



## wwPDB EM Validation Summary Report ⓘ

Dec 30, 2024 – 08:24 AM EST

PDB ID : 8AGU  
EMDB ID : EMD-15424  
Title : Yeast RQC complex in state E  
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.  
Deposited on : 2022-07-20  
Resolution : 2.70 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](mailto: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>.

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

EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

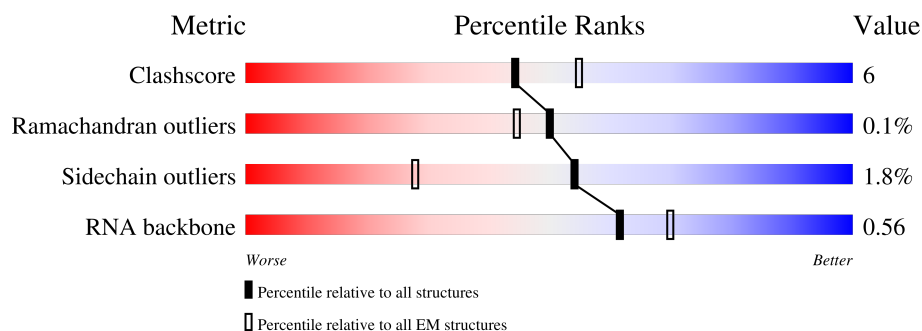
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.70 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.







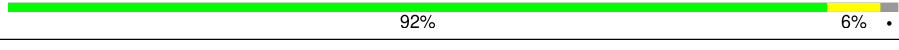
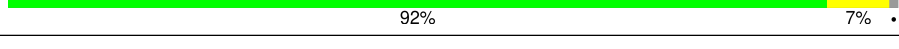
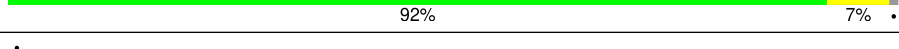
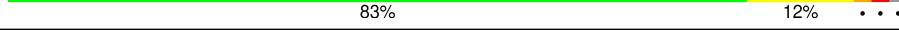
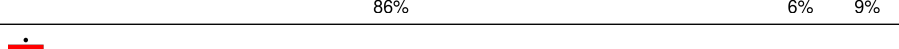
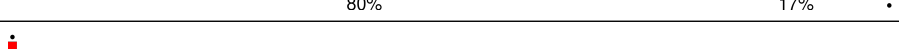
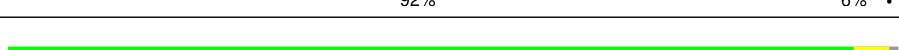
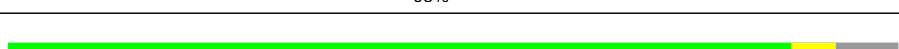
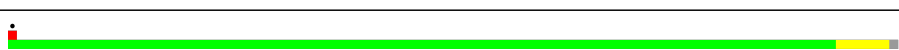
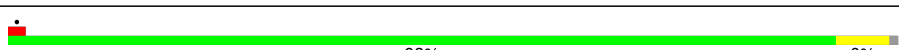
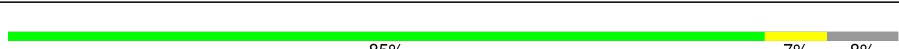

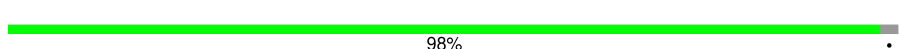

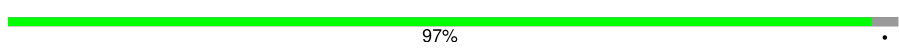
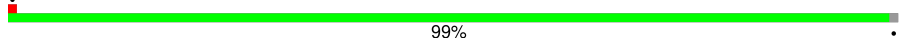
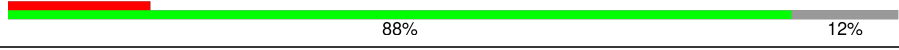
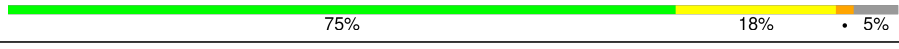



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	
4	D	186	
5	E	189	
6	F	172	
7	G	160	

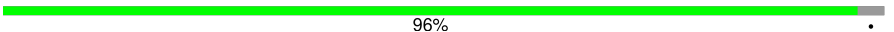

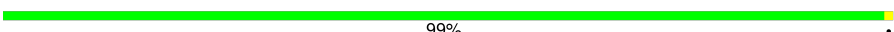
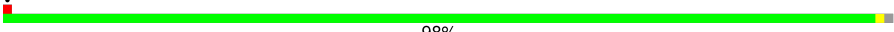










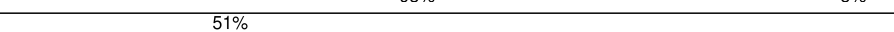

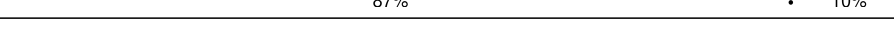
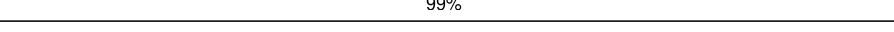
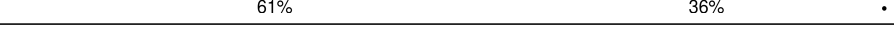


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Mol	Chain	Length	Quality of chain
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	
29	d	25	
30	f	3395	
31	h	121	
32	i	158	

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Mol	Chain	Length	Quality of chain
33	j	254	 96% .
34	k	387	 99% .
35	l	362	 99% .
36	m	297	 98% ..
37	n	176	 94% . 5%
38	o	244	 91% 9%
39	p	256	 89% . 9%
40	q	191	 98% ..
41	r	221	 98% ..
42	s	174	 95% .. .
43	t	199	 96% . .
44	u	138	 97% ..
45	a	1038	 14% 78% . 18%
46	e	1562	 68% 93% 5% .
47	g	245	 51% 91% 8%
48	v	157	 87% . 10%
49	w	217	 99%
50	y	76	 61% 36% .
51	z	165	 89% . 10%
52	0	312	 31% 7% . 61%
53	1	18	 94% 6%

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 149748 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 BJ4\_G0032190.mRNA.1.CDS.1.

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 RPL41A isoform 1.

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 BJ4\_G0008850.mRNA.1.CDS.1.

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 BJ4\_G0027750.mRNA.1.CDS.1.

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
			6569	4188	1138	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
			11509	7353	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 P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	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 peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 54 is MAGNESIUM ION (three-letter code: 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	
54	T	1	Total	Mg	0
			1	1	

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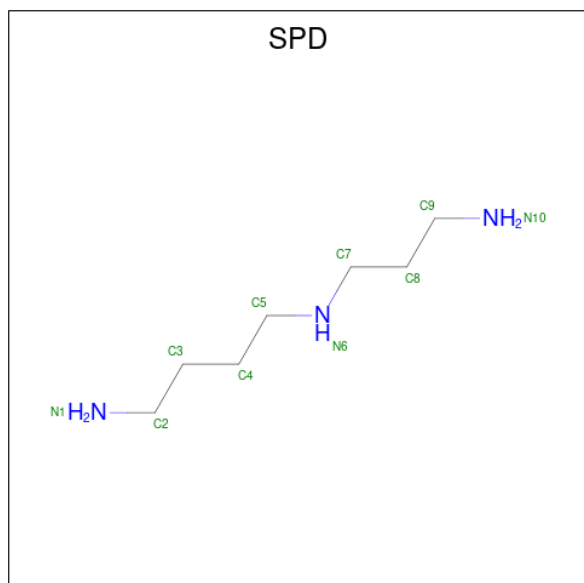
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Mol	Chain	Residues	Atoms		AltConf
54	f	3	Total 3	Mg 3	0
54	h	1	Total 1	Mg 1	0
54	j	2	Total 2	Mg 2	0
54	k	1	Total 1	Mg 1	0

- Molecule 55 is ZINC ION (three-letter code: 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 (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).

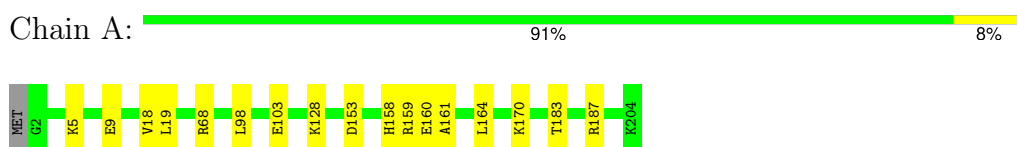


Mol	Chain	Residues	Atoms			AltConf
56	f	1	Total	C	N	0
			10	7	3	

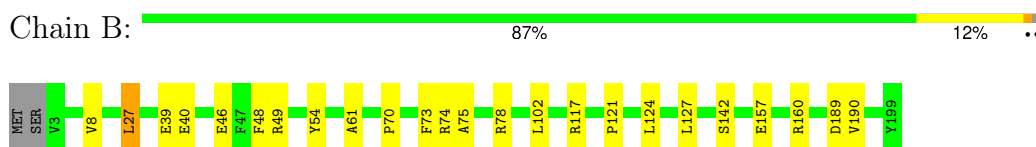
### 3 Residue-property plots [i](#)

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.

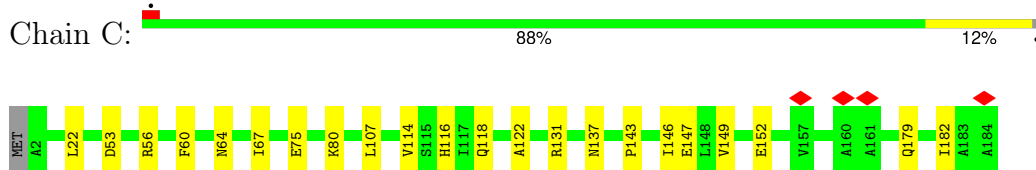
- Molecule 1: 60S ribosomal protein L15-A



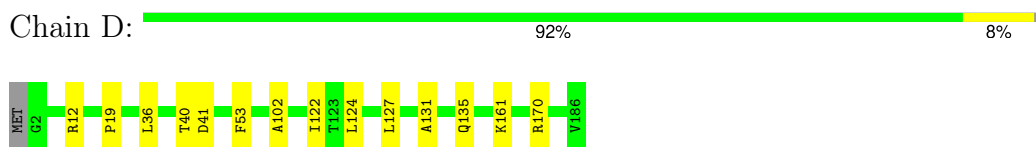
- Molecule 2: 60S ribosomal protein L16-A



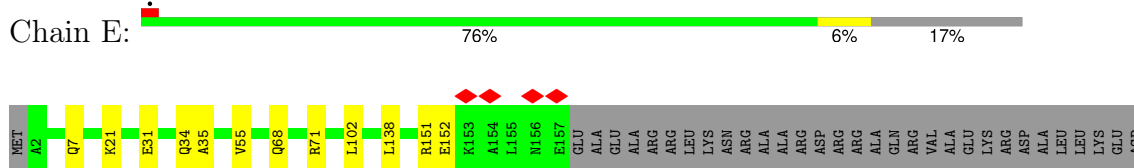
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A




- Molecule 5: 60S ribosomal protein L19-A



ALA

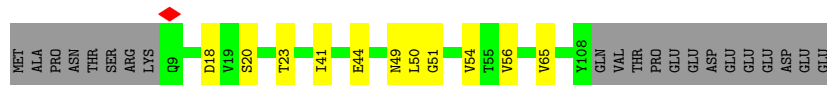
- Molecule 6: 60S ribosomal protein L20-A

Chain F:  87% 12%


- Molecule 7: 60S ribosomal protein L21-A

Chain G:  90% 9%

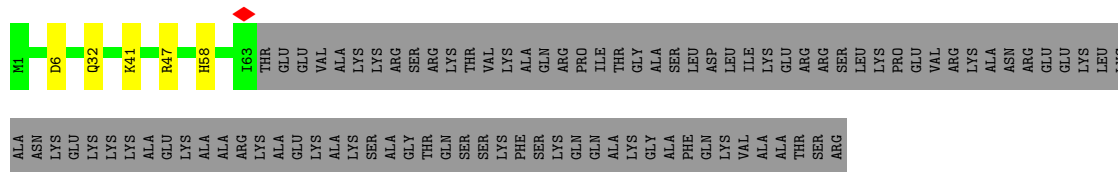
- Molecule 8: 60S ribosomal protein L22-A

Chain H:  74% 9% 17%


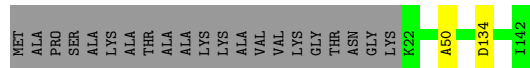
- Molecule 9: 60S ribosomal protein L23-A

Chain I:  88% 11%

- Molecule 10: 60S ribosomal protein L24-A

Chain J:  37% 59%

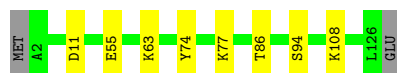
- Molecule 11: 60S ribosomal protein L25

Chain K:  84% 15%

- Molecule 12: 60S ribosomal protein L26-A



Chain L:  92% 6% .



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  92% 7% .




- Molecule 14: 60S ribosomal protein L28

Chain N:  92% 7% .




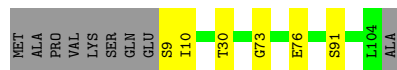
- Molecule 15: 60S ribosomal protein L29

Chain O:  83% 12% . . .




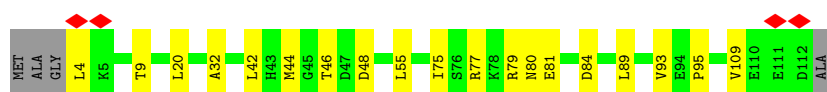
- Molecule 16: 60S ribosomal protein L30

Chain P:  86% 6% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  80% 17% .



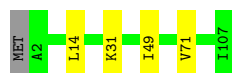
- Molecule 18: 60S ribosomal protein L32

Chain R:  92% 6% .




- Molecule 19: 60S ribosomal protein L33-A

Chain S:  95% . .



- Molecule 20: 60S ribosomal protein L34-A

Chain T:  88% 5% 7%



- Molecule 21: 60S ribosomal protein L35-A

Chain U:  93% 6% .




- Molecule 22: 60S ribosomal protein L36-A

Chain V:  93% 6% .




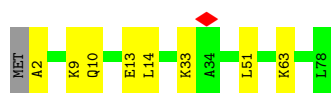
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  85% 7% 8%



- Molecule 24: BJ4\_G0032190.mRNA.1.CDS.1

Chain X:  88% 10% .



- Molecule 25: 60S ribosomal protein L39

Chain Y:  98% .



- Molecule 26: Ubiquitin-60S ribosomal protein L40

Chain Z:  41% 59%

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

ILE GLN LYS SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY I77 K128

- Molecule 27: 60S ribosomal protein L42-A

Chain b:  97%


MET V2 L104 GLN PHE

- Molecule 28: 60S ribosomal protein L43-A

Chain c:  99%

MET A2 A92

- Molecule 29: RPL41A isoform 1

Chain d:  16% 88% 12%

W4 R21 R22 V23 R24 A25 ARG SER LYS

- Molecule 30: 25S rRNA

Chain f:  75% 18% 5%

G U U3 A6 A13 U14 A26 C36 A40 A43 A211 A49 G59 A60 A65 A66 U78 U87 G92 U97 U98 A99 A109 G110 C111 U112 C113 A116 G120 A121 A122 U133 U134 C135 G136 C142 U149 G156 A157 A165

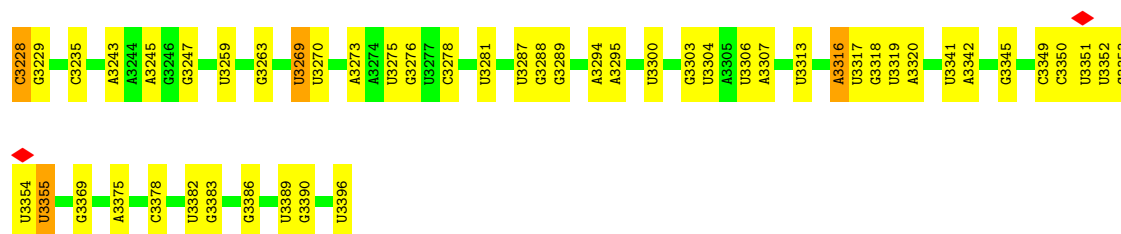
C166 G172 G173 A187 U190 U191 C192 C200 G206 U210 A211 G212 A213 G218 A219 A234 U240 G241 C242 G243 G244 U245 U249 U252 U257 G269 U270 G282 G283 U286 A295 U305 C315 A323 U329 C339 C350 U354 A165

A374 A375 G376 A398 G400 U401 A402 C403 G406 U411 G421 A422 A439 A440 U441 G442 G443 U444 U445 U446 U447 U448 U449 G450 U451 G C C C U C U C G U C C C U U U G C C C U U U G G G U A G G G A A U C

U C G A486 U488 U489 C490 G494 G518 A519 U520 A521 A522 A523 U524 G535 U536 C543 C544 U545 C546 G547 G548 A551 G552 U555 U556 A557 U558 A559 A578 G579 A589 G597 G604 G608 G609 G610 G611 U620 A621 A622 C637 C638 U874

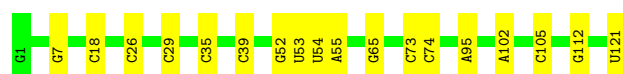
A649 A660 C667 A677 U681 G684 A690 A691 A705 A712 A715 A716 U719 A720 C758 G763 U764 C765 U766 U767 U776 U777 U780 G781 G785 A786 A806 A817 A830 G835 A846 C849 U850 A861 C861 U865 U874

G3059	A2845	G2590	U2537	A2402	A2223	C	U	U1760	A1566	G1349	A1217	U1028	
U3078	U2846	A2691	U2538	G2403	A2224	G	U	C1761	U1567	A1350	A1218	A1036	
G3080	C2849	A2694	C2539	A2404	U2225	C	A	U1764	U1568	U1351	C1219	A1036	
A3086	U2860	A2695	A2540	U2411	A2228	U	G	U1765	U1569	A1352		U1041	
C3092	C2867	A2696	U2541	A2419	C2235	G	C	G1766	U1572	U1353	G1222	U1041	
U3104	G2871	A2704	U2542	G2437	G2249	C	C	G1770	C1354	A1355	A1225	A1047	
A3113	G2872	G2714	U2543	C2444	U2254	U	U	G1775	U1573	U1356	A1226	A1047	
A3122	U2873	U2719	U2544	U2445	A	A	A	U1776	C1574	C1357	C1227	C1049	
U3130	U2874	C2726	U2545	U2446	C	C	C	U1777	U1575	A1386	U1235	G1063	
U3131	U2875	A2727	U2546	A2447	U	U	U	G1780	U1576	A1386	U1236	A1064	
A3142	A2887	U2728	U2547	G2450	A	A	A	U1781	C1577	G1392	G1237	A1065	
C3143	G2898	U2729	U2548	A2461	U	U	U	G1782	U1578	A1399	C1238	G1072	
U3148	C2899	A2730	U2549	G2462	A	A	A	U1783	U1579	G1400	U1241	U1081	
U3151	A2911	U2731	U2550	U2463	U	U	U	A1816	G1580	A1419	G1242	G1087	
U3152	G2914	C2753	U2551	U2464	A	A	A	U1819	C1581	U1425	G1243	A1083	
U3153	U2923	U2754	U2552	A2468	A	A	A	U1820	U1582	G1434	A1244	A1083	
C3154	U2935	C2755	U2553	G2469	U	U	U	U1821	C1583	A1434	A1245	U1094	
U3155	A2936	C2756	U2554	C2470	U	U	U	A1835	U1584	C1437	A1251	U1095	
U3156	G2937	U2757	U2555	U2471	U	U	U	U1839	U1585	A1446	U1252	U1096	
U3157	U2938	C2758	U2556	U2472	A	A	A	A1841	U1586	G1447	C1254	A1103	
A3165	U2941	U2759	U2557	G2473	U	U	U	A1842	C1608	A1449	U1258	G1104	
A3170	C2942	U2760	U2558	U2474	U	U	U	C1846	U1620	G1450	U1259	G1115	
G3173	U2943	C2761	U2559	A2479	G	G	G	U1629	U1642	A1481	A1263	G1116	
A3174	U2944	U2762	U2560	A2480	C	C	C	U1630	A1643	A1482	G1264	G1117	
G3176	C2945	U2763	U2561	U2481	G	G	G	A1644	U1645	G1483	U1265	G1131	
U3179	U2946	A2802	U2562	U2482	U	U	U	A1867	C1657	G1487	U1269	U1144	
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C3181	C2948	U2804	U2564	A2484	C	C	C	U1881	U1717	C1502	C1277	A1159	
A3186	U2949	U2805	U2565	A2485	U	U	U	A1883	A1688	C1508	G1282	C1160	
A3187	C2950	U2806	U2566	U2486	G	G	G	G1906	U1724	G1525	G1285	A1180	
U3196	U2951	G2807	U2567	U2487	U	U	U	C1907	C1725	G1536	A1286	U1181	
U3207	A3006	A2808	U2568	U2488	C	C	C	U1907	U1726	A1539	A1287	G1010	
G3208	A3012	U2809	U2569	U2489	U	U	U	G1943	U1727	U1554	G1295	A1190	
A3209	C3034	U2810	U2570	C2495	C	C	C	C1951	U1732	U1555	G1307	U1191	
U3214	A3048	U2811	U2571	C2496	U	U	U	G1952	U1736	C1556	A1308	A1192	
C3217	U3056	U2812	U2572	U2497	C	C	C	G1953	A1741	A1557	U1309	C1196	
A3218	U3057	U2813	U2573	U2498	U	U	U	U1954	U1955	G1560	G1313	A1197	
G3219	U3058	U2814	U2574	U2499	C	C	C	U1955	A1750	G1561	A1330	C1201	
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		U2816	U2576	U2501	C	C	C	U1957		C1563		U1208	
		U2817	U2577	U2502	G	G	G	U1958					
		U2818	U2578	U2503	U	U	U	U1959					
		U2819	U2579	U2504	C	C	C	U1960					
		U2820	U2580	U2505	U	U	U	U1961					
		U2821	U2581	U2506	C	C	C	U1962					
		U2822	U2582	U2507	U	U	U	U1963					
		U2823	U2583	U2508	C	C	C	U1964					
		U2824	U2584	U2509	U	U	U	U1965					
		U2825	U2585	U2510	C	C	C	U1966					
		U2826	U2586	U2511	U	U	U	U1967					
		U2827	U2587	U2512	C	C	C	U1968					
		U2828	U2588	U2513	U	U	U	U1969					
		U2829	U2589	U2514	C	C	C	U1970					
		U2830	U2590	U2515	U	U	U	U1971					
		U2831	U2591	U2516	C	C	C	U1972					
		U2832	U2592	U2517	U	U	U	U1973					
		U2833	U2593	U2518	C	C	C	U1974					
		U2834	U2594	U2519	U	U	U	U1975					
		U2835	U2595	U2520	C	C	C	U1976					
		U2836	U2596	U2521	U	U	U	U1977					
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		U2838	U2598	U2523	U	U	U	U1979					
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		U2841	U2601	U2526	C	C	C	U1982					
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		U2845	U2605	U2530	C	C	C	U1986					
		U2846	U2606	U2531	U	U	U	U1987					
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		U2848	U2608	U2533	U	U	U	U1989					
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		U2850	U2610	U2535	U	U	U	U1991					
		U2851	U2611	U2536	C	C	C	U1992					
		U2852	U2612	U2537	U	U	U	U1993					
		U2853	U2613	U2538	C	C	C	U1994					
		U2854	U2614	U2539	U	U	U	U1995					
		U2855	U2615	U2540	C	C	C	U1996					
		U2856	U2616	U2541	U	U	U	U1997					
		U2857	U2617	U2542	C	C	C	U1998					
		U2858	U2618	U2543	U	U	U	U1999					
		U2859	U2619	U2544	C	C	C	U2000					
		U2860	U2620	U2545	U	U	U	U2001					
		U2861	U2621	U2546	C	C	C	U2002					
		U2862	U2622	U2547	U	U	U	U2003					
		U2863	U2623	U2548	C	C	C	U2004					
		U2864	U2624	U2549	U	U	U	U2005					
		U2865	U2625	U2550	C	C	C	U2006					
		U2866	U2626	U2551	U	U	U	U2007					
		U2867	U2627	U2552	C	C	C	U2008					
		U2868	U2628	U2553	U	U	U	U2009					
		U2869	U2629	U2554	C	C	C	U2010					
		U2870	U2630	U2555	U	U	U	U2011					
		U2871	U2631	U2556	C	C	C	U2012					
		U2872	U2632	U2557	U	U	U	U2013					
		U2873	U2633	U2558	C	C	C	U2014					
		U2874	U2634	U2559	U	U	U	U2015					
		U2875	U2635	U2560	C	C	C	U2016					
		U2876	U2636	U2561	U	U	U	U2017					
		U2877	U2637	U2562	C	C	C	U2018					
		U2878	U2638	U2563	U	U	U	U2019					
		U2879	U2639	U2564	C	C	C	U2020					
		U2880	U2640	U2565	U	U	U	U2021					
		U2881	U2641	U2566	C	C	C	U2022					
		U2882	U2642	U2567	U	U	U	U2023					
		U2883	U2643	U2568	C	C	C	U2024					
		U2884	U2644	U2569	U	U	U	U2025					
		U2885	U2645	U2570	C	C	C	U2026					
		U2886	U2646	U2571	U	U	U	U2027					
		U2887	U2647	U2572	C	C	C	U2028					
		U2888	U2648	U2573	U	U	U	U2029					
		U2889	U2649	U2574	C	C	C	U2030					
		U2890	U2650	U2575	U	U	U	U2031					
		U2891	U2651	U2576	C	C	C	U2032					
		U2892	U2652	U2577	U	U	U	U2033					
		U2893	U2653	U2578	C	C	C	U2034					
		U2894	U2654	U2579	U	U	U	U2035					
		U2895	U2655	U2580	C	C	C	U2036					
		U2896	U2656	U2581	U	U	U	U2037					
		U2897	U2657	U2582	C	C	C	U2038					
		U2898	U2658	U2583	U	U	U	U2039					
		U2899	U2659	U2584	C	C	C	U2040					
		U2900	U2660	U2585	U	U	U	U2041					
		U2901	U2661	U2586	C	C	C	U2042					



• Molecule 31: 5S rRNA

Chain h: 85% 15%



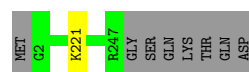
• Molecule 32: 5.8S rRNA

Chain i: 78% 20%



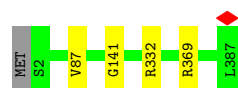
• Molecule 33: 60S ribosomal protein L2-A

Chain j: 96%



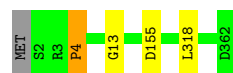
• Molecule 34: 60S ribosomal protein L3

Chain k: 99%



• Molecule 35: BJ4\_G0008850.mRNA.1.CDS.1

Chain l: 99%



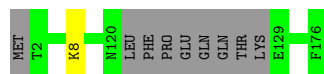
• Molecule 36: 60S ribosomal protein L5

Chain m: 98%



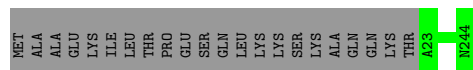
- Molecule 37: 60S ribosomal protein L6-B

Chain n:  94% • 5%




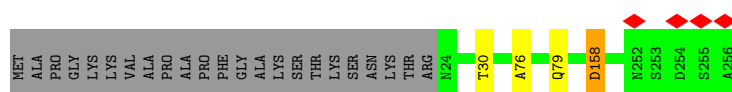
- Molecule 38: 60S ribosomal protein L7-A

Chain o:  91% 9%



- Molecule 39: 60S ribosomal protein L8-A

Chain p:  89% • 9%



- Molecule 40: 60S ribosomal protein L9-A

Chain q:  98% ..



- Molecule 41: 60S ribosomal protein L10

Chain r:  98% ..



- Molecule 42: BJ4\_G0027750.mRNA.1.CDS.1

Chain s:  95% ..



- Molecule 43: 60S ribosomal protein L13-A

Chain t:  96% ..




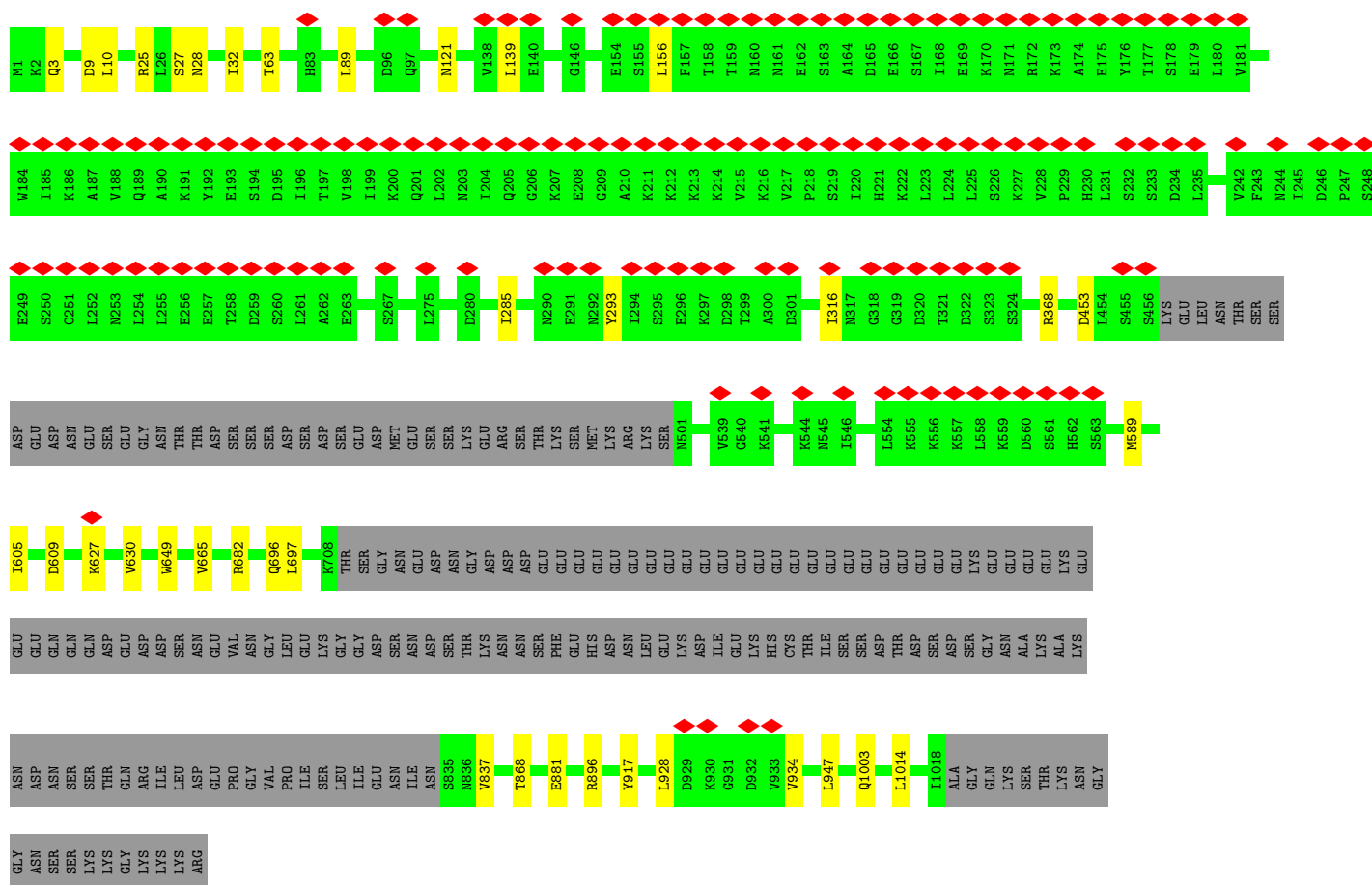
- Molecule 44: 60S ribosomal protein L14-A

Chain u:  97%

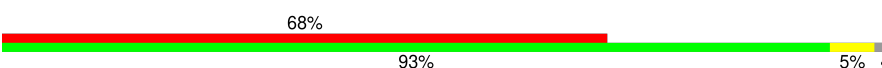


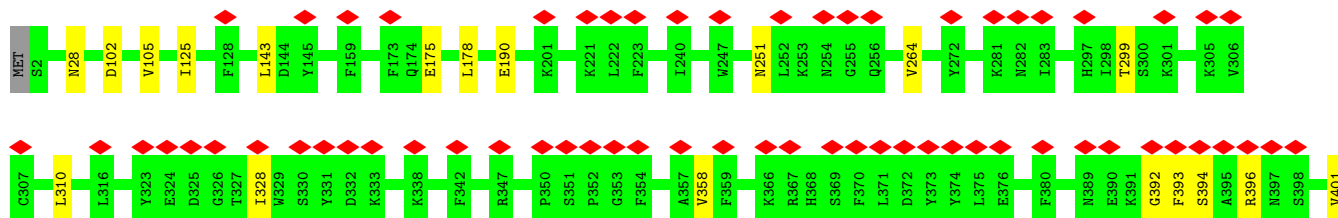
- Molecule 45: RQC2 isoform 1

Chain a:  14% 78% 18%



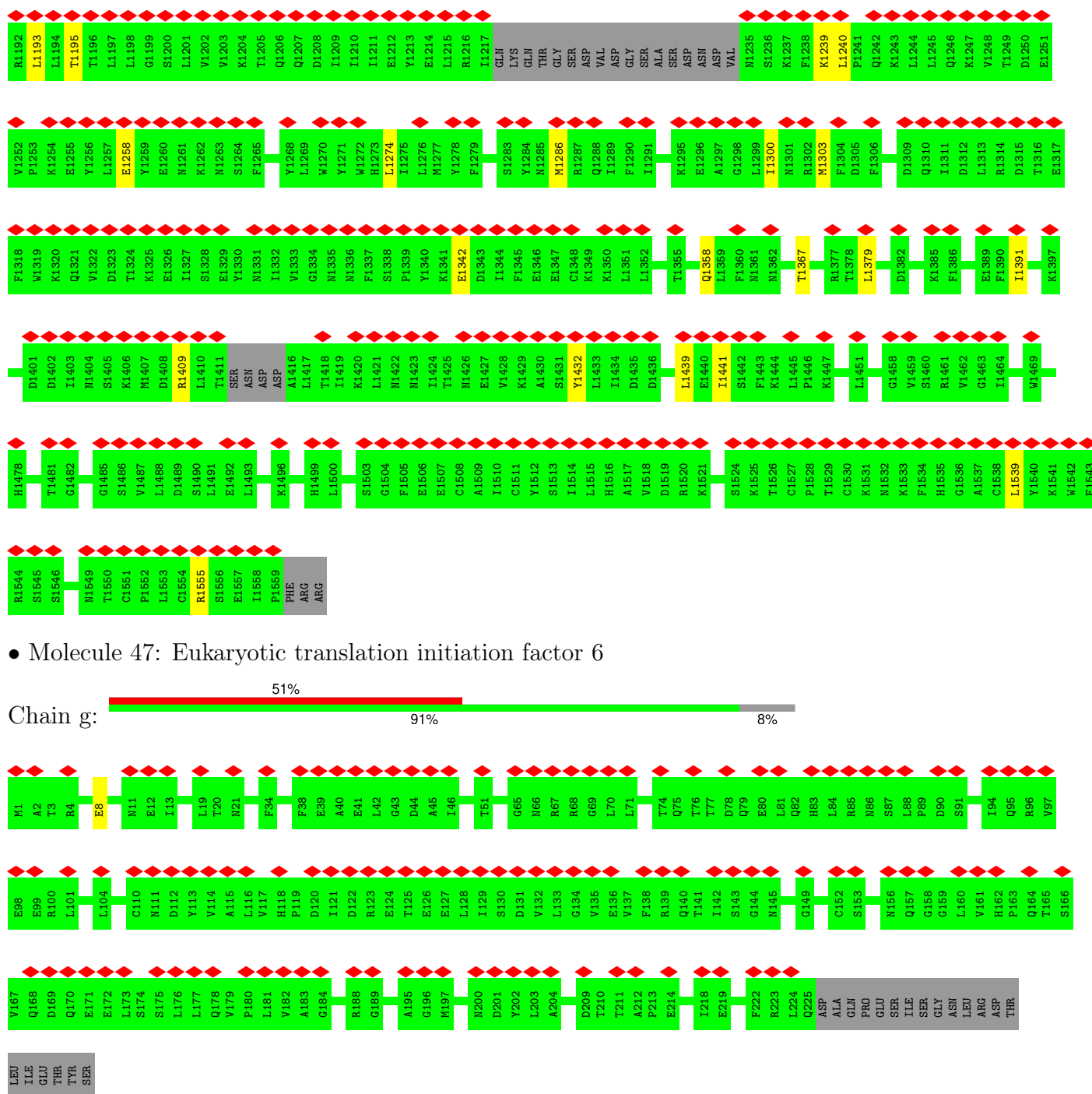
- Molecule 46: E3 ubiquitin-protein ligase listerin

Chain e:  68% 93% 5%



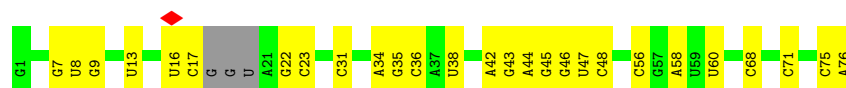
L1132	E1133	L1134	M1135	F1136	L1137	N1138	F1139	N1140	Q1141	E1142	R1143	N1144	N1145	Q1146	V1147	S1148	T1149	L1150	F1151	Y1152	Q1153	K1154	L1155	Y1156	K1157	V1158	I1159	S1160	S1161	M1162	E1163	L1164	K1165	K1166	L1167	E1168	S1169	Q1170	Y1171	K1172	R1173	I1174	F1175	E1176	V1177	V1178	L1179	N1180	D1181	K1182	L1183	I1184	G1185	S1186	N1187	I1188	N1189	Q1190	S1191	
A1072	F1073	E1074	L1075	S1076	E1077	R1078	L1079	L1080	A1081	D1082	S1083	L1084	S1085	M1086	C1087	Q1088	I1089	D1090	D1091	L1092	L1093	Y1094	L1095	L1096	E1097	L1098	R1099	S1100	S1101	C1102	L1103	N1104	L1105	Y1106	E1107	T1108	L1109	S1110	Q1111	GLY	VAL	SER	LYS	ASN	GLY	GLU	ILE	SER	E1122	Y1123	G1124	D1125	E1126	I1127	Q1128	E1129	N1130	L1131		
A1012	D1013	K1014	Q1015	F1016	V1017	P1018	I1019	A1020	P1021	Q1022	R1023	L1024	N1025	M1026	I1027	F1028	R1029	S1030	I1031	L1032	K1033	W1034	L1035	D1036	S1037	D1038	L1039	A1040	Y1041	E1042	P1043	S1044	F1045	S1046	T1047	V1048	R1049	L1050	L1051	L1052	L1053	D1054	F1055	F1056	T1057	K1058	L1059	M1060	R1061	F1062	E1063	G1064	V1065	R1066	D1067	M1068	I1069	P1010	Q1011	
K952	D953	Y954	L955	L956	C957	A958	I959	L960	L961	L962	M963	F964	N965	R966	S967	N968	S969	K970	D971	E972	I973	T974	K975	L976	R977	T978	L979	L980	A981	S982	Q983	L984	I985	G986	I987	R988	E989	V990	E991	L992	V993	D994	Q995	A996	E997	K998	S999	L1000	A1001	L1002	L1003	N1004	N1005	L1006	L1007	D1008	I1009	P1010	Q1011	
A892	N893	L894	T895	F896	D897	I898	A899	E900	S901	N902	S903	Y904	Y905	F906	F907	Y908	Y909	S910	R911	V912	L913	Y914	K915	V916	L917	L918	N919	S920	I921	D922	T923	V924	S925	S926	T927	T928	L929	N930	G931	L932	L933	A934	S935	V936	E937	S938	F939	V940	K941	K942	T943	V944	N945	D946	Q947	K948	S949	T950	D951	
N832	H833	I834	V835	A836	F837	I838	T839	W840	V841	S842	E843	L844	V845	T846	D847	Y848	N849	C850	L851	S852	E853	E854	P855	N856	D857	L858	Y859	Y860	D861	F862	G863	H864	T865	F866	F867	K868	H869	G870	K871	N872	N873	L874	N875	F876	S877	D878	T879	V880	N881	N882	V883	I884	Q885	P886	A887	N888	G889	Q890	D891	
V772	F773	A774	R775	Y776	M777	P778	A779	I780	D781	Y782	R783	S784	S785	L786	D787	S788	S789	L790	S791	T792	T793	T794	H795	L796	L797	L798	T799	D800	D801	K802	P803	L804	N805	L806	K807	N808	N809	Q810	K811	L812	L813	R814	Y815	A816	S817	F818	L819	D820	A821	L822	L823	D824	N825	L826	P827	E828	R829	V830	N831	
S712	L713	Q714	L715	A716	K717	G718	N719	S720	E721	I722	A723	M724	K725	L726	A727	Q728	V729	I730	L731	Y732	H733	A734	Q735	V736	Y737	F738	S739	P740	G741	A742	K743	E744	K745	Y746	V747	T748	H749	A750	V751	E752	L753	I754	N755	G756	G757	N758	D759	T760	S761	Q762	L763	F764	K764	N705	E706	K707	L708	F709	K710	L711
Q652	R653	T654	I655	T656	L657	L658	Y659	R660	S661	A662	V663	A664	N665	G666	Q667	V668	E669	Q670	F671	C672	A673	V674	L675	S676	L677	L678	D679	E680	T681	F682	F683	S684	T685	L686	L687	N688	N689	T690	D691	F692	L693	S694	C695	A696	L697	Y698	E699	V700	S701	E702	D703	T704	N705	E706	K707	L708	F709	K710	L711	
S592	F593	N594	L595	P596	K597	T598	I599	I600	L601	A602	T603	M604	N605	E606	L607	D608	N609	D610	I611	Y612	Q613	Q614	L615	M616	K617	S618	D619	S620	L621	E622	L623	E624	L625	Y626	I627	E628	D629	F630	M631	K632	N633	Y634	K635	F636	D637	D638	S639	G640	E641	I642	F643	E644	N645	N646	N647	K648	F649	L650	N651	
S532	D533	M534	I535	F536	L537	N538	G539	K540	I541	G542	K543	F544	I545	N546	E547	I548	P549	T550	L551	V552	Q553	E554	S555	T556	Y557	Q558	N559	F560	A561	G562	I563	M564	A565	Q566	Y567	S568	N569	S570	K571	F572	F573	K574	S575	N576	T577	D578	A579	I580	T581	S582	L583	E584	D585	F586	F587	I588	V589	A590	L591	
D471	I472	R473	K474	I475	K476	V477	S478	F479	E480	K481	M482	L483	F484	E485	L486	L487	V488	T489	S490	P491	M492	M493	E494	S495	Q496	I497	S498	R499	F500	F501	D502	F503	F504	V505	Q506	L507	I508	E509	T510	D511	P512	S513	N514	V515	T516	N517	D520	G521	V522	Y523	D524	A525	L526	N527	Y528	F529	L530	D531		

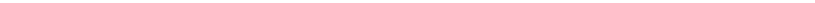


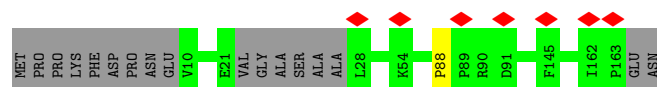


The diagram shows a segment of a protein backbone. The residues are MET (grey), S2 (green), E22 (green), K98 (yellow), and Y217 (green). A red diamond is positioned above the E22 residue, indicating a specific site of interest.

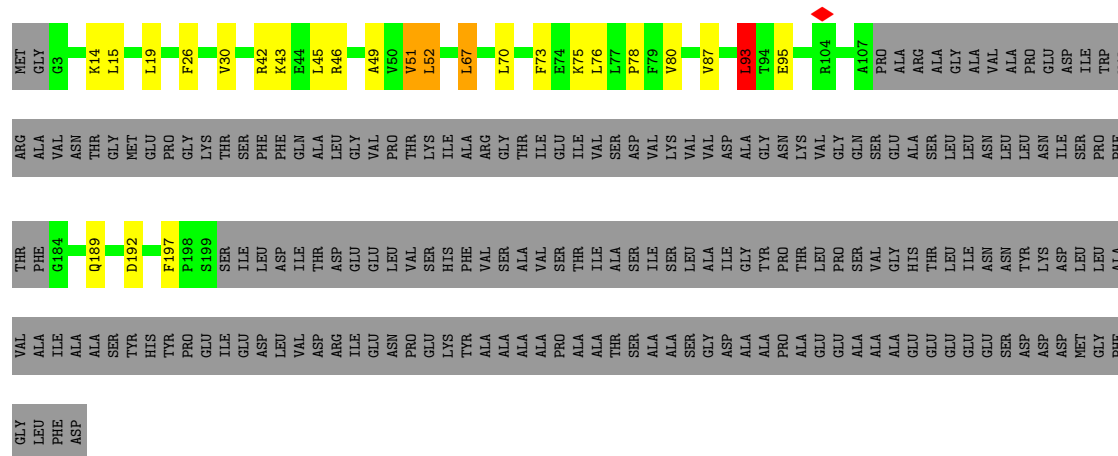
- Chain y: 



- Chain z:  89% 10%



- Chain 0:  31% 7% 61%



- Chain 1:  94% 6%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44241	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	3.554	Depositor
Minimum map value	-0.671	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.128	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: MG, 5CT, ZN, SPD

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	0.39	0/1757	0.70	1/2354 (0.0%)
2	B	0.39	0/1585	0.64	1/2128 (0.0%)
3	C	0.38	0/1439	0.71	2/1938 (0.1%)
4	D	0.34	0/1465	0.67	1/1965 (0.1%)
5	E	0.37	0/1275	0.67	0/1702
6	F	0.38	0/1473	0.65	0/1980
7	G	0.36	0/1296	0.62	0/1739
8	H	0.37	0/812	0.73	3/1099 (0.3%)
9	I	0.35	0/1018	0.64	0/1369
10	J	0.36	0/530	0.62	0/703
11	K	0.41	0/979	0.69	1/1321 (0.1%)
12	L	0.35	0/995	0.68	1/1329 (0.1%)
13	M	0.36	0/1106	0.61	0/1485
14	N	0.40	0/1200	0.62	0/1607
15	O	0.32	0/473	0.72	2/629 (0.3%)
16	P	0.35	0/745	0.67	0/1001
17	Q	0.39	0/890	0.77	2/1196 (0.2%)
18	R	0.32	0/1034	0.59	0/1385
19	S	0.38	0/868	0.61	0/1168
20	T	0.35	0/890	0.67	0/1189
21	U	0.34	0/978	0.65	1/1301 (0.1%)
22	V	0.34	0/772	0.66	0/1026
23	W	0.39	0/660	0.69	0/875
24	X	0.33	0/618	0.78	1/826 (0.1%)
25	Y	0.33	0/443	0.65	0/588
26	Z	0.33	0/416	0.70	0/553
27	b	0.36	0/836	0.66	0/1104
28	c	0.36	0/701	0.67	0/934
29	d	0.26	0/208	0.84	0/267
30	f	0.61	0/76989	1.03	289/120031 (0.2%)
31	h	0.53	0/2883	0.98	9/4491 (0.2%)
32	i	0.60	0/3746	0.96	7/5832 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	j	0.38	0/1908	0.68	0/2564
34	k	0.36	0/3146	0.64	1/4228 (0.0%)
35	l	0.36	0/2800	0.64	2/3790 (0.1%)
36	m	0.34	0/2400	0.67	4/3239 (0.1%)
37	n	0.36	0/1329	0.67	0/1794
38	o	0.37	0/1821	0.61	0/2451
39	p	0.34	0/1836	0.62	2/2481 (0.1%)
40	q	0.37	0/1529	0.68	2/2060 (0.1%)
41	r	0.33	0/1801	0.64	0/2416
42	s	0.33	0/1367	0.70	3/1834 (0.2%)
43	t	0.36	0/1568	0.69	1/2106 (0.0%)
44	u	0.34	0/1068	0.66	1/1438 (0.1%)
45	a	0.28	0/6679	0.48	0/9012
46	e	0.28	0/11708	0.48	0/15899
47	g	0.32	0/1672	0.63	0/2281
48	v	0.33	0/1084	0.63	1/1456 (0.1%)
49	w	0.33	0/1736	0.65	0/2332
50	y	0.23	0/1735	0.66	0/2701
51	z	0.38	0/726	0.61	0/1006
52	0	0.33	0/976	0.55	0/1313
All	All	0.50	0/159969	0.87	338/233516 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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

There are no bond length outliers.

The worst 5 of 338 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	f	3217	C	N1-C2-O2	12.15	126.19	118.90
30	f	3217	C	C2-N1-C1'	11.32	131.25	118.80
30	f	3217	C	N3-C2-O2	-9.76	115.07	121.90
11	K	134	ASP	CB-CG-OD1	9.69	127.02	118.30
17	Q	84	ASP	CB-CG-OD1	9.31	126.68	118.30

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1720	0	1779	10	0
2	B	1555	0	1659	13	0
3	C	1416	0	1433	11	0
4	D	1441	0	1543	7	0
5	E	1258	0	1342	6	0
6	F	1437	0	1475	15	0
7	G	1272	0	1312	9	0
8	H	796	0	812	4	0
9	I	1003	0	1048	8	0
10	J	518	0	542	3	0
11	K	964	0	1025	1	0
12	L	984	0	1075	4	0
13	M	1080	0	1122	5	0
14	N	1169	0	1211	7	0
15	O	462	0	491	6	0
16	P	737	0	792	3	0
17	Q	876	0	912	9	0
18	R	1013	0	1077	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	850	0	880	2	0
20	T	880	0	942	3	0
21	U	969	0	1078	3	0
22	V	766	0	844	4	0
23	W	645	0	645	3	0
24	X	612	0	682	3	0
25	Y	436	0	475	0	0
26	Z	410	0	442	0	0
27	b	824	0	888	0	0
28	c	694	0	734	0	0
29	d	207	0	250	0	0
30	f	68782	0	34563	0	0
31	h	2579	0	1304	0	0
32	i	3353	0	1695	0	0
33	j	1874	0	1943	0	0
34	k	3075	0	3142	0	0
35	l	2748	0	2859	0	0
36	m	2351	0	2294	0	0
37	n	1307	0	1377	0	0
38	o	1784	0	1862	0	0
39	p	1804	0	1877	0	0
40	q	1508	0	1572	0	0
41	r	1764	0	1804	0	0
42	s	1346	0	1370	0	0
43	t	1543	0	1608	0	0
44	u	1053	0	1149	0	0
45	a	6569	0	6459	0	0
46	e	11509	0	10765	0	0
47	g	1651	0	1613	0	0
48	v	1085	0	1086	0	0
49	w	1709	0	1799	0	0
50	y	1556	0	788	0	0
51	z	728	0	337	0	0
52	0	961	0	979	11	0
53	1	85	0	19	0	0
54	A	1	0	0	0	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	0	0
All	All	149748	0	112793	146	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 146 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)
15:O:16:ALA:O	15:O:20:GLY:HA3	1.69	0.90
15:O:16:ALA:O	15:O:20:GLY:CA	2.36	0.73
23:W:21:ARG:HE	23:W:39:TYR:HB2	1.58	0.69
2:B:46[A]:GLU:HB3	2:B:49[A]:ARG:HG3	1.75	0.68
52:O:26:PHE:HB2	52:O:87:VAL:HB	1.73	0.68

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	7	18
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%)	225 (92%)	19 (8%)	0	100	100
34	k	384/387 (99%)	364 (95%)	20 (5%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	37	61
36	m	292/297 (98%)	278 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	25	49
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	22	45
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	25	49
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	831 (99%)	11 (1%)	0	100	100
46	e	1519/1562 (97%)	1505 (99%)	11 (1%)	3 (0%)	44	68
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%)	137 (95%)	6 (4%)	1 (1%)	19	42
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	35
All	All	9314/10279 (91%)	8970 (96%)	334 (4%)	10 (0%)	50	73

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	e	393	PHE
51	z	88	PRO
46	e	396	ARG
35	l	4	PRO
40	q	107	ASP

### 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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	149 (99%)	1 (1%)	81	93
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%)	134 (99%)	1 (1%)	81	93
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%)	45 (98%)	1 (2%)	47	76
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%)	94 (99%)	1 (1%)	70	87
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%)	66 (97%)	2 (3%)	37	67
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%)	188 (100%)	1 (0%)	86	95
34	k	320/323 (99%)	318 (99%)	2 (1%)	84	94
35	l	288/289 (100%)	288 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	m	241/245 (98%)	241 (100%)	0	100	100
37	n	139/155 (90%)	138 (99%)	1 (1%)	81	93
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%)	183 (99%)	2 (1%)	70	87
42	s	145/150 (97%)	145 (100%)	0	100	100
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	676/949 (71%)	639 (94%)	37 (6%)	18	41
46	e	1150/1451 (79%)	1073 (93%)	77 (7%)	13	33
47	g	180/211 (85%)	180 (100%)	0	100	100
48	v	119/132 (90%)	116 (98%)	3 (2%)	42	72
49	w	197/198 (100%)	196 (100%)	1 (0%)	86	95
52	0	104/254 (41%)	95 (91%)	9 (9%)	8	20
All	All	7561/8690 (87%)	7422 (98%)	139 (2%)	54	80

5 of 139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1342	GLU
46	e	1391	ILE
52	0	30	VAL
45	a	1014	LEU
45	a	1003	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
46	e	254	ASN
46	e	1141	GLN
47	g	9	ASN
46	e	1138	ASN
46	e	1206	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3212/3395 (94%)	594 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
50	y	71/76 (93%)	27 (38%)	0
All	All	3560/3750 (94%)	665 (18%)	0

5 of 665 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	1.29	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	-2.19	108.85	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.

No monomer is involved in short contacts.

## 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.

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.

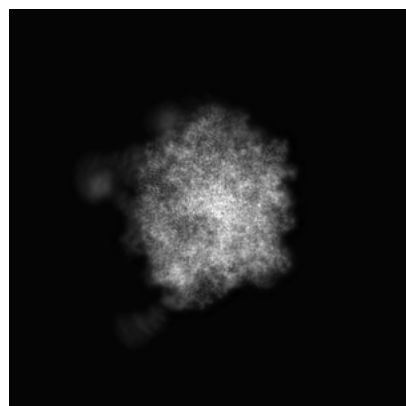
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15424. These allow visual inspection of the internal detail of the map and identification of artifacts.

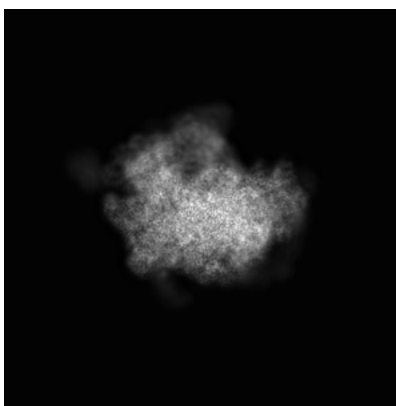
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

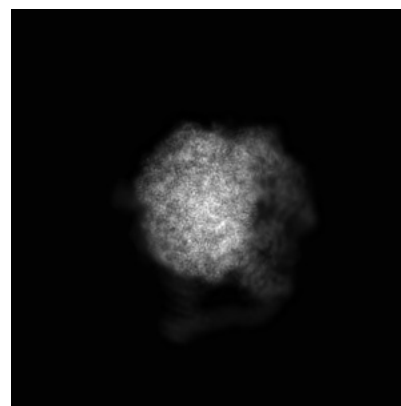
#### 6.1.1 Primary map



X

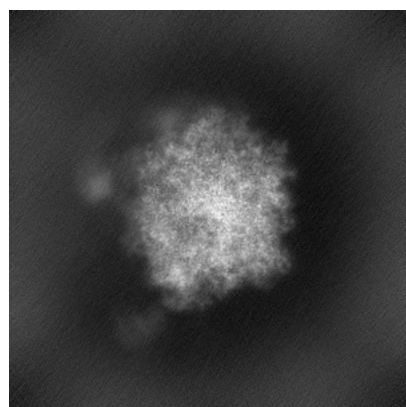


Y

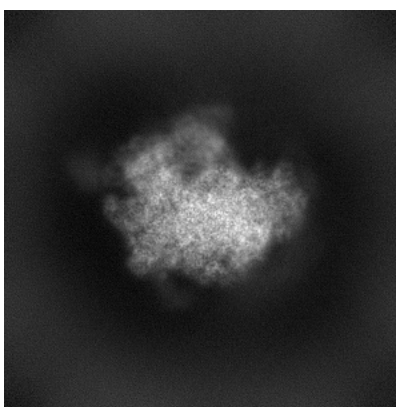


Z

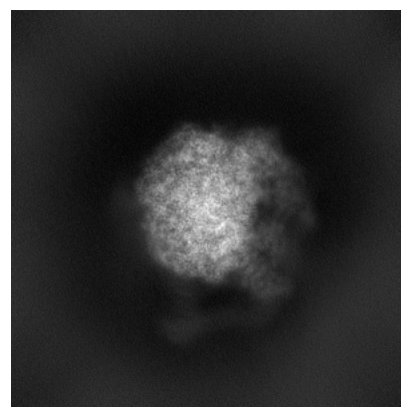
#### 6.1.2 Raw map



X



Y



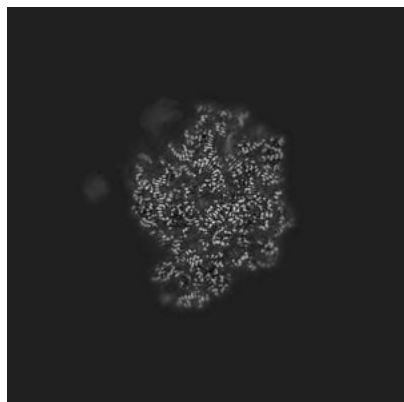
Z

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

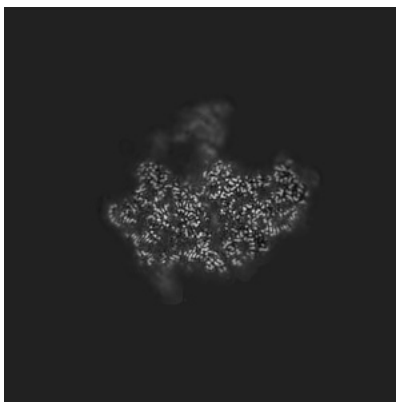


## 6.2 Central slices [i](#)

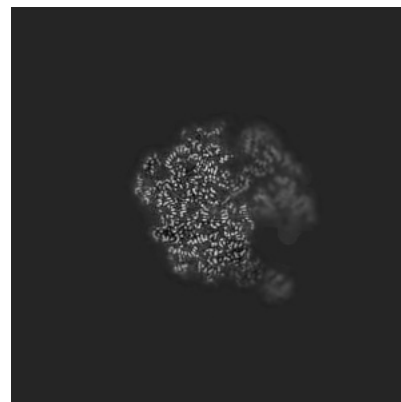
### 6.2.1 Primary map



X Index: 225

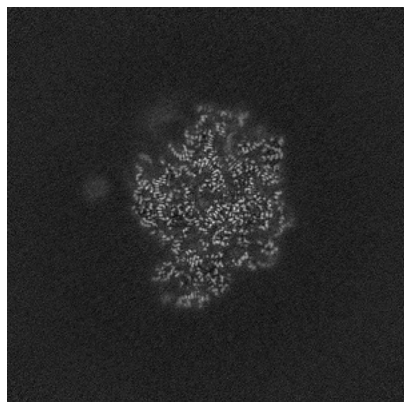


Y Index: 225

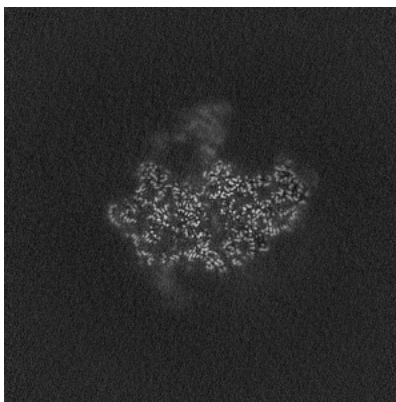


Z Index: 225

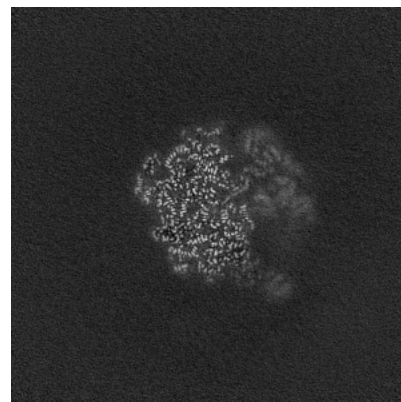
### 6.2.2 Raw map



X Index: 225



Y Index: 225

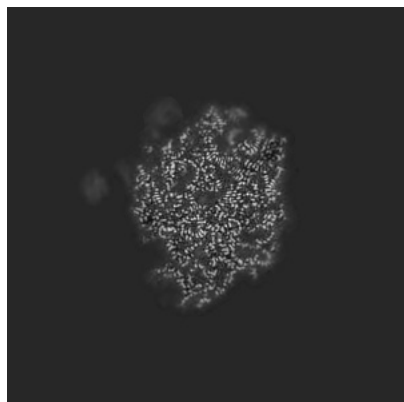


Z Index: 225

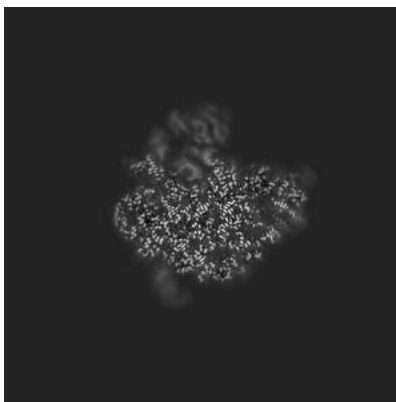
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

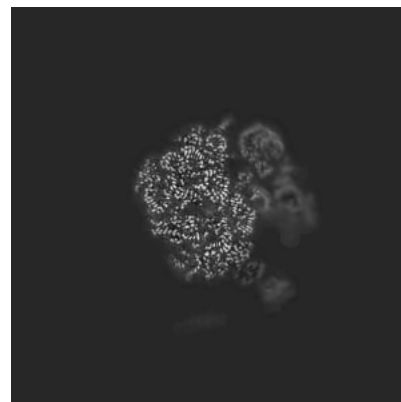
### 6.3.1 Primary map



X Index: 219

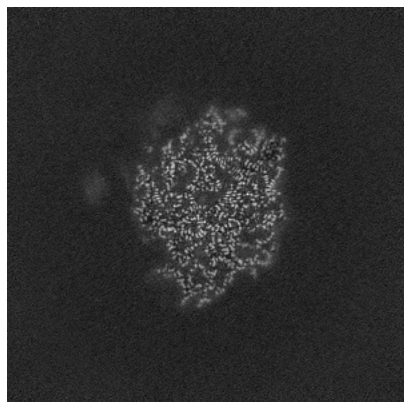


Y Index: 237

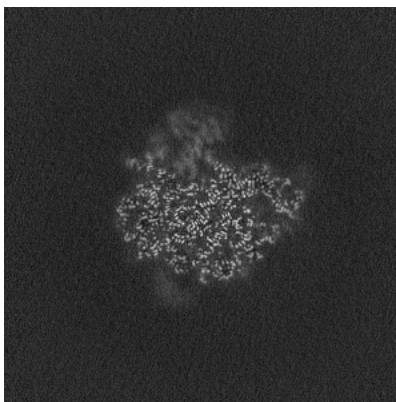


Z Index: 231

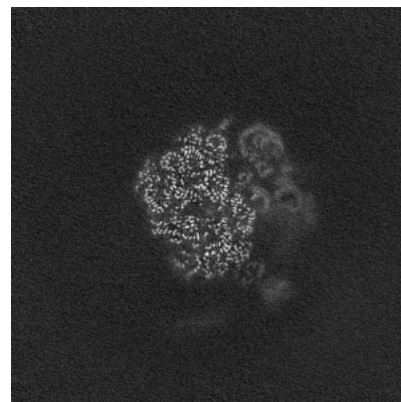
### 6.3.2 Raw map



X Index: 219



Y Index: 241

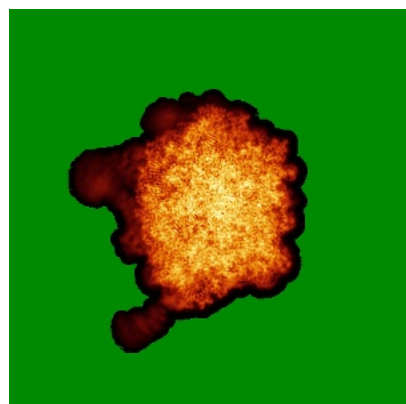


Z Index: 231

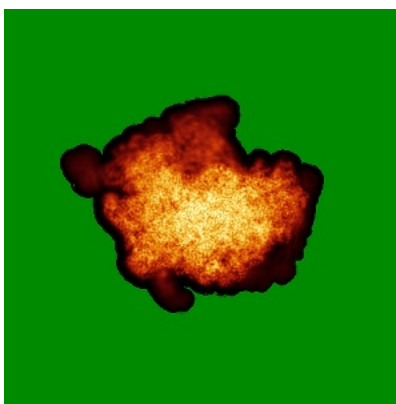
The images above show the largest variance slices of the map in three orthogonal directions.

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

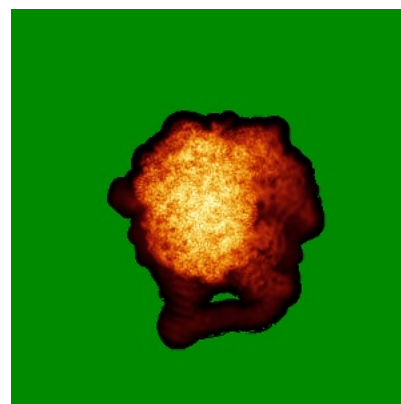
### 6.4.1 Primary map



X

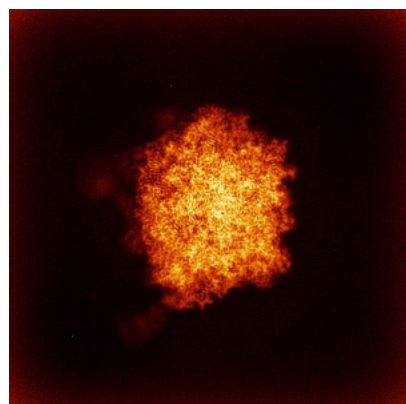


Y

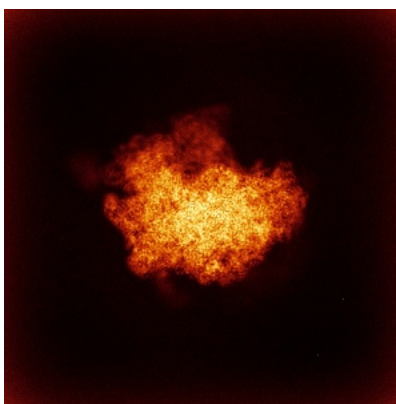


Z

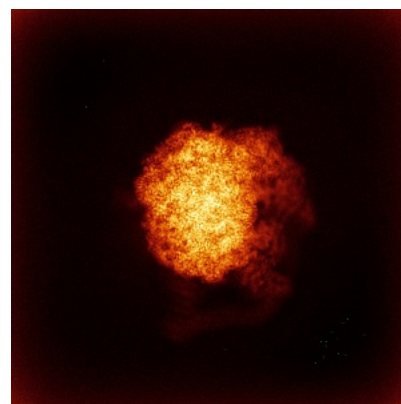
### 6.4.2 Raw map



X



Y

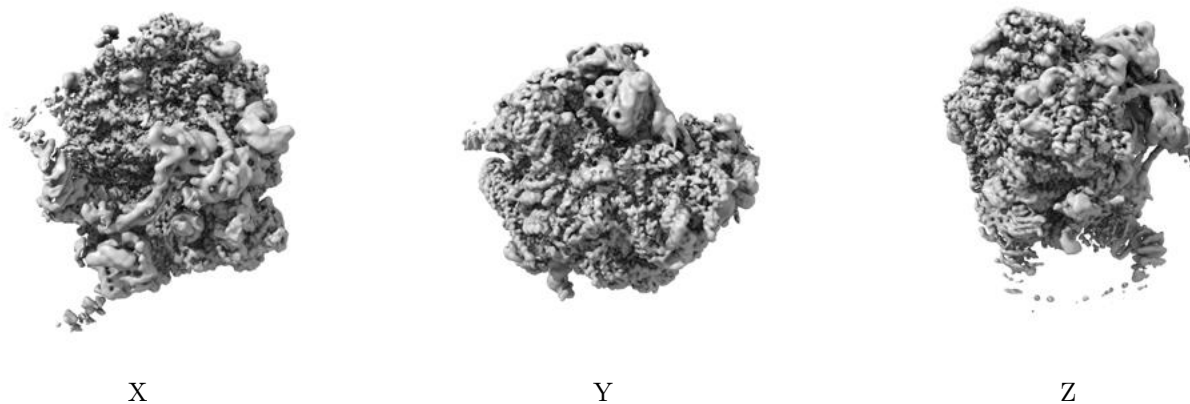


Z

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.

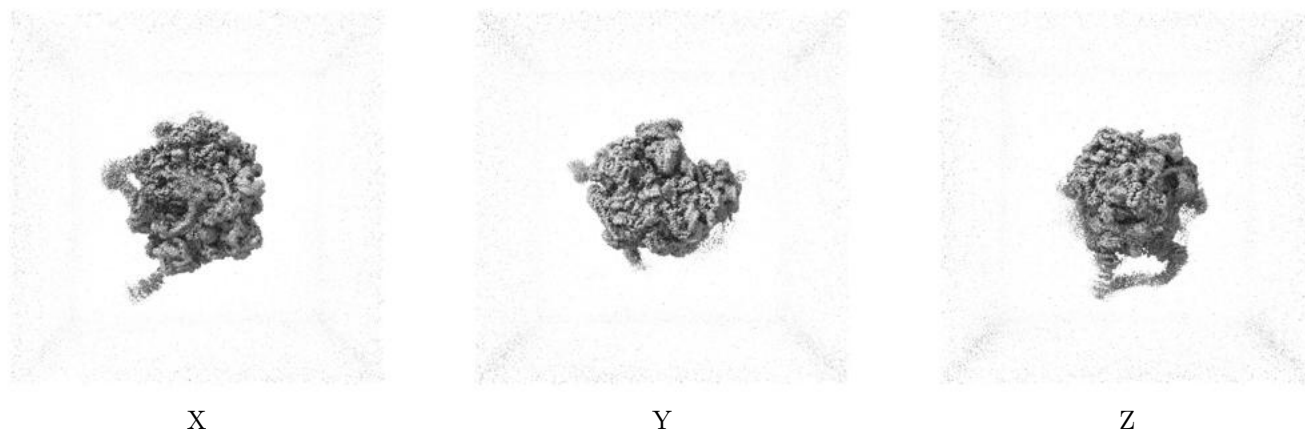
## 6.5 Orthogonal surface views [i](#)

### 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.

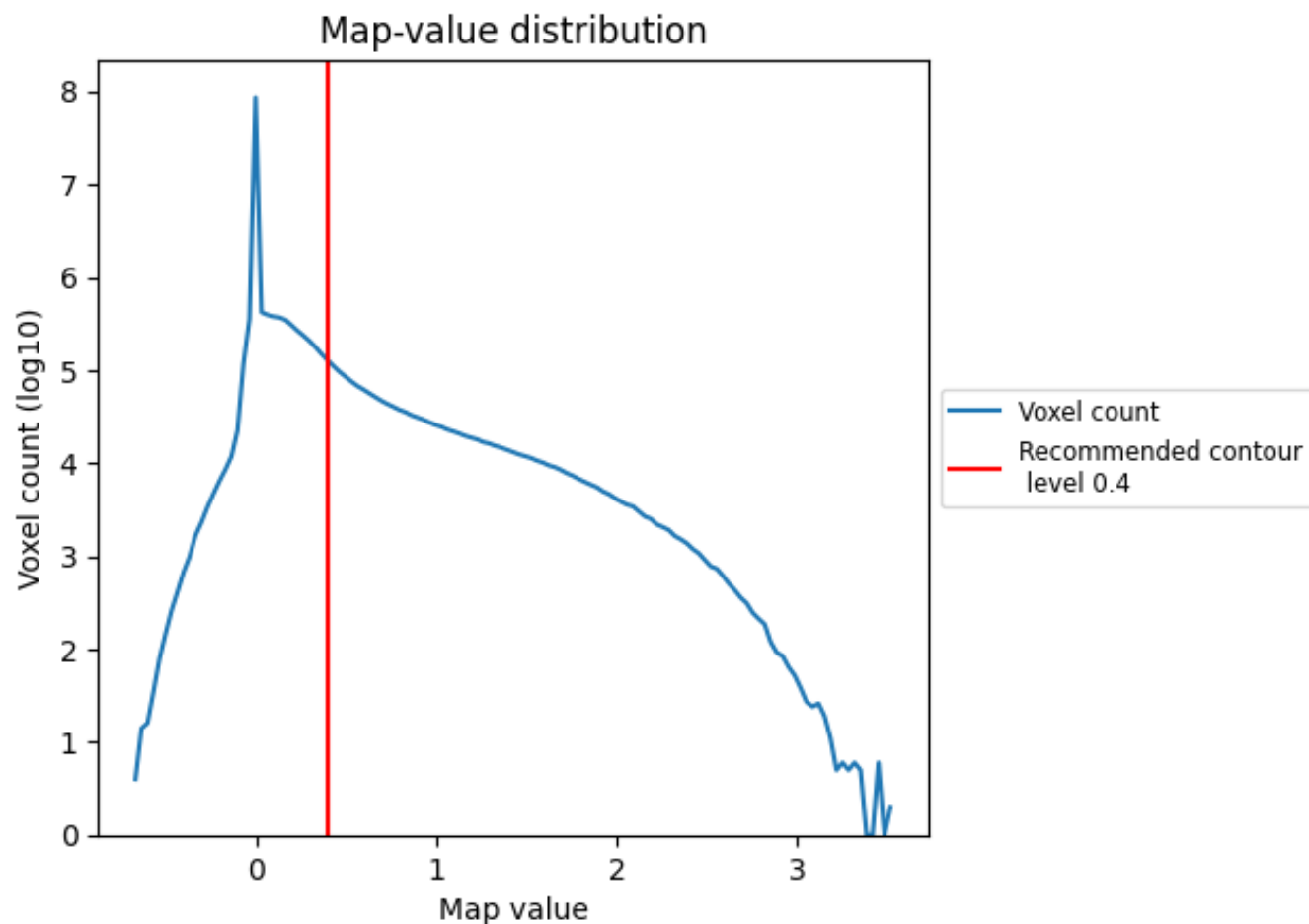
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

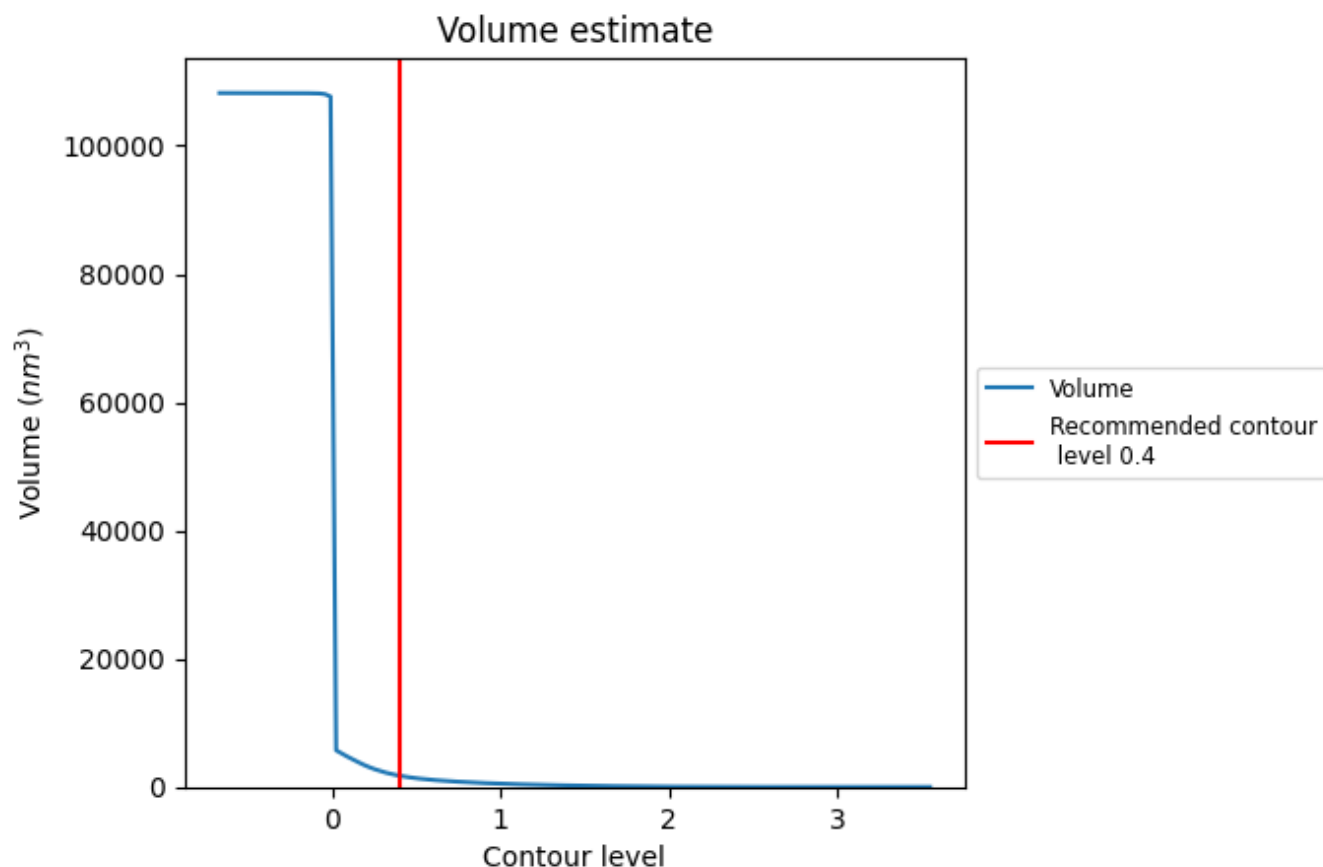
This section contains the results of statistical analysis of the map.

### 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.

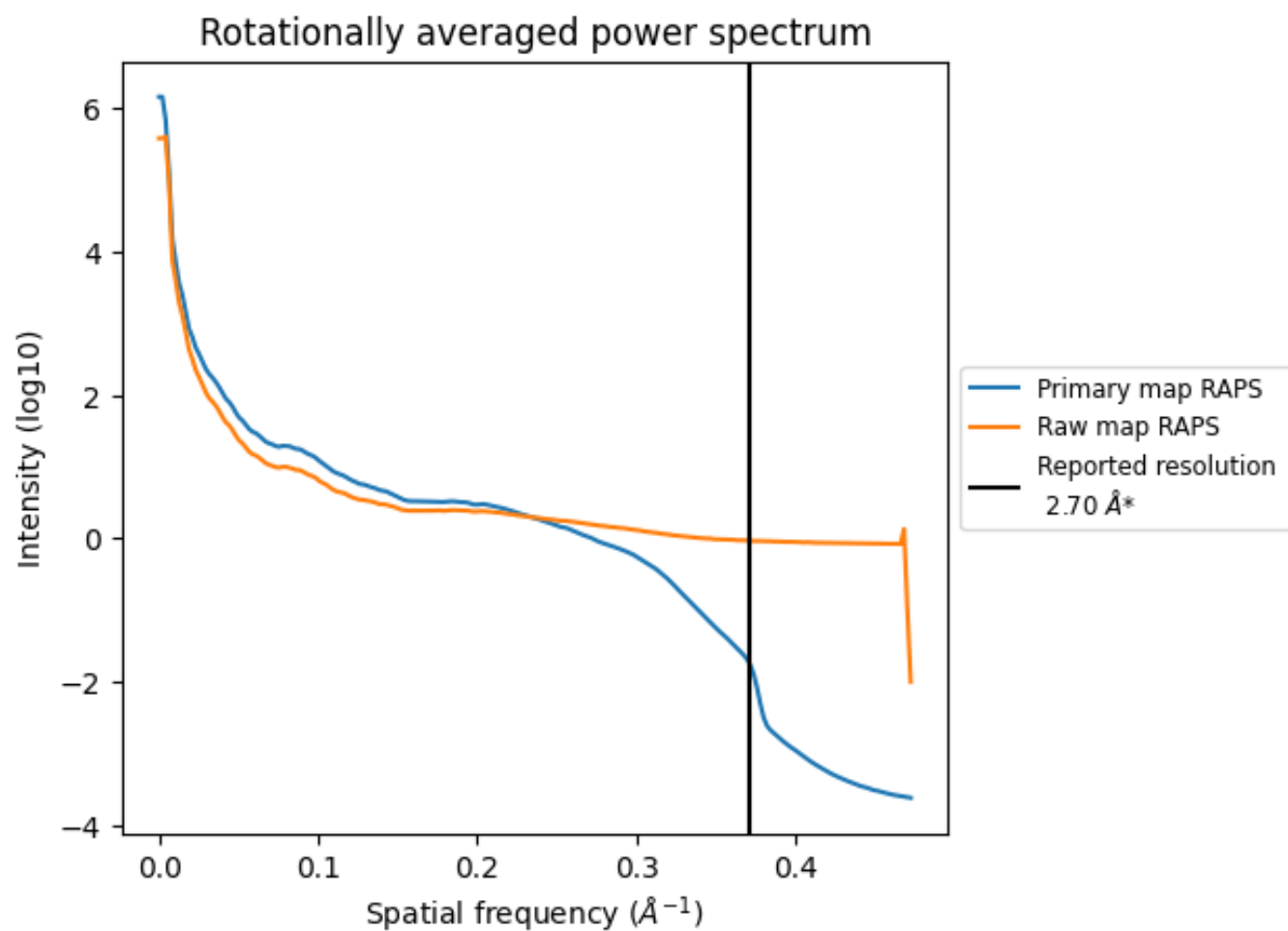
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1749  $\text{nm}^3$ ; this corresponds to an approximate mass of 1580 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 ⓘ

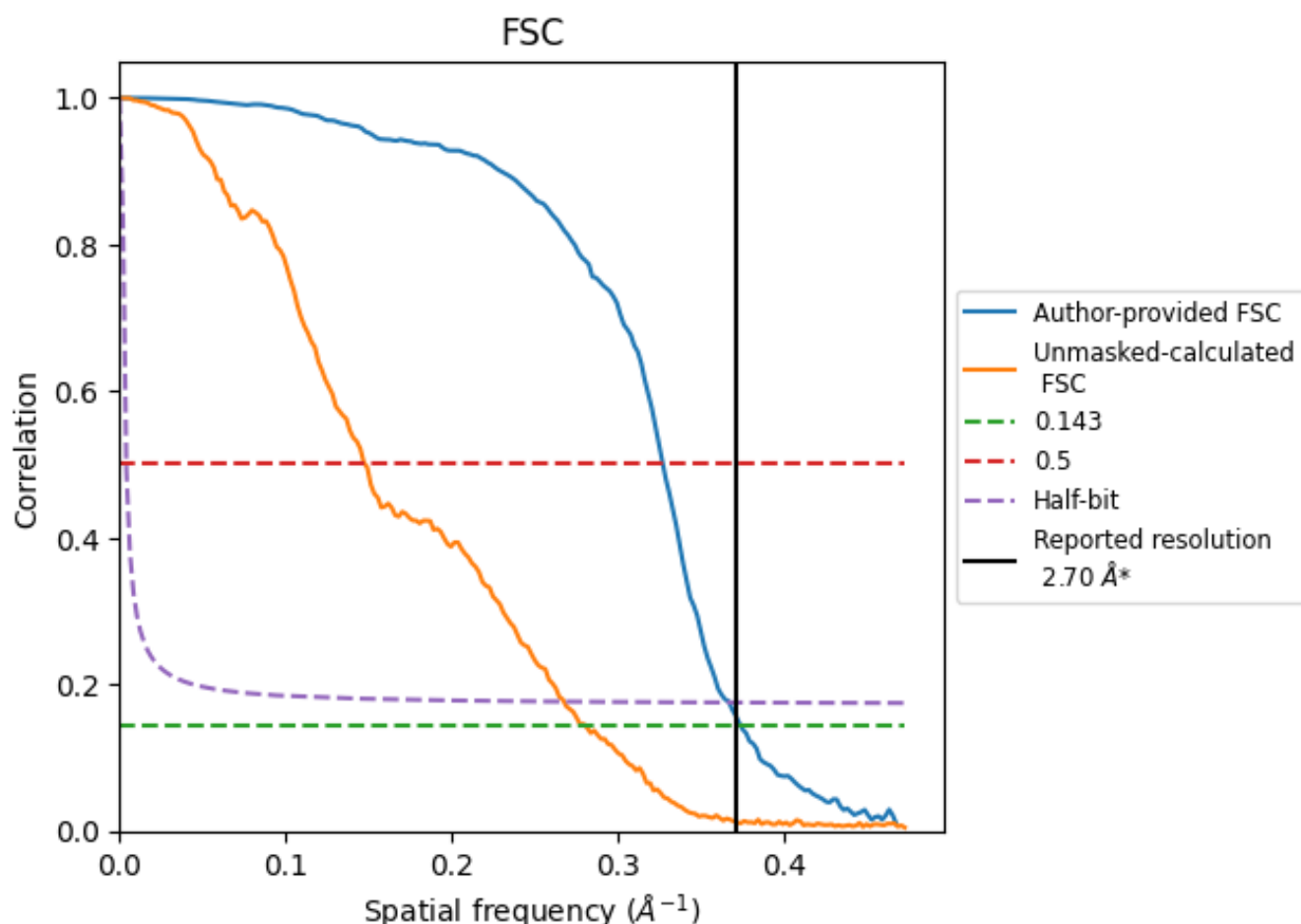


\*Reported resolution corresponds to spatial frequency of 0.370  $\text{\AA}^{-1}$

## 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 0.370  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

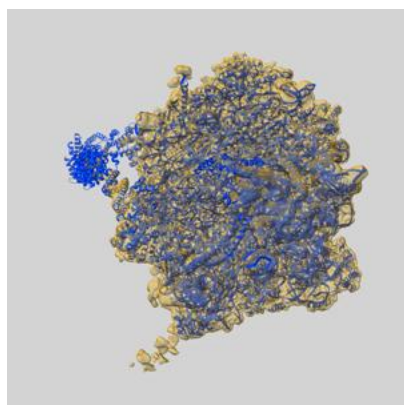
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.68	3.06	2.73
Unmasked-calculated*	3.57	6.78	3.74

\*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 3.57 differs from the reported value 2.7 by more than 10 %

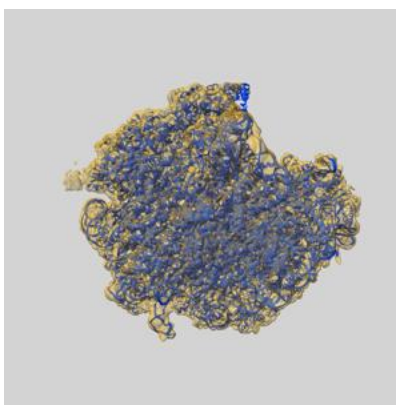
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15424 and PDB model 8AGU. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

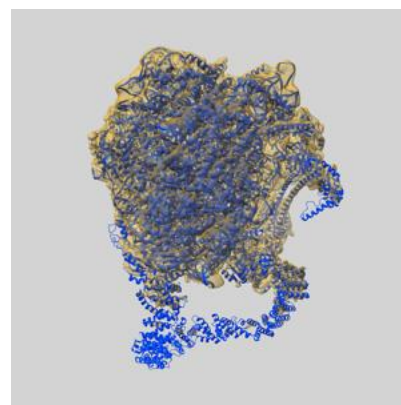
### 9.1 Map-model overlay [i](#)



X



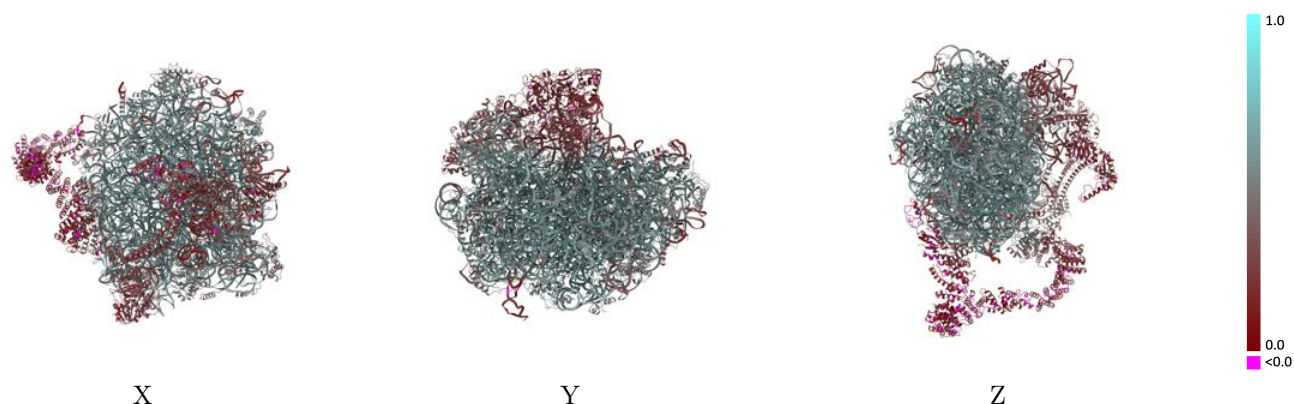
Y



Z

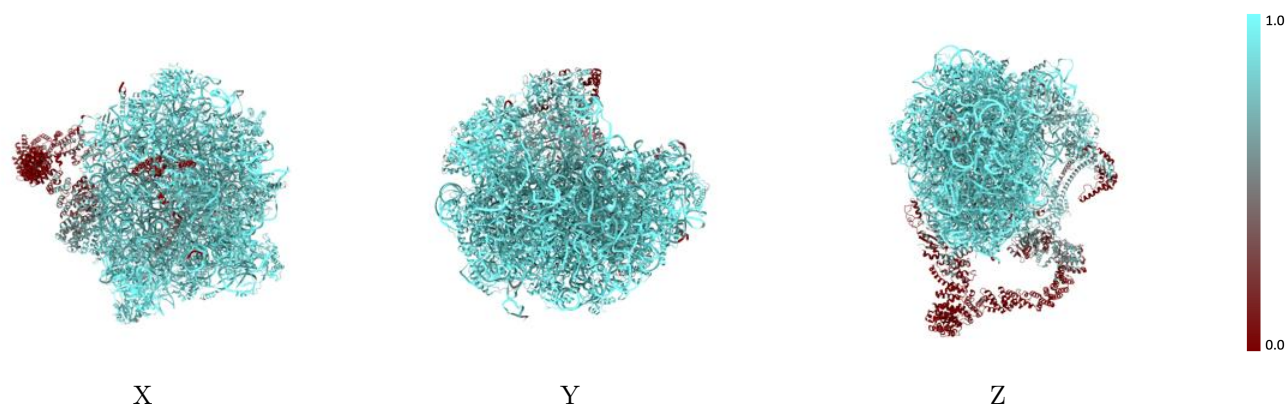
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



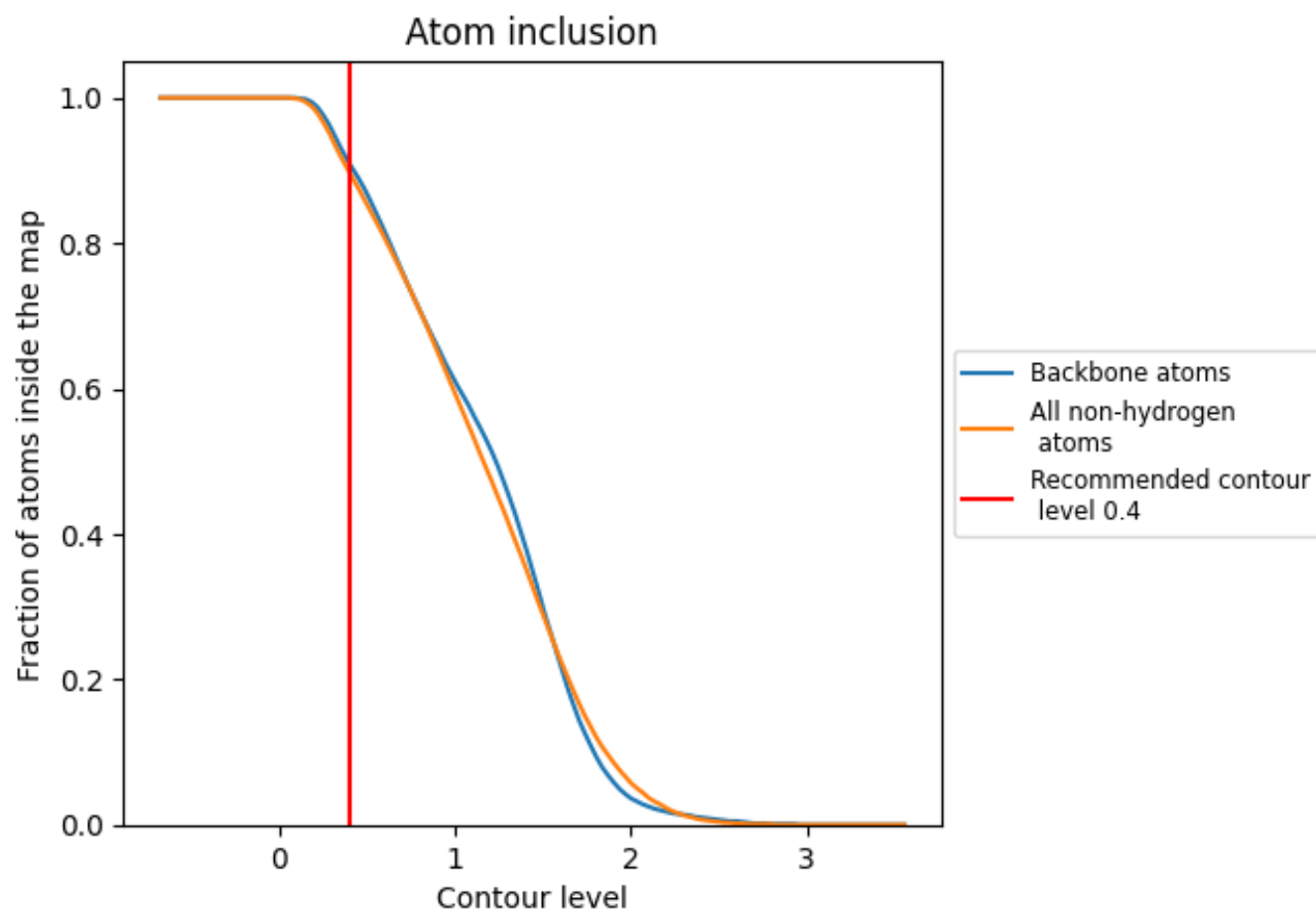
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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	 0.8980	 0.4960
0	 0.8070	 0.2580
1	 0.9880	 0.4550
A	 0.9920	 0.5990
B	 0.9790	 0.5770
C	 0.9680	 0.5790
D	 0.9760	 0.5700
E	 0.9340	 0.5360
F	 0.9720	 0.5680
G	 0.9650	 0.5510
H	 0.9130	 0.4540
I	 0.9560	 0.5630
J	 0.9580	 0.5570
K	 0.9690	 0.5560
L	 0.9680	 0.5530
M	 0.9400	 0.5040
N	 0.9750	 0.5820
O	 0.9450	 0.5240
P	 0.9370	 0.5070
Q	 0.9200	 0.5350
R	 0.9770	 0.5880
S	 0.9900	 0.6100
T	 0.9700	 0.5620
U	 0.9620	 0.5400
V	 0.9540	 0.5170
W	 1.0000	 0.6140
X	 0.9080	 0.4740
Y	 0.9980	 0.5930
Z	 0.9650	 0.5610
a	 0.6670	 0.2240
b	 0.9630	 0.5560
c	 0.9670	 0.5530
d	 0.7180	 0.3780
e	 0.2490	 0.1560
f	 0.9900	 0.5600



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Chain	Atom inclusion	Q-score
g	 0.3760	 0.3870
h	 0.9990	 0.5570
i	 0.9940	 0.5870
j	 0.9820	 0.5950
k	 0.9720	 0.5730
l	 0.9720	 0.5620
m	 0.9380	 0.4740
n	 0.9510	 0.5130
o	 0.9700	 0.5580
p	 0.9370	 0.5060
q	 0.9560	 0.5330
r	 0.9510	 0.5240
s	 0.9210	 0.4230
t	 0.9650	 0.5490
u	 0.9680	 0.5350
v	 0.8410	 0.3850
w	 0.8050	 0.2370
y	 0.9700	 0.2580
z	 0.9080	 0.2700