



wwPDB EM Validation Summary Report ⓘ

Nov 12, 2022 – 07:48 PM EST

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:

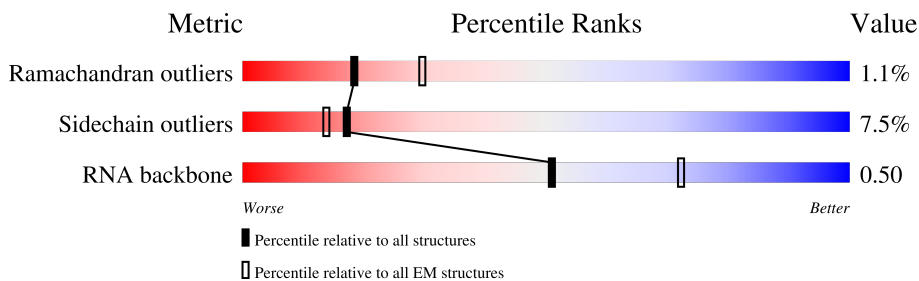
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	

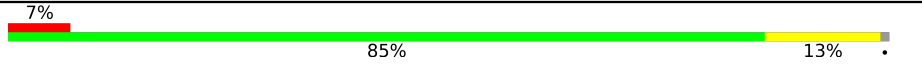
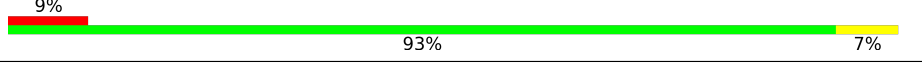
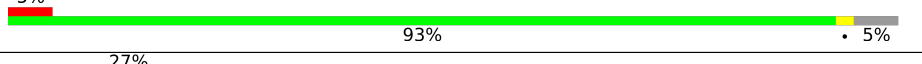

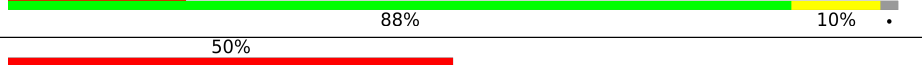

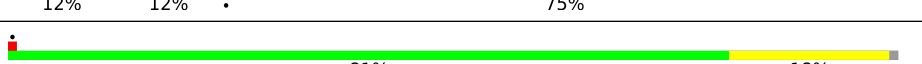
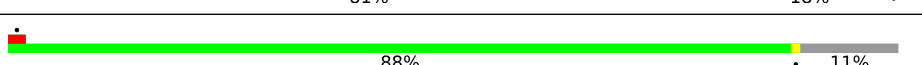
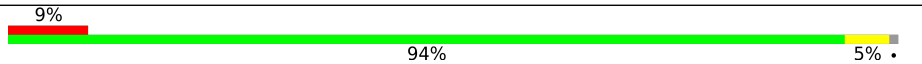

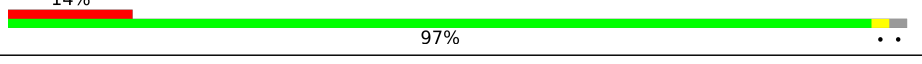
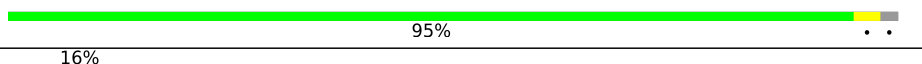
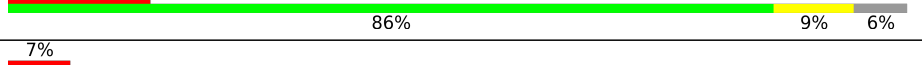
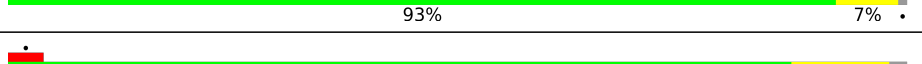
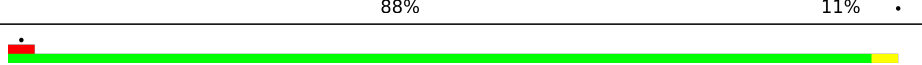
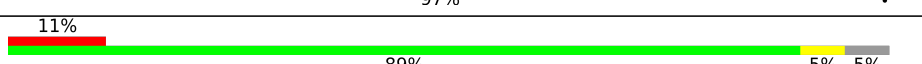
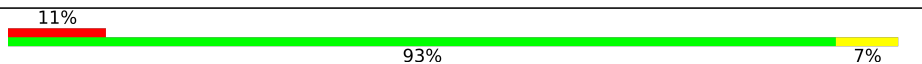
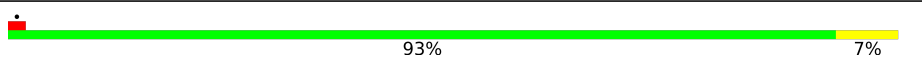

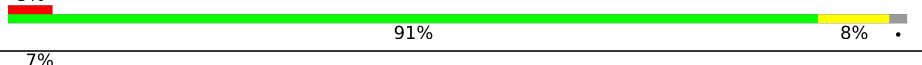
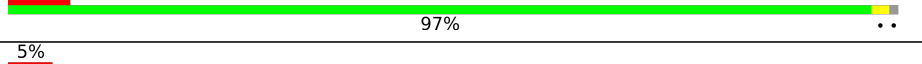
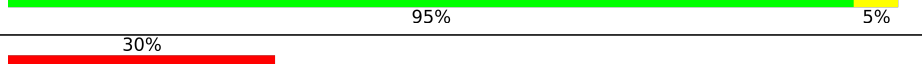
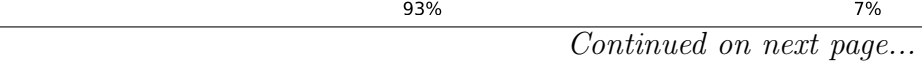


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Mol	Chain	Length	Quality of chain
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1358	
15	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	

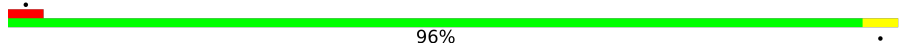
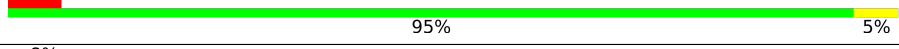
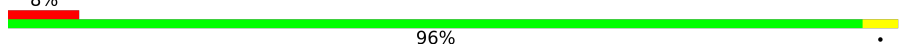
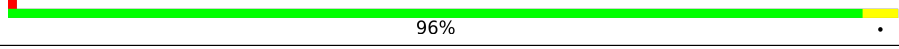

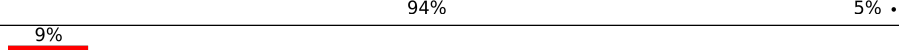
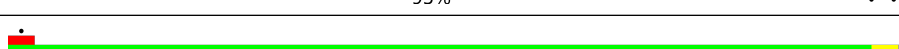

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Mol	Chain	Length	Quality of chain
32	T	89	
33	U	82	
34	V	84	
35	W	92	
36	X	118	
37	Y	142	
38	Z	121	
39	a	2904	
40	b	85	
41	c	78	
42	d	120	
43	e	63	
44	f	59	
45	g	70	
46	h	273	
47	i	57	
48	j	209	
49	k	55	
50	l	201	
51	m	46	
52	n	179	
53	o	65	
54	p	177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

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

2 Entry composition [i](#)

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	
			Total	C	H	N	O			S
1	0	103	1655	516	839	153	145	2	0	0

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
6	5	23	732	225	260	87	137	23	0	0

- 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	
			Total	C	H	N	O			S
13	AD	228	3556	1100	1789	312	349	6	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

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

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

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

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

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	
			Total	C	H	N	O			S
40	b	76	1181	360	599	117	104	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

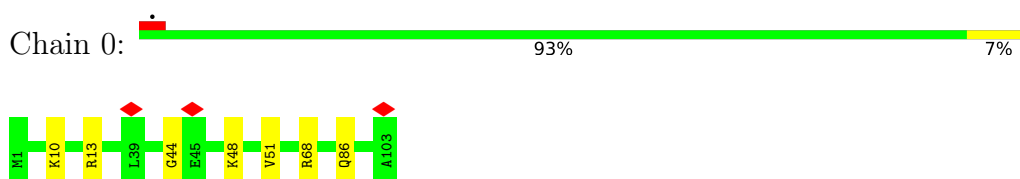
- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

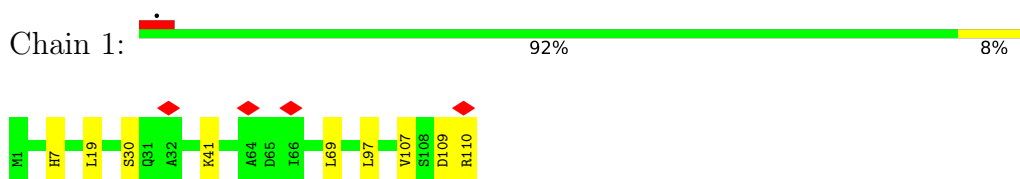
3 Residue-property plots [i](#)

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.

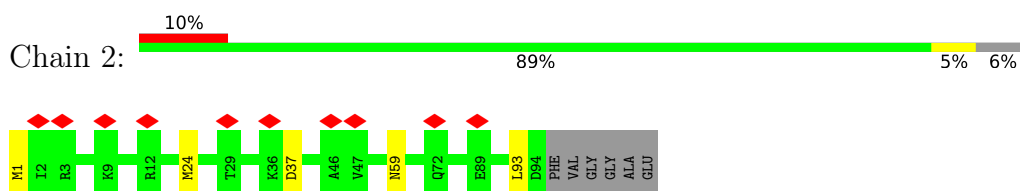
- Molecule 1: 50S ribosomal protein L21



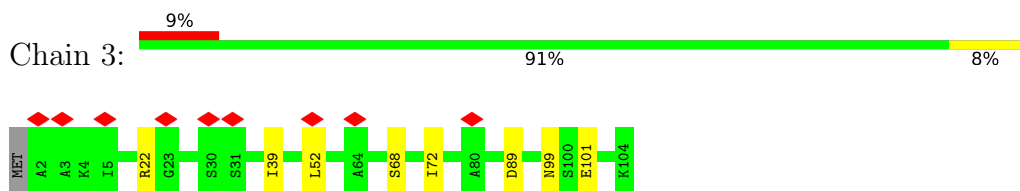
- Molecule 2: 50S ribosomal protein L22



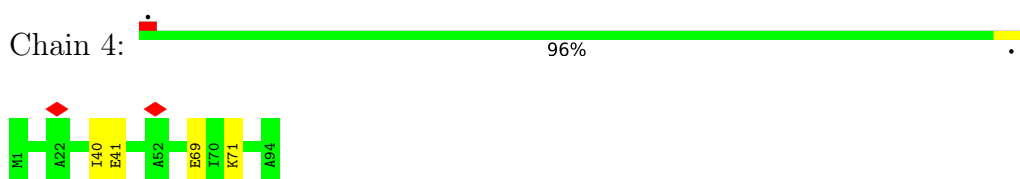
- Molecule 3: 50S ribosomal protein L23



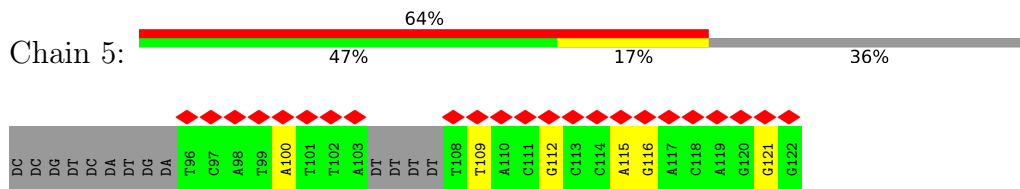
- Molecule 4: 50S ribosomal protein L24



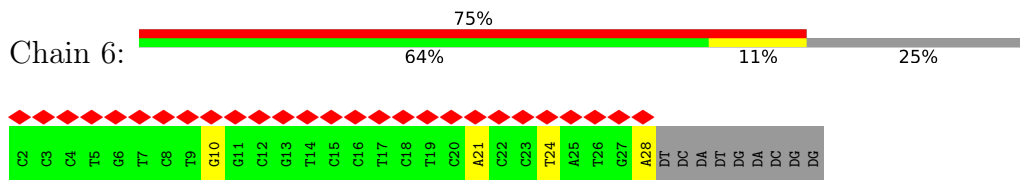
- Molecule 5: 50S ribosomal protein L25



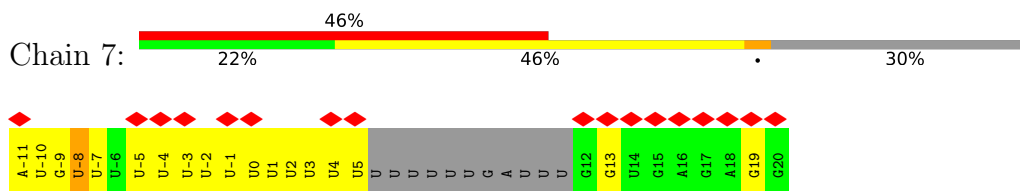
• Molecule 6: NT DNA



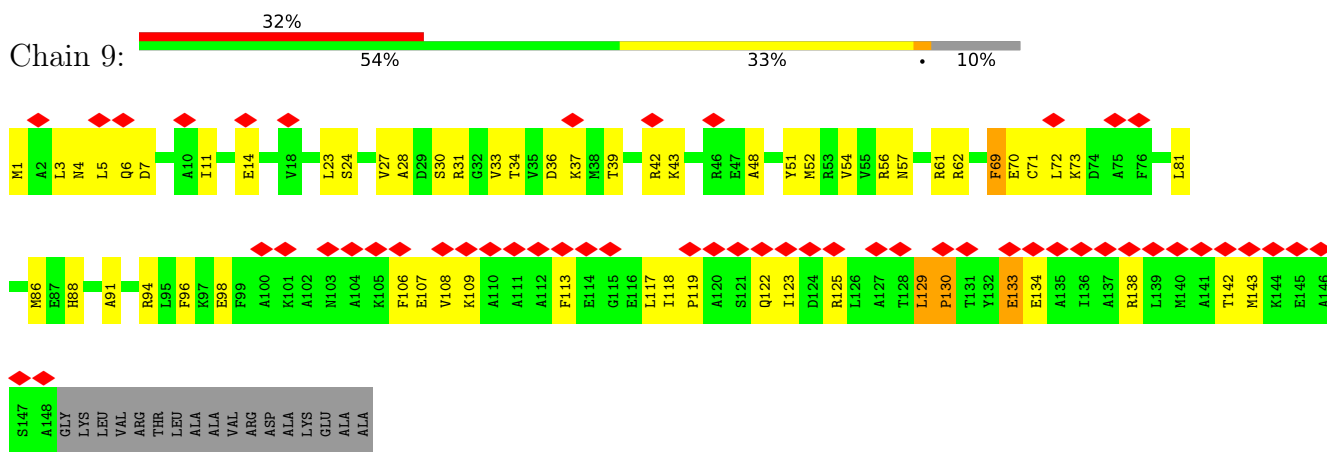
• Molecule 7: T DNA



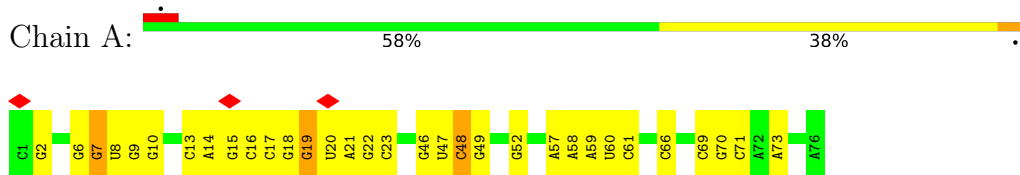
• Molecule 8: mRNA with 21 nt long spacer



• Molecule 9: 50S ribosomal protein L10

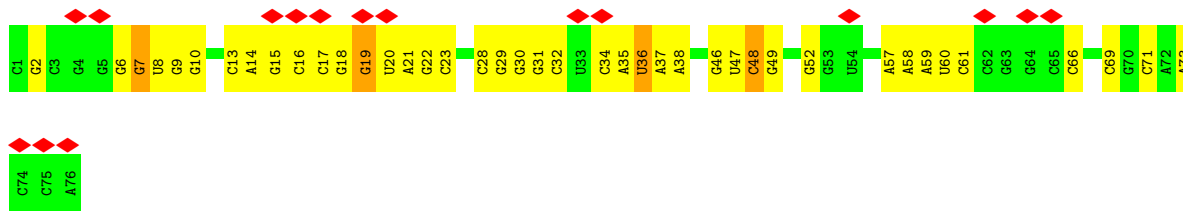


• Molecule 10: E-site and P-site tRNA (fMet)



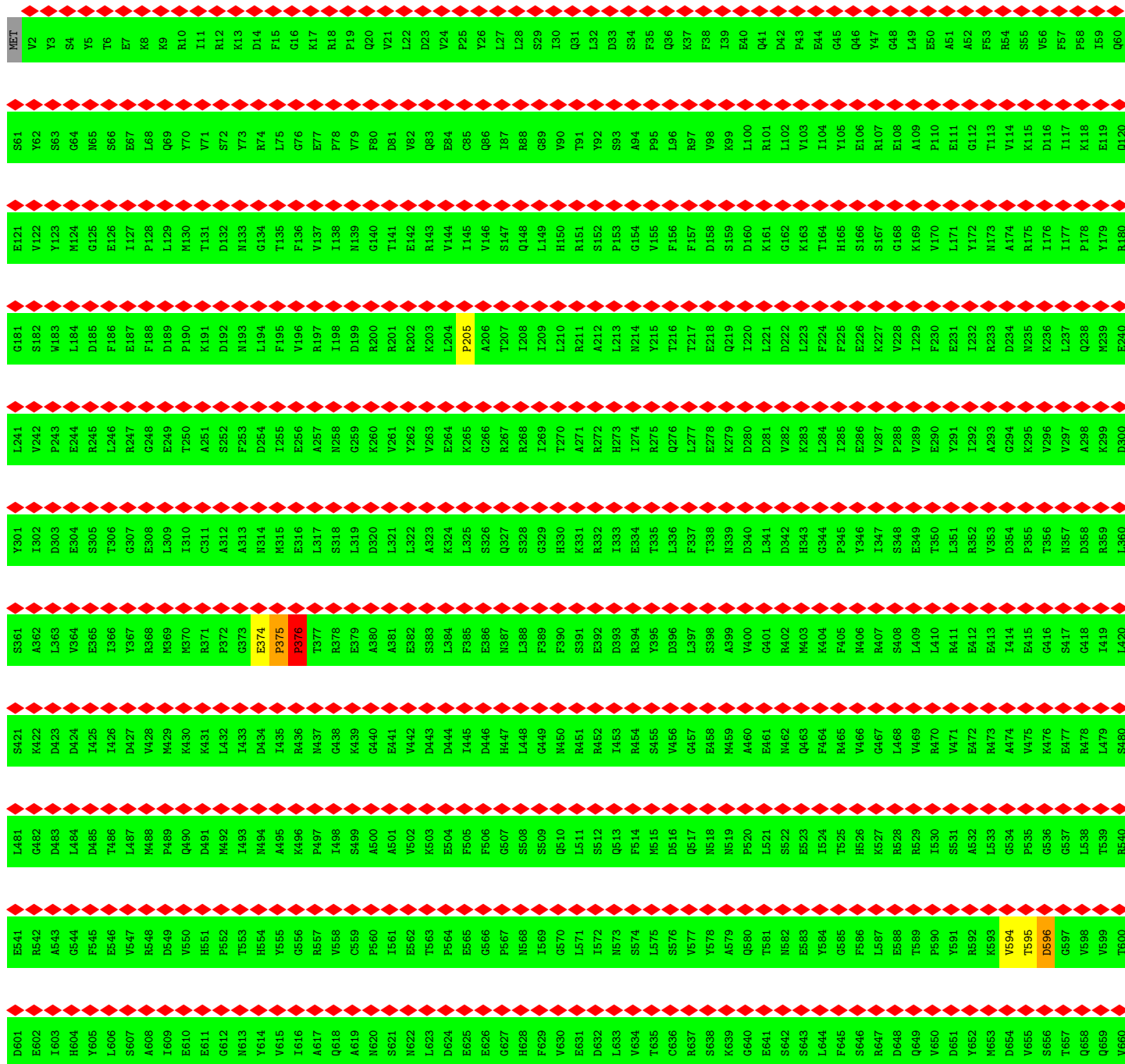
• Molecule 10: E-site and P-site tRNA (fMet)

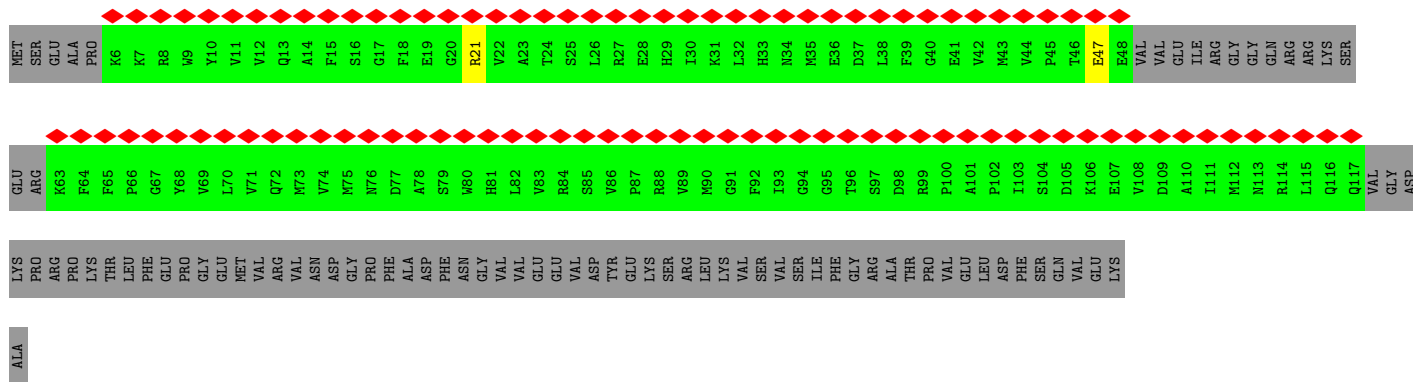




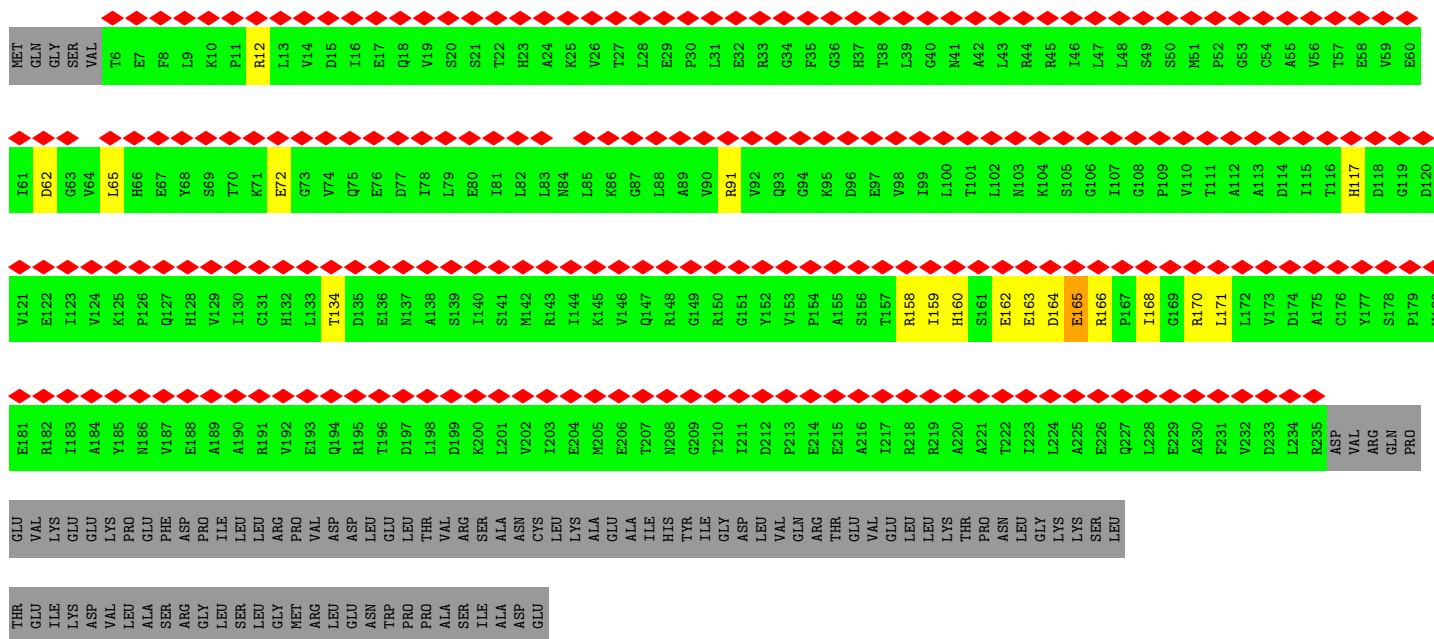
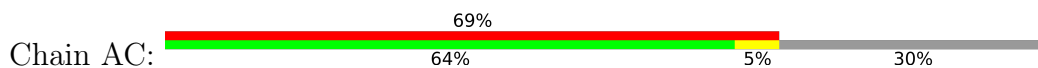
• Molecule 11: DNA-directed RNA polymerase subunit beta

Chain AA:

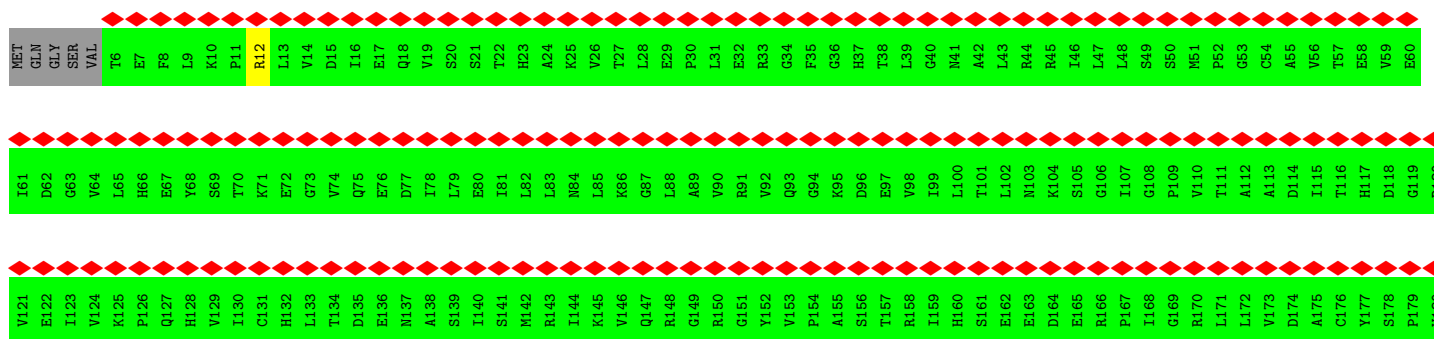
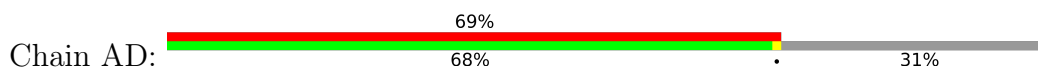




• Molecule 13: DNA-directed RNA polymerase subunit alpha



• Molecule 13: DNA-directed RNA polymerase subunit alpha

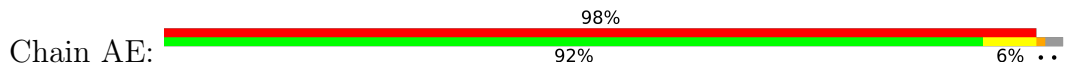


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GLU	VAL	LYS	GLY	LYS	PRO	PHE	ASP	PRO	ILE	LEU	ARG	MET	VAL	ASP	ASP	LEU	LEU	GLY	TRP	GLU	PRO	THR	VAL	ALA	ARG	SER	ALA	ALA	ASP	GLY	ASP	VAL	GLN	ARG	THR	VAL	GLY	LEU	LEU	LYS	THR	PRO	ASN	LEU	GLY	LYS	LYS	SER	LEU
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THR	GLU	ILE	LYS	ASP	VAL	LEU	ALA	SER	GLY	LEU	LEU	MET	ARG	LEU	GLY	ASN	TRP	PRO	PRO	VAL	ALA	SER	SER	ILE	ALA	ASP	GLU
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● Molecule 14: DNA-directed RNA polymerase subunit



E16	F17	D18	A19	K21	I22	A23	L24	A25	S26	P27	D28	M29	I30	R31	S32	W33	S34	F35	G36	V38	K39	K40	P41	E42	T43	I44	M45	Y46	R47	T48	F49	K50	P51	E52	R53	D54	G55	L56	F57	C58	K66	D67	Y68	E69	C70	L71	C72	G73	K74	Y75
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K76	R77	L78	K79	H80	R81	G82	V83	I84	C85	E86	K87	C88	G89	V90	E91	T93	Q94	T95	K96	R97	R98	R99	E100	R101	M102	G103	H104	I105	E106	L107	A108	S109	P110	T111	A112	H113	I114	W115	F116	L117	K118	S119	L120	P121	S122	R123	I124	G125	L126	L127	Y128	D129	M130	P131	L132	R133	D134	I135
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E136	R137	V138	L139	F141	E142	S143	I144	Y145	V146	I147	E148	G149	G150	M151	N152	M153	L154	E155	R156	Q157	Q158	I159	L160	T161	E162	E163	Q164	Y165	L166	D167	A168	L169	E170	E171	F172	G173	D174	E175	F176	D177	A178	K179	M180	G181	A182	E183	A184	I185	Q186	A187	L188	L189	K190	S191	M192	D193	L194	E195
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Q196	E197	C198	E199	Q200	L201	R202	E203	E204	L205	N206	E207	T208	N209	S210	E211	T212	K213	R214	K215	L216	K217	T218	K219	R220	I221	K222	L223	L224	E225	A226	F227	V228	Q229	D289	I290	S291	M292	K293	P294	E295	M296	R297	L298	L299	Q300	E301	L302	A303	V303	D304	A305	L306	L307	D308	N309	G310	R311	G312	R313	P254	L255
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D256	G257	G258	R259	F260	A261	T262	S263	D264	L265	M266	D267	L268	Y269	R270	R271	V272	L273	M274	R275	M276	N277	R278	L279	K280	R281	L282	L283	D284	L285	A286	A287	P288	D289	I290	V291	V292	R293	M294	E295	K296	R297	M298	L299	Q300	E301	A302	V303	D304	A305	L306	L307	D308	N309	G310	R311	G312	R313	P254	L255
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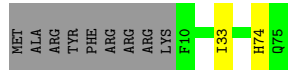
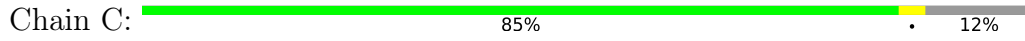
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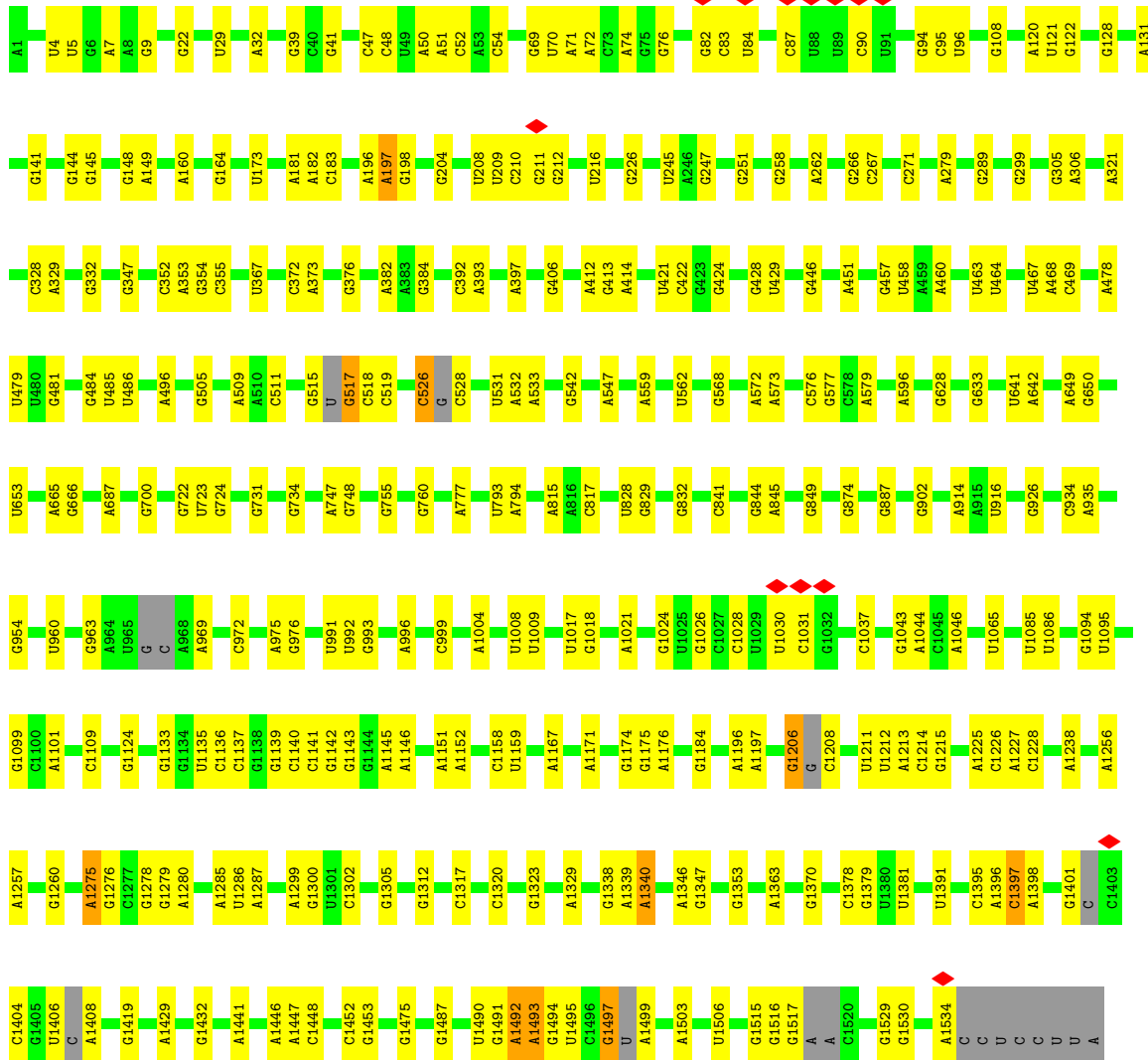
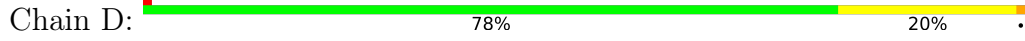
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L1156	A1157	E1158	I1159	S1160	G1161	V1163	S1164	F1165	G1166	K1167	L1168	T1169	K1170	G1171	K1172	R1173	R1174	L1175	V1176	I1177	T1178	P1179	V1180	T1181	G1182	S1183	D1184	Y1185	Y1186	E1187	E1188	M1189	I1190	K1251	H1252	I1253	E1254	V1255	I1256	V1257	R1258	Q1259	M1260	L1261	R1262	K1263	A1264	T1265	I1266	V1267	N1268	L1269	I1270	S1271	D1272	F1273	F1274	L1275							
P1096	A1097	Q1098	Y1099	F1100	L1101	P1102	G1103	K1104	T1045	I1106	V1107	L1108	L1109	E1110	D1111	G1112	V1113	Q1114	I1115	S1116	I1117	G1118	D1119	V1120	L1121	A1122	R1123	I1124	P1125	Q1126	GLU	SER	GLY	GLY	THR	LYS	ASP	ILE	THR	G1136	G1137	L1138	P1139	R1140	V1141	A1142	D1143	L1144	F1145	E1146	A1147	R1148	R1149	P1150	L1151	E1152	P1153	A1154	I1155						
R1036	F1037	T1038	D1039	M1040	I1041	P1042	G1043	Q1044	T1045	I1046	T1047	R1048	Q1049	T1050	D1051	E1052	L1053	T1054	G1055	L1056	S1057	S1058	L1059	V1060	V1061	L1062	D1063	S1064	A1065	E1066	R1067	T1068	A1069	G1070	G1071	K1072	D1073	L1074	R1075	P1076	A1077	L1078	K1079	I1080	V1081	D1082	A1083	Q1084	M1085	A1086	D1087	V1088	T1089	K1151	E1152	P1153	A1154	I1155							
G916	V917	R918	A919	R920	Q921	S922	I923	G924	E925	P926	G927	T928	Q929	L930	T931	M932	R933	THR	PHE	HIS	ILE	GLY	GLY	ALA	ALA	SER	ARG	ALA	M982	R983	S984	V985	S948	S949	R950	Q951	V952	K953	N954	K955	G956	S957	I958	K959	L960	S961	N962	V963	K964	S965	V966	V967	N968	S969	S970	G971	I908	K972	L973	N910	K911	G912	S913	A914	I915
I856	L857	V858	P859	R860	N861	T862	L863	L864	H865	E866	Q867	F868	C869	D870	L871	L872	E873	E874	N875	S876	V877	H817	E818	G819	I820	M821	M822	T823	P824	V825	I826	S887	C888	G889	T890	D891	F892	G893	V894	C895	A896	H897	C898	Y899	G900	R901	D902	L903	A904	R905	G906	H907	I908	I909	N910	K911	G912	S913	A914	I915					
L796	T797	R798	R799	L800	V801	D802	V803	A804	Q805	D806	L807	V808	V809	T810	E811	D812	D813	C814	G815	T816	H817	E818	G819	I820	M821	M822	T823	P824	V825	I826	S887	C888	G889	T890	D891	F892	G893	V894	C895	A896	H897	C898	Y899	G900	R901	D902	L903	A904	R905	G906	H907	I908	I909	N910	K911	G912	S913	A914	D855						
Q736	I737	R738	Q739	L740	A741	G742	M743	G744	T745	L746	M747	A748	K749	P750	D751	G752	S753	I754	I755	T756	T757	P758	I759	T760	A761	N762	F763	R764	E765	G766	L767	N768	V769	L770	Q771	F772	F773	I774	S775	T776	H777	G778	F779	A780	N781	G782	L783	A784	D785	T786	L787	K788	G789	T790	A791	N792	S793	G794	Y795						
G676	E677	R678	Y679	N680	K681	V682	I683	D684	I685	V686	A687	A688	A689	N690	D691	R692	V693	S694	K695	A696	M697	M698	D699	N700	L701	Q702	T703	E704	T705	V706	I707	N708	R709	D710	G711	Q712	E713	E714	K715	V716	V717	S718	F719	N720	G721	I722	Y723	M724	T725	A726	D727	S728	G729	A730	R731	G732	A733	A734	A735						
P616	T617	V618	I619	F620	A621	Q622	Q623	I624	M625	Y626	T627	G628	F629	A630	Y631	A632	A633	R634	S635	G636	A637	S638	V639	G640	I641	D642	D643	M644	V645	I646	P647	E648	K649	K650	H651	E652	I653	I654	S655	E656	A657	E658	A659	E660	A662	E663	I664	Q665	E666	Q667	F668	G669	S670	G671	L672	S673	T674	A675							

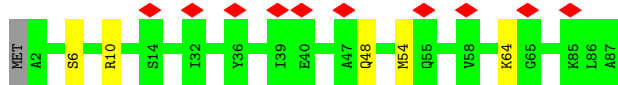
- Molecule 15: 30S ribosomal protein S18



• Molecule 16: 16S rRNA

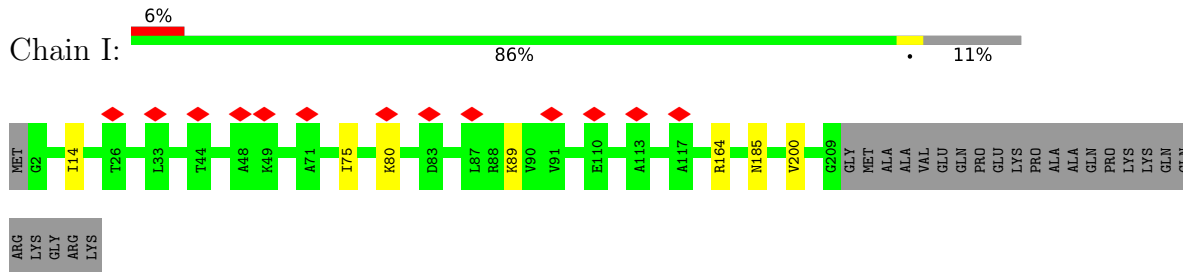


• Molecule 17: 30S ribosomal protein S20

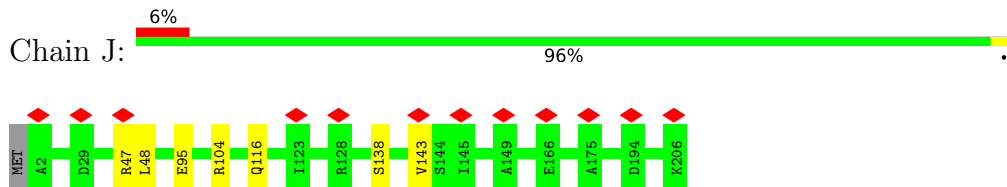


• Molecule 18: 30S ribosomal protein S21

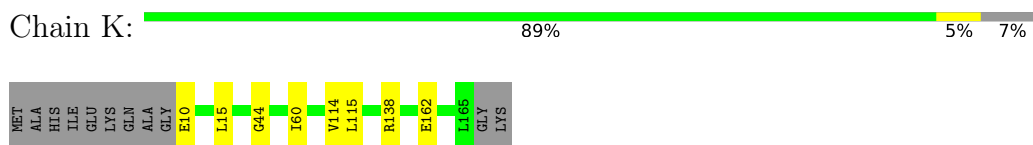
• Molecule 21: 30S ribosomal protein S3



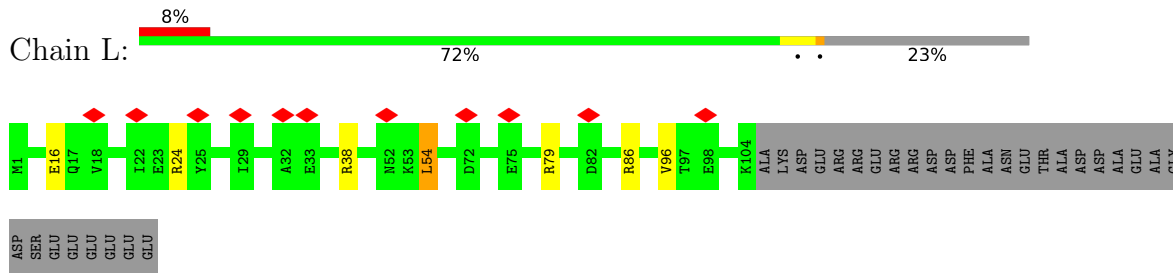
• Molecule 22: 30S ribosomal protein S4



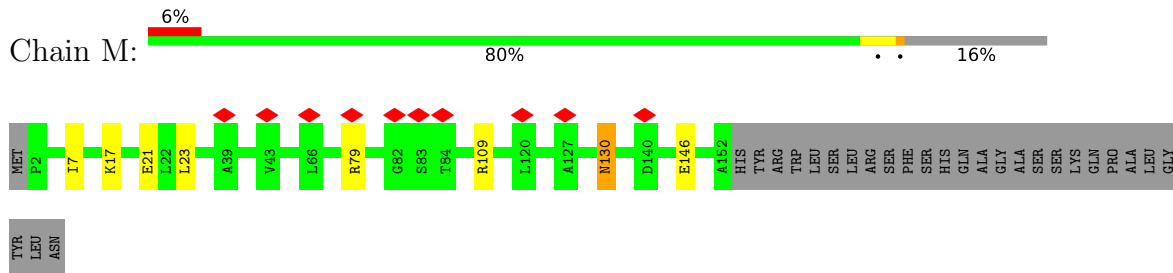
• Molecule 23: 30S ribosomal protein S5



• Molecule 24: 30S ribosomal protein S6

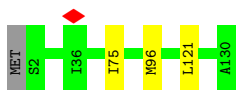


• Molecule 25: 30S ribosomal protein S7

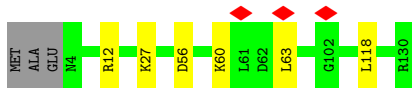


• Molecule 26: 30S ribosomal protein S8

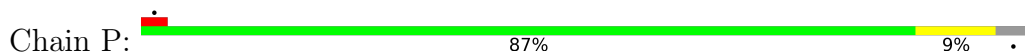




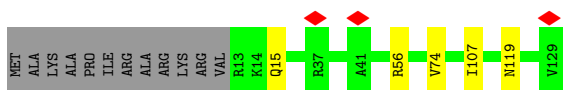
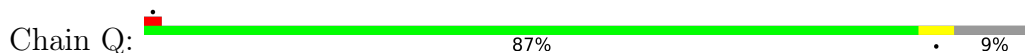
- Molecule 27: 30S ribosomal protein S9



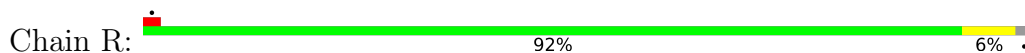
- Molecule 28: 30S ribosomal protein S10



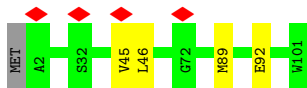
- Molecule 29: 30S ribosomal protein S11



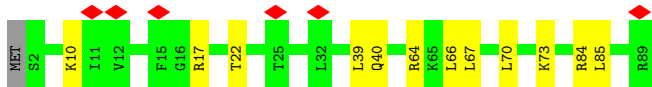
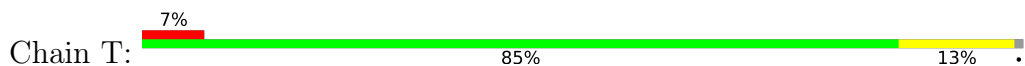
- Molecule 30: 30S ribosomal protein S12



- Molecule 31: 30S ribosomal protein S14

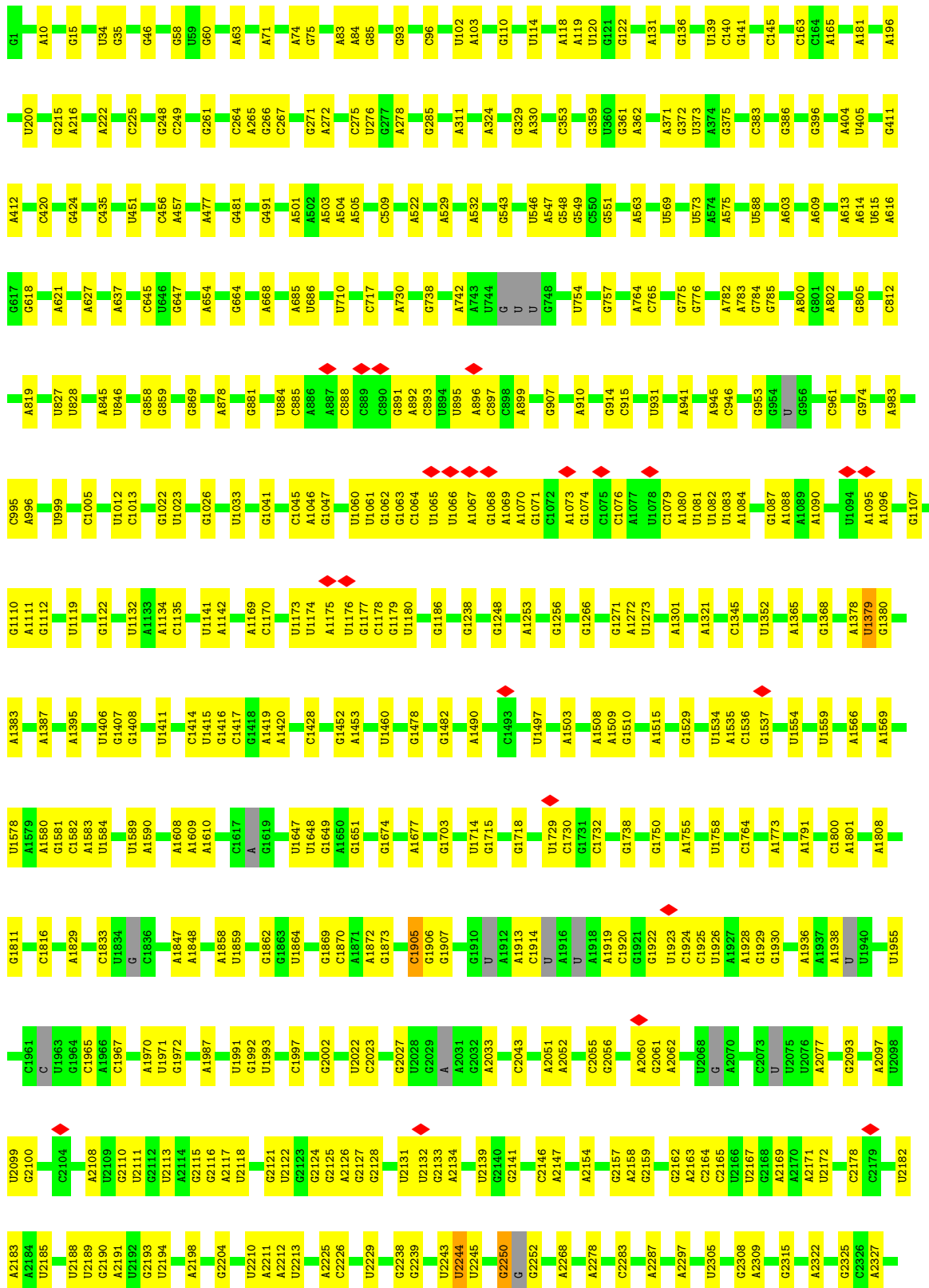
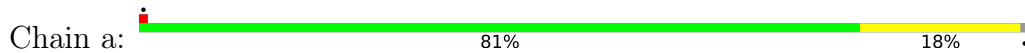


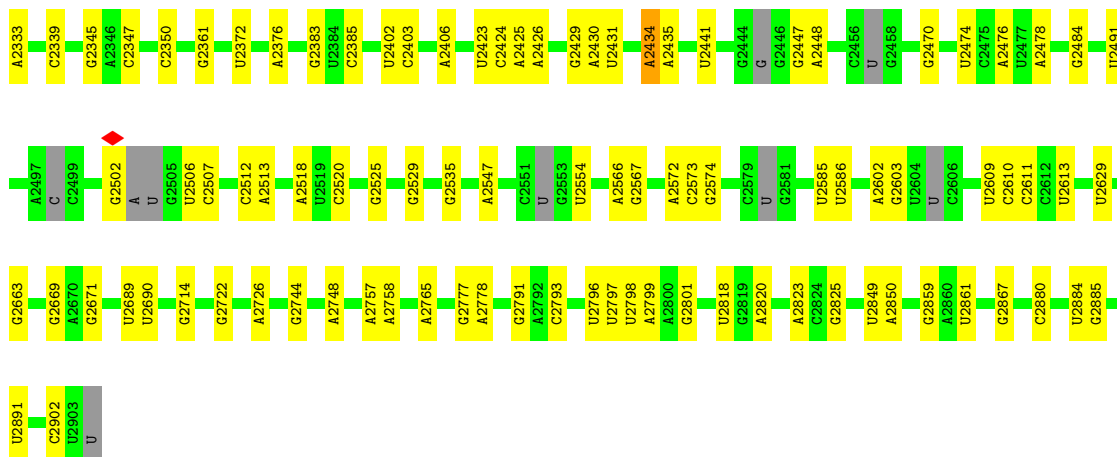
- Molecule 32: 30S ribosomal protein S15



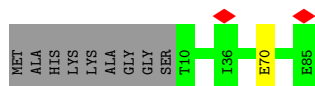
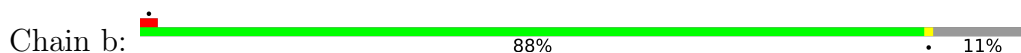
- Molecule 33: 30S ribosomal protein S16

• Molecule 39: 23S rRNA

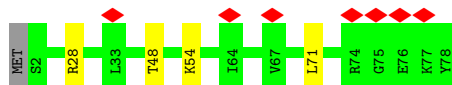
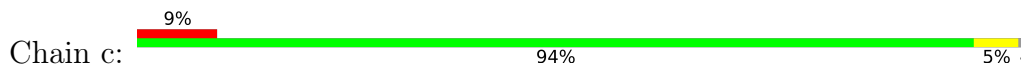




• Molecule 40: 50S ribosomal protein L27



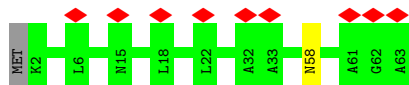
• Molecule 41: 50S ribosomal protein L28



• Molecule 42: 5S rRNA



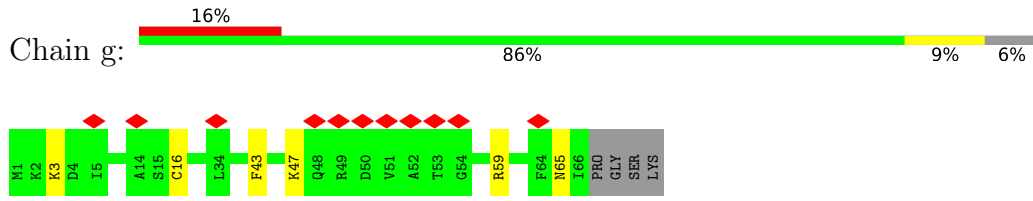
• Molecule 43: 50S ribosomal protein L29



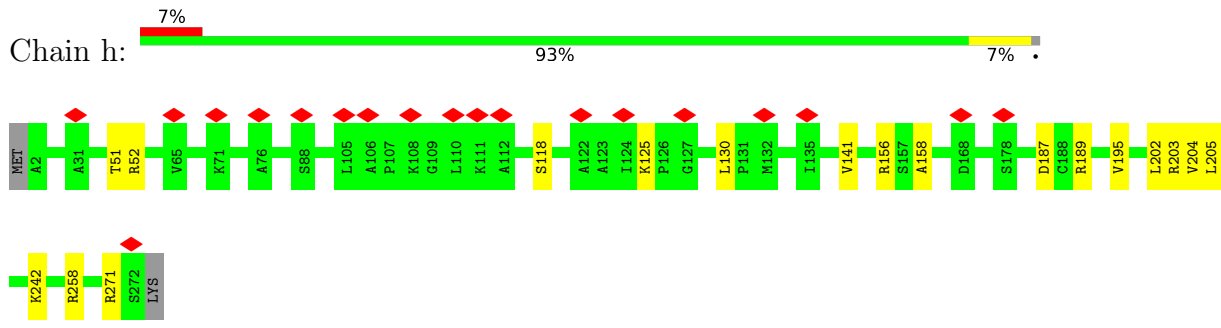
• Molecule 44: 50S ribosomal protein L30



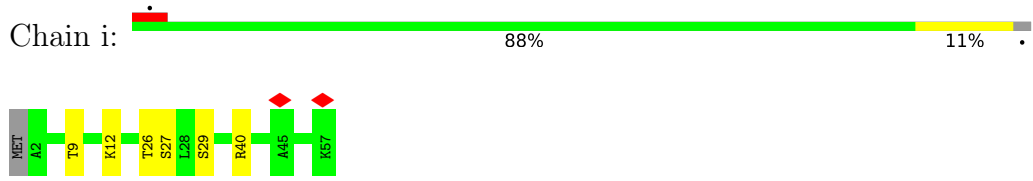
• Molecule 45: 50S ribosomal protein L31



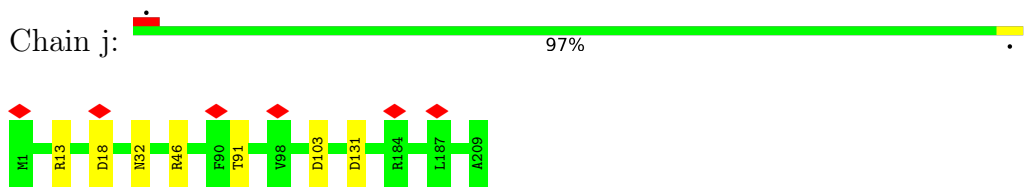
• Molecule 46: 50S ribosomal protein L2



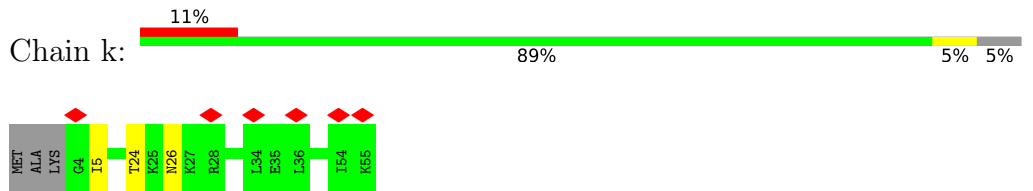
• Molecule 47: 50S ribosomal protein L32



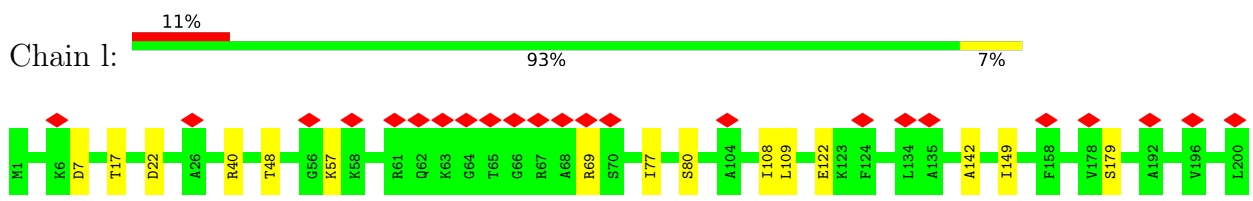
• Molecule 48: 50S ribosomal protein L3



• Molecule 49: 50S ribosomal protein L33



• Molecule 50: 50S ribosomal protein L4




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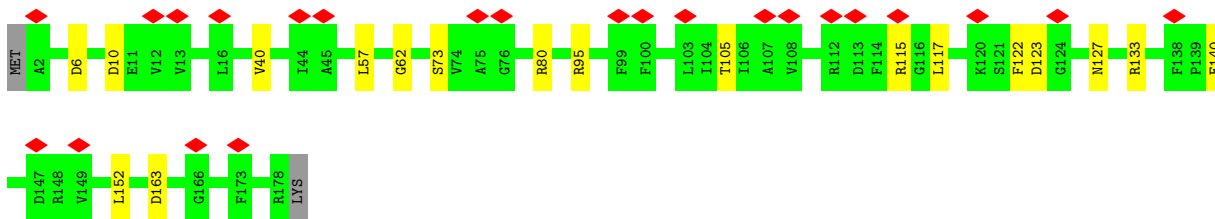
- Molecule 51: 50S ribosomal protein L34

Chain m:  93% 7%




- Molecule 52: 50S ribosomal protein L5

Chain n:  13% 89% 10%



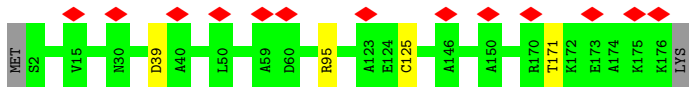
- Molecule 53: 50S ribosomal protein L35

Chain o:  5% 91% 8%

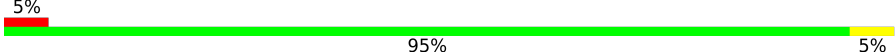


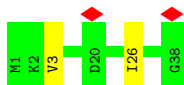
- Molecule 54: 50S ribosomal protein L6

Chain p:  7% 97%

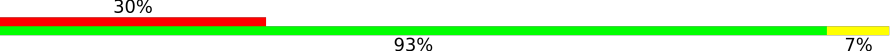


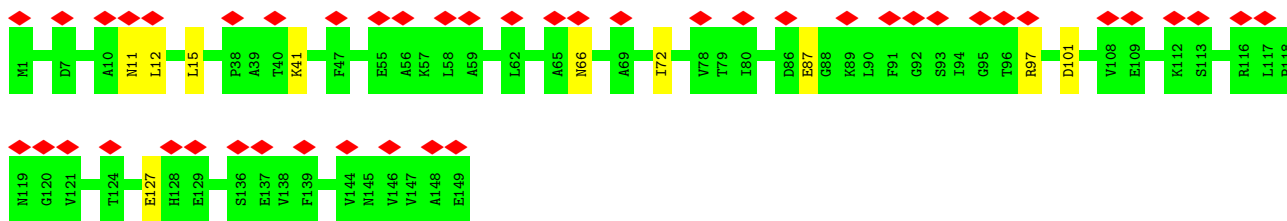
- Molecule 55: 50S ribosomal protein L36

Chain q:  5% 95% 5%

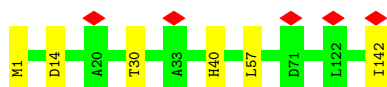


- Molecule 56: 50S ribosomal protein L9

Chain r:  30% 93% 7%



- Molecule 57: 50S ribosomal protein L13



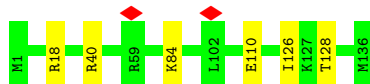
- Molecule 58: 50S ribosomal protein L14



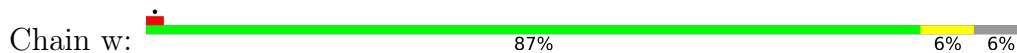
- Molecule 59: 50S ribosomal protein L15



- Molecule 60: 50S ribosomal protein L16

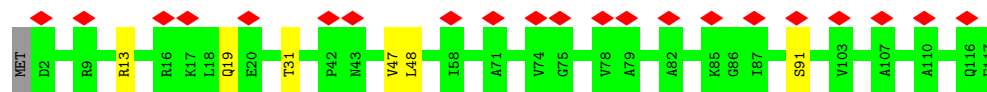


- Molecule 61: 50S ribosomal protein L17

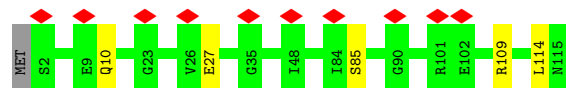


- Molecule 62: 50S ribosomal protein L18





- 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 i

5.1 Standard geometry i

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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Continued from previous page...

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%)	15	51
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%)	15	51
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	8
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	6	35
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	17	54
13	AD	226/329 (69%)	212 (94%)	13 (6%)	1 (0%)	34	69
14	AE	1329/1358 (98%)	1200 (90%)	120 (9%)	9 (1%)	22	59
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	23
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	29	66
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	25	62
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	15	51
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	22	59
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	19	56
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	19	56
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	15	51
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	9	42

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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%)	12	47
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%)	8	41
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	1	10
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	15
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%)	34	69
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%)	29	66
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	14	50
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%)	17	54
All	All	9368/10437 (90%)	8605 (92%)	660 (7%)	103 (1%)	18	50

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 [i](#)

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%)	14	45
2	1	93/93 (100%)	84 (90%)	9 (10%)	8	33
3	2	81/84 (96%)	76 (94%)	5 (6%)	18	49
4	3	84/85 (99%)	78 (93%)	6 (7%)	14	45
5	4	78/78 (100%)	74 (95%)	4 (5%)	24	55
9	9	112/123 (91%)	65 (58%)	47 (42%)	0	0
11	AA	1140/1157 (98%)	1039 (91%)	101 (9%)	9	37
12	AB	86/158 (54%)	84 (98%)	2 (2%)	50	71
13	AC	198/286 (69%)	182 (92%)	16 (8%)	11	41
13	AD	196/286 (68%)	194 (99%)	2 (1%)	76	86
14	AE	1120/1134 (99%)	1051 (94%)	69 (6%)	18	49
15	C	57/65 (88%)	55 (96%)	2 (4%)	36	63
17	E	65/66 (98%)	60 (92%)	5 (8%)	13	43
18	F	60/61 (98%)	57 (95%)	3 (5%)	24	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	178 (95%)	9 (5%)	25	56
20	H	137/461 (30%)	128 (93%)	9 (7%)	16	48
21	I	171/190 (90%)	165 (96%)	6 (4%)	36	63
22	J	172/173 (99%)	165 (96%)	7 (4%)	30	59
23	K	119/126 (94%)	112 (94%)	7 (6%)	19	51
24	L	91/116 (78%)	85 (93%)	6 (7%)	16	48
25	M	124/147 (84%)	116 (94%)	8 (6%)	17	48
26	N	104/105 (99%)	102 (98%)	2 (2%)	57	76
27	O	105/107 (98%)	100 (95%)	5 (5%)	25	56
28	P	86/90 (96%)	78 (91%)	8 (9%)	9	35
29	Q	90/99 (91%)	87 (97%)	3 (3%)	38	64
30	R	101/104 (97%)	94 (93%)	7 (7%)	15	46
31	S	83/84 (99%)	79 (95%)	4 (5%)	25	56
32	T	76/77 (99%)	64 (84%)	12 (16%)	2	16
33	U	65/65 (100%)	60 (92%)	5 (8%)	13	43
34	V	74/78 (95%)	72 (97%)	2 (3%)	44	68
35	W	72/79 (91%)	68 (94%)	4 (6%)	21	53
36	X	94/96 (98%)	85 (90%)	9 (10%)	8	34
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%)	60	79
41	c	67/68 (98%)	64 (96%)	3 (4%)	27	57
43	e	54/55 (98%)	53 (98%)	1 (2%)	57	76
44	f	48/49 (98%)	46 (96%)	2 (4%)	30	59
45	g	59/62 (95%)	53 (90%)	6 (10%)	7	31
46	h	216/218 (99%)	199 (92%)	17 (8%)	12	42
47	i	47/48 (98%)	41 (87%)	6 (13%)	4	23
48	j	164/164 (100%)	157 (96%)	7 (4%)	29	58
49	k	47/49 (96%)	44 (94%)	3 (6%)	17	48
50	l	165/165 (100%)	151 (92%)	14 (8%)	10	40
51	m	38/38 (100%)	35 (92%)	3 (8%)	12	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	134 (90%)	14 (10%)	8	34
53	o	51/52 (98%)	46 (90%)	5 (10%)	8	33
54	p	136/138 (99%)	132 (97%)	4 (3%)	42	66
55	q	34/34 (100%)	32 (94%)	2 (6%)	19	51
56	r	114/114 (100%)	104 (91%)	10 (9%)	10	38
57	s	116/116 (100%)	110 (95%)	6 (5%)	23	55
58	t	104/104 (100%)	98 (94%)	6 (6%)	20	52
59	u	103/103 (100%)	97 (94%)	6 (6%)	20	52
60	v	109/109 (100%)	103 (94%)	6 (6%)	21	53
61	w	99/103 (96%)	91 (92%)	8 (8%)	11	41
62	x	86/87 (99%)	80 (93%)	6 (7%)	15	45
63	y	99/100 (99%)	95 (96%)	4 (4%)	31	60
64	z	89/90 (99%)	87 (98%)	2 (2%)	52	72
All	All	7791/8630 (90%)	7209 (92%)	582 (8%)	17	43

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 monosaccharides 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

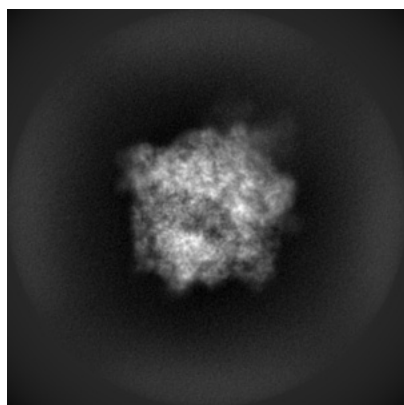
6 Map visualisation [i](#)

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

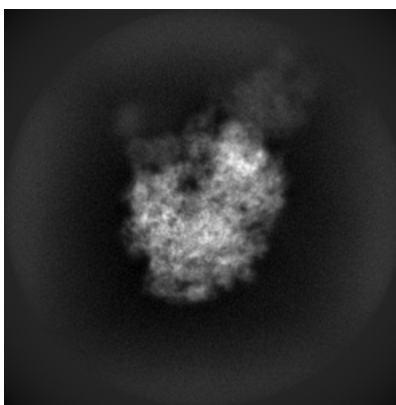
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

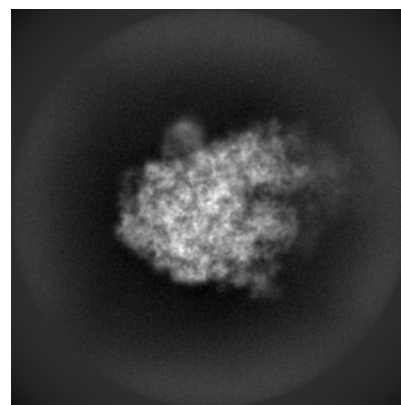
6.1.1 Primary map



X



Y

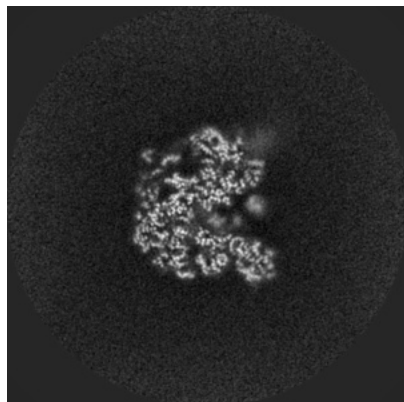


Z

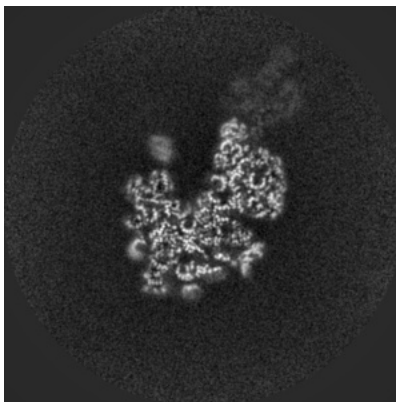
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

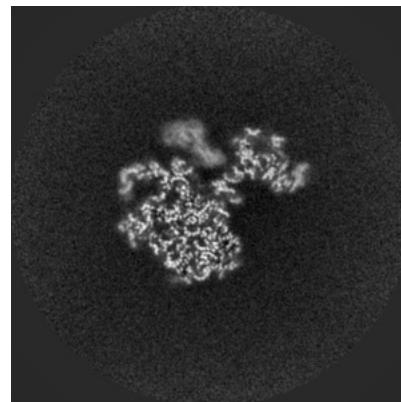
6.2.1 Primary map



X Index: 250



Y Index: 250

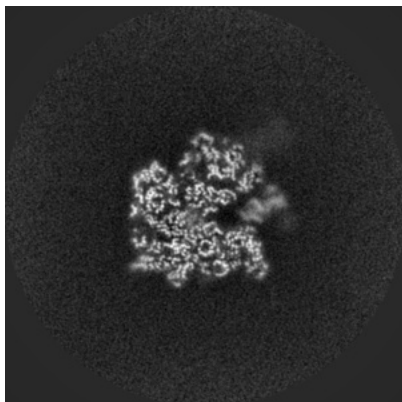


Z Index: 250

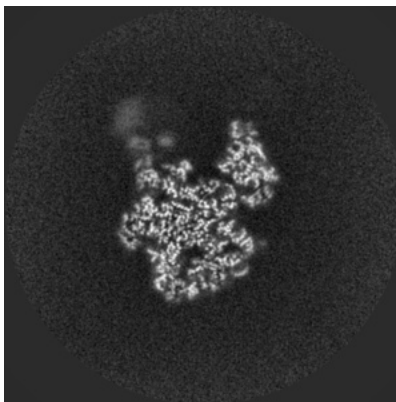
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

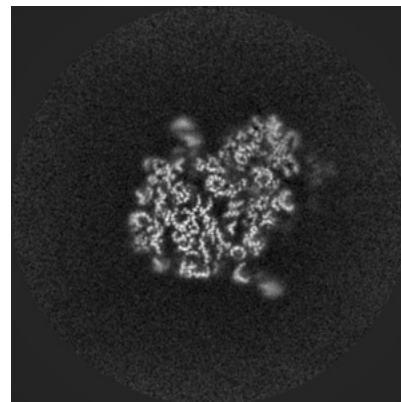
6.3.1 Primary map



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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

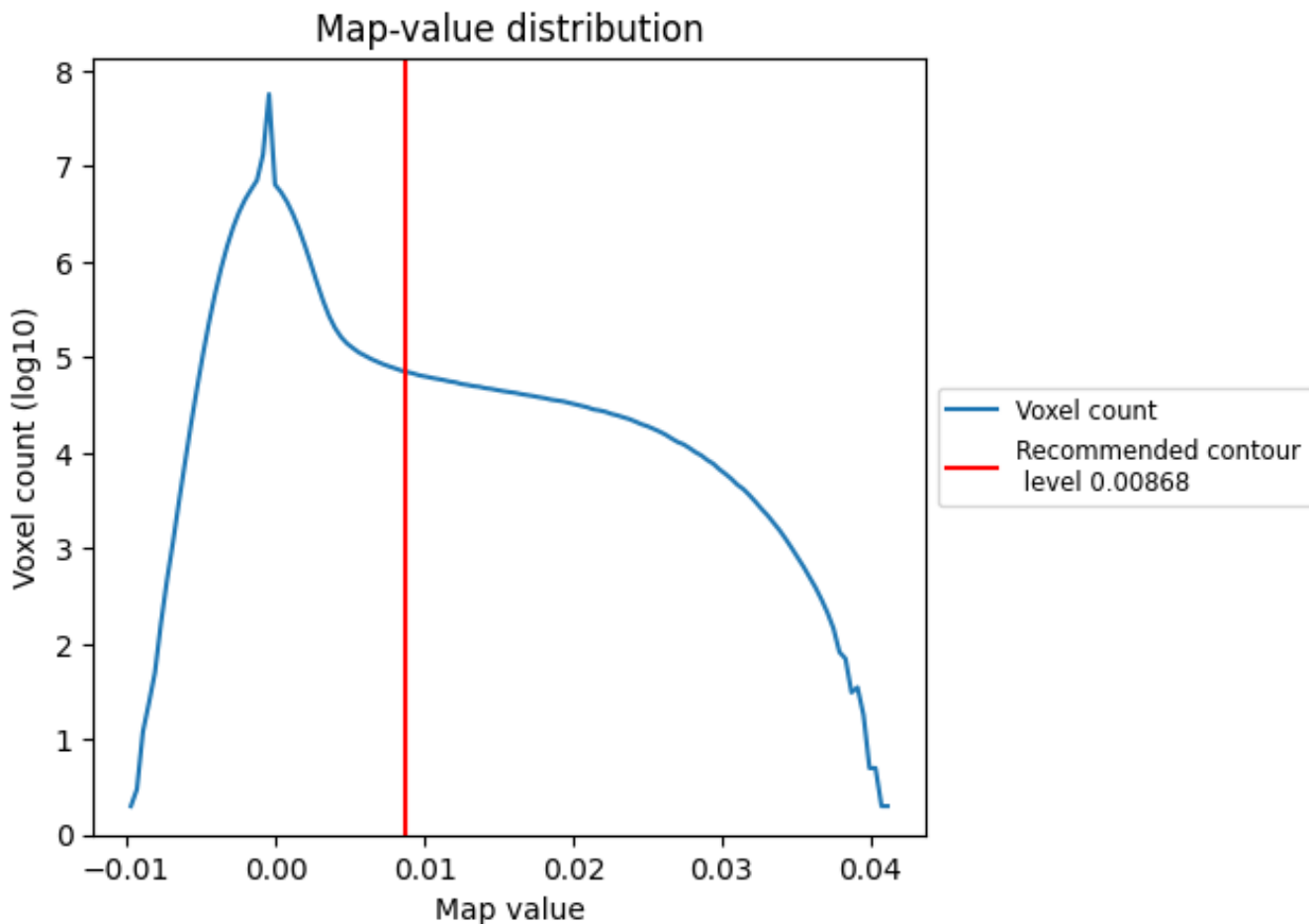
6.5 Mask visualisation

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

7 Map analysis [i](#)

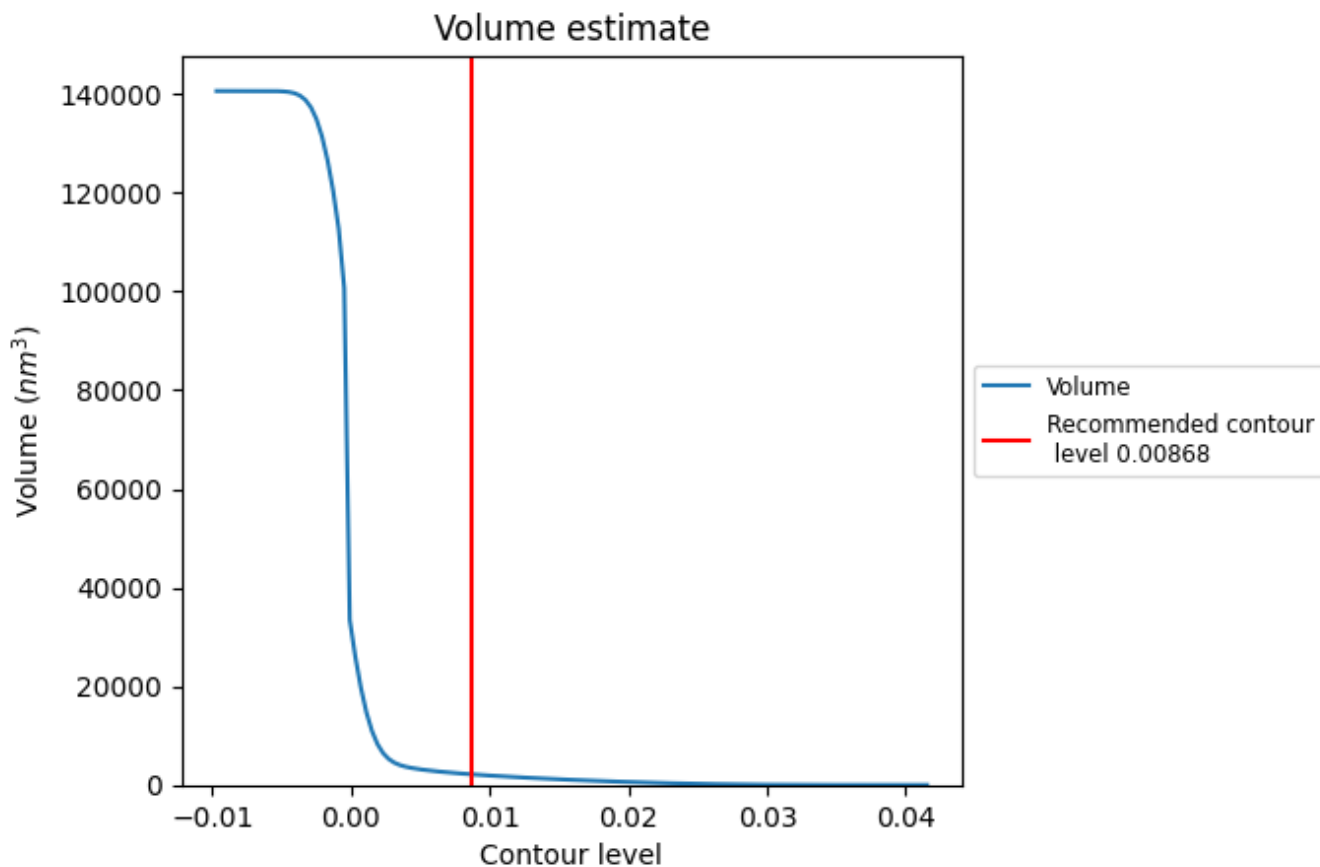
This section contains the results of statistical analysis of the map.

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.

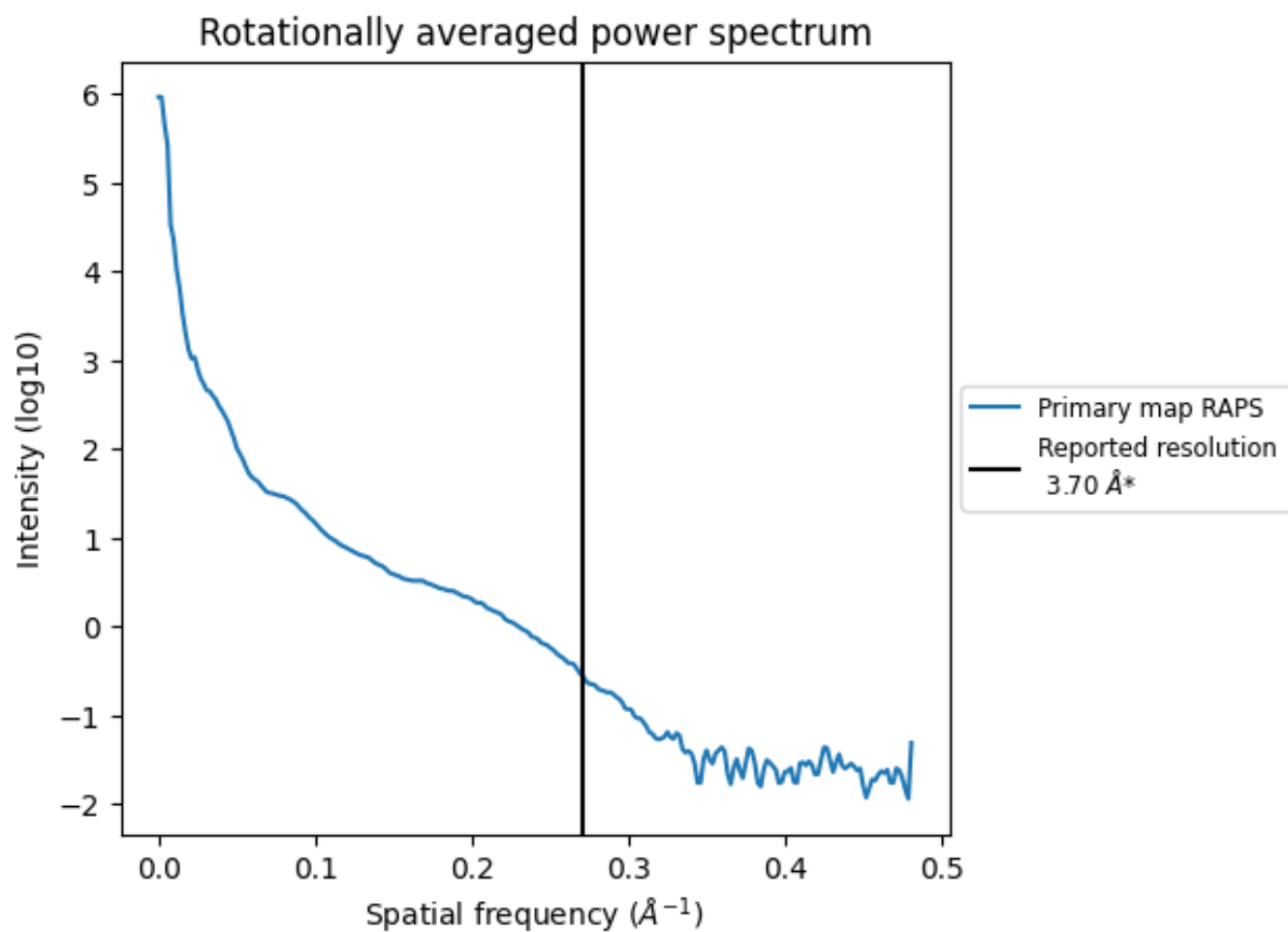
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2155 nm³; 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 [i](#)



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

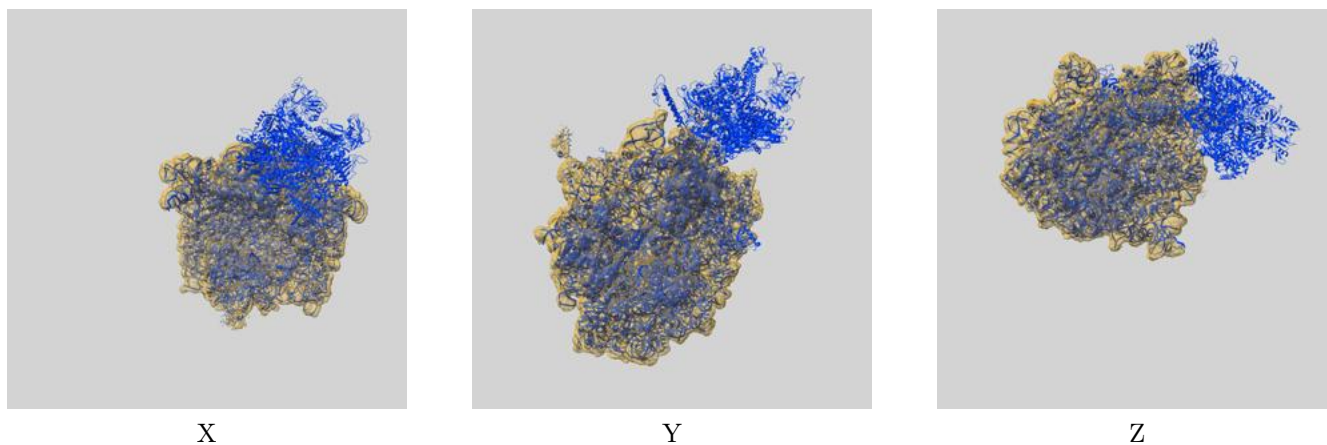
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

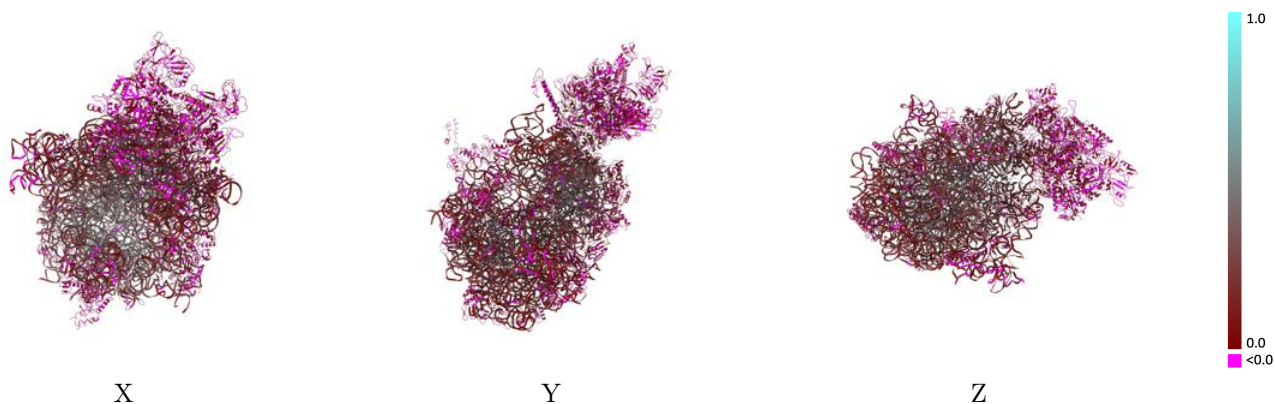
This section contains information regarding the fit between EMDB map EMD-21470 and PDB model 6VYS. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



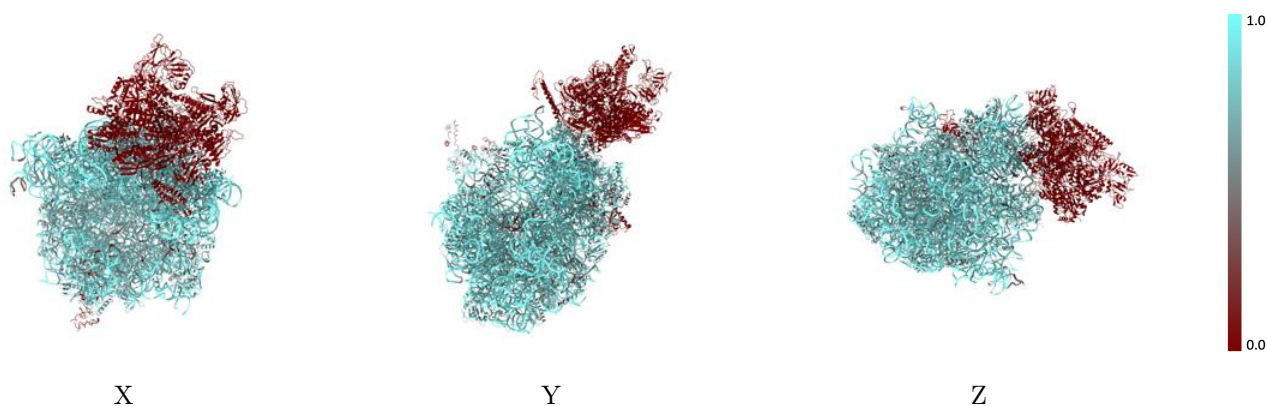
The images above show the 3D surface view of the map at the recommended contour level 0.00868 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



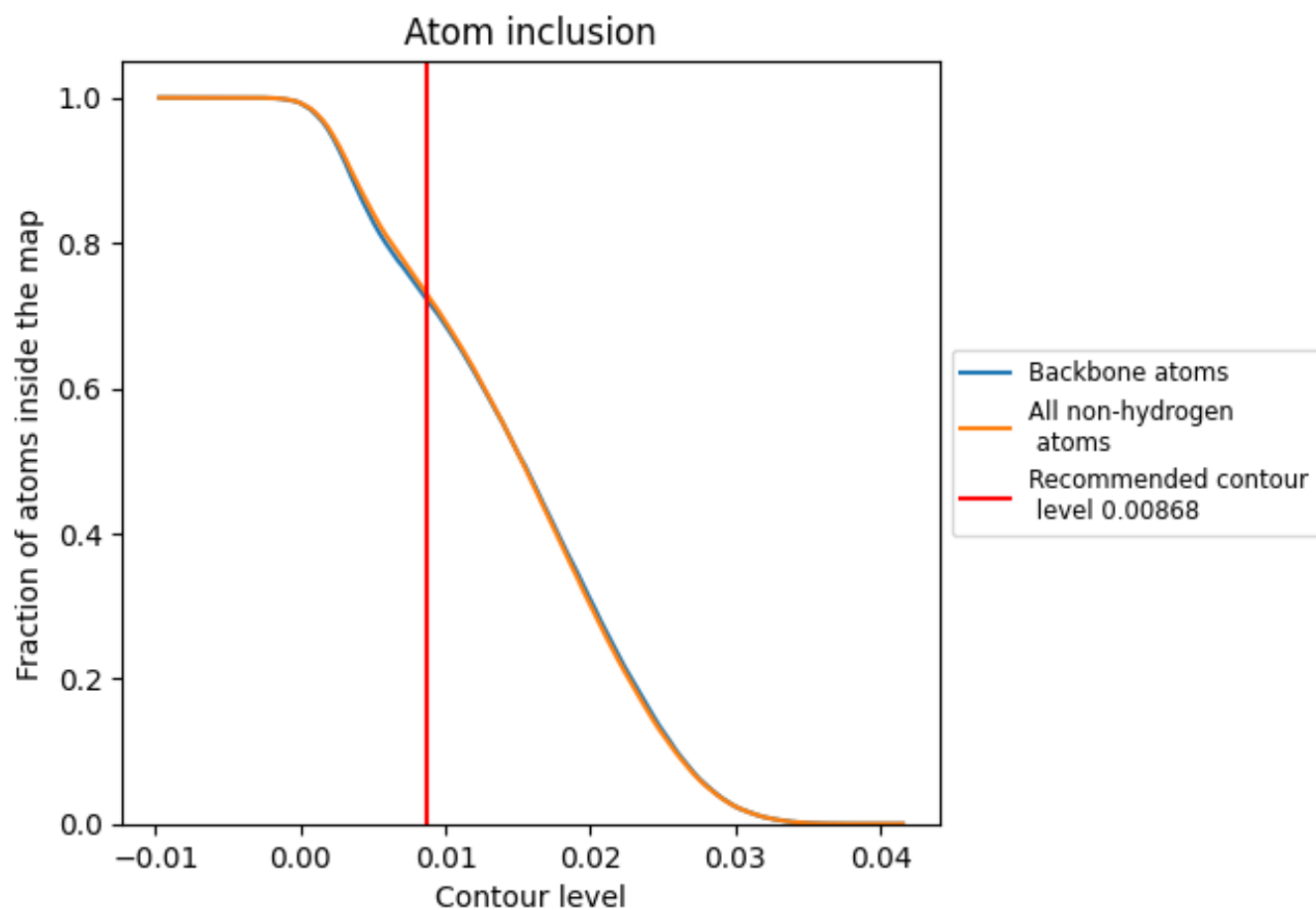
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.7316	 0.1950
0	 0.8143	 0.1990
1	 0.7811	 0.2550
2	 0.7000	 0.1110
3	 0.7655	 0.0900
4	 0.8103	 0.1990
5	 0.0000	 0.0130
6	 0.0185	 0.1500
7	 0.3071	 0.1010
9	 0.5585	 0.0400
A	 0.8901	 0.1870
AA	 0.0084	 0.0770
AB	 0.0000	 0.0340
AC	 0.0183	 0.1010
AD	 0.0000	 0.0460
AE	 0.0008	 0.0650
B	 0.6519	 0.0930
C	 0.7839	 0.1820
D	 0.9465	 0.2610
E	 0.7202	 0.0870
F	 0.7084	 0.2360
G	 0.7490	 0.1920
H	 0.1454	 0.0410
I	 0.7553	 0.2330
J	 0.7792	 0.1880
K	 0.8301	 0.3220
L	 0.7146	 0.1180
M	 0.7509	 0.1930
N	 0.8125	 0.2400
O	 0.8212	 0.1920
P	 0.7490	 0.1880
Q	 0.7691	 0.2140
R	 0.8287	 0.3250
S	 0.7933	 0.1770
T	 0.7797	 0.1690



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Chain	Atom inclusion	Q-score
U	 0.7368	 0.1070
V	 0.7785	 0.2040
W	 0.6275	 0.0470
X	 0.6820	 0.1050
Y	 0.4354	 0.0490
Z	 0.1762	 0.0610
a	 0.9342	 0.2370
b	 0.7898	 0.1940
c	 0.7388	 0.1720
d	 0.9288	 0.1880
e	 0.7485	 0.0770
f	 0.8096	 0.2460
g	 0.6967	 0.0790
h	 0.7386	 0.1500
i	 0.8107	 0.2560
j	 0.7952	 0.2150
k	 0.7033	 0.1200
l	 0.7296	 0.1640
m	 0.8282	 0.2680
n	 0.7174	 0.1030
o	 0.7434	 0.2070
p	 0.7692	 0.1100
q	 0.7979	 0.1930
r	 0.5712	 0.0620
s	 0.8145	 0.2330
t	 0.7318	 0.2060
u	 0.7803	 0.1890
v	 0.7812	 0.2590
w	 0.7930	 0.1840
x	 0.7520	 0.0520
y	 0.7421	 0.1430
z	 0.8414	 0.2700