



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:39 PM UTC

PDB ID : 9GFT / pdb_00009gft
EMDB ID : EMD-51318
Title : Structure of the HrpA-bound E. coli disome, Class I
Authors : Esser, H.F.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2024-08-12
Resolution : 3.10 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

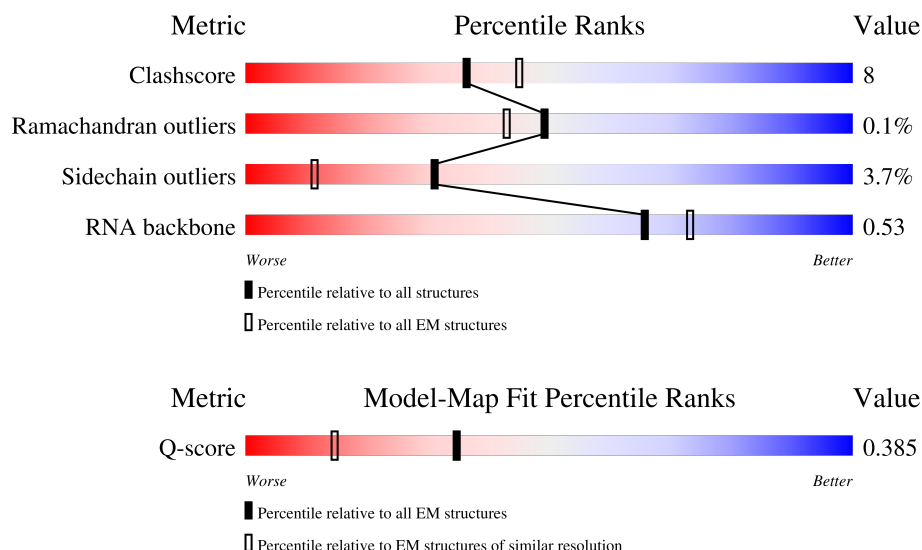
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	1542	
1	AA	1542	
2	1	241	

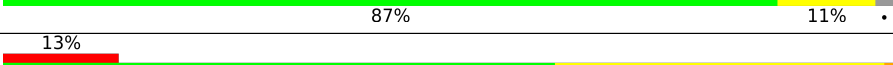
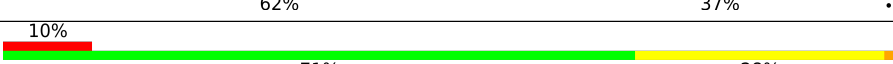
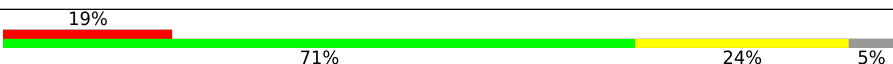
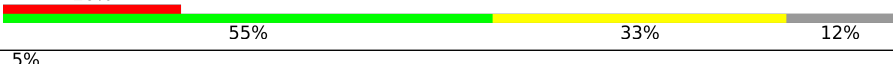
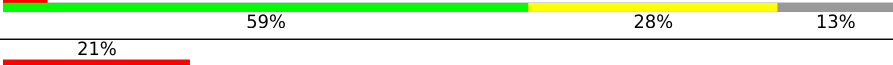
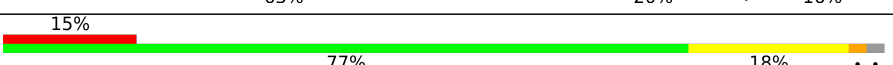
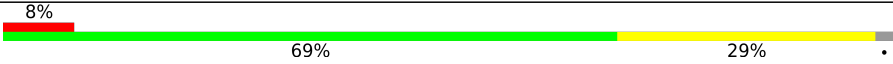
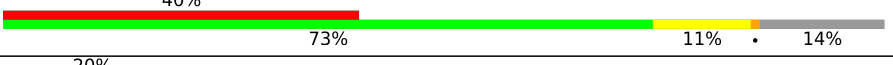
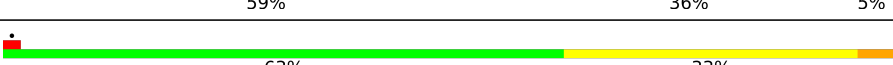
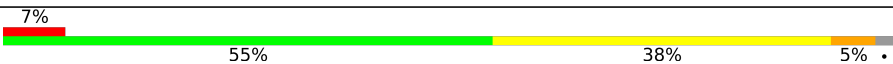
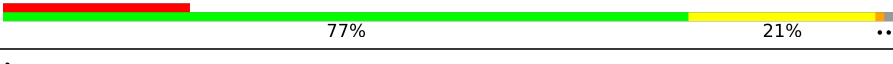
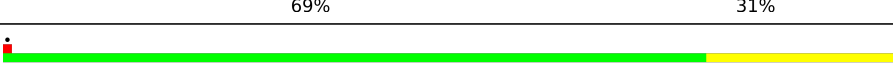
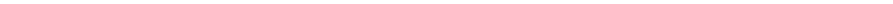
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	AB	241	
3	2	233	
3	AC	233	
4	3	206	
4	AD	206	
5	4	167	
5	AE	167	
6	5	135	
6	AF	135	
7	6	179	
7	AG	179	
8	7	130	
8	AH	130	
9	8	130	
9	AI	130	
10	9	103	
10	AJ	103	
11	A	76	
12	A1	71	
12	v	71	
13	A3	77	
14	AK	234	
14	C	234	
15	AL	118	
15	F	118	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
16	AM	101	
16	G	101	
17	AN	89	
17	H	89	
18	AO	82	
18	I	82	
19	AP	84	
19	J	84	
20	AQ	75	
20	K	75	
21	AR	92	
21	t	92	
22	AS	87	
22	u	87	
23	AT	70	
23	L	70	
24	AU	76	
25	AV	2903	
25	N	2903	
26	AW	120	
26	O	120	
27	AX	273	
27	P	273	
28	AY	209	
28	Q	209	

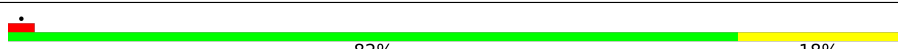
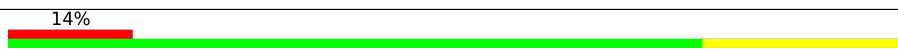
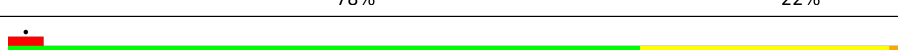
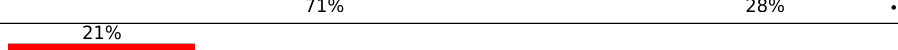
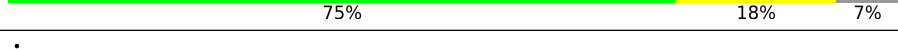
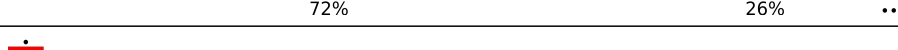
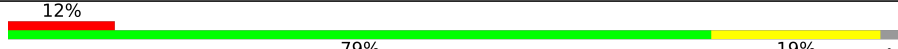
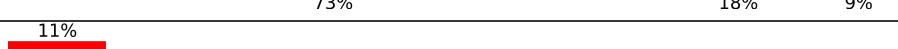
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	AZ	201	
29	R	201	
30	Aa	179	
30	S	179	
31	Ab	177	
31	T	177	
32	Ac	149	
32	U	149	
33	Ad	142	
33	V	142	
34	Ae	142	
34	W	142	
35	Af	123	
35	X	123	
36	Ag	144	
36	Y	144	
37	Ah	136	
37	Z	136	
38	Ai	127	
38	a	127	
39	Aj	117	
39	b	117	
40	Ak	115	
40	c	115	
41	Al	118	

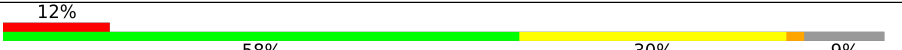
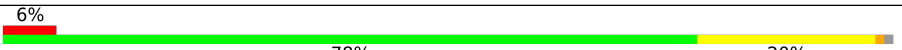
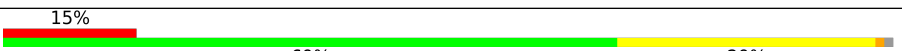
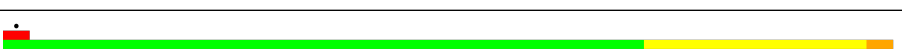
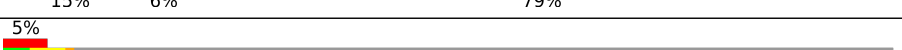
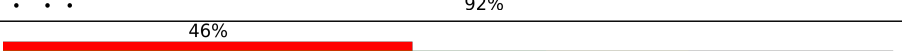
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
41	d	118	
42	Am	103	
42	e	103	
43	An	110	
43	f	110	
44	Ao	100	
44	g	100	
45	Ap	104	
45	h	104	
46	Aq	94	
46	i	94	
47	Ar	85	
47	j	85	
48	As	78	
48	k	78	
49	At	63	
49	l	63	
50	Au	59	
50	m	59	
51	Av	57	
52	Aw	55	
52	o	55	
53	Ax	46	
53	p	46	
54	Ay	65	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	q	65	
55	Az	38	
55	r	38	
56	B	1326	
57	D	129	
57	y	129	
58	E	124	
58	z	124	
59	M	75	
60	n	56	
61	s	179	
62	w	698	
63	x	165	

2 Entry composition [i](#)

There are 63 unique types of molecules in this entry. The entry contains 307377 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		
1	AA	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		
2	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		
3	AC	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		
4	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		
5	AE	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		
6	AF	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		
7	AG	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	129	Total	C	N	O	S	0	0
			979	616	173	184	6		
8	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		
9	AI	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 12 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A1	66	Total	C	N	O	S	0	0
			551	340	118	92	1		
12	v	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 13 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A3	77	Total	C	N	O	P	0	0
			1638	732	291	538	77		

- Molecule 14 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AK	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		
14	C	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 15 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AL	114	Total	C	N	O	S	0	0
			883	546	178	156	3		
15	F	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AM	96	Total	C	N	O	S	0	0
			774	483	160	128	3		
16	G	98	Total	C	N	O	S	0	0
			791	490	161	137	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AN	88	Total	C	N	O	S	0	0
			714	439	144	130	1		
17	H	87	Total	C	N	O	S	0	0
			702	433	140	128	1		

- Molecule 18 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AO	82	Total	C	N	O	S	0	0
			649	406	128	114	1		
18	I	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AP	80	Total	C	N	O	S	0	0
			648	411	121	113	3		
19	J	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 20 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AQ	66	Total	C	N	O	S	0	0
			544	345	102	96	1		
20	K	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 21 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AR	75	Total	C	N	O	S	0	0
			603	387	112	102	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
21	t	77	Total	C	N	O	S	0	0
			620	399	115	104	2		

- Molecule 22 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AS	85	Total	C	N	O	S	0	0
			665	411	137	114	3		
22	u	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 23 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AT	60	Total	C	N	O	S	0	0
			480	299	90	85	6		
23	L	62	Total	C	N	O	S	0	0
			499	309	95	89	6		

- Molecule 24 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AU	76	Total	C	N	O	P	0	0
			1625	724	293	532	76		

- Molecule 25 is a RNA chain called 23S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AV	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		
25	N	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AW	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		
26	O	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 27 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AX	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		
27	P	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AY	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		
28	Q	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AZ	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		
29	R	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 30 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Aa	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		
30	S	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ab	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		
31	T	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 32 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ac	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
32	U	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ad	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		
33	V	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 34 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ae	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		
34	W	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 35 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Af	122	Total	C	N	O	S	0	0
			938	587	180	165	6		
35	X	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ag	142	Total	C	N	O	S	0	0
			1034	643	202	188	1		
36	Y	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ah	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		
37	Z	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 38 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ai	118	Total	C	N	O	S	0	0
			945	585	194	161	5		
38	a	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Aj	116	Total	C	N	O	0	0
			892	552	178	162		
39	b	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 40 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ak	114	Total	C	N	O	S	0	0
			917	574	179	163	1		
40	c	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 41 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Al	117	Total	C	N	O	0	0
			947	604	192	151		
41	d	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 42 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Am	103	Total	C	N	O	S	0	0
			816	516	153	145	2		
42	e	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 43 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	An	110	Total	C	N	O	S	0	0
			857	532	166	156	3		
43	f	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 44 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ao	93	Total	C	N	O	S	0	0
			738	466	139	131	2		
44	g	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 45 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ap	102	Total	C	N	O		0	0
			779	492	146	141			
45	h	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 46 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aq	94	Total	C	N	O	S	0	0
			753	479	137	134	3		
46	i	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 47 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ar	75	Total	C	N	O	S	0	0
			575	356	116	102	1		
47	j	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 48 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	As	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
48	k	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 49 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	At	63	Total	C	N	O	S	0	0
			509	313	99	95	2		
49	l	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 50 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Au	56	Total	C	N	O	S	0	0
			435	272	84	77	2		
50	m	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 51 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Av	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 52 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	Aw	50	Total	C	N	O	0	0
			409	263	75	71		
52	o	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 53 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ax	46	Total	C	N	O	S	0	0
			377	228	90	57	2		
53	p	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Ay	64	Total	C	N	O	S	0	0
			504	323	105	74	2		
54	q	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Az	38	Total	C	N	O	S	0	0
			302	185	65	48	4		
55	r	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is a protein called ATP-dependent RNA helicase HrpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B	1295	Total	C	N	O	S	0	0
			10462	6619	1887	1924	32		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-25	MET	-	initiating methionine	UNP P43329
B	-24	GLY	-	expression tag	UNP P43329
B	-23	HIS	-	expression tag	UNP P43329
B	-22	HIS	-	expression tag	UNP P43329
B	-21	HIS	-	expression tag	UNP P43329
B	-20	HIS	-	expression tag	UNP P43329
B	-19	HIS	-	expression tag	UNP P43329
B	-18	HIS	-	expression tag	UNP P43329
B	-17	HIS	-	expression tag	UNP P43329
B	-16	HIS	-	expression tag	UNP P43329
B	-15	ASP	-	expression tag	UNP P43329
B	-14	TYR	-	expression tag	UNP P43329
B	-13	ASP	-	expression tag	UNP P43329
B	-12	ILE	-	expression tag	UNP P43329
B	-11	PRO	-	expression tag	UNP P43329
B	-10	THR	-	expression tag	UNP P43329
B	-9	THR	-	expression tag	UNP P43329
B	-8	LEU	-	expression tag	UNP P43329
B	-7	GLU	-	expression tag	UNP P43329
B	-6	VAL	-	expression tag	UNP P43329
B	-5	LEU	-	expression tag	UNP P43329

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	PHE	-	expression tag	UNP P43329
B	-3	GLN	-	expression tag	UNP P43329
B	-2	GLY	-	expression tag	UNP P43329
B	-1	PRO	-	expression tag	UNP P43329
B	0	GLY	-	expression tag	UNP P43329
B	1	THR	-	expression tag	UNP P43329

- Molecule 57 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	D	117	Total	C	N	O	S	0	0
			877	540	174	160	3		
57	y	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 58 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	E	123	Total	C	N	O	S	0	0
			955	590	196	165	4		
58	z	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 59 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	M	75	Total	C	N	O	P	0	0
			1593	711	281	526	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	n	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 61 is a protein called VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	s	37	Total	C	N	O	S	0	0
			316	198	58	58	2		

- Molecule 62 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	w	57	Total	C	N	O	P	0	0
			1175	527	165	426	57		

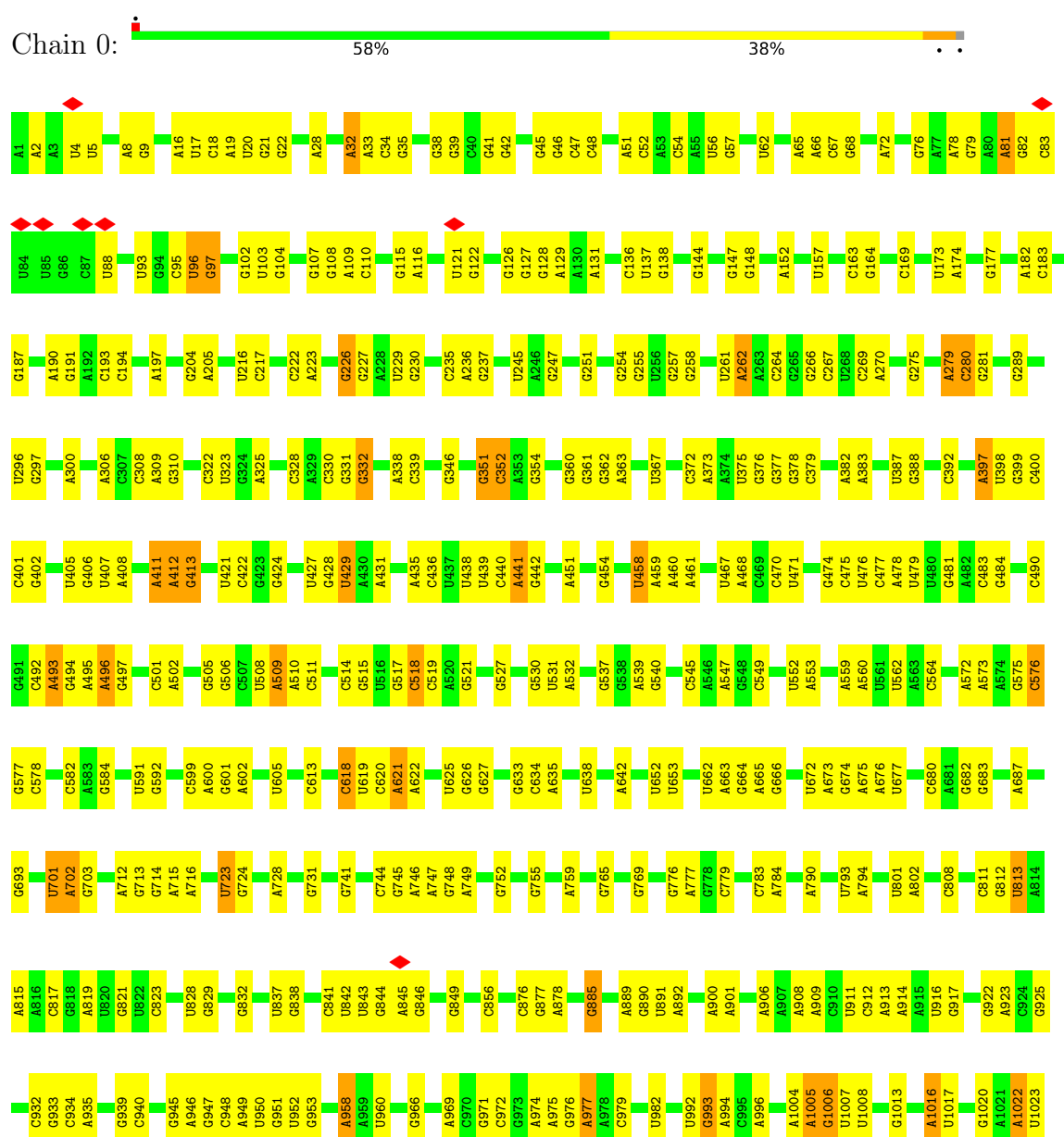
- Molecule 63 is a protein called Large ribosomal subunit protein uL10.

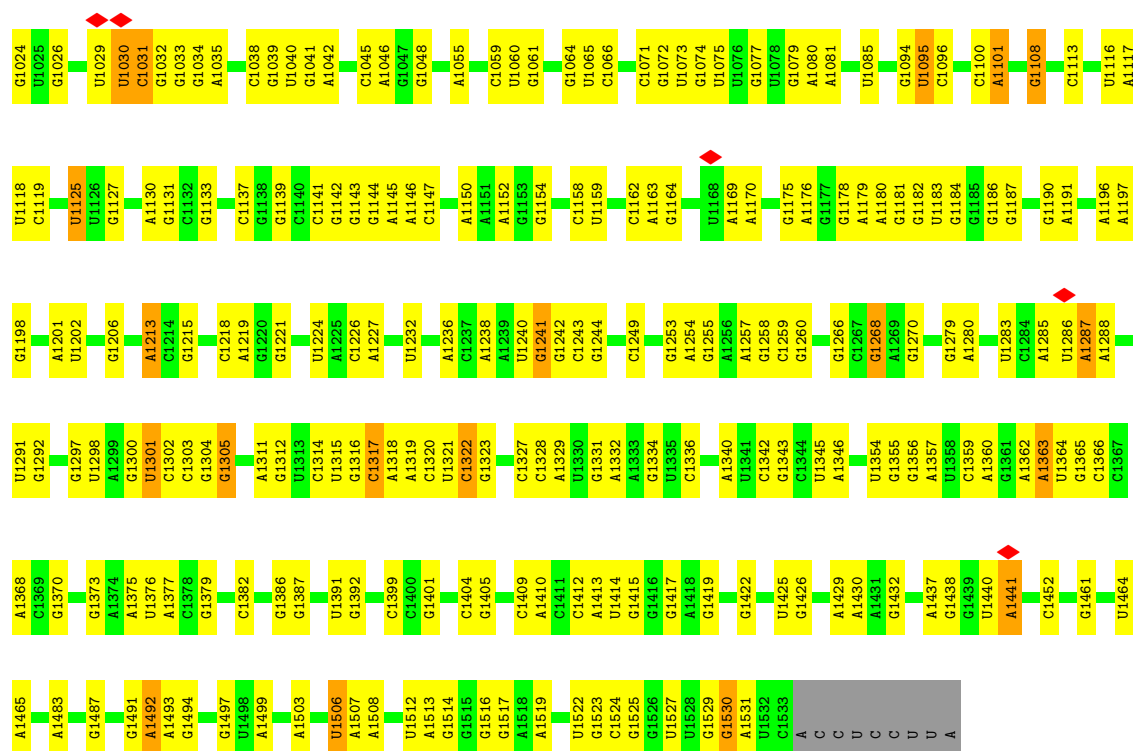
Mol	Chain	Residues	Atoms					AltConf	Trace
63	x	127	Total	C	N	O	S	0	0
			958	605	171	178	4		

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.

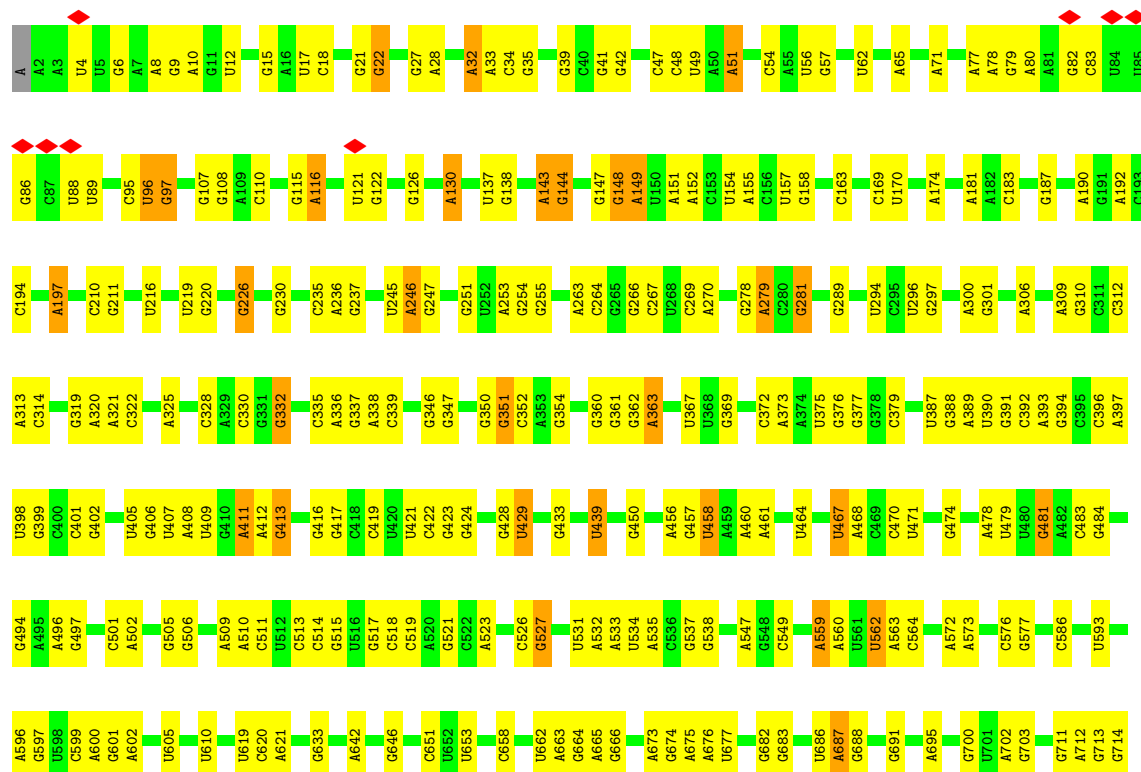
• Molecule 1: 16S ribosomal RNA

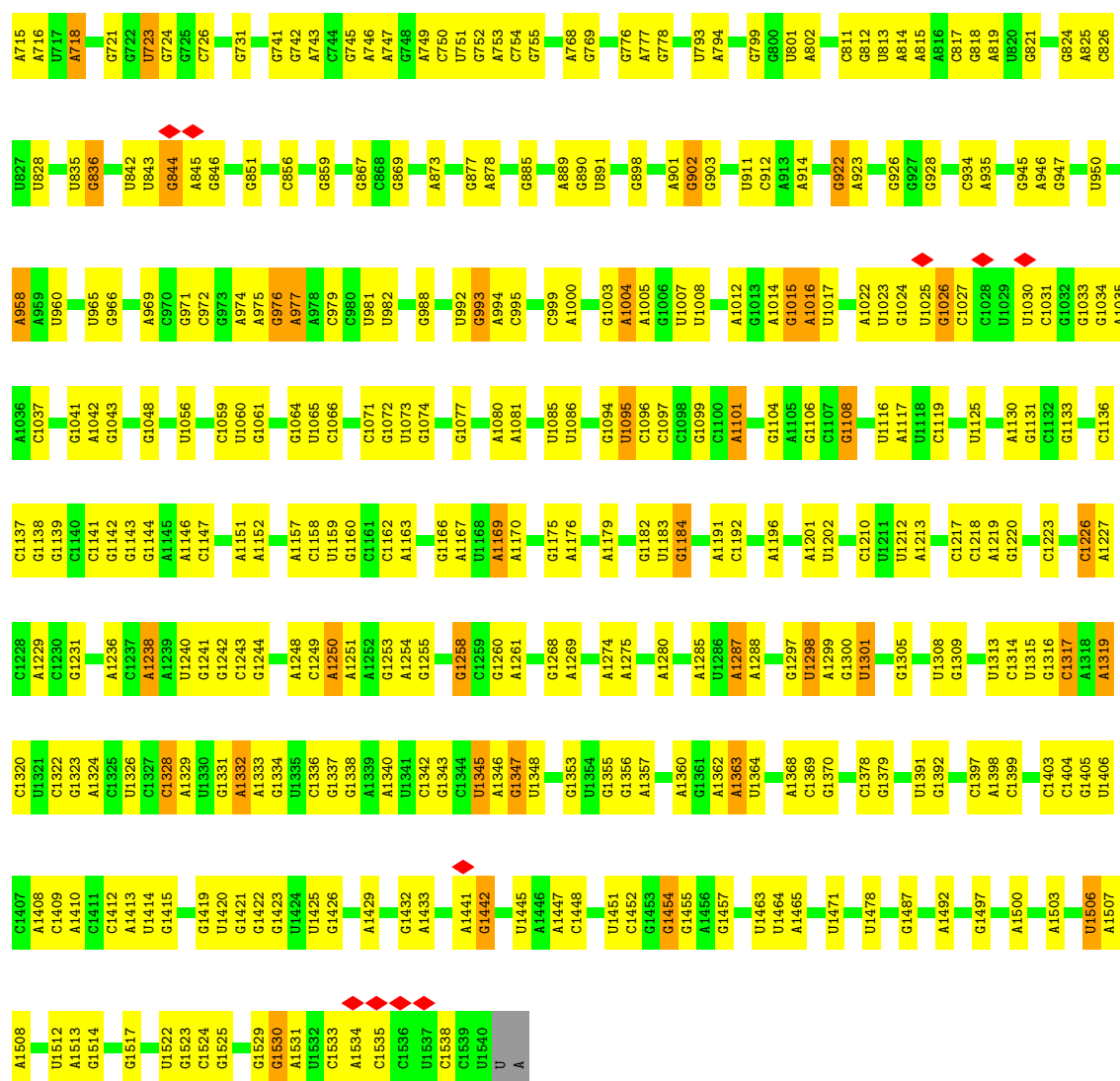




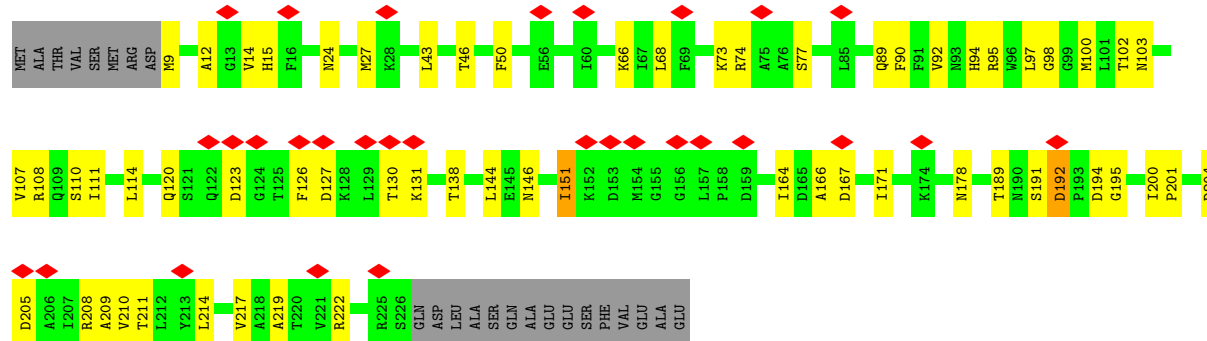
• Molecule 1: 16S ribosomal RNA

Chain AA: 60% 36%



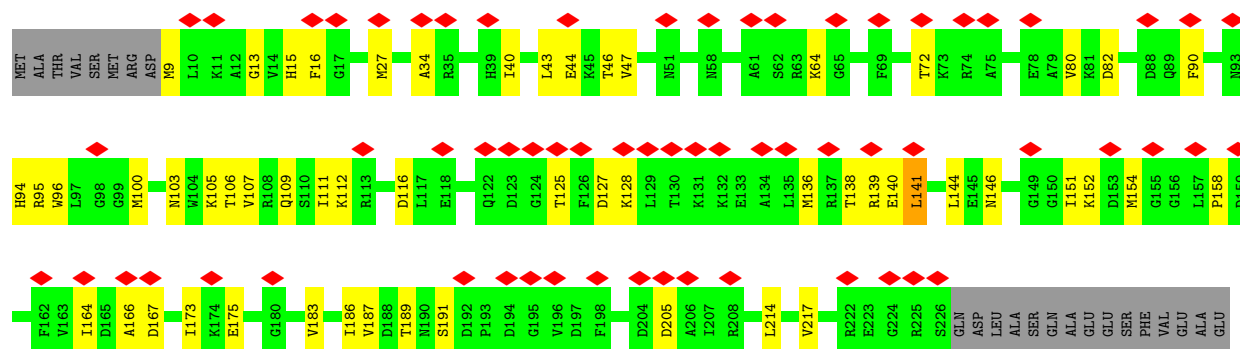


• Molecule 2: Small ribosomal subunit protein uS2

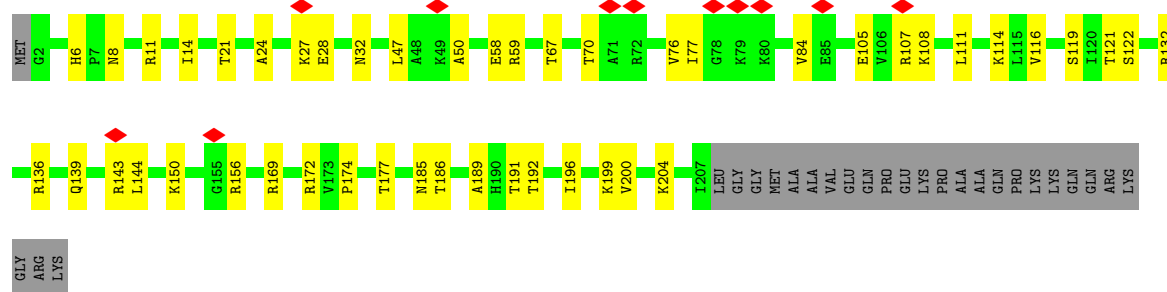


• Molecule 2: Small ribosomal subunit protein uS2

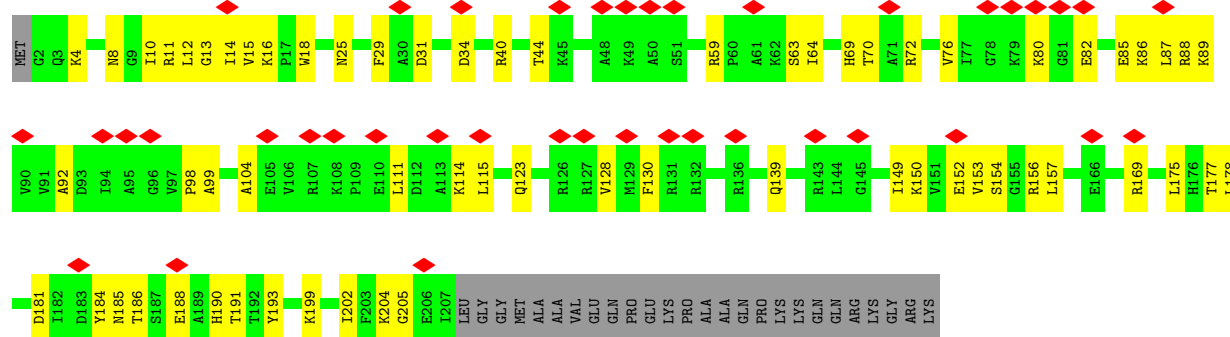




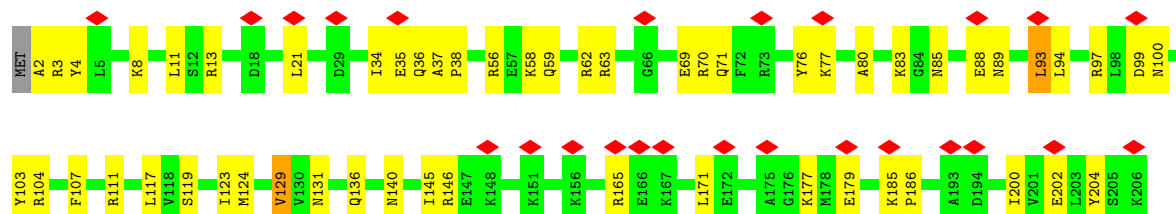
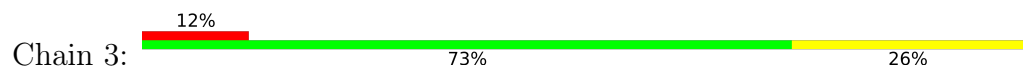
• Molecule 3: Small ribosomal subunit protein uS3



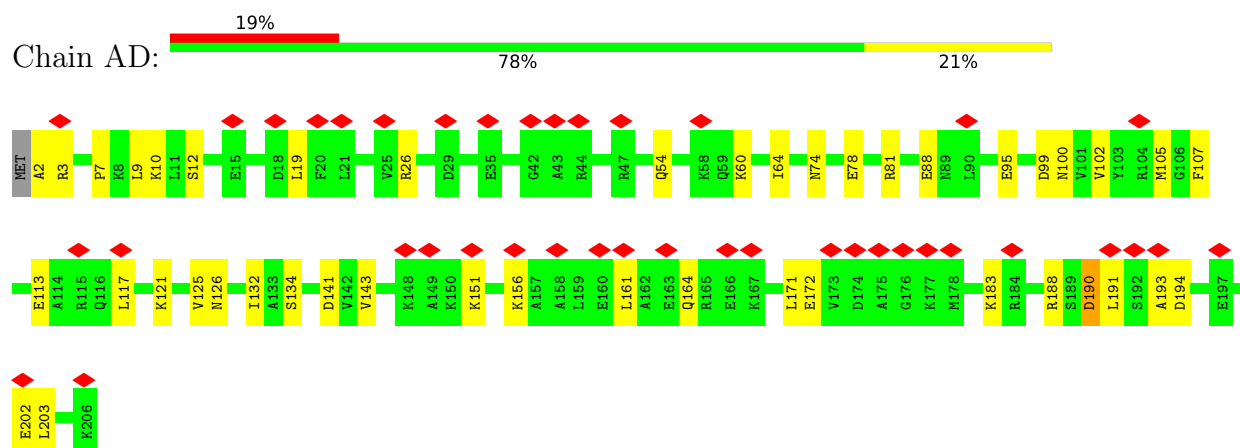
• Molecule 3: Small ribosomal subunit protein uS3



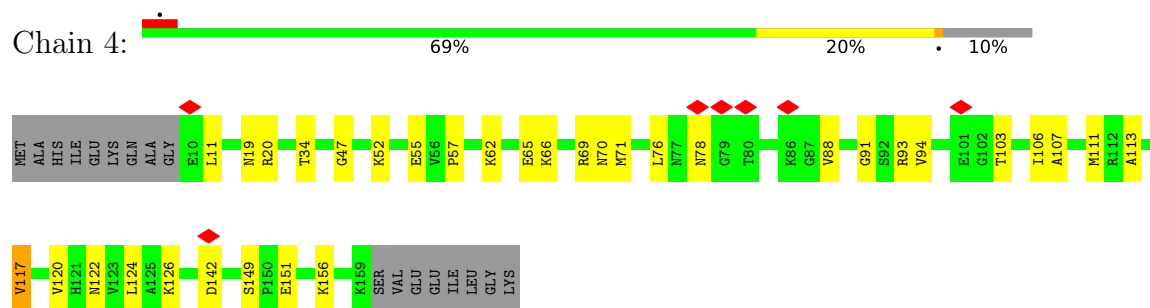
• Molecule 4: Small ribosomal subunit protein uS4



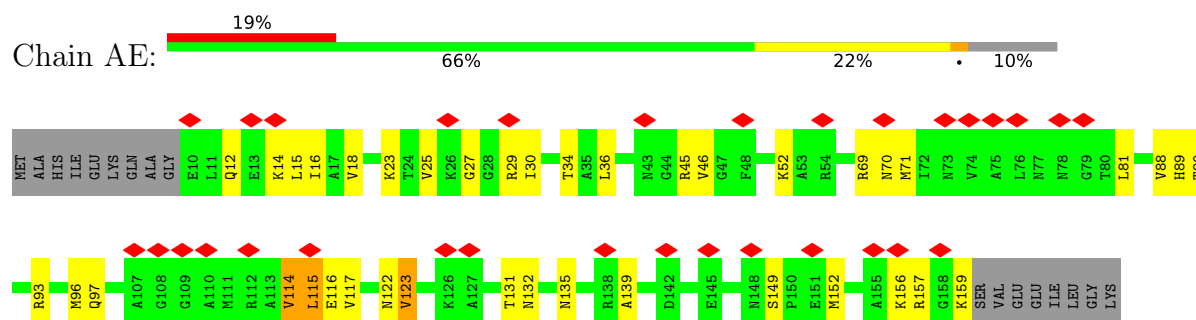
- Molecule 4: Small ribosomal subunit protein uS4



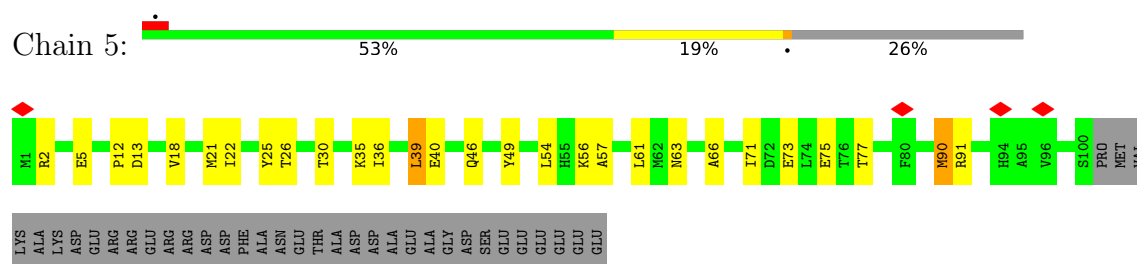
- Molecule 5: Small ribosomal subunit protein uS5



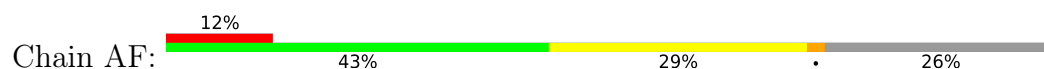
- Molecule 5: Small ribosomal subunit protein uS5

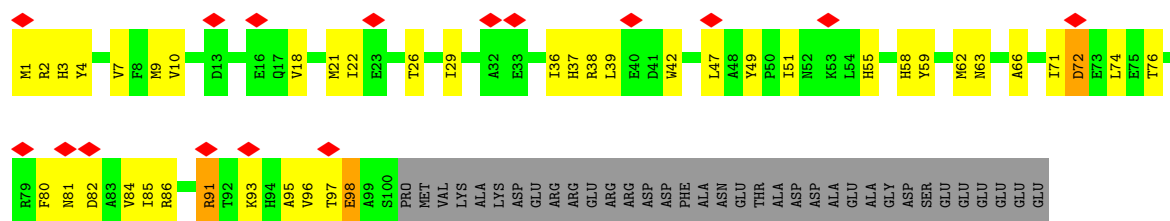


- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform

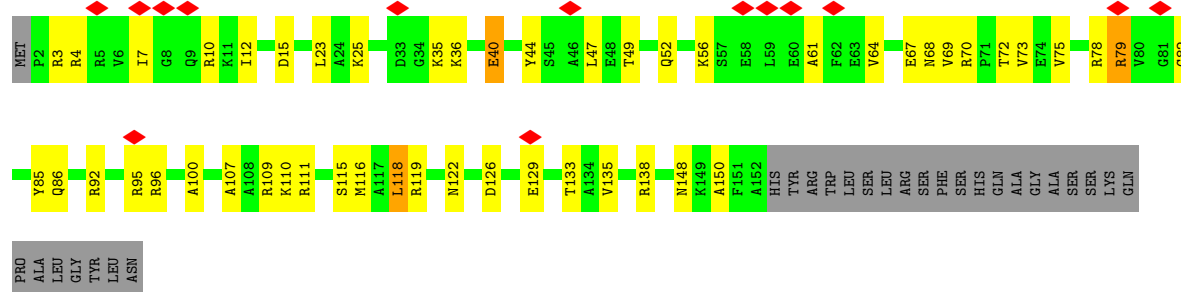


- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform

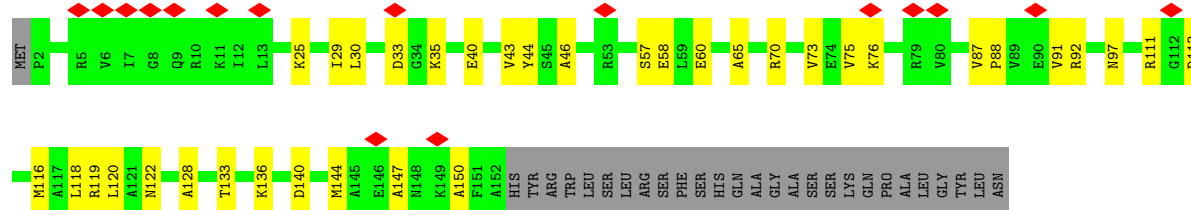




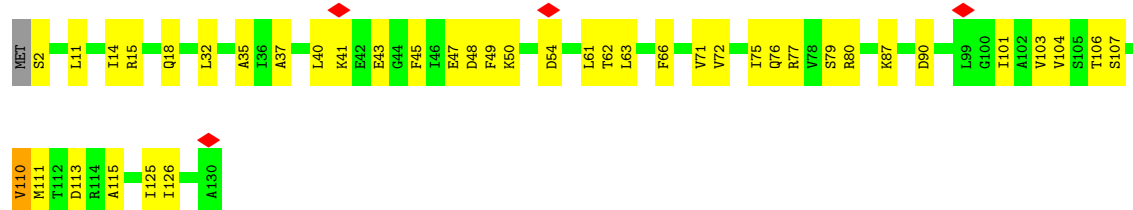
• Molecule 7: Small ribosomal subunit protein uS7



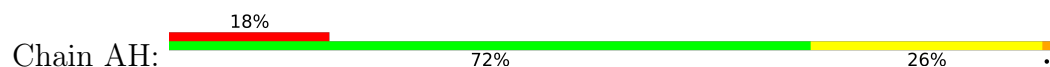
• Molecule 7: Small ribosomal subunit protein uS7

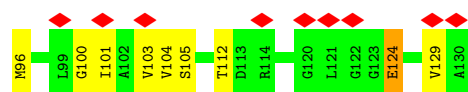


• Molecule 8: Small ribosomal subunit protein uS8



• Molecule 8: Small ribosomal subunit protein uS8

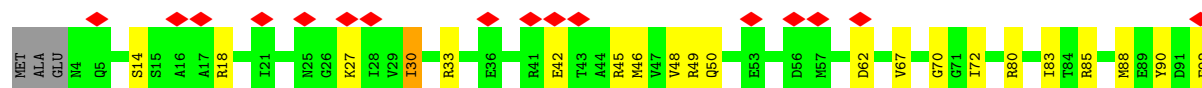
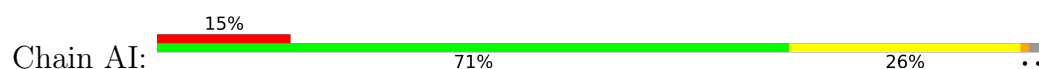




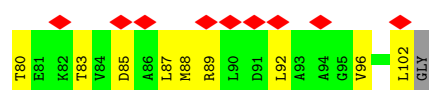
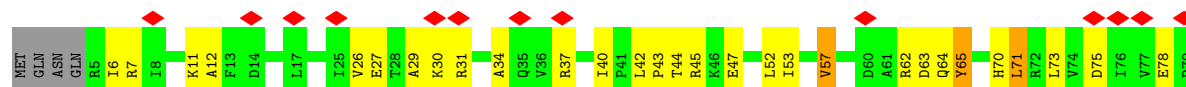
- Molecule 9: Small ribosomal subunit protein uS9



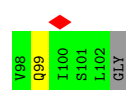
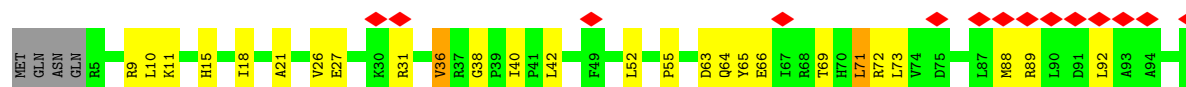
- Molecule 9: Small ribosomal subunit protein uS9



- Molecule 10: Small ribosomal subunit protein uS10



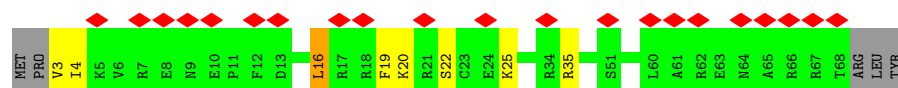
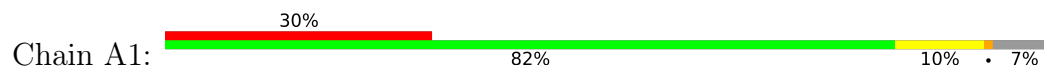
- Molecule 10: Small ribosomal subunit protein uS10



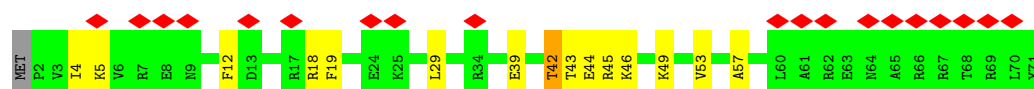
- Molecule 11: A-site tRNA



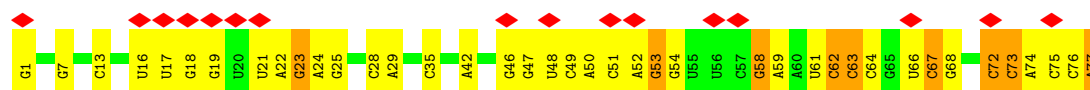
- Molecule 12: Small ribosomal subunit protein bS21



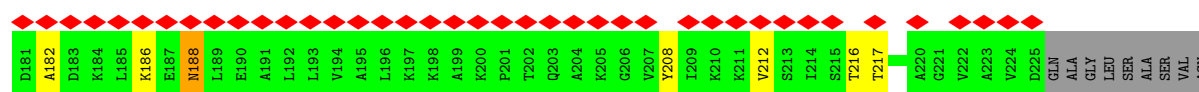
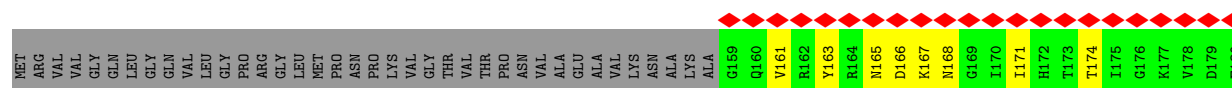
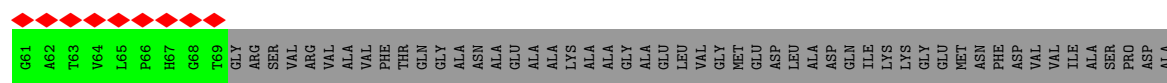
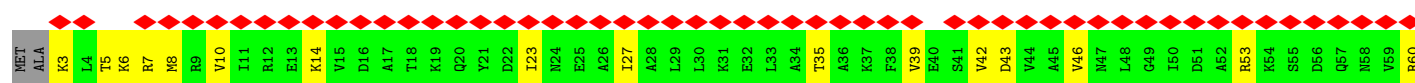
- Molecule 12: Small ribosomal subunit protein bS21



- Molecule 13: A-site tRNA

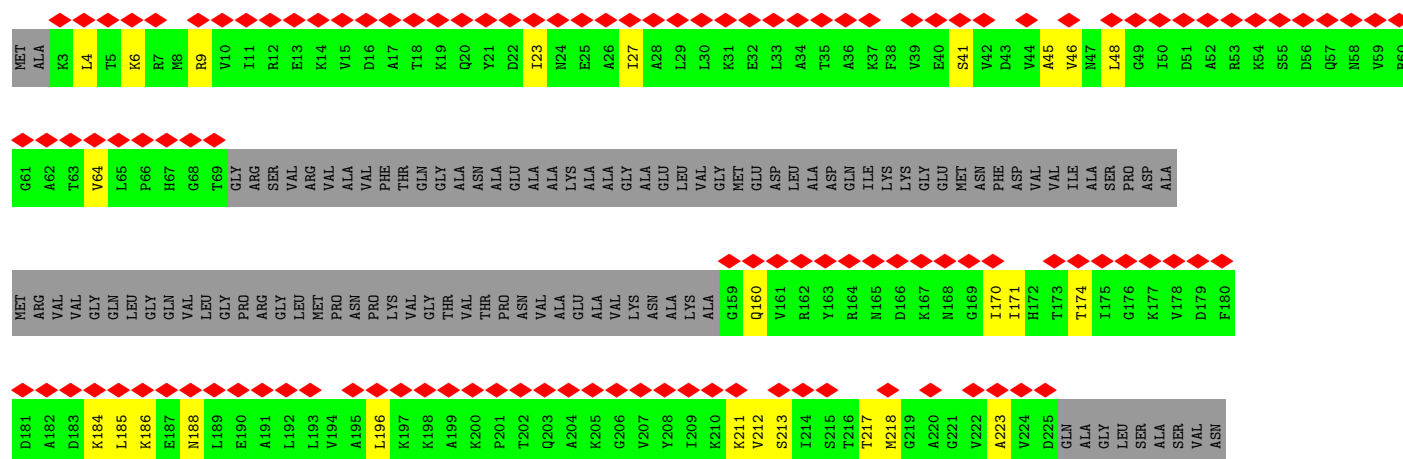


- Molecule 14: Large ribosomal subunit protein uL1

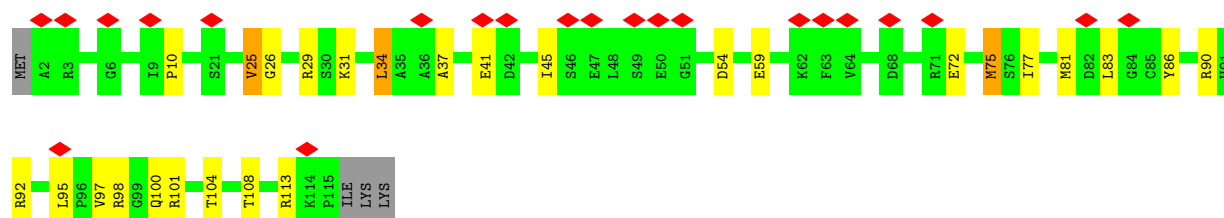
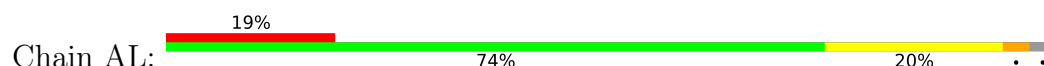


- Molecule 14: Large ribosomal subunit protein uL1

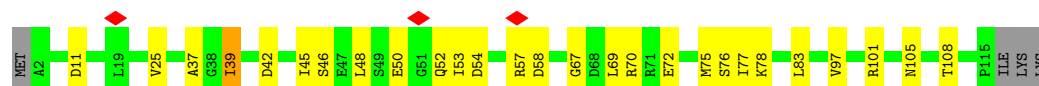




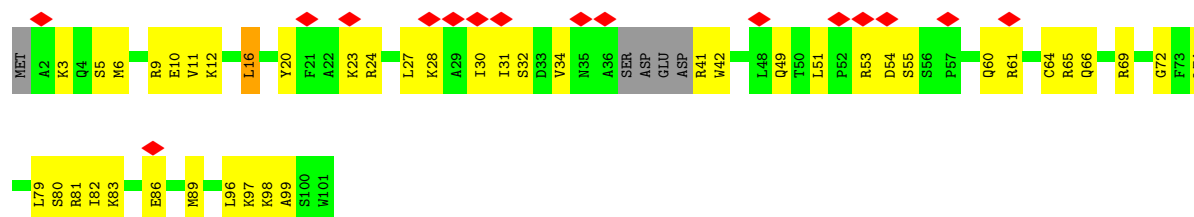
• Molecule 15: Small ribosomal subunit protein uS13



• Molecule 15: Small ribosomal subunit protein uS13

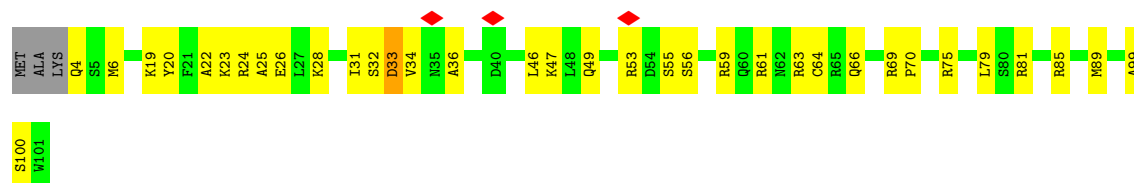


• Molecule 16: Small ribosomal subunit protein uS14

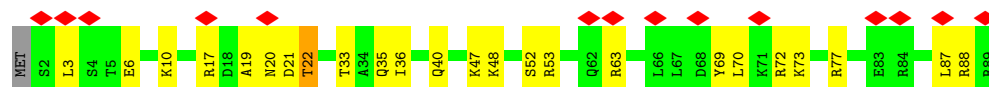


• Molecule 16: Small ribosomal subunit protein uS14

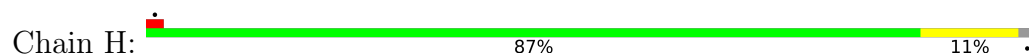




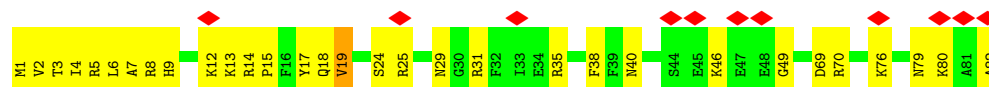
- Molecule 17: Small ribosomal subunit protein uS15



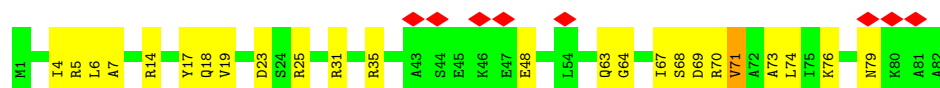
- Molecule 17: Small ribosomal subunit protein uS15



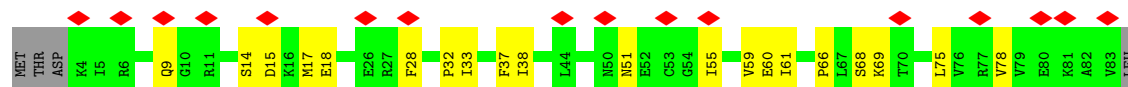
- Molecule 18: Small ribosomal subunit protein bS16



- Molecule 18: Small ribosomal subunit protein bS16



- Molecule 19: Small ribosomal subunit protein uS17

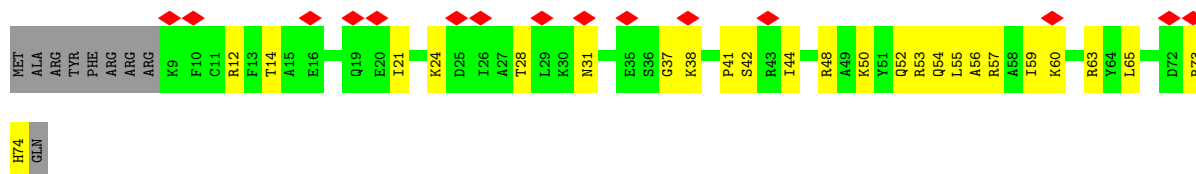


- Molecule 19: Small ribosomal subunit protein uS17

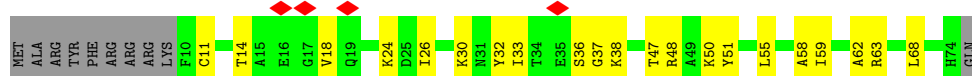




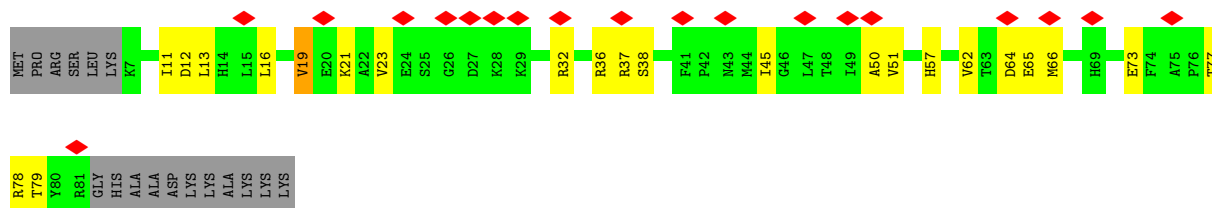
- Molecule 20: Small ribosomal subunit protein bS18



- Molecule 20: Small ribosomal subunit protein bS18



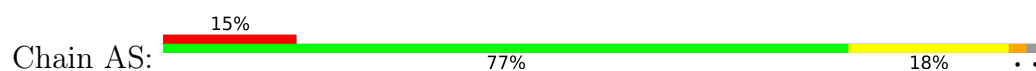
- Molecule 21: Small ribosomal subunit protein uS19



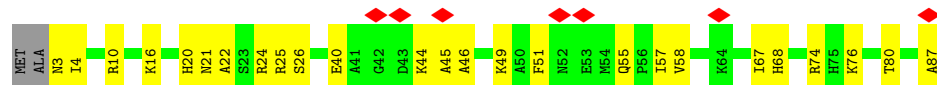
- Molecule 21: Small ribosomal subunit protein uS19



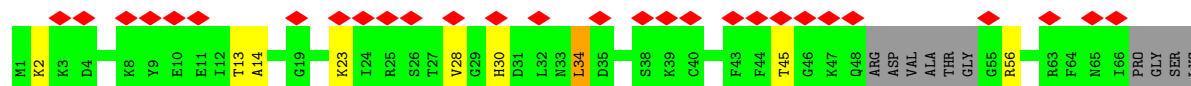
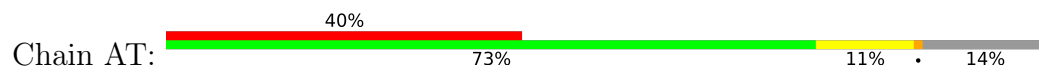
- Molecule 22: Small ribosomal subunit protein bS20



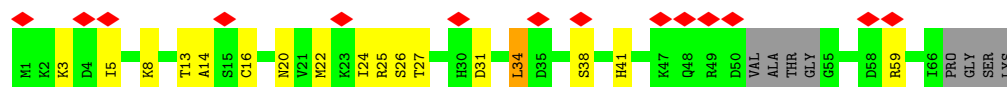
- Molecule 22: Small ribosomal subunit protein bS20



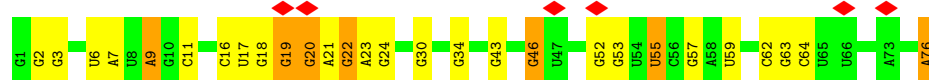
- Molecule 23: Large ribosomal subunit protein bL31A



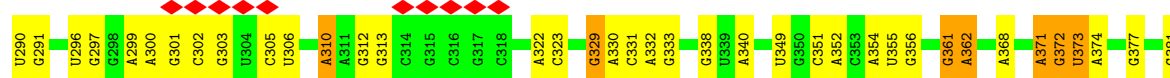
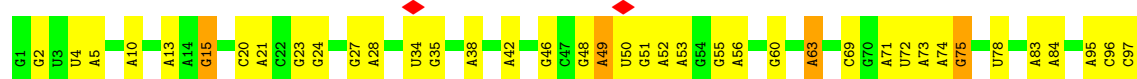
- Molecule 23: Large ribosomal subunit protein bL31A



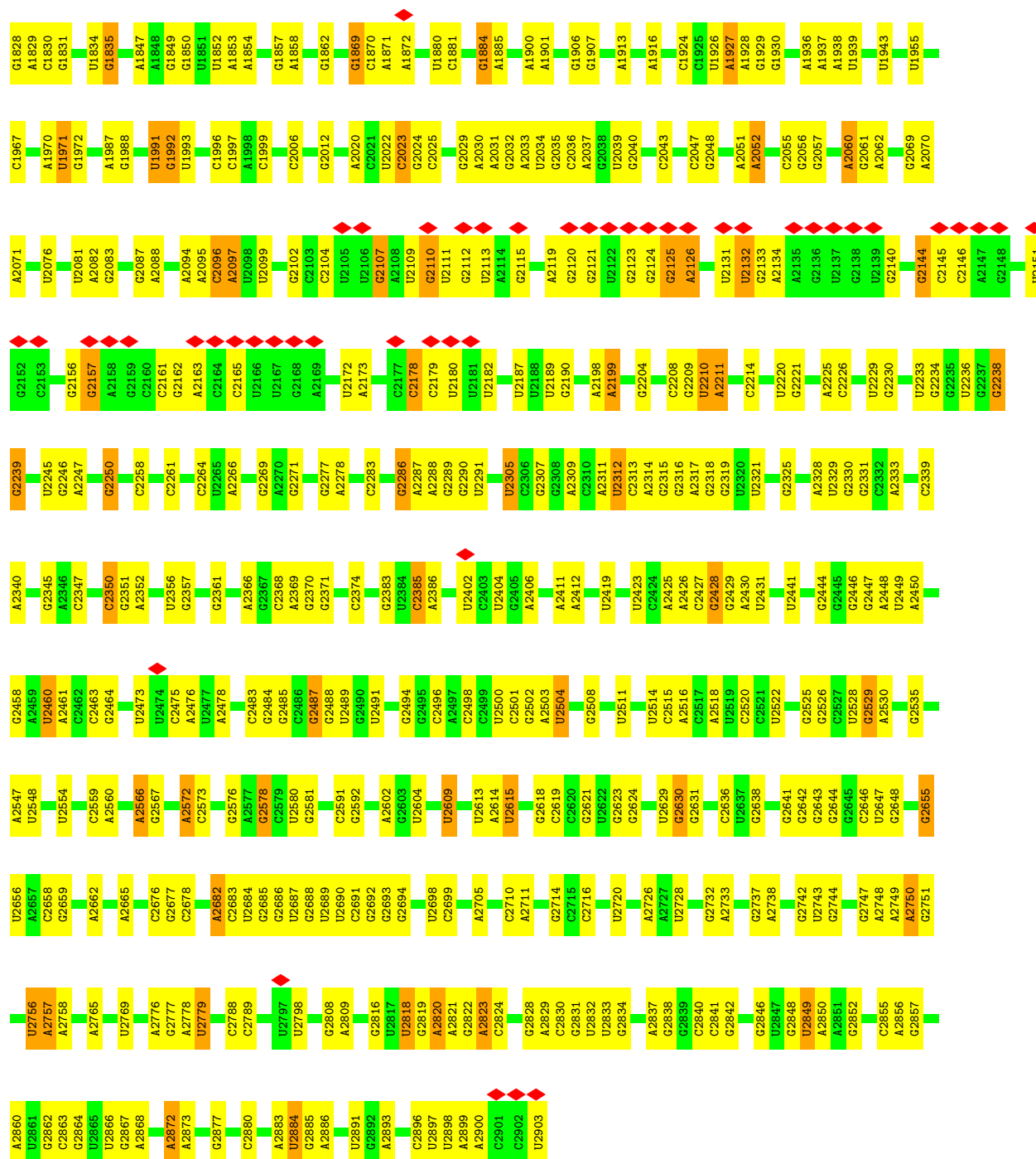
- Molecule 24: P-site tRNA



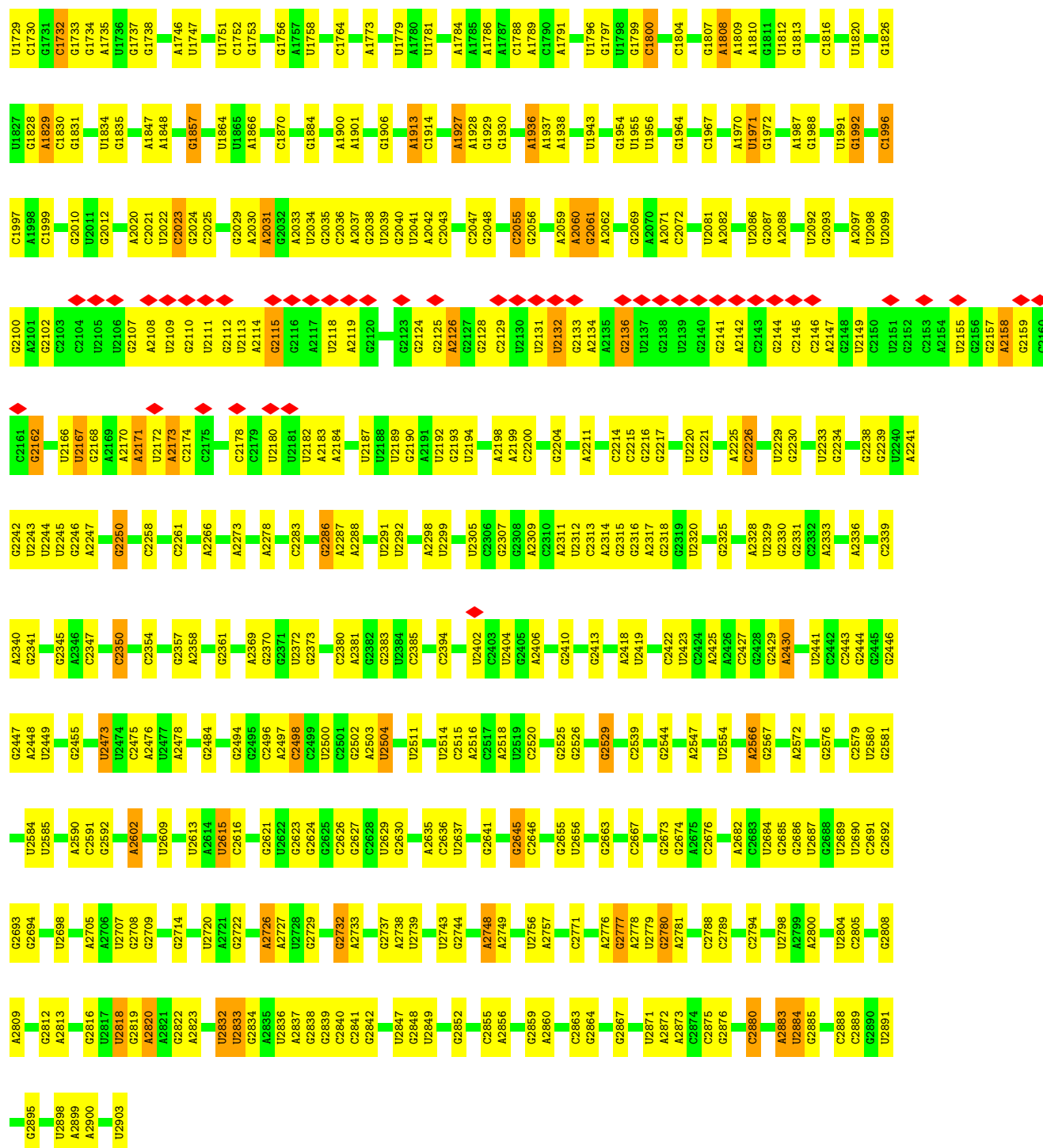
- Molecule 25: 23S RNA



U1709	C1585	G1492	U1406	C1278	G1186	U1105	A1039	A947	C765	C640	A563	G476
G1710	A1586	C1493	G1410	G1279	G1187	G1106	A1040	C948	U766	A643	A563	A479
A1711	G1587	A1494	U1411	G1280	G1190	G1107	G1041	G949	G767	A644	U568	A480
U1714	U1589	A1495	U1412	G1281	G1198	G1108	G1042	G953	U768	C645	U571	C481
G1715	A1590	A1496	A1413	U1282	U1198	C1110	C1043	G956	G774	U646	A572	A482
U1716	A1591	U1497	U1413	G1283	U1199	G1111	C1044	A960	G775	G647	U573	A483
A1717	C1592	A1504	G1416	A1286	A1204	G1112	U1046	A966	G776	G648	A574	G488
U1729	A1509	A1509	C1417	C1293	A1206	U1113	G1047	C961	A782	A654	A575	C490
G1730	G1510	G1510	A1418	G1294	G1206	G1116	G1051	G962	A783	A655	U580	G491
G1733	A1515	A1515	A1420	G1300	G1210	U1119	C1052	G969	G784	A656	U581	U499
A1735	G1516	G1517	G1421	A1301	C1211	G1122	A1054	U970	G785	A657	A582	A502
G1738	U1517	U1517	G1422	C1306	A1214	U1128	G1055	A972	G786	G663	A586	A503
G1743	G1519	G1519	A1427	C1319	A1214	G1128	U1056	G974	A787	G669	U589	A504
A1744	G1521	G1521	G1428	G1320	U1217	A1129	A1057	A980	A788	A670	A590	A505
G1752	U1522	U1522	G1430	A1321	U1217	U1130	U1058	A984	C672	C672	U591	G506
G1753	A1523	A1523	A1431	U1325	G1223	G1131	G1059	A988	A800	C680	A592	C509
G1756	G1524	G1524	G1432	U1326	U1224	U1132	U1060	G989	G805	G681	U593	U511
A1757	A1528	A1528	G1433	G1334	G1232	A1133	U1061	A994	U807	C681	U594	G512
U1758	G1530	G1530	A1434	C1335	G1232	G1136	G1062	A996	G808	C686	U596	G597
G1764	U1535	U1535	G1435	U1336	G1232	G1136	U1063	U999	G809	C691	C598	C516
A1773	A1536	A1536	G1436	C1336	G1232	G1136	G1064	A1000	U810	G712	A603	U521
U1779	G1537	G1537	C1437	C1336	G1232	G1136	U1065	U1004	A819	U720	G605	A528
A1780	U1542	U1542	G1445	A1354	A1244	C1150	A1071	C1005	A721	A721	C611	A529
U1781	G1543	G1543	C1446	G1355	G1248	C1153	G1072	U1009	A722	A722	G612	G530
A1783	A1544	A1544	G1448	G1356	U1249	G1154	C1075	A1010	A613	A613	A614	C531
A1784	U1545	U1545	G1449	G1360	G1250	A1155	C1076	G914	A532	A532	U615	A533
G1789	G1546	G1546	G1450	C1363	G1251	A1156	U1077	G916	U616	U616	G617	U534
C1790	C1547	C1547	C1451	G1364	G1252	A1157	U1078	U1012	U617	U617	G618	G535
A1791	A1548	A1548	G1452	A1365	A1253	C1158	U1081	G917	A730	A730	G619	G536
U1794	U1549	U1549	U1458	G1368	G1254	C1164	U1082	A918	G733	G733	G620	A538
C1795	C1557	C1557	G1459	C1376	G1255	A1165	U1083	A920	A734	A734	A621	G539
U1796	G1558	G1558	U1466	G1377	U1258	C1170	A1084	C922	A739	A739	G622	C544
G1797	A1566	A1566	A1469	A1378	G1259	G1171	A1085	G926	U741	U741	A627	U545
C1800	U1567	U1567	G1470	G1379	A1262	C1172	A1086	A927	A742	A742	G628	U546
A1808	G1568	G1568	G1471	G1380	A1265	U1173	U1087	U931	A743	A743	G629	A547
C1816	A1569	A1569	G1475	A1381	G1266	U1174	G1088	U934	U746	U746	G630	G548
G1817	U1570	U1570	U1476	G1382	U1267	U1175	A1089	U936	U747	U747	A631	G549
A1819	A1571	A1571	A1477	A1384	U1267	U1176	U1090	U937	A845	A845	A633	C550
U1820	A1572	A1572	G1478	C1385	C1270	G1177	U1094	U938	U846	U846	A634	G551
G1826	U1576	U1576	U1481	C1386	G1271	C1178	U1095	U939	U847	U847	C635	U552
U1827	C1577	C1577	G1482	A1387	A1272	U1180	A1096	A941	U754	U754	G636	G553
	A1578	A1578	G1483	U1396	U1273	U1181	U1097	U945	G757	G757	A637	U554
	A1579	A1579	U1491	U1405	A1274	U1182	U1098	A945	U852	U852	G638	U558
	U1583	U1583				G1185	G1099	C946	C853	C853	U639	G559
	U1584	U1584					U1101					
							C1102					
							A1103					
							C1104					

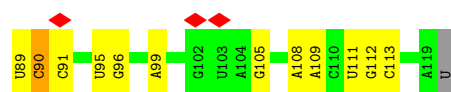


A1583	A1469	U1379	G1259	C1153	C946	A849	G726	A627	U534	U419	A320	A216
U1584	A1470	G1380	A1260	G1154	A947	U850	G729	A628	G535	C420	U321	A219
C1585	G1471	A1383	A1265	A1155	C948	U851	A730	G629	A538	C421	A322	A223
U1594	G1475	A1386	G1266	C1167	G956	G856	A734	A632	C540	A422	A324	U224
C1595	A1387	G1386	C1270	U1173	C957	G857	U741	A633	G543	A423	G329	A222
A1597	G1476	G1388	G1271	U1174	U958	G858	A742	C634	C544	A424	A330	U224
A1598	G1482	U1394	U1272	U1175	C961	G859	A743	G635	U546	U427	C331	C229
C1607	G1483	A1395	U1273	A1176	G964	A861	U746	A636	C435	C435	A340	U234
A1608	C1493	A1403	C1278	U1176	C964	G869	U747	G638	G438	G438	A345	A241
A1609	G1494	G1177	G1279	C1178	G971	A877	U748	U639	G548	A439	A346	A241
A1610	U1405	U1180	G1283	U1179	A972	A878	G748	C640	G549	C550	A347	G247
A1614	U1406	U1181	A1286	U1180	A973	G881	A764	C645	C554	C456	U355	G248
A1619	G1407	U1181	A1286	U1181	G974	U882	U766	U646	U546	A457	U356	C249
A1632	G1408	U1182	A1289	U1182	A975	G883	U767	G647	U558	U464	C357	A255
U1636	U1409	G1186	C1290	G1187	A980	G884	U768	G651	G559	G467	U358	A265
A1637	G1410	U1187	G1296	U1187	A983	U894	G770	U652	A563	C475	U360	G266
A1638	G1416	U1188	G1296	U1188	A984	C885	G776	A654	U569	A477	A362	C267
U1646	G1418	U1201	G1300	U1201	C987	U	G780	C660	A572	A478	C366	A272
U1647	A1419	G1202	A1301	U1202	A988	C	A781	G663	U573	A479	G367	C275
U1648	G1426	U1203	C1306	U1203	G989	C	A782	G664	A574	A480	U370	U276
U1649	A1427	A1205	A1307	U1204	U989	G	A783	A668	A575	G481	G371	G277
A1654	C1428	G1206	C1314	U1206	C995	A892	A784	A669	U576	A482	G372	A278
A1664	G1429	C1207	C1315	C1208	A996	C893	G785	G669	G577	G373	U373	C281
A1665	U1430	C1208	C1316	U1208	A1000	U894	A793	A670	G578	G374	U374	U284
A1668	G1432	G1212	G1317	U1212	A1006	A895	G805	C672	G579	G375	G375	G285
A1669	A1434	G1223	A1321	U1223	C1006	C897	G806	C673	U580	G491	G376	G286
A1670	G1435	U1224	U1326	U1224	A1009	U898	U807	A677	G494	G494	G377	G287
A1675	U1442	G1232	A1327	U1232	U1012	A900	G808	C680	A502	A502	G386	U288
A1683	U1443	U1233	G1332	G1233	C1013	G904	U811	G681	A503	A504	U399	G289
A1684	G1444	U1234	G1341	U1234	A1014	G907	C812	U686	A505	A505	U399	U290
A1689	G1445	G1235	C1345	U1235	U1019	A910	U813	C687	G506	G506	U395	G291
A1690	U1446	A1237	U1352	G1237	A1020	A911	C814	A688	C509	C509	G396	U296
A1704	G1447	G1112	U1352	G1237	G1022	G916	G818	A689	C510	C510	U397	G297
A1705	G1448	U1130	G1358	U1242	G1026	A917	A819	U688	U598	U511	G398	A300
A1709	G1449	U1131	C1363	C1243	C1030	A918	U827	A699	A599	G512	G398	G301
A1710	G1450	U1132	A1364	A1247	G1031	G926	U828	G700	G600	A513	A401	C302
A1711	G1451	A1133	A1365	G1250	A1032	A927	U832	G704	U594	A514	U403	U304
A1715	G1452	U1134	C1368	C1251	A1033	A928	A833	G604	U598	G518	A404	G306
A1716	G1453	G1135	U1372	U1252	U1034	U929	G834	G605	A599	U521	U405	U307
A1717	U1458	G1136	C1376	A1253	G1035	G930	G835	A612	G600	A522	G406	G308
A1718	C1461	U1139	G1377	A1254	G1036	U931	G836	A614	G600	A529	G407	G407
A1719	G1462	C1140	C1378	U1255	G1037	C937	A845	G622	U598	G530	G408	A309
A1724	C1463	U1141	G1377	U1256	G1038	U1141	U846	A621	U598	C531	G411	G313
A1725	G1464	A1142	A1378	G1257	A1039	A941	U847	A722	G622	A532	C414	G319
A1726		C1152		U1258	A1040		C848			G533	A415	



• Molecule 26: 5S ribosomal RNA





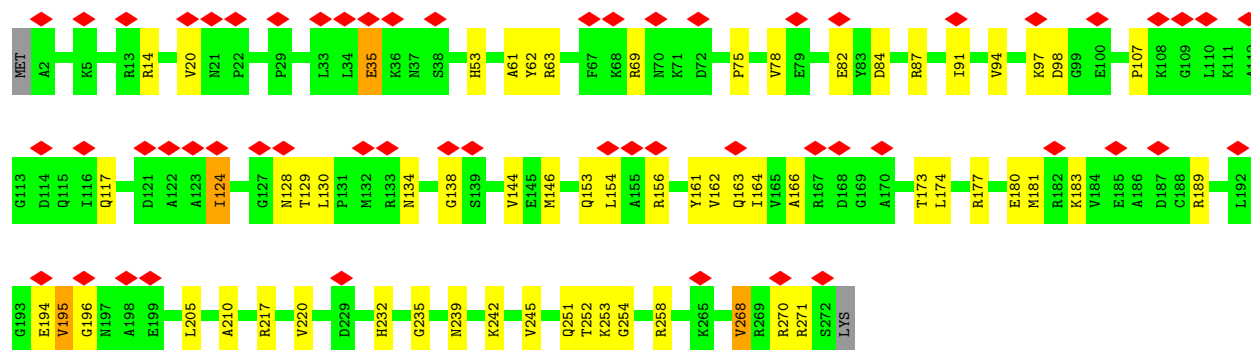
• Molecule 26: 5S ribosomal RNA

Chain O: 60% 38% ..



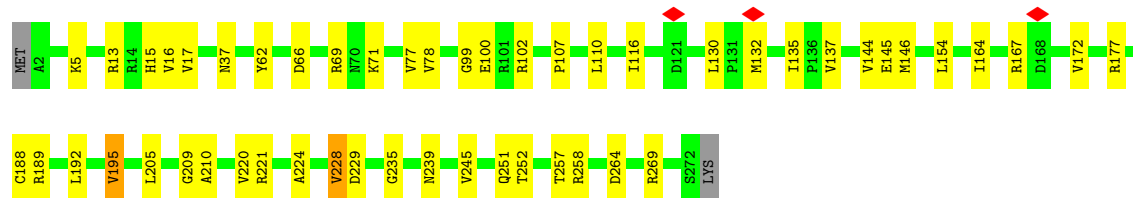
• Molecule 27: Large ribosomal subunit protein uL2

Chain AX: 21% 77% 21% ..



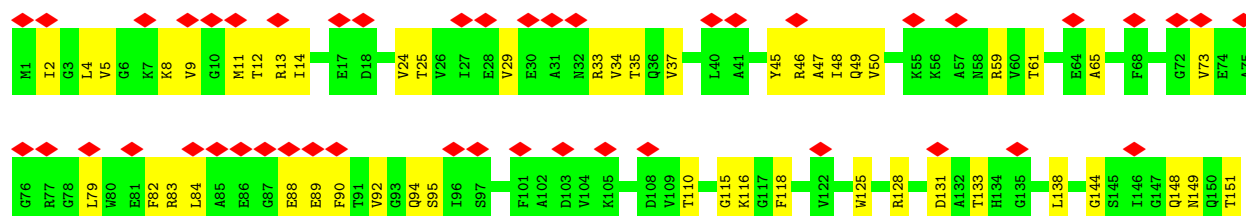
• Molecule 27: Large ribosomal subunit protein uL2

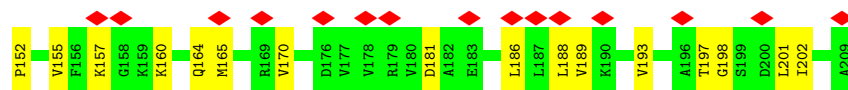
Chain P: 81% 18% ..



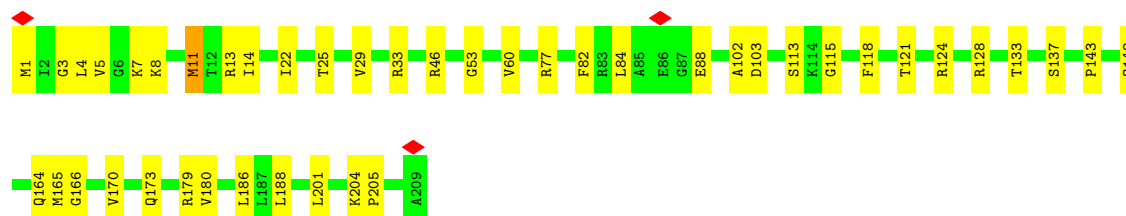
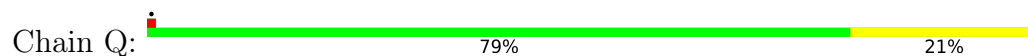
• Molecule 28: 50S ribosomal protein L3

Chain AY: 29% 69% 31%

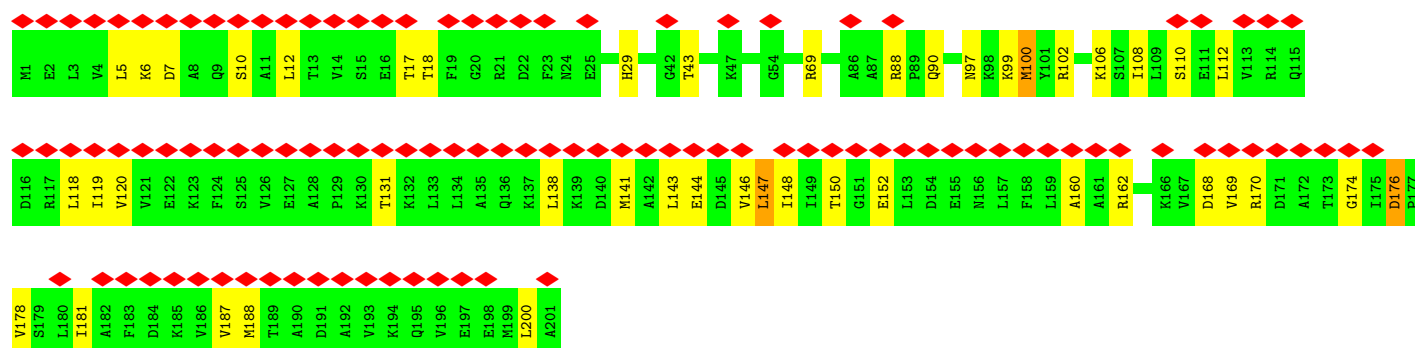
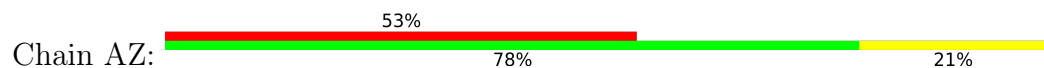




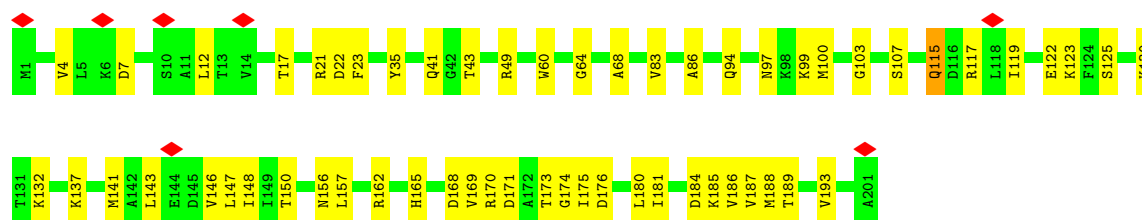
- Molecule 28: 50S ribosomal protein L3



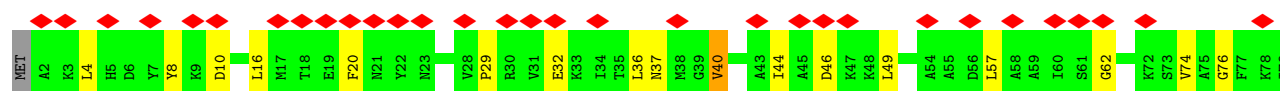
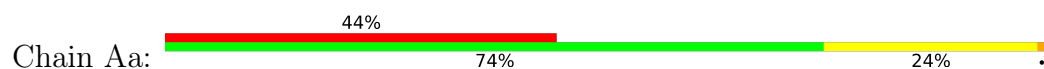
- Molecule 29: Large ribosomal subunit protein uL4

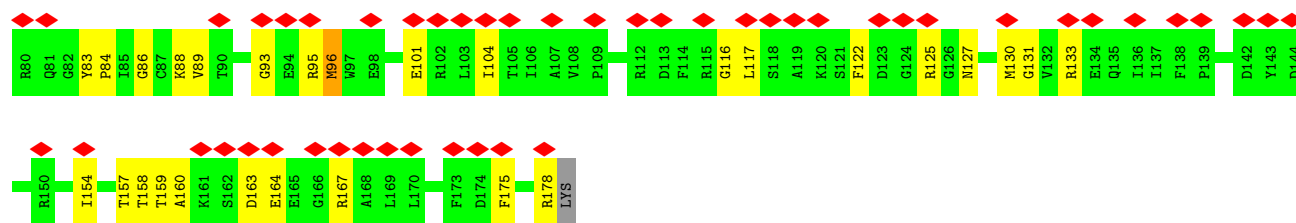


- Molecule 29: Large ribosomal subunit protein uL4

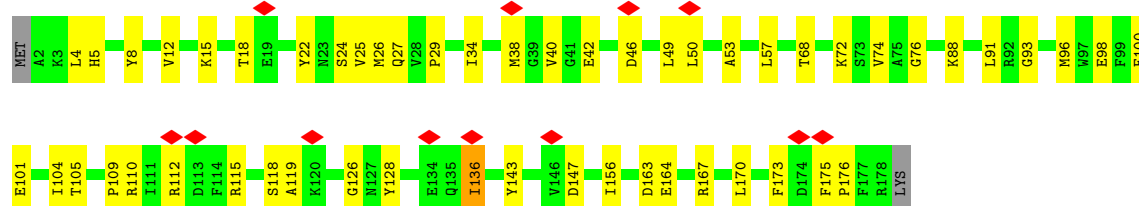


- Molecule 30: Large ribosomal subunit protein uL5

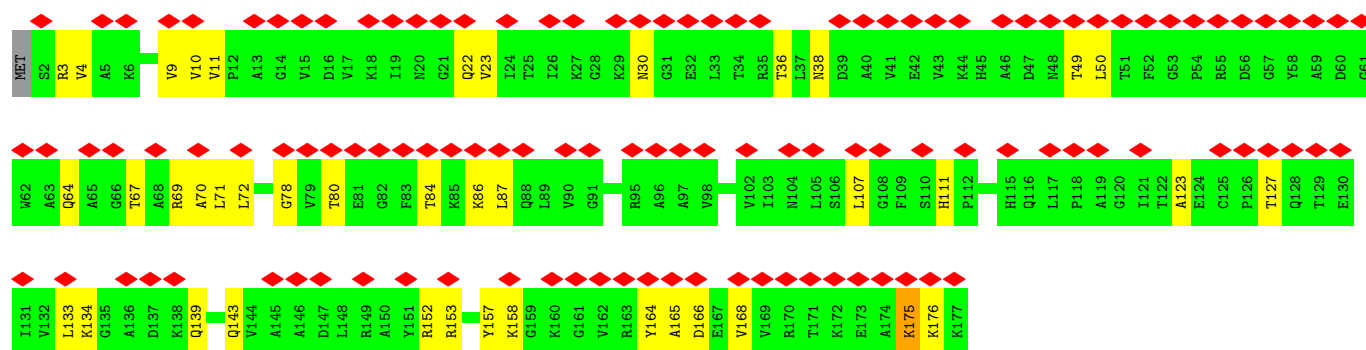
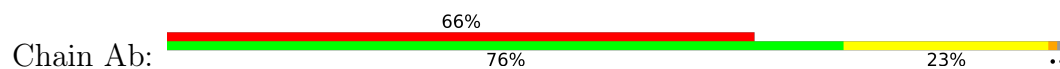




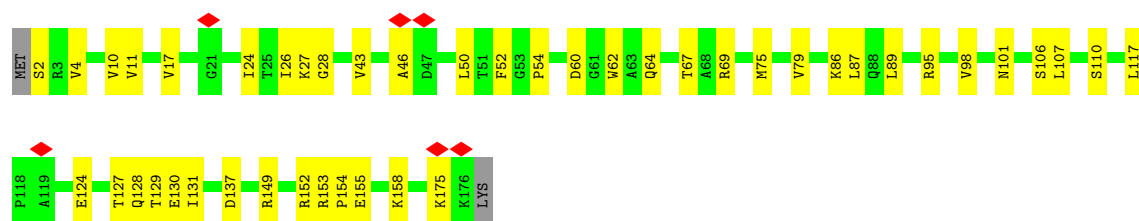
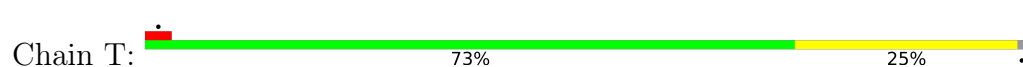
• Molecule 30: Large ribosomal subunit protein uL5



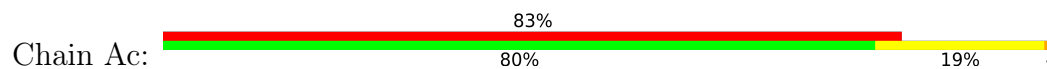
• Molecule 31: Large ribosomal subunit protein uL6

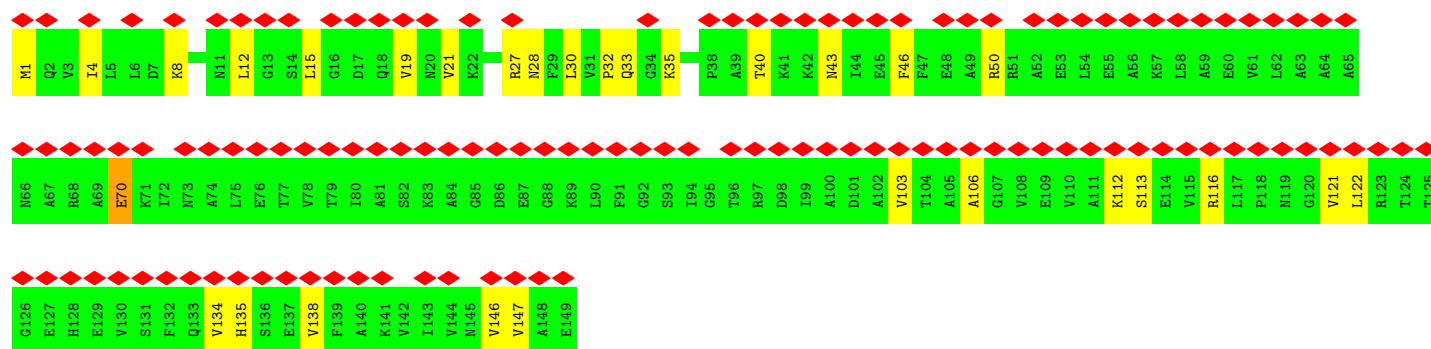


• Molecule 31: Large ribosomal subunit protein uL6

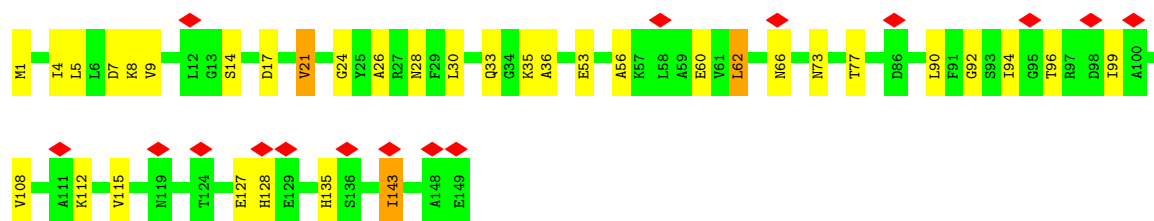
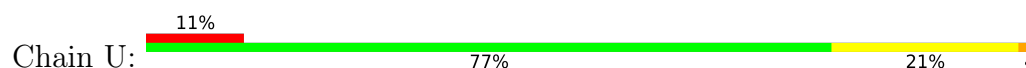


• Molecule 32: Large ribosomal subunit protein bL9

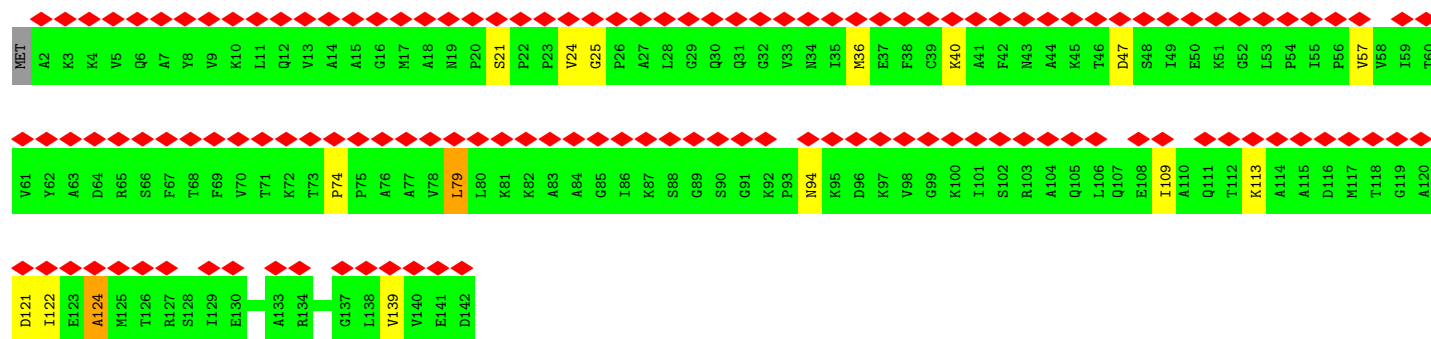
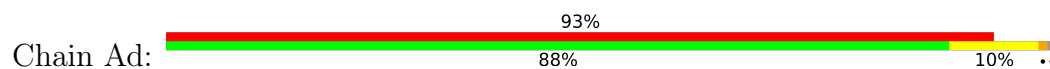




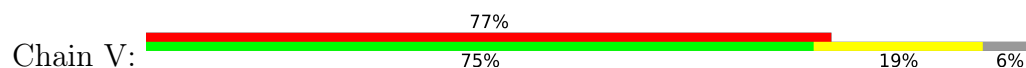
- Molecule 32: Large ribosomal subunit protein bL9

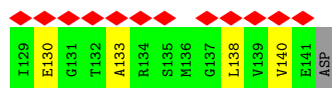


- Molecule 33: 50S ribosomal protein L11

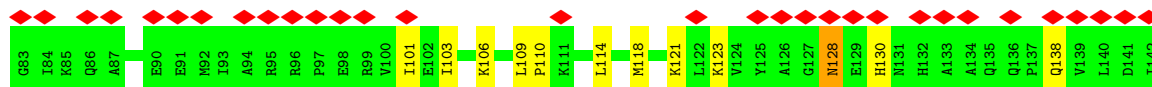
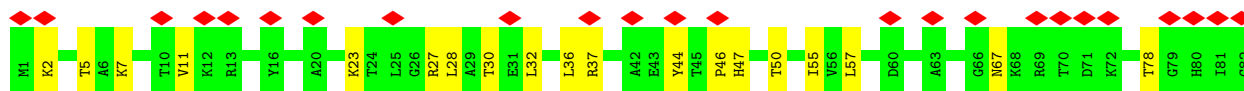
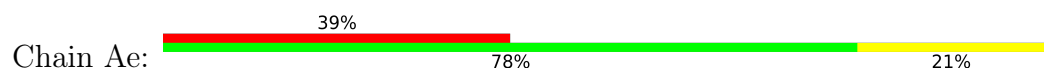


- Molecule 33: 50S ribosomal protein L11

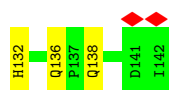
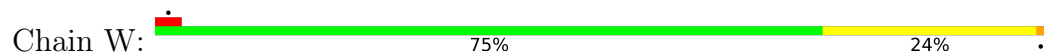




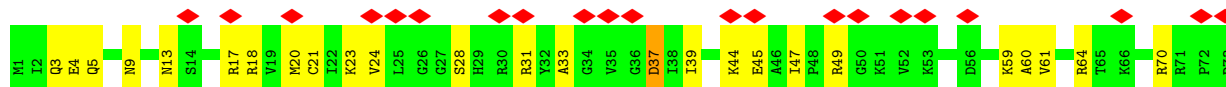
- Molecule 34: Large ribosomal subunit protein uL13



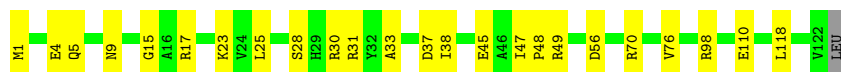
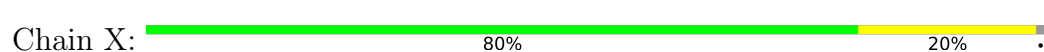
- Molecule 34: Large ribosomal subunit protein uL13



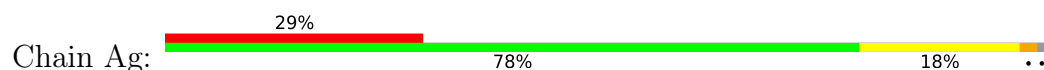
- Molecule 35: Large ribosomal subunit protein uL14

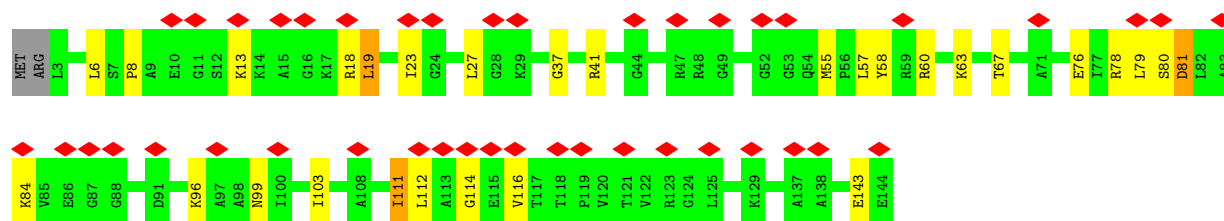


- Molecule 35: Large ribosomal subunit protein uL14

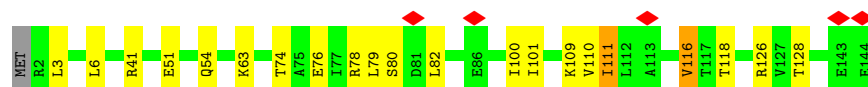
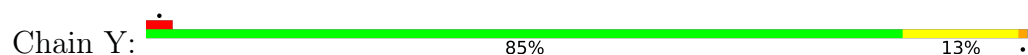


- Molecule 36: Large ribosomal subunit protein uL15

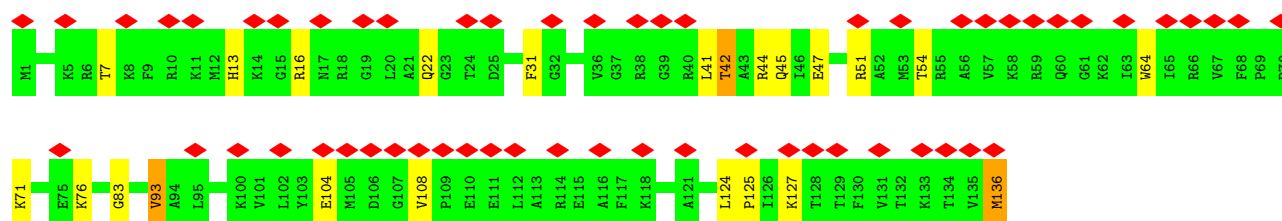
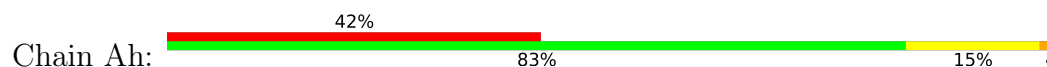




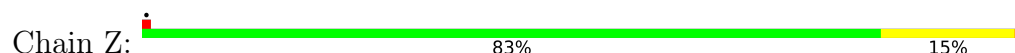
- Molecule 36: Large ribosomal subunit protein uL15



- Molecule 37: 50S ribosomal protein L16



- Molecule 37: 50S ribosomal protein L16



- Molecule 38: Large ribosomal subunit protein bL17

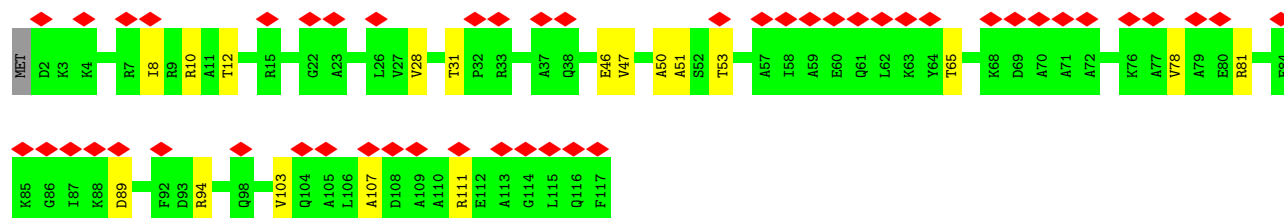
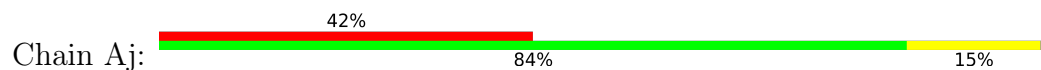


- Molecule 38: Large ribosomal subunit protein bL17





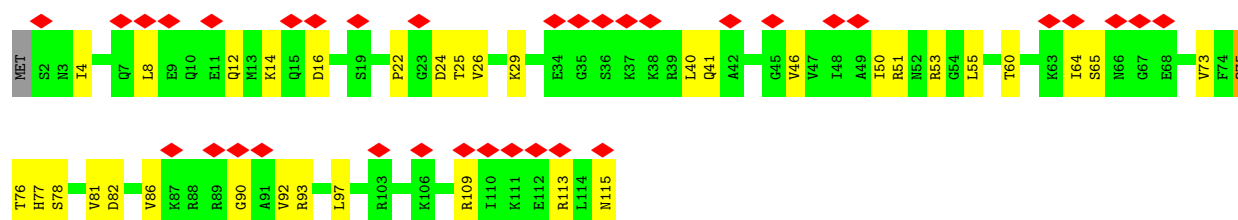
- Molecule 39: Large ribosomal subunit protein uL18



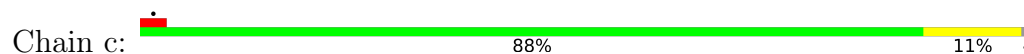
- Molecule 39: Large ribosomal subunit protein uL18



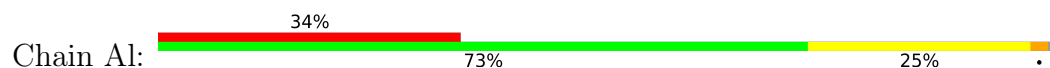
- Molecule 40: Large ribosomal subunit protein bL19

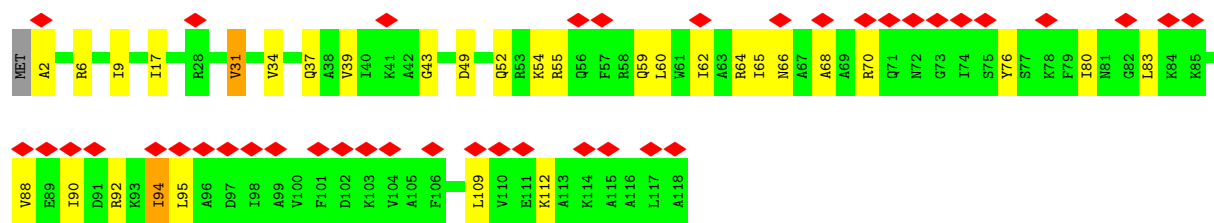


- Molecule 40: Large ribosomal subunit protein bL19

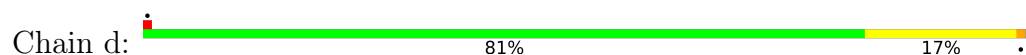


- Molecule 41: Large ribosomal subunit protein bL20

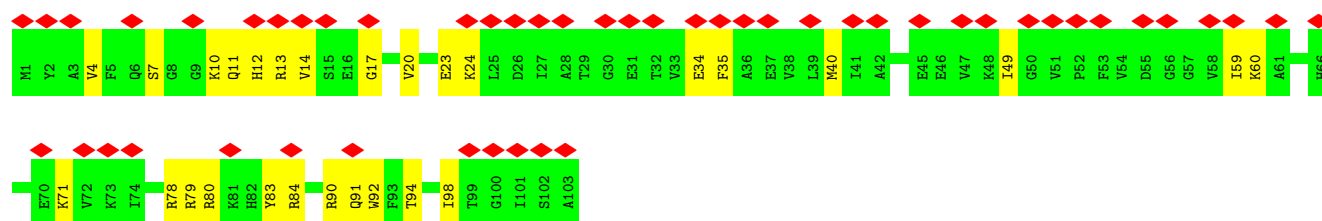
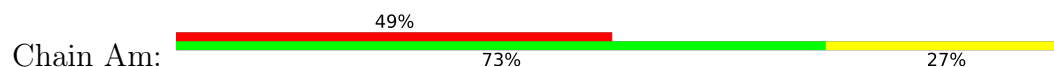




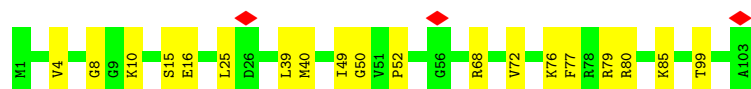
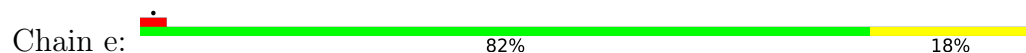
- Molecule 41: Large ribosomal subunit protein bL20



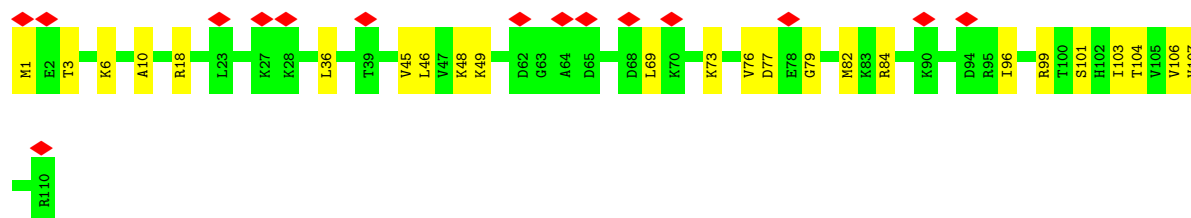
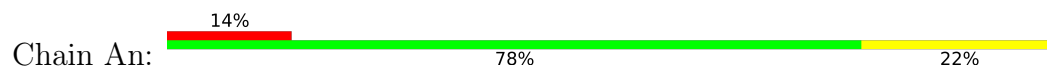
- Molecule 42: Large ribosomal subunit protein bL21



- Molecule 42: Large ribosomal subunit protein bL21



- Molecule 43: Large ribosomal subunit protein uL22

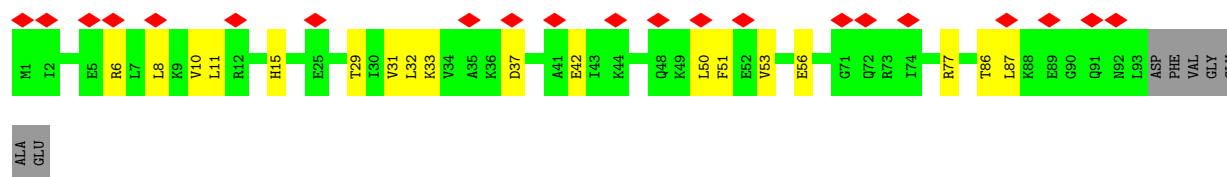
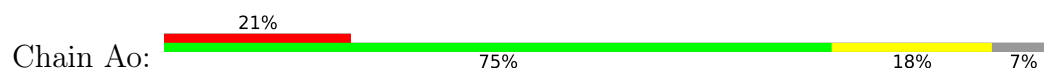


- Molecule 43: Large ribosomal subunit protein uL22

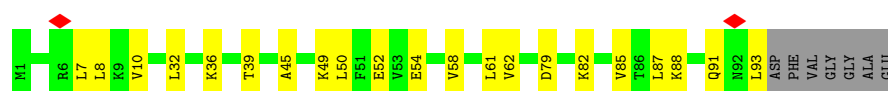




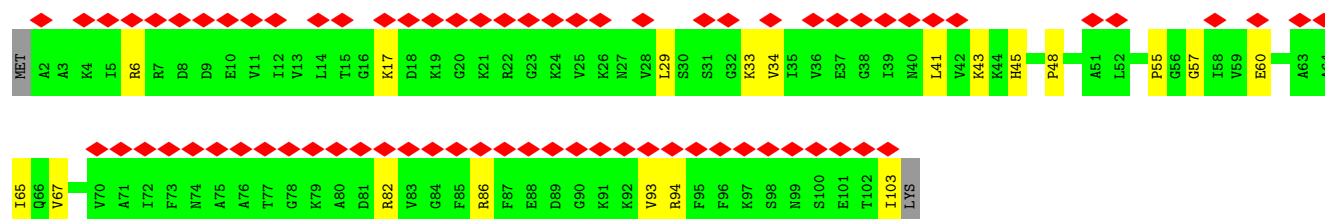
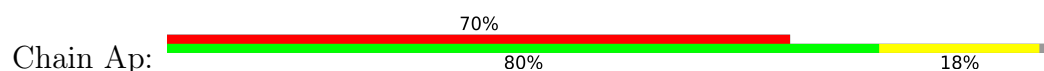
- Molecule 44: Large ribosomal subunit protein uL23



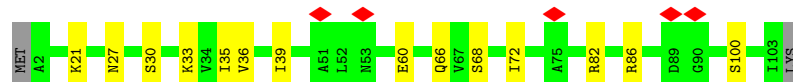
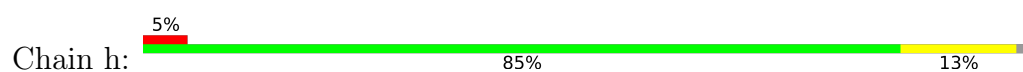
- Molecule 44: Large ribosomal subunit protein uL23



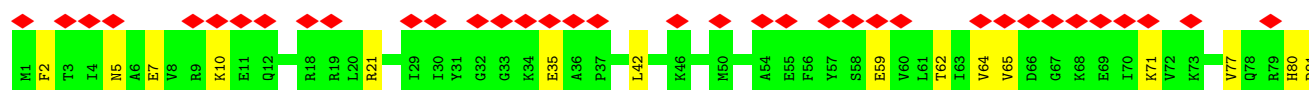
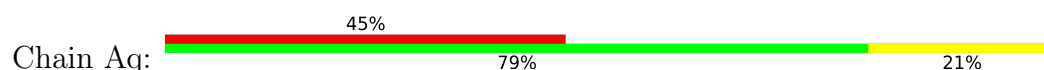
- Molecule 45: Large ribosomal subunit protein uL24

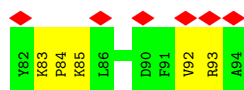


- Molecule 45: Large ribosomal subunit protein uL24

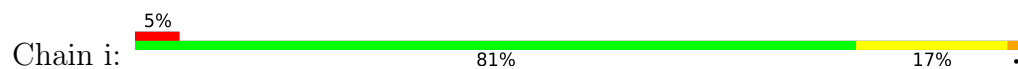


- Molecule 46: Large ribosomal subunit protein bL25

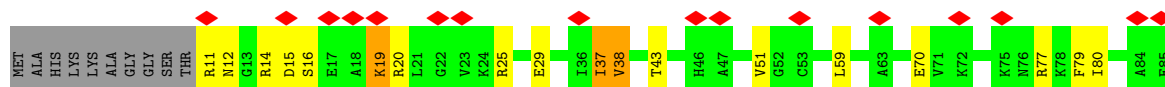




- Molecule 46: Large ribosomal subunit protein bL25



- Molecule 47: Large ribosomal subunit protein bL27



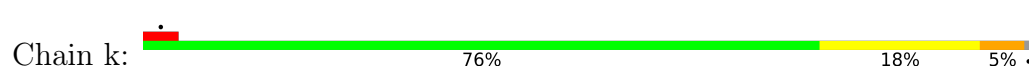
- Molecule 47: Large ribosomal subunit protein bL27



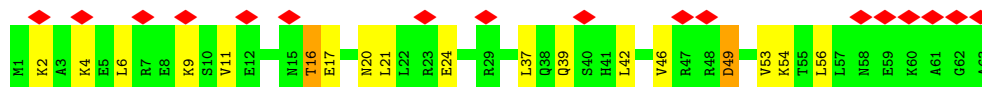
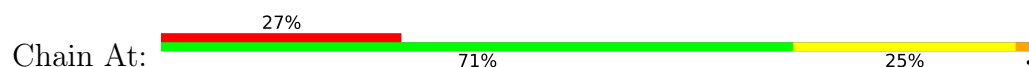
- Molecule 48: Large ribosomal subunit protein bL28



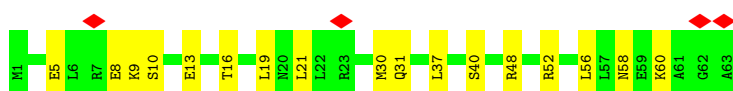
- Molecule 48: Large ribosomal subunit protein bL28



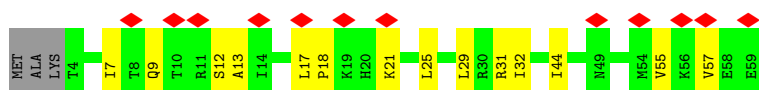
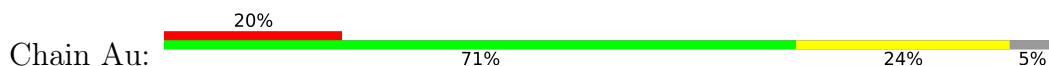
- Molecule 49: Large ribosomal subunit protein uL29



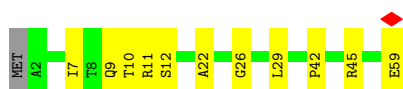
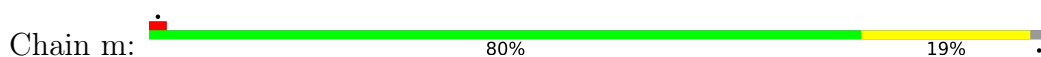
- Molecule 49: Large ribosomal subunit protein uL29



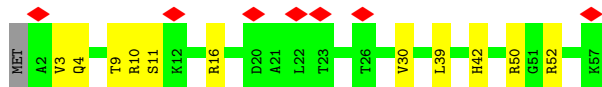
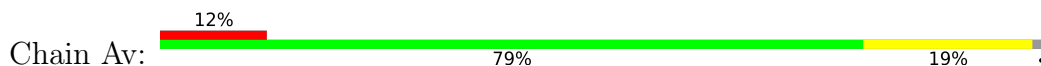
- Molecule 50: Large ribosomal subunit protein uL30



- Molecule 50: Large ribosomal subunit protein uL30



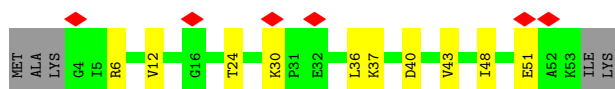
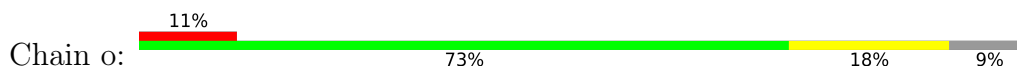
- Molecule 51: Large ribosomal subunit protein bL32



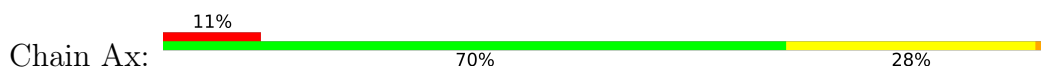
- Molecule 52: Large ribosomal subunit protein bL33



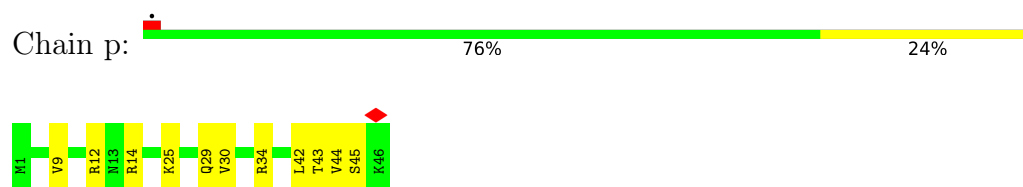
- Molecule 52: Large ribosomal subunit protein bL33



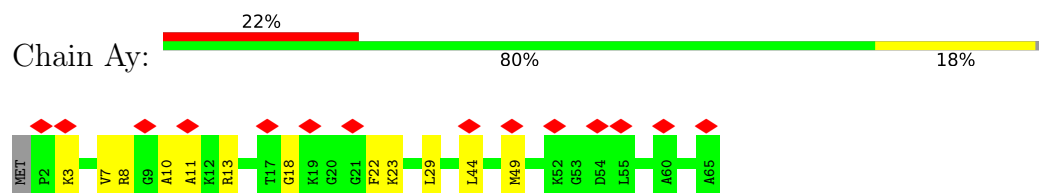
- Molecule 53: Large ribosomal subunit protein bL34



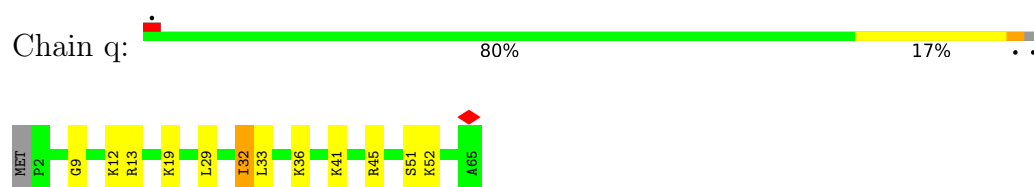
- Molecule 53: Large ribosomal subunit protein bL34



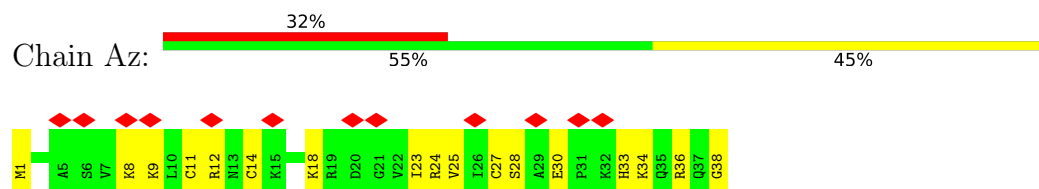
- Molecule 54: Large ribosomal subunit protein bL35



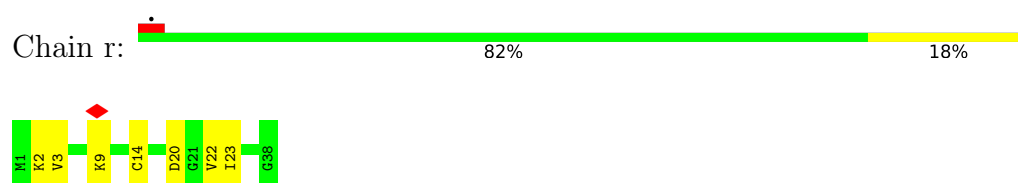
- Molecule 54: Large ribosomal subunit protein bL35



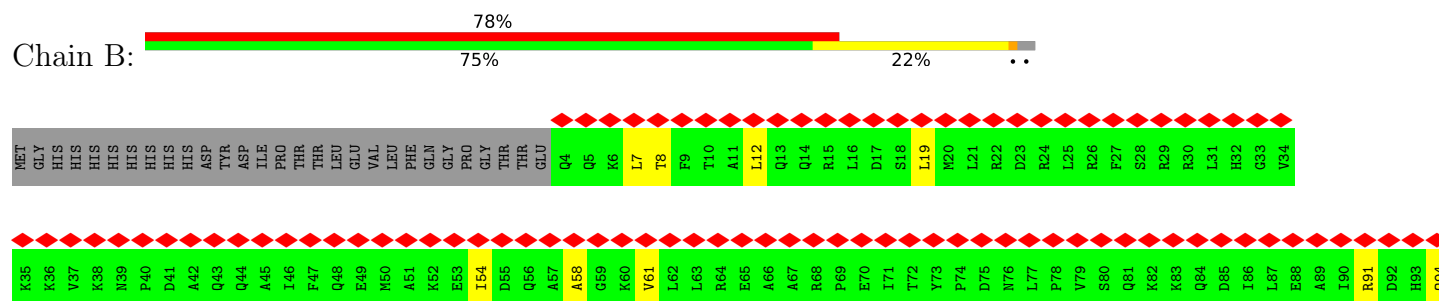
- Molecule 55: Large ribosomal subunit protein bL36A



- Molecule 55: Large ribosomal subunit protein bL36A



- Molecule 56: ATP-dependent RNA helicase HrpA



V95	V96	I97	V98	A99	G100	E101	T102	G103	S104	G105	K106	T107	T108	Q109	L110	P111	K112	I113	C114	M115	E116	L117	G118	R119	G120	I121	K122	G123	L124	I125	G126	H127	T128	Q129	P130	R131	R132	L133	A134	A135	R136	T137	V138	A139	N140	R141	I142	A143	E144	E145	L146	K147	T148	E149	P150	G151	C153	I154		
G155	Y156	K157	V158	R159	F160	S161	D162	H163	V164	S165	D166	M167	T168	M169	V170	K171	L172	M173	T174	D175	G176	L177	L178	L179	A180	H181	I182	Q183	Q184	D185	R186	L187	L188	M189	Q190	S260	G251	R252	T253	Y254	P255	V256	D197	E198	A199	H200	E201	R202	S203	V264	E265	E266	D207	F208	L209	L210	G211	Y212	L213	K214
E215	L216	L217	P218	R219	R220	P221	D222	L223	K224	I225	I226	I227	T228	S229	A230	T231	I232	D233	P234	E235	R236	F237	S238	R239	H240	F241	N242	N243	A244	P245	I246	I247	E248	V249	S260	G251	R252	T253	Y254	P255	V256	E257	V258	R259	Y260	R261	P262	I263	V264	E265	E266	A267	D268	D269	T270	E271	R272	D273	Q274	
L275	Q276	A277	I278	F279	D280	A281	V282	D283	E284	L285	S286	Q287	E288	S289	H290	G291	D292	I293	L294	F295	F296	M297	S298	G299	R300	E301	E302	I303	R304	D305	T306	E307	D308	A309	L310	K311	K312	L313	N314	L315	R316	H317	T318	E319	I320	L321	P322	L323	Y324	A325	R326	L327	S328	N329	S330	E331	N333	R334		
V335	F336	Q337	S338	H339	S340	G341	R342	R343	I344	V345	L346	A347	T348	N349	V350	A351	E352	T353	S354	L355	T356	V357	P358	G359	I360	K361	Y362	V363	I364	D365	P366	G367	T368	A369	R370	I371	S372	R373	Y374	S375	Y376	R377	T378	K379	V380	Q381	R382	L383	P384	I385	E386	P387	T388	S389	Q390	A391	S392	A393	N394	
Q395	R396	E397	G398	R399	C400	G401	R402	S403	Y404	E405	G406	T407	C408	I409	R410	L411	Y412	S413	E414	D415	D416	F417	L418	S419	R420	F421	E422	F423	T424	D425	P426	E427	L428	L429	R430	T431	N432	L433	A434	A435	V436	I437	L438	Q439	N440	T441	A442	L443	G444	L445	G446	D447	T448	A449	A450	F451	F452	F453	V454	
E455	A456	P457	D458	K459	R460	M461	L462	Q463	D464	G465	V466	R467	L468	L469	E470	E471	L472	G473	A474	L475	T476	T477	D478	GLU	GLN	A481	S482	A483	Y484	K485	L486	T487	P488	L489	G490	R491	Q492	L493	S494	Q495	L496	P497	V498	D499	P500	R501	L502	A503	Y504	N505	V506	L507	E508	A509	Q510	K511	H512	O513	G514	
V515	R516	E517	A518	Y519	I520	L521	T522	S523	A524	L525	S526	L527	Q528	D529	P530	R531	E532	R533	P534	M535	D536	K537	Q538	Q539	A540	S541	D542	E543	K544	H545	R546	R547	F548	H549	D550	K551	E552	S553	D554	F555	L556	A557	F558	V559	N560	L561	V562	N563	Y564	L565	G566	E567	Q568	Q569	K570	A571	L572	S573	S574	
M575	A576	F577	R578	R579	L580	C581	R582	T583	D584	Y585	L586	N587	Y588	L589	R590	Y591	R592	E593	Y594	Q595	D596	L597	Y598	T599	Q600	L601	R602	Q603	V604	V605	K606	E607	L608	G609	I610	P611	V612	N613	S614	E615	P616	A617	E618	Y619	R620	E621	T622	H623	L624	A625	L626	L627	T628	G629	L630	L631	S632	H633	L634	
G635	M636	K637	D638	A639	D640	K641	Q642	E643	G646	A647	R648	N649	A650	R651	F652	I654	F655	P656	G657	S658	G659	L660	F661	K662	K663	P664	P665	K666	K667	V668	M669	V670	A671	E672	L673	V674	E675	T676	S677	R678	L679	M680	C681	R682	H683	A684	A685	R686	T687	D688	P689	E690	W691	V692	E693	P694	V695			
A696	Q697	H698	L699	I700	K701	R702	T703	Y704	S705	E706	F707	H708	W709	E710	R711	A712	Q713	G714	A715	V716	R717	A718	T719	K720	Y721	Y722	T723	Y724	Y725	G726	L727	F728	T729	V730	A731	A732	R733	K734	Y737	S738	Q739	I740	D741	L744	L748	H752	A753	L754	Y755	E756	G757	D758	W759	Q760	T761					
R762	H763	A764	F765	F766	R767	E768	R769	L770	K771	L772	R773	A774	E775	Y776	E777	E778	L779	R784	R785	R786	D787	L788	L789	W790	D791	D792	E793	T794	L795	F796	E797	F798	Y799	D800	O801	R802	I803	S804	H805	D806	S809	A810	F813	D814	S815	K819	W820	S821	R822	E756	G757	D758	W759	Q760	T761					
M829	F830	E831	K832	S833	M834	L835	I836	K837	E838	G839	A840	E841	K842	I843	S844	K845	L846	M850	F851	W852	H853	Q854	G855	H861	W862	E866	P867	G868	A869	D870	A871	P879	L882	L883	M884	E887	P888	S889	G890	F891	E892	I895	P896	C897	L898	E901	W902	S901	I904	F918	W919	P920	A921							
P922	A925	R931	V932	L935	E936	L937	P938	L939	L940	D941	R945	R949	M950	T951	G952	V953	R957	E958	D959	W960	H961	W962	D963	Q964	V965	P966	D967	H968	L969	K970	F973	R974	V975	V976	D977	D978	K979	N980	K981	K982	L983	K984	E985	G986	R987	Q990	D991	L992	K993	D994	A995									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17182	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.831	Depositor
Minimum map value	-0.349	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.165	Depositor
Map size ($\text{\AA}$)	508.9, 508.9, 508.9	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.727, 0.727, 0.727	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	0.15	0/36834	0.31	0/57462
1	AA	0.14	0/36966	0.31	0/57666
2	1	0.25	0/1735	0.65	0/2338
2	AB	0.25	0/1735	0.68	2/2338 (0.1%)
3	2	0.23	0/1651	0.65	0/2225
3	AC	0.25	0/1651	0.64	0/2225
4	3	0.23	0/1665	0.68	1/2227 (0.0%)
4	AD	0.22	0/1665	0.71	0/2227
5	4	0.35	0/1118	0.75	0/1504
5	AE	0.31	0/1118	0.79	0/1504
6	5	0.40	1/835 (0.1%)	0.90	3/1128 (0.3%)
6	AF	0.47	0/835	0.95	2/1128 (0.2%)
7	6	0.23	0/1195	0.74	4/1602 (0.2%)
7	AG	0.35	0/1195	0.73	0/1602
8	7	0.21	0/989	0.62	0/1326
8	AH	0.29	0/989	0.69	0/1326
9	8	0.38	0/1034	0.87	0/1375
9	AI	0.26	0/1034	0.83	0/1375
10	9	0.30	0/796	0.78	0/1077
10	AJ	0.25	0/796	0.78	0/1077
11	A	0.15	0/1812	0.39	0/2823
12	A1	0.32	0/557	0.77	0/738
12	v	0.23	0/597	0.70	0/792
13	A3	0.17	0/1830	0.46	0/2849
14	AK	0.15	0/1033	0.48	0/1387
14	C	0.13	0/1033	0.46	0/1387
15	AL	0.23	0/892	0.75	1/1193 (0.1%)
15	F	0.29	0/892	0.76	0/1193
16	AM	0.24	0/785	0.77	0/1043
16	G	0.64	2/803 (0.2%)	0.92	1/1070 (0.1%)
17	AN	0.28	0/722	0.73	0/964
17	H	0.25	0/710	0.62	0/950
18	AO	0.31	0/659	0.86	2/884 (0.2%)
18	I	0.22	0/658	0.68	0/884

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	AP	0.23	0/657	0.71	0/881
19	J	0.27	0/657	0.70	0/881
20	AQ	0.26	0/553	0.76	1/742 (0.1%)
20	K	0.22	0/544	0.67	0/731
21	AR	0.24	0/618	0.64	0/833
21	t	0.29	0/635	0.71	0/855
22	AS	0.24	0/671	0.73	0/888
22	u	0.23	0/671	0.67	0/888
23	AT	0.21	0/488	0.63	0/649
23	L	0.29	0/507	0.69	0/674
24	AU	0.15	0/1816	0.33	0/2830
25	AV	0.14	0/69659	0.31	1/108672 (0.0%)
25	N	0.15	0/69659	0.31	0/108672
26	AW	0.14	0/2828	0.30	0/4410
26	O	0.14	0/2828	0.31	0/4410
27	AX	0.20	0/2121	0.60	1/2852 (0.0%)
27	P	0.26	0/2121	0.64	0/2852
28	AY	0.27	0/1586	0.60	0/2134
28	Q	0.25	0/1586	0.55	0/2134
29	AZ	0.18	0/1571	0.58	0/2113
29	R	0.21	0/1571	0.61	1/2113 (0.0%)
30	Aa	0.21	0/1434	0.60	0/1926
30	S	0.35	0/1434	0.74	0/1926
31	Ab	0.25	0/1343	0.60	1/1816 (0.1%)
31	T	0.21	0/1333	0.61	2/1805 (0.1%)
32	Ac	0.23	0/1122	0.67	0/1515
32	U	0.48	0/1122	0.86	0/1515
33	Ad	0.36	1/1046 (0.1%)	0.62	0/1410
33	V	0.23	0/993	0.61	0/1341
34	Ae	0.29	0/1152	0.66	0/1551
34	W	0.30	0/1152	0.64	0/1551
35	Af	0.24	0/947	0.65	0/1268
35	X	0.23	0/947	0.66	0/1268
36	Ag	0.19	0/1043	0.60	0/1389
36	Y	0.23	0/1054	0.68	0/1403
37	Ah	0.19	0/1093	0.58	0/1460
37	Z	0.23	0/1093	0.60	0/1460
38	Ai	0.26	0/958	0.73	0/1281
38	a	0.27	0/964	0.76	0/1289
39	Aj	0.19	0/902	0.56	0/1209
39	b	0.20	0/902	0.64	0/1209
40	Ak	0.45	1/929 (0.1%)	0.77	0/1242
40	c	0.23	0/929	0.70	1/1242 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	Al	0.21	0/960	0.66	0/1278
41	d	0.18	0/960	0.58	0/1278
42	Am	0.25	0/829	0.70	0/1107
42	e	0.24	0/829	0.69	1/1107 (0.1%)
43	An	0.31	0/864	0.67	0/1156
43	f	0.22	0/864	0.62	0/1156
44	Ao	0.19	0/744	0.59	0/994
44	g	0.40	0/744	0.79	1/994 (0.1%)
45	Ap	0.19	0/787	0.63	0/1051
45	h	0.19	0/787	0.58	0/1051
46	Aq	0.32	0/766	0.62	1/1025 (0.1%)
46	i	0.26	0/766	0.73	0/1025
47	Ar	0.24	0/582	0.75	1/769 (0.1%)
47	j	0.25	0/582	0.69	0/769
48	As	0.20	0/635	0.68	0/848
48	k	0.59	2/635 (0.3%)	0.81	1/848 (0.1%)
49	At	0.24	0/510	0.72	0/677
49	l	0.36	0/510	0.70	0/677
50	Au	0.24	0/439	0.69	0/587
50	m	0.22	0/453	0.65	0/605
51	Av	0.39	1/450 (0.2%)	0.69	0/599
52	Aw	0.25	0/416	0.66	1/554 (0.2%)
52	o	0.27	0/416	0.74	0/554
53	Ax	0.20	0/380	0.72	0/498
53	p	0.20	0/380	0.81	2/498 (0.4%)
54	Ay	0.21	0/513	0.66	0/676
54	q	0.22	0/513	0.58	0/676
55	Az	0.19	0/303	0.72	0/397
55	r	0.25	0/303	0.63	0/397
56	B	0.23	2/10668 (0.0%)	0.56	0/14419
57	D	0.25	0/893	0.69	0/1205
57	y	0.27	0/893	0.75	0/1205
58	E	0.27	0/969	0.77	1/1300 (0.1%)
58	z	0.38	0/969	0.81	0/1300
59	M	0.14	0/1778	0.30	0/2768
60	n	0.19	0/435	0.65	0/581
61	s	0.42	0/326	0.71	0/441
62	w	0.18	0/1302	0.45	0/2018
63	x	0.20	0/970	0.60	0/1307
All	All	0.19	10/333181 (0.0%)	0.45	33/496574 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	k	45	ARG	C-N	9.76	1.47	1.33
40	Ak	75	GLN	C-N	9.46	1.46	1.33
48	k	46	PHE	C-N	8.55	1.44	1.33
16	G	25	ALA	C-N	8.12	1.43	1.33
6	5	90	MET	C-N	-6.71	1.24	1.33

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	90	MET	CA-C-N	-10.46	104.76	122.33
6	5	90	MET	C-N-CA	-10.46	104.76	122.33
16	G	25	ALA	O-C-N	7.77	130.17	122.09
53	p	44	VAL	N-CA-CB	-7.52	103.59	112.39
27	AX	196	GLY	N-CA-C	7.07	121.21	112.73

There are no chirality outliers.

There are no planarity outliers.

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	32895	0	16553	390	0
1	AA	33015	0	16617	352	0
2	1	1704	0	1732	46	0
2	AB	1704	0	1732	44	0
3	2	1624	0	1696	25	0
3	AC	1624	0	1696	40	0
4	3	1643	0	1707	35	0
4	AD	1643	0	1707	27	0
5	4	1105	0	1148	23	0
5	AE	1105	0	1148	27	0
6	5	817	0	808	25	0
6	AF	817	0	808	40	0
7	6	1181	0	1238	41	0
7	AG	1181	0	1238	26	0
8	7	979	0	1031	32	0
8	AH	979	0	1031	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	8	1022	0	1070	33	0
9	AI	1022	0	1070	27	0
10	9	786	0	828	27	0
10	AJ	786	0	828	19	0
11	A	1622	0	821	11	0
12	A1	551	0	588	8	0
12	v	589	0	629	9	0
13	A3	1638	0	830	17	0
14	AK	1026	0	1092	26	0
14	C	1026	0	1092	14	0
15	AL	883	0	941	22	0
15	F	883	0	941	17	0
16	AM	774	0	824	32	0
16	G	791	0	826	42	0
17	AN	714	0	734	19	0
17	H	702	0	721	7	0
18	AO	649	0	666	28	0
18	I	648	0	666	20	0
19	AP	648	0	691	17	0
19	J	648	0	691	19	0
20	AQ	544	0	565	17	0
20	K	535	0	552	14	0
21	AR	603	0	623	16	0
21	t	620	0	647	14	0
22	AS	665	0	714	13	0
22	u	665	0	714	16	0
23	AT	480	0	482	5	0
23	L	499	0	499	12	0
24	AU	1625	0	822	23	0
25	AV	62195	0	31280	678	0
25	N	62195	0	31280	582	0
26	AW	2529	0	1281	26	0
26	O	2529	0	1281	25	0
27	AX	2082	0	2154	46	0
27	P	2082	0	2154	39	0
28	AY	1565	0	1616	63	0
28	Q	1565	0	1616	28	0
29	AZ	1552	0	1619	31	0
29	R	1552	0	1619	40	0
30	Aa	1410	0	1444	44	0
30	S	1410	0	1444	44	0
31	Ab	1323	0	1371	25	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	T	1313	0	1358	27	0
32	Ac	1111	0	1148	17	0
32	U	1111	0	1148	22	0
33	Ad	1032	0	1085	8	0
33	V	979	0	1028	19	0
34	Ae	1129	0	1162	24	0
34	W	1129	0	1162	27	0
35	Af	938	0	1012	24	0
35	X	938	0	1012	17	0
36	Ag	1034	0	1104	25	0
36	Y	1045	0	1117	15	0
37	Ah	1074	0	1155	34	0
37	Z	1074	0	1157	15	0
38	Ai	945	0	989	25	0
38	a	951	0	994	23	0
39	Aj	892	0	923	7	0
39	b	892	0	923	18	0
40	Ak	917	0	962	24	0
40	c	917	0	962	15	0
41	Al	947	0	1019	26	0
41	d	947	0	1019	17	0
42	Am	816	0	839	25	0
42	e	816	0	839	13	0
43	An	857	0	922	15	0
43	f	857	0	922	23	0
44	Ao	738	0	807	14	0
44	g	738	0	807	9	0
45	Ap	779	0	831	14	0
45	h	779	0	831	9	0
46	Aq	753	0	780	9	0
46	i	753	0	780	13	0
47	Ar	575	0	592	23	0
47	j	575	0	592	9	0
48	As	625	0	652	13	0
48	k	625	0	652	13	0
49	At	509	0	543	12	0
49	l	509	0	543	10	0
50	Au	435	0	470	8	0
50	m	449	0	488	7	0
51	Av	444	0	458	8	0
52	Aw	409	0	440	11	0
52	o	409	0	440	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Ax	377	0	418	9	0
53	p	377	0	418	9	0
54	Ay	504	0	572	9	0
54	q	504	0	572	9	0
55	Az	302	0	343	10	0
55	r	302	0	343	4	0
56	B	10462	0	10585	168	0
57	D	877	0	887	18	0
57	y	877	0	887	31	0
58	E	955	0	1016	18	0
58	z	955	0	1016	19	0
59	M	1593	0	810	6	0
60	n	429	0	440	10	0
61	s	316	0	283	9	0
62	w	1175	0	594	16	0
63	x	958	0	988	20	0
All	All	307377	0	211055	3829	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 8.

The worst 5 of 3829 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)
25:AV:1655:A:C1'	28:AY:118:PHE:CE2	1.85	1.57
25:AV:1655:A:C1'	28:AY:118:PHE:HE2	1.13	1.55
30:S:38:MET:SD	30:S:53:ALA:HB1	1.52	1.49
30:Aa:104:ILE:CG2	30:Aa:175:PHE:HD1	1.23	1.48
25:AV:1655:A:H1'	28:AY:118:PHE:CE2	0.92	1.43

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	
2	1	216/241 (90%)	203 (94%)	13 (6%)	0	100	100
2	AB	216/241 (90%)	203 (94%)	13 (6%)	0	100	100
3	2	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
3	AC	204/233 (88%)	198 (97%)	6 (3%)	0	100	100
4	3	203/206 (98%)	195 (96%)	8 (4%)	0	100	100
4	AD	203/206 (98%)	191 (94%)	12 (6%)	0	100	100
5	4	148/167 (89%)	139 (94%)	9 (6%)	0	100	100
5	AE	148/167 (89%)	135 (91%)	12 (8%)	1 (1%)	18	49
6	5	98/135 (73%)	90 (92%)	8 (8%)	0	100	100
6	AF	98/135 (73%)	94 (96%)	4 (4%)	0	100	100
7	6	149/179 (83%)	145 (97%)	4 (3%)	0	100	100
7	AG	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
8	7	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
8	AH	127/130 (98%)	123 (97%)	3 (2%)	1 (1%)	16	47
9	8	125/130 (96%)	113 (90%)	11 (9%)	1 (1%)	16	47
9	AI	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
10	9	96/103 (93%)	86 (90%)	9 (9%)	1 (1%)	12	41
10	AJ	96/103 (93%)	83 (86%)	13 (14%)	0	100	100
12	A1	64/71 (90%)	64 (100%)	0	0	100	100
12	v	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
14	AK	130/234 (56%)	126 (97%)	4 (3%)	0	100	100
14	C	130/234 (56%)	129 (99%)	1 (1%)	0	100	100
15	AL	112/118 (95%)	103 (92%)	9 (8%)	0	100	100
15	F	112/118 (95%)	108 (96%)	4 (4%)	0	100	100
16	AM	92/101 (91%)	79 (86%)	13 (14%)	0	100	100
16	G	96/101 (95%)	87 (91%)	8 (8%)	1 (1%)	12	41
17	AN	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
17	H	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
18	AO	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
18	I	80/82 (98%)	73 (91%)	7 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AP	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
19	J	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
20	AQ	64/75 (85%)	58 (91%)	6 (9%)	0	100	100
20	K	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
21	AR	73/92 (79%)	69 (94%)	4 (6%)	0	100	100
21	t	75/92 (82%)	70 (93%)	5 (7%)	0	100	100
22	AS	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
22	u	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
23	AT	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
23	L	58/70 (83%)	54 (93%)	4 (7%)	0	100	100
27	AX	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
27	P	269/273 (98%)	256 (95%)	13 (5%)	0	100	100
28	AY	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
28	Q	207/209 (99%)	199 (96%)	8 (4%)	0	100	100
29	AZ	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
29	R	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
30	Aa	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
30	S	175/179 (98%)	162 (93%)	13 (7%)	0	100	100
31	Ab	174/177 (98%)	167 (96%)	7 (4%)	0	100	100
31	T	173/177 (98%)	167 (96%)	6 (4%)	0	100	100
32	Ac	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
32	U	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
33	Ad	139/142 (98%)	120 (86%)	18 (13%)	1 (1%)	18	49
33	V	132/142 (93%)	119 (90%)	13 (10%)	0	100	100
34	Ae	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
34	W	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
35	Af	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
35	X	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
36	Ag	140/144 (97%)	134 (96%)	6 (4%)	0	100	100
36	Y	141/144 (98%)	133 (94%)	8 (6%)	0	100	100
37	Ah	134/136 (98%)	129 (96%)	5 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	Z	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
38	Ai	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
38	a	117/127 (92%)	111 (95%)	6 (5%)	0	100	100
39	Aj	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
39	b	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
40	Ak	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
40	c	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
41	Al	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
41	d	115/118 (98%)	115 (100%)	0	0	100	100
42	Am	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
42	e	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
43	An	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
43	f	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
44	Ao	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
44	g	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
45	Ap	100/104 (96%)	92 (92%)	8 (8%)	0	100	100
45	h	100/104 (96%)	93 (93%)	7 (7%)	0	100	100
46	Aq	92/94 (98%)	88 (96%)	3 (3%)	1 (1%)	11	39
46	i	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
47	Ar	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
47	j	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
48	As	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
48	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
49	At	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
49	l	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
50	Au	54/59 (92%)	50 (93%)	4 (7%)	0	100	100
50	m	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
51	Av	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
52	Aw	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
52	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
53	Ax	44/46 (96%)	42 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	p	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	Ay	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
54	q	62/65 (95%)	60 (97%)	1 (2%)	1 (2%)	7	30
55	Az	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
55	r	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	B	1291/1326 (97%)	1247 (97%)	44 (3%)	0	100	100
57	D	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
57	y	115/129 (89%)	104 (90%)	11 (10%)	0	100	100
58	E	121/124 (98%)	109 (90%)	12 (10%)	0	100	100
58	z	121/124 (98%)	115 (95%)	6 (5%)	0	100	100
60	n	52/56 (93%)	49 (94%)	3 (6%)	0	100	100
61	s	35/179 (20%)	33 (94%)	2 (6%)	0	100	100
63	x	125/165 (76%)	118 (94%)	7 (6%)	0	100	100
All	All	13095/14247 (92%)	12440 (95%)	647 (5%)	8 (0%)	49	78

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	Ad	47	ASP
9	8	39	PHE
5	AE	90	THR
8	AH	66	PHE
16	G	33	ASP

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	
2	1	180/199 (90%)	175 (97%)	5 (3%)	38	66
2	AB	180/199 (90%)	173 (96%)	7 (4%)	28	60
3	2	170/190 (90%)	163 (96%)	7 (4%)	27	59

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	170/190 (90%)	165 (97%)	5 (3%)	37	66
4	3	172/173 (99%)	166 (96%)	6 (4%)	32	62
4	AD	172/173 (99%)	166 (96%)	6 (4%)	32	62
5	4	113/126 (90%)	107 (95%)	6 (5%)	20	51
5	AE	113/126 (90%)	107 (95%)	6 (5%)	20	51
6	5	87/116 (75%)	84 (97%)	3 (3%)	32	63
6	AF	87/116 (75%)	83 (95%)	4 (5%)	24	55
7	6	124/147 (84%)	118 (95%)	6 (5%)	23	54
7	AG	124/147 (84%)	123 (99%)	1 (1%)	73	81
8	7	104/105 (99%)	99 (95%)	5 (5%)	23	54
8	AH	104/105 (99%)	98 (94%)	6 (6%)	18	48
9	8	105/107 (98%)	100 (95%)	5 (5%)	23	54
9	AI	105/107 (98%)	102 (97%)	3 (3%)	37	66
10	9	86/90 (96%)	78 (91%)	8 (9%)	8	31
10	AJ	86/90 (96%)	81 (94%)	5 (6%)	18	48
12	A1	56/61 (92%)	55 (98%)	1 (2%)	51	73
12	v	60/61 (98%)	57 (95%)	3 (5%)	22	53
14	AK	110/181 (61%)	103 (94%)	7 (6%)	16	44
14	C	110/181 (61%)	105 (96%)	5 (4%)	24	56
15	AL	92/96 (96%)	88 (96%)	4 (4%)	26	57
15	F	92/96 (96%)	88 (96%)	4 (4%)	26	57
16	AM	79/84 (94%)	74 (94%)	5 (6%)	16	45
16	G	82/84 (98%)	82 (100%)	0	100	100
17	AN	76/77 (99%)	74 (97%)	2 (3%)	40	68
17	H	75/77 (97%)	74 (99%)	1 (1%)	61	77
18	AO	65/65 (100%)	62 (95%)	3 (5%)	24	55
18	I	65/65 (100%)	62 (95%)	3 (5%)	24	55
19	AP	74/78 (95%)	72 (97%)	2 (3%)	39	67
19	J	74/78 (95%)	73 (99%)	1 (1%)	59	76
20	AQ	57/65 (88%)	55 (96%)	2 (4%)	32	62
20	K	56/65 (86%)	55 (98%)	1 (2%)	51	73

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AR	66/79 (84%)	62 (94%)	4 (6%)	17	46
21	t	68/79 (86%)	64 (94%)	4 (6%)	18	48
22	AS	65/66 (98%)	61 (94%)	4 (6%)	16	46
22	u	65/66 (98%)	62 (95%)	3 (5%)	24	55
23	AT	55/62 (89%)	53 (96%)	2 (4%)	31	62
23	L	57/62 (92%)	55 (96%)	2 (4%)	32	62
27	AX	216/218 (99%)	211 (98%)	5 (2%)	44	70
27	P	216/218 (99%)	210 (97%)	6 (3%)	38	66
28	AY	164/164 (100%)	159 (97%)	5 (3%)	36	65
28	Q	164/164 (100%)	159 (97%)	5 (3%)	36	65
29	AZ	165/165 (100%)	159 (96%)	6 (4%)	31	62
29	R	165/165 (100%)	160 (97%)	5 (3%)	36	65
30	Aa	148/150 (99%)	146 (99%)	2 (1%)	59	76
30	S	148/150 (99%)	139 (94%)	9 (6%)	17	46
31	Ab	137/138 (99%)	131 (96%)	6 (4%)	25	56
31	T	136/138 (99%)	132 (97%)	4 (3%)	37	66
32	Ac	114/114 (100%)	109 (96%)	5 (4%)	25	56
32	U	114/114 (100%)	107 (94%)	7 (6%)	17	46
33	Ad	109/110 (99%)	106 (97%)	3 (3%)	38	66
33	V	104/110 (94%)	102 (98%)	2 (2%)	50	73
34	Ae	116/116 (100%)	114 (98%)	2 (2%)	53	74
34	W	116/116 (100%)	114 (98%)	2 (2%)	53	74
35	Af	103/104 (99%)	97 (94%)	6 (6%)	18	48
35	X	103/104 (99%)	100 (97%)	3 (3%)	37	66
36	Ag	101/103 (98%)	96 (95%)	5 (5%)	22	53
36	Y	102/103 (99%)	96 (94%)	6 (6%)	18	48
37	Ah	109/109 (100%)	104 (95%)	5 (5%)	24	55
37	Z	109/109 (100%)	104 (95%)	5 (5%)	24	55
38	Ai	98/103 (95%)	95 (97%)	3 (3%)	35	64
38	a	99/103 (96%)	96 (97%)	3 (3%)	36	65
39	Aj	86/87 (99%)	81 (94%)	5 (6%)	18	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	b	86/87 (99%)	78 (91%)	8 (9%)	8	31
40	Ak	99/100 (99%)	96 (97%)	3 (3%)	36	65
40	c	99/100 (99%)	98 (99%)	1 (1%)	68	79
41	Al	89/90 (99%)	86 (97%)	3 (3%)	32	63
41	d	89/90 (99%)	87 (98%)	2 (2%)	45	71
42	Am	84/84 (100%)	84 (100%)	0	100	100
42	e	84/84 (100%)	80 (95%)	4 (5%)	23	54
43	An	93/93 (100%)	91 (98%)	2 (2%)	45	71
43	f	93/93 (100%)	90 (97%)	3 (3%)	34	64
44	Ao	80/84 (95%)	79 (99%)	1 (1%)	61	77
44	g	80/84 (95%)	76 (95%)	4 (5%)	22	53
45	Ap	83/85 (98%)	82 (99%)	1 (1%)	63	78
45	h	83/85 (98%)	81 (98%)	2 (2%)	43	69
46	Aq	78/78 (100%)	75 (96%)	3 (4%)	29	60
46	i	78/78 (100%)	75 (96%)	3 (4%)	29	60
47	Ar	57/63 (90%)	55 (96%)	2 (4%)	32	62
47	j	57/63 (90%)	54 (95%)	3 (5%)	20	51
48	As	67/68 (98%)	63 (94%)	4 (6%)	17	47
48	k	67/68 (98%)	61 (91%)	6 (9%)	9	33
49	At	55/55 (100%)	52 (94%)	3 (6%)	19	50
49	l	55/55 (100%)	53 (96%)	2 (4%)	31	62
50	Au	47/49 (96%)	44 (94%)	3 (6%)	16	44
50	m	48/49 (98%)	48 (100%)	0	100	100
51	Av	47/48 (98%)	47 (100%)	0	100	100
52	Aw	45/49 (92%)	44 (98%)	1 (2%)	45	71
52	o	45/49 (92%)	45 (100%)	0	100	100
53	Ax	38/38 (100%)	36 (95%)	2 (5%)	20	51
53	p	38/38 (100%)	38 (100%)	0	100	100
54	Ay	51/52 (98%)	51 (100%)	0	100	100
54	q	51/52 (98%)	49 (96%)	2 (4%)	28	60
55	Az	34/34 (100%)	33 (97%)	1 (3%)	37	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	r	34/34 (100%)	32 (94%)	2 (6%)	18	48
56	B	1130/1158 (98%)	1096 (97%)	34 (3%)	36	65
57	D	90/99 (91%)	84 (93%)	6 (7%)	15	43
57	y	90/99 (91%)	85 (94%)	5 (6%)	19	49
58	E	103/104 (99%)	100 (97%)	3 (3%)	37	66
58	z	103/104 (99%)	94 (91%)	9 (9%)	9	34
60	n	46/47 (98%)	43 (94%)	3 (6%)	15	44
61	s	34/158 (22%)	32 (94%)	2 (6%)	18	48
63	x	96/123 (78%)	96 (100%)	0	100	100
All	All	10949/11680 (94%)	10544 (96%)	405 (4%)	31	61

5 of 405 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	B	695	VAL
28	Q	113	SER
58	z	40	THR
56	B	919	VAL
57	D	97	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
53	Ax	13	ASN
60	n	6	ASN
56	B	1297	GLN
50	m	34	HIS
39	b	104	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	1532/1542 (99%)	232 (15%)	14 (0%)
1	AA	1538/1542 (99%)	250 (16%)	14 (0%)
11	A	75/76 (98%)	20 (26%)	5 (6%)
13	A3	76/77 (98%)	28 (36%)	6 (7%)
24	AU	75/76 (98%)	13 (17%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	AV	2895/2903 (99%)	498 (17%)	21 (0%)
25	N	2895/2903 (99%)	439 (15%)	15 (0%)
26	AW	117/120 (97%)	23 (19%)	0
26	O	117/120 (97%)	18 (15%)	1 (0%)
59	M	74/75 (98%)	14 (18%)	1 (1%)
62	w	56/698 (8%)	27 (48%)	0
All	All	9450/10132 (93%)	1562 (16%)	77 (0%)

5 of 1562 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	4	U
1	0	5	U
1	0	9	G
1	0	32	A
1	0	39	G

5 of 77 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	AV	2655	G
25	N	2311	A
25	AV	2776	A
25	N	481	G
25	N	2832	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

There are no chain breaks in this entry.

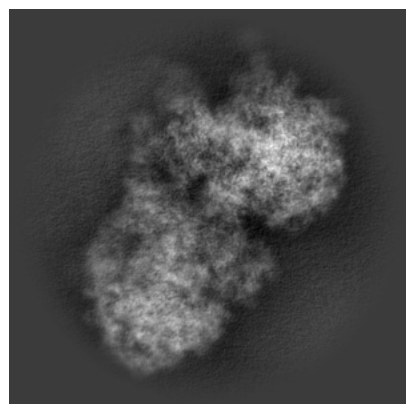
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51318. These allow visual inspection of the internal detail of the map and identification of artifacts.

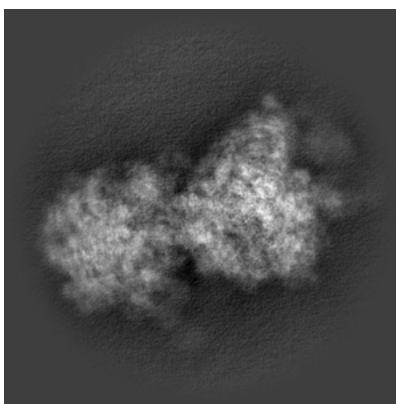
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

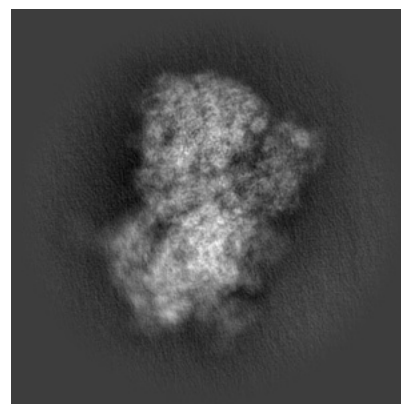
6.1.1 Primary map



X

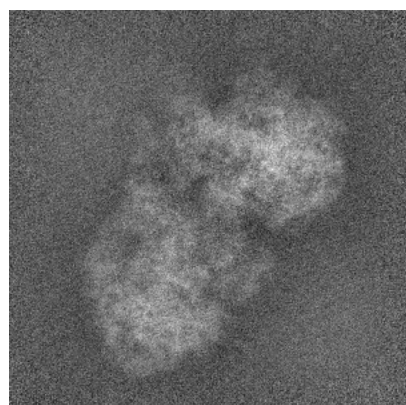


Y

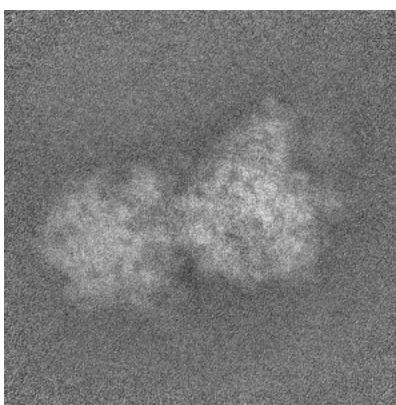


Z

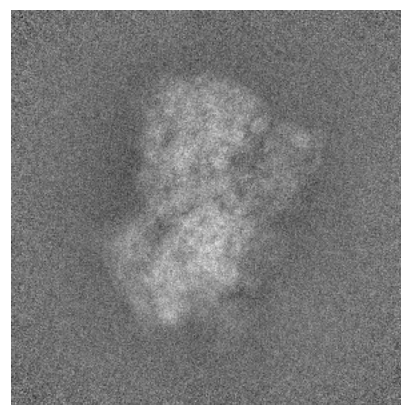
6.1.2 Raw map



X



Y

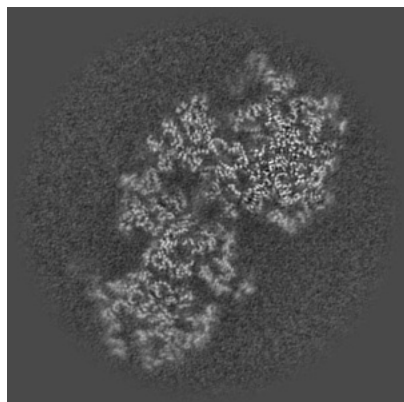


Z

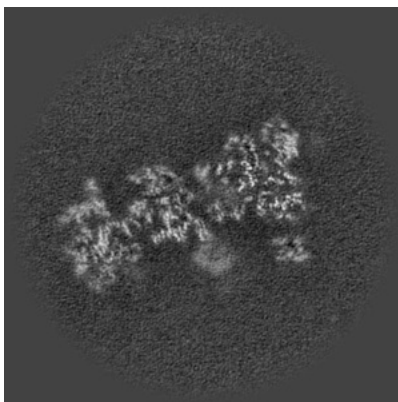
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

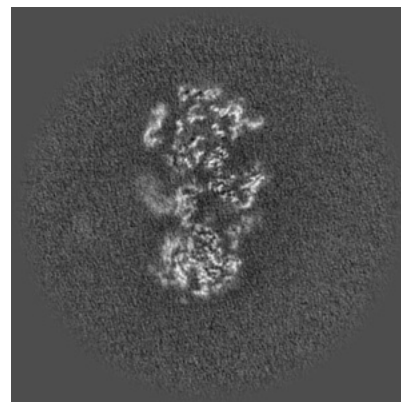
6.2.1 Primary map



X Index: 350

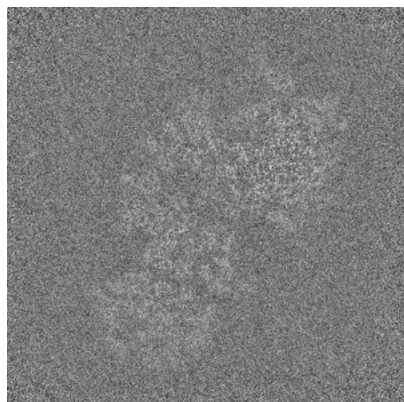


Y Index: 350

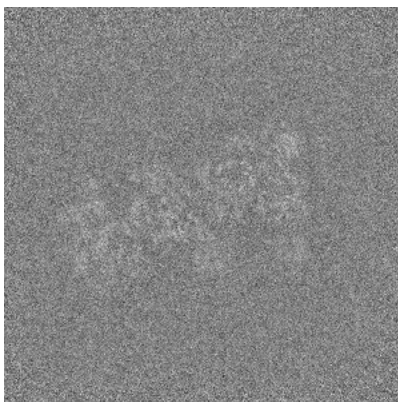


Z Index: 350

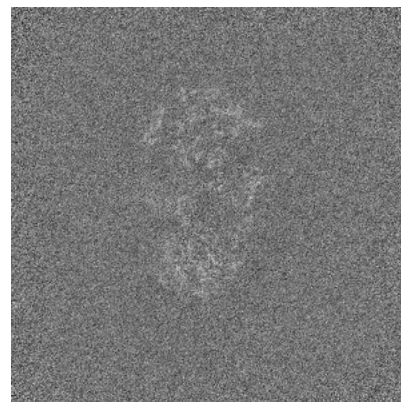
6.2.2 Raw map



X Index: 350



Y Index: 350

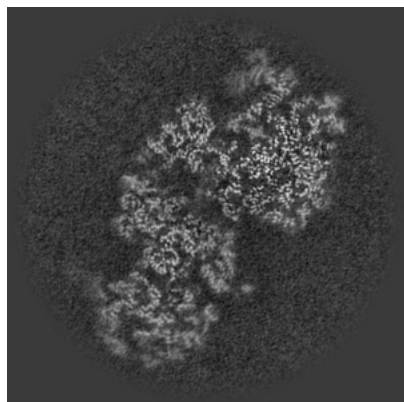


Z Index: 350

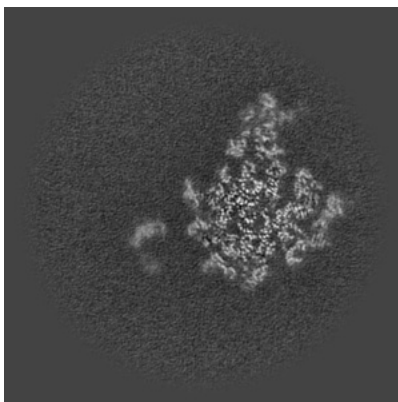
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

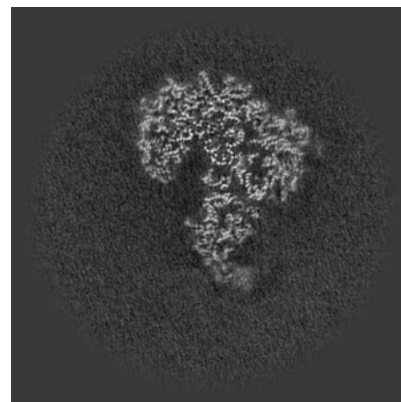
6.3.1 Primary map



X Index: 355

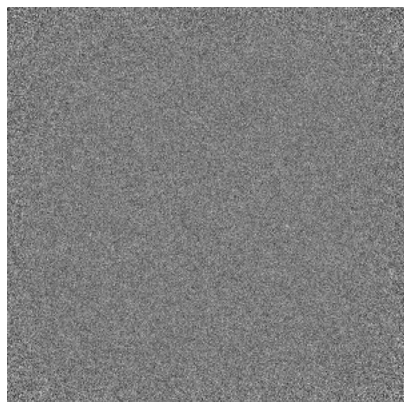


Y Index: 457

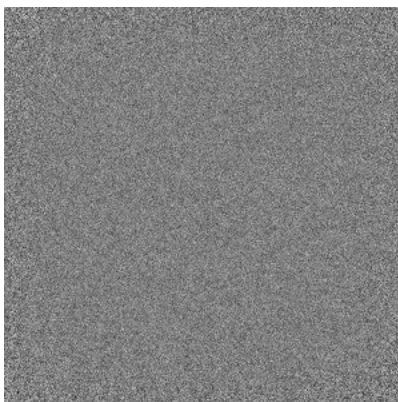


Z Index: 446

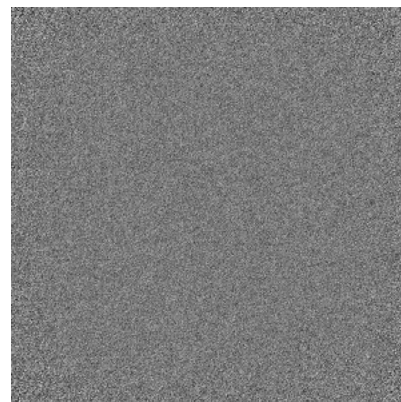
6.3.2 Raw map



X Index: 0



Y Index: 0

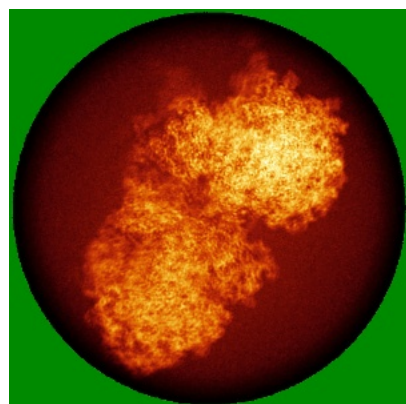


Z Index: 0

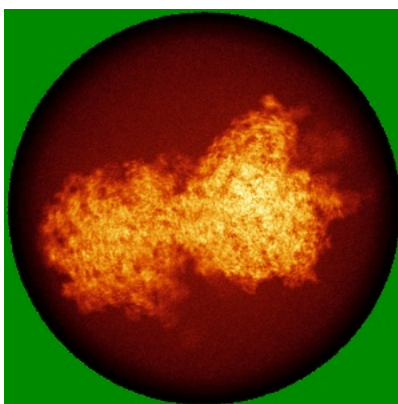
The images above show the largest variance slices of the map in three orthogonal directions.

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

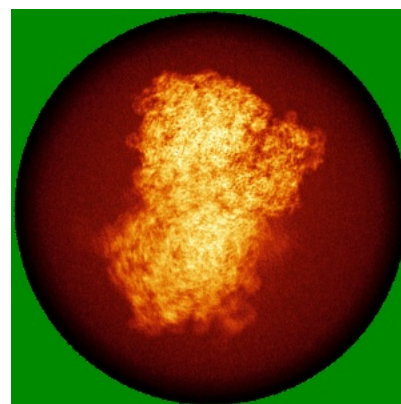
6.4.1 Primary map



X

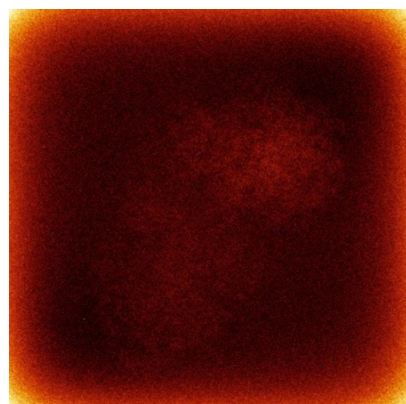


Y

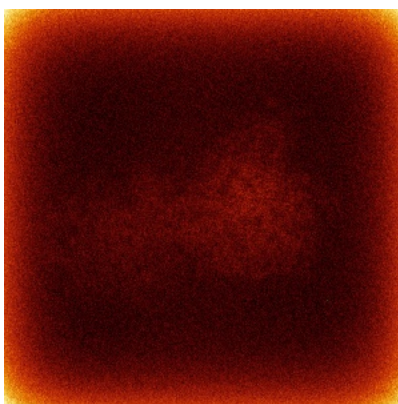


Z

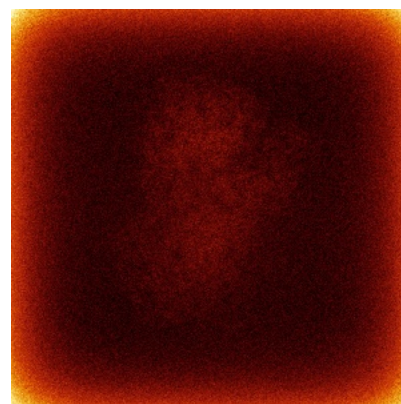
6.4.2 Raw map



X



Y

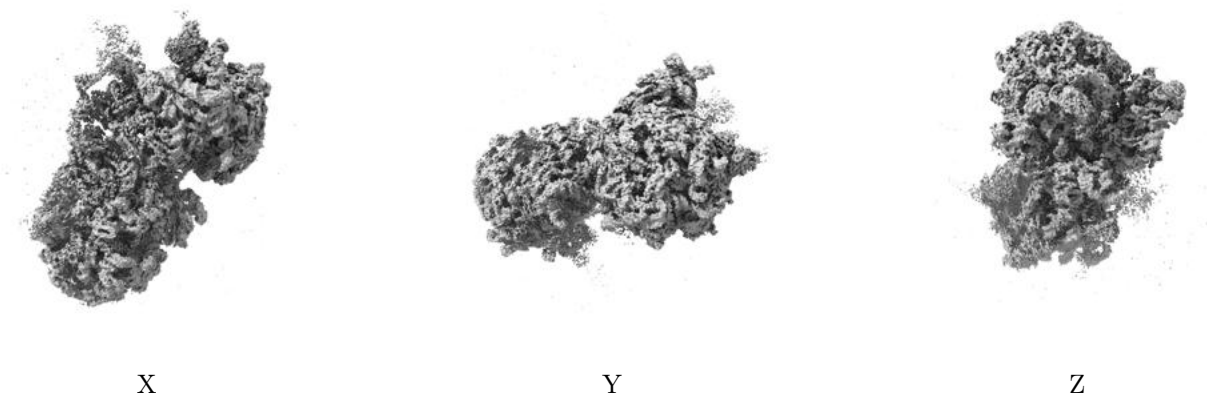


Z

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.

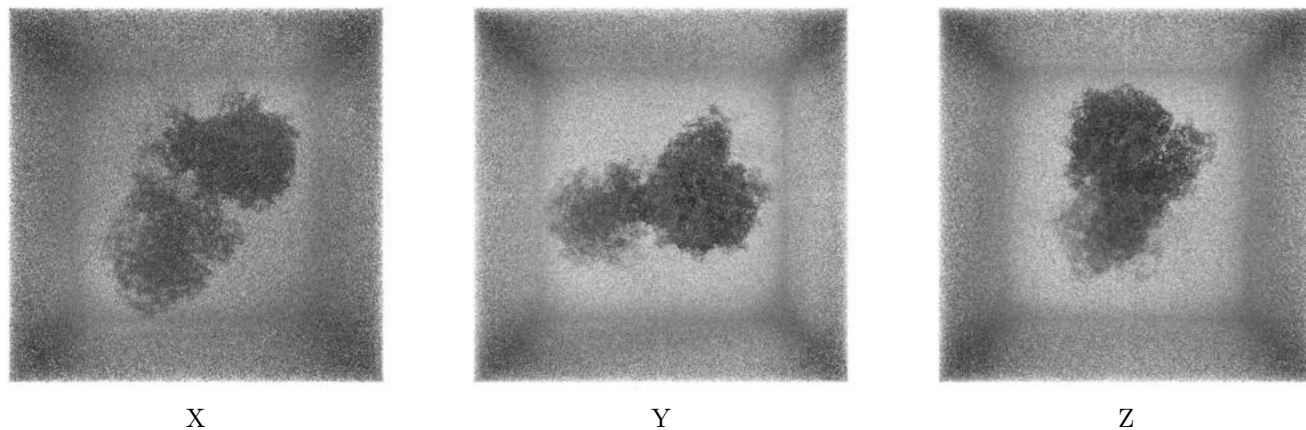
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.165. 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



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.

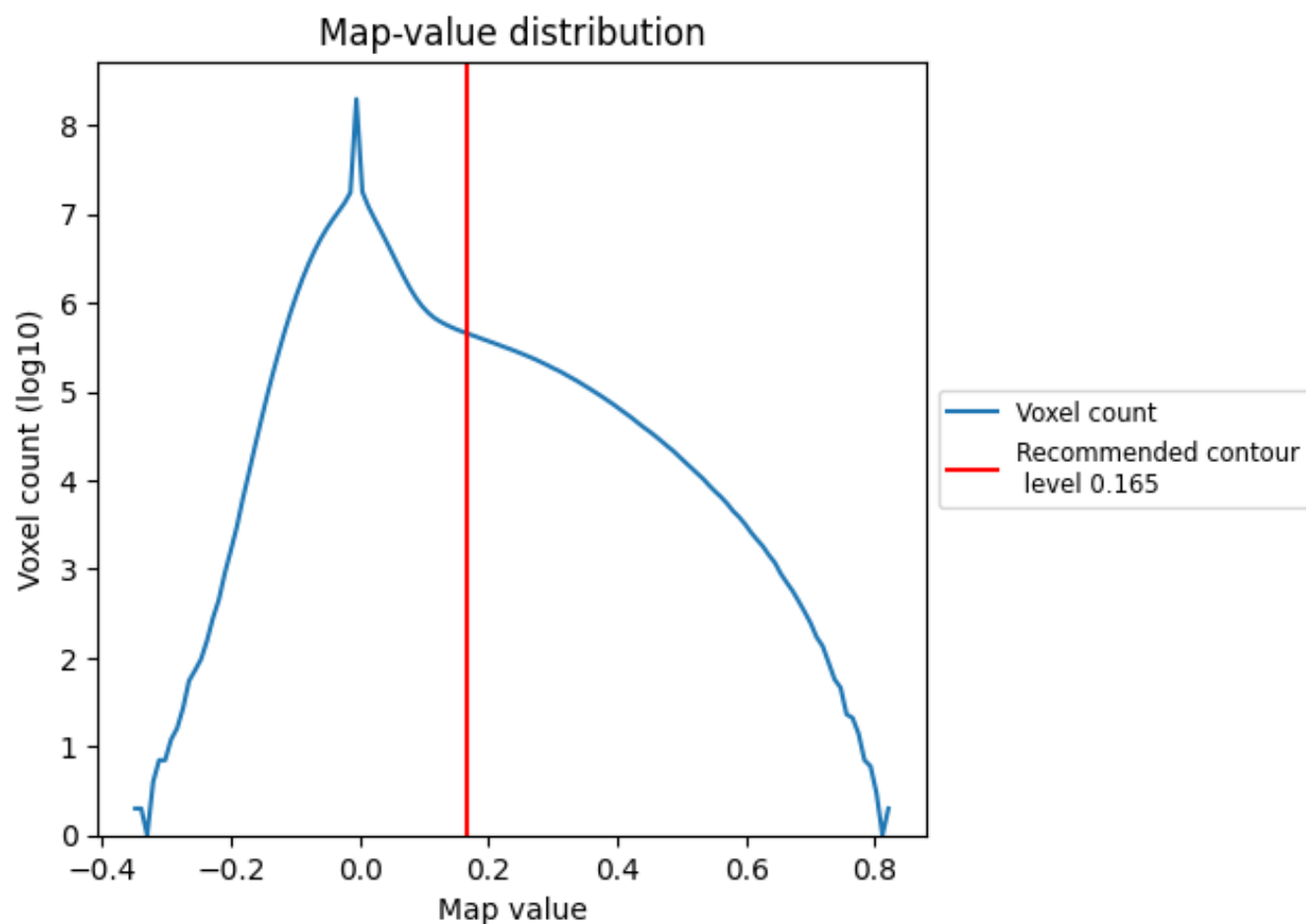
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

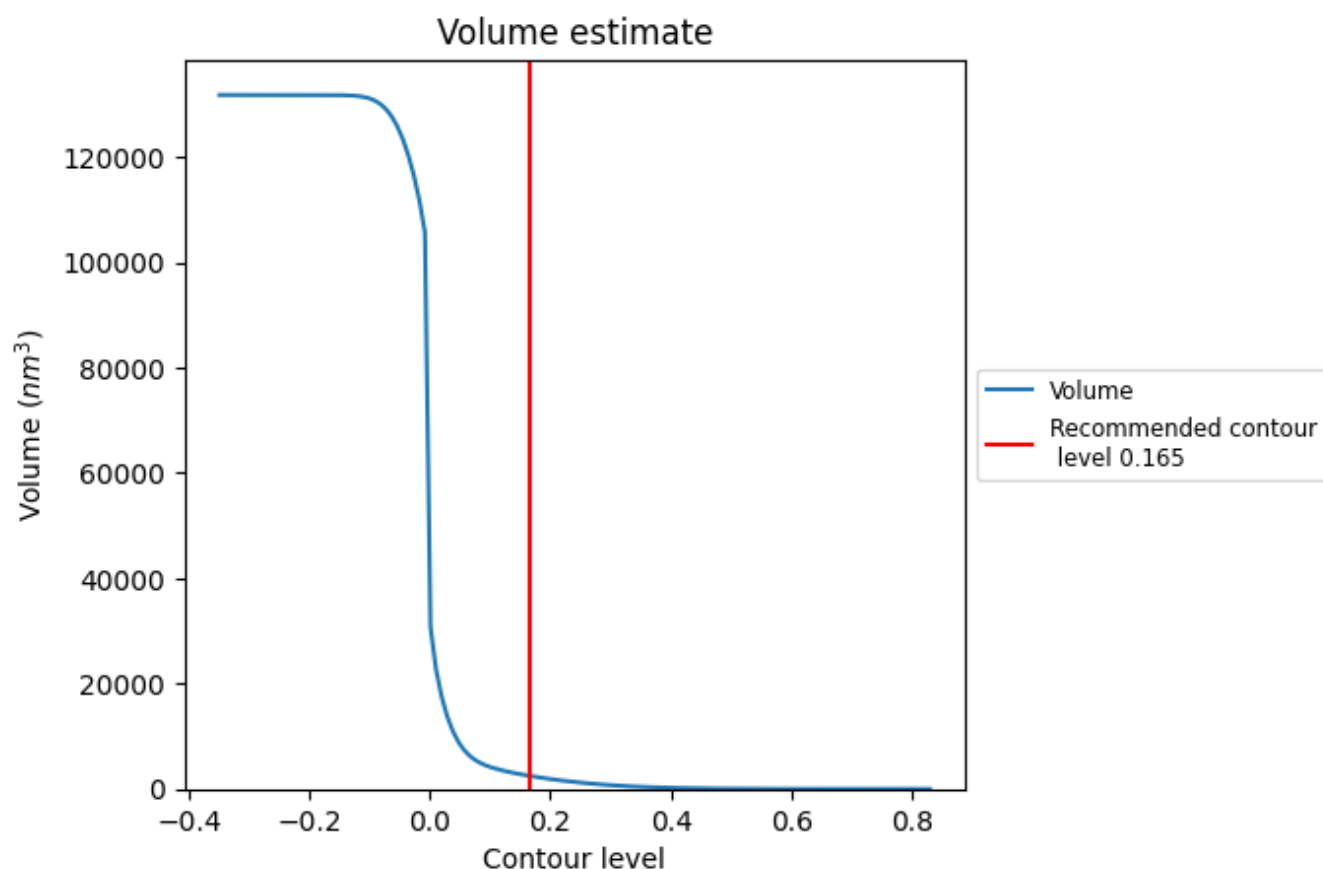
This section contains the results of statistical analysis of the map.

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.

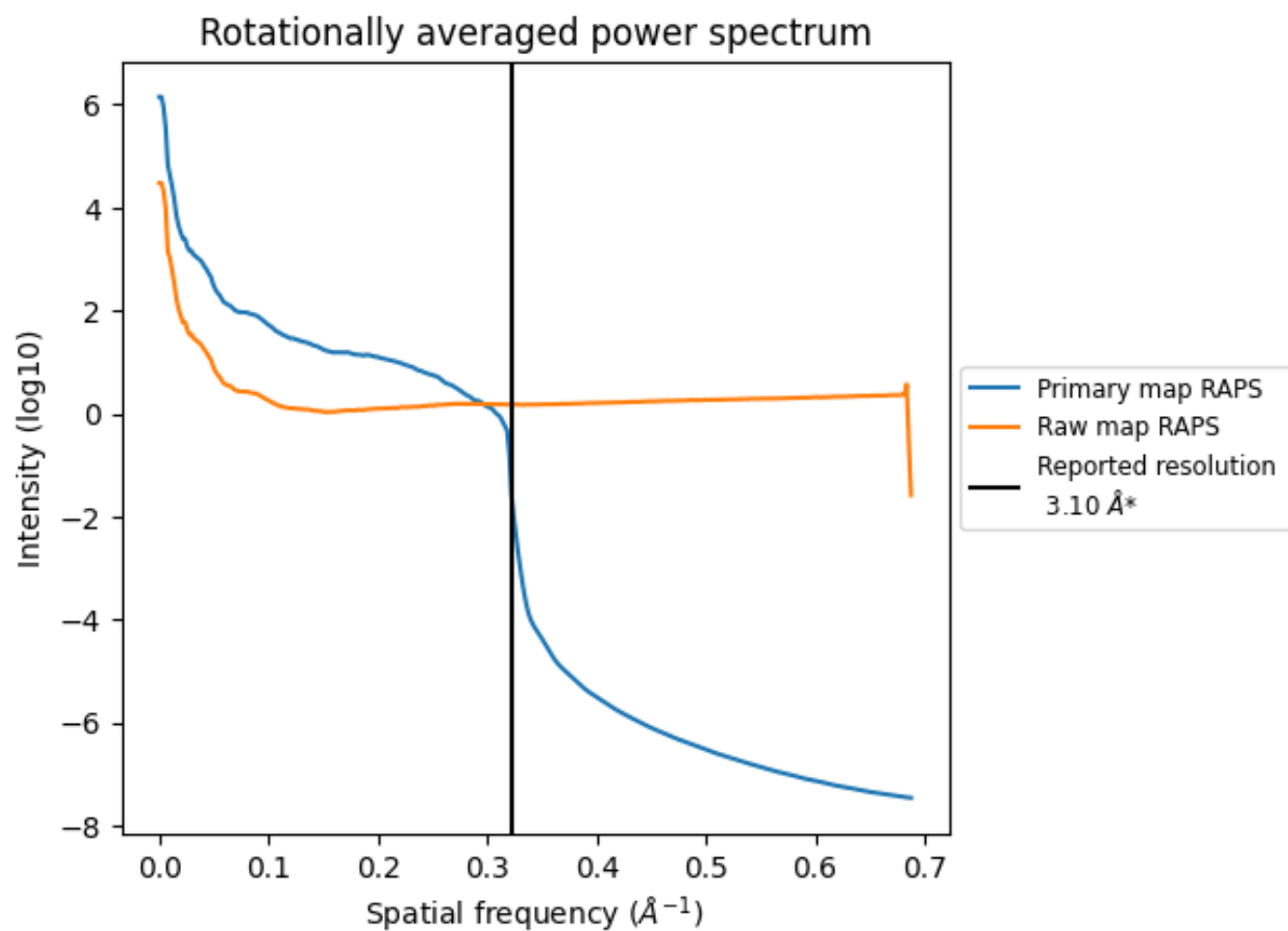
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2494 nm³; this corresponds to an approximate mass of 2253 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 ⓘ

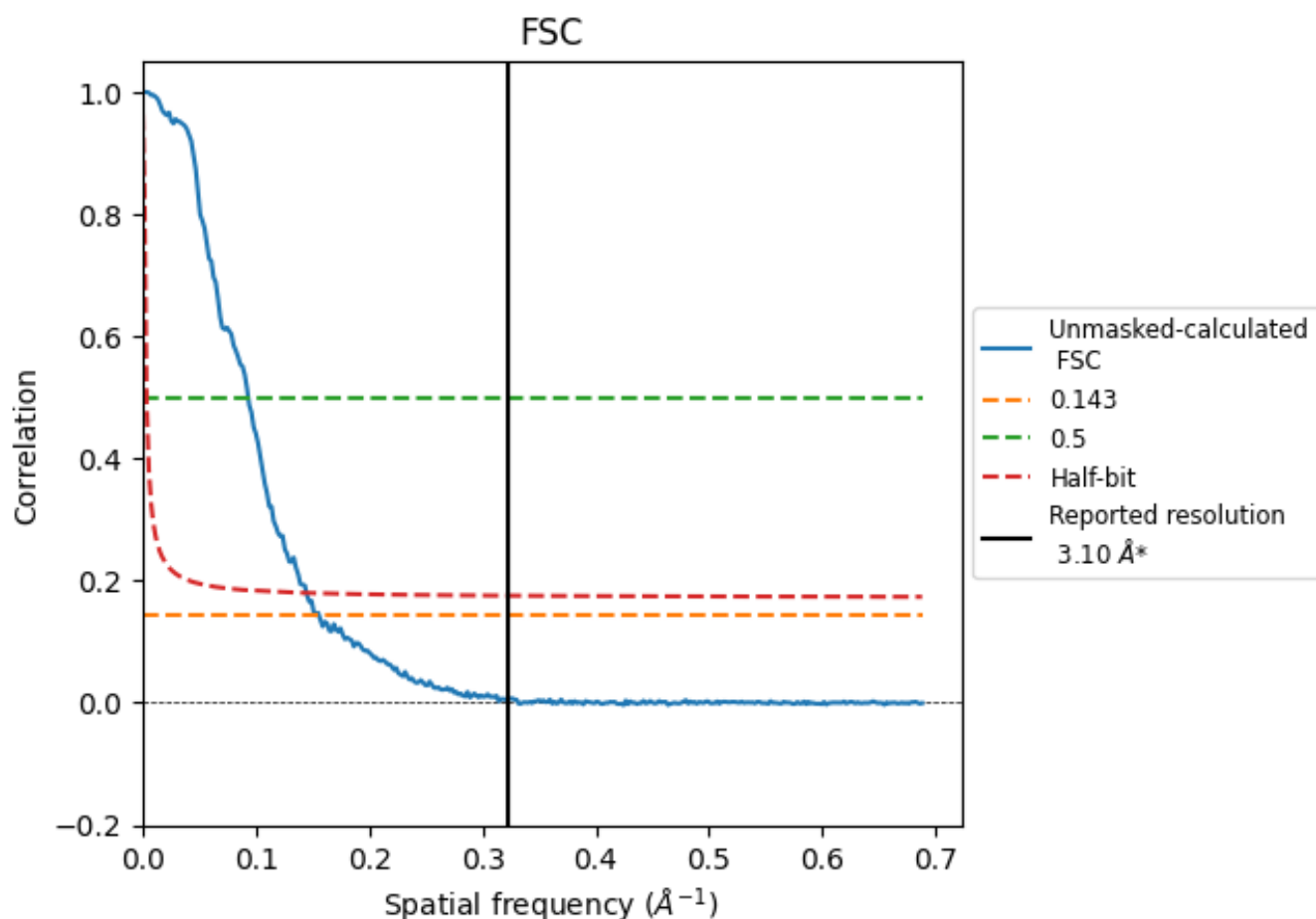


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.53	10.71	6.90

*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 6.53 differs from the reported value 3.1 by more than 10 %

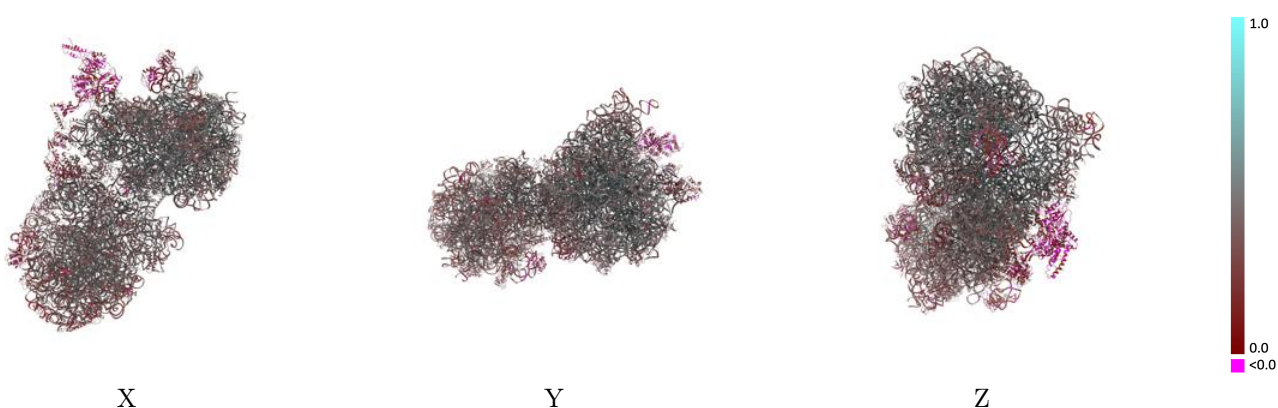
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51318 and PDB model 9GFT. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

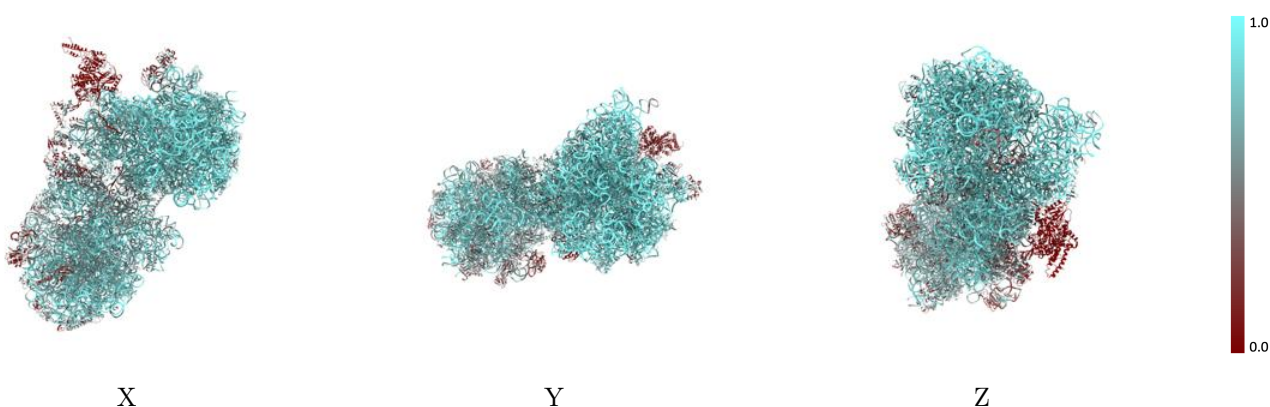
This section was not generated.

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



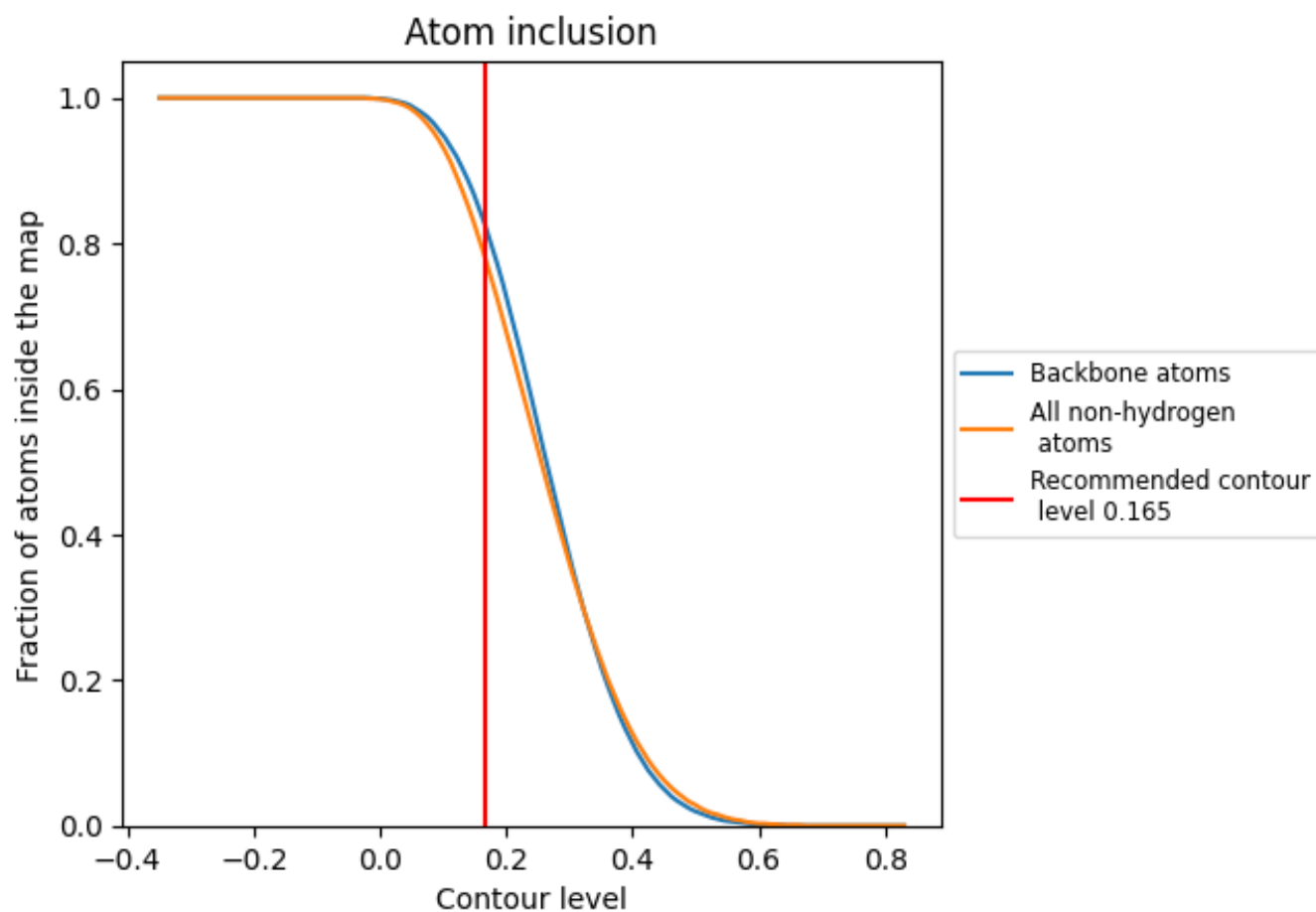
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.165).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (0.165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.3850
0	 0.9350	 0.4290
1	 0.6270	 0.3960
2	 0.6800	 0.4380
3	 0.6550	 0.3780
4	 0.7290	 0.4460
5	 0.7000	 0.4350
6	 0.6630	 0.4130
7	 0.7240	 0.4480
8	 0.7050	 0.4210
9	 0.5660	 0.4050
A	 0.8770	 0.4200
A1	 0.4960	 0.3940
A3	 0.6190	 0.3180
AA	 0.8990	 0.3990
AB	 0.5230	 0.3490
AC	 0.5870	 0.4120
AD	 0.5790	 0.4140
AE	 0.5890	 0.4050
AF	 0.5890	 0.3590
AG	 0.6480	 0.3750
AH	 0.5800	 0.3680
AI	 0.6320	 0.3690
AJ	 0.6030	 0.4190
AK	 0.1120	 0.1620
AL	 0.5970	 0.3250
AM	 0.6060	 0.3700
AN	 0.6250	 0.3540
AO	 0.6240	 0.3910
AP	 0.5970	 0.3730
AQ	 0.5990	 0.3760
AR	 0.5890	 0.3300
AS	 0.6090	 0.3140
AT	 0.4690	 0.3030
AU	 0.7460	 0.3420



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
AV	 0.8490	 0.3450
AW	 0.7780	 0.2440
AX	 0.6080	 0.4290
AY	 0.5270	 0.3630
AZ	 0.3710	 0.3120
Aa	 0.4650	 0.2850
Ab	 0.3150	 0.2550
Ac	 0.2020	 0.2500
Ad	 0.0810	 0.1470
Ae	 0.5090	 0.3040
Af	 0.5290	 0.4120
Ag	 0.5430	 0.3420
Ah	 0.4580	 0.3460
Ai	 0.6700	 0.3670
Aj	 0.4700	 0.2680
Ak	 0.5040	 0.3570
Al	 0.5660	 0.2940
Am	 0.4440	 0.2700
An	 0.6380	 0.3840
Ao	 0.5620	 0.3390
Ap	 0.2530	 0.2670
Aq	 0.4590	 0.2570
Ar	 0.6100	 0.2990
As	 0.6140	 0.3800
At	 0.5710	 0.2760
Au	 0.5440	 0.3220
Av	 0.6990	 0.3690
Aw	 0.5610	 0.3330
Ax	 0.6870	 0.4140
Ay	 0.6050	 0.3870
Az	 0.5620	 0.3460
B	 0.1950	 0.1830
C	 0.0920	 0.1490
D	 0.6690	 0.4580
E	 0.7590	 0.4890
F	 0.7520	 0.4030
G	 0.7210	 0.4080
H	 0.7540	 0.4430
I	 0.7010	 0.4090
J	 0.7250	 0.4380
K	 0.6980	 0.4560
L	 0.6310	 0.3590

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
M	 0.8960	 0.4310
N	 0.9340	 0.4420
O	 0.9470	 0.3970
P	 0.7830	 0.5070
Q	 0.8050	 0.4730
R	 0.7450	 0.4310
S	 0.6690	 0.3770
T	 0.7650	 0.3990
U	 0.6200	 0.3700
V	 0.1950	 0.1520
W	 0.8310	 0.4510
X	 0.7590	 0.4910
Y	 0.7690	 0.4550
Z	 0.7950	 0.4950
a	 0.8340	 0.4380
b	 0.7290	 0.3770
c	 0.7790	 0.4550
d	 0.8120	 0.4590
e	 0.7790	 0.4440
f	 0.7740	 0.4700
g	 0.7380	 0.4310
h	 0.7410	 0.4060
i	 0.7630	 0.4060
j	 0.8160	 0.4780
k	 0.7540	 0.4720
l	 0.7060	 0.3630
m	 0.8080	 0.4560
n	 0.8140	 0.4590
o	 0.6660	 0.4190
p	 0.7910	 0.5110
q	 0.7880	 0.4950
r	 0.7880	 0.4700
s	 0.7920	 0.4990
t	 0.8000	 0.4300
u	 0.7060	 0.3500
v	 0.5470	 0.4110
w	 0.3900	 0.2920
x	 0.3530	 0.2100
y	 0.6440	 0.4020
z	 0.6430	 0.4370