



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 12:42 am BST

PDB ID : 30RB / pdb_000030rb
EMDB ID : EMD-57975
Title : E. coli 70S ribosome with peptidyl-tRNA and Hsp15
Authors : Larsson, D.S.D.; Akbar, S.; Selmer, M.
Deposited on : 2026-05-10
Resolution : 2.92 Å(reported)
Based on initial models : 8CF1, 8CGJ, ., 7K00

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:

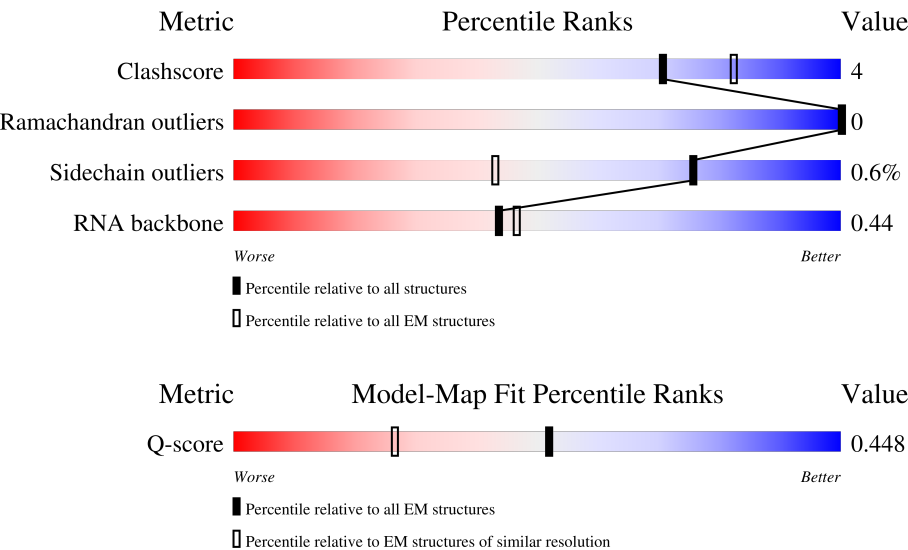
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal 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 i

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

The reported resolution of this entry is 2.92 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	13007 (2.42 - 3.42)

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	55	33% 82% 11% 7%
2	1	46	91% 9%
3	2	65	6% 83% 15%

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Mol	Chain	Length	Quality of chain
4	3	38	
5	A	1542	
6	B	241	
7	C	233	
8	D	206	
9	E	167	
10	F	135	
11	G	179	
12	H	130	
13	I	130	
14	J	103	
15	K	129	
16	L	124	
17	M	118	
18	N	101	
19	O	89	
20	P	82	
21	Q	84	
22	R	75	
23	S	92	
24	T	87	
25	U	71	
26	V	142	
27	Z	77	
28	a	2904	

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Mol	Chain	Length	Quality of chain
29	b	120	
30	c	273	
31	d	209	
32	e	201	
33	f	179	
34	g	177	
35	h	149	
36	i	142	
37	j	123	
38	k	144	
39	l	136	
40	m	127	
41	n	117	
42	o	115	
43	p	118	
44	q	103	
45	r	110	
46	s	100	
47	t	104	
48	u	94	
49	v	85	
50	w	78	
51	x	63	
52	y	59	
53	z	57	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 228734 atoms, of which 88883 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	H	N	O	0	0
			858	269	441	76	72		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	H	N	O S	0	0
			788	228	411	90	57 2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	H	N	O S	0	0
			1066	323	562	105	74 2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	H	N	O S	0	0
			639	185	337	65	48 4		

- Molecule 5 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	1514	Total	C	H	N	O P	0	0
			47328	14504	14825	5965	10520 1514		

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	224	Total	C	H	N	O S	0	0
			3504	1109	1751	315	321 8		

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	C	206	Total	C	H	N	O	S	0	0
			3293	1028	1669	305	288	3		

- Molecule 8 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	D	200	Total	C	H	N	O	S	0	0
			3245	1002	1640	307	292	4		

- Molecule 9 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	E	154	Total	C	H	N	O	S	0	0
			2295	706	1160	215	208	6		

- Molecule 10 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	F	101	Total	C	H	N	O	S	0	0
			1620	520	796	149	149	6		

- Molecule 11 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	G	134	Total	C	H	N	O	S	0	0
			2144	659	1087	204	190	4		

- Molecule 12 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	H	129	Total	C	H	N	O	S	0	0
			1994	616	1015	173	184	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	I	125	Total	C	H	N	O	S	0	0
			2028	622	1027	200	176	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	J	96	Total	C	H	N	O	S	0	0
			1581	487	806	148	139	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	K	117	Total	C	H	N	O	S	0	0
			1742	540	865	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 16 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	L	121	Total	C	H	N	O	S	0	0
			1918	582	976	193	162	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	M	115	Total	C	H	N	O	S	0	0
			1826	552	935	179	157	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	N	100	Total	C	H	N	O	S	0	0
			1637	499	832	164	139	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	O	88	Total	C	H	N	O	S	0	0
			1430	439	716	144	130	1		

- Molecule 20 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	P	79	Total	C	H	N	O	S	0	0
			1263	394	634	124	110	1		

- Molecule 21 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Q	79	Total	C	H	N	O	S	0	0
			1309	406	668	120	112	3		

- Molecule 22 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	R	64	Total	C	H	N	O	S	0	0
			1052	330	528	99	94	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	S	84	Total	C	H	N	O	S	0	0
			1346	427	678	127	112	2		

- Molecule 24 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	T	86	Total	C	H	N	O	S	0	0
			1380	414	710	138	115	3		

- Molecule 25 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	U	70	Total	C	H	N	O	S	0	0
			1210	366	621	125	97	1		

- Molecule 26 is a protein called Heat shock protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	V	109	Total	C	H	N	O	S	0	0
			1817	562	917	174	162	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	-8	MET	-	initiating methionine	UNP P0ACG8
V	-7	HIS	-	expression tag	UNP P0ACG8
V	-6	HIS	-	expression tag	UNP P0ACG8
V	-5	HIS	-	expression tag	UNP P0ACG8
V	-4	HIS	-	expression tag	UNP P0ACG8
V	-3	HIS	-	expression tag	UNP P0ACG8
V	-2	HIS	-	expression tag	UNP P0ACG8
V	-1	GLY	-	expression tag	UNP P0ACG8
V	0	SER	-	expression tag	UNP P0ACG8
V	1	GLY	-	expression tag	UNP P0ACG8

- Molecule 27 is a RNA chain called tRNA Asp.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Z	73	Total	C	H	N	O	P	0	0
			2271	693	714	275	516	73		

- Molecule 28 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	a	2753	Total	C	H	N	O	P	0	0
			86112	26384	26982	10897	19096	2753		

- Molecule 29 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	b	119	Total	C	H	N	O	P	0	0
			3720	1135	1171	466	829	119		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	c	271	Total	C	H	N	O	S	0	0
			4196	1288	2114	423	364	7		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	d	209	Total	C	H	N	O	S	0	0
			3152	980	1586	288	294	4		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	e	201	Total	C	H	N	O	S	0	0
			3142	974	1590	283	290	5		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	f	177	Total	C	H	N	O	S	0	0
			2831	899	1421	249	256	6		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	g	176	Total	C	H	N	O	S	0	0
			2670	832	1347	243	246	2		

- Molecule 35 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	h	41	Total	C	H	N	O	S	0	0
			627	194	324	54	54	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	i	142	Total	C	H	N	O	S	0	0
			2266	714	1137	212	199	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	j	123	Total	C	H	N	O	S	0	0
			1954	593	1008	181	166	6		

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	k	144	Total	C	H	N	O	S	0	0
			2164	654	1111	207	190	2		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	l	136	Total	C	H	N	O	S	0	0
			2217	686	1142	205	177	7		

- Molecule 40 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	m	118	Total	C	H	N	O	S	0	0
			1916	585	971	194	161	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	n	116	Total	C	H	N	O	S	0	0
			1800	552	908	178	162			

- Molecule 42 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	o	114	Total	C	H	N	O	S	0	0
			1864	574	947	179	163	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	p	117	Total	C	H	N	O	S	0	0
			1955	604	1008	192	151			

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	q	103	Total	C	H	N	O	S	0	0
			1641	516	825	153	145	2		

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	r	110	Total	C	H	N	O	S	0	0
			1761	532	904	166	156	3		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	s	93	Total	C	H	N	O	S	0	0
			1533	466	795	139	131	2		

- Molecule 47 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	t	102	Total	C	H	N	O		0	0
			1602	492	823	146	141			

- Molecule 48 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	u	94	Total	C	H	N	O	S	0	0
			1523	479	770	137	134	3		

- Molecule 49 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	v	78	Total	C	H	N	O	S	0	0
			1172	362	586	116	107	1		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	w	77	Total	C	H	N	O	S	0	0
			1263	388	638	129	106	2		

- Molecule 51 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	x	62	Total	C	H	N	O	S	0	0
			1027	308	526	98	94	1		

- Molecule 52 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	y	58	Total	C	H	N	O	S	0	0
			928	281	479	87	79	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	z	56	Total	C	H	N	O	S	0	0
			887	269	443	94	80	1		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

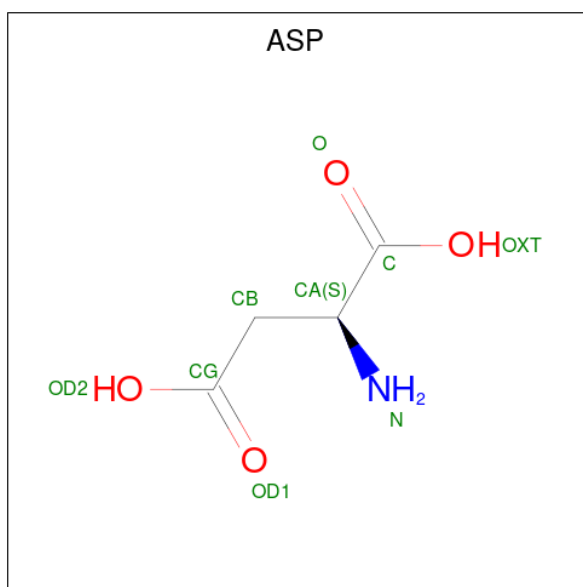
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	17	Total	Mg	0
			17	17	
55	Q	1	Total	Mg	0
			1	1	
55	a	185	Total	Mg	0
			185	185	
55	b	5	Total	Mg	0
			5	5	
55	c	1	Total	Mg	0
			1	1	
55	z	1	Total	Mg	0
			1	1	

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
56	A	1	Total	K	0
			1	1	
56	F	1	Total	K	0
			1	1	

- Molecule 57 is ASPARTIC ACID (CCD ID: ASP) (formula: C₄H₇NO₄).

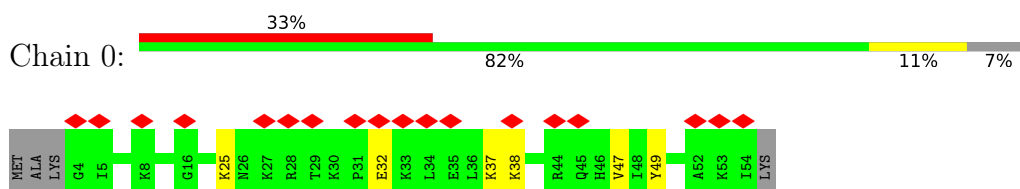


Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
57	Z	1	14	4	6	1	3	0

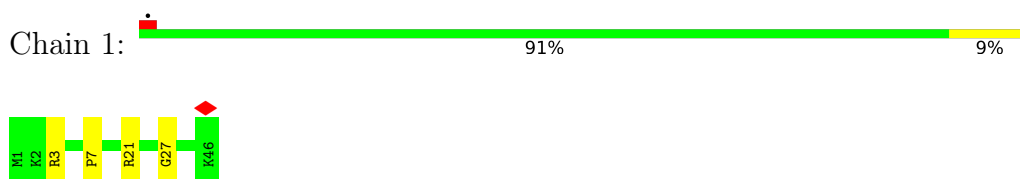
3 Residue-property plots [i](#)

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

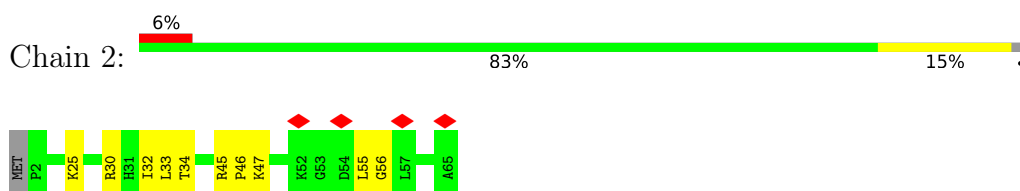
- Molecule 1: Large ribosomal subunit protein bL33



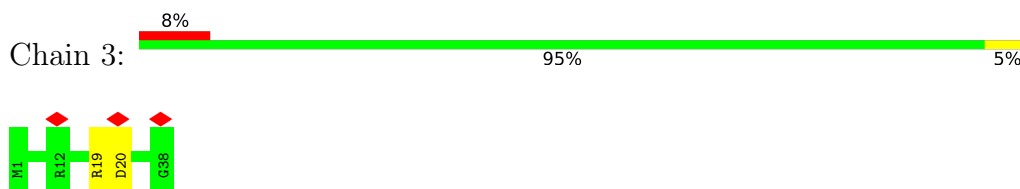
- Molecule 2: Large ribosomal subunit protein bL34



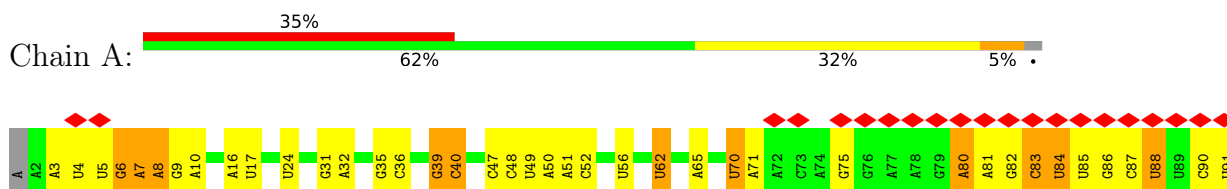
- Molecule 3: Large ribosomal subunit protein bL35

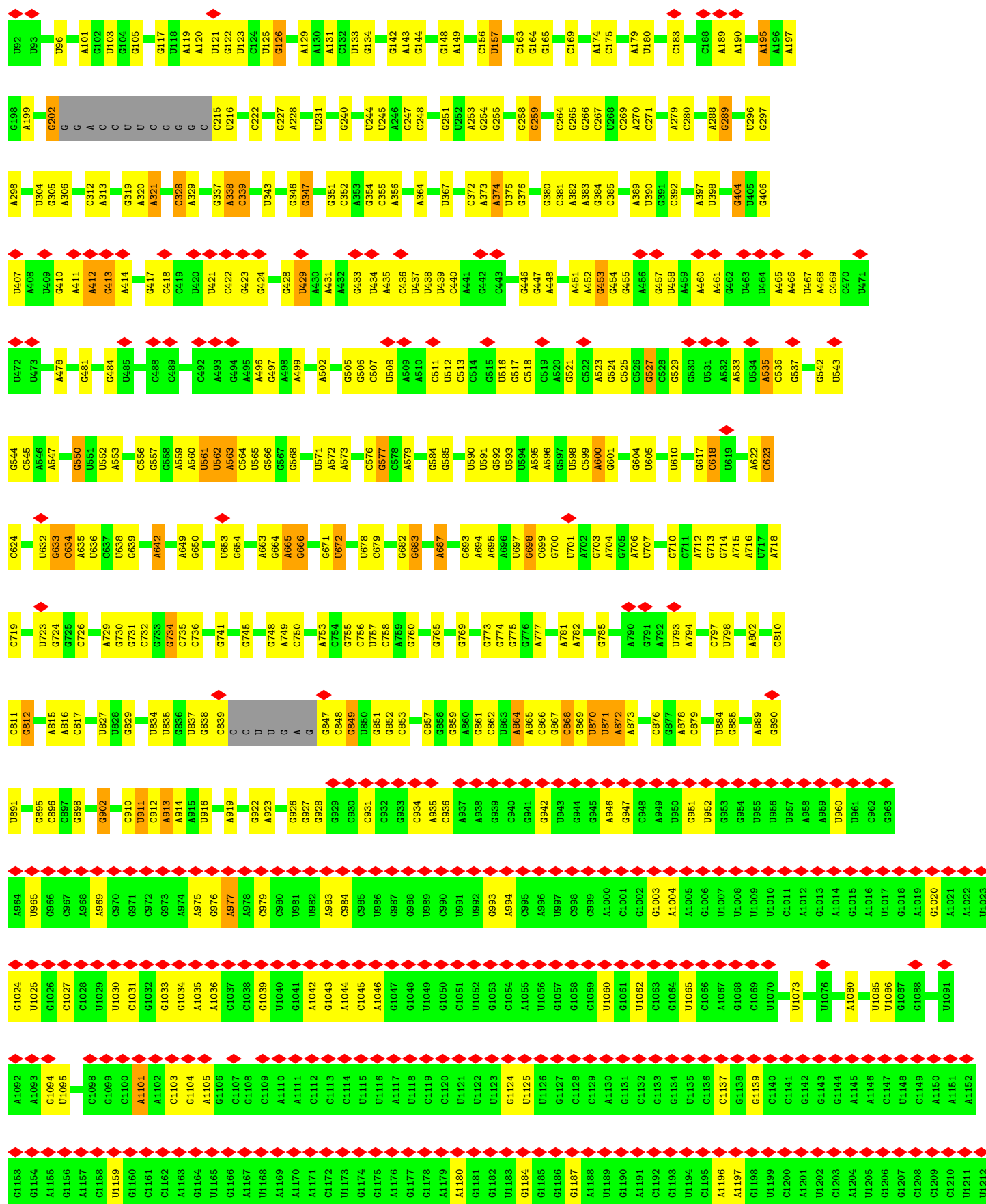


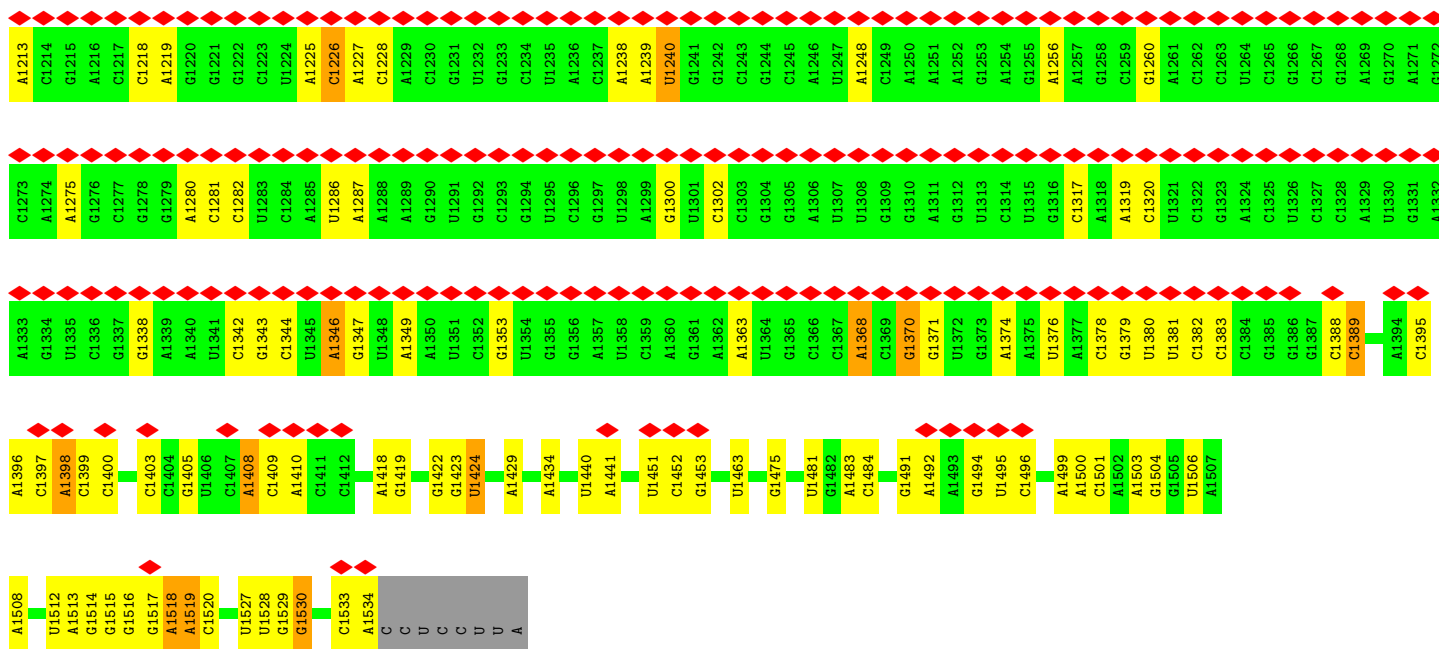
- Molecule 4: Large ribosomal subunit protein bL36A



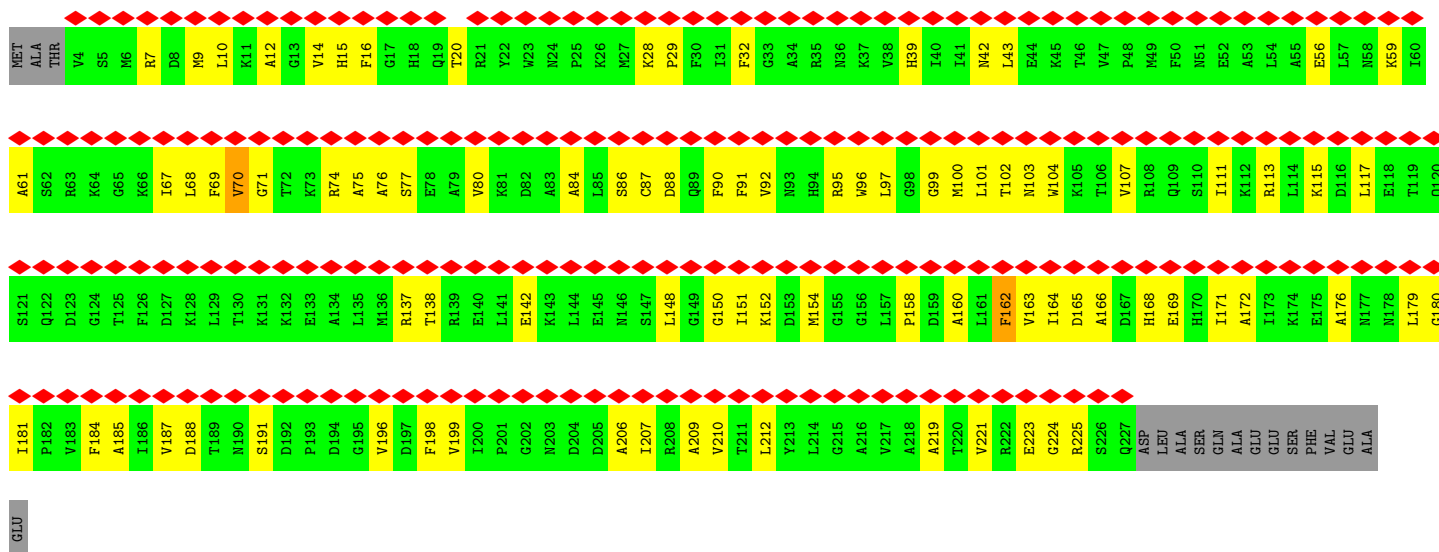
- Molecule 5: 16S rRNA



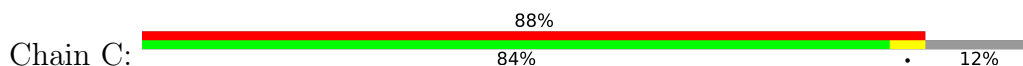


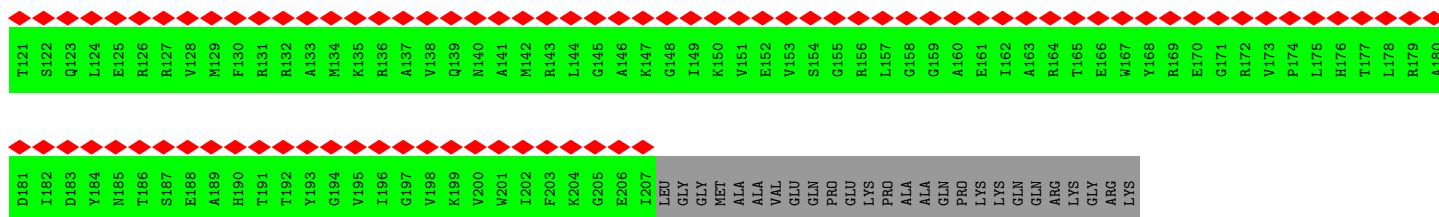


• Molecule 6: Small ribosomal subunit protein uS2

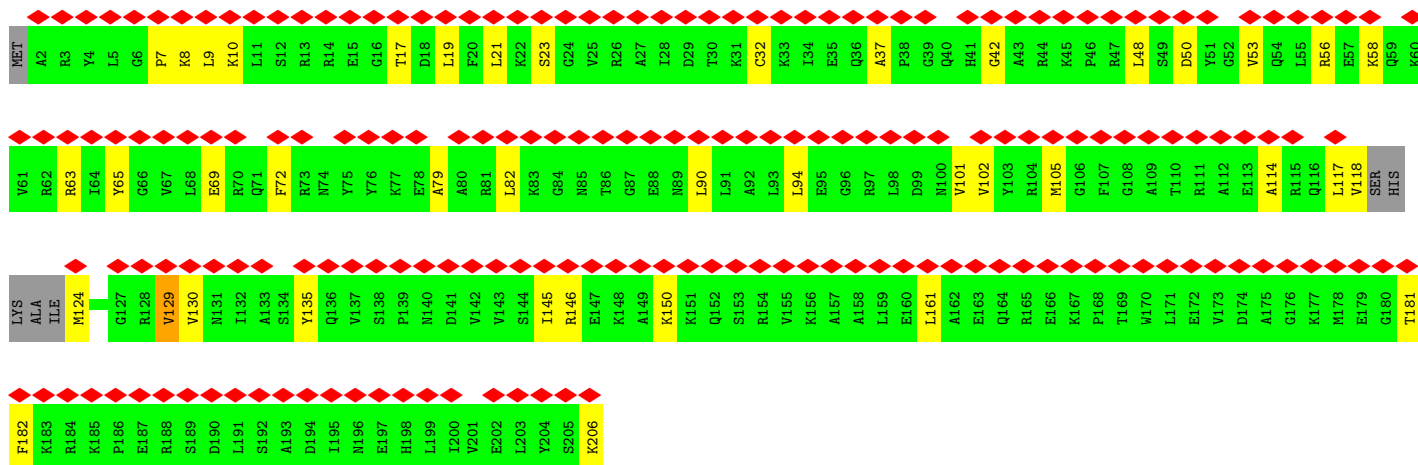
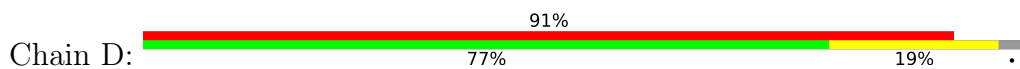


• Molecule 7: Small ribosomal subunit protein uS3

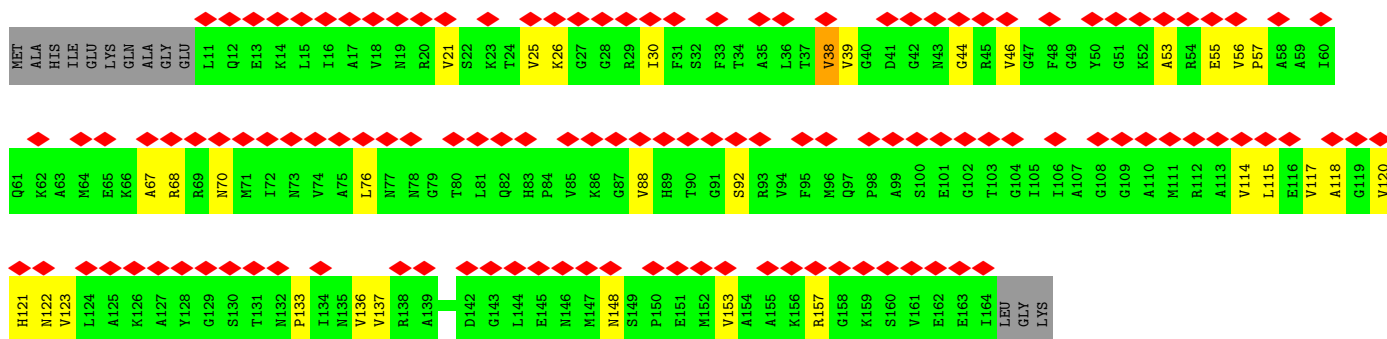
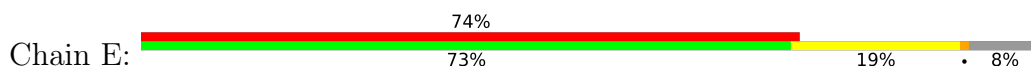




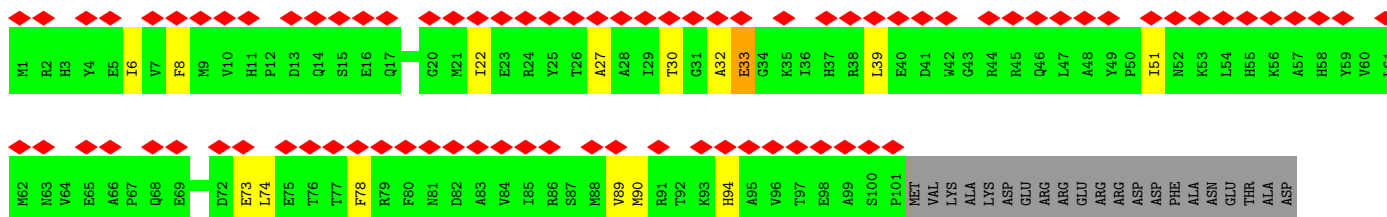
• Molecule 8: Small ribosomal subunit protein uS4



• Molecule 9: Small ribosomal subunit protein uS5

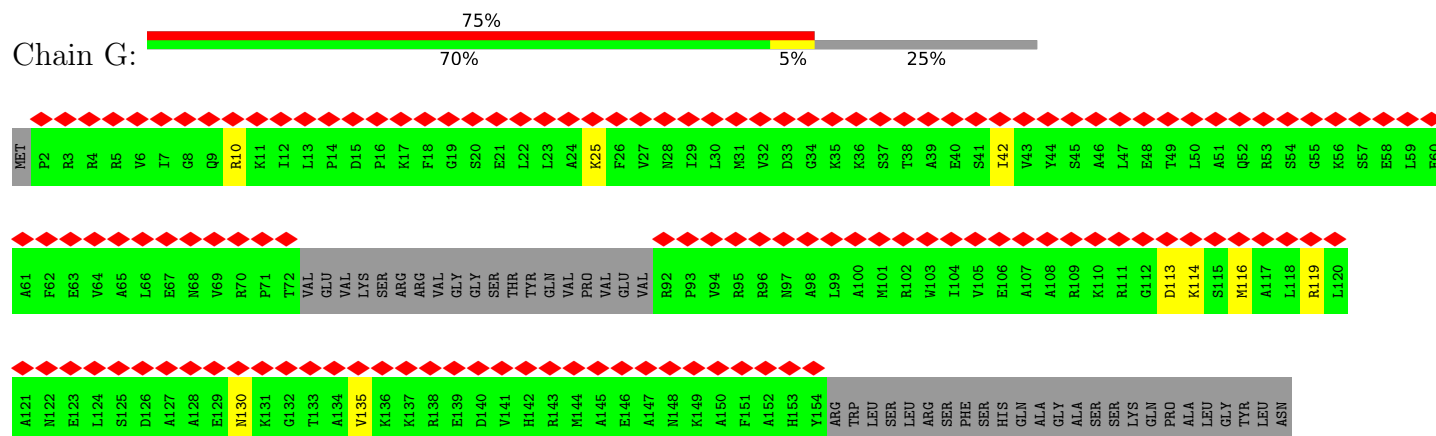


• Molecule 10: Small ribosomal subunit protein bS6, fully modified isoform

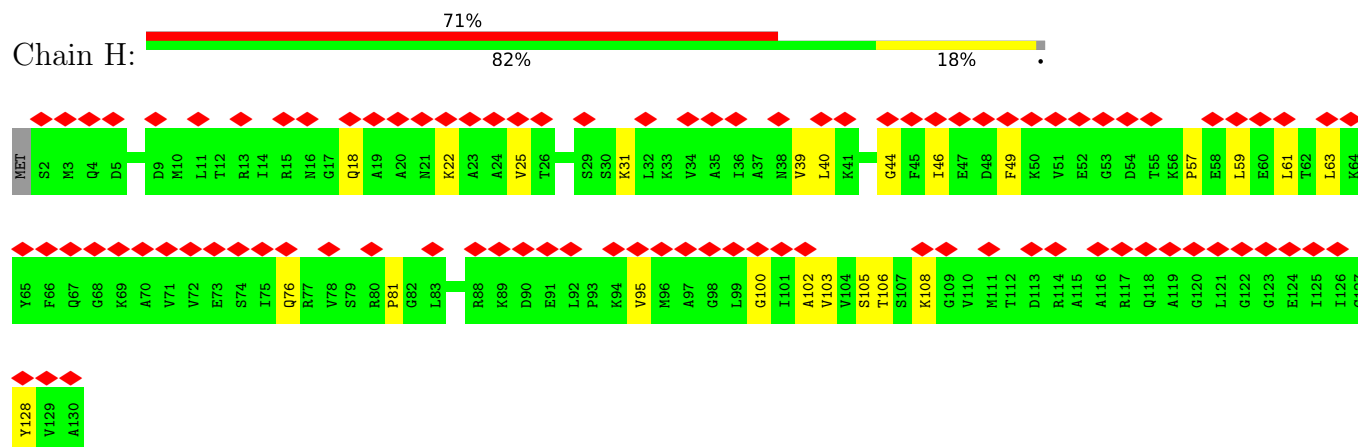


ASP
ALA
GLU
ALA
GLY
ASP
SER
GLU
GLU
GLU
GLU
GLU

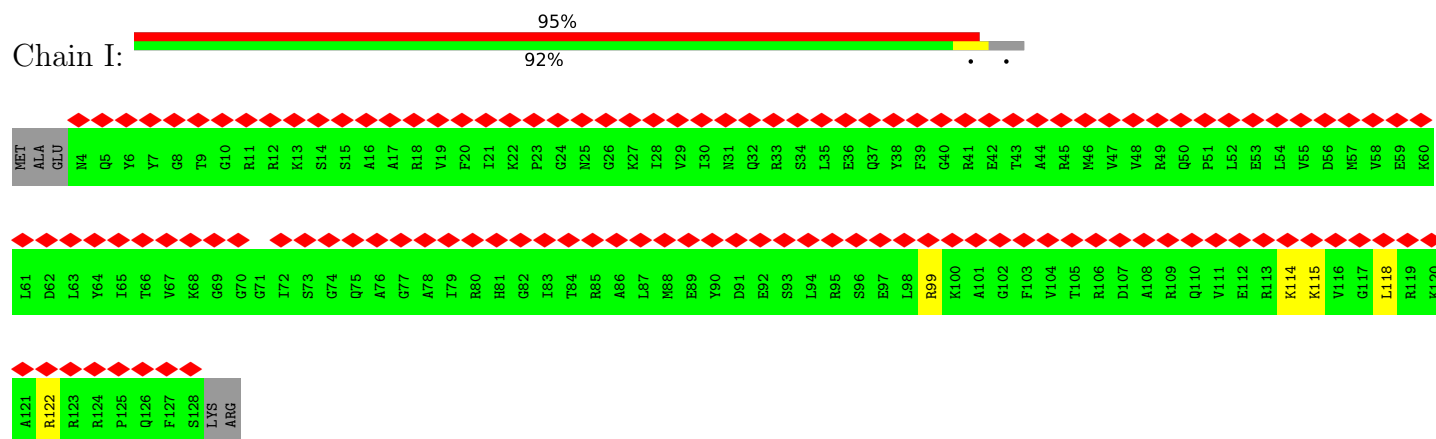
• Molecule 11: Small ribosomal subunit protein uS7



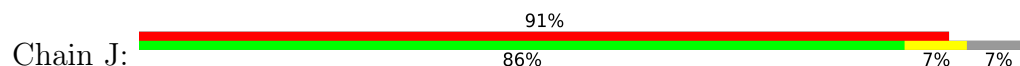
• Molecule 12: Small ribosomal subunit protein uS8

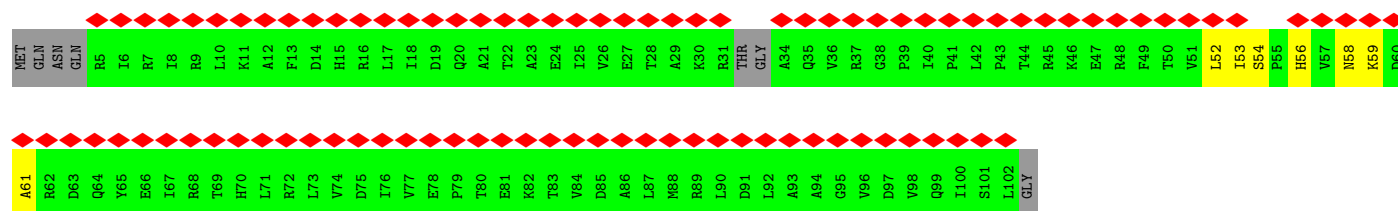


• Molecule 13: Small ribosomal subunit protein uS9

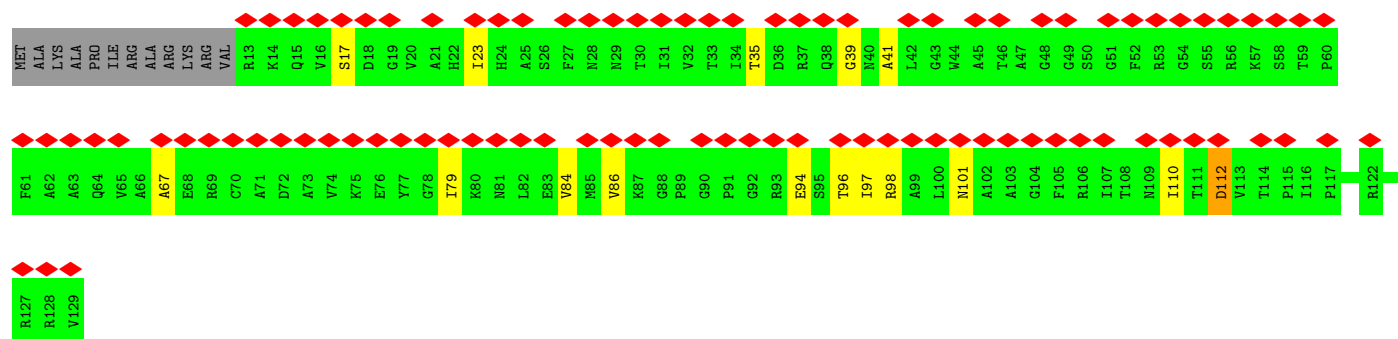
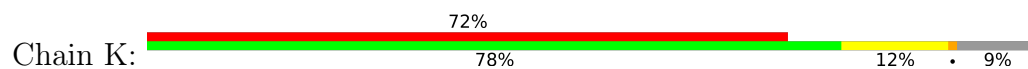


• Molecule 14: Small ribosomal subunit protein uS10

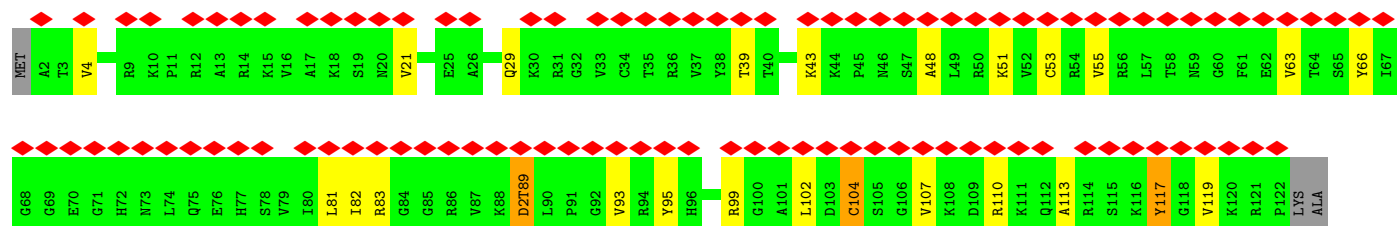
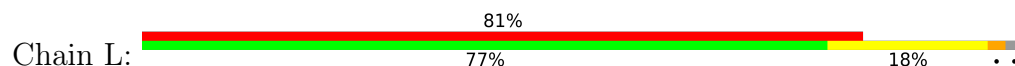




• Molecule 15: Small ribosomal subunit protein uS11



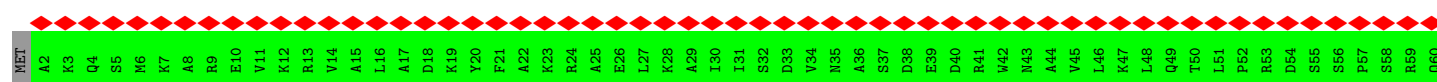
• Molecule 16: Small ribosomal subunit protein uS12

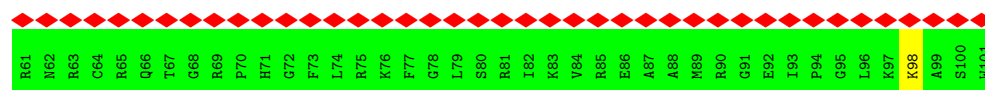


• Molecule 17: Small ribosomal subunit protein uS13

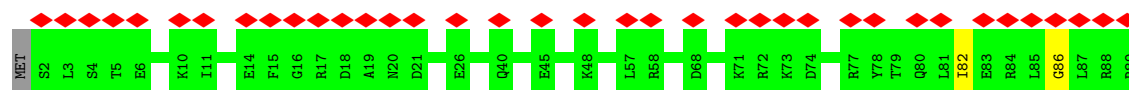
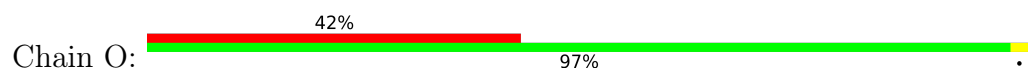


• Molecule 18: Small ribosomal subunit protein uS14

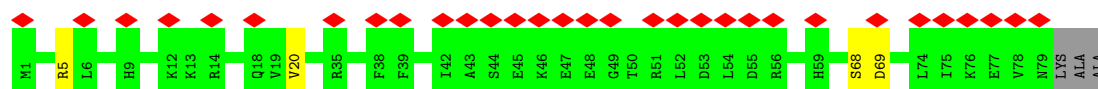
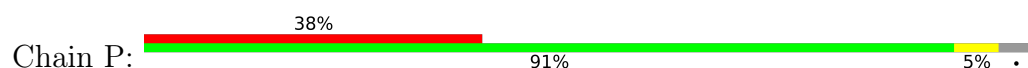




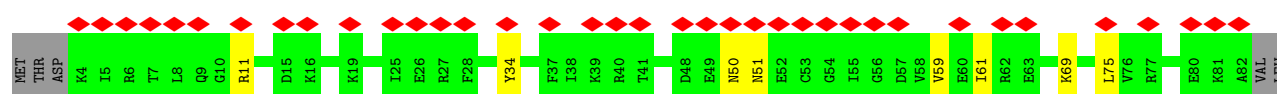
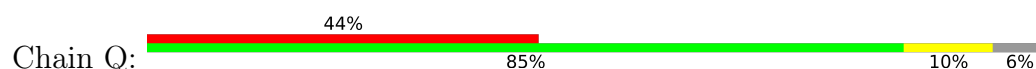
- Molecule 19: Small ribosomal subunit protein uS15



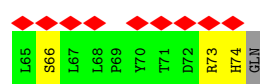
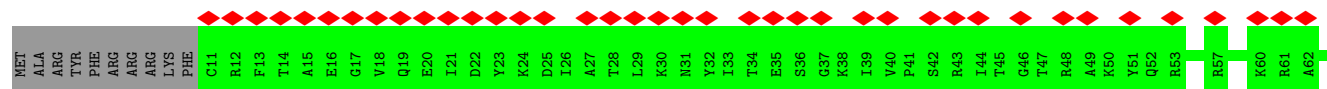
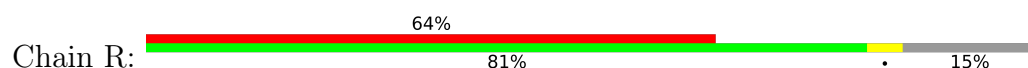
- Molecule 20: Small ribosomal subunit protein bS16



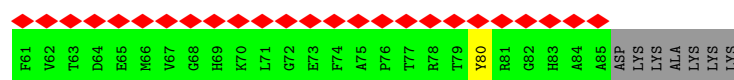
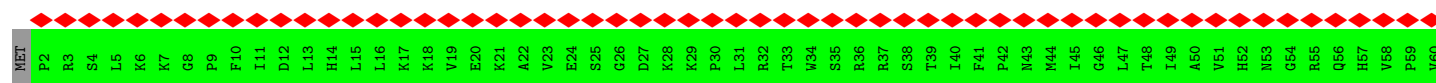
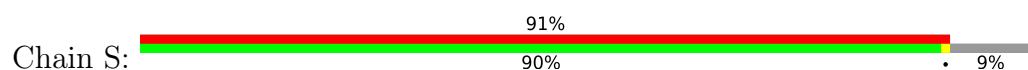
- Molecule 21: Small ribosomal subunit protein uS17



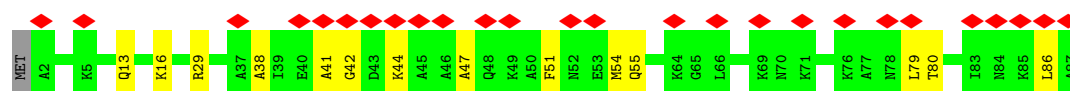
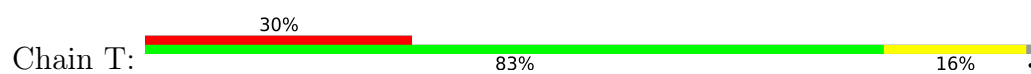
- Molecule 22: Small ribosomal subunit protein bS18



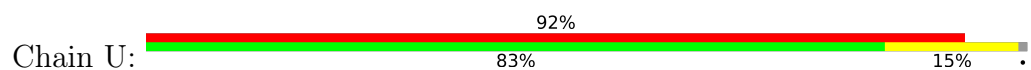
- Molecule 23: Small ribosomal subunit protein uS19



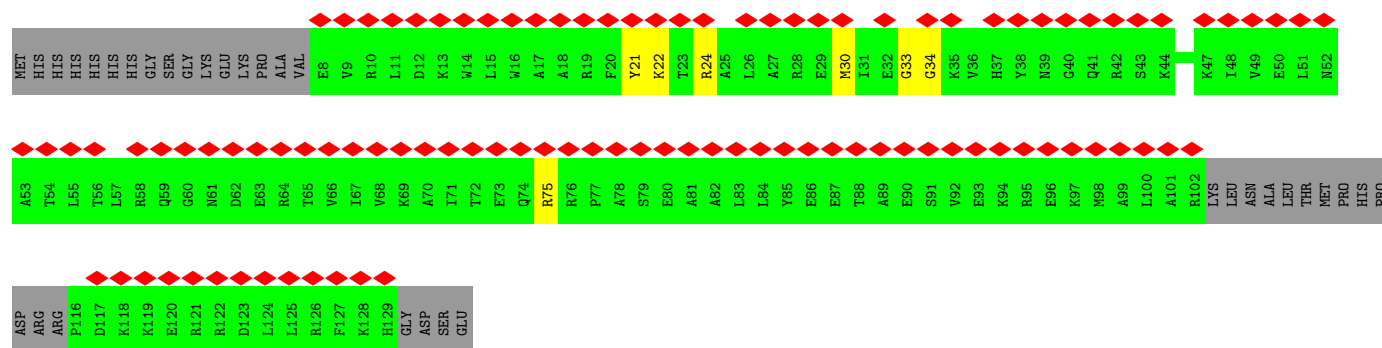
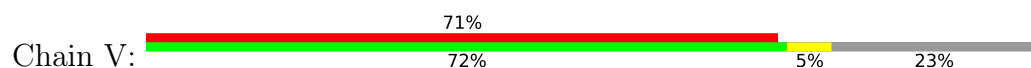
- Molecule 24: Small ribosomal subunit protein bS20



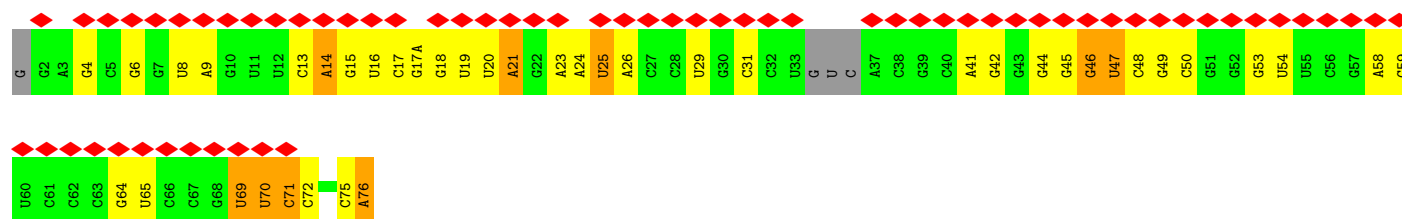
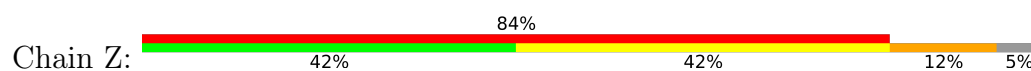
- Molecule 25: Small ribosomal subunit protein bS21



- Molecule 26: Heat shock protein 15

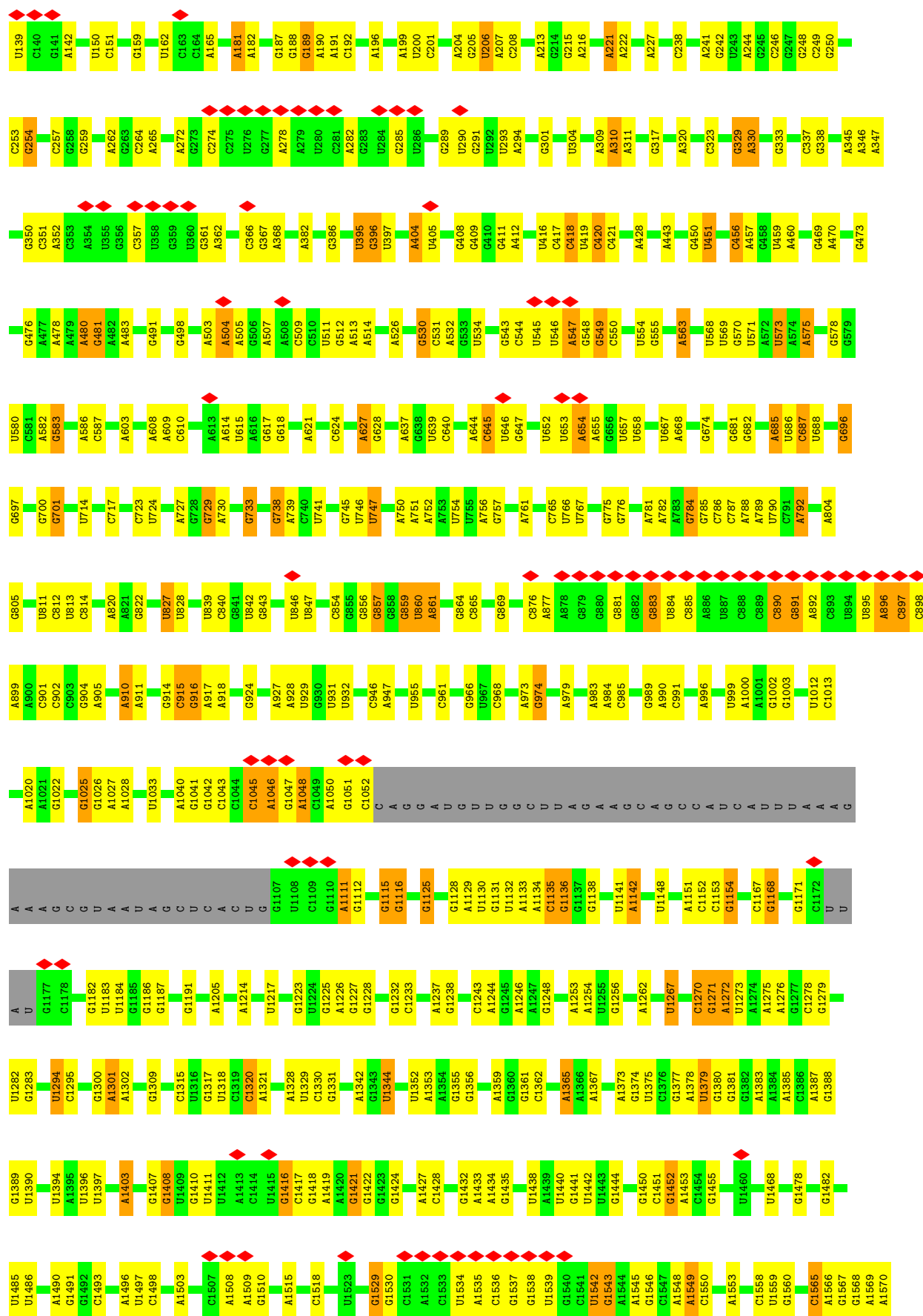


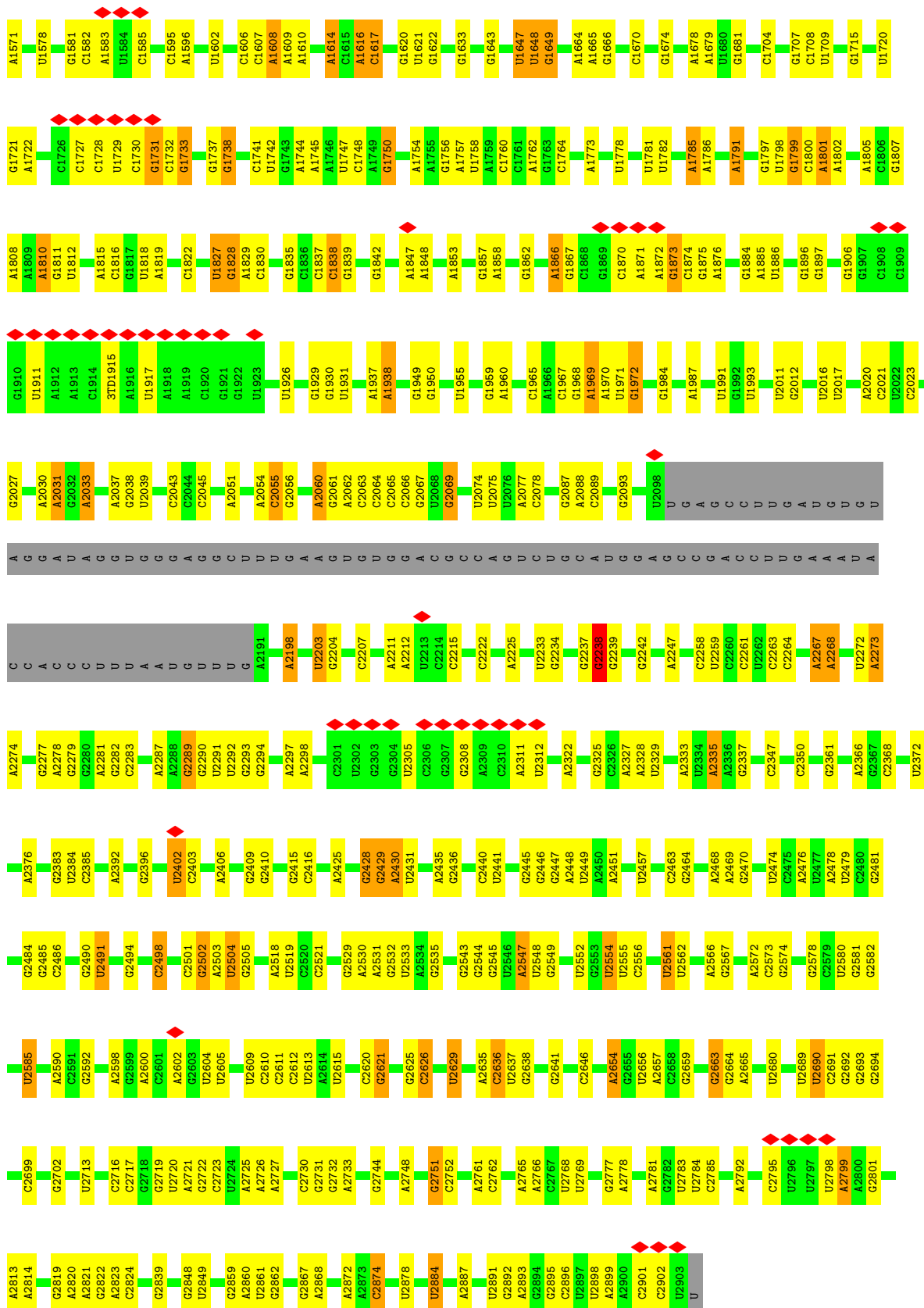
- Molecule 27: tRNA Asp



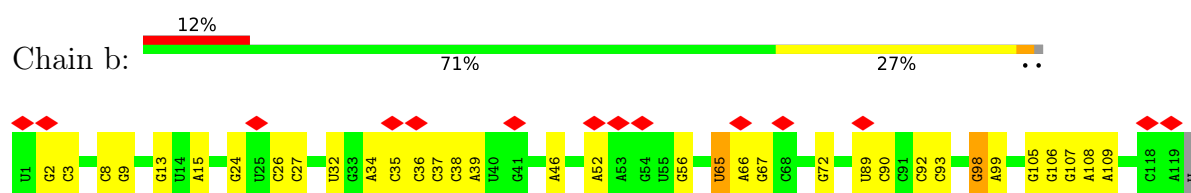
- Molecule 28: 23S rRNA



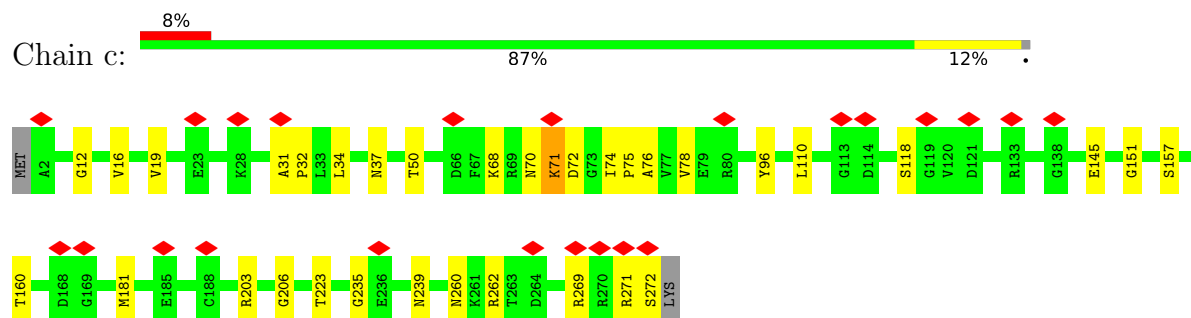




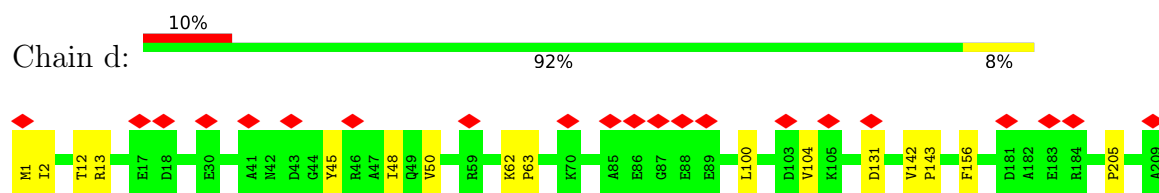
• Molecule 29: 5S rRNA



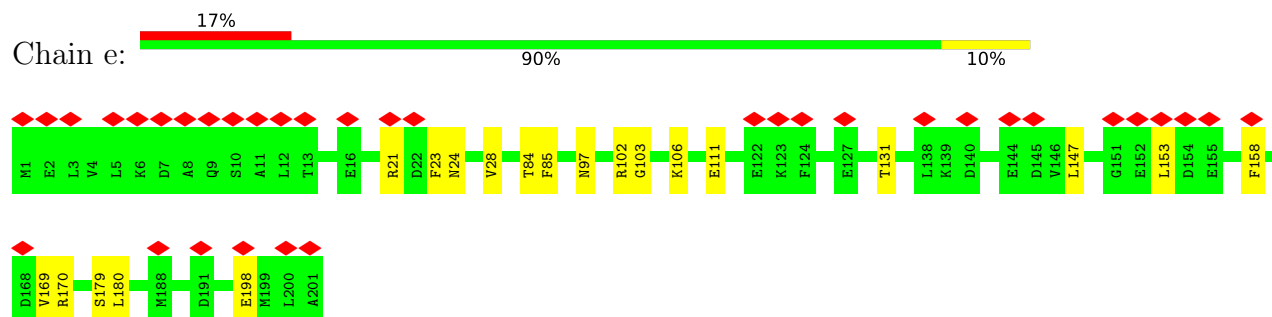
• Molecule 30: Large ribosomal subunit protein uL2



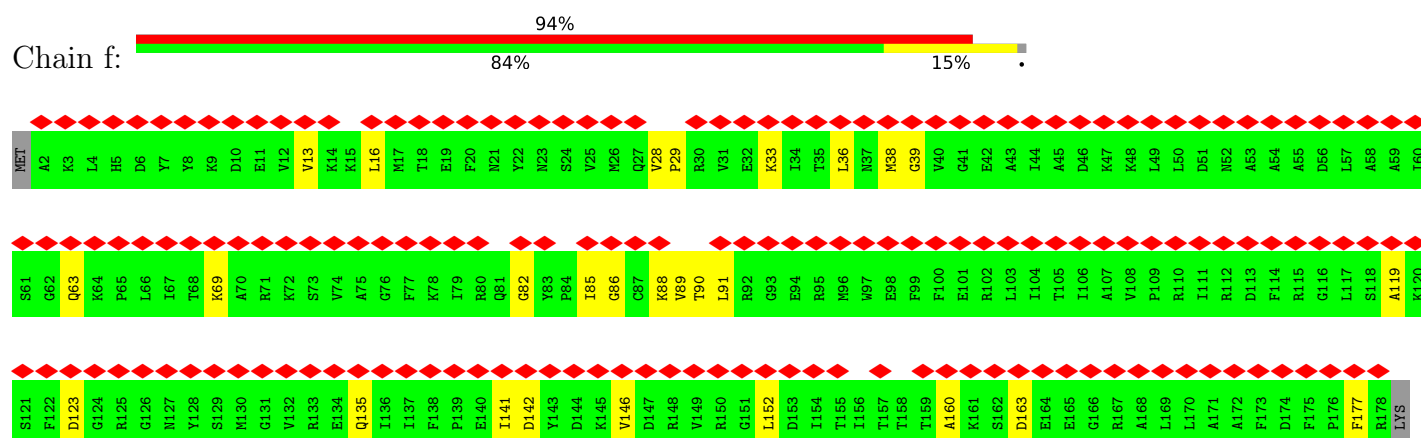
• Molecule 31: Large ribosomal subunit protein uL3



• Molecule 32: Large ribosomal subunit protein uL4

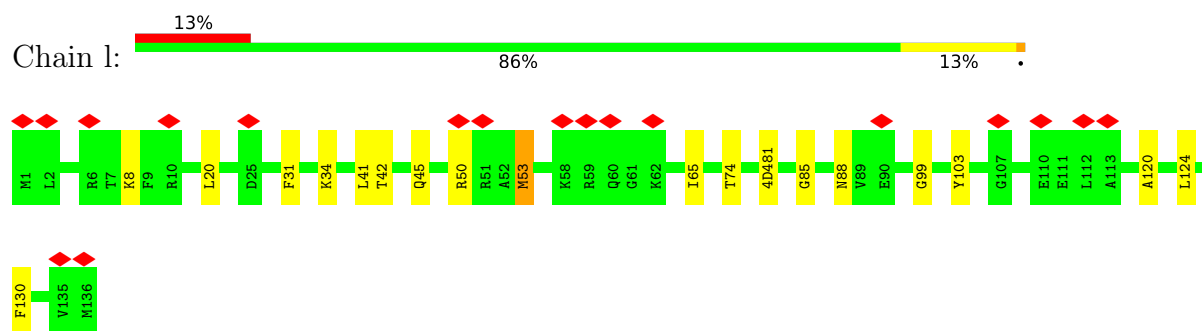


• Molecule 33: Large ribosomal subunit protein uL5

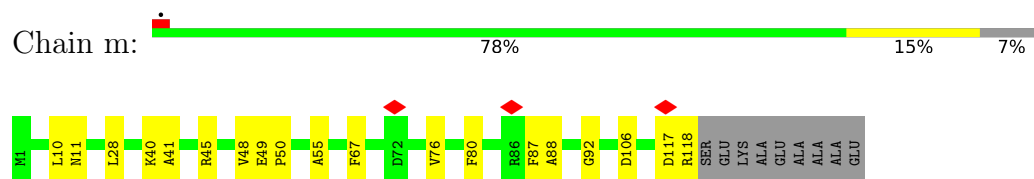


Chain k:

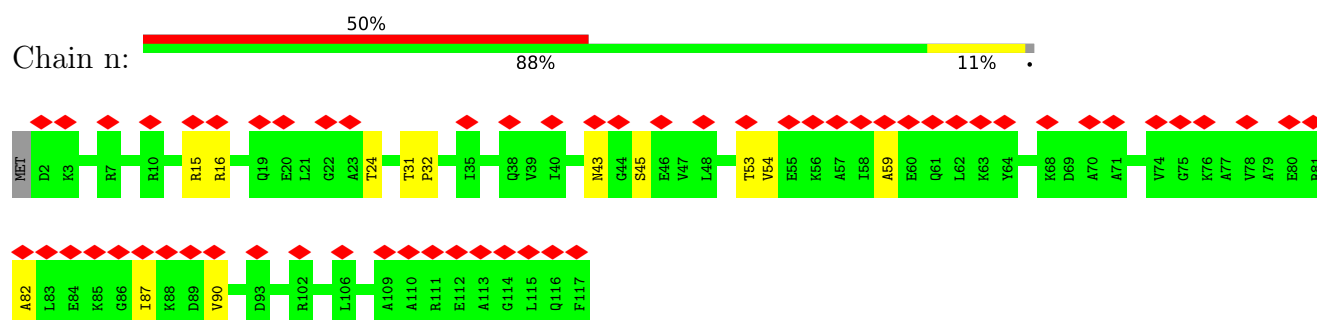
- Molecule 39: Large ribosomal subunit protein uL16



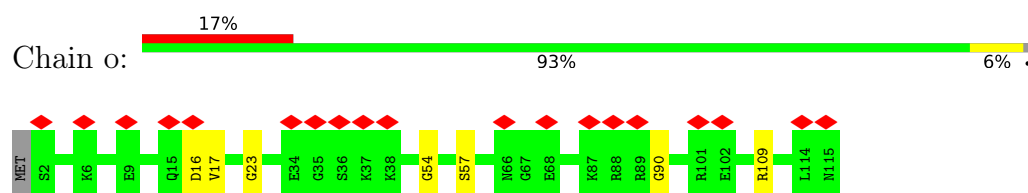
- Molecule 40: Large ribosomal subunit protein bL17



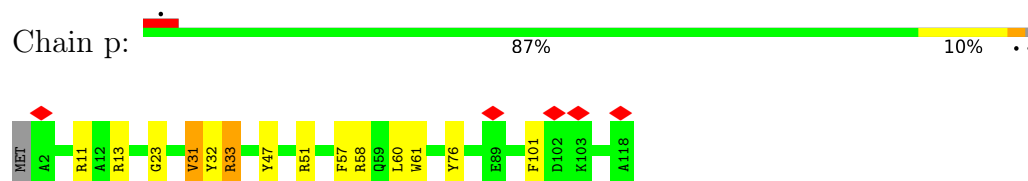
- Molecule 41: Large ribosomal subunit protein uL18



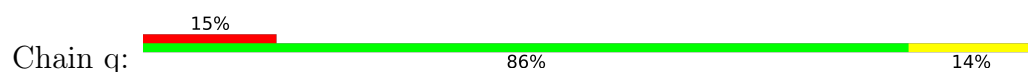
- Molecule 42: Large ribosomal subunit protein bL19

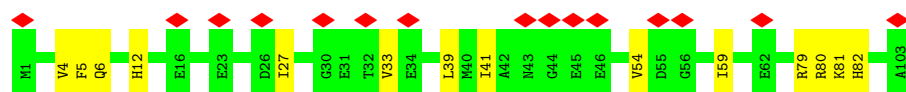


- Molecule 43: Large ribosomal subunit protein bL20

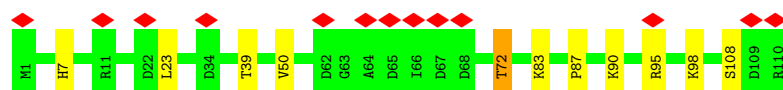
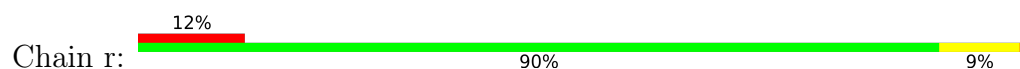


- Molecule 44: Large ribosomal subunit protein bL21

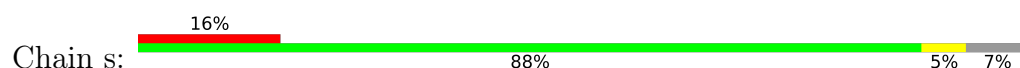




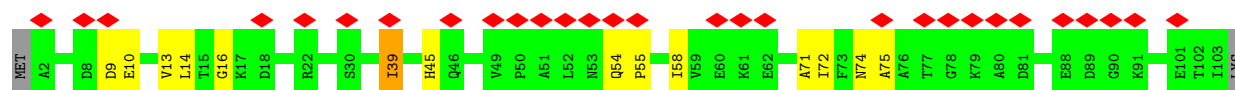
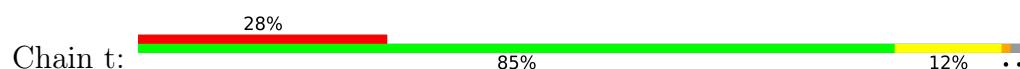
- Molecule 45: Large ribosomal subunit protein uL22



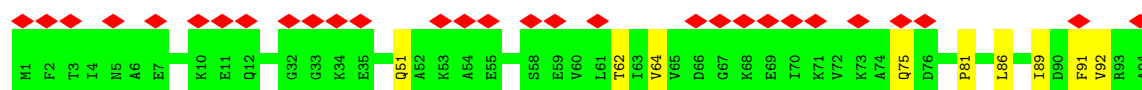
- Molecule 46: Large ribosomal subunit protein uL23



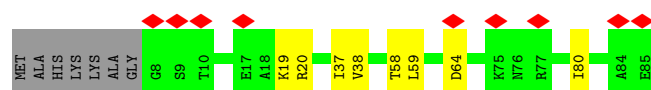
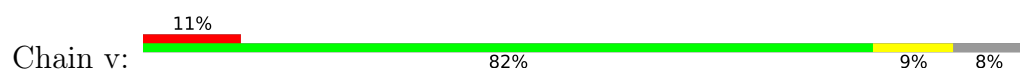
- Molecule 47: Large ribosomal subunit protein uL24



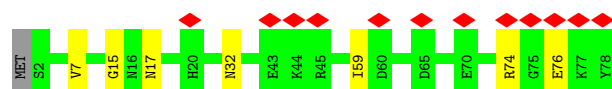
- Molecule 48: Large ribosomal subunit protein bL25



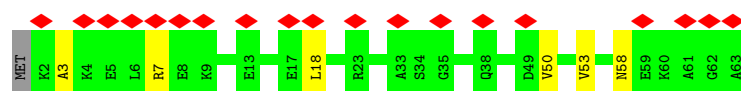
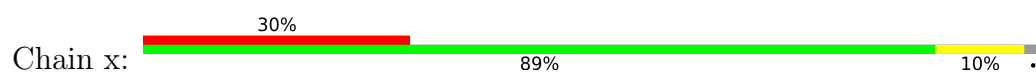
- Molecule 49: Large ribosomal subunit protein bL27



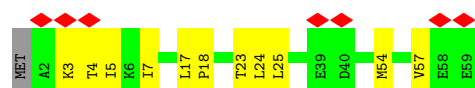
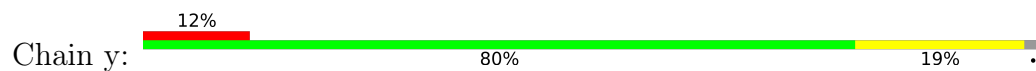
- Molecule 50: Large ribosomal subunit protein bL28



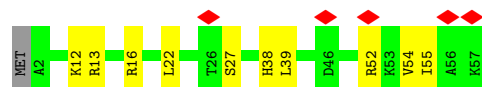
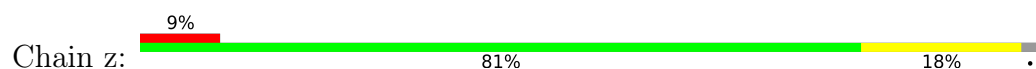
- Molecule 51: Large ribosomal subunit protein uL29



- Molecule 52: Large ribosomal subunit protein uL30



- Molecule 53: Large ribosomal subunit protein bL32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33268	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.215	Depositor
Minimum map value	-0.062	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	411.36, 411.36, 411.36	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8034375, 0.8034375, 0.8034375	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3TD, 5MC, 5MU, IAS, PSU, 2MA, D2T, H2U, 6MZ, MEQ, OMC, K, 4OC, 4D4, MG, 2MG, ZN, G7M, UR3, MS6, 1MG, MA6, OMU, OMG

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	0.57	0/424	1.14	0/565
2	1	0.69	0/380	1.26	0/498
3	2	0.65	0/513	1.21	0/676
4	3	0.61	0/303	1.13	0/397
5	A	0.60	1/36114 (0.0%)	0.92	28/56329 (0.0%)
6	B	0.54	0/1784	1.19	5/2403 (0.2%)
7	C	0.52	0/1651	0.94	0/2225
8	D	0.56	0/1625	1.24	2/2172 (0.1%)
9	E	0.58	0/1148	1.07	0/1545
10	F	0.52	0/843	1.10	2/1140 (0.2%)
11	G	0.50	0/1070	1.10	0/1431
12	H	0.56	0/989	1.14	1/1326 (0.1%)
13	I	0.51	0/1013	0.95	0/1350
14	J	0.53	0/784	1.01	1/1059 (0.1%)
15	K	0.60	0/884	1.10	1/1191 (0.1%)
16	L	0.60	0/945	1.09	1/1268 (0.1%)
17	M	0.52	0/900	0.98	0/1204
18	N	0.51	0/817	0.99	0/1088
19	O	0.53	0/722	1.15	0/964
20	P	0.56	0/639	1.14	1/859 (0.1%)
21	Q	0.55	0/650	1.04	1/871 (0.1%)
22	R	0.51	0/532	1.05	0/715
23	S	0.53	0/685	0.93	0/922
24	T	0.52	0/676	1.12	1/895 (0.1%)
25	U	0.52	0/597	1.18	0/792
26	V	0.52	0/912	0.98	0/1218
27	Z	0.61	0/1737	0.84	0/2704
28	a	0.63	1/65651 (0.0%)	1.10	293/102413 (0.3%)
29	b	0.62	0/2850	0.98	7/4444 (0.2%)
30	c	0.64	0/2121	1.19	3/2852 (0.1%)
31	d	0.63	0/1576	1.13	1/2119 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.59	0/1571	1.17	1/2113 (0.0%)
33	f	0.53	0/1434	1.15	2/1926 (0.1%)
34	g	0.56	0/1343	1.14	1/1816 (0.1%)
35	h	0.58	0/306	1.15	0/413
36	i	0.63	0/1152	1.15	3/1551 (0.2%)
37	j	0.59	0/955	1.15	1/1279 (0.1%)
38	k	0.64	0/1062	1.22	0/1413
39	l	0.58	0/1073	1.11	3/1433 (0.2%)
40	m	0.68	0/958	1.30	2/1281 (0.2%)
41	n	0.58	0/902	1.15	0/1209
42	o	0.58	0/929	1.06	0/1242
43	p	0.70	0/960	1.28	7/1278 (0.5%)
44	q	0.60	0/829	1.13	0/1107
45	r	0.69	0/864	1.20	2/1156 (0.2%)
46	s	0.60	0/744	1.15	0/994
47	t	0.63	0/787	1.19	1/1051 (0.1%)
48	u	0.56	0/766	1.13	1/1025 (0.1%)
49	v	0.60	0/593	1.13	2/785 (0.3%)
50	w	0.61	0/635	1.21	3/848 (0.4%)
51	x	0.53	0/502	1.24	0/667
52	y	0.60	0/453	1.11	1/605 (0.2%)
53	z	0.70	0/450	1.29	1/599 (0.2%)
All	All	0.61	2/150803 (0.0%)	1.06	379/225426 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	2552	OMU	O3'-P	5.94	1.62	1.56
5	A	527	G7M	O3'-P	5.67	1.61	1.56

The worst 5 of 379 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	a	786	C	O3'-P-O5'	-10.95	87.58	104.00
28	a	2730	C	O3'-P-O5'	-9.35	89.98	104.00
28	a	1328	A	O3'-P-O5'	-9.17	90.24	104.00
28	a	792	A	O3'-P-O5'	-9.12	90.32	104.00
28	a	1237	A	O3'-P-O5'	-8.98	90.53	104.00

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	417	441	451	3	0
2	1	377	411	418	3	0
3	2	504	562	572	6	0
4	3	302	337	340	1	0
5	A	32503	14825	16377	169	0
6	B	1753	1751	1780	60	0
7	C	1624	1669	1696	7	0
8	D	1605	1640	1665	24	0
9	E	1135	1160	1179	21	0
10	F	824	796	815	8	0
11	G	1057	1087	1101	8	0
12	H	979	1015	1031	17	0
13	I	1001	1027	1044	4	0
14	J	775	806	817	4	0
15	K	877	865	883	9	0
16	L	942	976	997	18	0
17	M	891	935	952	0	0
18	N	805	832	844	1	0
19	O	714	716	734	1	0
20	P	629	634	643	2	0
21	Q	641	668	682	6	0
22	R	524	528	543	2	0
23	S	668	678	693	1	0
24	T	670	710	719	7	0
25	U	589	621	629	6	0
26	V	900	917	931	6	0
27	Z	1557	714	789	18	0
28	a	59130	26982	29769	251	0
29	b	2549	1171	1291	10	0
30	c	2082	2114	2154	19	0
31	d	1566	1586	1618	10	0
32	e	1552	1590	1619	11	0
33	f	1410	1421	1444	17	0
34	g	1323	1347	1371	18	0
35	h	303	324	327	4	0
36	i	1129	1137	1162	13	0
37	j	946	1008	1023	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	1053	1111	1129	7	0
39	l	1075	1142	1145	10	0
40	m	945	971	989	10	0
41	n	892	908	923	8	0
42	o	917	947	962	4	0
43	p	947	1008	1019	7	0
44	q	816	825	839	7	0
45	r	857	904	922	7	0
46	s	738	795	807	4	0
47	t	779	823	831	9	0
48	u	753	770	780	4	0
49	v	586	586	596	4	0
50	w	625	638	652	3	0
51	x	501	526	531	3	0
52	y	449	479	488	6	0
53	z	444	443	458	5	0
54	3	1	0	0	0	0
55	A	17	0	0	0	0
55	Q	1	0	0	0	0
55	a	185	0	0	0	0
55	b	5	0	0	0	0
55	c	1	0	0	0	0
55	z	1	0	0	0	0
56	A	1	0	0	0	0
56	F	1	0	0	0	0
57	Z	8	6	3	1	0
All	All	139851	88883	94177	803	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 4.

The worst 5 of 803 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)
28:a:568:U:H1'	28:a:2030:6MZ:H9C1	1.61	0.82
28:a:1141:U:H4'	28:a:1142:A:O4'	1.80	0.82
5:A:1240:U:O4'	11:G:42:ILE:HD11	1.82	0.79
5:A:1346:A:C2	11:G:10:ARG:HD3	2.19	0.77
31:d:1:MET:HE2	31:d:205:PRO:HG3	1.67	0.77

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/55 (89%)	45 (92%)	4 (8%)	0	100	100
2	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
3	2	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
4	3	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
6	B	222/241 (92%)	218 (98%)	4 (2%)	0	100	100
7	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
8	D	196/206 (95%)	192 (98%)	4 (2%)	0	100	100
9	E	152/167 (91%)	141 (93%)	11 (7%)	0	100	100
10	F	99/135 (73%)	89 (90%)	10 (10%)	0	100	100
11	G	130/179 (73%)	126 (97%)	4 (3%)	0	100	100
12	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
13	I	123/130 (95%)	116 (94%)	7 (6%)	0	100	100
14	J	92/103 (89%)	90 (98%)	2 (2%)	0	100	100
15	K	113/129 (88%)	101 (89%)	12 (11%)	0	100	100
16	L	118/124 (95%)	111 (94%)	7 (6%)	0	100	100
17	M	113/118 (96%)	111 (98%)	2 (2%)	0	100	100
18	N	98/101 (97%)	98 (100%)	0	0	100	100
19	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
20	P	77/82 (94%)	71 (92%)	6 (8%)	0	100	100
21	Q	77/84 (92%)	67 (87%)	10 (13%)	0	100	100
22	R	62/75 (83%)	54 (87%)	8 (13%)	0	100	100
23	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
24	T	84/87 (97%)	74 (88%)	10 (12%)	0	100	100
25	U	68/71 (96%)	65 (96%)	3 (4%)	0	100	100
26	V	105/142 (74%)	101 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
31	d	206/209 (99%)	198 (96%)	8 (4%)	0	100	100
32	e	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
33	f	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
34	g	174/177 (98%)	168 (97%)	6 (3%)	0	100	100
35	h	39/149 (26%)	37 (95%)	2 (5%)	0	100	100
36	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
37	j	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
38	k	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
39	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
40	m	116/127 (91%)	108 (93%)	8 (7%)	0	100	100
41	n	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
42	o	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
43	p	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
44	q	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
45	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
46	s	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
47	t	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
48	u	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
49	v	76/85 (89%)	71 (93%)	5 (7%)	0	100	100
50	w	75/78 (96%)	75 (100%)	0	0	100	100
51	x	60/63 (95%)	60 (100%)	0	0	100	100
52	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
53	z	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
All	All	5486/5985 (92%)	5246 (96%)	240 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	34 (100%)	0	100	100
6	B	186/199 (94%)	185 (100%)	1 (0%)	81	93
7	C	170/190 (90%)	170 (100%)	0	100	100
8	D	168/173 (97%)	165 (98%)	3 (2%)	51	79
9	E	117/126 (93%)	114 (97%)	3 (3%)	40	72
10	F	88/116 (76%)	86 (98%)	2 (2%)	44	74
11	G	109/147 (74%)	108 (99%)	1 (1%)	70	88
12	H	104/105 (99%)	103 (99%)	1 (1%)	68	87
13	I	103/107 (96%)	103 (100%)	0	100	100
14	J	85/90 (94%)	85 (100%)	0	100	100
15	K	89/98 (91%)	88 (99%)	1 (1%)	65	86
16	L	101/103 (98%)	99 (98%)	2 (2%)	48	77
17	M	93/96 (97%)	93 (100%)	0	100	100
18	N	83/84 (99%)	83 (100%)	0	100	100
19	O	76/77 (99%)	76 (100%)	0	100	100
20	P	64/65 (98%)	64 (100%)	0	100	100
21	Q	73/78 (94%)	73 (100%)	0	100	100
22	R	55/65 (85%)	55 (100%)	0	100	100
23	S	72/79 (91%)	72 (100%)	0	100	100
24	T	65/66 (98%)	65 (100%)	0	100	100
25	U	60/61 (98%)	60 (100%)	0	100	100
26	V	93/121 (77%)	93 (100%)	0	100	100
30	c	216/218 (99%)	216 (100%)	0	100	100
31	d	163/163 (100%)	162 (99%)	1 (1%)	78	92
32	e	165/165 (100%)	164 (99%)	1 (1%)	78	92
33	f	148/150 (99%)	147 (99%)	1 (1%)	76	91
34	g	137/138 (99%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	h	32/114 (28%)	32 (100%)	0	100	100
36	i	116/116 (100%)	116 (100%)	0	100	100
37	j	104/104 (100%)	104 (100%)	0	100	100
38	k	103/103 (100%)	102 (99%)	1 (1%)	68	87
39	l	107/107 (100%)	107 (100%)	0	100	100
40	m	98/103 (95%)	97 (99%)	1 (1%)	68	87
41	n	86/87 (99%)	85 (99%)	1 (1%)	63	85
42	o	99/100 (99%)	99 (100%)	0	100	100
43	p	89/90 (99%)	88 (99%)	1 (1%)	65	86
44	q	84/84 (100%)	84 (100%)	0	100	100
45	r	93/93 (100%)	92 (99%)	1 (1%)	65	86
46	s	80/84 (95%)	80 (100%)	0	100	100
47	t	83/85 (98%)	82 (99%)	1 (1%)	63	85
48	u	78/78 (100%)	77 (99%)	1 (1%)	61	84
49	v	58/63 (92%)	58 (100%)	0	100	100
50	w	67/68 (98%)	67 (100%)	0	100	100
51	x	54/55 (98%)	53 (98%)	1 (2%)	50	78
52	y	48/49 (98%)	48 (100%)	0	100	100
53	z	47/48 (98%)	46 (98%)	1 (2%)	47	76
All	All	4578/4884 (94%)	4552 (99%)	26 (1%)	76	92

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	d	50	VAL
38	k	121	THR
51	x	58	ASN
33	f	88	LYS
40	m	48	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
26	V	52	ASN

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Mol	Chain	Res	Type
47	t	74	ASN
31	d	94	GLN
47	t	66	GLN
50	w	6	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	Z	71/77 (92%)	31 (43%)	0
28	a	2749/2904 (94%)	416 (15%)	0
29	b	118/120 (98%)	13 (11%)	0
5	A	1512/1542 (98%)	344 (22%)	54 (3%)
All	All	4450/4643 (95%)	804 (18%)	54 (1%)

5 of 804 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	3	A
5	A	4	U
5	A	6	G
5	A	8	A
5	A	9	G

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	847	G
5	A	1035	A
5	A	1440	U
5	A	870	U
5	A	983	A

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

40 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
28	PSU	a	2605	28	18,21,22	1.04	2 (11%)	22,30,33	0.75	0
28	H2U	a	2449	28	18,21,22	0.73	1 (5%)	21,30,33	1.37	3 (14%)
28	OMU	a	2552	28	19,22,23	0.41	0	26,31,34	0.64	0
28	5MU	a	747	28	19,22,23	0.42	0	28,32,35	0.65	0
28	5MU	a	1939	28	19,22,23	0.61	0	28,32,35	0.58	0
28	3TD	a	1915	28	18,22,23	0.94	1 (5%)	22,32,35	0.65	0
39	MS6	l	82	39	5,7,8	0.31	0	2,7,9	0.61	0
5	2MG	A	1207	5	23,26,27	0.40	0	32,38,41	0.41	0
28	PSU	a	2580	28	18,21,22	1.08	1 (5%)	22,30,33	1.23	1 (4%)
28	PSU	a	2604	28	18,21,22	0.91	1 (5%)	22,30,33	0.81	0
28	2MA	a	2503	28,55	22,25,26	0.88	1 (4%)	33,37,40	1.19	4 (12%)
28	OMC	a	2498	28,55	19,22,23	0.57	0	26,31,34	0.67	1 (3%)
5	MA6	A	1519	5	23,26,27	0.31	0	34,38,41	0.71	1 (2%)
28	PSU	a	1917	28	18,21,22	0.88	1 (5%)	22,30,33	0.64	0
5	5MC	A	1407	5	18,22,23	0.36	0	26,32,35	0.56	0
28	2MG	a	2445	28	23,26,27	0.51	0	32,38,41	0.69	0
28	5MC	a	1962	28	18,22,23	0.50	0	26,32,35	0.52	0
28	2MG	a	1835	28	23,26,27	0.36	0	32,38,41	0.53	1 (3%)
5	5MC	A	967	5	18,22,23	0.34	0	26,32,35	0.49	0
5	4OC	A	1402	5	20,23,24	0.42	0	26,32,35	0.47	0
28	PSU	a	2504	28	18,21,22	0.95	1 (5%)	22,30,33	1.01	1 (4%)
5	PSU	A	516	5	18,21,22	0.92	1 (5%)	22,30,33	1.13	1 (4%)
31	MEQ	d	150	31	8,9,10	0.53	0	5,10,12	0.65	0
39	4D4	l	81	39	9,11,12	0.69	0	8,13,15	1.19	1 (12%)
16	D2T	L	89	16	7,9,10	0.89	0	6,11,13	1.79	3 (50%)
28	PSU	a	2457	28	18,21,22	0.94	1 (5%)	22,30,33	0.61	0
5	2MG	A	1516	5	23,26,27	0.42	0	32,38,41	0.50	0
5	UR3	A	1498	5	19,22,23	0.34	0	26,32,35	0.66	0
5	G7M	A	527	5	23,26,27	0.74	1 (4%)	35,39,42	0.57	1 (2%)
28	OMG	a	2251	28,27	23,26,27	0.39	0	33,38,41	0.53	0
28	6MZ	a	2030	28	22,25,26	0.55	0	30,36,39	0.67	0
28	6MZ	a	1618	28	22,25,26	0.56	0	30,36,39	0.56	0
28	G7M	a	2069	28	23,26,27	0.62	0	35,39,42	0.87	1 (2%)
28	1MG	a	745	28	22,26,27	0.82	1 (4%)	33,39,42	0.70	1 (3%)
28	PSU	a	1911	28	18,21,22	0.95	1 (5%)	22,30,33	0.59	0
15	IAS	K	119	15	6,7,8	0.98	0	6,8,10	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	PSU	a	746	28,55	18,21,22	0.97	2 (11%)	22,30,33	0.82	0
5	2MG	A	966	5	23,26,27	0.40	0	32,38,41	0.37	0
28	PSU	a	955	28	18,21,22	0.92	2 (11%)	22,30,33	0.73	0
5	MA6	A	1518	5	23,26,27	0.28	0	34,38,41	0.74	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	PSU	a	2605	28	-	0/7/25/26	0/2/2/2
28	H2U	a	2449	28	-	0/7/38/39	0/2/2/2
28	OMU	a	2552	28	-	0/9/27/28	0/2/2/2
28	5MU	a	747	28	-	0/7/25/26	0/2/2/2
28	5MU	a	1939	28	-	0/7/25/26	0/2/2/2
28	3TD	a	1915	28	-	0/7/25/26	0/2/2/2
39	MS6	l	82	39	-	2/4/6/8	-
5	2MG	A	1207	5	-	0/9/27/28	0/3/3/3
28	PSU	a	2580	28	-	0/7/25/26	0/2/2/2
28	PSU	a	2604	28	-	0/7/25/26	0/2/2/2
28	2MA	a	2503	28,55	-	3/7/25/26	0/3/3/3
28	OMC	a	2498	28,55	-	0/9/27/28	0/2/2/2
5	MA6	A	1519	5	-	0/11/29/30	0/3/3/3
28	PSU	a	1917	28	-	1/7/25/26	0/2/2/2
5	5MC	A	1407	5	-	2/7/25/26	0/2/2/2
28	2MG	a	2445	28	-	2/9/27/28	0/3/3/3
28	5MC	a	1962	28	-	0/7/25/26	0/2/2/2
28	2MG	a	1835	28	-	0/9/27/28	0/3/3/3
5	5MC	A	967	5	-	0/7/25/26	0/2/2/2
5	4OC	A	1402	5	-	0/9/29/30	0/2/2/2
28	PSU	a	2504	28	-	2/7/25/26	0/2/2/2
5	PSU	A	516	5	-	0/7/25/26	0/2/2/2
31	MEQ	d	150	31	-	5/8/9/11	-
39	4D4	l	81	39	-	3/11/12/14	-
16	D2T	L	89	16	-	1/7/12/14	-
28	PSU	a	2457	28	-	0/7/25/26	0/2/2/2
5	2MG	A	1516	5	-	0/9/27/28	0/3/3/3
5	UR3	A	1498	5	-	2/7/25/26	0/2/2/2
5	G7M	A	527	5	-	2/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	OMG	a	2251	28,27	-	0/9/27/28	0/3/3/3
28	6MZ	a	2030	28	-	2/9/27/28	0/3/3/3
28	6MZ	a	1618	28	-	0/9/27/28	0/3/3/3
28	G7M	a	2069	28	-	2/7/25/26	0/3/3/3
28	1MG	a	745	28	-	0/7/25/26	0/3/3/3
28	PSU	a	1911	28	-	0/7/25/26	0/2/2/2
15	IAS	K	119	15	-	2/7/7/8	-
28	PSU	a	746	28,55	-	1/7/25/26	0/2/2/2
5	2MG	A	966	5	-	0/9/27/28	0/3/3/3
28	PSU	a	955	28	-	0/7/25/26	0/2/2/2
5	MA6	A	1518	5	-	0/11/29/30	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	1915	3TD	C6-C5	3.62	1.39	1.35
28	a	1911	PSU	C6-C5	3.60	1.39	1.35
28	a	1917	PSU	C6-C5	3.52	1.39	1.35
5	A	516	PSU	C6-C5	3.50	1.39	1.35
28	a	2504	PSU	C6-C5	3.26	1.39	1.35

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	a	2449	H2U	N3-C2-N1	4.03	120.91	116.65
5	A	516	PSU	C3'-C2'-C1'	3.79	106.05	101.64
28	a	2580	PSU	C3'-C2'-C1'	3.27	105.45	101.64
28	a	2504	PSU	C2'-C3'-C4'	-3.16	96.50	102.64
28	a	2503	2MA	C5-C4-N3	-2.94	123.88	127.19

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	527	G7M	C3'-C4'-C5'-O5'
39	l	81	4D4	O-C-CA-CB
39	l	81	4D4	NH2-CZ-NE-CD
39	l	81	4D4	NH1-CZ-NE-CD
39	l	82	MS6	C-CA-CB-CG

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	a	2498	OMC	1	0
5	A	1519	MA6	3	0
16	L	89	D2T	1	0
5	A	1516	2MG	2	0
28	a	2030	6MZ	2	0
5	A	1518	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 214 ligands modelled in this entry, 213 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	ASP	Z	101	-	6,7,8	1.08	0	5,8,10	1.03	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	ASP	Z	101	-	-	0/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	Z	101	ASP	1	0

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.

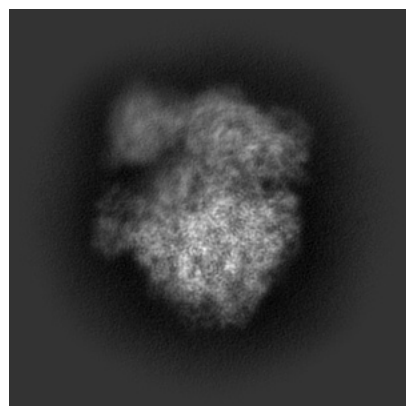
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-57975. These allow visual inspection of the internal detail of the map and identification of artifacts.

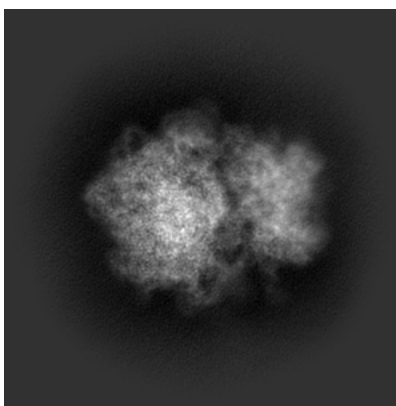
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

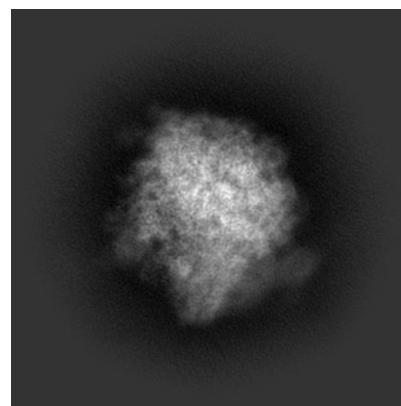
6.1.1 Primary map



X

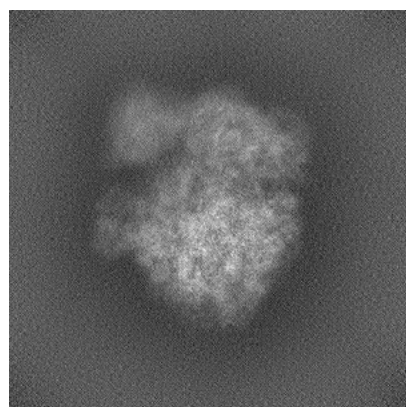


Y

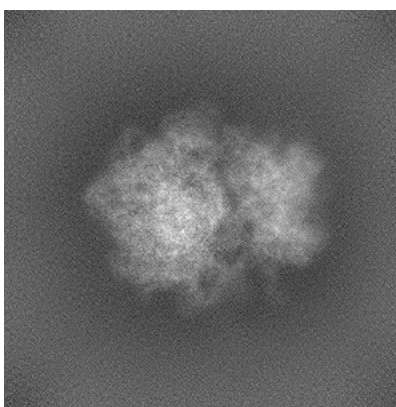


Z

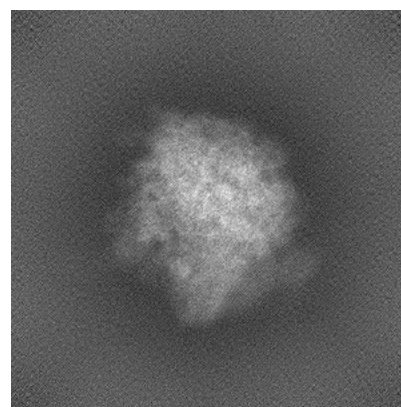
6.1.2 Raw map



X



Y

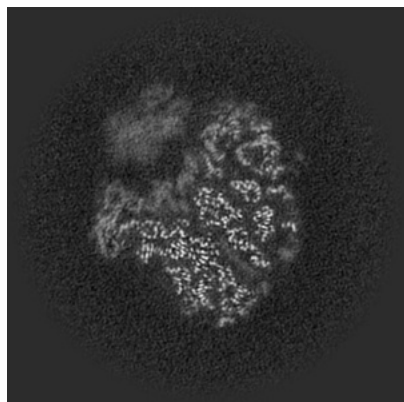


Z

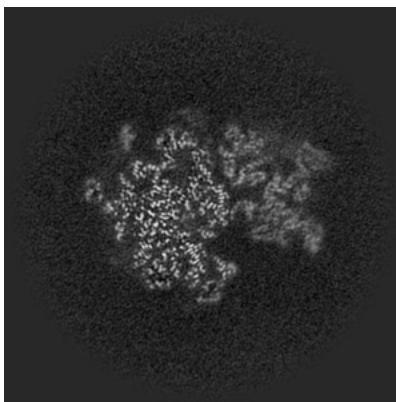
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

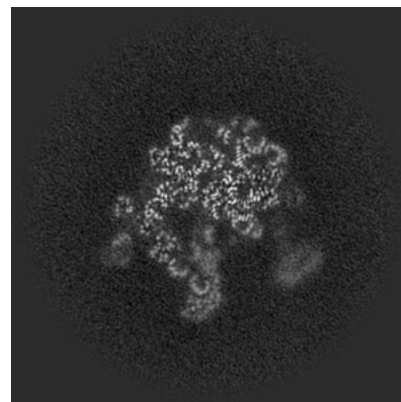
6.2.1 Primary map



X Index: 256

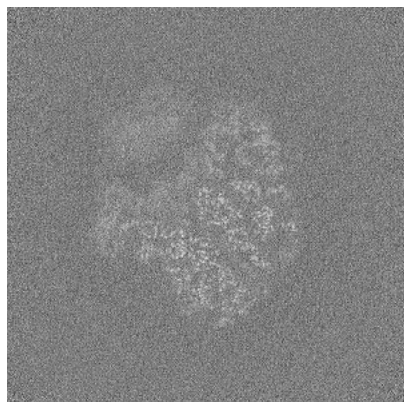


Y Index: 256

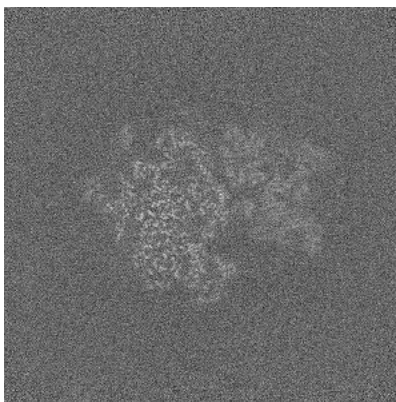


Z Index: 256

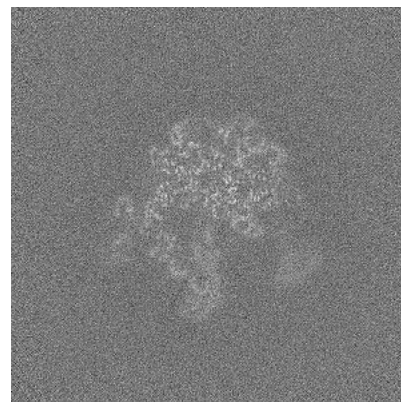
6.2.2 Raw map



X Index: 256



Y Index: 256

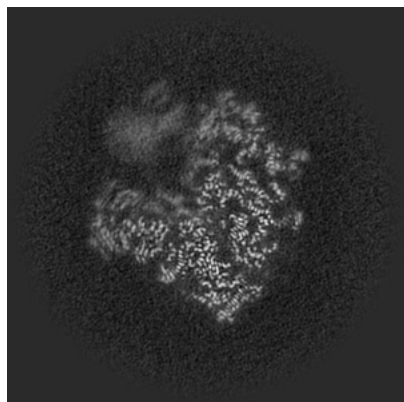


Z Index: 256

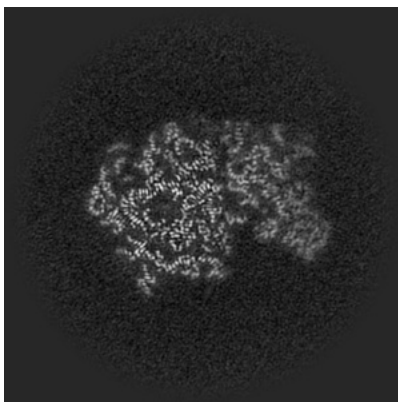
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

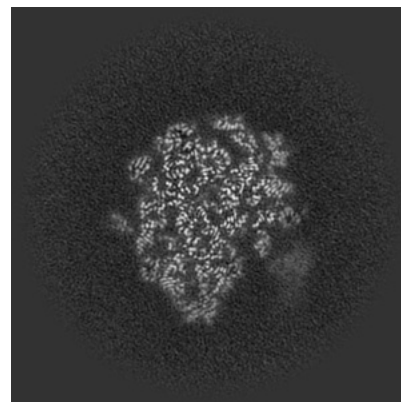
6.3.1 Primary map



X Index: 247

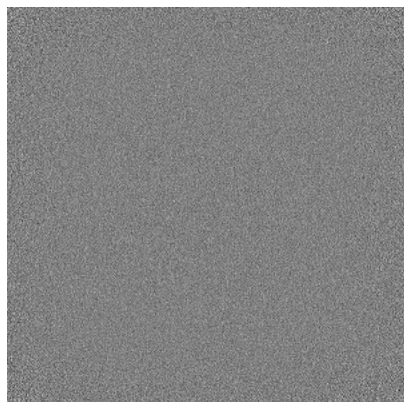


Y Index: 278

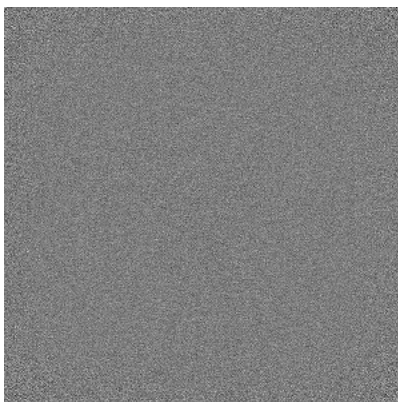


Z Index: 221

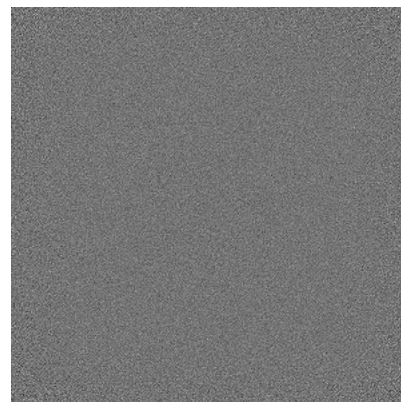
6.3.2 Raw map



X Index: 0



Y Index: 0

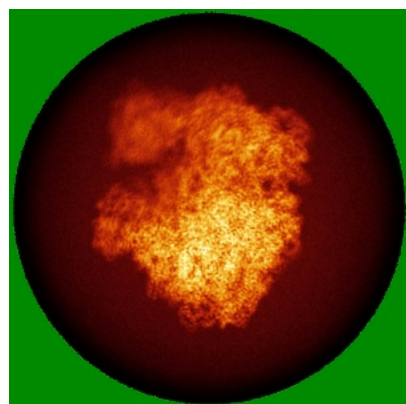


Z Index: 0

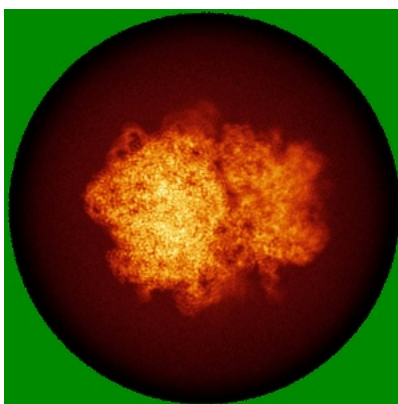
The images above show the largest variance slices of the map in three orthogonal directions.

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

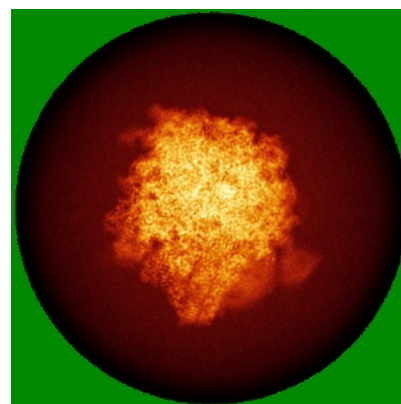
6.4.1 Primary map



X

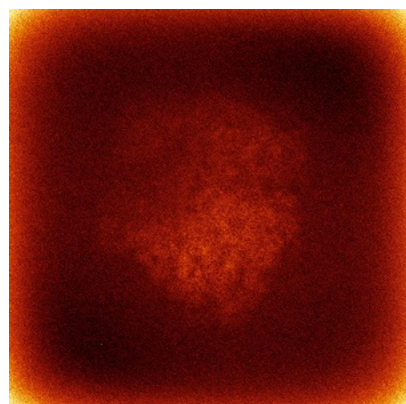


Y

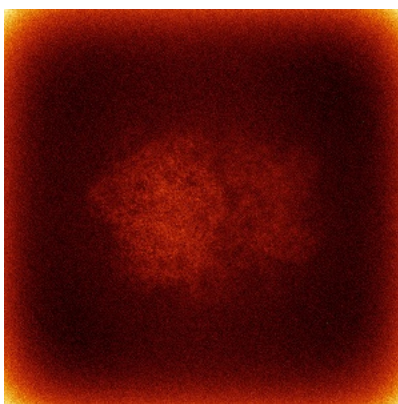


Z

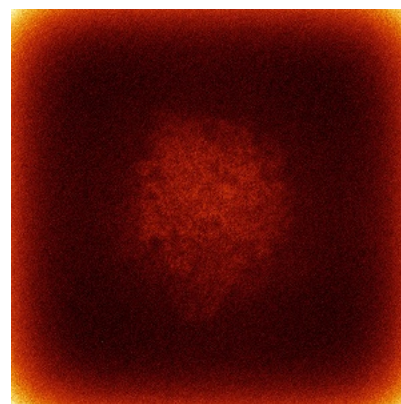
6.4.2 Raw map



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



X



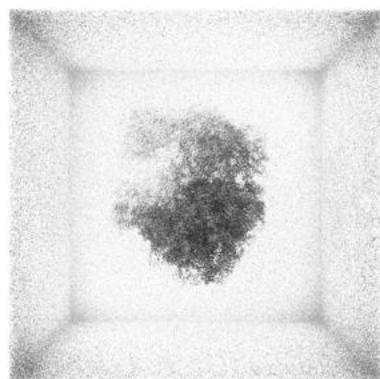
Y



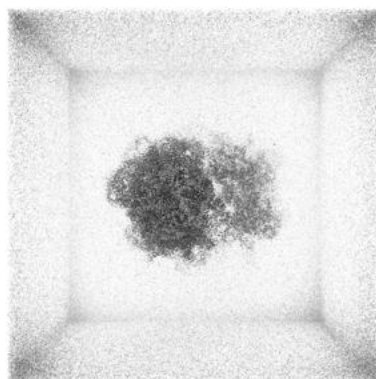
Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

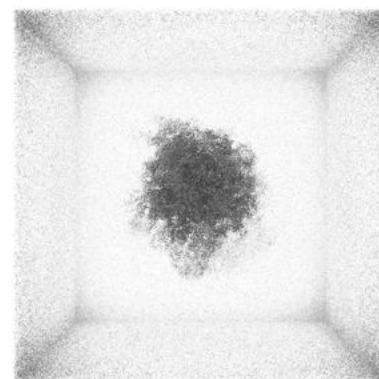
6.5.2 Raw map



X



Y



Z

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

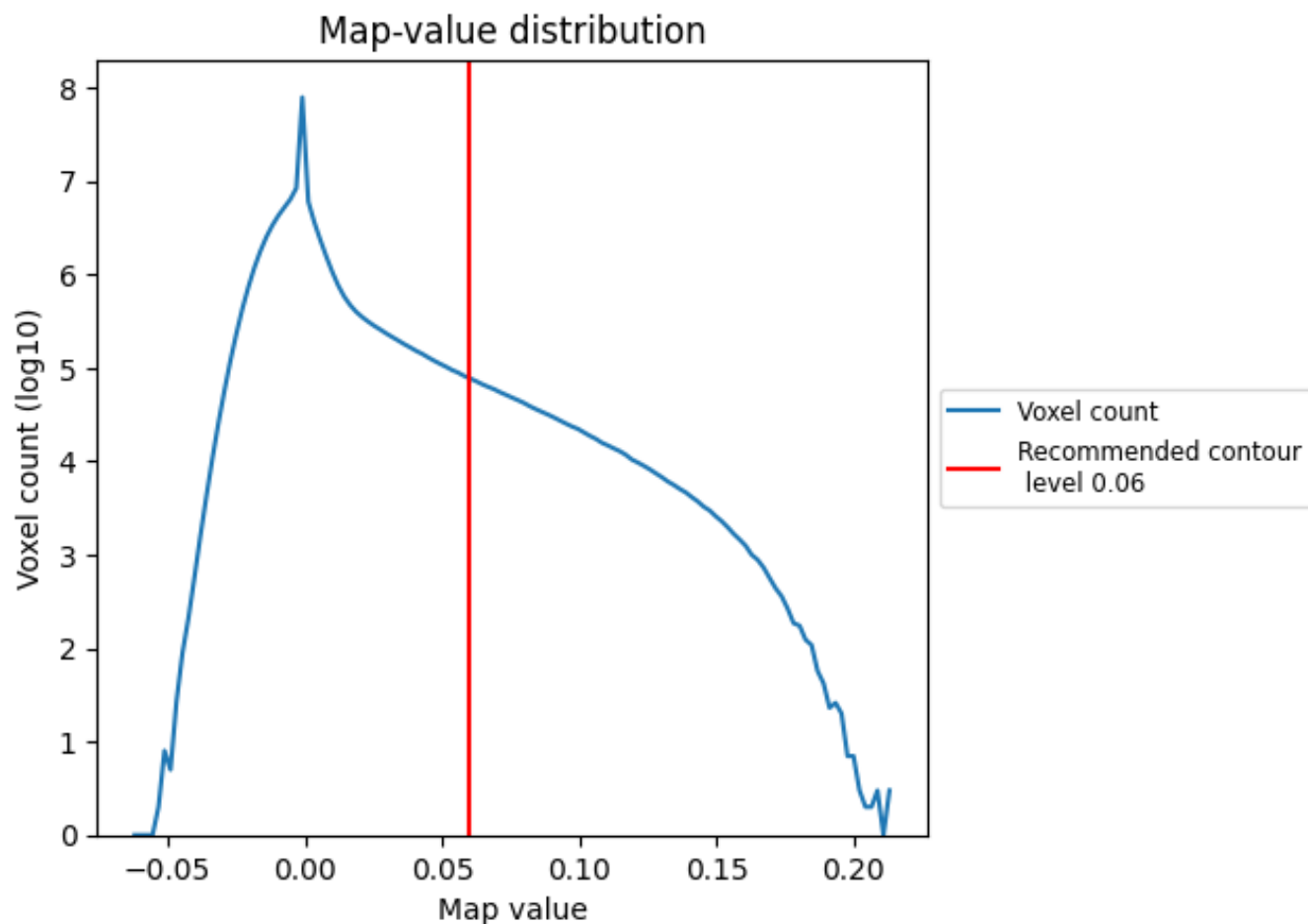
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

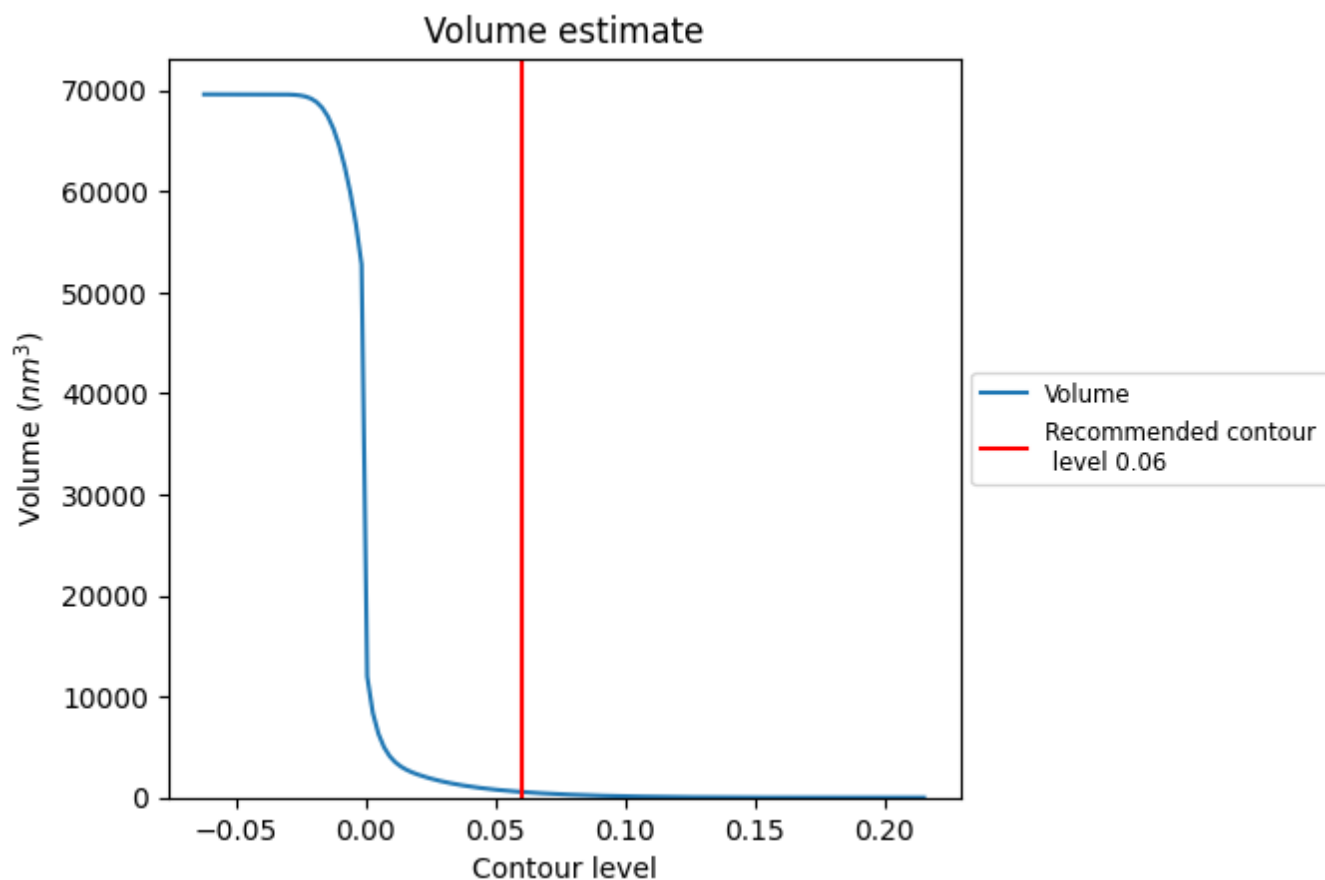
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

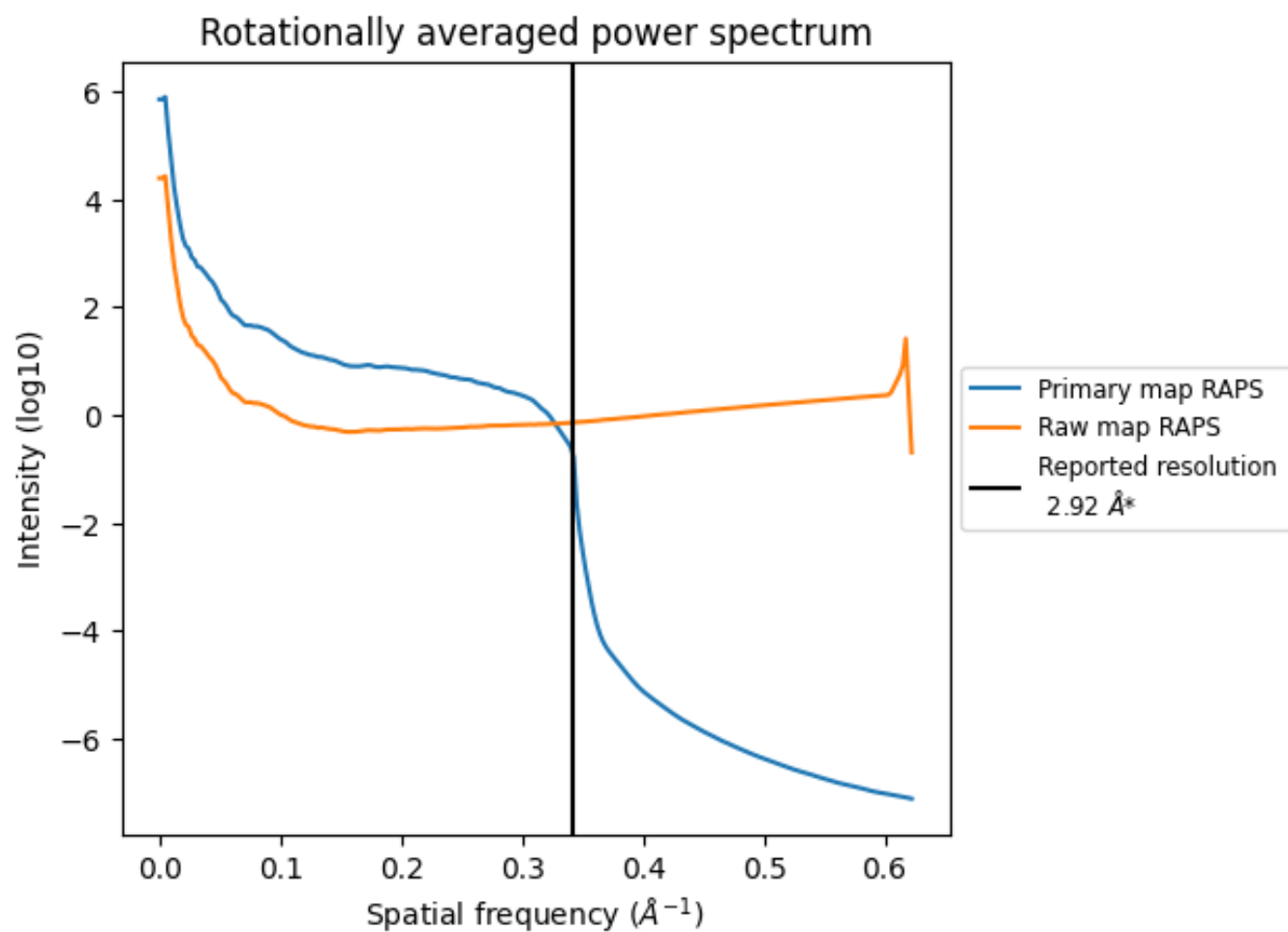
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 561 nm³; this corresponds to an approximate mass of 507 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 ⓘ

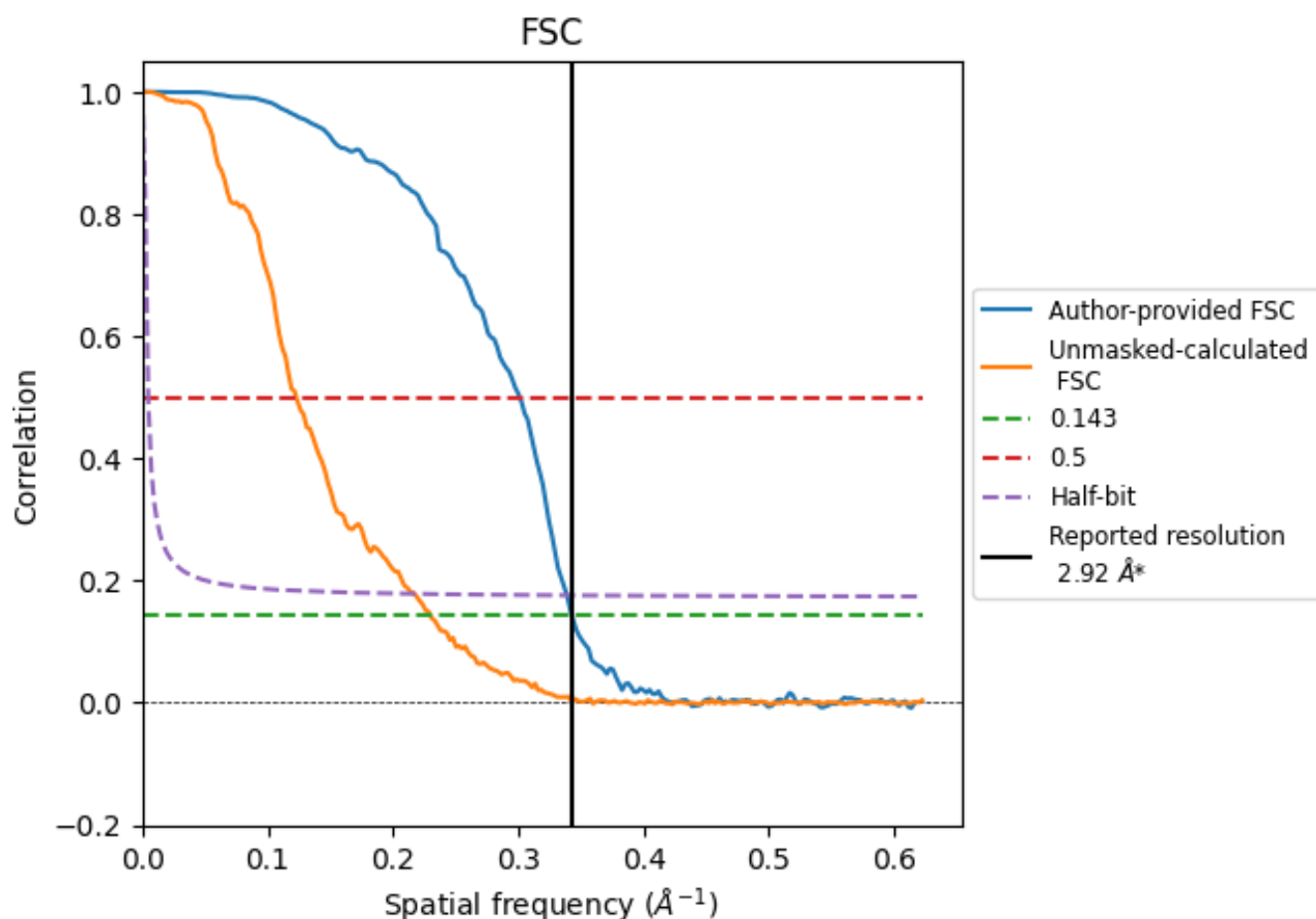


*Reported resolution corresponds to spatial frequency of 0.342 $\text{\AA}^{-1}$

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 0.342 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

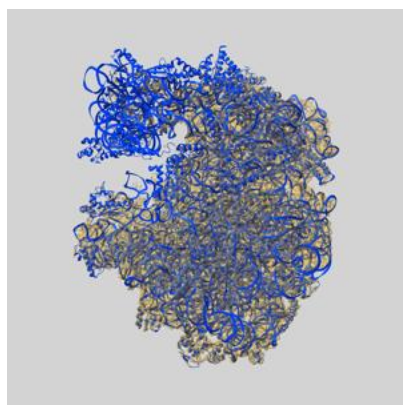
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.92	-	-
Author-provided FSC curve	2.92	3.32	2.95
Unmasked-calculated*	4.35	8.14	4.61

*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 4.35 differs from the reported value 2.92 by more than 10 %

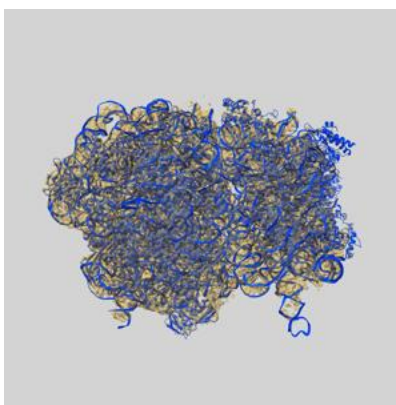
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-57975 and PDB model 30RB. Per-residue inclusion information can be found in section [3](#) on page [15](#).

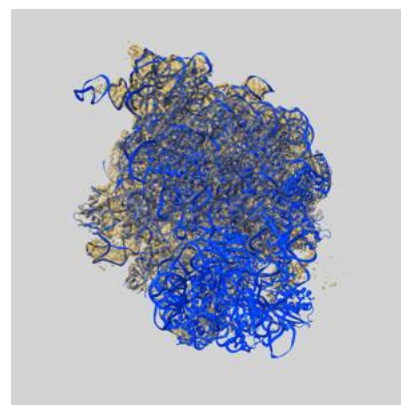
9.1 Map-model overlay [i](#)



X



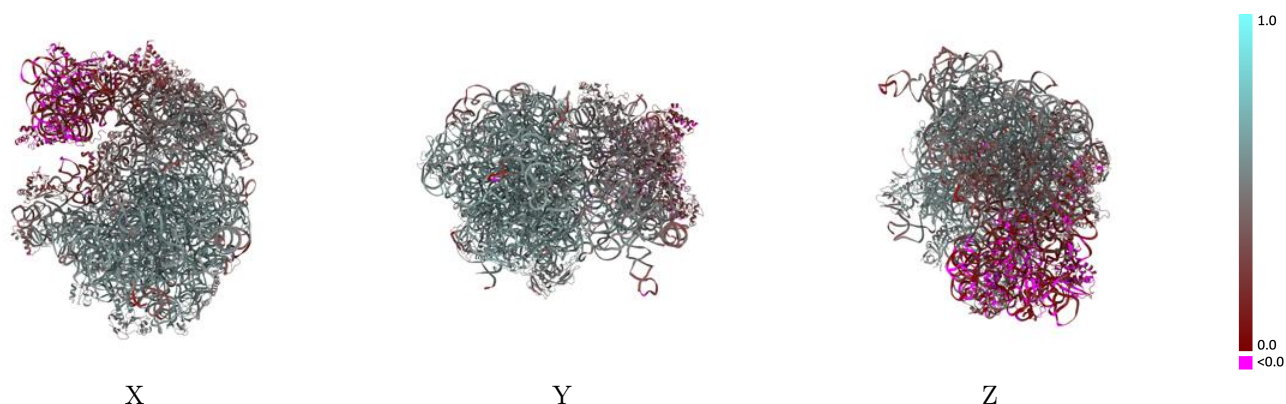
Y



Z

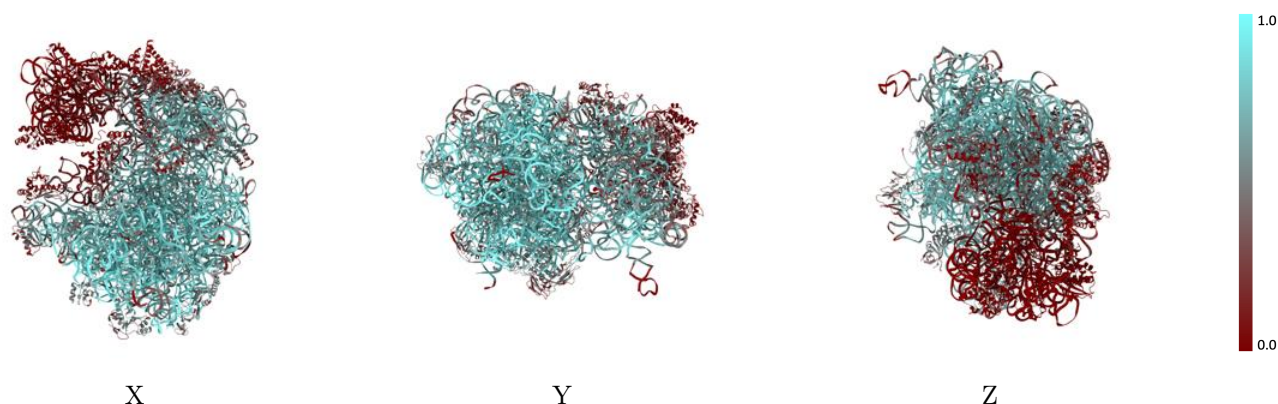
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



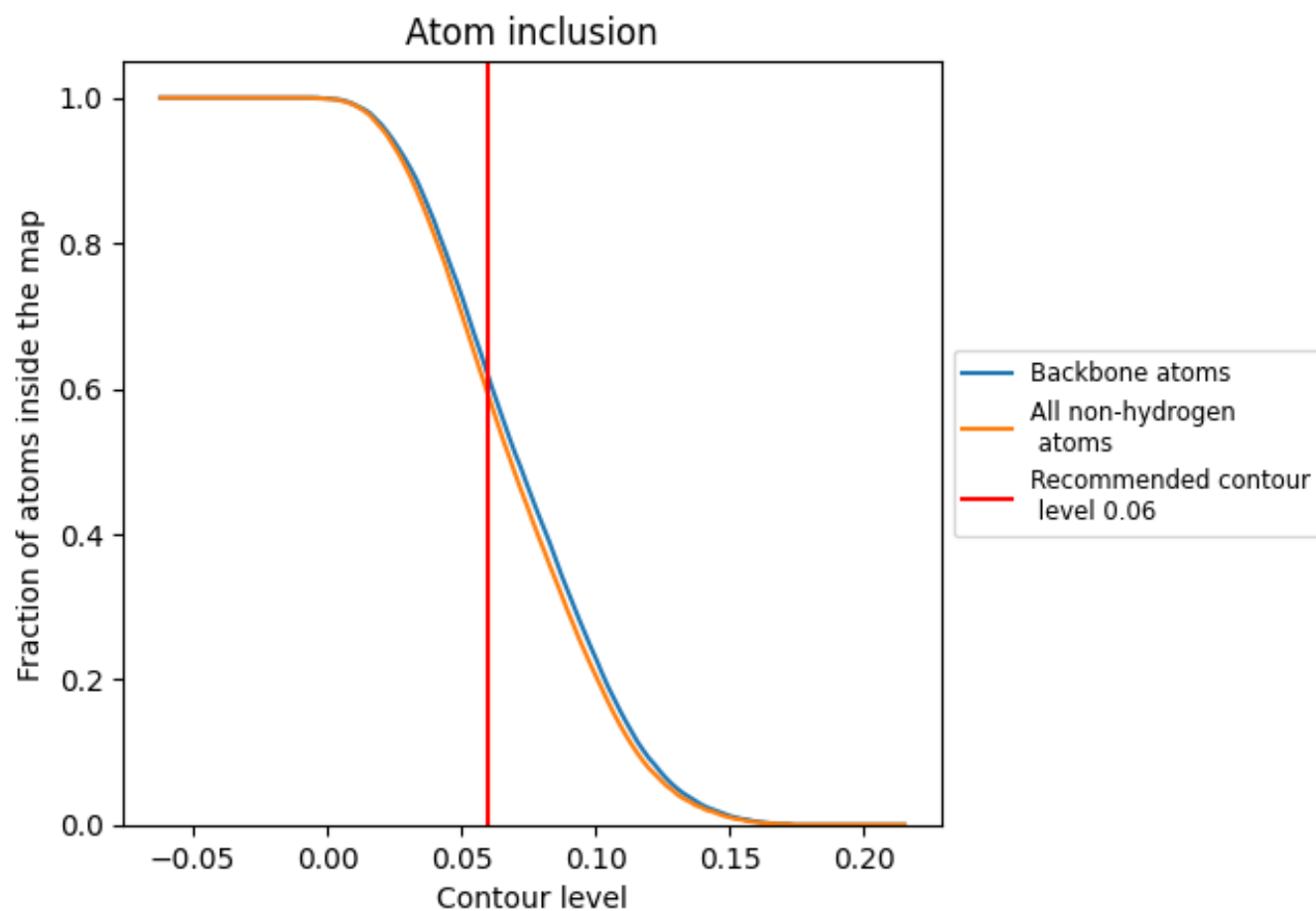
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 59% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5910	 0.4480
0	 0.4990	 0.5080
1	 0.7580	 0.5740
2	 0.7150	 0.5640
3	 0.6110	 0.5440
A	 0.4970	 0.3470
B	 0.0380	 0.1890
C	 0.0000	 0.1000
D	 0.1350	 0.2970
E	 0.2170	 0.3230
F	 0.2250	 0.3950
G	 0.0010	 0.1120
H	 0.3030	 0.3680
I	 0.0060	 0.0380
J	 0.0130	 0.0730
K	 0.2010	 0.3870
L	 0.2240	 0.3880
M	 0.0000	 0.0080
N	 0.0000	 0.0470
O	 0.4360	 0.4440
P	 0.4500	 0.4660
Q	 0.4310	 0.4630
R	 0.2460	 0.3860
S	 0.0000	 0.0380
T	 0.4810	 0.4800
U	 0.1270	 0.3520
V	 0.1420	 0.3340
Z	 0.1710	 0.2370
a	 0.8510	 0.5460
b	 0.6620	 0.4640
c	 0.6670	 0.5580
d	 0.6540	 0.5530
e	 0.6070	 0.5260
f	 0.1050	 0.2860
g	 0.3730	 0.4600



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Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.2570	 0.4280
i	 0.6800	 0.5540
j	 0.5790	 0.5430
k	 0.6420	 0.5390
l	 0.5860	 0.5290
m	 0.7080	 0.5570
n	 0.3940	 0.4140
o	 0.5920	 0.5420
p	 0.7240	 0.5610
q	 0.6220	 0.5280
r	 0.6530	 0.5440
s	 0.5570	 0.5060
t	 0.4800	 0.4770
u	 0.4850	 0.4990
v	 0.6430	 0.5500
w	 0.6420	 0.5430
x	 0.4850	 0.4570
y	 0.6220	 0.5320
z	 0.6690	 0.5560