



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:44 AM UTC

PDB ID : 8AGV / pdb_00008agv
EMDB ID : EMD-15425
Title : Yeast RQC complex in state H
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:

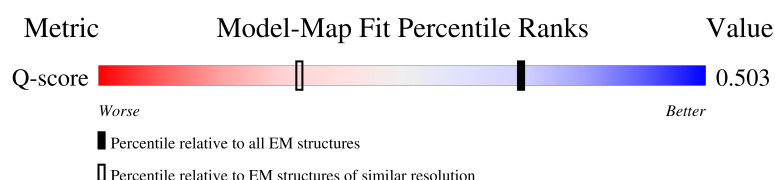
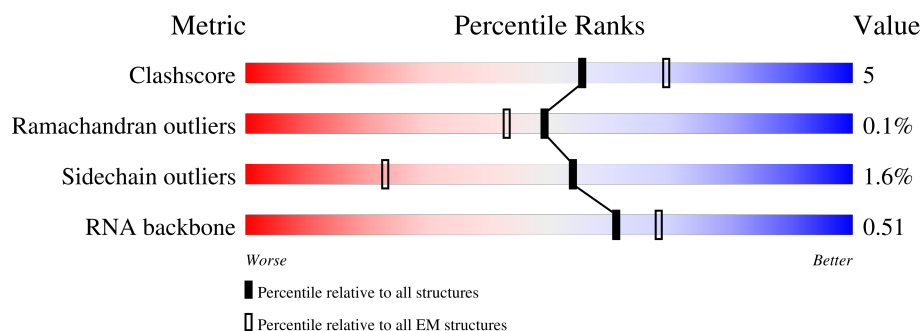
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13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



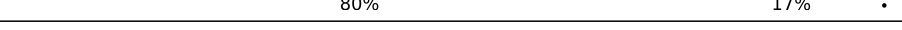
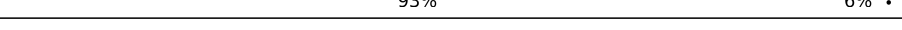
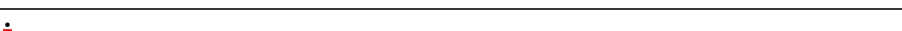
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	 88% 12%
2	B	199	 85% 14%
3	C	184	 87% 12%

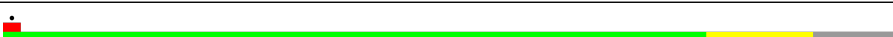
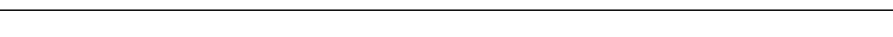
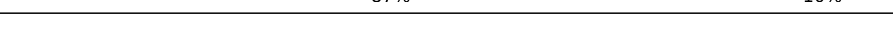
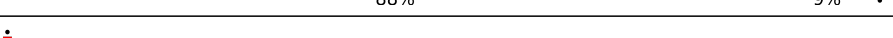
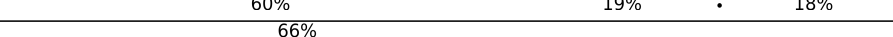
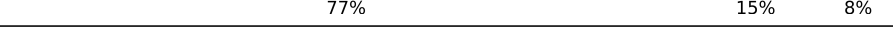
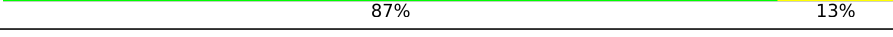
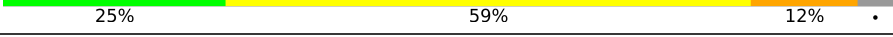
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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	189	
6	F	172	
7	G	160	
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	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	w	217	
49	x	76	
49	y	76	
50	z	165	
51	0	312	
52	1	18	

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Mol	Chain	Length	Quality of chain
53	v	157	 75% 14% 10%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151349 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		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		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		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	1	0
			68802	30732	12391	22462	3217		

- 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
			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
			11516	7358	1937	2183	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 60S ribosomal protein L1-A.

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

- Molecule 49 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	74	Total	C	N	O	P	0	0
			1579	702	278	525	74		
49	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

- Molecule 50 is a protein called 60S ribosomal protein L12-B.

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

- Molecule 51 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 52 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	1	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 53 is a protein called Eukaryotic translation initiation factor 5A-1.

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

- 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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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

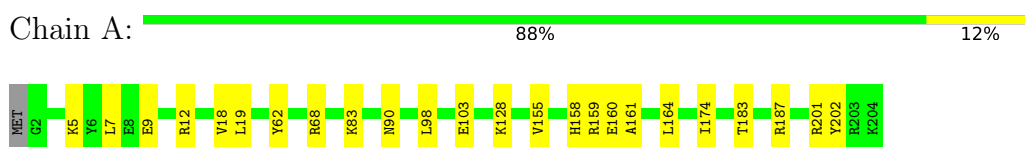
- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

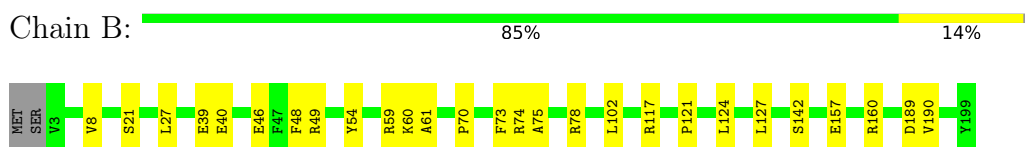
3 Residue-property plots [i](#)

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.

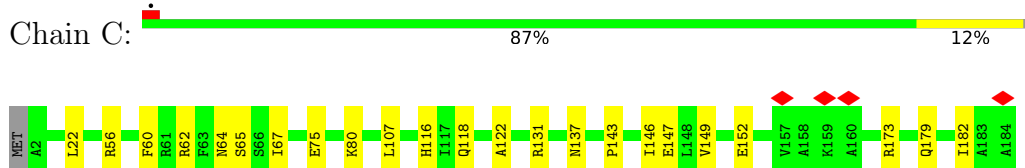
- Molecule 1: 60S ribosomal protein L15-A



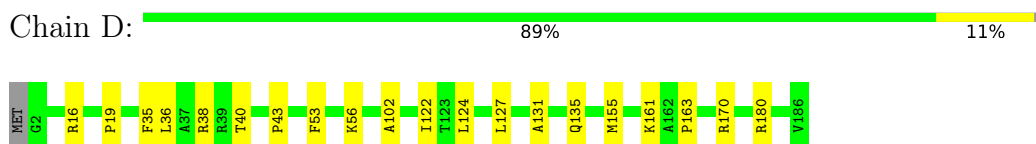
- Molecule 2: 60S ribosomal protein L16-A



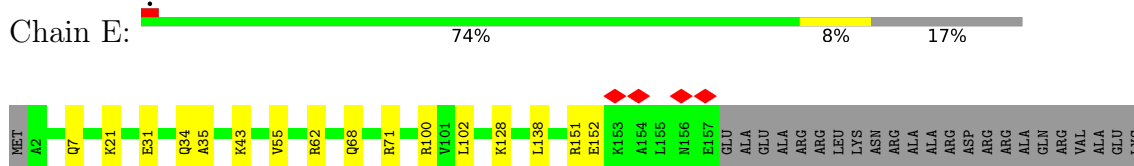
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A



- Molecule 5: 60S ribosomal protein L19-A



ARG
ASP
ALA
LEU
LYS
GLU
ASP
ALA

- Molecule 6: 60S ribosomal protein L20-A

Chain F:  84% 15%

MET A2 Q8 P22 S32 I36 R40 Y43 I64 T70 V77 R80 T87 H90 E93 I94 R95 D96 V97 L106 M110 H122 I123 L124 K125 V126 R137 V140 R155 V156 Y172

- Molecule 7: 60S ribosomal protein L21-A

Chain G:  89% 10%

MET G2 R17 H22 G73 Y84 R88 L89 R102 R108 M112 R116 A133 R136 R139 M146 P155 T188 F189 I160

- Molecule 8: 60S ribosomal protein L22-A

Chain H:  74% 9% 17%

MET ALA PRO THR SER ARG LYS D9 S20 T23 I41 E44 M49 L50 Q51 V54 F55 V56 V65 R90 D91 W92 Y108 GLN VAL THR PRO GLU GLU ASP GLU GLU GLU 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 GLY THR ARG LYS VAL LYS ALA GLN ARG PRO ILE THR GLY ALA SER LEU ASP LEU ILE LYS GLU ARG ARG SER LEU LYS PRO GLU VAL ARG LYS ALA ASN

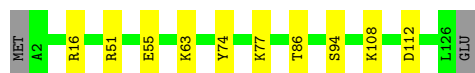
- Molecule 11: 60S ribosomal protein L25

Chain K:  85% 15%

MET ALA PRO SER ALA LYS ALA THR K22 A50 I142

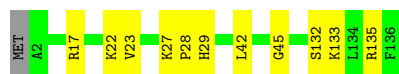
- Molecule 12: 60S ribosomal protein L26-A

Chain L:  91% 8% .



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  91% 8% .



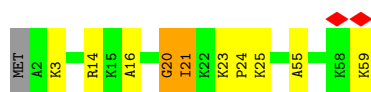
- Molecule 14: 60S ribosomal protein L28

Chain N:  87% 13% .



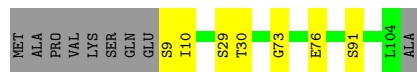
- Molecule 15: 60S ribosomal protein L29

Chain O:  81% 14% . .



- Molecule 16: 60S ribosomal protein L30

Chain P:  85% 7% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  80% 17% .

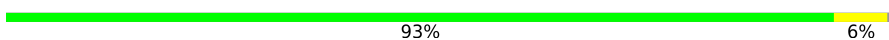


- Molecule 18: 60S ribosomal protein L32

Chain R:  89% 8% .



- Molecule 19: 60S ribosomal protein L33-A

Chain S:  93% 6%

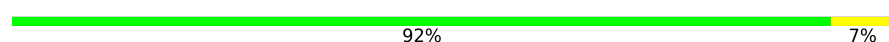


- Molecule 20: 60S ribosomal protein L34-A

Chain T:  85% 7% 7%

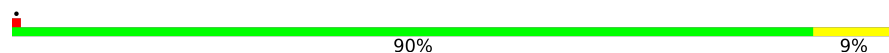


- Molecule 21: 60S ribosomal protein L35-A

Chain U:  92% 7%



- Molecule 22: 60S ribosomal protein L36-A

Chain V:  90% 9%

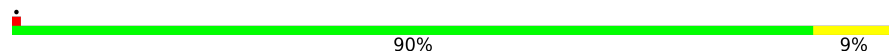


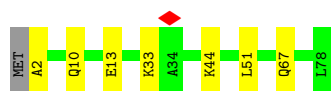
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  76% 16% 8%

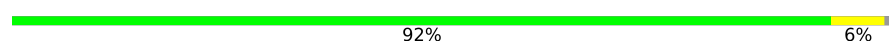


- Molecule 24: 60S ribosomal protein L38

Chain X:  90% 9%

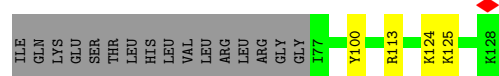


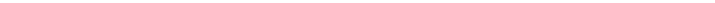
- Molecule 25: 60S ribosomal protein L39

Chain Y:  92% 6%



- Molecule 26: Ubiquitin-60S ribosomal protein L40



- Chain b:  81% 16% .



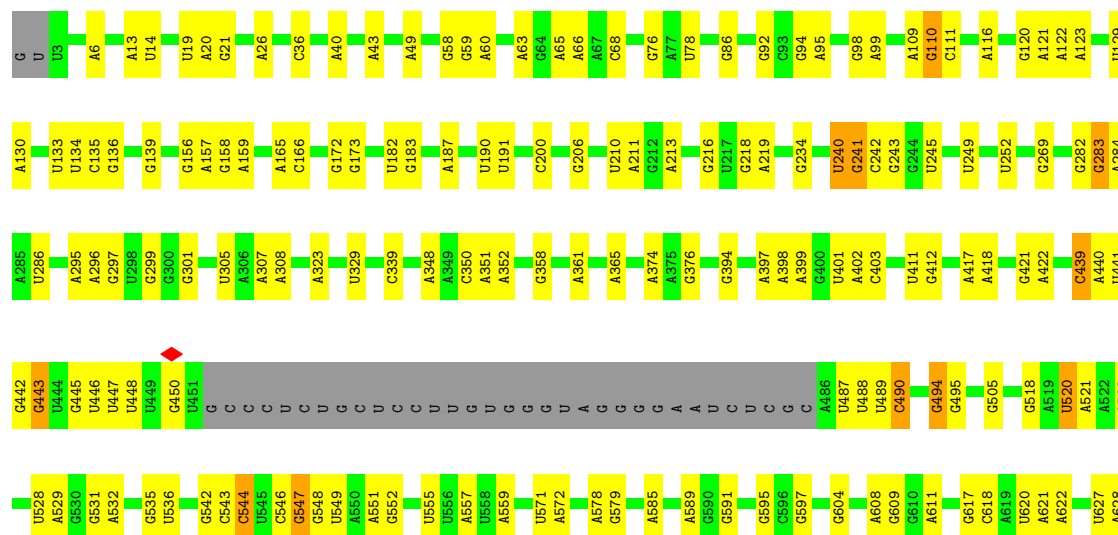
- Chain c: 91% 8%



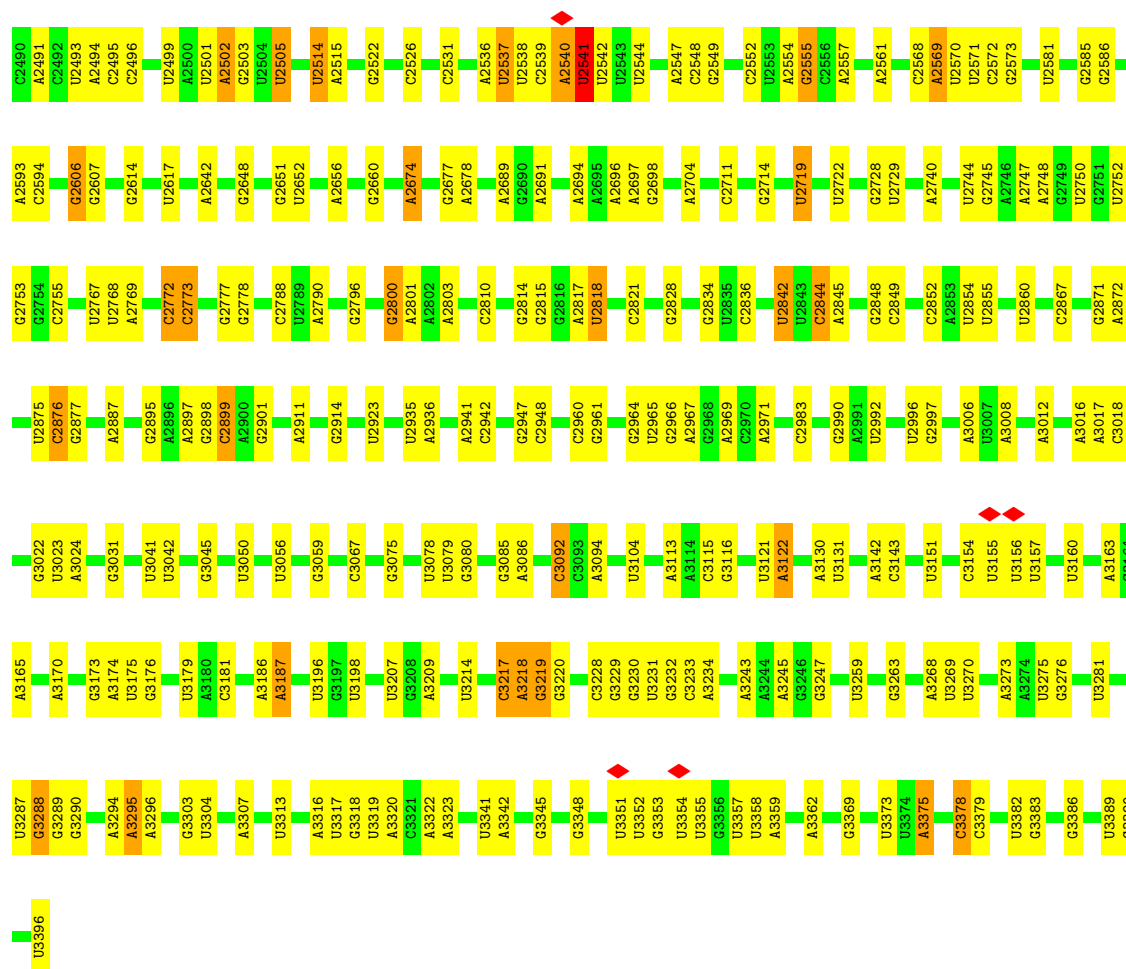
- Chain d:  20% 72% 12% 12%



- Chain f: 68% 24% 5%

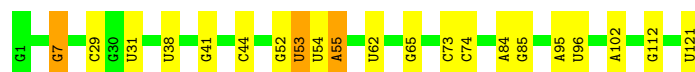


U2368	A2222	G2111	G1736	A1583	G1420	U1265	U1191	A1047	G913	U763	G637
C2392	A2223	U2112	G1741	A1589	G1421	G1268	C1192	A1048	A914	U764	C638
G2393	U2225	A2113	A1741	A1590	G1422	U1269	G1193	C1049	A915	C765	G639
A2397	A2228	G2115	G1747	A1593	G1434	A1270	C1196	G1063	A917	U766	U640
A2402	C2245	G2116	A1750	C1596	C1437	C1272	A1197	A1065	A920	G770	A649
A2404	G2249	A2117	G1751	G1598	A1446	A1278	A1201	G1072	A921	U776	C655
U2411	U2254	U1871	A1760	G1598	G1447	C1279	A1202	U1081	A925	U777	A656
G2412	A	U1880	C1761	A1606	G1450	G1280	A1204	U1082	A780	A780	A660
A2413	C	A1881	C1762	U1607	A1477	G1281	U1208	G1083	G937	G781	U664
G2414	C	U1764	U1763	A1613	G1480	G1282	G1213	A1084	C938	G785	A665
G2415	U	U1765	G1766	U1620	A1481	G1285	G1213	G1087	C944	A786	A665
U2417	A	G1766	G1770	U1629	A1482	U1287	A1217	U1093	C945	U799	U673
G2418	U	G1771	U1772	G1634	G1483	U1288	U1218	U1094	U946	G799	G674
A2419	A	U1772	G1775	G1639	G1487	U1289	C1219	U1095	G947	C804	C675
A2424	G	G1775	G1778	A1642	G1488	G1295	U1220	U1096	C959	G805	G676
G2437	G	G1778	C1779	A1643	A1497	G1295	A1221	G1097	U960	A806	U679
G2442	U	G1780	G1786	C1657	A1498	G1307	G1222	A1098	G974	G815	G680
A2443	C	U1786	A1787	G1660	C1502	A1308	A1225	A1103	A816	A817	U681
U2446	G	G1786	A1787	G1662	C1508	U1309	G1227	G1104	C982	G854	G684
A2447	U	G1787	C1793	G1666	G1536	G1313	G1230	U1107	C991	U829	U687
G2450	A	C1793	A1797	A1667	G1557	A1330	A1231	U1108	G994	G831	G688
G2451	G	A1797	A1798	G1675	U1555	U1348	G1233	G1117	G1001	G835	U689
G2452	C	U1798	A1799	A1676	C1556	G1349	U1234	C1118	A1002	A896	A690
C2284	C	A1800	A1801	G1676	A1557	A1350	G1236	C1119	U1008	A897	A692
G2461	U	G1802	G1807	A1683	G1560	U1351	G1237	A1120	A1009	G838	C696
U2462	C	C1802	G1808	G1683	G1561	A1352	C1238	G1131	G1010	A846	A705
G2463	C	A1813	A1814	C1693	G1562	G1354	C1239	G1134	U1015	C849	A710
U2464	C	U1814	U1815	U1716	C1562	A1355	A1240	U1139	C1016	U850	A711
G2465	A	G1815	A1816	G1718	C1563	U1356	U1241	G1139	C1017	G857	G712
G2466	C	U1816	U1819	G1721	G1573	G1357	G1242	U1144	G1018	G860	A715
U2467	C	U1819	U1820	U1722	G1574	A1369	A1244	G1145	G1019	C861	A716
G2468	C	A1835	U1821	A1723	A1575	G1383	A1245	G1152	G1021	U874	U719
G2469	C	A1839	A1840	U1724	G1576	A1386	G1250	A1153	G1024	U879	A720
U2470	U	U1841	U1842	G1725	G1577	G1387	A1251	C1156	A1025	G728	G728
G2471	A	A1841	A1842	C1726	C1579	U1388	U1252	U1159	A1026	A895	C745
U2472	C	A1842	A1843	G1727	A1580	G1389	C1254	C1160	A1027	A896	A746
G2473	C	A1843	A1844	U1727	A1581	G1391	G1255	G1177	U1028	A904	C752
G2474	C	A1844	A1845	G1730	C1581	G1392	C1257	G1177	U1033	G907	C752
C2479	A	A1845	A1846	G1730	C1582	A1399	U1258	U1180	U1034	G908	C758
A2480	C	A1846	A1847	G1730	C1582	G1400	A1259	U1181	A1036	C911	U759
U2481	C	A1847	A1848	G1730	C1582	A1418	A1263	A1190	U1041	G912	G760
G2482	C	A1848	A1849	G1730	C1582	A1419	G1264	A1190	U1041	G912	G760



- Molecule 31: 5S rRNA

Chain h: 83% 15% .



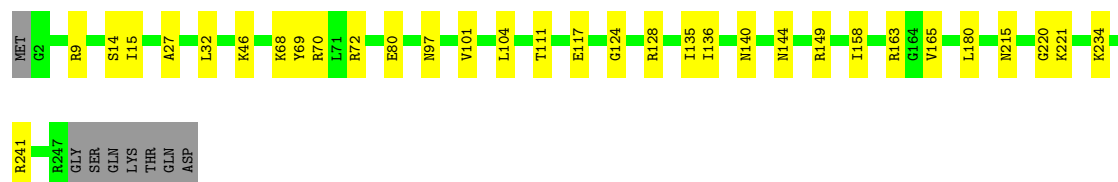
- Molecule 32: 5.8S rRNA

Chain i: 73% 23% .

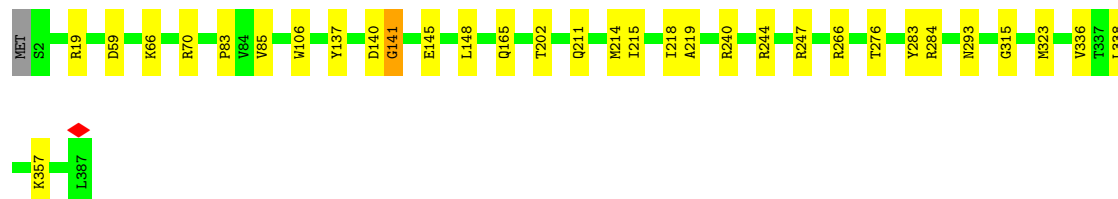


- Molecule 33: 60S ribosomal protein L2-A

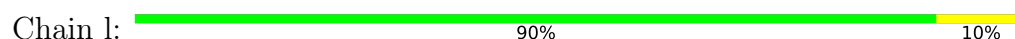
Chain j: 84% 13% .



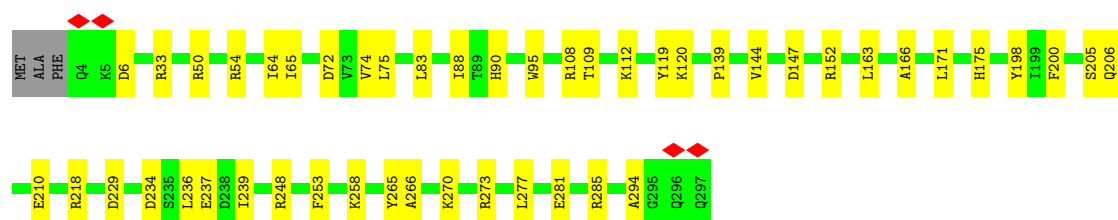
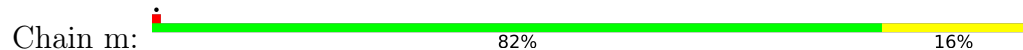
- Molecule 34: 60S ribosomal protein L3



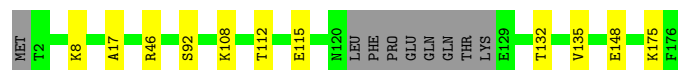
- Molecule 35: 60S ribosomal protein L4-A



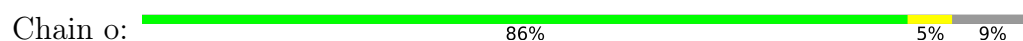
- Molecule 36: 60S ribosomal protein L5

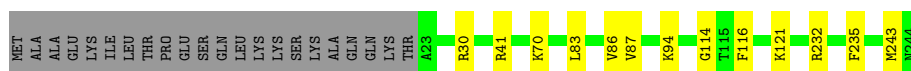


- Molecule 37: 60S ribosomal protein L6-B

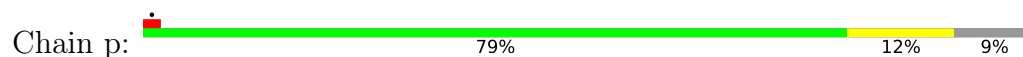


- Molecule 38: 60S ribosomal protein L7-A

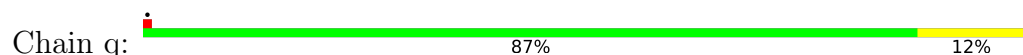




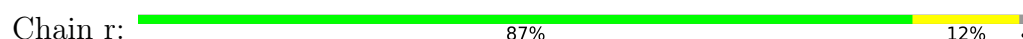
- Molecule 39: 60S ribosomal protein L8-A



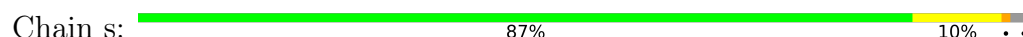
- Molecule 40: 60S ribosomal protein L9-A



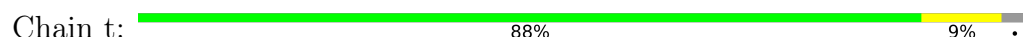
- Molecule 41: 60S ribosomal protein L10



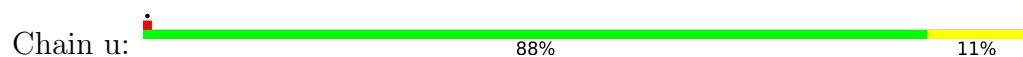
- Molecule 42: 60S ribosomal protein L11-A



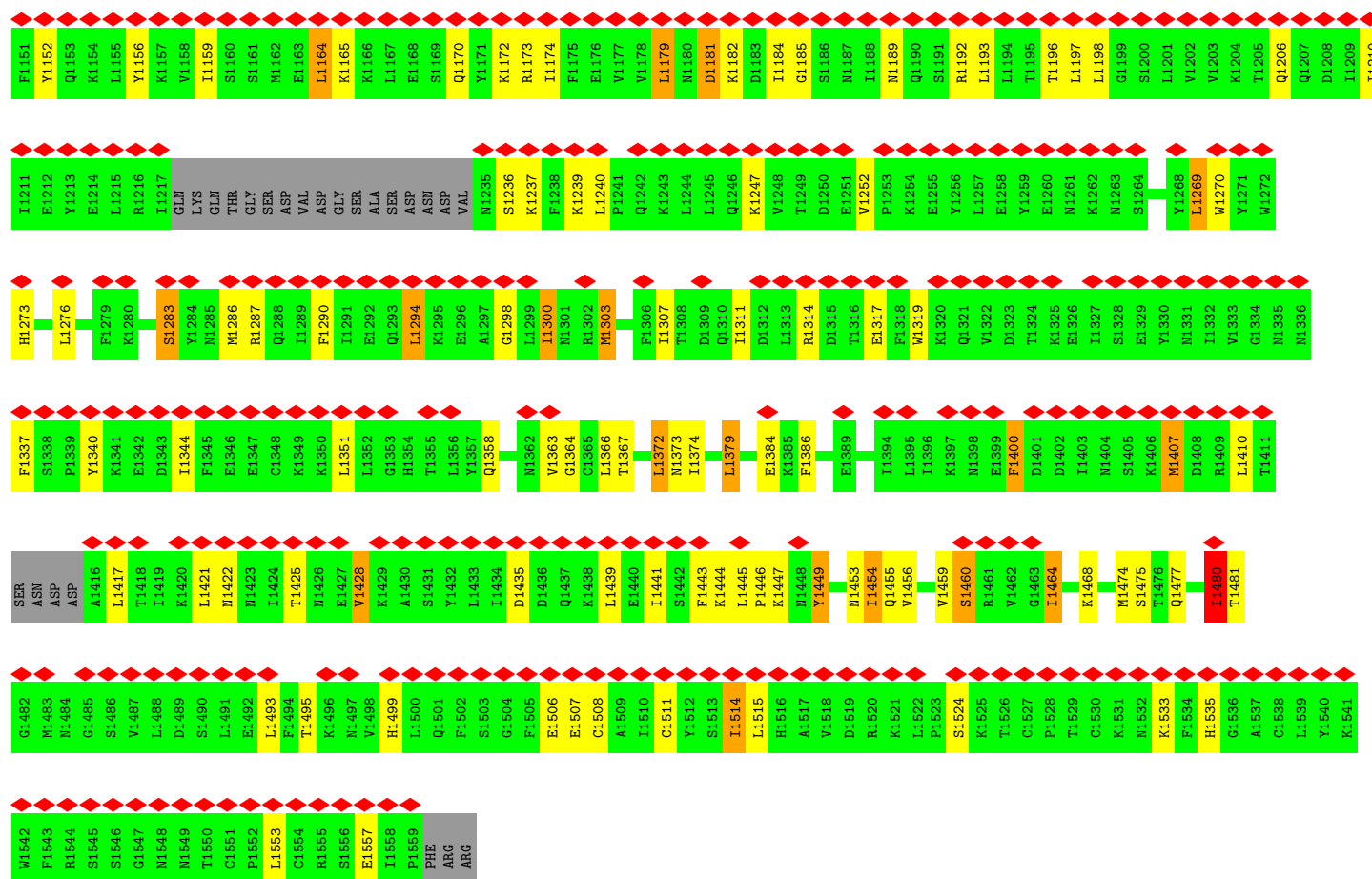
- Molecule 43: 60S ribosomal protein L13-A



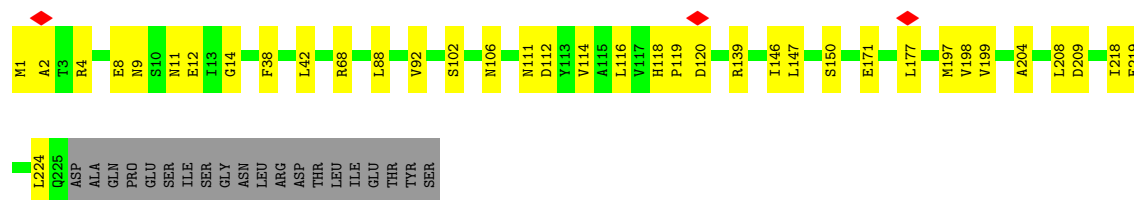
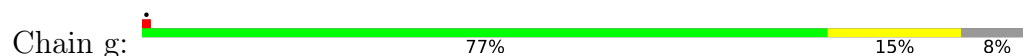
- Molecule 44: 60S ribosomal protein L14-A



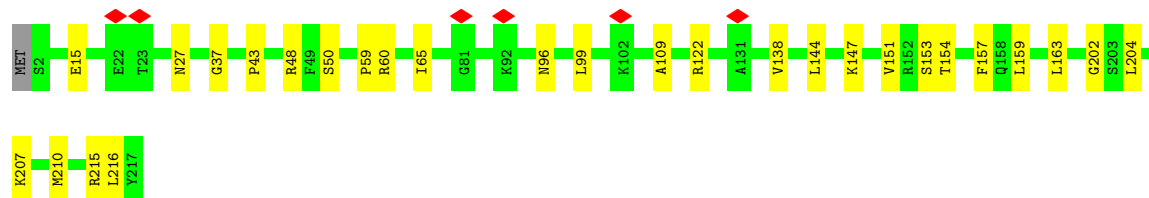
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I1031	L1032	K1033	W1034	L1035	D1036	S1037	D1038	L1039	A1040	Y1041	E1042	P1043	S1044	F1045	S1046	T1047	V1048	R1049	L1050	L1051	L1052	VAL	SER	LVS	ASN	GLY	GLU	GLU	ILE	SER	E1122	Y1123	G1124	D1125	E1126	I1127	Q1128	E1129	M1130	L1131	I1132	E1133	L1134	M1135	F1073	E1074	L1075	S1076	E1077	R1078	L1079	L1080	A1081	D1082	S1083	L1084	S1085	M1086	C1087	Q1088	I1089
D971	E972	I973	T974	K975	L976	R977	T978	L979	L980	A981	S982	L1103	S1044	L985	G986	I987	R988	E989	V990	E991	L992	V993	D994	F995	Q996	E997	K998	S999	L1000	A1001	L1002	L1003	N1004	N1005	L1006	L1007	D1008	I1009	P1010	Q1011	A1012	D1013	K1014	Q1015	F1016	V1017	P1018	I1019	A1020	P1021	Q1022	R1023	L1024	N1025	M1026	I1027	F1028	I1029	S1030		
L851	S852	E853	E854	P855	N856	D857	L858	Y859	Y860	D861	F862	G863	H864	T865	F866	F867	K868	H869	G870	K871	H872	N873	L874	N875	F876	S877	D878	L879	V880	S881	N882	N883	L884	Q885	P886	A887	N888	G889	G890	D891	A892	H893	L894	T895	F896	D897	C957	A958	I959	L960	L961	L962	N963	F964	N965	R966	S967	N968	S969	K970	
R911	V912	L913	Y914	K915	V916	L917	L918	N919	S920	I921	D922	T923	V924	S925	S926	T927	L928	L929	N930	G931	L932	L933	A934	S935	V936	E937	S938	F939	V940	T941	K942	T943	V944	R945	D946	Q947	N948	S949	T950	D951	K952	D953	Y954	L955	L956	C957	A958	I959	L960	L961	L962	N963	F964	N965	R966	S967	N968	S969	K970		
S791	T792	N793	T794	H795	L796	L797	L798	T799	D800	D801	K802	P803	L804	N805	L806	K807	N808	N809	Q810	K811	L812	T813	R814	Y815	A816	L817	F818	L819	D820	A821	L822	N823	D824	A825	L826	P827	E828	R829	W830	N831	N832	H833	L834	R835	A836	F837	L838	T839	W841	S842	R843	L844	Y845	T846	D847	Y848	N849	C850			
L731	Q732	H733	A734	Q735	T736	Y737	F738	S739	P740	G741	A742	K743	E744	K745	Y746	T747	T748	H749	A750	V751	E752	L753	I754	N755	G756	C757	N758	D759	T760	S761	Q762	I763	F764	F765	P766	A767	N768	A769	I770	E771	V772	F773	A774	R775	T776	M777	P778	A779	I780	D781	Y782	R783	S785	L786	V787	S788	S789	L790			
F671	C672	A673	V674	L675	S676	K677	L678	D679	E680	T681	F682	F683	S684	T685	L686	L687	L688	N689	T690	D691	F692	L693	S694	C695	A696	L697	Y698	E699	V700	S701	E702	D703	T704	M705	E706	K707	L708	F709	K710	L711	S712	L713	Q714	L715	A716	K717	G718	M719	S720	E721	I722	A723	N724	K725	L726	A727	Q728	V729	I730		
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	K644	G645	N646	N647	K648	F649	L650	N651	Q652	R653	T654	I655	T656	T657	L658	Y659	R660	S661	A662	V663	A664	N665	G666	Q667	V668	E669	Q670		
S490	P491	M492	M493	E544	S495	A496	T497	S498	R499	L500	F501	D502	F503	F504	V505	Q506	L507	I508	E509	T510	P512	S513	N514	V515	F516	N517	K518	Y519	D520	G521	V522	Y523	D524	A525	L526	N527	Y528	F529	L530	D531	S532	D533	M534	I535	F536	L537	N538	G539	K540	T541	G542	K543	F544	I545	N546	E547	T548	P549			
T550	L551	V552	Q553	E554	S555	T556	Y557	Q558	N559	F560	A561	G562	I563	M564	A565	Q566	N569	S570	K571	F572	F573	K574	N575	N576	T577	D578	A579	I580	T581	S582	L583	E584	D585	F586	F587	I588	V589	A590	L591	S592	F593	N594	L595	P596	K597	T598	I599	I600	L601	A602	T603	M604	N605	E606	L607	D608	N609	D610			
K411	F412	A413	E414	D415	S416	S417	E418	E419	R420	L421	S432	L433	S434	C435	G436	K437	S438	L439	S440	E441	Y442	T443	K444	S450	G451	V452	F453	P454	P455	D456	K457	W458	E459	R460	E461	I462	E463	D464	Y465	F466	T467	S468	D469	E470	D471	I472	R473	K474	I475	K476	V477	E480	L487	V488	T489						
D322	Y323	E324	D325	G326	T327	I328	V329	S330	Y331	D332	K333	S334	S335	K338	F342	R347	F354	V358	T365	K366	R367	H368	S369	F370	L371	D372	Y373	Y374	L375	E376	W377	L378	P379	F380	K383	R387	L388	N389	E390	K391	G392	F393	S394	A395	R396	N397	S398	A399	E400	L410											



• Molecule 47: Eukaryotic translation initiation factor 6

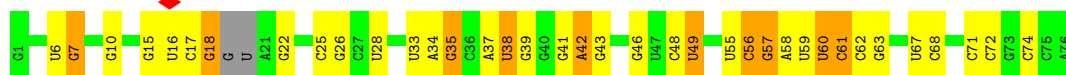


• Molecule 48: 60S ribosomal protein L1-A



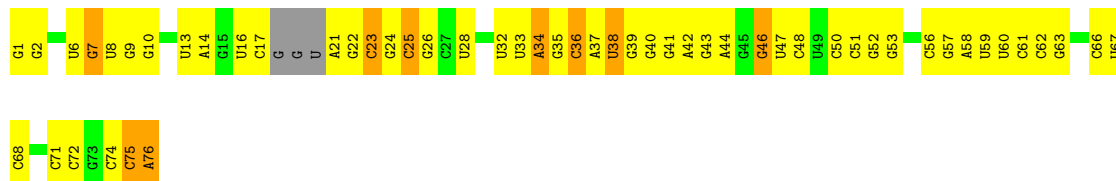
• Molecule 49: Ala tRNA

Chain x: 



• Molecule 49: Ala tRNA

Chain y: 



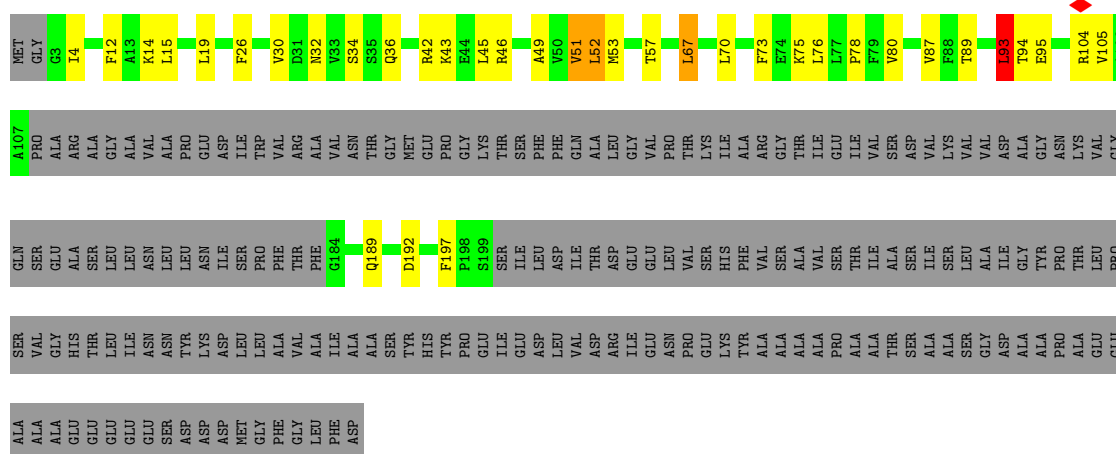
• Molecule 50: 60S ribosomal protein L12-B

Chain z: 



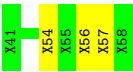
• Molecule 51: 60S acidic ribosomal protein P0

Chain 0: 



• Molecule 52: CAT-tailed nascent peptide

Chain 1: 



- Molecule 53: Eukaryotic translation initiation factor 5A-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54175	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	3.799	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.132	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: ZN, MG, 5CT

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	0.31	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	0.29	0/812	0.75	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	0.25	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	0.29	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	0.52	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	0/77011	0.39	5/120065 (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	0.35	0/1908	0.54	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	0.56	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	0.63	2/2060 (0.1%)
41	r	0.25	0/1801	0.49	0/2416
42	s	0.26	0/1367	0.69	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	0.45	0/6679	0.85	20/9012 (0.2%)
46	e	0.60	0/11715	0.91	53/15908 (0.3%)
47	g	0.24	0/1672	0.59	1/2281 (0.0%)
48	w	0.27	0/1736	0.61	1/2332 (0.0%)
49	x	0.35	0/1761	0.60	0/2742
49	y	0.36	0/1735	0.64	0/2701
50	z	0.67	0/726	1.24	13/1006 (1.3%)
51	0	0.49	0/976	0.95	3/1313 (0.2%)
53	v	0.29	0/1084	0.64	1/1456 (0.1%)
All	All	0.34	0/161759	0.54	119/236301 (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
47	g	0	1
All	All	0	11

There are no bond length outliers.

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	e	1364	GLY	N-CA-C	12.23	127.29	112.49
45	a	116	PHE	N-CA-C	-10.36	99.52	112.88
46	e	1460	SER	N-CA-C	10.01	122.27	111.36
46	e	1181	ASP	N-CA-C	8.85	120.93	111.28
46	e	1141	GLN	N-CA-C	8.76	120.83	111.28

There are no chirality outliers.

5 of 11 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	17	0
3	C	1416	0	1433	14	0
4	D	1441	0	1543	16	0
5	E	1258	0	1342	11	0
6	F	1437	0	1475	20	0
7	G	1272	0	1312	12	0
8	H	796	0	812	6	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
14	N	1169	0	1211	14	0
15	O	462	0	491	9	0
16	P	737	0	792	4	0
17	Q	876	0	912	10	0
18	R	1013	0	1077	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	850	0	880	4	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	11	0
28	c	694	0	734	8	0
29	d	207	0	250	3	0
30	f	68802	0	34573	340	0
31	h	2579	0	1304	9	0
32	i	3353	0	1695	13	0
33	j	1874	0	1943	23	0
34	k	3075	0	3142	20	0
35	l	2748	0	2859	23	0
36	m	2351	0	2294	31	0
37	n	1307	0	1377	8	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	9	0
43	t	1543	0	1608	14	0
44	u	1053	0	1149	11	0
45	a	6569	0	6460	246	0
46	e	11516	0	10776	279	0
47	g	1651	0	1613	22	0
48	w	1709	0	1799	17	0
49	x	1579	0	799	49	0
49	y	1556	0	789	39	0
50	z	728	0	337	19	0
51	0	961	0	979	45	0
52	1	90	0	21	3	0
53	v	1085	0	1087	15	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
All	All	151349	0	113599	1309	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 5.

The worst 5 of 1309 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:272:TYR:HA	46:e:277:MET:SD	1.28	1.66
46:e:277:MET:SD	46:e:278:PRO:HD3	1.34	1.62
46:e:751:VAL:HA	46:e:754:ILE:CD1	1.30	1.59
49:x:67:U:H2'	49:x:68:C:C5	1.26	1.59
45:a:90:THR:HB	45:a:104:GLN:CB	1.35	1.56

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%)	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
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

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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%)	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%)	830 (99%)	12 (1%)	0	100	100
46	e	1519/1562 (97%)	1495 (98%)	22 (1%)	2 (0%)	48	70
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
50	z	144/165 (87%)	135 (94%)	8 (6%)	1 (1%)	18	38
51	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	30
53	v	139/157 (88%)	139 (100%)	0	0	100	100
All	All	9314/10279 (91%)	8956 (96%)	349 (4%)	9 (0%)	49	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
50	z	88	PRO
46	e	437	LYS
46	e	855	PRO
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

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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%)	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%)	188 (100%)	1 (0%)	81	92
34	k	321/323 (99%)	321 (100%)	0	100	100
35	l	288/289 (100%)	288 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	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%)	633 (94%)	43 (6%)	16	35
46	e	1152/1451 (79%)	1091 (95%)	61 (5%)	20	43
47	g	180/211 (85%)	180 (100%)	0	100	100
48	w	197/198 (100%)	197 (100%)	0	100	100
51	0	104/254 (41%)	94 (90%)	10 (10%)	8	17
53	v	119/132 (90%)	117 (98%)	2 (2%)	53	78
All	All	7564/8690 (87%)	7446 (98%)	118 (2%)	54	79

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	319	THR
51	0	76	LEU
46	e	867	PHE
51	0	67	LEU
46	e	1428	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
45	a	417	ASN
46	e	251	ASN
45	a	532	GLN
46	e	79	ASN
46	e	869	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	591 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
49	x	72/76 (94%)	23 (31%)	0
49	y	71/76 (93%)	32 (45%)	0
All	All	3631/3826 (94%)	690 (19%)	0

5 of 690 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	$\# Z > 2$
53	5CT	v	51	53	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
53	5CT	v	51	53	-	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(°)
53	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
53	v	51	5CT	NZ-C1-C2-C3
53	v	51	5CT	O1-C2-C3-C4
53	v	51	5CT	C2-C3-C4-N1
53	v	51	5CT	C-CA-CB-CG
53	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
53	v	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 20 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

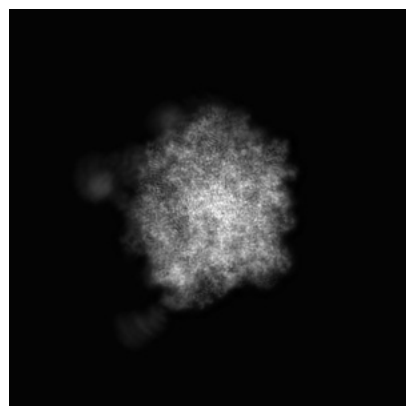
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15425. These allow visual inspection of the internal detail of the map and identification of artifacts.

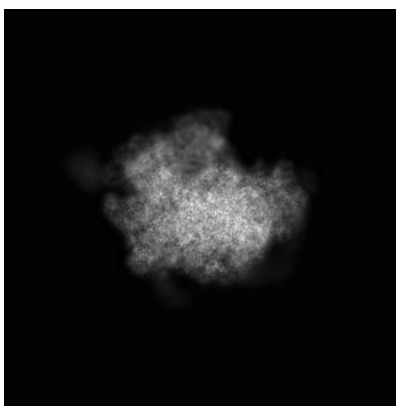
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

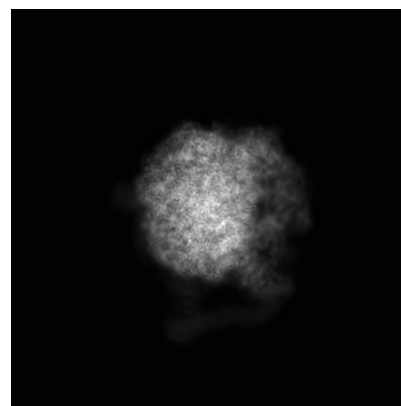
6.1.1 Primary map



X

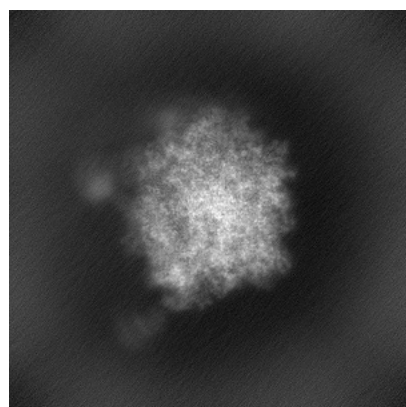


Y

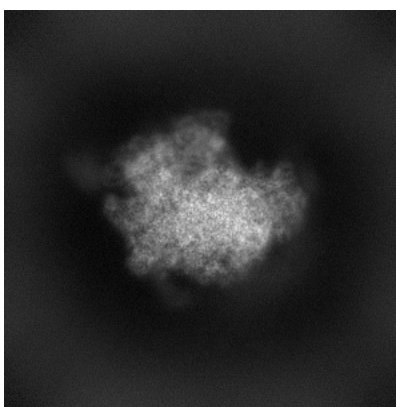


Z

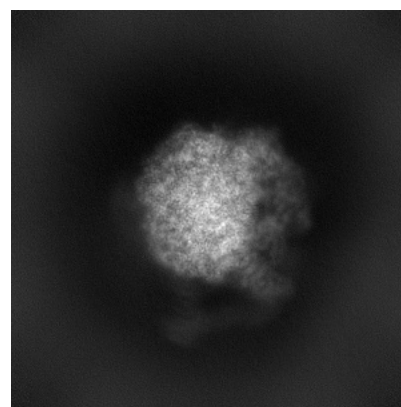
6.1.2 Raw map



X



Y

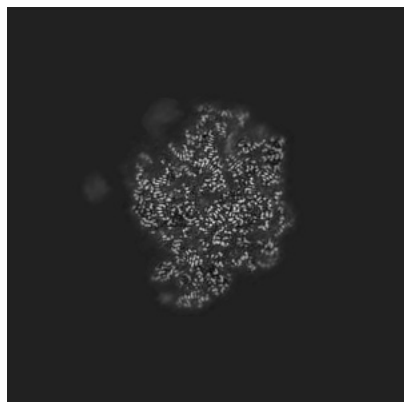


Z

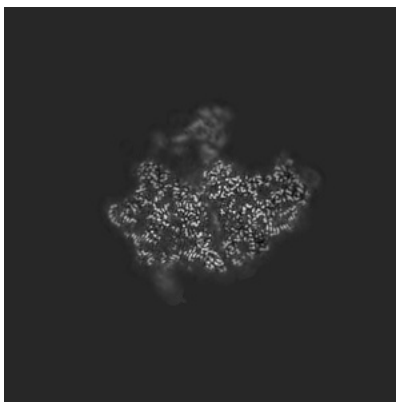
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

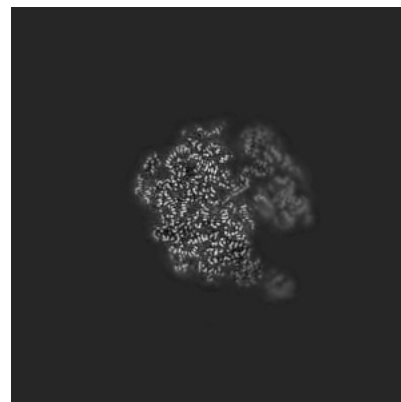
6.2.1 Primary map



X Index: 225

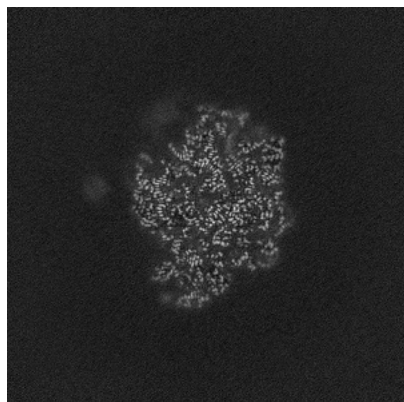


Y Index: 225

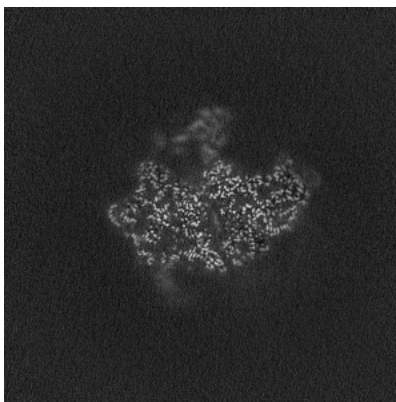


Z Index: 225

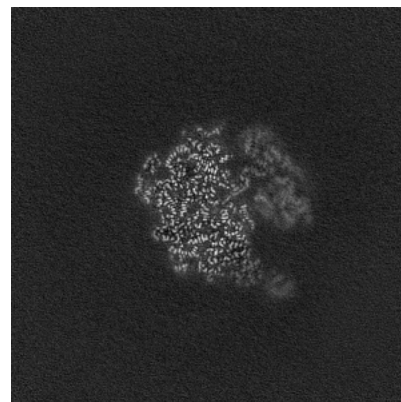
6.2.2 Raw map



X Index: 225



Y Index: 225

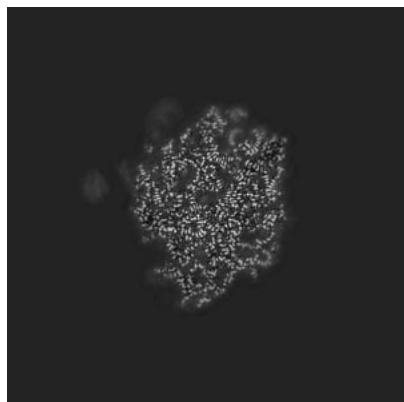


Z Index: 225

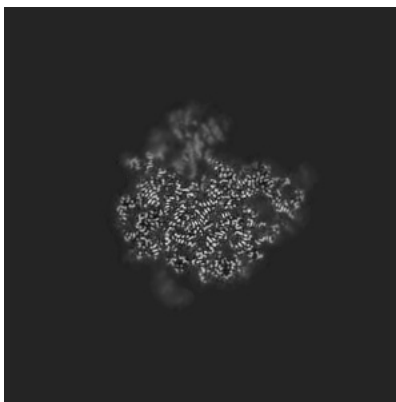
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

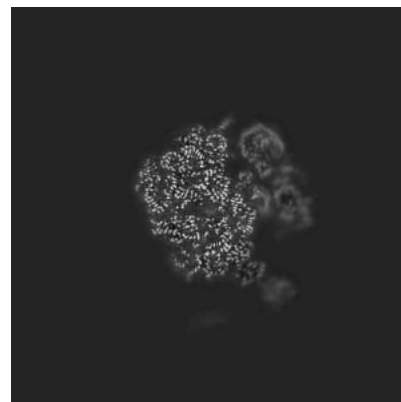
6.3.1 Primary map



X Index: 219

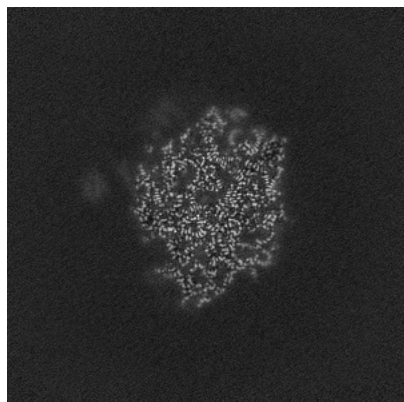


Y Index: 242

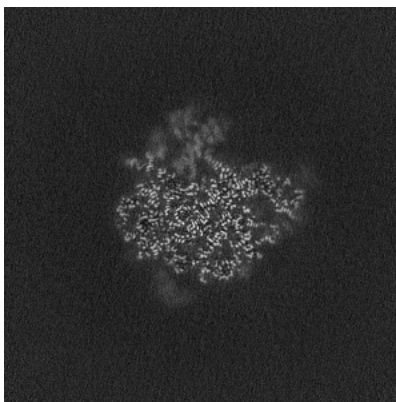


Z Index: 231

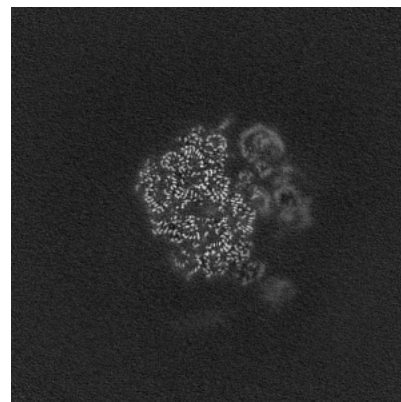
6.3.2 Raw map



X Index: 219



Y Index: 241

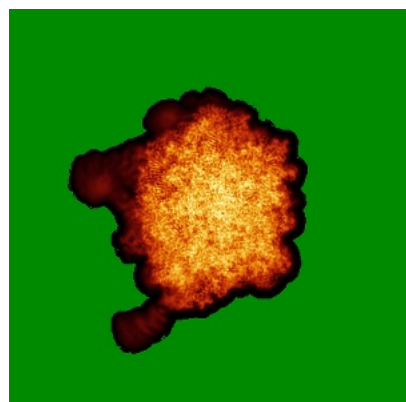


Z Index: 231

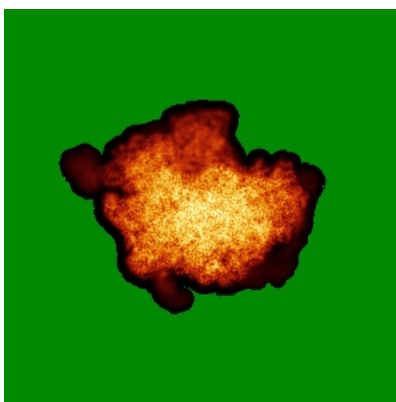
The images above show the largest variance slices of the map in three orthogonal directions.

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

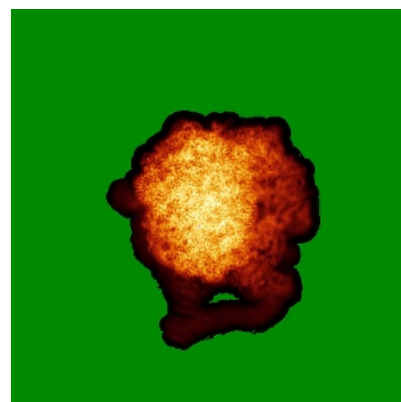
6.4.1 Primary map



X

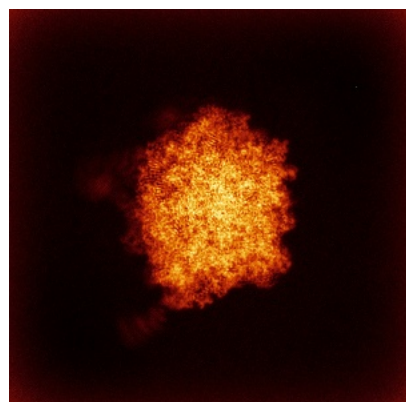


Y

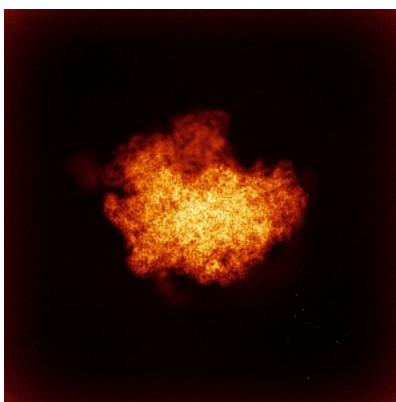


Z

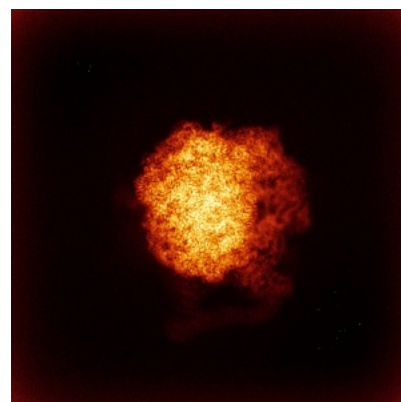
6.4.2 Raw map



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.

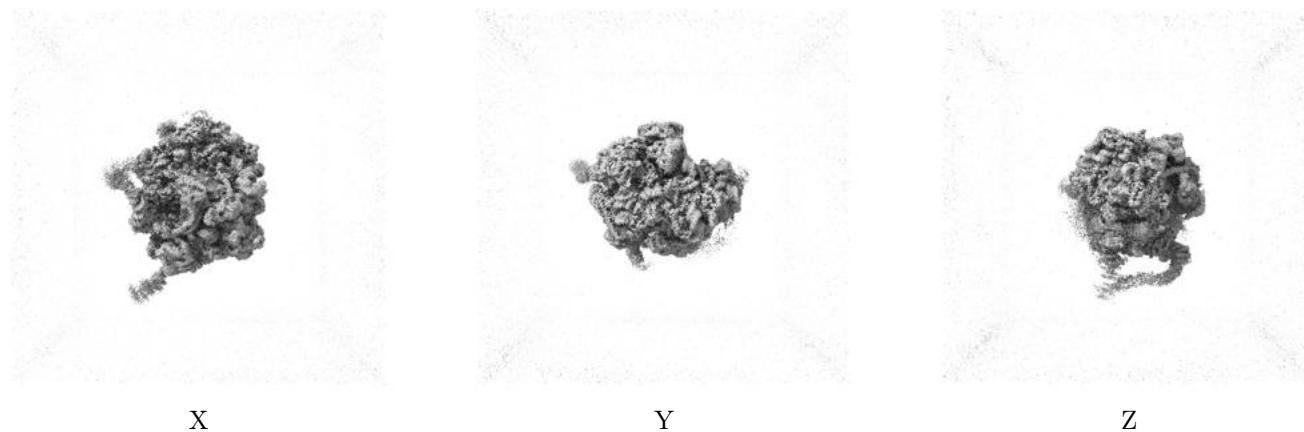
6.5 Orthogonal surface views [i](#)

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.

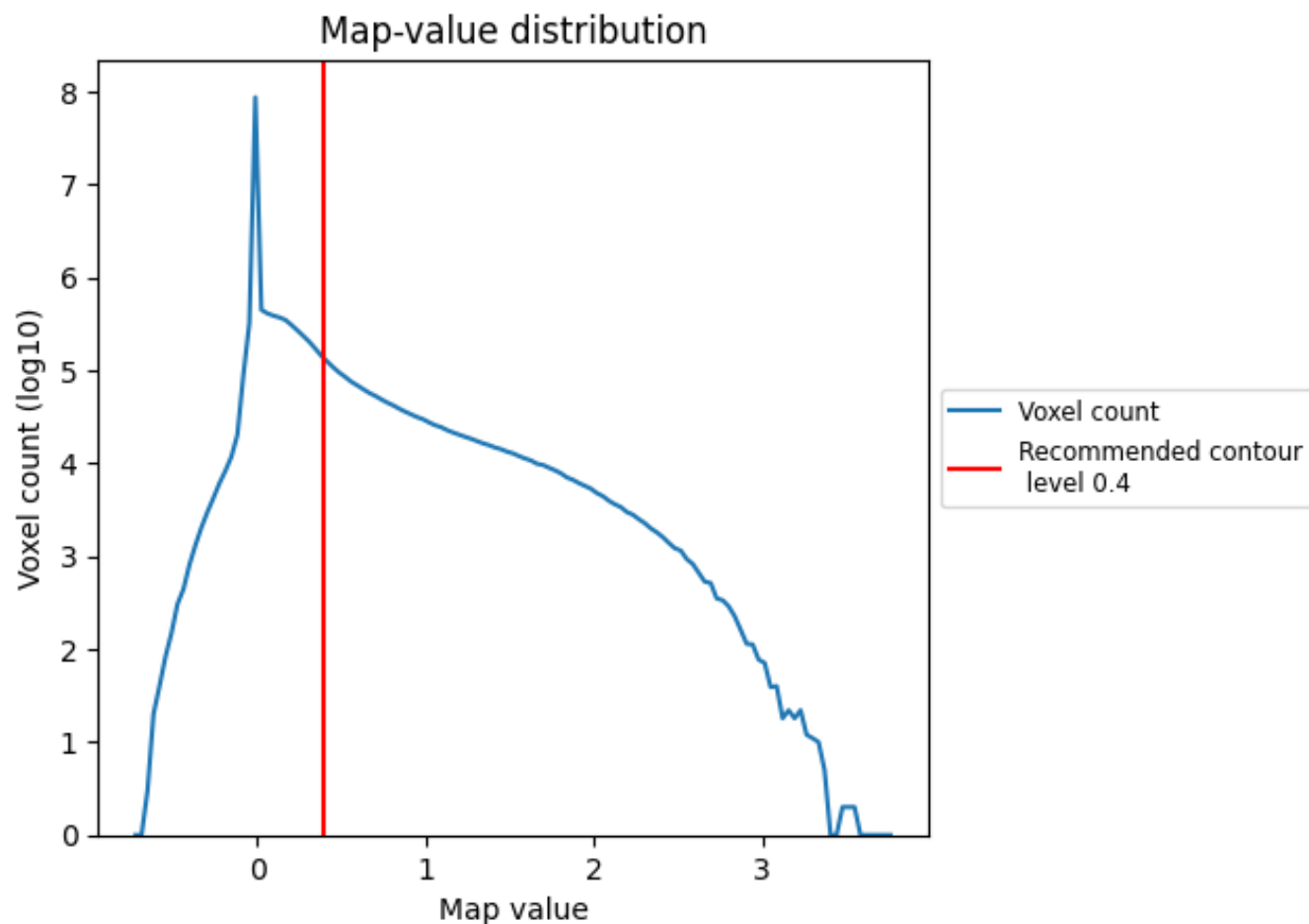
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

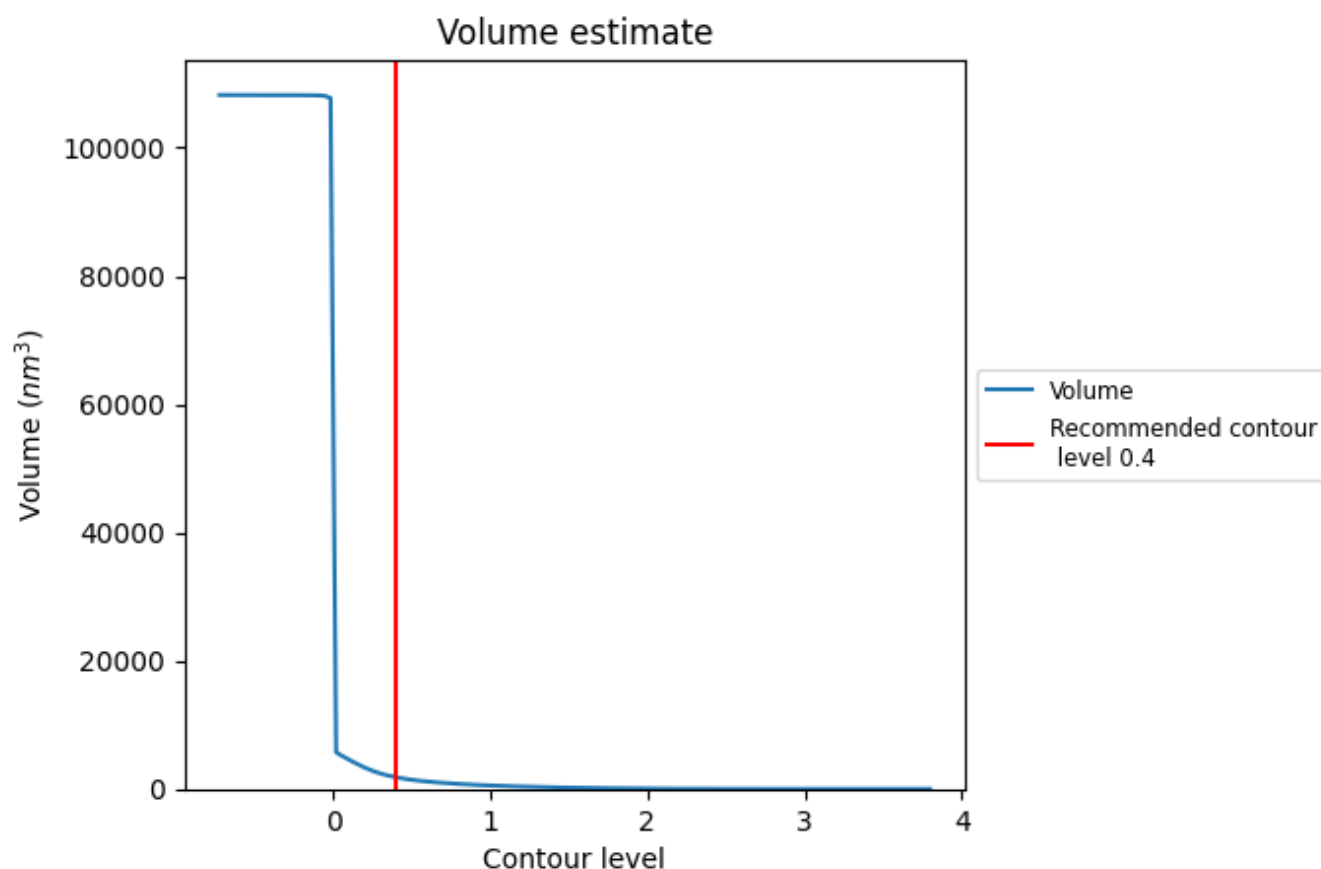
This section contains the results of statistical analysis of the map.

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.

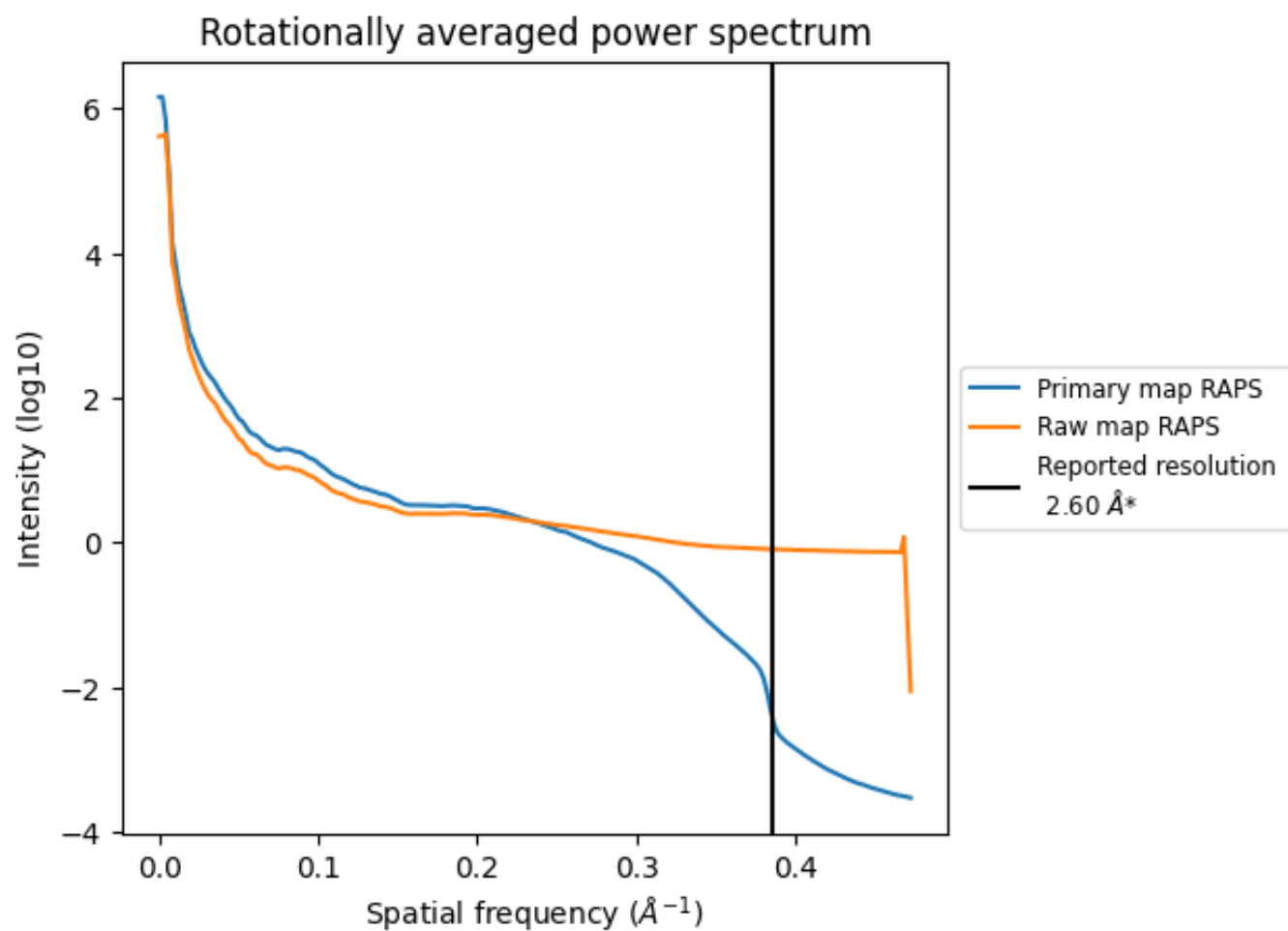
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1819 nm³; this corresponds to an approximate mass of 1643 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 ⓘ

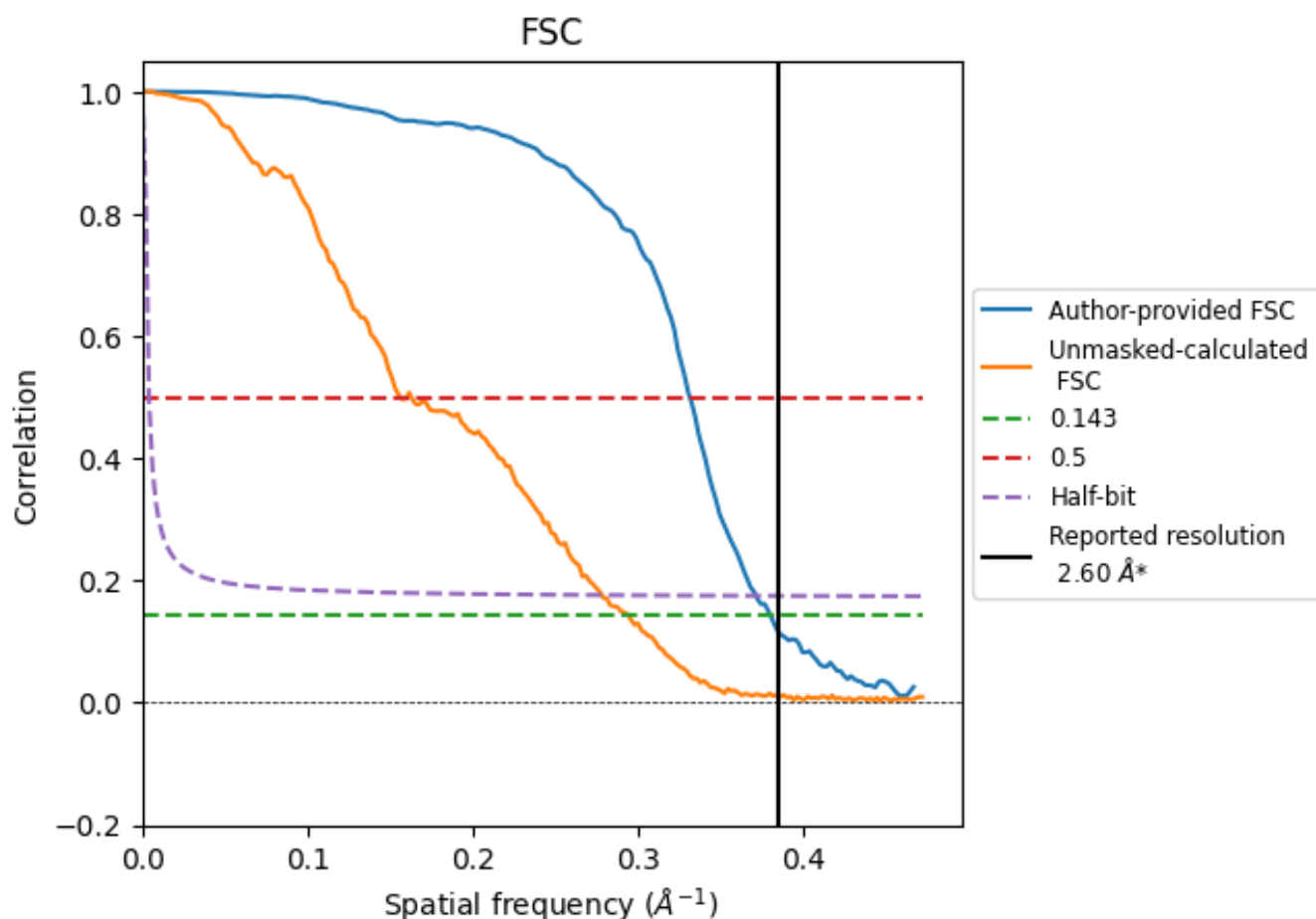


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

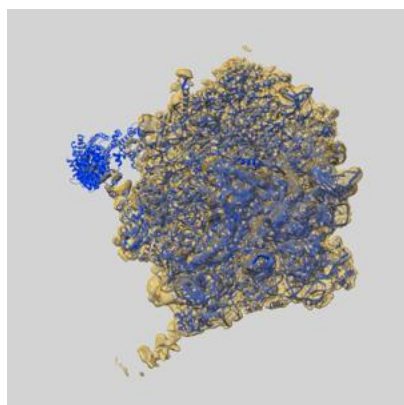
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.63	3.02	2.69
Unmasked-calculated*	3.40	6.40	3.59

*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 3.40 differs from the reported value 2.6 by more than 10 %

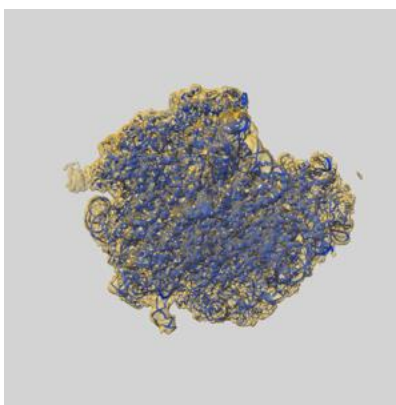
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15425 and PDB model 8AGV. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

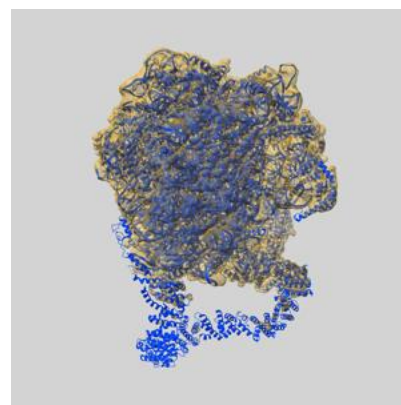
9.1 Map-model overlay [i](#)



X



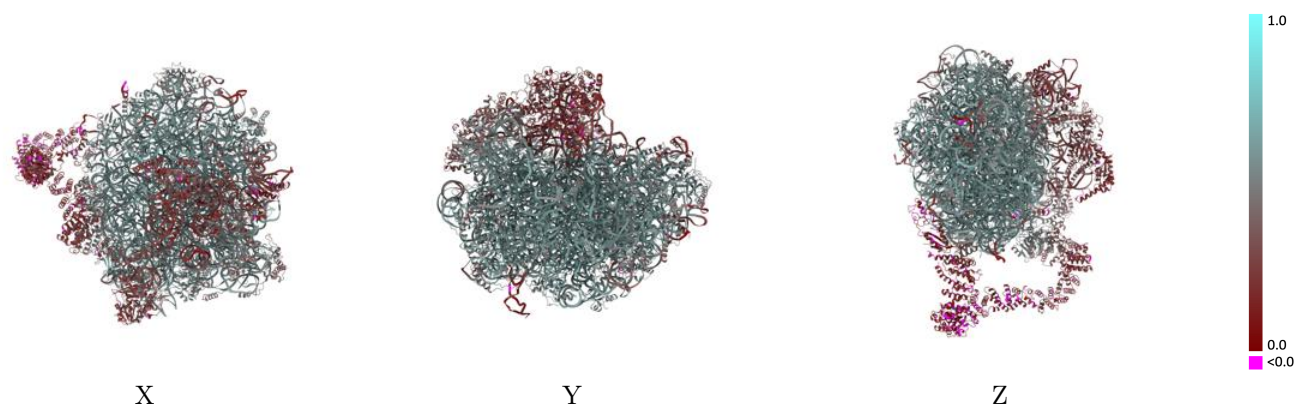
Y



Z

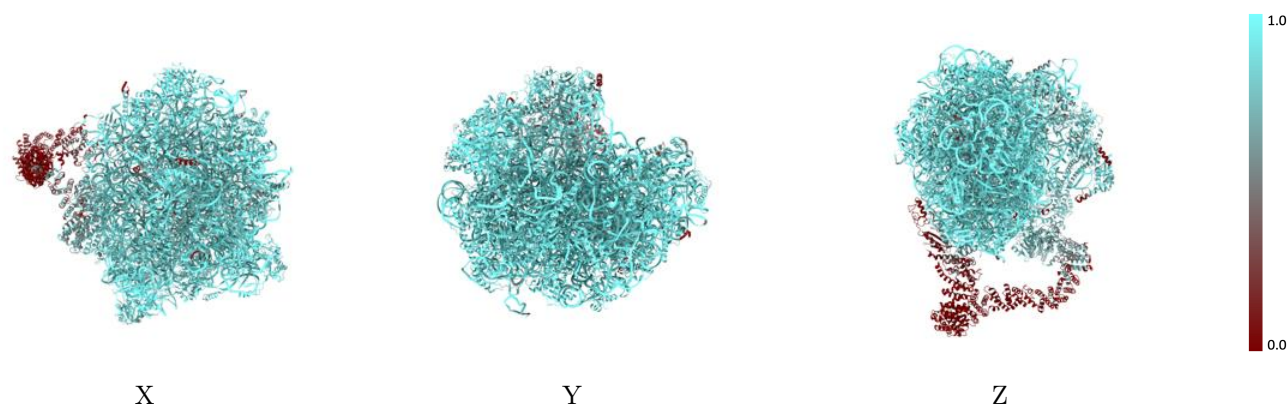
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



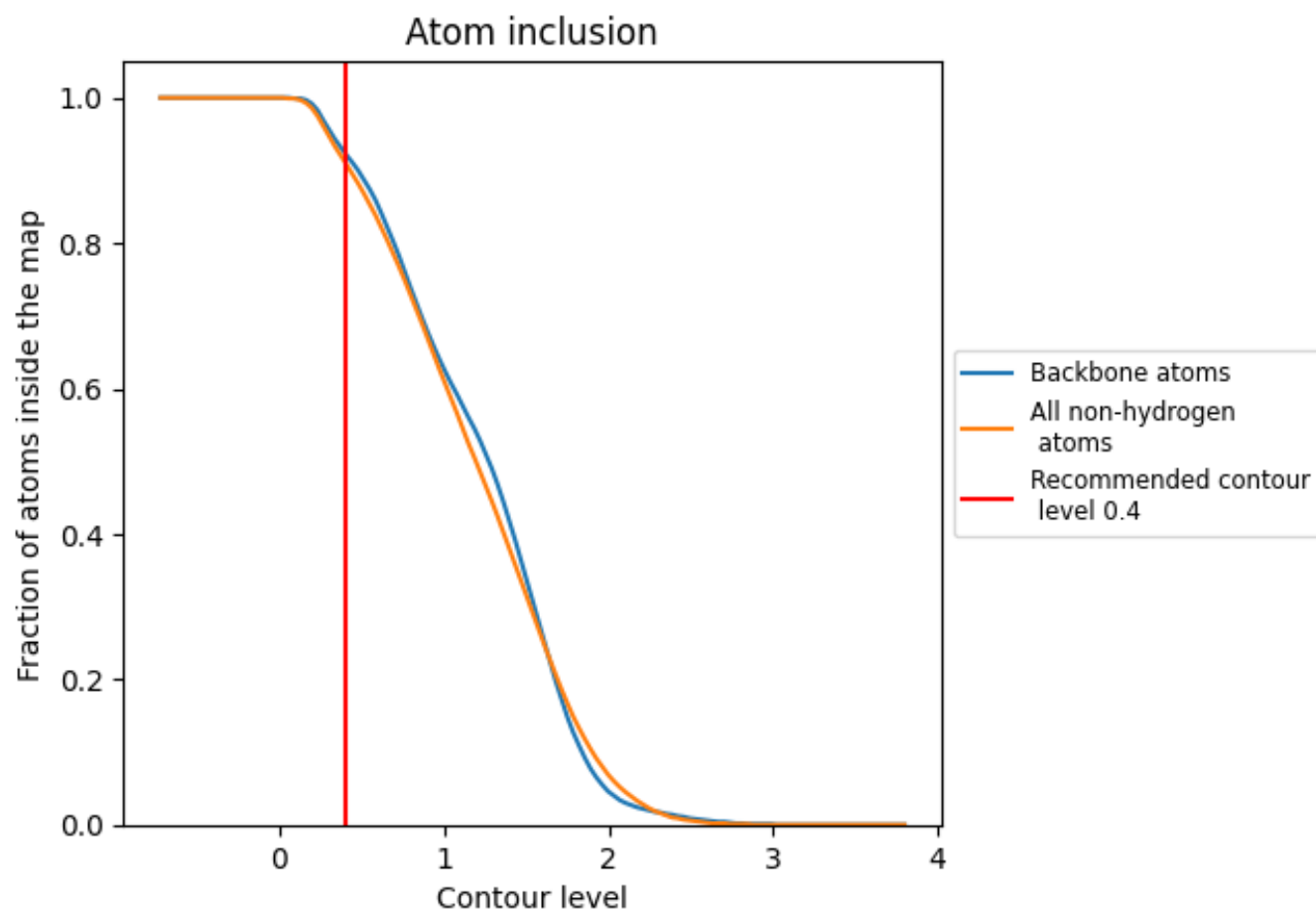
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 92% of all backbone atoms, 91% 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	 0.9110	 0.5030
0	 0.8290	 0.2900
1	 1.0000	 0.4570
A	 0.9930	 0.6050
B	 0.9760	 0.5790
C	 0.9670	 0.5860
D	 0.9790	 0.5790
E	 0.9420	 0.5390
F	 0.9770	 0.5730
G	 0.9690	 0.5580
H	 0.9310	 0.4750
I	 0.9640	 0.5630
J	 0.9600	 0.5600
K	 0.9660	 0.5650
L	 0.9730	 0.5580
M	 0.9550	 0.5190
N	 0.9800	 0.5870
O	 0.9560	 0.5330
P	 0.9420	 0.5100
Q	 0.9250	 0.5480
R	 0.9810	 0.5950
S	 0.9900	 0.6120
T	 0.9660	 0.5690
U	 0.9670	 0.5480
V	 0.9570	 0.5200
W	 1.0000	 0.6200
X	 0.9200	 0.4970
Y	 0.9950	 0.5950
Z	 0.9670	 0.5650
a	 0.8080	 0.2780
b	 0.9640	 0.5640
c	 0.9720	 0.5620
d	 0.7130	 0.3910
e	 0.2590	 0.1800
f	 0.9910	 0.5650



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Chain	Atom inclusion	Q-score
g	 0.7570	 0.4630
h	 0.9990	 0.5600
i	 0.9950	 0.5920
j	 0.9860	 0.5960
k	 0.9790	 0.5810
l	 0.9760	 0.5680
m	 0.9350	 0.4780
n	 0.9450	 0.5190
o	 0.9690	 0.5640
p	 0.9410	 0.5120
q	 0.9590	 0.5410
r	 0.9530	 0.5300
s	 0.9250	 0.4200
t	 0.9670	 0.5540
u	 0.9680	 0.5400
v	 0.8470	 0.3530
w	 0.7890	 0.2020
x	 0.9770	 0.2800
y	 0.9760	 0.2610
z	 0.9130	 0.2760