



wwPDB EM Validation Summary Report ⓘ

Dec 28, 2024 – 09:32 AM EST

PDB ID : 6VU3
EMDB ID : EMD-21386
Title : Cryo-EM structure of Escherichia coli transcription-translation complex A (TTC-A) containing mRNA with a 12 nt long spacer
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.
Deposited on : 2020-02-14
Resolution : 3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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

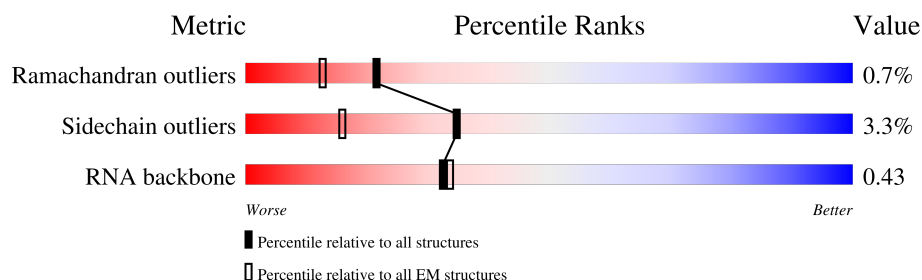
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



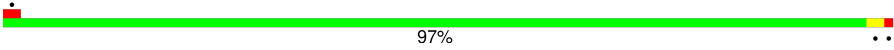







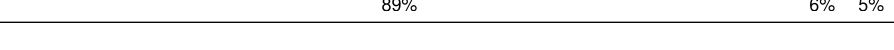
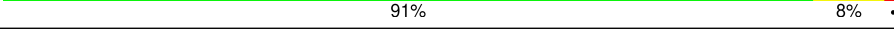

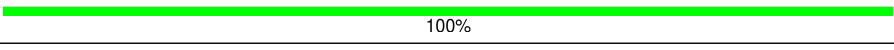
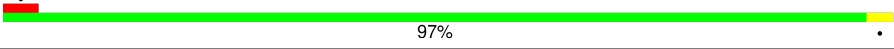
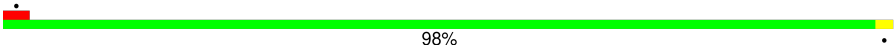

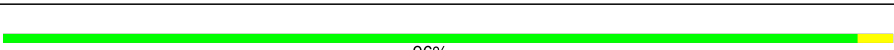

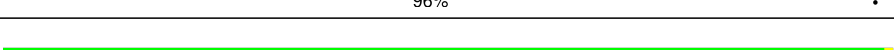
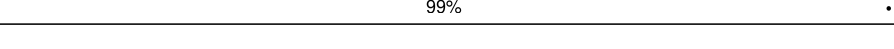
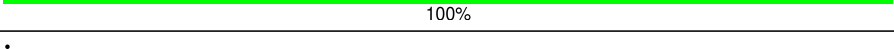
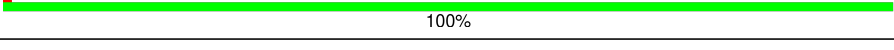
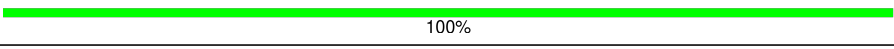
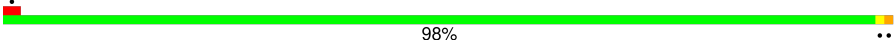

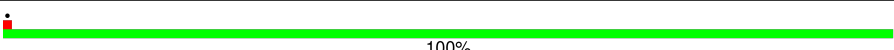
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	
4	3	103	
5	4	94	
6	5	36	
7	6	27	
8	7	29	

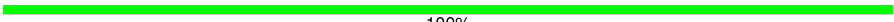













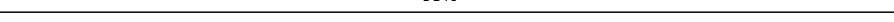
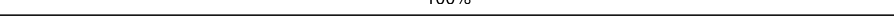
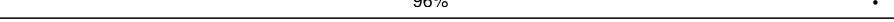
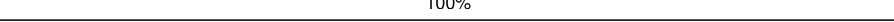
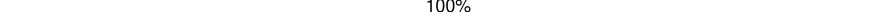
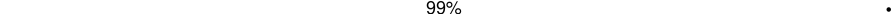

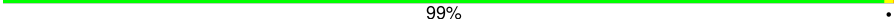
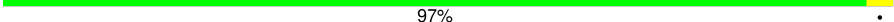
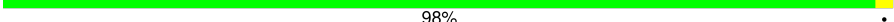

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Mol	Chain	Length	Quality of chain
9	9	148	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	230	
13	AD	230	
14	AE	1407	
15	C	66	
16	D	1542	
17	E	86	
18	F	70	
19	G	225	
20	H	557	
21	I	208	
22	J	205	
23	K	156	
24	L	104	
25	M	151	
26	N	129	
27	O	127	
28	P	99	
29	Q	117	
30	R	124	
31	S	100	

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Mol	Chain	Length	Quality of chain
32	T	88	 100%
33	U	82	 99%
34	V	80	 99%
35	W	83	 100%
36	X	116	 99%
37	Y	141	 99%
38	Z	30	 100%
39	a	2904	 75% 22%
40	b	76	 5% 97%
41	c	77	 100%
42	d	120	 83% 17%
43	e	62	 100%
44	f	58	 100%
45	g	66	 6% 98%
46	h	271	 100%
47	i	56	 96%
48	j	209	 100%
49	k	52	 100%
50	l	201	 99%
51	m	46	 93% 7%
52	n	177	 99%
53	o	64	 97%
54	p	175	 98%
55	q	38	 95% 5%
56	r	149	 100%

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Mol	Chain	Length	Quality of chain
57	s	142	 100%
58	t	123	 100%
59	u	144	 100%
60	v	136	 99% .
61	w	119	 99% .
62	x	116	 100%
63	y	114	 99% .
64	z	117	 99% .

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300609 atoms, of which 124724 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
			732	225	260	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
			848	259	306	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 12 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	29	Total	C	H	N	O	P	0	0
			709	273	97	94	216	29		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and A-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AA	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	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
13	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	conflict	UNP A0A4S1NBU2

- 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	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- 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 protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 39 is a RNA chain called 23S rRNA.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 40 is a protein called 50S ribosomal protein L27.

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

- Molecule 41 is a protein called 50S ribosomal protein L28.

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

- Molecule 42 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 43 is a protein called 50S ribosomal protein L29.

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

- Molecule 44 is a protein called 50S ribosomal protein L30.

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

- Molecule 45 is a protein called 50S ribosomal protein L31.

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

- Molecule 46 is a protein called 50S ribosomal protein L2.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L3.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L5.

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

- Molecule 53 is a protein called 50S ribosomal protein L35.

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

- Molecule 54 is a protein called 50S ribosomal protein L6.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a protein called 50S ribosomal protein L13.

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

- Molecule 58 is a protein called 50S ribosomal protein L14.

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

- Molecule 59 is a protein called 50S ribosomal protein L15.

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

- Molecule 60 is a protein called 50S ribosomal protein L16.

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

- Molecule 61 is a protein called 50S ribosomal protein L17.

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

- Molecule 62 is a protein called 50S ribosomal protein L18.

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

- Molecule 63 is a protein called 50S ribosomal protein L19.

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

- Molecule 64 is a protein called 50S ribosomal protein L20.

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

- Molecule 65 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
65	7	1	Total	Mg	0
			1	1	

- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
66	AA	2	Total	Zn	0
			2	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: 50S ribosomal protein L21

Chain 0:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: 50S ribosomal protein L22

Chain 1:  100%

There are no outlier residues recorded for this chain.

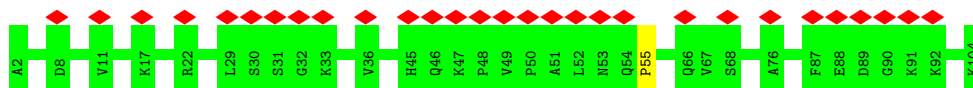
- Molecule 3: 50S ribosomal protein L23

Chain 2:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 50S ribosomal protein L24

Chain 3:  28% 99%



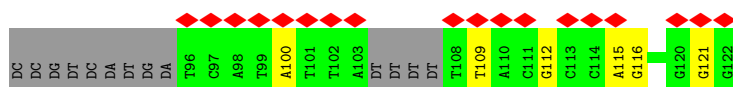
- Molecule 5: 50S ribosomal protein L25

Chain 4:  100%

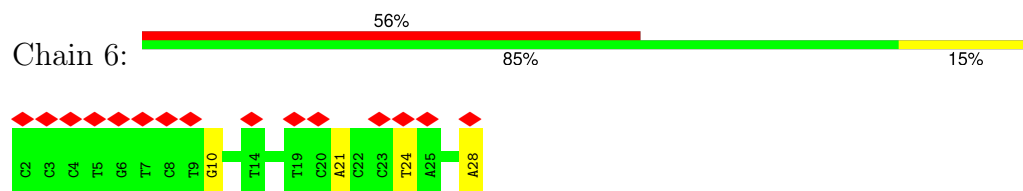
There are no outlier residues recorded for this chain.

- Molecule 6: NT DNA

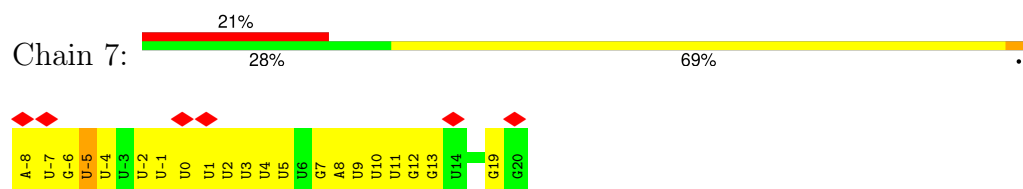
Chain 5:  50% 47% 17% 36%



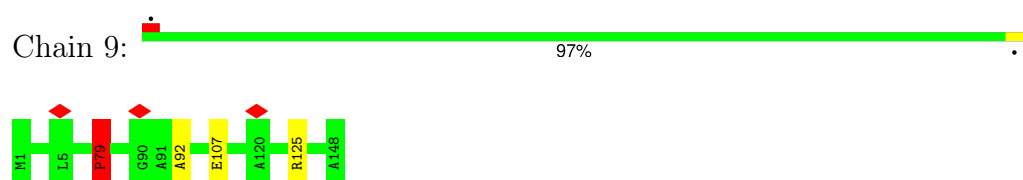
- Molecule 7: T DNA



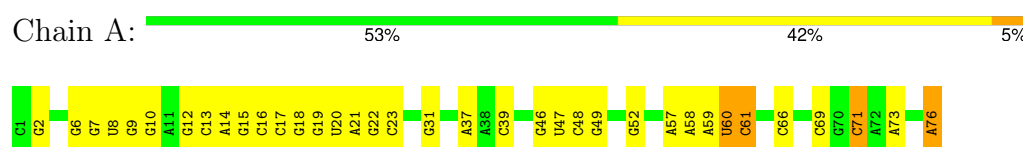
- Molecule 8: mRNA with 12 nt long spacer



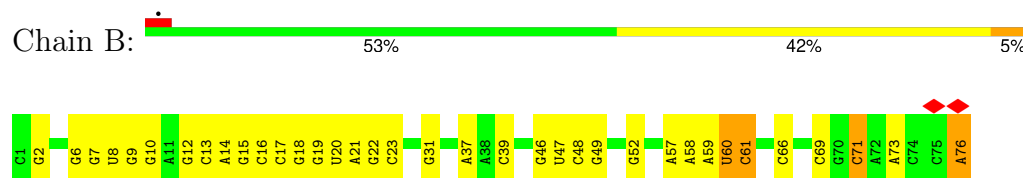
- Molecule 9: 50S ribosomal protein L10



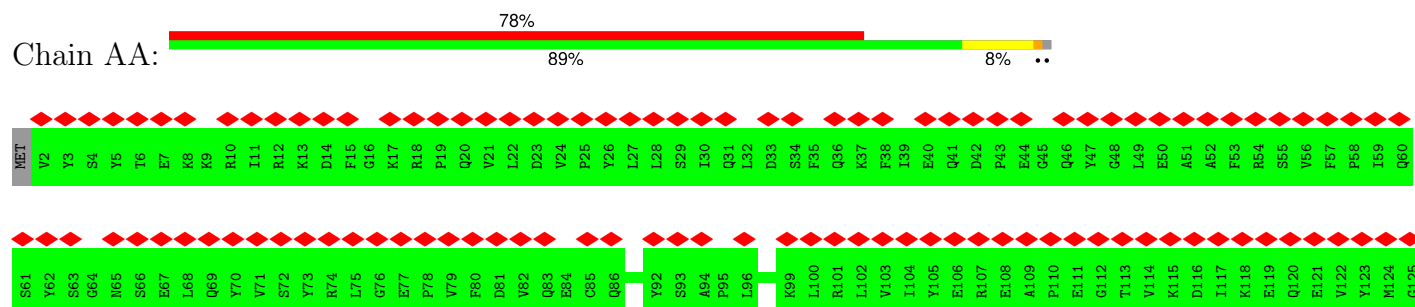
- Molecule 10: E-site and A-site tRNA (fMet)



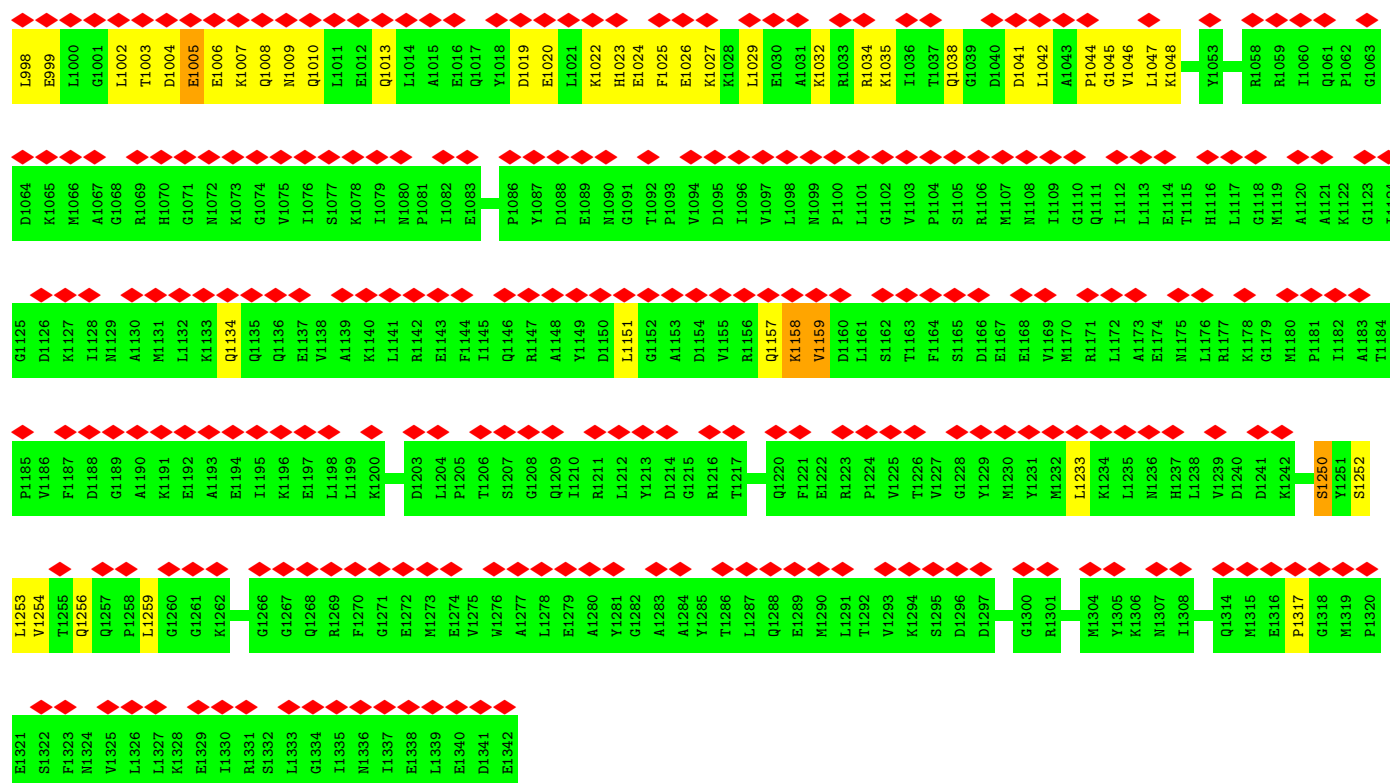
- Molecule 10: E-site and A-site tRNA (fMet)



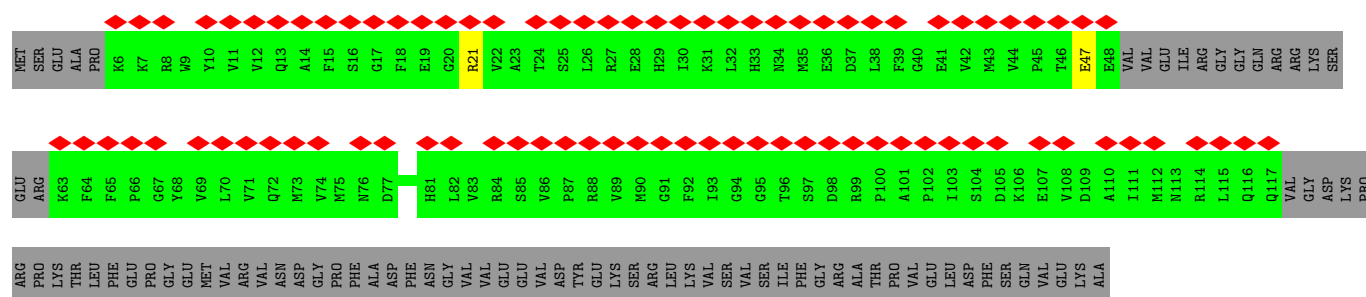
- Molecule 11: DNA-directed RNA polymerase subunit beta



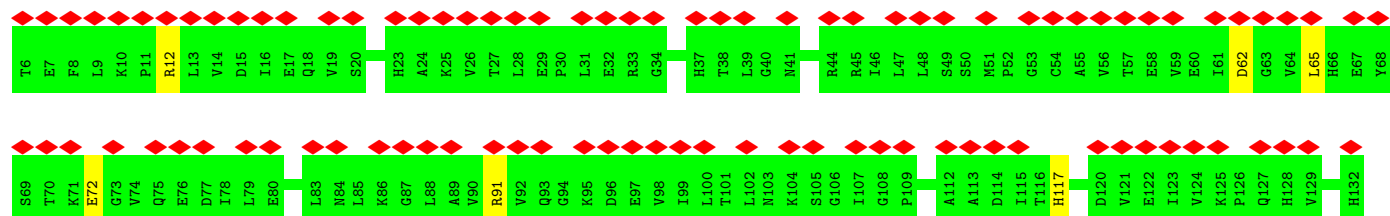
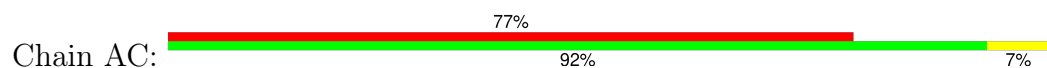
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E940	S868	R802	V736	D675	H613	T553	M492	L432	P372	C311	T250	P190	P128
K941	G869	V802	N737	A676	V614	H554	L493	L433	G373	A312	S252	D192	L129
D942	V871	A803	E738	N677	V615	Y555	M494	D434	E374	A313	F253	N193	M130
K943	I872	F804	D739	N678	L616	G556	A495	L435	P375	N314	D254	L194	H132
R944	I873	M805	E740	A679	A617	R557	K496	K436	P376	N315	L255	F195	N133
A945	G874	Q809	H741	L680	D618	V558	P497	N437	T377	E316	E256	V196	G134
L946	A875	Y810	V742	N681	A619	C559	L498	G438	R378	L317	A257	R197	T135
E947	E876	N811	P743	G682	N620	P560	T498	K439	E379	S318	N258	I198	F136
V948	V877	F812	G744	A683	S621	L561	A500	G440	A380	L319	G259	D199	V137
E949	L883	E813	E745	N684	N622	E582	A501	E441	A381	D320	K260	R200	I138
E950	V884	D814	A746	M685	L623	T563	V502	V442	E382	L321	V261	R201	
M951	G885	S815	G747	Q686	D624	P564	K503	D443	L384	L322	Y262	R202	T141
L953	K886	I816	I748	R687	E625	E585	E504	D444	F385	A323	V263	K203	E142
K954	P889	L817	D749	Q688	E626	P567	F505	I445	E386	K324	E264	L204	R143
Q955	V839	V818	I750	A699	G627	N568	F506	D446	N387	L325	K265	V144	V144
A956	G891	W819	Y751	V690	H628	T569	G507	H447	L388	S326	G266	A206	I145
K957	GLU	S819	N752	P691	F629	G570	S508	L448	F389	Q327	R267	T207	V146
K958	THR	E820	L753	T692	V630	L571	S509	G449	F389	H330	R268	I208	S147
D959	LEU	R821	T754	R694	E631	L572	Q510	L450	F390	L210	I209	L209	Q148
L960	THR	V822	T754	A695	D632	M573	L511	R451	S391	K331	T270	R211	L149
S961		E825	S759	D696	L633	S574	S512	R452	E392	R332	A271	R211	H150
E962	GLU	D826	M760	K697	V634	L575	Q513	L453	D393	L333	R272	A212	R151
E963	GLU	R827	Q761	P698	T635	S576	F514	R454	R394	E334	H273	L213	S152
L964	LEU	F828	N762	L699	C636	V577	M515	S455	Y395	T335	I274	M214	P153
Q965	LEU	T829	T763	R637	V636	Y578	D516	V456	D396	L336	R275	Y215	G154
V966	ARG	T830	C764	V700	S638	Y578	Q517	G457	L397	F337	Q276	T216	
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E968	ILE	T702	N766	T702	G640	Q580	N519	M459	A399	N339	E278	E218	D158
A969	PHE	G703	Q767	G703	E641	T581	N582	M459	V400	D340	K279	Q219	S159
GLY	GLY	M768	M768	M704	S642	N582	P520	A460	G401	D340	D280	I220	D160
GLU	GLU	L836	M769	E705	S643	E583	L521	E461	R402	L341	K161		K161
LYS	LYS	A837	P769	R706	S643	G585	S522	N462	R402	D342	D221		G162
ALA	ALA	A837	C770	R706	L644	G585	E523	Q463	K404	H343	D222		K163
S911	S911	S840	V771	A707	F645	F586	E523	Q463	K404	H343	D222		T164
D912	D912	T843	S772	V708	S646	L587	T525	R465	F405	G344	K283	F224	H165
V913	V913	K844	L773	A709	R647	E588	H526	V466	N406	P345	L284	F225	S166
K914	K914	L845	G774	V710	D647	T589	K527	G467	R407	Y346	I285	E226	S166
		G846	E775	D711	R647	P590	R528	L468	S408	T347	E286	E226	S167
S917	S917	P847	P776	S712	Q649	V591	R529	V469	L409	S348	K227	G168	
L918	L918	E848	V777	G713	V650	R592	L530	R470	L410	E349	V228	G169	
		V849	E778	V714	D651	R592	L530	R470	L410	E349	V228	G169	
S925	S925	T850	E778	V714	D651	R592	L530	R470	L410	E349	V228	G169	
G926	G926	E849	E778	V714	D651	R592	L530	R470	L410	E349	V228	G169	
V990	V990	I850	G713	T715	Y652	K593	S531	V471	R411	T350	L229	F230	V170
A981	A981	T851	G780	A716	M653	Y594	A532	E472	E412	R352	E231	E231	L171
V928	V928	A852	D781	V717	V655	T595	L533	R473	E413	V353	I232	I232	Y172
G983	G983	D853	D781	V717	V655	D596	L533	R473	E413	V353	I232	I232	N173
V984	V984	I854	V782	A718	V655	G597	G536	V475	E415	D354	A293	D234	A174
		P855	K719	R718	S656	G597	G536	V475	E415	D354	A293	D234	A174
E985	E985	N856	R720	A784	T657	V598	G537	K476	G416	P355	G294	N235	R175
F934	F934	H857	D785	V657	T657	V599	G537	K476	G416	P355	G294	N235	R175
A986	A986	V857	D785	V657	T657	V599	G537	K476	G416	P355	G294	N235	R175
E987	E987	T935	G786	Q658	Q658	V599	L538	E477	S417	K357	V296	K236	I176
R936	R936	G858	G786	Q658	Q658	V599	L538	E477	S417	K357	V296	K236	I176
K988	K988	E859	G786	Q658	Q658	V599	L538	E477	S417	K357	V296	K236	I176
L989	L989	A860	P787	V659	V659	D601	R540	L479	I419	D358	L237	Q238	P178
		R861	V787	V659	V659	D601	R540	L479	I419	D358	L237	Q238	P178
D990	D990	A861	S788	V659	V659	D601	R540	L479	I419	D358	L237	Q238	P178
		L862	V789	V659	V659	D601	R540	L479	I419	D358	L237	Q238	P178
K991	K991	S863	T789	V659	V659	D601	R540	L479	I419	D358	L237	Q238	P178
L992	L992	H604	V664	A665	G664	E602	E541	S480	L420	S361	A298	M239	R180
P993	P993	L791	A665	A665	G664	E602	E541	S480	L420	S361	A298	M239	R180
		L791	A665	A665	G664	E602	E541	S480	L420	S361	A298	M239	R180
R994	R994	A729	S666	S666	G664	E602	E541	S480	L420	S361	A298	M239	R180
		L791	A665	A665	G664	E602	E541	S480	L420	S361	A298	M239	R180
D995	D995	G792	L667	L667	S666	E602	E541	S480	L420	S361	A298	M239	R180
		E793	L667	L667	S666	E602	E541	S480	L420	S361	A298	M239	R180
K995	K995	L794	T668	T668	S666	E602	E541	S480	L420	S361	A298	M239	R180
		L794	T668	T668	S666	E602	E541	S480	L420	S361	A298	M239	R180
D996	D996	A795	F670	F670	S666	E602	E541	S480	L420	S361	A298	M239	R180
		L671	F670	F670	S666	E602	E541	S480	L420	S361	A298	M239	R180
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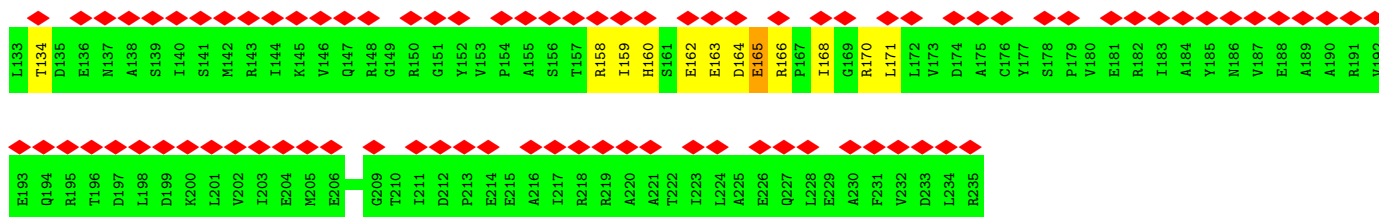


• Molecule 12: Transcription termination/antitermination protein NusG

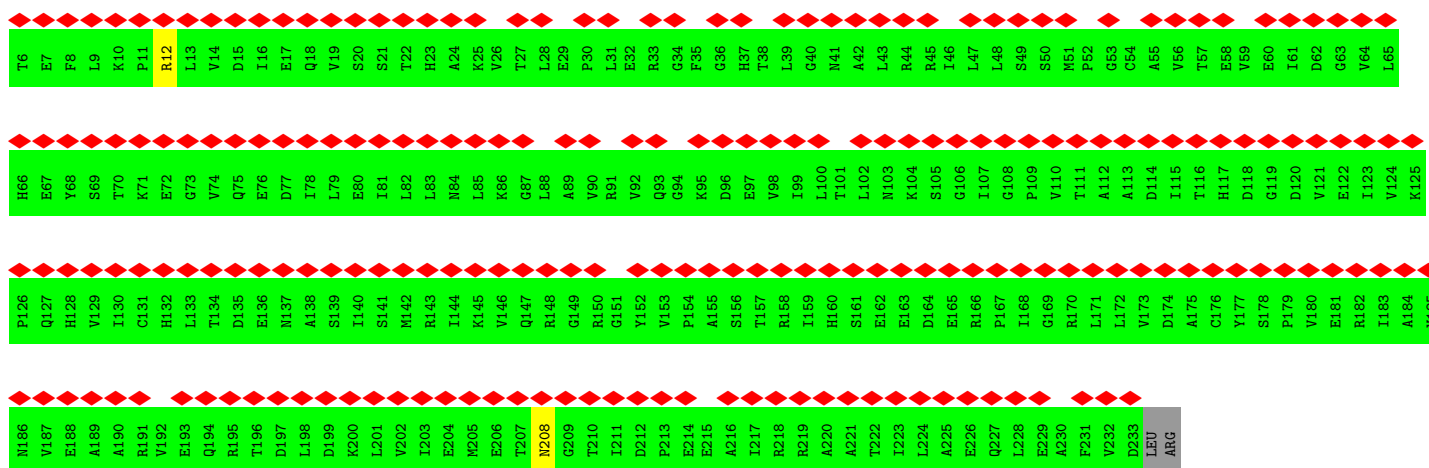


• Molecule 13: DNA-directed RNA polymerase subunit alpha

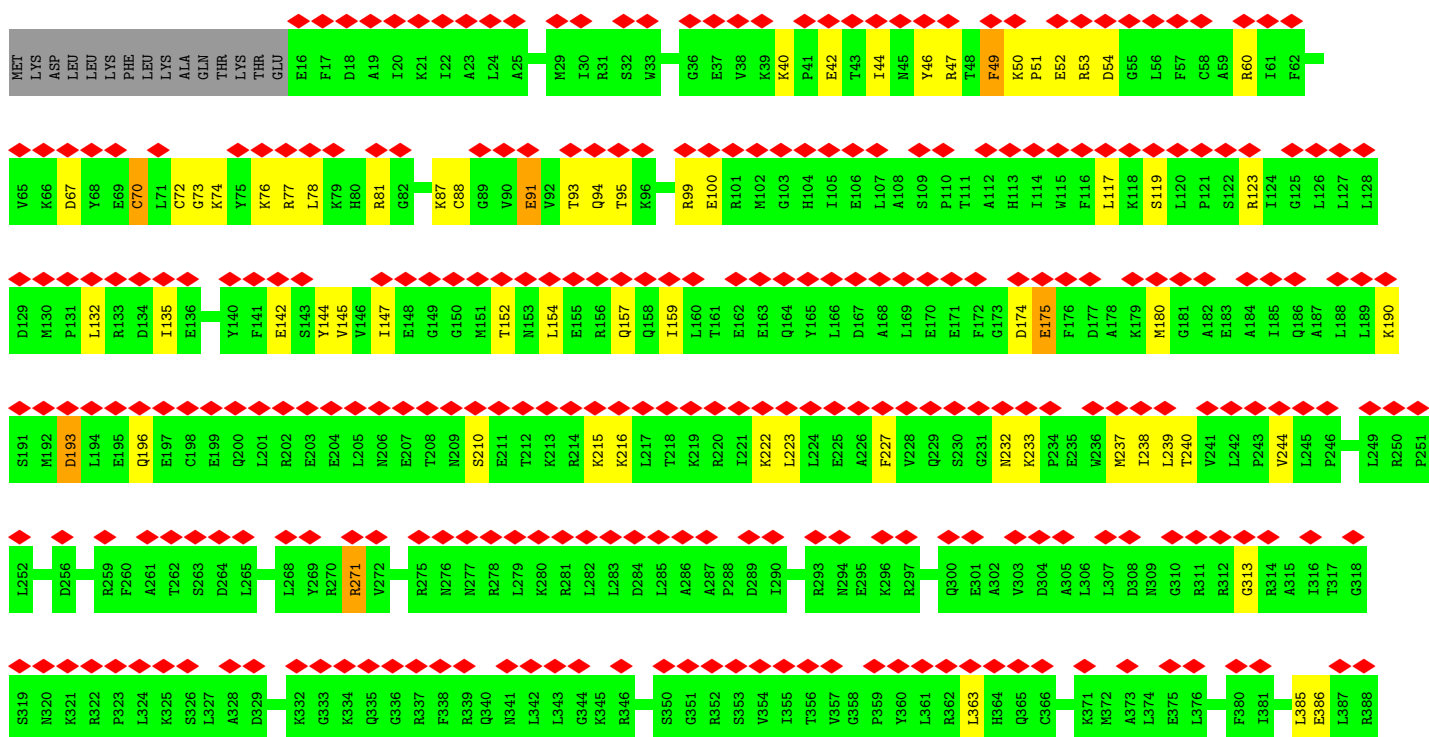
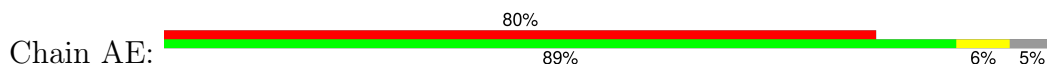




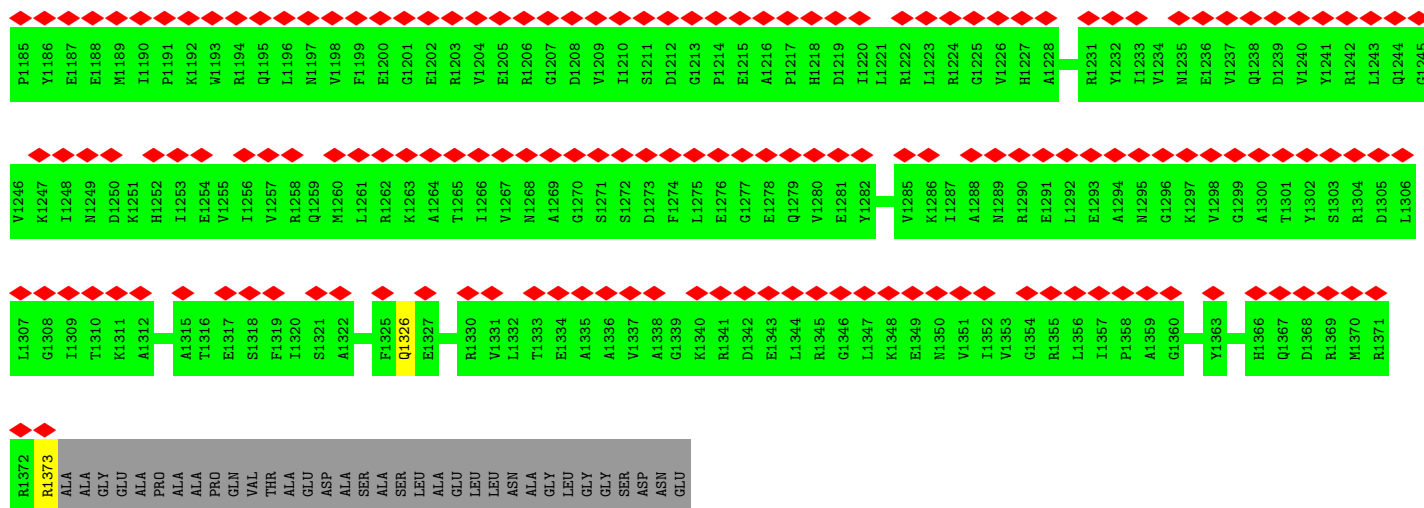
• Molecule 13: DNA-directed RNA polymerase subunit alpha



• Molecule 14: DNA-directed RNA polymerase subunit beta'

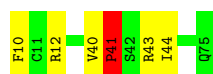


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Q702	T703	E704	T705	V706	I707	M708	R709	D710	G711	Q712	E713	E714	K715	Q716	V717	S718	F719	N720	S721	I722	V723	M724	M725	A726	D727	S728	G729	A730	R731	G732	S733	A734	T735	Q736	I737	R738	Q739	L740	A741	G742	M743	R744	G745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	E756	T757	P758	I759	T760	A761	
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W580	M581	I582	V583	P584	K585	G586	L587	P588	Y589	S590	V591	V592	N593	Q594	A595	L596	G597	K598	K599	A600	K603	M604	L605	N606	T607	C608	R610	I611	L612	G613	L614	K615	P616	T617	V618	I619	F620	A621	D622	Q623	I624	M625	Y626	T627	G628	F629	A630	Y631	A632	A633	R634	S635	G636	A637	S638	V639	G640			
N519	A520	K521	G522	E523	G524	M525	V526	L527	T528	G529	P530	K531	E532	A533	E534	R535	L536	Y537	R538	S539	G540	L541	A542	S543	L544	H545	A546	R547	V548	K549	R550	L551	I552	T553	E554	Y555	E556	K557	D558	A559	N560	G561	E562	L563	V564	A565	S566	T567	S568	L569	K570	D571	T572	G575	R576	A577	I578	L579		
A459	D460	F461	D462	G463	D464	Q465	M466	A467	V468	H469	P470	V471	L472	T473	L474	E475	A476	Q477	L478	E479	A480	R481	A482	L483	M484	M485	S486	T487	M488	L489	I490	L491	S492	P493	A494	M495	G496	E497	P498	I499	I500	V501	P502	S503	Q504	D505	V506	V507	L508	G509	L510	Y511	Y512	M513	T514	R515	D516	C517	V518	
G389	L390	A391	T392	T393	I394	K395	K398	V401	A406	W409	D410	I411	L412	D413	I416	R417	E418	V421	L422	L423	M424	R425	A426	P427	T428	L429	H430	R431	L432	G433	I434	Q435	A436	V440	L441	I442	E443	G444	K445	A446	I447	Q448	L449	H450	P451	L452	V453	C454	A455	A456	Y457	R458								



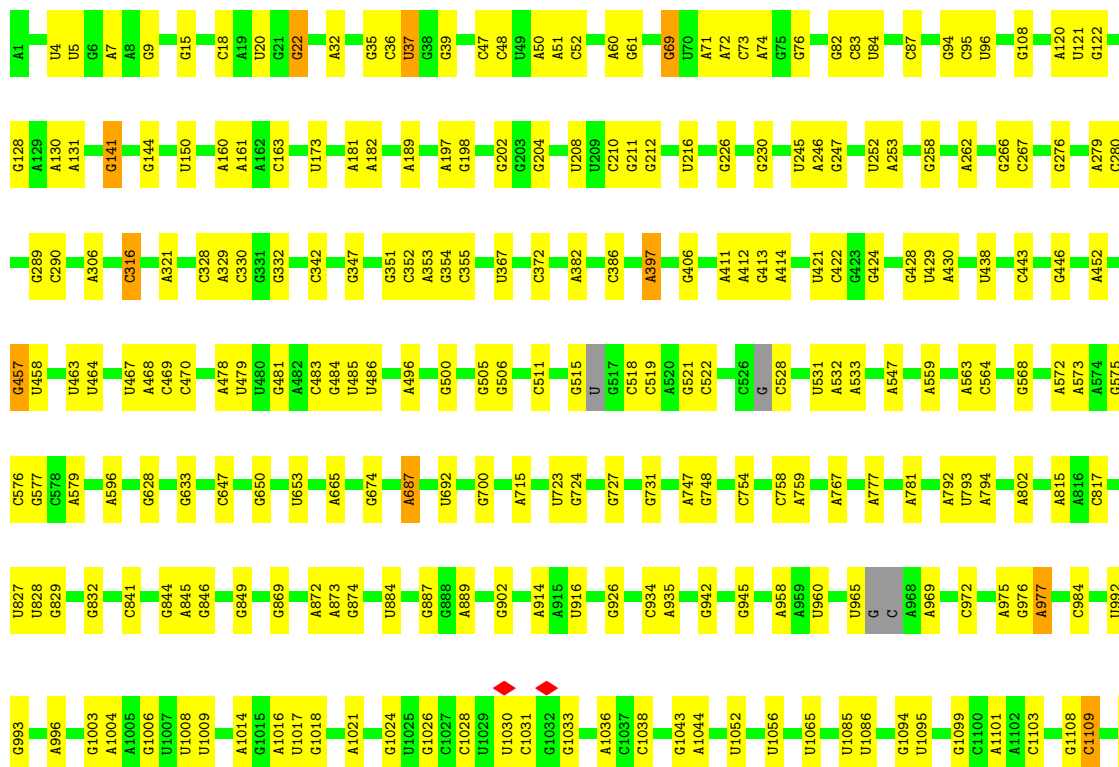
- Molecule 15: 30S ribosomal protein S18

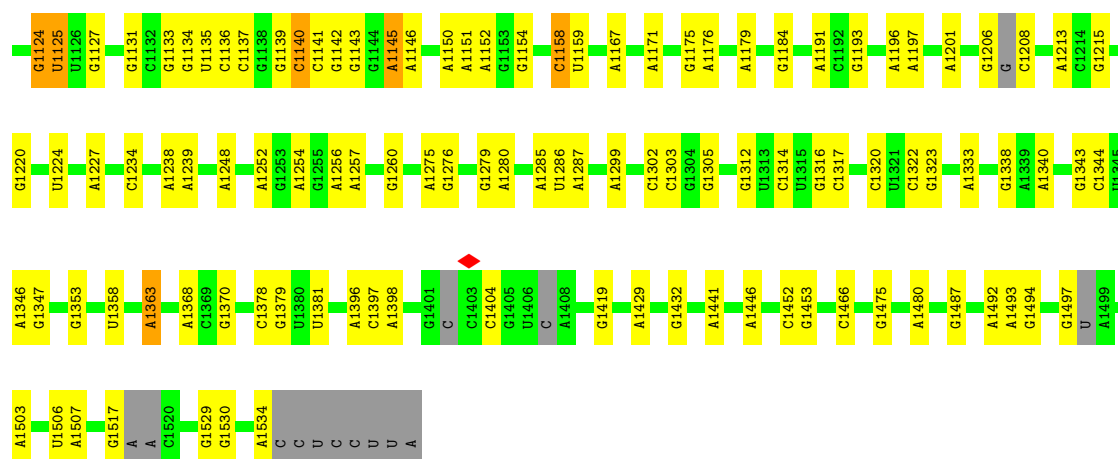
Chain C: 91% 8%



- Molecule 16: 16S rRNA

Chain D: 76% 22%





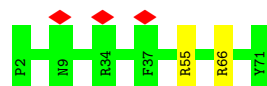
- Molecule 17: 30S ribosomal protein S20

Chain E: 100%

There are no outlier residues recorded for this chain.

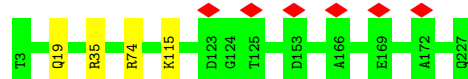
- Molecule 18: 30S ribosomal protein S21

Chain F: 97%



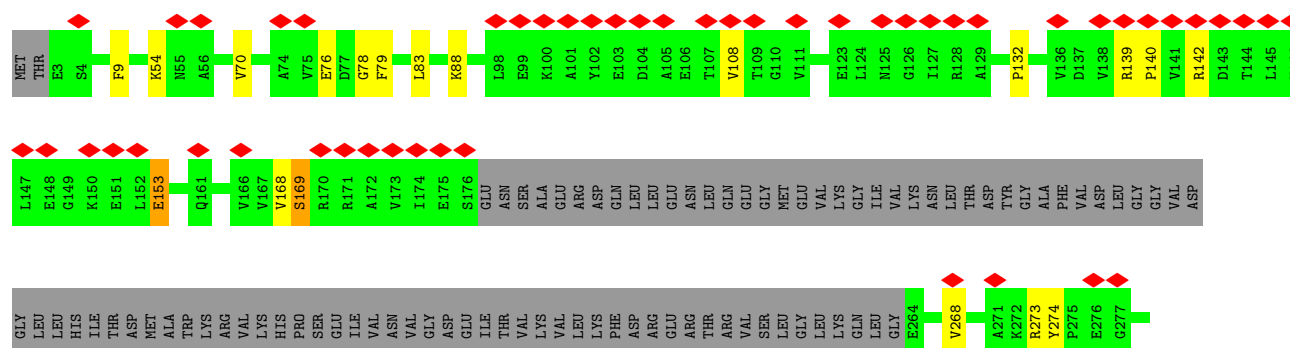
- Molecule 19: 30S ribosomal protein S2

Chain G: 98%



- Molecule 20: 30S ribosomal protein S1

Chain H: 41% 54%

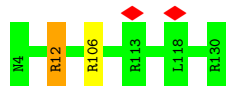


Chain N:  100%


There are no outlier residues recorded for this chain.

- Molecule 27: 30S ribosomal protein S9

Chain O:  98%



- Molecule 28: 30S ribosomal protein S10

Chain P:  90% 10%



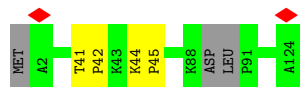
- Molecule 29: 30S ribosomal protein S11

Chain Q:  100%



- Molecule 30: 30S ribosomal protein S12

Chain R:  94%



- Molecule 31: 30S ribosomal protein S14

Chain S:  96%



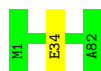
- Molecule 32: 30S ribosomal protein S15

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 33: 30S ribosomal protein S16

Chain U:  99%



- Molecule 34: 30S ribosomal protein S17

Chain V: 99%



- Molecule 35: 30S ribosomal protein S19

Chain W: 100%

There are no outlier residues recorded for this chain.

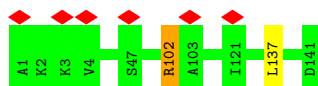
- Molecule 36: 30S ribosomal protein S13

Chain X: 99%



- Molecule 37: 50S ribosomal protein L11

Chain Y: 99%



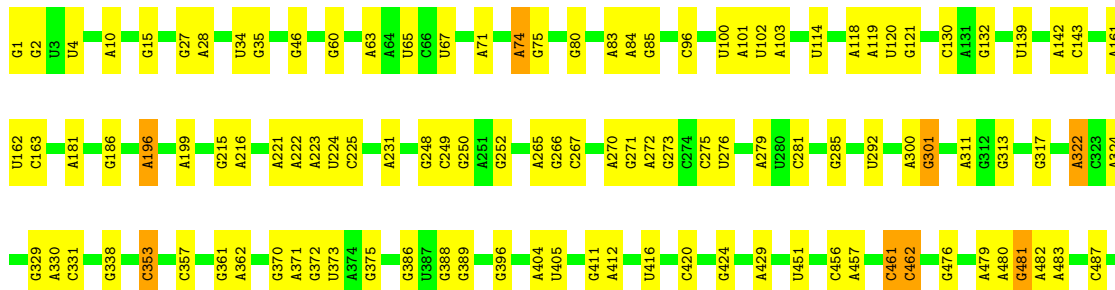
- Molecule 38: 50S ribosomal protein L7/L12

Chain Z: 100%

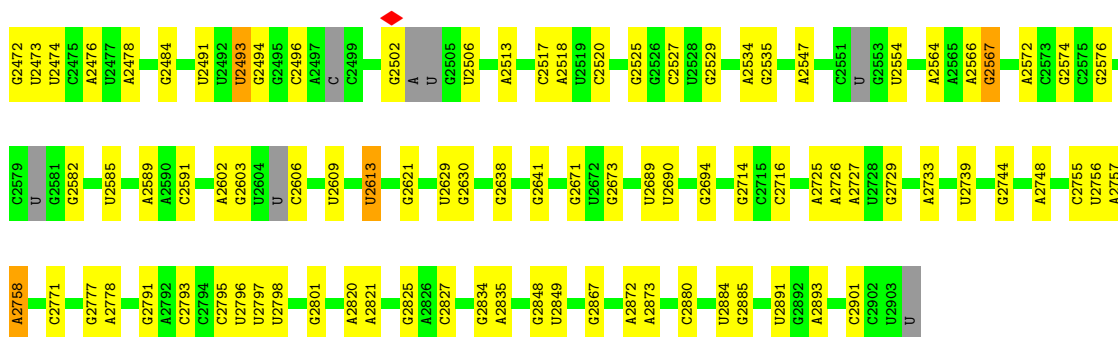
There are no outlier residues recorded for this chain.

- Molecule 39: 23S rRNA

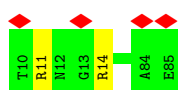
Chain a: 75% 22%







- Molecule 40: 50S ribosomal protein L27

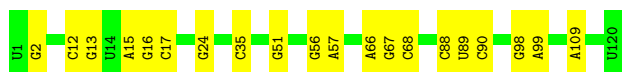
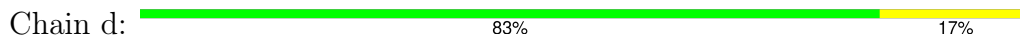


- Molecule 41: 50S ribosomal protein L28



There are no outlier residues recorded for this chain.

- Molecule 42: 5S rRNA



- Molecule 43: 50S ribosomal protein L29



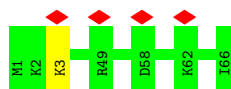
There are no outlier residues recorded for this chain.

- Molecule 44: 50S ribosomal protein L30



There are no outlier residues recorded for this chain.

- Molecule 45: 50S ribosomal protein L31



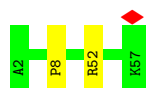
- Molecule 46: 50S ribosomal protein L2

Chain h:  100%



- Molecule 47: 50S ribosomal protein L32

Chain i:  96%



- Molecule 48: 50S ribosomal protein L3

Chain j:  100%



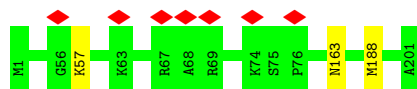
- Molecule 49: 50S ribosomal protein L33

Chain k:  100%

There are no outlier residues recorded for this chain.

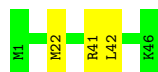
- Molecule 50: 50S ribosomal protein L4

Chain l:  99%



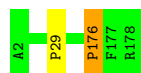
- Molecule 51: 50S ribosomal protein L34

Chain m:  93%



- Molecule 52: 50S ribosomal protein L5

Chain n:  99%



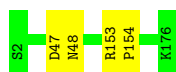
- Molecule 53: 50S ribosomal protein L35

Chain o:  97%



- Molecule 54: 50S ribosomal protein L6

Chain p:  98%



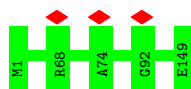
- Molecule 55: 50S ribosomal protein L36

Chain q:  95% 5%



- Molecule 56: 50S ribosomal protein L9

Chain r:  100%



- Molecule 57: 50S ribosomal protein L13

Chain s:  100%

There are no outlier residues recorded for this chain.

- Molecule 58: 50S ribosomal protein L14

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 59: 50S ribosomal protein L15

Chain u:  100%

There are no outlier residues recorded for this chain.

- Molecule 60: 50S ribosomal protein L16

Chain v:  99%



- Molecule 61: 50S ribosomal protein L17

Chain w:  99% .



- Molecule 62: 50S ribosomal protein L18

Chain x:  100%

There are no outlier residues recorded for this chain.

- Molecule 63: 50S ribosomal protein L19

Chain y:  99% .



- Molecule 64: 50S ribosomal protein L20

Chain z:  99% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24959	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	0.093	Depositor
Minimum map value	-0.039	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	548.05, 548.05, 548.05	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	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	0.51	0/829	0.70	0/1107
2	1	0.48	0/864	0.62	0/1156
3	2	0.48	0/752	0.63	0/1005
4	3	0.46	0/796	0.65	0/1062
5	4	0.47	0/766	0.60	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.60	2/681 (0.3%)	0.92	3/1058 (0.3%)
9	9	0.34	0/1131	0.63	1/1524 (0.1%)
10	A	0.55	0/1810	1.28	11/2821 (0.4%)
10	B	0.55	0/1810	1.28	11/2821 (0.4%)
11	AA	0.58	2/10591 (0.0%)	0.75	15/14289 (0.1%)
12	AB	0.43	0/808	0.59	0/1088
13	AC	0.48	0/1808	0.62	1/2450 (0.0%)
13	AD	0.39	0/1789	0.56	0/2425
14	AE	0.50	3/10545 (0.0%)	0.66	4/14236 (0.0%)
15	C	0.88	3/553 (0.5%)	0.86	2/743 (0.3%)
16	D	0.69	9/36610 (0.0%)	1.21	107/57091 (0.2%)
17	E	0.50	0/675	0.64	0/895
18	F	0.53	0/597	0.63	0/792
19	G	0.47	0/1791	0.61	0/2413
20	H	0.57	1/1746 (0.1%)	1.05	13/2382 (0.5%)
21	I	0.44	0/1663	0.71	0/2241
22	J	0.48	0/1665	0.74	0/2227
23	K	0.52	0/1165	0.67	0/1568
24	L	0.54	0/867	0.70	0/1171
25	M	0.51	0/1195	0.63	0/1602
26	N	0.50	0/989	0.68	0/1326
27	O	0.59	0/1034	0.78	0/1375
28	P	0.44	0/800	0.77	0/1082
29	Q	0.47	0/893	0.65	0/1205
30	R	0.72	2/952 (0.2%)	0.80	1/1274 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.48	0/817	0.69	0/1088
32	T	0.47	0/722	0.62	0/964
33	U	0.58	2/659 (0.3%)	0.67	0/884
34	V	0.50	0/657	0.64	0/881
35	W	0.46	0/680	0.62	0/915
36	X	0.43	0/909	0.59	0/1215
37	Y	0.37	0/1046	0.59	2/1410 (0.1%)
38	Z	0.28	0/227	0.47	0/304
39	a	0.69	12/69247 (0.0%)	1.19	226/107985 (0.2%)
40	b	0.49	0/589	0.59	0/779
41	c	0.47	0/635	0.67	0/848
42	d	0.67	0/2872	1.10	2/4478 (0.0%)
43	e	0.44	0/502	0.59	0/667
44	f	0.43	0/452	0.66	0/605
45	g	0.44	0/531	0.62	0/709
46	h	0.61	2/2121 (0.1%)	0.76	4/2852 (0.1%)
47	i	0.65	1/450 (0.2%)	0.86	2/599 (0.3%)
48	j	0.50	0/1586	0.67	0/2134
49	k	0.51	0/433	0.60	0/576
50	l	0.47	0/1571	0.65	1/2113 (0.0%)
51	m	0.55	0/380	0.98	0/498
52	n	0.77	4/1434 (0.3%)	0.91	7/1926 (0.4%)
53	o	0.47	0/513	0.73	0/676
54	p	0.60	3/1333 (0.2%)	0.78	4/1805 (0.2%)
55	q	0.77	1/303 (0.3%)	0.84	1/397 (0.3%)
56	r	0.43	0/1122	0.60	0/1515
57	s	0.50	0/1152	0.64	0/1551
58	t	0.51	0/955	0.69	0/1279
59	u	0.50	0/1062	0.71	0/1413
60	v	0.53	0/1093	0.68	0/1460
61	w	0.51	0/964	0.69	0/1289
62	x	0.46	0/902	0.61	0/1209
63	y	0.54	0/929	0.65	0/1242
64	z	0.53	0/960	0.80	2/1278 (0.2%)
All	All	0.63	57/189114 (0.0%)	1.04	421/278734 (0.2%)

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	9	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	AA	0	10
14	AE	0	5
20	H	0	1
27	O	0	1
30	R	0	1
36	X	0	1
40	b	0	1
52	n	0	1
53	o	0	1
54	p	0	1
All	All	0	26

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	C	41	PRO	N-CA	14.00	1.71	1.47
46	h	107	PRO	CG-CD	-14.00	1.04	1.50
30	R	42	PRO	N-CA	13.72	1.70	1.47
52	n	176	PRO	CG-CD	-13.50	1.06	1.50
52	n	29	PRO	CG-CD	-11.86	1.11	1.50

The worst 5 of 421 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	37	U	C5-C4-O4	34.28	146.47	125.90
39	a	1141	U	C5-C4-O4	33.53	146.02	125.90
16	D	1358	U	C5-C4-O4	31.93	145.06	125.90
16	D	37	U	N3-C4-O4	-31.78	97.16	119.40
39	a	1019	U	C5-C4-O4	31.05	144.53	125.90

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	89 (88%)	12 (12%)	0	100	100
2	1	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
3	2	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
4	3	101/103 (98%)	93 (92%)	7 (7%)	1 (1%)	13	44
5	4	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
9	9	146/148 (99%)	112 (77%)	33 (23%)	1 (1%)	19	51
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	5	30
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/230 (99%)	215 (94%)	11 (5%)	2 (1%)	14	47
13	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	19	51
15	C	64/66 (97%)	59 (92%)	4 (6%)	1 (2%)	8	37
17	E	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	201 (90%)	22 (10%)	0	100	100
20	H	255/557 (46%)	187 (73%)	56 (22%)	12 (5%)	2	19
21	I	206/208 (99%)	197 (96%)	8 (4%)	1 (0%)	25	57
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	140 (91%)	13 (8%)	1 (1%)	22	54
24	L	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
25	M	149/151 (99%)	142 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	N	127/129 (98%)	110 (87%)	17 (13%)	0	100	100
27	O	125/127 (98%)	111 (89%)	14 (11%)	0	100	100
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	13	44
29	Q	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
30	R	117/124 (94%)	105 (90%)	11 (9%)	1 (1%)	14	47
31	S	98/100 (98%)	95 (97%)	2 (2%)	1 (1%)	13	44
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
34	V	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
35	W	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
36	X	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
37	Y	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
38	Z	28/30 (93%)	27 (96%)	1 (4%)	0	100	100
40	b	74/76 (97%)	67 (90%)	7 (10%)	0	100	100
41	c	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
43	e	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
44	f	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
45	g	64/66 (97%)	58 (91%)	6 (9%)	0	100	100
46	h	269/271 (99%)	241 (90%)	28 (10%)	0	100	100
47	i	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
48	j	207/209 (99%)	188 (91%)	19 (9%)	0	100	100
49	k	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
50	l	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/177 (99%)	161 (92%)	14 (8%)	0	100	100
53	o	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	8	37
54	p	173/175 (99%)	156 (90%)	16 (9%)	1 (1%)	22	54
55	q	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	127 (91%)	13 (9%)	0	100	100
58	t	121/123 (98%)	108 (89%)	13 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	u	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
60	v	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
61	w	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
62	x	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
63	y	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
64	z	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
All	All	9368/9974 (94%)	8467 (90%)	836 (9%)	65 (1%)	21	51

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU
11	AA	873	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	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/81 (100%)	81 (100%)	0	100	100
4	3	84/84 (100%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/112 (100%)	111 (99%)	1 (1%)	75	84
11	AA	1140/1157 (98%)	1039 (91%)	101 (9%)	8	31
12	AB	86/158 (54%)	84 (98%)	2 (2%)	45	64
13	AC	198/198 (100%)	182 (92%)	16 (8%)	9	34
13	AD	196/198 (99%)	194 (99%)	2 (1%)	73	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	AE	1120/1168 (96%)	1051 (94%)	69 (6%)	15	42
15	C	57/57 (100%)	53 (93%)	4 (7%)	12	39
17	E	65/65 (100%)	65 (100%)	0	100	100
18	F	60/60 (100%)	58 (97%)	2 (3%)	33	57
19	G	187/187 (100%)	183 (98%)	4 (2%)	48	67
20	H	137/461 (30%)	125 (91%)	12 (9%)	8	32
21	I	171/171 (100%)	164 (96%)	7 (4%)	26	52
22	J	172/172 (100%)	163 (95%)	9 (5%)	19	46
23	K	119/119 (100%)	118 (99%)	1 (1%)	79	85
24	L	91/91 (100%)	91 (100%)	0	100	100
25	M	124/124 (100%)	124 (100%)	0	100	100
26	N	104/104 (100%)	104 (100%)	0	100	100
27	O	105/105 (100%)	103 (98%)	2 (2%)	52	70
28	P	86/86 (100%)	77 (90%)	9 (10%)	5	25
29	Q	90/90 (100%)	90 (100%)	0	100	100
30	R	101/104 (97%)	101 (100%)	0	100	100
31	S	83/83 (100%)	80 (96%)	3 (4%)	30	55
32	T	76/76 (100%)	76 (100%)	0	100	100
33	U	65/65 (100%)	65 (100%)	0	100	100
34	V	74/74 (100%)	73 (99%)	1 (1%)	62	76
35	W	72/72 (100%)	72 (100%)	0	100	100
36	X	94/94 (100%)	94 (100%)	0	100	100
37	Y	109/109 (100%)	108 (99%)	1 (1%)	75	84
38	Z	26/26 (100%)	26 (100%)	0	100	100
40	b	58/58 (100%)	57 (98%)	1 (2%)	56	73
41	c	67/67 (100%)	67 (100%)	0	100	100
43	e	54/54 (100%)	54 (100%)	0	100	100
44	f	48/48 (100%)	48 (100%)	0	100	100
45	g	59/59 (100%)	58 (98%)	1 (2%)	56	73
46	h	216/216 (100%)	216 (100%)	0	100	100
47	i	47/47 (100%)	46 (98%)	1 (2%)	48	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	j	164/164 (100%)	163 (99%)	1 (1%)	84	90
49	k	47/47 (100%)	47 (100%)	0	100	100
50	l	165/165 (100%)	163 (99%)	2 (1%)	67	79
51	m	38/38 (100%)	35 (92%)	3 (8%)	10	36
52	n	148/148 (100%)	148 (100%)	0	100	100
53	o	51/51 (100%)	51 (100%)	0	100	100
54	p	136/136 (100%)	136 (100%)	0	100	100
55	q	34/34 (100%)	34 (100%)	0	100	100
56	r	114/114 (100%)	114 (100%)	0	100	100
57	s	116/116 (100%)	116 (100%)	0	100	100
58	t	104/104 (100%)	104 (100%)	0	100	100
59	u	103/103 (100%)	103 (100%)	0	100	100
60	v	109/109 (100%)	107 (98%)	2 (2%)	54	71
61	w	99/99 (100%)	98 (99%)	1 (1%)	73	82
62	x	86/86 (100%)	86 (100%)	0	100	100
63	y	99/99 (100%)	98 (99%)	1 (1%)	73	82
64	z	89/89 (100%)	89 (100%)	0	100	100
All	All	7791/8257 (94%)	7532 (97%)	259 (3%)	35	57

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	O	106	ARG
28	P	72	ARG
11	AA	1252	SER
11	AA	1151	LEU
31	S	98	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
56	r	18	GLN
60	v	13	HIS
64	z	20	GLN
41	c	34	HIS

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Mol	Chain	Res	Type
41	c	6	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	30 (40%)	8 (10%)
10	B	75/76 (98%)	30 (40%)	8 (10%)
16	D	1514/1542 (98%)	304 (20%)	10 (0%)
39	a	2859/2904 (98%)	582 (20%)	0
42	d	119/120 (99%)	19 (15%)	0
8	7	28/29 (96%)	18 (64%)	3 (10%)
All	All	4670/4747 (98%)	983 (21%)	29 (0%)

5 of 983 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-6	G
8	7	-5	U
8	7	-4	U
8	7	-2	U
8	7	-1	U

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	22	G
16	D	1492	A
10	B	57	A
16	D	992	U
10	B	48	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

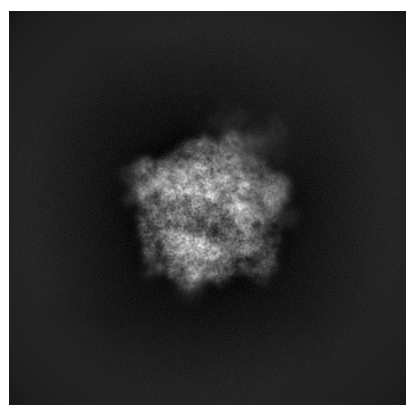
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21386. These allow visual inspection of the internal detail of the map and identification of artifacts.

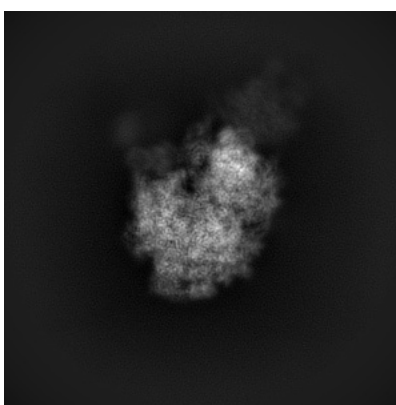
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

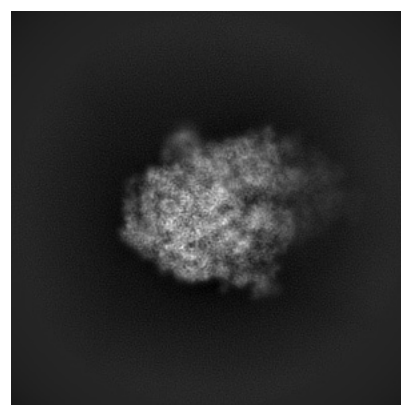
6.1.1 Primary map



X



Y

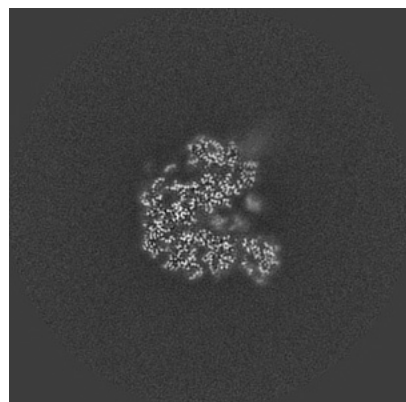


Z

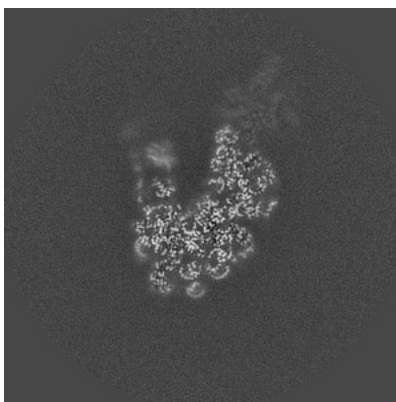
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

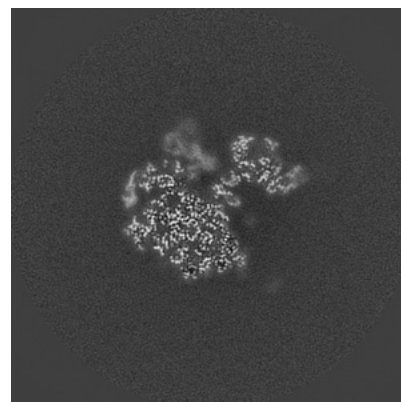
6.2.1 Primary map



X Index: 250



Y Index: 250

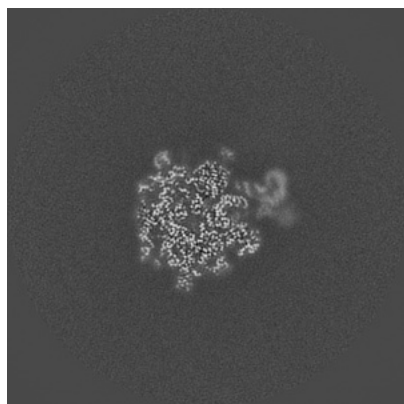


Z Index: 250

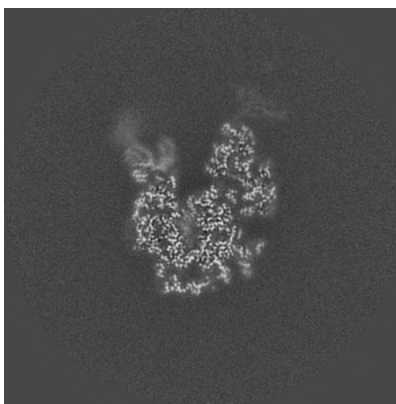
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

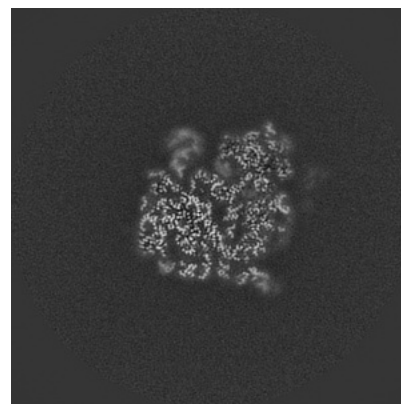
6.3.1 Primary map



X Index: 215



Y Index: 233

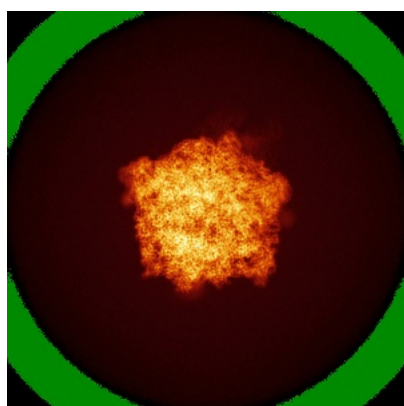


Z Index: 271

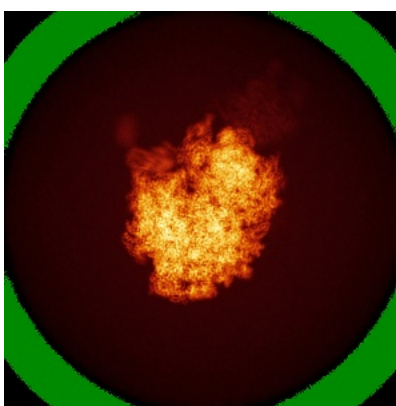
The images above show the largest variance slices of the map in three orthogonal directions.

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

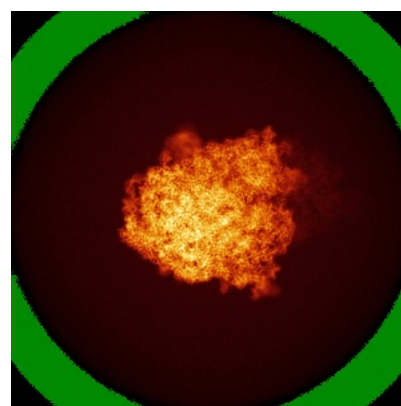
6.4.1 Primary map



X



Y

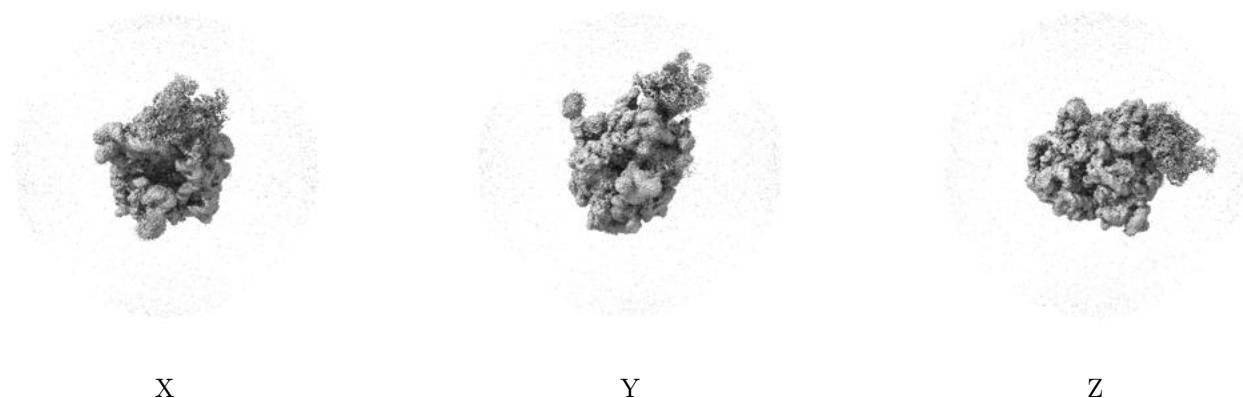


Z

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

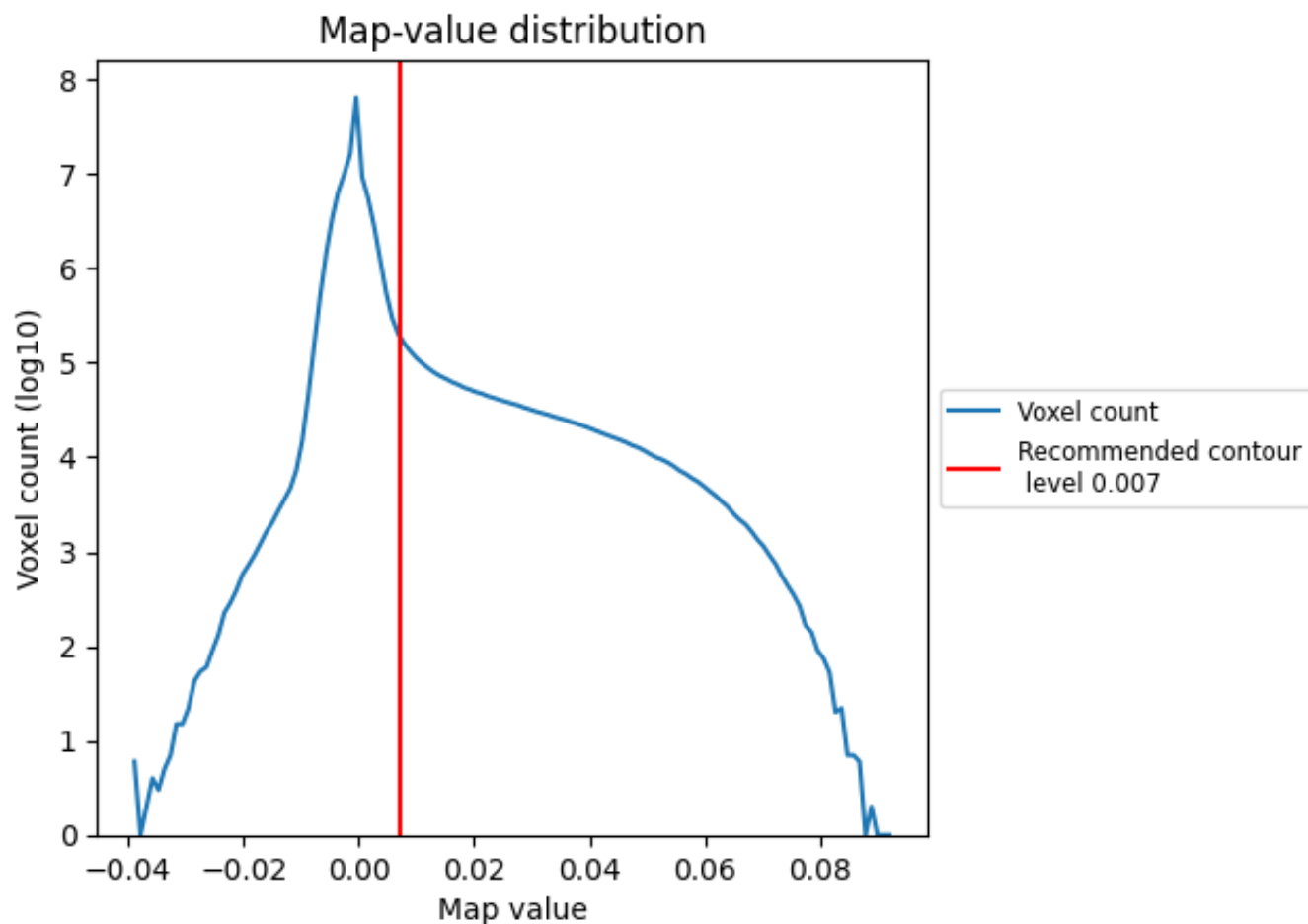
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

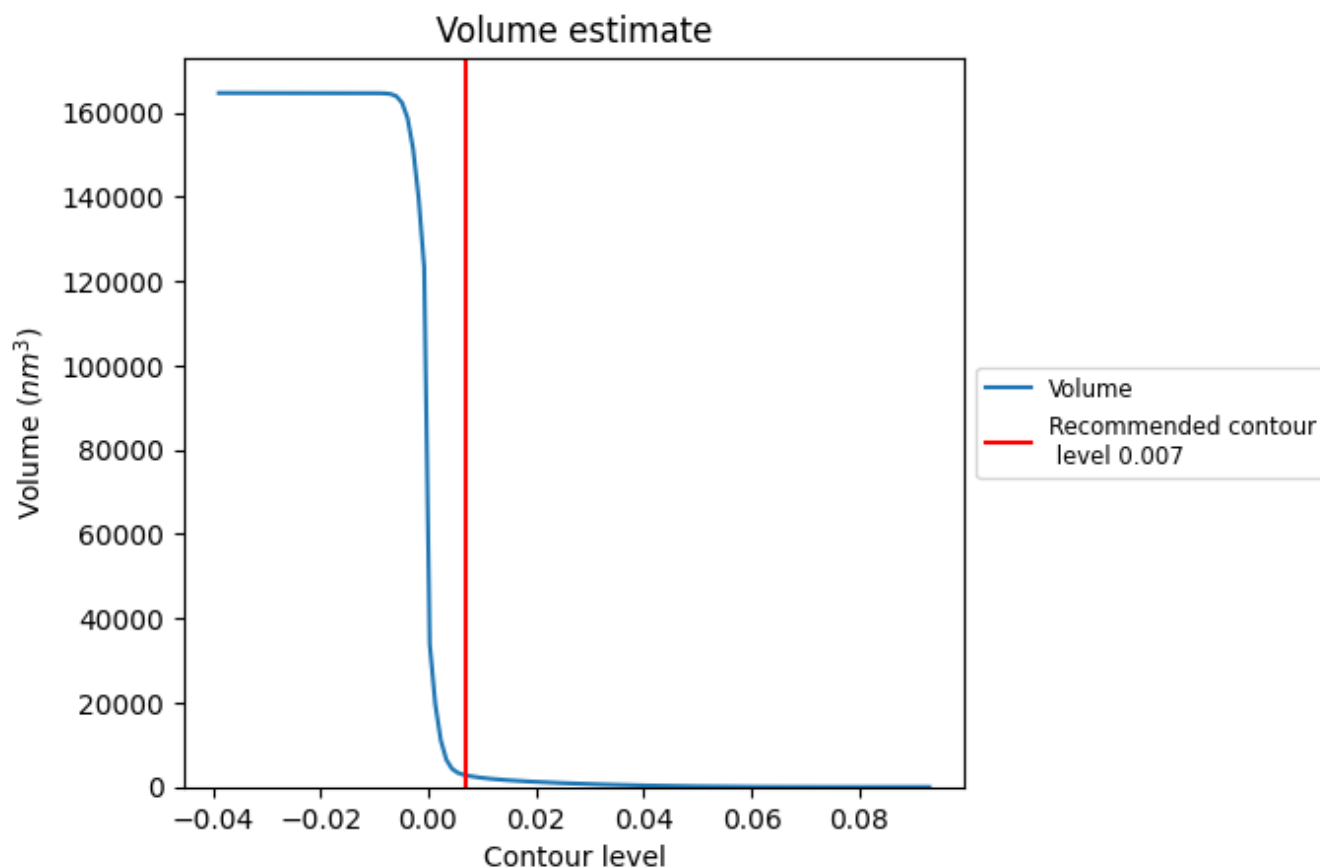
This section contains the results of statistical analysis of the map.

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.

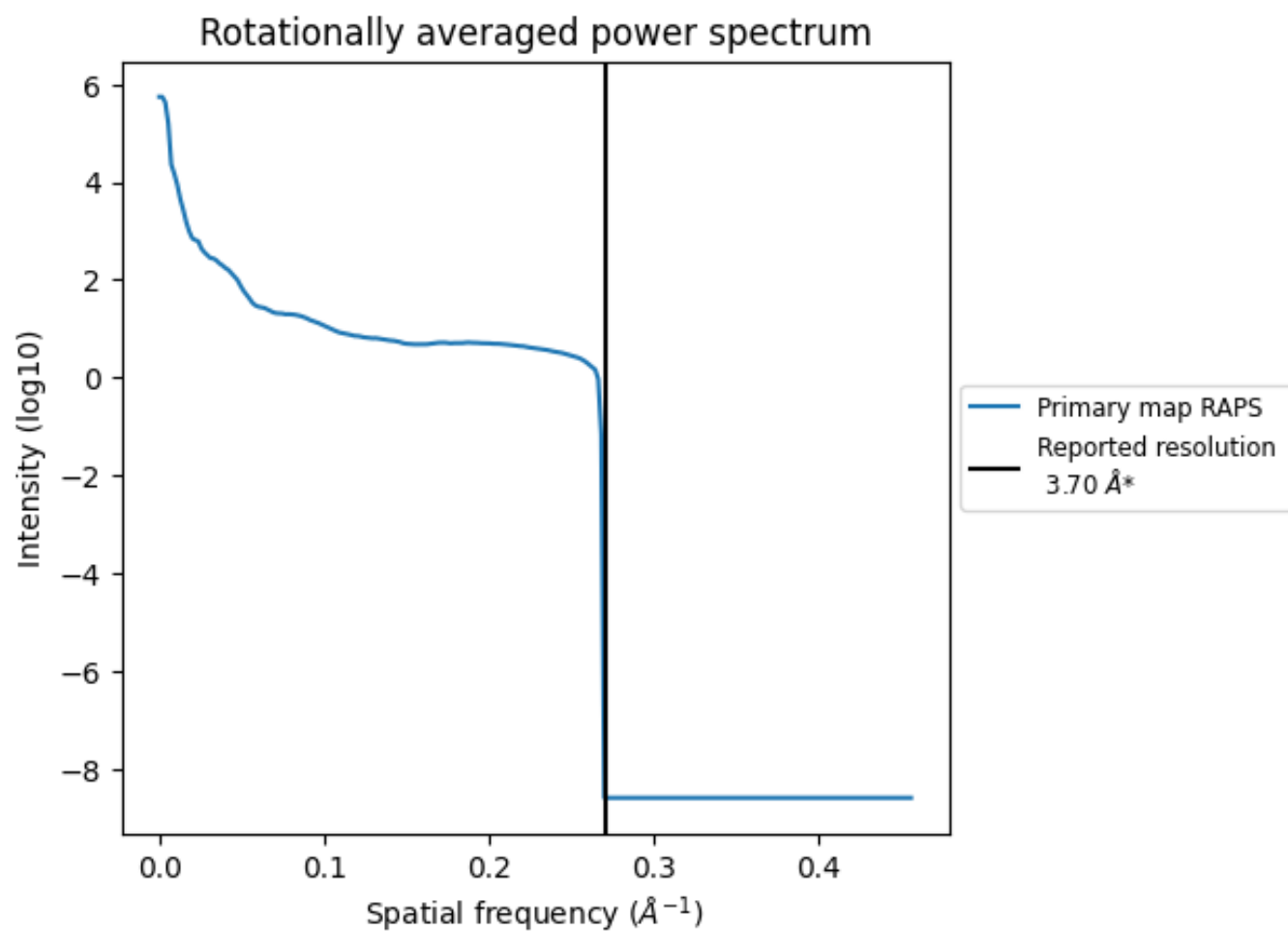
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm³; this corresponds to an approximate mass of 2518 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 ⓘ

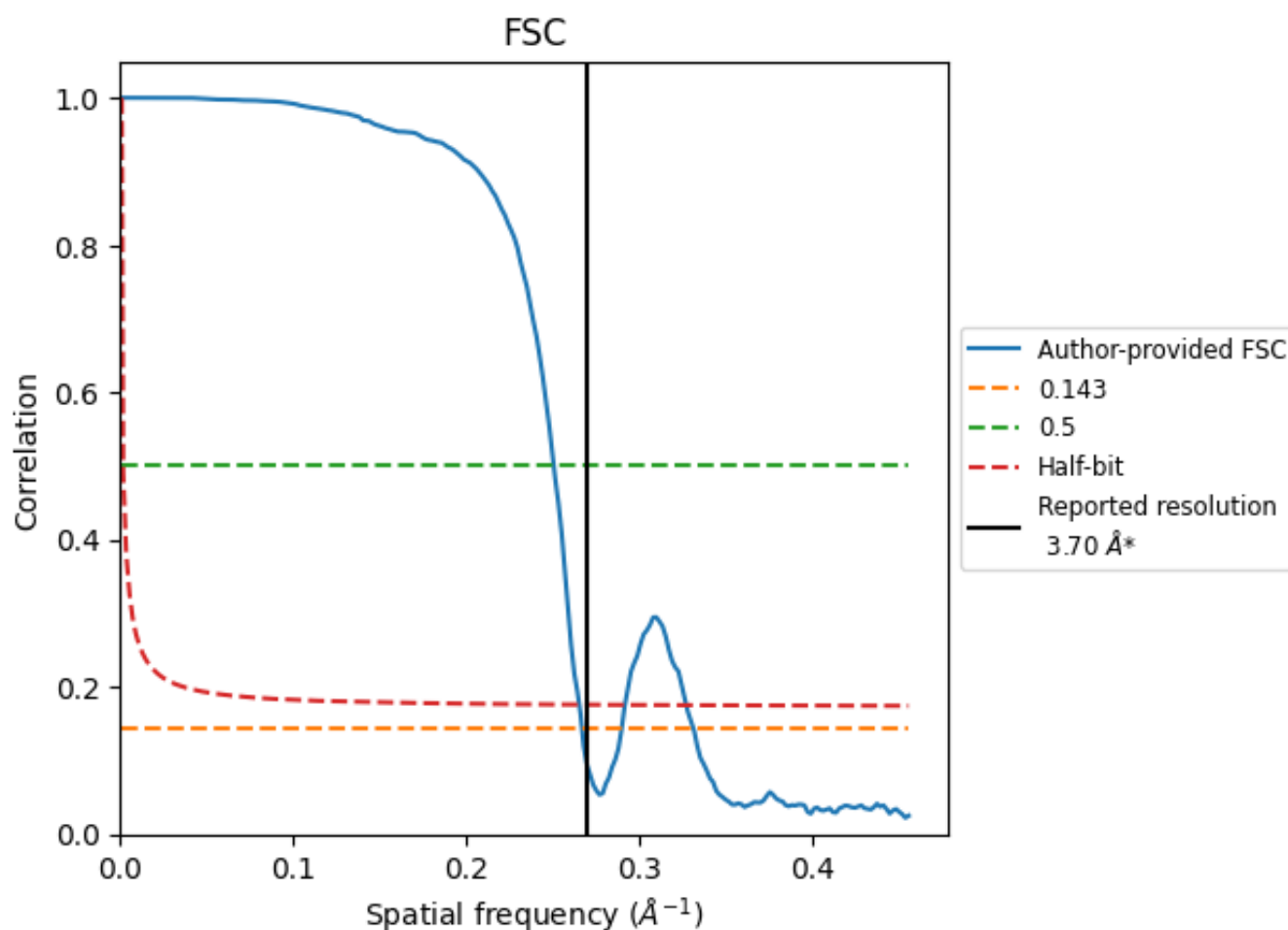


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

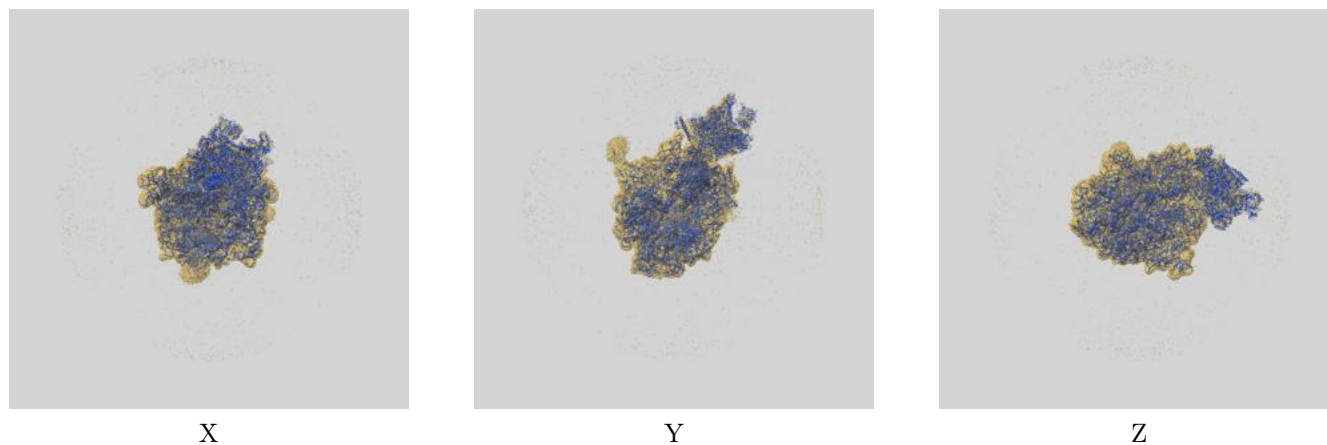
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.74	3.99	3.77
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

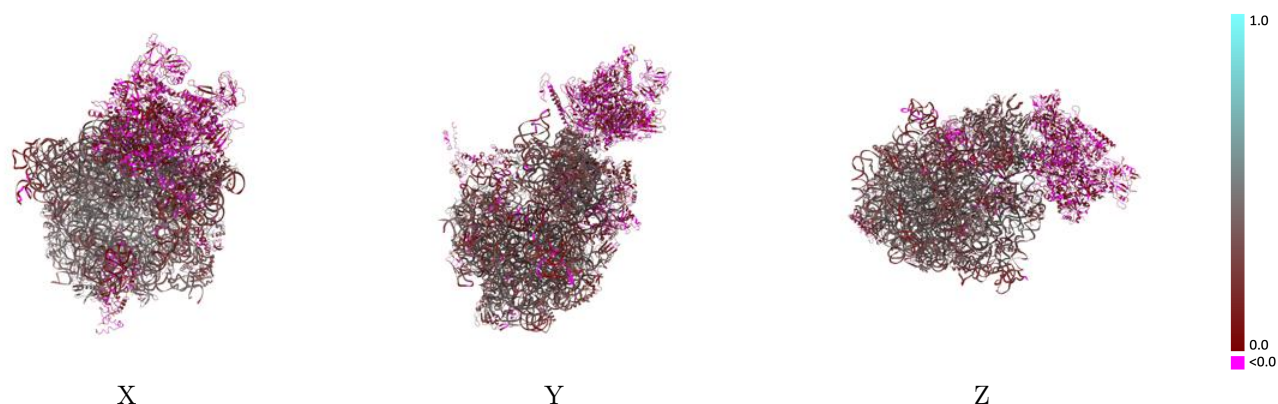
This section contains information regarding the fit between EMDB map EMD-21386 and PDB model 6VU3. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



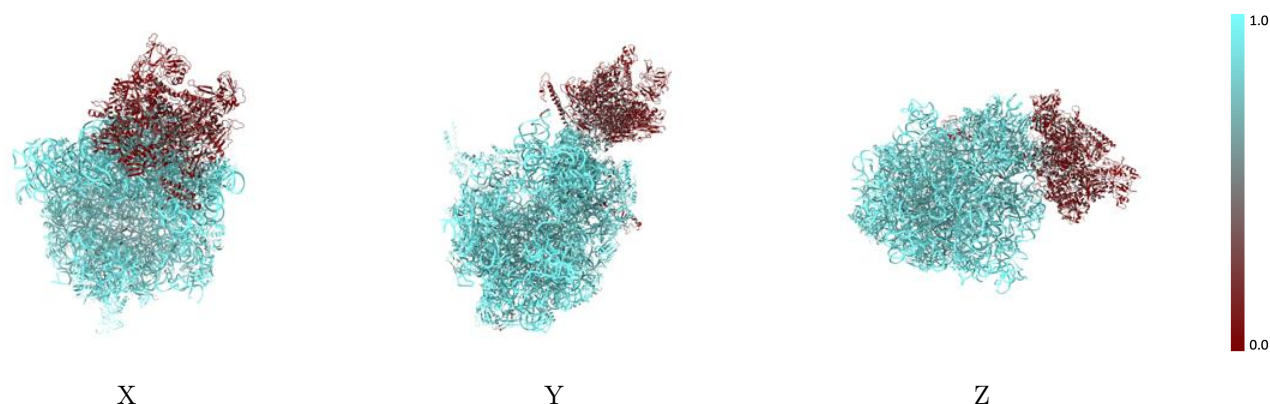
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



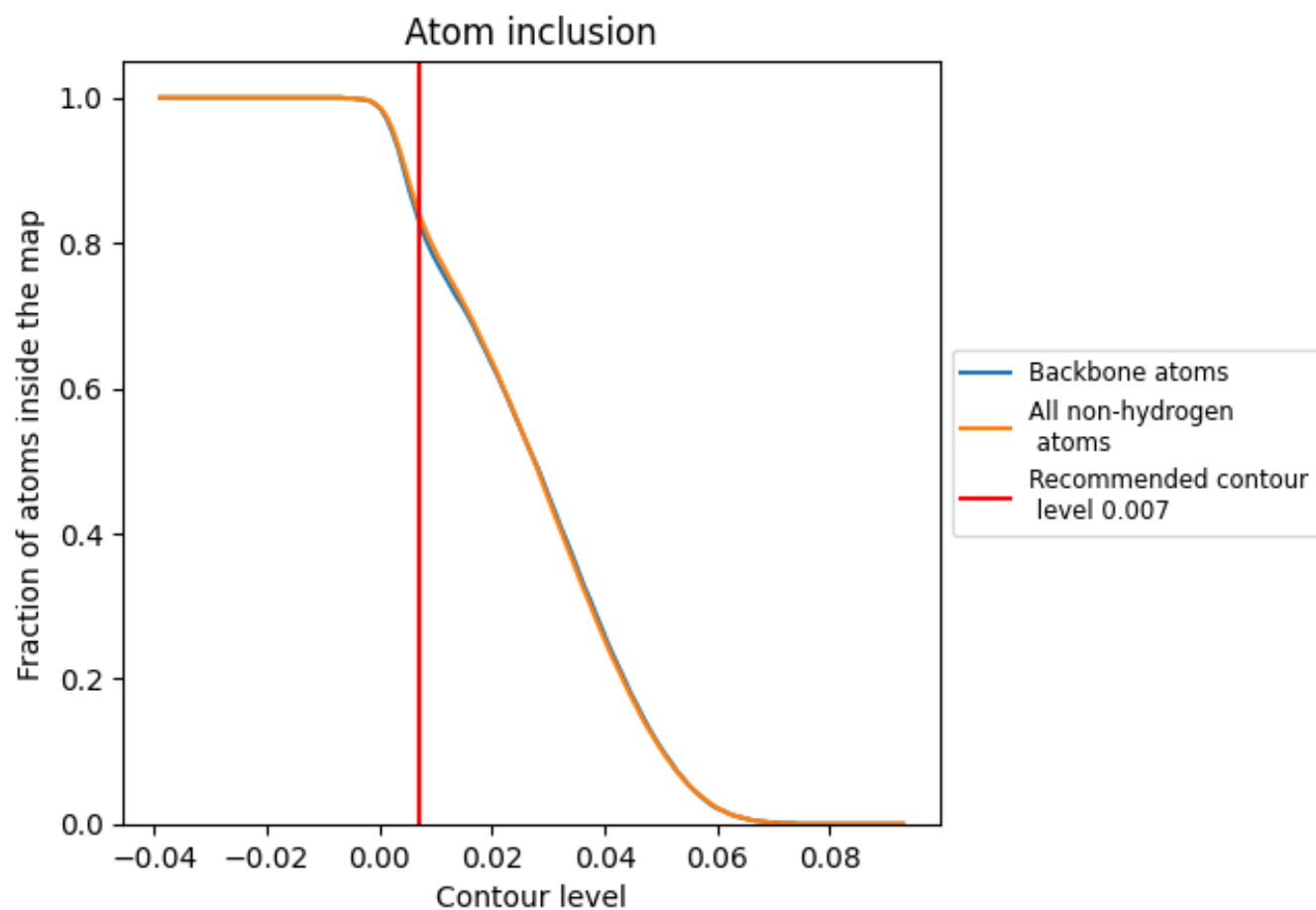
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 84% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.2760
0	 0.8630	 0.1500
1	 0.9110	 0.3400
2	 0.9110	 0.2660
3	 0.6280	 0.0310
4	 0.9420	 0.3370
5	 0.2100	 0.0920
6	 0.3360	 0.0790
7	 0.6430	 0.0640
9	 0.9420	 0.1200
A	 0.9890	 0.2070
AA	 0.2260	 0.0620
AB	 0.1630	 0.1010
AC	 0.2250	 0.0630
AD	 0.1360	 0.0640
AE	 0.1910	 0.0790
B	 0.9170	 0.1670
C	 0.8680	 0.1580
D	 0.9890	 0.3430
E	 0.9480	 0.3300
F	 0.8230	 0.0680
G	 0.8700	 0.1600
H	 0.6290	 0.0360
I	 0.9350	 0.3890
J	 0.9180	 0.2940
K	 0.8750	 0.1820
L	 0.9190	 0.2480
M	 0.9170	 0.2680
N	 0.8870	 0.2180
O	 0.9100	 0.1900
P	 0.9310	 0.3190
Q	 0.9030	 0.2490
R	 0.8880	 0.2860
S	 0.9110	 0.2460
T	 0.9130	 0.2380



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Chain	Atom inclusion	Q-score
U	 0.9280	 0.2700
V	 0.8810	 0.2100
W	 0.9460	 0.3250
X	 0.9290	 0.3180
Y	 0.8830	 0.0510
Z	 0.9210	 0.0010
a	 0.9850	 0.3450
b	 0.8550	 0.1810
c	 0.9150	 0.3260
d	 0.9950	 0.3210
e	 0.8850	 0.1590
f	 0.9130	 0.3480
g	 0.8400	 0.0960
h	 0.9530	 0.4140
i	 0.8760	 0.2890
j	 0.9270	 0.3660
k	 0.8900	 0.2720
l	 0.8740	 0.2520
m	 0.9270	 0.3560
n	 0.9300	 0.2780
o	 0.9230	 0.3850
p	 0.9530	 0.3550
q	 0.9310	 0.3900
r	 0.8750	 0.2450
s	 0.9260	 0.3160
t	 0.9250	 0.3760
u	 0.9430	 0.3710
v	 0.9300	 0.3530
w	 0.9210	 0.2700
x	 0.9270	 0.2180
y	 0.9090	 0.2750
z	 0.9060	 0.2850