



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:05 PM UTC

PDB ID : 6VU3 / pdb_00006vu3
EMDB ID : EMD-21386
Title : Cryo-EM structure of Escherichia coli transcription-translation complex A (TTC-A) containing mRNA with a 12 nt long spacer
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.
Deposited on : 2020-02-14
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

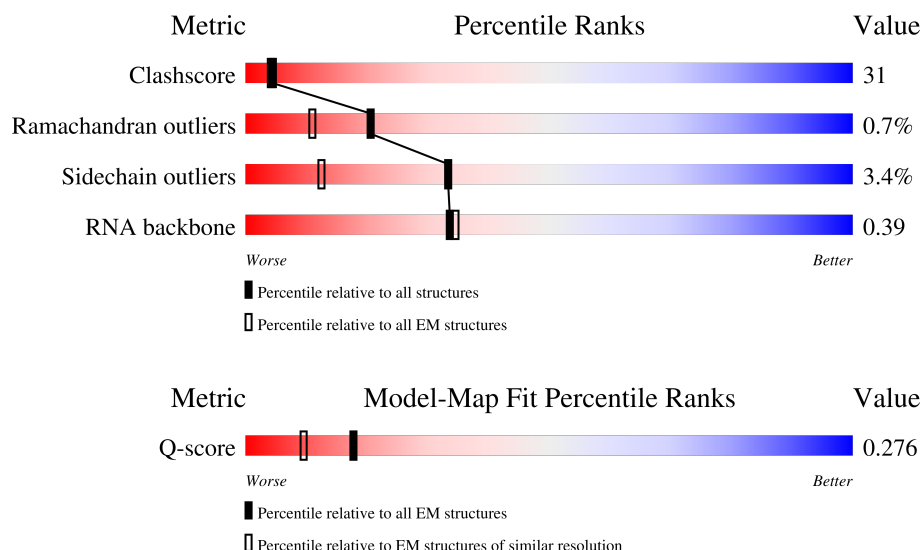
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 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.



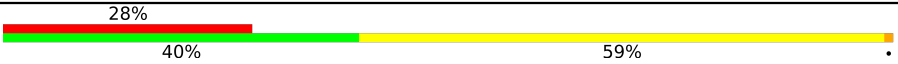
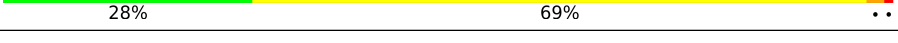
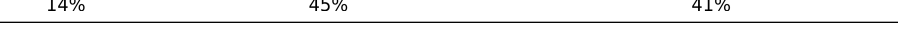
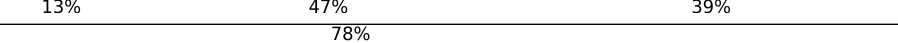
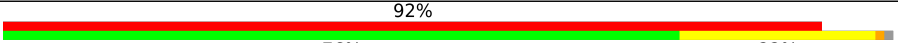
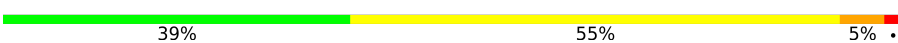
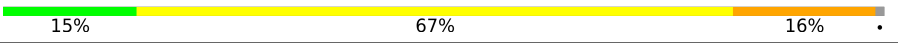
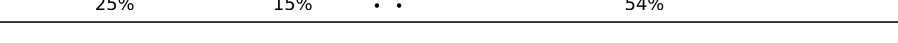
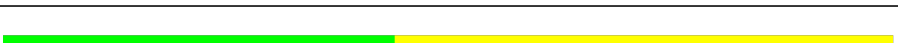
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	94	

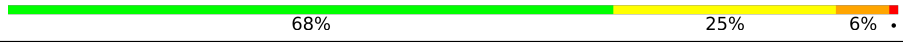
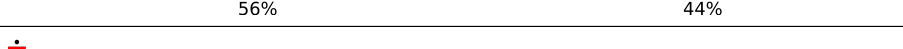
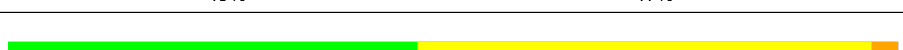
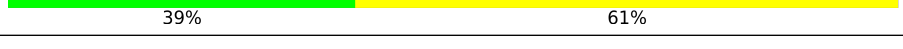
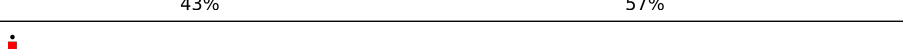
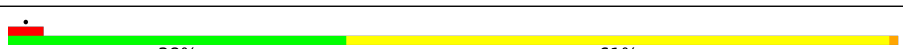
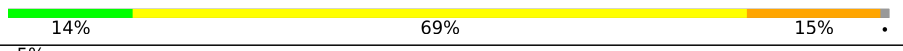
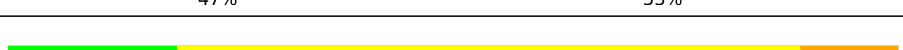
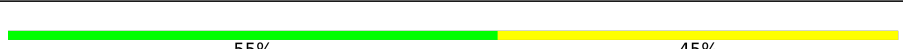
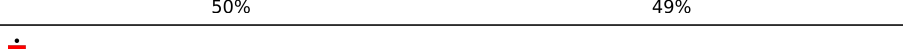
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Mol	Chain	Length	Quality of chain
4	3	103	
5	4	94	
6	5	36	
7	6	27	
8	7	29	
9	9	148	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	230	
13	AD	230	
14	AE	1407	
15	C	66	
16	D	1542	
17	E	86	
18	F	70	
19	G	225	
20	H	557	
21	I	208	
22	J	205	
23	K	156	
24	L	104	
25	M	151	
26	N	129	

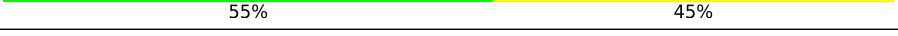
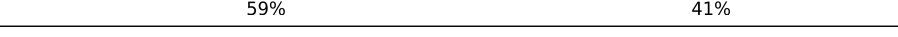
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Mol	Chain	Length	Quality of chain
27	O	127	
28	P	99	
29	Q	117	
30	R	124	
31	S	100	
32	T	88	
33	U	82	
34	V	80	
35	W	83	
36	X	116	
37	Y	141	
38	Z	30	
39	a	2904	
40	b	76	
41	c	77	
42	d	120	
43	e	62	
44	f	58	
45	g	66	
46	h	271	
47	i	56	
48	j	209	
49	k	52	
50	l	201	
51	m	46	

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Mol	Chain	Length	Quality of chain
52	n	177	 54%45%..
53	o	64	 36%61%.
54	p	175	 50%49%.
55	q	38	 45%55%
56	r	149	 55%45%
57	s	142	 53%47%
58	t	123	 50%50%
59	u	144	 62%38%
60	v	136	 55%45%
61	w	119	 31%69%
62	x	116	 59%41%
63	y	114	 49%51%
64	z	117	 52%47%.

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300609 atoms, of which 124724 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L21.

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

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

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

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

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

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

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

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

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

- Molecule 6 is a DNA chain called NT DNA.

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

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			848	259	306	89	167	27		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

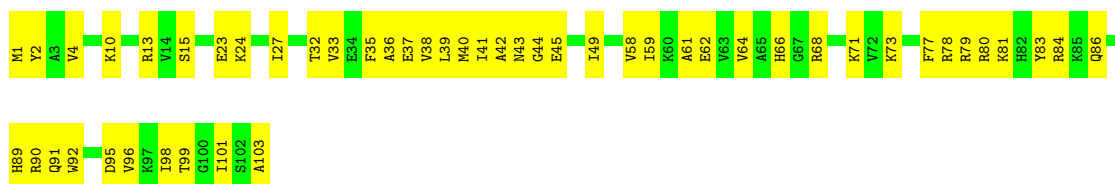
Mol	Chain	Residues	Atoms		AltConf
66	AA	2	Total	Zn	0
			2	2	

3 Residue-property plots

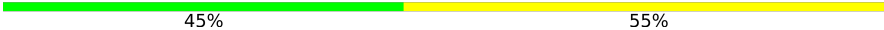
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

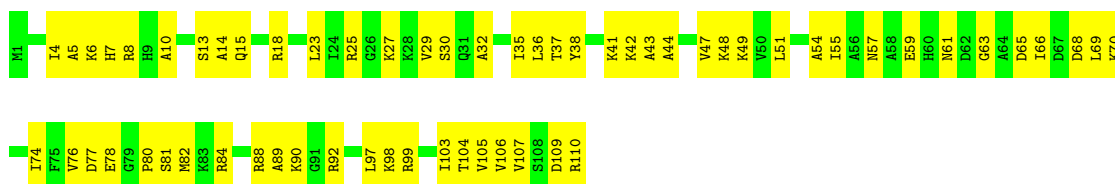
• Molecule 1: 50S ribosomal protein L21

Chain 0: 



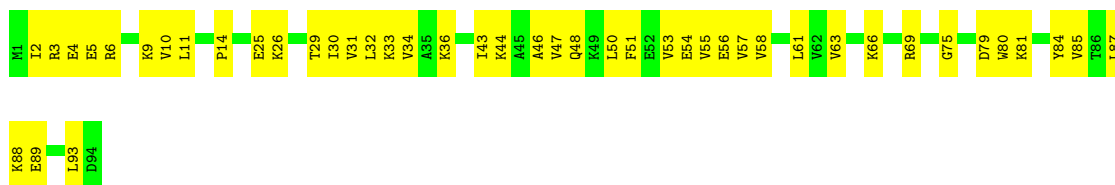
• Molecule 2: 50S ribosomal protein L22

Chain 1: 



• Molecule 3: 50S ribosomal protein L23

Chain 2: 



• Molecule 4: 50S ribosomal protein L24

Chain 3: 

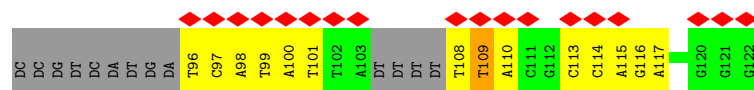
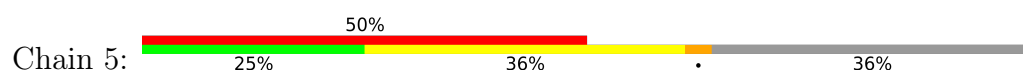




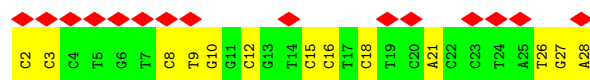
- Molecule 5: 50S ribosomal protein L25



- Molecule 6: NT DNA



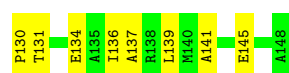
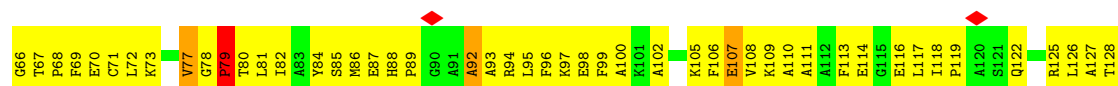
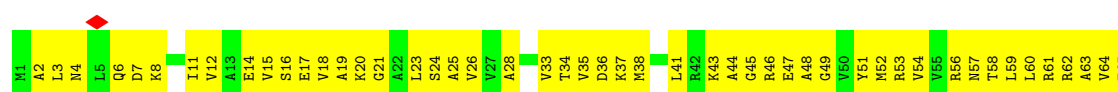
- Molecule 7: T DNA



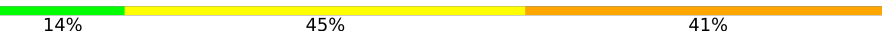
- Molecule 8: mRNA with 12 nt long spacer



- Molecule 9: 50S ribosomal protein L10

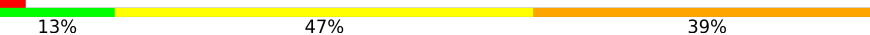


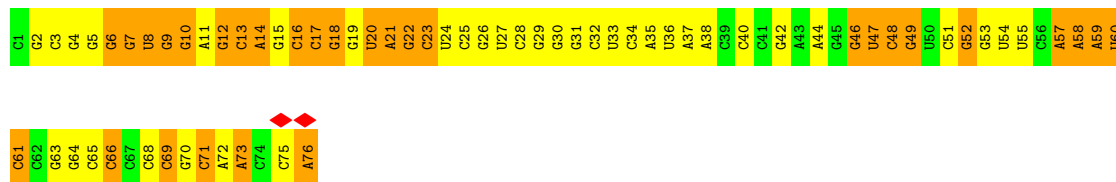
- Molecule 10: E-site and A-site tRNA (fMet)

Chain A: 



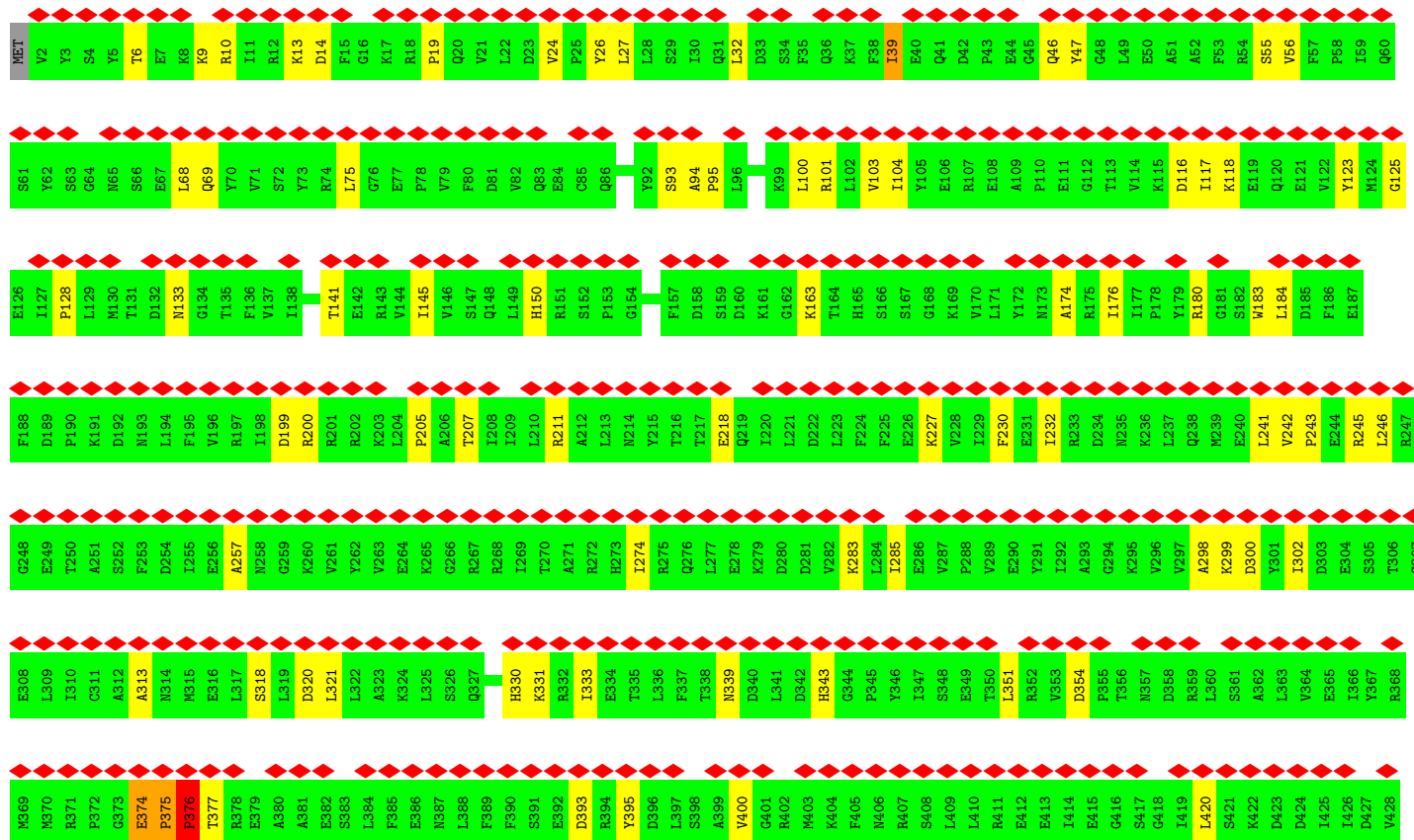
- Molecule 10: E-site and A-site tRNA (fMet)

Chain B: 

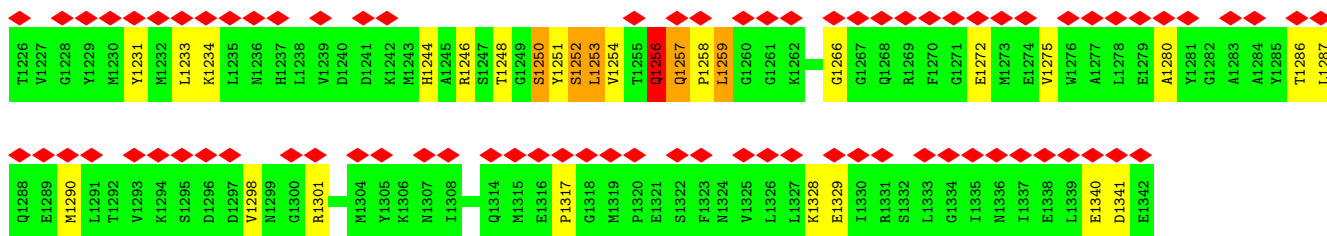


- Molecule 11: DNA-directed RNA polymerase subunit beta

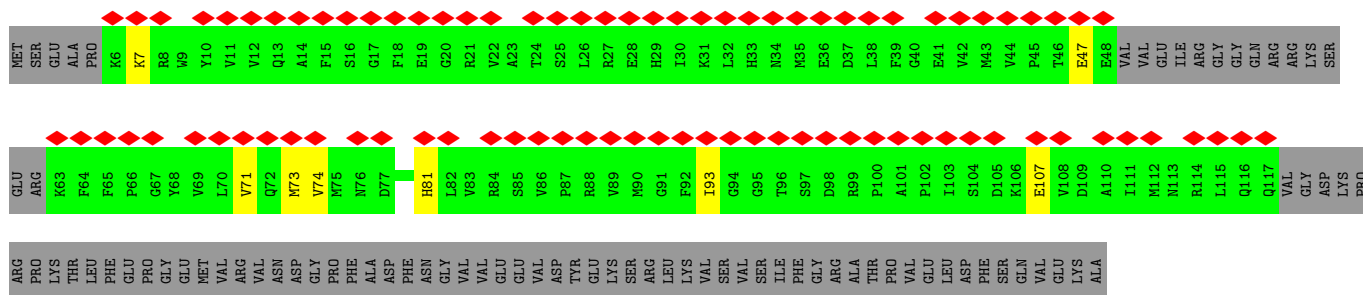
Chain AA: 



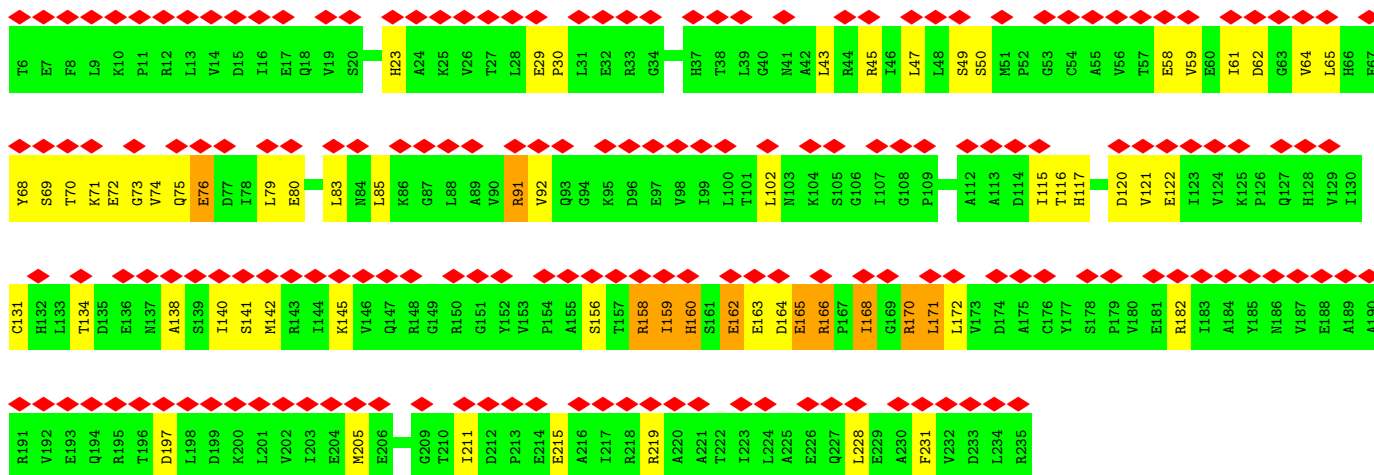
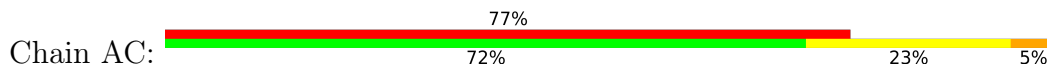
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P1104	S1105	R1106	M1107	N1108	I1109	G1110	Q1111	I1112	L1113	E1114	T1115	H1116	L1117	G1118	M1119	A1120	K1121	G1122	A1123	I1124	G1125	D1126	K1127	I1128	M1129	A1130	M1131	L1132	K1133	Q1134	Q1135	Q1136	E1137	V1138	A1139	K1140	L1141	R1142	E1143	F1144	T1145	S1207	G1208	Q1209	I1210	R1211	L1212	Y1213	D1214	G1215	R1216	T1217	Q1220	F1221	E1222	R1223	P1224	V1225	
D1041	L1042	A1043	P1044	G1045	V1046	L1047	K1048	I1049	V1050	K1051	V1052	Y1053	R1058	I1059	I1060	Q1061	P1062	G1063	D1064	K1065	M1066	A1067	G1068	R1069	H1070	G1071	N1072	K1073	G1074	V1075	I1076	S1077	K1078	I1079	M1080	P1081	I1082	E1083	D1084	M1085	P1086	Y1087	D1088	E1089	M1090	G1091	T1092	P1093	V1094	I1095	I1096	V1097	L1098	M1099	P1100	L1101	G1102	V1103	
A981	G982	G983	V984	E985	A986	E987	K988	L989	D990	K991	L992	P993	R994	D995	R996	W997	L998	E999	L1000	G1001	L1002	T1003	D1004	E1005	E1006	K1007	Q1008	N1009	Q1010	L1011	E1012	Q1013	L1014	A1015	E1016	Q1017	Y1018	D1019	E1020	L1021	K1022	H1023	E1024	F1025	E1026	K1027	K1028	L1029	E1030	A1031	K1032	R1033	K1034	K1035	L1036	T1037	Q1038	G1039	D1040
S917	L918	R919	V920	S925	G926	T927	V928	D930	V933	F934	T935	R936	D937	G938	V939	E940	K941	D942	R943	R944	A945	L946	E947	I948	E949	E950	R951	Q952	L953	K954	Q955	A956	K957	K958	D959	L960	S961	E962	E963	L964	Q965	L967	E968	A969	G970	L971	F972	S973	R974	L975	R976	A977	V978	L979	V980				
N956	V957	G958	E959	A960	A961	S963	K964	L965	D966	E967	S968	V971	Y972	L973	G974	A975	E976	V977	T978	G979	C980	D981	T982	L983	V984	C985	K986	V987	T988	P989	K990	G991	GLU	THR	GLN	LEU	THR	PRO	GLU	GLU	LYS	LEU	LEU	ARG	ALA	ILE	PHE	GLY	LYS	ALA	S911	D912	V913	K914					
L791	G792	E793	L794	A795	L796	N799	M800	R801	V802	A803	F804	M805	N808	G809	H810	N811	F812	E813	D814	S815	T816	L817	V818	S819	E820	R821	V822	E825	D826	R827	F828	T829	T830	L831	E835	L836	A837	C838	V839	S840	R841	D842	T843	K844	L845	G846	P847	E848	E849	T850	T851	A852	D853	L854	P855				
S730	R731	I732	V733	L734	K735	V736	N737	E738	D739	E740	S668	M741	Y742	P743	G744	E745	A746	G747	I748	D749	L750	Y751	N752	L753	T754	K755	Y756	S759	N760	Q761	N762	T763	C764	I765	T766	M768	P769	C770	V771	S772	L773	G774	E775	P776	V777	E778	R779	D780	V782	L783	A784	D785	G786	P787	T788	T789	D790		
F670	L671	E672	H673	D674	A676	N677	R678	A679	L680	M681	G682	A683	N684	M685	Q686	R687	Q688	A689	V690	P691	T692	L693	R694	A695	D696	K697	P698	L699	V700	G701	T702	G703	M704	E705	R706	A707	V708	A709	V710	D711	S712	G713	V714	T715	A716	S717	A718	K719	G720	G721	G722	V723	Q725	Y726	T727	D728	A729		
E610	E611	G612	N613	Y614	V615	I616	A617	Q618	A619	N620	S621	N622	L623	D624	E625	E626	G627	H628	F629	V630	E631	D632	L633	L634	T635	C636	R637	S638	K639	G640	E641	S642	S643	L644	F645	S646	R647	D648	Q649	V650	D651	V652	M653	D654	V655	T657	Q658	Q659	V660	V661	S662	V663	G664	A665	S666	L667	I668	P669	
V550	H551	P552	H554	Y555	G556	R557	V558	C559	P560	I561	E562	T563	P564	E565	G566	P567	N568	I569	G570	L571	I572	N573	S574	L575	S576	V577	Y578	A579	Q580	T581	N582	E583	Y584	G585	F586	L587	E588	T589	P590	Y591	R592	K593	V594	T595	D596	G597	V598	T599	D600	E601	E602	I603	H604	Y605	L606	S607	I608	I609	
P489	Q490	D491	M492	I493	M494	A495	R496	P497	V498	S499	A500	A501	V502	K503	E504	F505	F506	G507	S508	S509	Q510	L511	S512	Q513	F514	M515	D516	Q517	N518	N519	P520	L521	S522	E523	I524	T525	H526	K527	R528	R529	I530	S531	A532	L533	G536	G537	L538	T539	R540	E541	R542	A543	G544	F545	E546	V547	D549		
M429	K430	K431	L432	I433	D434	I435	R436	V437	G438	K439	G440	E441	V442	D443	D444	I445	D446	H447	L448	G449	M450	R451	R452	I453	R454	S455	V456	G457	E458	M459	A460	E461	N462	Q463	F464	R465	V466	L468	V469	R470	V471	E472	R473	A474	V475	K476	E477	L478	L479	S480	L481	G482	D483	L484	D485	T486	R487	M488	



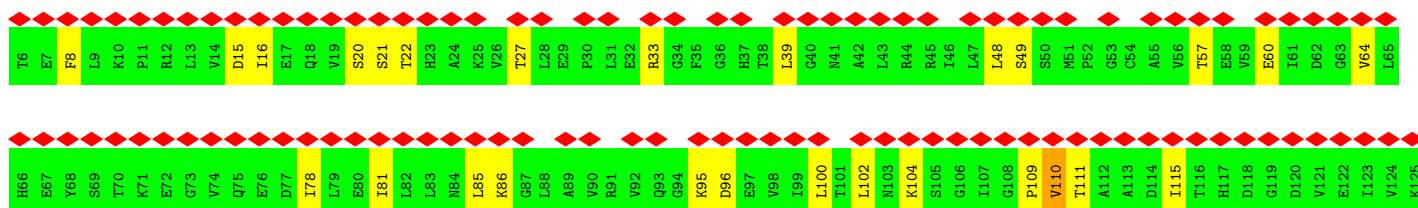
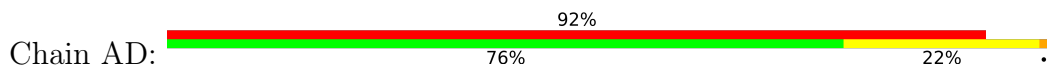
• Molecule 12: Transcription termination/antitermination protein NusG

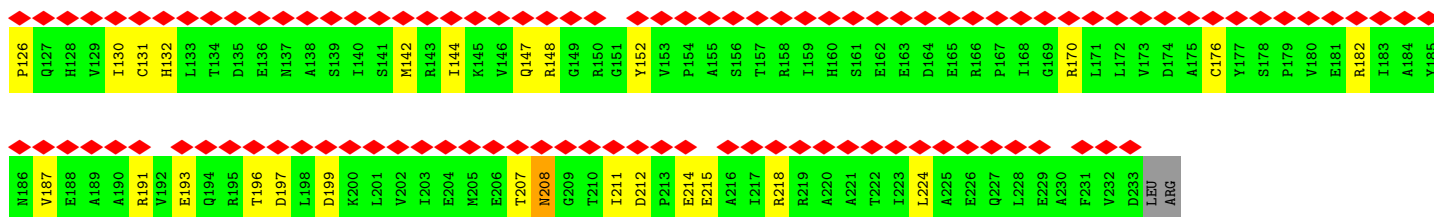


• Molecule 13: DNA-directed RNA polymerase subunit alpha

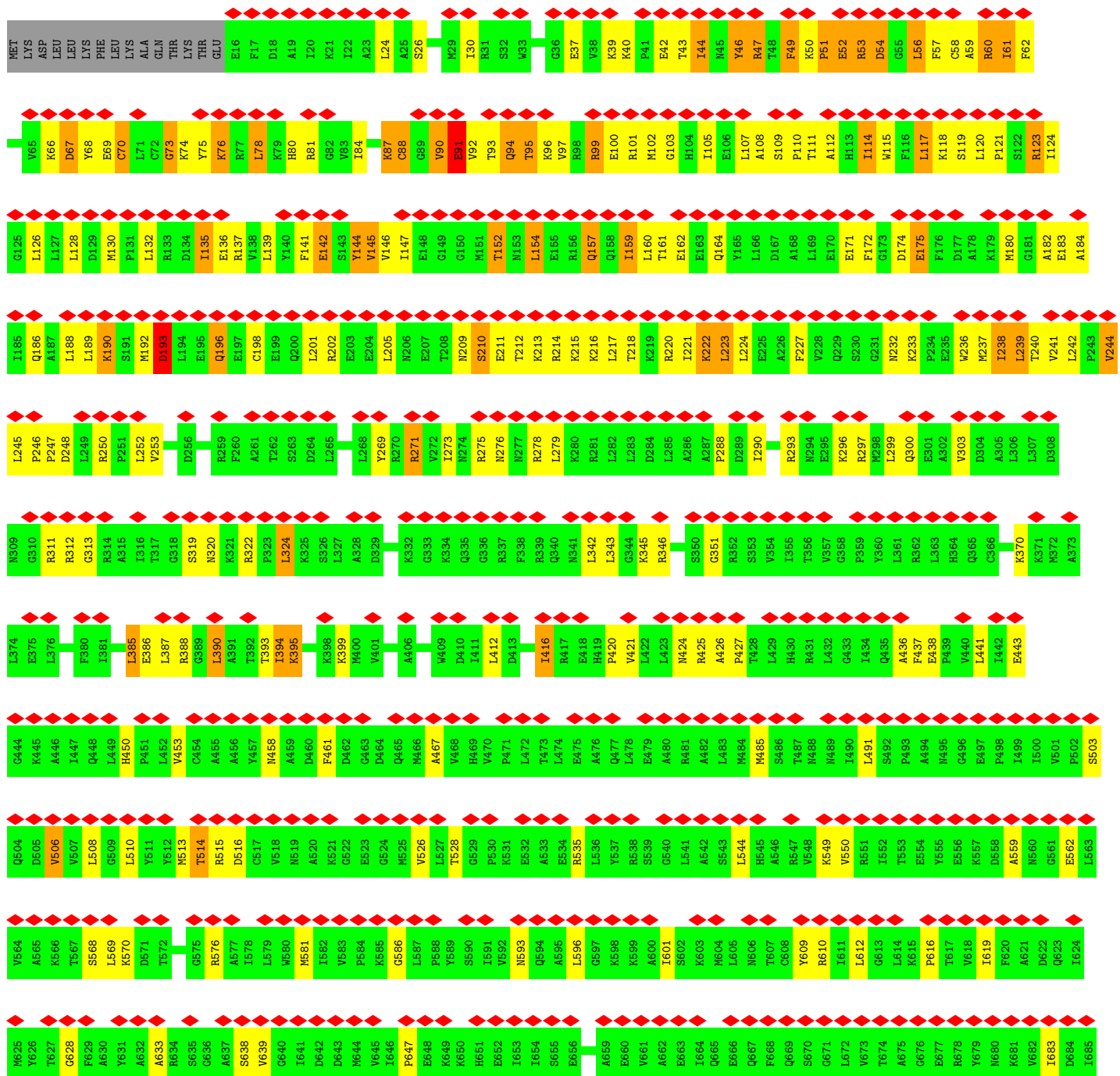
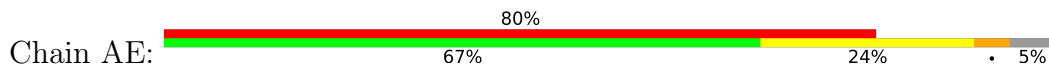


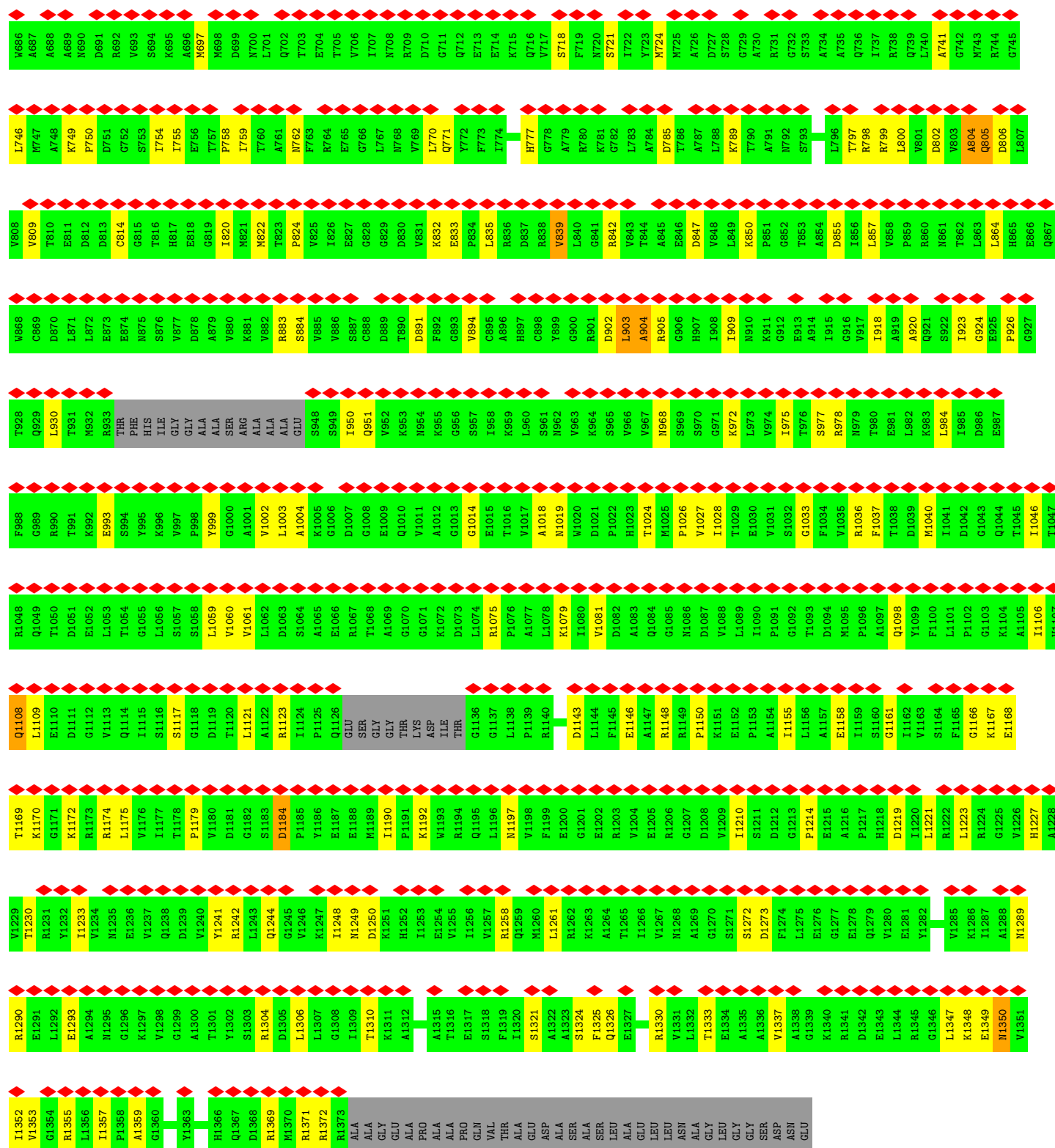
• Molecule 13: DNA-directed RNA polymerase subunit alpha

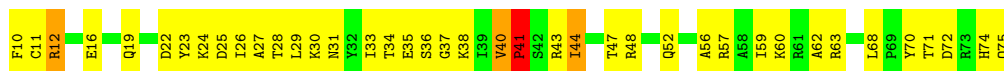




• Molecule 14: DNA-directed RNA polymerase subunit beta'

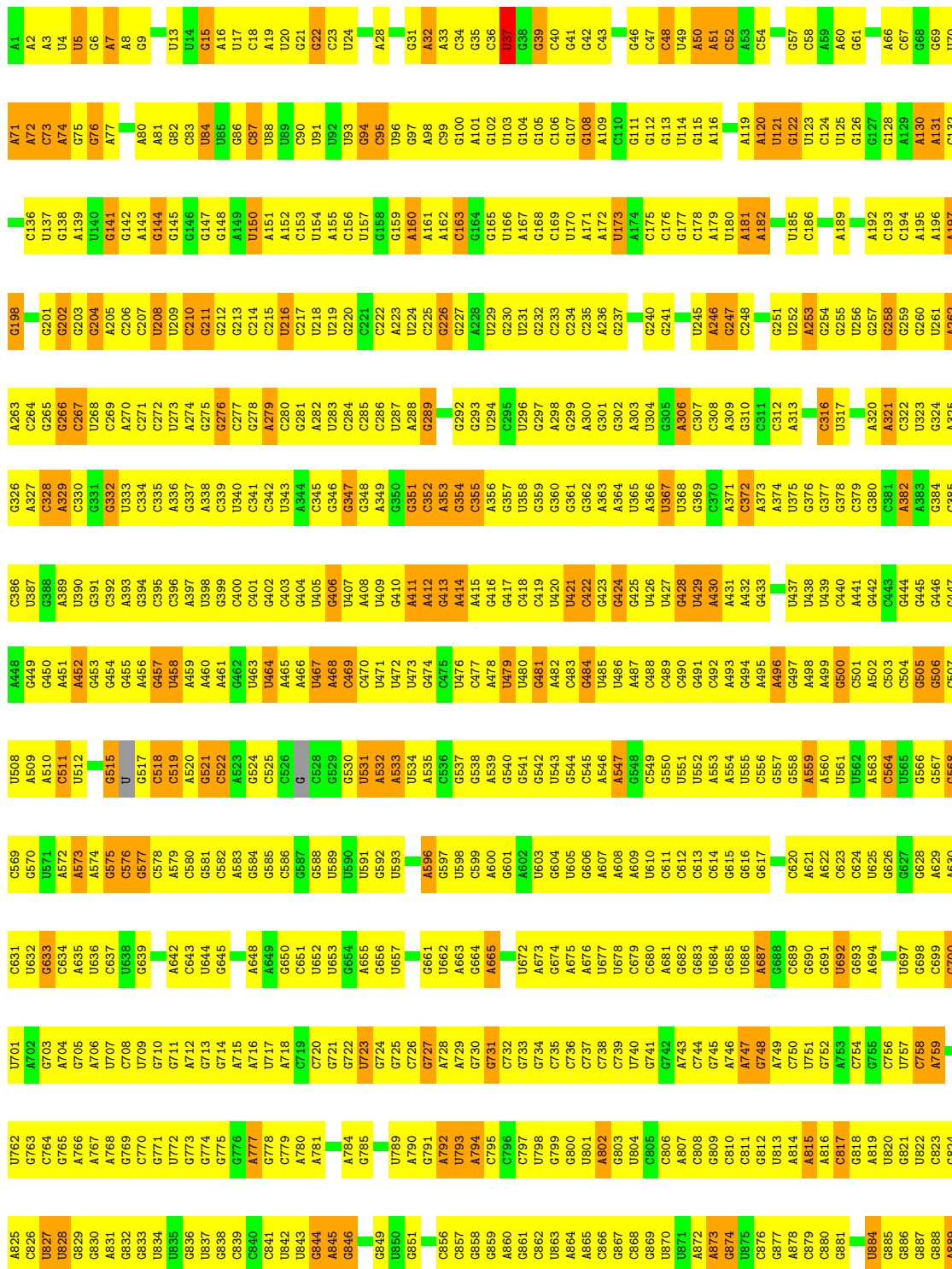


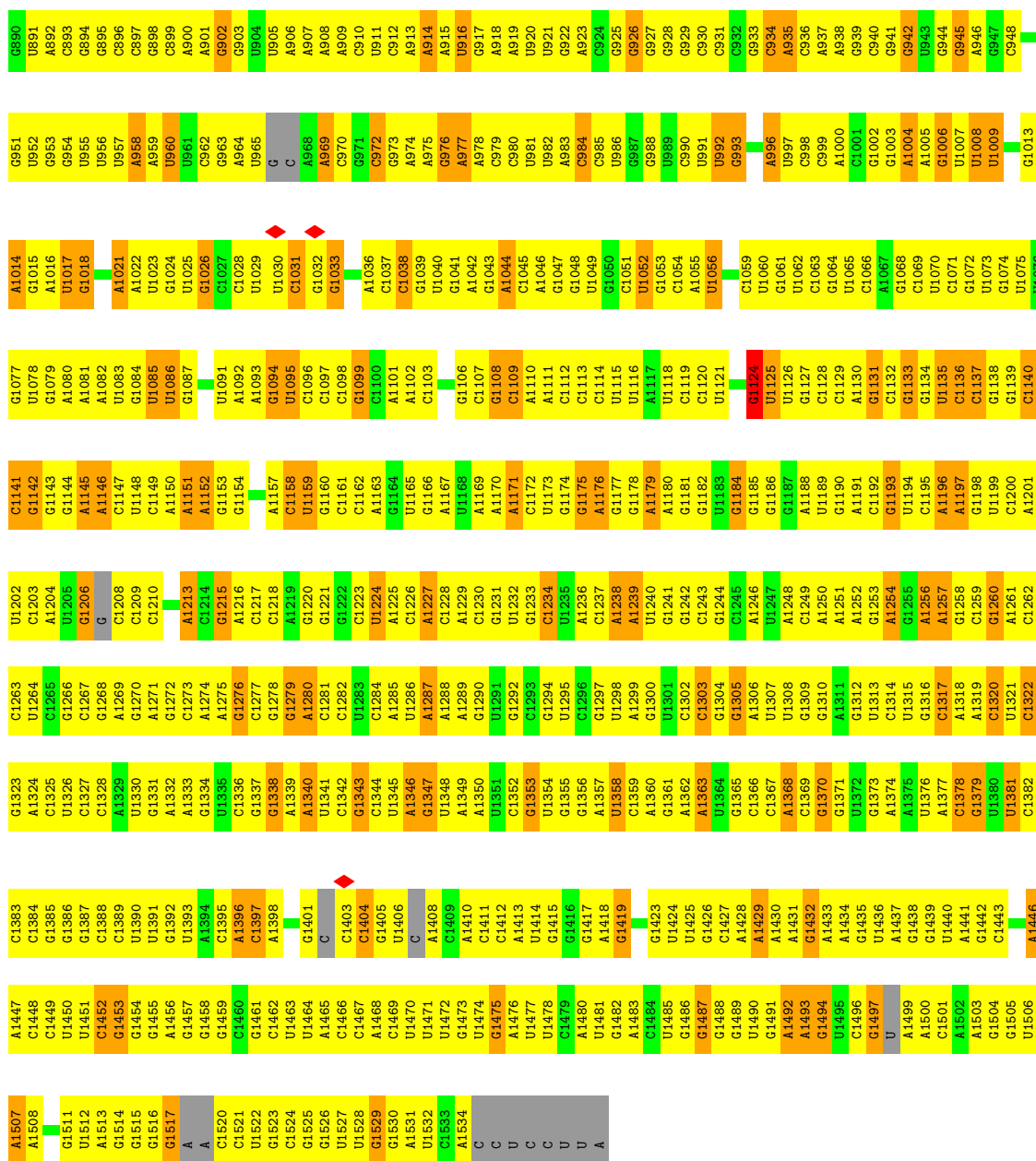




• Molecule 16: 16S rRNA

Chain D: 15% 67% 16%





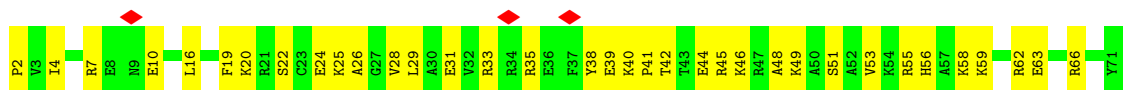
• Molecule 17: 30S ribosomal protein S20

Chain E:



• Molecule 18: 30S ribosomal protein S21

Chain F:



Chain G:

48%

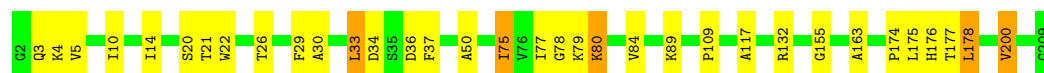
51%

Nodes in Chain G (48 nodes):

- T3, V4, S5, M6, R7, D8, M9, L10, K11, A12, G13, V14, H15, Q19, R21, Y22, W23, N24, P25, K28, I31, F32, R35, N36, K37, V38, H39, I40, I41, M42, L43, V47, P48, E56, L57, N58, K59, I60, A61, S62, G65, V70, G71, T72, K73, R74, D82, L85, S86, C87, D88, Q89, F90, F91, V92, A93, H94, R95, V96, L97, G98, G99, M100, T102, M103, W104, K105, T106, V107, R108, I111, K112, R113, L114, K115, D116, L117, Q120, D123, G124, T125, F126, K128, L129, T130, K131, K132, E133, A134, L135, M136, R137, L141, L144, E145, G149, G150, I151, K152, D153, M154.

[illegible]

Chain I: 84% 14%



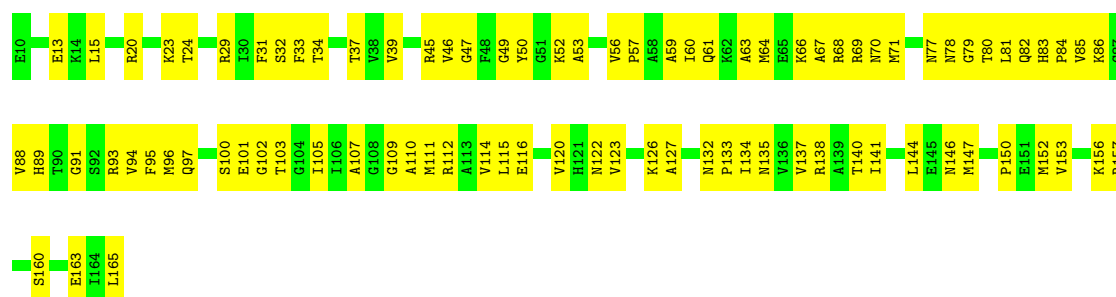
- Molecule 22: 30S ribosomal protein S4

Chain J: 84% 15% .



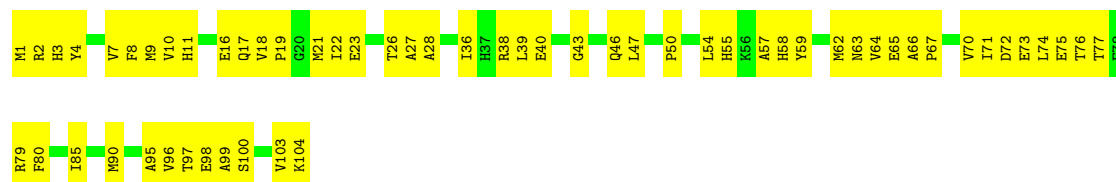
- Molecule 23: 30S ribosomal protein S5

Chain K: 44% 56%



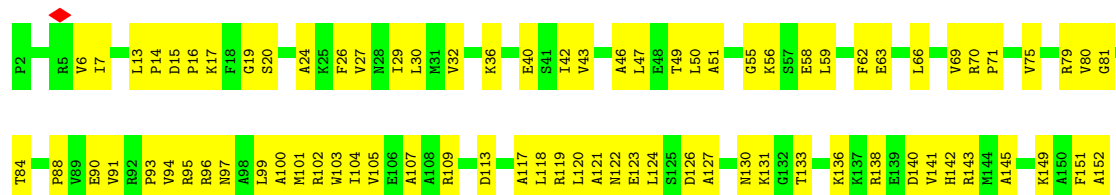
- Molecule 24: 30S ribosomal protein S6

Chain L: 44% 56%



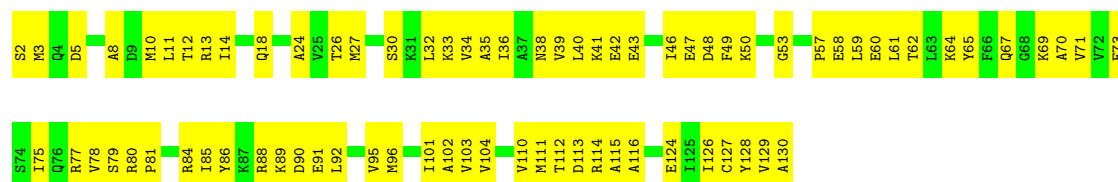
- Molecule 25: 30S ribosomal protein S7

Chain M: 47% 53%

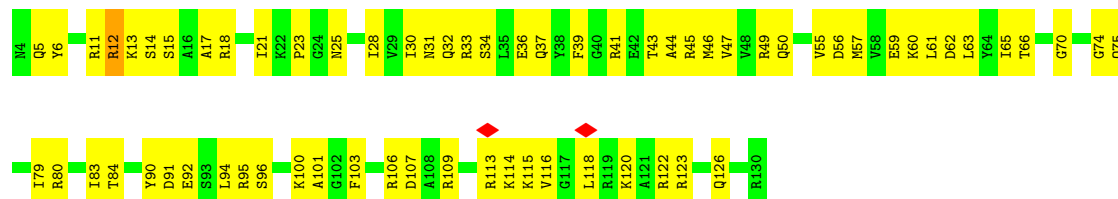


- Molecule 26: 30S ribosomal protein S8

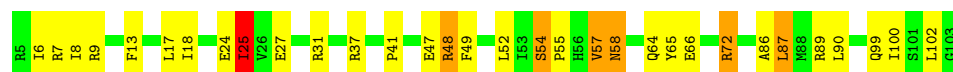
Chain N: 40% 60%



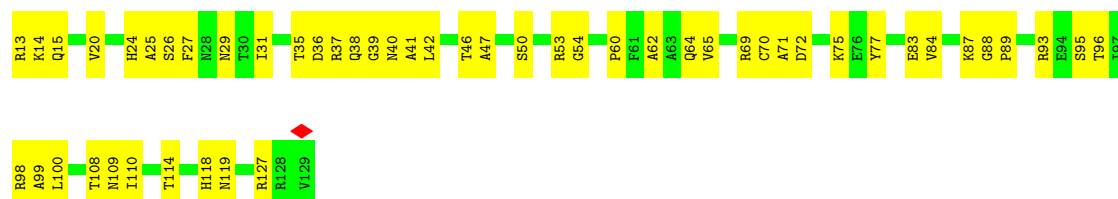
- Molecule 27: 30S ribosomal protein S9



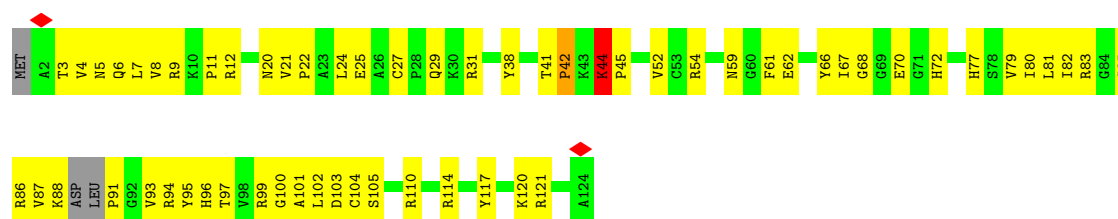
- Molecule 28: 30S ribosomal protein S10



- Molecule 29: 30S ribosomal protein S11

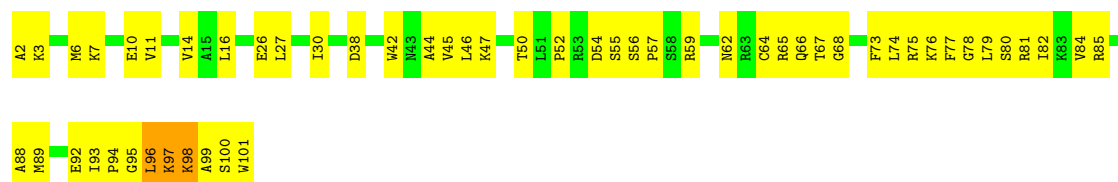


- Molecule 30: 30S ribosomal protein S12



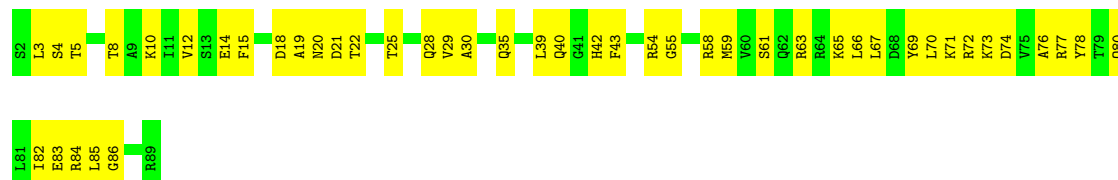
- Molecule 31: 30S ribosomal protein S14





- Molecule 32: 30S ribosomal protein S15

Chain T: 48% 52%



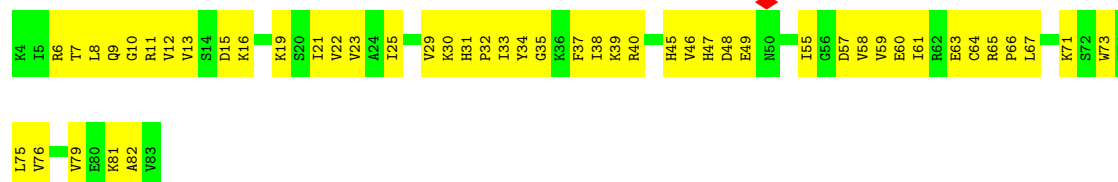
- Molecule 33: 30S ribosomal protein S16

Chain U: 54% 45%



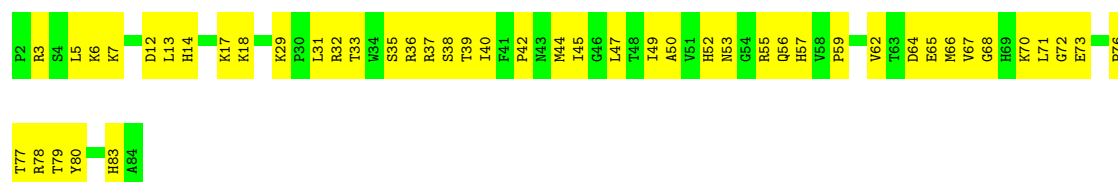
- Molecule 34: 30S ribosomal protein S17

Chain V: 39% 61%



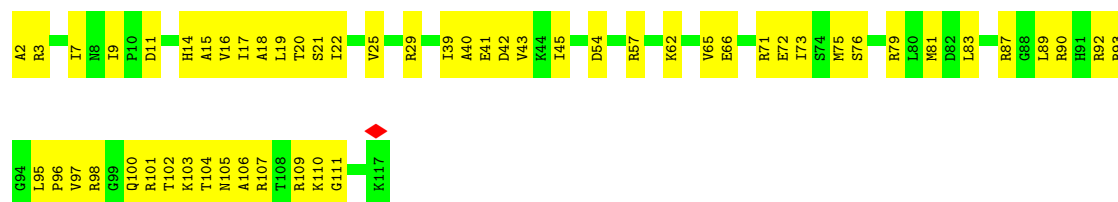
- Molecule 35: 30S ribosomal protein S19

Chain W: 43% 57%

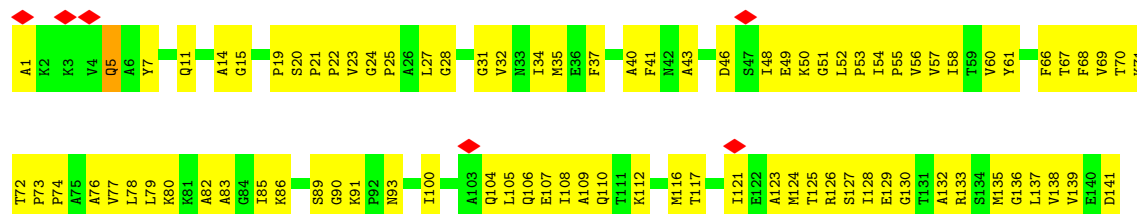


- Molecule 36: 30S ribosomal protein S13

Chain X: 53% 47%



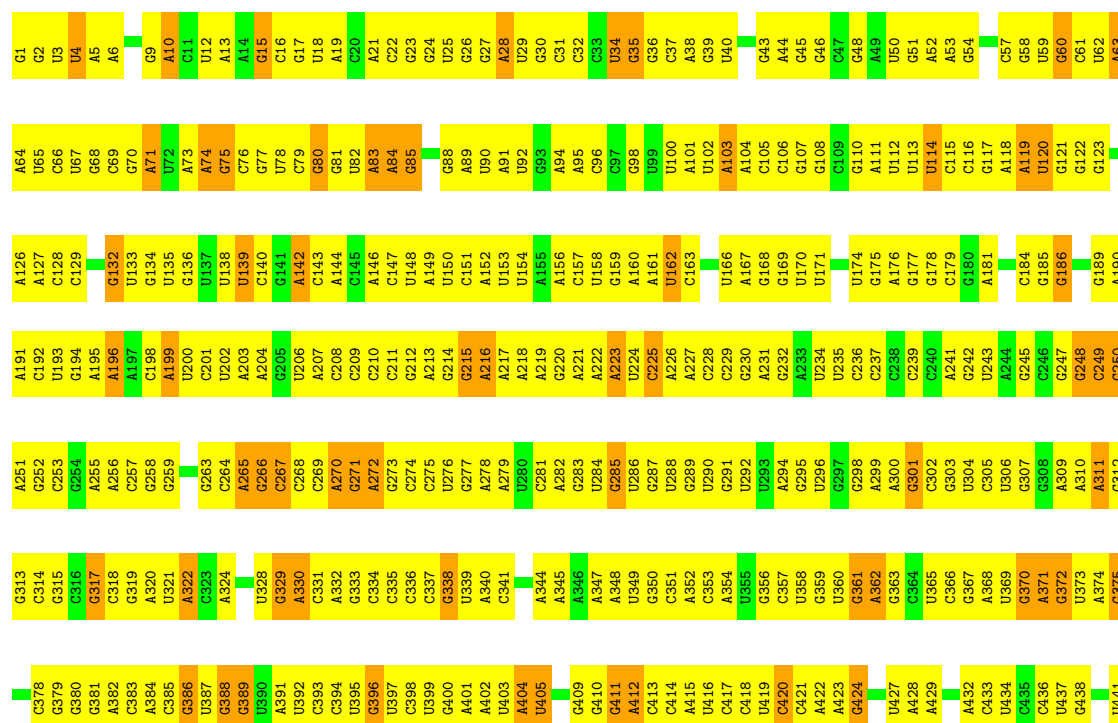
• Molecule 37: 50S ribosomal protein L11



• Molecule 38: 50S ribosomal protein L7/L12

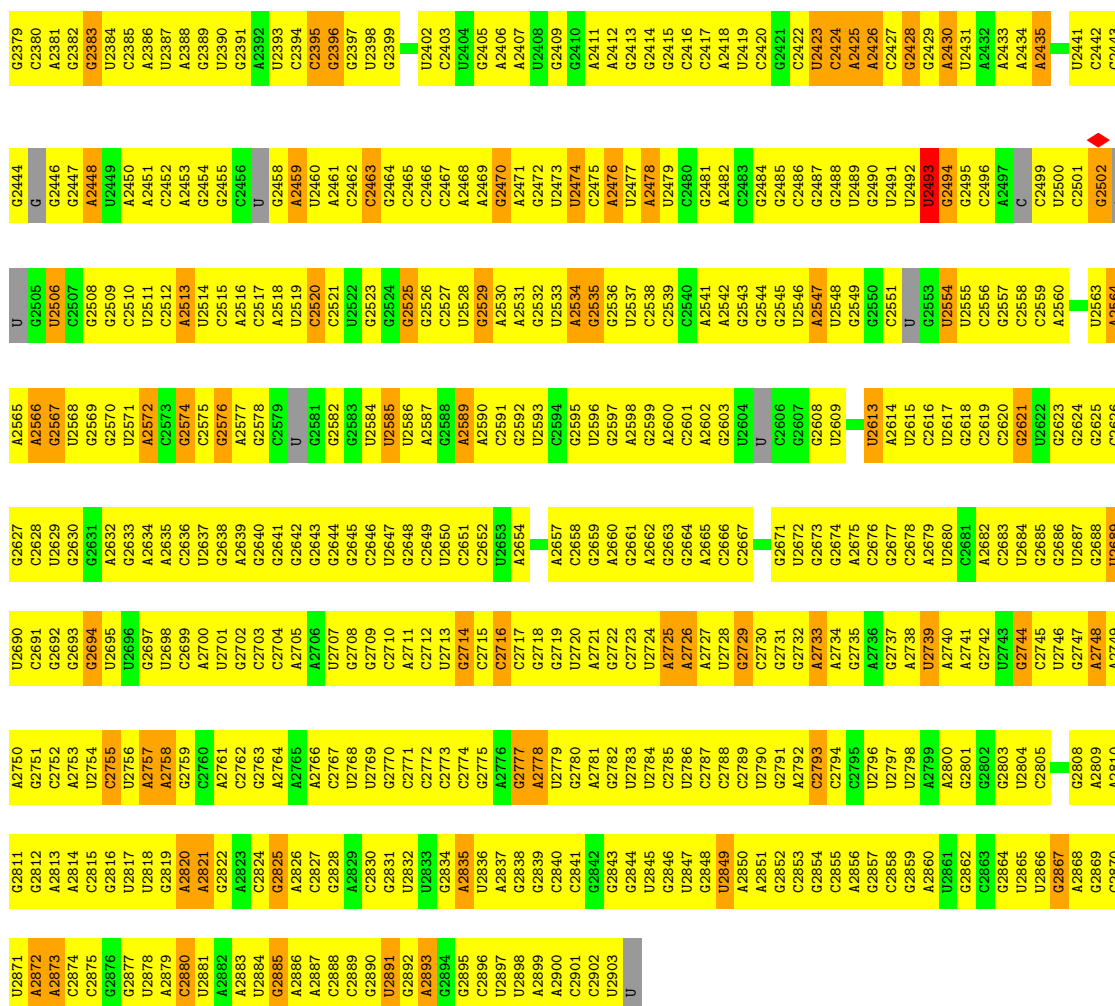


• Molecule 39: 23S rRNA

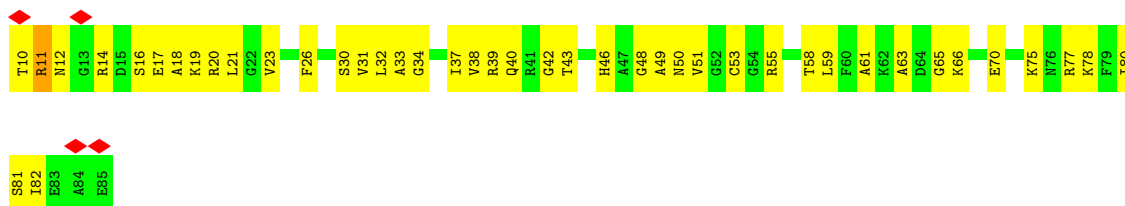


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G2341	G2280	G2156	U2092	G2026	A1966	G1904	C1843	U1782	G1719	A1654	C1592	G1530	C1461
C2342	A2281	G2157	G2093	G2027	C1967	C1905	C1844	U1783	U1720	A1655	A1593	C1531	C1462
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C2344	C2283	G2159	A2095	G2029	A1969	G1907	G1846	A1785	G1722	U1657	C1595	C1533	G1464
C2345	A2284	C2160	C2096	A	A1970	G1910	A1847	A1786	G1723	U1658	A1596	U1534	C1471
A2346	C2285	G2161	U2097	A2031	U1971	U	A1848	A1787	G1726	G1660	A1597	A1535	U1466
C2347	G2286	G2162	U2098	G2032	G1972	C1912	G1849	C1788	C1727	G1661	A1598	U1467	
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G2350	G2289	A2101	A2101	C2036	U1976	C1914	U1852	A1791	U1729	G1664	A1602	G1540	
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	G2292	U2105	U2105	U2039	U1979	A1918	U1856	C1795	G1732	G1667	C1605	A1544	U1474
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A2358	U2298	A2176	U2109	C2045	G1984	U1923	G1861	C1800	G1738	A1672	A1610	A1549	G1479
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C2362	C2302	U2113	U2113	G2048	G1988	A1927	U1865	C1804	U1742	A1676	A1614	A1553	
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A2365	U2244	A2183	G2116	A2051	U1991	G1930	C1868	A1808	U1680	A1679	A	C1556	G1492
C2366	U2245	A2184	C2117	A2052	U1992	U1931	G1869	A1809	A1746		C1617	C1557	C1493
G2367	G2246	U2185	U2118		G1993	A1932	C1870	A1810	U1747	G1681	G1619		A1494
C2368	A2247	G2186	G2121	C2055	U1994	G1933	C1871	U1811	U1748	G1682	U1620	G1560	A1495
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G2370	A2249	U2188	G2057	G2057	U1997	U1937	G1873	G1813	G1750	G1684	G1622	U1562	U1497
C2371	G2250	U2189	C1996		C1998	A1937		G1814	U1751	G1623	G1623	U1563	C1498
U2372	G	G2123	A1997	A2060	U1998	A1938		A1815	C1752	U1688	G1624	C1564	C1499
C2373	G2124	G2124	C1998	G2061	C1999	U	A1876	C1816	G1753	A1689	C1625	C1565	G1500
U2374	G2125	G2125	C1999	A2062	C1999	U1940	A1877	G1817	A1754	A1690	G1626	A1566	G1501
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G2376	G2127	G2127	C2001	C2064	C2001	C1942	G1879	G1755		U1692		G1568	A1503
A2377	G2128	G2128	G2002	C2065	G2002		U1880	A1819	G1756				
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• Molecule 40: 50S ribosomal protein L27

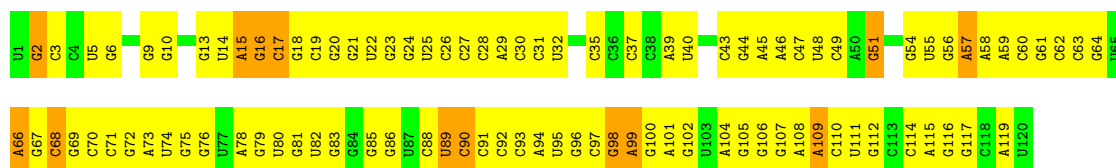


• Molecule 41: 50S ribosomal protein L28



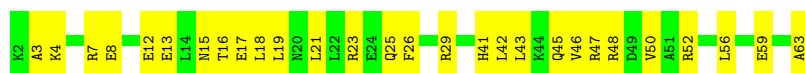
• Molecule 42: 5S rRNA





- Molecule 43: 50S ribosomal protein L29

Chain e: 55% 45%



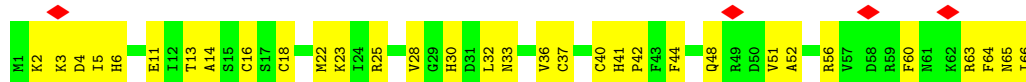
- Molecule 44: 50S ribosomal protein L30

Chain f: 41% 59%



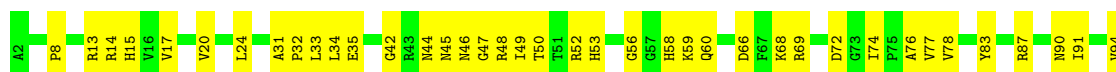
- Molecule 45: 50S ribosomal protein L31

Chain g: 6% 52% 48%



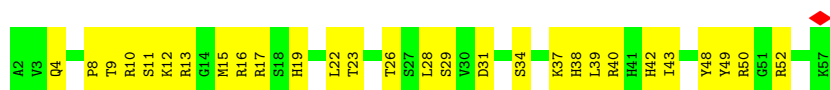
- Molecule 46: 50S ribosomal protein L2

Chain h: 50% 49%



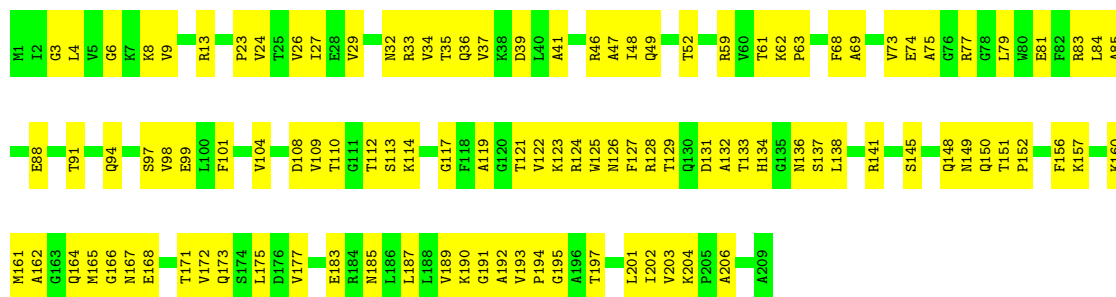
- Molecule 47: 50S ribosomal protein L32

Chain i: 50% 50%



- Molecule 48: 50S ribosomal protein L3

Chain j: 48% 52%



- Molecule 49: 50S ribosomal protein L33

Chain k: 40% 60%



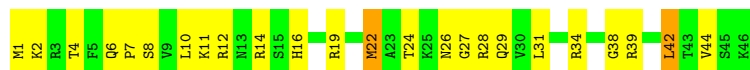
- Molecule 50: 50S ribosomal protein L4

Chain l: 45% 55%



- Molecule 51: 50S ribosomal protein L34

Chain m: 48% 48%

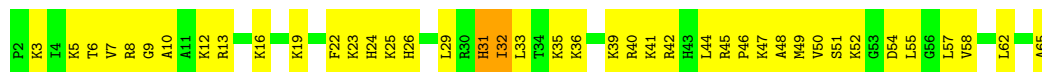


- Molecule 52: 50S ribosomal protein L5

Chain n: 54% 45%



• Molecule 53: 50S ribosomal protein L35



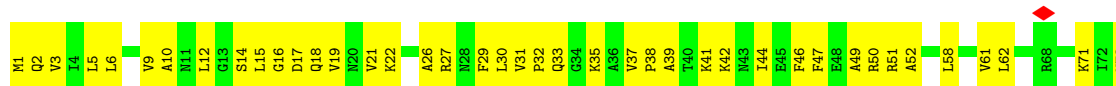
• Molecule 54: 50S ribosomal protein L6



• Molecule 55: 50S ribosomal protein L36

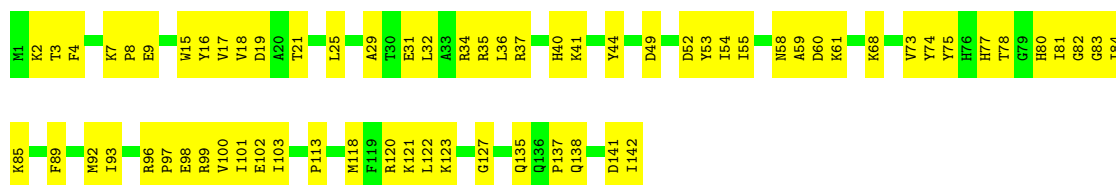


• Molecule 56: 50S ribosomal protein L9



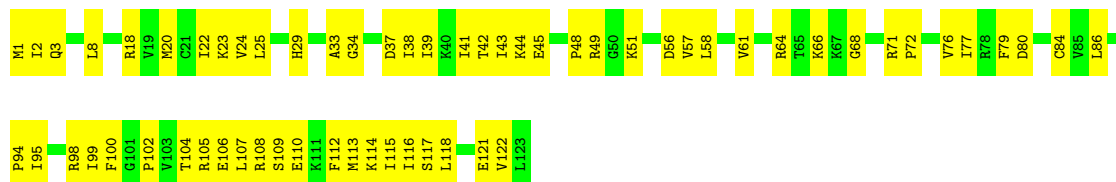
• Molecule 57: 50S ribosomal protein L13





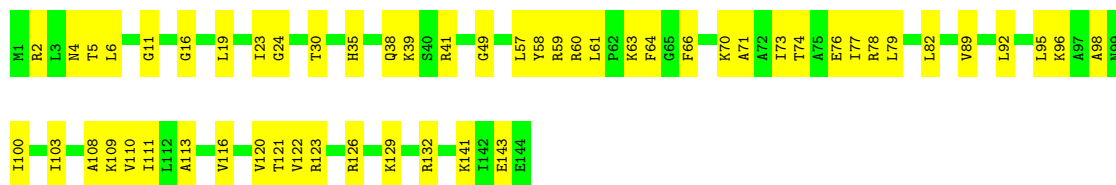
- Molecule 58: 50S ribosomal protein L14

Chain t: 50% 50%



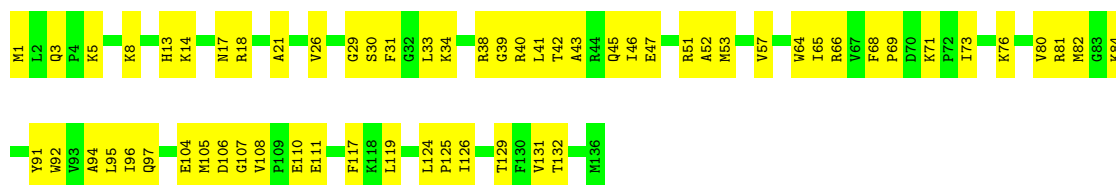
- Molecule 59: 50S ribosomal protein L15

Chain u: 62% 38%



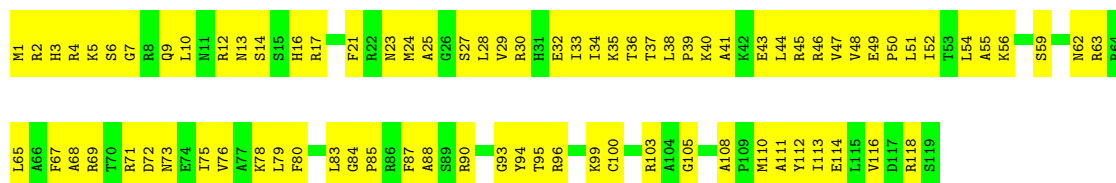
- Molecule 60: 50S ribosomal protein L16

Chain v: 55% 45%



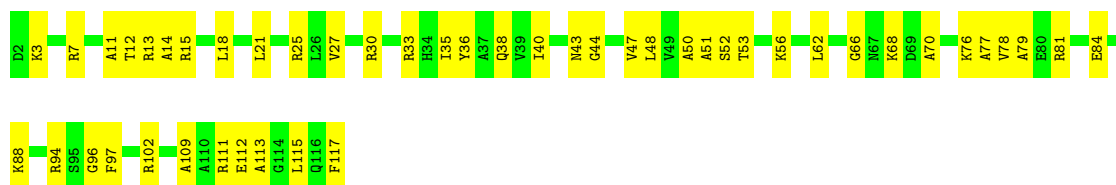
- Molecule 61: 50S ribosomal protein L17

Chain w: 31% 69%

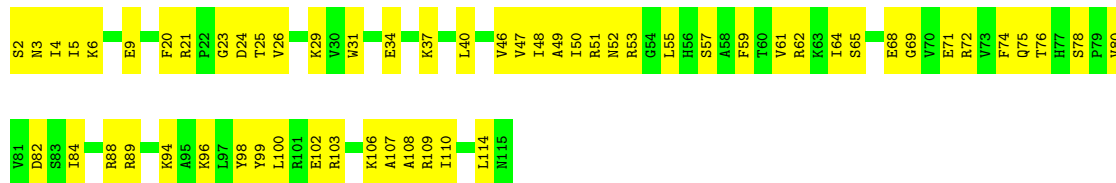


- Molecule 62: 50S ribosomal protein L18

Chain x: 59% 41%



- 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	24959	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.039	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	548.05, 548.05, 548.05	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.48	0/829	0.67	0/1107
2	1	0.49	0/864	0.63	0/1156
3	2	0.44	0/752	0.60	0/1005
4	3	0.45	0/796	0.66	0/1062
5	4	0.46	0/766	0.59	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.59	2/681 (0.3%)	0.88	3/1058 (0.3%)
9	9	0.30	0/1131	0.72	2/1524 (0.1%)
10	A	0.28	0/1810	0.61	0/2821
10	B	0.28	0/1810	0.61	0/2821
11	AA	0.67	11/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AB	0.42	1/808 (0.1%)	0.70	2/1088 (0.2%)
13	AC	0.60	3/1808 (0.2%)	0.73	9/2450 (0.4%)
13	AD	0.39	0/1789	0.55	0/2425
14	AE	0.53	7/10545 (0.1%)	0.74	22/14236 (0.2%)
15	C	1.04	2/553 (0.4%)	1.30	5/743 (0.7%)
16	D	0.34	0/36610	0.49	10/57091 (0.0%)
17	E	0.52	0/675	0.70	0/895
18	F	0.51	0/597	0.69	0/792
19	G	0.48	0/1791	0.70	1/2413 (0.0%)
20	H	0.81	4/1746 (0.2%)	1.63	39/2382 (1.6%)
21	I	0.58	0/1663	0.98	0/2241
22	J	0.64	0/1665	1.10	3/2227 (0.1%)
23	K	0.51	0/1165	0.72	0/1568
24	L	0.51	0/867	0.73	0/1171
25	M	0.49	0/1195	0.64	0/1602
26	N	0.49	0/989	0.64	0/1326
27	O	0.58	0/1034	0.81	0/1375
28	P	0.62	0/800	1.18	9/1082 (0.8%)
29	Q	0.47	0/893	0.65	0/1205
30	R	0.90	2/952 (0.2%)	1.06	3/1274 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.49	0/817	0.75	2/1088 (0.2%)
32	T	0.48	0/722	0.62	0/964
33	U	0.52	0/659	0.72	1/884 (0.1%)
34	V	0.47	0/657	0.66	0/881
35	W	0.44	0/680	0.59	0/915
36	X	0.42	0/909	0.64	0/1215
37	Y	0.39	1/1046 (0.1%)	0.70	0/1410
38	Z	0.22	0/227	0.56	0/304
39	a	0.34	0/69247	0.50	10/107985 (0.0%)
40	b	0.45	0/589	0.65	0/779
41	c	0.44	0/635	0.69	0/848
42	d	0.32	0/2872	0.44	0/4478
43	e	0.44	0/502	0.58	0/667
44	f	0.46	0/452	0.66	1/605 (0.2%)
45	g	0.39	0/531	0.59	0/709
46	h	0.60	2/2121 (0.1%)	0.76	4/2852 (0.1%)
47	i	0.68	1/450 (0.2%)	0.88	2/599 (0.3%)
48	j	0.47	0/1586	0.67	0/2134
49	k	0.46	0/433	0.59	0/576
50	l	0.44	0/1571	0.63	0/2113
51	m	0.71	0/380	1.26	0/498
52	n	0.77	4/1434 (0.3%)	0.94	8/1926 (0.4%)
53	o	0.48	0/513	0.71	0/676
54	p	0.62	3/1333 (0.2%)	0.79	4/1805 (0.2%)
55	q	0.75	0/303	0.83	0/397
56	r	0.39	0/1122	0.59	0/1515
57	s	0.45	0/1152	0.67	0/1551
58	t	0.53	0/955	0.69	0/1279
59	u	0.47	0/1062	0.71	0/1413
60	v	0.53	0/1093	0.68	0/1460
61	w	0.51	0/964	0.70	0/1289
62	x	0.45	0/902	0.64	0/1209
63	y	0.51	0/929	0.67	0/1242
64	z	0.54	0/960	0.78	2/1278 (0.2%)
All	All	0.44	45/189114 (0.0%)	0.63	196/278734 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3

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

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	R	42	PRO	N-CA	19.82	1.70	1.47
15	C	41	PRO	N-CA	18.54	1.71	1.47
11	AA	374	GLU	C-N	17.49	1.54	1.33
46	h	107	PRO	CG-CD	-13.62	1.04	1.50
52	n	176	PRO	CG-CD	-13.13	1.06	1.50

The worst 5 of 196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AA	727	VAL	N-CA-C	-17.25	95.05	110.74
20	H	88	LYS	CA-C-N	16.88	143.50	120.38
20	H	88	LYS	C-N-CA	16.88	143.50	120.38
46	h	107	PRO	N-CD-CG	-16.88	77.88	103.20
30	R	41	THR	CA-C-N	16.66	136.53	120.03

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	52	0
2	1	857	922	922	67	0
3	2	746	811	811	42	0
4	3	788	844	844	77	0
5	4	753	780	780	32	0
6	5	472	260	261	22	0
7	6	542	306	306	26	0
8	7	612	97	302	99	0
9	9	1117	0	1155	221	0
10	A	1620	826	827	100	0
10	B	1620	813	827	106	0
11	AA	10425	10426	10427	370	0
12	AB	790	783	783	7	0
13	AC	1786	1813	1813	59	0
13	AD	1767	1789	1789	46	0
14	AE	10388	10612	10611	363	0
15	C	544	559	560	62	0
16	D	32703	16423	16456	1805	0
17	E	669	719	719	43	0
18	F	589	629	629	45	0
19	G	1760	1785	1787	123	0
20	H	1730	1454	1454	224	0
21	I	1636	1710	1709	147	0
22	J	1643	1707	1707	41	0
23	K	1152	1196	1196	111	0
24	L	848	846	846	56	0
25	M	1181	1235	1238	71	0
26	N	979	1031	1031	81	0
27	O	1022	1070	1070	83	0
28	P	790	831	831	55	0
29	Q	877	887	887	41	0
30	R	939	1001	1001	59	0
31	S	805	844	844	173	0
32	T	714	734	734	40	0
33	U	649	666	666	33	0
34	V	648	691	691	58	0
35	W	663	688	688	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	X	900	964	965	54	0
37	Y	1032	0	1088	133	0
38	Z	227	0	237	15	0
39	a	61841	31077	31119	3354	0
40	b	582	599	599	41	0
41	c	625	652	652	39	0
42	d	2569	1301	1301	123	0
43	e	501	531	531	23	0
44	f	448	488	488	29	0
45	g	522	520	520	32	0
46	h	2082	2154	2154	151	0
47	i	444	459	458	30	0
48	j	1565	1617	1616	117	0
49	k	426	464	464	28	0
50	l	1552	1619	1619	108	0
51	m	377	418	418	42	0
52	n	1410	1443	1444	80	0
53	o	504	572	572	48	0
54	p	1313	1358	1358	69	0
55	q	302	343	343	29	0
56	r	1111	1148	1148	63	0
57	s	1129	1162	1162	69	0
58	t	946	1023	1023	58	0
59	u	1053	1129	1129	60	0
60	v	1074	1157	1157	64	0
61	w	951	994	994	92	0
62	x	892	923	923	41	0
63	y	917	962	962	55	0
64	z	947	1020	1019	60	0
65	7	1	0	0	0	0
66	AA	2	0	0	0	0
All	All	175885	124724	127504	9290	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

The worst 5 of 9290 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.56
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:P:66:GLU:CG	31:S:99:ALA:HB2	1.43	1.43
18:F:25:LYS:HD2	20:H:336:ASP:CG	1.41	1.43
30:R:42:PRO:N	30:R:42:PRO:CA	1.70	1.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
2	1	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
3	2	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
4	3	101/103 (98%)	93 (92%)	7 (7%)	1 (1%)	12	43
5	4	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
9	9	146/148 (99%)	112 (77%)	33 (23%)	1 (1%)	18	50
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	4	29
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/230 (99%)	215 (94%)	11 (5%)	2 (1%)	14	45
13	AD	226/230 (98%)	212 (94%)	14 (6%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	121 (9%)	9 (1%)	18	50
15	C	64/66 (97%)	59 (92%)	4 (6%)	1 (2%)	7	35
17	E	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
18	F	68/70 (97%)	68 (100%)	0	0	100	100
19	G	223/225 (99%)	201 (90%)	22 (10%)	0	100	100
20	H	255/557 (46%)	187 (73%)	56 (22%)	12 (5%)	2	18
21	I	206/208 (99%)	197 (96%)	8 (4%)	1 (0%)	24	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	J	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
23	K	154/156 (99%)	140 (91%)	13 (8%)	1 (1%)	21	52
24	L	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
25	M	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
26	N	127/129 (98%)	110 (87%)	17 (13%)	0	100	100
27	O	125/127 (98%)	111 (89%)	14 (11%)	0	100	100
28	P	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	12	43
29	Q	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
30	R	117/124 (94%)	105 (90%)	11 (9%)	1 (1%)	14	45
31	S	98/100 (98%)	95 (97%)	2 (2%)	1 (1%)	12	43
32	T	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
34	V	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
35	W	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
36	X	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
37	Y	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
38	Z	28/30 (93%)	27 (96%)	1 (4%)	0	100	100
40	b	74/76 (97%)	67 (90%)	7 (10%)	0	100	100
41	c	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
43	e	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
44	f	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
45	g	64/66 (97%)	58 (91%)	6 (9%)	0	100	100
46	h	269/271 (99%)	241 (90%)	28 (10%)	0	100	100
47	i	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
48	j	207/209 (99%)	188 (91%)	19 (9%)	0	100	100
49	k	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
50	l	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/177 (99%)	161 (92%)	14 (8%)	0	100	100
53	o	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	35
54	p	173/175 (99%)	156 (90%)	16 (9%)	1 (1%)	21	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	q	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	127 (91%)	13 (9%)	0	100	100
58	t	121/123 (98%)	108 (89%)	13 (11%)	0	100	100
59	u	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
60	v	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
61	w	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
62	x	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
63	y	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
64	z	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
All	All	9368/9974 (94%)	8467 (90%)	836 (9%)	65 (1%)	20	50

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU
11	AA	873	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/81 (100%)	81 (100%)	0	100	100
4	3	84/84 (100%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/112 (100%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7	30
12	AB	86/158 (54%)	85 (99%)	1 (1%)	63	72
13	AC	198/198 (100%)	183 (92%)	15 (8%)	12	38
13	AD	196/198 (99%)	193 (98%)	3 (2%)	57	68
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	15	42
15	C	57/57 (100%)	53 (93%)	4 (7%)	14	41
17	E	65/65 (100%)	65 (100%)	0	100	100
18	F	60/60 (100%)	59 (98%)	1 (2%)	53	67
19	G	187/187 (100%)	185 (99%)	2 (1%)	65	73
20	H	137/461 (30%)	121 (88%)	16 (12%)	5	24
21	I	171/171 (100%)	162 (95%)	9 (5%)	20	46
22	J	172/172 (100%)	162 (94%)	10 (6%)	18	45
23	K	119/119 (100%)	119 (100%)	0	100	100
24	L	91/91 (100%)	91 (100%)	0	100	100
25	M	124/124 (100%)	124 (100%)	0	100	100
26	N	104/104 (100%)	104 (100%)	0	100	100
27	O	105/105 (100%)	105 (100%)	0	100	100
28	P	86/86 (100%)	76 (88%)	10 (12%)	5	24
29	Q	90/90 (100%)	90 (100%)	0	100	100
30	R	101/104 (97%)	100 (99%)	1 (1%)	68	74
31	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
32	T	76/76 (100%)	76 (100%)	0	100	100
33	U	65/65 (100%)	65 (100%)	0	100	100
34	V	74/74 (100%)	74 (100%)	0	100	100
35	W	72/72 (100%)	72 (100%)	0	100	100
36	X	94/94 (100%)	94 (100%)	0	100	100
37	Y	109/109 (100%)	109 (100%)	0	100	100
38	Z	26/26 (100%)	26 (100%)	0	100	100
40	b	58/58 (100%)	58 (100%)	0	100	100
41	c	67/67 (100%)	67 (100%)	0	100	100
43	e	54/54 (100%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	f	48/48 (100%)	48 (100%)	0	100	100
45	g	59/59 (100%)	59 (100%)	0	100	100
46	h	216/216 (100%)	216 (100%)	0	100	100
47	i	47/47 (100%)	47 (100%)	0	100	100
48	j	164/164 (100%)	163 (99%)	1 (1%)	78	79
49	k	47/47 (100%)	47 (100%)	0	100	100
50	l	165/165 (100%)	165 (100%)	0	100	100
51	m	38/38 (100%)	36 (95%)	2 (5%)	20	46
52	n	148/148 (100%)	148 (100%)	0	100	100
53	o	51/51 (100%)	51 (100%)	0	100	100
54	p	136/136 (100%)	136 (100%)	0	100	100
55	q	34/34 (100%)	33 (97%)	1 (3%)	37	57
56	r	114/114 (100%)	114 (100%)	0	100	100
57	s	116/116 (100%)	116 (100%)	0	100	100
58	t	104/104 (100%)	104 (100%)	0	100	100
59	u	103/103 (100%)	103 (100%)	0	100	100
60	v	109/109 (100%)	109 (100%)	0	100	100
61	w	99/99 (100%)	99 (100%)	0	100	100
62	x	86/86 (100%)	86 (100%)	0	100	100
63	y	99/99 (100%)	99 (100%)	0	100	100
64	z	89/89 (100%)	89 (100%)	0	100	100
All	All	7791/8257 (94%)	7527 (97%)	264 (3%)	33	55

5 of 264 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	I	33	LEU
22	J	47	ARG
48	j	173	GLN
11	AA	1041	ASP
11	AA	1035	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
47	i	5	GLN
58	t	3	GLN
48	j	49	GLN
54	p	38	ASN
61	w	9	GLN

5.3.3 RNA ⓘ

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

5 of 983 RNA backbone outliers are listed below:

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

5 of 29 RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [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.

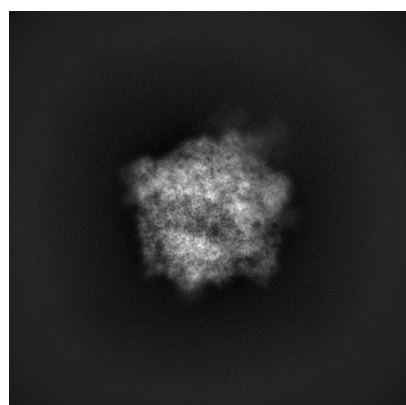
6 Map visualisation [i](#)

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

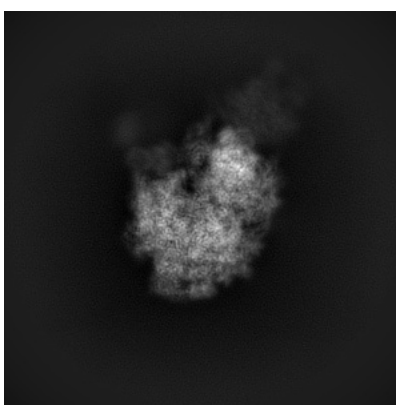
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

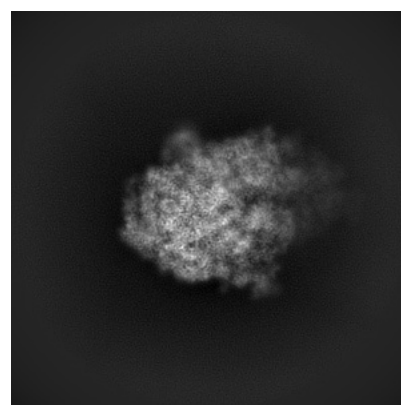
6.1.1 Primary map



X



Y

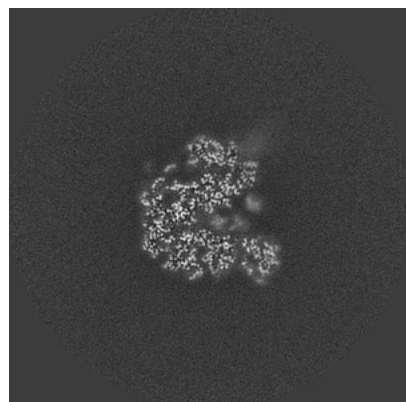


Z

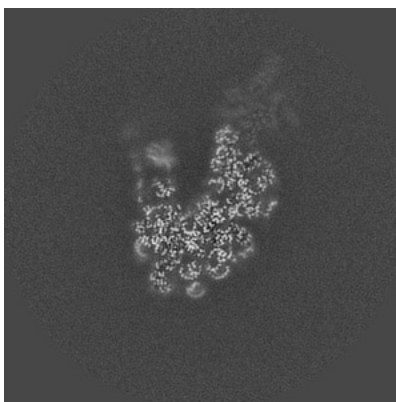
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

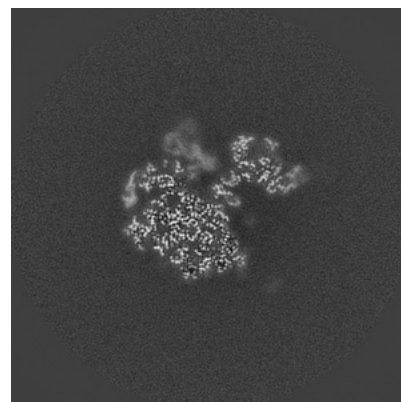
6.2.1 Primary map



X Index: 250



Y Index: 250

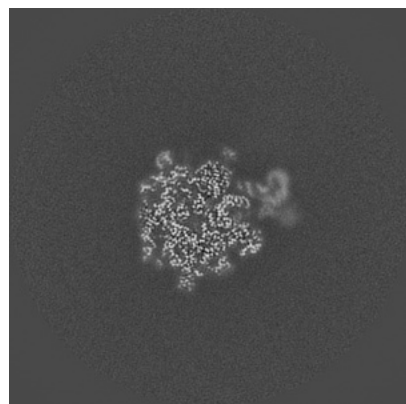


Z Index: 250

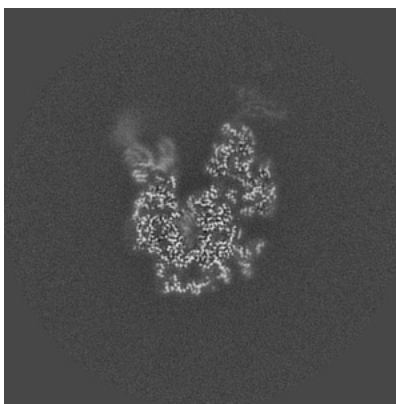
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

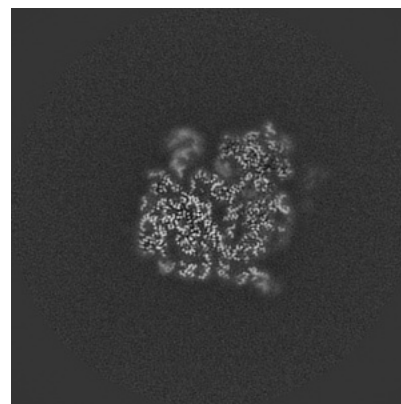
6.3.1 Primary map



X Index: 215



Y Index: 233

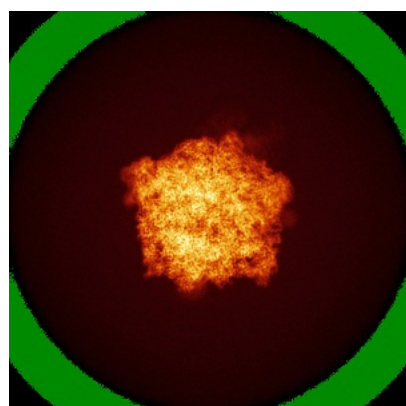


Z Index: 271

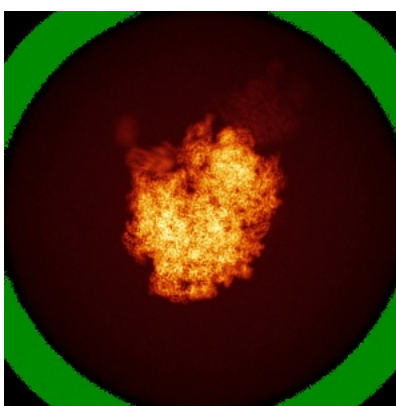
The images above show the largest variance slices of the map in three orthogonal directions.

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

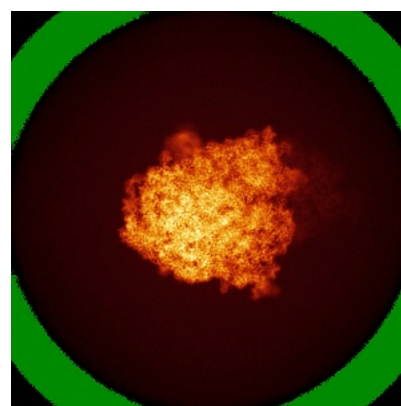
6.4.1 Primary map



X



Y

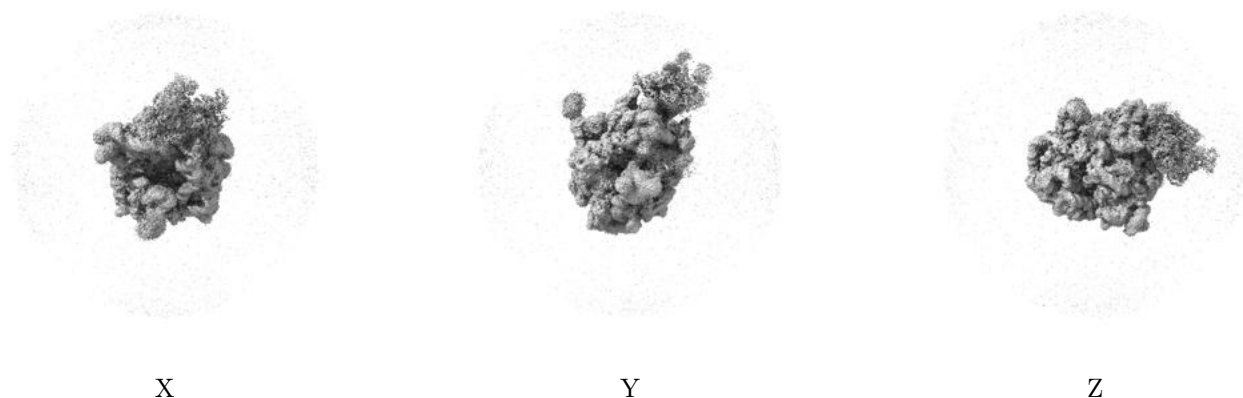


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

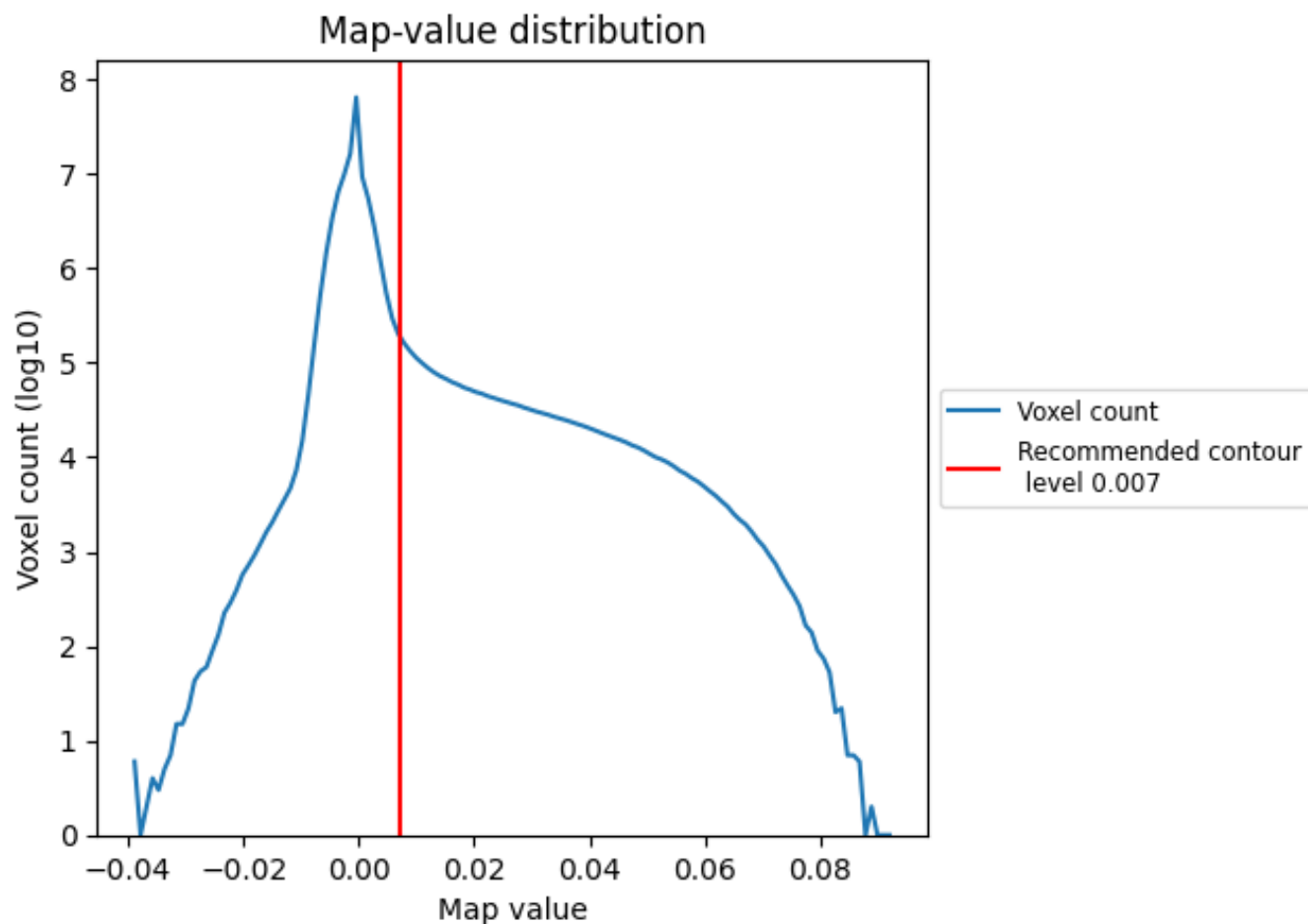
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

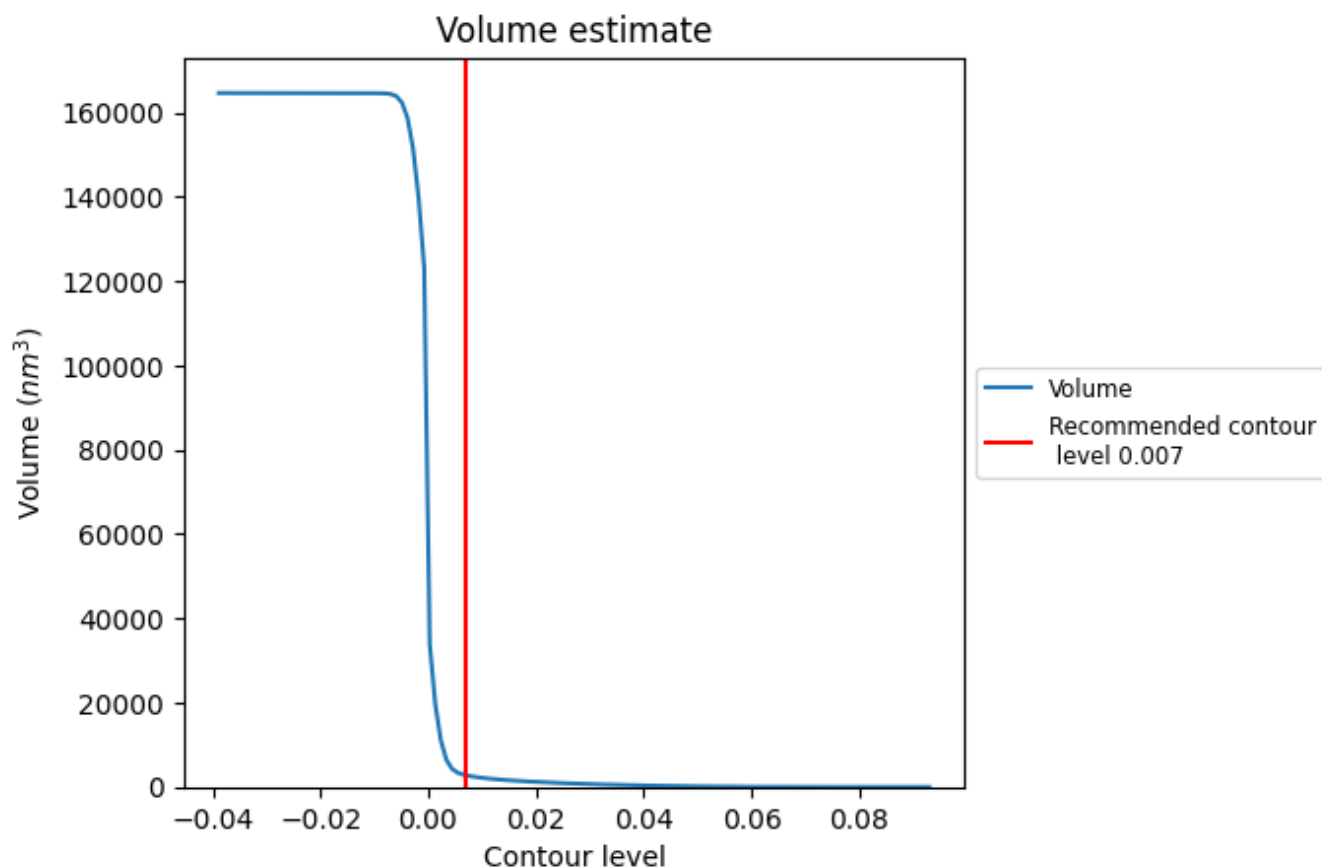
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

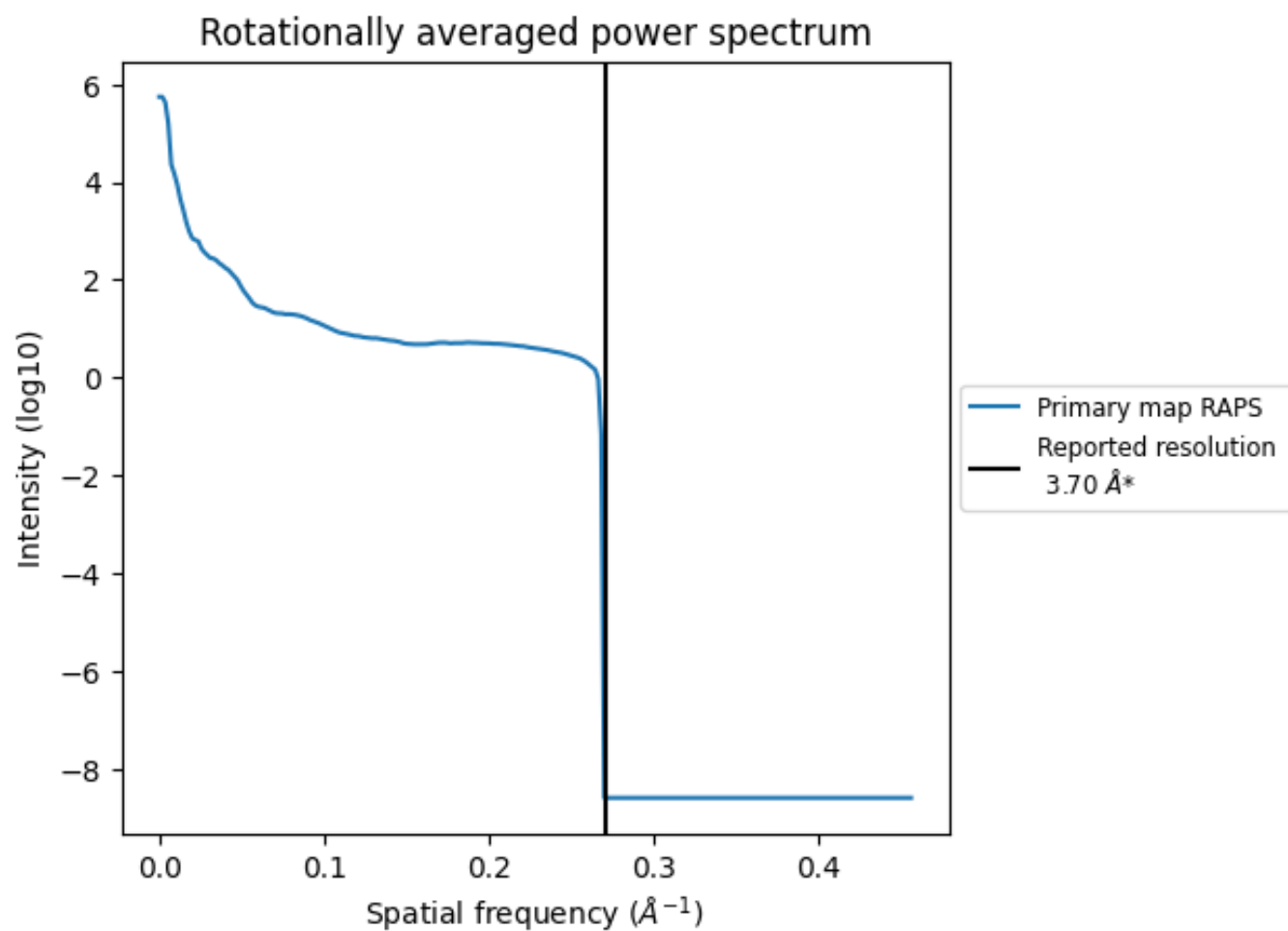
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm^3 ; this corresponds to an approximate mass of 2518 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

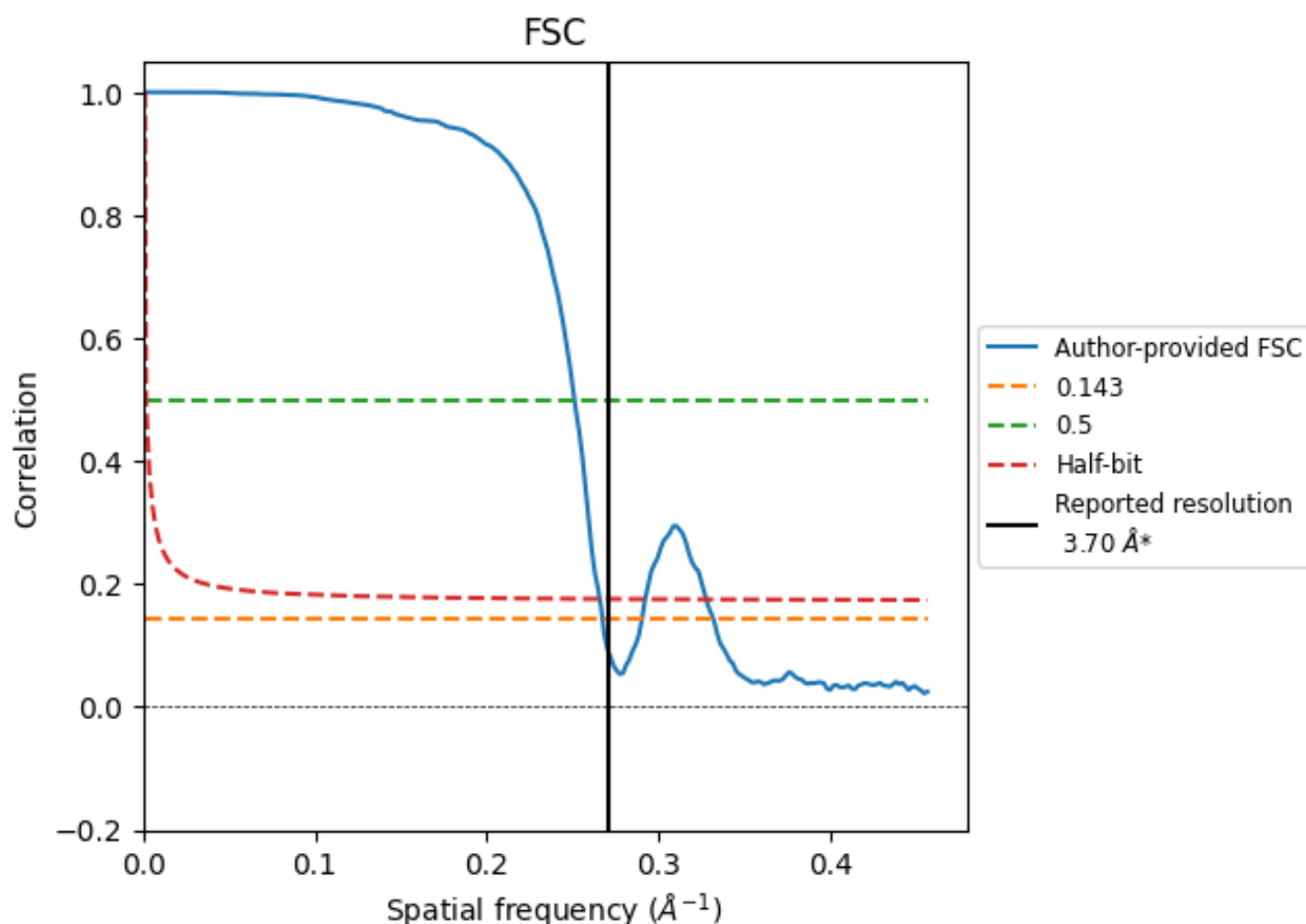


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

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

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

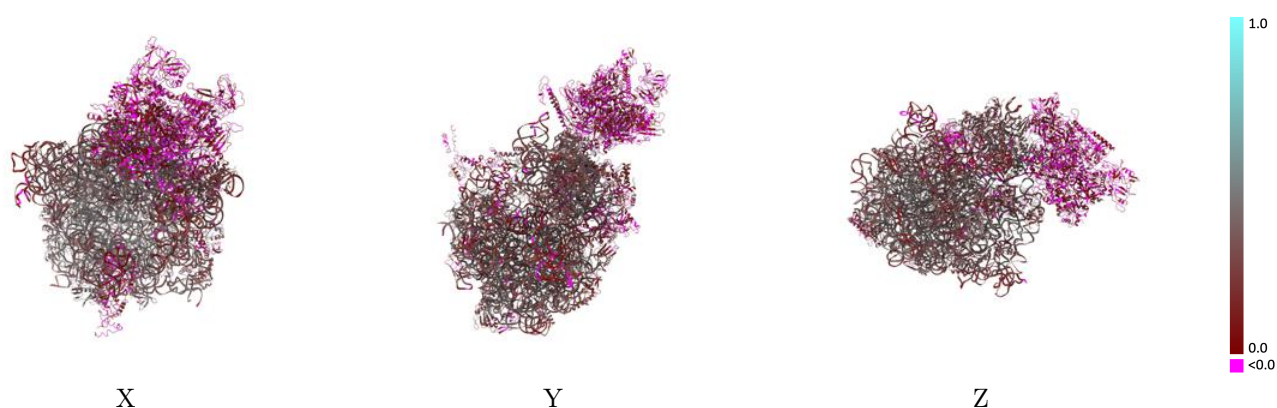
9 Map-model fit [i](#)

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

9.1 Map-model overlay [i](#)

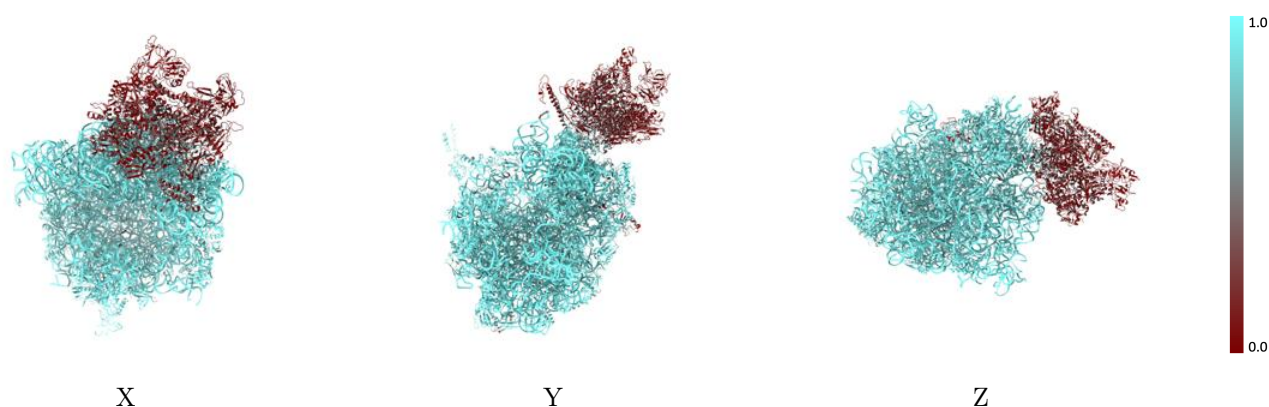
This section was not generated.

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



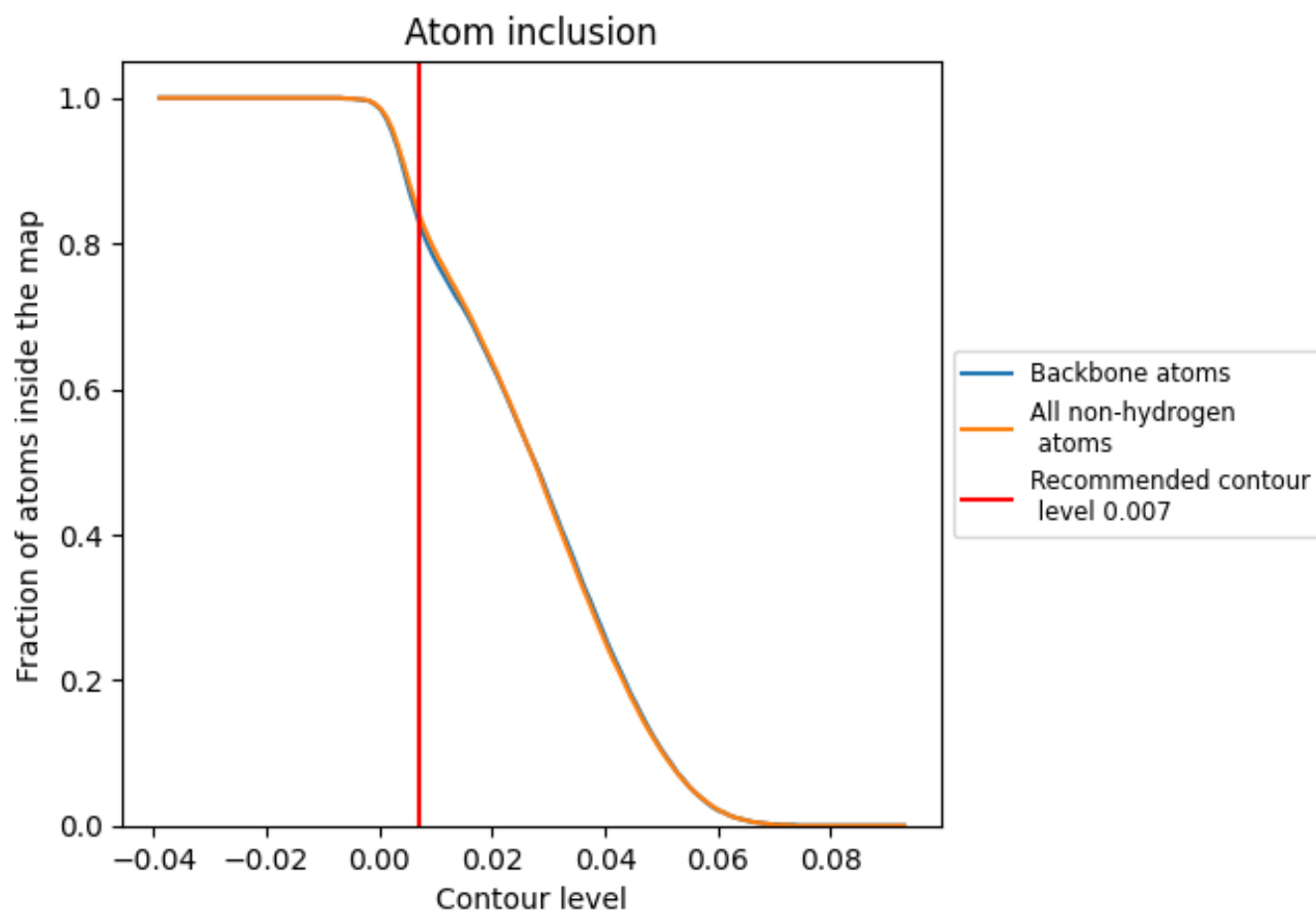
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.007) and Q-score for the entire model and for each chain.

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



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