



## wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 09:54 PM EST

PDB ID : 6XDQ  
EMDB ID : EMD-22141  
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B3 (TTC-B3) containing an mRNA with a 30 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site  
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.  
Deposited on : 2020-06-11  
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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

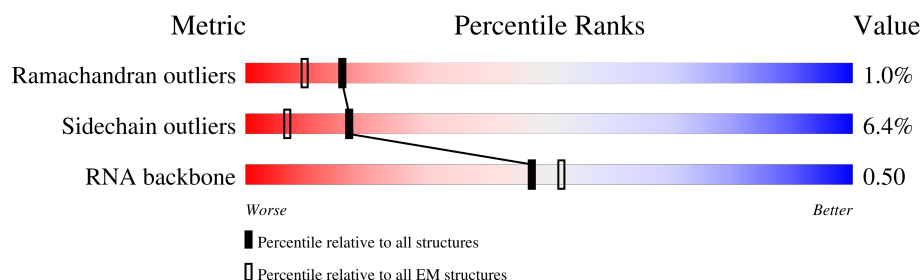
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 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  $\geq 3$ , 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	100	
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	46	

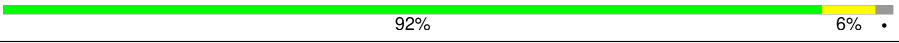
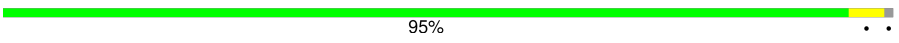

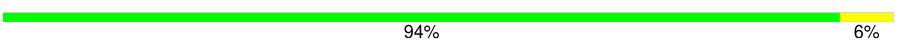






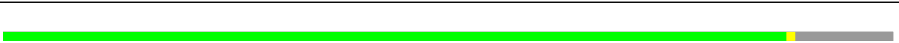



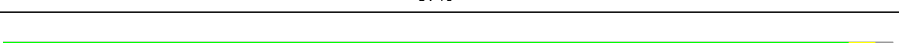
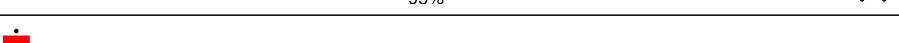
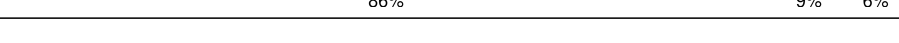
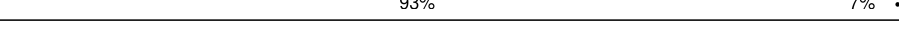

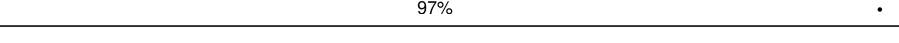

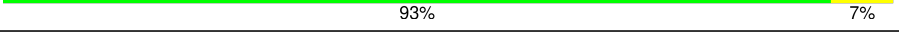
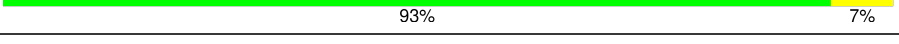

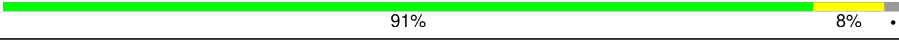
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Mol	Chain	Length	Quality of chain
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	


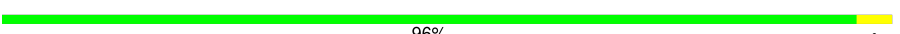

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Mol	Chain	Length	Quality of chain
32	R	124	 92% 6%
33	S	101	 95%
34	T	89	 85% 13%
35	U	82	 94% 6%
36	V	84	 93% 5%
37	W	92	 86% 10%
38	X	118	 88% 10%
39	Y	142	 21% 69% 27%
40	Z	121	 12% 12% 75%
41	a	2904	 81% 18%
42	b	85	 88% 11%
43	c	78	 94% 5%
44	d	120	 86% 14%
45	e	63	 5% 97%
46	f	59	 95%
47	g	70	 86% 9% 6%
48	h	273	 93% 7%
49	i	57	 88% 11%
50	j	209	 97%
51	k	55	 89% 5% 5%
52	l	201	 93% 7%
53	m	46	 93% 7%
54	n	179	 89% 10%
55	o	65	 91% 8%
56	p	177	 97%

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Mol	Chain	Length	Quality of chain
57	q	38	 95% 5%
58	r	149	 93% 7% 5%
59	s	142	 96% .
60	t	123	 95% 5%
61	u	144	 96% .
62	v	136	 96% .
63	w	127	 87% 6% 6%
64	x	117	 94% 5% .
65	y	115	 95% . .
66	z	118	 96% . .

## 2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 290243 atoms, of which 109912 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
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 30 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	35	Total	C	H	N	O	P	0	0
			824	325	97	100	267	35		

- 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 P-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	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2091	1295	379	411	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	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	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AG	494	Total	C	N	O	0	0
			2442	1454	494	494		

- Molecule 17 is a protein called 30S ribosomal protein S18.

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

- Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 19 is a protein called 30S ribosomal protein S20.



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

- Molecule 20 is a protein called 30S ribosomal protein S21.

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

- Molecule 21 is a protein called 30S ribosomal protein S2.

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

- Molecule 22 is a protein called 30S ribosomal protein S1.

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

- Molecule 23 is a protein called 30S ribosomal protein S3.

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

- Molecule 24 is a protein called 30S ribosomal protein S4.

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

- Molecule 25 is a protein called 30S ribosomal protein S5.

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

- Molecule 26 is a protein called 30S ribosomal protein S6.

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

- Molecule 27 is a protein called 30S ribosomal protein S7.

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

- Molecule 28 is a protein called 30S ribosomal protein S8.

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

- Molecule 29 is a protein called 30S ribosomal protein S9.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S11.

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

- Molecule 32 is a protein called 30S ribosomal protein S12.

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

- Molecule 33 is a protein called 30S ribosomal protein S14.

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

- Molecule 34 is a protein called 30S ribosomal protein S15.

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

- Molecule 35 is a protein called 30S ribosomal protein S16.

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

- Molecule 36 is a protein called 30S ribosomal protein S17.

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

- Molecule 37 is a protein called 30S ribosomal protein S19.

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

- Molecule 38 is a protein called 30S ribosomal protein S13.

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

- Molecule 39 is a protein called 50S ribosomal protein L11.

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

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	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	variant	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

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

- Molecule 43 is a protein called 50S ribosomal protein L28.

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

- Molecule 44 is a RNA chain called 5S rRNA.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L2.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33.

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

- Molecule 52 is a protein called 50S ribosomal protein L4.

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

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

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

- Molecule 56 is a protein called 50S ribosomal protein L6.

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

- Molecule 57 is a protein called 50S ribosomal protein L36.

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

- Molecule 58 is a protein called 50S ribosomal protein L9.

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

- Molecule 59 is a protein called 50S ribosomal protein L13.

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

- Molecule 60 is a protein called 50S ribosomal protein L14.

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

- Molecule 61 is a protein called 50S ribosomal protein L15.

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

- Molecule 62 is a protein called 50S ribosomal protein L16.

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

- Molecule 63 is a protein called 50S ribosomal protein L17.

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

- Molecule 64 is a protein called 50S ribosomal protein L18.

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

- Molecule 65 is a protein called 50S ribosomal protein L19.

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

- Molecule 66 is a protein called 50S ribosomal protein L20.

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

- Molecule 67 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	AE	1	Total 1	Mg 1	0

- Molecule 68 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

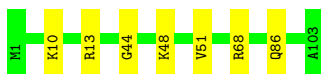


### 3 Residue-property plots

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.

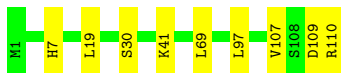
- Molecule 1: 50S ribosomal protein L21

Chain 0:  93% 7%




- Molecule 2: 50S ribosomal protein L22

Chain 1:  92% 8%



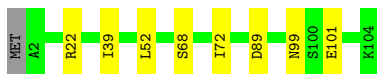
- Molecule 3: 50S ribosomal protein L23

Chain 2:  89% 5% 6%



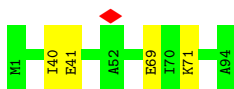
- Molecule 4: 50S ribosomal protein L24

Chain 3:  91% 8%



- Molecule 5: 50S ribosomal protein L25

Chain 4:  96%



- Molecule 6: NT DNA

A horizontal bar chart showing the distribution of 15 categories. The categories are: DC, DC, DG, DT, DT, DC, DA, DG, DT, DA, T96, A100, A103, DT, DT, DT, DT, T108, T109, G112, A115, G116, G121, and G122. The bars are colored in a repeating pattern of grey, green, and yellow. A red diamond marker is placed above the T96 bar.

- Chain 6:  64% 11% 25%

C2		G10	A21	T24	A28	DT	DC	DA	DT	DG	DA	DC	DG	DG
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- Chain 7:  22% 50% 2% 24%

A-20
U-19
G-18
U-17
U-16
U-15
U-14
U-13
U-12
U-11
U-10
U-9
U-8
U-7
U-6
U-5
U-4
U-3
U-2
U-1
U0
U1
U2
U3
U4
U
U
U
U
U
U
U
U
U
U
A
A
U
U
U11
G12
G13
G19
G20

- Chain 9:  7% 54% 33% 10%

R94	R95	R96	R97	R98	R99	R100	R101	R102	R103	R104	R105	R106	R107	R108	R109	R110	R111	R112	R113	R114	R115	R116	R117	R118	R119	R120	R121	R122	R123	R124	R125	R126	R127	R128	R129	R130	R131	R132	R133	R134	R135	R136	R137	R138	R139	R140	R141	R142	R143	R144	R145	R146	R147	R148	R149	R150	R151	R152	R153	R154	R155	R156	R157	R158	R159	R160	R161	R162	R163	R164	R165	R166	R167	R168	R169	R170	R171	R172	R173	R174	R175	R176	R177	R178	R179	R180	R181	R182	R183	R184	R185	R186	R187	R188	R189	R190	R191	R192	R193	R194	R195	R196	R197	R198	R199	R200	R201	R202	R203	R204	R205	R206	R207	R208	R209	R210	R211	R212	R213	R214	R215	R216	R217	R218	R219	R220	R221	R222	R223	R224	R225	R226	R227	R228	R229	R230	R231	R232	R233	R234	R235	R236	R237	R238	R239	R240	R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300	R301	R302	R303	R304	R305	R306	R307	R308	R309	R310	R311	R312	R313	R314	R315	R316	R317	R318	R319	R320	R321	R322	R323	R324	R325	R326	R327	R328	R329	R330	R331	R332	R333	R334	R335	R336	R337	R338	R339	R340	R341	R342	R343	R344	R345	R346	R347	R348	R349	R350	R351	R352	R353	R354	R355	R356	R357	R358	R359	R360	R361	R362	R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385	R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408	R409	R410	R411	R412	R413	R414	R415	R416	R417	R418	R419	R420	R421	R422	R423	R424	R425	R426	R427	R428	R429	R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452	R453	R454	R455	R456	R457	R458	R459	R460	R461	R462	R463	R464	R465	R466	R467	R468	R469	R470	R471	R472	R473	R474	R475	R476	R477	R478	R479	R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502	R503	R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R525	R526	R527	R528	R529	R530	R531	R532	R533	R534	R535	R536	R537	R538	R539	R540	R541	R542	R543	R544	R545	R546	R547	R548	R549	R550	R551	R552	R553	R554	R555	R556	R557	R558	R559	R560	R561	R562	R563	R564	R565	R566	R567	R568	R569	R570	R571	R572	R573	R574	R575	R576	R577	R578	R579	R580	R581	R582	R583	R584	R585	R586	R587	R588	R589	R590	R591	R592	R593	R594	R595	R596	R597	R598	R599	R600	R601	R602	R603	R604	R605
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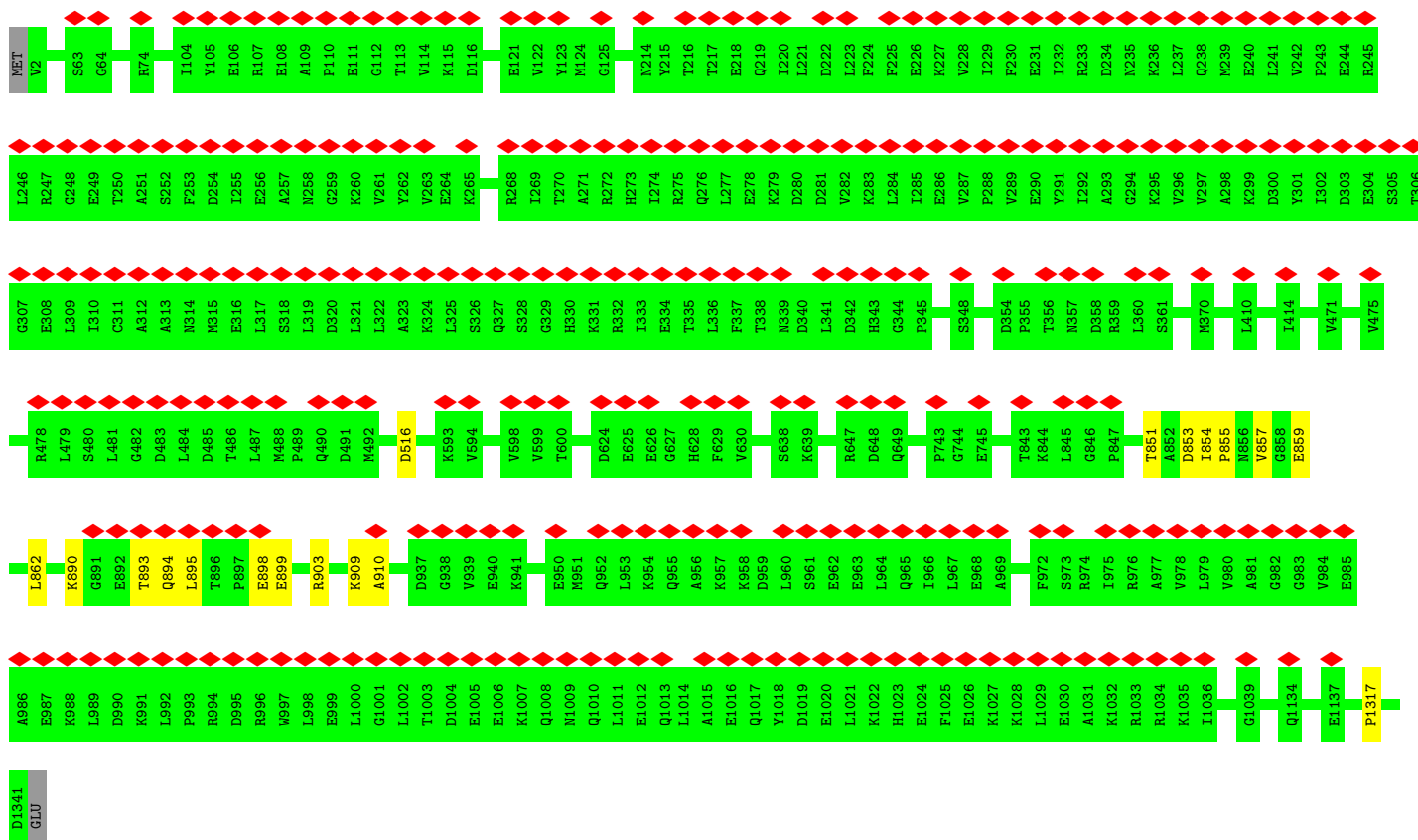
- Chain A:  58% 38%

G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50	G51	G52	G53	G54	G55	G56	G57	G58	G59	G60	G61	G62	G63	G64	G65	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78	G79	G80	G81	G82	G83	G84	G85	G86	G87	G88	G89	G90	G91	G92	G93	G94	G95	G96	G97	G98	G99	G100	G101	G102	G103	G104	G105	G106	G107	G108	G109	G110	G111	G112	G113	G114	G115	G116	G117	G118	G119	G120	G121	G122	G123	G124	G125	G126	G127	G128	G129	G130	G131	G132	G133	G134	G135	G136	G137	G138	G139	G140	G141	G142	G143	G144	G145	G146	G147	G148	G149	G150	G151	G152	G153	G154	G155	G156	G157	G158	G159	G160	G161	G162	G163	G164	G165	G166	G167	G168	G169	G170	G171	G172	G173	G174	G175	G176	G177	G178	G179	G180	G181	G182	G183	G184	G185	G186	G187	G188	G189	G190	G191	G192	G193	G194	G195	G196	G197	G198	G199	G200	G201	G202	G203	G204	G205	G206	G207	G208	G209	G210	G211	G212	G213	G214	G215	G216	G217	G218	G219	G220	G221	G222	G223	G224	G225	G226	G227	G228	G229	G230	G231	G232	G233	G234	G235	G236	G237	G238	G239	G240	G241	G242	G243	G244	G245	G246	G247	G248	G249	G250	G251	G252	G253	G254	G255	G256	G257	G258	G259	G260	G261	G262	G263	G264	G265	G266	G267	G268	G269	G270	G271	G272	G273	G274	G275	G276	G277	G278	G279	G280	G281	G282	G283	G284	G285	G286	G287	G288	G289	G290	G291	G292	G293	G294	G295	G296	G297	G298	G299	G300	G301	G302	G303	G304	G305	G306	G307	G308	G309	G310	G311	G312	G313	G314	G315	G316	G317	G318	G319	G320	G321	G322	G323	G324	G325	G326	G327	G328	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	G352	G353	G354	G355	G356	G357	G358	G359	G360	G361	G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455	G456	G457	G458	G459	G460	G461	G462	G463	G464	G465	G466	G467	G468	G469	G470	G471	G472	G473	G474	G475	G476	G477	G478	G479	G480	G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G5
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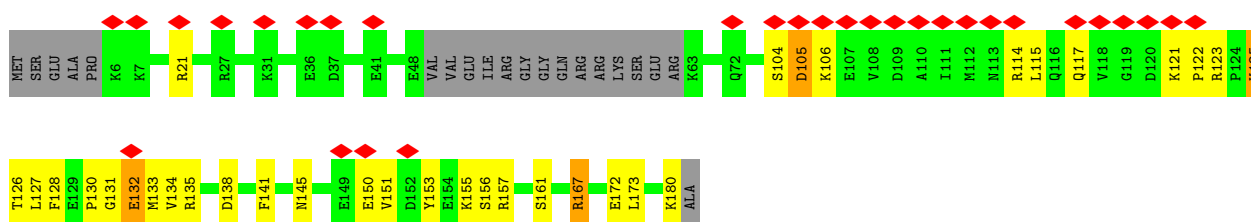
- Chain B:  46% 49% 5%

Category	Count
G1	100
G2	50
G3	100
G4	100
G5	100
G6	100
G7	100
G8	100
G9	100
G10	100
G11	100
G12	100
G13	100
G14	100
G15	100
G16	100
G17	100
G18	100
G19	100
G20	100
G21	100
G22	100
G23	100
G24	100
G25	100

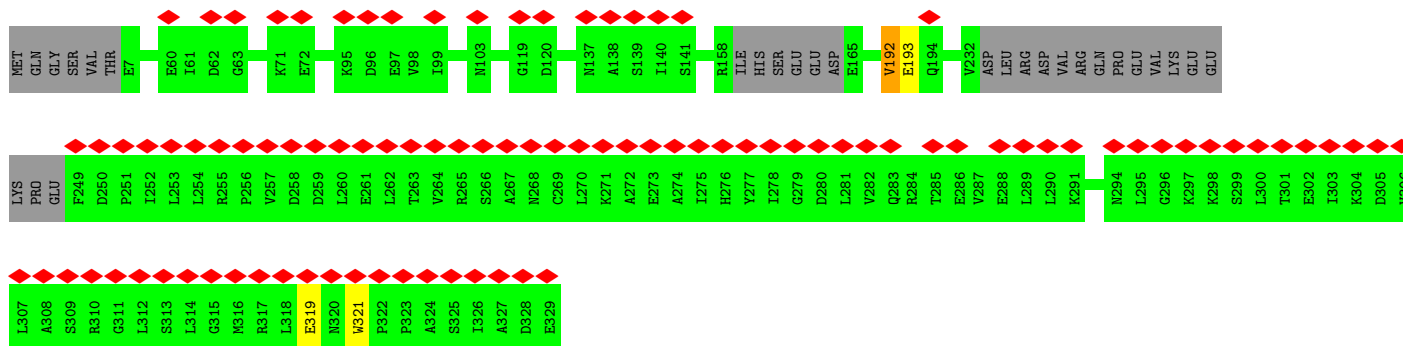
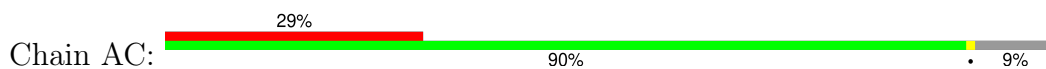
- Chain AA:  22% 99%



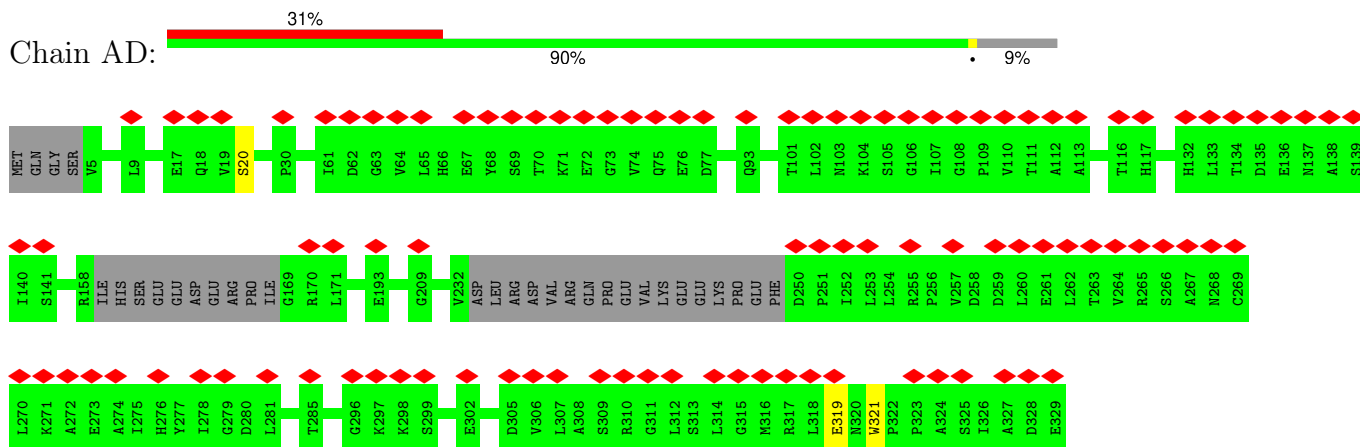
- Molecule 12: Transcription termination/antitermination protein NusG



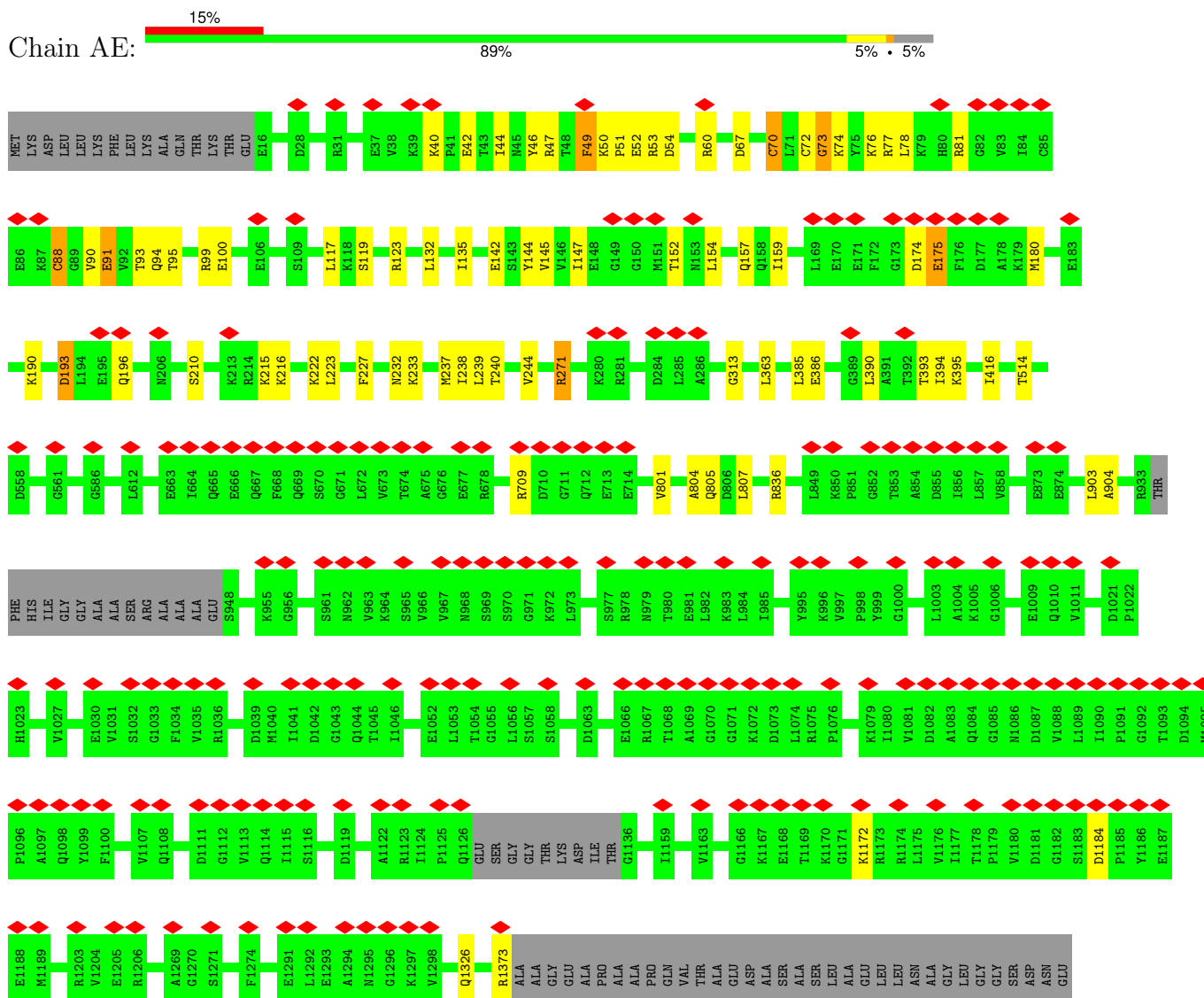
- Molecule 13: DNA-directed RNA polymerase subunit alpha



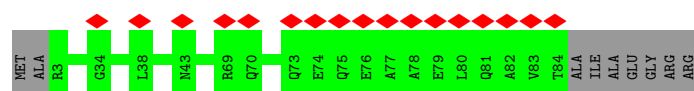
- Molecule 13: DNA-directed RNA polymerase subunit alpha



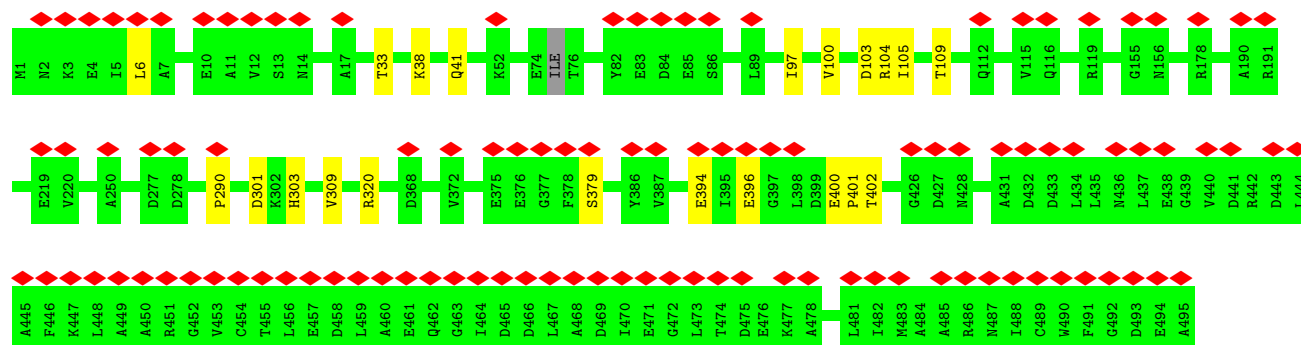
- Molecule 14: DNA-directed RNA polymerase subunit beta'



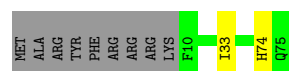
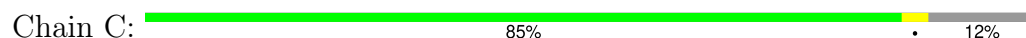
- Molecule 15: DNA-directed RNA polymerase subunit omega



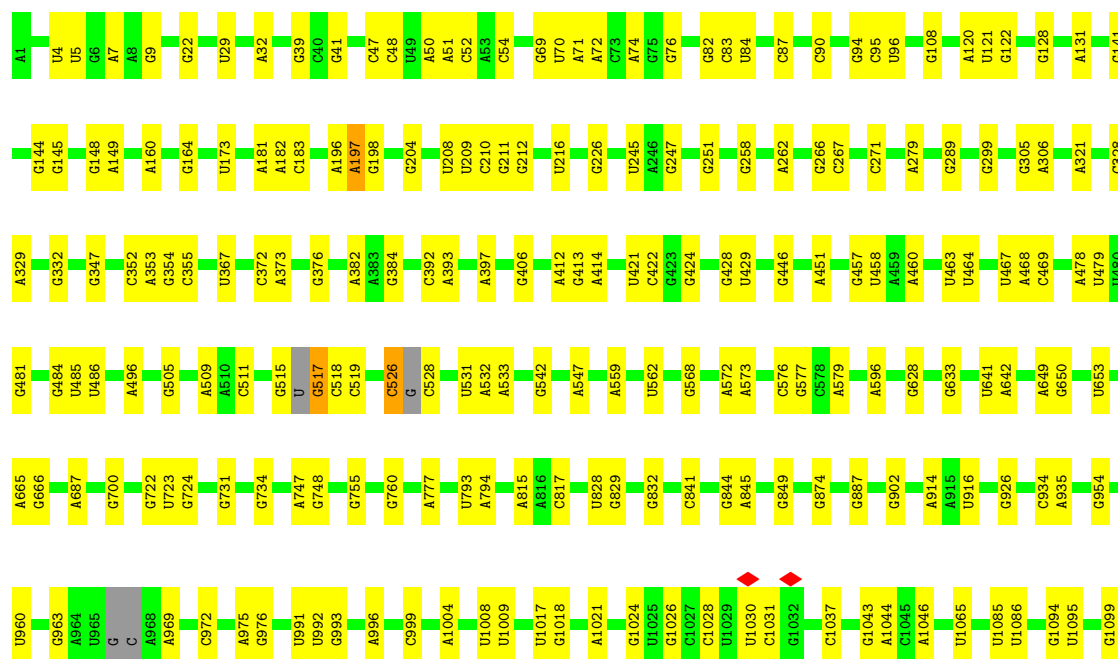
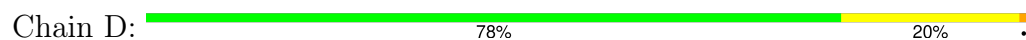
- Molecule 16: Transcription termination/antitermination protein NusA

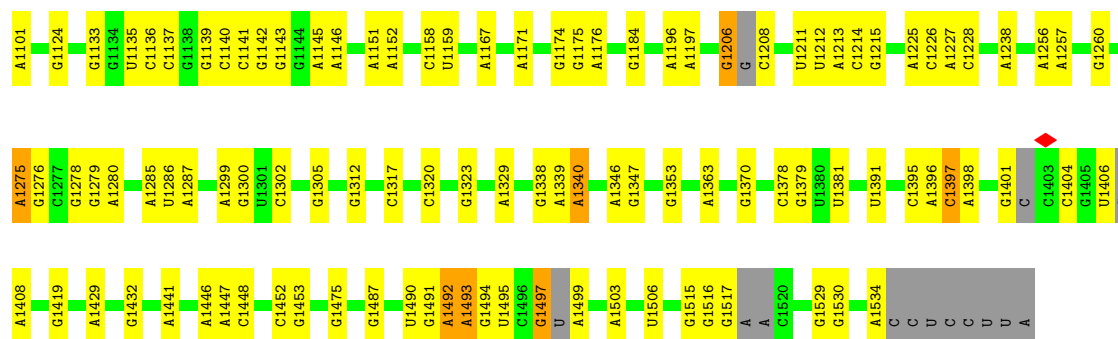


- Molecule 17: 30S ribosomal protein S18



- Molecule 18: 16S rRNA





• Molecule 19: 30S ribosomal protein S20

Chain E: 93% 6%



• Molecule 20: 30S ribosomal protein S21

Chain F: 94%



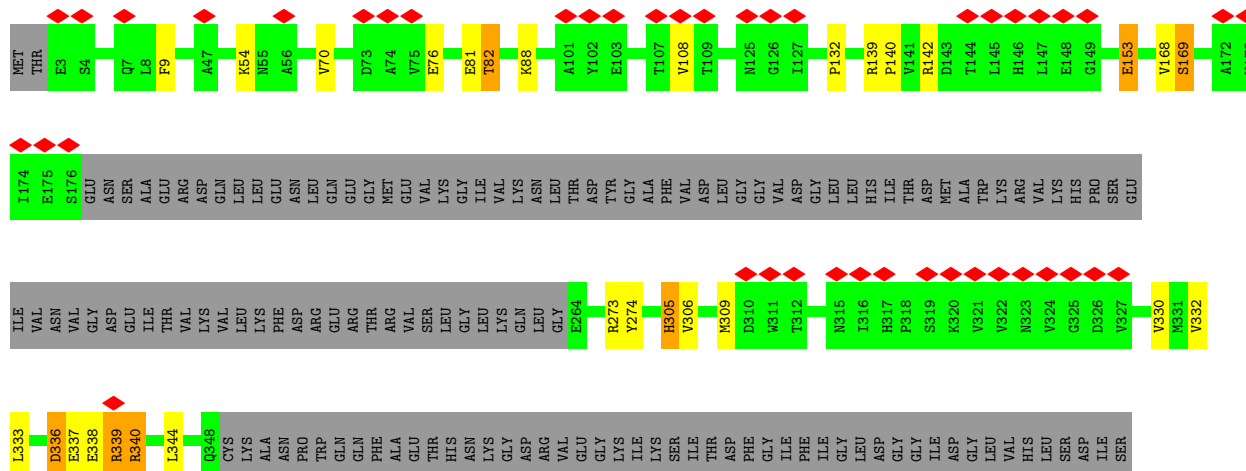
• Molecule 21: 30S ribosomal protein S2

Chain G: 90% 7%




• Molecule 22: 30S ribosomal protein S1

Chain H: 8% 41% 54%



TRP	ASN	VAL	ALA	GLY	GLU	ALA	VAL	ARG	GLU	TYR	LYS	GLY	ASP	GLU	ILE	ALA	ALA	VAL	VAL	GLN	VAL	ASP	ALA	GLU	ARG	GLU	ARG	GLU	ILE	ASP	LEU	GLY	VAL	LEU	ASN	LEU	GLN	ALA	GLY	ASP	PRO	PHE	ASN	TRP	VAL	ALA	LEU	ASN	LYS	LYS	GLY	ASN	ALA	ILE	VAL	THR	GLY	LEU	LYS
VAL	THR	ALA	VAL	ASP	ALA	LYS	GLY	ALA	ASP	GLU	VAL	THR	ASP	GLY	VAL	ASN	LYS	GLN	TYR	LEU	ARG	ALA	VAL	GLU	LYS	ASP	ALA	VAL	GLU	GLY	ALA	GLY	VAL	LEU	SER	VAL	GLY	VAL	GLU	GLY	ASP	GLY	VAL	THR	GLY	VAL	ASP	ARG	LYS	ASN	ARG	ALA	ILE	VAL	THR	GLY	SER	LEU	LYS
SER	VAL	ARG	ALA	LYS	ASP	GLU	ALA	ASP	GLU	THR	LYS	ASP	GLU	ILE	ALA	THR	VAL	ASN	LYS	GLN	GLY	ALA	VAL	GLU	LYS	ASP	ALA	VAL	GLU	GLY	ALA	GLY	VAL	LEU	GLN	PRO	PHE	ASN	GLU	GLY	ASP	GLY	VAL	THR	GLY	VAL	ASP	ARG	LYS	ASN	ARG	ALA	ILE	VAL	THR	GLY	SER	LEU	LYS

- Molecule 23: 30S ribosomal protein S3

Chain I:  86% 11%


MET	G2	I14	I75	K80	K89	R164	M185	V200	G209	GLY	MET	ALA	ALA	VAL	GLU	GLN	PRO	GLY	LYS	PRO	ALA	GLN	PRO	LYS	LYS	GLN	GLN	ARG	LYS	GLY	ARG	LYS
-----	----	-----	-----	-----	-----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 24: 30S ribosomal protein S4

Chain J:  96%

MET	A2	R47	L48	E95	R104	Q116	S138	V143	A149	R206
-----	----	-----	-----	-----	------	------	------	------	------	------

- Molecule 25: 30S ribosomal protein S5

Chain K:  89% 5% 7%


MET	ALA	HIS	ILE	GLU	LYS	GLN	ALA	GLY	E10	L15	G44	I60	V114	L115	R139	E162	L165	GLY	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	-----	-----

- Molecule 26: 30S ribosomal protein S6

Chain L:  72% 23%

M1	E16	R24	R38	L64	R79	R86	V96	K104	ALA	LYS	ASP	GLU	ARG	ARG	GLU	ARG	ARG	ASP	PHE	ALA	ASN	GLU	THR	ALA	ASP	ASP	ALA	GLU	ALA	GLY	ASP	SER	GLU	GLU	GLU	GLU	GLU
----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 27: 30S ribosomal protein S7

Chain M:  80% 16%

MET	F2	I7	K17	E21	L22	L23	R79	R109	M130	E146	A182	HIS	TYR	ARG	TRP	LEU	SER	LEU	ARG	SER	PHE	ALA	ASN	GLU	THR	ALA	GLY	ALA	ALA	SER	SER	LYS	GLN	PRO	ALA	LEU	GLY	TYR	LEU	ASN
-----	----	----	-----	-----	-----	-----	-----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 28: 30S ribosomal protein S8

Chain N:  97%

MET	S2	I75	N96	L121	A130
-----	----	-----	-----	------	------

- Molecule 29: 30S ribosomal protein S9

Chain O:  93% 5%




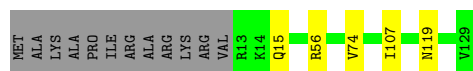
- Molecule 30: 30S ribosomal protein S10

Chain P:  87% 9%



- Molecule 31: 30S ribosomal protein S11

Chain Q:  87% 9%



- Molecule 32: 30S ribosomal protein S12

Chain R:  92% 6%




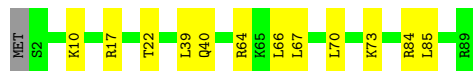
- Molecule 33: 30S ribosomal protein S14

Chain S:  95%



- Molecule 34: 30S ribosomal protein S15

Chain T:  85% 13%



- Molecule 35: 30S ribosomal protein S16

Chain U:  94% 6%

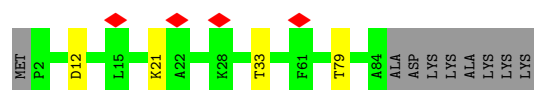


- Molecule 36: 30S ribosomal protein S17

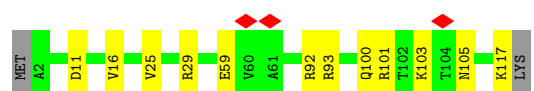


MET  
 THR  
 ASP  
 K4  
 L75  
 K81  
 A82  
 V83  
 LEU

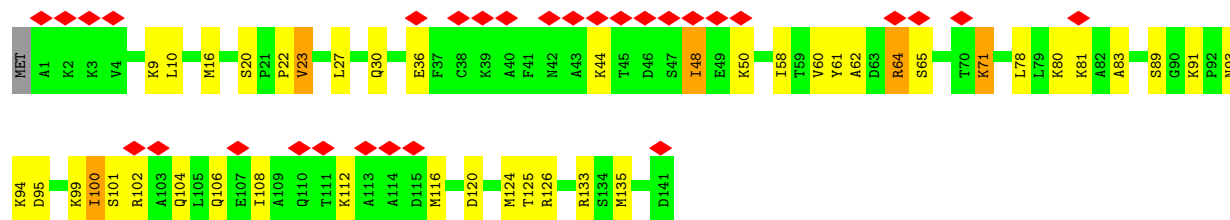
- Chain W:  86% 10%



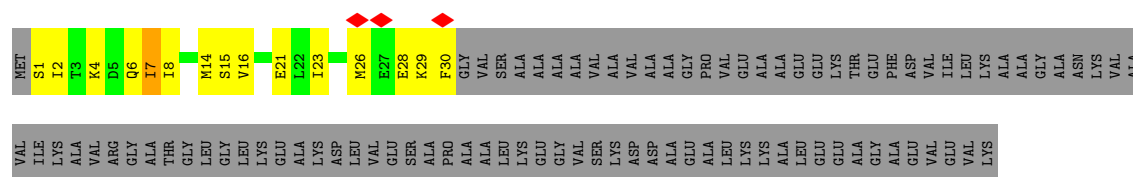
- Chain X: 



- Chain Y: 




- Chain Z: 

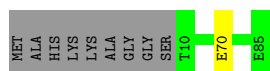


- Chain a:  81% 18%



- Molecule 42: 50S ribosomal protein L27

Chain b:  88% 11%




- Molecule 43: 50S ribosomal protein L28

Chain c:  94% 5%



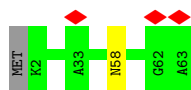
- Molecule 44: 5S rRNA

Chain d:  86% 14%



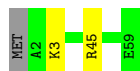
- Molecule 45: 50S ribosomal protein L29

Chain e:  5% 97%




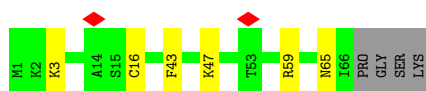
- Molecule 46: 50S ribosomal protein L30

Chain f:  95%



- Molecule 47: 50S ribosomal protein L31

Chain g:  86% 9% 6%




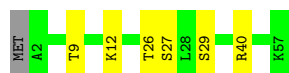
- Molecule 48: 50S ribosomal protein L2

Chain h:  93% 7%



- Molecule 49: 50S ribosomal protein L32

Chain i:  88% 11%




- Molecule 50: 50S ribosomal protein L3

Chain j:  97%



- Molecule 51: 50S ribosomal protein L33

Chain k:  89% 5% 5%



- Molecule 52: 50S ribosomal protein L4

Chain l:  93% 7%




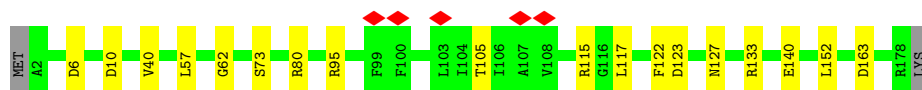
- Molecule 53: 50S ribosomal protein L34

Chain m:  93% 7%



- Molecule 54: 50S ribosomal protein L5

Chain n:  89% 10%



- Molecule 55: 50S ribosomal protein L35

Chain o:  91% 8%



- Molecule 56: 50S ribosomal protein L6

Chain p:  97% ..




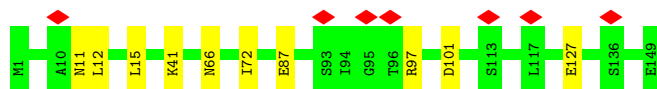
- Molecule 57: 50S ribosomal protein L36

Chain q:  95% 5%



- Molecule 58: 50S ribosomal protein L9

Chain r:  5% 93% 7%



- Molecule 59: 50S ribosomal protein L13

Chain s:  96% .



- Molecule 60: 50S ribosomal protein L14

Chain t:  95% 5%



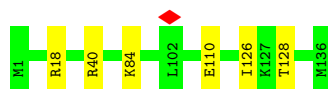
- Molecule 61: 50S ribosomal protein L15

Chain u:  96% .




- Molecule 62: 50S ribosomal protein L16

Chain v:  96% .



- Molecule 63: 50S ribosomal protein L17

Chain w:  87% 6% 6%



- Molecule 64: 50S ribosomal protein L18

Chain x:  94% 5% .

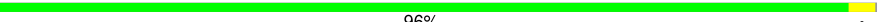


- Molecule 65: 50S ribosomal protein L19

Chain y:  95% . .



- Molecule 66: 50S ribosomal protein L20

Chain z:  96% . .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19967	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	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	0.039	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00359	Depositor
Map size ( $\text{\AA}$ )	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.04, 1.04, 1.04	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.38	0/829	0.67	0/1107
2	1	0.48	0/864	0.82	0/1156
3	2	0.42	0/752	0.71	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.40	0/766	0.68	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	0.59	3/805 (0.4%)	0.90	3/1246 (0.2%)
9	9	0.79	2/1131 (0.2%)	0.64	1/1524 (0.1%)
10	A	0.39	0/1810	0.75	1/2821 (0.0%)
10	B	0.46	1/1810 (0.1%)	0.86	7/2821 (0.2%)
11	AA	0.43	0/10736	0.61	1/14487 (0.0%)
12	AB	0.55	0/1304	0.63	1/1759 (0.1%)
13	AC	0.38	0/2110	0.58	0/2873
13	AD	0.34	0/2091	0.59	0/2847
14	AE	0.52	4/10545 (0.0%)	0.66	6/14236 (0.0%)
15	AF	0.33	0/652	0.57	0/879
16	AG	0.46	0/2440	0.56	2/3396 (0.1%)
17	C	0.48	0/553	0.83	0/743
18	D	0.34	10/36610 (0.0%)	0.73	30/57091 (0.1%)
19	E	0.57	0/675	0.86	0/895
20	F	0.56	0/597	0.87	0/792
21	G	0.48	0/1791	0.71	0/2413
22	H	0.54	1/1746 (0.1%)	1.03	13/2382 (0.5%)
23	I	0.44	0/1663	0.71	0/2241
24	J	0.47	0/1665	0.73	0/2227
25	K	0.45	0/1165	0.75	0/1568
26	L	0.43	0/867	0.75	1/1171 (0.1%)
27	M	0.50	0/1195	0.81	0/1602
28	N	0.41	0/989	0.69	0/1326
29	O	0.43	0/1034	0.75	0/1375
30	P	0.44	0/800	0.76	0/1082



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	Q	0.40	0/893	0.70	0/1205
32	R	0.35	0/952	0.74	0/1274
33	S	0.49	0/817	0.79	0/1088
34	T	0.53	0/722	0.86	0/964
35	U	0.44	0/659	0.78	0/884
36	V	0.34	0/657	0.61	0/881
37	W	0.38	0/680	0.62	0/915
38	X	0.49	0/909	0.87	0/1215
39	Y	0.67	0/1046	0.58	0/1410
40	Z	0.69	0/227	0.57	0/304
41	a	0.38	3/69247 (0.0%)	0.72	17/107985 (0.0%)
42	b	0.39	0/589	0.71	0/779
43	c	0.48	0/635	0.81	1/848 (0.1%)
44	d	0.29	0/2872	0.69	0/4478
45	e	0.54	0/502	0.82	0/667
46	f	0.45	0/452	0.78	0/605
47	g	0.43	0/531	0.68	0/709
48	h	0.39	0/2121	0.78	0/2852
49	i	0.40	0/450	0.79	0/599
50	j	0.44	0/1586	0.70	0/2134
51	k	0.35	0/433	0.65	0/576
52	l	0.46	0/1571	0.77	0/2113
53	m	0.53	0/380	0.99	0/498
54	n	0.49	0/1434	0.88	3/1926 (0.2%)
55	o	0.45	0/513	0.83	0/676
56	p	0.39	0/1333	0.67	0/1805
57	q	0.37	0/303	0.77	0/397
58	r	0.44	0/1122	0.69	0/1515
59	s	0.50	0/1152	0.75	0/1551
60	t	0.41	0/955	0.78	0/1279
61	u	0.40	0/1062	0.76	0/1413
62	v	0.47	0/1093	0.81	0/1460
63	w	0.52	0/964	0.87	0/1289
64	x	0.46	0/902	0.81	0/1209
65	y	0.41	0/929	0.73	1/1242 (0.1%)
66	z	0.60	0/960	0.92	1/1278 (0.1%)
All	All	0.42	34/193575 (0.0%)	0.73	92/284911 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	A	0	2
10	B	0	2
11	AA	0	1
13	AC	0	3
13	AD	0	3
14	AE	0	5
16	AG	0	1
22	H	0	3
38	X	0	1
All	All	0	21

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	13.71	1.70	1.47
18	D	1516	G	O3'-P	-13.41	1.45	1.61
18	D	1339	A	O3'-P	10.49	1.73	1.61
14	AE	88	CYS	CB-SG	-10.21	1.64	1.82
6	5	109	DT	O3'-P	8.68	1.71	1.61

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1516	G	P-O3'-C3'	-18.97	96.93	119.70
18	D	1516	G	O3'-P-O5'	13.78	130.18	104.00
41	a	2252	G	N9-C1'-C2'	-10.95	99.76	114.00
18	D	1401	G	N9-C1'-C2'	-10.69	100.10	114.00
54	n	73	SER	N-CA-CB	-10.60	94.60	110.50

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	910	ALA	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	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%)	97 (96%)	3 (3%)	1 (1%)	13	44
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	13	44
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1338/1342 (100%)	1209 (90%)	126 (9%)	3 (0%)	44	72
12	AB	157/181 (87%)	128 (82%)	22 (14%)	7 (4%)	2	19
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	19	51
13	AD	292/329 (89%)	270 (92%)	22 (8%)	0	100	100
14	AE	1329/1407 (94%)	1198 (90%)	122 (9%)	9 (1%)	19	51
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	490/495 (99%)	421 (86%)	51 (10%)	18 (4%)	2	24
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	19
23	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	25	57
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	54
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	44
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	51
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	49
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	P	97/103 (94%)	87 (90%)	9 (9%)	1 (1%)	13	44
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	36
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	40
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	7	35
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	9
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	13
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	62
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	25	57
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	43
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	47
All	All	10154/11072 (92%)	9318 (92%)	738 (7%)	98 (1%)	16	44

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
16	AG	6	LEU
16	AG	100	VAL
16	AG	400	GLU
16	AG	401	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	78 (93%)	6 (7%)	12	39
2	1	93/93 (100%)	84 (90%)	9 (10%)	6	28
3	2	81/84 (96%)	76 (94%)	5 (6%)	15	42
4	3	84/85 (99%)	78 (93%)	6 (7%)	12	39
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	47
9	9	112/123 (91%)	65 (58%)	47 (42%)	0	0
11	AA	1155/1157 (100%)	1142 (99%)	13 (1%)	70	80
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	6
13	AC	185/286 (65%)	185 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1052 (94%)	68 (6%)	15	43
15	AF	70/75 (93%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	C	57/65 (88%)	55 (96%)	2 (4%)	31	56
19	E	65/66 (98%)	60 (92%)	5 (8%)	10	37
20	F	60/61 (98%)	57 (95%)	3 (5%)	20	47
21	G	187/199 (94%)	178 (95%)	9 (5%)	21	48
22	H	137/461 (30%)	128 (93%)	9 (7%)	14	41
23	I	171/190 (90%)	164 (96%)	7 (4%)	26	52
24	J	172/173 (99%)	165 (96%)	7 (4%)	26	52
25	K	119/126 (94%)	112 (94%)	7 (6%)	16	44
26	L	91/116 (78%)	85 (93%)	6 (7%)	14	41
27	M	124/147 (84%)	116 (94%)	8 (6%)	14	41
28	N	104/105 (99%)	102 (98%)	2 (2%)	52	70
29	O	105/107 (98%)	100 (95%)	5 (5%)	21	48
30	P	86/90 (96%)	78 (91%)	8 (9%)	7	30
31	Q	90/99 (91%)	87 (97%)	3 (3%)	33	57
32	R	101/104 (97%)	94 (93%)	7 (7%)	13	39
33	S	83/84 (99%)	79 (95%)	4 (5%)	21	48
34	T	76/77 (99%)	64 (84%)	12 (16%)	2	14
35	U	65/65 (100%)	61 (94%)	4 (6%)	15	42
36	V	74/78 (95%)	72 (97%)	2 (3%)	40	61
37	W	72/79 (91%)	68 (94%)	4 (6%)	17	45
38	X	94/96 (98%)	85 (90%)	9 (10%)	7	28
39	Y	109/110 (99%)	73 (67%)	36 (33%)	0	1
40	Z	26/85 (31%)	12 (46%)	14 (54%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	56	73
43	c	67/68 (98%)	64 (96%)	3 (4%)	23	50
45	e	54/55 (98%)	53 (98%)	1 (2%)	52	70
46	f	48/49 (98%)	46 (96%)	2 (4%)	25	51
47	g	59/62 (95%)	53 (90%)	6 (10%)	6	26
48	h	216/218 (99%)	199 (92%)	17 (8%)	10	36
49	i	47/48 (98%)	41 (87%)	6 (13%)	3	19
50	j	164/164 (100%)	157 (96%)	7 (4%)	25	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	k	47/49 (96%)	44 (94%)	3 (6%)	14	42
52	l	165/165 (100%)	151 (92%)	14 (8%)	8	33
53	m	38/38 (100%)	35 (92%)	3 (8%)	10	36
54	n	148/150 (99%)	134 (90%)	14 (10%)	7	29
55	o	51/52 (98%)	46 (90%)	5 (10%)	6	27
56	p	136/138 (99%)	132 (97%)	4 (3%)	37	59
57	q	34/34 (100%)	32 (94%)	2 (6%)	16	44
58	r	114/114 (100%)	104 (91%)	10 (9%)	8	32
59	s	116/116 (100%)	110 (95%)	6 (5%)	19	46
60	t	104/104 (100%)	98 (94%)	6 (6%)	17	44
61	u	103/103 (100%)	97 (94%)	6 (6%)	17	44
62	v	109/109 (100%)	103 (94%)	6 (6%)	18	45
63	w	99/103 (96%)	91 (92%)	8 (8%)	9	34
64	x	86/87 (99%)	80 (93%)	6 (7%)	12	39
65	y	99/100 (99%)	95 (96%)	4 (4%)	27	52
66	z	89/90 (99%)	87 (98%)	2 (2%)	47	65
All	All	7904/8739 (90%)	7401 (94%)	503 (6%)	17	42

5 of 503 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	K	15	LEU
56	p	39	ASP
34	T	66	LEU
55	o	8	ARG
61	u	48	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
13	AD	66	HIS
14	AE	294	ASN
13	AD	227	GLN
15	AF	31	GLN
11	AA	580	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
18	D	1514/1542 (98%)	288 (19%)	34 (2%)
41	a	2859/2904 (98%)	533 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	34/46 (73%)	21 (61%)	4 (11%)
All	All	4676/4764 (98%)	923 (19%)	50 (1%)

5 of 923 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U
8	7	-14	U
8	7	-13	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	531	U
18	D	992	U
18	D	1493	A
18	D	532	A
18	D	722	G

## 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.

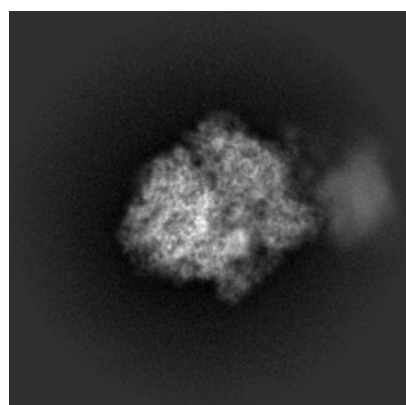
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22141. These allow visual inspection of the internal detail of the map and identification of artifacts.

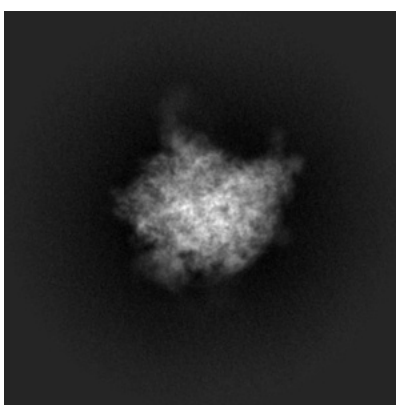
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

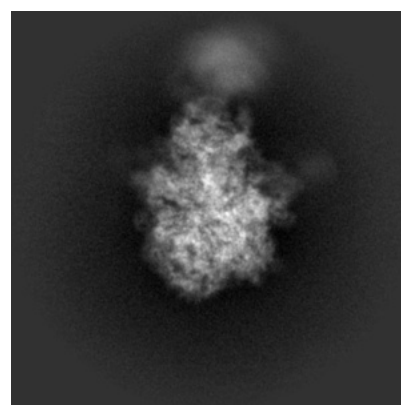
#### 6.1.1 Primary map



X



Y

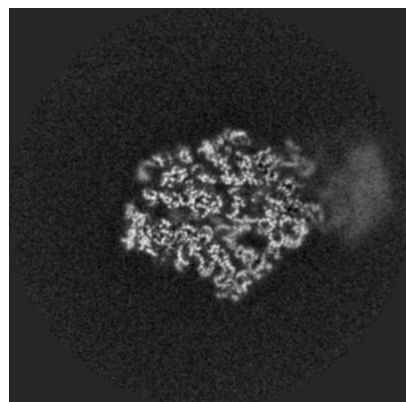


Z

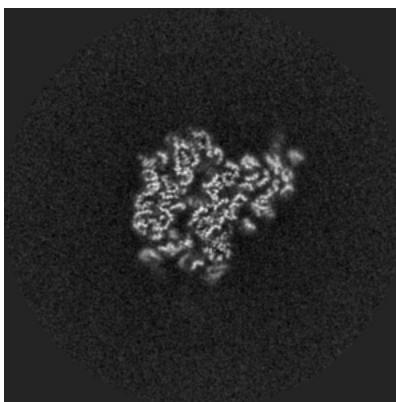
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

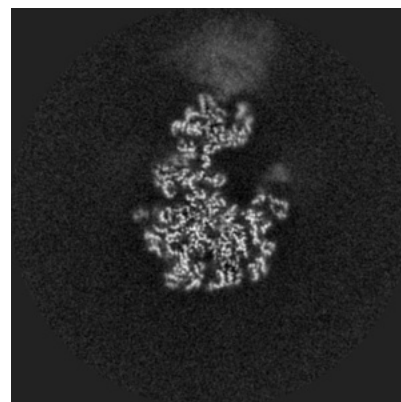
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

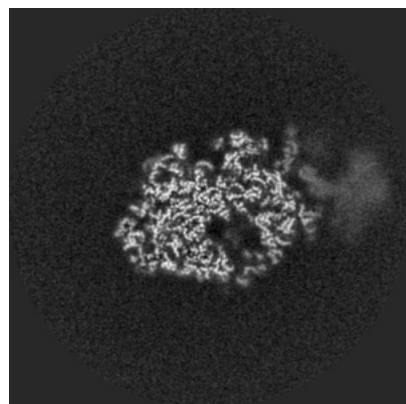


Z Index: 256

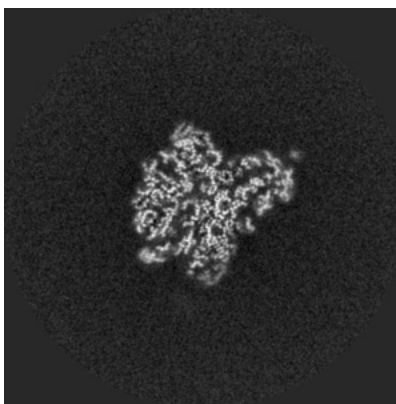
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

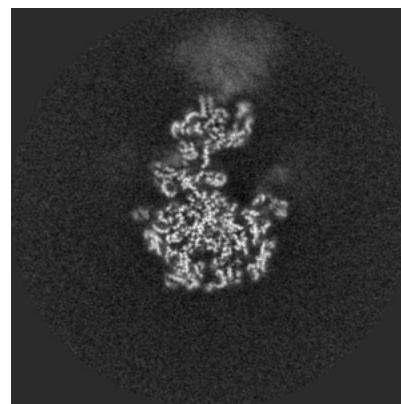
### 6.3.1 Primary map



X Index: 239



Y Index: 251

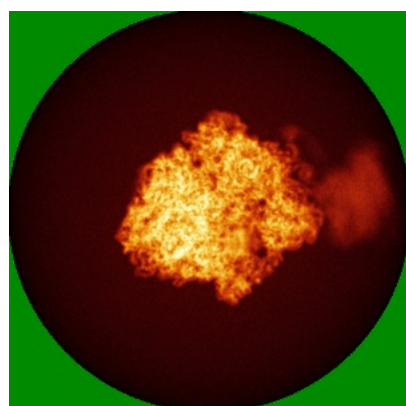


Z Index: 258

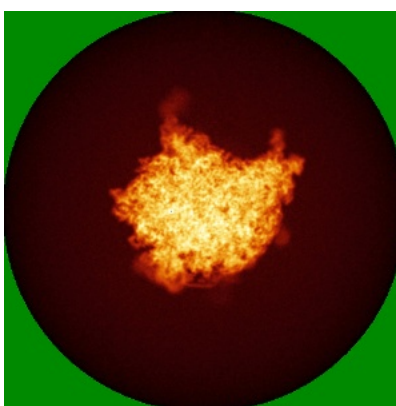
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X



Y

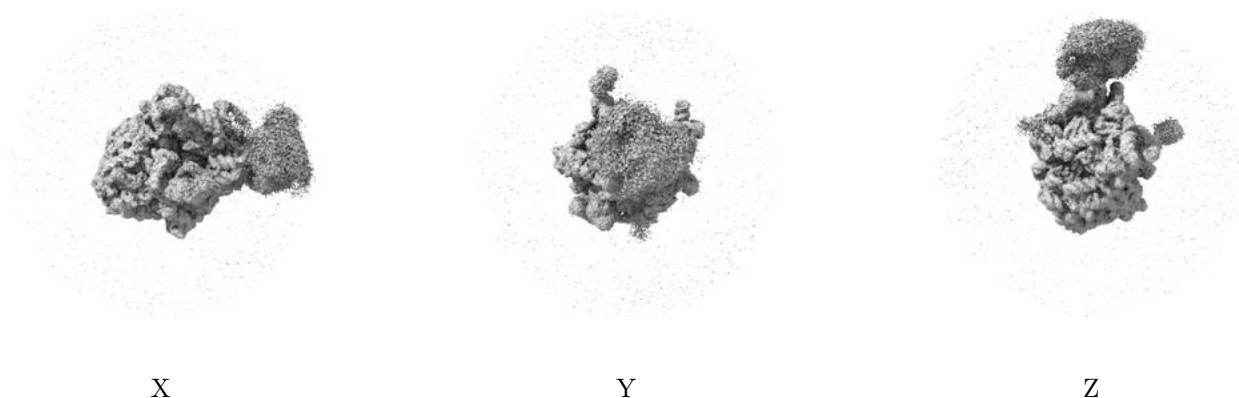


Z

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 0.00359. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

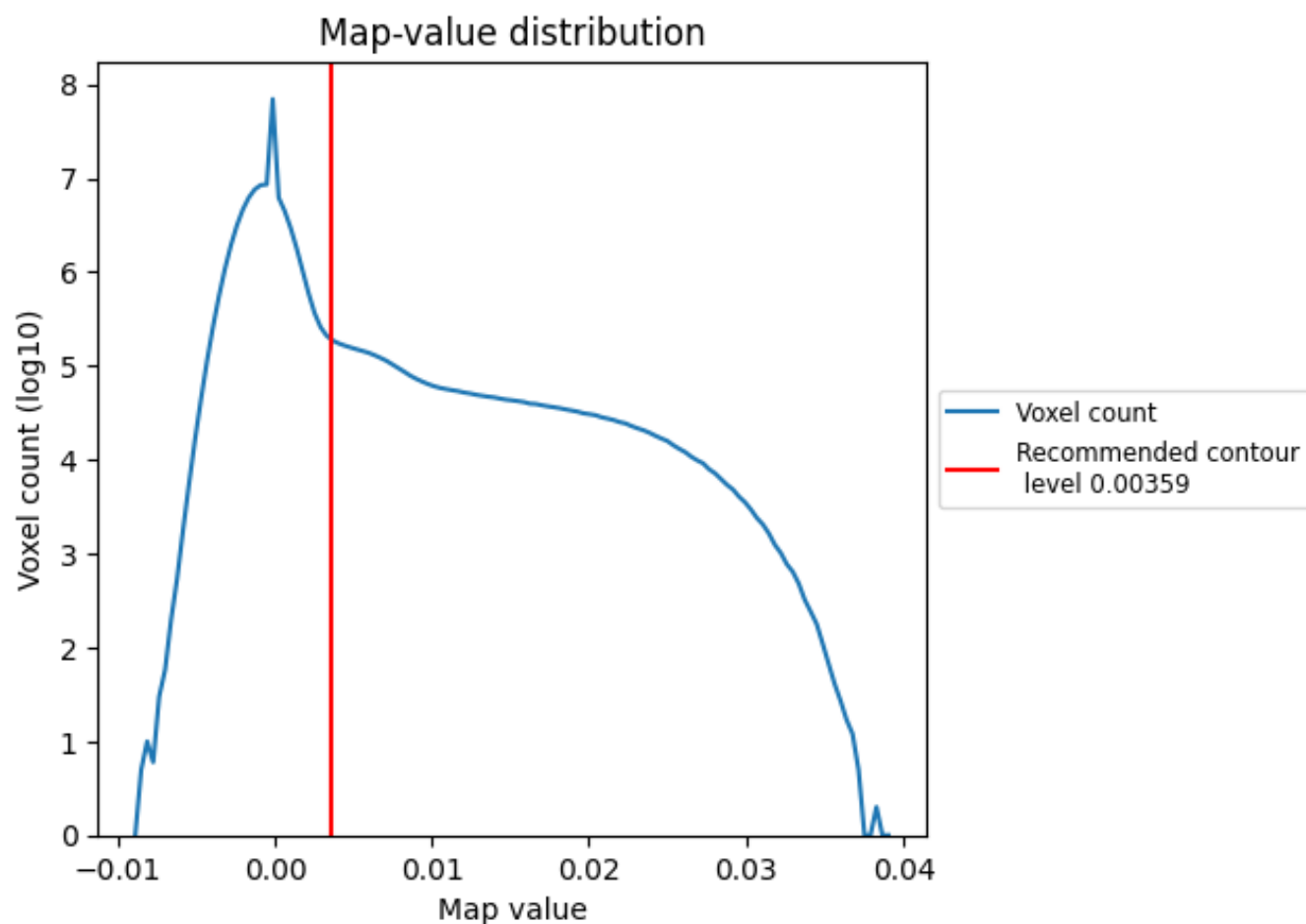
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

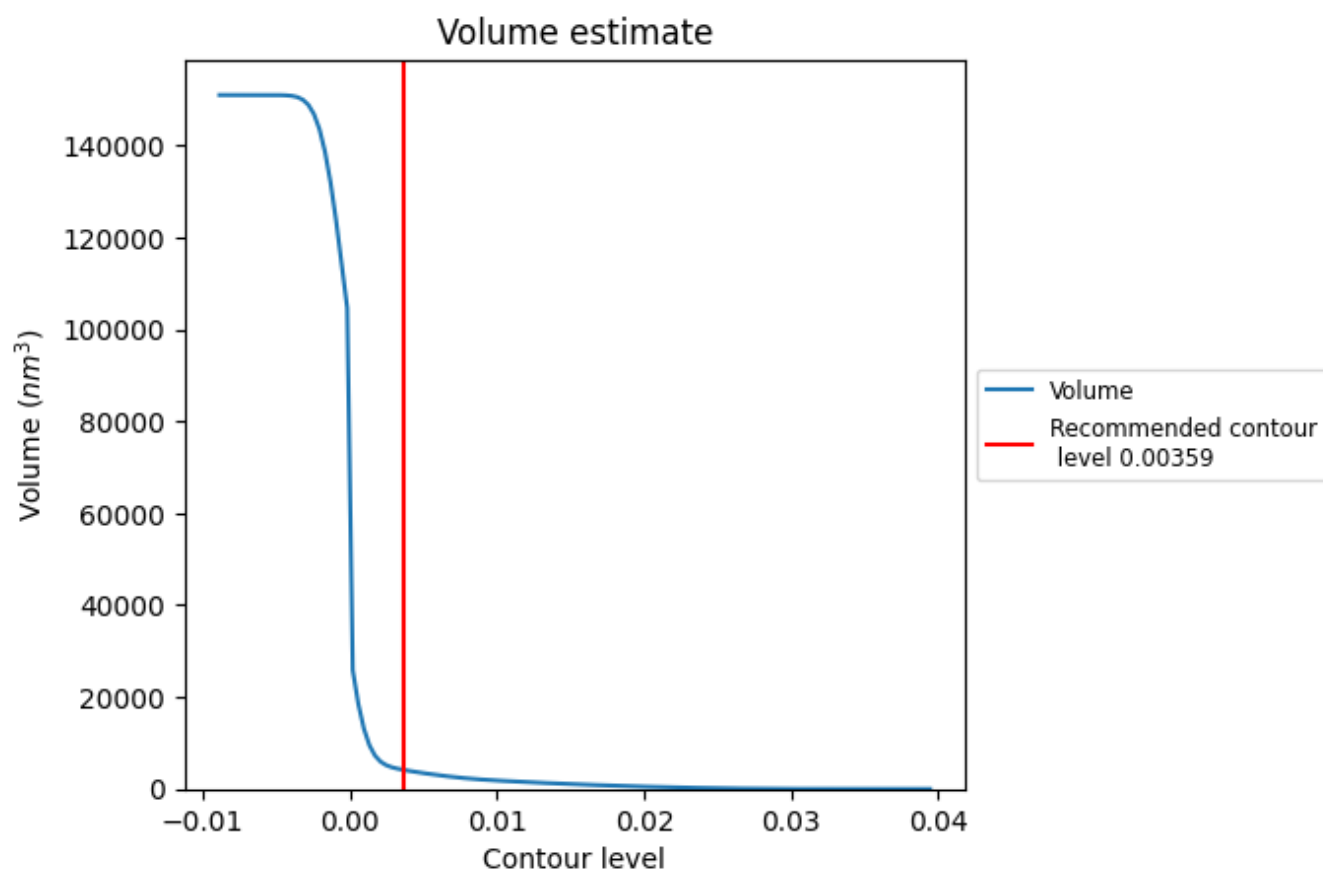
This section contains the results of statistical analysis of the map.

### 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.

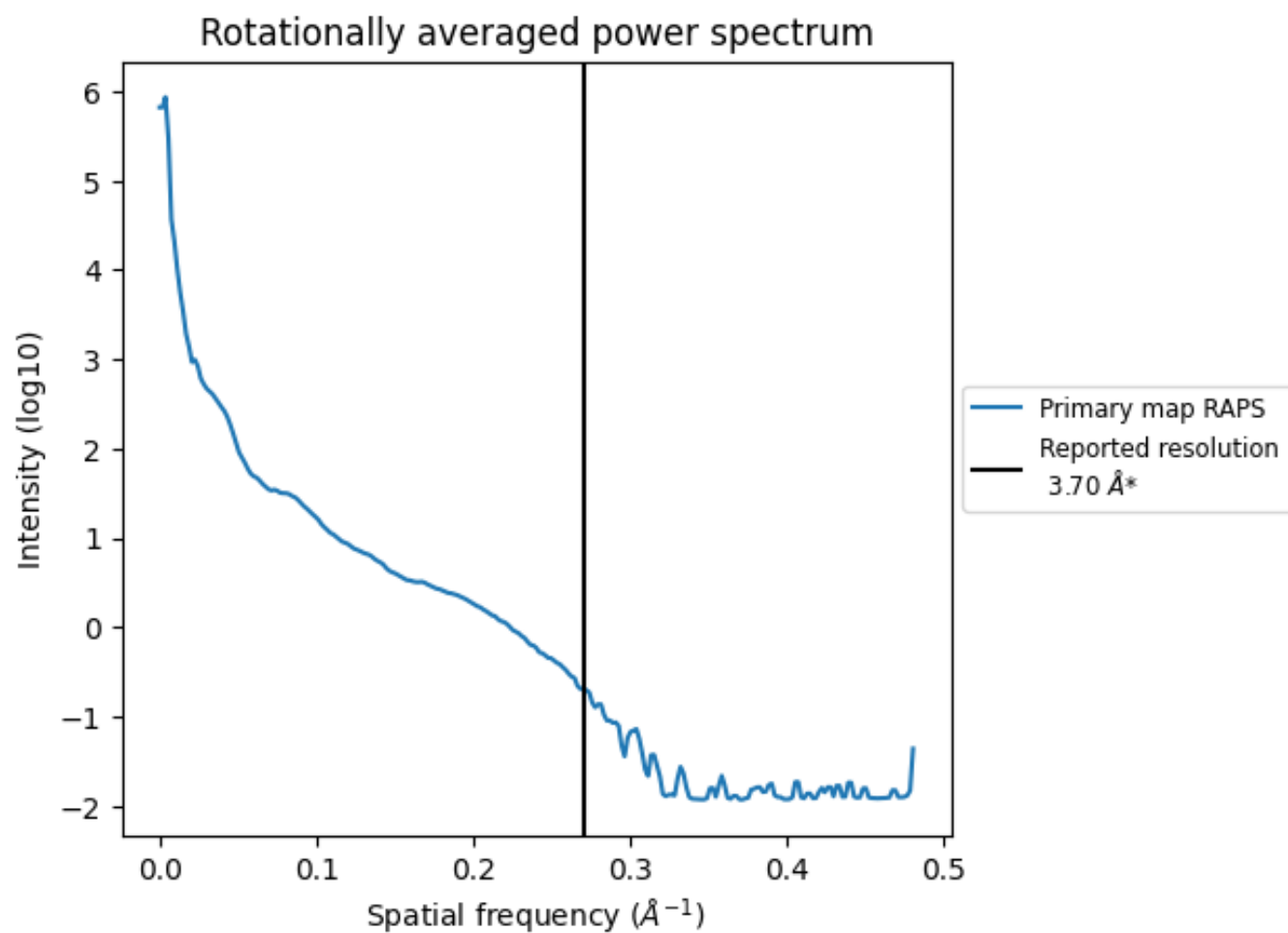
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4172 nm<sup>3</sup>; this corresponds to an approximate mass of 3769 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<sup>-1</sup>

## 8 Fourier-Shell correlation

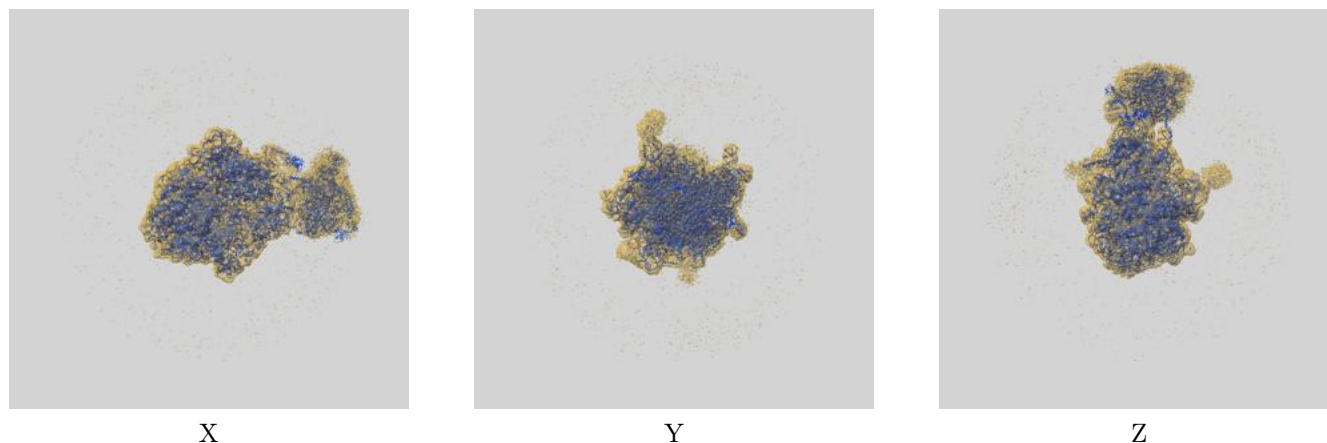
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

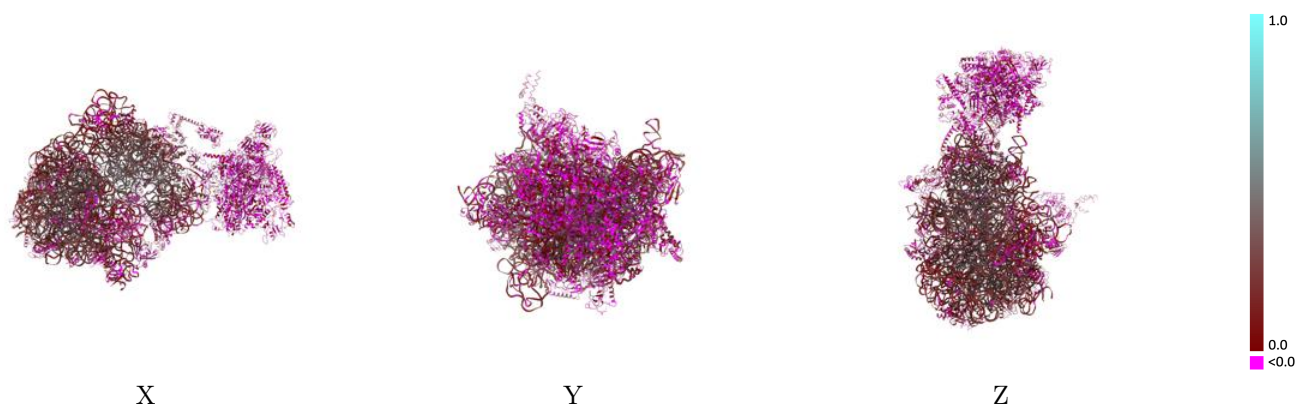
This section contains information regarding the fit between EMDB map EMD-22141 and PDB model 6XDQ. Per-residue inclusion information can be found in section [3](#) on page [17](#).

### 9.1 Map-model overlay [i](#)



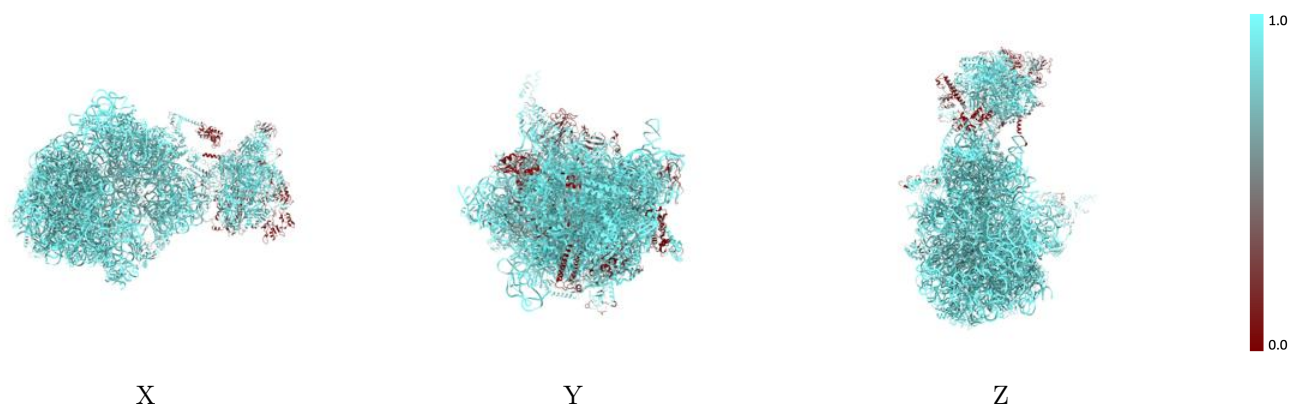
The images above show the 3D surface view of the map at the recommended contour level 0.00359 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



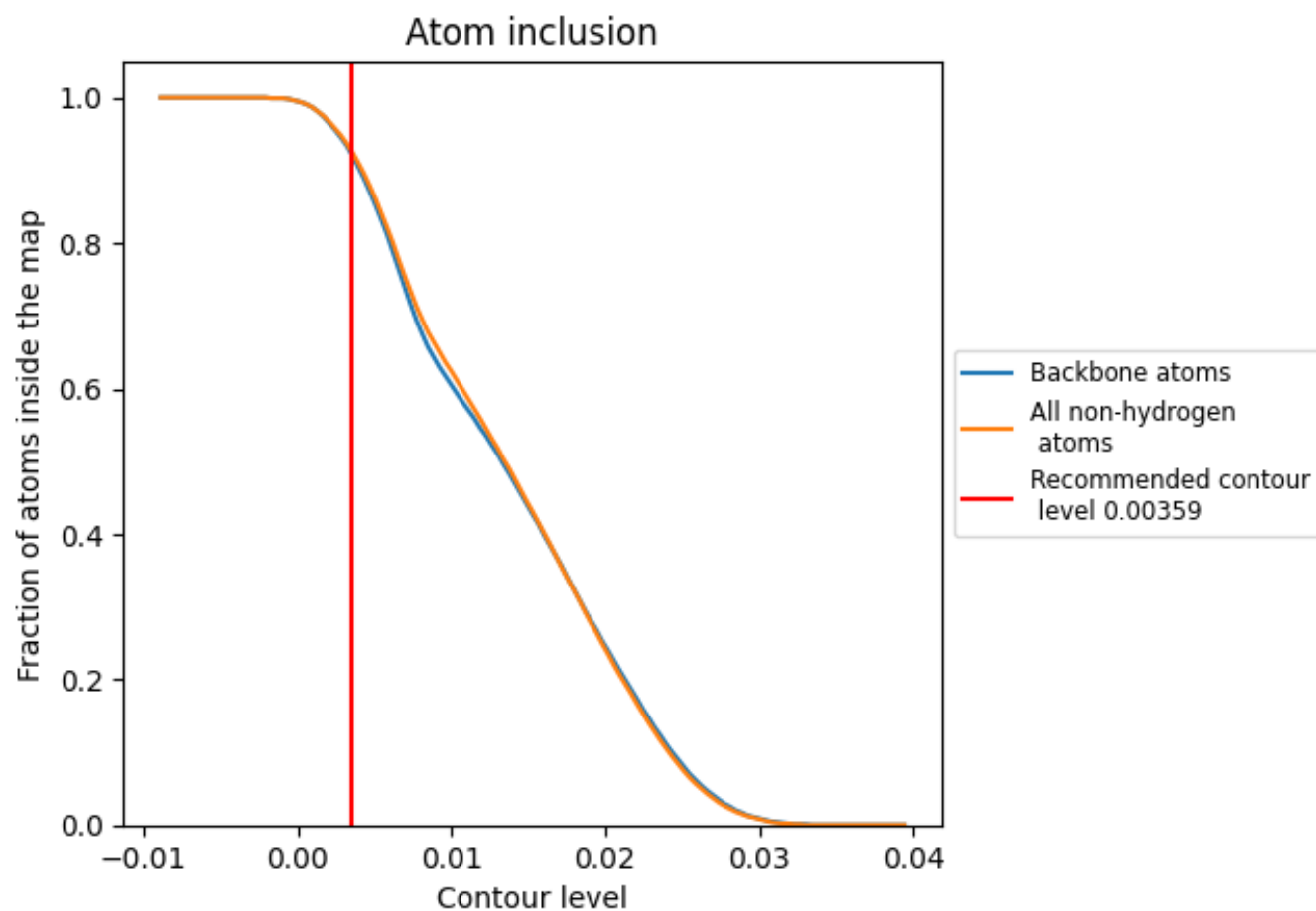
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00359).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.00359) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.1750
0	 0.9360	 0.1880
1	 0.9380	 0.2750
2	 0.9140	 0.1340
3	 0.9450	 0.1200
4	 0.9400	 0.1220
5	 0.8900	 0.0180
6	 0.9610	 0.0240
7	 0.9440	 0.0680
9	 0.8770	 0.0300
A	 0.9980	 0.1920
AA	 0.7490	 0.0110
AB	 0.7330	 0.0390
AC	 0.7050	 0.0230
AD	 0.6300	 0.0140
AE	 0.8150	 0.0130
AF	 0.7080	 -0.0110
AG	 0.7700	 0.0870
B	 0.8930	 0.0740
C	 0.9560	 0.1710
D	 0.9930	 0.2500
E	 0.9620	 0.1080
F	 0.9450	 0.2240
G	 0.9230	 0.1830
H	 0.7990	 0.0360
I	 0.9400	 0.2120
J	 0.9500	 0.1860
K	 0.9660	 0.3140
L	 0.9180	 0.1040
M	 0.9340	 0.1710
N	 0.9540	 0.2430
O	 0.9480	 0.1460
P	 0.9230	 0.1430
Q	 0.9630	 0.1940
R	 0.9750	 0.3010



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Chain	Atom inclusion	Q-score
S	 0.9560	 0.1410
T	 0.9640	 0.2030
U	 0.9590	 0.1030
V	 0.9480	 0.2250
W	 0.8690	 0.0450
X	 0.9020	 0.0720
Y	 0.7380	 0.0150
Z	 0.8330	 0.0180
a	 0.9930	 0.2350
b	 0.9470	 0.1360
c	 0.9470	 0.1970
d	 0.9880	 0.1350
e	 0.9120	 0.0940
f	 0.9500	 0.1830
g	 0.9290	 0.0380
h	 0.9490	 0.1910
i	 0.9580	 0.2310
j	 0.9490	 0.1660
k	 0.9280	 0.0880
l	 0.9340	 0.1680
m	 0.9750	 0.3110
n	 0.9130	 0.0610
o	 0.9470	 0.1880
p	 0.9320	 0.0620
q	 0.9520	 0.1030
r	 0.8490	 0.0530
s	 0.9510	 0.1750
t	 0.9140	 0.1690
u	 0.9470	 0.1790
v	 0.9550	 0.1880
w	 0.9440	 0.1840
x	 0.9320	 0.0210
y	 0.9230	 0.1170
z	 0.9630	 0.2310