



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:16 AM UTC

PDB ID : 8V9J / pdb_00008v9j
EMDB ID : EMD-43074
Title : Cryo-EM structure of the Mycobacterium smegmatis 70S ribosome in complex with hibernation factor Msmeg1130 (Balon) (Structure 4)
Authors : Rybak, M.Y.; Helena-Bueno, K.; Hill, C.H.; Melnikov, S.V.; Gagnon, M.G.
Deposited on : 2023-12-08
Resolution : 3.10 Å(reported)
Based on initial model : 5o61

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:

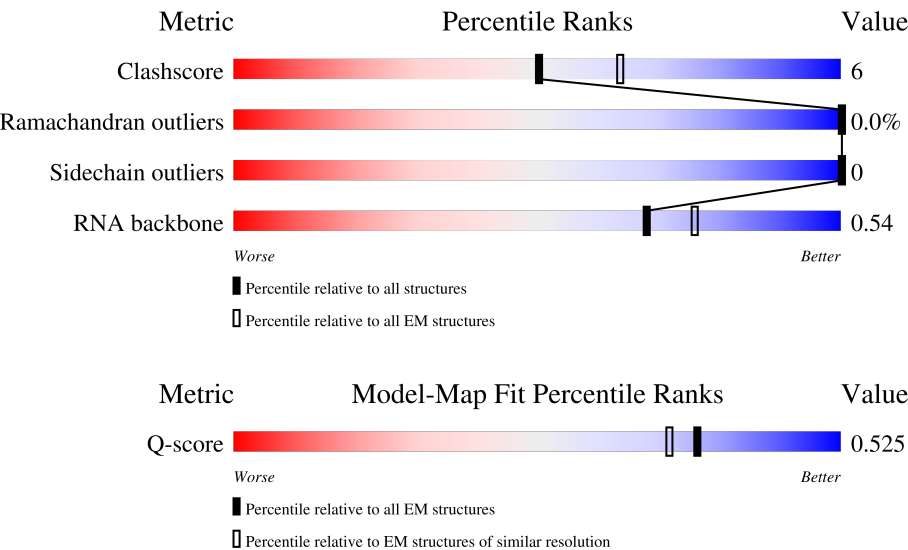
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.10 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.



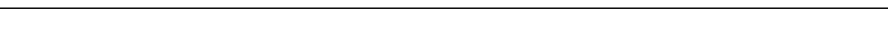
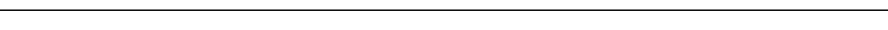
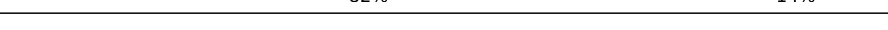
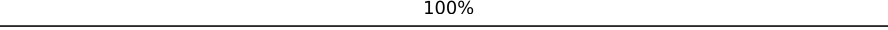
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1528	61%32%6%• 82%
2	b	277	68%14%18% 82%
3	c	275	63%13%24% 82%

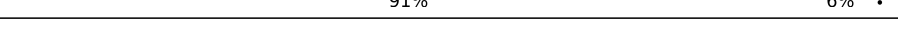
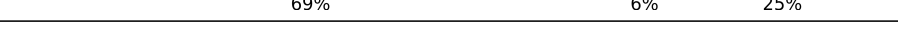
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Mol	Chain	Length	Quality of chain
4	d	201	
5	e	214	
6	f	96	
7	g	156	
8	h	132	
9	i	150	
10	j	101	
11	k	138	
12	l	124	
13	m	124	
14	n	61	
15	o	89	
16	p	156	
17	q	98	
18	r	84	
19	s	93	
20	t	86	
21	u	33	
22	v	3	
23	y	76	
24	z	375	
25	A	3164	
26	B	118	
27	C	278	
28	D	217	

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Mol	Chain	Length	Quality of chain
29	E	215	
30	F	187	
31	G	179	
32	H	151	
33	I	175	
34	J	142	
35	K	235	
36	L	147	
37	M	122	
38	N	147	
39	O	137	
40	P	199	
41	Q	127	
42	R	113	
43	S	129	
44	T	103	
45	U	153	
46	V	100	
47	W	105	
48	X	215	
49	Y	88	
50	Z	64	
51	1	77	
52	2	61	
53	3	75	

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Mol	Chain	Length	Quality of chain
54	4	57	 77% 18% 5%
55	5	55	 73% 16% 11%
56	6	47	 89% 9% .
57	7	64	 77% 22% .
58	8	37	 89% 11%
59	9	24	 75% 21% .

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153055 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	i	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			954	591	196	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	o	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	p	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	t	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 21 is a protein called 30S Ribosomal Protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called poly-U mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	3	Total	C	N	O	P	0	0
			60	27	6	24	3		

- Molecule 23 is a RNA chain called pe/E deacylated phenylalanine-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	y	74	Total	C	N	O	P	S	0	0
			1581	707	285	515	73	1		

- Molecule 24 is a protein called Ribosome hibernation factor Balon (MSMEG_1130).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	362	Total	C	N	O	S	0	0
			2812	1743	528	532	9		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	3073	Total	C	N	O	P	0	0
			65997	29416	12137	21371	3073		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	182	Total	C	N	O	S	0	0
			1439	904	268	261	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 35 is a protein called 50S Ribosomal Protein L01.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	K	102	Total	C	N	O	0	0
			531	316	109	106		

- Molecule 36 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	L	146	Total	C	N	O	S	0
			1130	722	207	200	1	0

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	M	122	Total	C	N	O	S	0
			938	586	179	170	3	0

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	N	145	Total	C	N	O	S	0
			1078	676	205	194	3	0

- Molecule 39 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	O	136	Total	C	N	O	S	0
			1092	690	213	187	2	0

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	P	118	Total	C	N	O	S	0
			928	583	180	163	2	0

- Molecule 41 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Q	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 43 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	S	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 44 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	T	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 45 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	U	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 46 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	V	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	X	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	Y	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 50 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 53 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	59	Total	C	N	O	S	0	0
			436	273	75	83	5		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 55 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 59 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	9	23	Total	C	N	O	S	0	0
			189	111	50	28			

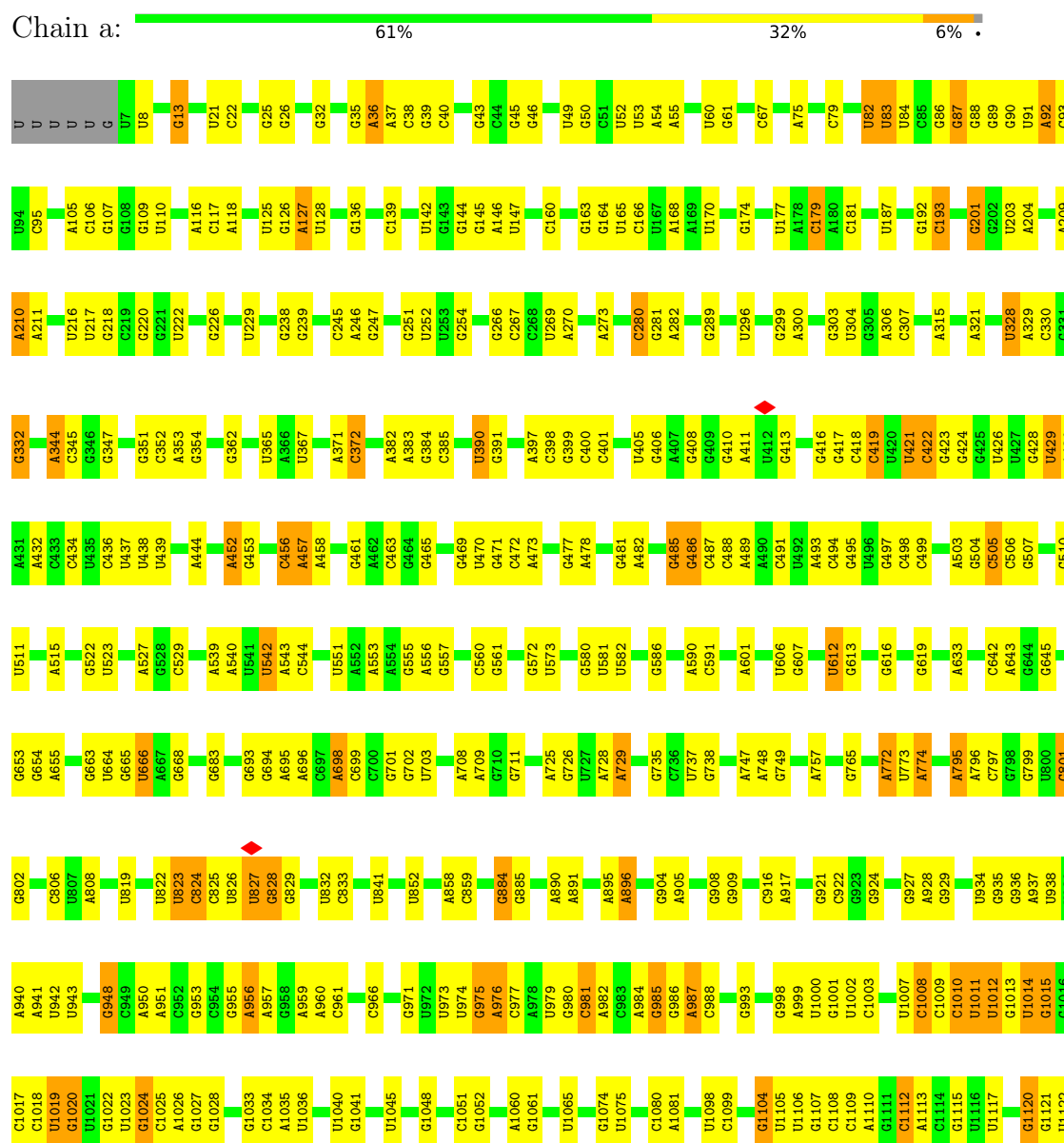
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

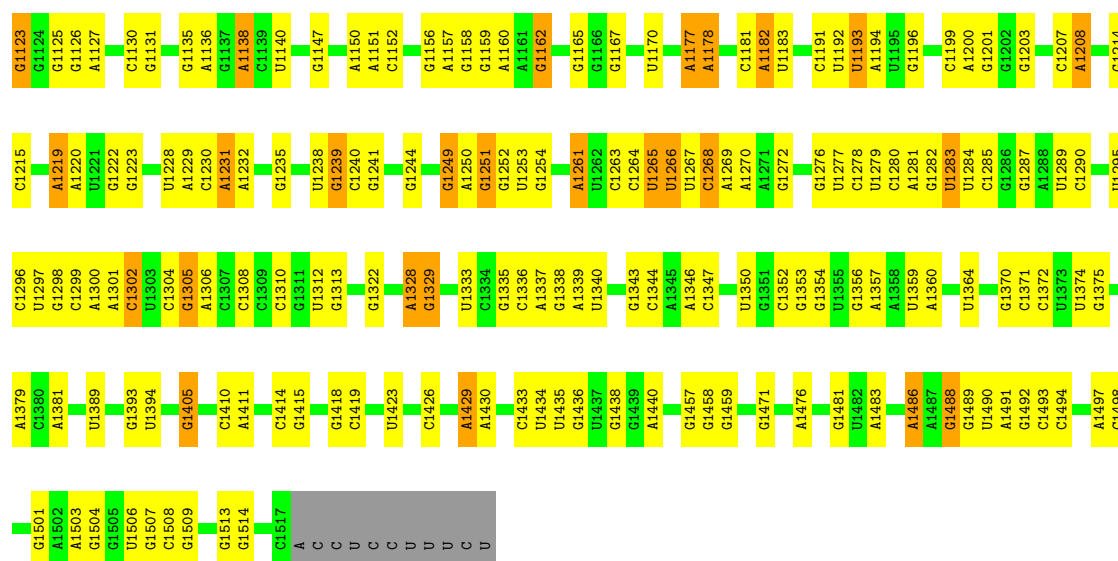
Mol	Chain	Residues	Atoms		AltConf
60	Z	1	Total	Zn	0
			1	1	
60	5	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

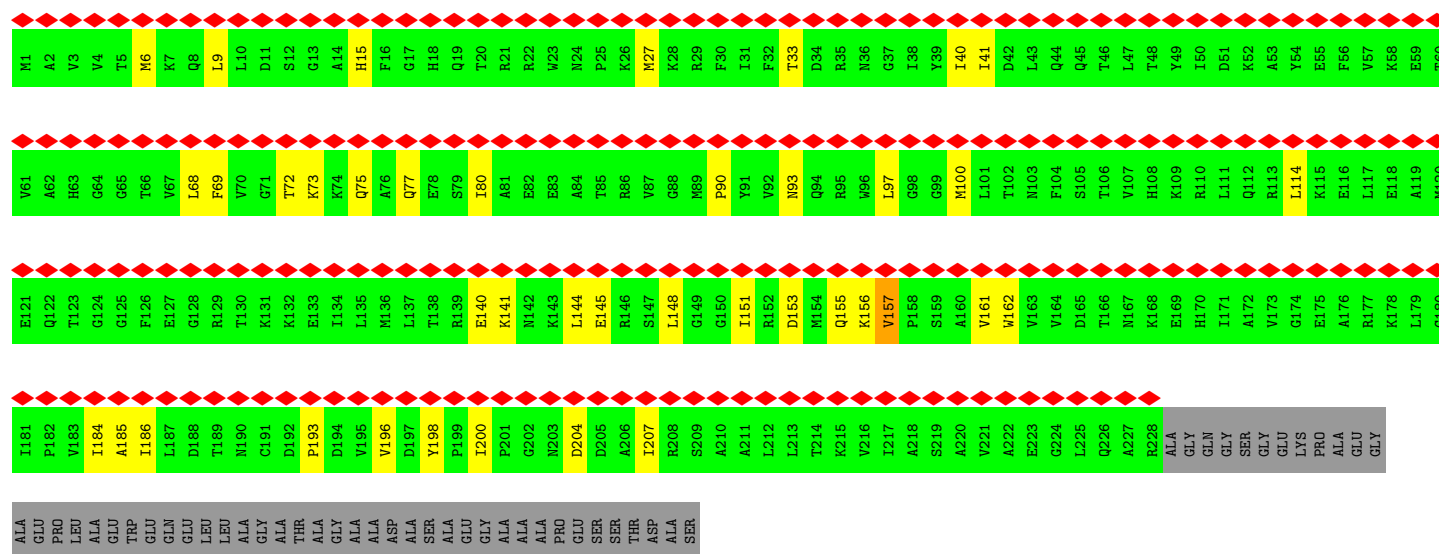
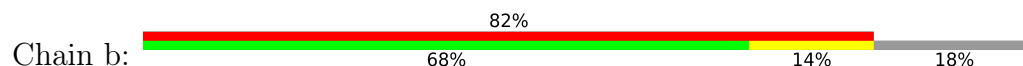
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA

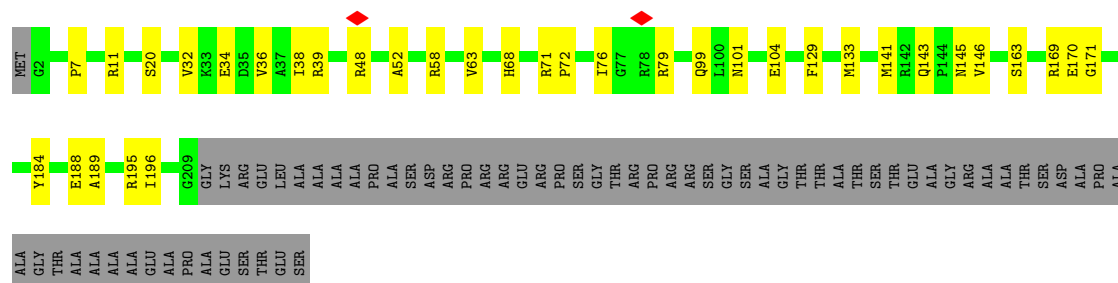




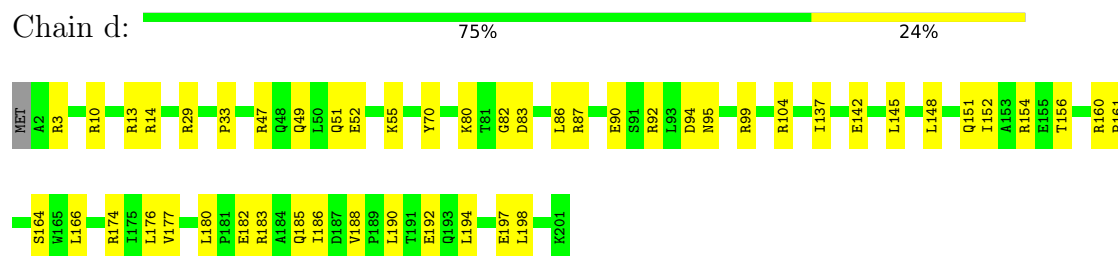
• Molecule 2: 30S Ribosomal Protein S2



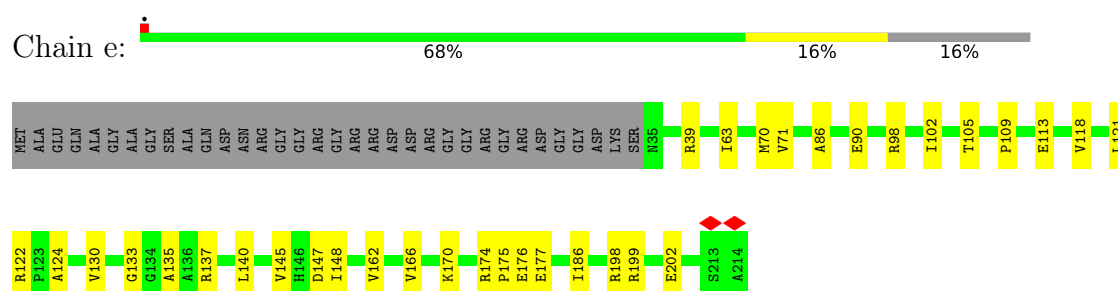
• Molecule 3: 30S ribosomal protein S3



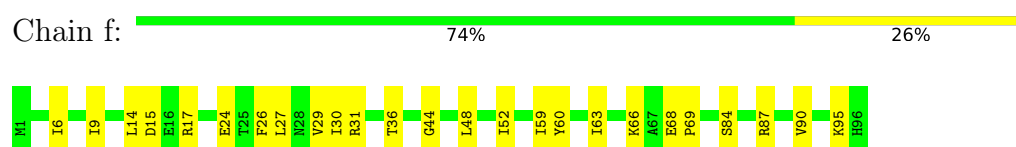
- Molecule 4: 30S ribosomal protein S4



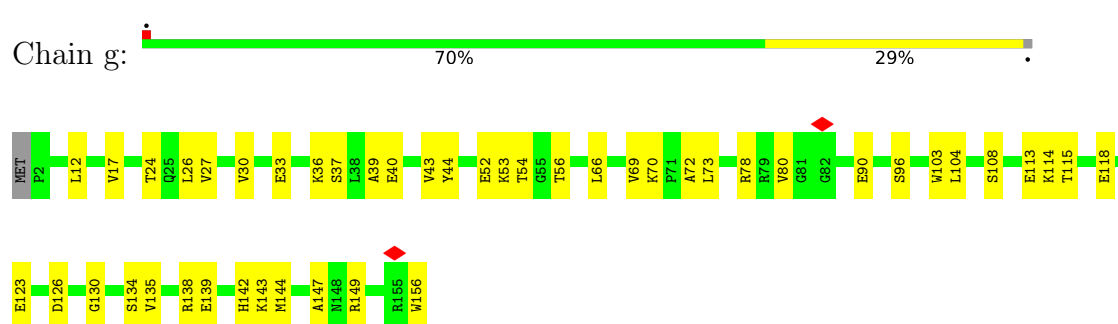
- Molecule 5: 30S Ribosomal Protein S5



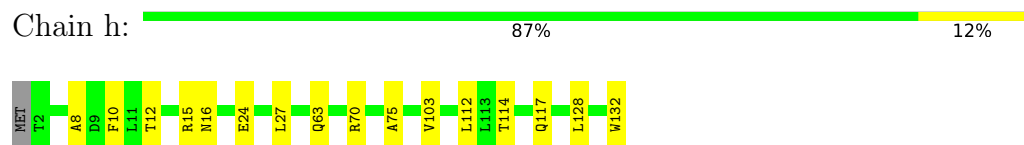
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7

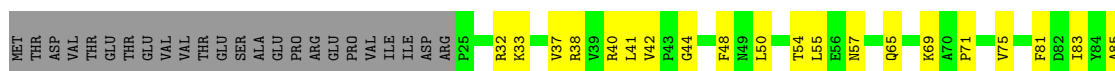


- Molecule 8: 30S Ribosomal Protein S8



- Molecule 9: 30S ribosomal protein S9





- Molecule 10: 30S ribosomal protein S10

Chain j: 77% 21% .



- Molecule 11: 30S ribosomal protein S11

Chain k: 70% 14% 17%



- Molecule 12: 30S ribosomal protein S12

Chain l: 74% 24% .



- Molecule 13: 30S ribosomal protein S13

Chain m: 56% 37% 6%



- Molecule 14: 30S Ribosomal Protein S14

Chain n: 79% 20% .

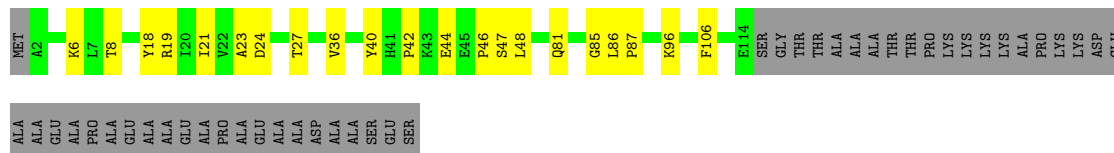


- Molecule 15: 30S Ribosomal Protein S15

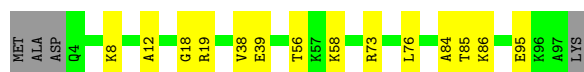
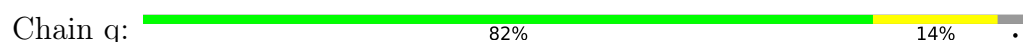
Chain o: 83% 16% .



- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S Ribosomal Protein S18



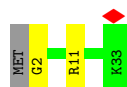
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S Ribosomal Protein S22



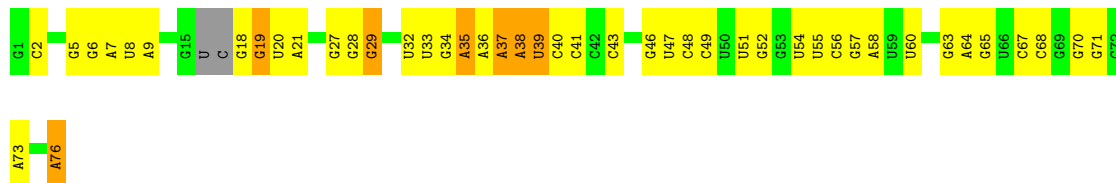
- Molecule 22: poly-U mRNA

Chain v:  100%

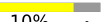
There are no outlier residues recorded for this chain.

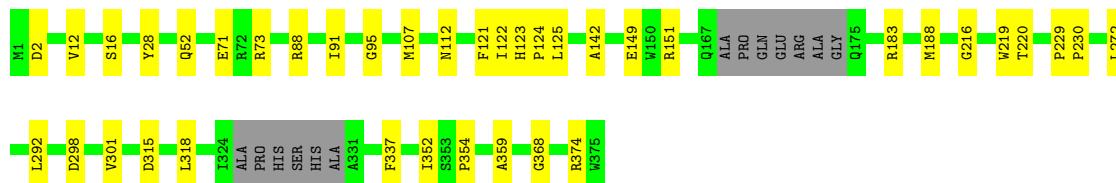
- Molecule 23: pe/E deacylated phenylalanine-tRNA

Chain y:  38%  50%  9% .



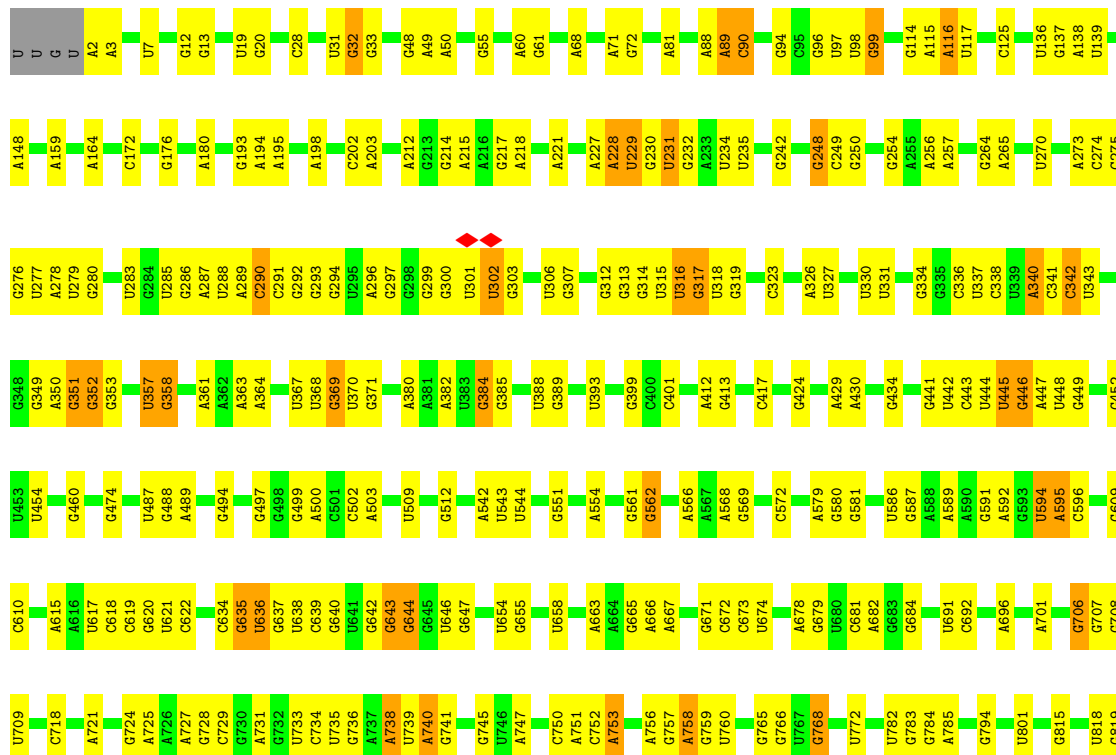
- Molecule 24: Ribosome hibernation factor Balon (MSMEG_1130)

Chain z:  86%  10% .

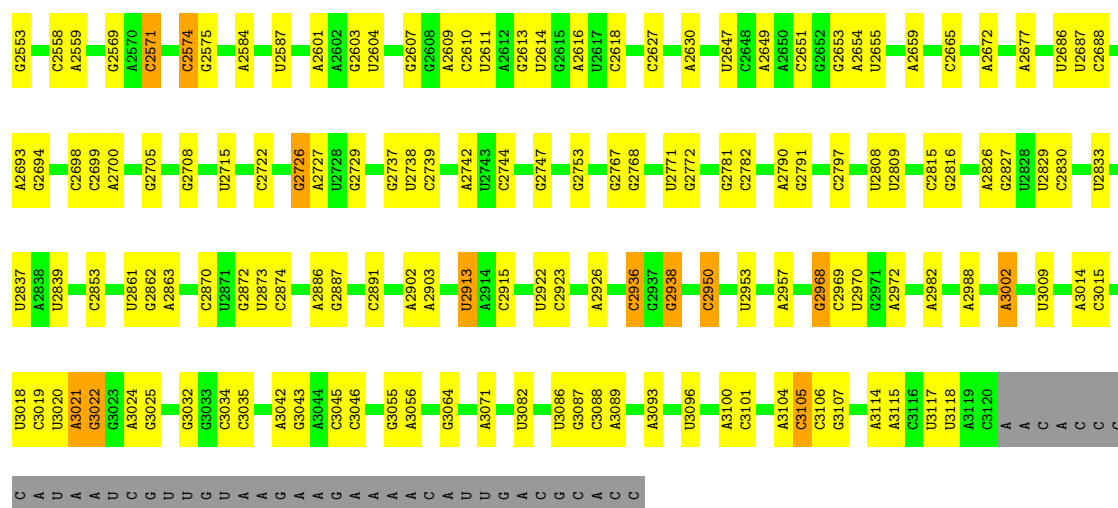


- Molecule 25: 23S Ribosomal RNA

Chain A:  66%  27% . .

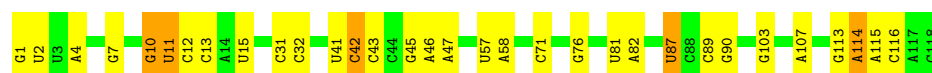






• Molecule 26: 5S Ribosomal RNA

Chain B: 73% 23% .



• Molecule 27: 50S ribosomal protein L2

Chain C: 87% 12% .



• Molecule 28: 50S ribosomal protein L3

Chain D: 84% 14% .

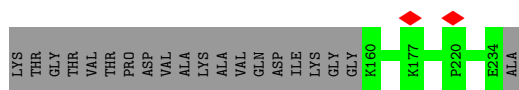


• Molecule 29: 50S Ribosomal Protein L4

Chain E: 87% 11% .



• Molecule 30: 50S Ribosomal Protein L5



- Molecule 36: 50S Ribosomal Protein L13

Chain L: 88% 11% .



- Molecule 37: 50S ribosomal protein L14

Chain M: 88% 12% .



- Molecule 38: 50S ribosomal protein L15

Chain N: 82% 16% .



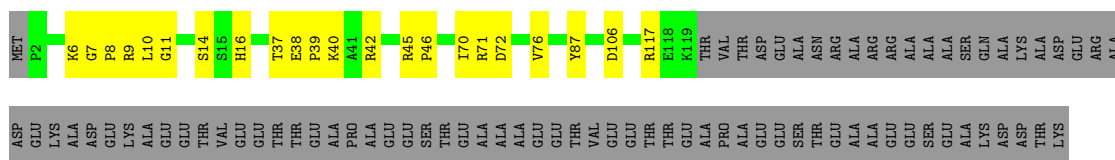
- Molecule 39: 50S Ribosomal Protein L16

Chain O: 85% 14% .



- Molecule 40: 50S ribosomal protein L17

Chain P: 48% 11% 41% .

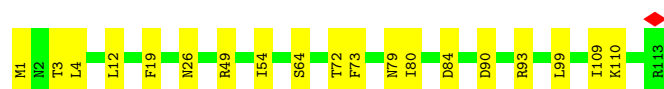
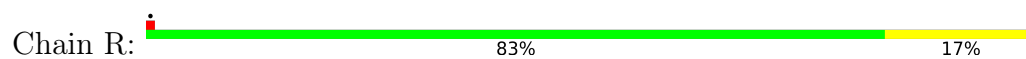


- Molecule 41: 50S Ribosomal Protein L18

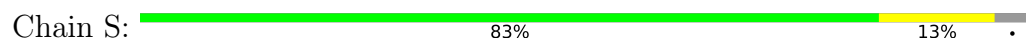
Chain Q: 87% 13% .



- Molecule 42: 50S ribosomal protein L19



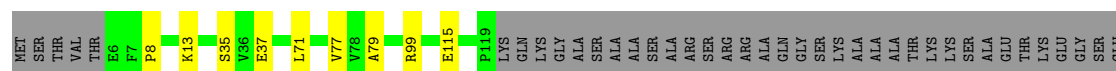
- Molecule 43: 50S Ribosomal Protein L20



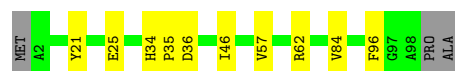
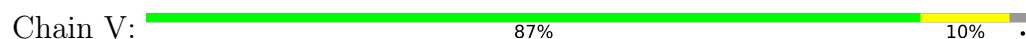
- Molecule 44: 50S Ribosomal Protein L21



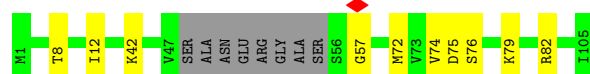
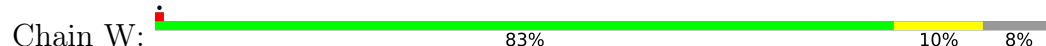
- Molecule 45: 50S Ribosomal Protein L22



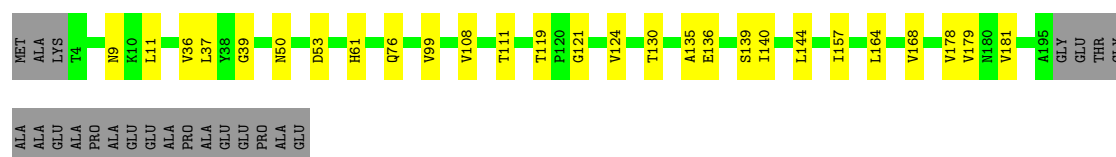
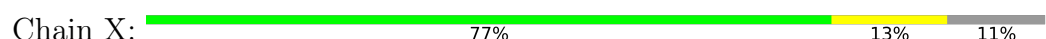
- Molecule 46: 50S Ribosomal Protein L23



- Molecule 47: 50S ribosomal protein L24



- Molecule 48: 50S ribosomal protein L25



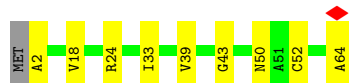
- Molecule 49: 50S ribosomal protein L27

Chain Y:  83% 7% 10%



- Molecule 50: 50S Ribosomal Protein L28

Chain Z:  84% 14% .



- Molecule 51: 50S ribosomal protein L29

Chain 1:  66% 17% 17%



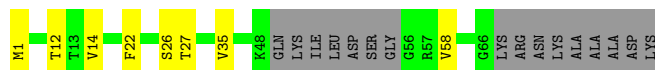
- Molecule 52: 50S ribosomal protein L30

Chain 2:  90% 7% .



- Molecule 53: 50S Ribosomal Protein L31

Chain 3:  68% 11% 21%



- Molecule 54: 50S ribosomal protein L32

Chain 4:  77% 18% 5%



- Molecule 55: 50S Ribosomal Protein L33

Chain 5:  73% 16% 11%



- Molecule 56: 50S ribosomal protein L34

Chain 6:  89% 9% .



- Molecule 57: 50S ribosomal protein L35

Chain 7:  77% 22% .



- Molecule 58: 50S ribosomal protein L36

Chain 8:  89% 11% .



- Molecule 59: 50S Ribosomal Protein L37

Chain 9:  75% 21% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	302401	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.10	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.657	Depositor
Minimum map value	-0.336	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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: 7MG, 5MU, PSU, ZN, 4SU

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	0.15	0/36309	0.27	0/56657
2	b	0.09	0/1822	0.28	0/2457
3	c	0.11	0/1684	0.28	0/2261
4	d	0.13	0/1672	0.34	0/2251
5	e	0.15	0/1312	0.31	0/1772
6	f	0.15	0/782	0.38	0/1059
7	g	0.16	0/1252	0.43	0/1690
8	h	0.15	0/1025	0.30	0/1385
9	i	0.12	0/1012	0.34	0/1362
10	j	0.13	0/802	0.34	0/1086
11	k	0.17	0/873	0.34	0/1180
12	l	0.15	0/965	0.32	0/1290
13	m	0.14	0/942	0.38	0/1260
14	n	0.11	0/488	0.30	0/650
15	o	0.18	0/729	0.31	0/977
16	p	0.16	0/908	0.41	0/1226
17	q	0.13	0/759	0.31	0/1016
18	r	0.15	0/518	0.26	0/693
19	s	0.11	0/680	0.34	0/915
20	t	0.17	0/663	0.28	0/882
21	u	0.16	0/280	0.29	0/359
22	v	0.12	0/65	0.15	0/98
23	y	0.17	0/1628	0.28	0/2536
24	z	0.14	0/2852	0.29	0/3859
25	A	0.19	0/73900	0.29	0/115307
26	B	0.15	0/2821	0.26	0/4396
27	C	0.21	0/2153	0.31	0/2895
28	D	0.20	0/1609	0.36	0/2165
29	E	0.18	0/1592	0.29	0/2153
30	F	0.13	0/1461	0.26	0/1966
31	G	0.14	0/1369	0.27	0/1848
32	H	0.10	0/1027	0.28	0/1398

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.10	0/925	0.28	0/1246
34	J	0.13	0/1006	0.33	0/1364
35	K	0.07	0/530	0.22	0/731
36	L	0.18	0/1157	0.28	0/1567
37	M	0.18	0/946	0.29	0/1268
38	N	0.20	0/1091	0.36	0/1457
39	O	0.17	0/1118	0.31	0/1506
40	P	0.19	0/945	0.32	0/1267
41	Q	0.13	0/966	0.24	0/1298
42	R	0.18	0/921	0.36	0/1236
43	S	0.20	0/1000	0.26	0/1341
44	T	0.17	0/764	0.25	0/1030
45	U	0.19	0/887	0.30	0/1204
46	V	0.17	0/766	0.24	0/1030
47	W	0.14	0/738	0.29	0/987
48	X	0.14	0/1443	0.27	0/1970
49	Y	0.18	0/595	0.27	0/798
50	Z	0.20	0/478	0.30	0/641
51	1	0.15	0/534	0.23	0/713
52	2	0.18	0/477	0.25	0/640
53	3	0.10	0/445	0.29	0/600
54	4	0.21	0/427	0.28	0/572
55	5	0.17	0/413	0.26	0/553
56	6	0.21	0/380	0.27	0/500
57	7	0.20	0/507	0.30	0/672
58	8	0.17	0/303	0.30	0/401
59	9	0.21	0/191	0.29	0/247
All	All	0.17	0/165907	0.29	0/247888

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
7	g	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	g	113	GLU	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	a	32439	0	16321	338	0
2	b	1793	0	1839	26	0
3	c	1660	0	1707	24	0
4	d	1641	0	1668	35	0
5	e	1296	0	1360	22	0
6	f	771	0	797	17	0
7	g	1232	0	1282	36	0
8	h	1010	0	1046	11	0
9	i	994	0	1050	24	0
10	j	788	0	819	17	0
11	k	855	0	863	15	0
12	l	954	0	1034	22	0
13	m	935	0	986	32	0
14	n	477	0	503	10	0
15	o	720	0	760	8	0
16	p	891	0	935	18	0
17	q	748	0	795	11	0
18	r	513	0	540	7	0
19	s	662	0	677	15	0
20	t	660	0	712	4	0
21	u	280	0	342	2	0
22	v	60	0	31	0	0
23	y	1581	0	808	30	0
24	z	2812	0	2804	26	0
25	A	65997	0	33205	469	0
26	B	2522	0	1285	16	0
27	C	2110	0	2165	25	0
28	D	1587	0	1630	22	0
29	E	1569	0	1607	13	0
30	F	1439	0	1465	25	0
31	G	1348	0	1399	13	0
32	H	1018	0	988	12	0
33	I	918	0	959	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	J	990	0	1021	16	0
35	K	531	0	271	1	0
36	L	1130	0	1167	12	0
37	M	938	0	1000	12	0
38	N	1078	0	1151	17	0
39	O	1092	0	1128	12	0
40	P	928	0	972	16	0
41	Q	956	0	991	9	0
42	R	907	0	938	14	0
43	S	988	0	1038	14	0
44	T	754	0	802	4	0
45	U	873	0	909	7	0
46	V	756	0	802	7	0
47	W	732	0	782	8	0
48	X	1428	0	1443	15	0
49	Y	586	0	601	6	0
50	Z	470	0	480	8	0
51	1	531	0	541	8	0
52	2	474	0	500	2	0
53	3	436	0	410	7	0
54	4	423	0	463	13	0
55	5	405	0	407	7	0
56	6	377	0	411	2	0
57	7	502	0	541	11	0
58	8	299	0	324	2	0
59	9	189	0	205	4	0
60	5	1	0	0	0	0
60	Z	1	0	0	0	0
All	All	153055	0	103680	1410	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 6.

The worst 5 of 1410 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)
1:a:993:G:H1	1:a:1002:U:H3	1.05	1.00
1:a:1010:C:N4	1:a:1014:U:H3	1.60	0.99
1:a:410:G:H21	1:a:432:A:H62	1.11	0.98
1:a:1232:A:H62	1:a:1268:C:N4	1.62	0.96
23:y:51:U:H3	23:y:63:G:H1	1.00	0.93

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	
2	b	226/277 (82%)	216 (96%)	9 (4%)	1 (0%)	30	61
3	c	206/275 (75%)	198 (96%)	8 (4%)	0	100	100
4	d	198/201 (98%)	186 (94%)	12 (6%)	0	100	100
5	e	178/214 (83%)	171 (96%)	7 (4%)	0	100	100
6	f	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
7	g	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
8	h	129/132 (98%)	128 (99%)	1 (1%)	0	100	100
9	i	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
10	j	97/101 (96%)	92 (95%)	4 (4%)	1 (1%)	12	41
11	k	113/138 (82%)	106 (94%)	7 (6%)	0	100	100
12	l	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
13	m	114/124 (92%)	107 (94%)	7 (6%)	0	100	100
14	n	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
15	o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	p	111/156 (71%)	103 (93%)	8 (7%)	0	100	100
17	q	92/98 (94%)	88 (96%)	4 (4%)	0	100	100
18	r	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
19	s	80/93 (86%)	74 (92%)	6 (8%)	0	100	100
20	t	83/86 (96%)	83 (100%)	0	0	100	100
21	u	30/33 (91%)	29 (97%)	1 (3%)	0	100	100
24	z	356/375 (95%)	342 (96%)	14 (4%)	0	100	100
27	C	273/278 (98%)	260 (95%)	13 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	D	212/217 (98%)	203 (96%)	9 (4%)	0	100	100
29	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
30	F	180/187 (96%)	171 (95%)	9 (5%)	0	100	100
31	G	174/179 (97%)	168 (97%)	6 (3%)	0	100	100
32	H	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
33	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
34	J	131/142 (92%)	121 (92%)	10 (8%)	0	100	100
35	K	98/235 (42%)	88 (90%)	10 (10%)	0	100	100
36	L	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
37	M	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
38	N	143/147 (97%)	124 (87%)	19 (13%)	0	100	100
39	O	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
40	P	116/199 (58%)	112 (97%)	4 (3%)	0	100	100
41	Q	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
42	R	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
43	S	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
44	T	98/103 (95%)	97 (99%)	1 (1%)	0	100	100
45	U	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
46	V	95/100 (95%)	91 (96%)	4 (4%)	0	100	100
47	W	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
48	X	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
49	Y	77/88 (88%)	71 (92%)	6 (8%)	0	100	100
50	Z	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
51	1	62/77 (80%)	62 (100%)	0	0	100	100
52	2	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
53	3	55/75 (73%)	52 (94%)	3 (6%)	0	100	100
54	4	52/57 (91%)	52 (100%)	0	0	100	100
55	5	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
56	6	44/47 (94%)	44 (100%)	0	0	100	100
57	7	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
58	8	35/37 (95%)	33 (94%)	2 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	9	21/24 (88%)	21 (100%)	0	0	100	100
All	All	6433/7288 (88%)	6149 (96%)	282 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	j	57	LYS
2	b	157	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	191/218 (88%)	191 (100%)	0	100	100
3	c	170/212 (80%)	170 (100%)	0	100	100
4	d	175/176 (99%)	175 (100%)	0	100	100
5	e	127/147 (86%)	127 (100%)	0	100	100
6	f	85/85 (100%)	85 (100%)	0	100	100
7	g	131/132 (99%)	131 (100%)	0	100	100
8	h	107/108 (99%)	107 (100%)	0	100	100
9	i	102/125 (82%)	102 (100%)	0	100	100
10	j	89/90 (99%)	89 (100%)	0	100	100
11	k	89/105 (85%)	89 (100%)	0	100	100
12	l	102/105 (97%)	102 (100%)	0	100	100
13	m	99/104 (95%)	99 (100%)	0	100	100
14	n	49/50 (98%)	49 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	92/118 (78%)	92 (100%)	0	100	100
17	q	80/83 (96%)	80 (100%)	0	100	100
18	r	55/72 (76%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	s	73/84 (87%)	73 (100%)	0	100	100
20	t	69/70 (99%)	69 (100%)	0	100	100
21	u	30/31 (97%)	30 (100%)	0	100	100
24	z	288/297 (97%)	288 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100
28	D	160/163 (98%)	160 (100%)	0	100	100
29	E	169/173 (98%)	169 (100%)	0	100	100
30	F	150/156 (96%)	150 (100%)	0	100	100
31	G	148/150 (99%)	148 (100%)	0	100	100
32	H	90/116 (78%)	90 (100%)	0	100	100
33	I	89/120 (74%)	89 (100%)	0	100	100
34	J	102/108 (94%)	102 (100%)	0	100	100
35	K	6/184 (3%)	6 (100%)	0	100	100
36	L	119/120 (99%)	119 (100%)	0	100	100
37	M	100/100 (100%)	100 (100%)	0	100	100
38	N	112/114 (98%)	112 (100%)	0	100	100
39	O	114/115 (99%)	114 (100%)	0	100	100
40	P	97/158 (61%)	97 (100%)	0	100	100
41	Q	93/94 (99%)	93 (100%)	0	100	100
42	R	100/100 (100%)	100 (100%)	0	100	100
43	S	97/99 (98%)	97 (100%)	0	100	100
44	T	81/83 (98%)	81 (100%)	0	100	100
45	U	90/117 (77%)	90 (100%)	0	100	100
46	V	83/85 (98%)	83 (100%)	0	100	100
47	W	81/86 (94%)	81 (100%)	0	100	100
48	X	155/168 (92%)	155 (100%)	0	100	100
49	Y	58/63 (92%)	58 (100%)	0	100	100
50	Z	50/51 (98%)	50 (100%)	0	100	100
51	1	58/66 (88%)	58 (100%)	0	100	100
52	2	52/54 (96%)	52 (100%)	0	100	100
53	3	47/63 (75%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	4	43/46 (94%)	43 (100%)	0	100	100
55	5	47/52 (90%)	47 (100%)	0	100	100
56	6	35/36 (97%)	35 (100%)	0	100	100
57	7	53/54 (98%)	53 (100%)	0	100	100
58	8	35/35 (100%)	35 (100%)	0	100	100
59	9	18/19 (95%)	18 (100%)	0	100	100
All	All	5226/5855 (89%)	5226 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
36	L	103	ASN
58	8	34	GLN
41	Q	56	ASN
58	8	20	HIS
49	Y	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1510/1528 (98%)	259 (17%)	0
22	v	2/3 (66%)	0	0
23	y	72/76 (94%)	15 (20%)	0
25	A	3071/3164 (97%)	499 (16%)	15 (0%)
26	B	117/118 (99%)	13 (11%)	1 (0%)
All	All	4772/4889 (97%)	786 (16%)	16 (0%)

5 of 786 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	U
1	a	13	G
1	a	36	A
1	a	43	G
1	a	52	U

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	2381	A
25	A	2094	G
25	A	980	C
25	A	1730	U
25	A	974	G

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

6 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
23	4SU	y	8	23	18,21,22	1.90	4 (22%)	25,30,33	2.16	4 (16%)
23	7MG	y	46	23	23,26,27	1.32	3 (13%)	27,39,42	2.59	7 (25%)
23	PSU	y	32	23	18,21,22	1.36	2 (11%)	21,30,33	1.96	3 (14%)
23	PSU	y	55	23	18,21,22	1.36	2 (11%)	21,30,33	2.06	4 (19%)
23	PSU	y	39	23	18,21,22	1.40	3 (16%)	21,30,33	1.93	3 (14%)
23	5MU	y	54	23	19,22,23	1.39	5 (26%)	27,32,35	2.13	6 (22%)

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
23	4SU	y	8	23	-	0/7/25/26	0/2/2/2
23	7MG	y	46	23	-	5/7/37/38	0/3/3/3
23	PSU	y	32	23	-	0/7/25/26	0/2/2/2
23	PSU	y	55	23	-	0/7/25/26	0/2/2/2
23	PSU	y	39	23	-	2/7/25/26	0/2/2/2
23	5MU	y	54	23	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	8	4SU	C4-S4	-5.10	1.59	1.68
23	y	8	4SU	C4-N3	-3.56	1.33	1.37
23	y	39	PSU	C6-C5	3.46	1.39	1.35
23	y	55	PSU	C6-C5	3.30	1.38	1.35
23	y	46	7MG	C5-C4	3.21	1.47	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	y	46	7MG	N9-C4-N3	8.77	138.31	125.46
23	y	55	PSU	N1-C2-N3	6.40	121.92	115.17
23	y	8	4SU	C4-N3-C2	-6.34	121.23	127.31
23	y	32	PSU	N1-C2-N3	6.13	121.63	115.17
23	y	39	PSU	N1-C2-N3	6.02	121.52	115.17

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	y	39	PSU	C3'-C4'-C5'-O5'
23	y	39	PSU	O4'-C4'-C5'-O5'
23	y	46	7MG	C2'-C1'-N9-C8
23	y	46	7MG	O4'-C4'-C5'-O5'
23	y	46	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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.

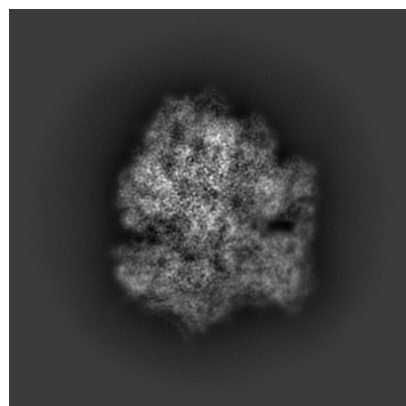
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43074. These allow visual inspection of the internal detail of the map and identification of artifacts.

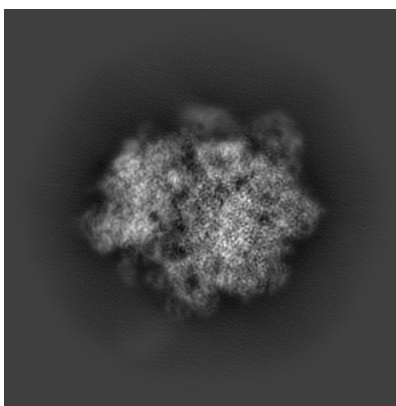
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

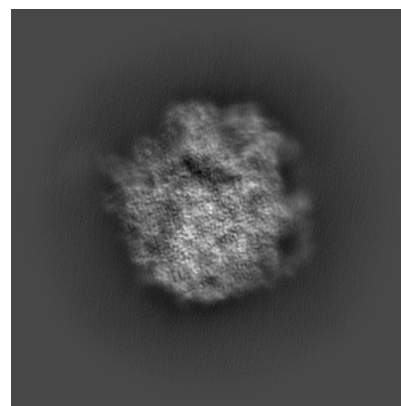
6.1.1 Primary map



X

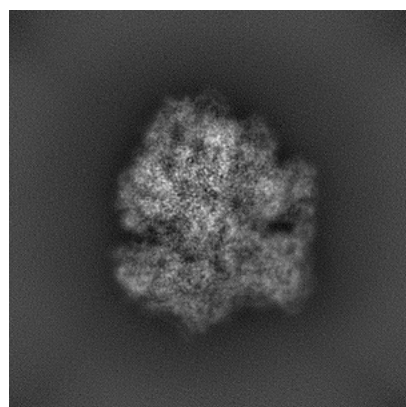


Y

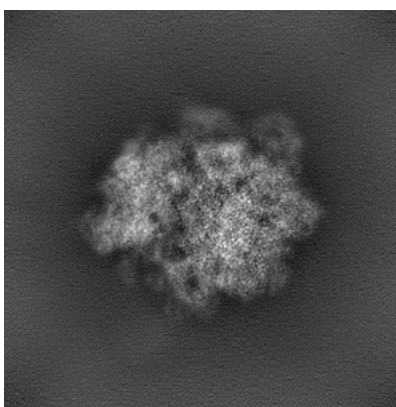


Z

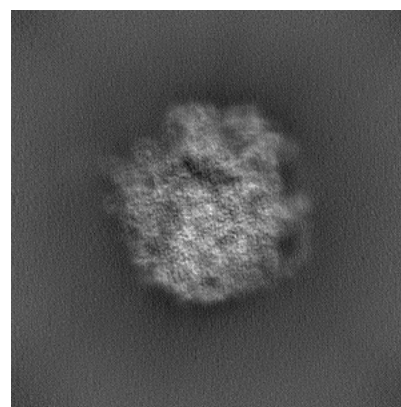
6.1.2 Raw map



X



Y

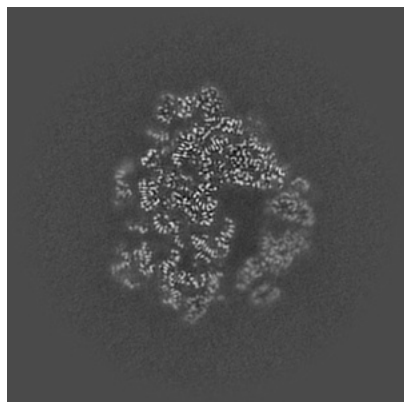


Z

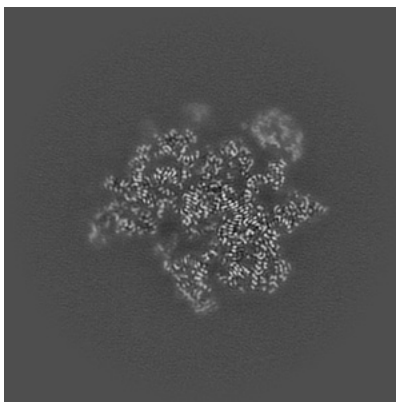
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

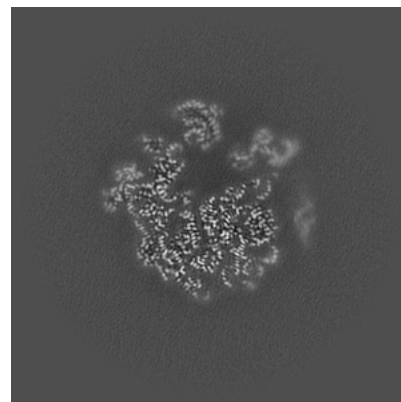
6.2.1 Primary map



X Index: 256

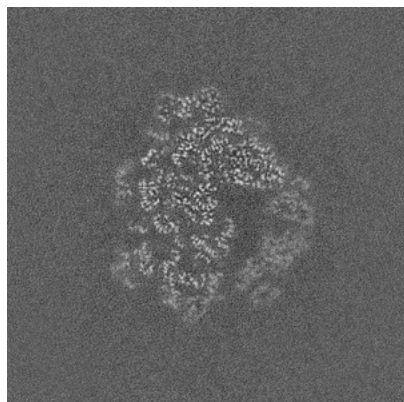


Y Index: 256

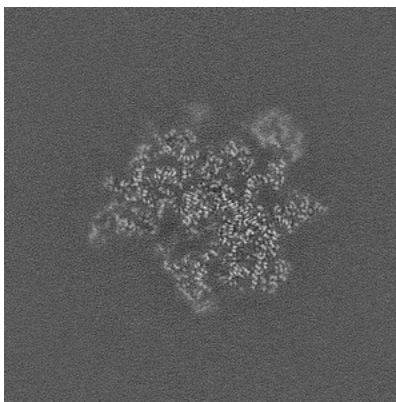


Z Index: 256

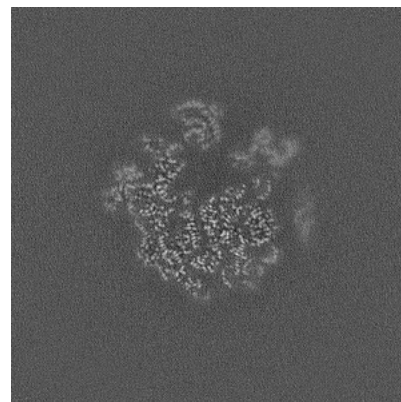
6.2.2 Raw map



X Index: 256



Y Index: 256

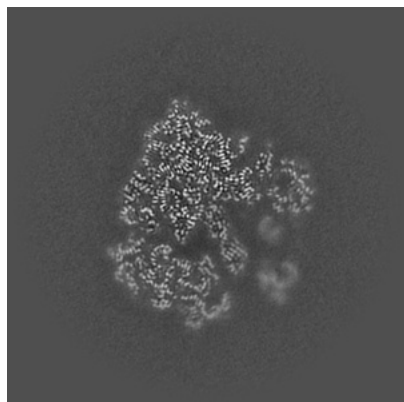


Z Index: 256

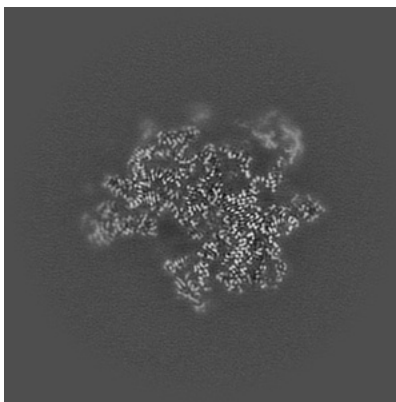
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

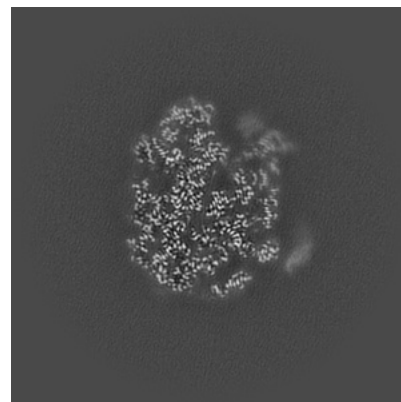
6.3.1 Primary map



X Index: 223

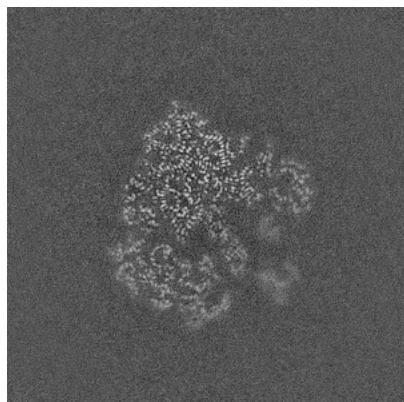


Y Index: 252

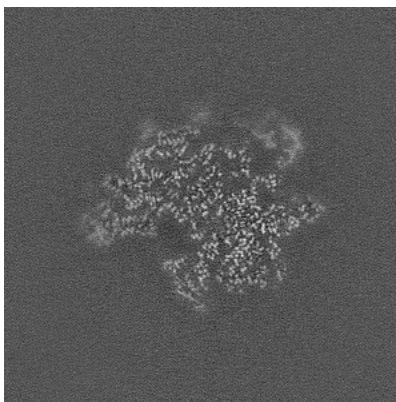


Z Index: 282

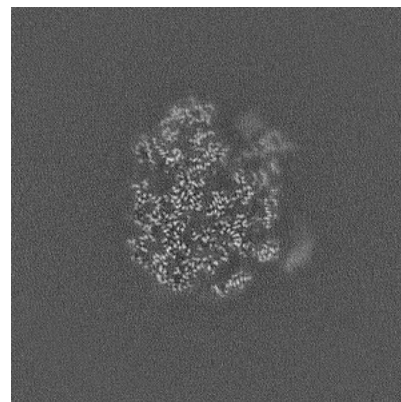
6.3.2 Raw map



X Index: 222



Y Index: 251

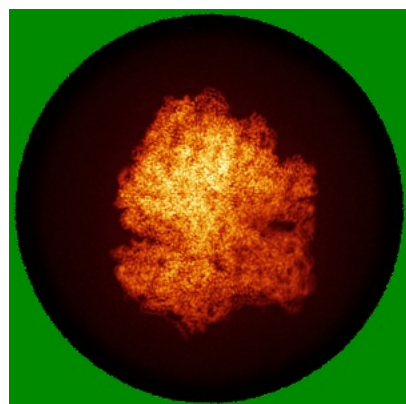


Z Index: 282

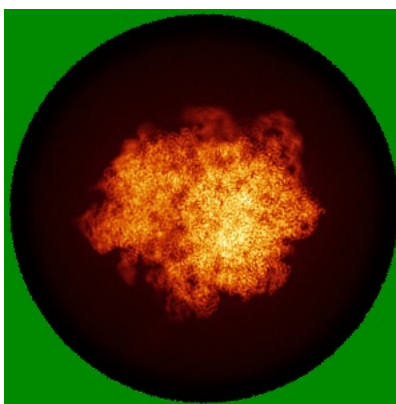
The images above show the largest variance slices of the map in three orthogonal directions.

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

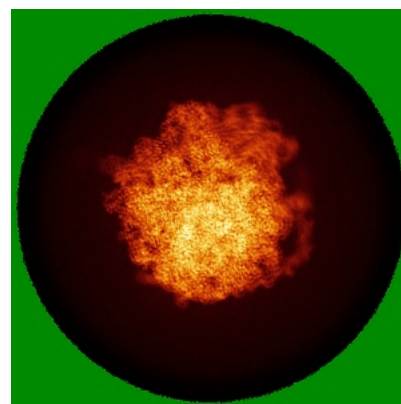
6.4.1 Primary map



X

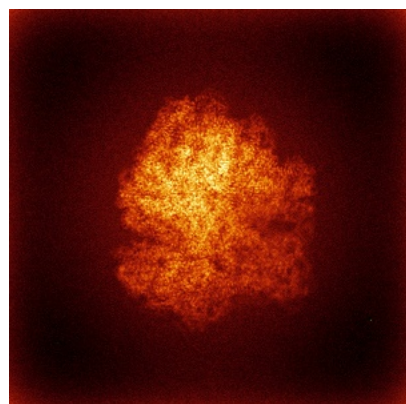


Y

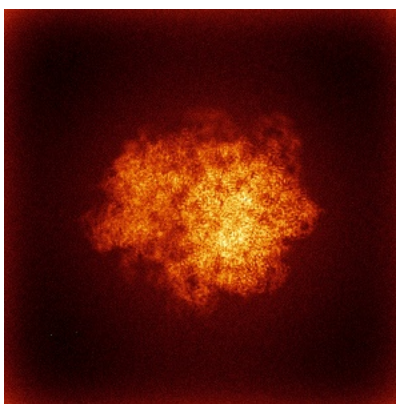


Z

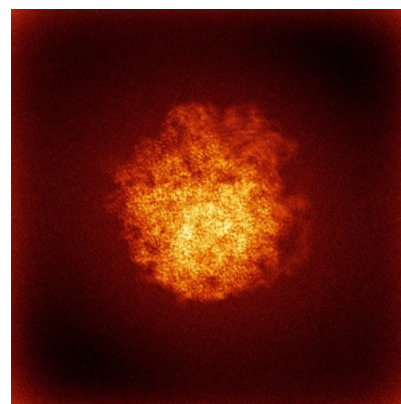
6.4.2 Raw map



X



Y

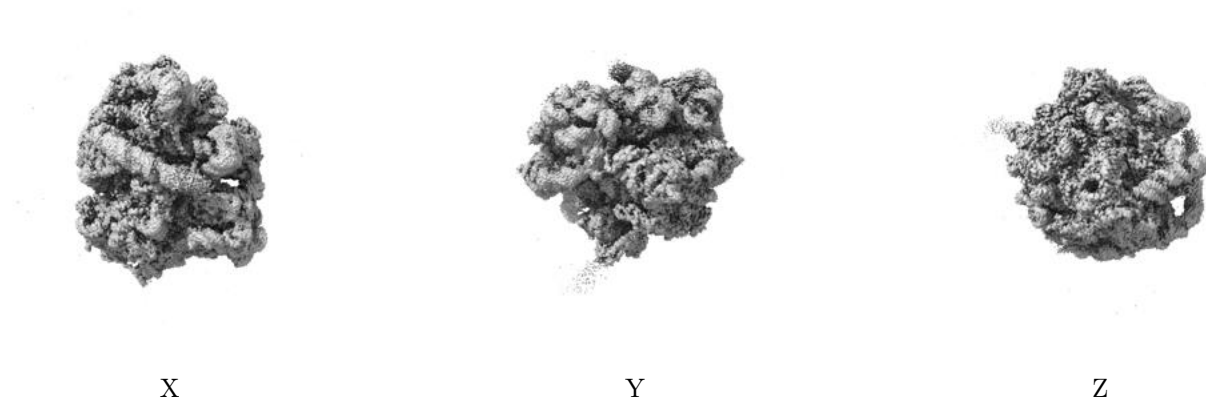


Z

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.

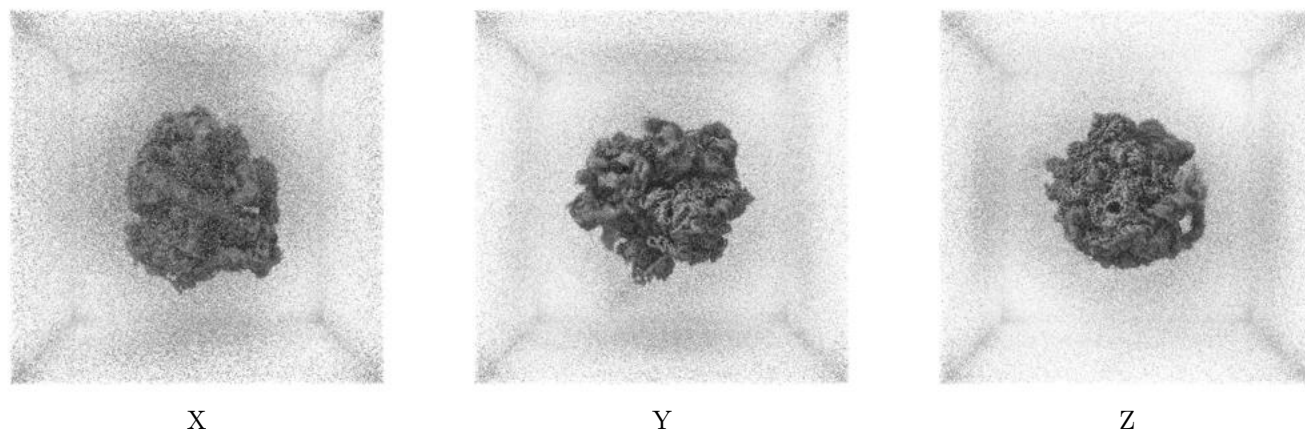
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

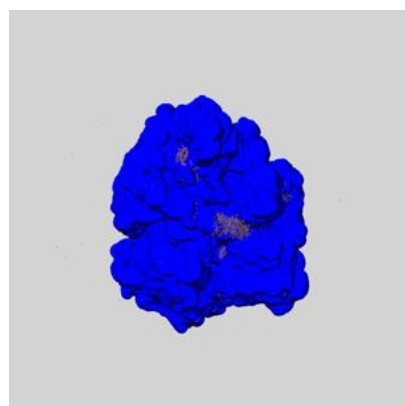
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

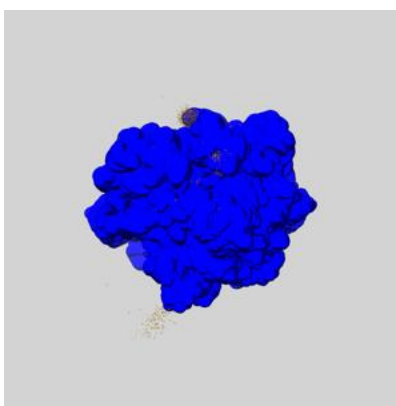
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

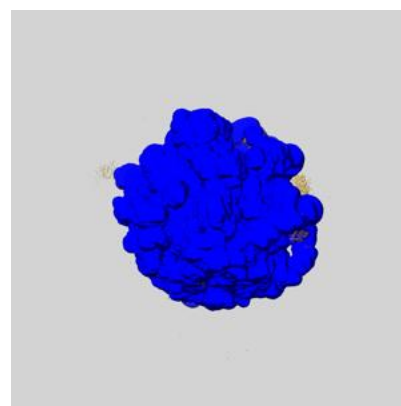
6.6.1 emd_43074_msk_1.map [i](#)



X



Y

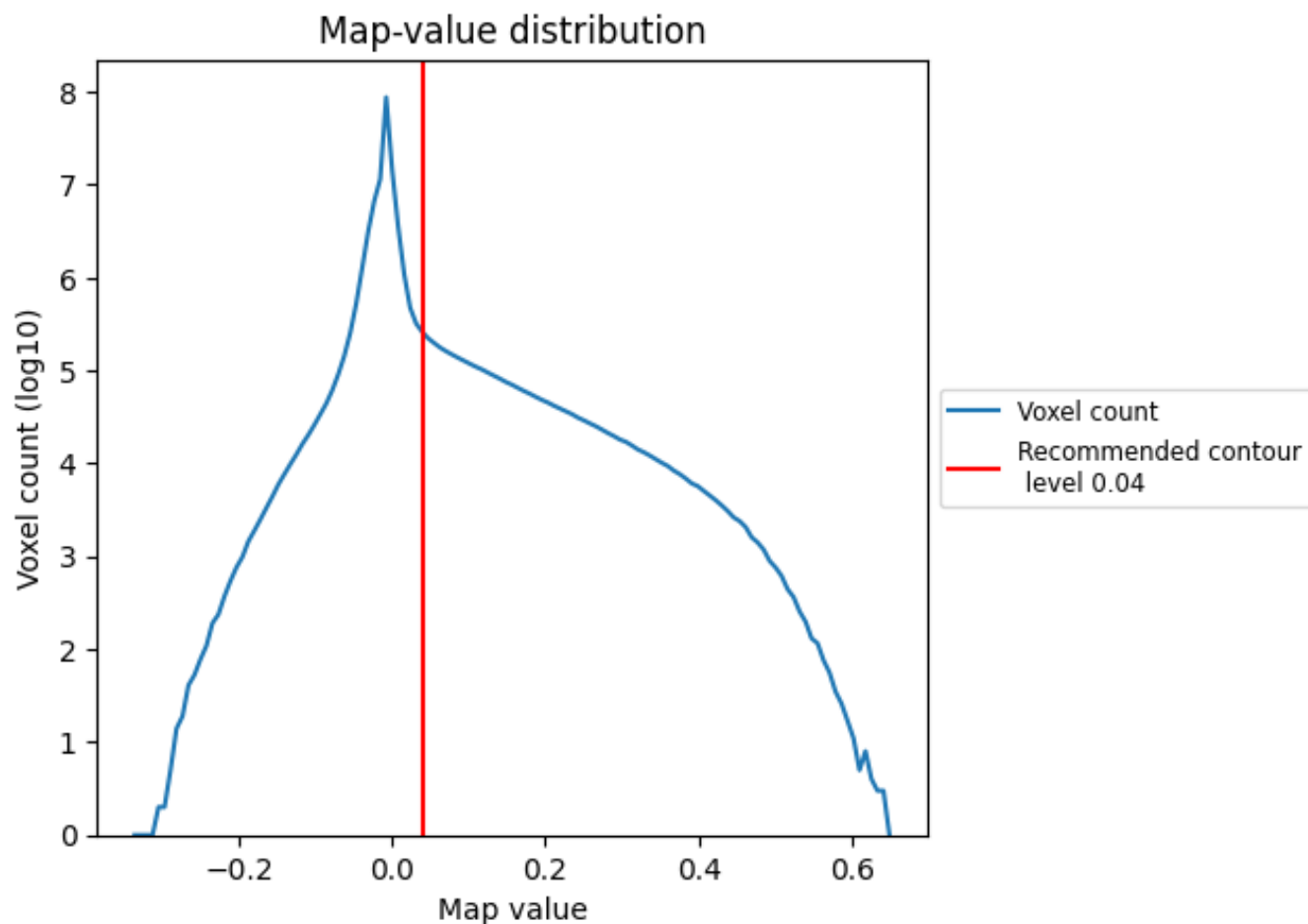


Z

7 Map analysis [i](#)

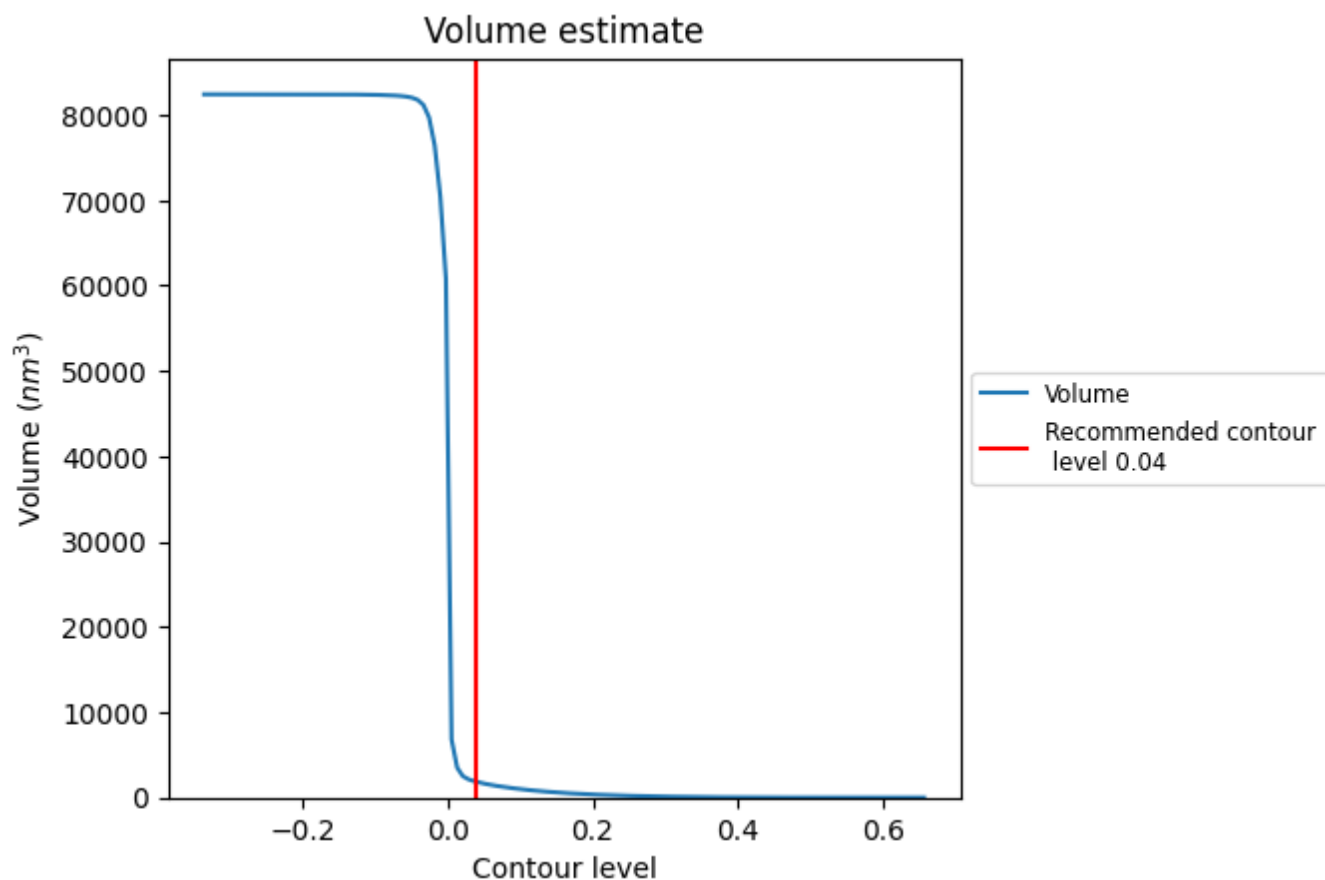
This section contains the results of statistical analysis of the map.

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.

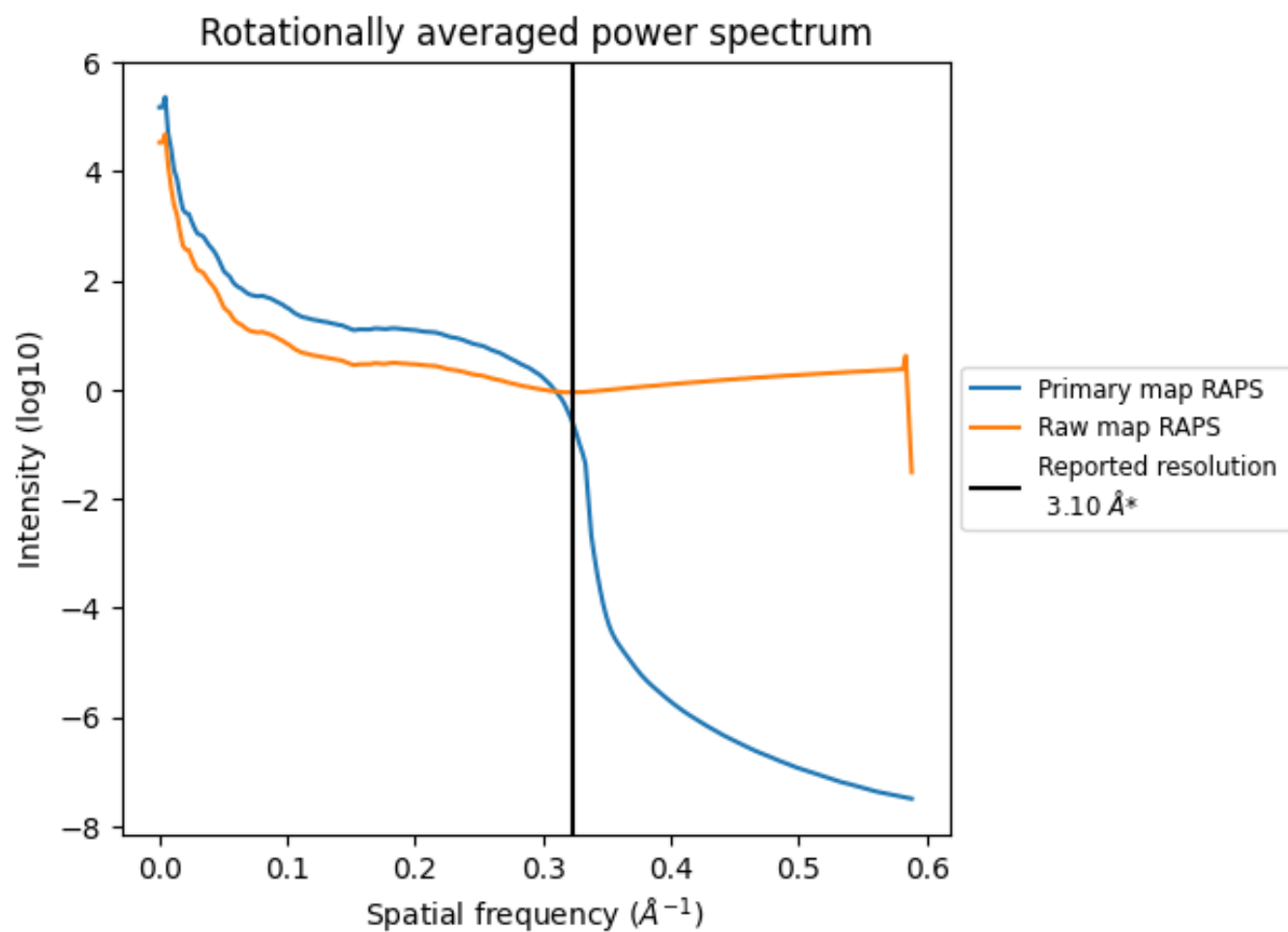
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1842 nm³; this corresponds to an approximate mass of 1664 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 ⓘ

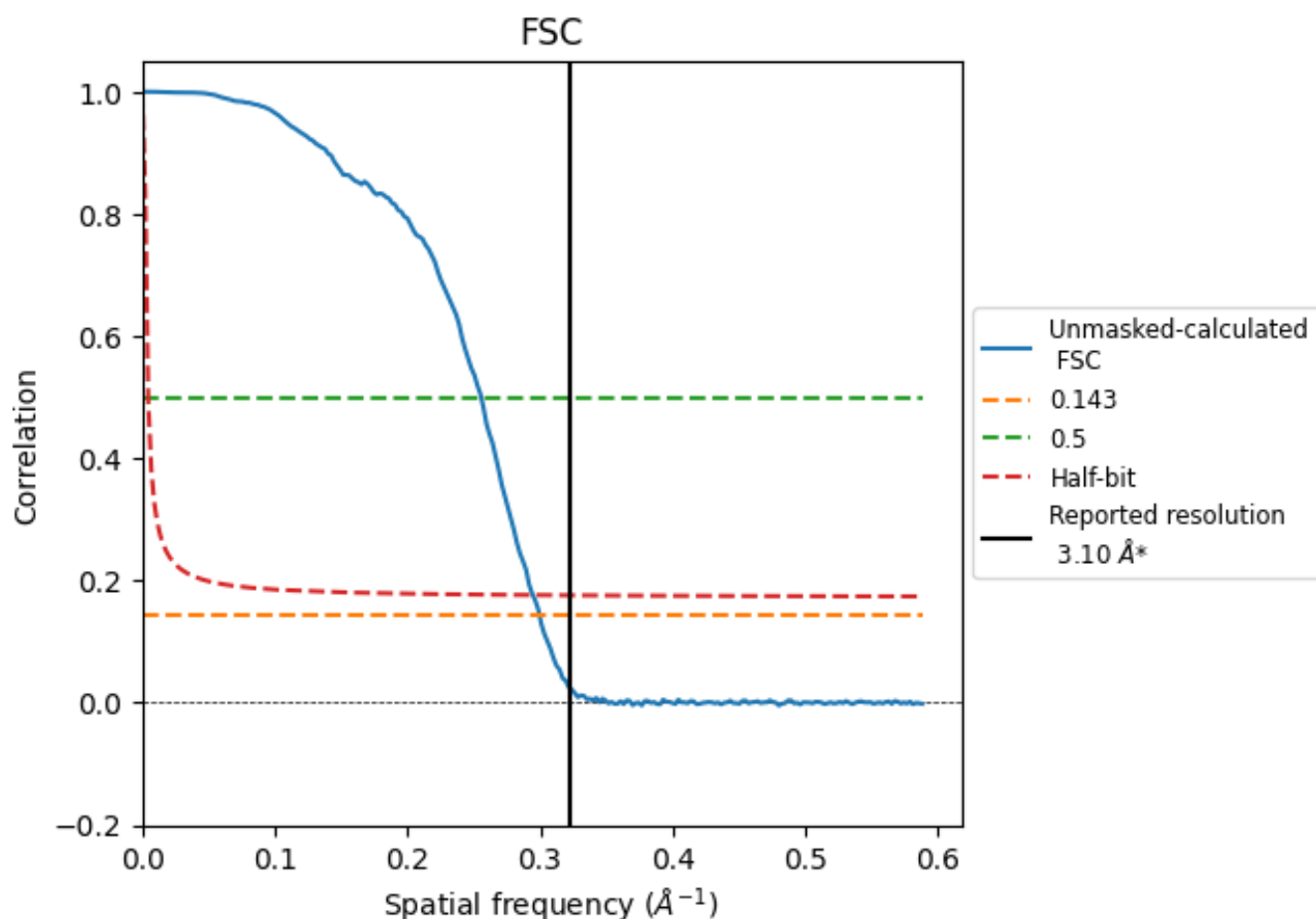


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

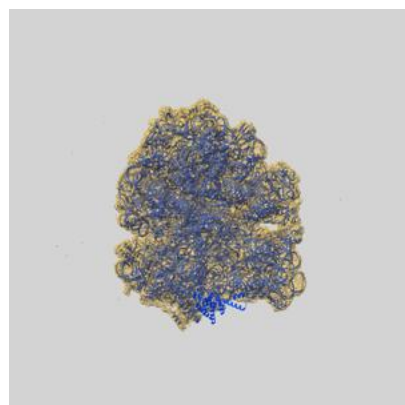
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.34	3.91	3.39

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

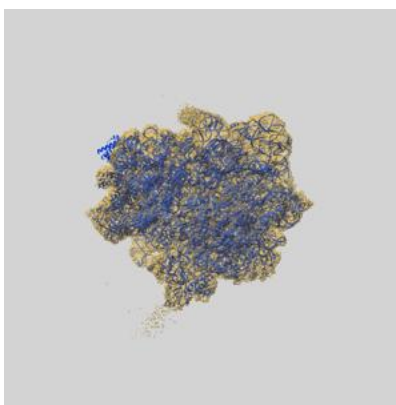
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43074 and PDB model 8V9J. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

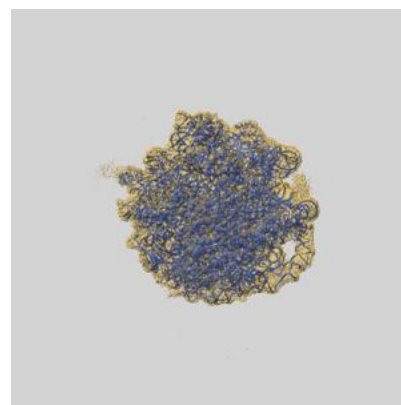
9.1 Map-model overlay [i](#)



X



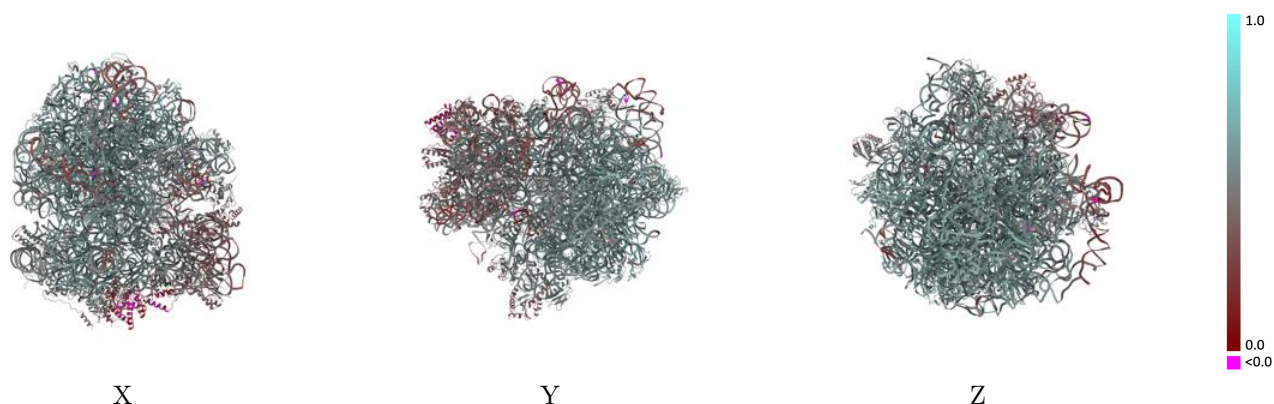
Y



Z

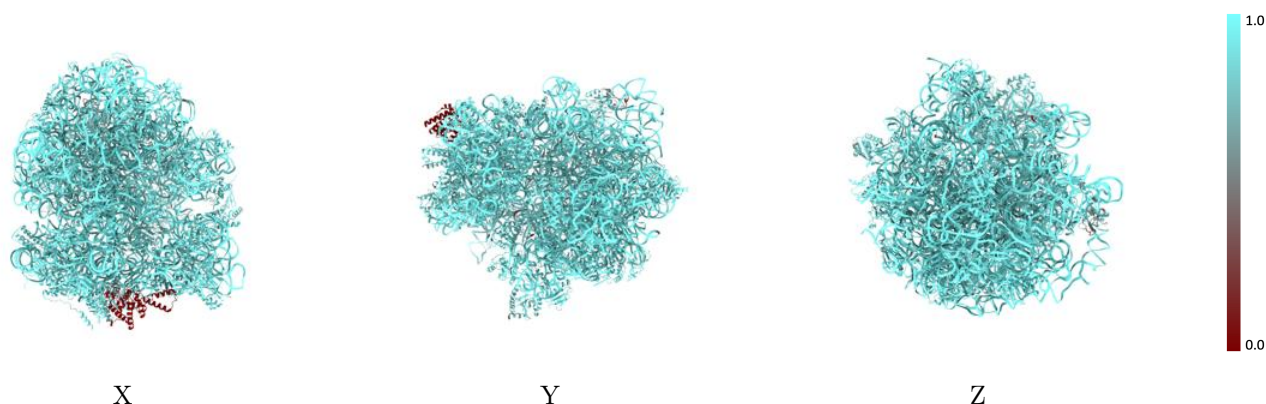
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



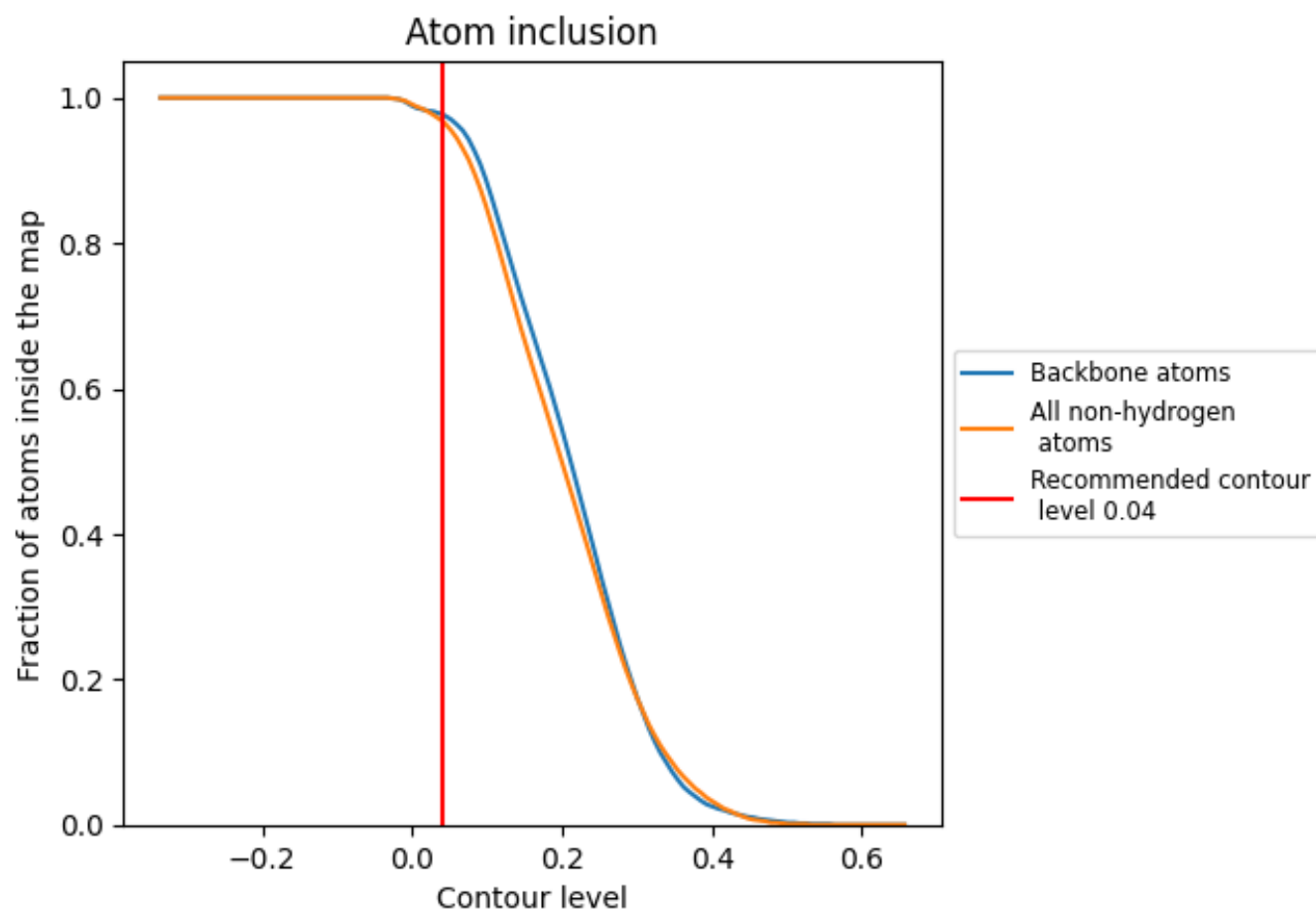
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.5250
1	 0.9710	 0.5610
2	 0.9760	 0.5830
3	 0.9770	 0.4610
4	 0.9730	 0.5820
5	 0.9770	 0.5760
6	 0.9860	 0.5970
7	 0.9770	 0.5950
8	 0.9790	 0.5840
9	 0.9780	 0.6030
A	 0.9930	 0.5500
B	 0.9960	 0.5370
C	 0.9740	 0.5920
D	 0.9800	 0.5780
E	 0.9770	 0.5720
F	 0.9490	 0.4940
G	 0.9710	 0.5330
H	 0.7360	 0.4730
I	 0.8370	 0.4080
J	 0.9460	 0.4330
K	 0.9750	 0.4690
L	 0.9770	 0.5770
M	 0.9400	 0.5710
N	 0.9730	 0.5750
O	 0.9600	 0.5780
P	 0.9780	 0.5860
Q	 0.9830	 0.5490
R	 0.9490	 0.5650
S	 0.9830	 0.5920
T	 0.9920	 0.5890
U	 0.9790	 0.5840
V	 0.9570	 0.5580
W	 0.9740	 0.5490
X	 0.9600	 0.5400
Y	 0.9740	 0.5850



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Chain	Atom inclusion	Q-score
Z	 0.9820	 0.5850
a	 0.9950	 0.5010
b	 0.0030	 0.1260
c	 0.9140	 0.4360
d	 0.9240	 0.4330
e	 0.9410	 0.5260
f	 0.9450	 0.5210
g	 0.8850	 0.3620
h	 0.9810	 0.5500
i	 0.9500	 0.4120
j	 0.9030	 0.4070
k	 0.9520	 0.5390
l	 0.9310	 0.5460
m	 0.9090	 0.3610
n	 0.9350	 0.4630
o	 0.9610	 0.5420
p	 0.9400	 0.4990
q	 0.9440	 0.5260
r	 0.9780	 0.5300
s	 0.9320	 0.3910
t	 0.9560	 0.5100
u	 0.8850	 0.5580
v	 1.0000	 0.5280
y	 0.9840	 0.4760
z	 0.9340	 0.5170