



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 07:04 AM UTC

PDB ID : 8AGZ / pdb_00008agz
EMDB ID : EMD-15428
Title : Yeast RQC complex in state with the RING domain of Ltn1 in the OUT position
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.
Deposited on : 2022-07-20
Resolution : 2.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

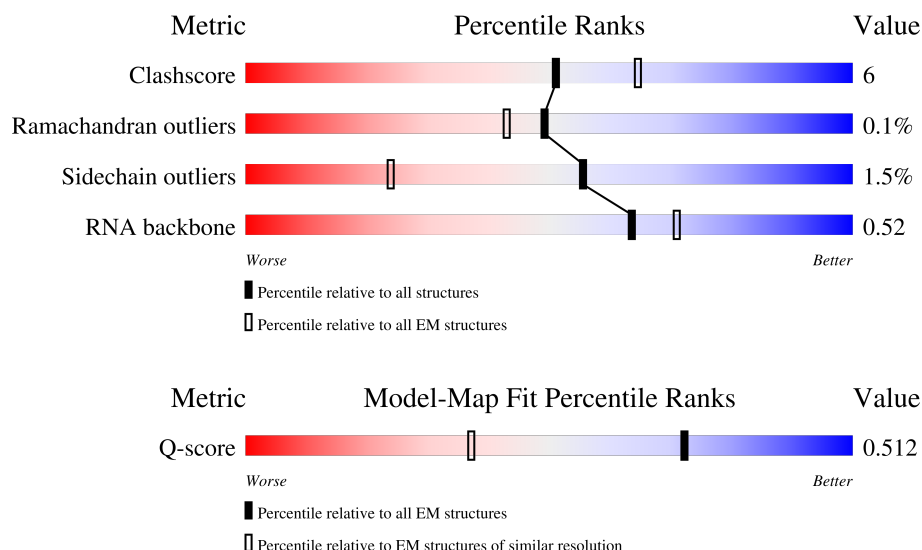
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

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

The reported resolution of this entry is 2.60 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.



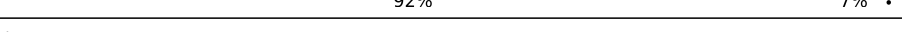
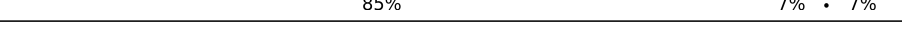
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	204	
2	B	199	
3	C	184	

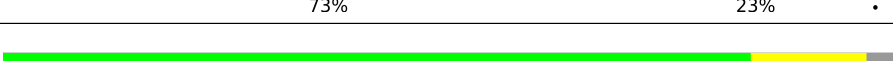
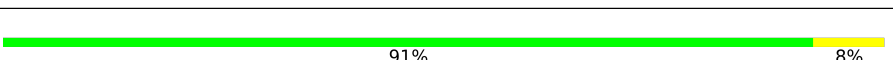
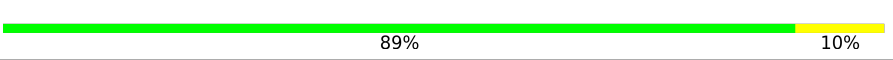
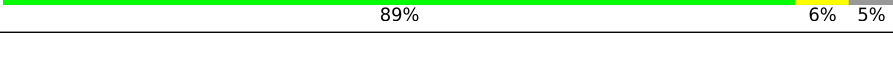
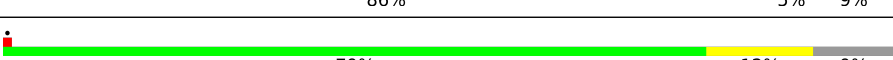
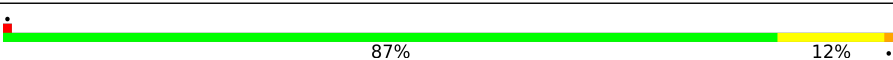
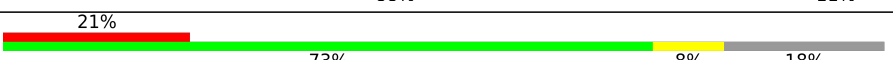
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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	189	
6	F	172	
7	G	160	
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	

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Mol	Chain	Length	Quality of chain
29	d	25	
30	f	3395	
31	h	121	
32	i	158	
33	j	254	
34	k	387	
35	l	362	
36	m	297	
37	n	176	
38	o	244	
39	p	256	
40	q	191	
41	r	221	
42	s	174	
43	t	199	
44	u	138	
45	a	1038	
46	e	1562	
47	g	245	
48	v	157	
49	w	217	
50	x	76	
50	y	76	
51	z	165	
52	0	312	

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Mol	Chain	Length	Quality of chain
53	1	18	 61% 39%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 151339 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 2 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 3 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 4 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 5 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 6 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 7 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 8 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 9 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 10 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	63	Total	C	N	O	S	0	0
			518	333	102	82	1		

- Molecule 11 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	125	Total	C	N	O	S	0	0
			984	620	191	173			

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	135	Total	C	N	O	S	0	0
			1080	701	199	180			

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 15 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 18 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 24 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 25 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 27 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 29 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 30 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	3216	Total	C	N	O	P	0	0
			68782	30723	12389	22454	3216		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 32 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 34 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 35 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 36 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 37 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	167	Total	C	N	O		0	0
			1307	843	234	230			

- Molecule 38 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 39 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 40 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 41 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 43 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 44 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 45 is a protein called RQC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6579	4194	1142	1226	17		

- Molecule 46 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	1527	Total	C	N	O	S	0	0
			11506	7350	1937	2181	38		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	142	Total	C	N	O	S	0	0
			1085	676	183	217	9		

- Molecule 49 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 50 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	74	Total	C	N	O	P	0	0
			1579	702	277	526	74		
50	y	73	Total	C	N	O	P	0	0
			1556	692	272	519	73		

- Molecule 51 is a protein called 60S ribosomal protein L12-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	148	Total	C	N	O	0	0
			728	432	148	148		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 53 is a protein called CAT-tailed nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	1	Total	Mg	0
			1	1	
54	C	1	Total	Mg	0
			1	1	
54	E	1	Total	Mg	0
			1	1	
54	I	1	Total	Mg	0
			1	1	
54	R	1	Total	Mg	0
			1	1	

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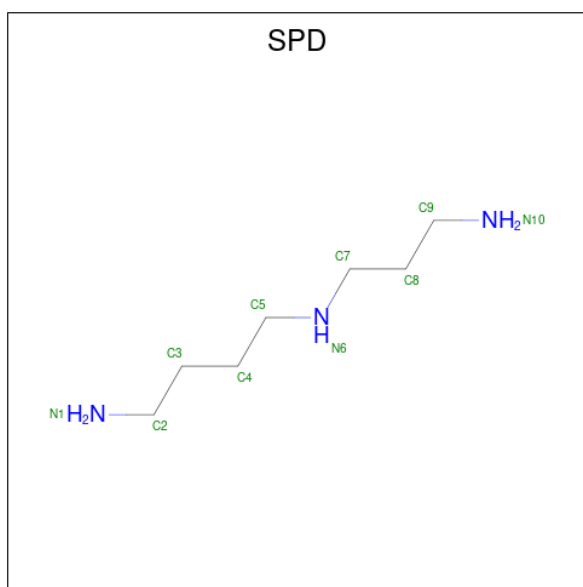
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Mol	Chain	Residues	Atoms		AltConf
54	T	1	Total 1	Mg 1	0
54	f	3	Total 3	Mg 3	0
54	h	1	Total 1	Mg 1	0
54	j	2	Total 2	Mg 2	0
54	k	1	Total 1	Mg 1	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	T	1	Total 1	Zn 1	0
55	W	1	Total 1	Zn 1	0
55	Z	1	Total 1	Zn 1	0
55	b	1	Total 1	Zn 1	0
55	c	1	Total 1	Zn 1	0
55	e	2	Total 2	Zn 2	0

- Molecule 56 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).

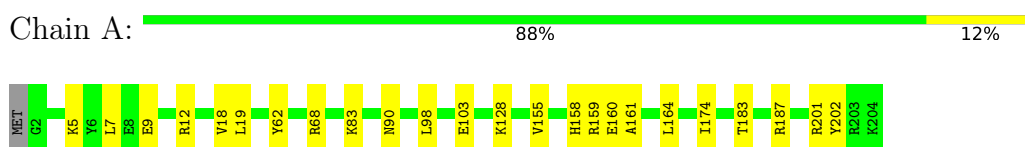


Mol	Chain	Residues	Atoms			AltConf
56	f	1	Total	C	N	0
			10	7	3	

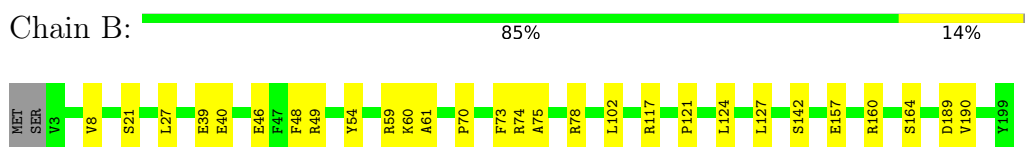
3 Residue-property plots [i](#)

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.

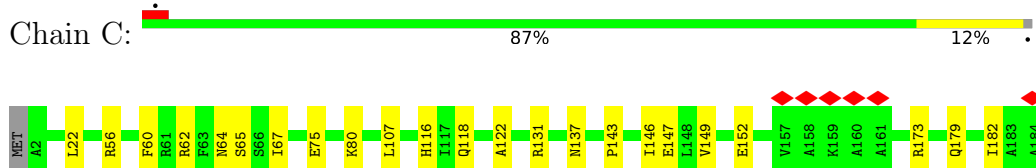
- Molecule 1: 60S ribosomal protein L15-A



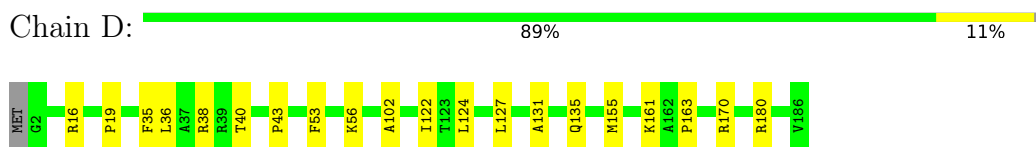
- Molecule 2: 60S ribosomal protein L16-A



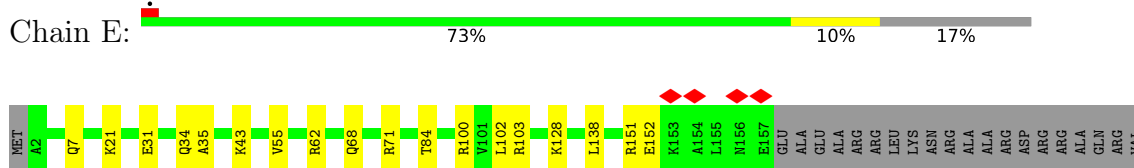
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A



- Molecule 5: 60S ribosomal protein L19-A



ALA
GLU
LYS
ARG
ASP
ALA
LEU
LEU
LYS
GLU
ASP
ALA

• Molecule 6: 60S ribosomal protein L20-A

Chain F:  85% 15% .

MET A2 Q8 P22 S32 I36 Y43 I64 T70 V77 R80 T87 M90 E93 I94 R95 D96 V97 L106 M110 H122 I123 L124 R125 V126 R137 V140 R155 V156 Y172

• Molecule 7: 60S ribosomal protein L21-A

Chain G:  87% 12% .

MET G2 R17 H22 T68 K69 G73 Y84 R88 L89 S99 K100 C101 R102 R108 M112 R116 A133 R136 R139 M146 P155 T168 F169 I160

• Molecule 8: 60S ribosomal protein L22-A

Chain H:  69% 14% 17%

MET ALA PRO ASN THR SER ARG LYS D9 V19 S20 T23 I41 K42 V43 E44 N49 L50 G51 V54 T55 V56 V65 K81 R90 D91 L105 A106 F107 Y108 G1N VAL THR PRO GLU GLU ASP GLU GLU ASP GLU

• Molecule 9: 60S ribosomal protein L23-A

Chain I:  88% 11% .

MET S2 R12 I13 S14 P18 A38 A51 M59 R80 Q81 Y94 A99 P117 R128 V129 S133 G134 V135 V136 V137

• Molecule 10: 60S ribosomal protein L24-A

Chain J:  35% 5% 59%

M1 D6 G16 Q32 R33 S34 K41 K44 R47 H58 I63 THR GLU GLU VAL ALA LYS LYS ARG SER THR VAL ALA GLN ARG PRO ILE THR GLY ALA SER LEU ASP LEU ILE LYS GLU ARG SER LEU LYS PRO GLU VAL ARG LYS ALA ASN
ARG GLU LYS LEU LYS ALA ASN GLU LYS LYS ALA VAL VAL LYS GLY THR ASN GLY LYS ARG ALA ALA LYS SER GLY THR GLN SER LYS PHE SER LYS GLN GLN ALA LYS GLY ALA PHE GLN LYS VAL ALA ALA THR SER ARG

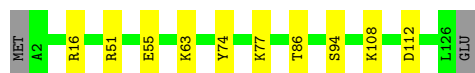
• Molecule 11: 60S ribosomal protein L25

Chain K:  85% 15%

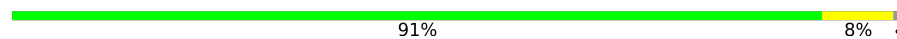
MET ALA PRO SER LYS LYS ALA ALA THR ALA LYS LYS VAL VAL LYS GLY THR ASN GLY LYS K22 A50 I142

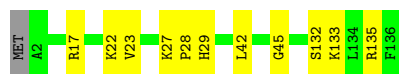
• Molecule 12: 60S ribosomal protein L26-A

Chain L:  91% 8% .



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  91% 8% .



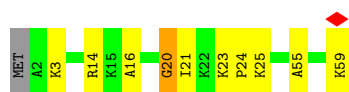
- Molecule 14: 60S ribosomal protein L28

Chain N:  87% 13% .



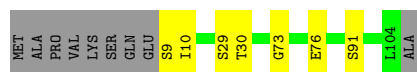
- Molecule 15: 60S ribosomal protein L29

Chain O:  81% 15% . .



- Molecule 16: 60S ribosomal protein L30

Chain P:  85% 7% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  80% 17% .

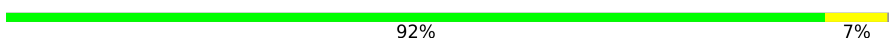


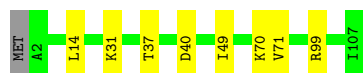
- Molecule 18: 60S ribosomal protein L32

Chain R:  89% 8% .



- Molecule 19: 60S ribosomal protein L33-A

Chain S:  92% 7%

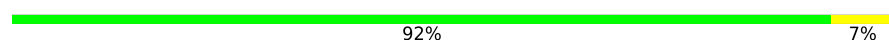


- Molecule 20: 60S ribosomal protein L34-A

Chain T:  85% 7% 7%

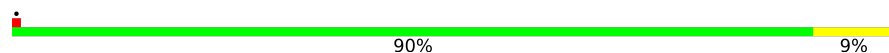


- Molecule 21: 60S ribosomal protein L35-A

Chain U:  92% 7%



- Molecule 22: 60S ribosomal protein L36-A

Chain V:  90% 9%

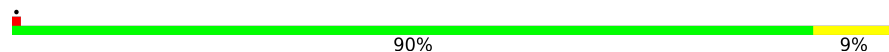


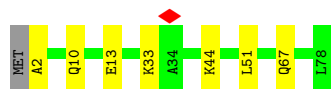
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  76% 16% 8%

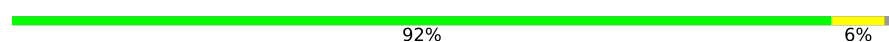


- Molecule 24: 60S ribosomal protein L38

Chain X:  90% 9%

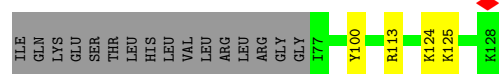


- Molecule 25: 60S ribosomal protein L39

Chain Y:  92% 6%



- Molecule 26: Ubiquitin-60S ribosomal protein L40



- [illegible]

-

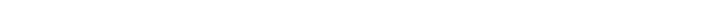
- Chain d: 

Diagram illustrating the 20 amino acids in the genetic code, arranged in a 4x5 grid. The amino acids are color-coded: orange (M4), yellow (R20, R21, V23), green (K22, R24, A25), and grey (ARG, SER, LYS). Red diamonds are placed above the amino acids K22, V23, R24, and A25.

- Chain f: 68% 24% 5%

G	U	U	A6	A13	U14	U19	A20	G21	A26	C36	A40	A43	A49	G58	G59	A60	A63	G64	A65	A66	A67	G68	G76	U77	U78	G86	G92	G93	G94	A95	G98	A99	A109	G110	C111	A116	G120	A121	A122	A123	...
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U130	U133	U134	U135	G136	G139	G156	A157	G158	A159	A165	G166	G172	G173	U182	G183	A187	U190	U191	G200	G206	U210	A211	G212	A213	G216	U217	G218	A219	G234	U240	G241	G242	G243	G244	U245	U249	U252	G269	G282	G283
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A285	A286	A287	A288	A289	A290	A291	A292	A293	A294	A295	A296	A297	A298	A299	A300	A301	A302	A303	A304	A305	A306	A307	A308	A309	A310	A311	A312	A313	A314	A315	A316	A317	A318	A319	A320	A321	A322	A323	A324	A325	A326	A327	A328	A329	A330	A331	A332	A333	A334	A335	A336	A337	A338	A339	A340	A341	A342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500
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[illegible]

U528
A529
G530
G531
A532

G535
U536

G542
G543
G544
U545
G546
G547
G548
U549

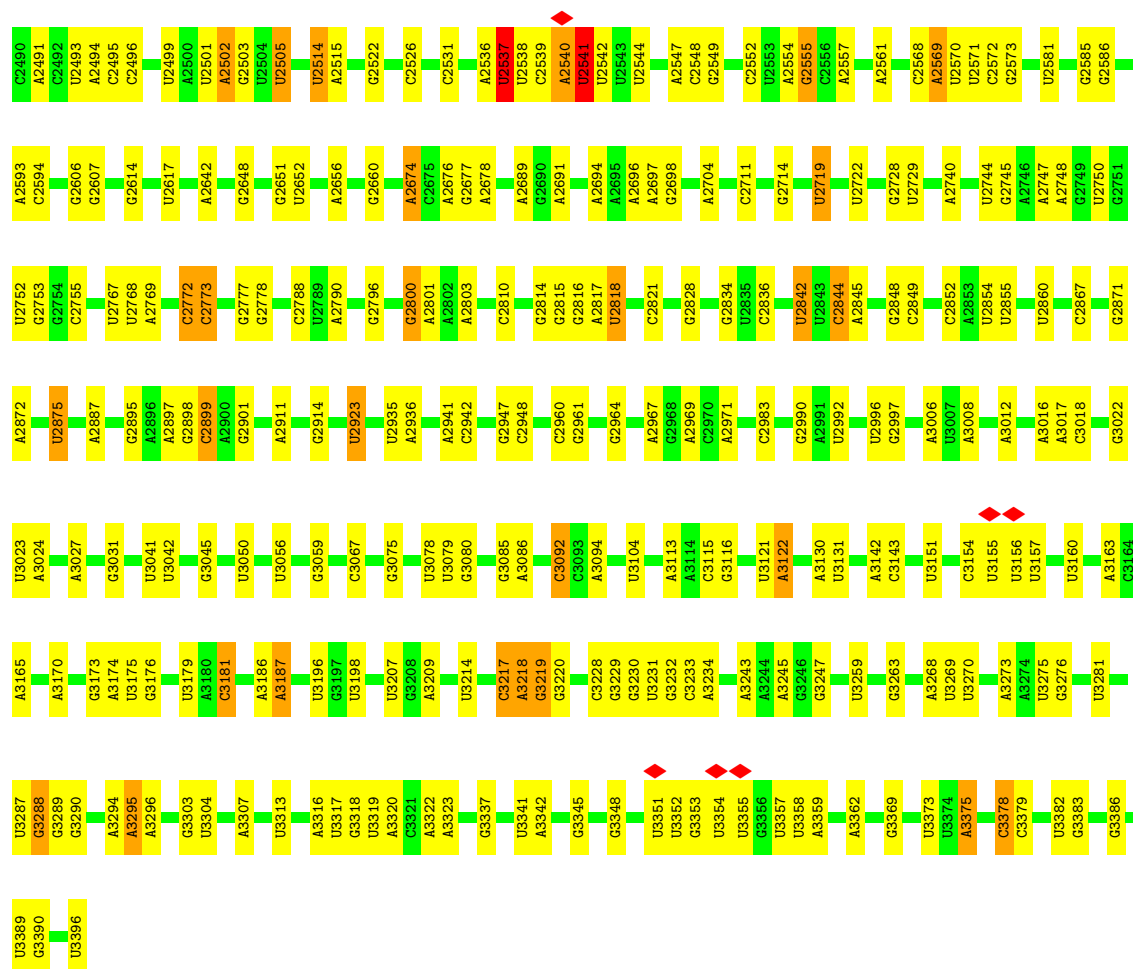
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A559

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A572
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A589
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G591
G595
G596
G597
A598
G599

G604
A608
G609
G610
A611
G618
A619
U620
A621
A622
G623

A2397	A2402	G2403	A2404	U2411	G2412	A2413	G2414	A2419	A2424	G2437	G2442	A2443	U2446	A2447	G2450	G2451	G2452	U2453	G2454	U2455	A2458	A2459	U2460	A2461	G2462	G2463	U2464	G2465	G2466	G2467	A2468	G2469	C2470	U2471	U2472	C2473	G2474	G2475	G2476	U2479	A2480	A2484	A2485		
A2224	U2225	A2228	G2239	C2245	G2249	G2249	U2254	U	A	A	C	U	A	U	U2268	G2272	G2273	U2274	A2281	U2282	G2283	C2284	G2288	G2307	C2308	A2309	U2310	A2313	U2314	G2315	U2334	G2335	U2336	A2357	A2358	U2209	A2094	G2095	A2096	U2097	C2101	U2102	G2111		
U2112	A2113	C2114	G2115	A2116	G2117	C2118	G2121	G2122	U2129	G2130	A2131	G2134	U2137	A2138	G2139	U2140	U2141	A2142	A2143	A2144	G2155	A2158	U2159	G2160	G2161	U2162	G2169	U2176	G2177	G2185	U2193	G2194	G2201	U2205	G2206	A2207	A2208	U2209	A2094	G2095	A2096	U2097	C2101	U2102	G2111
G	U	U	G	U	U	C	U	U	C	U	U	C	U	U	C	U	U	U	U	U	U	U	U	U	C	C	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
A1850	A1864	G1865	C1866	A1867	U1871	U1880	A1881	U1888	A1893	G1899	G1906	C1907	A1915	G1940	C1943	G1949	U1952	G1953	G1954	U1955	U	A	G	U	G	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
G1736	A1741	G1747	A1750	G1751	A1760	C1761	U1764	U1765	G1766	G1770	C1771	U1772	G1775	G1778	C1779	G1780	G1786	A1787	C1793	A1797	C1802	C1805	A1806	G1807	G1808	A1813	A1814	U1815	A1816	U1819	U1820	U1821	A1835	A1839	U1840	A1841	A1842	C1846	C1849						
A1589	G1590	A1593	C1596	C1597	A1605	U1606	U1607	A1613	U1620	U1629	G1634	C1639	A1642	A1643	U1644	U1645	C1657	C1660	G1661	G1662	G1666	A1667	G1675	A1676	A1683	U1686	C1693	U1716	U1717	G1718	U1721	U1722	A1723	U1724	C1725	G1726	G1727	G1730							
G1421	G1422	G1434	C1437	A1446	G1447	G1450	A1477	G1480	A1481	A1482	G1483	G1487	G1488	C1497	A1498	C1502	C1508	C1536	A1539	U1555	C1556	A1557	G1560	G1561	C1562	C1563	U1566	U1567	U1568	U1569	A1571	U1572	C1574	A1575	G1576	G1577	C1578	C1579	A1580	C1581	C1582	A1583			
U1265	G1268	U1269	C1272	A1273	C1277	A1278	C1279	A1280	G1281	G1282	G1285	A1286	A1287	U1288	G1289	G1295	G1307	A1308	U1309	G1313	G1330	U1348	G1349	A1350	U1351	A1352	U1353	G1354	A1355	U1356	G1357	A1369	G1383	A1386	G1387	U1388	G1389	A1390	G1391	G1392	A1399	G1400	A1418	A1419	C1420
U1191	C1192	G1193	A1047	C1048	C1049	G1063	A1064	A1065	G1072	U1081	U1082	G1083	A1084	G1087	A1093	U1094	U1095	U1096	G1097	A1098	A1103	G1104	A1105	G1106	C1107	U1108	U1109	G1117	C1118	C1119	A1120	G1131	G1134	G1139	U1144	G1145	A1153	C1156	A1159	C1160	G1177	A1180	U1181	A1190	
G912	A913	A914	A915	G916	A917	A920	A921	G924	A925	G937	C938	C944	C945	U946	G947	C804	G805	A806	G815	A816	A817	U829	G830	G831	G835	A836	A837	G838	A846	C849	U850	A710	A711	G712	A715	A716	U719	A720	G728	A895	A896	A904	C907	G908	C911
A628	G763	U764	C765	G766	U767	G770	U776	U777	A656	A780	G781	G785	A786	U673	G674	C675	G676	A677	G678	U679	G680	U681	G684	U687	G688	U689	A690	A691	A692	C896	A705	A710	A711	G712	A715	A716	U719	A720	G728	A895	A896	A904	C907	G908	C911



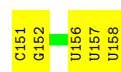
- Molecule 31: 5S rRNA

Chain h: 82% 16%



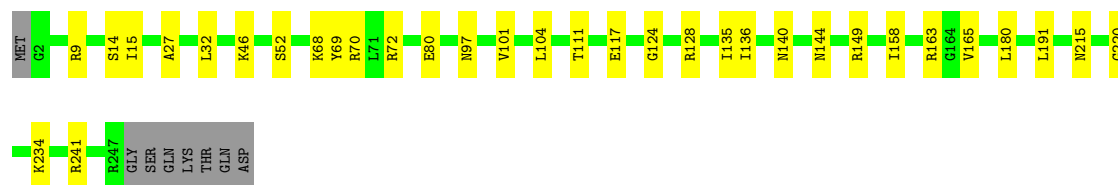
- Molecule 32: 5.8S rRNA

Chain i: 73% 23%

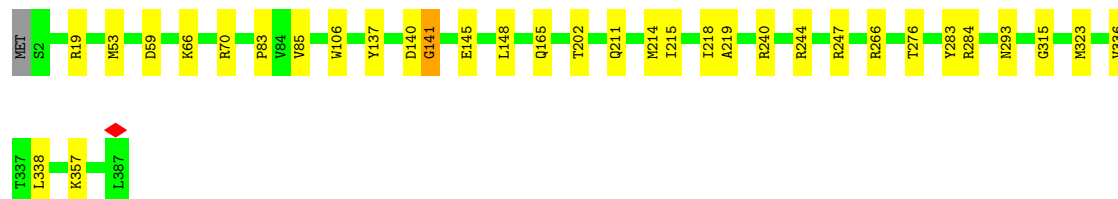


- Molecule 33: 60S ribosomal protein L2-A

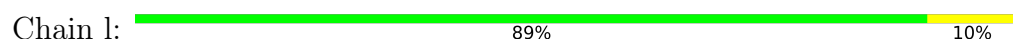
Chain j: 84% 13%



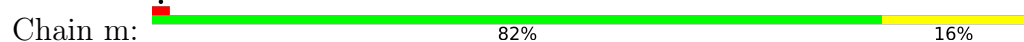
- Molecule 34: 60S ribosomal protein L3



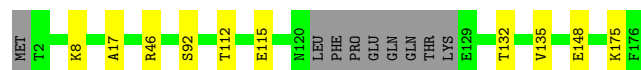
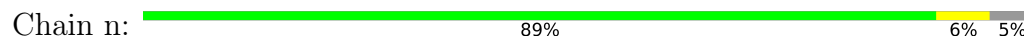
- Molecule 35: 60S ribosomal protein L4-A



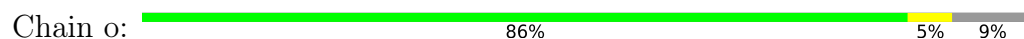
- Molecule 36: 60S ribosomal protein L5

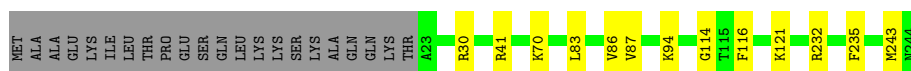


- Molecule 37: 60S ribosomal protein L6-B

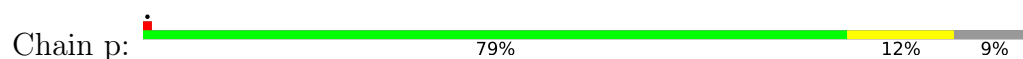


- Molecule 38: 60S ribosomal protein L7-A

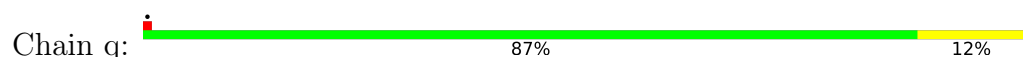




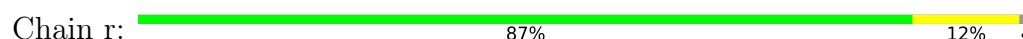
- Molecule 39: 60S ribosomal protein L8-A



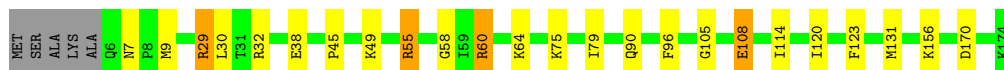
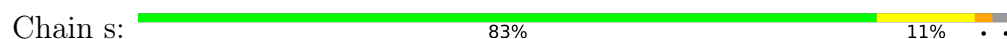
- Molecule 40: 60S ribosomal protein L9-A



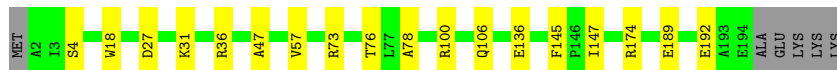
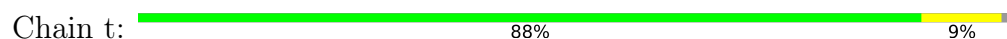
- Molecule 41: 60S ribosomal protein L10



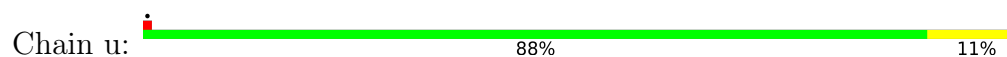
- Molecule 42: 60S ribosomal protein L11-A



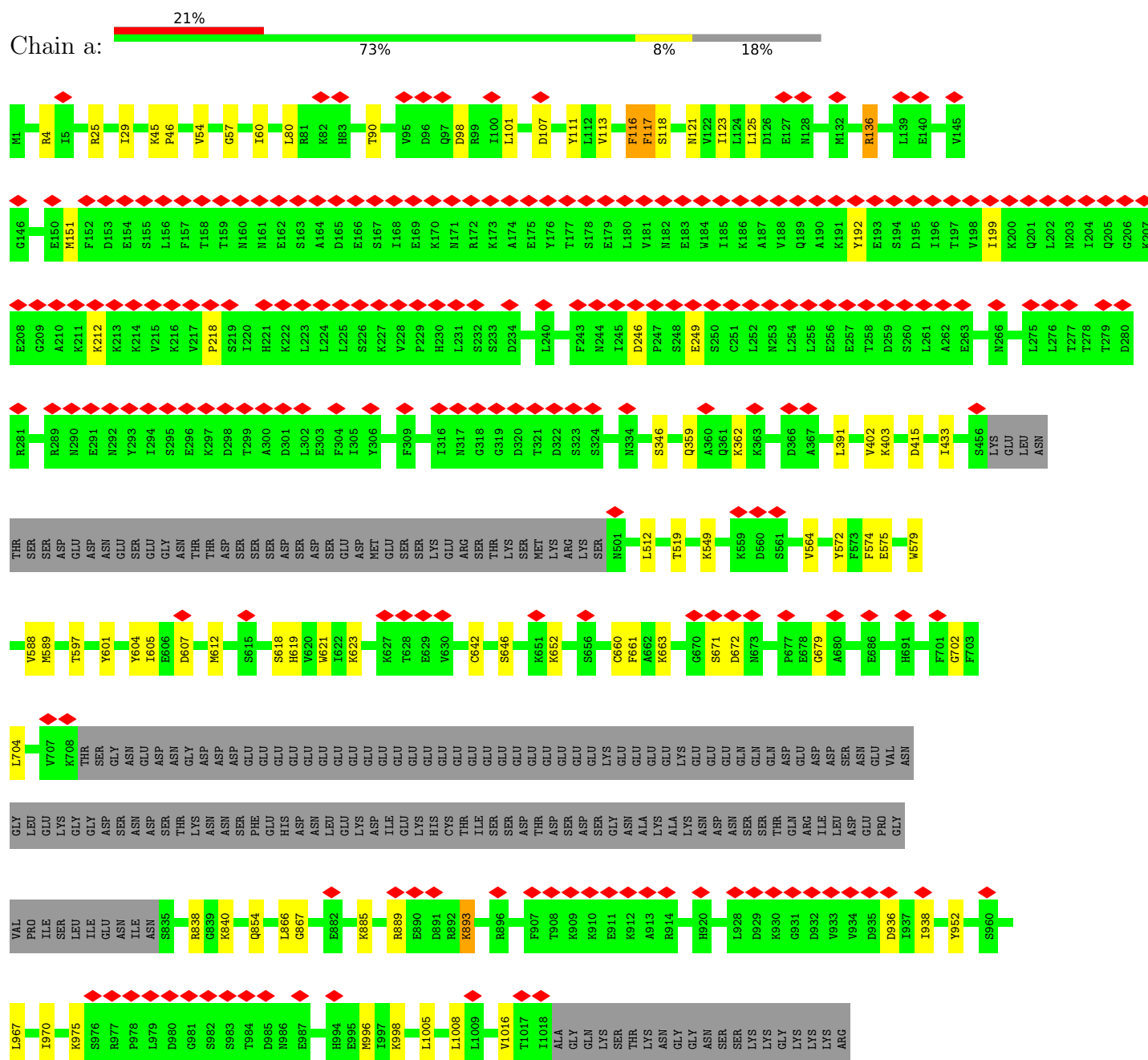
- Molecule 43: 60S ribosomal protein L13-A



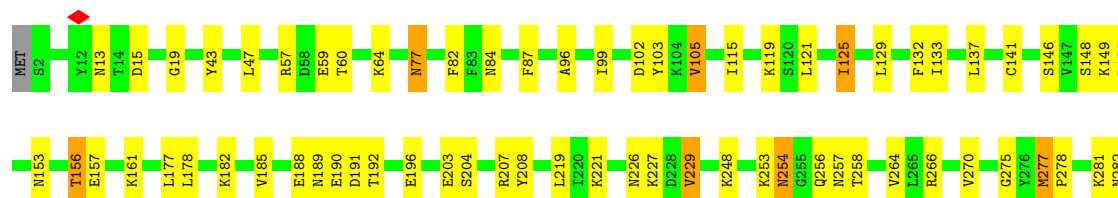
- Molecule 44: 60S ribosomal protein L14-A



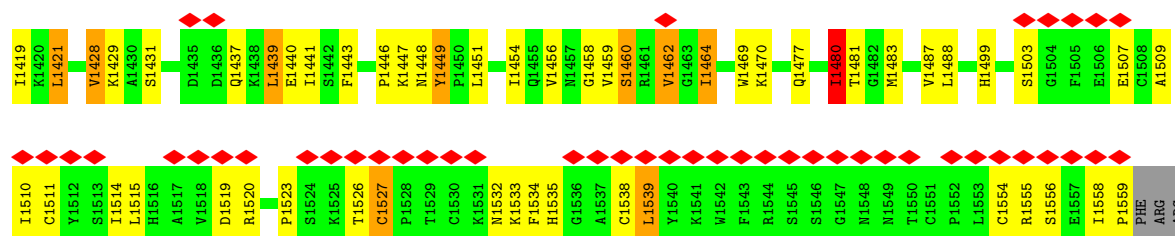
• Molecule 45: RQC2 isoform 1



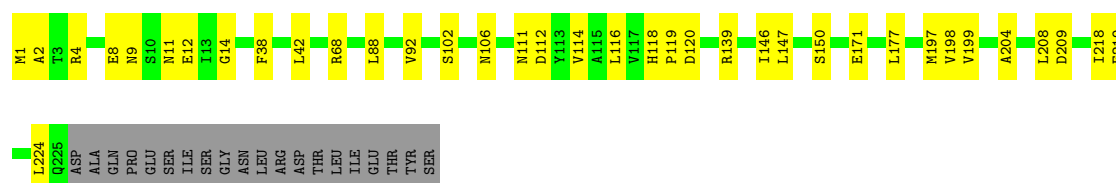
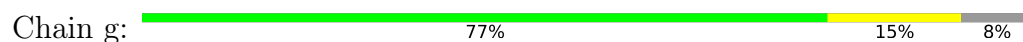
• Molecule 46: E3 ubiquitin-protein ligase listerin



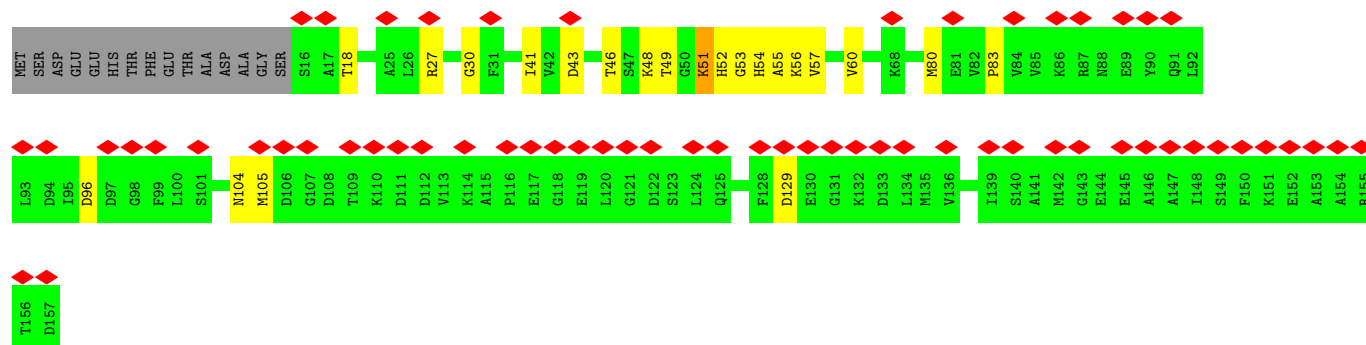
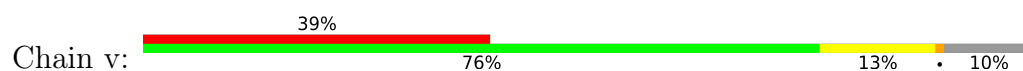




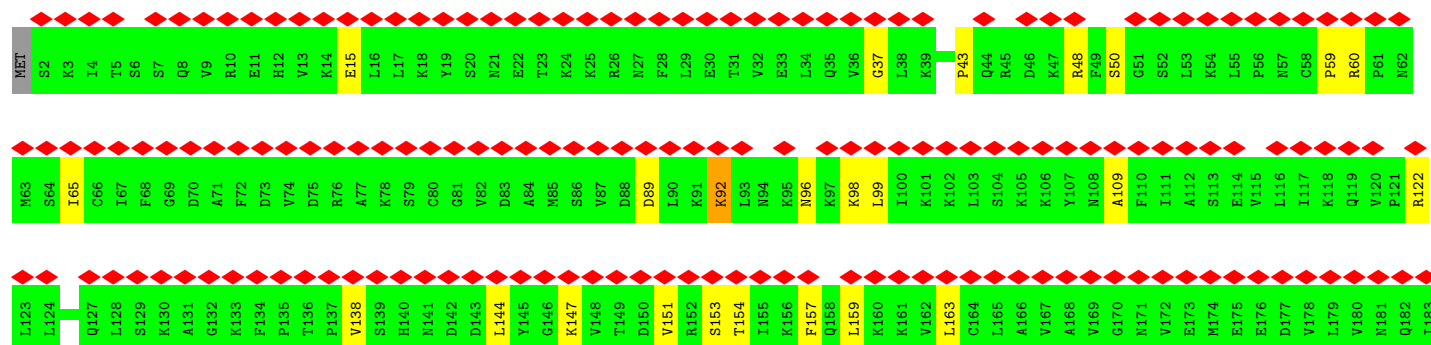
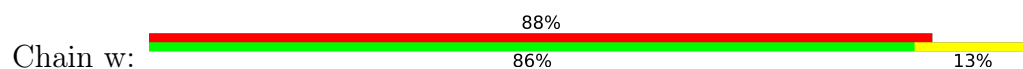
• Molecule 47: Eukaryotic translation initiation factor 6



• Molecule 48: Eukaryotic translation initiation factor 5A-1

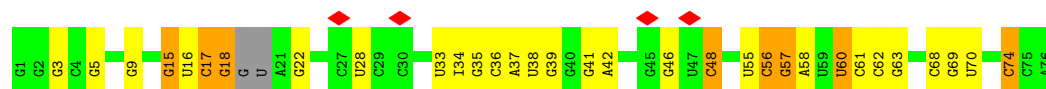


• Molecule 49: 60S ribosomal protein L1-A

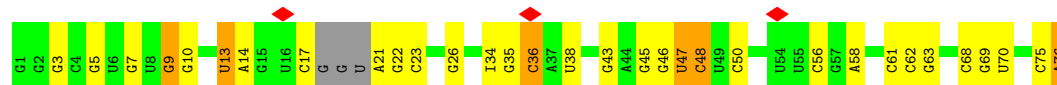




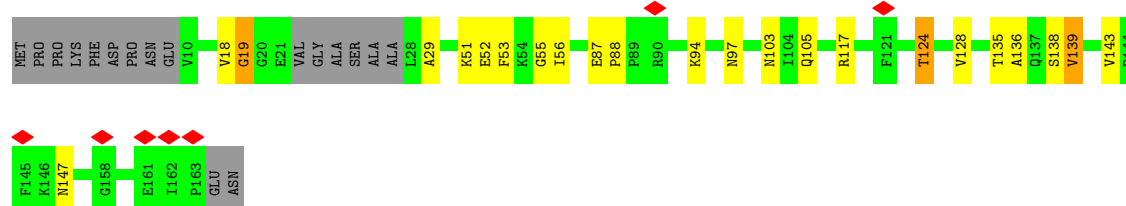
• Molecule 50: Ala tRNA



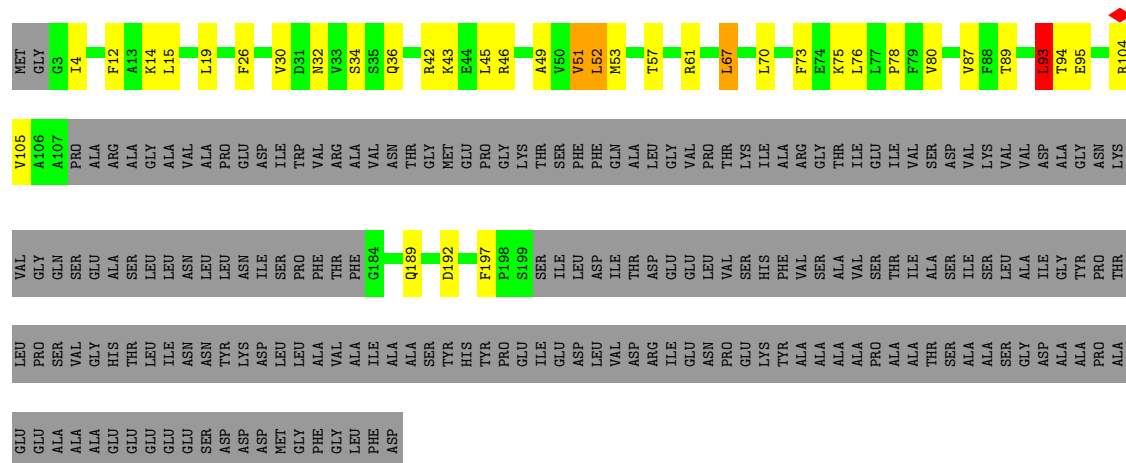
• Molecule 50: Ala tRNA



• Molecule 51: 60S ribosomal protein L12-B



• Molecule 52: 60S acidic ribosomal protein P0



• Molecule 53: CAT-tailed nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	79267	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.680	Depositor
Minimum map value	-0.672	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, ZN, 5CT, MG

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	0.31	0/1757	0.54	0/2354
2	B	0.32	0/1585	0.54	0/2128
3	C	0.30	0/1439	0.61	0/1938
4	D	0.28	0/1465	0.57	0/1965
5	E	0.29	0/1275	0.56	0/1702
6	F	0.31	0/1473	0.56	0/1980
7	G	0.27	0/1296	0.56	0/1739
8	H	0.37	0/812	0.77	2/1099 (0.2%)
9	I	0.27	0/1018	0.50	0/1369
10	J	0.27	0/530	0.52	0/703
11	K	0.31	0/979	0.57	0/1321
12	L	0.27	0/995	0.53	0/1329
13	M	0.27	0/1106	0.56	0/1485
14	N	0.32	0/1200	0.56	1/1607 (0.1%)
15	O	0.25	0/473	0.62	0/629
16	P	0.26	0/745	0.60	0/1001
17	Q	0.31	0/890	0.68	2/1196 (0.2%)
18	R	0.26	0/1034	0.47	0/1385
19	S	0.30	0/868	0.47	0/1168
20	T	0.29	0/890	0.58	2/1189 (0.2%)
21	U	0.27	0/978	0.53	0/1301
22	V	0.28	0/772	0.57	0/1026
23	W	0.32	0/660	0.60	0/875
24	X	0.28	0/618	0.65	1/826 (0.1%)
25	Y	0.29	0/443	0.46	0/588
26	Z	0.28	0/416	0.60	0/553
27	b	0.28	0/836	0.53	0/1104
28	c	0.27	0/701	0.56	0/934
29	d	0.22	0/208	0.81	2/267 (0.7%)
30	f	0.30	0/76989	0.39	6/120031 (0.0%)
31	h	0.26	0/2883	0.32	0/4491
32	i	0.30	0/3746	0.36	0/5832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	j	0.31	0/1908	0.53	0/2564
34	k	0.29	0/3146	0.53	0/4228
35	l	0.29	0/2800	0.57	4/3790 (0.1%)
36	m	0.27	0/2400	0.57	0/3239
37	n	0.28	0/1329	0.60	0/1794
38	o	0.31	0/1821	0.58	0/2451
39	p	0.27	0/1836	0.58	1/2481 (0.0%)
40	q	0.30	0/1529	0.64	2/2060 (0.1%)
41	r	0.25	0/1801	0.49	0/2416
42	s	0.33	0/1367	0.73	4/1834 (0.2%)
43	t	0.29	0/1568	0.62	1/2106 (0.0%)
44	u	0.30	0/1068	0.53	0/1438
45	a	0.26	0/6689	0.56	2/9023 (0.0%)
46	e	0.60	0/11705	0.96	65/15895 (0.4%)
47	g	0.24	0/1672	0.59	1/2281 (0.0%)
48	v	0.25	0/1084	0.61	1/1456 (0.1%)
49	w	0.29	0/1736	0.62	1/2332 (0.0%)
50	x	0.26	0/1760	0.41	0/2738
50	y	0.31	1/1734 (0.1%)	0.44	0/2697
51	z	0.66	0/726	1.24	13/1006 (1.3%)
52	0	0.49	0/976	0.94	3/1313 (0.2%)
All	All	0.33	1/161735 (0.0%)	0.52	114/236257 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	O	0	1
21	U	0	1
34	k	0	1
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
46	e	0	1
47	g	0	1
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	y	34	I	O3'-P	7.21	1.63	1.56

The worst 5 of 114 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	e	884	ILE	N-CA-C	-9.16	101.28	110.62
46	e	19	GLY	N-CA-C	9.15	122.07	111.36
46	e	1182	LYS	N-CA-C	8.97	121.06	111.28
46	e	1364	GLY	N-CA-C	8.39	122.64	112.49
46	e	868	LYS	N-CA-C	8.32	120.35	111.28

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
34	k	141	GLY	Peptide
35	l	13	GLY	Peptide
35	l	318	LEU	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	1720	0	1779	18	0
2	B	1555	0	1659	18	0
3	C	1416	0	1433	14	0
4	D	1441	0	1543	15	0
5	E	1258	0	1342	13	0
6	F	1437	0	1475	19	0
7	G	1272	0	1312	14	0
8	H	796	0	812	9	0
9	I	1003	0	1048	10	0
10	J	518	0	542	6	0
11	K	964	0	1025	1	0
12	L	984	0	1075	7	0
13	M	1080	0	1122	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	N	1169	0	1211	14	0
15	O	462	0	491	8	0
16	P	737	0	792	4	0
17	Q	876	0	912	10	0
18	R	1013	0	1077	8	0
19	S	850	0	880	5	0
20	T	880	0	942	8	0
21	U	969	0	1078	5	0
22	V	766	0	844	7	0
23	W	645	0	645	12	0
24	X	612	0	682	6	0
25	Y	436	0	475	2	0
26	Z	410	0	442	5	0
27	b	824	0	888	13	0
28	c	694	0	734	8	0
29	d	207	0	250	3	0
30	f	68782	0	34563	334	0
31	h	2579	0	1304	10	0
32	i	3353	0	1695	14	0
33	j	1874	0	1943	25	0
34	k	3075	0	3142	21	0
35	l	2748	0	2859	25	0
36	m	2351	0	2294	32	0
37	n	1307	0	1377	7	0
38	o	1784	0	1862	9	0
39	p	1804	0	1877	17	0
40	q	1508	0	1572	16	0
41	r	1764	0	1804	18	0
42	s	1346	0	1370	17	0
43	t	1543	0	1608	14	0
44	u	1053	0	1149	11	0
45	a	6579	0	6482	62	0
46	e	11506	0	10754	633	0
47	g	1651	0	1613	20	0
48	v	1085	0	1087	16	0
49	w	1709	0	1799	21	0
50	x	1579	0	798	14	0
50	y	1556	0	788	16	0
51	z	728	0	337	16	0
52	0	961	0	979	46	0
53	1	90	0	23	7	0
54	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	C	1	0	0	0	0
54	E	1	0	0	0	0
54	I	1	0	0	0	0
54	R	1	0	0	0	0
54	T	1	0	0	0	0
54	f	3	0	0	0	0
54	h	1	0	0	0	0
54	j	2	0	0	0	0
54	k	1	0	0	0	0
55	T	1	0	0	0	0
55	W	1	0	0	0	0
55	Z	1	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	e	2	0	0	0	0
56	f	10	0	19	1	0
All	All	151339	0	113608	1439	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 1439 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)
46:e:368:HIS:CE1	46:e:370:PHE:HB2	1.29	1.62
46:e:989:GLU:HG2	46:e:1034:TRP:CA	1.21	1.61
46:e:838:ILE:CD1	46:e:864:HIS:HB2	1.29	1.60
46:e:545:ILE:CB	46:e:579:ALA:HB1	1.32	1.58
46:e:972:GLU:HA	46:e:975:LYS:CE	1.18	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
3	C	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
4	D	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
5	E	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
6	F	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
7	G	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
8	H	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
9	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
10	J	61/155 (39%)	61 (100%)	0	0	100	100
11	K	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	14
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
24	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	Z	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
27	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
28	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
29	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
33	j	244/254 (96%)	226 (93%)	18 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	k	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	36	58
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
37	n	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
38	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
39	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
40	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	24	46
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	21	42
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	24	46
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	827 (98%)	15 (2%)	0	100	100
46	e	1519/1562 (97%)	1501 (99%)	16 (1%)	2 (0%)	48	70
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	v	139/157 (88%)	139 (100%)	0	0	100	100
49	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
51	z	144/165 (87%)	134 (93%)	9 (6%)	1 (1%)	18	38
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	30
All	All	9314/10279 (91%)	8958 (96%)	347 (4%)	9 (0%)	49	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
51	z	88	PRO
35	l	4	PRO
40	q	107	ASP
42	s	108	GLU
46	e	437	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	
1	A	175/176 (99%)	175 (100%)	0	100	100
2	B	160/162 (99%)	160 (100%)	0	100	100
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	150 (100%)	0	100	100
5	E	129/154 (84%)	129 (100%)	0	100	100
6	F	155/156 (99%)	155 (100%)	0	100	100
7	G	135/137 (98%)	135 (100%)	0	100	100
8	H	87/107 (81%)	87 (100%)	0	100	100
9	I	104/105 (99%)	104 (100%)	0	100	100
10	J	54/129 (42%)	54 (100%)	0	100	100
11	K	104/118 (88%)	104 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	46 (100%)	0	100	100
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	95 (100%)	0	100	100
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100
23	W	67/71 (94%)	67 (100%)	0	100	100
24	X	68/69 (99%)	68 (100%)	0	100	100
25	Y	45/46 (98%)	45 (100%)	0	100	100
26	Z	45/116 (39%)	45 (100%)	0	100	100
27	b	87/91 (96%)	87 (100%)	0	100	100
28	c	71/72 (99%)	71 (100%)	0	100	100
29	d	20/23 (87%)	20 (100%)	0	100	100
33	j	189/196 (96%)	189 (100%)	0	100	100
34	k	321/323 (99%)	321 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	l	288/289 (100%)	288 (100%)	0	100	100
36	m	241/245 (98%)	241 (100%)	0	100	100
37	n	139/155 (90%)	139 (100%)	0	100	100
38	o	186/205 (91%)	186 (100%)	0	100	100
39	p	187/208 (90%)	187 (100%)	0	100	100
40	q	168/171 (98%)	168 (100%)	0	100	100
41	r	185/187 (99%)	184 (100%)	1 (0%)	81	92
42	s	145/150 (97%)	142 (98%)	3 (2%)	47	73
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	678/949 (71%)	675 (100%)	3 (0%)	84	93
46	e	1149/1451 (79%)	1055 (92%)	94 (8%)	10	24
47	g	180/211 (85%)	180 (100%)	0	100	100
48	v	119/132 (90%)	118 (99%)	1 (1%)	73	88
49	w	197/198 (100%)	196 (100%)	1 (0%)	81	92
52	0	104/254 (41%)	94 (90%)	10 (10%)	8	17
All	All	7563/8690 (87%)	7450 (98%)	113 (2%)	55	80

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	987	ILE
52	0	95	GLU
46	e	1123	TYR
52	0	93	LEU
46	e	1527	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
46	e	13	ASN
46	e	1145	ASN
46	e	174	GLN
46	e	805	ASN
47	g	9	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3212/3395 (94%)	591 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
50	x	70/76 (92%)	19 (27%)	0
50	y	69/76 (90%)	18 (26%)	0
All	All	3628/3826 (94%)	672 (18%)	0

5 of 672 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	f	6	A
30	f	13	A
30	f	14	U
30	f	26	A
30	f	40	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
48	5CT	v	51	48	13,14,15	0.78	0	8,15,17	1.28	1 (12%)

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
48	5CT	v	51	48	-	9/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	v	51	5CT	C4-C3-C2	-2.20	108.84	113.47

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	v	51	5CT	NZ-C1-C2-C3
48	v	51	5CT	O1-C2-C3-C4
48	v	51	5CT	C2-C3-C4-N1
48	v	51	5CT	C-CA-CB-CG
48	v	51	5CT	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	v	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

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
56	SPD	f	3401	-	9,9,9	0.32	0	8,8,8	0.85	0

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
56	SPD	f	3401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	f	3401	SPD	C3-C4-C5-N6
56	f	3401	SPD	N6-C7-C8-C9
56	f	3401	SPD	C2-C3-C4-C5
56	f	3401	SPD	C4-C5-N6-C7
56	f	3401	SPD	C8-C7-N6-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	f	3401	SPD	1	0

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.

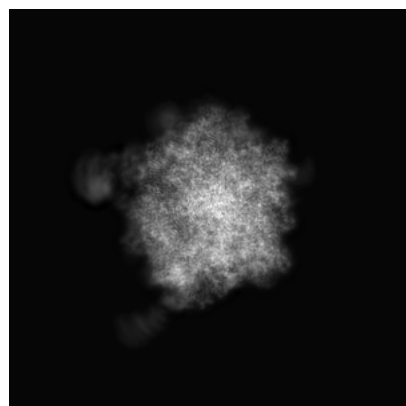
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15428. These allow visual inspection of the internal detail of the map and identification of artifacts.

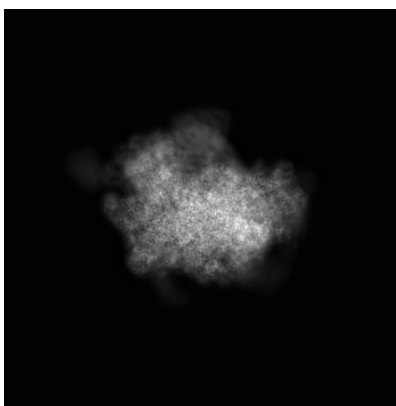
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

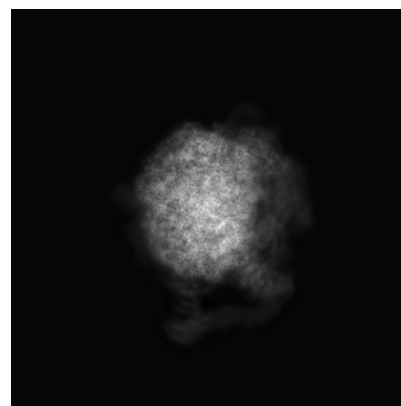
6.1.1 Primary map



X

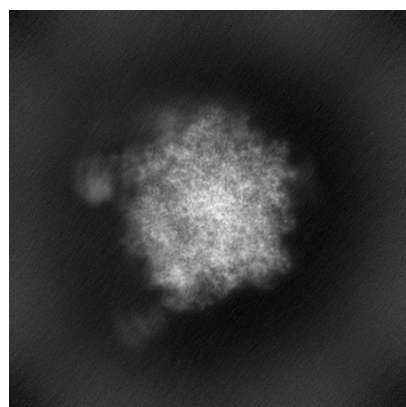


Y

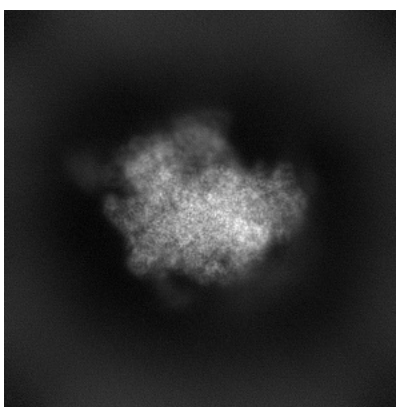


Z

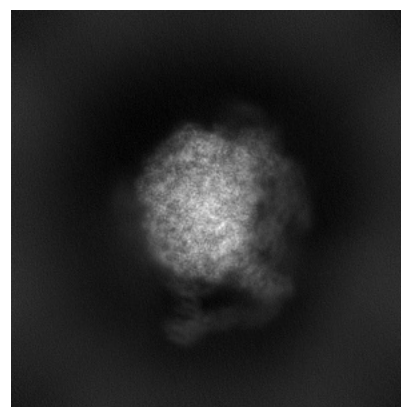
6.1.2 Raw map



X



Y

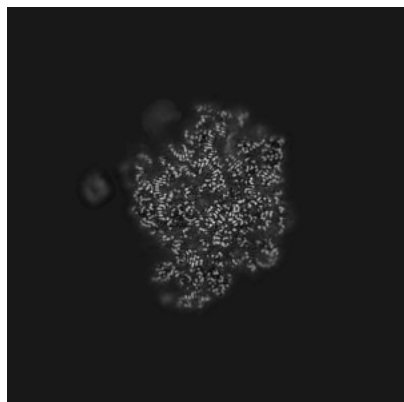


Z

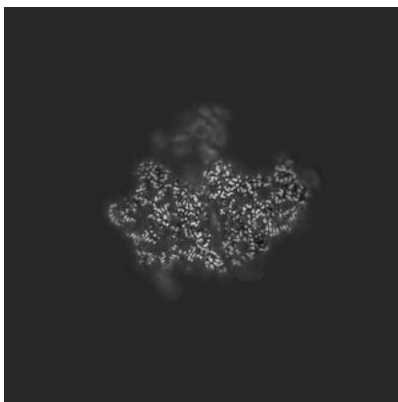
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

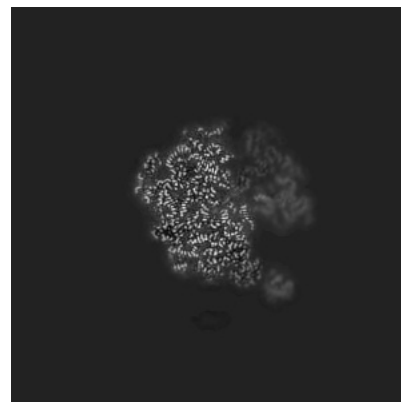
6.2.1 Primary map



X Index: 225

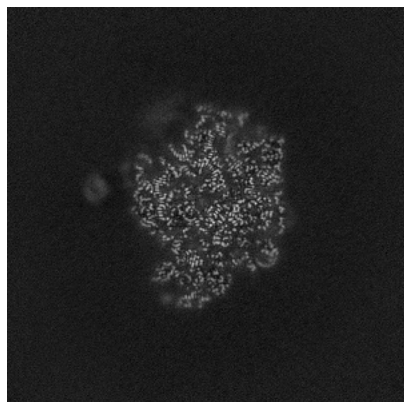


Y Index: 225

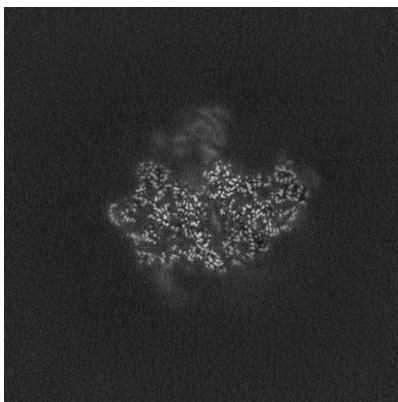


Z Index: 225

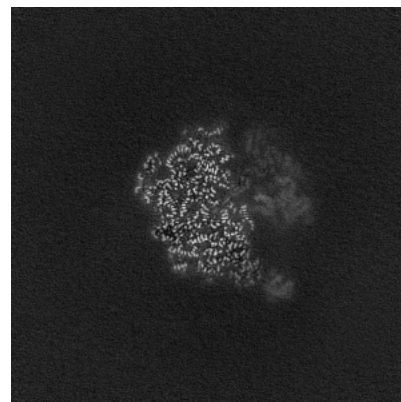
6.2.2 Raw map



X Index: 225



Y Index: 225

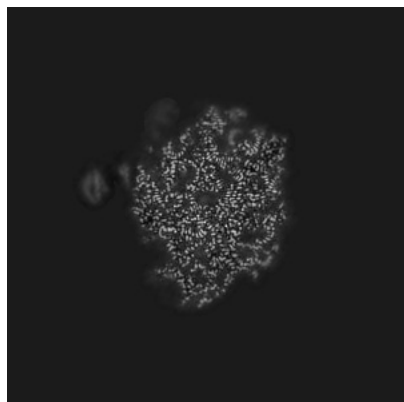


Z Index: 225

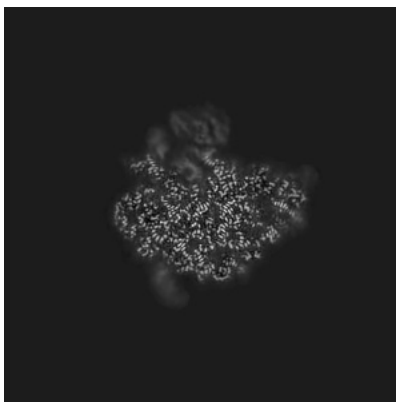
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

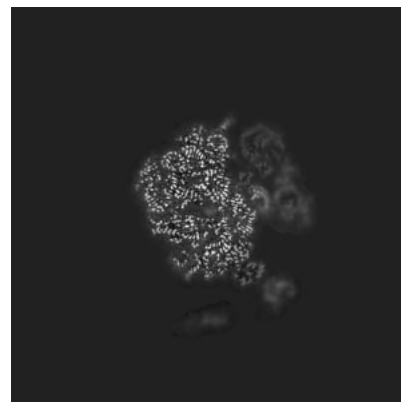
6.3.1 Primary map



X Index: 219

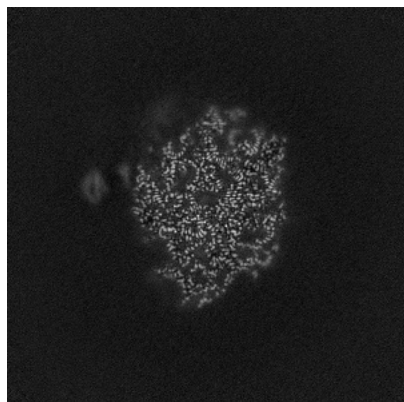


Y Index: 237

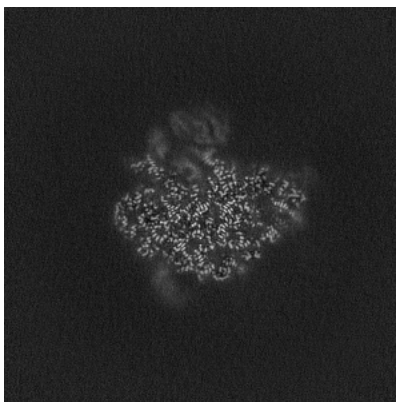


Z Index: 231

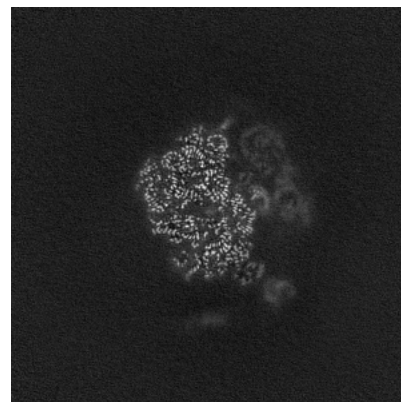
6.3.2 Raw map



X Index: 219



Y Index: 237

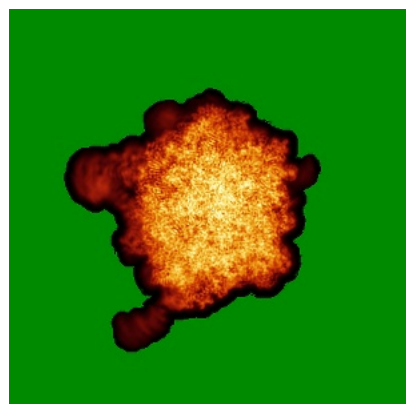


Z Index: 231

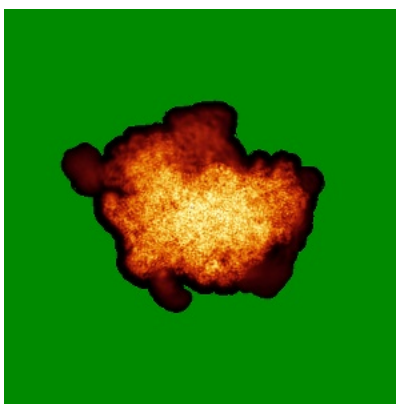
The images above show the largest variance slices of the map in three orthogonal directions.

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

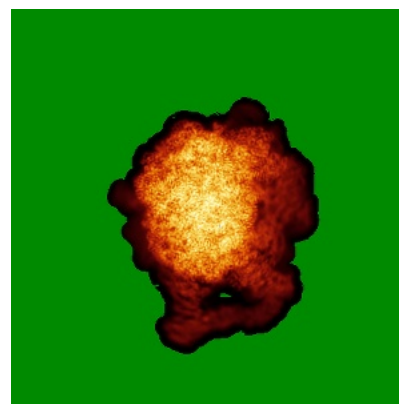
6.4.1 Primary map



X

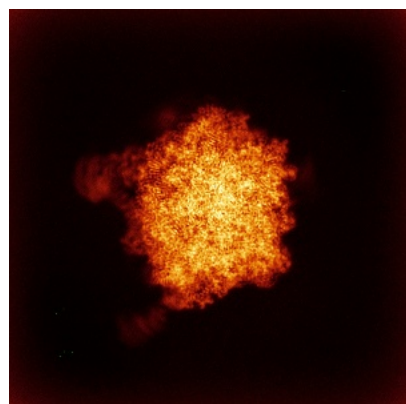


Y

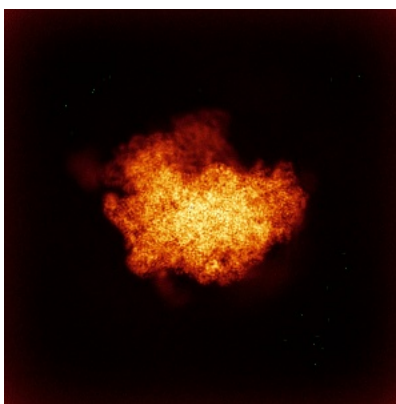


Z

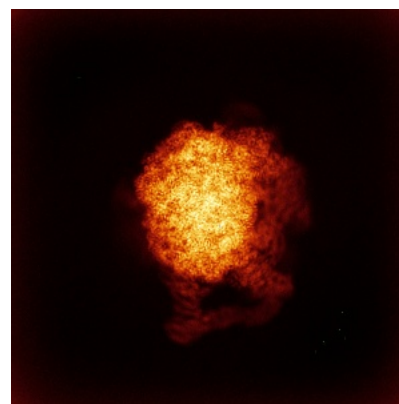
6.4.2 Raw map



X



Y

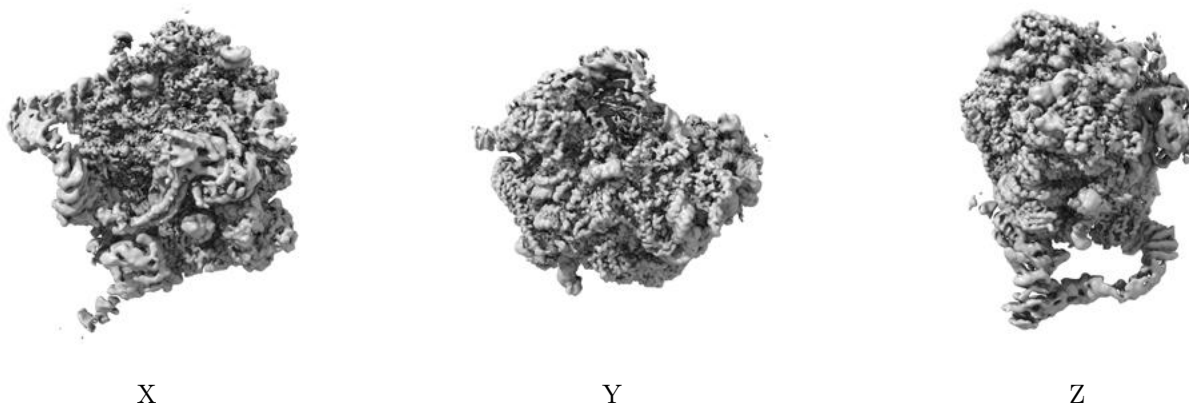


Z

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.

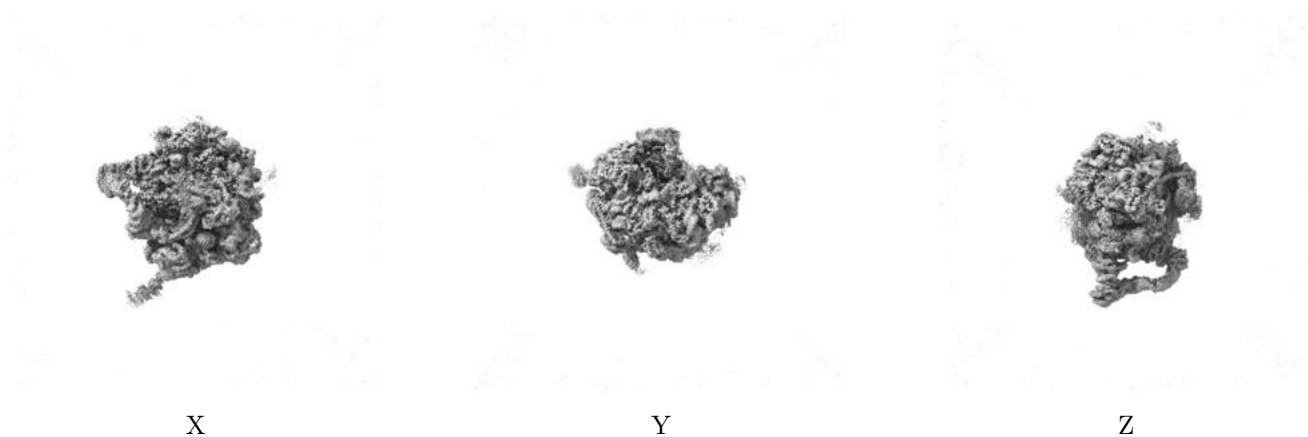
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

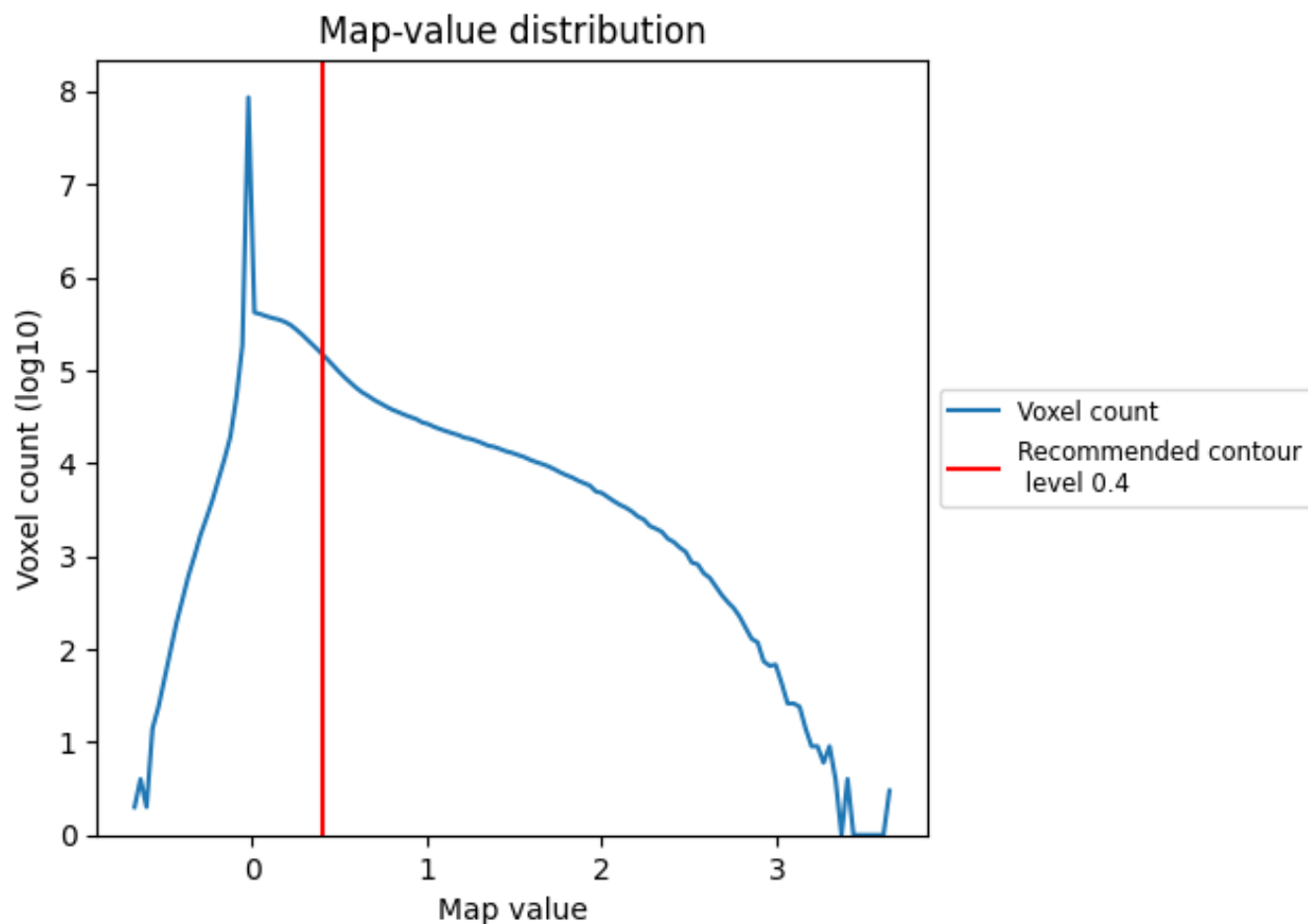
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

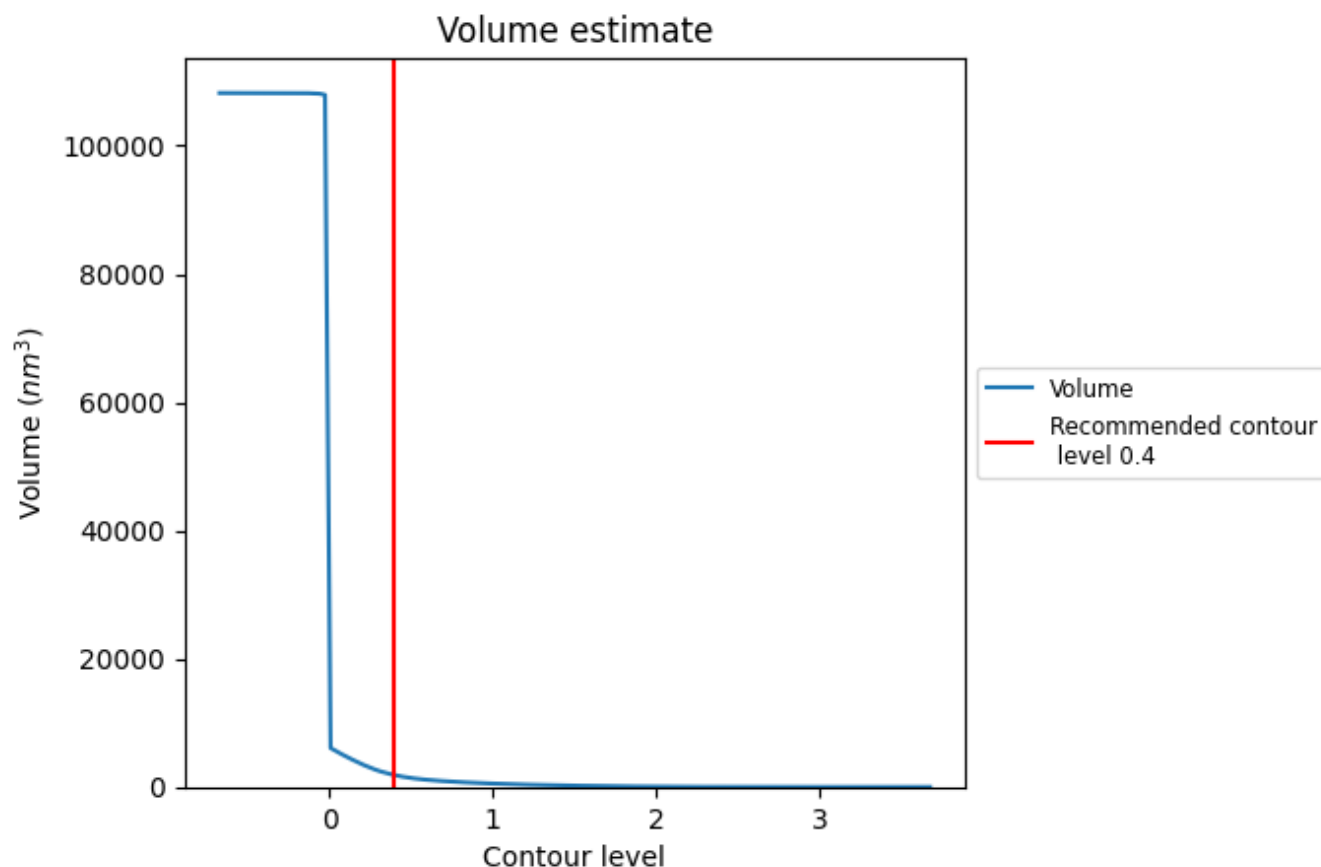
This section contains the results of statistical analysis of the map.

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.

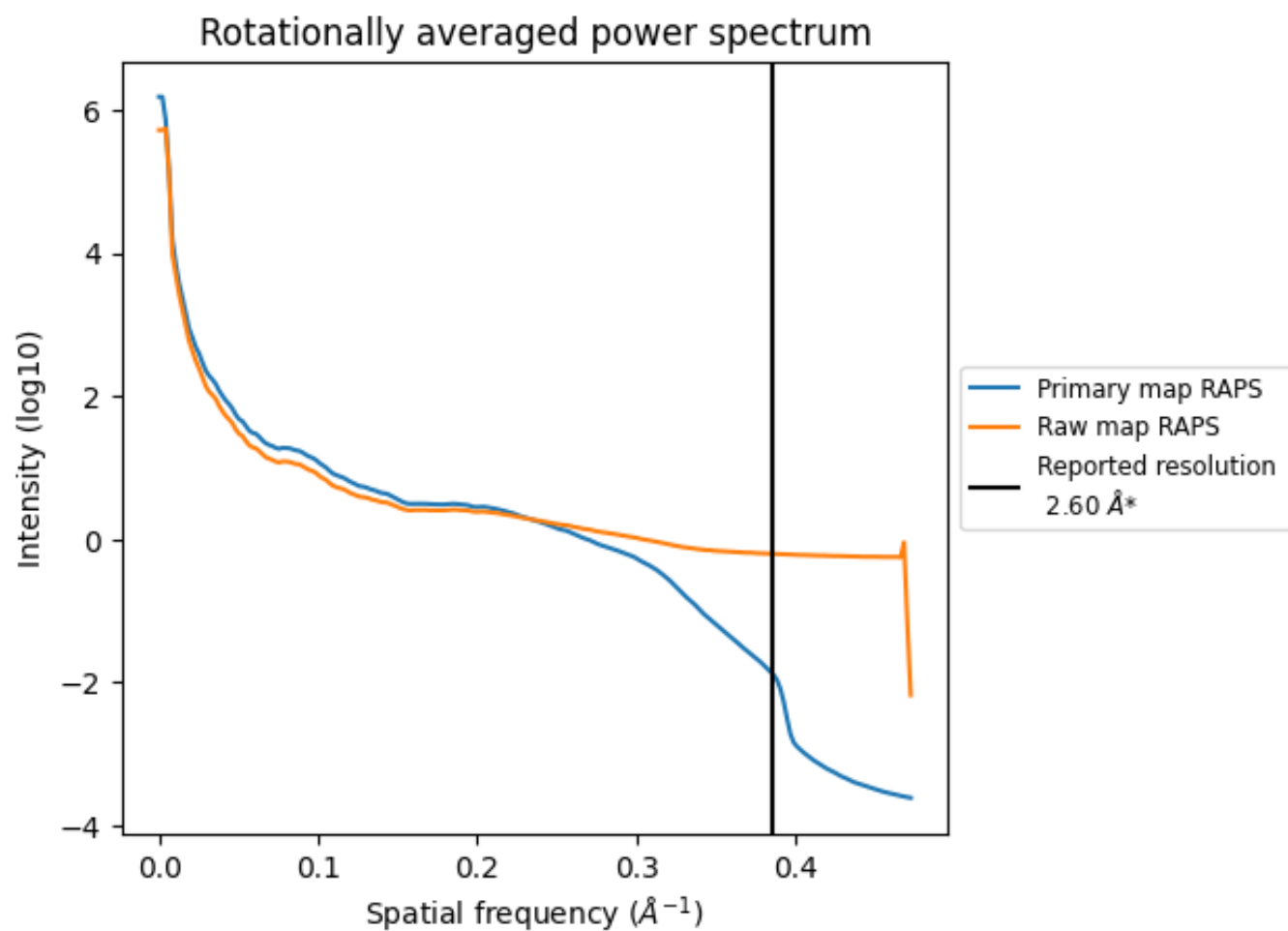
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1851 nm^3 ; this corresponds to an approximate mass of 1672 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 ⓘ

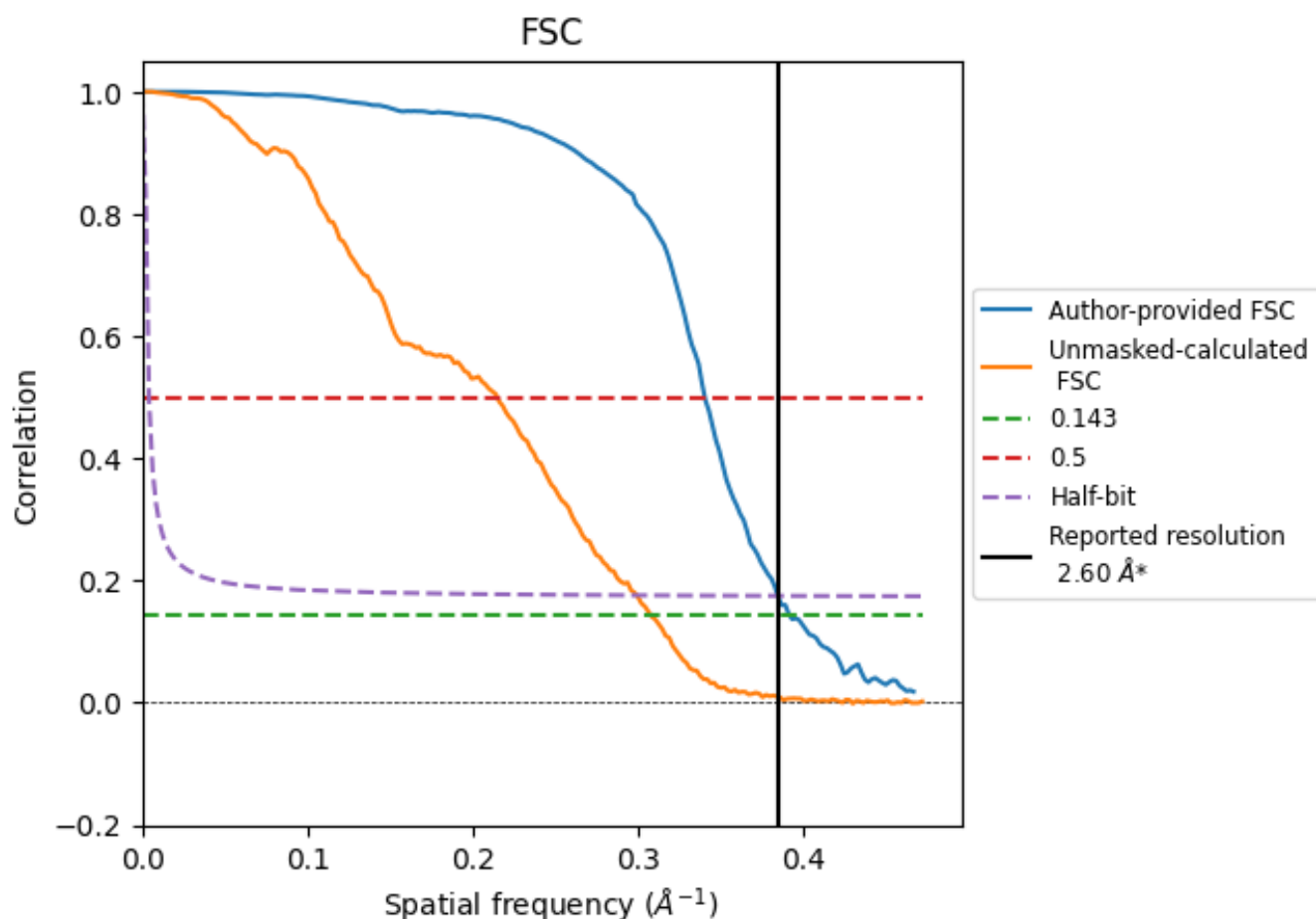


*Reported resolution corresponds to spatial frequency of $0.385 \text{ \AA}^{-1}$

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 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

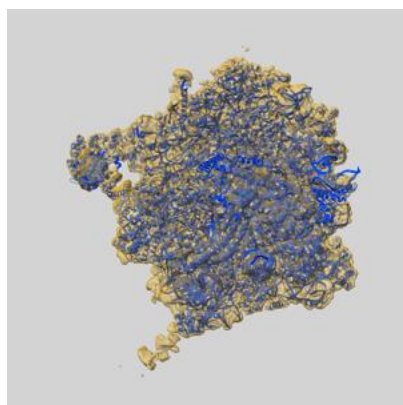
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.55	2.94	2.60
Unmasked-calculated*	3.25	4.65	3.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.25 differs from the reported value 2.6 by more than 10 %

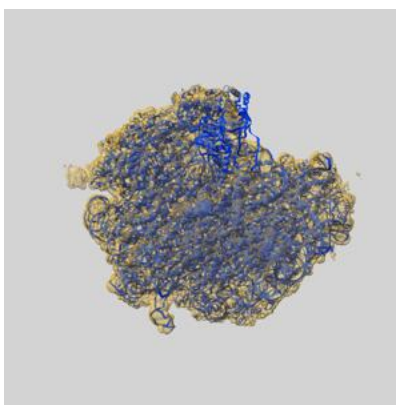
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15428 and PDB model 8AGZ. Per-residue inclusion information can be found in section 3 on page 16.

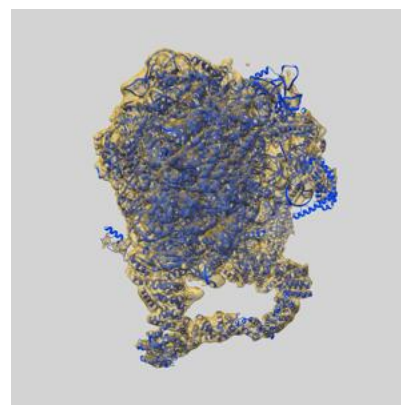
9.1 Map-model overlay [i](#)



X



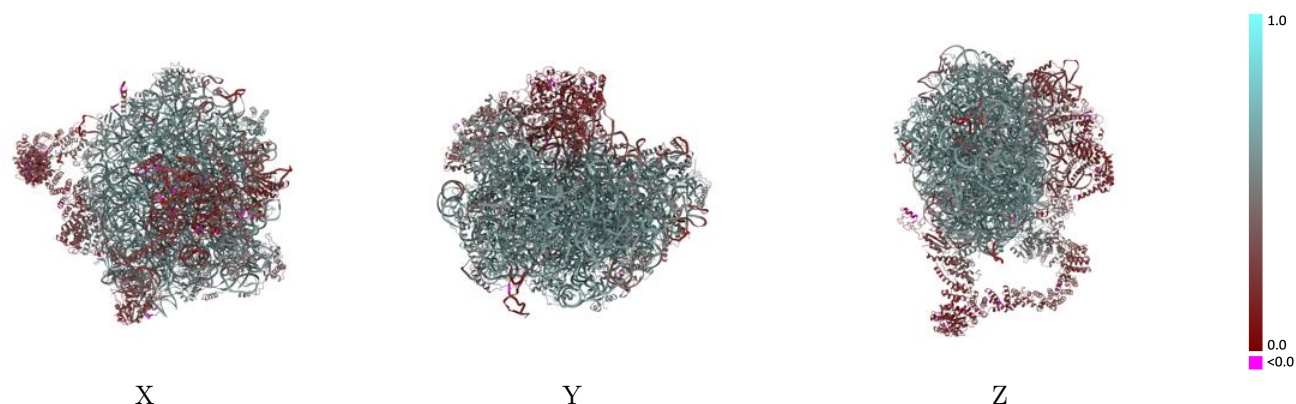
Y



Z

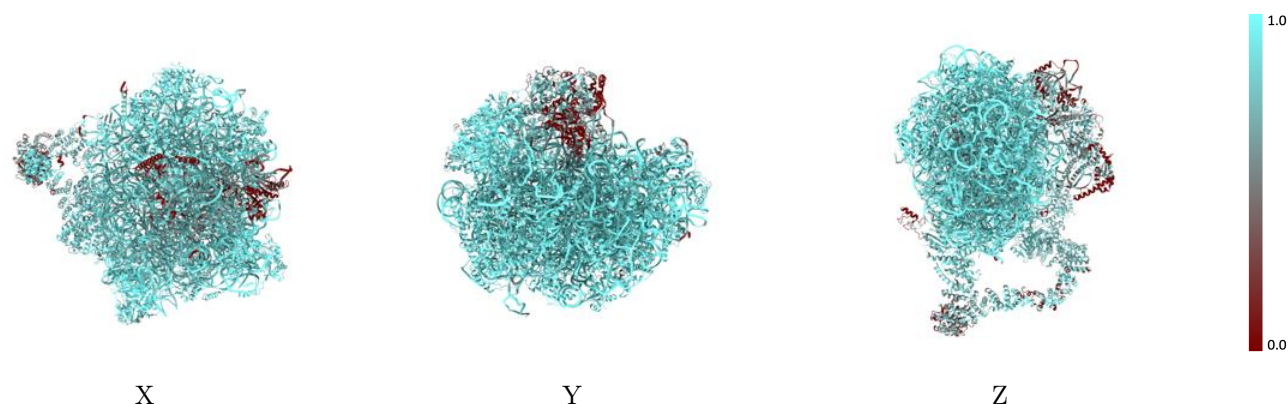
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



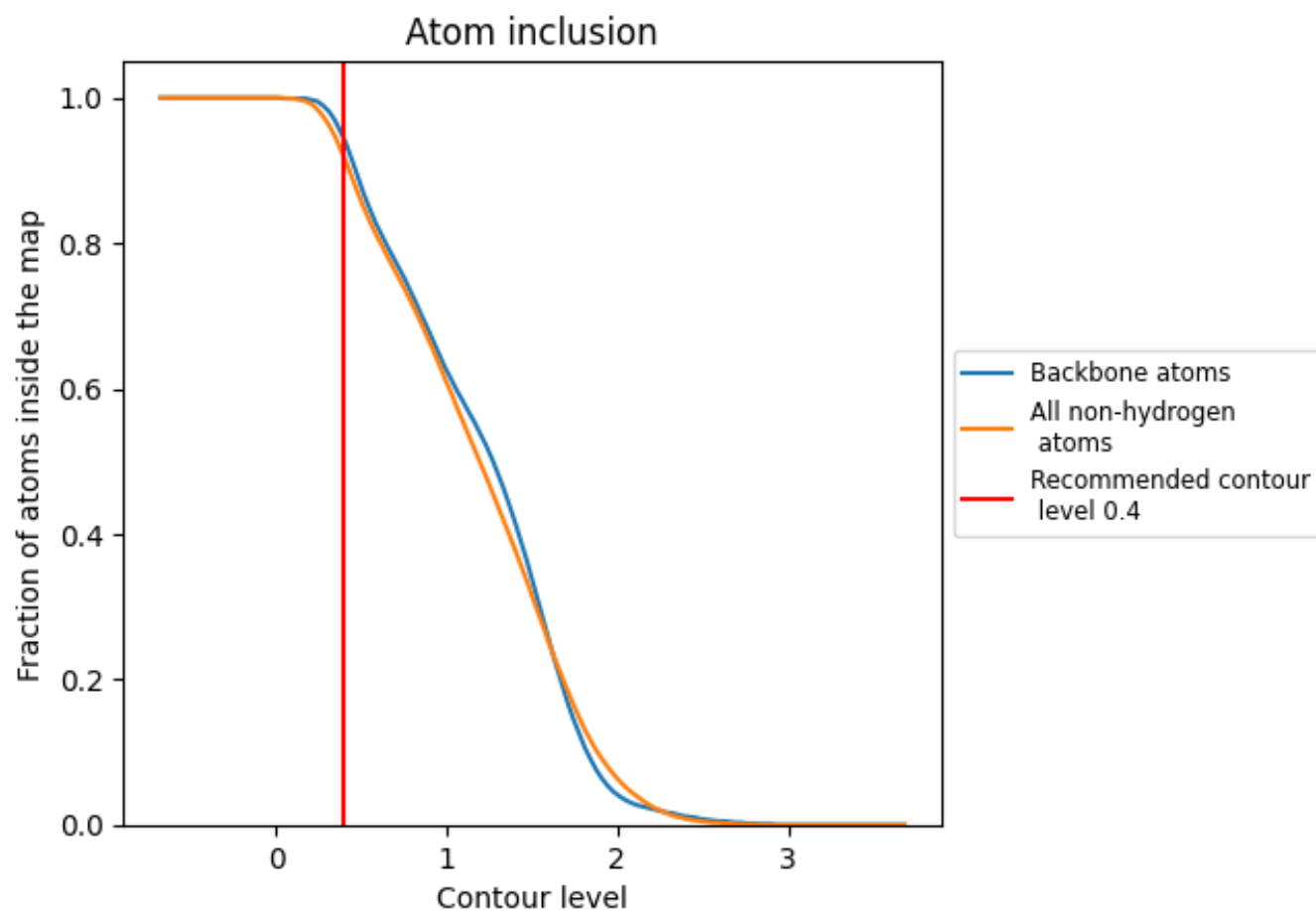
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.5120
0	 0.8470	 0.2900
1	 1.0000	 0.4020
A	 0.9930	 0.6120
B	 0.9790	 0.5890
C	 0.9640	 0.5890
D	 0.9820	 0.5850
E	 0.9390	 0.5500
F	 0.9810	 0.5800
G	 0.9680	 0.5650
H	 0.9220	 0.4640
I	 0.9680	 0.5780
J	 0.9660	 0.5780
K	 0.9660	 0.5740
L	 0.9770	 0.5700
M	 0.9560	 0.5210
N	 0.9810	 0.5940
O	 0.9580	 0.5420
P	 0.9390	 0.5230
Q	 0.9260	 0.5490
R	 0.9820	 0.5990
S	 0.9920	 0.6150
T	 0.9770	 0.5760
U	 0.9670	 0.5580
V	 0.9600	 0.5300
W	 1.0000	 0.6280
X	 0.9210	 0.4970
Y	 1.0000	 0.6020
Z	 0.9700	 0.5760
a	 0.5850	 0.2180
b	 0.9640	 0.5730
c	 0.9720	 0.5700
d	 0.7610	 0.4030
e	 0.6980	 0.2570
f	 0.9820	 0.5700



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Chain	Atom inclusion	Q-score
g	 0.8440	 0.4880
h	 0.9990	 0.5720
i	 0.9970	 0.5980
j	 0.9910	 0.6050
k	 0.9790	 0.5880
l	 0.9780	 0.5770
m	 0.9400	 0.4870
n	 0.9500	 0.5290
o	 0.9690	 0.5710
p	 0.9460	 0.5210
q	 0.9610	 0.5500
r	 0.9610	 0.5470
s	 0.9300	 0.4480
t	 0.9710	 0.5610
u	 0.9700	 0.5500
v	 0.4610	 0.3610
w	 0.1230	 0.2290
x	 0.7470	 0.2550
y	 0.8690	 0.2310
z	 0.9090	 0.2990