



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:33 AM UTC

PDB ID : 8BPO / pdb_00008bpo
EMDB ID : EMD-16155
Title : Structure of rabbit 80S ribosome translating beta-tubulin in complex with tetratricopeptide protein 5 (TTC5) and S-phase Cyclin A Associated Protein residing in the ER (SCAPER)
Authors : Hopfler, M.; Absmeier, E.; Passmore, L.A.; Hegde, R.S.
Deposited on : 2022-11-17
Resolution : 2.80 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
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

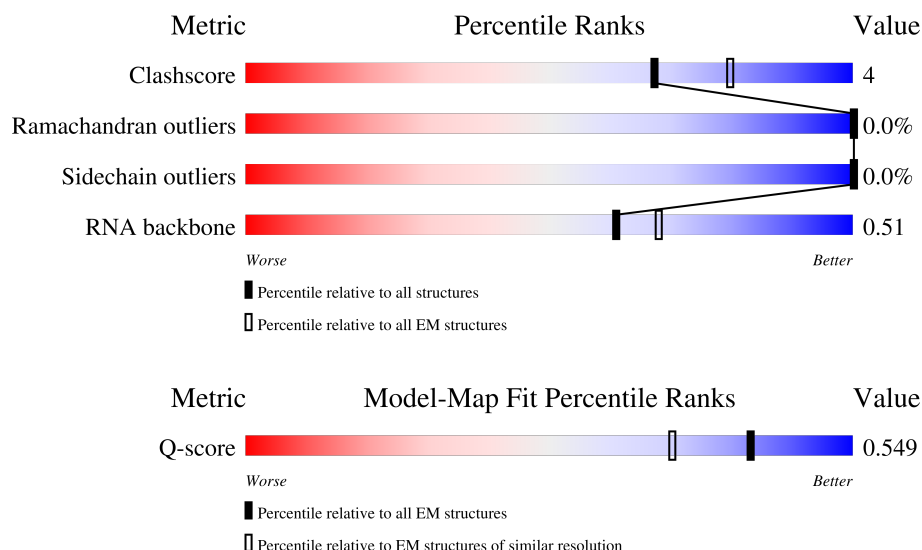
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	A1	4380	
2	B1	120	
3	C1	156	

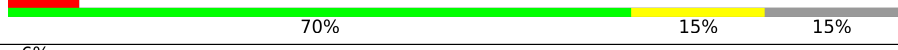
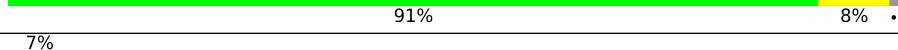
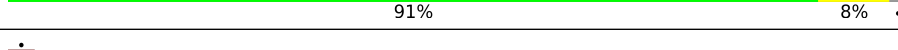
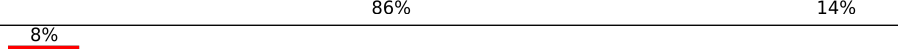
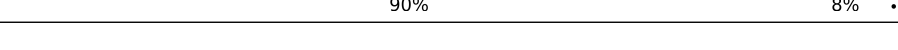
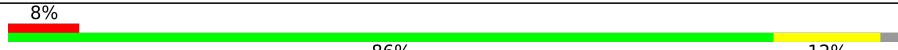
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Mol	Chain	Length	Quality of chain
4	D1	29	
5	A2	257	
6	B2	403	
7	C2	425	
8	D2	297	
9	E2	291	
10	F2	247	
11	G2	319	
12	H2	192	
13	I2	214	
14	J2	178	
15	K2	211	
16	L2	218	
17	M2	204	
18	N2	203	
19	O2	184	
20	P2	187	
21	Q2	196	
22	R2	176	
23	S2	160	
24	T2	128	
25	U2	140	
26	V2	157	
27	W2	156	
28	X2	145	

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Mol	Chain	Length	Quality of chain
29	Y2	136	
30	Z2	148	
31	a2	226	
32	b2	115	
33	c2	125	
34	d2	135	
35	e2	110	
36	f2	116	
37	g2	122	
38	h2	105	
39	i2	97	
40	j2	70	
41	k2	51	
42	l2	102	
43	m2	25	
44	n2	106	
45	o2	92	
46	p2	137	
47	q2	318	
48	r2	165	
49	s2	1411	
50	t2	489	
51	u2	64	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 143326 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B1	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C1	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a protein called Nascent polypeptide-associated complex subunit alpha N-terminal region.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D1	29	Total	C	N	O	0	0
			150	92	29	29		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A2	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B2	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C2	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D2	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E2	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F2	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G2	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G2	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H2	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 13 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I2	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J2	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K2	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K2	74	ARG	HIS	conflict	UNP G1TKB3
K2	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L2	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M2	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 18 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N2	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O2	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 20 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P2	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q2	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R2	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S2	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T2	102	Total	C	N	O	S	0	0
			834	534	146	152	2		

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U2	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 26 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V2	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 27 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W2	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 28 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X2	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y2	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z2	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a2	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b2	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c2	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 34 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d2	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 35 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e2	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f2	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g2	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h2	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j2	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j2	24	LYS	ASN	conflict	UNP G1U001

- Molecule 41 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k2	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l2	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m2	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 44 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n2	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 45 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o2	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p2	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q2	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 48 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r2	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 49 is a protein called S phase cyclin A-associated protein in the endoplasmic reticulum.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s2	395	Total	C	N	O	S	0	0
			3050	1943	525	557	25		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s2	-10	MET	-	initiating methionine	UNP Q9BY12
s2	-9	ASP	-	expression tag	UNP Q9BY12
s2	-8	TYR	-	expression tag	UNP Q9BY12
s2	-7	LYS	-	expression tag	UNP Q9BY12
s2	-6	ASP	-	expression tag	UNP Q9BY12
s2	-5	ASP	-	expression tag	UNP Q9BY12
s2	-4	ASP	-	expression tag	UNP Q9BY12
s2	-3	ASP	-	expression tag	UNP Q9BY12
s2	-2	LYS	-	expression tag	UNP Q9BY12
s2	-1	GLY	-	expression tag	UNP Q9BY12
s2	0	SER	-	expression tag	UNP Q9BY12

- Molecule 50 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t2	418	Total	C	N	O	S	0	0
			3262	2050	573	626	13		

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t2	-48	MET	-	initiating methionine	UNP Q8N0Z6
t2	-47	GLY	-	expression tag	UNP Q8N0Z6
t2	-46	HIS	-	expression tag	UNP Q8N0Z6
t2	-45	HIS	-	expression tag	UNP Q8N0Z6
t2	-44	HIS	-	expression tag	UNP Q8N0Z6
t2	-43	HIS	-	expression tag	UNP Q8N0Z6
t2	-42	HIS	-	expression tag	UNP Q8N0Z6
t2	-41	HIS	-	expression tag	UNP Q8N0Z6
t2	-40	GLU	-	expression tag	UNP Q8N0Z6
t2	-39	ASN	-	expression tag	UNP Q8N0Z6
t2	-38	LEU	-	expression tag	UNP Q8N0Z6
t2	-37	TYR	-	expression tag	UNP Q8N0Z6
t2	-36	PHE	-	expression tag	UNP Q8N0Z6
t2	-35	GLN	-	expression tag	UNP Q8N0Z6
t2	-34	GLY	-	expression tag	UNP Q8N0Z6
t2	-33	SER	-	expression tag	UNP Q8N0Z6
t2	-32	ALA	-	expression tag	UNP Q8N0Z6
t2	-31	TRP	-	expression tag	UNP Q8N0Z6
t2	-30	SER	-	expression tag	UNP Q8N0Z6
t2	-29	HIS	-	expression tag	UNP Q8N0Z6
t2	-28	PRO	-	expression tag	UNP Q8N0Z6
t2	-27	GLN	-	expression tag	UNP Q8N0Z6
t2	-26	PHE	-	expression tag	UNP Q8N0Z6
t2	-25	GLU	-	expression tag	UNP Q8N0Z6
t2	-24	LYS	-	expression tag	UNP Q8N0Z6
t2	-23	GLY	-	expression tag	UNP Q8N0Z6
t2	-22	GLY	-	expression tag	UNP Q8N0Z6
t2	-21	GLY	-	expression tag	UNP Q8N0Z6
t2	-20	SER	-	expression tag	UNP Q8N0Z6
t2	-19	GLY	-	expression tag	UNP Q8N0Z6
t2	-18	GLY	-	expression tag	UNP Q8N0Z6
t2	-17	GLY	-	expression tag	UNP Q8N0Z6
t2	-16	SER	-	expression tag	UNP Q8N0Z6
t2	-15	GLY	-	expression tag	UNP Q8N0Z6
t2	-14	GLY	-	expression tag	UNP Q8N0Z6
t2	-13	SER	-	expression tag	UNP Q8N0Z6
t2	-12	ALA	-	expression tag	UNP Q8N0Z6
t2	-11	TRP	-	expression tag	UNP Q8N0Z6
t2	-10	SER	-	expression tag	UNP Q8N0Z6
t2	-9	HIS	-	expression tag	UNP Q8N0Z6
t2	-8	PRO	-	expression tag	UNP Q8N0Z6
t2	-7	GLN	-	expression tag	UNP Q8N0Z6

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Chain	Residue	Modelled	Actual	Comment	Reference
t2	-6	PHE	-	expression tag	UNP Q8N0Z6
t2	-5	GLU	-	expression tag	UNP Q8N0Z6
t2	-4	LYS	-	expression tag	UNP Q8N0Z6
t2	-3	GLY	-	expression tag	UNP Q8N0Z6
t2	-2	SER	-	expression tag	UNP Q8N0Z6
t2	-1	SER	-	expression tag	UNP Q8N0Z6
t2	0	GLY	-	expression tag	UNP Q8N0Z6

- Molecule 51 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u2	11	Total	C	N	O	S	0	0
			82	50	18	13	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u2	61	MET	-	expression tag	UNP P07437
u2	62	LYS	-	expression tag	UNP P07437
u2	63	LEU	-	expression tag	UNP P07437
u2	64	VAL	-	expression tag	UNP P07437

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	A1	194	Total	Mg	0
			194	194	
52	B1	7	Total	Mg	0
			7	7	
52	C1	6	Total	Mg	0
			6	6	
52	B2	1	Total	Mg	0
			1	1	
52	I2	1	Total	Mg	0
			1	1	
52	O2	2	Total	Mg	0
			2	2	
52	U2	1	Total	Mg	0
			1	1	
52	Z2	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
52	f2	1	Total	Mg	0
			1	1	

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

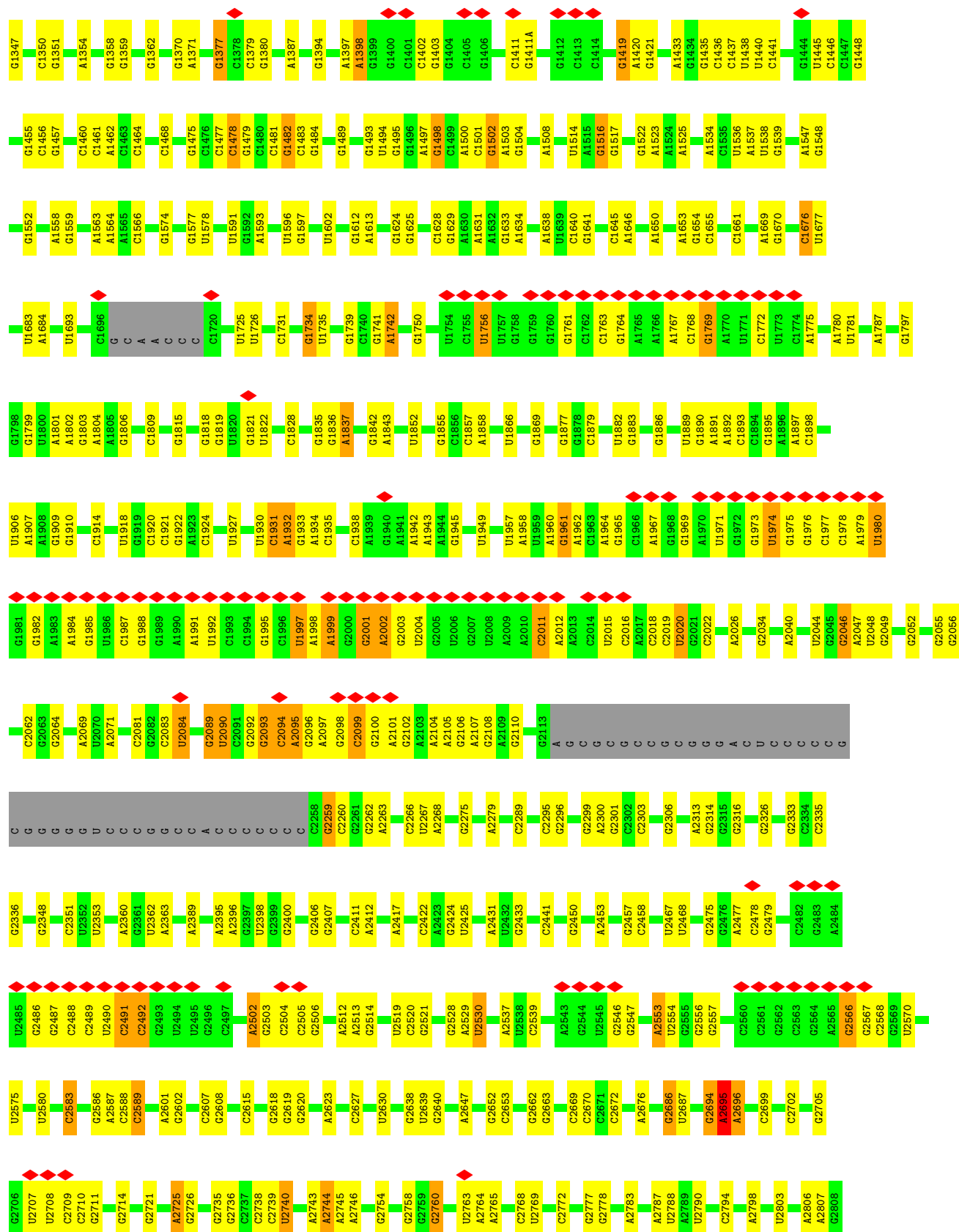
Mol	Chain	Residues	Atoms		AltConf
53	f2	1	Total	Zn	0
			1	1	
53	i2	1	Total	Zn	0
			1	1	
53	l2	1	Total	Zn	0
			1	1	
53	n2	1	Total	Zn	0
			1	1	
53	o2	1	Total	Zn	0
			1	1	

3 Residue-property plots

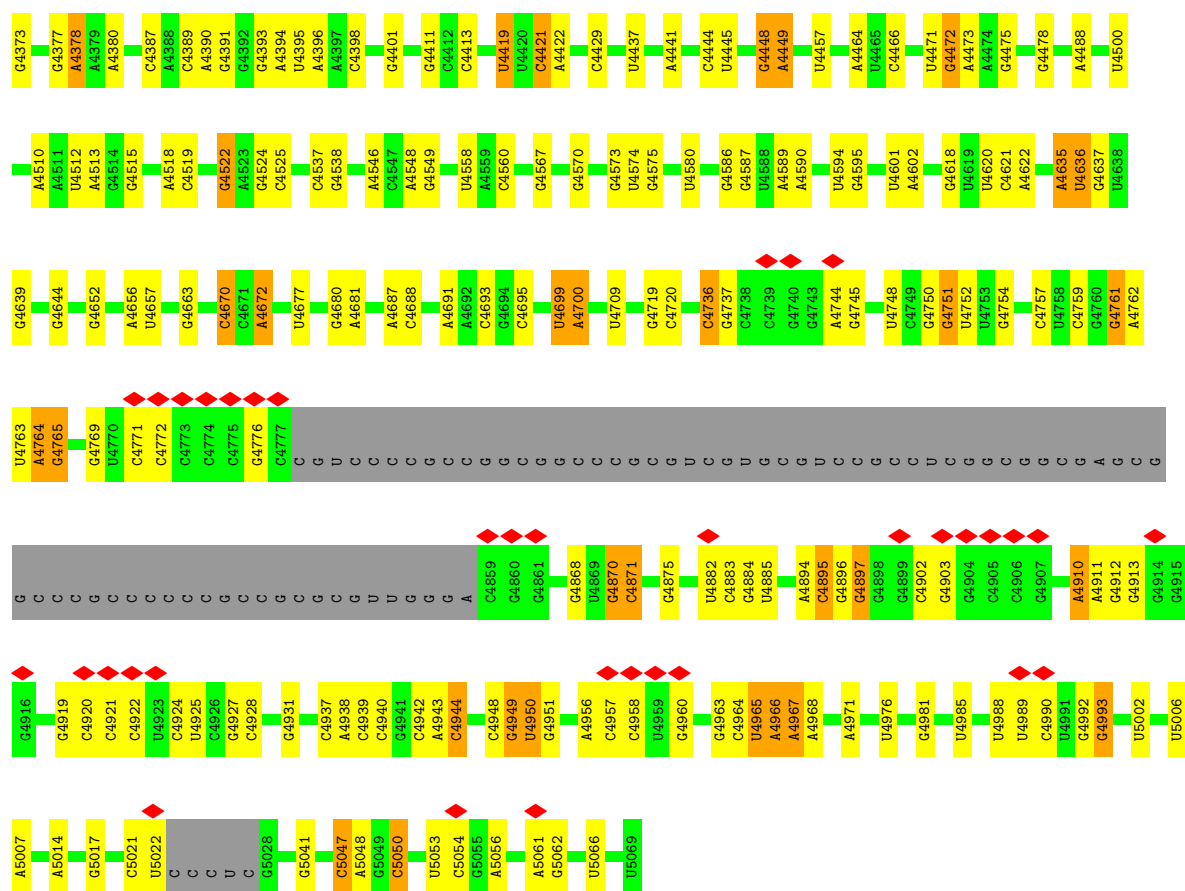
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S ribosomal RNA

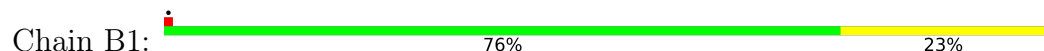




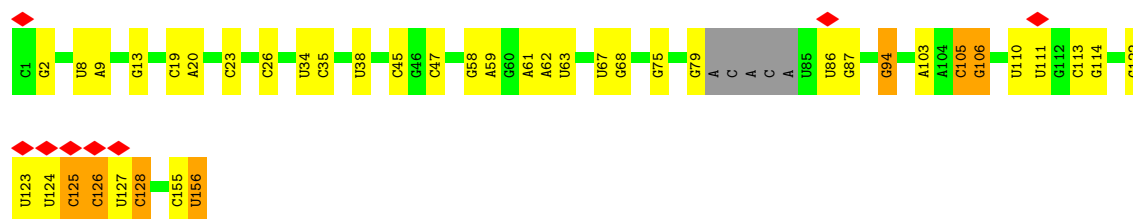
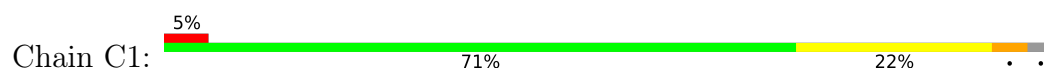
[illegible]



- Molecule 2: 5S ribosomal RNA

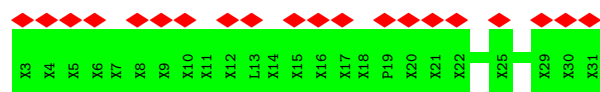


- Molecule 3: 5.8S ribosomal RNA

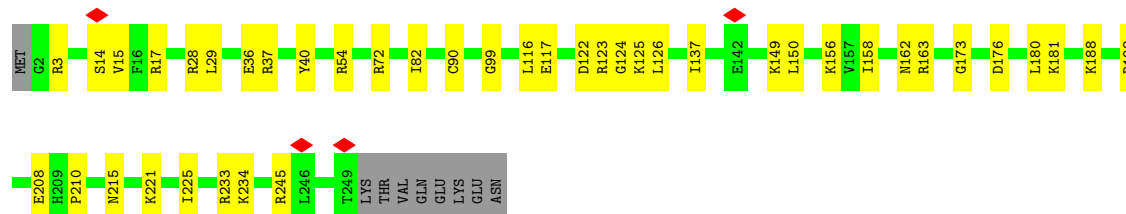
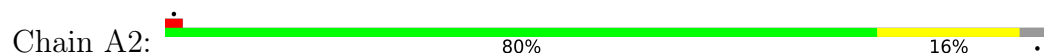


- Molecule 4: Nascent polypeptide-associated complex subunit alpha N-terminal region

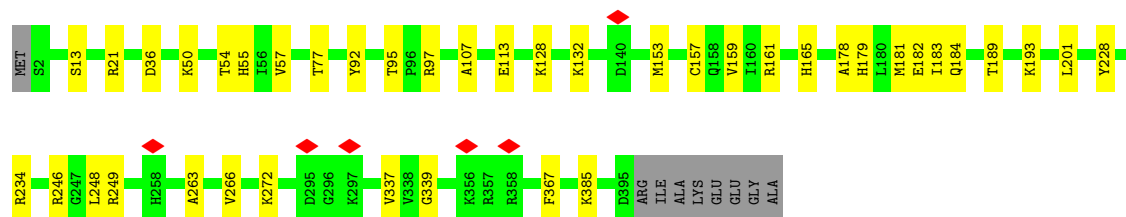
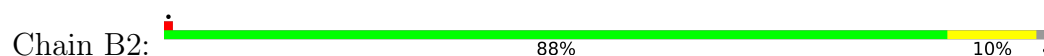




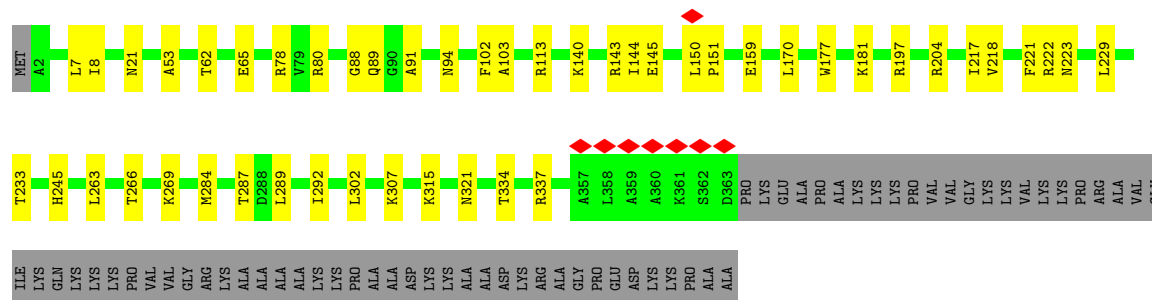
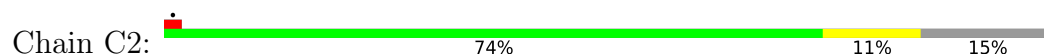
- Molecule 5: 60S ribosomal protein L8



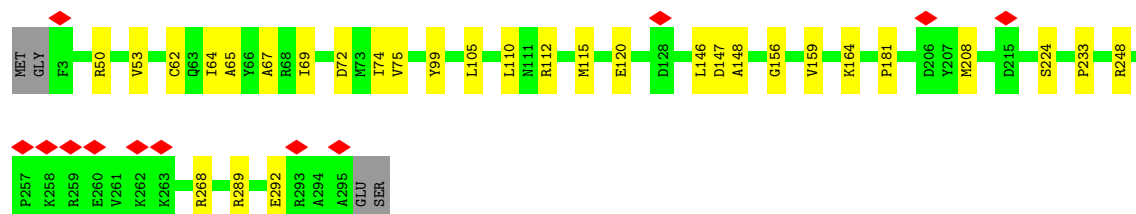
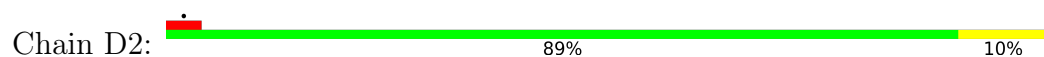
- Molecule 6: Ribosomal protein L3



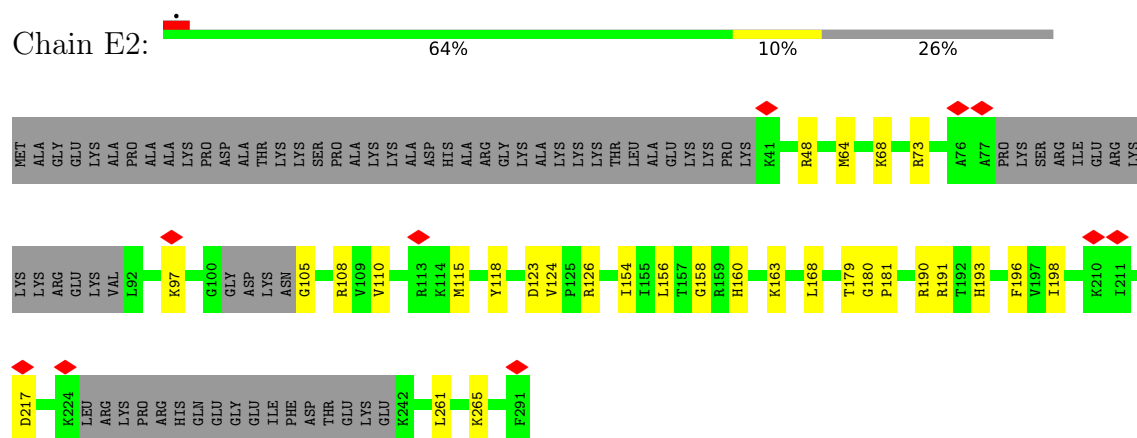
- Molecule 7: 60S ribosomal protein L4



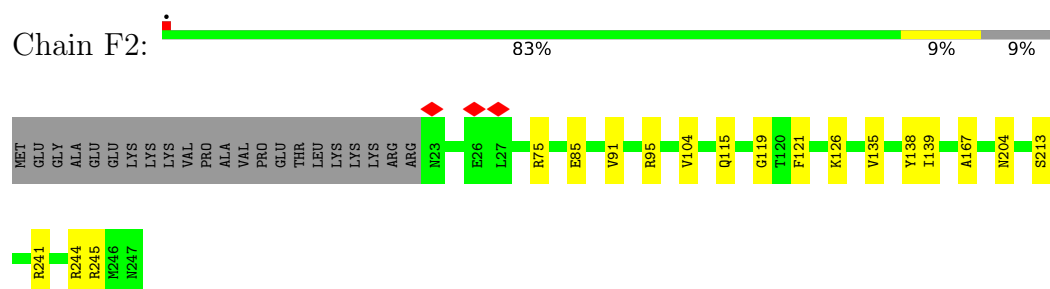
- Molecule 8: Ribosomal_L18_c domain-containing protein



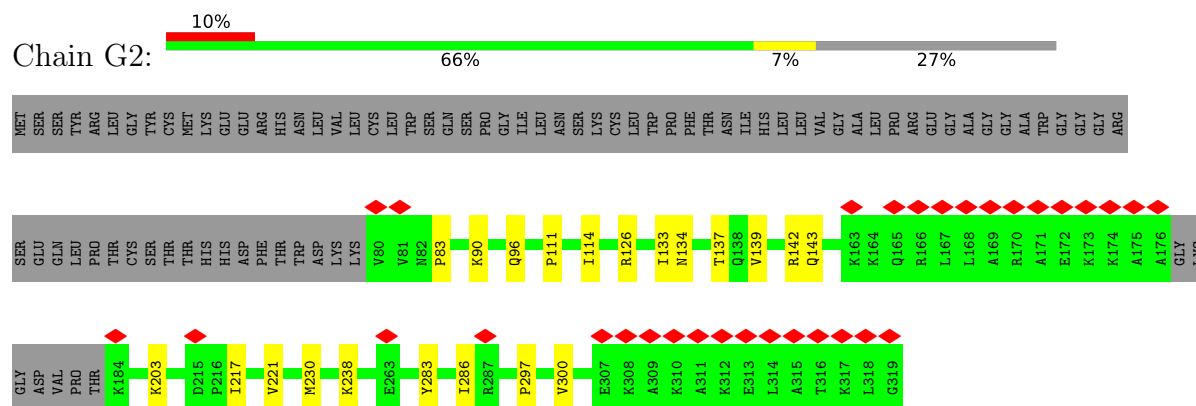
- Molecule 9: 60S ribosomal protein L6



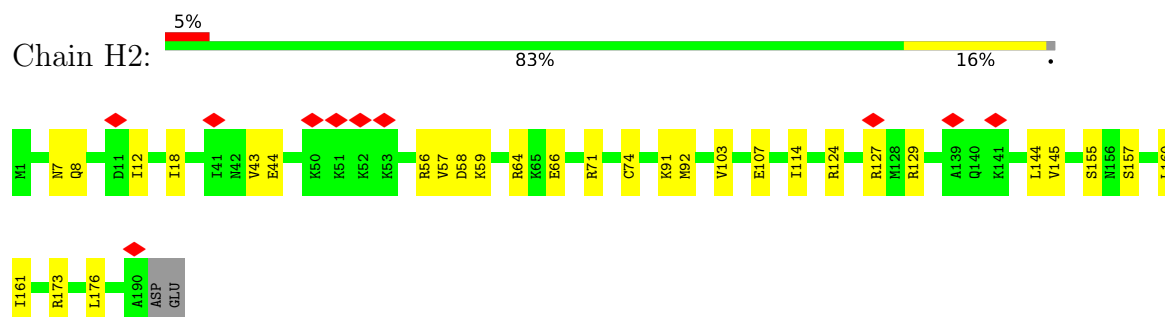
- Molecule 10: 60S ribosomal protein L7



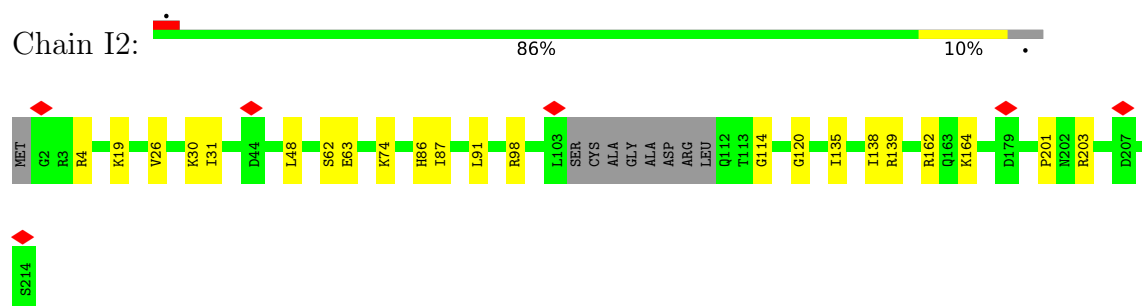
- Molecule 11: 60S ribosomal protein L7a



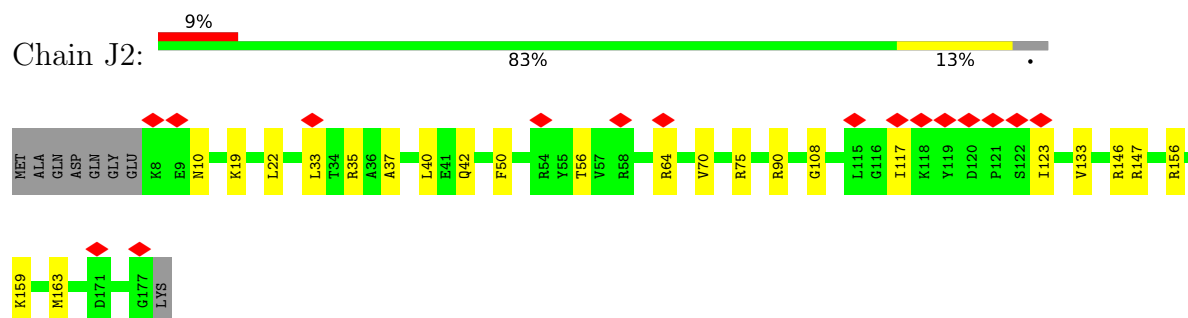
- Molecule 12: 60S ribosomal protein L9



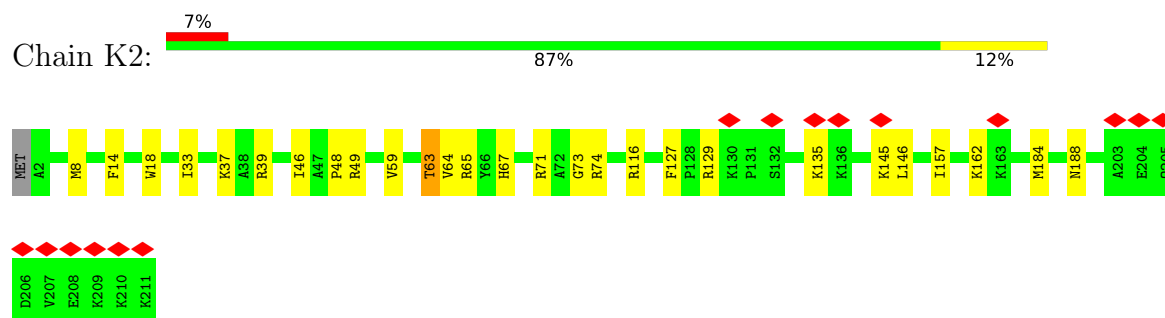
- Molecule 13: Ribosomal protein L10



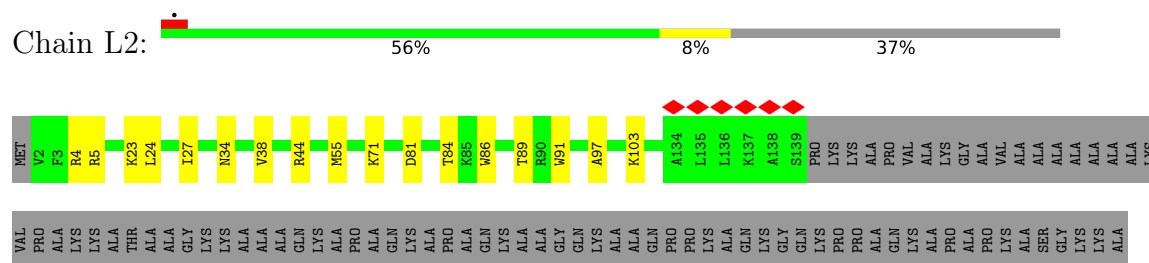
- Molecule 14: 60S ribosomal protein L11



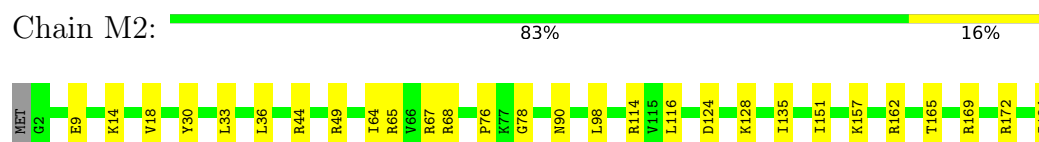
- Molecule 15: 60S ribosomal protein L13



- Molecule 16: 60S ribosomal protein L14



- Molecule 17: Ribosomal protein L15





- Molecule 18: 60S ribosomal protein L13a

Chain N2: 89% 9%



- Molecule 19: 60S ribosomal protein L17

Chain O2: 69% 14% 17%



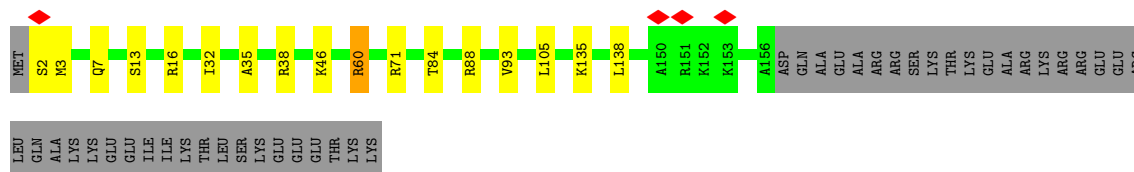
- Molecule 20: Ribosomal protein L18

Chain P2: 87% 13%



- Molecule 21: 60S ribosomal protein L19

Chain Q2: 70% 8% 21%



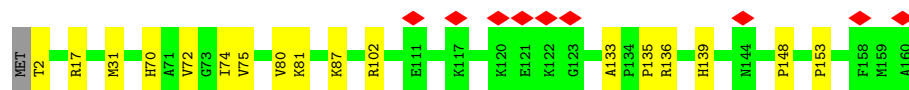
- Molecule 22: 60S ribosomal protein L18a

Chain R2: 85% 15%

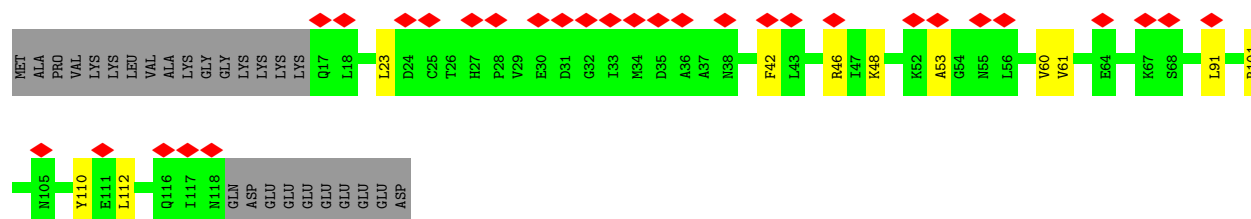
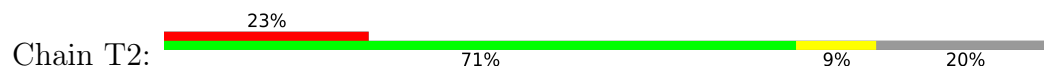


- Molecule 23: 60S ribosomal protein L21

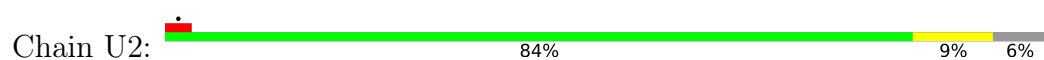
Chain S2: 6% 89% 11%



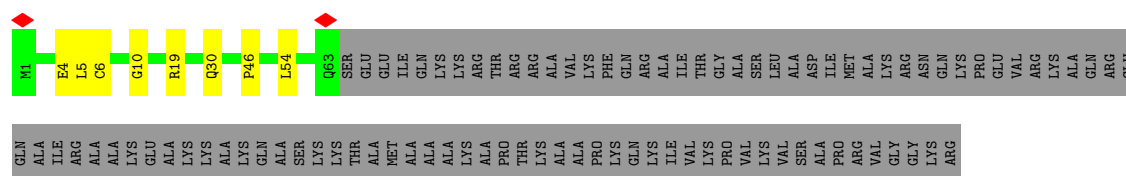
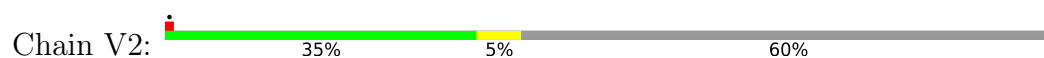
- Molecule 24: 60S ribosomal protein L22



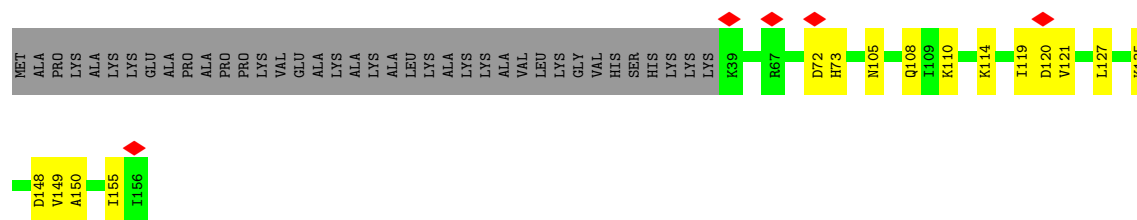
- Molecule 25: 60S ribosomal protein L23



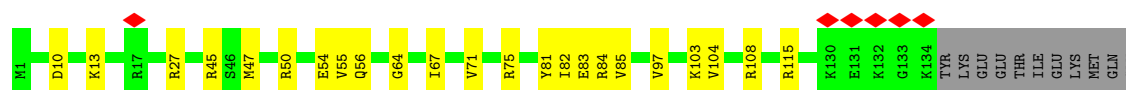
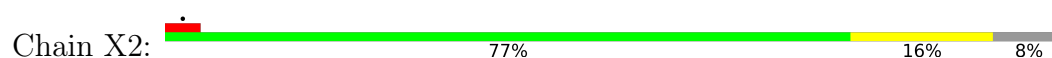
- Molecule 26: Ribosomal protein L24



- Molecule 27: Ribosomal_L23eN domain-containing protein



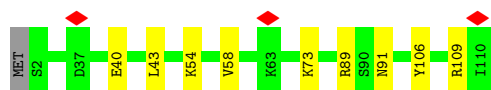
- Molecule 28: Ribosomal protein L26



-

- Molecule 35: 60S ribosomal protein L35a

Chain e2:  91% 8%



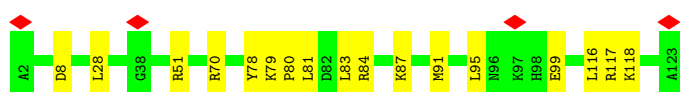
- Molecule 36: 60S ribosomal protein L34

Chain f2:  7% 91% 8%

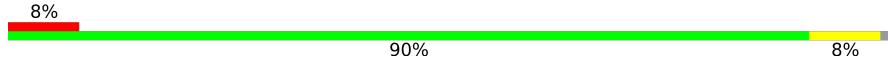


- Molecule 37: 60S ribosomal protein L35

Chain g2:  86% 14%



- Molecule 38: 60S ribosomal protein L36

Chain h2:  8% 90% 8%



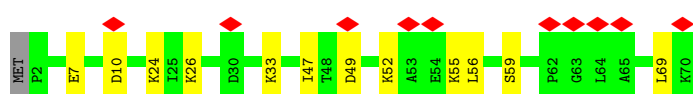
- Molecule 39: Ribosomal protein L37

Chain i2:  79% 9% 11%



- Molecule 40: 60S ribosomal protein L38

Chain j2:  14% 81% 17%

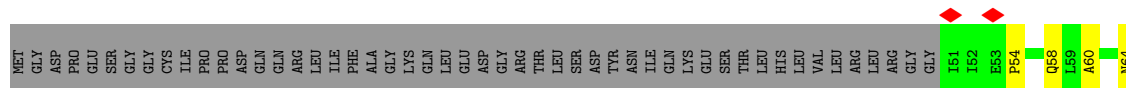


- Molecule 41: 60S ribosomal protein L39-like

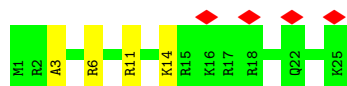
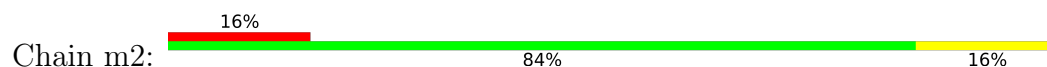
Chain k2:  6% 82% 16%



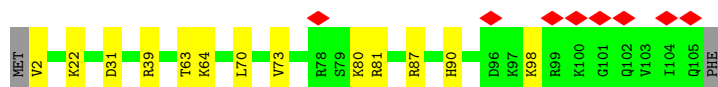
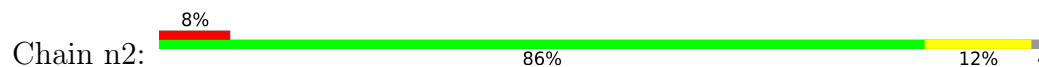
- Molecule 42: Ubiquitin-60S ribosomal protein L40



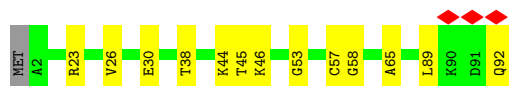
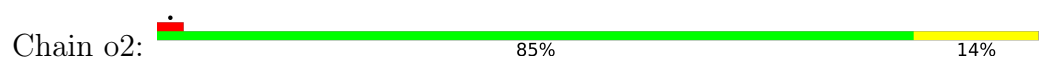
- Molecule 43: 60S ribosomal protein L41



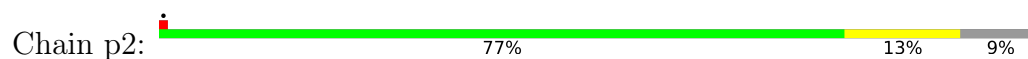
- Molecule 44: 60S ribosomal protein L36a-like



- Molecule 45: 60S ribosomal protein L37a

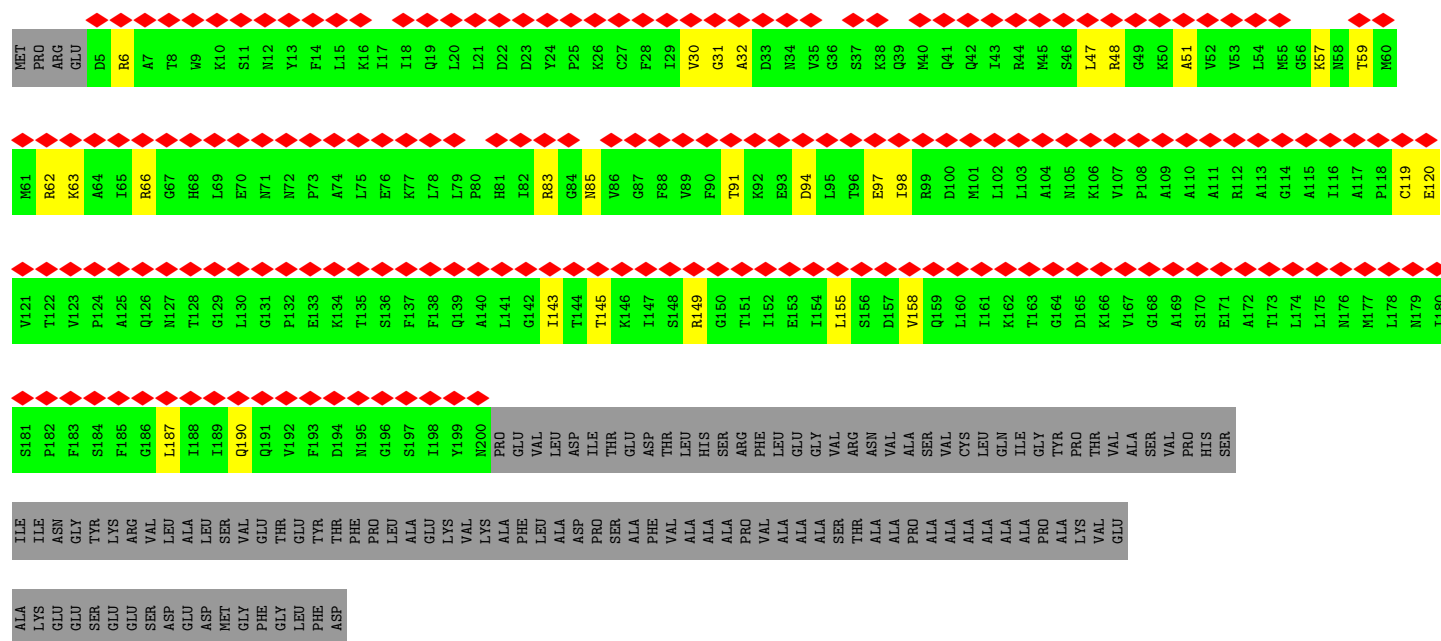


- Molecule 46: 60S ribosomal protein L28

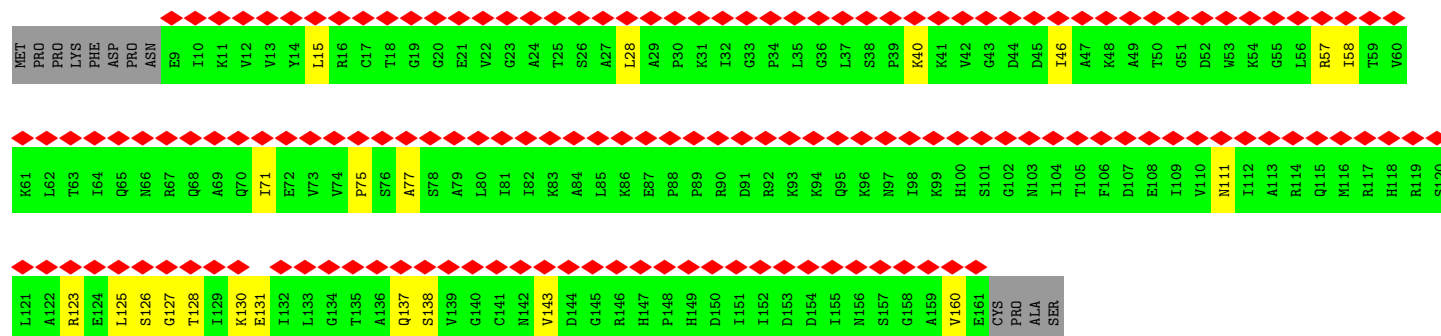
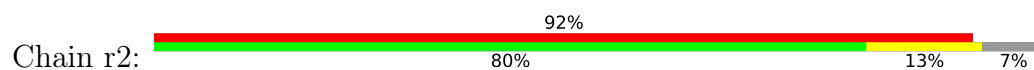


- Molecule 47: 60S acidic ribosomal protein P0

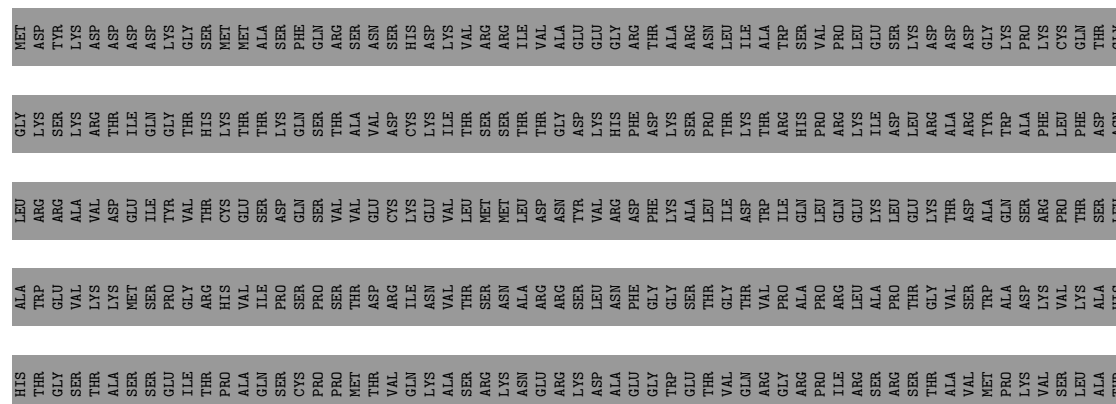




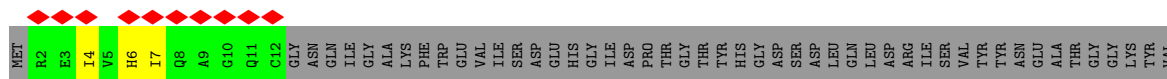
• Molecule 48: 60S ribosomal protein L12



• Molecule 49: S phase cyclin A-associated protein in the endoplasmic reticulum







MET
LYS
LEU
VAL

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18949	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 ($e^-/\text{\AA}^2$)	44.7	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	431.08, 431.08, 431.08	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	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, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A1	0.17	0/84976	0.37	5/132520 (0.0%)
2	B1	0.15	0/2858	0.30	0/4455
3	C1	0.16	0/3581	0.33	0/5577
4	D1	0.30	0/14	0.73	0/16
5	A2	0.23	0/1936	0.53	0/2596
6	B2	0.20	0/3240	0.52	0/4339
7	C2	0.21	0/2937	0.56	0/3946
8	D2	0.22	0/2437	0.53	0/3264
9	E2	0.22	0/1762	0.55	0/2362
10	F2	0.24	0/1911	0.58	0/2549
11	G2	0.21	0/1910	0.54	0/2569
12	H2	0.23	0/1535	0.63	0/2063
13	I2	0.18	0/1702	0.47	0/2272
14	J2	0.24	0/1385	0.66	2/1852 (0.1%)
15	K2	0.23	0/1733	0.55	0/2316
16	L2	0.21	0/1158	0.57	2/1547 (0.1%)
17	M2	0.23	0/1746	0.60	1/2338 (0.0%)
18	N2	0.24	0/1662	0.59	0/2222
19	O2	0.25	0/1268	0.60	0/1700
20	P2	0.22	0/1538	0.55	0/2054
21	Q2	0.31	1/1310 (0.1%)	0.68	2/1734 (0.1%)
22	R2	0.21	0/1501	0.58	0/2012
23	S2	0.21	0/1326	0.53	0/1770
24	T2	0.31	0/848	0.73	0/1138
25	U2	0.21	0/993	0.55	0/1332
26	V2	0.24	0/541	0.59	0/720
27	W2	0.20	0/984	0.54	0/1323
28	X2	0.21	0/1132	0.57	0/1504
29	Y2	0.23	0/1130	0.61	1/1507 (0.1%)
30	Z2	0.20	0/1191	0.54	0/1590
31	a2	0.19	0/861	0.50	0/1138
32	b2	0.25	0/771	0.59	0/1034

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c2	0.22	0/903	0.57	0/1216
34	d2	0.19	0/1071	0.58	0/1429
35	e2	0.20	0/895	0.50	0/1198
36	f2	0.20	0/916	0.51	0/1220
37	g2	0.22	0/1021	0.58	0/1348
38	h2	0.24	0/841	0.60	1/1112 (0.1%)
39	i2	0.18	0/720	0.55	0/952
40	j2	0.26	0/575	0.61	0/761
41	k2	0.20	0/459	0.53	0/608
42	l2	0.21	0/435	0.50	0/575
43	m2	0.24	0/240	0.60	0/305
44	n2	0.17	0/864	0.48	0/1140
45	o2	0.20	0/718	0.61	0/953
46	p2	0.22	0/1010	0.64	2/1354 (0.1%)
47	q2	0.23	0/1530	0.60	0/2064
48	r2	0.27	0/1174	0.68	0/1582
49	s2	0.34	0/3090	0.77	0/4169
50	t2	0.24	0/3323	0.60	0/4494
51	u2	0.26	0/82	0.60	0/109
All	All	0.20	1/153744 (0.0%)	0.46	16/225948 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	K2	0	1
17	M2	0	2
23	S2	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Q2	60	ARG	CA-C	6.35	1.60	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	J2	22	LEU	CA-C-N	-5.83	112.77	122.21
14	J2	22	LEU	C-N-CA	-5.83	112.77	122.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	245	C	C2'-C3'-O3'	5.62	117.94	109.50
46	p2	32	LEU	CA-C-N	5.54	132.13	121.54
46	p2	32	LEU	C-N-CA	5.54	132.13	121.54

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	K2	63	THR	Peptide
17	M2	76	PRO	Peptide
17	M2	78	GLY	Peptide
23	S2	80	VAL	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	A1	75972	0	38389	425	0
2	B1	2558	0	1296	13	0
3	C1	3208	0	1629	14	0
4	D1	150	0	51	0	0
5	A2	1898	0	1993	32	0
6	B2	3172	0	3310	30	0
7	C2	2883	0	3053	31	0
8	D2	2391	0	2424	21	0
9	E2	1729	0	1887	24	0
10	F2	1875	0	1995	15	0
11	G2	1879	0	2027	14	0
12	H2	1516	0	1597	20	0
13	I2	1664	0	1712	14	0
14	J2	1362	0	1399	14	0
15	K2	1702	0	1820	21	0
16	L2	1137	0	1211	12	0
17	M2	1701	0	1749	24	0
18	N2	1630	0	1778	13	0
19	O2	1242	0	1274	16	0
20	P2	1514	0	1634	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Q2	1294	0	1434	12	0
22	R2	1462	0	1508	18	0
23	S2	1298	0	1366	13	0
24	T2	834	0	858	8	0
25	U2	979	0	1039	8	0
26	V2	528	0	541	5	0
27	W2	967	0	1040	8	0
28	X2	1115	0	1205	16	0
29	Y2	1107	0	1182	15	0
30	Z2	1162	0	1209	13	0
31	a2	848	0	920	7	0
32	b2	761	0	794	9	0
33	c2	888	0	930	6	0
34	d2	1053	0	1147	13	0
35	e2	876	0	912	8	0
36	f2	906	0	998	7	0
37	g2	1013	0	1147	13	0
38	h2	830	0	916	5	0
39	i2	705	0	736	8	0
40	j2	569	0	637	8	0
41	k2	447	0	480	8	0
42	l2	429	0	465	8	0
43	m2	239	0	289	2	0
44	n2	851	0	920	9	0
45	o2	708	0	757	9	0
46	p2	994	0	1051	13	0
47	q2	1507	0	1564	16	0
48	r2	1160	0	1218	16	0
49	s2	3050	0	3128	36	0
50	t2	3262	0	3261	38	0
51	u2	82	0	81	2	0
52	A1	194	0	0	0	0
52	B1	7	0	0	0	0
52	B2	1	0	0	0	0
52	C1	6	0	0	0	0
52	I2	1	0	0	0	0
52	O2	2	0	0	0	0
52	U2	1	0	0	0	0
52	Z2	1	0	0	0	0
52	f2	1	0	0	0	0
53	f2	1	0	0	0	0
53	i2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	l2	1	0	0	0	0
53	n2	1	0	0	0	0
53	o2	1	0	0	0	0
All	All	143326	0	105961	898	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 898 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)
49:s2:1104:SER:O	49:s2:1108:ASN:HB2	1.84	0.77
1:A1:2486:G:H1	1:A1:2492:C:H42	1.33	0.76
1:A1:1628:C:H42	5:A2:3:ARG:HD3	1.50	0.76
1:A1:3692:A:H62	1:A1:3823:G:H21	1.34	0.74
17:M2:165:THR:O	17:M2:169:ARG:HB2	1.87	0.73

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D1	2/29 (7%)	1 (50%)	1 (50%)	0	100	100
5	A2	246/257 (96%)	234 (95%)	12 (5%)	0	100	100
6	B2	392/403 (97%)	384 (98%)	8 (2%)	0	100	100
7	C2	360/425 (85%)	343 (95%)	17 (5%)	0	100	100
8	D2	291/297 (98%)	283 (97%)	8 (3%)	0	100	100
9	E2	208/291 (72%)	201 (97%)	7 (3%)	0	100	100
10	F2	223/247 (90%)	215 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	G2	229/319 (72%)	223 (97%)	6 (3%)	0	100	100
12	H2	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
13	I2	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
14	J2	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
15	K2	208/211 (99%)	197 (95%)	10 (5%)	1 (0%)	24	55
16	L2	136/218 (62%)	131 (96%)	5 (4%)	0	100	100
17	M2	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
18	N2	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
19	O2	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
20	P2	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
21	Q2	153/196 (78%)	148 (97%)	5 (3%)	0	100	100
22	R2	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
23	S2	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
24	T2	100/128 (78%)	96 (96%)	4 (4%)	0	100	100
25	U2	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
26	V2	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
27	W2	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
28	X2	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
29	Y2	133/136 (98%)	125 (94%)	7 (5%)	1 (1%)	16	44
30	Z2	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
31	a2	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
32	b2	96/115 (84%)	96 (100%)	0	0	100	100
33	c2	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
34	d2	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
35	e2	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
36	f2	112/116 (97%)	110 (98%)	2 (2%)	0	100	100
37	g2	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
38	h2	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
39	i2	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
40	j2	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
41	k2	48/51 (94%)	45 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	l2	50/102 (49%)	49 (98%)	1 (2%)	0	100	100
43	m2	23/25 (92%)	23 (100%)	0	0	100	100
44	n2	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
45	o2	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
46	p2	122/137 (89%)	117 (96%)	5 (4%)	0	100	100
47	q2	194/318 (61%)	185 (95%)	9 (5%)	0	100	100
48	r2	151/165 (92%)	133 (88%)	18 (12%)	0	100	100
49	s2	377/1411 (27%)	368 (98%)	9 (2%)	0	100	100
50	t2	414/489 (85%)	402 (97%)	12 (3%)	0	100	100
51	u2	9/64 (14%)	9 (100%)	0	0	100	100
All	All	7482/9782 (76%)	7227 (97%)	253 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	K2	64	VAL
29	Y2	90	PRO

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	
4	D1	2/2 (100%)	2 (100%)	0	100	100
5	A2	190/199 (96%)	190 (100%)	0	100	100
6	B2	342/348 (98%)	342 (100%)	0	100	100
7	C2	302/347 (87%)	302 (100%)	0	100	100
8	D2	247/250 (99%)	247 (100%)	0	100	100
9	E2	190/251 (76%)	190 (100%)	0	100	100
10	F2	196/215 (91%)	196 (100%)	0	100	100
11	G2	200/272 (74%)	199 (100%)	1 (0%)	81	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	H2	169/171 (99%)	169 (100%)	0	100	100
13	I2	175/181 (97%)	175 (100%)	0	100	100
14	J2	143/149 (96%)	143 (100%)	0	100	100
15	K2	175/176 (99%)	175 (100%)	0	100	100
16	L2	117/161 (73%)	117 (100%)	0	100	100
17	M2	171/172 (99%)	171 (100%)	0	100	100
18	N2	171/173 (99%)	171 (100%)	0	100	100
19	O2	134/163 (82%)	134 (100%)	0	100	100
20	P2	164/164 (100%)	164 (100%)	0	100	100
21	Q2	138/175 (79%)	138 (100%)	0	100	100
22	R2	157/157 (100%)	157 (100%)	0	100	100
23	S2	139/140 (99%)	139 (100%)	0	100	100
24	T2	92/114 (81%)	92 (100%)	0	100	100
25	U2	101/107 (94%)	101 (100%)	0	100	100
26	V2	55/126 (44%)	55 (100%)	0	100	100
27	W2	106/134 (79%)	106 (100%)	0	100	100
28	X2	124/135 (92%)	124 (100%)	0	100	100
29	Y2	117/118 (99%)	117 (100%)	0	100	100
30	Z2	119/120 (99%)	119 (100%)	0	100	100
31	a2	84/172 (49%)	84 (100%)	0	100	100
32	b2	84/98 (86%)	84 (100%)	0	100	100
33	c2	98/110 (89%)	98 (100%)	0	100	100
34	d2	114/121 (94%)	114 (100%)	0	100	100
35	e2	88/89 (99%)	88 (100%)	0	100	100
36	f2	98/99 (99%)	98 (100%)	0	100	100
37	g2	109/109 (100%)	109 (100%)	0	100	100
38	h2	86/89 (97%)	86 (100%)	0	100	100
39	i2	73/80 (91%)	73 (100%)	0	100	100
40	j2	64/65 (98%)	64 (100%)	0	100	100
41	k2	47/48 (98%)	47 (100%)	0	100	100
42	l2	48/90 (53%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	m2	24/24 (100%)	24 (100%)	0	100	100
44	n2	92/94 (98%)	92 (100%)	0	100	100
45	o2	74/75 (99%)	74 (100%)	0	100	100
46	p2	108/121 (89%)	108 (100%)	0	100	100
47	q2	164/258 (64%)	164 (100%)	0	100	100
48	r2	126/137 (92%)	126 (100%)	0	100	100
49	s2	342/1239 (28%)	342 (100%)	0	100	100
50	t2	360/416 (86%)	359 (100%)	1 (0%)	86	95
51	u2	8/53 (15%)	8 (100%)	0	100	100
All	All	6527/8307 (79%)	6525 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	G2	143	GLN
50	t2	266	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
49	s2	1100	GLN
49	s2	1330	GLN
19	O2	28	ASN
18	N2	199	HIS
49	s2	1331	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A1	3519/4380 (80%)	724 (20%)	45 (1%)
2	B1	119/120 (99%)	11 (9%)	0
3	C1	149/156 (95%)	28 (18%)	1 (0%)
All	All	3787/4656 (81%)	763 (20%)	46 (1%)

5 of 763 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A1	12	A
1	A1	13	U
1	A1	17	A
1	A1	25	A
1	A1	30	C

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A1	2089	G
1	A1	3876	A
1	A1	2266	C
1	A1	2695	A
1	A1	4119	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 219 ligands modelled in this entry, 219 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A1	19

The worst 5 of 19 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1252:C	O3'	1271:G	P	37.11
1	A1	1219:G	O3'	1233:G	P	19.96
1	A1	990:C	O3'	1064:G	P	18.26
1	A1	523:C	O3'	638:G	P	16.85
1	A1	1406(C):G	O3'	1411:C	P	16.23

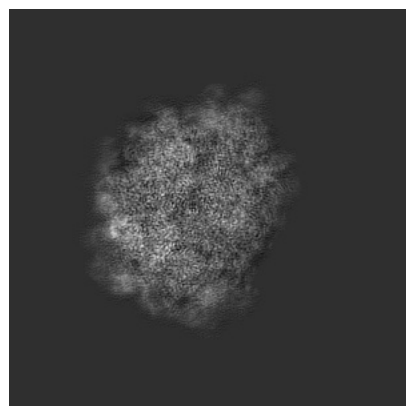
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16155. These allow visual inspection of the internal detail of the map and identification of artifacts.

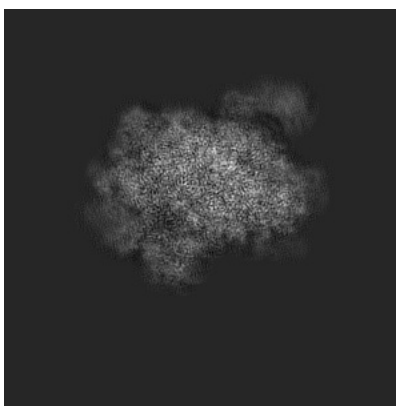
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

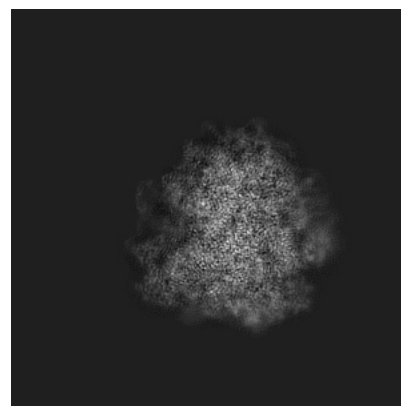
6.1.1 Primary map



X

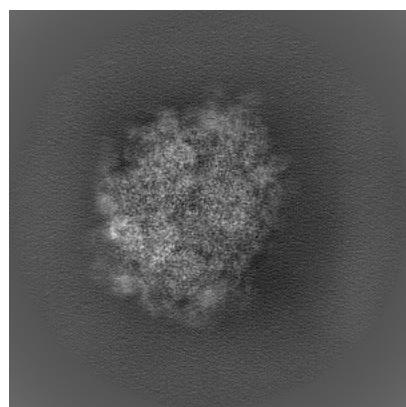


Y

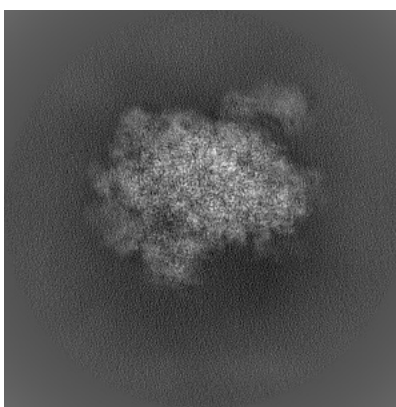


Z

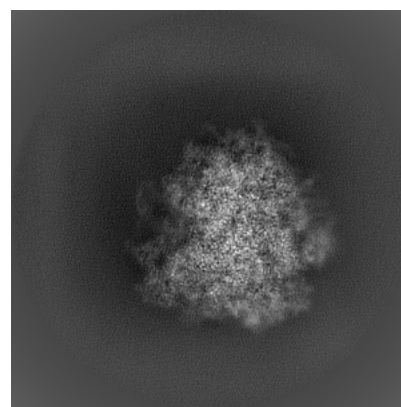
6.1.2 Raw map



X



Y

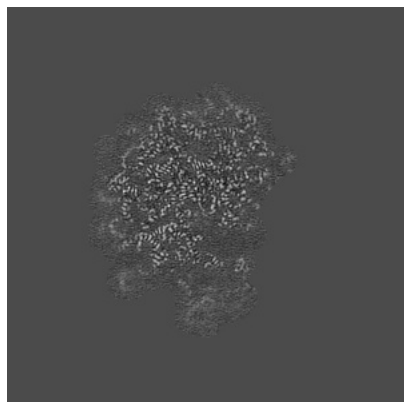


Z

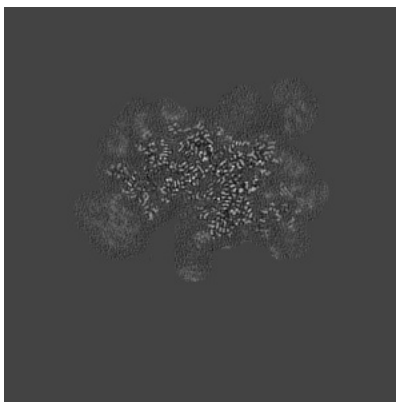
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

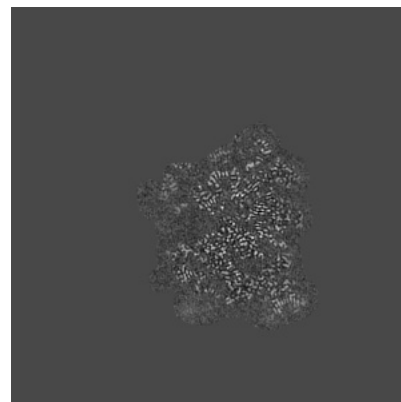
6.2.1 Primary map



X Index: 260

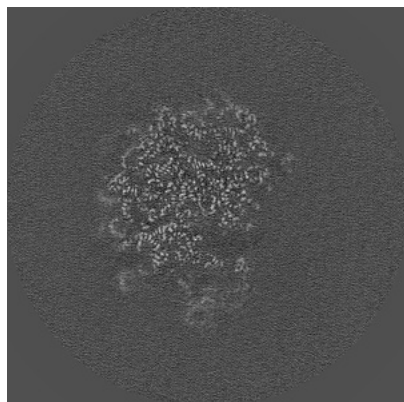


Y Index: 260

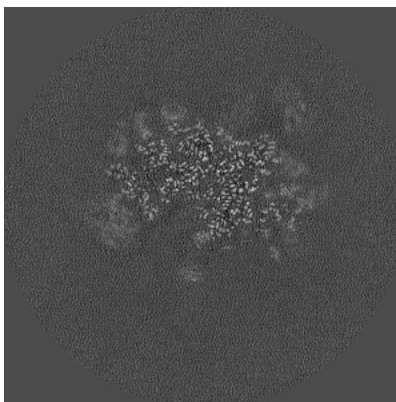


Z Index: 260

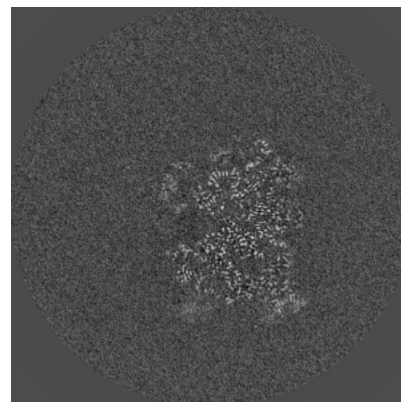
6.2.2 Raw map



X Index: 260



Y Index: 260

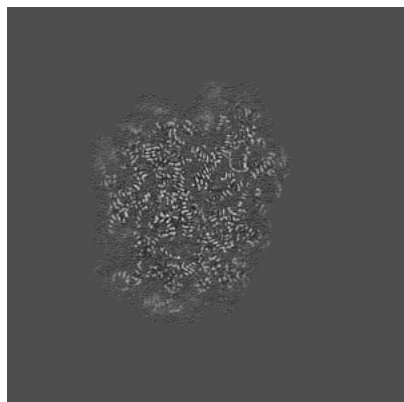


Z Index: 260

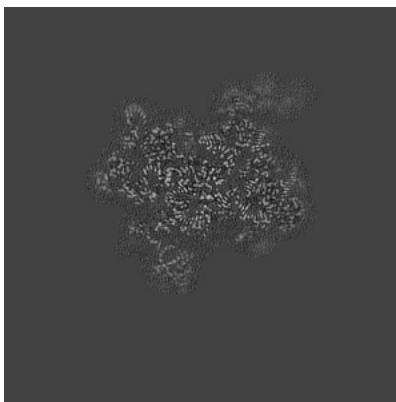
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

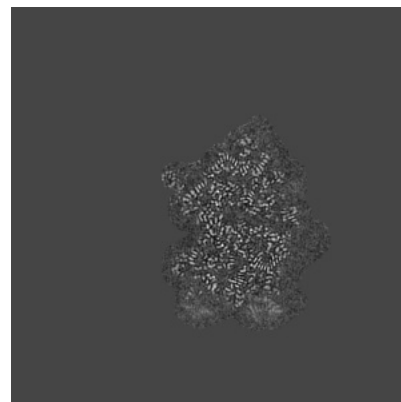
6.3.1 Primary map



X Index: 282

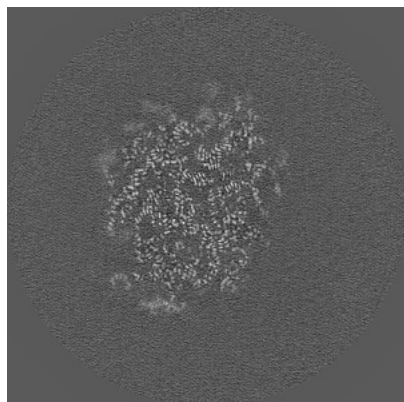


Y Index: 210

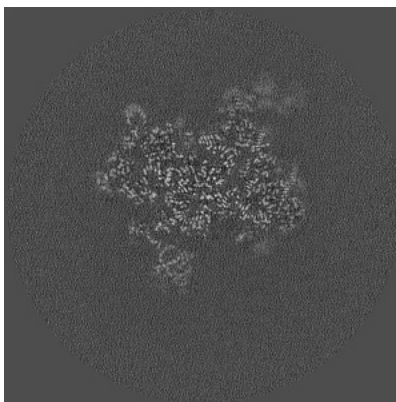


Z Index: 275

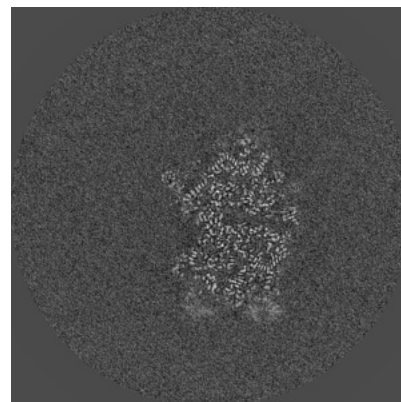
6.3.2 Raw map



X Index: 285



Y Index: 210

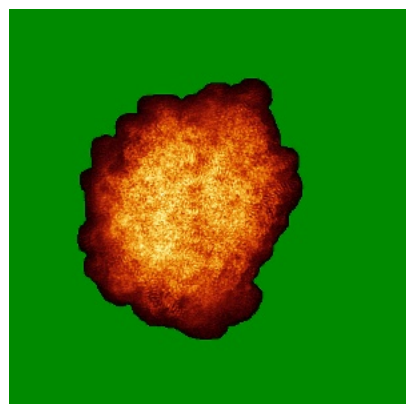


Z Index: 275

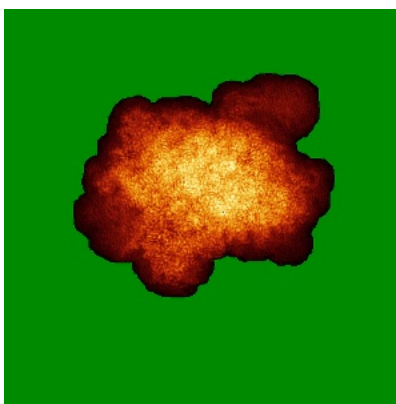
The images above show the largest variance slices of the map in three orthogonal directions.

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

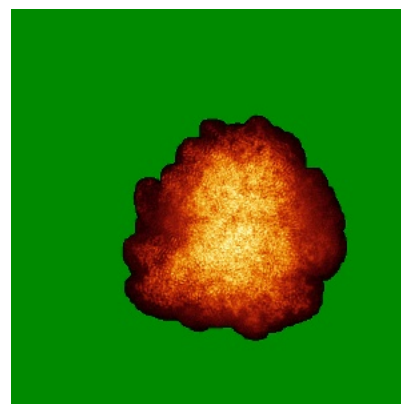
6.4.1 Primary map



X

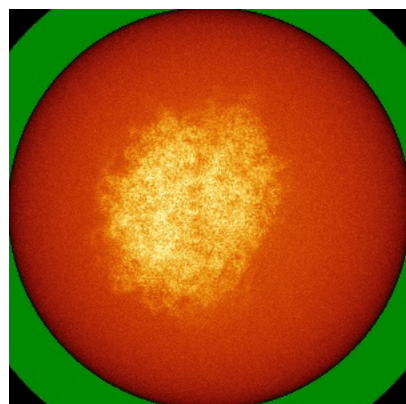


Y

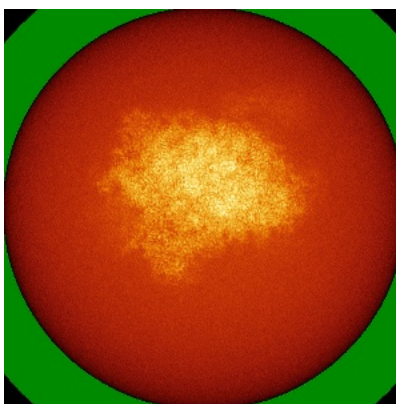


Z

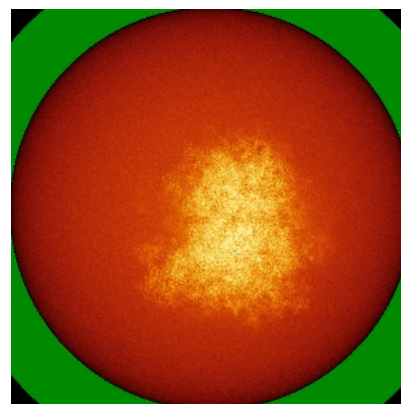
6.4.2 Raw map



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



X



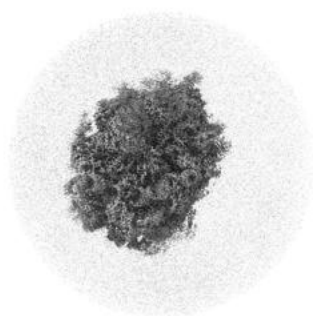
Y



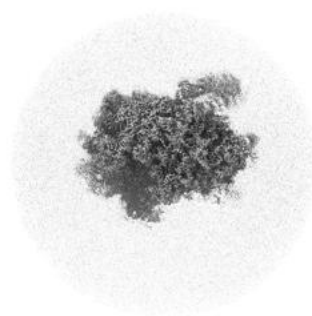
Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

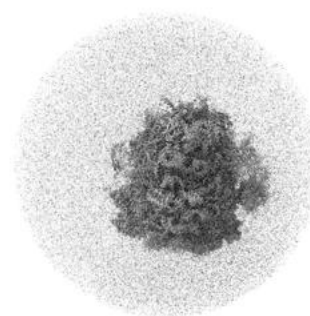
6.5.2 Raw map



X



Y



Z

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

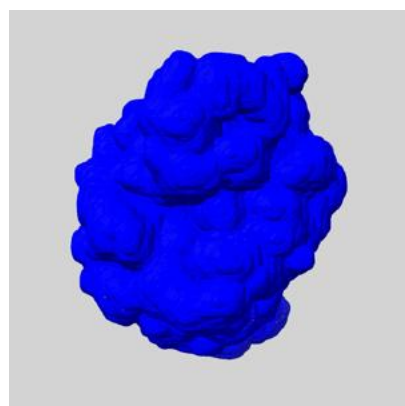
6.6 Mask visualisation [i](#)

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

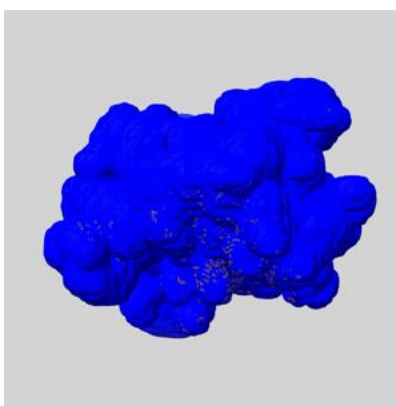
A mask typically either:

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

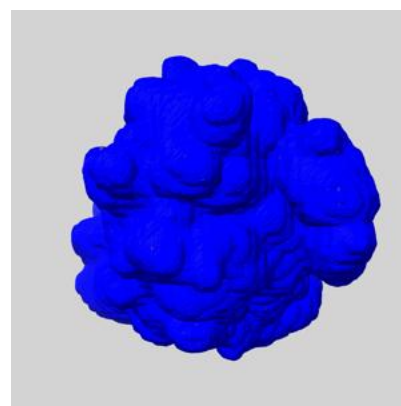
6.6.1 emd_16155_msk_1.map [i](#)



X



Y

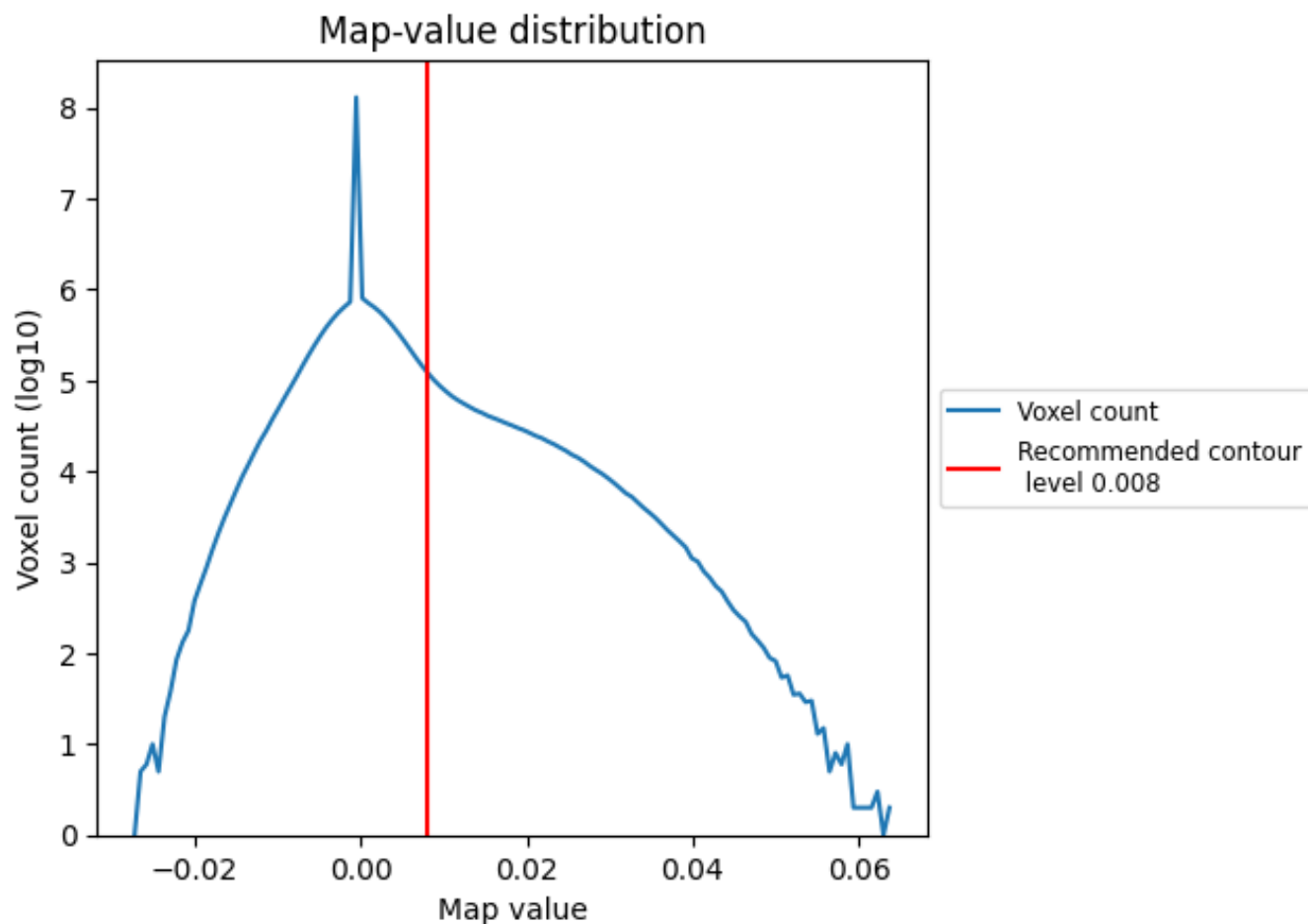


Z

7 Map analysis [i](#)

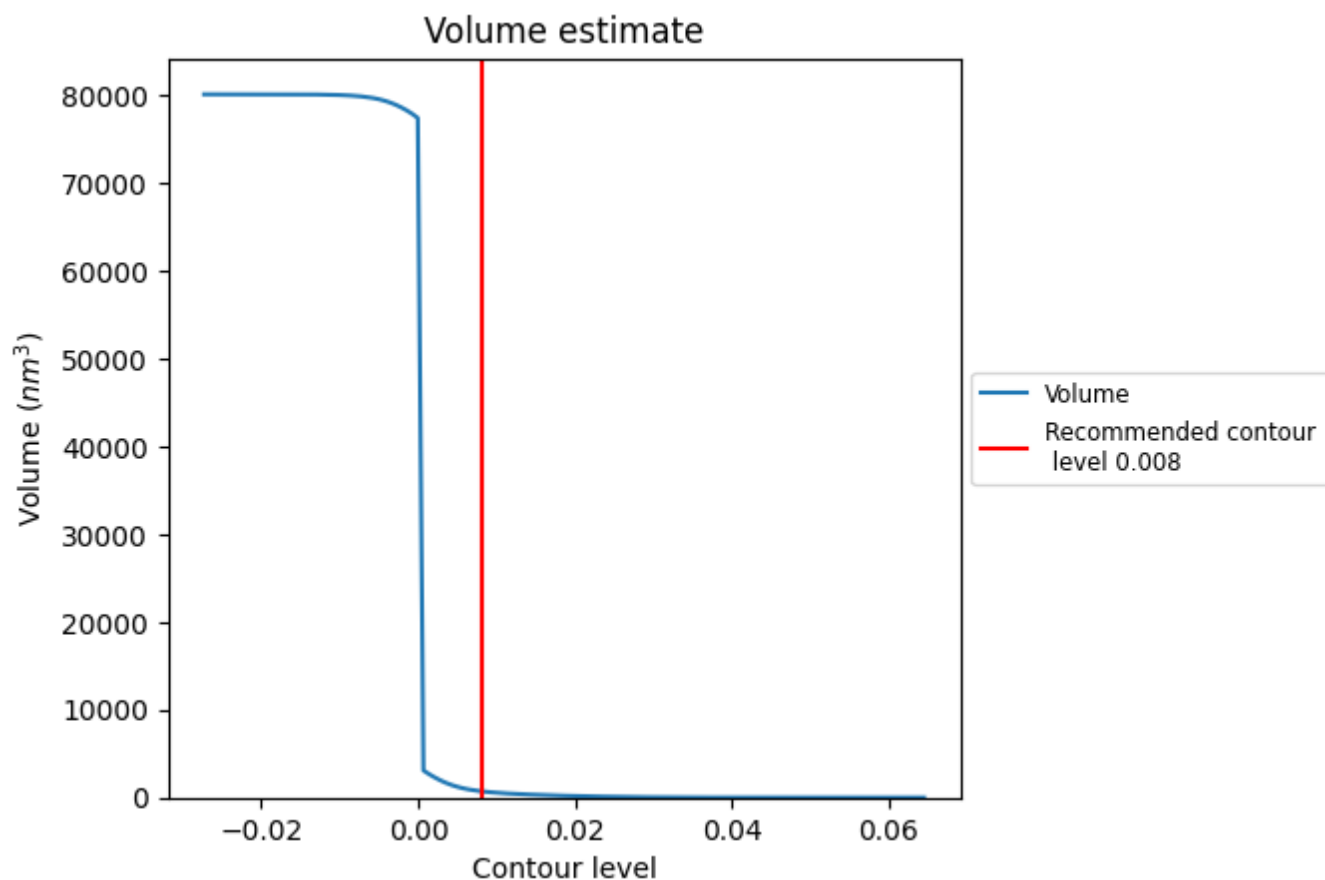
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

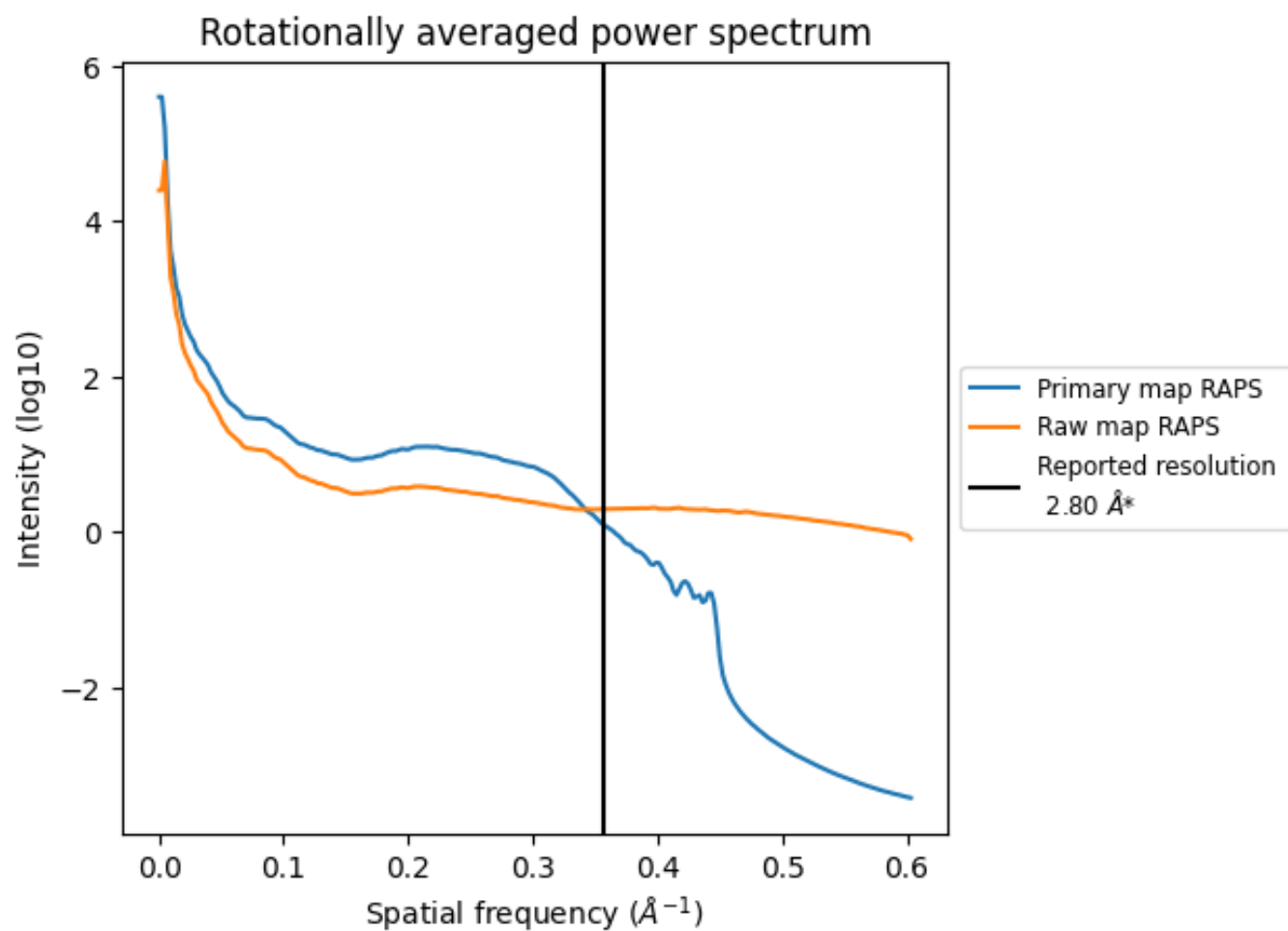
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 717 nm³; this corresponds to an approximate mass of 648 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 ⓘ

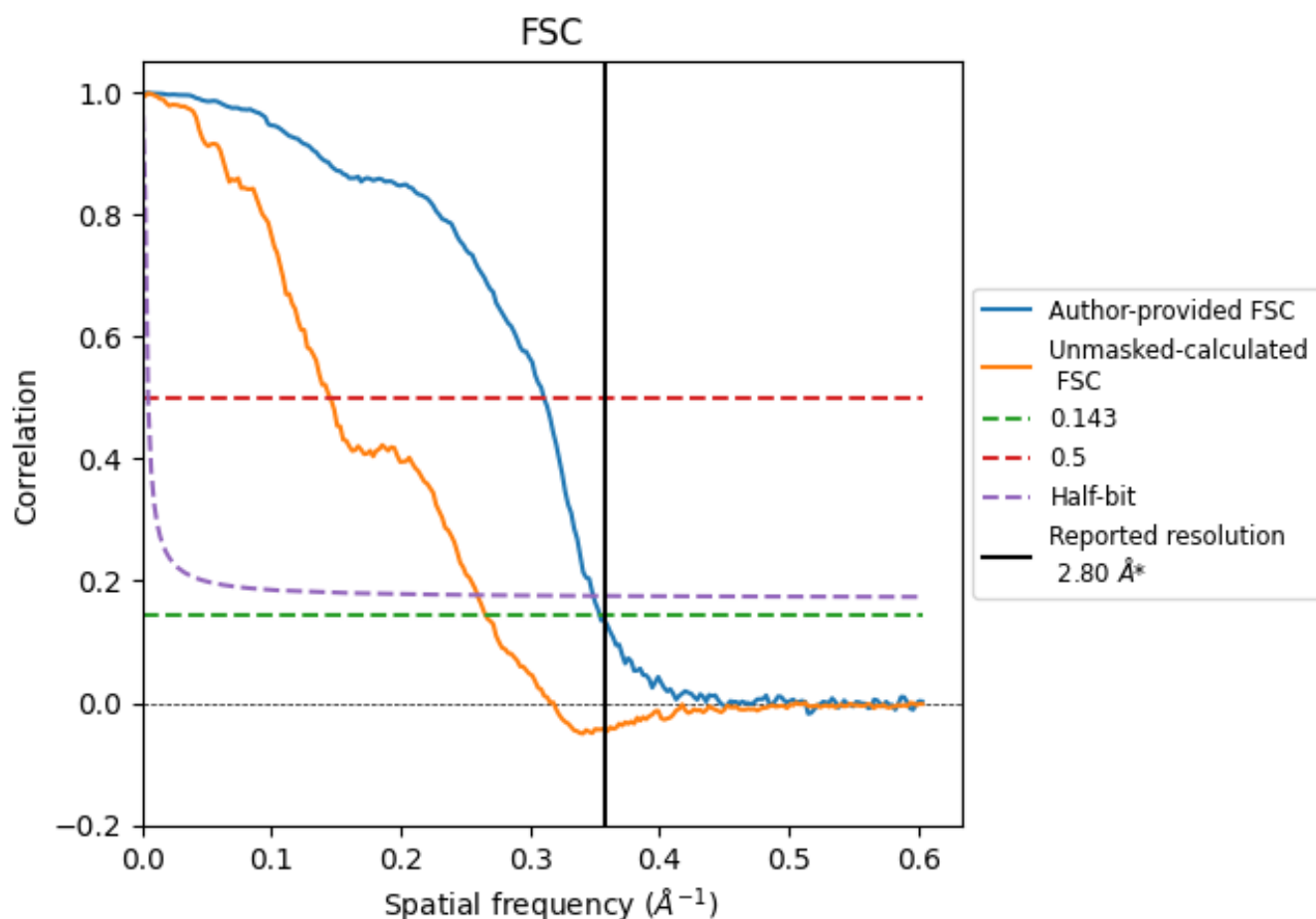


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 $0.357 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

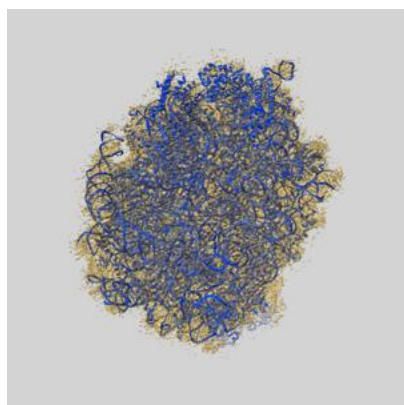
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.83	3.22	2.87
Unmasked-calculated*	3.76	6.87	3.86

*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 3.76 differs from the reported value 2.8 by more than 10 %

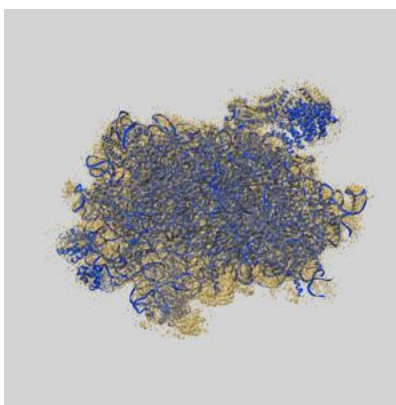
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16155 and PDB model 8BPO. Per-residue inclusion information can be found in section 3 on page 16.

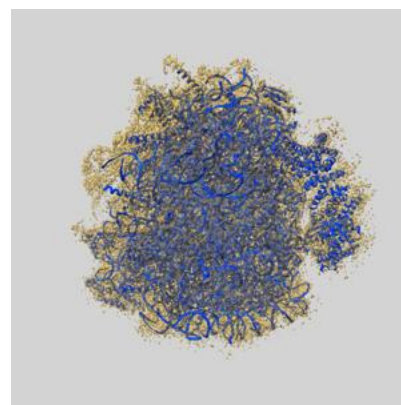
9.1 Map-model overlay [i](#)



X



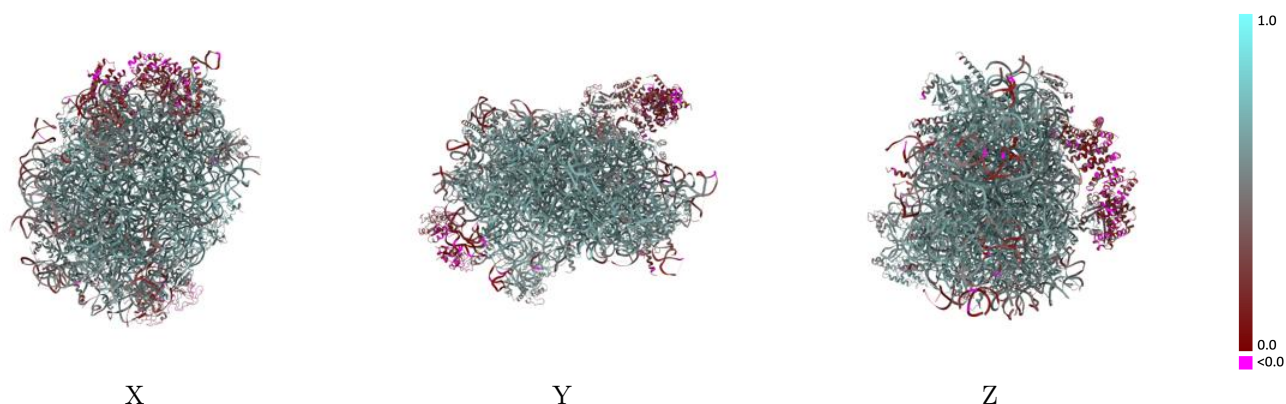
Y



Z

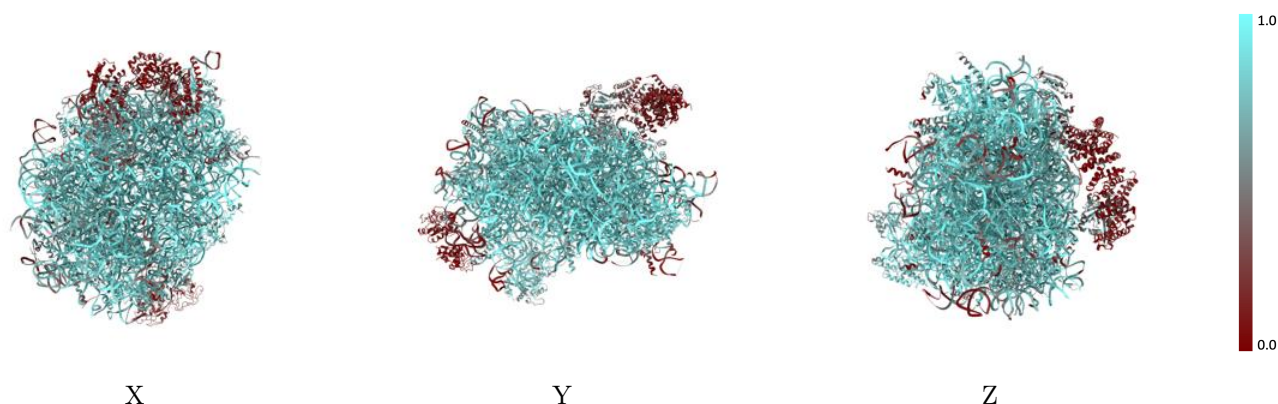
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



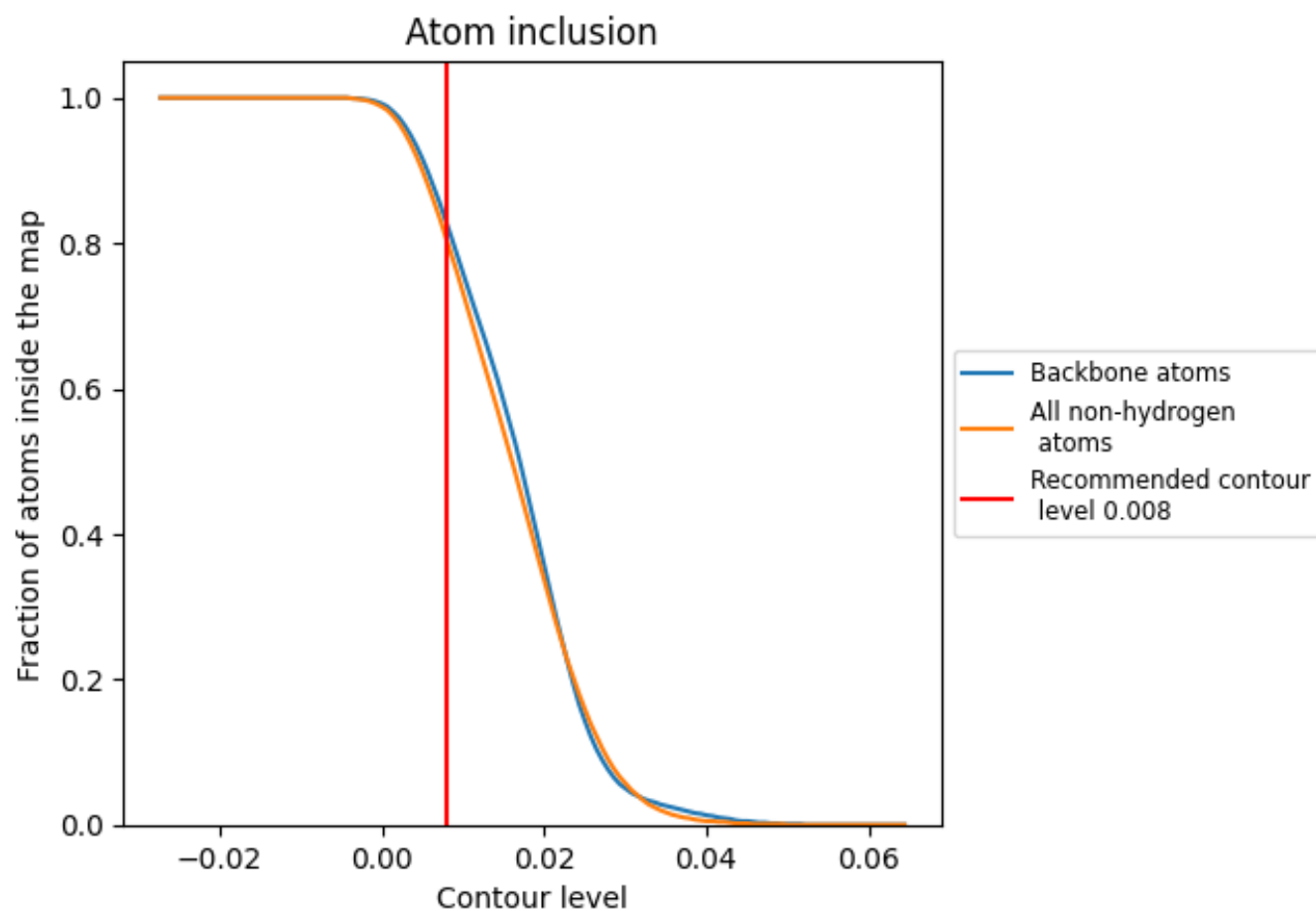
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8040	 0.5490
A1	 0.8560	 0.5610
A2	 0.8830	 0.6230
B1	 0.9580	 0.6180
B2	 0.8650	 0.6080
C1	 0.8970	 0.5890
C2	 0.8700	 0.6000
D1	 0.3130	 0.3710
D2	 0.8190	 0.5710
E2	 0.7860	 0.5580
F2	 0.8760	 0.6160
G2	 0.7120	 0.5270
H2	 0.7650	 0.5660
I2	 0.8470	 0.6040
J2	 0.6960	 0.5040
K2	 0.8050	 0.5680
L2	 0.8270	 0.5780
M2	 0.9070	 0.6300
N2	 0.8680	 0.6050
O2	 0.8660	 0.6140
P2	 0.8900	 0.6180
Q2	 0.8310	 0.5890
R2	 0.8740	 0.6070
S2	 0.8140	 0.5760
T2	 0.5580	 0.4390
U2	 0.8390	 0.6030
V2	 0.8070	 0.6030
W2	 0.7950	 0.5720
X2	 0.8150	 0.5800
Y2	 0.8100	 0.5680
Z2	 0.9110	 0.6270
a2	 0.6750	 0.5250
b2	 0.7660	 0.5320
c2	 0.8060	 0.5720
d2	 0.8850	 0.6240



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Chain	Atom inclusion	Q-score
e2	 0.8970	 0.6220
f2	 0.8260	 0.5860
g2	 0.7890	 0.5720
h2	 0.7650	 0.5490
i2	 0.9140	 0.6270
j2	 0.6500	 0.5190
k2	 0.8150	 0.5820
l2	 0.8150	 0.5860
m2	 0.6240	 0.4990
n2	 0.8150	 0.5990
o2	 0.8100	 0.5920
p2	 0.8740	 0.5970
q2	 0.1120	 0.1880
r2	 0.0370	 0.1160
s2	 0.1280	 0.1880
t2	 0.3250	 0.2750
u2	 0.2370	 0.2500