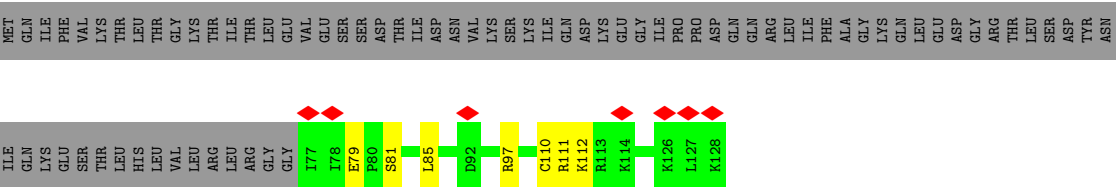


• Molecule 45: 60S ribosomal protein L10

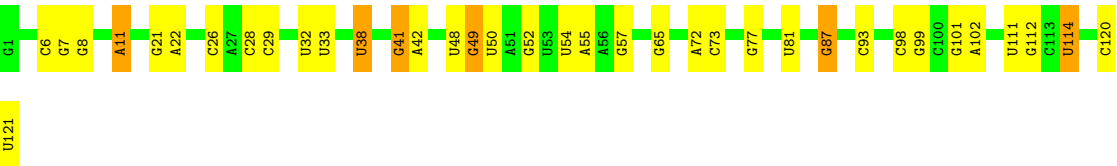




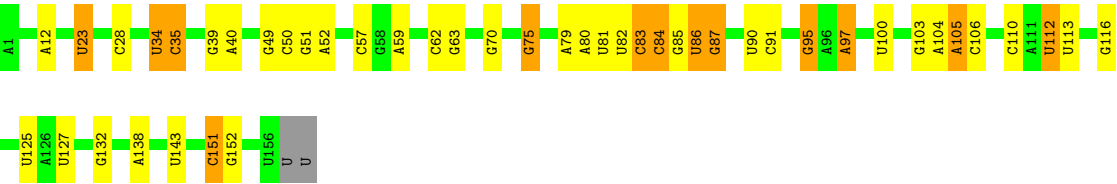
● Molecule 46: Ubiquitin-60S ribosomal protein L40



● Molecule 47: 5S rRNA



● Molecule 48: 5.8S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48239	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.451	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	A	0.24	1/75323 (0.0%)	0.37	0/117432
2	B	0.36	0/1912	0.55	0/2569
3	C	0.35	0/3110	0.55	2/4184 (0.0%)
4	D	0.33	0/2800	0.49	0/3791
5	E	0.27	0/1373	0.65	5/1841 (0.3%)
6	F	0.24	0/1523	0.47	0/2051
7	G	0.25	0/1423	0.44	0/1911
8	H	0.30	0/1774	0.70	6/2395 (0.3%)
9	J	0.33	0/1593	0.46	0/2137
10	K	0.32	0/1511	0.54	0/2031
11	L	0.32	0/1017	0.48	0/1368
12	M	0.28	0/1060	0.48	0/1428
13	N	0.37	0/1203	0.58	1/1611 (0.1%)
14	O	0.36	0/1756	0.49	0/2353
15	P	0.27	0/2225	0.48	0/3004
16	Q	0.33	0/1464	0.49	0/1964
17	R	0.31	0/1226	0.52	0/1637
18	S	0.31	0/1472	0.46	0/1979
19	T	0.30	0/1299	0.50	0/1742
20	U	0.34	0/1245	0.49	0/1676
21	V	0.25	0/802	0.47	0/1087
22	W	0.29	0/973	0.51	0/1313
23	X	0.30	0/995	0.48	0/1329
24	Y	0.25	0/1117	0.51	0/1496
25	Z	0.29	0/972	0.45	0/1293
26	a	0.28	0/426	0.46	0/570
27	b	0.35	0/1797	0.54	2/2419 (0.1%)
28	c	0.25	0/749	0.50	0/1007
29	d	0.32	0/886	0.51	0/1190
30	e	0.33	0/1041	0.54	1/1393 (0.1%)
31	f	0.36	0/867	0.57	0/1167
32	g	0.39	0/822	0.59	0/1099

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.26	0/770	0.50	0/1023
34	i	0.39	0/680	0.61	0/901
35	j	0.26	0/617	0.51	0/825
36	k	0.35	0/442	0.46	0/587
37	l	0.38	0/768	0.74	0/1016
38	m	0.39	0/687	0.70	1/915 (0.1%)
39	n	0.22	0/1712	0.49	0/2330
40	z	0.24	0/494	0.56	0/654
41	w	0.38	0/3135	0.65	4/4255 (0.1%)
42	v	0.27	0/512	0.54	0/680
43	o	0.39	0/2669	0.73	5/3612 (0.1%)
45	q	0.24	0/1707	0.46	0/2288
46	t	0.26	0/423	0.52	0/562
47	x	0.22	0/2880	0.32	0/4487
48	y	0.25	0/3699	0.35	0/5760
All	All	0.28	1/138951 (0.0%)	0.44	27/204362 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2258	U	C1'-N1	5.74	1.57	1.48

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	159	PRO	CA-N-CD	-13.66	92.87	112.00
3	C	18	PRO	CA-N-CD	-10.35	97.52	112.00
8	H	159	PRO	CB-CA-C	8.66	125.84	111.56
13	N	95	SER	N-CA-C	-8.65	101.85	111.28
5	E	167	TYR	CB-CA-C	8.43	118.18	109.83

There are no chirality outliers.

There are no planarity outliers.

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	A	67289	0	33823	412	0
2	B	1878	0	1946	24	0
3	C	3039	0	3113	41	0
4	D	2748	0	2863	32	0
5	E	1352	0	1383	26	0
6	F	1502	0	1572	18	0
7	G	1399	0	1501	8	0
8	H	1742	0	1834	15	0
9	J	1563	0	1665	25	0
10	K	1486	0	1554	20	0
11	L	1002	0	1048	8	0
12	M	1045	0	1136	15	0
13	N	1172	0	1215	21	0
14	O	1719	0	1779	29	0
15	P	2176	0	2116	21	0
16	Q	1440	0	1543	16	0
17	R	1209	0	1295	23	0
18	S	1436	0	1475	10	0
19	T	1275	0	1323	9	0
20	U	1222	0	1231	13	0
21	V	786	0	799	8	0
22	W	958	0	1023	7	0
23	X	984	0	1075	10	0
24	Y	1091	0	1155	8	0
25	Z	963	0	1073	7	0
26	a	415	0	429	3	0
27	b	1760	0	1843	19	0
28	c	741	0	797	8	0
29	d	872	0	914	6	0
30	e	1020	0	1091	11	0
31	f	849	0	880	6	0
32	g	812	0	874	12	0
33	h	763	0	842	7	0
34	i	665	0	668	13	0
35	j	611	0	682	4	0
36	k	435	0	475	8	0
37	l	756	0	817	9	0
38	m	680	0	725	12	0
39	n	1691	0	1689	32	0
40	z	491	0	518	6	0
41	w	3076	0	3105	76	0
42	v	500	0	524	9	0
43	o	2615	0	2644	63	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	p	1050	0	256	7	0
45	q	1671	0	1712	11	0
46	t	417	0	457	5	0
47	x	2576	0	1305	18	0
48	y	3310	0	1676	24	0
49	g	1	0	0	0	0
49	i	1	0	0	0	0
49	l	1	0	0	0	0
49	m	1	0	0	0	0
49	t	1	0	0	0	0
49	w	2	0	0	0	0
All	All	130259	0	95463	929	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 929 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)
41:w:64:PHE:CE2	41:w:81:LEU:HD11	1.81	1.15
41:w:57:PHE:CD1	41:w:64:PHE:HB3	1.80	1.09
32:g:46:ASP:OD2	32:g:88:ARG:NH2	1.86	1.07
43:o:180:PRO:O	43:o:392:VAL:HG21	1.51	1.06
43:o:180:PRO:O	43:o:392:VAL:CG2	2.03	1.05

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	245/254 (96%)	226 (92%)	18 (7%)	1 (0%)	30 62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	379/387 (98%)	346 (91%)	31 (8%)	2 (0%)	24	57
4	D	359/362 (99%)	339 (94%)	20 (6%)	0	100	100
5	E	167/174 (96%)	159 (95%)	7 (4%)	1 (1%)	21	54
6	F	187/191 (98%)	175 (94%)	12 (6%)	0	100	100
7	G	173/176 (98%)	156 (90%)	17 (10%)	0	100	100
8	H	221/256 (86%)	210 (95%)	9 (4%)	2 (1%)	14	47
9	J	195/198 (98%)	192 (98%)	3 (2%)	0	100	100
10	K	184/199 (92%)	170 (92%)	14 (8%)	0	100	100
11	L	134/137 (98%)	125 (93%)	9 (7%)	0	100	100
12	M	133/138 (96%)	126 (95%)	7 (5%)	0	100	100
13	N	146/149 (98%)	127 (87%)	19 (13%)	0	100	100
14	O	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
15	P	267/297 (90%)	243 (91%)	24 (9%)	0	100	100
16	Q	183/186 (98%)	172 (94%)	11 (6%)	0	100	100
17	R	148/189 (78%)	144 (97%)	4 (3%)	0	100	100
18	S	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
19	T	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
20	U	152/184 (83%)	142 (93%)	10 (7%)	0	100	100
21	V	97/121 (80%)	89 (92%)	8 (8%)	0	100	100
22	W	118/142 (83%)	107 (91%)	11 (9%)	0	100	100
23	X	123/127 (97%)	116 (94%)	7 (6%)	0	100	100
24	Y	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
25	Z	116/120 (97%)	112 (97%)	4 (3%)	0	100	100
26	a	50/59 (85%)	43 (86%)	7 (14%)	0	100	100
27	b	217/244 (89%)	205 (94%)	12 (6%)	0	100	100
28	c	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
29	d	105/113 (93%)	87 (83%)	18 (17%)	0	100	100
30	e	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	16	49
31	f	104/107 (97%)	93 (89%)	11 (11%)	0	100	100
32	g	101/121 (84%)	92 (91%)	9 (9%)	0	100	100
33	h	96/100 (96%)	91 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	i	82/88 (93%)	74 (90%)	8 (10%)	0	100	100
35	j	75/78 (96%)	68 (91%)	7 (9%)	0	100	100
36	k	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
37	l	92/106 (87%)	88 (96%)	3 (3%)	1 (1%)	11	43
38	m	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
39	n	222/245 (91%)	203 (91%)	19 (9%)	0	100	100
40	z	56/432 (13%)	50 (89%)	6 (11%)	0	100	100
41	w	387/518 (75%)	354 (92%)	33 (8%)	0	100	100
42	v	58/155 (37%)	56 (97%)	2 (3%)	0	100	100
43	o	319/640 (50%)	254 (80%)	59 (18%)	6 (2%)	6	33
45	q	200/221 (90%)	189 (94%)	11 (6%)	0	100	100
46	t	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
All	All	6956/8392 (83%)	6431 (92%)	511 (7%)	14 (0%)	44	74

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
5	E	169	ALA
8	H	159	PRO
8	H	160	ILE
37	l	78	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	189/196 (96%)	188 (100%)	1 (0%)	81	80
3	C	317/323 (98%)	316 (100%)	1 (0%)	86	83
4	D	288/289 (100%)	288 (100%)	0	100	100
5	E	147/150 (98%)	146 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	169/171 (99%)	169 (100%)	0	100	100
7	G	152/153 (99%)	152 (100%)	0	100	100
8	H	183/208 (88%)	180 (98%)	3 (2%)	55	70
9	J	163/164 (99%)	163 (100%)	0	100	100
10	K	149/159 (94%)	148 (99%)	1 (1%)	76	78
11	L	104/105 (99%)	103 (99%)	1 (1%)	68	75
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	118/119 (99%)	118 (100%)	0	100	100
14	O	175/176 (99%)	175 (100%)	0	100	100
15	P	227/245 (93%)	227 (100%)	0	100	100
16	Q	150/151 (99%)	150 (100%)	0	100	100
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	154 (99%)	1 (1%)	78	79
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	125/146 (86%)	125 (100%)	0	100	100
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	103 (99%)	1 (1%)	68	75
23	X	108/110 (98%)	108 (100%)	0	100	100
24	Y	115/116 (99%)	114 (99%)	1 (1%)	70	76
25	Z	104/105 (99%)	104 (100%)	0	100	100
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	182 (99%)	2 (1%)	65	74
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	94 (100%)	0	100	100
30	e	109/111 (98%)	109 (100%)	0	100	100
31	f	90/91 (99%)	90 (100%)	0	100	100
32	g	88/103 (85%)	85 (97%)	3 (3%)	32	57
33	h	80/82 (98%)	79 (99%)	1 (1%)	61	72
34	i	69/71 (97%)	69 (100%)	0	100	100
35	j	68/69 (99%)	67 (98%)	1 (2%)	57	71
36	k	45/46 (98%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	l	81/91 (89%)	80 (99%)	1 (1%)	63	73
38	m	70/72 (97%)	69 (99%)	1 (1%)	59	71
39	n	192/211 (91%)	192 (100%)	0	100	100
40	z	53/392 (14%)	53 (100%)	0	100	100
41	w	348/467 (74%)	344 (99%)	4 (1%)	65	74
42	v	53/129 (41%)	53 (100%)	0	100	100
43	o	286/555 (52%)	271 (95%)	15 (5%)	21	47
45	q	177/187 (95%)	177 (100%)	0	100	100
46	t	47/116 (40%)	47 (100%)	0	100	100
All	All	5951/7097 (84%)	5912 (99%)	39 (1%)	73	78

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	o	168	HIS
43	o	399	ASN
43	o	169	LEU
43	o	176	LEU
43	o	402	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
20	U	145	HIS
41	w	403	GLN
27	b	194	HIS
43	o	170	GLN
35	j	57	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3140/3396 (92%)	678 (21%)	15 (0%)
47	x	120/121 (99%)	22 (18%)	0
48	y	155/158 (98%)	33 (21%)	0
All	All	3415/3675 (92%)	733 (21%)	15 (0%)

5 of 733 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	14	U
1	A	26	A
1	A	40	A
1	A	43	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1629	U
1	A	3206	C
1	A	1815	U
1	A	3353	G
1	A	2404	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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.

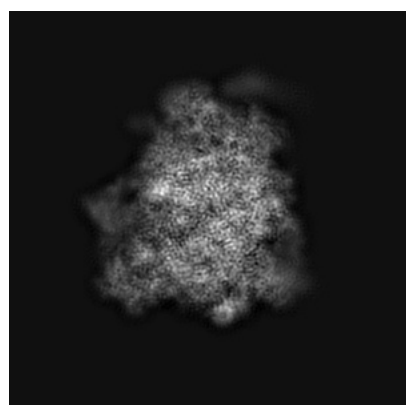
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4636. These allow visual inspection of the internal detail of the map and identification of artifacts.

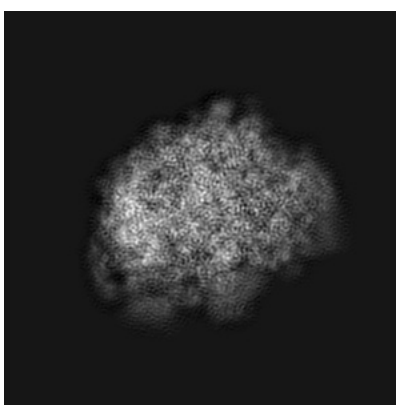
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

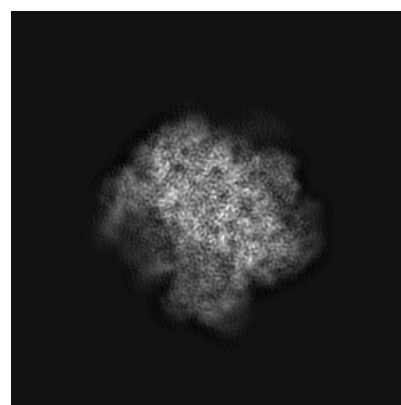
6.1.1 Primary map



X



Y

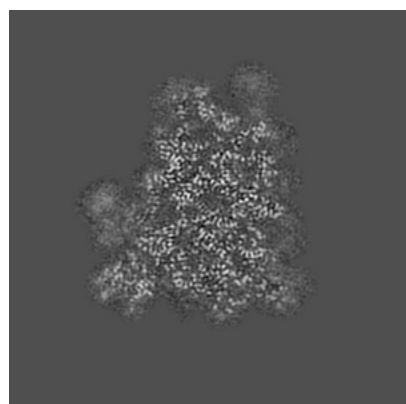


Z

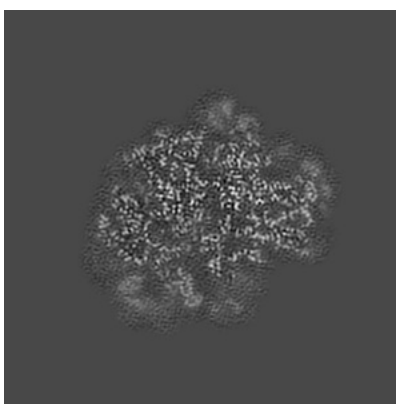
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 180



Y Index: 180

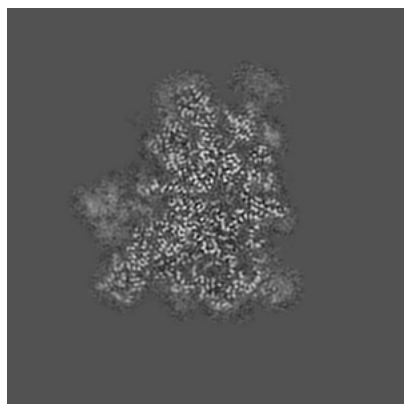


Z Index: 180

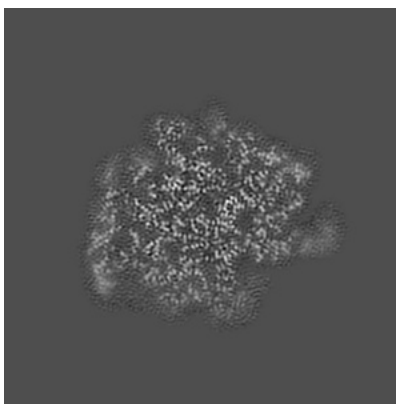
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

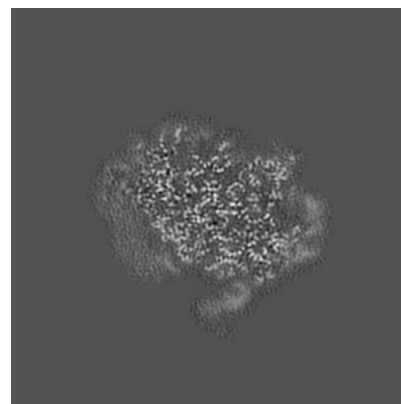
6.3.1 Primary map



X Index: 189



Y Index: 196

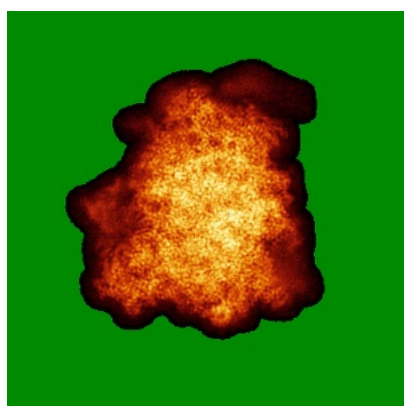


Z Index: 199

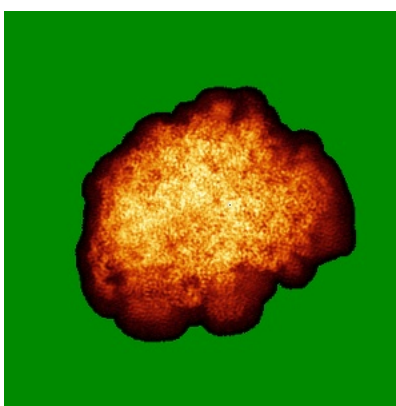
The images above show the largest variance slices of the map in three orthogonal directions.

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

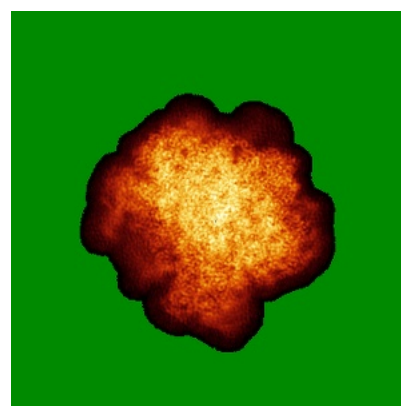
6.4.1 Primary map



X



Y

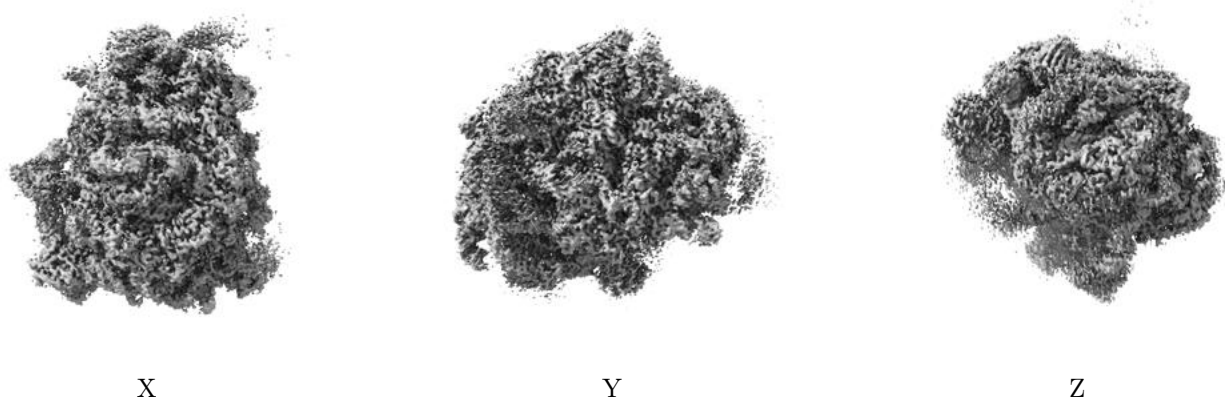


Z

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.

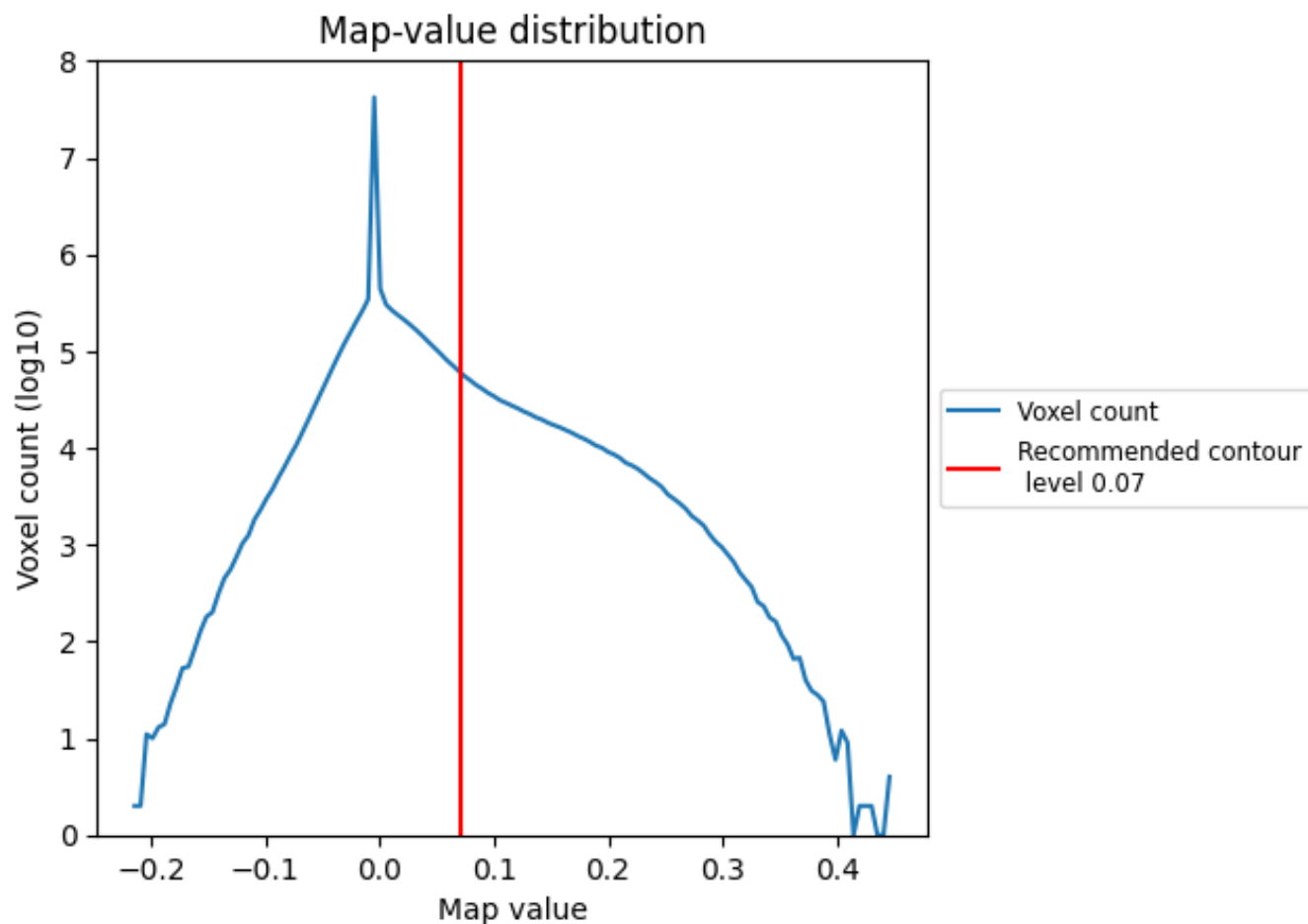
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

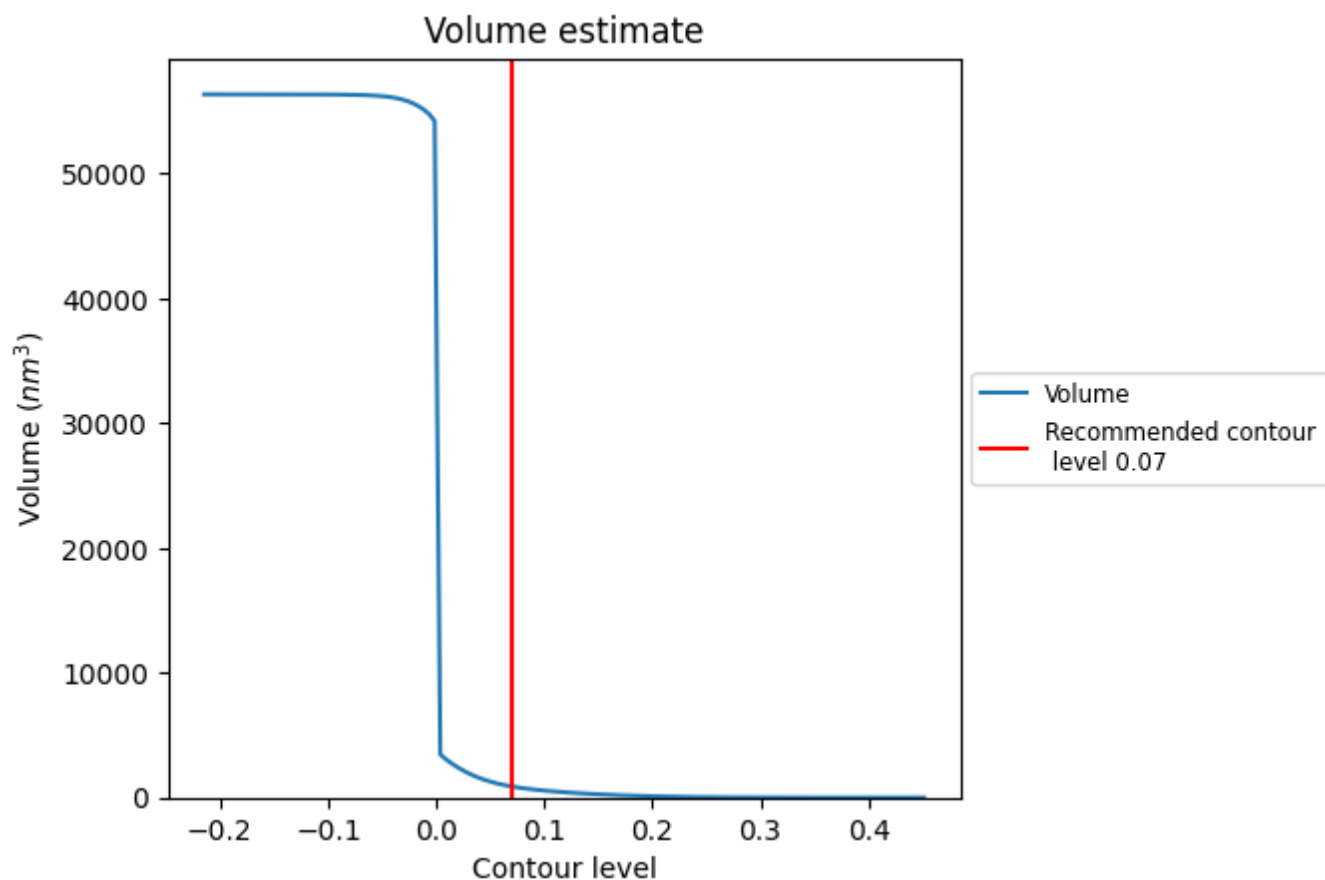
This section contains the results of statistical analysis of the map.

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.

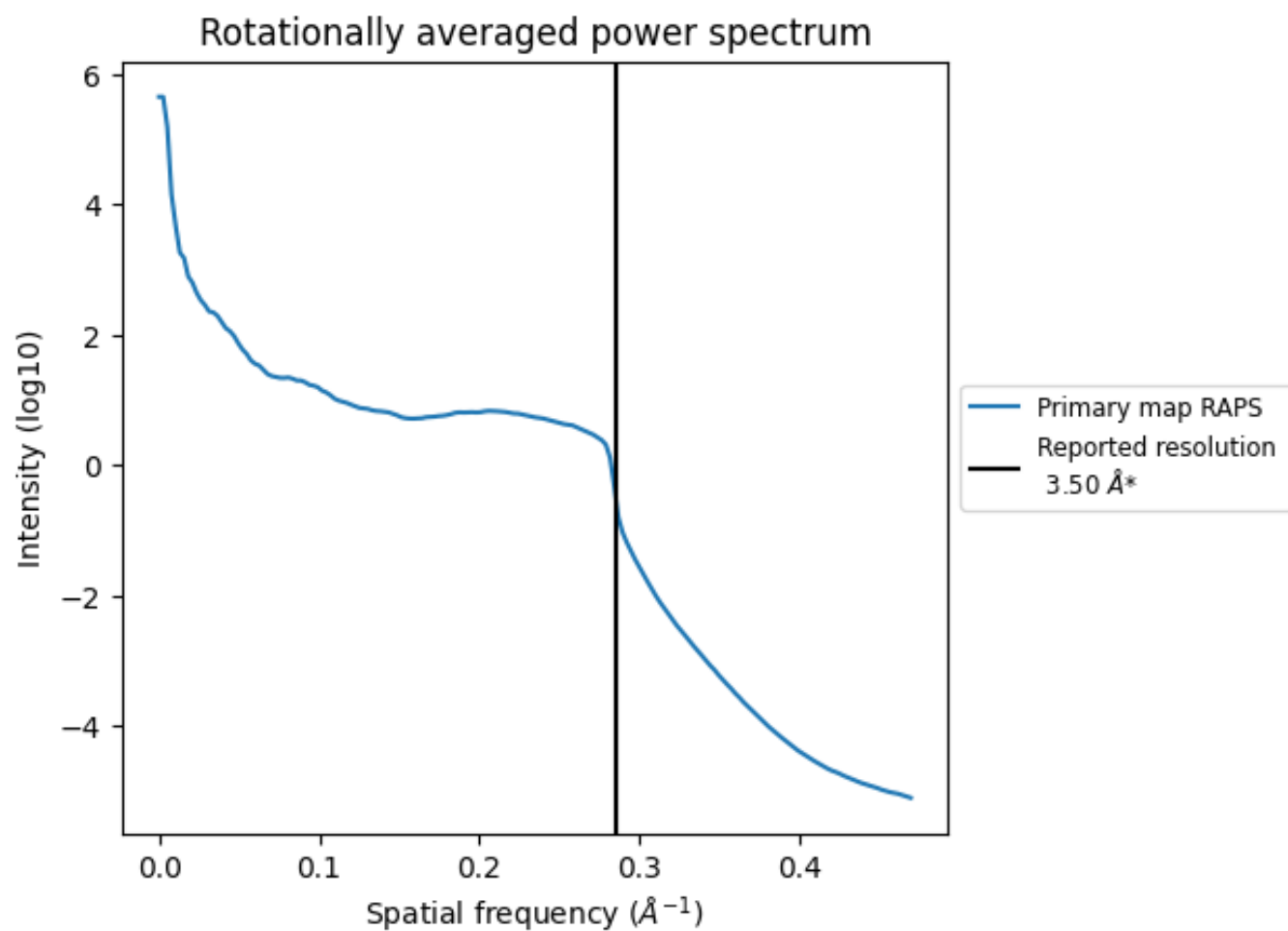
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 889 nm³; this corresponds to an approximate mass of 803 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 0.286 $\text{\AA}^{-1}$

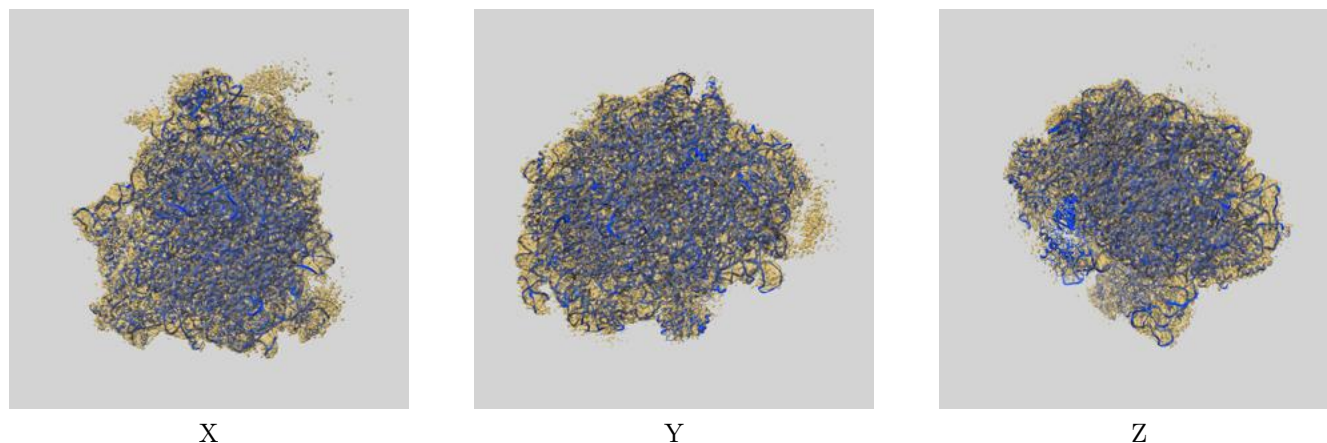
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

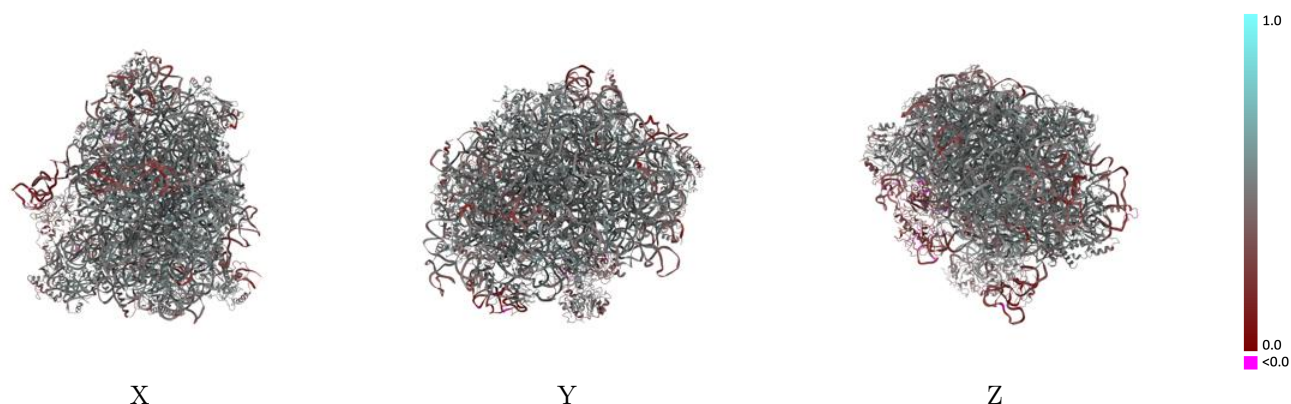
This section contains information regarding the fit between EMDB map EMD-4636 and PDB model 6QTZ. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



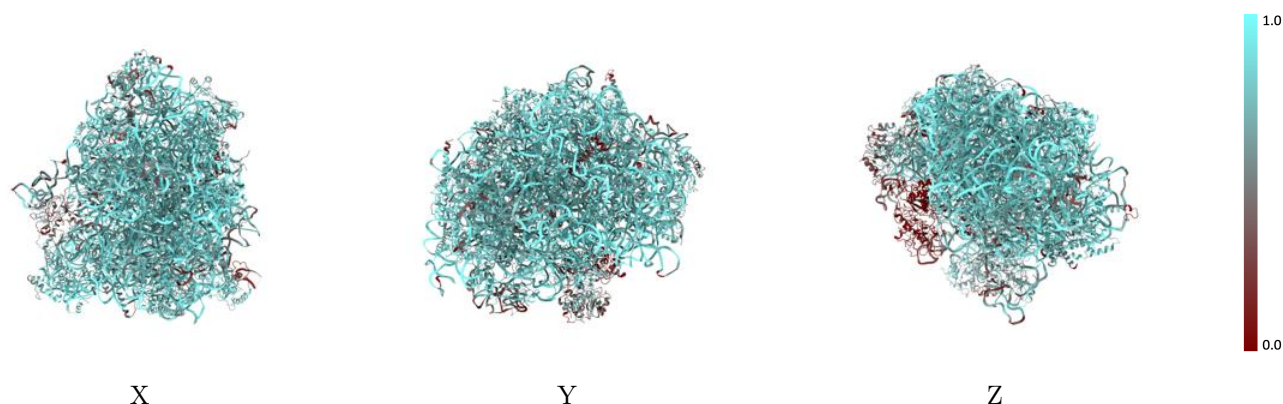
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



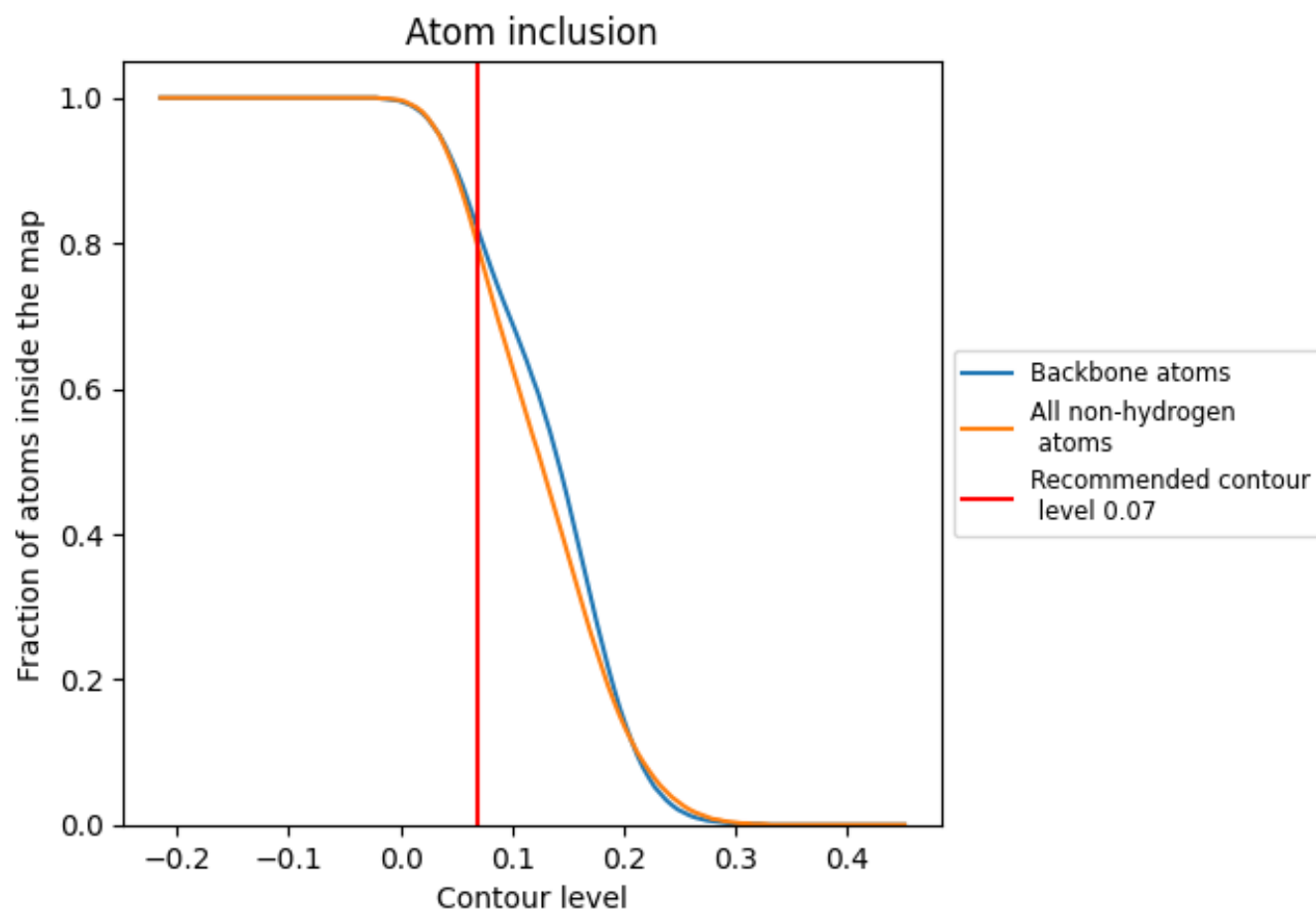
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 82% of all backbone atoms, 79% 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	 0.7930	 0.4630
A	 0.8710	 0.4540
B	 0.8050	 0.5260
C	 0.8040	 0.5100
D	 0.7900	 0.5170
E	 0.7090	 0.4200
F	 0.7600	 0.4820
G	 0.6330	 0.4390
H	 0.7280	 0.4660
J	 0.7770	 0.5030
K	 0.7580	 0.5020
L	 0.7530	 0.5100
M	 0.7530	 0.4890
N	 0.8180	 0.5180
O	 0.8070	 0.5360
P	 0.7950	 0.4760
Q	 0.7890	 0.5220
R	 0.8100	 0.5120
S	 0.8000	 0.5190
T	 0.7590	 0.5060
U	 0.8120	 0.5250
V	 0.7230	 0.4520
W	 0.7730	 0.5110
X	 0.7940	 0.5130
Y	 0.7410	 0.4540
Z	 0.7910	 0.5000
a	 0.7510	 0.5020
b	 0.7930	 0.5060
c	 0.7120	 0.4510
d	 0.7270	 0.4960
e	 0.7650	 0.5230
f	 0.7900	 0.5290
g	 0.7870	 0.5170
h	 0.6020	 0.4520
i	 0.8160	 0.5380



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Chain	Atom inclusion	Q-score
j	 0.6810	 0.4640
k	 0.7900	 0.5310
l	 0.8100	 0.5300
m	 0.7490	 0.4970
n	 0.4930	 0.4150
o	 0.0700	 0.2550
p	 0.4420	 0.3380
q	 0.6610	 0.4810
t	 0.6260	 0.4770
v	 0.3120	 0.3970
w	 0.2900	 0.3340
x	 0.9430	 0.4720
y	 0.9230	 0.4830
z	 0.1820	 0.4250