



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 04:44 AM EDT

PDB ID : 6VYS
EMDB ID : EMD-21470
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing a 21 nt long mRNA spacer, NusG, and fMet-tRNAs at E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-02-27
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:

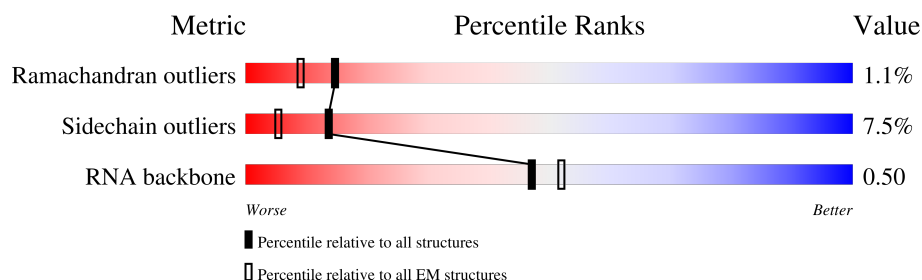
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :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

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 ≥ 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	37	

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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	1358	
15	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	

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Mol	Chain	Length	Quality of chain
32	T	89	
33	U	82	
34	V	84	
35	W	92	
36	X	118	
37	Y	142	
38	Z	121	
39	a	2904	
40	b	85	
41	c	78	
42	d	120	
43	e	63	
44	f	59	
45	g	70	
46	h	273	
47	i	57	
48	j	209	
49	k	55	
50	l	201	
51	m	46	
52	n	179	
53	o	65	
54	p	177	
55	q	38	
56	r	149	

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Mol	Chain	Length	Quality of chain
57	s	142	<div><div></div><div>96%</div><div></div></div>
58	t	123	<div><div>6%</div><div>95%</div><div>5%</div></div>
59	u	144	<div><div>8%</div><div>96%</div><div></div></div>
60	v	136	<div><div></div><div>96%</div><div></div></div>
61	w	127	<div><div></div><div>87%</div><div>6%</div><div>6%</div></div>
62	x	117	<div><div>18%</div><div>94%</div><div>5%</div></div>
63	y	115	<div><div>9%</div><div>95%</div><div></div></div>
64	z	118	<div><div></div><div>97%</div><div></div></div>

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300543 atoms, of which 124723 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 21 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	26	Total	C	H	N	O	P	0	0
			644	244	97	82	195	26		

- 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	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.

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

- 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	variant	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	AE	1	Total	Mg	0
			1	1	

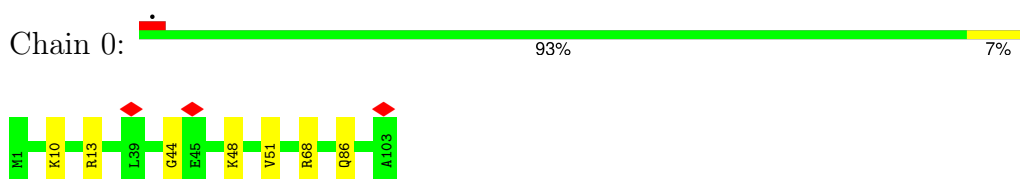
- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

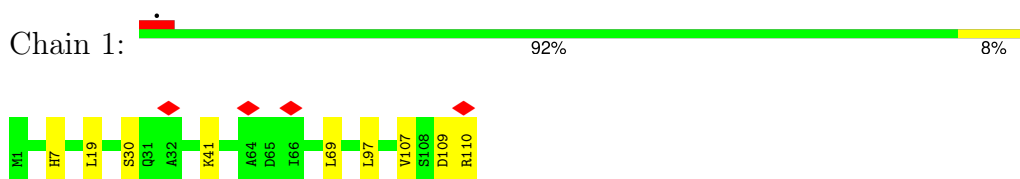
3 Residue-property plots [i](#)

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

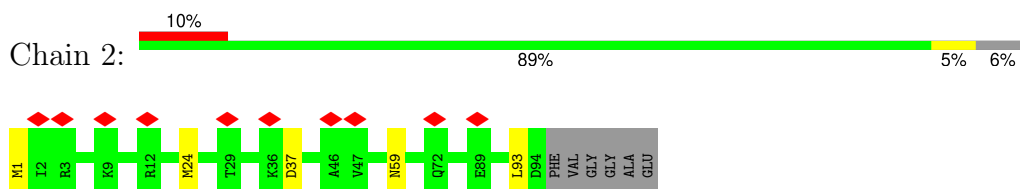
- Molecule 1: 50S ribosomal protein L21



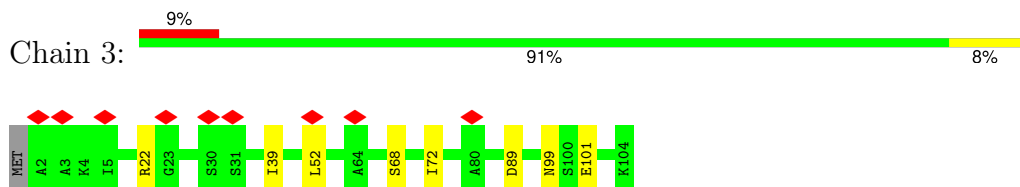
- Molecule 2: 50S ribosomal protein L22



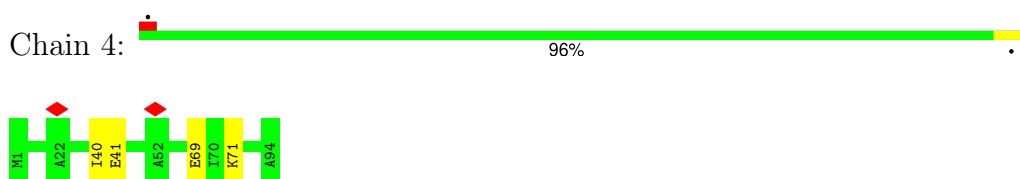
- Molecule 3: 50S ribosomal protein L23



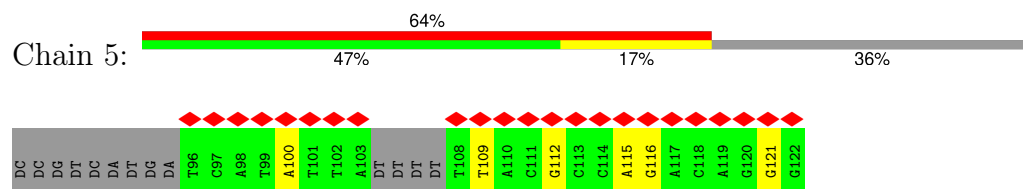
- Molecule 4: 50S ribosomal protein L24



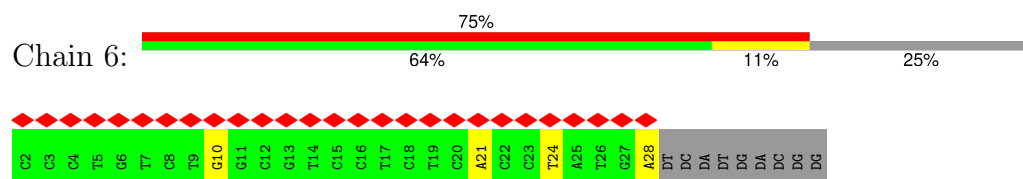
- Molecule 5: 50S ribosomal protein L25



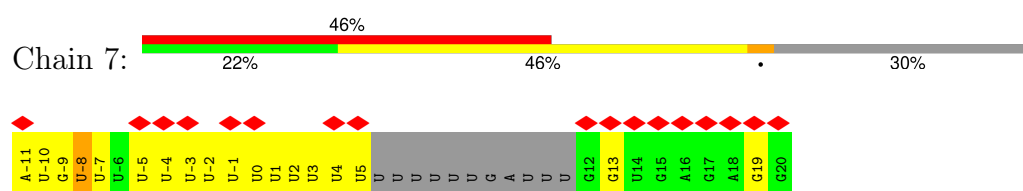
- Molecule 6: NT DNA



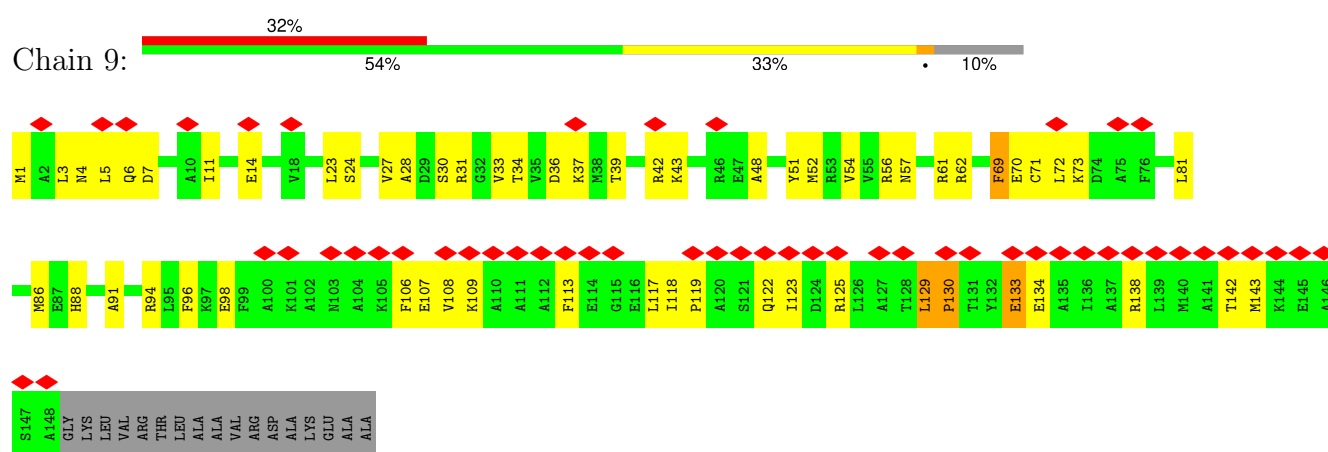
- Molecule 7: T DNA



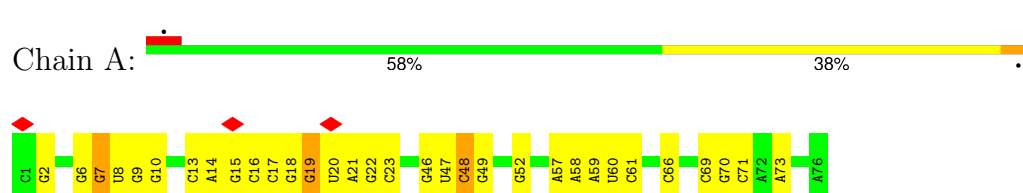
- Molecule 8: mRNA with 21 nt long spacer



- Molecule 9: 50S ribosomal protein L10

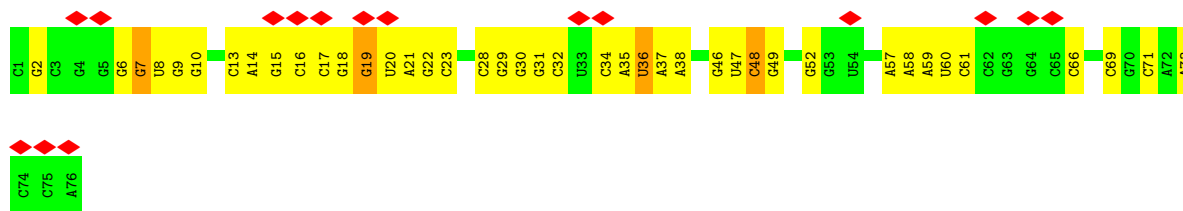


- Molecule 10: E-site and P-site tRNA (fMet)



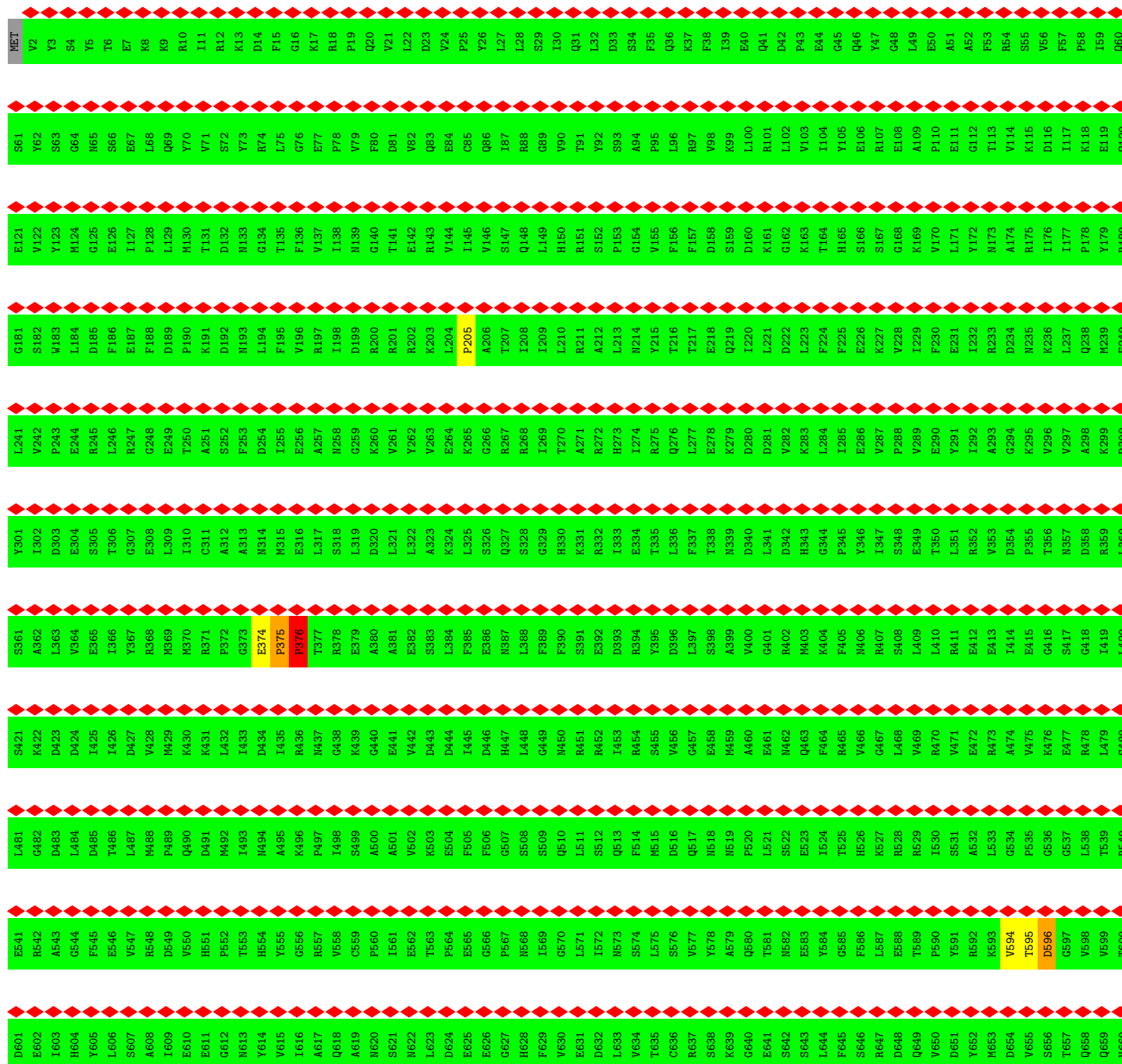
- Molecule 10: E-site and P-site tRNA (fMet)

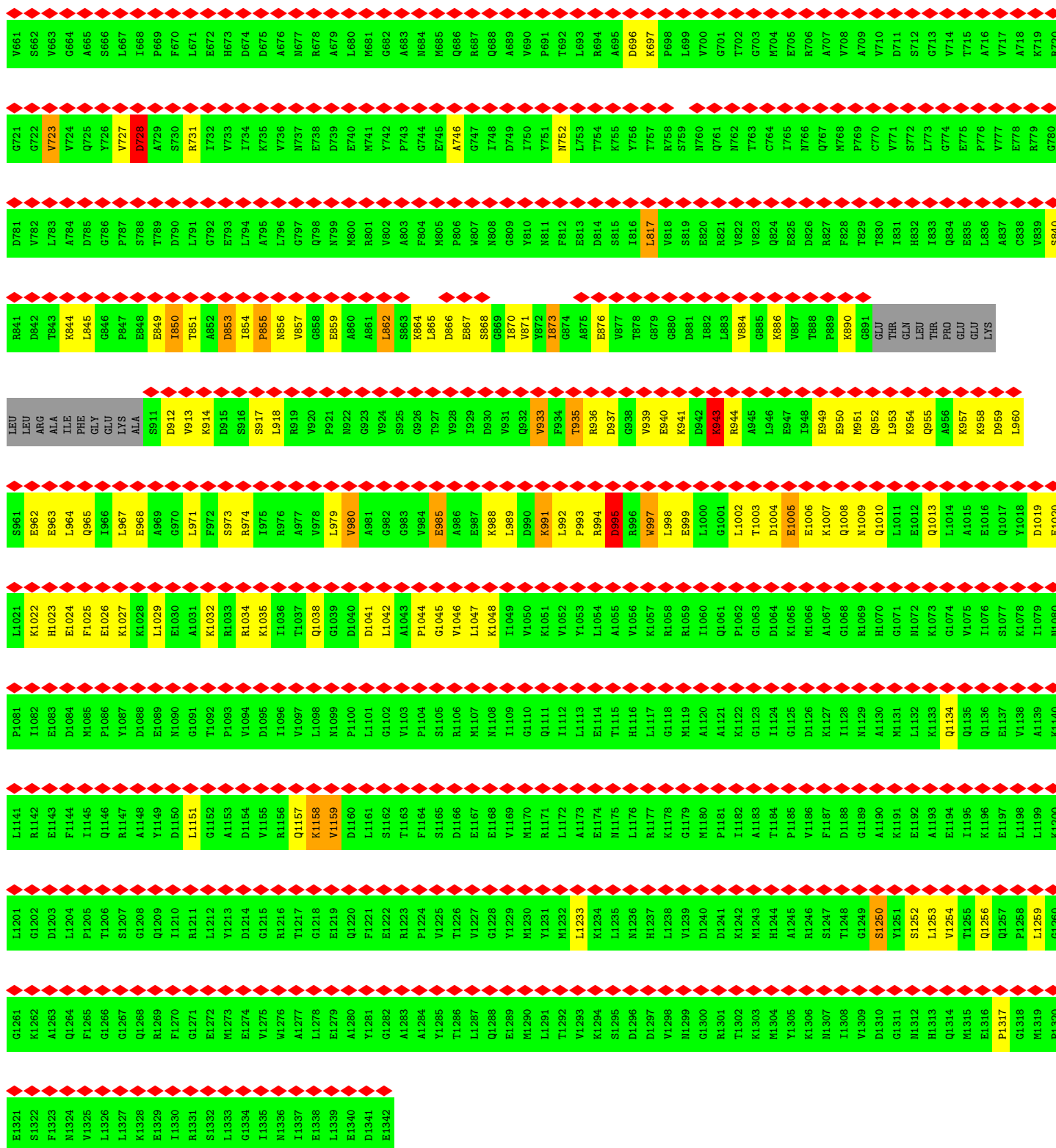




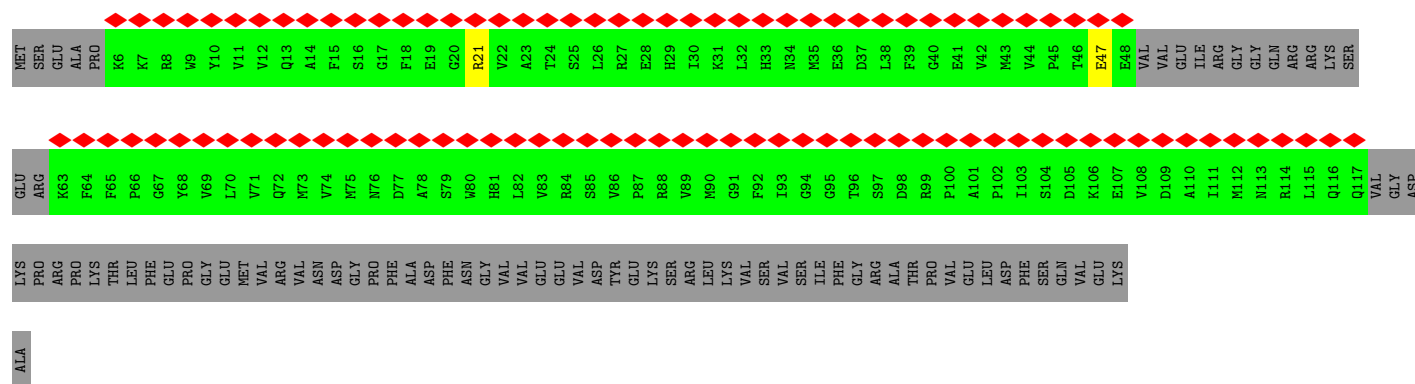
● Molecule 11: DNA-directed RNA polymerase subunit beta

Chain AA: 98% 89% 8% ..



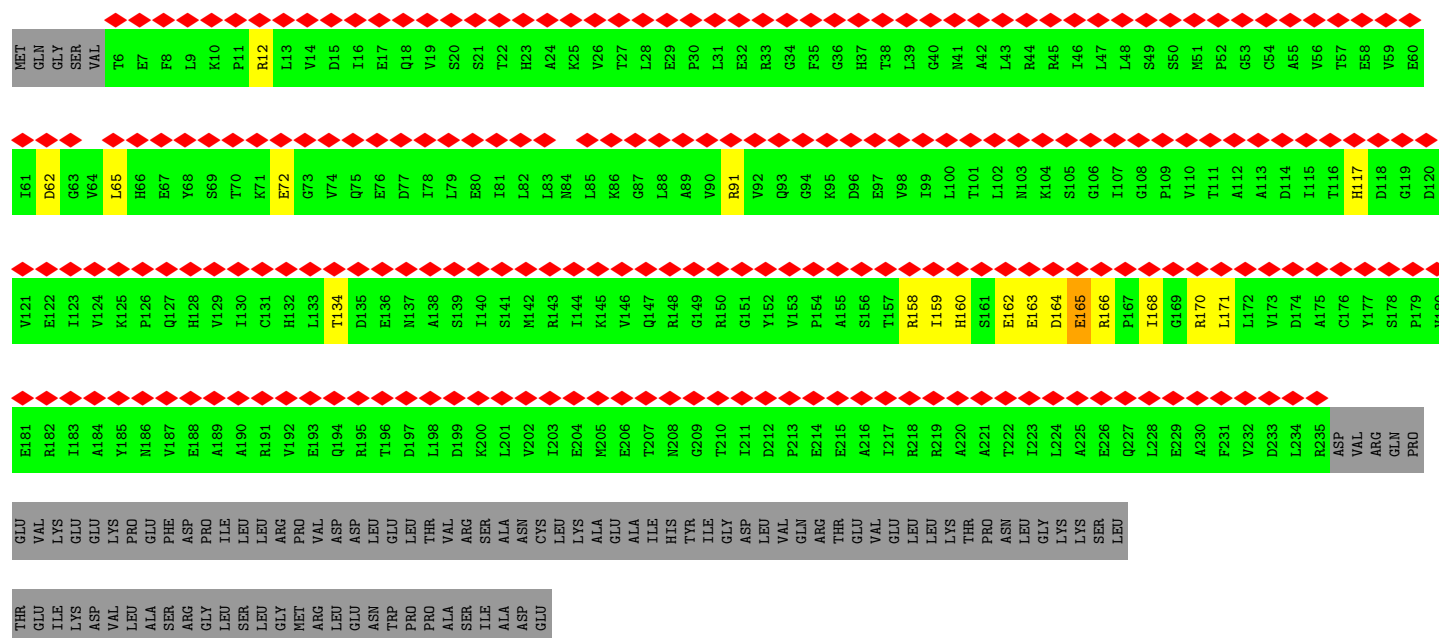


• Molecule 12: Transcription termination/antitermination protein NusG



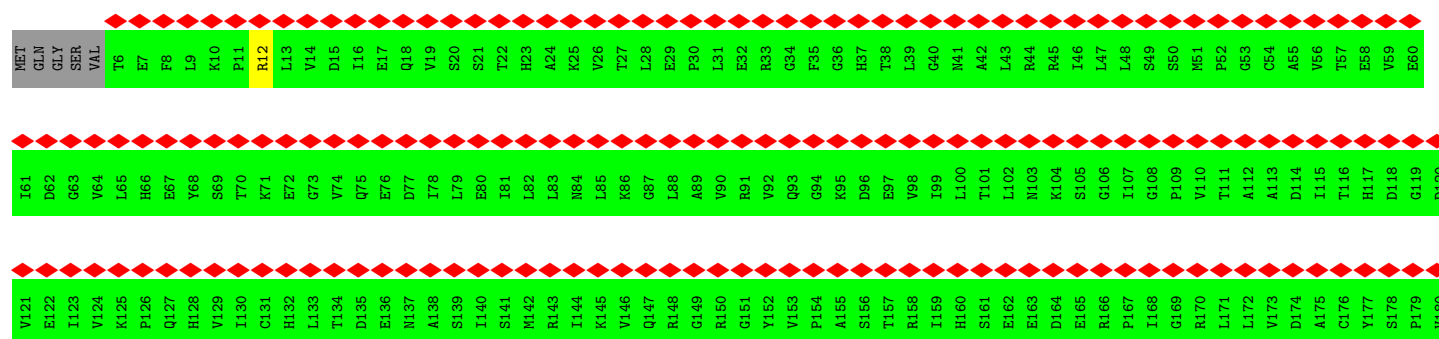
• Molecule 13: DNA-directed RNA polymerase subunit alpha

Chain AC:



• Molecule 13: DNA-directed RNA polymerase subunit alpha

Chain AD:



GLU	THR
VAL	GLU
ILE	ILE
LYS	LYS
GLY	ASP
GLY	VAL
LYS	LEU
PRO	ALA
GLU	GLY
PHE	SER
I22	ARG
A23	PRO
PRO	VAL
ASP	VAL
ILE	ARG
L24	LEU
SER	SER
LEU	LEU
S26	LEU
P27	GLY
ARG	MET
V192	PRO
E193	ARG
Q194	VAL
R195	LEU
ASP	GLU
T196	ASN
GLU	TRP
D197	PRO
L198	THR
D199	VAL
K200	ARG
L201	SER
V202	ILE
I203	ASN
E204	CYS
M205	LYS
E206	ALA
T207	GLU
N208	ALA
G209	ILE
T210	TTR
I211	ILE
D212	ASP
P213	GLY
E214	VAL
E215	GLN
A216	ARG
L217	THR
R218	VAL
R219	GLU
A220	LEU
A221	LEU
T222	LYS
I223	THR
L224	PRO
A225	ASN
E226	LEU
Q227	GLY
L228	LYS
E229	SER
A230	LYS
F231	LYS
V232	LYS
D233	LEU
LEU	ASP
ASP	ARG
VAL	VAL
ARG	ARG
GLN	GLN
PRO	PRO


• Molecule 14: DNA-directed RNA polymerase subunit

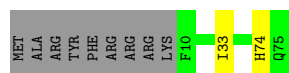


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F17	R77	R137	E197	G257	T317	F377	F437	E497	K557
D18	L78	V138	C198	G258	G318	K378	E438	P498	D558
A19	K79	L139	E199	R259	S319	P379	P439	T499	A559
I20	H80	Y140	Q200	F260	N320	F380	V440	I500	R560
K21	R81	F141	L201	A261	K321	L381	L441	V501	G561
I22	G82	E142	R202	T262	K322	Y382	L442	P502	E562
A23	V83	S143	E203	S263	P323	G383	E443	S503	L563
L24	I84	L204	E204	D264	L324	K384	G444	Q504	V564
A25	C85	Y145	L205	L265	K325	L385	K445	D505	A565
S26	E86	V146	N206	N266	S326	E386	A446	V506	K566
P27	K87	I147	E207	D267	L327	L387	T447	V507	T567
D28	C88	E148	T208	L268	A328	R388	Q448	S508	S568
M29	G89	G149	N209	Y269	K329	G389	L449	O509	L569
I30	V90	G150	S210	R270	M330	L390	H450	L510	K570
R31	E91	M151	E211	R271	I331	A391	P451	V511	D571
S32	T92	T152	T212	V272	K332	T392	L452	V512	T572
W33	V93	N153	K213	L273	G333	T393	V453	M513	T573
S34	Q94	L154	R214	M274	K334	I394	C454	T514	V574
F35	T95	E155	K215	R275	Q335	K395	A455	B515	G575
G36	K96	R156	L216	N276	G336	A396	A456	D516	R576
V38	R98	Q157	K217	N277	F338	A397	Y457	C517	A577
K39	I99	Q158	T218	R278	Q338	K398	N458	V518	L578
K40	E100	I159	K219	L279	R340	K399	A459	N519	L579
P41	R101	T160	R220	K280	Q340	M400	D460	A520	W580
E42	M102	E162	L221	R281	N341	V401	P461	K521	H581
T43	G103	E163	K222	L282	L342	E402	D462	G522	L582
I44	H104	Q164	L223	L283	G344	R403	G463	E523	V583
M45	I105	Y165	E224	L285	G345	E404	D464	G524	P584
Y46	E106	L166	A225	A286	R346	A405	Q465	K525	K585
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T48	A108	A168	V228	R288	D348	V407	A467	L527	L587
F49	S109	L169	Q229	P288	Y349	W408	W468	T528	P588
K50	P110	E170	S230	I290	S350	D410	H469	O529	Y589
P51	T111	E171	G231	I291	G351	T411	V470	P530	S590
E52	A112	F172	N232	V292	R352	L412	P471	K531	I591
R53	H113	E52	K233	R293	S353	D413	L472	E532	V592
D54	I114	D174	P234	N294	V354	E414	L474	E534	Q594
G55	W115	E175	E235	E295	I355	V415	E475	R535	A595
L56	F116	F176	M236	K296	T356	I416	A476	L536	L596
F57	L117	D177	M237	R297	V357	R417	Q477	V537	G597
C58	K118	A178	I238	M298	G358	E418	L478	R538	K598
A59	S119	K179	L239	L299	P359	H419	E479	S539	K599
R60	L120	M180	T240	Q300	Y360	V420	A480	G540	A600
I61	P121	L121	V241	E301	L361	V421	R481	L541	T601
F62	S122	A182	L242	A302	R362	L422	A482	A542	S602
G63	R123	E183	P243	V303	L363	L423	L483	S543	K603
P64	I124	A184	V244	D304	H364	N424	M484	L544	M604
V65	G125	I185	L245	A305	Q365	R425	M485	H545	L605
K66	L126	Q186	P246	L306	C366	A426	S486	A546	M606
D67	L127	A187	D247	L307	G367	P427	T487	R547	T607
Y68	L128	L188	D248	D308	L368	T428	N488	V548	C608
E69	D129	L189	L249	N309	P369	L429	Y489	K549	Y609
C70	M130	K190	R250	G310	K370	H430	T490	V550	R610
L71	P131	S191	P251	R311	K371	R431	L491	R551	T611
C72	L132	M192	L252	R312	M372	A432	S492	I552	L612
K74	R133	D193	V253	G313	A373	Q433	P493	T553	G613
Y75	D134	L194	P254	R314	L374	T434	A494	E554	L614
	I135	E195	L255	A315	E375	Q435	N495	Y555	K615


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A1338	E1278	H1218	E1158	Q1098	T1038	S978	A918	V858	R797	R738	E678	V618
G1339	Q1279	D1219	T1159	Y1099	D1039	N979	I919	P859	R799	Q739	Y679	I619
K1340	V1280	L1220	S1160	F1100	M1040	T980	A920	R860	L800	L740	K681	F620
R1341	E1281	L1221	G1161	L1101	I1041	E981	Q921	N861	V801	A741	K681	A621
D1342	P1282	R1222	T1162	P1102	D1042	L982	S922	T862	D802	G742	V682	D622
E1343	S1283	L1223	V1163	G1103	G1043	K983	I923	L863	V803	M743	I683	Q623
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R1345	V1285	G1225	F1165	A1105	T1045	I985	E925	H865	Q805	G745	I685	M625
G1346	K1286	V1226	G1166	I1106	I1046	D986	P926	E866	D806	L746	W686	M626
L1347	I1287	H1227	K1167	V1107	T1047	E987	G927	Q867	L807	M747	A687	T627
K1348	A1288	A1228	E1168	Q1108	R1048	F988	T928	W868	V808	A748	A688	G628
E1349	N1289	V1229	T1169	L1109	Q1049	G989	Q929	C869	V809	K749	A689	F629
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V1351	E1291	R1231	G1171	D1111	D1051	T991	T931	L871	E811	D751	D691	Y631
I1352	L1292	L1232	K1172	G1112	E1052	K992	M932	L872	D812	G752	R692	A632
V1353	E1293	I1233	R1173	V1113	L1053	E993	R933	E873	D813	S753	V693	A633
G1354	A1294	V1234	R1174	Q1114	T1054	S994	THR	E874	C814	I754	S694	R634
R1355	N1295	M1235	L1175	I1115	G1055	Y995	PHE	N875	G815	I755	K695	A635
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V1357	K1297	V1237	I1177	S1117	S1057	V997	GLY	V877	H817	T757	M697	A637
P1358	V1298	Q1238	T1178	G1118	S1058	P998	GLY	D878	E818	P758	M698	V638
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Y1363	S1303	L1243	S1183	R1123	D1063	L1003	ALA	R883	T823	F763	T703	D643
A1364	R1304	Q1244	D1184	I1124	S1064	A1004	GLU	S884	P824	R764	E704	M644
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G1368	G1308	L1248	E1188	GLY	T1068	G1008	Q951	C888	G828	N768	N708	E648
R1369	I1309	N1249	M1189	GLY	A1069	E1009	V952	D889	G829	V769	R709	K649
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Q1326	R1206	I1266	R1206	R1148	N1086	P1026	S969	G906	E846	T786	A726	E666
	G1207	V1267	G1207	R1149	D1087	V1027	S970	H907	D847	A787	D727	Q667
T1328	N1268	V1267	D1208	P1150	V1088	I1028	G971	I908	V848	L788	S728	F668
N1329	A1269	A1269	V1209	K1151	L1089	T1029	K972	I909	L849	K789	G729	Q669
R1330	G1270	G1270	I1210	E1152	I1090	E1030	L973	N910	R850	T790	A730	S670
V1331	S1271	S1271	S1211	P1153	P1091	V1031	V974	K911	P851	A791	R731	G671
L1332	D1272	S1272	D1212	A1154	G1092	S1032	I975	E913	T853	N792	G732	L672
T1333	G1273	D1273	G1213	T1093	T1093	G1033	I975	E913	T853	S793	S733	V673
A1334	F1274	L1274	P1214	D1094	D1094	F1034	T915	T915	D855	V795	A734	A675

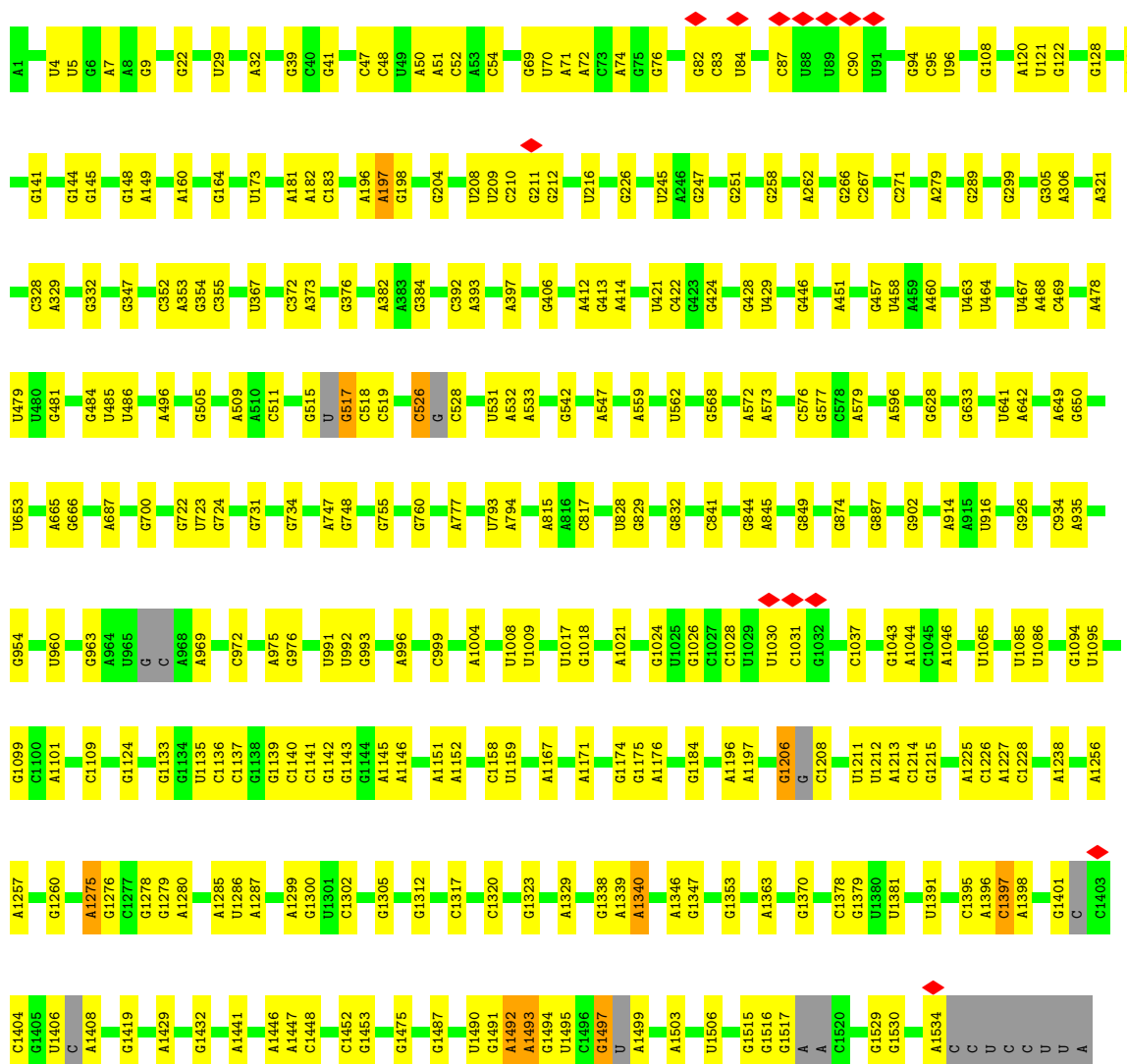
- Molecule 15: 30S ribosomal protein S18

Chain C:  85% 12%



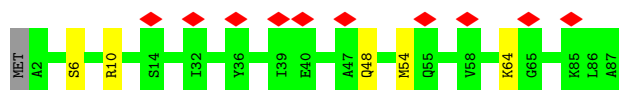
• Molecule 16: 16S rRNA

Chain D:  78% 20%



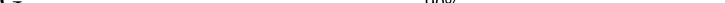
• Molecule 17: 30S ribosomal protein S20

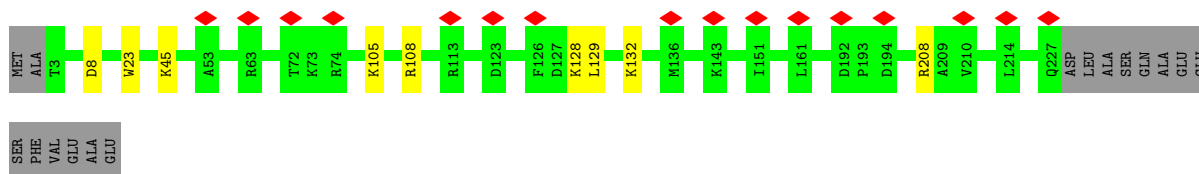
Chain E:  11% 93% 6%

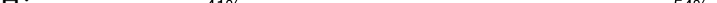


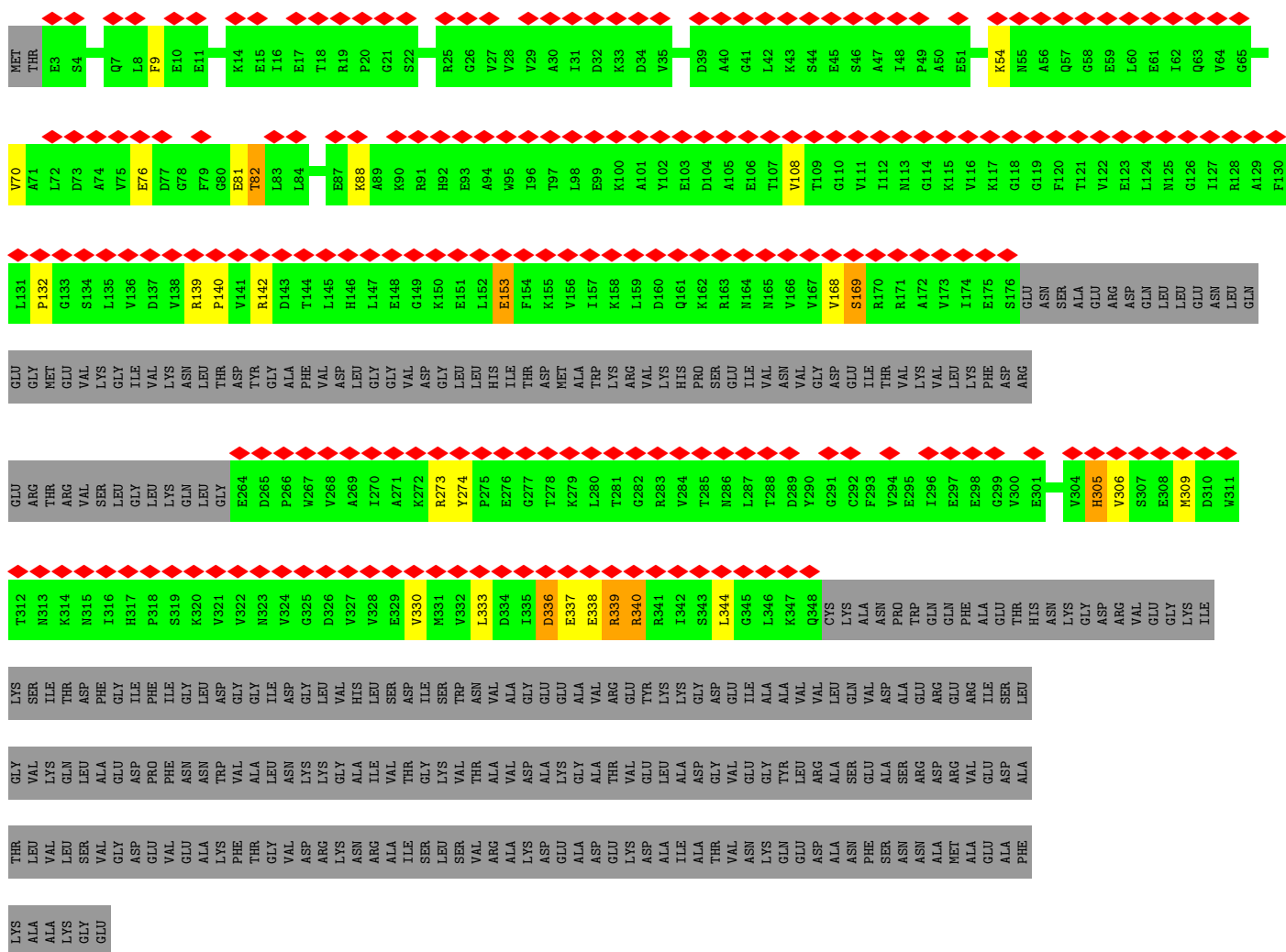
• Molecule 18: 30S ribosomal protein S21



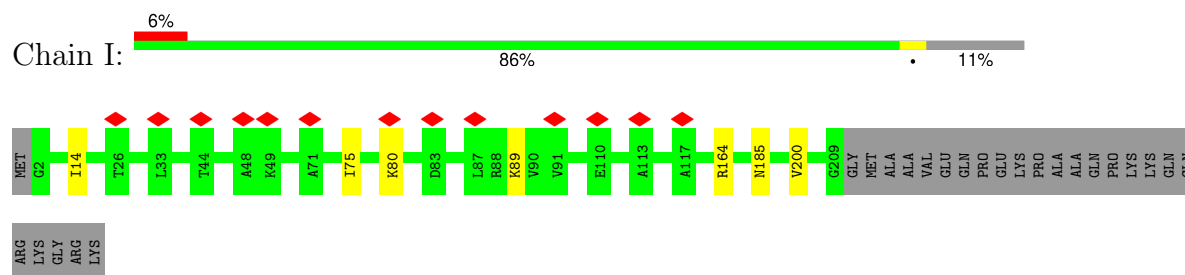
- Chain G:  7% 90% 7%



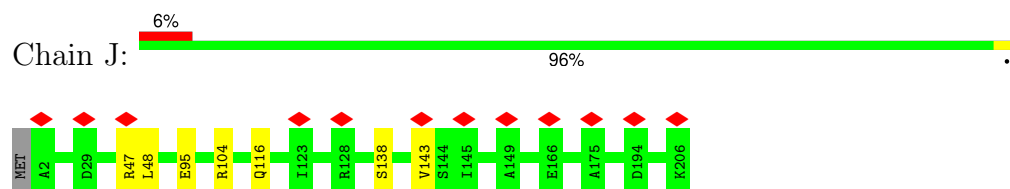
- Chain H:  40% 41% 54%



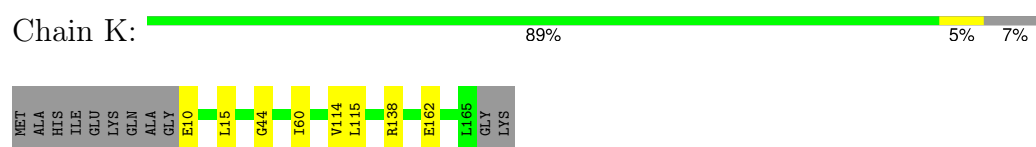
- Molecule 21: 30S ribosomal protein S3



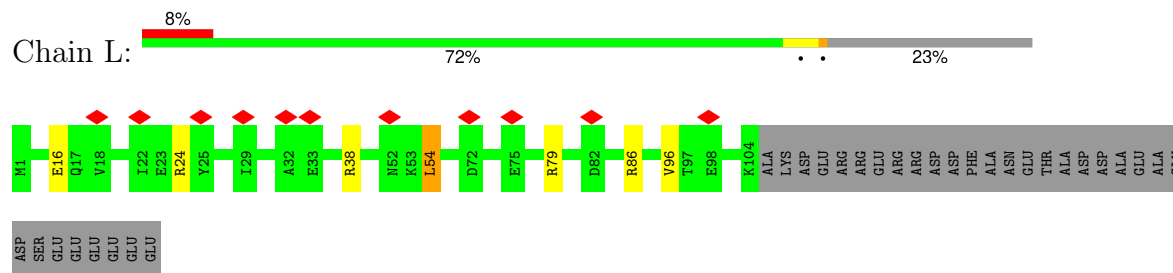
- Molecule 22: 30S ribosomal protein S4



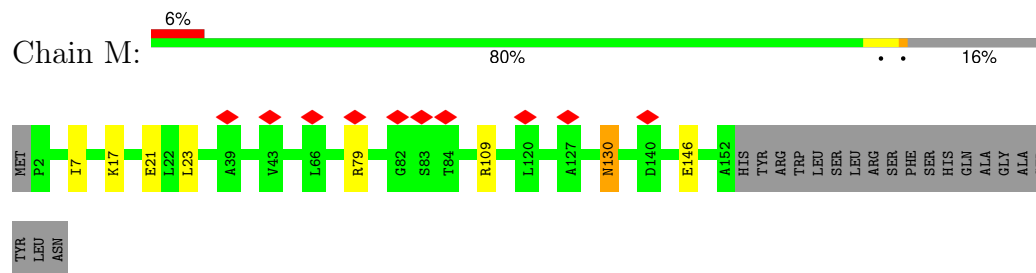
- Molecule 23: 30S ribosomal protein S5



- Molecule 24: 30S ribosomal protein S6

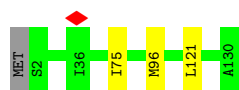


- Molecule 25: 30S ribosomal protein S7

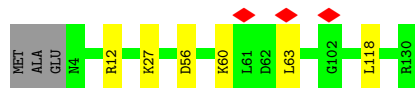


- Molecule 26: 30S ribosomal protein S8

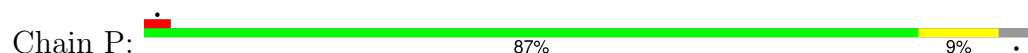




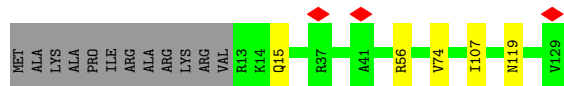
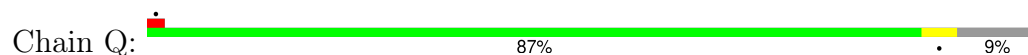
- Molecule 27: 30S ribosomal protein S9



- Molecule 28: 30S ribosomal protein S10



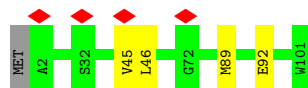
- Molecule 29: 30S ribosomal protein S11



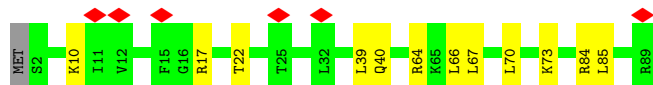
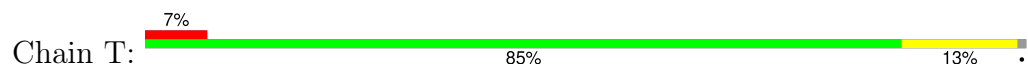
- Molecule 30: 30S ribosomal protein S12



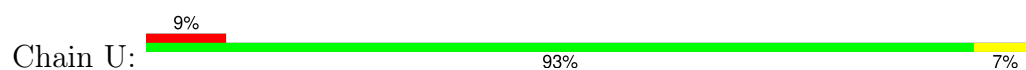
- Molecule 31: 30S ribosomal protein S14



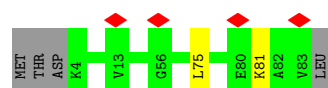
- Molecule 32: 30S ribosomal protein S15



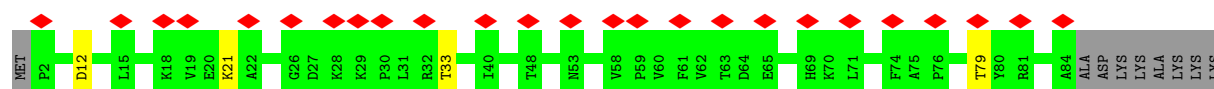
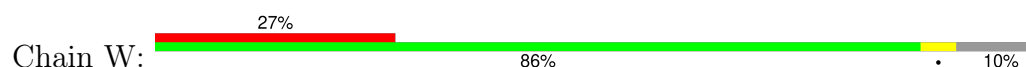
- Molecule 33: 30S ribosomal protein S16



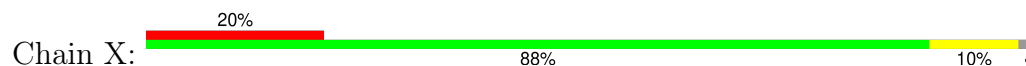
- Molecule 34: 30S ribosomal protein S17



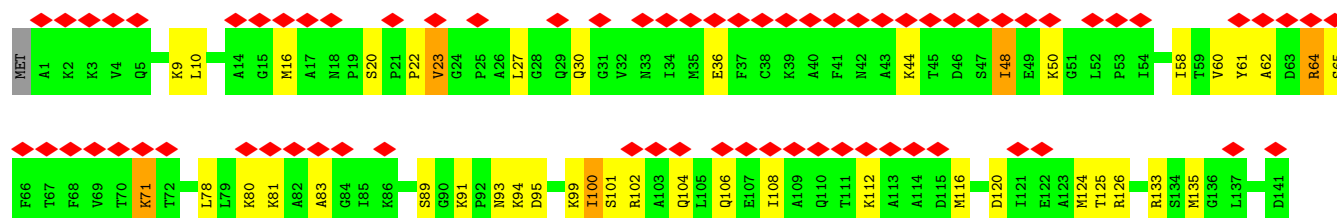
- Molecule 35: 30S ribosomal protein S19



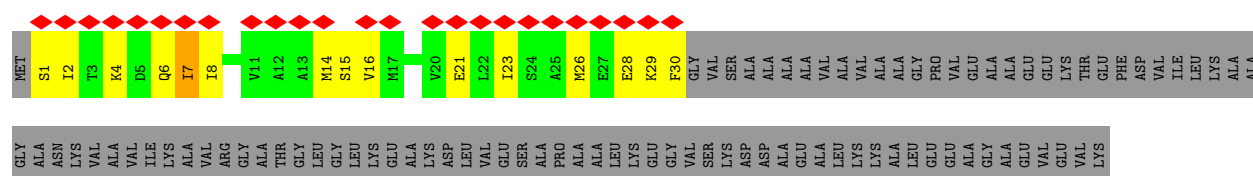
- Molecule 36: 30S ribosomal protein S13




- Molecule 37: 50S ribosomal protein L11

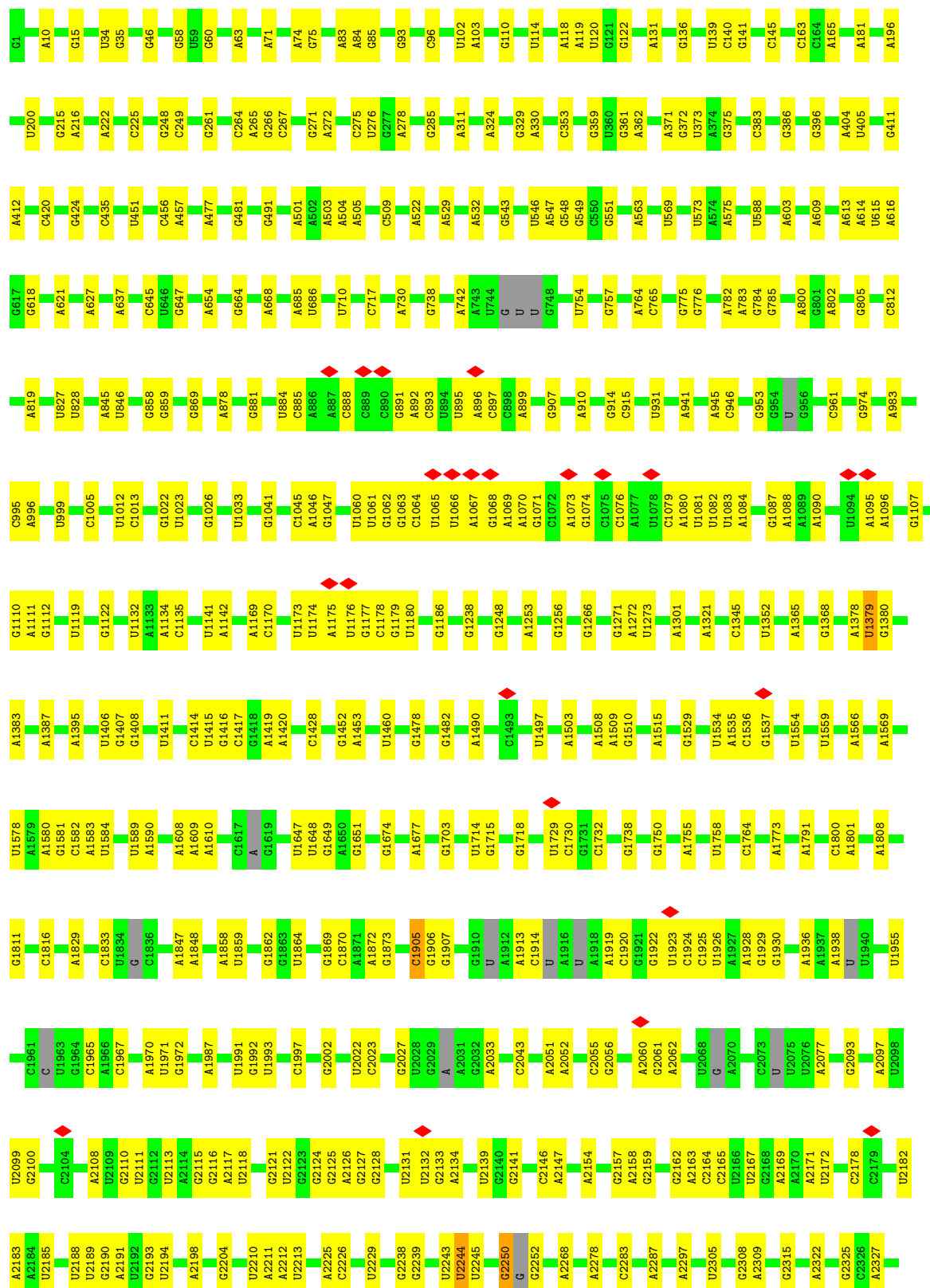


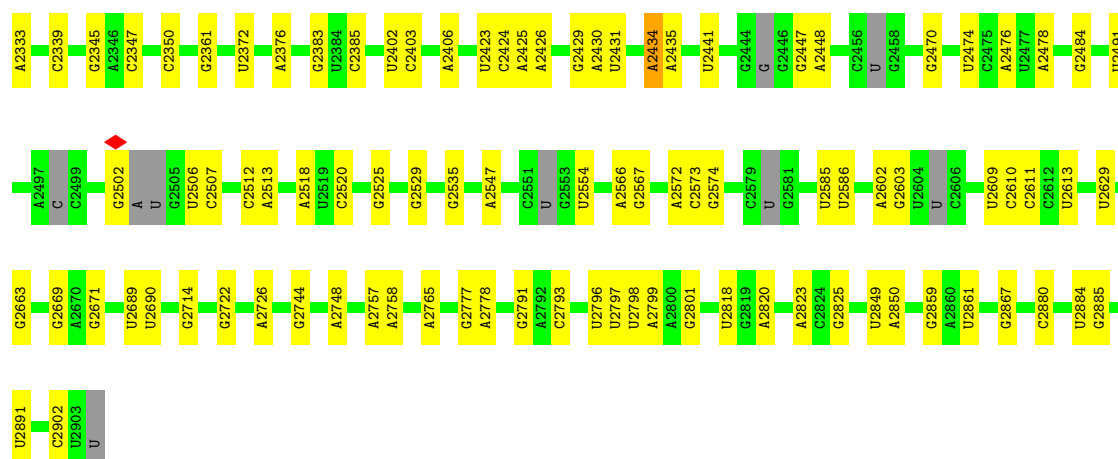
- Molecule 38: 50S ribosomal protein L7/L12



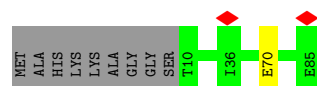
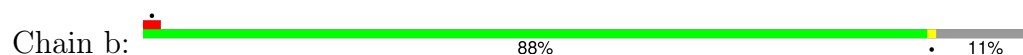
● Molecule 39: 23S rRNA

Chain a:  81% 18%

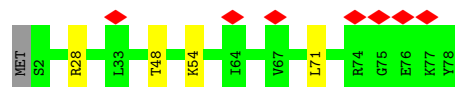




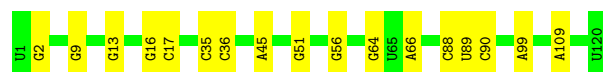
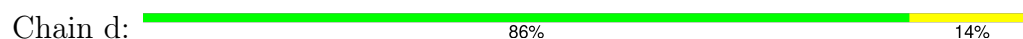
- Molecule 40: 50S ribosomal protein L27



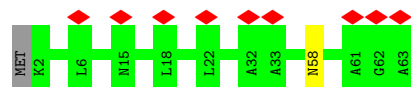
- Molecule 41: 50S ribosomal protein L28



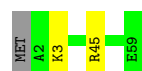
- Molecule 42: 5S rRNA



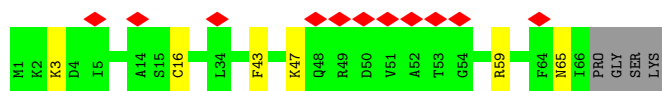
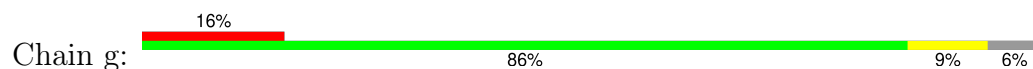
- Molecule 43: 50S ribosomal protein L29



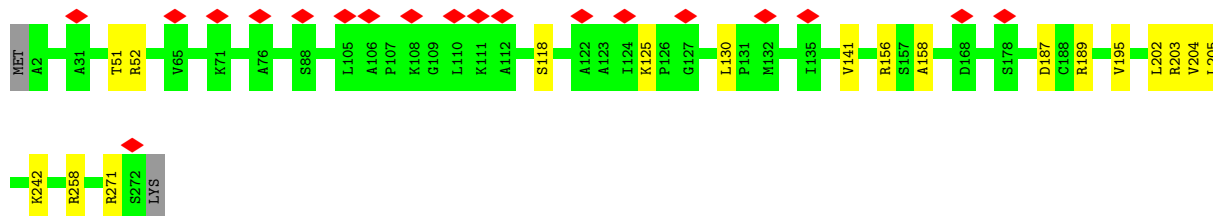
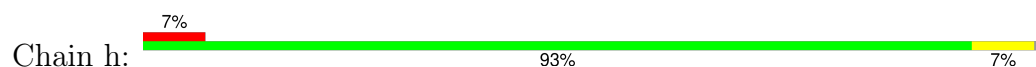
- Molecule 44: 50S ribosomal protein L30



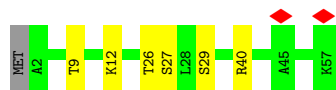
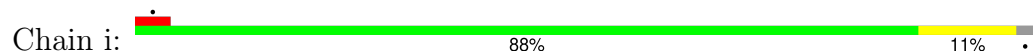
- Molecule 45: 50S ribosomal protein L31



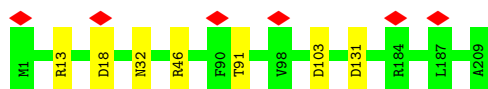
- Molecule 46: 50S ribosomal protein L2



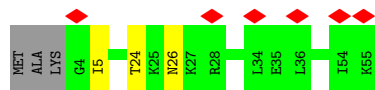
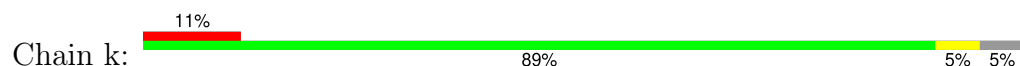
- Molecule 47: 50S ribosomal protein L32



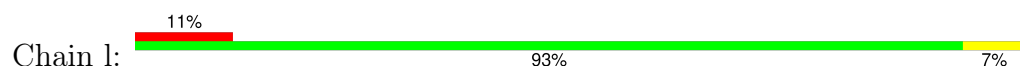
- Molecule 48: 50S ribosomal protein L3



- Molecule 49: 50S ribosomal protein L33



- Molecule 50: 50S ribosomal protein L4




A201

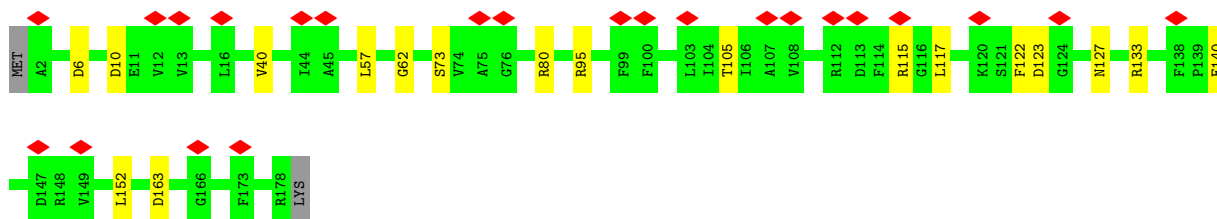
- Molecule 51: 50S ribosomal protein L34

Chain m:  93% 7%




- Molecule 52: 50S ribosomal protein L5

Chain n:  13% 89% 10%



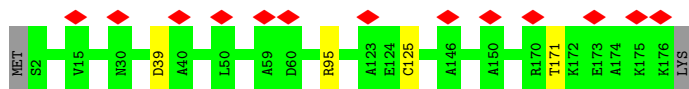
- Molecule 53: 50S ribosomal protein L35

Chain o:  5% 91% 8%



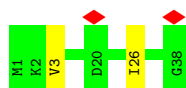
- Molecule 54: 50S ribosomal protein L6

Chain p:  7% 97%




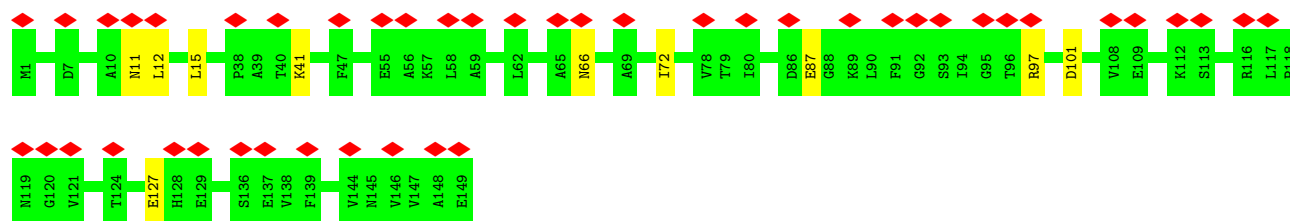
- Molecule 55: 50S ribosomal protein L36

Chain q:  5% 95% 5%

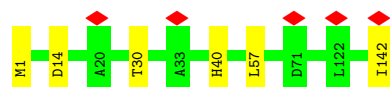


- Molecule 56: 50S ribosomal protein L9

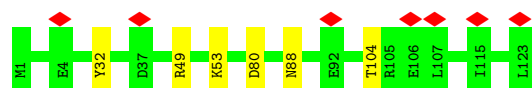
Chain r:  30% 93% 7%



- Molecule 57: 50S ribosomal protein L13



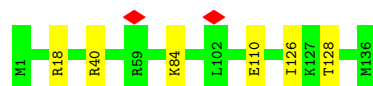
- Molecule 58: 50S ribosomal protein L14



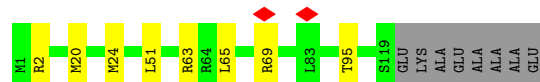
- Molecule 59: 50S ribosomal protein L15



- Molecule 60: 50S ribosomal protein L16

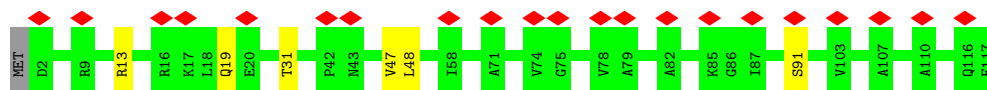


- Molecule 61: 50S ribosomal protein L17

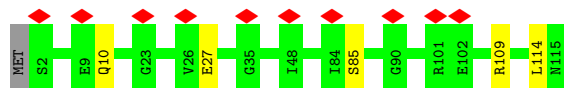


- Molecule 62: 50S ribosomal protein L18





- Molecule 63: 50S ribosomal protein L19



- Molecule 64: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29704	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	0.042	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00868	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.67	2/1062 (0.2%)
5	4	0.41	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%)	0.96	0/926
8	7	0.62	2/607 (0.3%)	0.93	3/940 (0.3%)
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	0.59	2/10591 (0.0%)	0.75	15/14289 (0.1%)
12	AB	0.43	0/808	0.60	0/1088
13	AC	0.48	0/1808	0.62	1/2450 (0.0%)
13	AD	0.40	0/1789	0.57	0/2425
14	AE	0.52	3/10545 (0.0%)	0.66	5/14236 (0.0%)
15	C	0.48	0/553	0.83	0/743
16	D	0.34	10/36610 (0.0%)	0.74	30/57091 (0.1%)
17	E	0.57	0/675	0.86	0/895
18	F	0.56	0/597	0.87	0/792
19	G	0.49	0/1791	0.71	0/2413
20	H	0.54	1/1746 (0.1%)	1.03	12/2382 (0.5%)
21	I	0.44	0/1663	0.71	0/2241
22	J	0.47	0/1665	0.73	0/2227
23	K	0.45	0/1165	0.75	0/1568
24	L	0.43	0/867	0.75	1/1171 (0.1%)
25	M	0.50	0/1195	0.81	0/1602
26	N	0.41	0/989	0.69	0/1326
27	O	0.43	0/1034	0.75	0/1375
28	P	0.43	0/800	0.75	0/1082
29	Q	0.40	0/893	0.70	0/1205
30	R	0.35	0/952	0.74	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.50	0/817	0.79	0/1088
32	T	0.53	0/722	0.86	0/964
33	U	0.44	0/659	0.78	0/884
34	V	0.34	0/657	0.61	0/881
35	W	0.38	0/680	0.62	0/915
36	X	0.49	0/909	0.86	0/1215
37	Y	0.67	0/1046	0.59	0/1410
38	Z	0.69	0/227	0.57	0/304
39	a	0.38	3/69247 (0.0%)	0.72	18/107985 (0.0%)
40	b	0.39	0/589	0.71	0/779
41	c	0.48	0/635	0.81	1/848 (0.1%)
42	d	0.30	0/2872	0.70	0/4478
43	e	0.54	0/502	0.83	0/667
44	f	0.45	0/452	0.78	0/605
45	g	0.43	0/531	0.68	0/709
46	h	0.39	0/2121	0.78	0/2852
47	i	0.40	0/450	0.79	0/599
48	j	0.44	0/1586	0.69	0/2134
49	k	0.35	0/433	0.64	0/576
50	l	0.46	0/1571	0.77	0/2113
51	m	0.53	0/380	0.99	0/498
52	n	0.49	0/1434	0.88	3/1926 (0.2%)
53	o	0.45	0/513	0.83	0/676
54	p	0.39	0/1333	0.67	0/1805
55	q	0.37	0/303	0.77	0/397
56	r	0.44	0/1122	0.69	0/1515
57	s	0.50	0/1152	0.76	0/1551
58	t	0.41	0/955	0.78	0/1279
59	u	0.40	0/1062	0.75	0/1413
60	v	0.47	0/1093	0.81	0/1460
61	w	0.52	0/964	0.87	0/1289
62	x	0.46	0/902	0.81	0/1209
63	y	0.41	0/929	0.72	1/1242 (0.1%)
64	z	0.60	0/960	0.92	0/1278
All	All	0.43	34/189040 (0.0%)	0.74	102/278616 (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

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
14	AE	0	5
20	H	0	3
36	X	0	1
All	All	0	23

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	13.78	1.70	1.47
16	D	1516	G	O3'-P	-13.54	1.44	1.61
16	D	1339	A	O3'-P	10.62	1.73	1.61
11	AA	374	GLU	C-N	10.48	1.54	1.34
14	AE	88	CYS	CB-SG	-10.15	1.65	1.82

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	P-O3'-C3'	-18.95	96.97	119.70
16	D	1516	G	O3'-P-O5'	13.80	130.22	104.00
11	AA	1250	SER	C-N-CA	11.15	149.59	121.70
39	a	2252	G	N9-C1'-C2'	-10.92	99.81	114.00
16	D	1401	G	N9-C1'-C2'	-10.66	100.14	114.00

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	Peptide

5.2 Too-close contacts [i](#)

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	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	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	47
13	AD	226/329 (69%)	212 (94%)	13 (6%)	1 (0%)	30	62
14	AE	1329/1358 (98%)	1200 (90%)	120 (9%)	9 (1%)	19	51
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
18	F	68/71 (96%)	68 (100%)	0	0	100	100
19	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	19
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	25	57
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	54
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	44
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	51
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	49
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	49
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	13	44
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
31	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
32	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	76 (95%)	3 (4%)	1 (1%)	10	40
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
35	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
36	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	7	35
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	9
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	13
40	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
45	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
46	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	62
47	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	25	57
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	43
53	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
54	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
58	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
59	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
62	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	47
All	All	9368/10437 (90%)	8605 (92%)	660 (7%)	103 (1%)	15	43

5 of 103 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU

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	1140/1157 (98%)	1039 (91%)	101 (9%)	8	31
12	AB	86/158 (54%)	84 (98%)	2 (2%)	45	64
13	AC	198/286 (69%)	182 (92%)	16 (8%)	9	34
13	AD	196/286 (68%)	194 (99%)	2 (1%)	73	82
14	AE	1120/1134 (99%)	1051 (94%)	69 (6%)	15	42
15	C	57/65 (88%)	55 (96%)	2 (4%)	31	56
17	E	65/66 (98%)	60 (92%)	5 (8%)	10	37
18	F	60/61 (98%)	57 (95%)	3 (5%)	20	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	178 (95%)	9 (5%)	21	48
20	H	137/461 (30%)	128 (93%)	9 (7%)	14	41
21	I	171/190 (90%)	165 (96%)	6 (4%)	31	56
22	J	172/173 (99%)	165 (96%)	7 (4%)	26	52
23	K	119/126 (94%)	112 (94%)	7 (6%)	16	44
24	L	91/116 (78%)	85 (93%)	6 (7%)	14	41
25	M	124/147 (84%)	116 (94%)	8 (6%)	14	41
26	N	104/105 (99%)	102 (98%)	2 (2%)	52	70
27	O	105/107 (98%)	100 (95%)	5 (5%)	21	48
28	P	86/90 (96%)	78 (91%)	8 (9%)	7	30
29	Q	90/99 (91%)	87 (97%)	3 (3%)	33	57
30	R	101/104 (97%)	94 (93%)	7 (7%)	13	39
31	S	83/84 (99%)	79 (95%)	4 (5%)	21	48
32	T	76/77 (99%)	64 (84%)	12 (16%)	2	14
33	U	65/65 (100%)	60 (92%)	5 (8%)	10	37
34	V	74/78 (95%)	72 (97%)	2 (3%)	40	61
35	W	72/79 (91%)	68 (94%)	4 (6%)	17	45
36	X	94/96 (98%)	85 (90%)	9 (10%)	7	28
37	Y	109/110 (99%)	73 (67%)	36 (33%)	0	1
38	Z	26/85 (31%)	12 (46%)	14 (54%)	0	0
40	b	58/63 (92%)	57 (98%)	1 (2%)	56	73
41	c	67/68 (98%)	64 (96%)	3 (4%)	23	50
43	e	54/55 (98%)	53 (98%)	1 (2%)	52	70
44	f	48/49 (98%)	46 (96%)	2 (4%)	25	51
45	g	59/62 (95%)	53 (90%)	6 (10%)	6	26
46	h	216/218 (99%)	199 (92%)	17 (8%)	10	36
47	i	47/48 (98%)	41 (87%)	6 (13%)	3	19
48	j	164/164 (100%)	157 (96%)	7 (4%)	25	50
49	k	47/49 (96%)	44 (94%)	3 (6%)	14	42
50	l	165/165 (100%)	151 (92%)	14 (8%)	8	33
51	m	38/38 (100%)	35 (92%)	3 (8%)	10	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	134 (90%)	14 (10%)	7	29
53	o	51/52 (98%)	46 (90%)	5 (10%)	6	27
54	p	136/138 (99%)	132 (97%)	4 (3%)	37	59
55	q	34/34 (100%)	32 (94%)	2 (6%)	16	44
56	r	114/114 (100%)	104 (91%)	10 (9%)	8	32
57	s	116/116 (100%)	110 (95%)	6 (5%)	19	46
58	t	104/104 (100%)	98 (94%)	6 (6%)	17	44
59	u	103/103 (100%)	97 (94%)	6 (6%)	17	44
60	v	109/109 (100%)	103 (94%)	6 (6%)	18	45
61	w	99/103 (96%)	91 (92%)	8 (8%)	9	34
62	x	86/87 (99%)	80 (93%)	6 (7%)	12	39
63	y	99/100 (99%)	95 (96%)	4 (4%)	27	52
64	z	89/90 (99%)	87 (98%)	2 (2%)	47	65
All	All	7791/8630 (90%)	7209 (92%)	582 (8%)	14	37

5 of 582 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	h	202	LEU
62	x	47	VAL
48	j	13	ARG
46	h	195	VAL
53	o	54	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
9	9	103	ASN
19	G	18	HIS
23	K	70	ASN
36	X	105	ASN
59	u	4	ASN

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%)
16	D	1515/1542 (98%)	288 (19%)	35 (2%)
39	a	2859/2904 (98%)	532 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	24/37 (64%)	15 (62%)	3 (12%)
All	All	4667/4755 (98%)	916 (19%)	50 (1%)

5 of 916 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-9	G
8	7	-8	U
8	7	-7	U
8	7	-5	U
8	7	-4	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	532	A
16	D	1109	C
16	D	1493	A
16	D	562	U
16	D	793	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

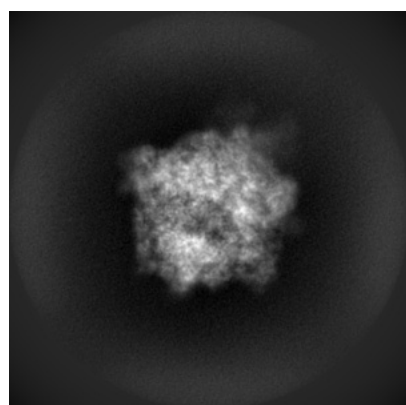
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21470. These allow visual inspection of the internal detail of the map and identification of artifacts.

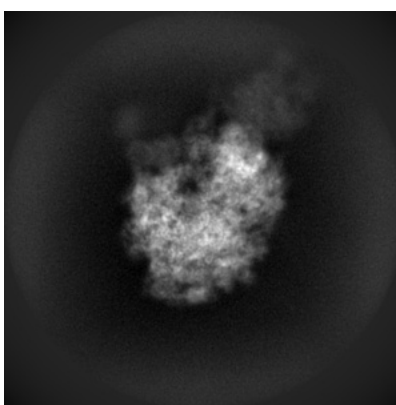
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

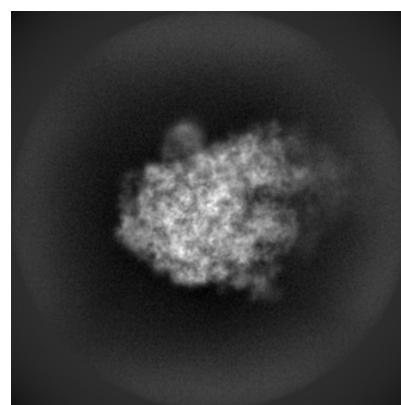
6.1.1 Primary map



X



Y

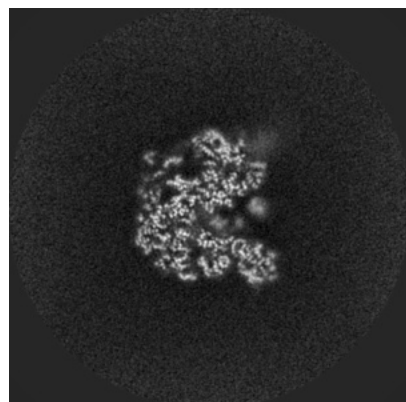


Z

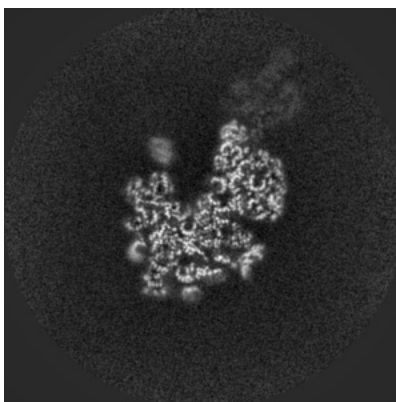
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

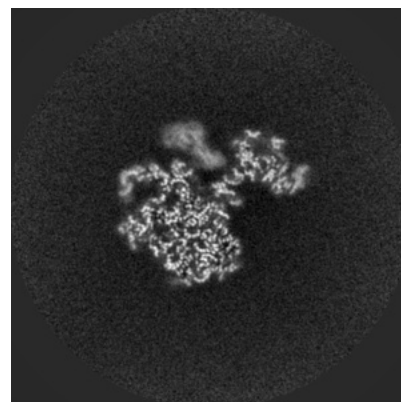
6.2.1 Primary map



X Index: 250



Y Index: 250

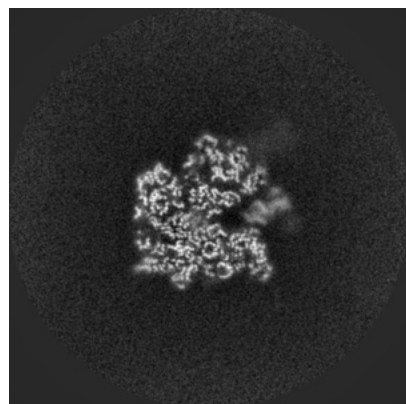


Z Index: 250

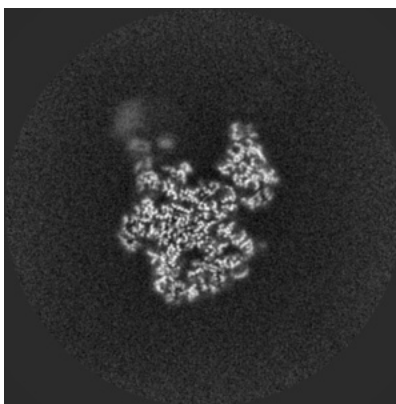
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

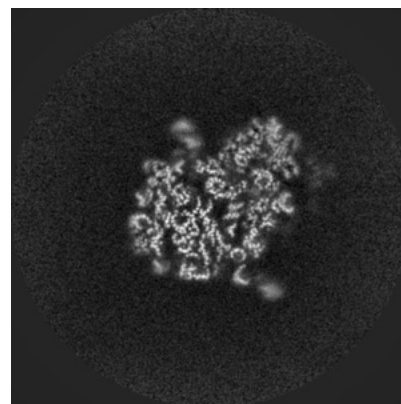
6.3.1 Primary map



X Index: 238



Y Index: 213

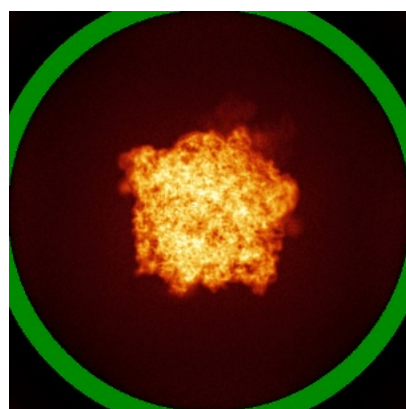


Z Index: 276

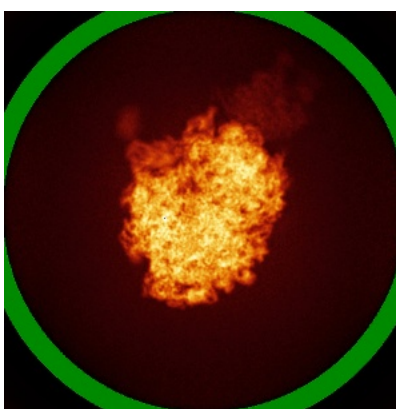
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.00868. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

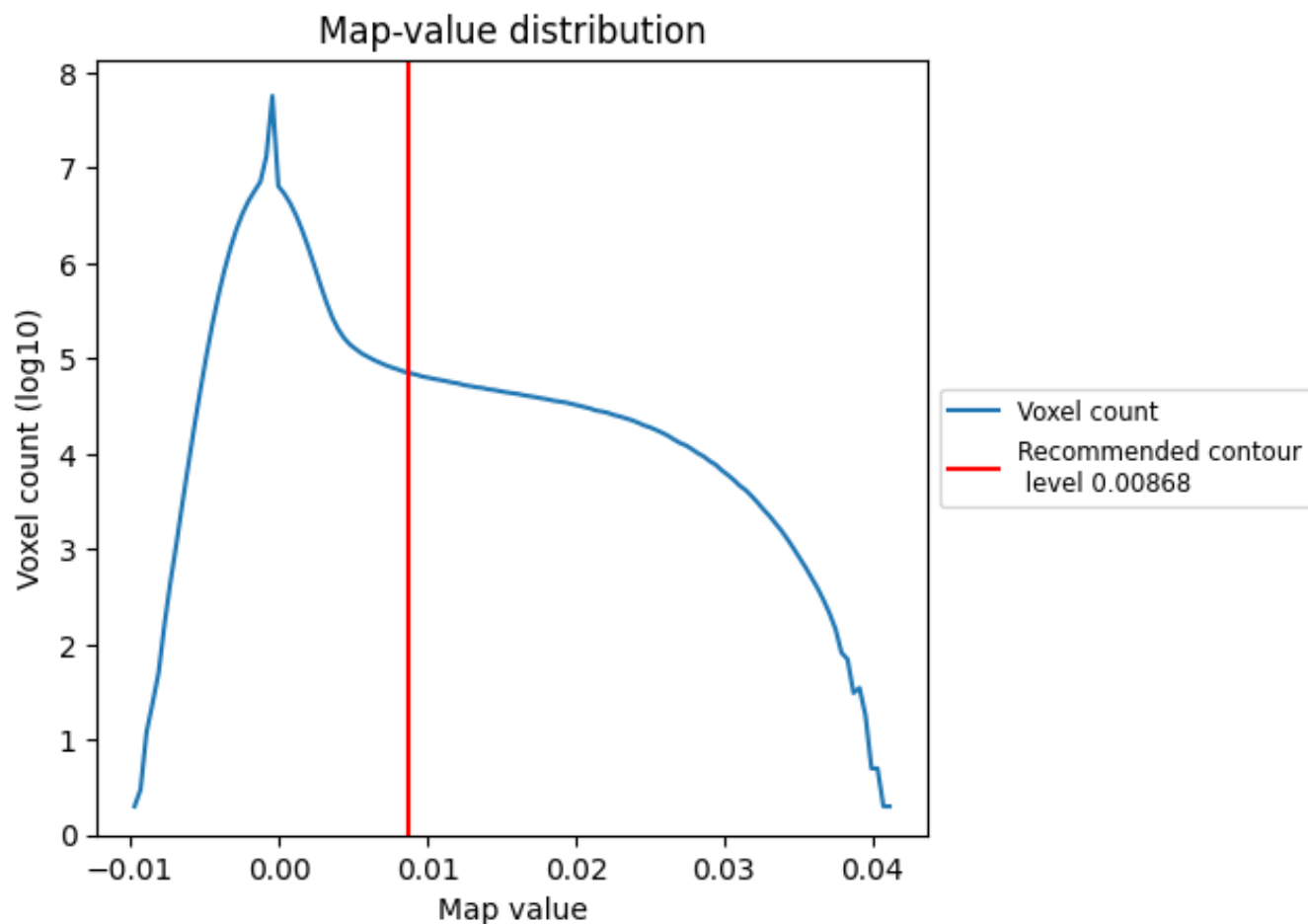
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

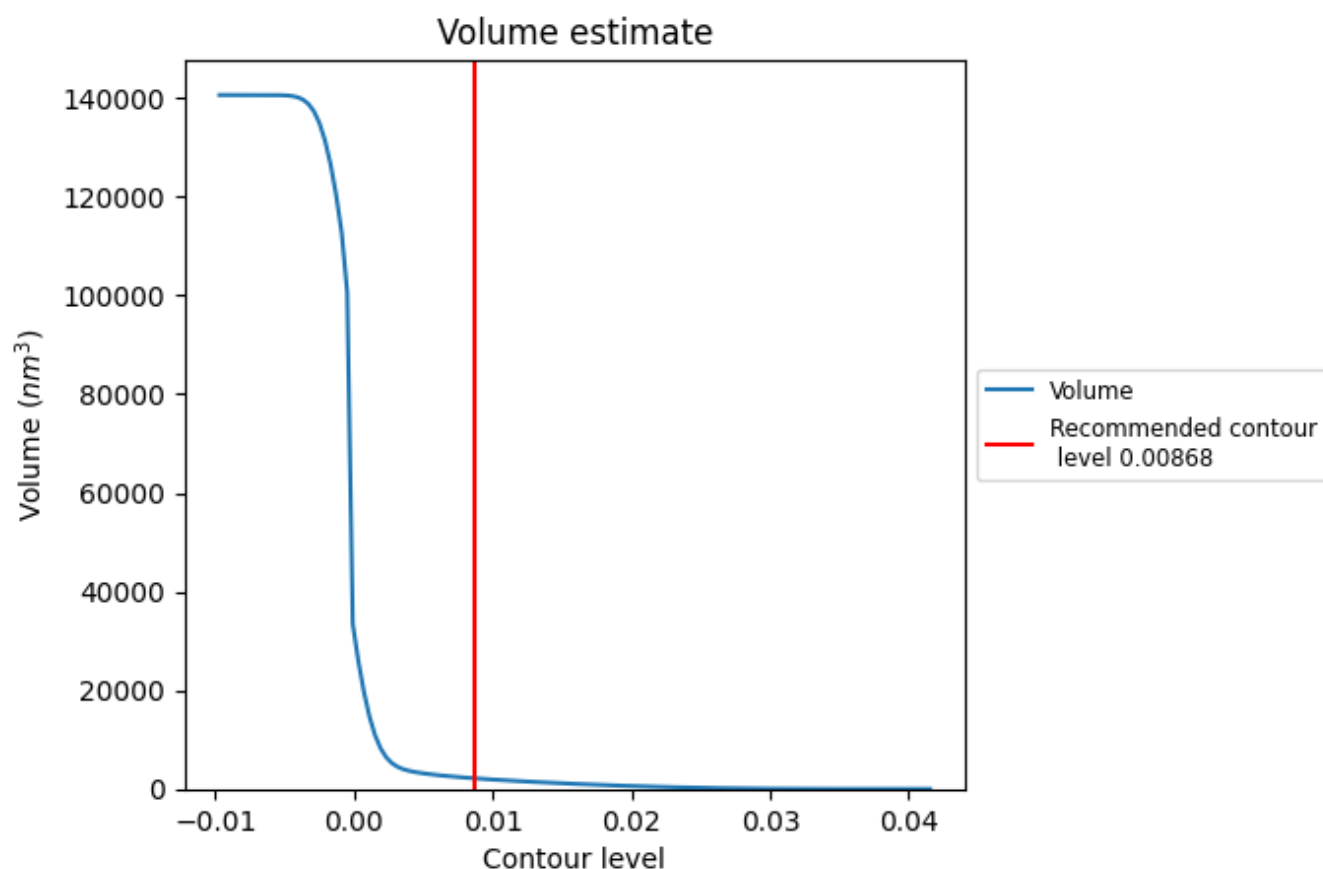
This section contains the results of statistical analysis of the map.

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.

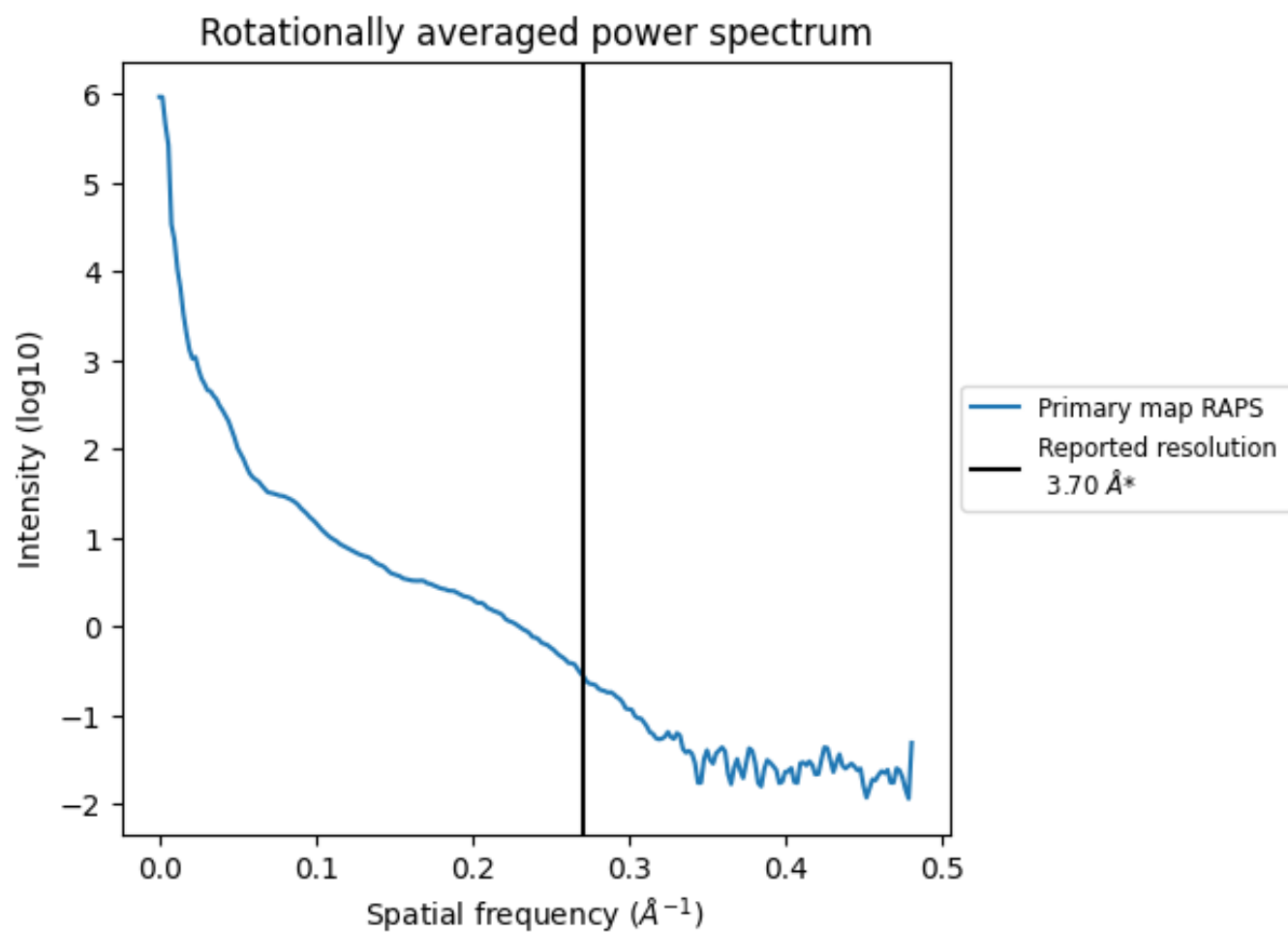
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2155 nm^3 ; this corresponds to an approximate mass of 1947 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

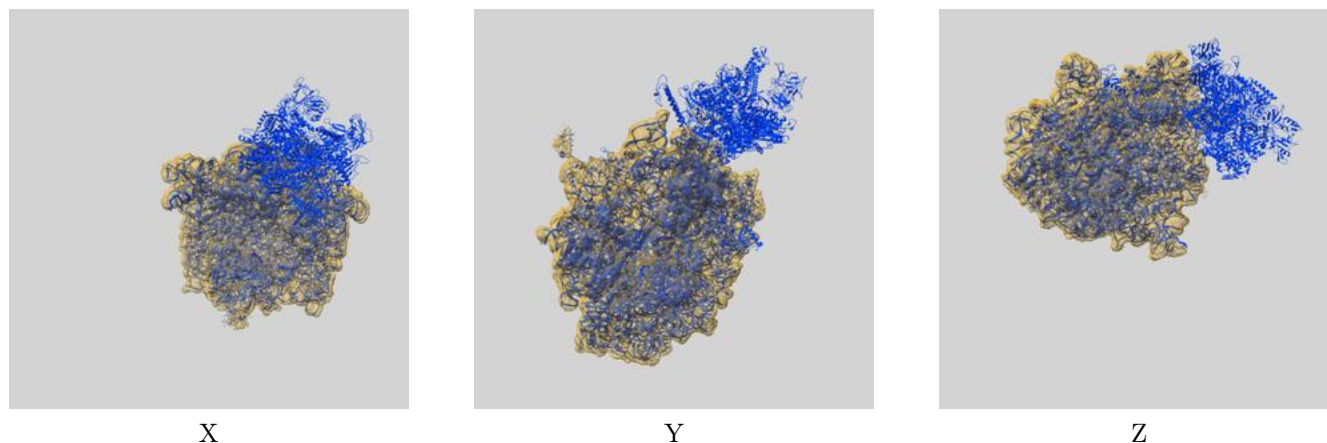
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

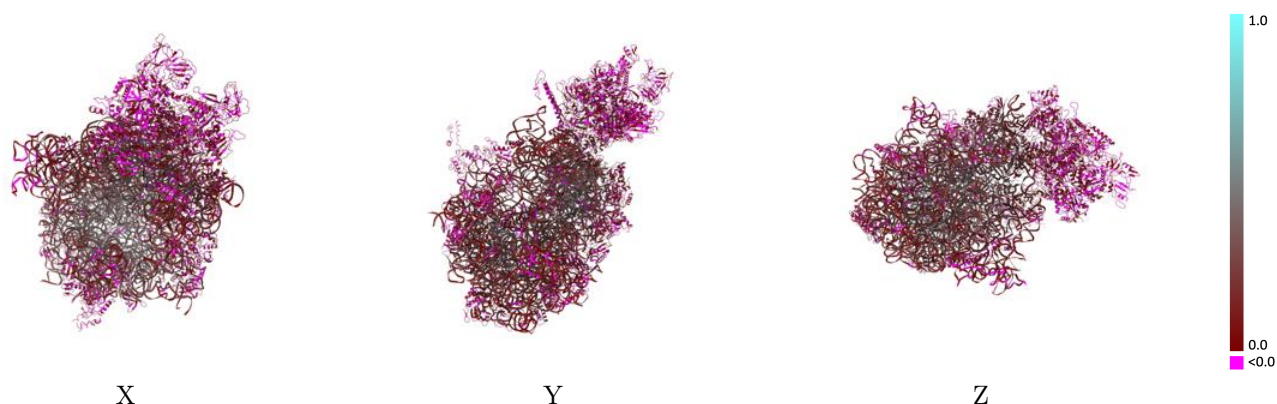
This section contains information regarding the fit between EMDB map EMD-21470 and PDB model 6VYS. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



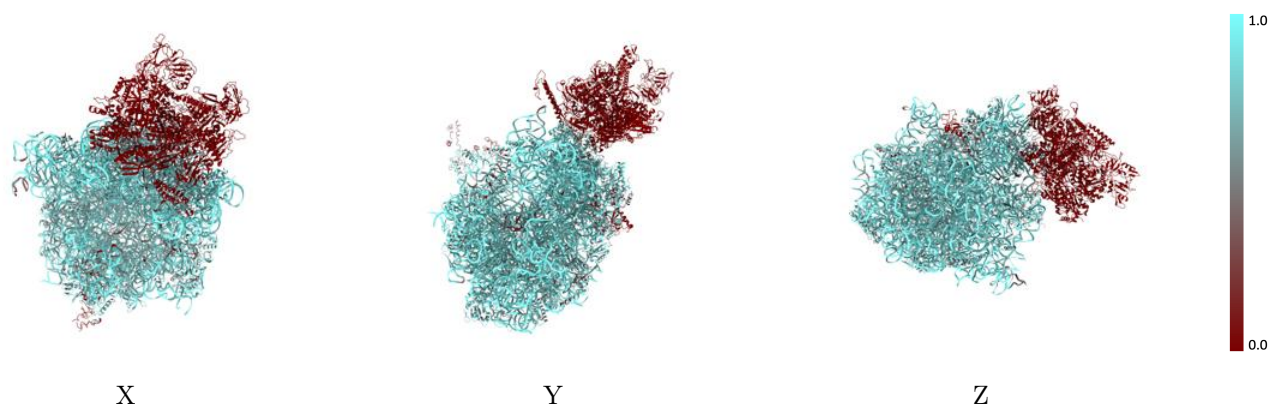
The images above show the 3D surface view of the map at the recommended contour level 0.00868 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



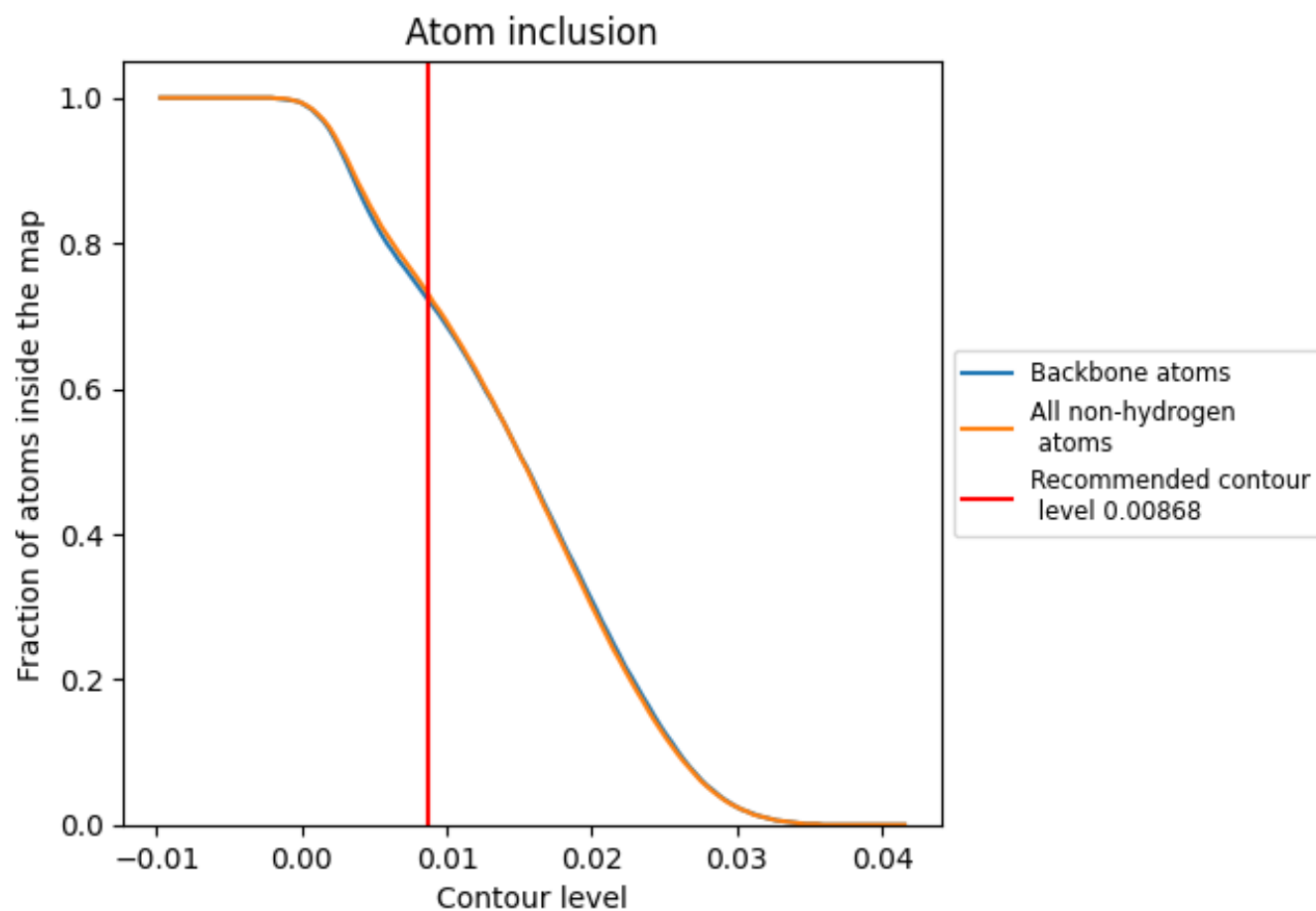
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00868).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 72% of all backbone atoms, 73% 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 (0.00868) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7320	 0.1950
0	 0.8140	 0.1990
1	 0.7810	 0.2550
2	 0.7000	 0.1110
3	 0.7650	 0.0900
4	 0.8100	 0.1990
5	 0.0000	 0.0130
6	 0.0180	 0.1500
7	 0.3070	 0.1010
9	 0.5580	 0.0400
A	 0.8900	 0.1870
AA	 0.0080	 0.0770
AB	 0.0000	 0.0340
AC	 0.0180	 0.1010
AD	 0.0000	 0.0460
AE	 0.0010	 0.0650
B	 0.6520	 0.0930
C	 0.7840	 0.1820
D	 0.9470	 0.2610
E	 0.7200	 0.0870
F	 0.7080	 0.2360
G	 0.7490	 0.1920
H	 0.1450	 0.0410
I	 0.7550	 0.2330
J	 0.7790	 0.1880
K	 0.8300	 0.3220
L	 0.7150	 0.1180
M	 0.7510	 0.1930
N	 0.8120	 0.2400
O	 0.8210	 0.1920
P	 0.7490	 0.1880
Q	 0.7690	 0.2140
R	 0.8290	 0.3250
S	 0.7930	 0.1770
T	 0.7800	 0.1690



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Chain	Atom inclusion	Q-score
U	 0.7370	 0.1070
V	 0.7780	 0.2040
W	 0.6270	 0.0470
X	 0.6820	 0.1050
Y	 0.4350	 0.0490
Z	 0.1760	 0.0610
a	 0.9340	 0.2370
b	 0.7900	 0.1940
c	 0.7390	 0.1720
d	 0.9290	 0.1880
e	 0.7490	 0.0770
f	 0.8100	 0.2460
g	 0.6970	 0.0790
h	 0.7390	 0.1500
i	 0.8110	 0.2560
j	 0.7950	 0.2150
k	 0.7030	 0.1200
l	 0.7300	 0.1640
m	 0.8280	 0.2680
n	 0.7170	 0.1030
o	 0.7430	 0.2070
p	 0.7690	 0.1100
q	 0.7980	 0.1930
r	 0.5710	 0.0620
s	 0.8150	 0.2330
t	 0.7320	 0.2060
u	 0.7800	 0.1890
v	 0.7810	 0.2590
w	 0.7930	 0.1840
x	 0.7520	 0.0520
y	 0.7420	 0.1430
z	 0.8410	 0.2700