



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 05:19 AM EDT

PDB ID : 6VZ3 / pdb_00006vz3
EMDB ID : EMD-21483
Title : Escherichia coli transcription-translation complex D2 (TTC-D2) containing mRNA with a 27 nt long spacer
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
Resolution : 8.90 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:

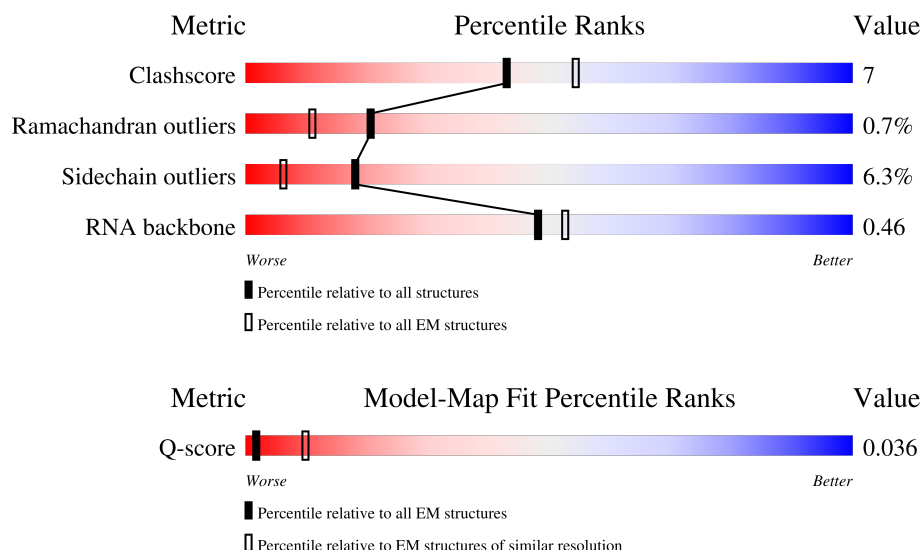
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.90 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.



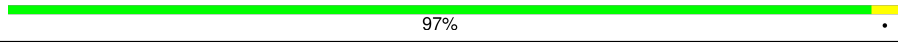
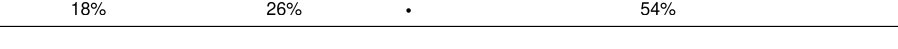
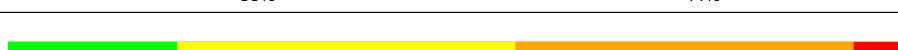
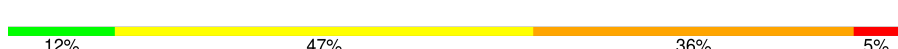
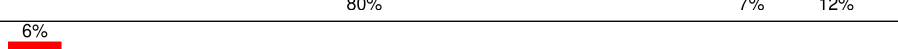
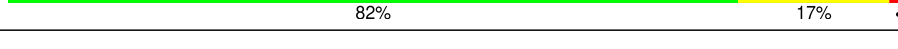
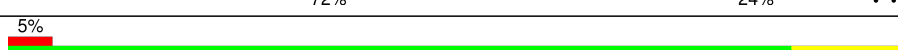
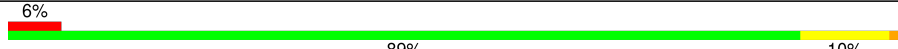
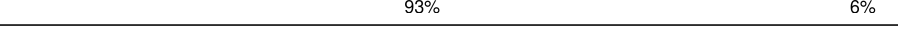
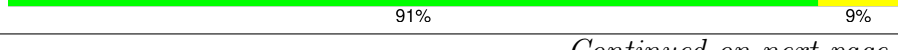
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	258 (8.40 - 9.40)

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	0	103	
2	1	110	
3	2	94	

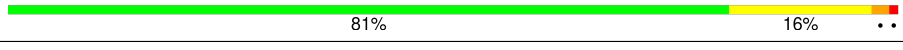
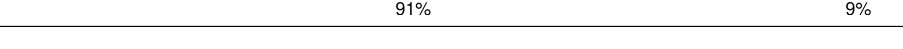
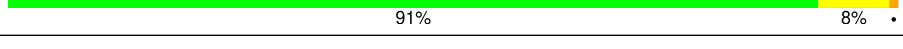
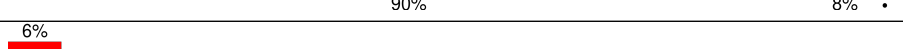
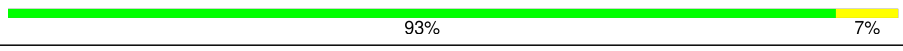
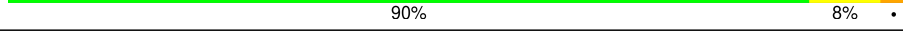
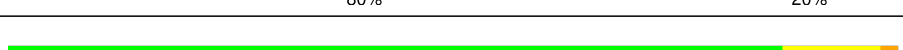
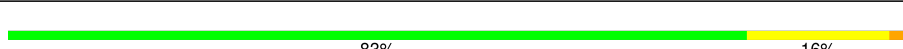
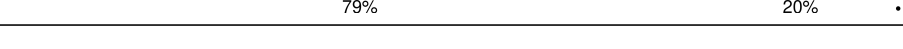
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Mol	Chain	Length	Quality of chain
4	3	103	
5	4	94	
6	5	50	
7	6	27	
8	7	16	
9	A	76	
9	B	76	
10	AA	1342	
11	AB	112	
12	AC	230	
12	AD	230	
13	AE	1358	
14	AF	83	
15	C	66	
16	D	1534	
17	E	86	
18	F	70	
19	G	225	
20	H	346	
21	I	208	
22	J	205	
23	K	156	
24	L	104	
25	M	151	
26	N	129	

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Mol	Chain	Length	Quality of chain
27	O	127	
28	P	99	
29	Q	117	
30	R	123	
31	S	100	
32	T	88	
33	U	82	
34	V	80	
35	W	83	
36	X	116	
37	Y	3	
38	a	2903	
39	b	76	
40	c	77	
41	d	120	
42	e	62	
43	f	58	
44	g	66	
45	h	271	
46	i	56	
47	j	209	
48	k	52	
49	l	201	
50	m	46	
51	n	177	

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Mol	Chain	Length	Quality of chain
52	o	64	 89% 8% •
53	p	175	 91% 9%
54	q	38	 89% 8% •
55	r	149	 9% 89% 9% •
56	s	142	 81% 18% •
57	t	123	 80% 18% •
58	u	144	 90% 10%
59	v	136	 91% 8% •
60	w	119	 81% 19%
61	x	116	 83% 16% •
62	y	114	 89% 11%
63	z	117	 85% 15%

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 297772 atoms, of which 124652 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 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			731	225	259	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	16	Total	C	H	N	O	P	0	0
			516	154	169	62	115	16		

- Molecule 9 is a RNA chain called E-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A	76	Total	C	H	N	O	P	0	0
			2445	723	825	295	527	75		
9	B	76	Total	C	H	N	O	P	0	0
			2432	723	812	295	527	75		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	U	deletion	GB 1126835761
B	?	-	U	deletion	GB 1126835761

- Molecule 10 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AA	1223	Total	C	H	N	O	S	0	0
			19198	6029	9588	1672	1867	42		

- Molecule 11 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
12	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	83	Total	C	H	N	O	S	0	0
			1318	399	663	123	132	1		

- Molecule 15 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
16	D	1523	Total	C	H	N	O	P	0	0
			49110	14575	16431	5998	10583	1523		

- Molecule 17 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 18 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 20 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 21 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 22 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 23 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 24 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 25 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 26 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 27 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 28 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 29 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 31 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 32 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 33 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 34 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 35 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 36 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 37 is a RNA chain called mRNA in the ribosomal RNA entrance pore.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Y	3	Total	C	H	N	O	P	0	0
			88	27	28	6	24	3		

- Molecule 38 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 40 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 41 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	d	120	Total	C	H	N	O	P	0	0
			3869	1144	1300	468	837	120		

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 44 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 45 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 47 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 49 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 53 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 55 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 56 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 57 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 58 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 59 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 60 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 61 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	x	116	Total	C	H	N	O	0	0
			1815	552	923	178	162		

- Molecule 62 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 63 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	z	117	Total	C	H	N	O	0	0
			1967	604	1020	192	151		

- Molecule 64 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	7	1	Total	Mg	0
			1	1	

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

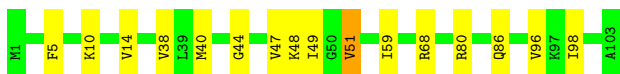
Mol	Chain	Residues	Atoms		AltConf
65	AE	2	Total	Zn	0
			2	2	

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L21

Chain 0: 



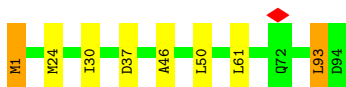
- Molecule 2: 50S ribosomal protein L22

Chain 1: 



- Molecule 3: 50S ribosomal protein L23

Chain 2: 

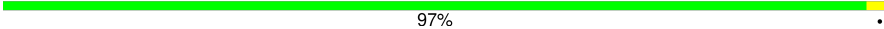


- Molecule 4: 50S ribosomal protein L24

Chain 3: 



- Molecule 5: 50S ribosomal protein L25

Chain 4: 



- Molecule 6: NT DNA

[illegible]

A diagram of a 16-bit bus structure. It consists of 16 yellow rectangular blocks arranged in a single row, separated by small gaps. The blocks are labeled as follows from left to right: C2, C3, C8, T9, G10, G11, C12, C15, C16, A21, T26, G27, and A28. The block labeled G11 is highlighted in green, while all other blocks are yellow.

U55	U56	G57	A58	U59	U60	U61	G62	G63	U64	G65	A66		G69	G70
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----

C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	A72	A73	A76	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	A14	C15	C16	C17	C18	C19	C20	A21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	A35	C36	C37	A38	C39	C40	C41	C42	A43	A44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	A57	A58	A59
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

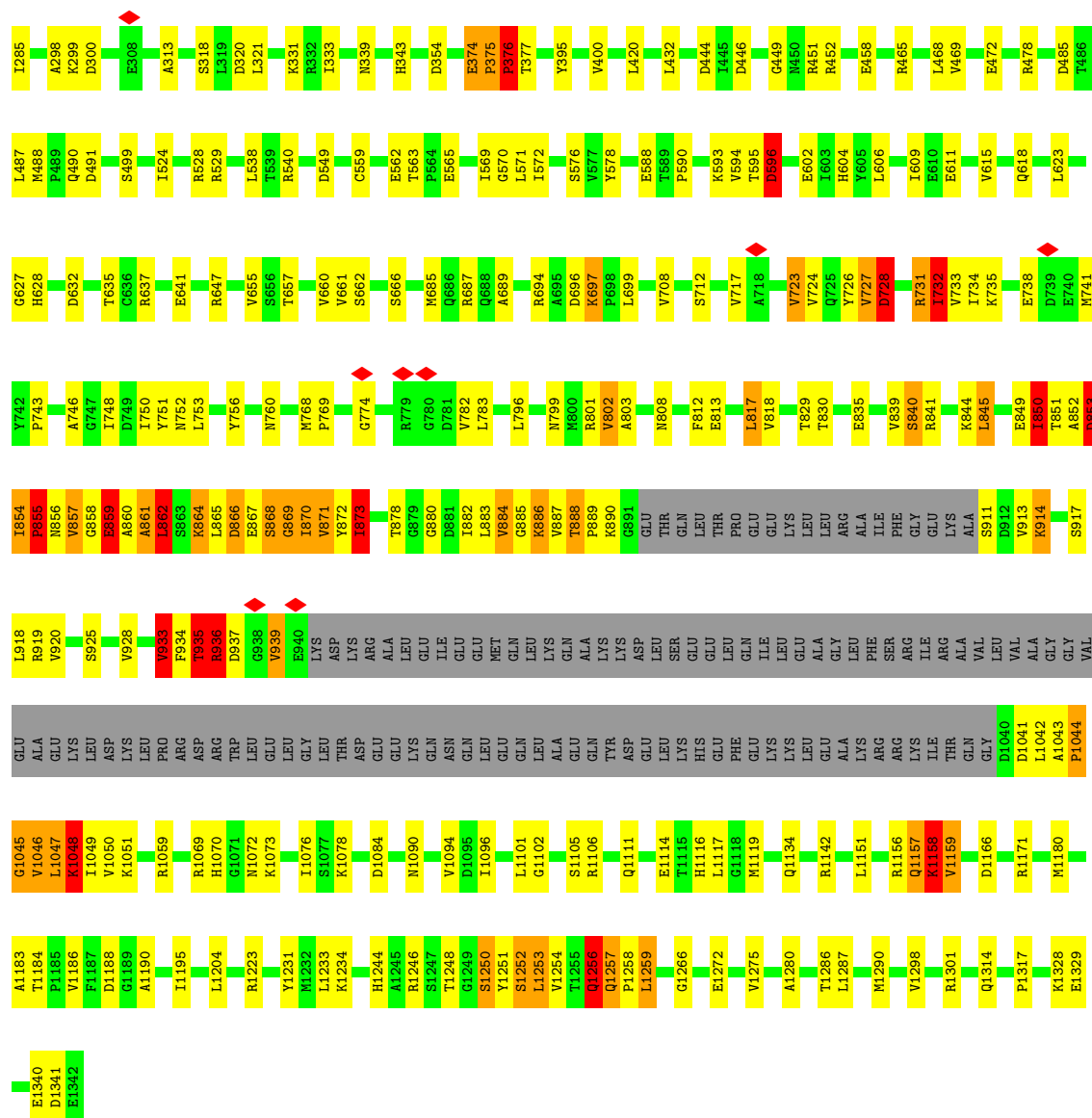
The diagram illustrates a network of nodes and their connections. The nodes are represented by colored squares and are labeled with IDs. The connections are shown as lines between nodes. Some nodes have red diamond markers above them, indicating a specific status or type of node.

Node Legend:

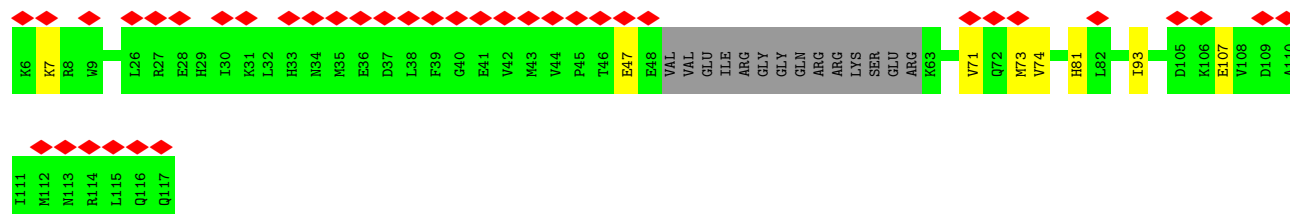
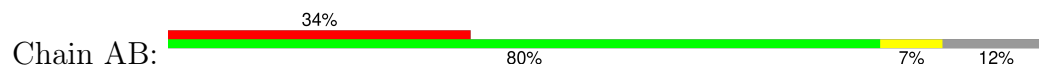
- Green:** V2, K9, R10, K13, D14, P19, V24, L27, L32, L39, Q46, V47, S55, V56, L68, Q69, R74, L75, G76, E77, P78, V79, F80, D81, V82, S93, A94, P95, L96, A97, L100, R101, L102, V103, I104, E108, A109, P110, E111, G112, T113, V114, D116, I117, K118, E119, Q120, E121, V122, Y123, H124, G125, P128, D132, I138, T141, I145, H150, K163, A174, R175, I176, W183, L184, D199, R200, P205, A206, T207, E218, K227, F230, F231, I232, L241, V242, P243, E244, R245, L246, A257, I274, K283, L284.
- Yellow:** T6, K9, R10, K13, D14, P19, V24, L27, L32, L39, Q46, V47, S55, V56, L68, Q69, R74, L75, G76, E77, P78, V79, F80, D81, V82, S93, A94, P95, L96, A97, L100, R101, L102, V103, I104, E108, A109, P110, E111, G112, T113, V114, D116, I117, K118, E119, Q120, E121, V122, Y123, H124, G125, P128, D132, I138, T141, I145, H150, K163, A174, R175, I176, W183, L184, D199, R200, P205, A206, T207, E218, K227, F230, F231, I232, L241, V242, P243, E244, R245, L246, A257, I274, K283, L284.
- Orange:** L39.
- Grey:** MET.

Connections:

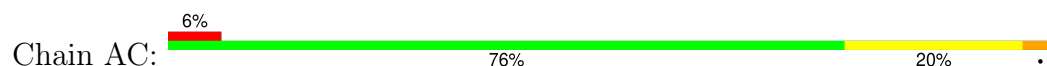
- Grey node (MET) connects to V2.
- V2 connects to T6.
- T6 connects to K9.
- K9 connects to R10.
- R10 connects to K13.
- K13 connects to D14.
- D14 connects to P19.
- P19 connects to V24.
- V24 connects to L27.
- L27 connects to L32.
- L32 connects to L39.
- L39 connects to Q46.
- Q46 connects to V47.
- V47 connects to S55.
- S55 connects to V56.
- V56 connects to L68.
- L68 connects to Q69.
- Q69 connects to R74.
- R74 connects to L75.
- L75 connects to G76.
- G76 connects to E77.
- E77 connects to P78.
- P78 connects to V79.
- V79 connects to F80.
- F80 connects to D81.
- D81 connects to V82.
- V82 connects to S93.
- S93 connects to A94.
- A94 connects to P95.
- P95 connects to L96.
- L96 connects to A97.
- A97 connects to L100.
- L100 connects to R101.
- R101 connects to L102.
- L102 connects to V103.
- V103 connects to I104.
- I104 connects to E108.
- E108 connects to A109.
- A109 connects to P110.
- P110 connects to E111.
- E111 connects to G112.
- G112 connects to T113.
- T113 connects to V114.
- V114 connects to D116.
- D116 connects to I117.
- I117 connects to K118.
- K118 connects to E119.
- E119 connects to Q120.
- Q120 connects to E121.
- E121 connects to V122.
- V122 connects to Y123.
- Y123 connects to H124.
- H124 connects to G125.
- G125 connects to P128.
- P128 connects to D132.
- D132 connects to I138.
- I138 connects to T141.
- T141 connects to I145.
- I145 connects to H150.
- H150 connects to K163.
- K163 connects to A174.
- A174 connects to R175.
- R175 connects to I176.
- I176 connects to W183.
- W183 connects to L184.
- L184 connects to D199.
- D199 connects to R200.
- R200 connects to P205.
- P205 connects to A206.
- A206 connects to T207.
- T207 connects to E218.
- E218 connects to K227.
- K227 connects to F230.
- F230 connects to F231.
- F231 connects to I232.
- I232 connects to L241.
- L241 connects to V242.
- V242 connects to P243.
- P243 connects to E244.
- E244 connects to R245.
- R245 connects to L246.
- L246 connects to A257.
- A257 connects to I274.
- I274 connects to K283.
- K283 connects to L284.

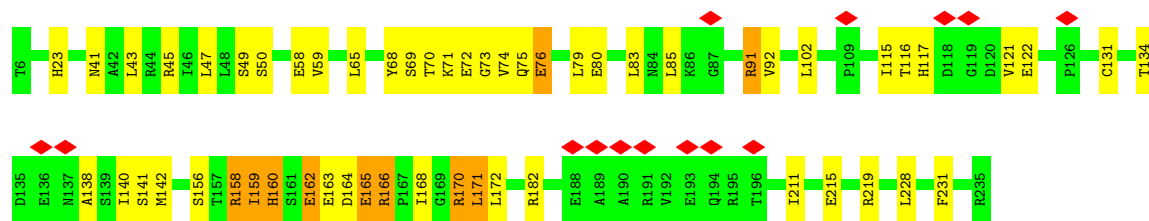


• Molecule 11: Transcription termination/antitermination protein NusG

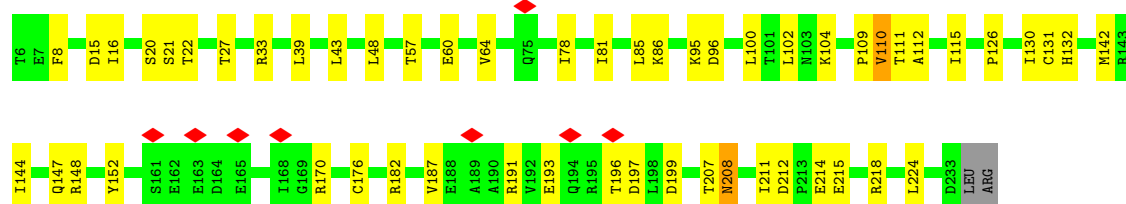
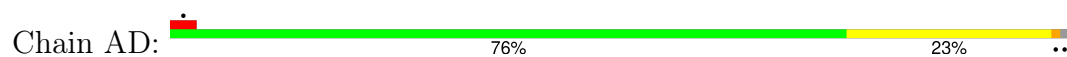


• Molecule 12: DNA-directed RNA polymerase subunit alpha

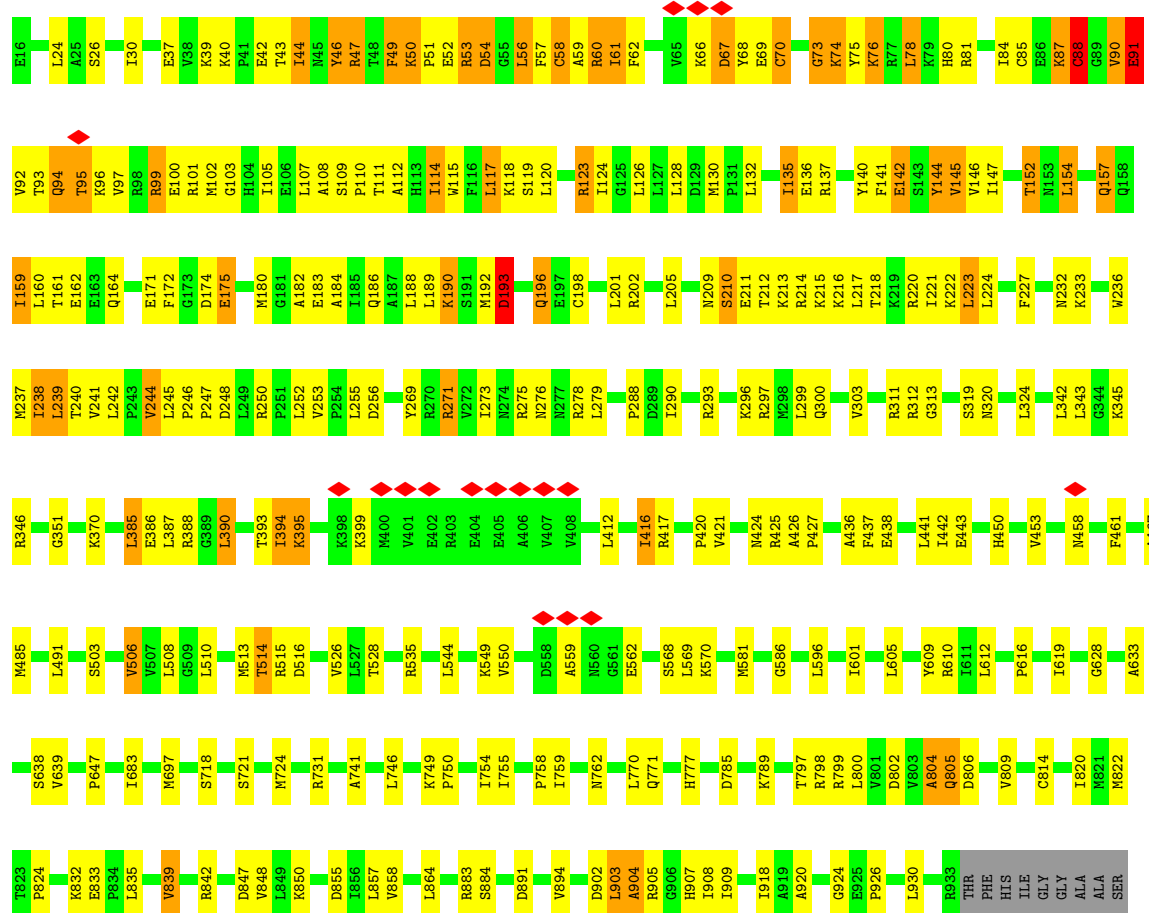


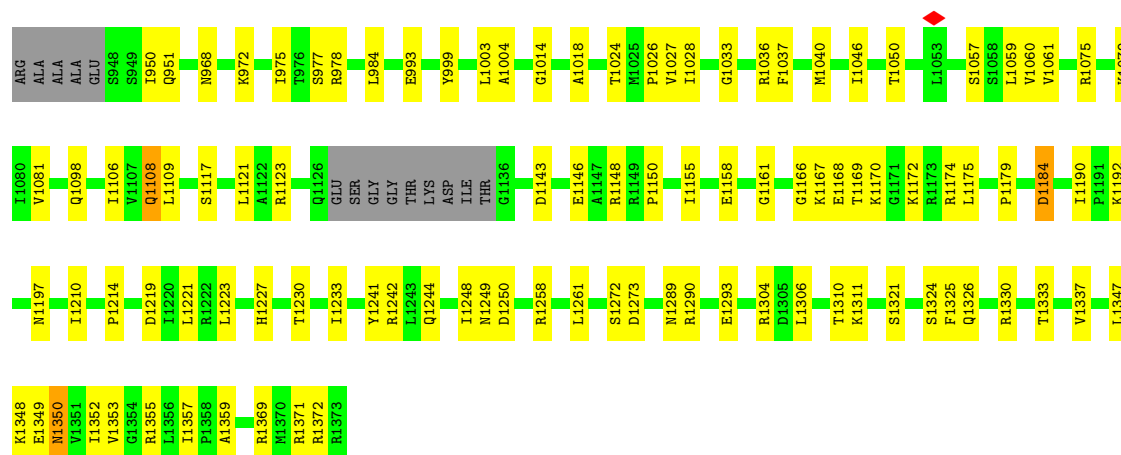


• Molecule 12: DNA-directed RNA polymerase subunit alpha

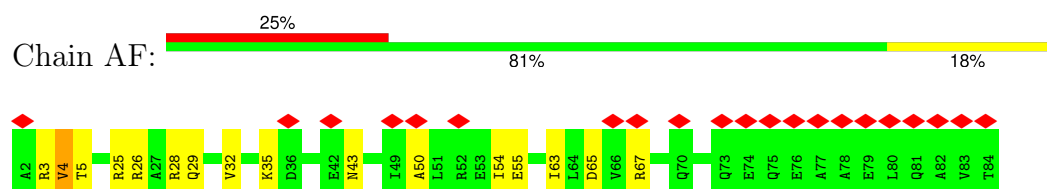


• Molecule 13: DNA-directed RNA polymerase subunit beta

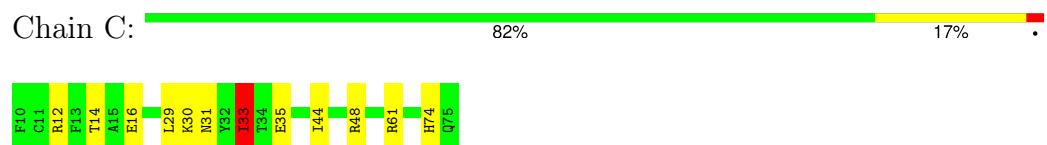




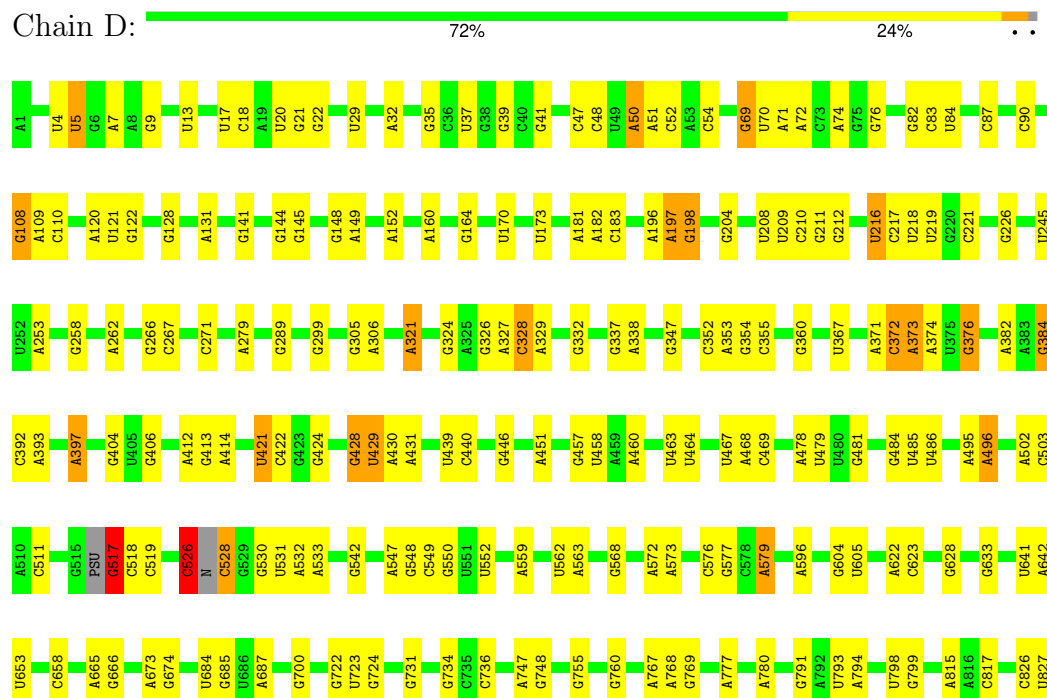
- Molecule 14: DNA-directed RNA polymerase subunit omega

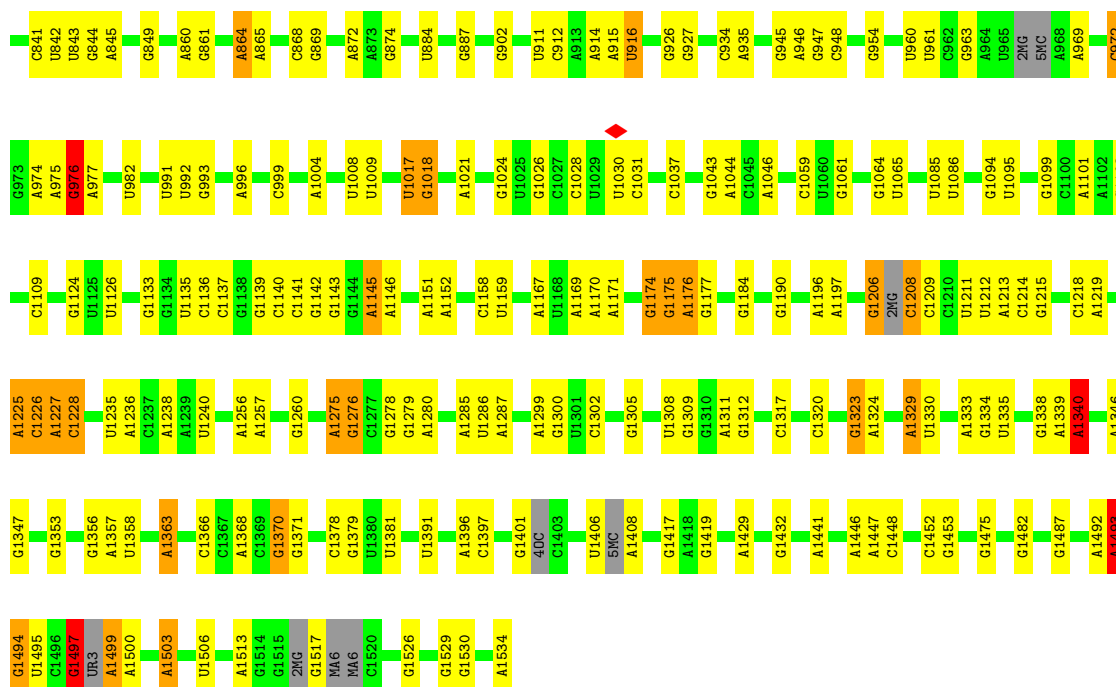


- Molecule 15: 30S ribosomal protein S18

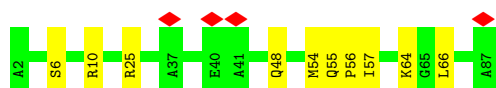
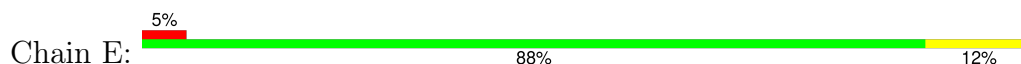


- Molecule 16: 16S rRNA

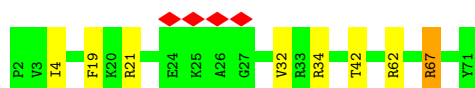
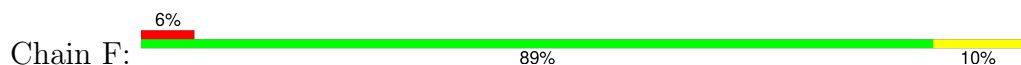




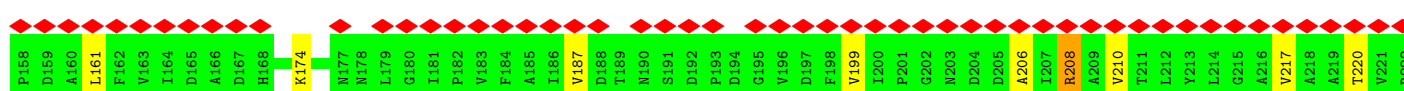
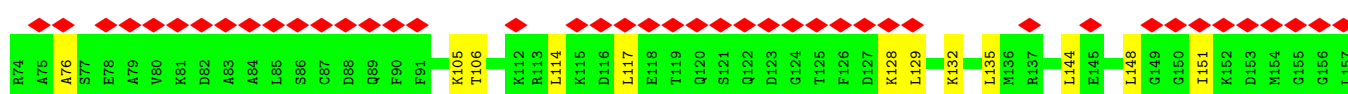
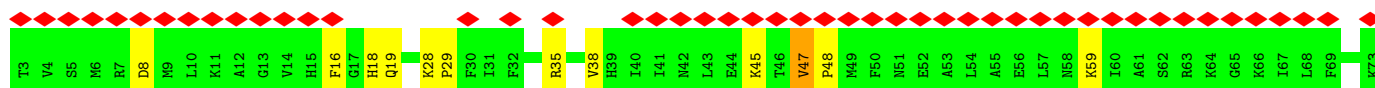
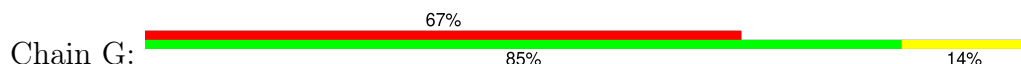
• Molecule 17: 30S ribosomal protein S20

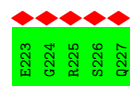


• Molecule 18: 30S ribosomal protein S21

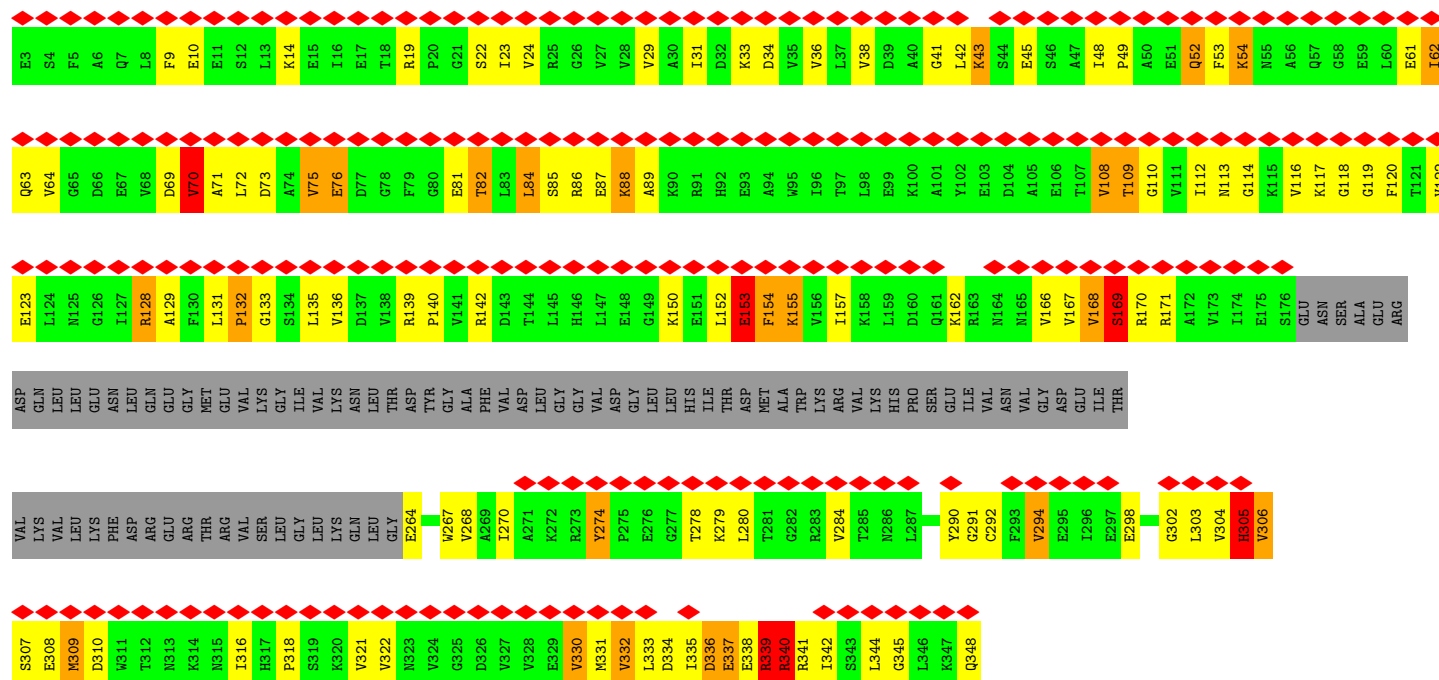
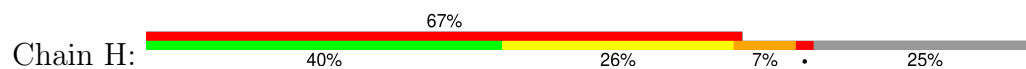


• Molecule 19: 30S ribosomal protein S2





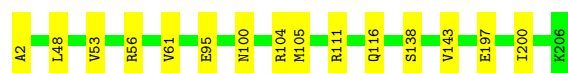
• Molecule 20: 30S ribosomal protein S1



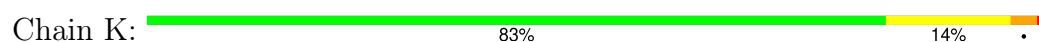
• Molecule 21: 30S ribosomal protein S3



• Molecule 22: 30S ribosomal protein S4

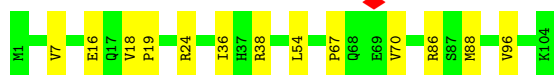


• Molecule 23: 30S ribosomal protein S5



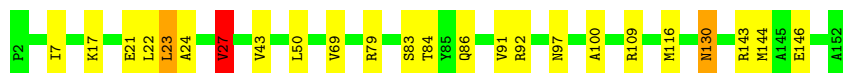
• Molecule 24: 30S ribosomal protein S6

Chain L:  88% 12%



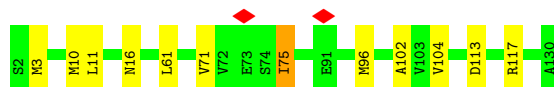
- Molecule 25: 30S ribosomal protein S7

Chain M:  84% 14% ..



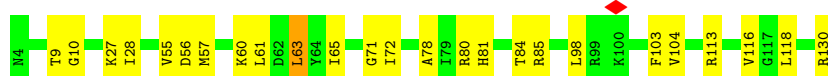
- Molecule 26: 30S ribosomal protein S8

Chain N:  91% 9% .



- Molecule 27: 30S ribosomal protein S9

Chain O:  80% 19% .



- Molecule 28: 30S ribosomal protein S10

Chain P:  81% 16% ..



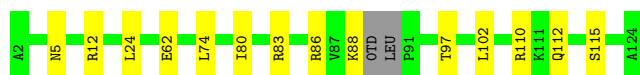
- Molecule 29: 30S ribosomal protein S11

Chain Q:  91% 9%



- Molecule 30: 30S ribosomal protein S12

Chain R:  87% 11% .



- Molecule 31: 30S ribosomal protein S14

Chain S:  92% 6% ..



- Molecule 32: 30S ribosomal protein S15

Chain T:  80% 18% .



- Molecule 33: 30S ribosomal protein S16

Chain U:  87% 12% .



- Molecule 34: 30S ribosomal protein S17

Chain V:  91% 8% .



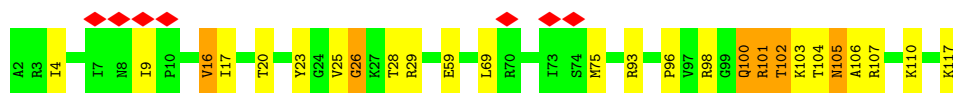
- Molecule 35: 30S ribosomal protein S19

Chain W:  90% 8% .

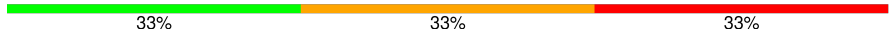


- Molecule 36: 30S ribosomal protein S13

Chain X:  6% 78% 17% 5%



- Molecule 37: mRNA in the ribosomal RNA entrance pore

Chain Y:  33% 33% 33%



- Molecule 38: 23S rRNA

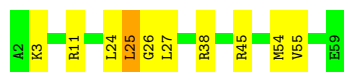
73% 23%





- Molecule 43: 50S ribosomal protein L30

Chain f: 83% 16%



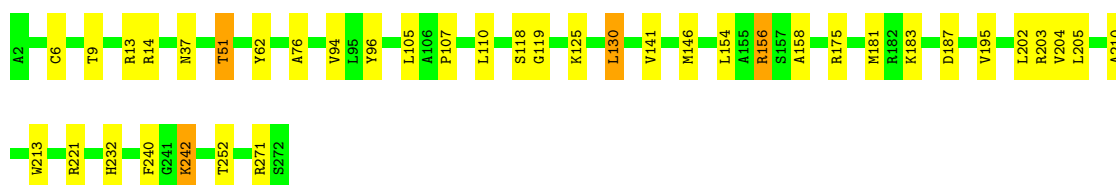
- Molecule 44: 50S ribosomal protein L31

Chain g: 85% 14%



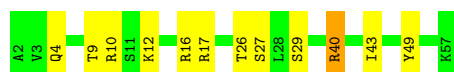
- Molecule 45: 50S ribosomal protein L2

Chain h: 86% 13%



- Molecule 46: 50S ribosomal protein L32

Chain i: 79% 20%



- Molecule 47: 50S ribosomal protein L3

Chain j: 87% 12%



- Molecule 48: 50S ribosomal protein L33

Chain k: 94% 6%



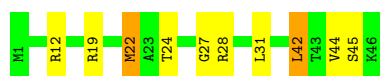
- Molecule 49: 50S ribosomal protein L4

Chain l:  85% 14%



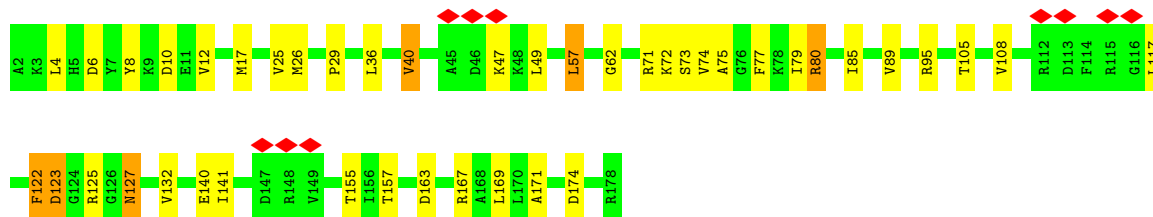
- Molecule 50: 50S ribosomal protein L34

Chain m:  78% 17%



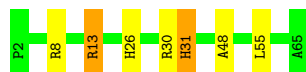
- Molecule 51: 50S ribosomal protein L5

Chain n:  6% 76% 21%



- Molecule 52: 50S ribosomal protein L35

Chain o:  89% 8%



- Molecule 53: 50S ribosomal protein L6

Chain p:  91% 9%

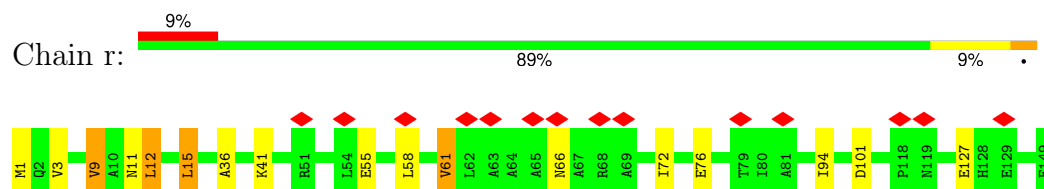


- Molecule 54: 50S ribosomal protein L36

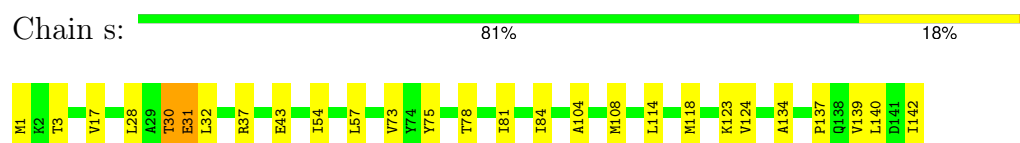
Chain q:  89% 8%



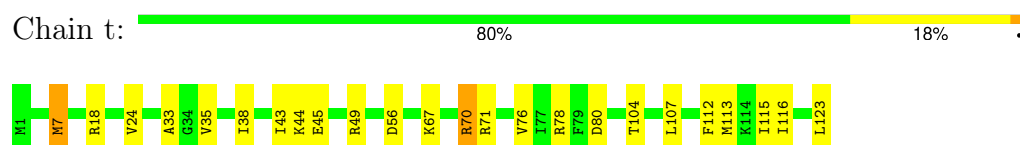
- Molecule 55: 50S ribosomal protein L9



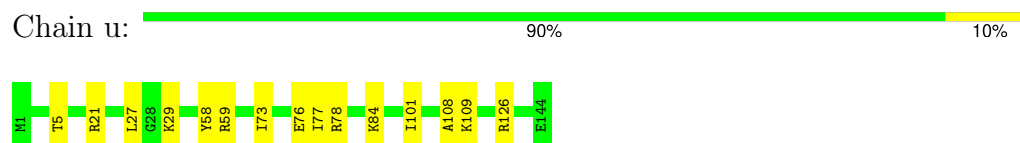
- Molecule 56: 50S ribosomal protein L13



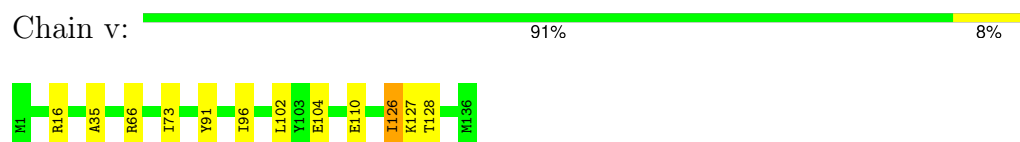
- Molecule 57: 50S ribosomal protein L14



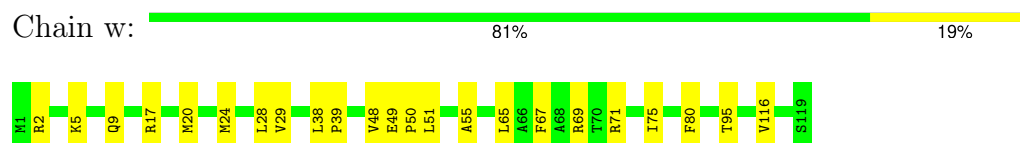
- Molecule 58: 50S ribosomal protein L15



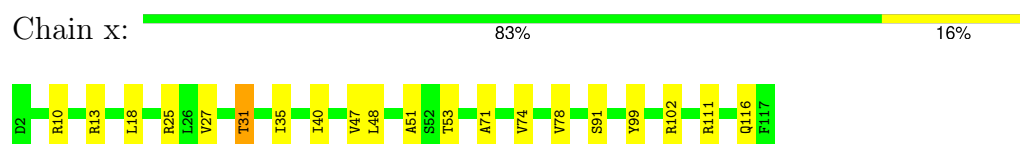
- Molecule 59: 50S ribosomal protein L16



- Molecule 60: 50S ribosomal protein L17

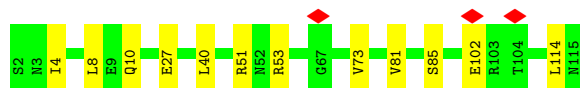


- Molecule 61: 50S ribosomal protein L18



- Molecule 62: 50S ribosomal protein L19

Chain y:  89% 11%



- Molecule 63: 50S ribosomal protein L20

Chain z:  85% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6237	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.334	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.0197	Depositor
Map size ($\text{\AA}$)	564.48, 564.48, 564.48	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.9399998, 2.9399998, 2.9399998	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	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.53	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.75	4/388 (1.0%)	0.55	0/604
9	A	0.35	0/1810	0.72	3/2821 (0.1%)
9	B	0.41	0/1810	0.86	8/2821 (0.3%)
10	AA	0.64	12/9768 (0.1%)	0.92	46/13191 (0.3%)
11	AB	0.43	1/808 (0.1%)	0.70	2/1088 (0.2%)
12	AC	0.57	5/1808 (0.3%)	0.71	9/2450 (0.4%)
12	AD	0.39	0/1789	0.55	0/2425
13	AE	0.54	7/10545 (0.1%)	0.74	25/14236 (0.2%)
14	AF	0.47	0/657	0.73	0/886
15	C	0.66	0/553	1.14	2/743 (0.3%)
16	D	0.38	4/36582 (0.0%)	0.74	30/57043 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.71	0/597	1.20	0/792
19	G	0.63	0/1791	1.06	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.57	0/1663	0.97	0/2241
22	J	0.61	0/1665	1.05	0/2227
23	K	0.64	0/1165	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.67	0/1195	1.19	3/1602 (0.2%)
26	N	0.54	0/989	0.91	0/1326
27	O	0.58	0/1034	1.02	1/1375 (0.1%)
28	P	0.54	0/800	1.05	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.68	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.45	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	0.89	1/65 (1.5%)	1.00	1/98 (1.0%)
38	a	0.40	3/69247 (0.0%)	0.75	57/107985 (0.1%)
39	b	0.50	0/589	0.76	0/779
40	c	0.63	0/635	0.97	0/848
41	d	0.37	0/2872	0.69	0/4478
42	e	0.69	0/502	1.19	0/667
43	f	0.62	0/452	1.02	0/605
44	g	0.55	0/531	0.99	1/709 (0.1%)
45	h	0.53	0/2121	0.85	0/2852
46	i	0.52	0/450	0.94	0/599
47	j	0.59	0/1586	0.87	0/2134
48	k	0.46	0/433	0.80	0/576
49	l	0.61	0/1571	1.03	1/2113 (0.0%)
50	m	0.68	0/380	1.22	0/498
51	n	0.62	0/1434	1.18	10/1926 (0.5%)
52	o	0.63	0/513	1.11	1/676 (0.1%)
53	p	0.57	0/1333	0.89	0/1805
54	q	0.50	0/303	0.88	0/397
55	r	0.63	0/1122	0.97	1/1515 (0.1%)
56	s	0.68	0/1152	1.02	2/1551 (0.1%)
57	t	0.57	0/955	0.88	0/1279
58	u	0.54	0/1062	0.95	1/1413 (0.1%)
59	v	0.59	0/1093	0.96	0/1460
60	w	0.67	0/964	1.13	0/1289
61	x	0.60	0/902	1.09	0/1209
62	y	0.52	0/929	0.79	0/1242
63	z	0.80	0/960	1.25	0/1278
All	All	0.48	43/186288 (0.0%)	0.83	249/274880 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	A	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	B	0	2
10	AA	0	11
13	AE	0	5
14	AF	0	1
20	H	0	3
36	X	0	1
All	All	0	25

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	AA	374	GLU	C-N	17.53	1.54	1.33
10	AA	850	ILE	N-CA	-13.22	1.29	1.46
13	AE	93	THR	CA-C	12.16	1.69	1.52
20	H	169	SER	N-CA	11.77	1.61	1.46
13	AE	70	CYS	CA-CB	-8.64	1.41	1.53

The worst 5 of 249 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	AA	727	VAL	N-CA-C	-17.23	95.06	110.74
20	H	88	LYS	CA-C-N	16.94	143.58	120.38
20	H	88	LYS	C-N-CA	16.94	143.58	120.38
9	B	29	G	C3'-C2'-O2'	15.97	134.66	110.70
10	AA	374	GLU	CA-C-N	15.00	135.83	120.38

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A	19	G	Sidechain
9	A	7	G	Sidechain
10	AA	205	PRO	Peptide
10	AA	594	VAL	Peptide
10	AA	595	THR	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	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	259	261	22	0
7	6	542	305	306	15	0
8	7	347	169	169	17	0
9	A	1620	825	826	178	0
9	B	1620	812	827	137	0
10	AA	9610	9588	9587	269	0
11	AB	790	783	783	7	0
12	AC	1786	1813	1813	47	0
12	AD	1767	1789	1789	47	0
13	AE	10388	10612	10611	367	0
14	AF	655	663	663	15	0
15	C	544	559	560	23	0
16	D	32679	16431	16450	178	0
17	E	669	719	719	3	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	213	0
21	I	1636	1710	1710	4	0
22	J	1643	1707	1707	8	0
23	K	1152	1196	1196	17	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	35	0
26	N	979	1031	1031	6	0
27	O	1022	1070	1070	13	0
28	P	790	831	831	13	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	7	0
31	S	805	844	844	4	0
32	T	714	734	734	8	0
33	U	649	666	666	4	0
34	V	648	691	691	4	0
35	W	663	688	688	2	0
36	X	900	964	964	57	0
37	Y	60	28	31	22	0
38	a	61841	31077	31124	275	0
39	b	582	599	599	3	0
40	c	625	652	652	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	d	2569	1300	1301	4	0
42	e	501	531	531	5	0
43	f	448	488	488	6	0
44	g	522	520	520	11	0
45	h	2082	2154	2154	19	0
46	i	444	459	458	6	0
47	j	1565	1617	1616	16	0
48	k	426	464	464	0	0
49	l	1552	1619	1619	14	0
50	m	377	418	418	10	0
51	n	1410	1443	1444	28	0
52	o	504	572	572	3	0
53	p	1313	1358	1358	7	0
54	q	302	343	343	1	0
55	r	1111	1148	1148	5	0
56	s	1129	1162	1162	15	0
57	t	946	1023	1023	12	0
58	u	1053	1129	1129	7	0
59	v	1074	1157	1157	5	0
60	w	951	994	994	9	0
61	x	892	923	923	10	0
62	y	917	962	962	4	0
63	z	947	1020	1019	12	0
64	7	1	0	0	0	0
65	AE	2	0	0	0	0
All	All	173120	124652	124738	1964	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 7.

The worst 5 of 1964 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.60
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.53
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.49
10:AA:743:PRO:HB3	37:Y:73:U:C1'	1.42	1.44
20:H:71:ALA:C	20:H:72:LEU:HD12	1.49	1.36

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	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	49
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
4	3	101/103 (98%)	96 (95%)	4 (4%)	1 (1%)	12	49
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
10	AA	1217/1342 (91%)	1071 (88%)	124 (10%)	22 (2%)	6	34
11	AB	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
12	AC	228/230 (99%)	214 (94%)	12 (5%)	2 (1%)	14	51
12	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
13	AE	1329/1358 (98%)	1198 (90%)	122 (9%)	9 (1%)	18	56
14	AF	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
15	C	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
17	E	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
20	H	255/346 (74%)	189 (74%)	54 (21%)	12 (5%)	2	16
21	I	206/208 (99%)	196 (95%)	9 (4%)	1 (0%)	24	63
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	146 (95%)	7 (4%)	1 (1%)	21	59
24	L	102/104 (98%)	97 (95%)	4 (4%)	1 (1%)	12	49
25	M	149/151 (99%)	144 (97%)	4 (3%)	1 (1%)	18	56
26	N	127/129 (98%)	121 (95%)	5 (4%)	1 (1%)	16	54
27	O	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	54
28	P	97/99 (98%)	89 (92%)	7 (7%)	1 (1%)	12	49
29	Q	115/117 (98%)	104 (90%)	9 (8%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/123 (95%)	116 (99%)	1 (1%)	0	100	100
31	S	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	42
34	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
35	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
36	X	114/116 (98%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	b	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
40	c	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
42	e	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
43	f	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
44	g	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
45	h	269/271 (99%)	259 (96%)	9 (3%)	1 (0%)	30	67
46	i	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
47	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
48	k	50/52 (96%)	50 (100%)	0	0	100	100
49	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	63
50	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
51	n	175/177 (99%)	162 (93%)	11 (6%)	2 (1%)	11	46
52	o	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
53	p	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
54	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
56	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
57	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
58	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
59	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
60	w	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
61	x	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
62	y	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
63	z	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9035/9408 (96%)	8383 (93%)	588 (6%)	64 (1%)	20	56

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	AA	596	ASP
10	AA	853	ASP
10	AA	859	GLU
10	AA	862	LEU
10	AA	937	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	25
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	33
3	2	81/81 (100%)	77 (95%)	4 (5%)	22	43
4	3	84/84 (100%)	79 (94%)	5 (6%)	17	39
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	50
10	AA	1054/1157 (91%)	998 (95%)	56 (5%)	20	41
11	AB	86/98 (88%)	85 (99%)	1 (1%)	63	75
12	AC	198/198 (100%)	185 (93%)	13 (7%)	15	37
12	AD	196/198 (99%)	193 (98%)	3 (2%)	57	72
13	AE	1120/1134 (99%)	1046 (93%)	74 (7%)	15	37
14	AF	70/70 (100%)	68 (97%)	2 (3%)	37	58
15	C	57/57 (100%)	55 (96%)	2 (4%)	32	53
17	E	65/65 (100%)	61 (94%)	4 (6%)	16	38
18	F	60/60 (100%)	57 (95%)	3 (5%)	22	43
19	G	187/187 (100%)	175 (94%)	12 (6%)	16	37
20	H	137/297 (46%)	124 (90%)	13 (10%)	8	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	I	171/171 (100%)	164 (96%)	7 (4%)	27	49
22	J	172/172 (100%)	166 (96%)	6 (4%)	32	53
23	K	119/119 (100%)	111 (93%)	8 (7%)	15	36
24	L	91/91 (100%)	84 (92%)	7 (8%)	12	32
25	M	124/124 (100%)	113 (91%)	11 (9%)	9	28
26	N	104/104 (100%)	101 (97%)	3 (3%)	37	58
27	O	105/105 (100%)	99 (94%)	6 (6%)	18	40
28	P	86/86 (100%)	78 (91%)	8 (9%)	8	26
29	Q	90/90 (100%)	88 (98%)	2 (2%)	45	64
30	R	101/102 (99%)	95 (94%)	6 (6%)	18	39
31	S	83/83 (100%)	79 (95%)	4 (5%)	23	44
32	T	76/76 (100%)	65 (86%)	11 (14%)	3	13
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	32
34	V	74/74 (100%)	71 (96%)	3 (4%)	27	49
35	W	72/72 (100%)	66 (92%)	6 (8%)	10	30
36	X	94/94 (100%)	87 (93%)	7 (7%)	13	33
39	b	58/58 (100%)	57 (98%)	1 (2%)	53	69
40	c	67/67 (100%)	64 (96%)	3 (4%)	24	46
42	e	54/54 (100%)	51 (94%)	3 (6%)	19	40
43	f	48/48 (100%)	43 (90%)	5 (10%)	7	22
44	g	59/59 (100%)	54 (92%)	5 (8%)	10	29
45	h	216/216 (100%)	199 (92%)	17 (8%)	11	32
46	i	47/47 (100%)	41 (87%)	6 (13%)	4	15
47	j	164/164 (100%)	156 (95%)	8 (5%)	22	43
48	k	47/47 (100%)	44 (94%)	3 (6%)	16	37
49	l	165/165 (100%)	151 (92%)	14 (8%)	10	29
50	m	38/38 (100%)	36 (95%)	2 (5%)	20	41
51	n	148/148 (100%)	130 (88%)	18 (12%)	5	17
52	o	51/51 (100%)	47 (92%)	4 (8%)	11	32
53	p	136/136 (100%)	130 (96%)	6 (4%)	25	47
54	q	34/34 (100%)	31 (91%)	3 (9%)	9	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	r	114/114 (100%)	102 (90%)	12 (10%)	6	21
56	s	116/116 (100%)	106 (91%)	10 (9%)	10	29
57	t	104/104 (100%)	97 (93%)	7 (7%)	15	36
58	u	103/103 (100%)	96 (93%)	7 (7%)	14	36
59	v	109/109 (100%)	105 (96%)	4 (4%)	30	51
60	w	99/99 (100%)	91 (92%)	8 (8%)	11	31
61	x	86/86 (100%)	80 (93%)	6 (7%)	14	35
62	y	99/99 (100%)	91 (92%)	8 (8%)	11	31
63	z	89/89 (100%)	85 (96%)	4 (4%)	24	46
All	All	7528/7820 (96%)	7054 (94%)	474 (6%)	18	37

5 of 474 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	L	7	VAL
58	u	84	LYS
32	T	73	LYS
58	u	27	LEU
63	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
45	h	70	ASN
52	o	28	ASN
62	y	15	GLN
13	AE	1249	ASN
13	AE	1238	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	D	1513/1534 (98%)	286 (18%)	33 (2%)
37	Y	2/3 (66%)	2 (100%)	0
38	a	2859/2903 (98%)	541 (18%)	0
41	d	119/120 (99%)	17 (14%)	0
8	7	15/16 (93%)	7 (46%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	A	75/76 (98%)	29 (38%)	6 (8%)
9	B	75/76 (98%)	34 (45%)	5 (6%)
All	All	4658/4728 (98%)	916 (19%)	44 (0%)

5 of 916 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	56	U
8	7	57	G
8	7	58	A
8	7	59	U
8	7	60	U

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	793	U
16	D	1212	U
16	D	991	U
16	D	1145	A
16	D	1214	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 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

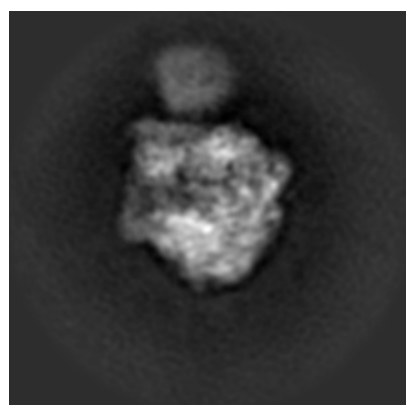
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21483. These allow visual inspection of the internal detail of the map and identification of artifacts.

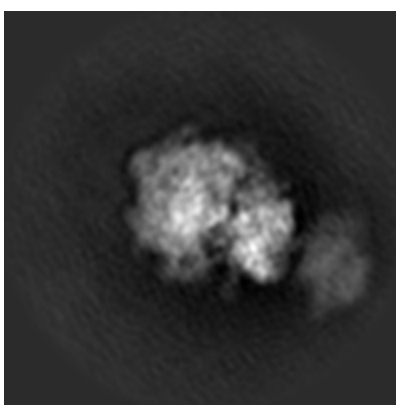
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

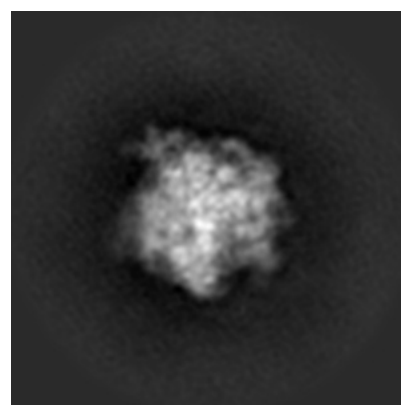
6.1.1 Primary map



X



Y

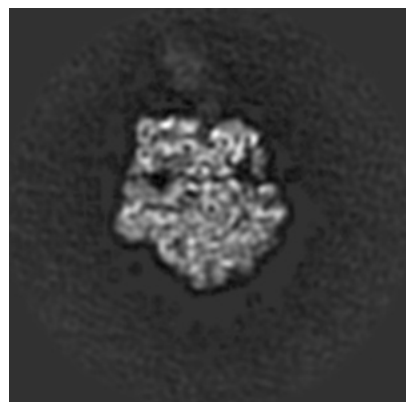


Z

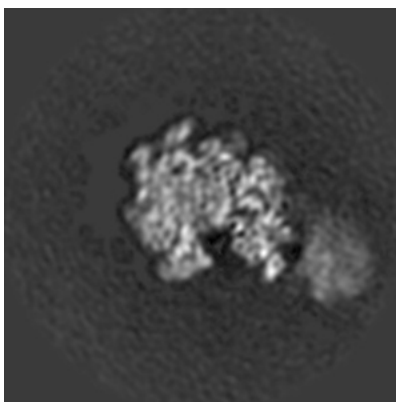
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

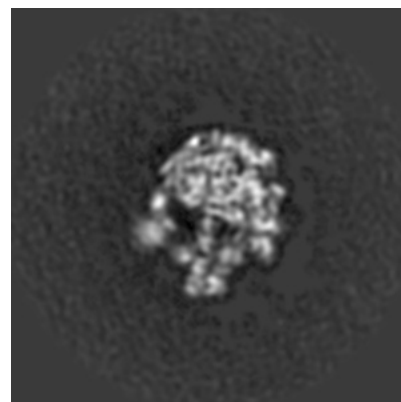
6.2.1 Primary map



X Index: 96



Y Index: 96

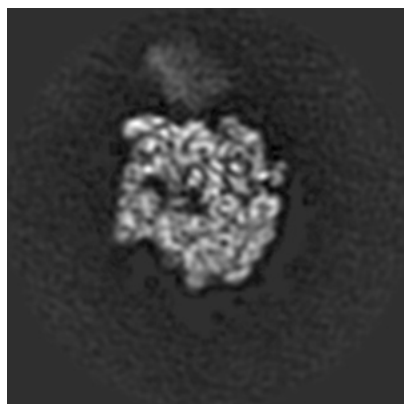


Z Index: 96

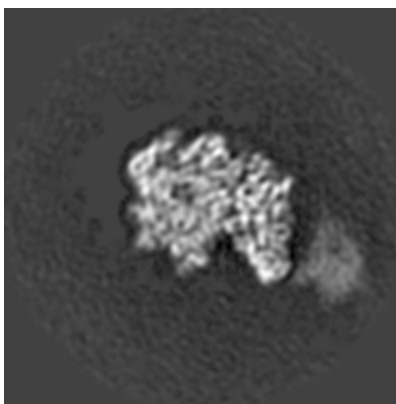
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

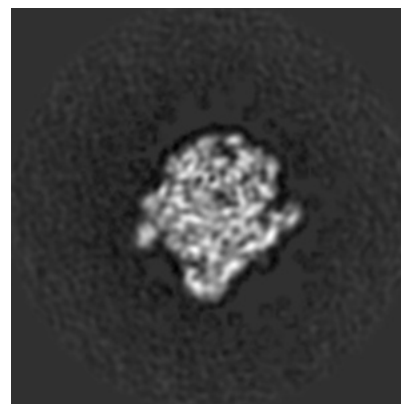
6.3.1 Primary map



X Index: 89



Y Index: 102

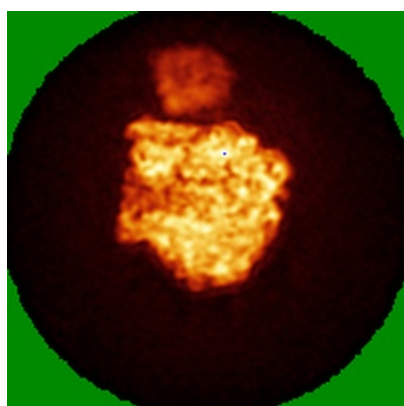


Z Index: 89

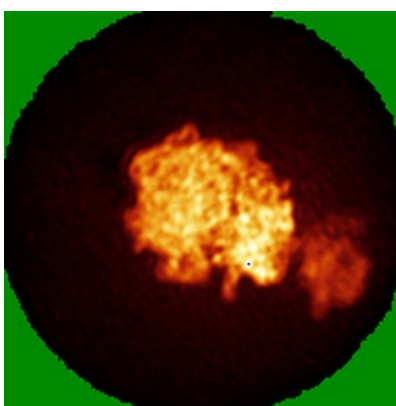
The images above show the largest variance slices of the map in three orthogonal directions.

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

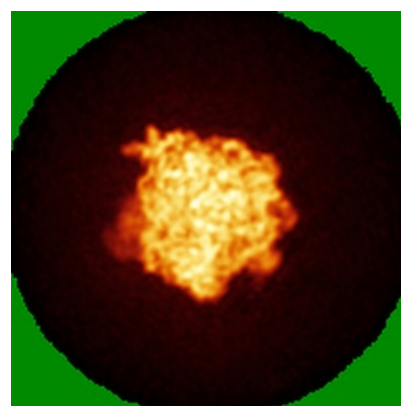
6.4.1 Primary map



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 0.0197. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

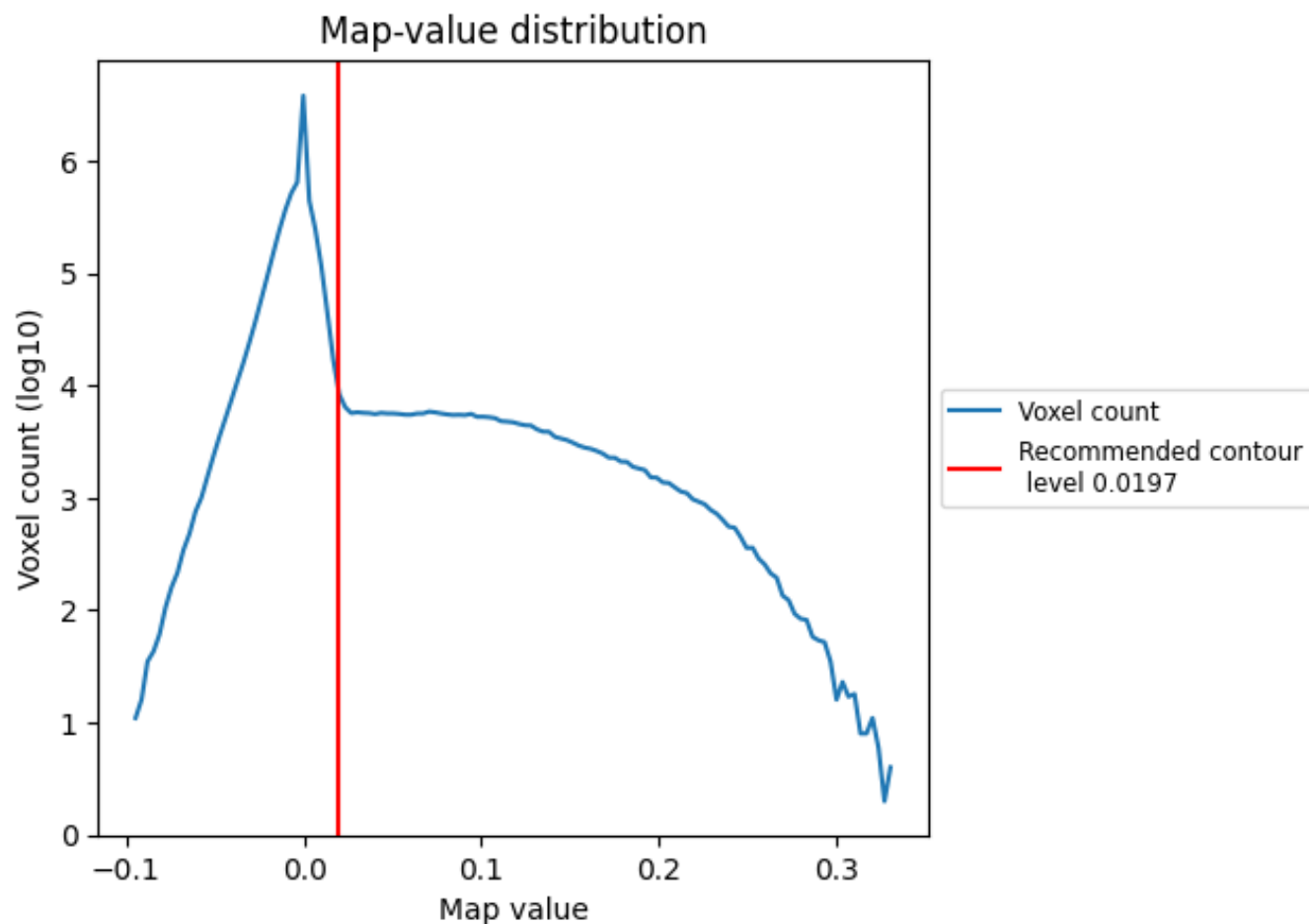
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

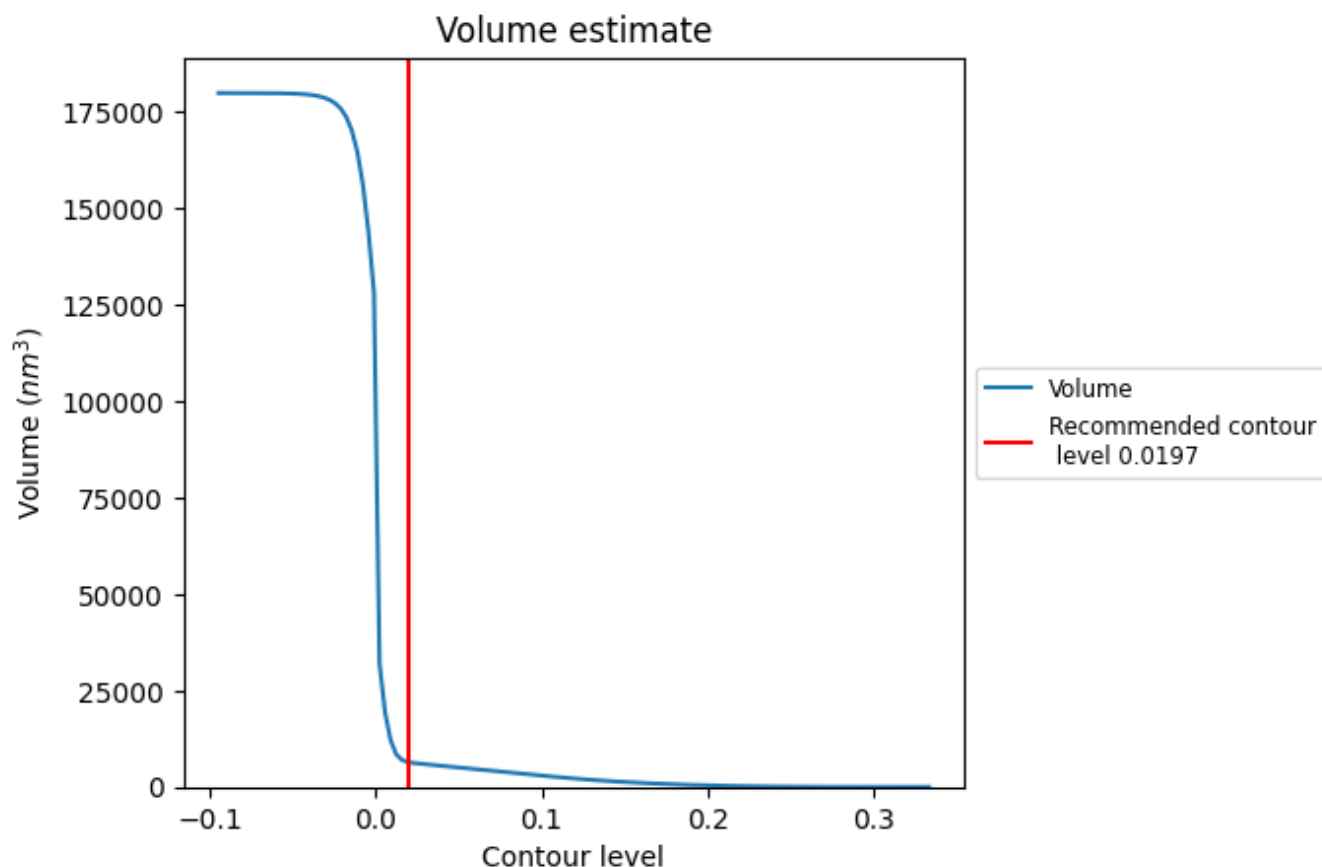
This section contains the results of statistical analysis of the map.

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.

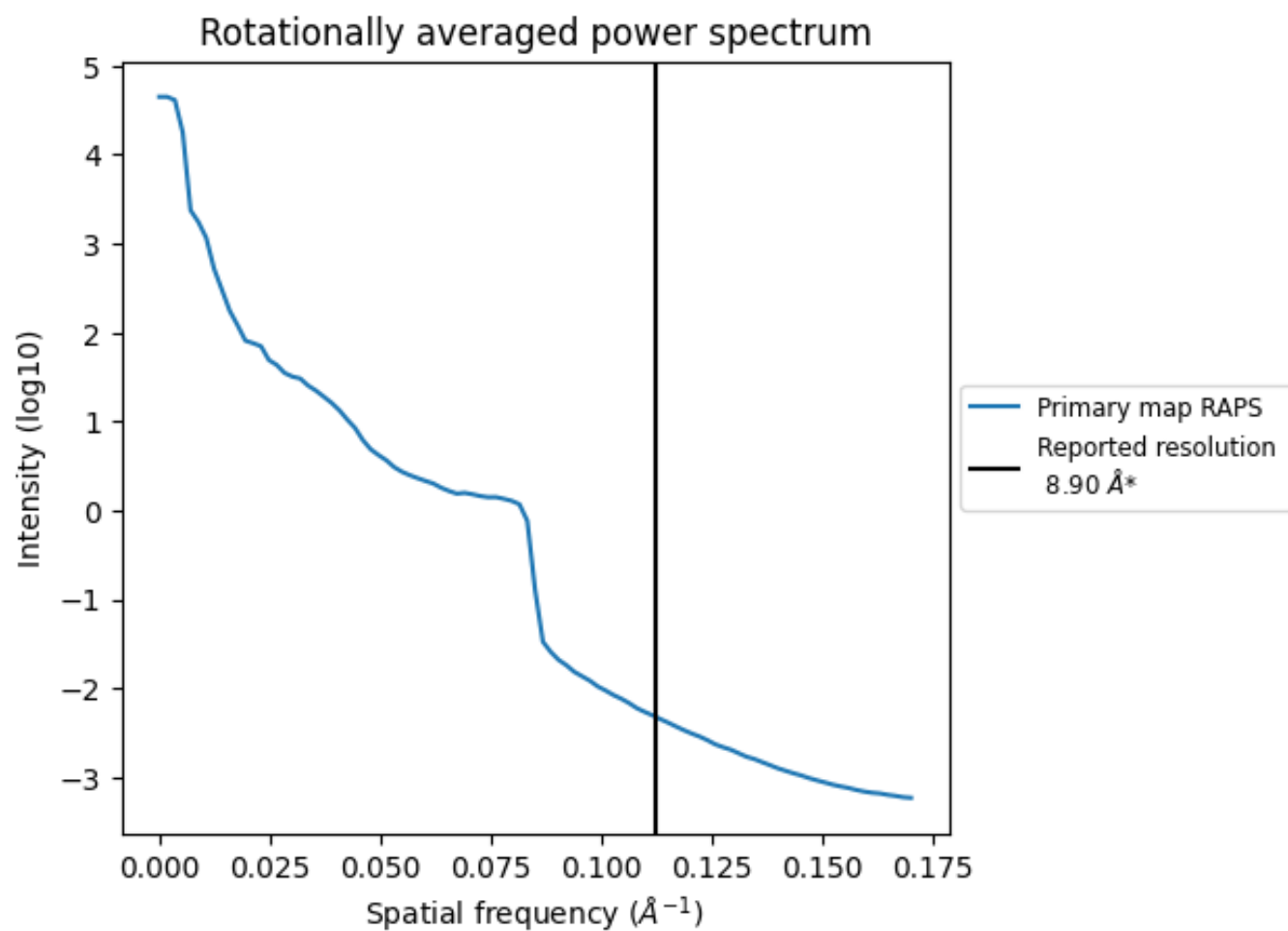
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6434 nm³; this corresponds to an approximate mass of 5812 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 0.112 Å⁻¹

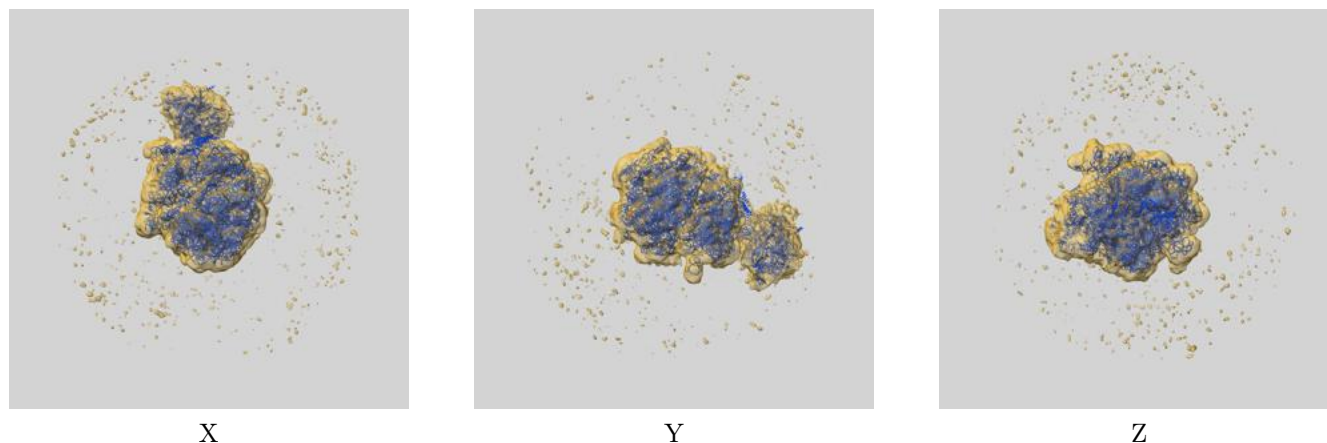
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

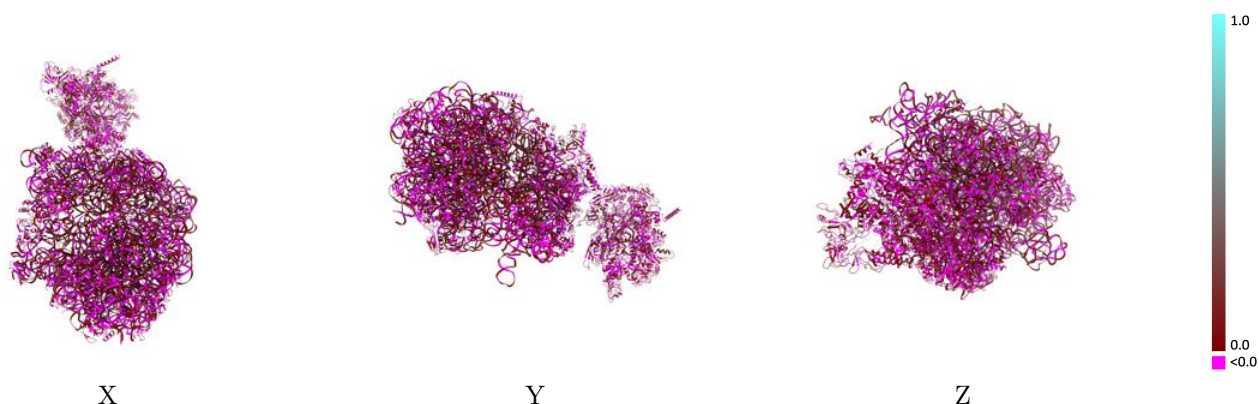
This section contains information regarding the fit between EMDB map EMD-21483 and PDB model 6VZ3. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



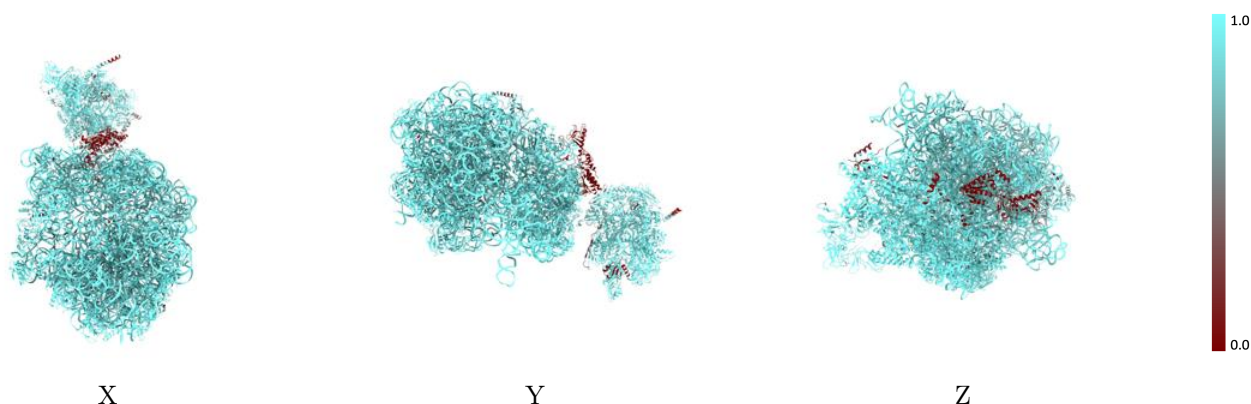
The images above show the 3D surface view of the map at the recommended contour level 0.0197 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



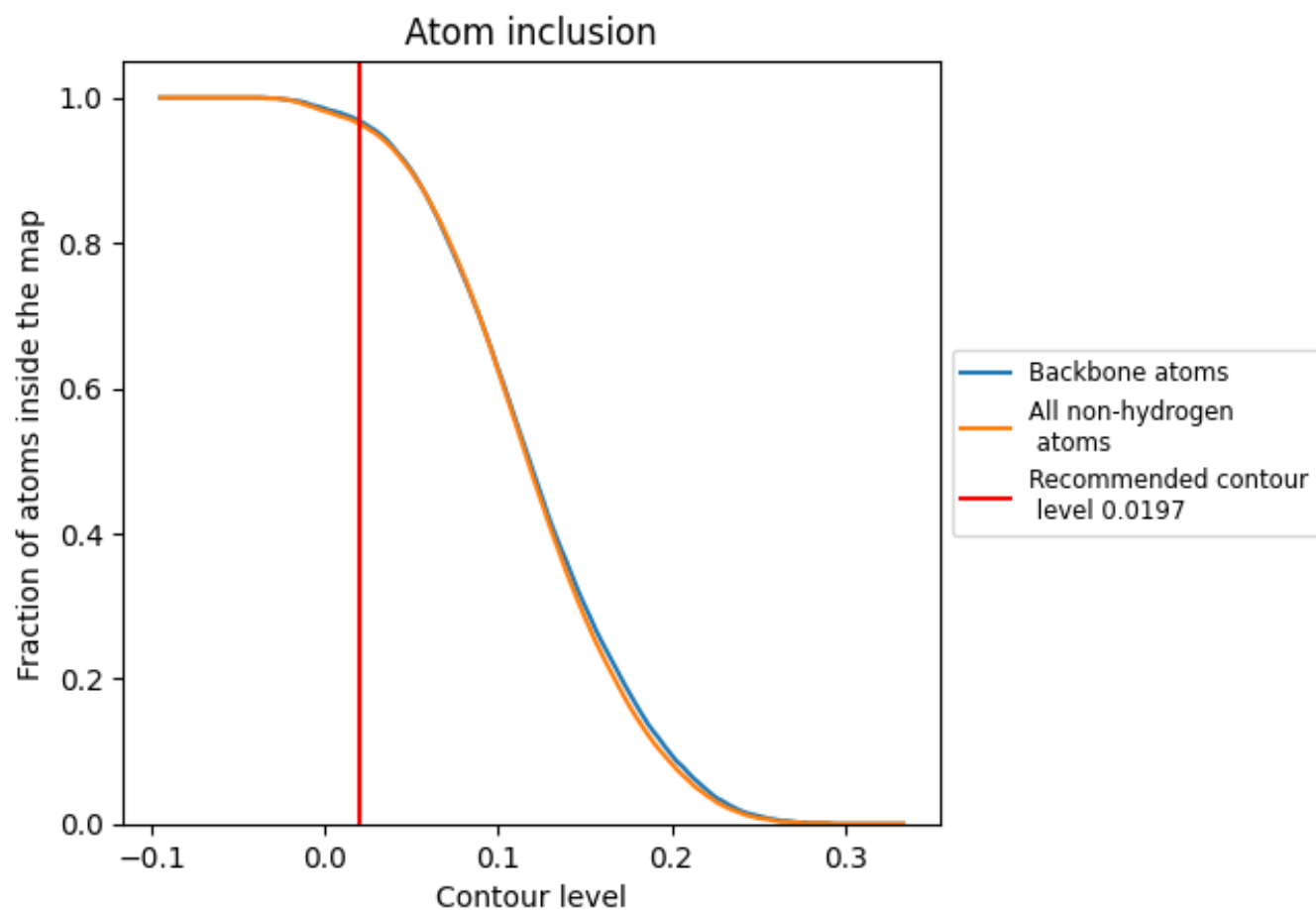
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0197).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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 (0.0197) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.0360
0	 1.0000	 0.0130
1	 0.9990	 0.0250
2	 0.9670	 -0.0180
3	 0.9520	 0.0010
4	 1.0000	 -0.0000
5	 1.0000	 0.0730
6	 1.0000	 0.0440
7	 0.9540	 0.0090
A	 0.9590	 0.0810
AA	 0.9710	 0.0400
AB	 0.5750	 0.0040
AC	 0.9150	 0.0330
AD	 0.9500	 0.0270
AE	 0.9790	 0.0280
AF	 0.7320	 0.0140
B	 0.9330	 0.0560
C	 1.0000	 -0.0030
D	 0.9940	 0.0540
E	 0.9560	 0.0050
F	 0.9160	 0.0160
G	 0.3210	 -0.0110
H	 0.1170	 -0.0150
I	 0.9790	 0.0010
J	 0.9960	 -0.0040
K	 0.9990	 0.0330
L	 0.9710	 0.0180
M	 0.9860	 0.0160
N	 0.9780	 -0.0090
O	 0.9800	 -0.0120
P	 1.0000	 0.0170
Q	 0.9980	 0.0410
R	 0.9850	 0.0570
S	 1.0000	 -0.0100
T	 0.9970	 0.0270



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Chain	Atom inclusion	Q-score
U	 1.0000	 -0.0030
V	 0.9680	 0.0380
W	 0.9800	 0.0130
X	 0.9200	 0.0010
Y	 0.9830	 0.0490
a	 0.9910	 0.0480
b	 1.0000	 -0.0500
c	 0.9670	 0.0210
d	 0.9940	 0.0220
e	 0.9880	 -0.0240
f	 1.0000	 -0.0180
g	 0.9800	 0.0450
h	 0.9990	 0.0270
i	 1.0000	 -0.0160
j	 0.9920	 -0.0040
k	 0.9760	 0.0090
l	 0.9890	 0.0100
m	 0.9940	 0.0080
n	 0.9340	 0.0220
o	 1.0000	 -0.0110
p	 0.9970	 0.0250
q	 1.0000	 -0.0170
r	 0.8620	 -0.0060
s	 0.9960	 -0.0100
t	 0.9980	 0.0200
u	 1.0000	 -0.0030
v	 0.9890	 0.0390
w	 1.0000	 -0.0080
x	 0.9990	 0.0190
y	 0.9750	 -0.0080
z	 1.0000	 -0.0240