



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 03:40 pm BST

PDB ID : 9SL4 / pdb_00009sl4
EMDB ID : EMD-53668
Title : Model of M. pneumoniae 70S eT-TC (collided)
Authors : Dobbs, J.M.; Mahamid, J.
Deposited on : 2025-09-03
Resolution : 7.20 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:

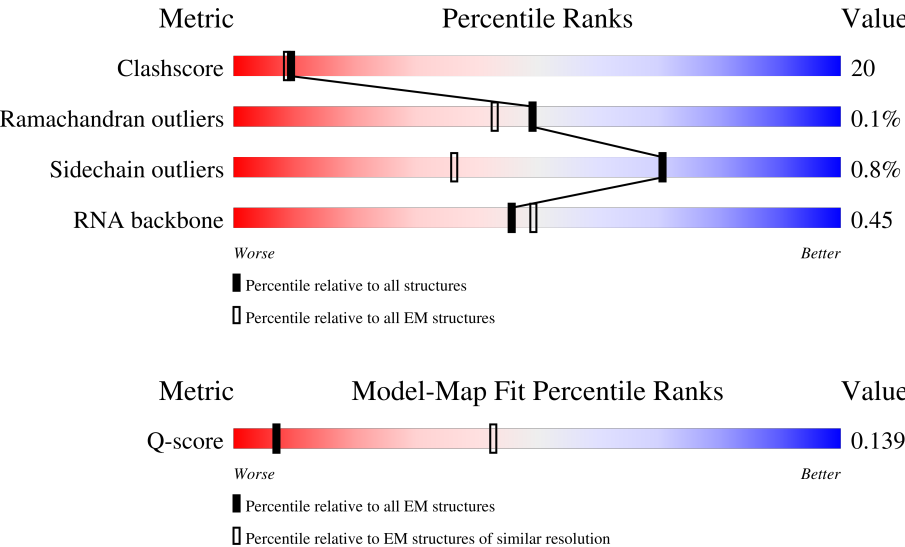
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 7.20 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.



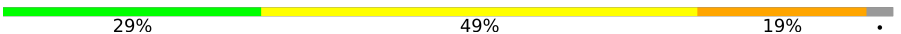
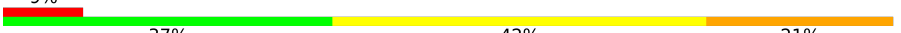
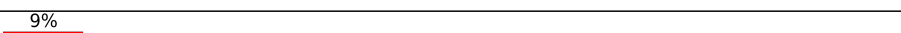
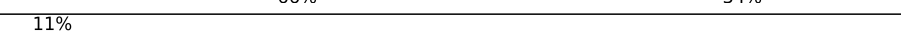
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	444 (6.70 - 7.70)

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	47	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	3	2893	
5	4	108	
6	5	1505	
7	6	247	
7	AA	247	
8	7	76	
9	8	1391	
10	9	89	
11	A	240	
12	AB	32	
13	AC	32	
14	AD	160	
15	B	215	
16	C	203	
17	D	153	
18	E	167	
19	F	154	
20	G	141	
21	H	128	
22	I	101	
23	J	114	
24	K	136	
25	L	118	
26	M	60	
27	N	83	

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Mol	Chain	Length	Quality of chain
28	O	80	
29	P	83	
30	Q	65	
31	R	84	
32	S	77	
33	T	53	
34	U	161	
35	V	29	
35	W	29	
35	X	29	
35	Y	29	
36	Z	1276	
37	a	285	
38	b	229	
39	c	210	
40	d	175	
41	e	176	
42	f	145	
43	h	128	
44	i	144	
45	j	122	
46	k	148	
47	l	136	
48	m	119	
49	n	116	

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Mol	Chain	Length	Quality of chain
50	o	115	
51	p	114	
52	q	99	
53	r	139	
54	s	92	
55	t	111	
56	u	86	
57	v	63	
58	w	108	
59	x	44	
60	y	56	
61	z	50	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 173941 atoms, of which 0 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 Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 5 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	247	Total	C	N	O	S	0	0
			1920	1236	313	362	9		
7	AA	247	Total	C	N	O	S	0	0
			1920	1236	313	362	9		

- Molecule 8 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	1391	Total	C	N	O	S	0	0
			10948	6905	1892	2114	37		

- Molecule 10 is a protein called Probable DNA-directed RNA polymerase subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	89	Total	C	N	O	S	0	0
			770	505	122	140	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 12 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	32	Total	C	N	O	P	0	0
			663	317	124	190	32		

- Molecule 13 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	32	Total	C	N	O	P	0	0
			649	313	110	194	32		

- Molecule 14 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AD	160	Total	C	N	O	S	0	0
			1277	821	220	233	3		

- Molecule 15 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 16 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 20 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 21 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 24 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 25 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	L	118	Total	C	N	O	0	0
			951	594	191	166		

- Molecule 26 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	N	83	Total	C	N	O	0	0
			673	428	125	120		

- Molecule 28 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 29 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P	83	Total	C	N	O	S	0	0
			675	425	135	115			

- Molecule 30 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 31 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 32 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	77	Total	C	N	O	S	0	0
			629	383	135	111			

- Molecule 33 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 34 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	U	161	Total	C	N	O	S	0	0
			1239	796	213	225	5		

- Molecule 35 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	V	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
35	W	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
35	X	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
35	Y	29	Total	C	N	O	S	0	0
			232	146	34	50	2		

- Molecule 36 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	1276	Total	C	N	O	S	0	0
			10085	6431	1752	1872	30		

- Molecule 37 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 38 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 39 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 40 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 41 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 42 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 43 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 44 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 45 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 46 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 47 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 48 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 50 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 51 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 52 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 53 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 54 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 55 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 56 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 57 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 58 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	w	100	Total	C	N	O		0	0
			818	517	153	148			

- Molecule 59 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 60 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

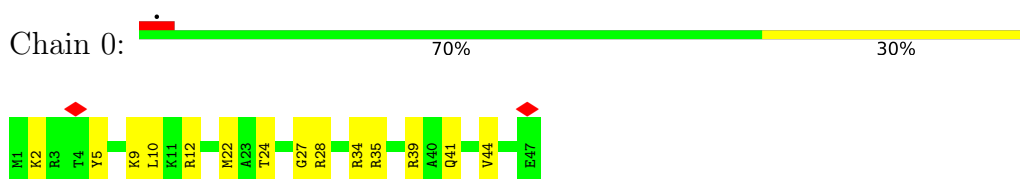
- Molecule 61 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

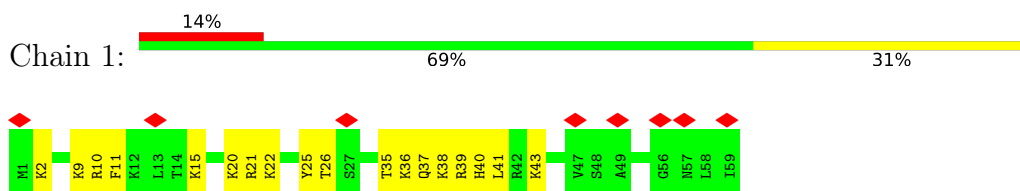
3 Residue-property plots

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.

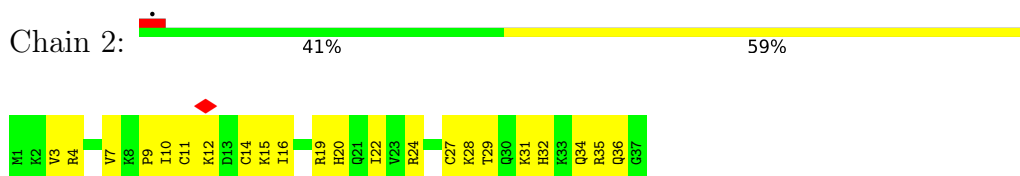
- Molecule 1: Large ribosomal subunit protein bL34



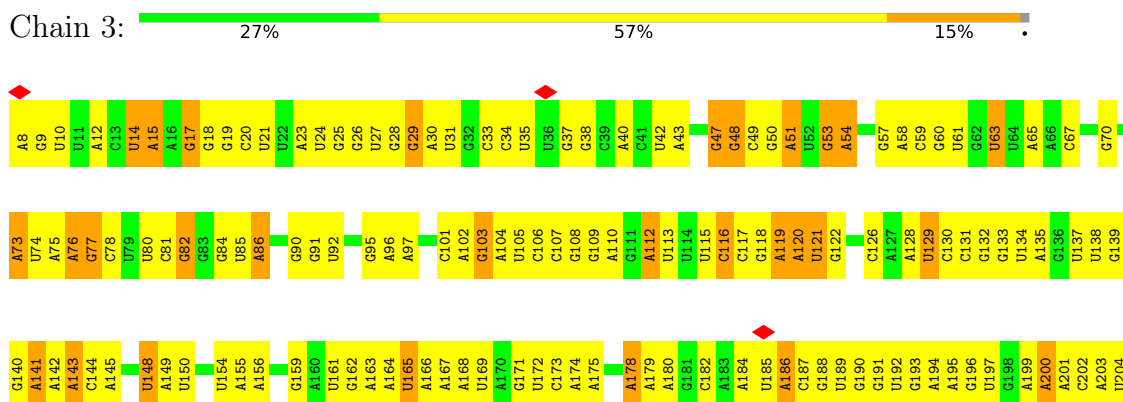
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

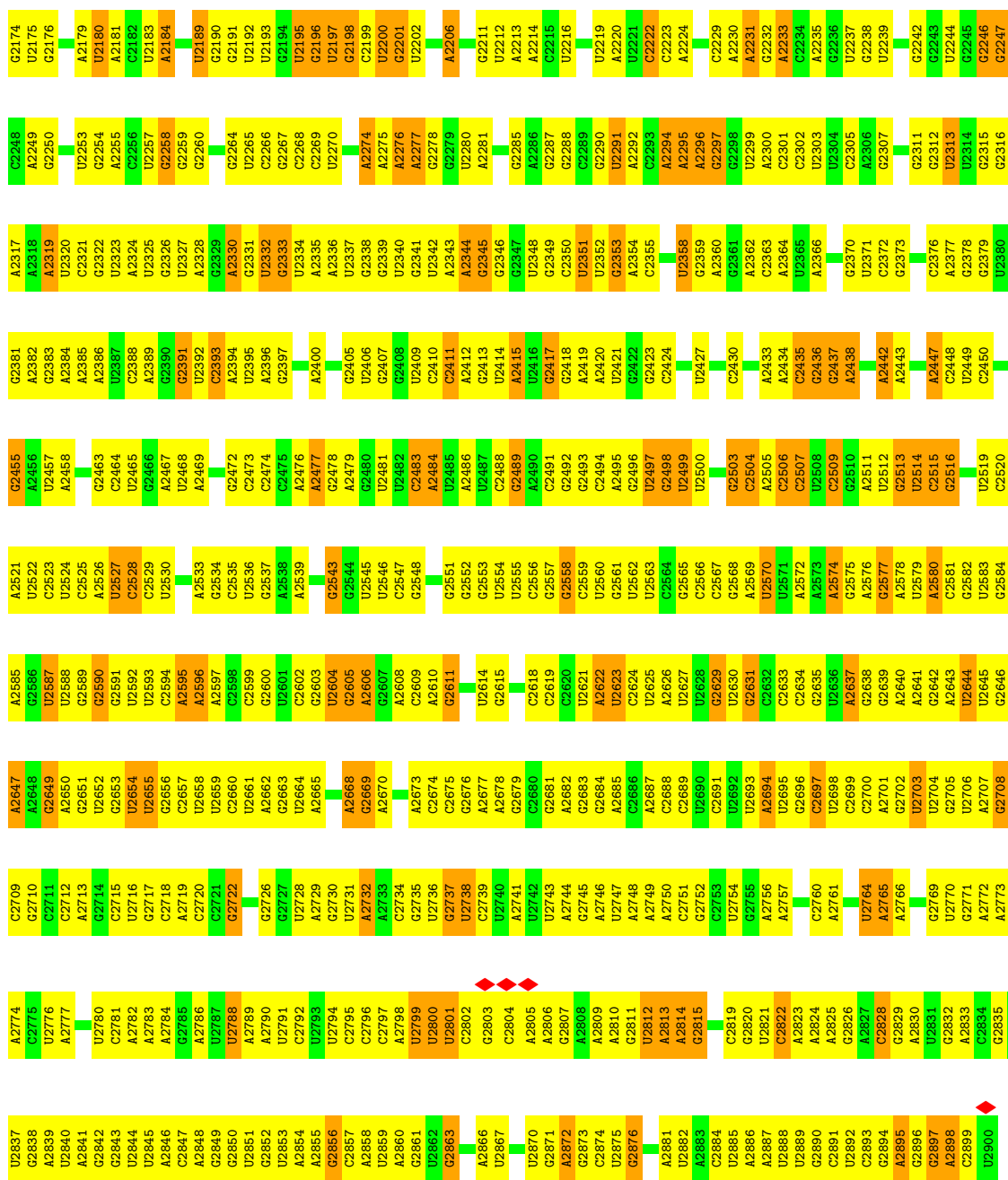


- Molecule 4: 23S ribosomal RNA



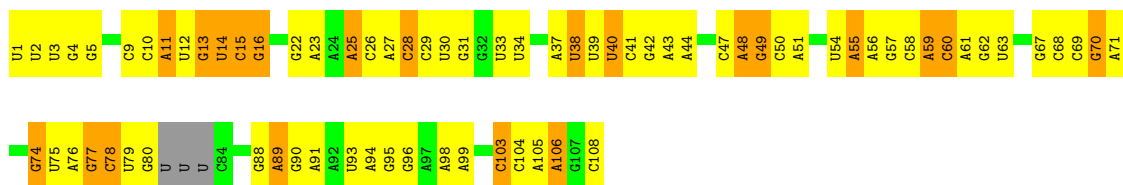
U143	U1079	G1013	U945	G875	G811	G742	U676	G610	U544	C480	U411	A343	A274	C205
C144	A1080	A1016	A946	A876	G815	G743	A679	A611	C545	C481	A412	A344	A275	
G145	A1081	A1017	A947	A877	G816	U744	A680	G612	U546	G482	G413	A345	A276	
A146	A1082	A1018	A948	A878	U745	G746	A681	C613	G547	A483		G346		G209
G147	A1083	G1018	C949	A817	U746	A747	A682	C614	A548	U484	G418	C347	U279	U210
U148	C1084	U1019	U950	A818	U747		A683	C615	A549	U485	A419	A348	A280	A211
A149	A1085	G1020	C951	C882	U819		G683	G616	A550	A486	A420	G349	A281	G212
U150	C1086	G1021	U952	A883	U820	G752	A684	C617	C551	C486	A421	C350		G213
U151	G1087	C1022	G953	U886	C821	A753	G685		C552	G488	A422	G351	U284	C214
	A955	A954	A955		A823	U754	C686		A553	A489	C423	C352	U285	A215
U154	A1088	A1024		G891	A824	C755	C687	G620		A490	G424	C353	A286	C216
G155	G1090	G1025	C958	G892	U825	A756	U688	A622	C558	A491	U425	C354	G287	A217
C156	G1091	A1026	C959	G893	U826	G758	U689	A623	U560	A492	U426	A355	A288	G218
G157	A1092	U1027	C959	A893	G827		U690	U634	A493		A427	A356	U289	G219
C158	C1093	C1028	A960	G894	U759		G691	G625	A561	G494	U428	A357	A290	A220
C159	A1094	A1029	U961	G895	A828	G760	U692	A626	C562	U495	U429	A358	G291	A221
G160	U1095	U1030	U962	U896	A829	G761	U693	G627	A563	A496	U430	G359	G292	A222
A161	U1096	G1031	U963	A897	A830	A762	U694	A628	A564	C497	U431	G360	A293	A223
G162	G1097	A1032	A964	A898	U831	G763	G695	G629	C565	C498	G432		G294	G224
C163	G1098	A1033	U965	A899	C832	G764	U696	G630	G566	G499	A433	G363	U295	A225
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• Molecule 5: 5S ribosomal RNA

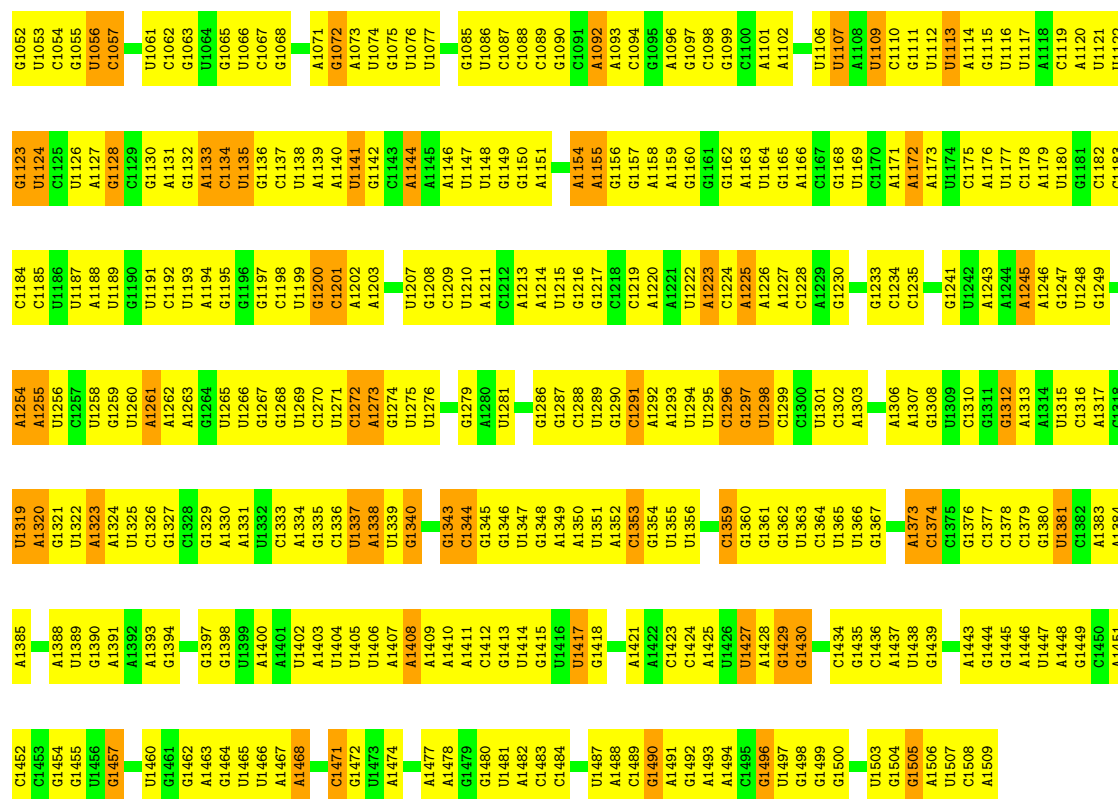
Chain 4: 29% 49% 19%



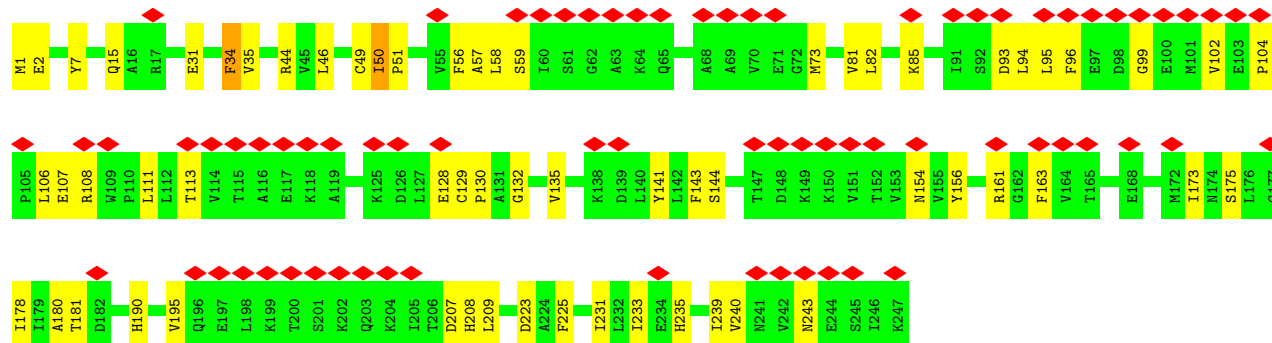
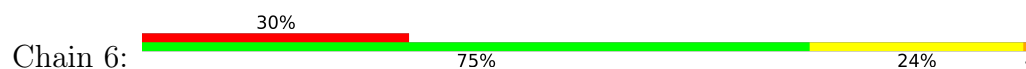
• Molecule 6: 16S ribosomal RNA

Chain 5:  29% 58% 13%

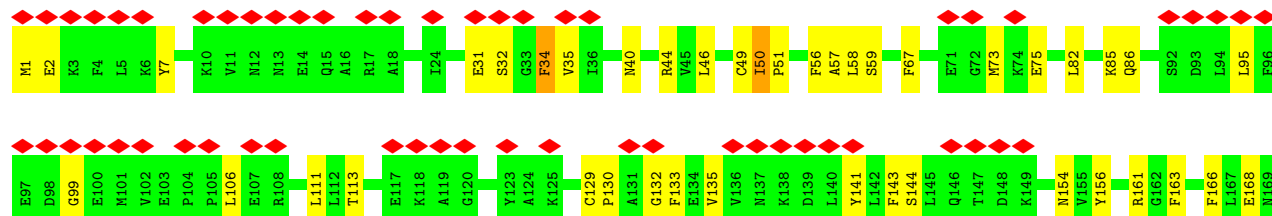
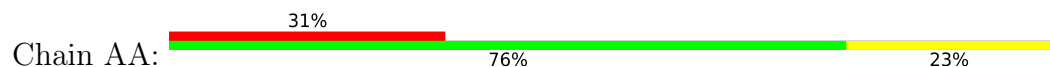
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C215	G216	U217	U218	A219	U220	U221	U222	U223	A224	U225	G226	A227	G230	U231	C232	C233	G236	A237	U238	A239	C241	A242	G243	C244	U245	A246	G247	U248	U249	G250	G251	U252	G253	G254	G255	U256	A257	A258	C259	G260	G261	C262	G263	C264	U265	A266	A269	U270	G271	C272	G273	A274	U275	G276						
G280	U281	G282	U283	A284	G285	C286	U287	A288	U289	G290	C291	U292	G293	A294	C295	A296	U299	A302	U303	A304	C305	C306	C307	C308	A309	C310	A311	A312	U313	G316	A317	C318	U319	G320	A323	C324	A325	C326	G327	G328	C329	C330	C331	A332	U333	A334	C335	U336	C337	C338	U339	A340	C341	G342	U343	A344				
G344	A345	C348	U349	A350	C351	A352	G353	U354	A355	G356	C357	G358	A359	C360	U361	U362	U363	U364	U365	C366	A367	C368	A369	A370	U371	G372	A373	C374	C375	G376	A377	A378	A379	G380	U381	U382	U383	C384	A385	U386	C387	G388	A393	U394	C395	G396	C397	G398	C399	G400	U401	G402	A403	A404	C405	G406	A407			
U408	G409	A410	A411	G412	C413	U416	U417	U418	A419	A420	G421	A422	U423	U424	G425	U426	A429	G430	U431	U432	C433	U434	U435	U436	U437	U440	U441	G442	G443	U444	A445	A446	G447	A448	A449	U450	G451	A452	C453	U454	U455	U456	A457	G458	C459	A460	G461	G462	U463	A464	G467	A471	G472	A473						
G474	U475	U476	U477	G478	A479	C480	U481	G482	U483	A484	U488	U489	U490	U491	G492	A493	A494	U495	U498	G500	A501	C502	G503	A504	U505	U506	A507	U508	C509	U510	A511	U512	G515	C516	C517	A518	G519	U523	C524	G525	C526	G527	G528	U529	A530	U531	U532	A533	U536	A537	G538	U539	U540							
C541	G542	C543	A544	A545	G548	U549	U550	A551	C554	A555	G556	A557	U558	U559	U560	A561	U562	U563	G564	A565	U569	A570	A571	A572	G573	C574	A575	U576	G577	U578	A579	G585	G586	A587	U588	U589	G590	A591	A592	U593	G594	U595	A596	U597	G600	U601	G602	U603	U604	A605	A606	U607	G608							
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U745	A746	C747	U748	G749	U750	G751	G752	C753	A763	U767	G768	G773	A774	G775	A778	U779	U780	A781	G782	U786	A789	A790	C791	U792	A793	U794	C795	A796	U797	U798	U799	C802	A806	A807	C808	G809	U810	A811	A812	U813	C814	G815	A816	U817	A818	G819	A820	U821	A822	C823	U824	A825								
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A970	A971	A972	C973	U977	A978	C979	G980	U981	A982	U983	A984	U987	G988	C989	A1000	A1001	A1002	G1003	A1010	A1011	A1012	C1013	A1014	U1015	A1016	A1017	U1018	G1019	G	A	G	G	U	U	A	A	C1028	A1031	G1032	U1033	A1037	G1038	U1039	G1044	C1045	A1046	U1047	G1048	U1051											



• Molecule 7: DNA-directed RNA polymerase subunit alpha

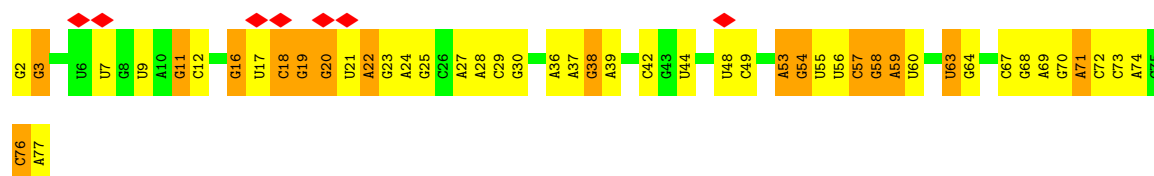


• Molecule 7: DNA-directed RNA polymerase subunit alpha

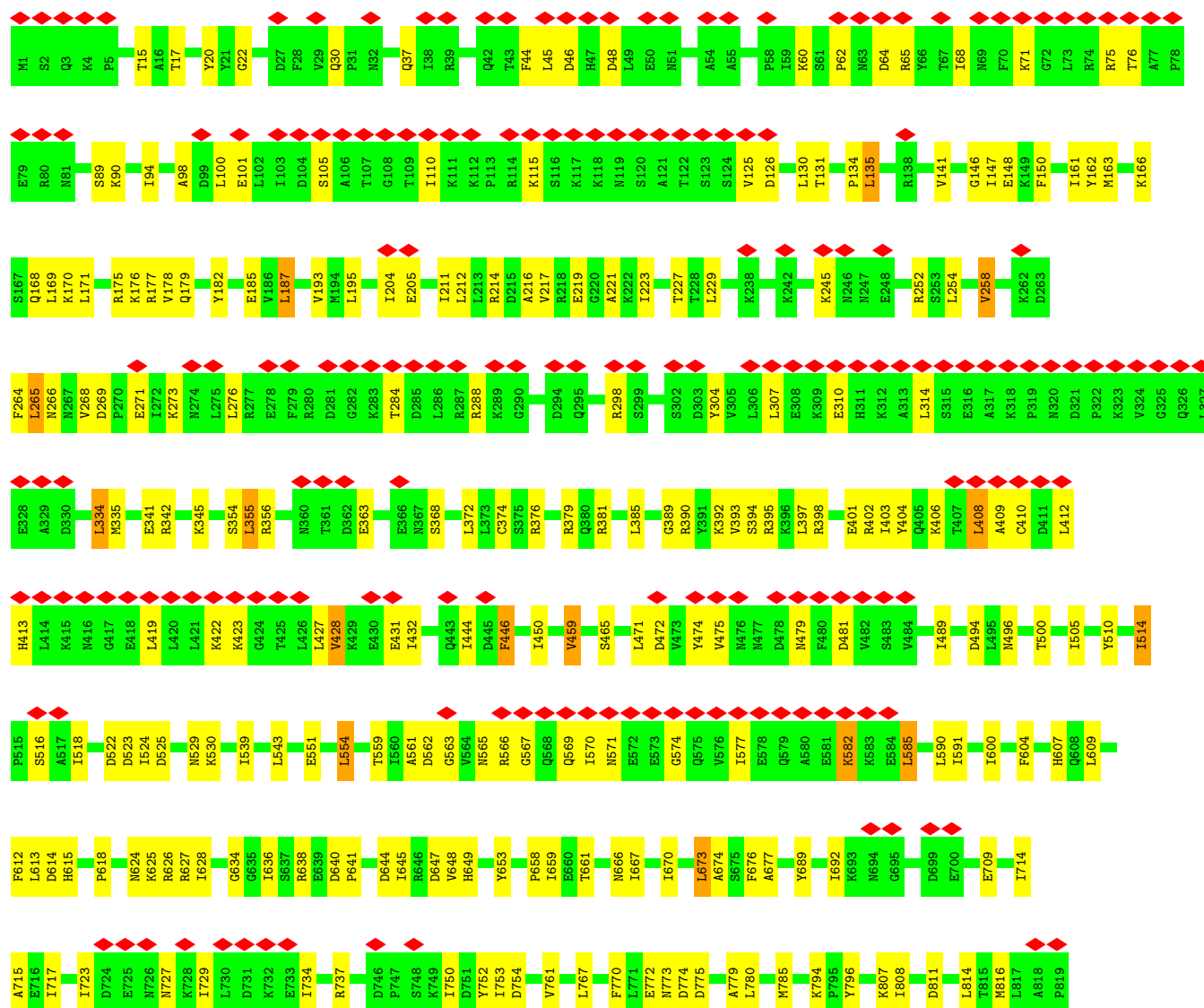


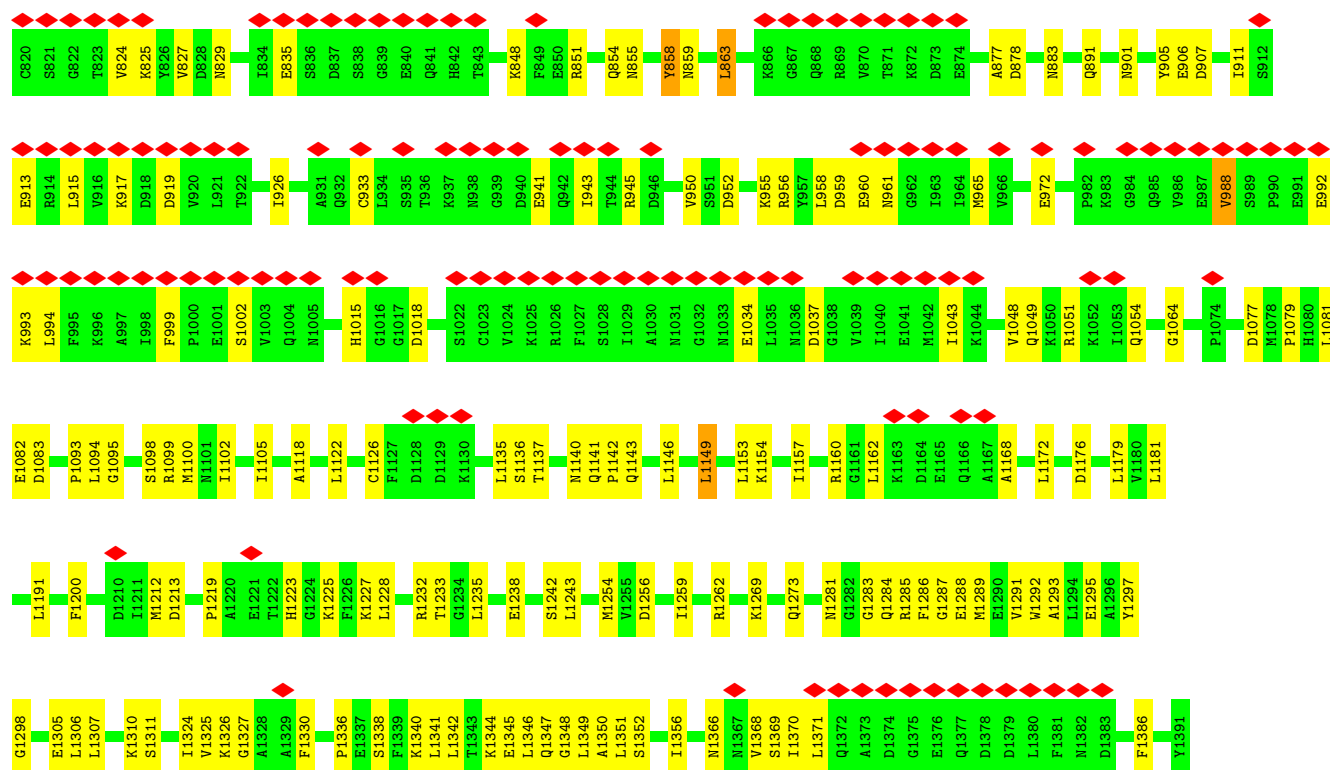


• Molecule 8: tRNA-Phe

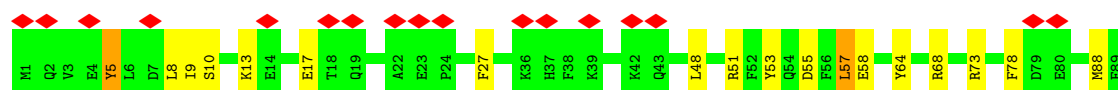
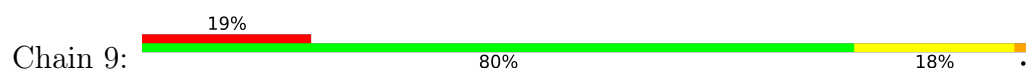


• Molecule 9: DNA-directed RNA polymerase subunit beta

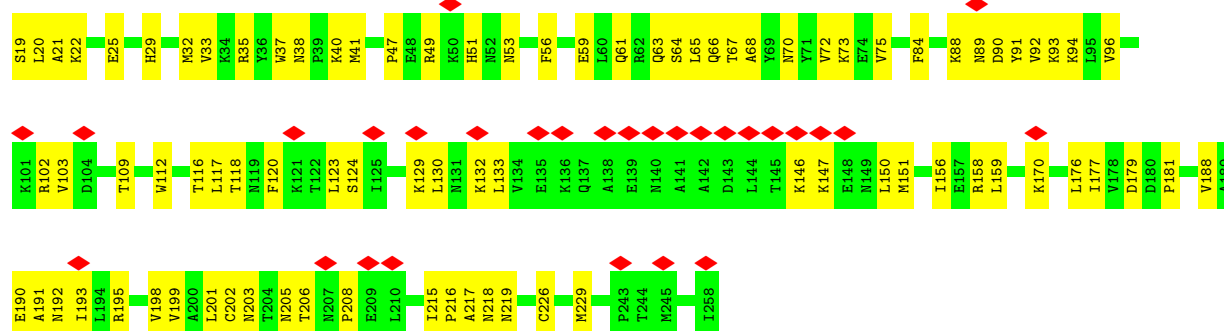




• Molecule 10: Probable DNA-directed RNA polymerase subunit delta



• Molecule 11: Small ribosomal subunit protein uS2

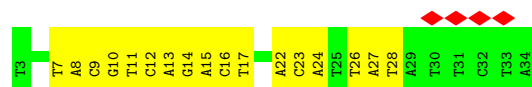


• Molecule 12: DNA

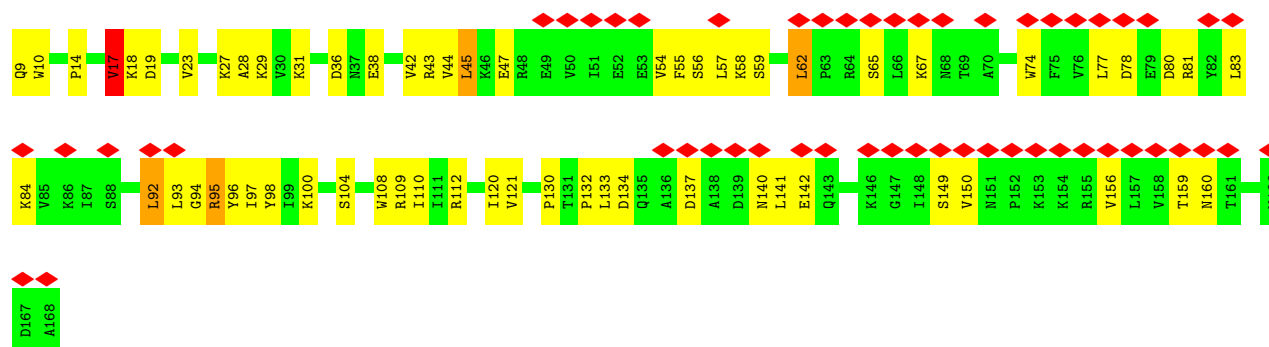




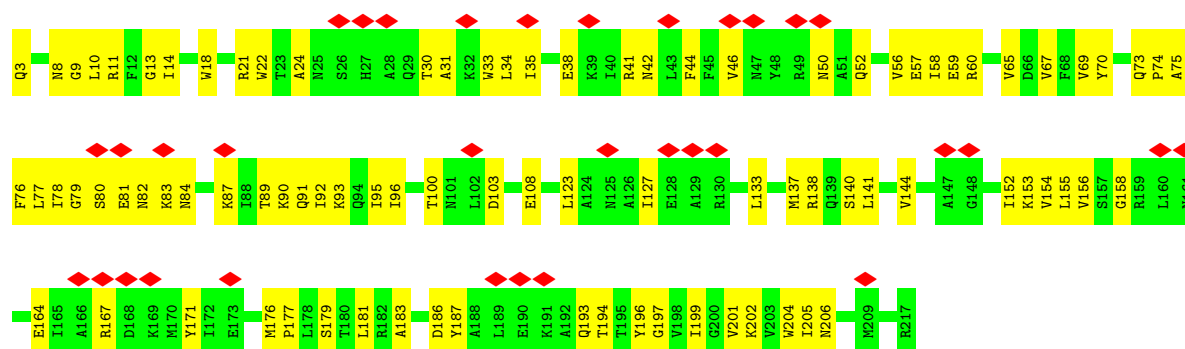
- Molecule 13: DNA



- Molecule 14: Transcription termination/antitermination protein NusG

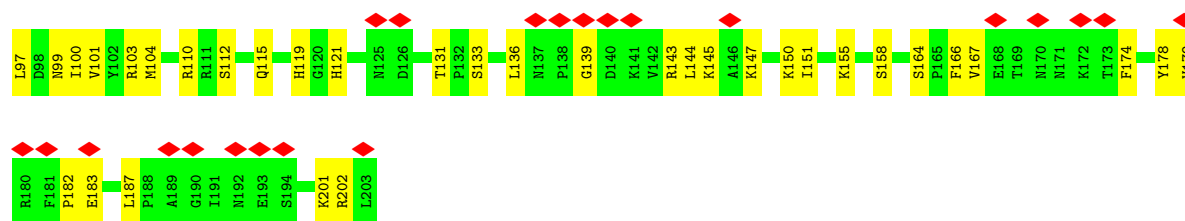


- Molecule 15: Small ribosomal subunit protein uS3

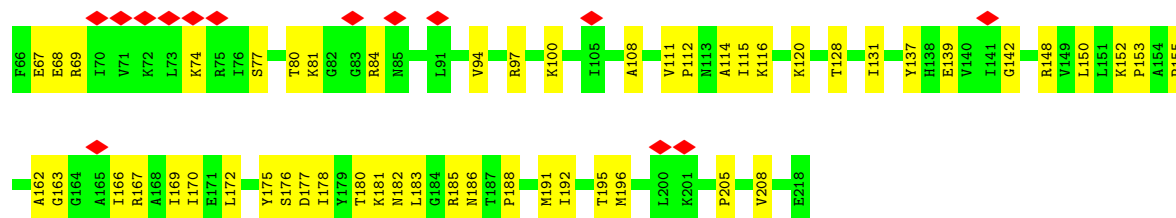


- Molecule 16: Small ribosomal subunit protein uS4

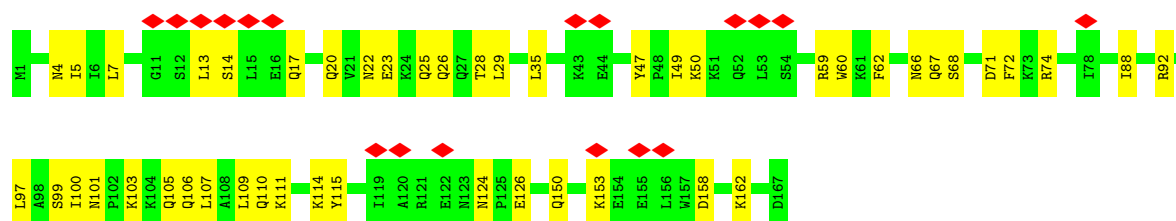




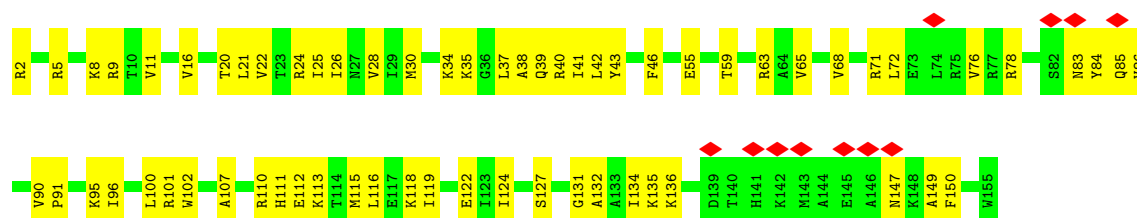
- Molecule 17: Small ribosomal subunit protein uS5



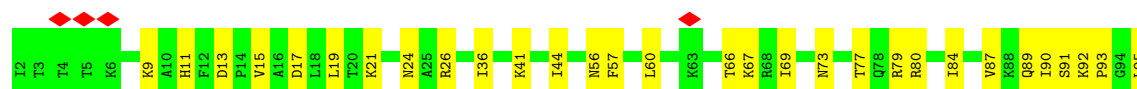
- Molecule 18: Small ribosomal subunit protein bS6



- Molecule 19: Small ribosomal subunit protein uS7



- Molecule 20: Small ribosomal subunit protein uS8

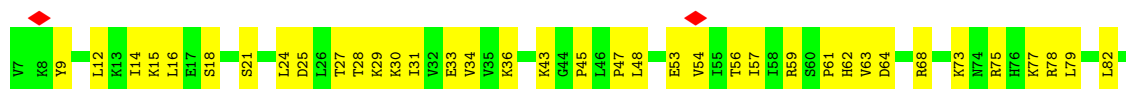




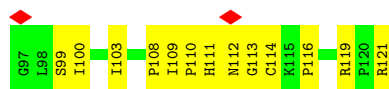
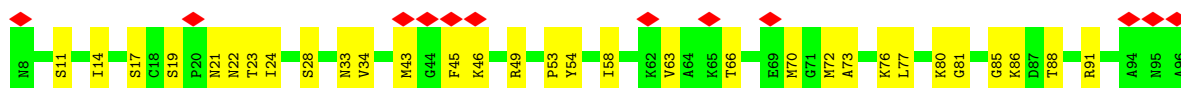
- Molecule 21: Small ribosomal subunit protein uS9



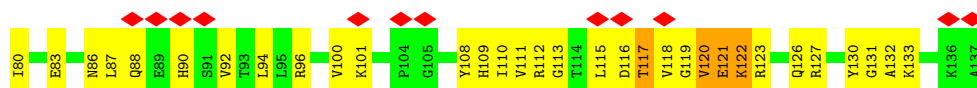
- Molecule 22: Small ribosomal subunit protein uS10



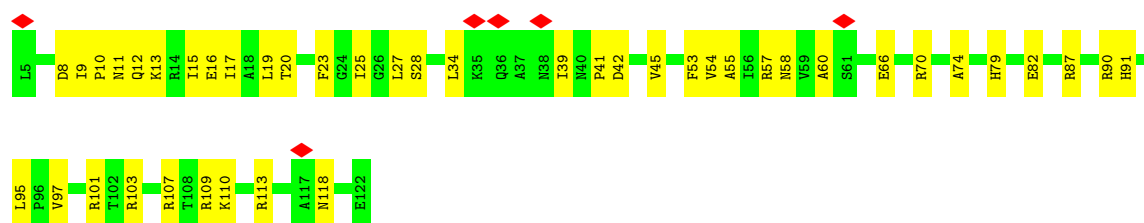
- Molecule 23: Small ribosomal subunit protein uS11



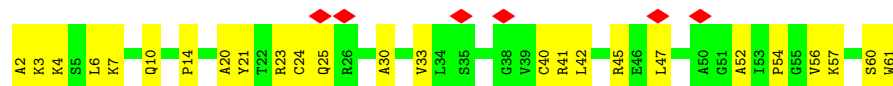
- Molecule 24: Small ribosomal subunit protein uS12



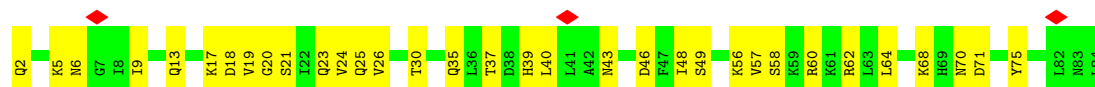
- Molecule 25: Small ribosomal subunit protein uS13



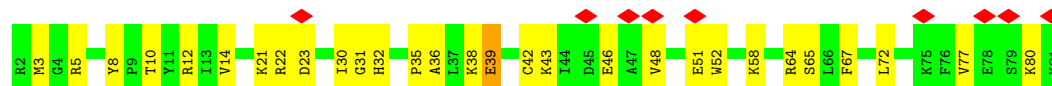
- Molecule 26: Small ribosomal subunit protein uS14



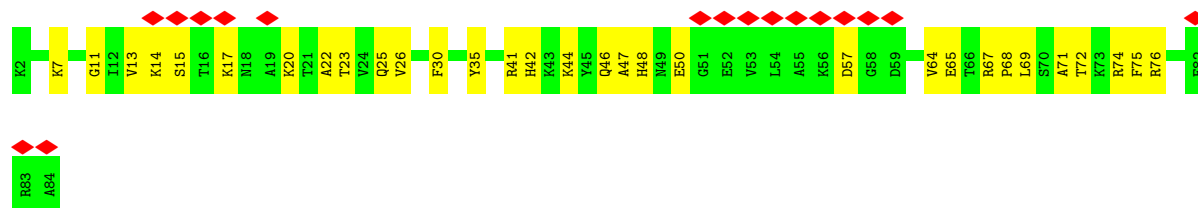
- Molecule 27: Small ribosomal subunit protein uS15



- Molecule 28: Small ribosomal subunit protein bS16



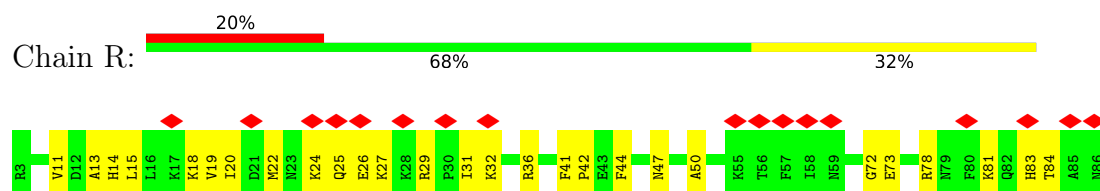
- Molecule 29: Small ribosomal subunit protein uS17



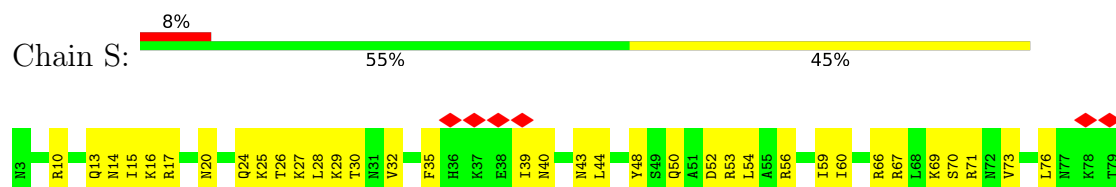
- Molecule 30: Small ribosomal subunit protein bS18



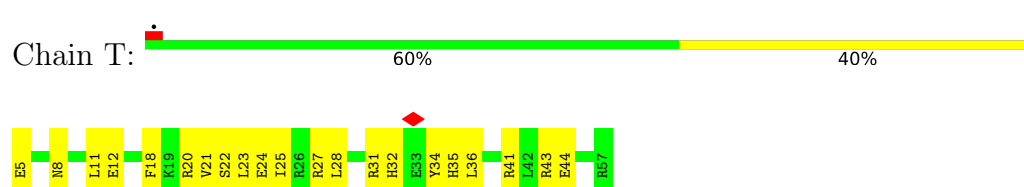
- Molecule 31: Small ribosomal subunit protein uS19



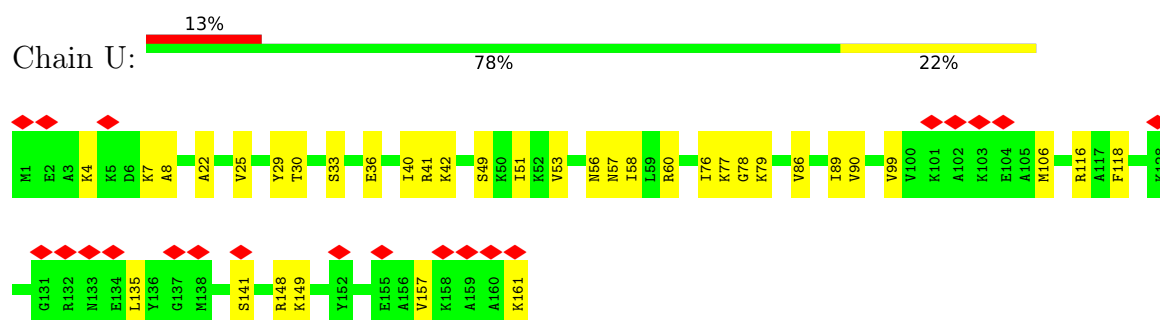
- Molecule 32: Small ribosomal subunit protein bS20



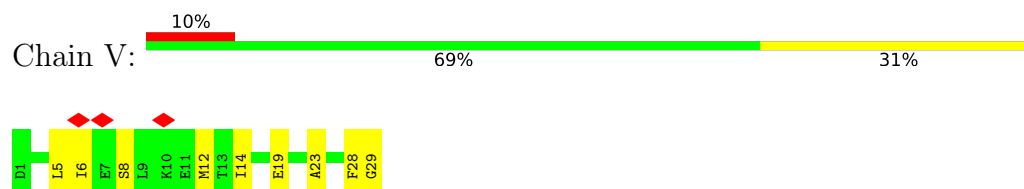
- Molecule 33: Small ribosomal subunit protein bS21



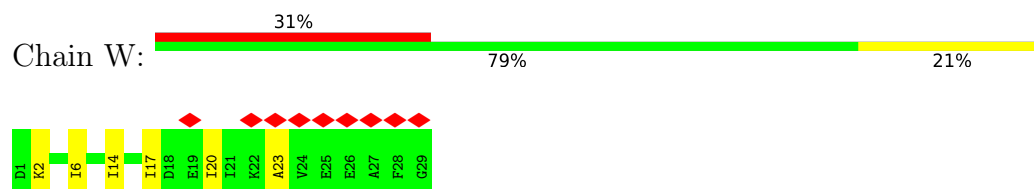
- Molecule 34: 50S ribosomal protein L10



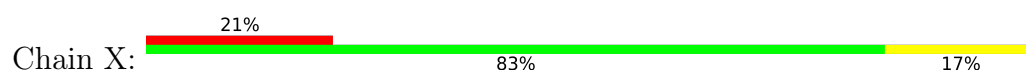
- Molecule 35: Large ribosomal subunit protein bL12



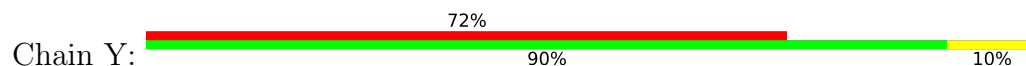
- Molecule 35: Large ribosomal subunit protein bL12



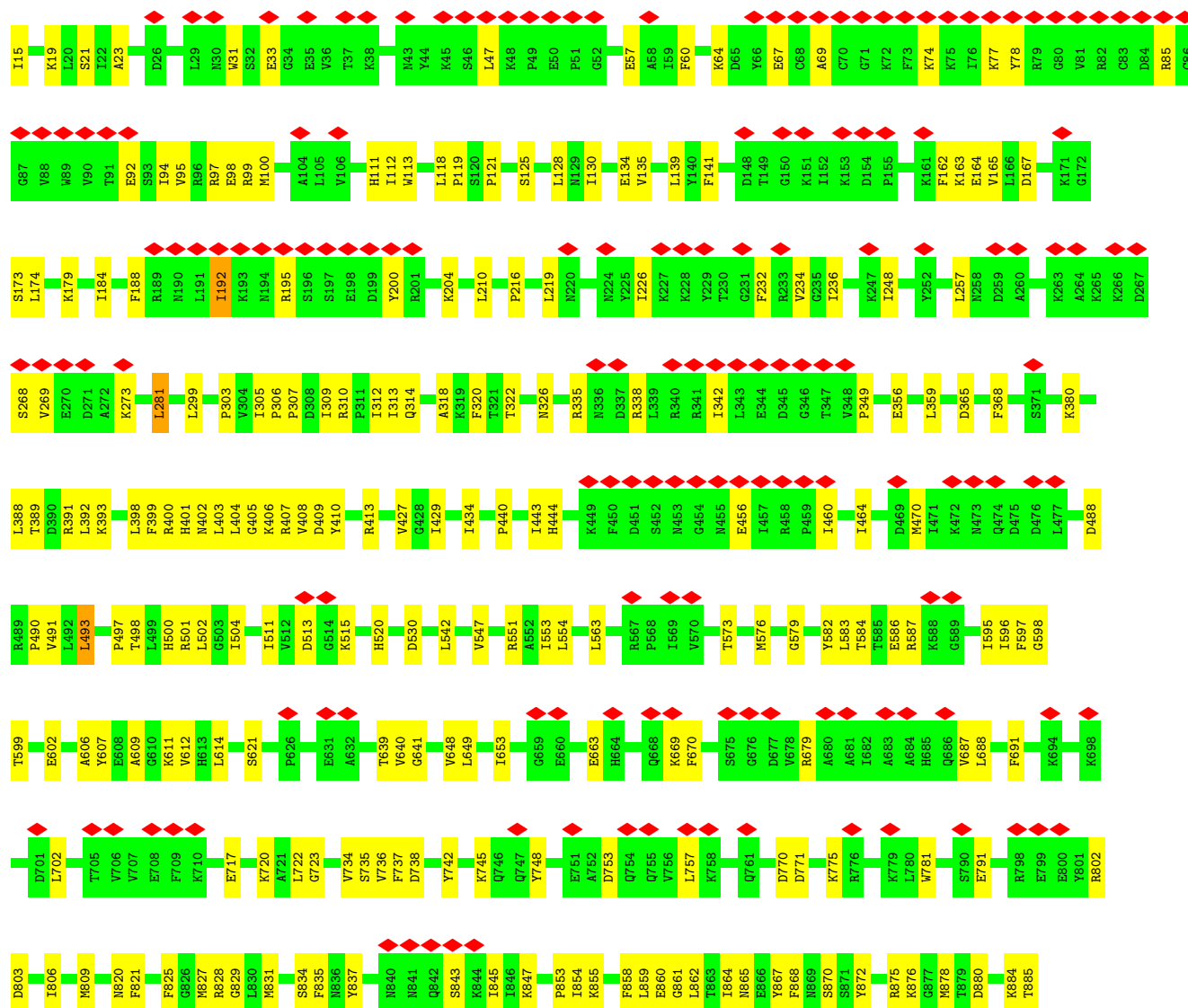
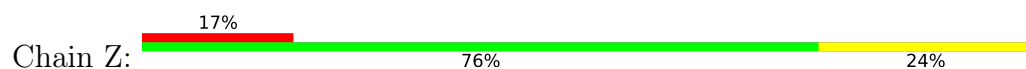
- Molecule 35: Large ribosomal subunit protein bL12

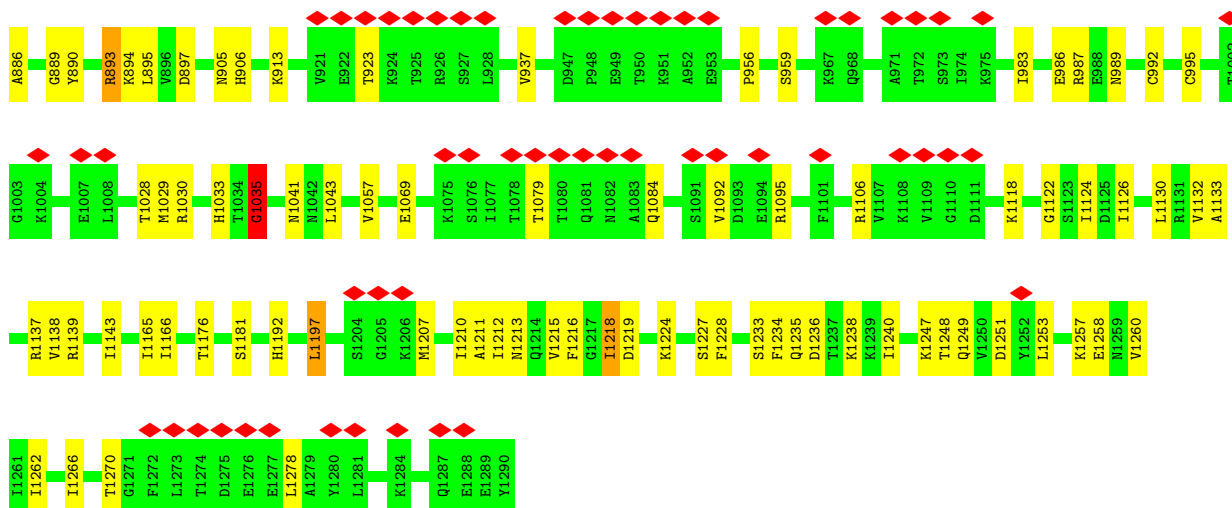


- Molecule 35: Large ribosomal subunit protein bL12

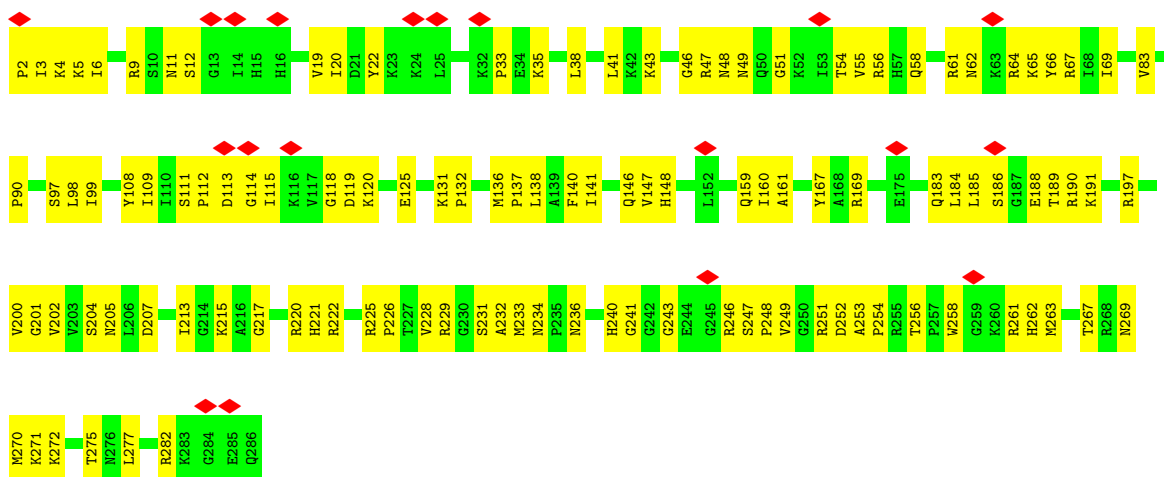


- Molecule 36: DNA-directed RNA polymerase subunit beta'

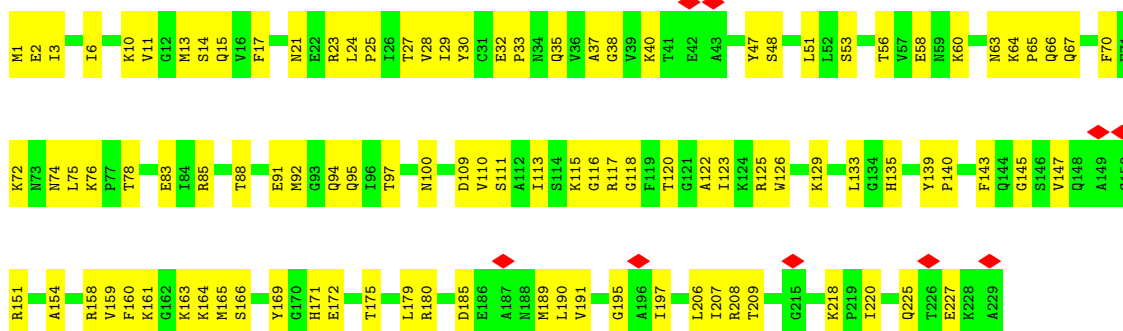




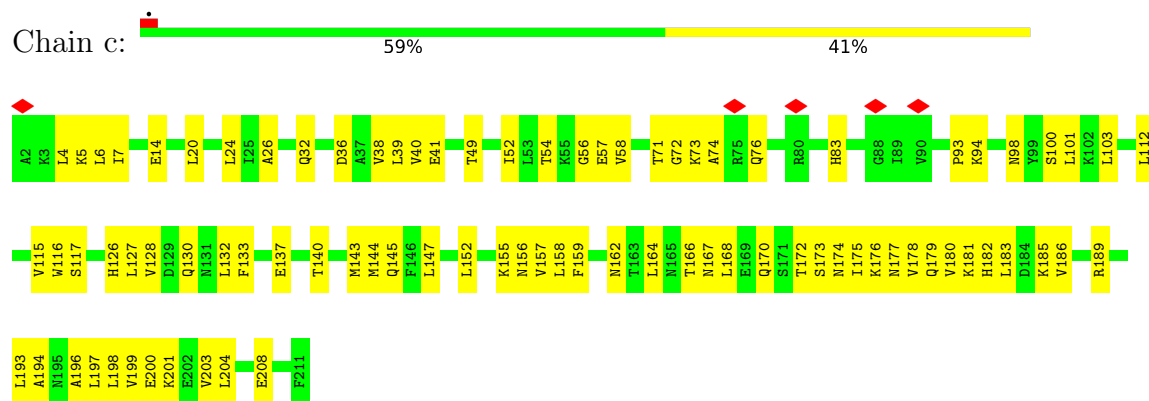
• Molecule 37: Large ribosomal subunit protein uL2



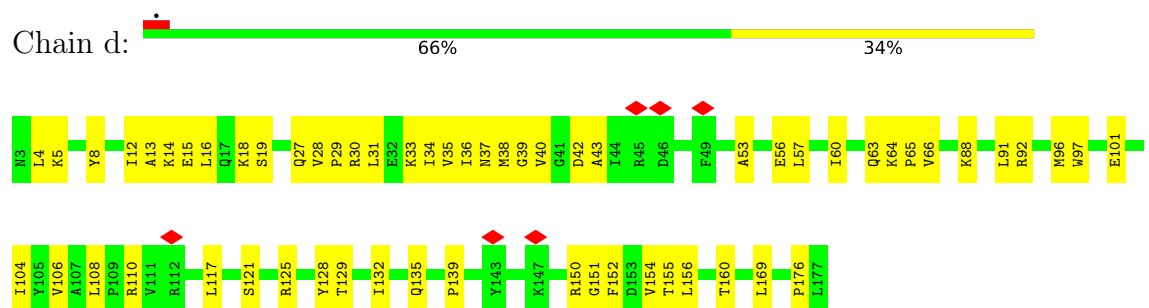
• Molecule 38: Large ribosomal subunit protein uL3



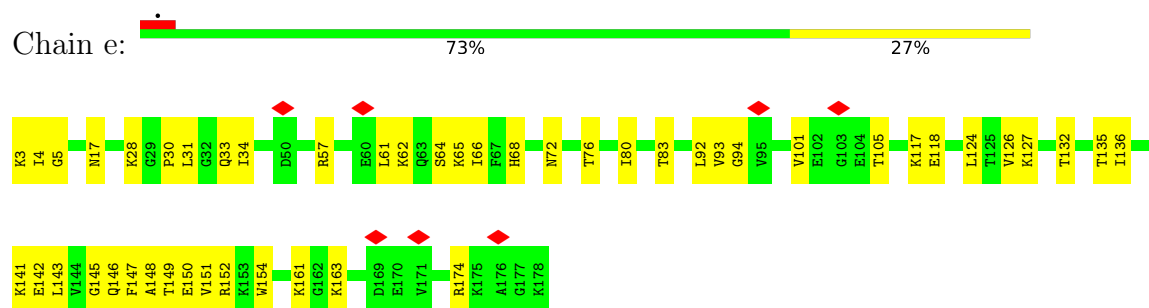
• Molecule 39: Large ribosomal subunit protein uL4



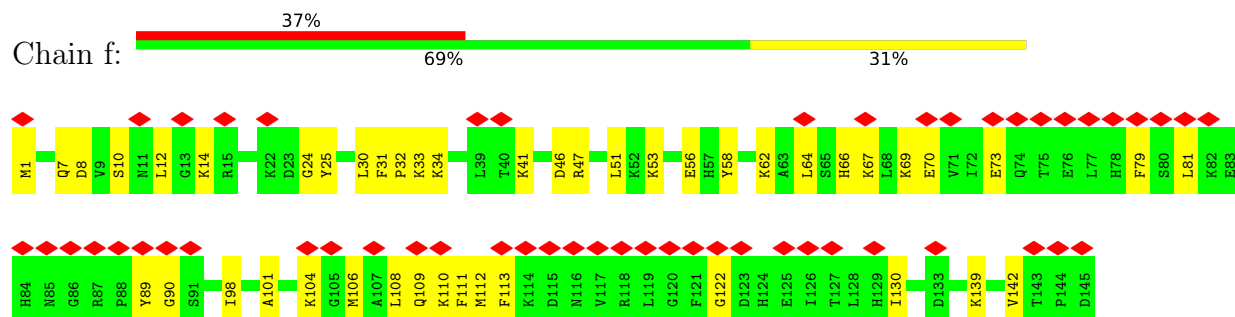
- Molecule 40: Large ribosomal subunit protein uL5



- Molecule 41: Large ribosomal subunit protein uL6

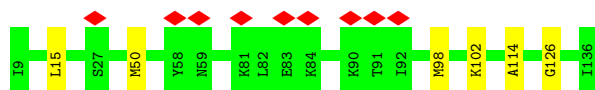


- Molecule 42: Large ribosomal subunit protein bL9



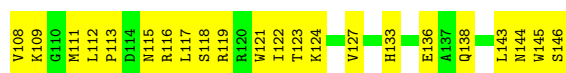
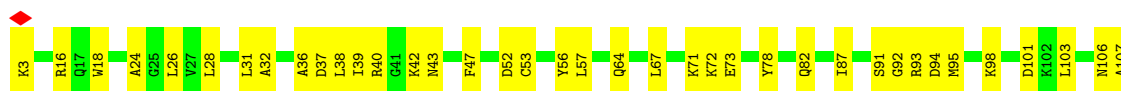
- Molecule 43: Large ribosomal subunit protein uL11





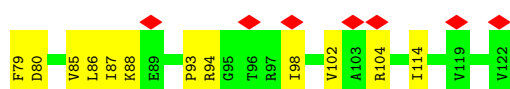
- Molecule 44: Large ribosomal subunit protein uL13

Chain i: 58% 42%



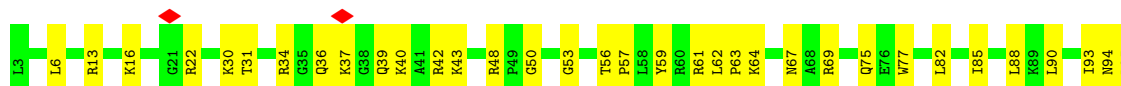
- Molecule 45: 50S ribosomal protein L14

Chain j: 15% 57% 43%



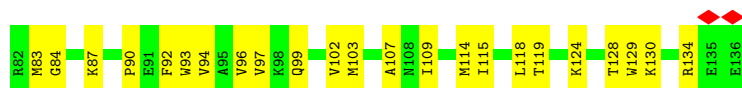
- Molecule 46: Large ribosomal subunit protein uL15

Chain k: 66% 34%



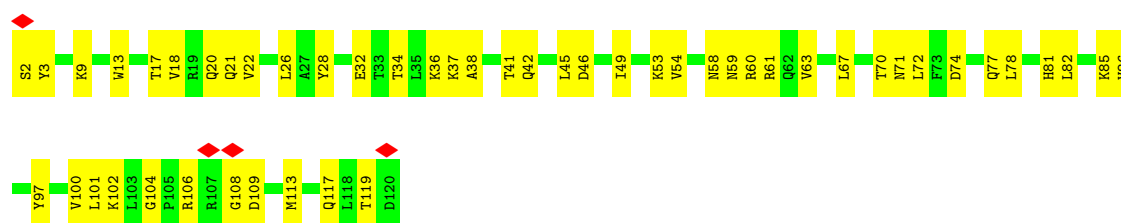
- Molecule 47: Large ribosomal subunit protein uL16

Chain l: 6% 60% 40%



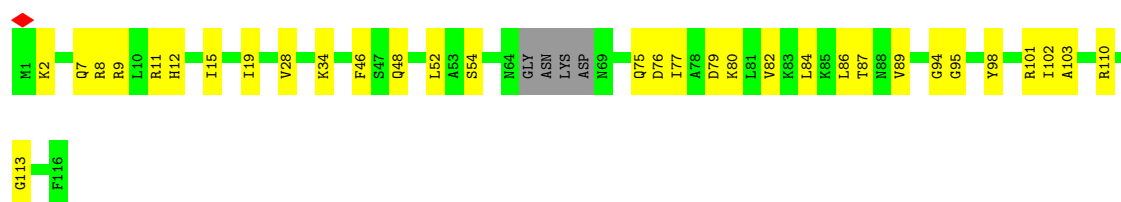
- Molecule 48: Large ribosomal subunit protein bL17

Chain m:  58% 42%



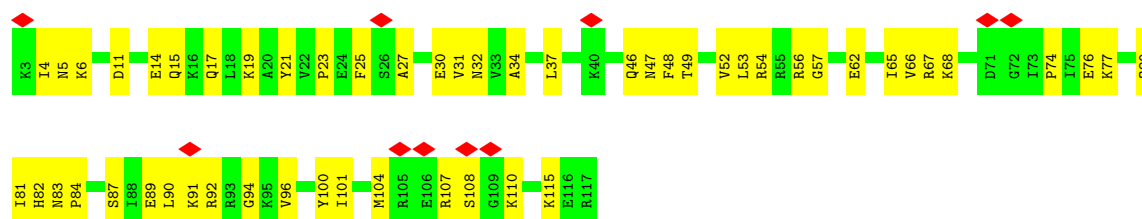
- Molecule 49: Large ribosomal subunit protein uL18

Chain n:  69% 28%



- Molecule 50: Large ribosomal subunit protein bL19

Chain o:  9% 54% 46%



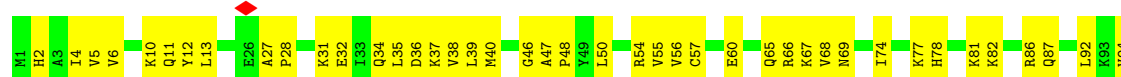
- Molecule 51: Large ribosomal subunit protein bL20

Chain p:  54% 46%



- Molecule 52: Large ribosomal subunit protein bL21

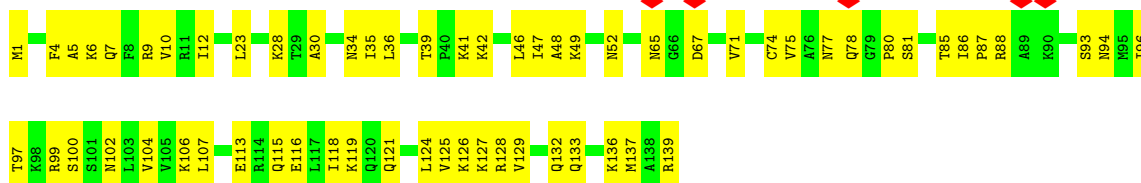
Chain q:  55% 45%





- Molecule 53: Large ribosomal subunit protein uL22

Chain r:



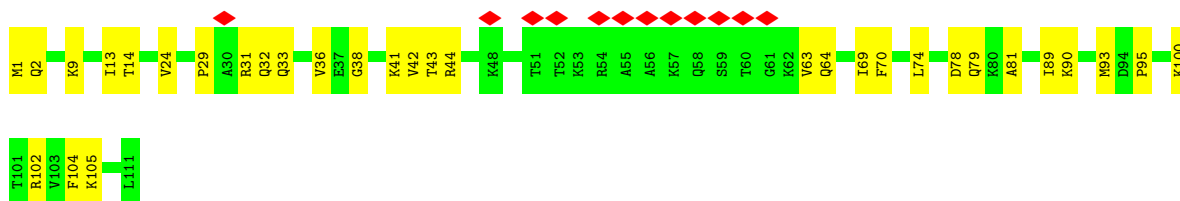
- Molecule 54: Large ribosomal subunit protein uL23

Chain s:



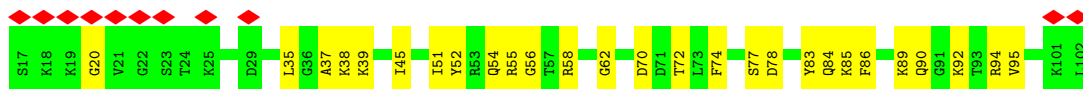
- Molecule 55: 50S ribosomal protein L24

Chain t:



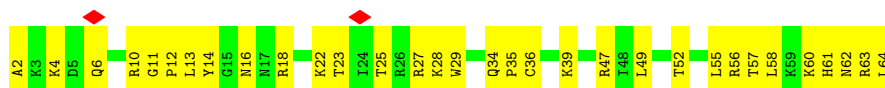
- Molecule 56: Large ribosomal subunit protein bL27

Chain u:



- Molecule 57: Large ribosomal subunit protein bL28

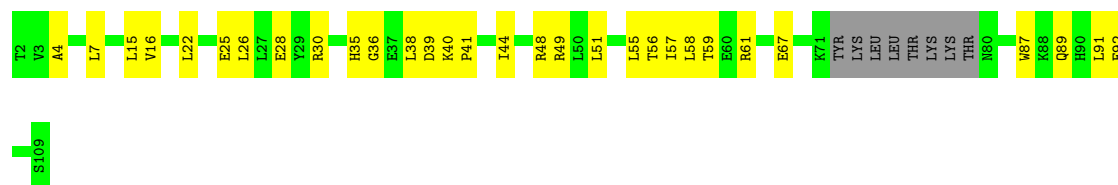
Chain v:



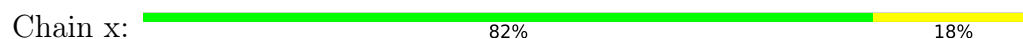
- Molecule 58: Large ribosomal subunit protein uL29

Chain w:

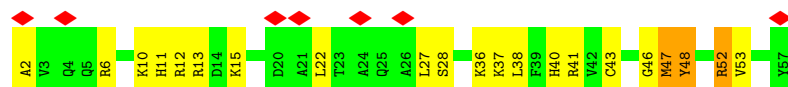




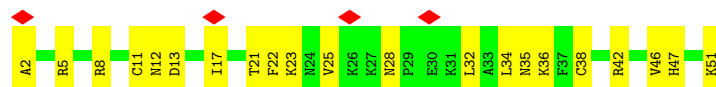
- Molecule 59: Large ribosomal subunit protein bL31



- Molecule 60: Large ribosomal subunit protein bL32



- Molecule 61: Large ribosomal subunit protein bL33A



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2584	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.017	Depositor
Minimum map value	-0.008	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00124	Depositor
Map size (Å)	600.0, 600.0, 600.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0, 2.0, 2.0	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.14	0/383	0.38	0/504
2	1	0.18	0/484	0.54	0/637
3	2	0.16	0/306	0.46	0/401
4	3	0.10	0/69073	0.23	0/107710
5	4	0.11	0/2505	0.28	0/3902
6	5	0.09	0/35768	0.22	0/55764
7	6	0.67	0/1954	0.98	0/2645
7	AA	0.67	0/1954	0.98	0/2645
8	7	0.11	0/1808	0.28	0/2817
9	8	0.70	0/11124	1.06	0/15014
10	9	0.69	0/792	1.05	0/1065
11	A	0.15	0/1954	0.43	0/2642
12	AB	0.47	0/745	0.61	1/1149 (0.1%)
13	AC	0.65	1/725 (0.1%)	0.75	2/1115 (0.2%)
14	AD	0.71	0/1298	1.00	0/1752
15	B	0.18	0/1721	0.49	0/2323
16	C	0.17	0/1691	0.49	0/2267
17	D	0.19	0/1188	0.52	1/1593 (0.1%)
18	E	0.16	0/1384	0.48	2/1867 (0.1%)
19	F	0.19	0/1266	0.56	1/1700 (0.1%)
20	G	0.17	0/1126	0.53	0/1517
21	H	0.17	0/1044	0.47	0/1395
22	I	0.20	0/820	0.58	1/1103 (0.1%)
23	J	0.15	0/844	0.44	0/1136
24	K	0.28	0/1094	0.60	2/1468 (0.1%)
25	L	0.18	0/962	0.50	0/1289
26	M	0.18	0/483	0.51	0/643
27	N	0.15	0/679	0.49	1/907 (0.1%)
28	O	0.18	0/659	0.57	1/885 (0.1%)
29	P	0.15	0/684	0.42	0/913
30	Q	0.20	0/545	0.60	0/730
31	R	0.16	0/698	0.49	0/936
32	S	0.17	0/631	0.46	0/838
33	T	0.20	0/475	0.56	0/621

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	U	0.68	0/1254	1.11	0/1677
35	V	0.64	0/232	1.16	2/307 (0.7%)
35	W	0.60	0/232	1.09	0/307
35	X	0.64	0/232	1.04	0/307
35	Y	0.63	0/232	1.07	0/307
36	Z	0.71	0/10259	1.06	2/13846 (0.0%)
37	a	0.16	0/2267	0.43	0/3044
38	b	0.17	0/1795	0.51	0/2412
39	c	0.19	0/1671	0.51	1/2246 (0.0%)
40	d	0.16	0/1409	0.44	0/1894
41	e	0.15	0/1420	0.43	0/1912
42	f	0.19	0/1183	0.56	2/1587 (0.1%)
43	h	0.16	0/968	0.43	0/1298
44	i	0.15	0/1186	0.46	0/1592
45	j	0.16	0/953	0.47	0/1275
46	k	0.17	0/1170	0.46	0/1559
47	l	0.18	0/1104	0.47	0/1481
48	m	0.22	0/973	0.58	0/1309
49	n	0.18	0/897	0.53	0/1198
50	o	0.17	0/948	0.50	0/1262
51	p	0.19	0/961	0.48	0/1278
52	q	0.18	0/828	0.56	0/1111
53	r	0.18	0/1077	0.52	0/1441
54	s	0.17	0/732	0.52	1/988 (0.1%)
55	t	0.15	0/879	0.44	0/1165
56	u	0.15	0/665	0.43	0/884
57	v	0.22	0/519	0.53	0/695
58	w	0.18	0/826	0.47	0/1104
59	x	0.17	0/353	0.40	0/474
60	y	0.32	0/457	0.68	0/601
61	z	0.15	0/412	0.48	0/547
All	All	0.30	1/186961 (0.0%)	0.50	20/275001 (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
9	8	0	1
20	G	0	1
23	J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	O	0	1
36	Z	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	AC	22	DA	O3'-P	-15.40	1.38	1.61

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	AC	22	DA	P-O3'-C3'	14.74	142.31	120.20
12	AB	17	DT	P-O3'-C3'	8.55	133.03	120.20
13	AC	22	DA	O3'-P-O5'	-8.22	91.67	104.00
19	F	16	VAL	N-CA-C	-6.76	107.28	113.71
18	E	162	LYS	CA-C-N	6.26	133.50	121.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	8	858	TYR	Sidechain
20	G	108	LEU	Peptide
23	J	111	HIS	Peptide
28	O	39	GLU	Peptide
36	Z	893	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	380	0	429	10	0
2	1	477	0	530	24	0
3	2	304	0	350	16	0
4	3	61664	0	30953	1941	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	4	2239	0	1137	64	0
6	5	31943	0	16058	939	0
7	6	1920	0	1957	97	0
7	AA	1920	0	1959	86	0
8	7	1618	0	821	43	0
9	8	10948	0	11059	949	0
10	9	770	0	742	30	0
11	A	1921	0	1973	64	0
12	AB	663	0	361	86	0
13	AC	649	0	364	128	0
14	AD	1277	0	1329	137	0
15	B	1698	0	1762	144	0
16	C	1660	0	1718	69	0
17	D	1173	0	1267	33	0
18	E	1362	0	1377	41	0
19	F	1246	0	1308	54	0
20	G	1110	0	1226	41	0
21	H	1028	0	1094	35	0
22	I	809	0	889	79	0
23	J	829	0	855	39	0
24	K	1076	0	1170	48	0
25	L	951	0	1014	34	0
26	M	474	0	509	23	0
27	N	673	0	730	30	0
28	O	646	0	677	25	0
29	P	675	0	728	25	0
30	Q	535	0	562	23	0
31	R	682	0	691	24	0
32	S	629	0	681	34	0
33	T	471	0	522	18	0
34	U	1239	0	1301	128	0
35	V	232	0	237	9	0
35	W	232	0	237	7	0
35	X	232	0	237	9	0
35	Y	232	0	237	7	0
36	Z	10085	0	10377	782	0
37	a	2225	0	2301	106	0
38	b	1762	0	1808	91	0
39	c	1644	0	1731	70	0
40	d	1388	0	1469	46	0
41	e	1396	0	1481	33	0
42	f	1160	0	1172	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	h	959	0	1039	9	0
44	i	1164	0	1192	52	0
45	j	944	0	1019	45	0
46	k	1153	0	1256	46	0
47	l	1079	0	1134	48	0
48	m	958	0	1011	40	0
49	n	889	0	952	26	0
50	o	938	0	1008	47	0
51	p	947	0	1028	64	0
52	q	811	0	858	38	0
53	r	1068	0	1150	53	0
54	s	720	0	803	20	0
55	t	872	0	972	18	0
56	u	657	0	695	22	0
57	v	513	0	560	29	0
58	w	818	0	870	20	0
59	x	344	0	333	4	0
60	y	452	0	472	22	0
61	z	408	0	440	16	0
All	All	173941	0	128182	5778	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 20.

The worst 5 of 5778 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)
4:3:1081:A:C4	34:U:7:LYS:HD3	1.25	1.70
9:8:1344:LYS:HG3	36:Z:309:ILE:CD1	1.26	1.57
9:8:965:MET:HE2	15:B:78:ILE:CG2	1.19	1.57
9:8:1342:LEU:CD1	36:Z:392:LEU:CD2	1.79	1.56
9:8:1342:LEU:CB	36:Z:398:LEU:CD2	1.84	1.54

There are no symmetry-related clashes.

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	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
7	6	245/247 (99%)	242 (99%)	3 (1%)	0	100	100
7	AA	245/247 (99%)	242 (99%)	3 (1%)	0	100	100
9	8	1389/1391 (100%)	1355 (98%)	33 (2%)	1 (0%)	48	83
10	9	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
11	A	238/240 (99%)	222 (93%)	16 (7%)	0	100	100
14	AD	158/160 (99%)	155 (98%)	1 (1%)	2 (1%)	9	42
15	B	213/215 (99%)	196 (92%)	17 (8%)	0	100	100
16	C	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
17	D	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
18	E	165/167 (99%)	147 (89%)	18 (11%)	0	100	100
19	F	152/154 (99%)	135 (89%)	17 (11%)	0	100	100
20	G	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
21	H	126/128 (98%)	115 (91%)	11 (9%)	0	100	100
22	I	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
23	J	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
24	K	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
25	L	116/118 (98%)	104 (90%)	12 (10%)	0	100	100
26	M	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
27	N	81/83 (98%)	81 (100%)	0	0	100	100
28	O	78/80 (98%)	70 (90%)	8 (10%)	0	100	100
29	P	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
30	Q	63/65 (97%)	52 (82%)	11 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	R	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
32	S	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
33	T	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
34	U	159/161 (99%)	154 (97%)	4 (2%)	1 (1%)	21	59
35	V	27/29 (93%)	27 (100%)	0	0	100	100
35	W	27/29 (93%)	27 (100%)	0	0	100	100
35	X	27/29 (93%)	27 (100%)	0	0	100	100
35	Y	27/29 (93%)	27 (100%)	0	0	100	100
36	Z	1274/1276 (100%)	1252 (98%)	21 (2%)	1 (0%)	48	83
37	a	283/285 (99%)	265 (94%)	18 (6%)	0	100	100
38	b	227/229 (99%)	214 (94%)	13 (6%)	0	100	100
39	c	208/210 (99%)	197 (95%)	11 (5%)	0	100	100
40	d	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
41	e	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
42	f	143/145 (99%)	125 (87%)	18 (13%)	0	100	100
43	h	126/128 (98%)	114 (90%)	12 (10%)	0	100	100
44	i	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
45	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
46	k	146/148 (99%)	139 (95%)	7 (5%)	0	100	100
47	l	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
48	m	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
49	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
50	o	113/115 (98%)	101 (89%)	12 (11%)	0	100	100
51	p	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
52	q	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
53	r	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
54	s	90/92 (98%)	88 (98%)	2 (2%)	0	100	100
55	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
56	u	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
57	v	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
58	w	96/108 (89%)	89 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	x	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
60	y	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
61	z	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
All	All	9361/9495 (99%)	8905 (95%)	451 (5%)	5 (0%)	49	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	AD	95	ARG
9	8	582	LYS
36	Z	1035	GLY
34	U	106	MET
14	AD	17	VAL

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	40/40 (100%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
7	6	212/212 (100%)	206 (97%)	6 (3%)	38	59
7	AA	212/212 (100%)	207 (98%)	5 (2%)	43	64
9	8	1213/1213 (100%)	1188 (98%)	25 (2%)	47	65
10	9	83/83 (100%)	79 (95%)	4 (5%)	23	44
11	A	212/212 (100%)	211 (100%)	1 (0%)	81	83
14	AD	140/140 (100%)	134 (96%)	6 (4%)	26	47
15	B	180/180 (100%)	180 (100%)	0	100	100
16	C	181/181 (100%)	181 (100%)	0	100	100
17	D	123/123 (100%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	E	150/150 (100%)	150 (100%)	0	100	100
19	F	131/131 (100%)	131 (100%)	0	100	100
20	G	123/123 (100%)	123 (100%)	0	100	100
21	H	111/111 (100%)	111 (100%)	0	100	100
22	I	95/95 (100%)	95 (100%)	0	100	100
23	J	91/91 (100%)	91 (100%)	0	100	100
24	K	117/117 (100%)	114 (97%)	3 (3%)	40	62
25	L	100/100 (100%)	99 (99%)	1 (1%)	68	78
26	M	47/47 (100%)	47 (100%)	0	100	100
27	N	76/76 (100%)	76 (100%)	0	100	100
28	O	69/69 (100%)	69 (100%)	0	100	100
29	P	73/73 (100%)	73 (100%)	0	100	100
30	Q	56/56 (100%)	56 (100%)	0	100	100
31	R	74/74 (100%)	74 (100%)	0	100	100
32	S	70/70 (100%)	70 (100%)	0	100	100
33	T	49/49 (100%)	49 (100%)	0	100	100
34	U	129/129 (100%)	129 (100%)	0	100	100
35	V	26/26 (100%)	26 (100%)	0	100	100
35	W	26/26 (100%)	26 (100%)	0	100	100
35	X	26/26 (100%)	26 (100%)	0	100	100
35	Y	26/26 (100%)	26 (100%)	0	100	100
36	Z	1113/1113 (100%)	1100 (99%)	13 (1%)	63	75
37	a	241/241 (100%)	241 (100%)	0	100	100
38	b	186/186 (100%)	186 (100%)	0	100	100
39	c	182/182 (100%)	182 (100%)	0	100	100
40	d	150/150 (100%)	150 (100%)	0	100	100
41	e	153/153 (100%)	153 (100%)	0	100	100
42	f	123/131 (94%)	123 (100%)	0	100	100
43	h	102/102 (100%)	102 (100%)	0	100	100
44	i	126/126 (100%)	126 (100%)	0	100	100
45	j	103/103 (100%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	k	123/123 (100%)	123 (100%)	0	100	100
47	l	113/113 (100%)	113 (100%)	0	100	100
48	m	105/105 (100%)	105 (100%)	0	100	100
49	n	96/99 (97%)	96 (100%)	0	100	100
50	o	101/101 (100%)	101 (100%)	0	100	100
51	p	100/100 (100%)	100 (100%)	0	100	100
52	q	90/90 (100%)	90 (100%)	0	100	100
53	r	116/116 (100%)	116 (100%)	0	100	100
54	s	82/82 (100%)	82 (100%)	0	100	100
55	t	96/96 (100%)	96 (100%)	0	100	100
56	u	69/69 (100%)	69 (100%)	0	100	100
57	v	58/58 (100%)	58 (100%)	0	100	100
58	w	87/95 (92%)	87 (100%)	0	100	100
59	x	41/41 (100%)	41 (100%)	0	100	100
60	y	48/48 (100%)	45 (94%)	3 (6%)	16	37
61	z	47/47 (100%)	47 (100%)	0	100	100
All	All	8198/8217 (100%)	8131 (99%)	67 (1%)	70	80

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	Z	757	LEU
36	Z	937	VAL
60	y	48	TYR
9	8	863	LEU
9	8	673	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
29	P	5	GLN
57	v	16	ASN
36	Z	500	HIS
57	v	6	GLN
49	n	75	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	3	2875/2893 (99%)	733 (25%)	25 (0%)
5	4	103/108 (95%)	34 (33%)	5 (4%)
6	5	1490/1505 (99%)	349 (23%)	6 (0%)
8	7	75/76 (98%)	25 (33%)	2 (2%)
All	All	4543/4582 (99%)	1141 (25%)	38 (0%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	12	A
4	3	14	U
4	3	15	A
4	3	17	G
4	3	29	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	4	59	A
6	5	1373	A
5	4	70	G
6	5	448	A
8	7	19	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	AC	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AC	22:DA	O3'	23:DC	P	1.38

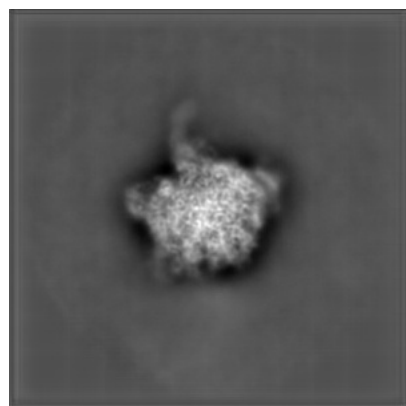
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53668. These allow visual inspection of the internal detail of the map and identification of artifacts.

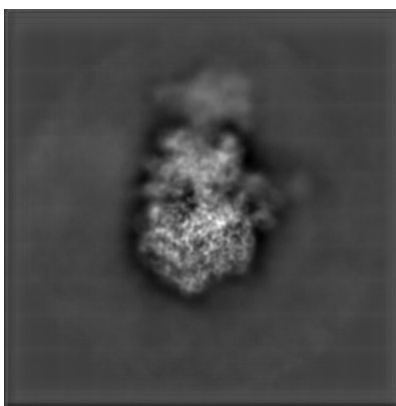
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

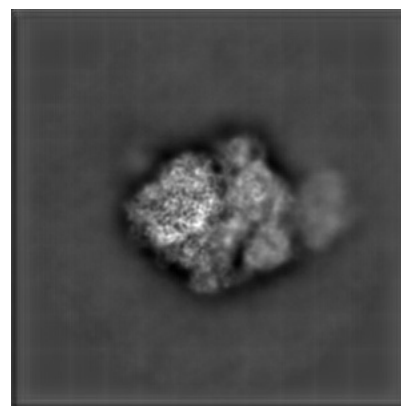
6.1.1 Primary map



X

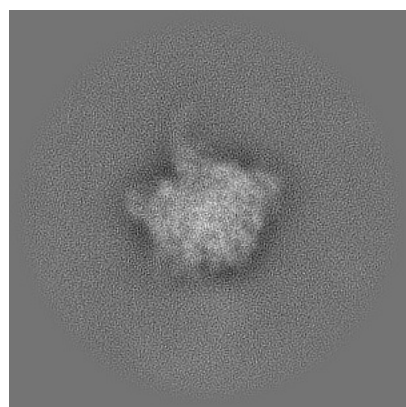


Y

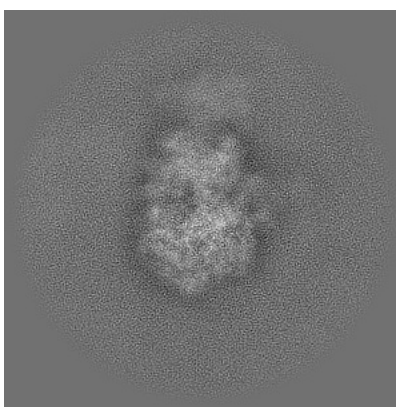


Z

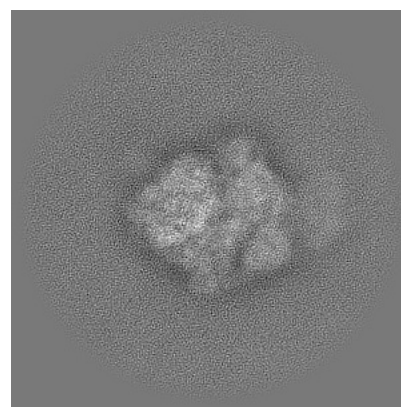
6.1.2 Raw map



X



Y

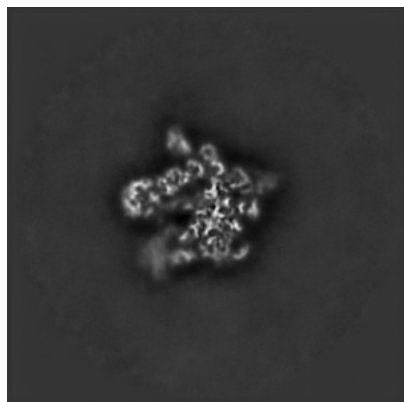


Z

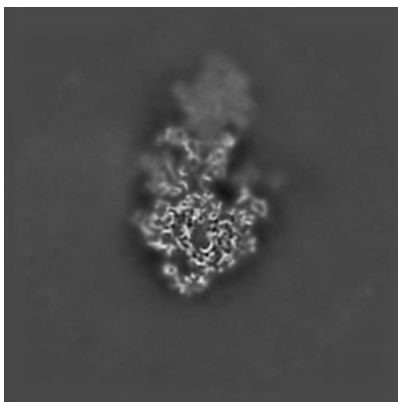
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

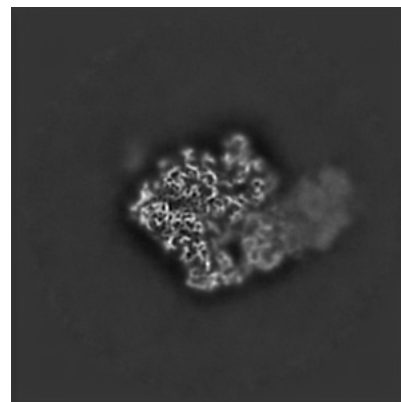
6.2.1 Primary map



X Index: 150

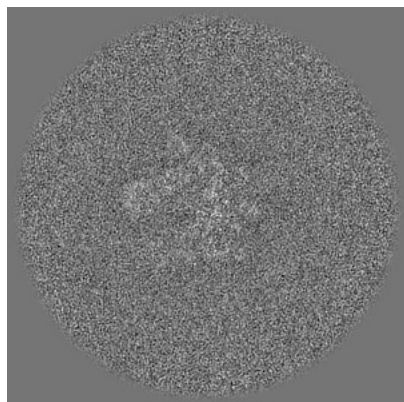


Y Index: 150

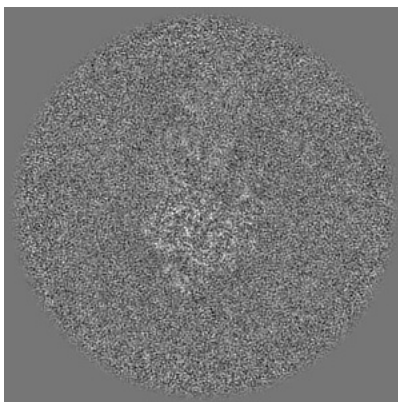


Z Index: 150

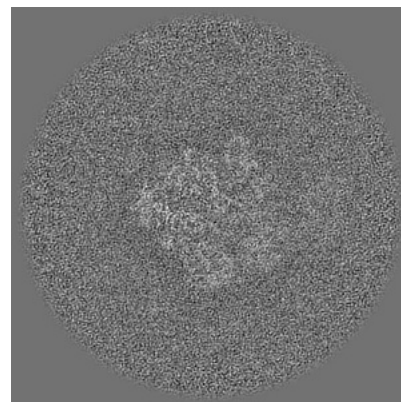
6.2.2 Raw map



X Index: 150



Y Index: 150

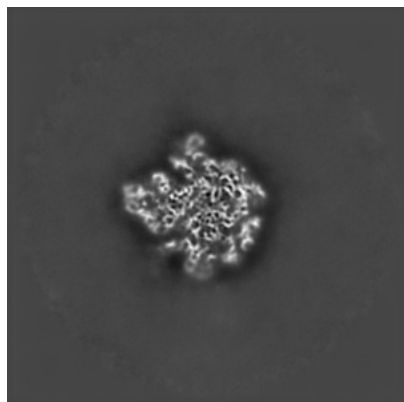


Z Index: 150

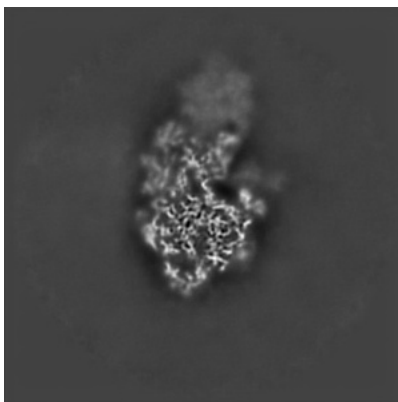
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

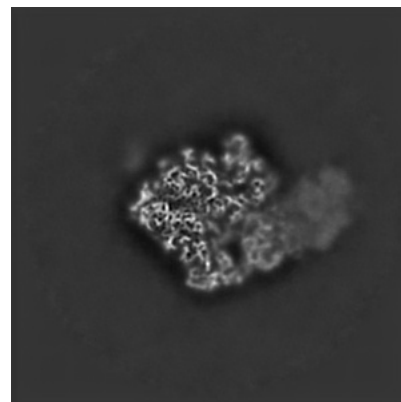
6.3.1 Primary map



X Index: 139

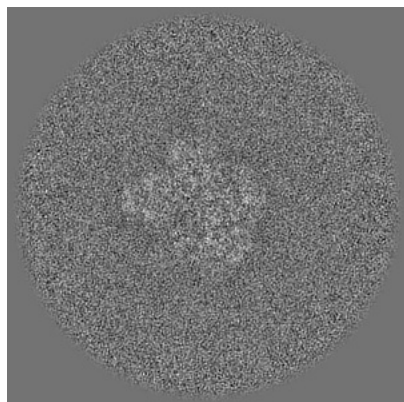


Y Index: 154

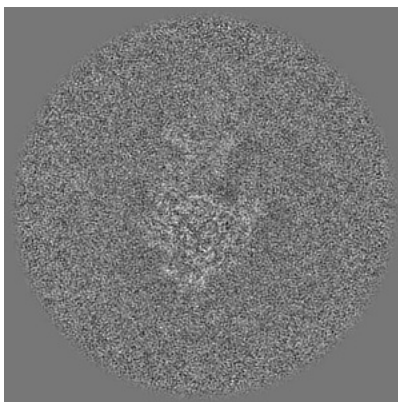


Z Index: 150

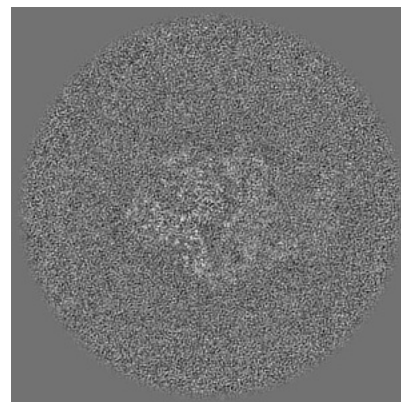
6.3.2 Raw map



X Index: 145



Y Index: 149

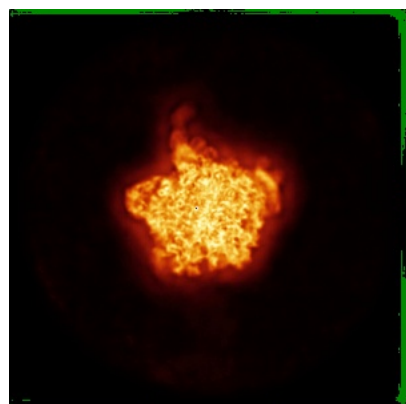


Z Index: 144

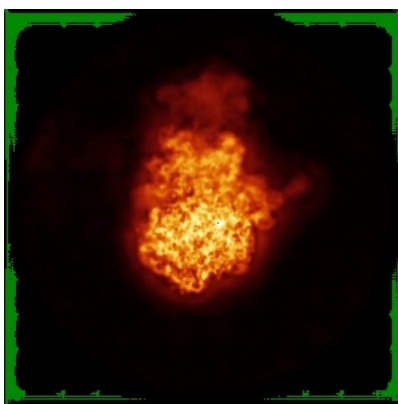
The images above show the largest variance slices of the map in three orthogonal directions.

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

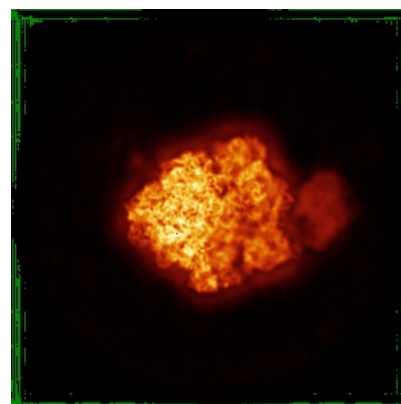
6.4.1 Primary map



X

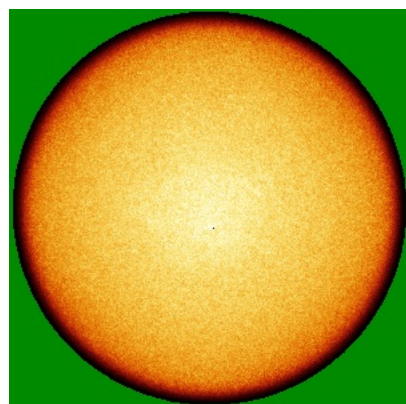


Y

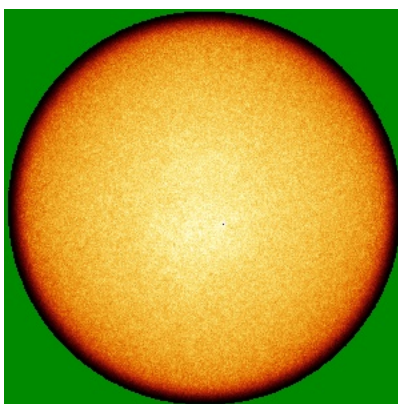


Z

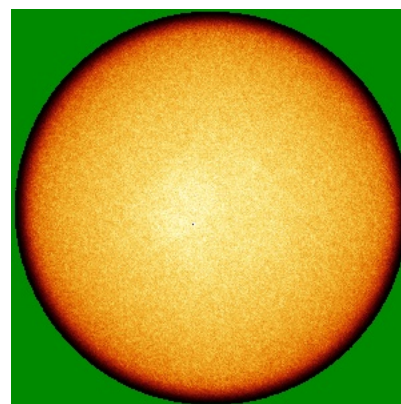
6.4.2 Raw map



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](#)

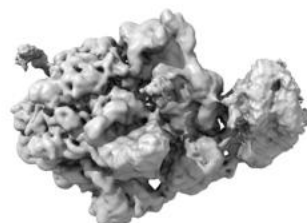
6.5.1 Primary map



X



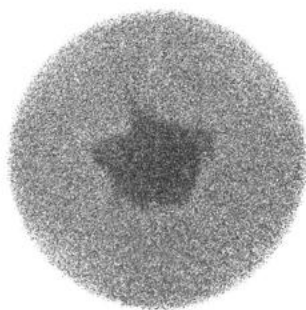
Y



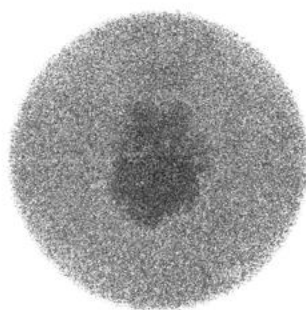
Z

The images above show the 3D surface view of the map at the recommended contour level 0.00124. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

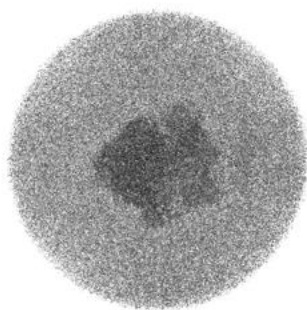
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

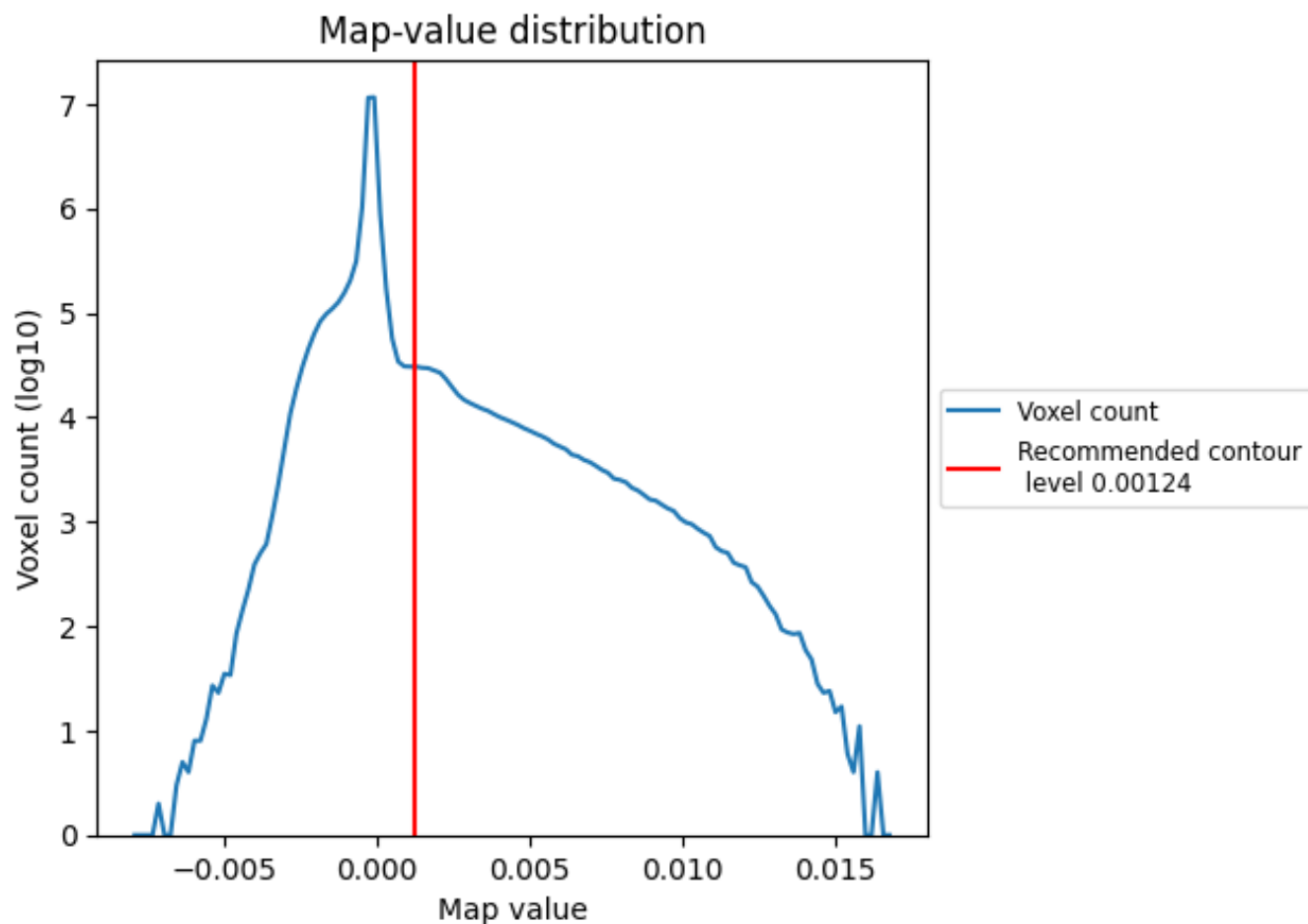
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

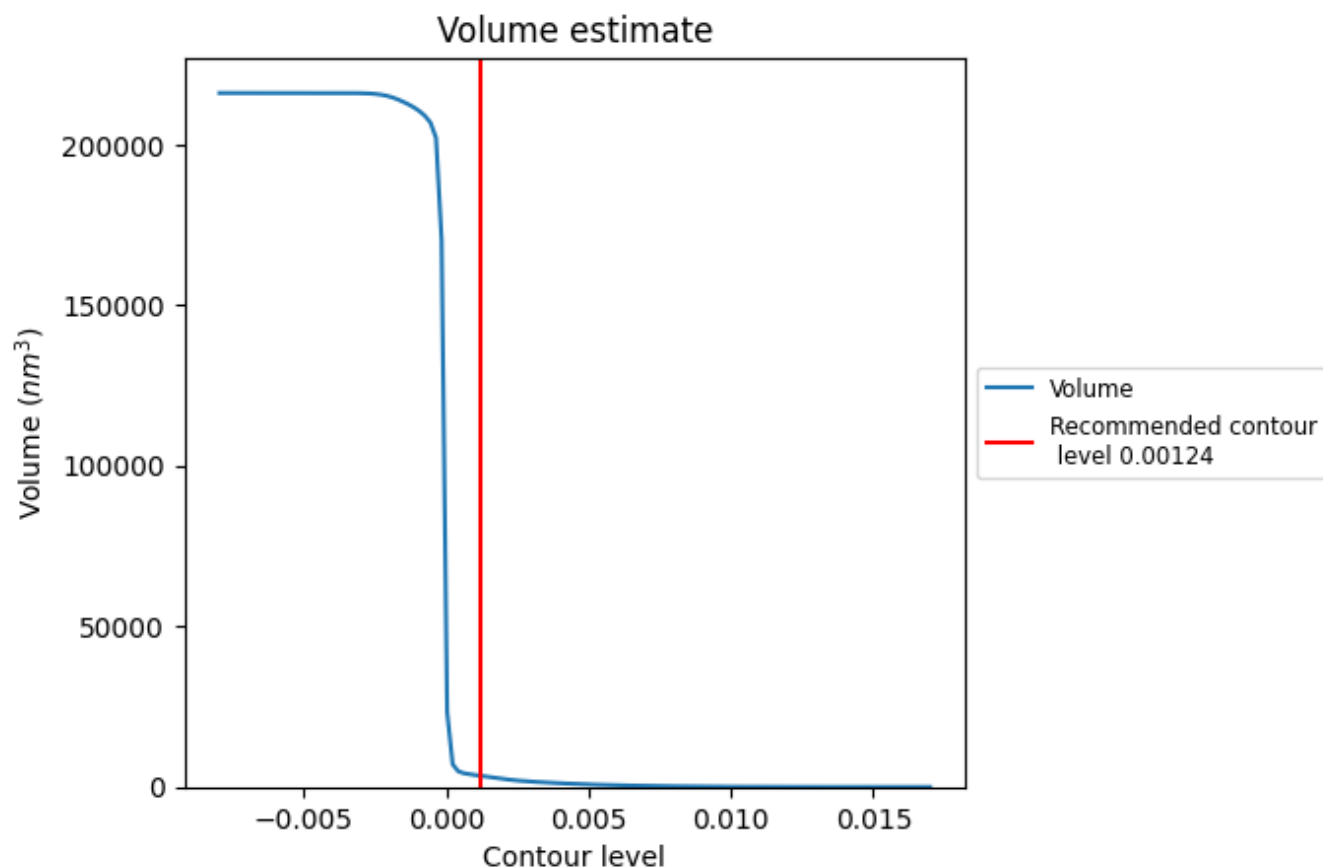
This section contains the results of statistical analysis of the map.

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.

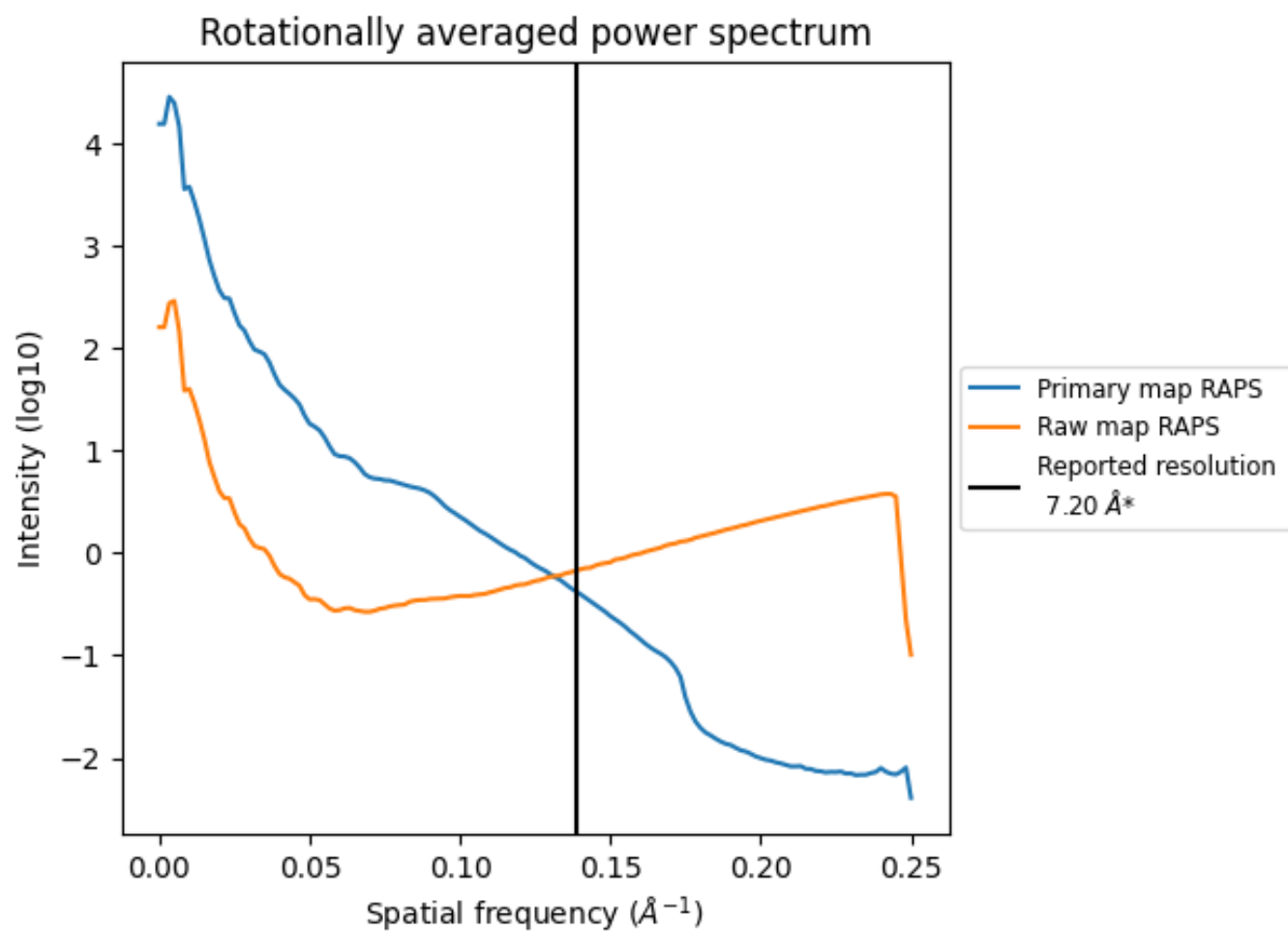
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3433 nm³; this corresponds to an approximate mass of 3101 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 ⓘ

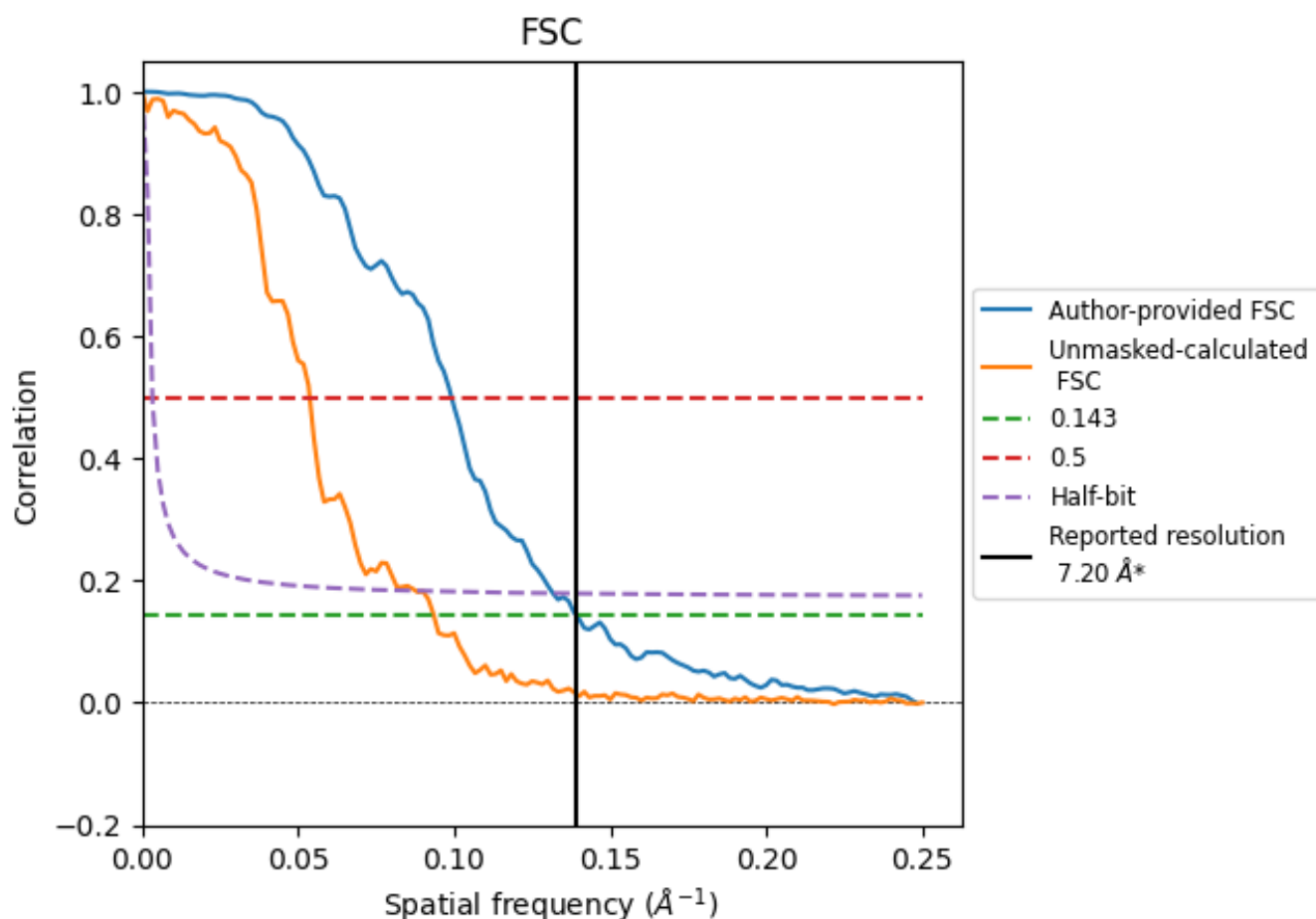


*Reported resolution corresponds to spatial frequency of 0.139 $\text{\AA}^{-1}$

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 0.139 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

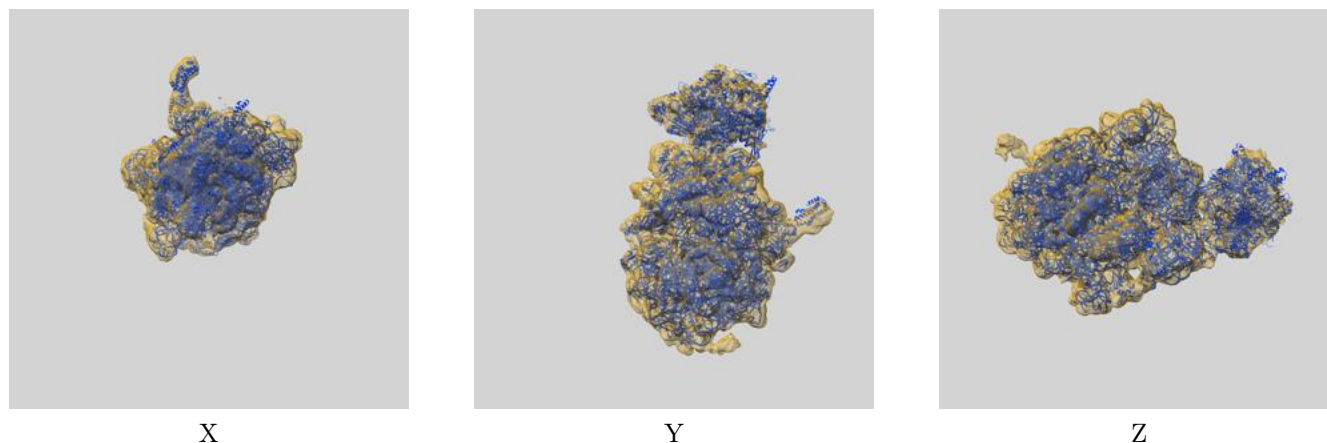
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.20	-	-
Author-provided FSC curve	7.19	10.08	7.60
Unmasked-calculated*	10.70	18.62	11.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.70 differs from the reported value 7.2 by more than 10 %

9 Map-model fit [i](#)

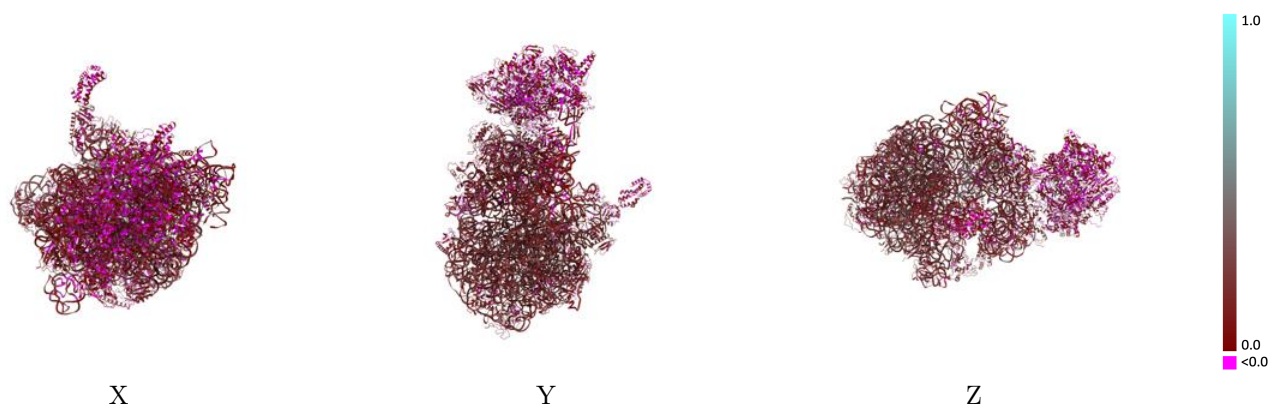
This section contains information regarding the fit between EMDB map EMD-53668 and PDB model 9SL4. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



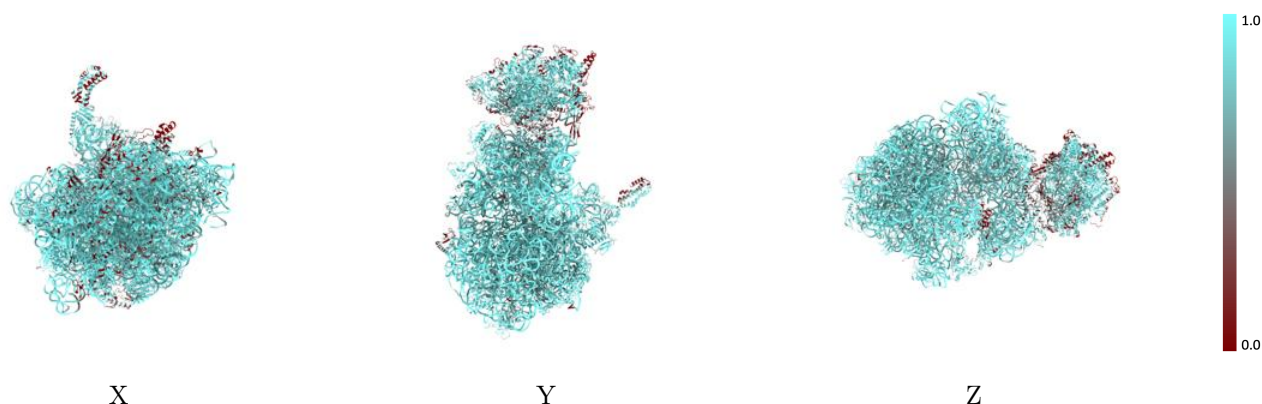
The images above show the 3D surface view of the map at the recommended contour level 0.00124 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



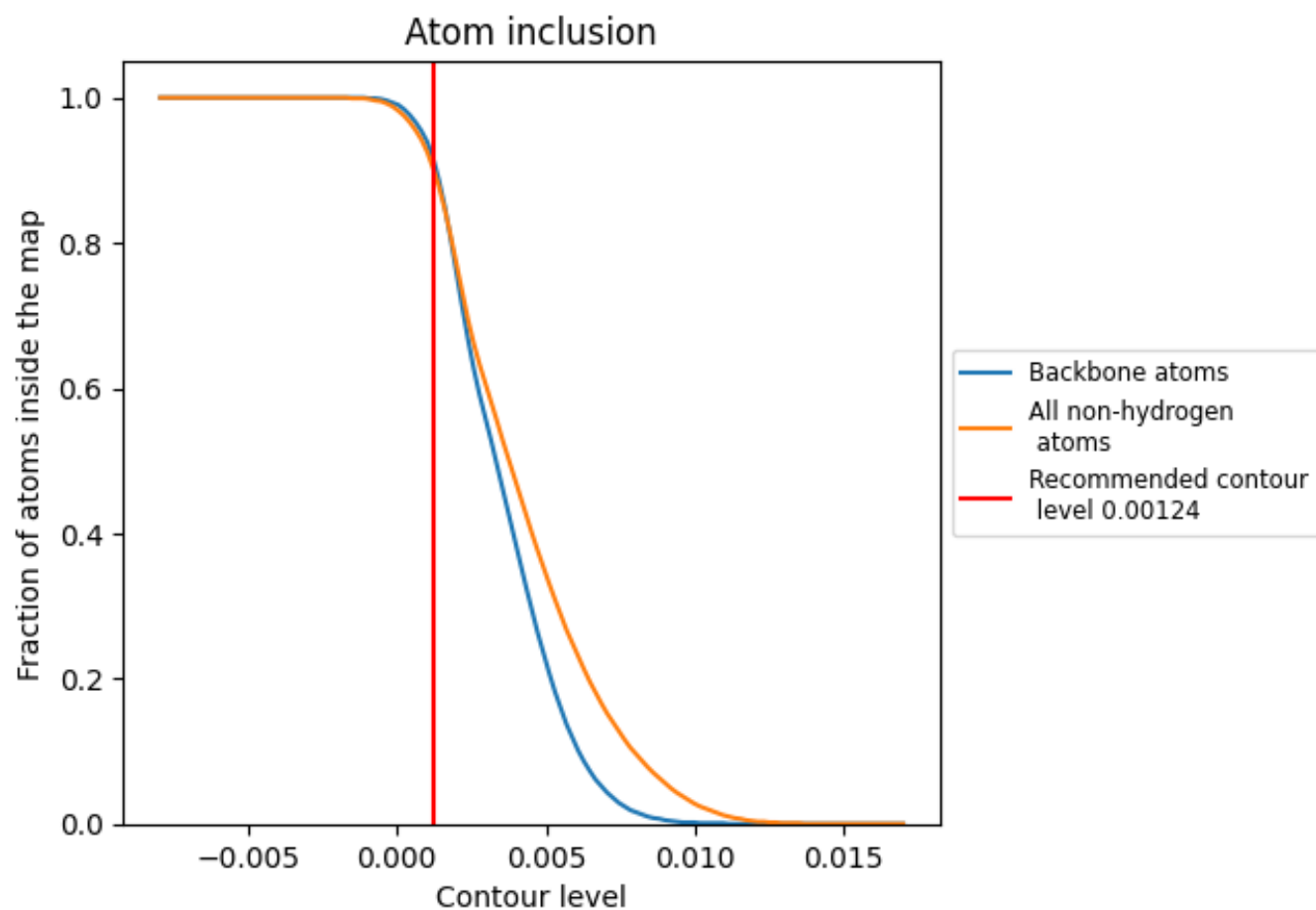
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00124).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.00124) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8990	 0.1390
0	 0.7560	 0.1500
1	 0.7080	 0.1190
2	 0.8010	 0.1000
3	 0.9750	 0.1970
4	 0.9950	 0.1780
5	 0.9730	 0.1430
6	 0.6690	 0.0490
7	 0.7640	 0.1290
8	 0.7400	 0.0330
9	 0.7640	 0.0550
A	 0.8360	 0.1260
AA	 0.6650	 0.0530
AB	 0.9140	 0.0700
AC	 0.8690	 0.0760
AD	 0.6300	 0.0430
B	 0.7860	 0.1080
C	 0.8500	 0.0760
D	 0.8060	 0.1210
E	 0.8380	 0.1190
F	 0.9200	 0.1190
G	 0.8880	 0.1000
H	 0.9700	 0.0820
I	 0.9010	 0.0900
J	 0.8210	 0.1050
K	 0.7590	 0.0730
L	 0.8900	 0.0970
M	 0.8660	 0.0440
N	 0.9000	 0.1330
O	 0.8120	 0.0580
P	 0.7610	 0.0740
Q	 0.9440	 0.0940
R	 0.7790	 0.0850
S	 0.8790	 0.1260
T	 0.8260	 0.1190



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Chain	Atom inclusion	Q-score
U	 0.8250	 0.0850
V	 0.8280	 0.0520
W	 0.6680	 0.0600
X	 0.7200	 0.0400
Y	 0.2800	 0.0270
Z	 0.7950	 0.0440
a	 0.8150	 0.1350
b	 0.8660	 0.1440
c	 0.8700	 0.1480
d	 0.9150	 0.1110
e	 0.8940	 0.1370
f	 0.5740	 0.1040
h	 0.9020	 0.0710
i	 0.8830	 0.1480
j	 0.7160	 0.1330
k	 0.8800	 0.1420
l	 0.8340	 0.1340
m	 0.8240	 0.1320
n	 0.9260	 0.1230
o	 0.8200	 0.1330
p	 0.8610	 0.1400
q	 0.8960	 0.1460
r	 0.8160	 0.1500
s	 0.8340	 0.1320
t	 0.8330	 0.1130
u	 0.8030	 0.1190
v	 0.8360	 0.1400
w	 0.9000	 0.1530
x	 0.9480	 0.1230
y	 0.7810	 0.1190
z	 0.8440	 0.1430