



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:45 PM UTC

PDB ID : 5H5U / pdb_00005h5u
EMDB ID : EMD-6667
Title : Mechanistic insights into the alternative translation termination by ArfA and RF2
Authors : Ma, C.; Kurita, D.; Li, N.; Chen, Y.; Himeno, H.; Gao, N.
Deposited on : 2016-11-09
Resolution : 3.01 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:

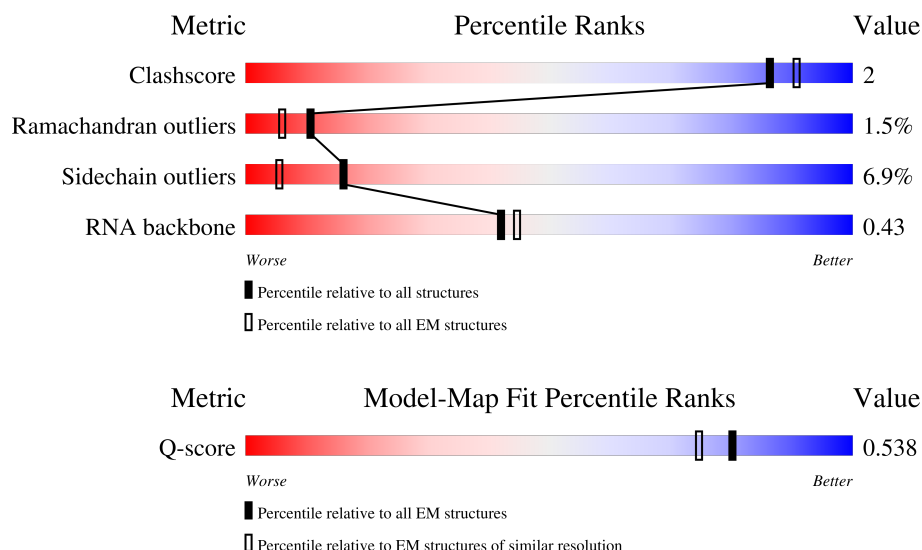
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

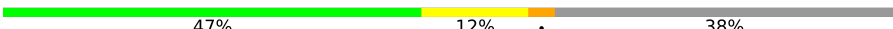
The reported resolution of this entry is 3.01 Å.

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	13882 (2.51 - 3.51)

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	1	86	 92% 7%
2	2	70	 69% 11% 20%
3	3	72	 47% 12% 38%

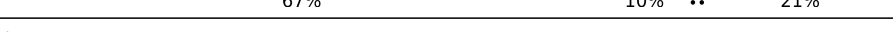
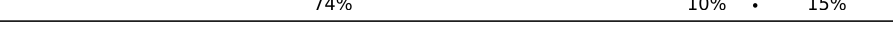
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Mol	Chain	Length	Quality of chain
4	4	365	
5	5	76	
6	7	6	
7	A	2903	
8	B	120	
9	C	272	
10	D	209	
11	E	201	
12	F	178	
13	G	176	
14	H	149	
15	I	164	
16	J	141	
17	K	142	
18	L	123	
19	M	144	
20	N	136	
21	O	127	
22	P	117	
23	Q	114	
24	R	117	
25	S	103	
26	T	110	
27	U	100	
28	V	103	

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Mol	Chain	Length	Quality of chain
29	W	94	
30	X	84	
31	Y	77	
32	Z	63	
33	a	58	
34	b	56	
35	c	54	
36	d	46	
37	e	64	
38	f	38	
39	h	1534	
40	i	240	
41	j	232	
42	k	205	
43	l	166	
44	m	135	
45	n	178	
46	o	129	
47	p	129	
48	q	103	
49	r	128	
50	s	123	
51	t	117	
52	u	100	
53	v	88	

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Mol	Chain	Length	Quality of chain
54	w	82	84% 15%
55	x	83	81% 12%
56	y	74	69% 5% 26%
57	z	91	74% 12%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148128 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 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 2 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	56	Total	C	N	O	S	0	0
			465	290	96	78	1		

- Molecule 3 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	45	Total	C	N	O	S	0	0
			369	229	76	63	1		

- Molecule 4 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	357	Total	C	N	O	S	0	0
			2829	1740	499	580	10		

- Molecule 5 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	76	Total	C	N	O	P	0	0
			1620	723	294	528	75		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	6	Total	C	N	O	P	0	0
			127	57	22	42	6		

- Molecule 7 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2897	Total	C	N	O	P	3	0
			62240	27765	11457	20119	2899		

- Molecule 8 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	148	Total	C	N	O	S	0	0
			1101	694	196	210	1		

- Molecule 15 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	135	Total	C	N	O	S	0	0
			1023	649	179	192	3		

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	71	Total	C	N	O	S	0	0
			509	313	93	100	3		

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	136	Total	C	N	O	S	1	0
			1082	691	208	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	117	Total	C	N	O		
			947	604	192	151	0	0

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	V	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	94	Total	C	N	O	S	
			753	479	137	134	3	0

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	X	76	Total	C	N	O	S	
			591	365	121	104	1	0

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Y	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Z	62	Total	C	N	O	S	
			501	308	98	94	1	0

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	a	58	Total	C	N	O	S	
			463	290	90	81	2	0

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	b	56	Total	C	N	O	S	
			444	269	94	80	1	0

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 36 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 37 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 39 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	1534	Total	C	N	O	P	0	0
			32917	14681	6041	10661	1534		

- Molecule 40 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 41 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 42 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 43 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	155	Total	C	N	O	S	0	0
			1144	711	216	211	6		

- Molecule 44 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 45 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 46 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 47 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 48 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	99	Total	C	N	O	S	0	0
			795	498	152	144	1		

- Molecule 49 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 50 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 51 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 52 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 53 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 54 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 55 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 56 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	y	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 57 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	z	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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: 30S ribosomal protein S20

Chain 1: 

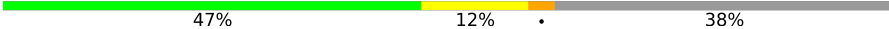


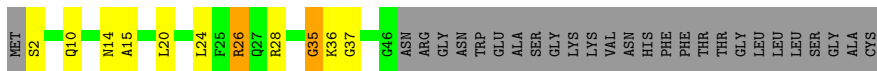
- Molecule 2: 30S ribosomal protein S21

Chain 2: 



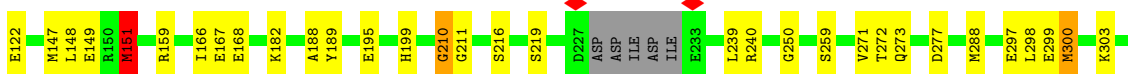
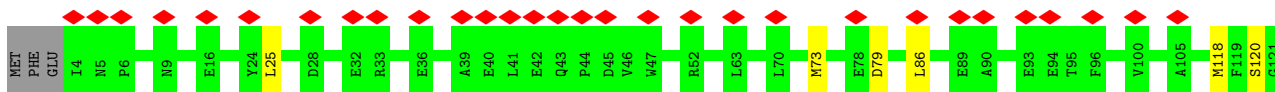
- Molecule 3: Alternative ribosome-rescue factor A

Chain 3: 



- Molecule 4: Peptide chain release factor 2

Chain 4: 



- Molecule 5: P-site tRNA

Chain 5:  70% 30%

C1 C9 A14 G15 G16 U17A G18 G19 U20 A21 G22 C25 G30 G31 G32 U33 A44 U47 C48 G53 G62 G63 G64 C69 A73 C74 C75 A76

• Molecule 6: mRNA

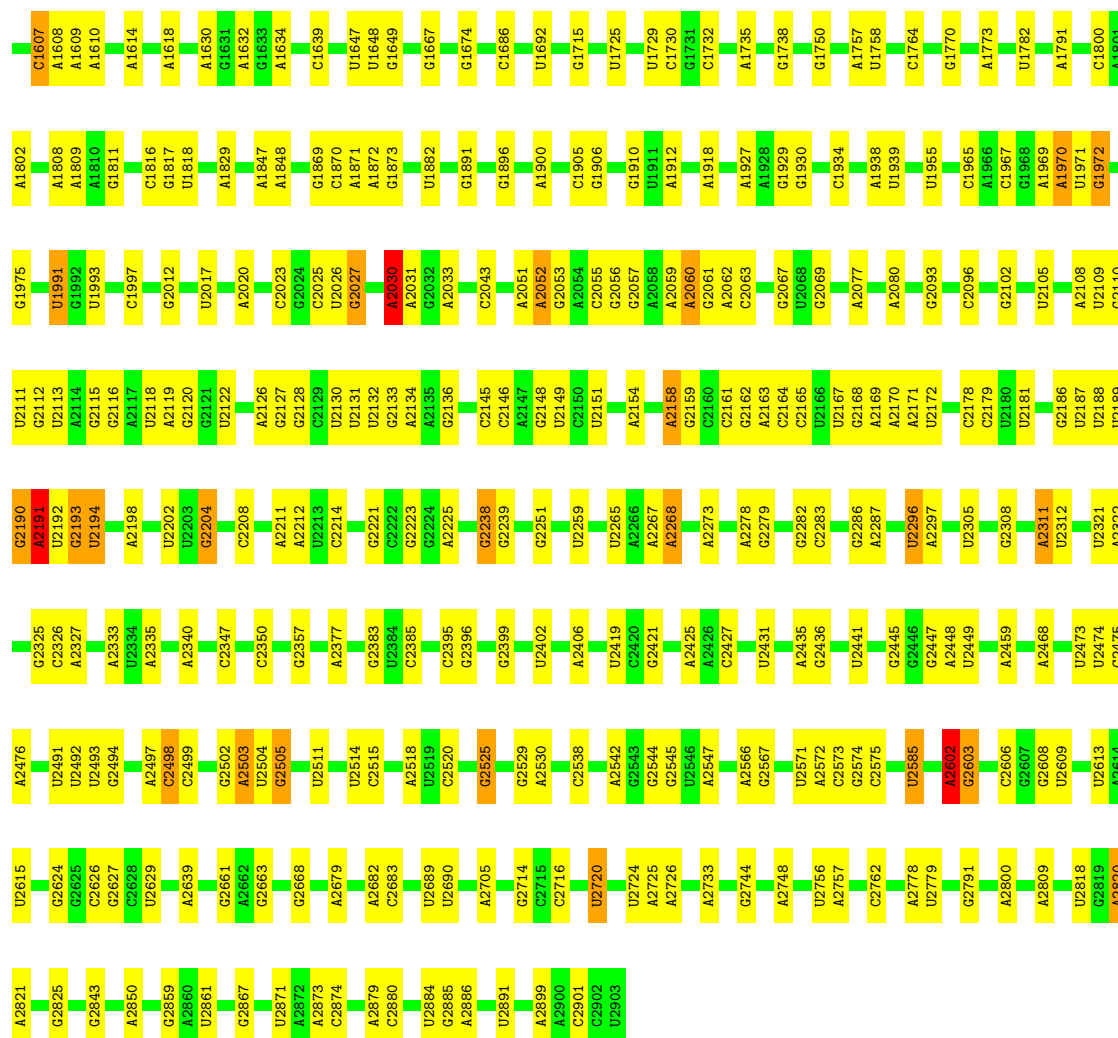
Chain 7:  50% 33% 17%

A13 C14 U15 A16 U17 G18

• Molecule 7: 23S rRNA

Chain A:  76% 22% .

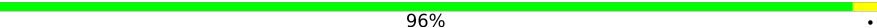
G1 U4 A10 C11 U12 G17 U18 U34 G35 G46 A49 G58 A63 C66 A71 A74 G75 A84 G88 A89 C96 C97 G98 A101 U102 A118 A119 U120 A125 A126 A131 A132 U133 G134 U137 U138 U139 C140 G141 A142 A160 C163 C164 A165 U166 A167 U171 A181 G186 A196 A197 C198 A199 U200 G201 U202 G215 A216 A221 A222 G248 C249 G283 C284 G285 G286 A272 U276 U280 C281 A282 G283 U284 U290 G301 C302 A310 A311 A322 C323 G329 A330 C331 A332 G333 A340 A348 U349 A362 G367 G370 A371 G372 G380 G381 G386 U387 U399 U403 G411 A412 A423 G424 A429 G446 U451 C455 C456 A479 A480 G481 G491 A492 G493 G494 U499 G500 A501 A502 A503 A504 A505 C508 C509 C510 C511 G512 A513 A529 G530 C531 A532 G533 A538 C544 G545 U546 A547 G548 G549 C550 G555 U556 G559 A563 C564 C565 U566 G570 U573 A574 A575 G585 A602 A603 A613 A614 U615 G620 A621 A627 A637 C645 U646 G647 U653 A654 A655 A670 U686 G700 A722 G726 A730 G738 U746 U747 G748 A761 A764 C765 G775 G776 A781 A782 G783 G784 G785 A789 U790 A791 A792 A804 G805 C806 U807 U811 C812 A819 U826 U827 U828 C835 A845 U846 C851 G858 C859 U860 A861 A866 G869 U870 U871 C876 A877 A878 G879 G880 C881 G882 C883 U884 C885 A A U C C C C A892 A896 C897 C898 A910 A911 G914 C915 G916 A917 U931 U932 U933 U934 C944 A945 C946 U955 C961 G962 U963 C964 G974 A981 C982 A983 A984 C985 A996 U999 G1002 C1005 A1009 U1012 C1013 U1017 A1071 U1072 U1073 U1078 C1079 U1082 U1083 A1084 G1087 A1088 A1089 A1090 G1091 A1098 A1111 G1112 U1119 G1128 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 G1138 U1141 A1142 C1153 C1172 U1173 U1174 A1175 U1176 A1189 G1206 U1209 G1210 A1214 U1239 G1238 U1240 A1253 G1256 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1274 A1275 A1286 A1287 G1288 C1289 A1301 G1310 U1313 A1321 A1327 G1328 U1329 C1330 G1331 C1345 G1346 A1347 U1352 C1357 G1358 A1365 G1371 A1378 U1379 G1380 A1383 A1394 A1395 G1401 G1416 G1417 G1418 A1419 G1424 G1425 G1426 A1427 C1428 A1431 A1435 G1449 G1450 G1451 G1452 A1453 G1454 G1455 U1460 A1469 A1470 G1478 G1482 G1488 C1489 A1490 G1491 G1492 G1493 A1494 A1495 A1496 U1497 C1498 A1502 A1503 A1504 C1507 G1510 A1515 U1523 G1524 G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1540 C1557 A1569 A1570 U1578 U1584 C1585 G1586 A1593



Chain D:  87% 11% .



- Molecule 11: 50S ribosomal protein L4

Chain E:  96% .



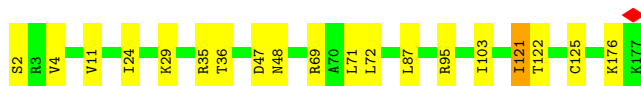
- Molecule 12: 50S ribosomal protein L5

Chain F:  87% 11% ..

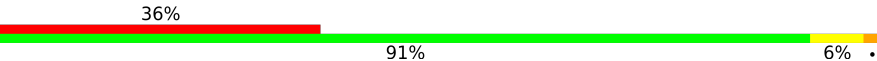


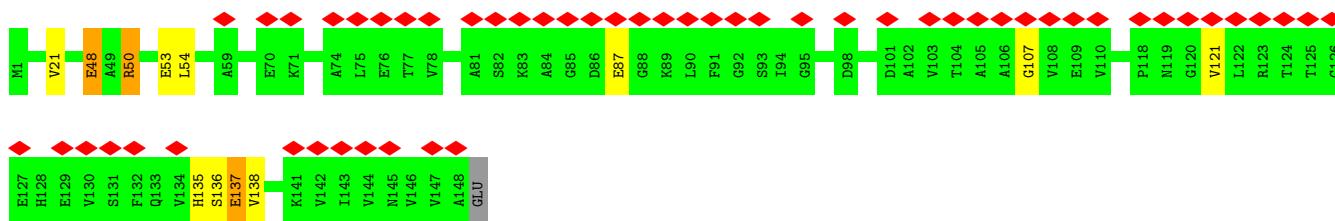
- Molecule 13: 50S ribosomal protein L6

Chain G:  89% 10% .



- Molecule 14: 50S ribosomal protein L9

Chain H:  36% 91% 6% ..



- Molecule 15: 50S ribosomal protein L10

Chain I:  55% 77% 18%



- Molecule 16: 50S ribosomal protein L11



ALA	LYS	LYS	VAL	GLN	ALA	TYR	VAL	LYS	GLN	VAL	ALA	ALA	GLY	MET	ALA	ASN	PRO	SER	PRO	PRO	PRO	VAL	GLY	GLY	PRO	ALA	LEU	GLN	GLN	GLN	GLY	VAL	VAL	ASN	PHE	GLU	CYS	LYS	ALA	ALA	PHE	ASN	ASN	THR	THR	SER	ILE	GLU	LYS	GLY	LEU	PRO	ILE	PRO	ILE	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

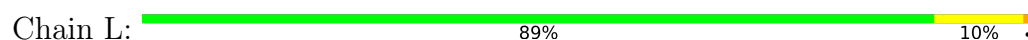
Figure 1 shows a schematic representation of the protein structure of the 120 kDa subunit of the 20S proteasome. The diagram displays a linear sequence of amino acids from TYR to ASP. Specific residues are highlighted in colored boxes: yellow for P75, A76, and M117; red for E123; and green for A77, V78, K81, K82, A83, A84, G85, I86, K87, S88, K100, A104, A120, D121, I122, A124, M125, V129, V140, and E141. Red diamonds above the sequence indicate the positions of the 120 kDa subunit in the 20S proteasome structure.

- Molecule 17: 50S ribosomal protein L13



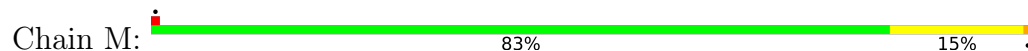
Genotype	Number of Samples
M1	1
K12	2
T24	2
K39	3
H40	3
E43	4
T50	2
I81	3
E90	2
I101	2
V124	3
I142	3

- Molecule 18: 50S ribosomal protein L14



Category	Count
M1	100
M7	100
L8	100
R17	100
I22	100
I41	100
K44	100
L58	100
R70	100
S75	100
D80	100
R105	100
R108	100
S109	100
E110	100
L123	100

- Molecule 19: 50S ribosomal protein L15



W1	S7	K14	R21	G22	I23	G24	S25	G45	V46	G53	S68	I77	R78	L112	V116	R123	G124	L125	R126	V127	T128	K129	G130	A131	R132	A133	A134	F144
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- Molecule 20: 50S ribosomal protein L16



M1
L2
Q3
R6
L33
R59
P77
L78
A79
V80
R81
M82
K86
M105
T129
M136

- Molecule 21: 50S ribosomal protein L17



- Molecule 22: 50S ribosomal protein L18

Chain P:  91% 7% .



- Molecule 23: 50S ribosomal protein L19

Chain Q:  89% 11%



- Molecule 24: 50S ribosomal protein L20

Chain R:  91% 7% .



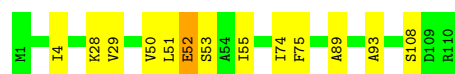
- Molecule 25: 50S ribosomal protein L21

Chain S:  77% 19% . .



- Molecule 26: 50S ribosomal protein L22

Chain T:  88% 11% .



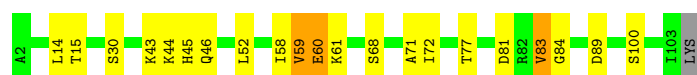
- Molecule 27: 50S ribosomal protein L23

Chain U:  77% 14% 7%



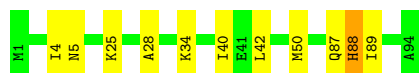
- Molecule 28: 50S ribosomal protein L24

Chain V:  79% 17% . .



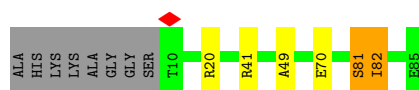
- Molecule 29: 50S ribosomal protein L25

Chain W:  88% 11%



- Molecule 30: 50S ribosomal protein L27

Chain X:  83% 5% 10%



- Molecule 31: 50S ribosomal protein L28

Chain Y:  82% 14%



- Molecule 32: 50S ribosomal protein L29

Chain Z:  90% 8%



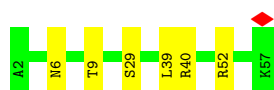
- Molecule 33: 50S ribosomal protein L30

Chain a:  88% 12%



- Molecule 34: 50S ribosomal protein L32

Chain b:  89% 11%



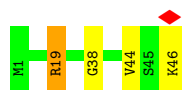
- Molecule 35: 50S ribosomal protein L33

Chain c:  80% 13% 6%



- Molecule 36: 50S ribosomal protein L34

Chain d:  91% 7%



- Molecule 37: 50S ribosomal protein L35

Chain e:  91% 9%



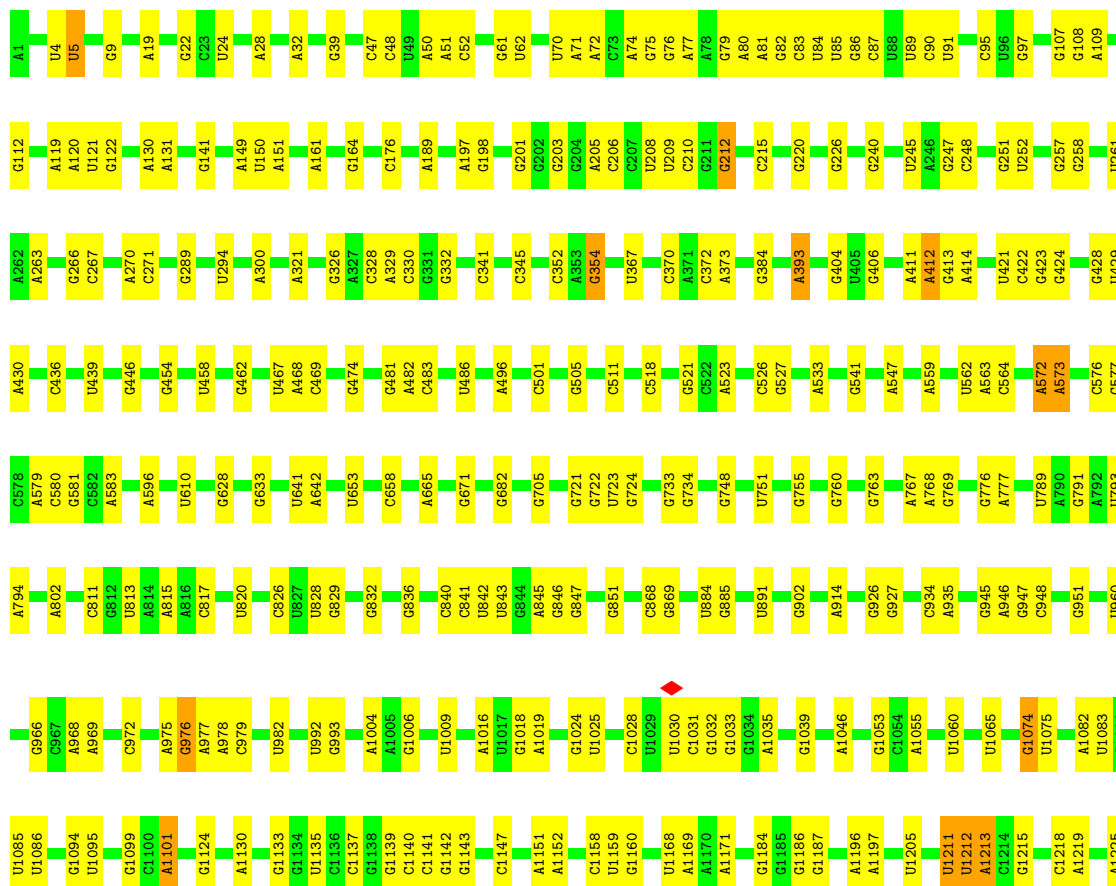
- Molecule 38: 50S ribosomal protein L36

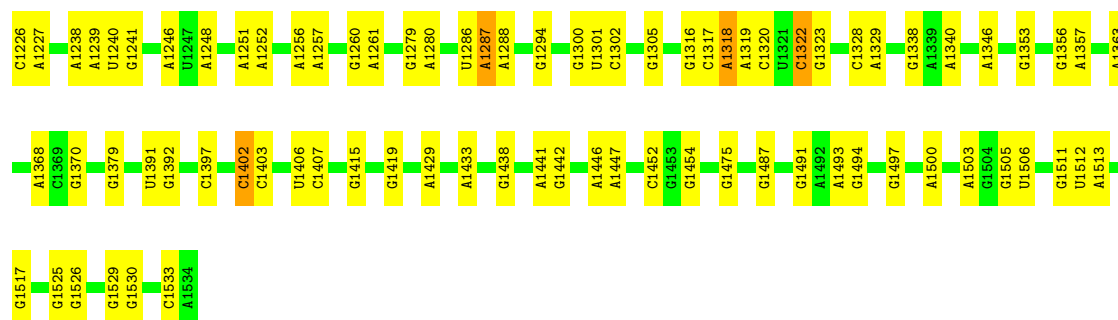
Chain f:  92% 8%



- Molecule 39: 16S rRNA

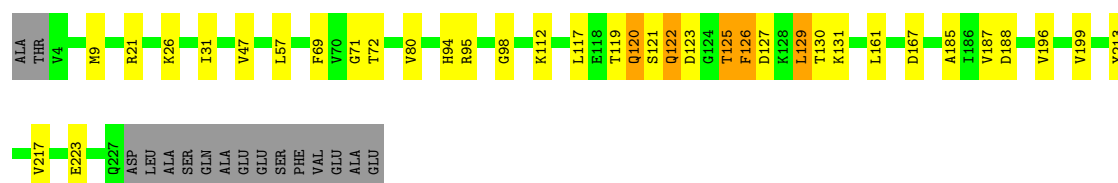
Chain h:  76% 23%





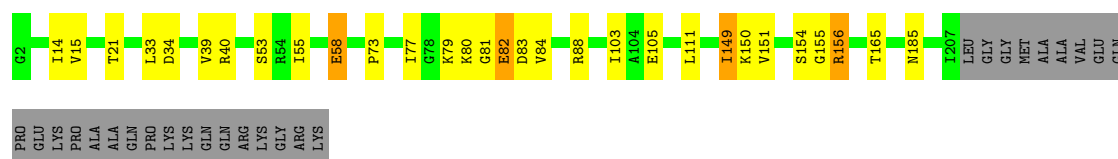
• Molecule 40: 30S ribosomal protein S2

Chain i: 78% 13% 7%



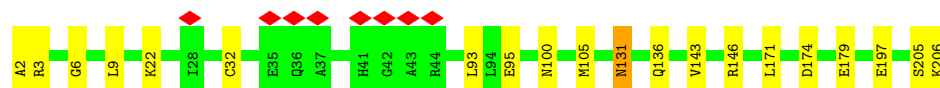
• Molecule 41: 30S ribosomal protein S3

Chain j: 76% 11% 11%



• Molecule 42: 30S ribosomal protein S4

Chain k: 90% 9% 1%



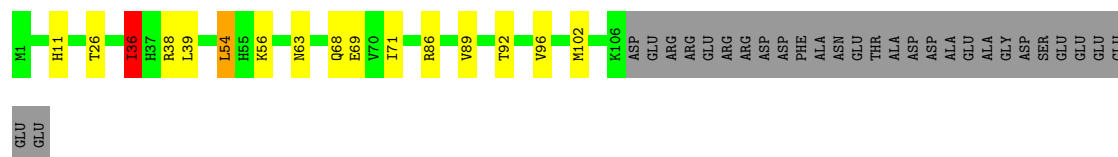
• Molecule 43: 30S ribosomal protein S5

Chain l: 81% 12% 7%

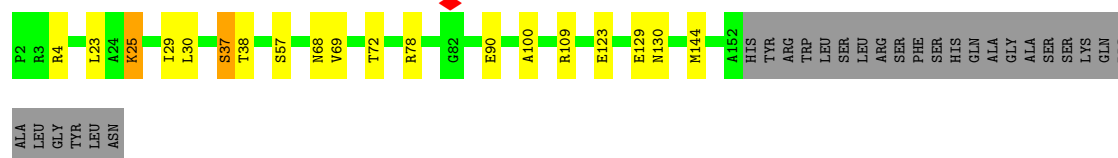


• Molecule 44: 30S ribosomal protein S6

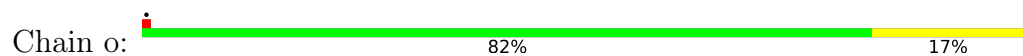
Chain m: 67% 10% 21%



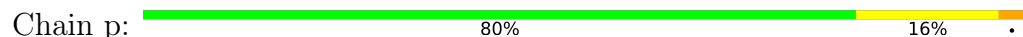
- Molecule 45: 30S ribosomal protein S7



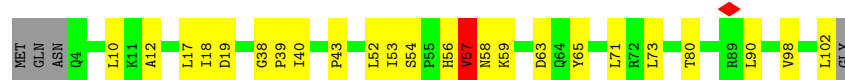
- Molecule 46: 30S ribosomal protein S8



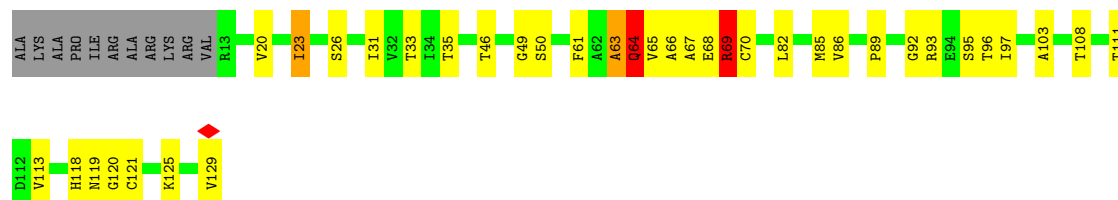
- Molecule 47: 30S ribosomal protein S9



- Molecule 48: 30S ribosomal protein S10



- Molecule 49: 30S ribosomal protein S11



- Molecule 50: 30S ribosomal protein S12

Chain s:  88% 10% ..



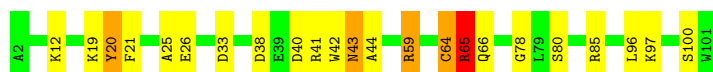
- Molecule 51: 30S ribosomal protein S13

Chain t:  74% 18% . . .

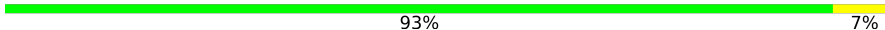


- Molecule 52: 30S ribosomal protein S14

Chain u:  77% 18% . .



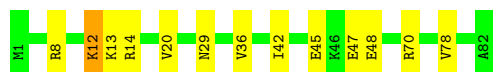
- Molecule 53: 30S ribosomal protein S15

Chain v:  93% 7%



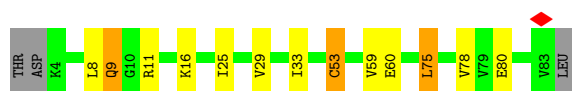
- Molecule 54: 30S ribosomal protein S16

Chain w:  84% 15% .



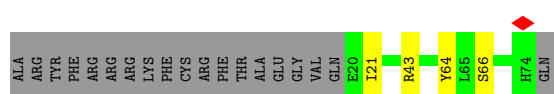
- Molecule 55: 30S ribosomal protein S17

Chain x:  81% 12% . .



- Molecule 56: 30S ribosomal protein S18

Chain y:  69% 5% 26%



- Molecule 57: 30S ribosomal protein S19



PRO	R3	S4	L5	K6	K7	G8	F9	F10	I11	L15	D27	S38	T39	T63	R78	R81	GLY	HIS	ALA	ALA	ASP	LYS	LYS	ALA	LYS	LYS	LYS
-----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13693	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.456	Depositor
Minimum map value	-0.203	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.026	Depositor
Map size ($\text{\AA}$)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1	0.56	0/676	0.89	0/895
2	2	0.62	0/472	0.85	0/627
3	3	0.60	0/375	0.89	0/494
4	4	0.64	1/2868 (0.0%)	0.81	4/3861 (0.1%)
5	5	0.41	0/1810	0.75	1/2821 (0.0%)
6	7	0.48	0/141	1.07	1/217 (0.5%)
7	A	0.41	0/69735	0.78	62/108791 (0.1%)
8	B	0.40	0/2872	0.71	0/4478
9	C	0.58	0/2121	0.87	1/2852 (0.0%)
10	D	0.60	0/1586	0.84	1/2134 (0.0%)
11	E	0.52	0/1571	0.78	0/2113
12	F	0.57	0/1434	0.77	0/1926
13	G	0.59	0/1343	0.81	1/1816 (0.1%)
14	H	0.67	0/1112	0.76	1/1503 (0.1%)
15	I	0.69	0/1037	0.77	0/1402
16	J	0.68	0/511	0.84	0/683
17	K	0.56	0/1152	0.83	0/1551
18	L	0.56	0/955	0.80	0/1279
19	M	0.56	0/1062	0.84	0/1413
20	N	0.60	0/1104	0.80	0/1474
21	O	0.62	0/1006	0.89	0/1345
22	P	0.53	0/910	0.85	1/1219 (0.1%)
23	Q	0.55	0/929	0.77	0/1242
24	R	0.60	0/960	0.93	0/1278
25	S	0.54	0/829	0.77	2/1107 (0.2%)
26	T	0.62	0/864	0.82	0/1156
27	U	0.61	0/744	0.82	0/994
28	V	0.53	0/787	0.76	0/1051
29	W	0.54	0/766	0.76	0/1025
30	X	0.64	0/598	0.87	1/790 (0.1%)
31	Y	0.59	0/635	0.83	0/848
32	Z	0.50	0/502	0.90	0/667
33	a	0.53	0/467	0.84	0/623
34	b	0.56	0/450	0.83	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	c	0.59	0/421	0.79	0/561
36	d	0.65	0/380	1.10	0/498
37	e	0.55	0/513	0.84	0/676
38	f	0.50	0/303	0.77	0/397
39	h	0.41	0/36859	0.78	24/57501 (0.0%)
40	i	0.58	0/1784	0.82	0/2403
41	j	0.60	0/1651	0.83	0/2225
42	k	0.57	0/1665	0.81	2/2227 (0.1%)
43	l	0.63	0/1157	0.87	0/1557
44	m	0.62	0/881	0.88	0/1189
45	n	0.62	0/1195	0.86	0/1602
46	o	0.55	0/989	0.84	0/1326
47	p	0.59	0/1034	0.84	0/1375
48	q	0.59	0/805	0.81	1/1089 (0.1%)
49	r	0.59	0/893	0.88	1/1205 (0.1%)
50	s	0.65	0/969	0.84	1/1300 (0.1%)
51	t	0.62	0/892	0.85	1/1193 (0.1%)
52	u	0.60	0/817	0.83	0/1088
53	v	0.54	0/722	0.85	0/964
54	w	0.62	0/659	0.84	0/884
55	x	0.56	0/657	0.71	0/881
56	y	0.66	0/462	0.88	0/621
57	z	0.62	0/652	0.81	0/877
All	All	0.47	1/160744 (0.0%)	0.79	106/239913 (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
1	1	0	1
2	2	0	1
3	3	0	4
4	4	0	6
9	C	0	6
10	D	0	3
11	E	0	3
12	F	0	4
13	G	0	6
14	H	0	1
15	I	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	L	0	1
19	M	0	2
20	N	0	2
21	O	0	1
22	P	0	1
23	Q	0	2
25	S	0	3
26	T	0	1
27	U	0	3
28	V	0	1
29	W	0	1
31	Y	0	2
32	Z	0	1
35	c	0	2
36	d	0	1
40	i	0	4
41	j	0	4
42	k	0	4
43	l	0	1
44	m	0	2
45	n	0	3
46	o	0	4
47	p	0	5
48	q	0	3
49	r	0	4
50	s	0	1
51	t	0	4
52	u	0	3
53	v	0	1
54	w	0	2
55	x	0	1
56	y	0	1
57	z	0	2
All	All	0	111

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	332	ARG	CA-C	5.81	1.59	1.53

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1607	C	C2'-C3'-O3'	11.61	126.92	109.50
39	h	1211	U	C2'-C3'-O3'	9.06	123.08	109.50
4	4	332	ARG	N-CA-C	8.97	120.46	108.07
7	A	2030	A	C2'-C3'-O3'	8.84	122.76	109.50
39	h	428	G	C4'-C3'-O3'	8.83	122.64	109.40

There are no chirality outliers.

5 of 111 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	42	GLY	Peptide
2	2	55	ARG	Peptide
3	3	2	SER	Peptide
3	3	35	GLY	Peptide
3	3	36	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	670	0	719	3	0
2	2	465	0	491	4	0
3	3	369	0	381	3	0
4	4	2829	0	2734	38	0
5	5	1620	0	826	1	0
6	7	127	0	65	0	0
7	A	62240	0	31297	96	0
8	B	2569	0	1301	1	0
9	C	2082	0	2154	13	0
10	D	1565	0	1616	26	0
11	E	1552	0	1619	0	0
12	F	1410	0	1444	19	0
13	G	1323	0	1371	9	0
14	H	1101	0	1142	4	0
15	I	1023	0	1052	1	0
16	J	509	0	547	5	0
17	K	1129	0	1162	3	0
18	L	946	0	1023	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	M	1053	0	1129	24	0
20	N	1082	0	1170	7	0
21	O	993	0	1034	4	0
22	P	900	0	935	5	0
23	Q	917	0	962	2	0
24	R	947	0	1019	4	0
25	S	816	0	839	35	0
26	T	857	0	922	9	0
27	U	738	0	807	5	0
28	V	779	0	831	12	0
29	W	753	0	780	5	0
30	X	591	0	606	4	0
31	Y	625	0	652	8	0
32	Z	501	0	531	1	0
33	a	463	0	504	2	0
34	b	444	0	458	0	0
35	c	414	0	442	1	0
36	d	377	0	418	1	0
37	e	504	0	572	2	0
38	f	302	0	343	1	0
39	h	32917	0	16564	49	0
40	i	1753	0	1780	16	0
41	j	1624	0	1696	15	0
42	k	1643	0	1707	5	0
43	l	1144	0	1185	1	0
44	m	862	0	864	4	0
45	n	1181	0	1238	2	0
46	o	979	0	1031	6	0
47	p	1022	0	1070	4	0
48	q	795	0	836	7	0
49	r	877	0	885	21	0
50	s	955	0	1016	10	0
51	t	883	0	941	53	0
52	u	805	0	844	15	0
53	v	714	0	734	1	0
54	w	649	0	666	6	0
55	x	648	0	691	5	0
56	y	455	0	478	1	0
57	z	637	0	665	2	0
All	All	148128	0	100789	515	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 2.

The worst 5 of 515 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)
25:S:37:GLU:CB	25:S:53:PHE:HE1	1.04	1.67
25:S:37:GLU:HB3	25:S:53:PHE:CE1	1.25	1.64
51:t:19:LEU:CD1	51:t:34:LEU:HD21	1.46	1.43
25:S:37:GLU:CB	25:S:53:PHE:CE1	1.88	1.39
7:A:1061:U:H1'	7:A:1070:A:C1'	1.54	1.34

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	1	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	10	38
2	2	54/70 (77%)	51 (94%)	3 (6%)	0	100	100
3	3	43/72 (60%)	32 (74%)	8 (19%)	3 (7%)	1	4
4	4	353/365 (97%)	316 (90%)	31 (9%)	6 (2%)	7	30
9	C	269/272 (99%)	245 (91%)	24 (9%)	0	100	100
10	D	207/209 (99%)	189 (91%)	16 (8%)	2 (1%)	12	43
11	E	199/201 (99%)	188 (94%)	10 (5%)	1 (0%)	24	59
12	F	175/178 (98%)	157 (90%)	15 (9%)	3 (2%)	7	30
13	G	174/176 (99%)	156 (90%)	18 (10%)	0	100	100
14	H	146/149 (98%)	131 (90%)	13 (9%)	2 (1%)	9	34
15	I	133/164 (81%)	116 (87%)	14 (10%)	3 (2%)	5	23
16	J	69/141 (49%)	61 (88%)	7 (10%)	1 (1%)	9	34
17	K	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
18	L	121/123 (98%)	108 (89%)	11 (9%)	2 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	M	142/144 (99%)	127 (89%)	14 (10%)	1 (1%)	18	51
20	N	135/136 (99%)	125 (93%)	6 (4%)	4 (3%)	3	18
21	O	123/127 (97%)	110 (89%)	12 (10%)	1 (1%)	16	48
22	P	115/117 (98%)	112 (97%)	2 (2%)	1 (1%)	14	46
23	Q	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
24	R	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
25	S	101/103 (98%)	93 (92%)	6 (6%)	2 (2%)	6	26
26	T	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
27	U	91/100 (91%)	83 (91%)	4 (4%)	4 (4%)	2	11
28	V	100/103 (97%)	88 (88%)	8 (8%)	4 (4%)	2	12
29	W	92/94 (98%)	83 (90%)	8 (9%)	1 (1%)	11	41
30	X	75/84 (89%)	66 (88%)	9 (12%)	0	100	100
31	Y	75/77 (97%)	66 (88%)	6 (8%)	3 (4%)	2	12
32	Z	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
33	a	57/58 (98%)	52 (91%)	5 (9%)	0	100	100
34	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
35	c	49/54 (91%)	45 (92%)	4 (8%)	0	100	100
36	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
37	e	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
38	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
40	i	222/240 (92%)	196 (88%)	17 (8%)	9 (4%)	2	12
41	j	204/232 (88%)	176 (86%)	25 (12%)	3 (2%)	8	33
42	k	203/205 (99%)	193 (95%)	10 (5%)	0	100	100
43	l	153/166 (92%)	130 (85%)	20 (13%)	3 (2%)	6	26
44	m	104/135 (77%)	91 (88%)	11 (11%)	2 (2%)	6	28
45	n	149/178 (84%)	130 (87%)	16 (11%)	3 (2%)	6	26
46	o	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
47	p	125/129 (97%)	106 (85%)	14 (11%)	5 (4%)	2	12
48	q	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	25
49	r	115/128 (90%)	94 (82%)	17 (15%)	4 (4%)	3	15
50	s	121/123 (98%)	106 (88%)	13 (11%)	2 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	t	112/117 (96%)	94 (84%)	12 (11%)	6 (5%)	1	8
52	u	98/100 (98%)	83 (85%)	10 (10%)	5 (5%)	1	9
53	v	86/88 (98%)	78 (91%)	8 (9%)	0	100	100
54	w	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	9	36
55	x	78/83 (94%)	73 (94%)	5 (6%)	0	100	100
56	y	53/74 (72%)	49 (92%)	3 (6%)	1 (2%)	6	28
57	z	77/91 (85%)	69 (90%)	7 (9%)	1 (1%)	9	36
All	All	6117/6556 (93%)	5506 (90%)	519 (8%)	92 (2%)	11	33

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	E	73	ILE
14	H	50	ARG
19	M	132	ARG
20	N	81	ARG
27	U	2	ILE

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	1	65/65 (100%)	61 (94%)	4 (6%)	16	47
2	2	48/60 (80%)	45 (94%)	3 (6%)	16	46
3	3	38/59 (64%)	35 (92%)	3 (8%)	11	37
4	4	303/311 (97%)	278 (92%)	25 (8%)	10	35
9	C	216/217 (100%)	199 (92%)	17 (8%)	11	37
10	D	164/164 (100%)	151 (92%)	13 (8%)	11	37
11	E	165/165 (100%)	160 (97%)	5 (3%)	36	68
12	F	148/149 (99%)	140 (95%)	8 (5%)	20	52
13	G	137/137 (100%)	132 (96%)	5 (4%)	31	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	H	113/114 (99%)	106 (94%)	7 (6%)	16	47
15	I	103/122 (84%)	102 (99%)	1 (1%)	68	83
16	J	53/109 (49%)	51 (96%)	2 (4%)	29	62
17	K	116/116 (100%)	106 (91%)	10 (9%)	10	34
18	L	104/104 (100%)	96 (92%)	8 (8%)	12	38
19	M	103/103 (100%)	96 (93%)	7 (7%)	14	43
20	N	110/109 (101%)	108 (98%)	2 (2%)	51	76
21	O	102/103 (99%)	98 (96%)	4 (4%)	28	61
22	P	87/87 (100%)	86 (99%)	1 (1%)	65	82
23	Q	99/99 (100%)	92 (93%)	7 (7%)	13	42
24	R	89/89 (100%)	82 (92%)	7 (8%)	11	37
25	S	84/84 (100%)	77 (92%)	7 (8%)	10	35
26	T	93/93 (100%)	90 (97%)	3 (3%)	34	66
27	U	80/84 (95%)	74 (92%)	6 (8%)	12	39
28	V	83/84 (99%)	75 (90%)	8 (10%)	8	29
29	W	78/78 (100%)	77 (99%)	1 (1%)	61	80
30	X	58/62 (94%)	55 (95%)	3 (5%)	21	53
31	Y	67/67 (100%)	62 (92%)	5 (8%)	12	39
32	Z	54/55 (98%)	52 (96%)	2 (4%)	30	63
33	a	49/48 (102%)	45 (92%)	4 (8%)	10	36
34	b	47/47 (100%)	41 (87%)	6 (13%)	4	18
35	c	45/48 (94%)	40 (89%)	5 (11%)	6	23
36	d	38/38 (100%)	35 (92%)	3 (8%)	11	37
37	e	51/51 (100%)	48 (94%)	3 (6%)	18	49
38	f	34/34 (100%)	33 (97%)	1 (3%)	37	68
40	i	186/198 (94%)	176 (95%)	10 (5%)	20	52
41	j	170/189 (90%)	160 (94%)	10 (6%)	18	49
42	k	172/172 (100%)	164 (95%)	8 (5%)	23	56
43	l	118/125 (94%)	101 (86%)	17 (14%)	3	14
44	m	92/116 (79%)	83 (90%)	9 (10%)	7	29
45	n	124/146 (85%)	113 (91%)	11 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	o	104/104 (100%)	95 (91%)	9 (9%)	9	34
47	p	105/106 (99%)	91 (87%)	14 (13%)	4	17
48	q	87/90 (97%)	79 (91%)	8 (9%)	8	31
49	r	90/98 (92%)	77 (86%)	13 (14%)	3	14
50	s	103/103 (100%)	93 (90%)	10 (10%)	8	29
51	t	92/95 (97%)	89 (97%)	3 (3%)	33	65
52	u	83/83 (100%)	75 (90%)	8 (10%)	8	29
53	v	76/76 (100%)	72 (95%)	4 (5%)	20	52
54	w	65/65 (100%)	60 (92%)	5 (8%)	12	38
55	x	74/77 (96%)	67 (90%)	7 (10%)	8	30
56	y	48/64 (75%)	47 (98%)	1 (2%)	47	74
57	z	70/78 (90%)	63 (90%)	7 (10%)	7	28
All	All	5083/5340 (95%)	4733 (93%)	350 (7%)	16	43

5 of 350 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	l	73	ASN
48	q	57	VAL
43	l	137	VAL
45	n	144	MET
49	r	108	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
40	i	94	HIS
50	s	6	GLN
40	i	227	GLN
44	m	94	HIS
53	v	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
39	h	1533/1534 (99%)	293 (19%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	5	75/76 (98%)	20 (26%)	2 (2%)
6	7	5/6 (83%)	3 (60%)	1 (20%)
7	A	2892/2903 (99%)	541 (18%)	62 (2%)
8	B	119/120 (99%)	17 (14%)	0
All	All	4624/4639 (99%)	874 (18%)	65 (1%)

5 of 874 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	5	9	G
5	5	14	A
5	5	17(A)	U
5	5	18	G
5	5	19	G

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	2468	A
7	A	2498	C
7	A	961	C
7	A	871	U
7	A	2529	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

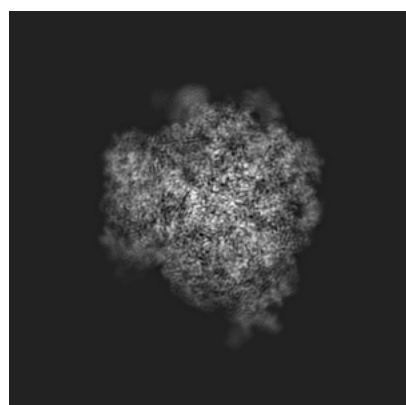
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6667. These allow visual inspection of the internal detail of the map and identification of artifacts.

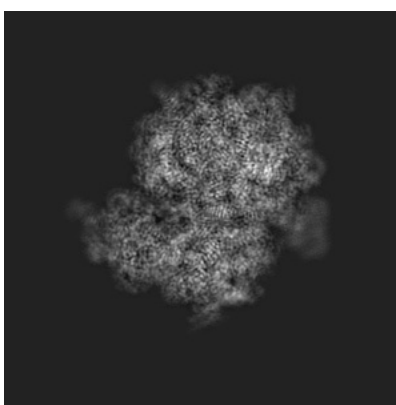
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

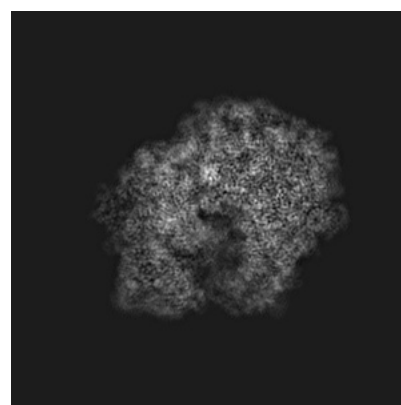
6.1.1 Primary map



X



Y

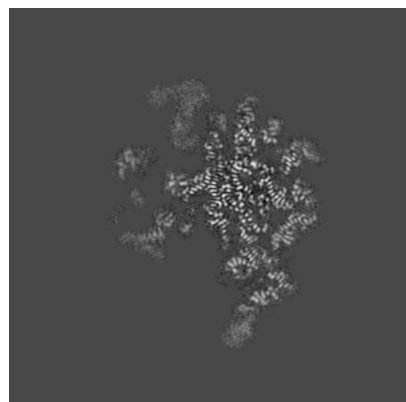


Z

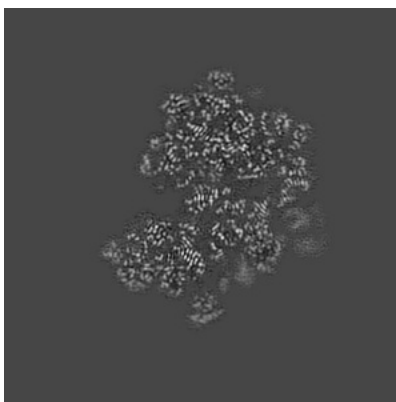
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

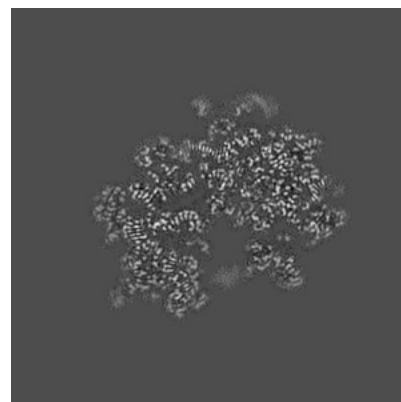
6.2.1 Primary map



X Index: 180



Y Index: 180

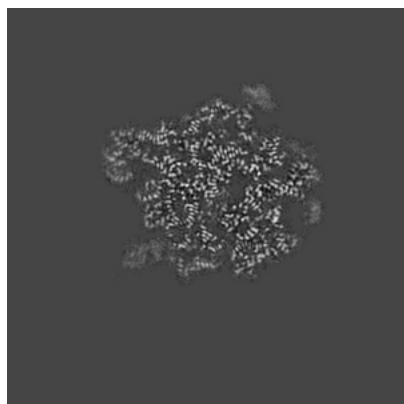


Z Index: 180

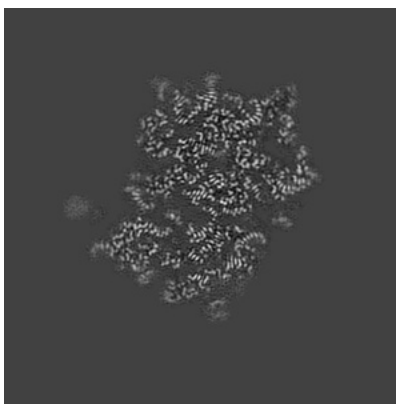
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

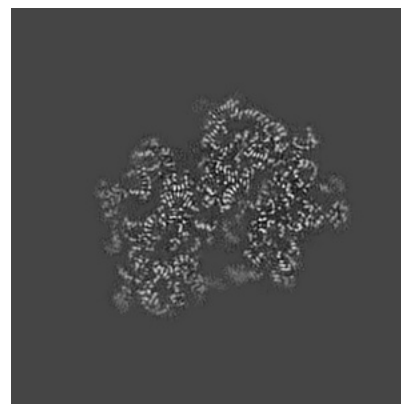
6.3.1 Primary map



X Index: 222



Y Index: 200

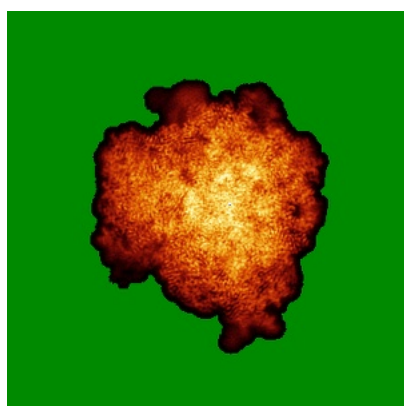


Z Index: 191

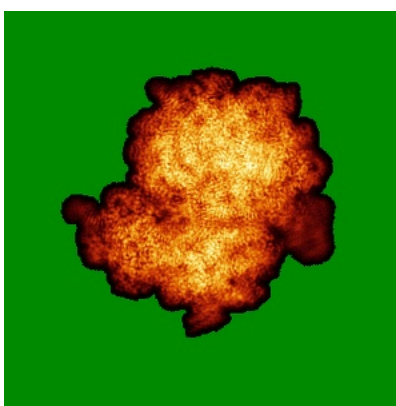
The images above show the largest variance slices of the map in three orthogonal directions.

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

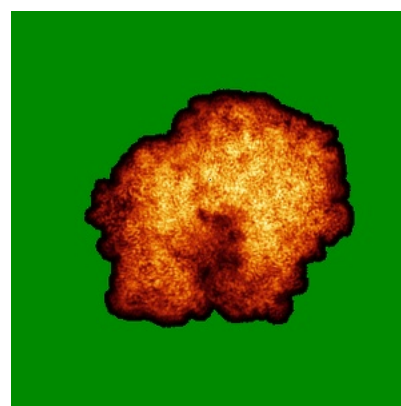
6.4.1 Primary map



X



Y

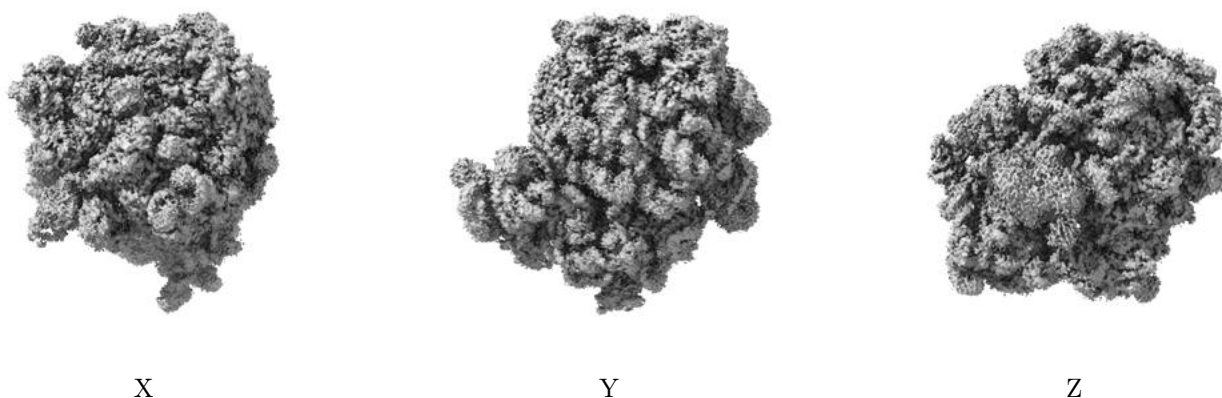


Z

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 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

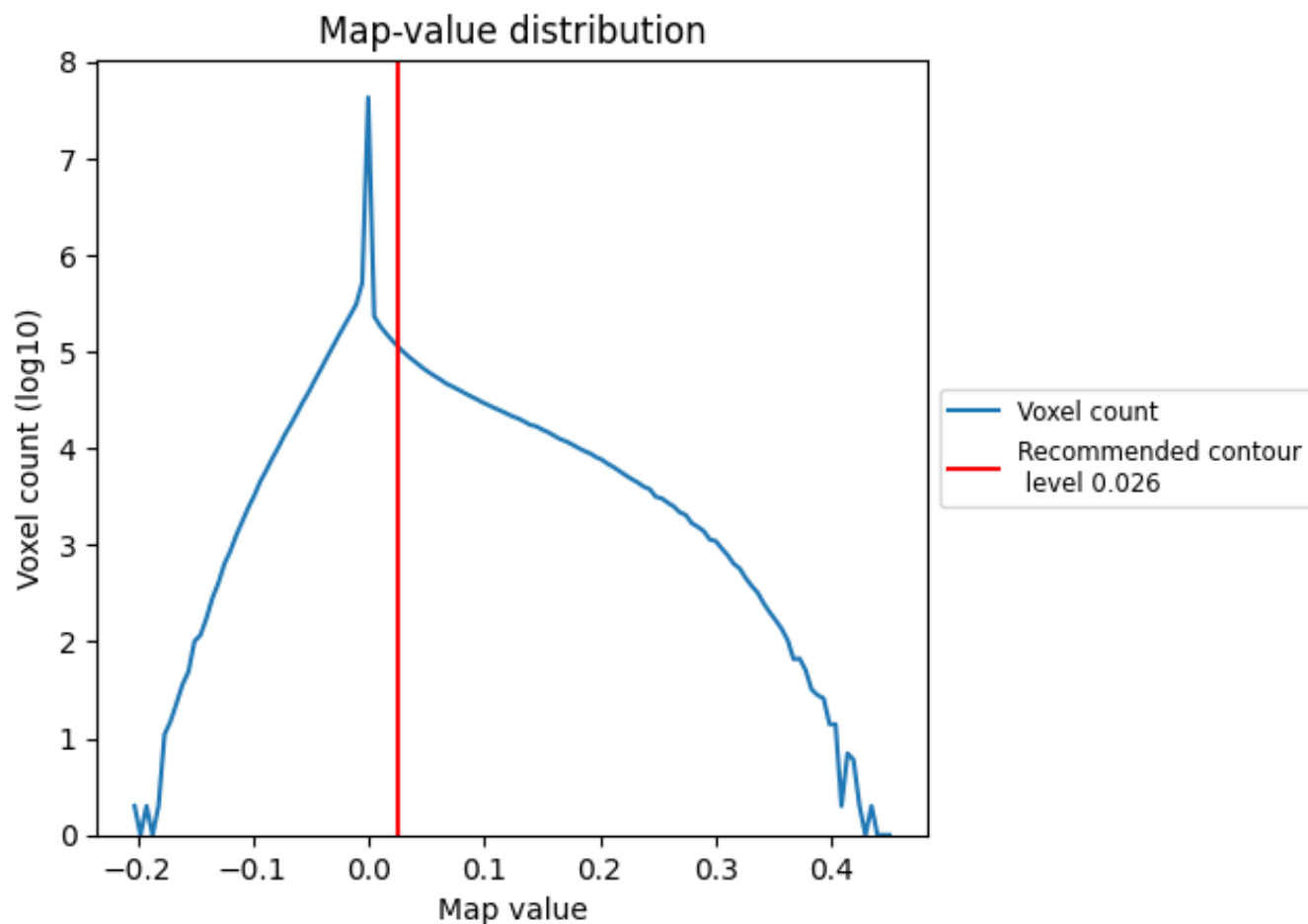
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

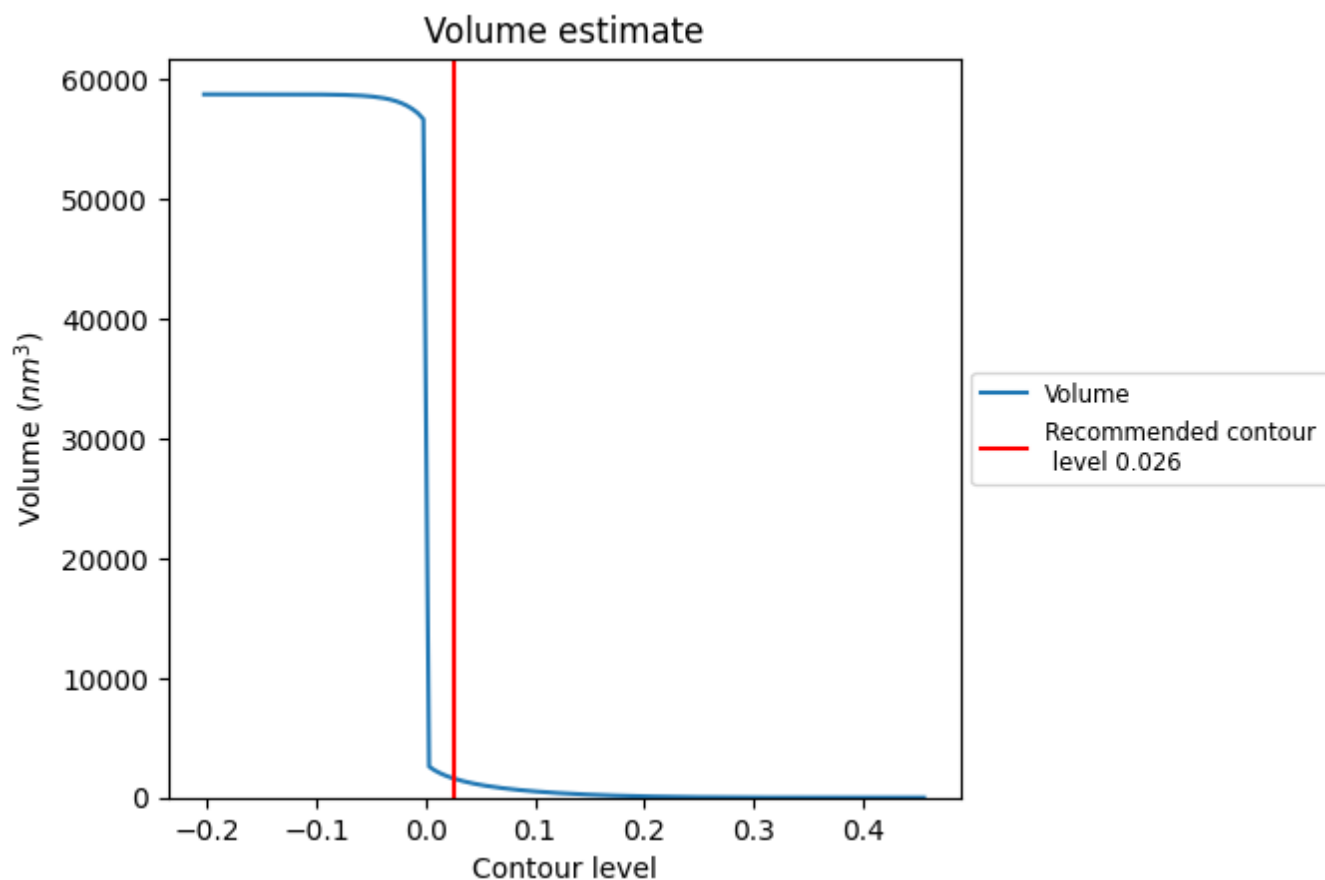
This section contains the results of statistical analysis of the map.

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.

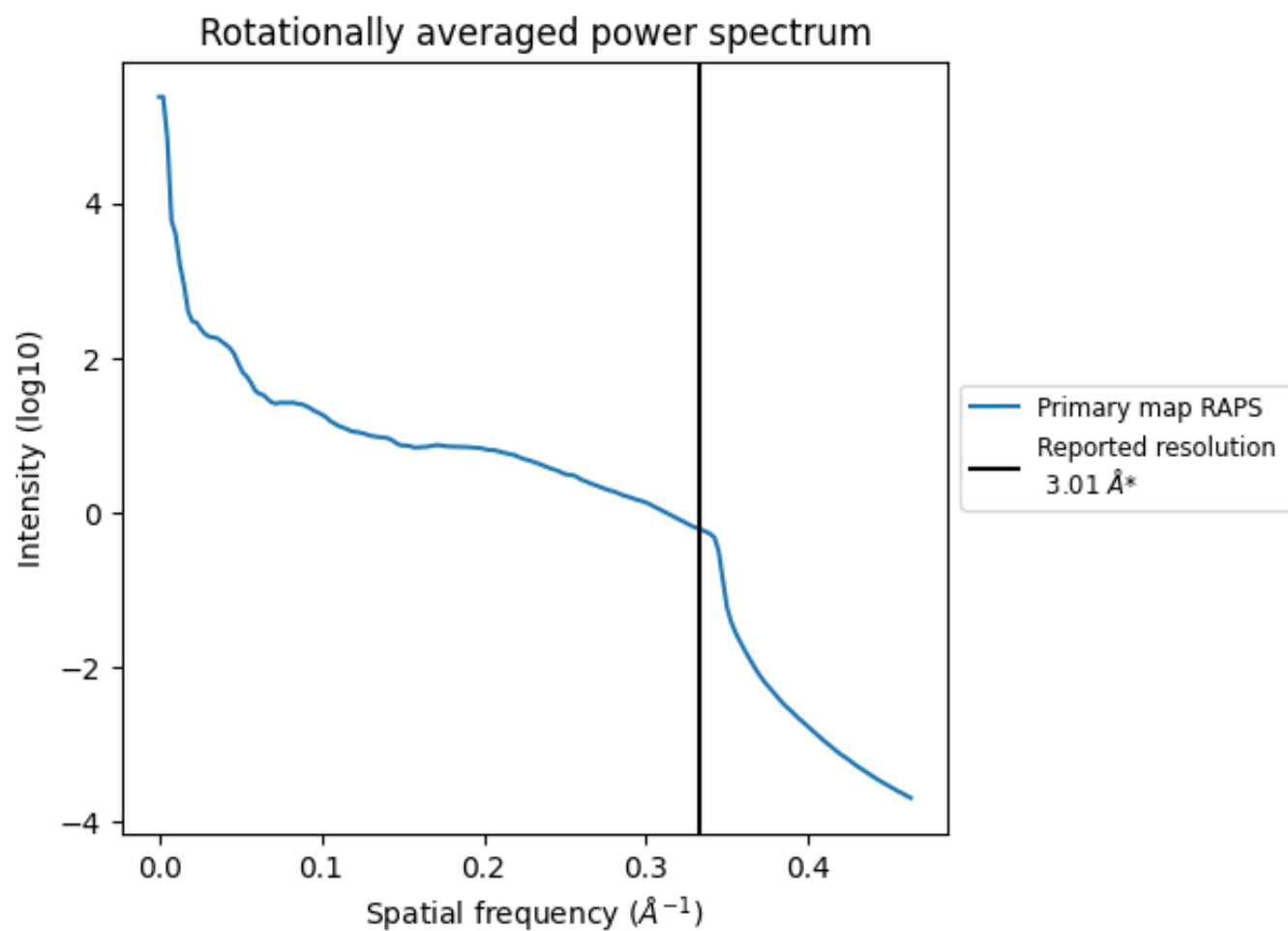
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1587 nm³; this corresponds to an approximate mass of 1434 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 0.332 Å⁻¹

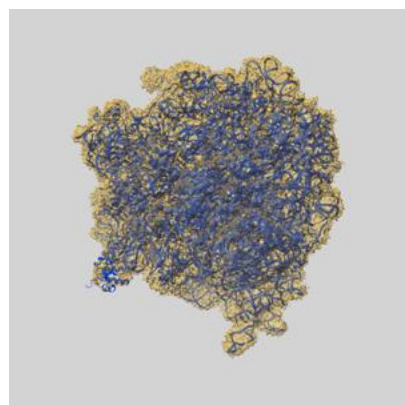
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

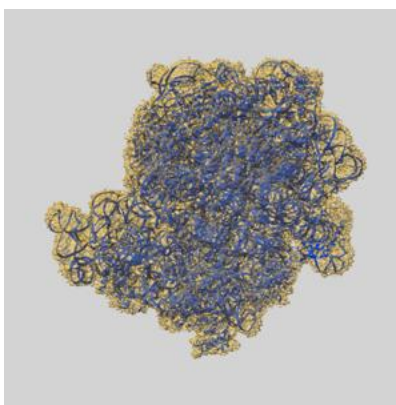
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6667 and PDB model 5H5U. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

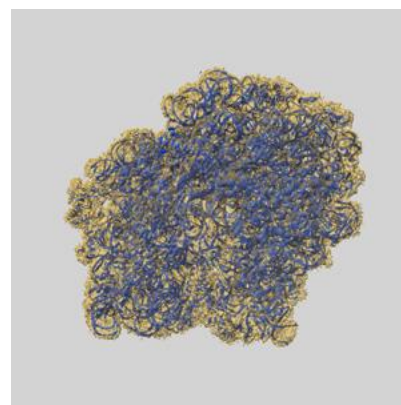
9.1 Map-model overlay [i](#)



X



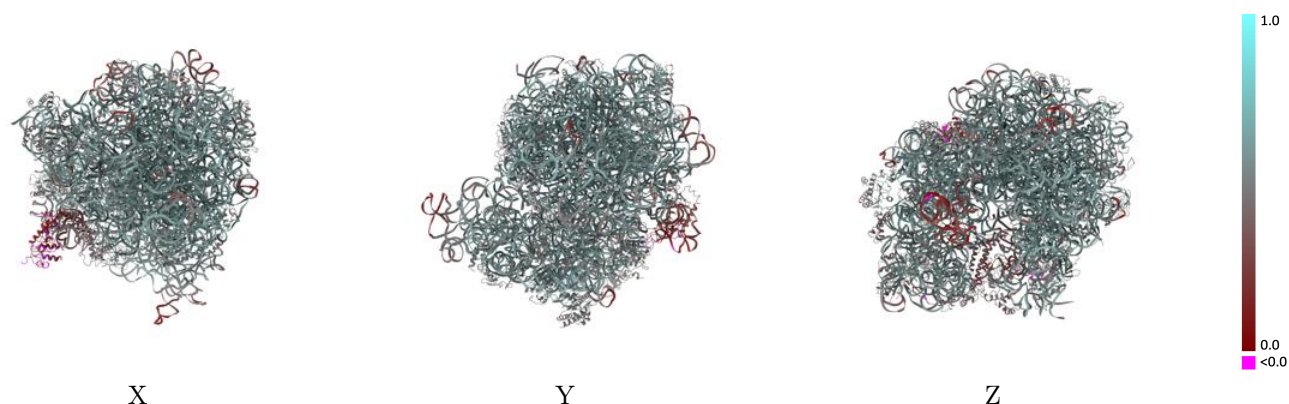
Y



Z

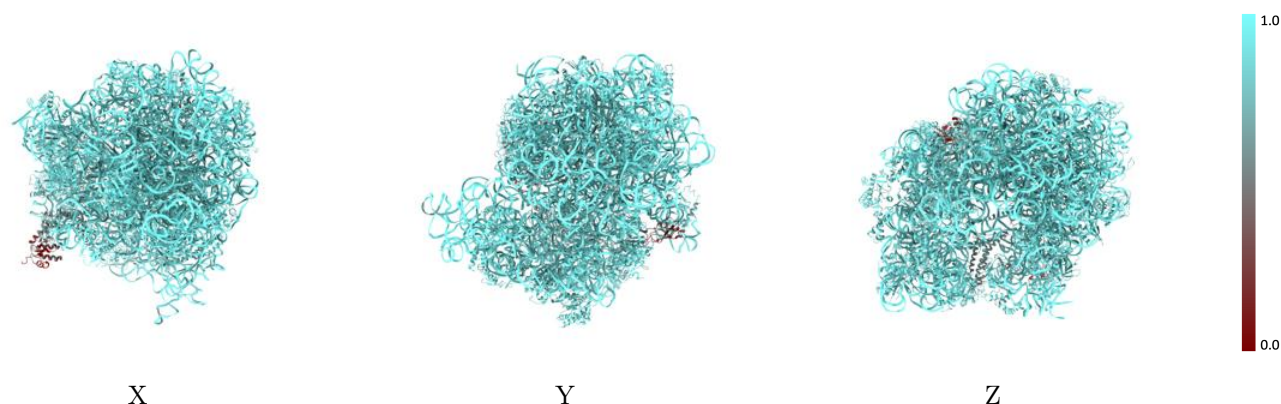
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



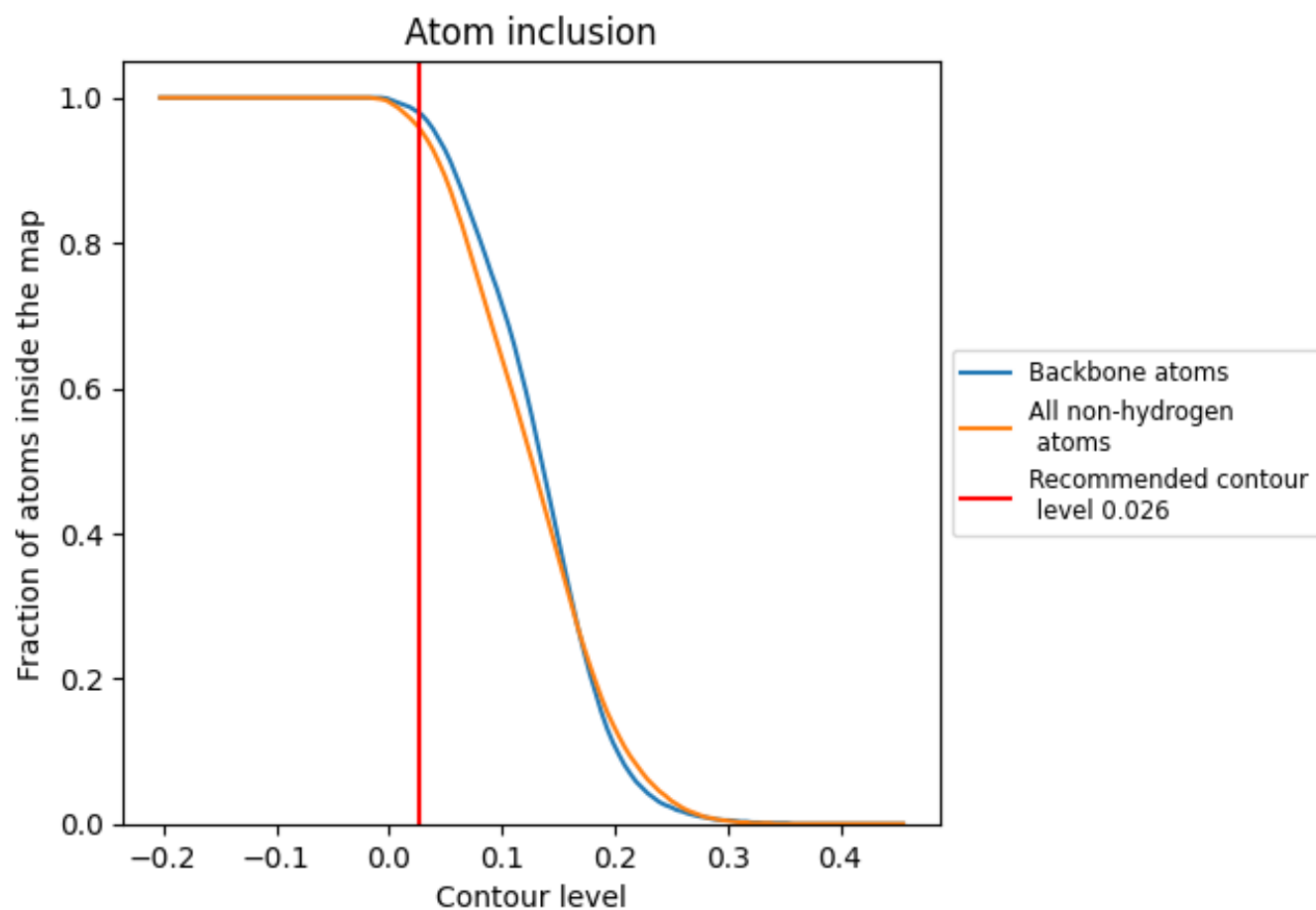
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.5380
1	 0.9500	 0.5340
2	 0.8650	 0.4780
3	 0.9280	 0.5630
4	 0.7590	 0.4140
5	 0.9690	 0.5080
7	 0.9450	 0.5010
A	 0.9900	 0.5540
B	 0.9970	 0.5480
C	 0.9490	 0.5760
D	 0.9490	 0.5650
E	 0.9180	 0.5210
F	 0.9100	 0.4490
G	 0.9310	 0.4730
H	 0.5520	 0.3180
I	 0.2920	 0.1140
J	 0.6080	 0.2110
K	 0.9420	 0.5560
L	 0.9350	 0.5560
M	 0.9400	 0.5520
N	 0.9440	 0.5670
O	 0.9340	 0.5600
P	 0.9400	 0.5130
Q	 0.9230	 0.5450
R	 0.9670	 0.5710
S	 0.9350	 0.5390
T	 0.9370	 0.5590
U	 0.9320	 0.5310
V	 0.9470	 0.5100
W	 0.9350	 0.5250
X	 0.9450	 0.5750
Y	 0.9370	 0.5140
Z	 0.9280	 0.5000
a	 0.9270	 0.5480
b	 0.9420	 0.5590



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Chain	Atom inclusion	Q-score
c	 0.9240	 0.5430
d	 0.9470	 0.5780
e	 0.9550	 0.5850
f	 0.9380	 0.5540
h	 0.9940	 0.5600
i	 0.9200	 0.4840
j	 0.9350	 0.5260
k	 0.8860	 0.5080
l	 0.9500	 0.5460
m	 0.9170	 0.4940
n	 0.8980	 0.4740
o	 0.9470	 0.5590
p	 0.9350	 0.5120
q	 0.8900	 0.4800
r	 0.9450	 0.5310
s	 0.9360	 0.5660
t	 0.9260	 0.4920
u	 0.9110	 0.5210
v	 0.9360	 0.5250
w	 0.9490	 0.5500
x	 0.9130	 0.4990
y	 0.9360	 0.5340
z	 0.9440	 0.4940