



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:42 AM UTC

PDB ID : 7QGH / pdb_00007qgh
EMDB ID : EMD-13955
Title : Structure of the E. coli disome - collided 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-08
Resolution : 4.48 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:

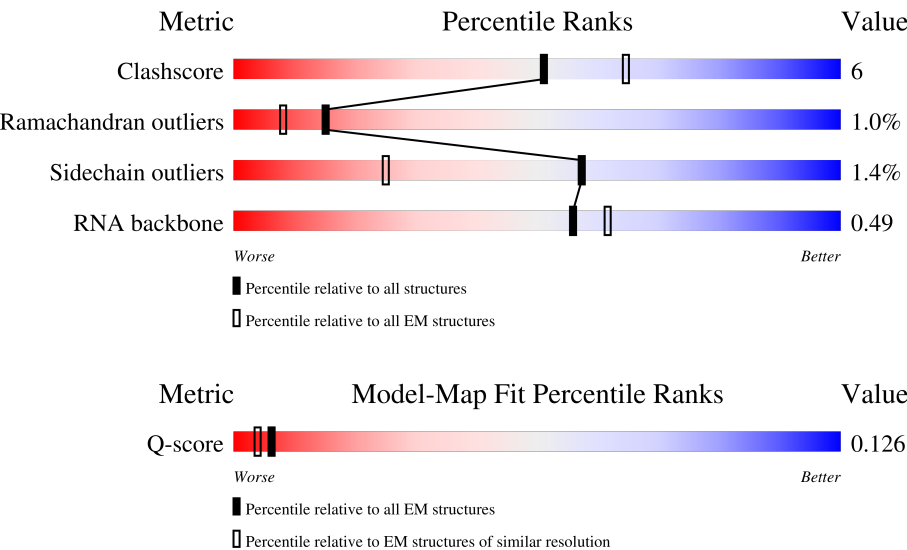
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.48 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	2912 (3.99 - 4.98)

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	O	120	
2	P	275	
3	Q	209	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	R	201	
5	S	179	
6	T	177	
7	V	142	
8	W	142	
9	X	123	
10	Y	144	
11	Z	137	
12	a	127	
13	b	117	
14	c	115	
15	d	118	
16	e	103	
17	f	110	
18	g	100	
19	h	104	
20	i	94	
21	j	85	
22	k	78	
23	l	63	
24	m	59	
25	n	57	
26	o	55	
27	p	47	
28	q	67	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	r	55	
30	N	2903	
31	L	70	
32	C	223	
33	U	149	
34	M	75	
35	x	692	
36	0	1539	
37	1	244	
38	2	237	
39	3	206	
40	4	162	
41	5	131	
42	6	152	
43	7	130	
44	8	130	
45	9	110	
46	A	129	
47	B	124	
48	D	118	
49	E	101	
50	F	89	
51	G	100	
52	H	84	
53	I	75	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	J	92	25% 65% 16% • • 14%
55	K	87	8% 74% 22% • • •
56	s	88	15% 43% 13% • 42%
57	t	557	24% 24% • 74%
58	u	73	21% 67% 27% 5%

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 147973 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 5S rRNA.

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

- Molecule 2 is a protein called 50S ribosomal protein L2.

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 4 is a protein called 50S ribosomal protein L4.

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

- Molecule 5 is a protein called 50S ribosomal protein L5.

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

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 7 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 9 is a protein called 50S ribosomal protein L14.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	a	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	conflict	UNP P0AG44

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	b	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	c	114	Total	C	N	O	S	0	0
			915	573	179	162	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	d	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	conflict	UNP P0ADZ0

- Molecule 19 is a protein called 50S ribosomal protein L24.

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

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	i	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	j	75	Total	C	N	O	S	0	0
			568	353	113	101	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	3	UNK	HIS	conflict	UNP P0A7L8

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	k	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	m	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	n	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 26 is a protein called 50S ribosomal protein L33.

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

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	p	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	q	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	2897	Total	C	N	O	P	1	0
			62215	27754	11448	20115	2898		

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L	52	Total	C	N	O	S	0	0
			404	250	73	75	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	conflict	UNP P0A7M9

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	C	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	75	Total	C	N	O	P	0	0
			1594	711	281	527	75		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	x	14	Total	C	N	O	P	0	0
			294	132	51	97	14		

- Molecule 36 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	0	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	conflict	UNP P0A7W1

- Molecule 41 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	101	SER	PRO	conflict	UNP P02358

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	conflict	UNP P0A7X3

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	ALA	PRO	conflict	UNP P0A7R9

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	D	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	VAL	MET	conflict	UNP P0A7S9

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	E	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	ALA	ASP	conflict	UNP P0AG59

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	G	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	H	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	2	ALA	THR	conflict	UNP P0AG63

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	I	55	Total	C	N	O	0	0
			455	288	86	81		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	15	THR	ALA	conflict	UNP P0A7T7
I	19	VAL	GLN	conflict	UNP P0A7T7

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	J	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	K	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	LEU	MET	conflict	UNP P0A7U7

- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	s	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 57 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	t	143	Total	C	N	O		0	0
			704	418	143	143			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	241	VAL	ILE	conflict	UNP P0AG67

- Molecule 58 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	73	Total	C	N	O	P	0	0
			1561	695	279	514	73		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	3	G	C	conflict	GB 1851743410
u	70	C	G	conflict	GB 1851743410

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	u	2	Total	Mg	0
			2	2	

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
60	u	1	Total	K	0
			1	1	

- Molecule 61 is water.

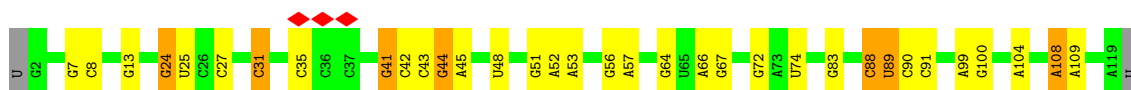
Mol	Chain	Residues	Atoms		AltConf
61	u	9	Total	O	0
			9	9	

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.

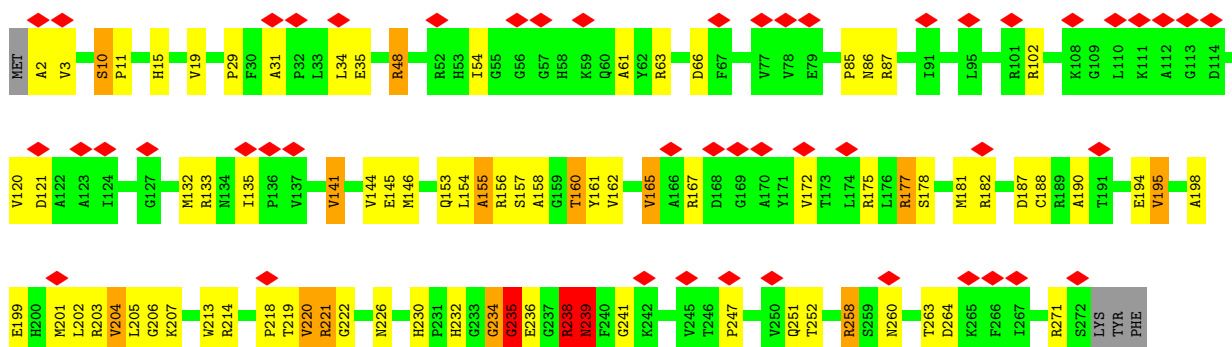
• Molecule 1: 5S rRNA

Chain O: 



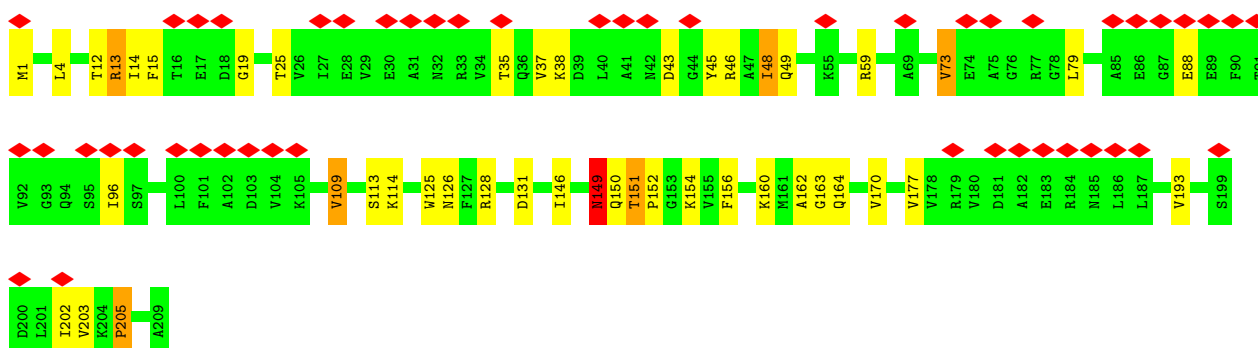
• Molecule 2: 50S ribosomal protein L2

Chain P: 

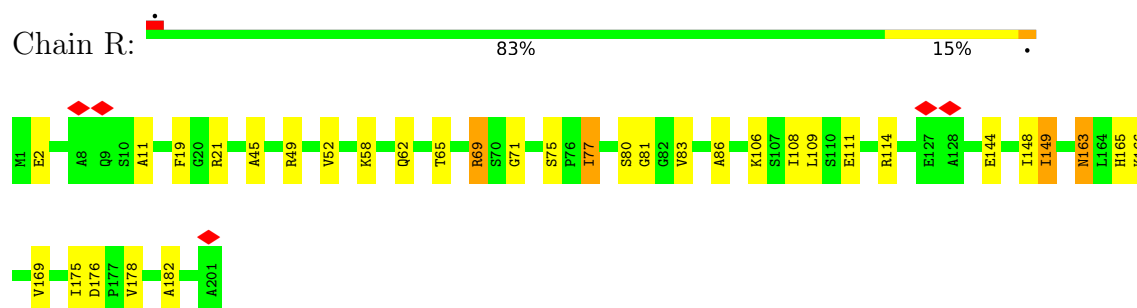


• Molecule 3: 50S ribosomal protein L3

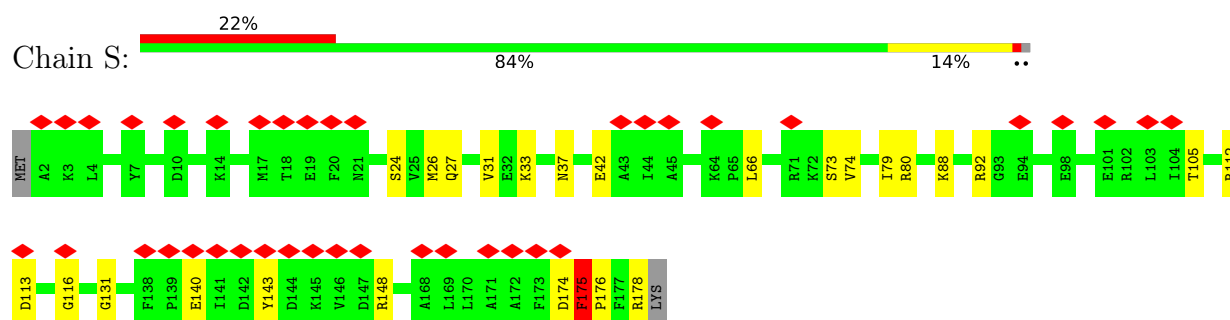
Chain Q: 



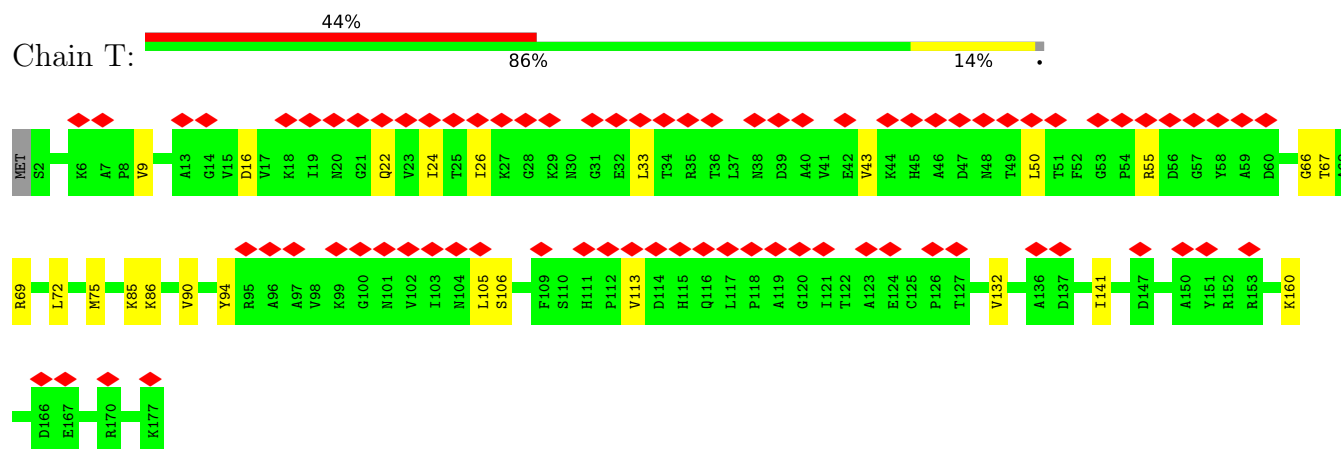
- Molecule 4: 50S ribosomal protein L4



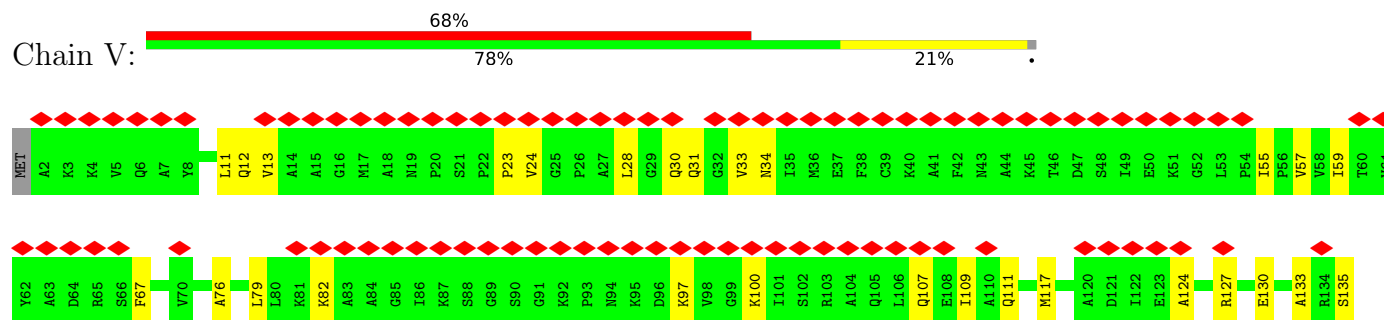
- Molecule 5: 50S ribosomal protein L5

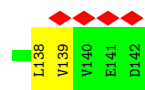


- Molecule 6: 50S ribosomal protein L6

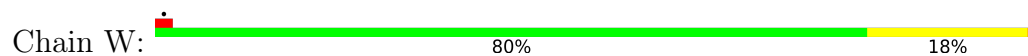


- Molecule 7: 50S ribosomal protein L11

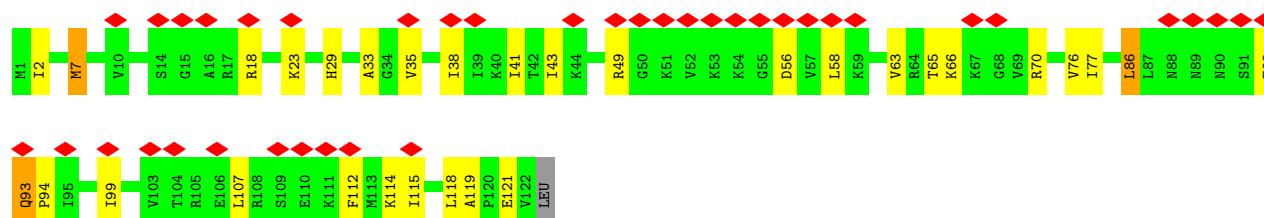
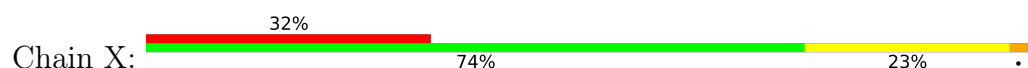




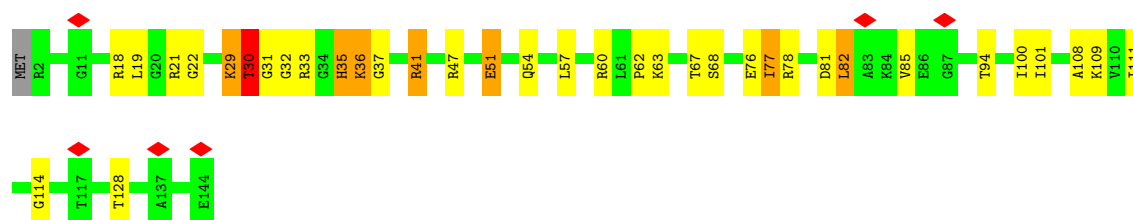
- Molecule 8: 50S ribosomal protein L13



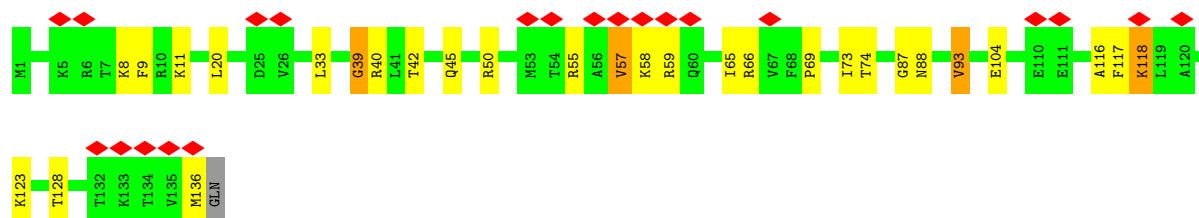
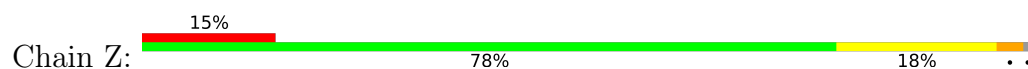
- Molecule 9: 50S ribosomal protein L14



- Molecule 10: 50S ribosomal protein L15

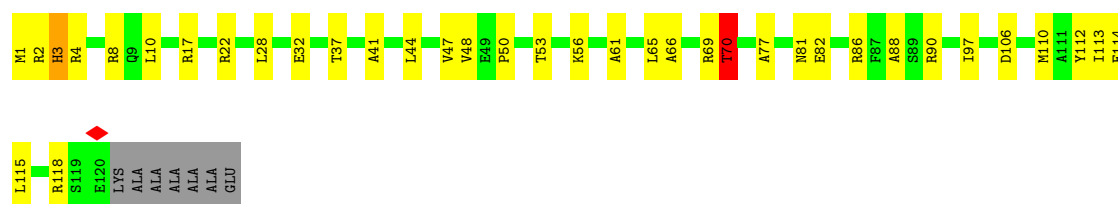


- Molecule 11: 50S ribosomal protein L16



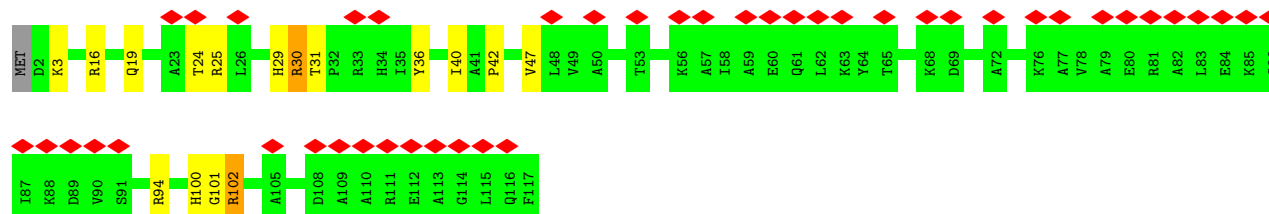
- Molecule 12: 50S ribosomal protein L17





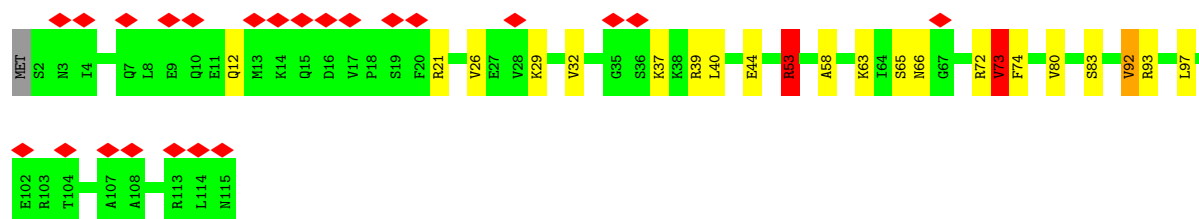
- Molecule 13: 50S ribosomal protein L18

Chain b: 38% 85% 12% ..



- Molecule 14: 50S ribosomal protein L19

Chain c: 20% 80% 17% ...



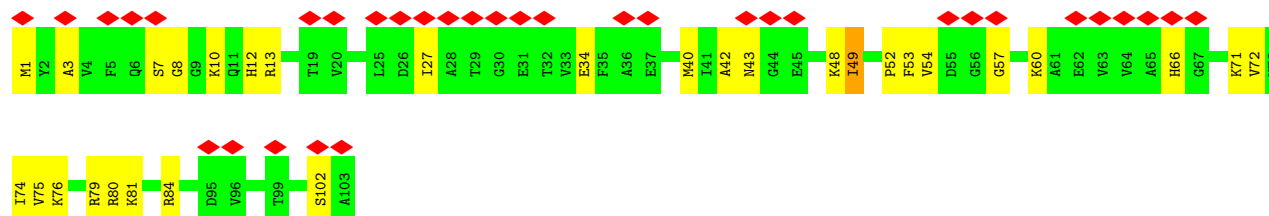
- Molecule 15: 50S ribosomal protein L20

Chain d: 8% 77% 18% ..

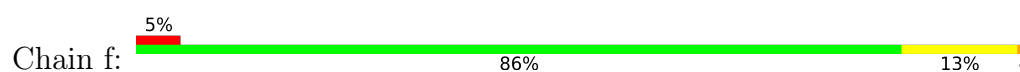


- Molecule 16: 50S ribosomal protein L21

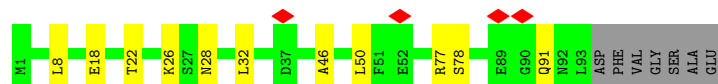
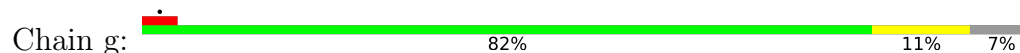
Chain e: 33% 71% 28% .



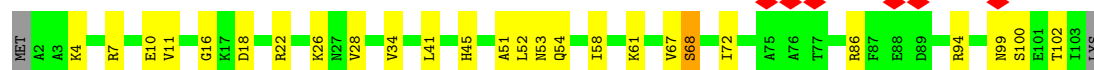
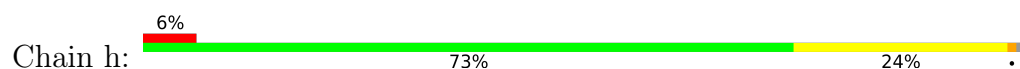
- Molecule 17: 50S ribosomal protein L22



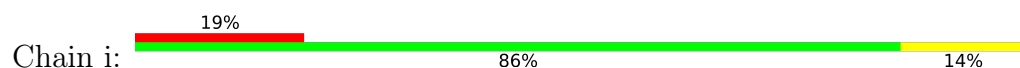
- Molecule 18: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L24



- Molecule 20: 50S ribosomal protein L25



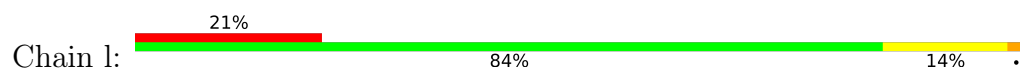
- Molecule 21: 50S ribosomal protein L27

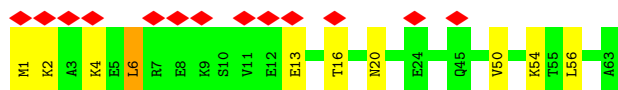


- Molecule 22: 50S ribosomal protein L28



- Molecule 23: 50S ribosomal protein L29

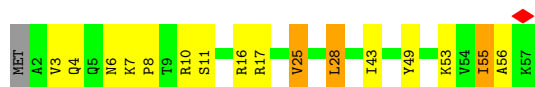




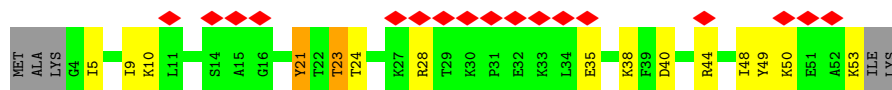
- Molecule 24: 50S ribosomal protein L30



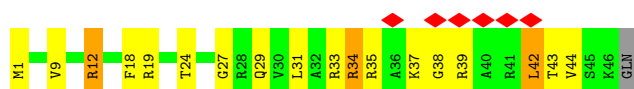
- Molecule 25: 50S ribosomal protein L32



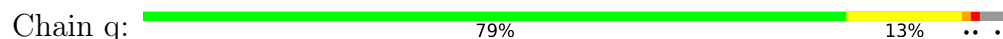
- Molecule 26: 50S ribosomal protein L33



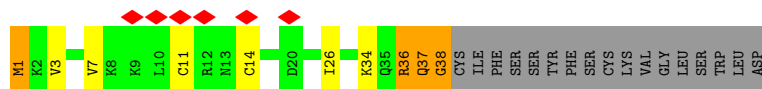
- Molecule 27: 50S ribosomal protein L34



- Molecule 28: 50S ribosomal protein L35

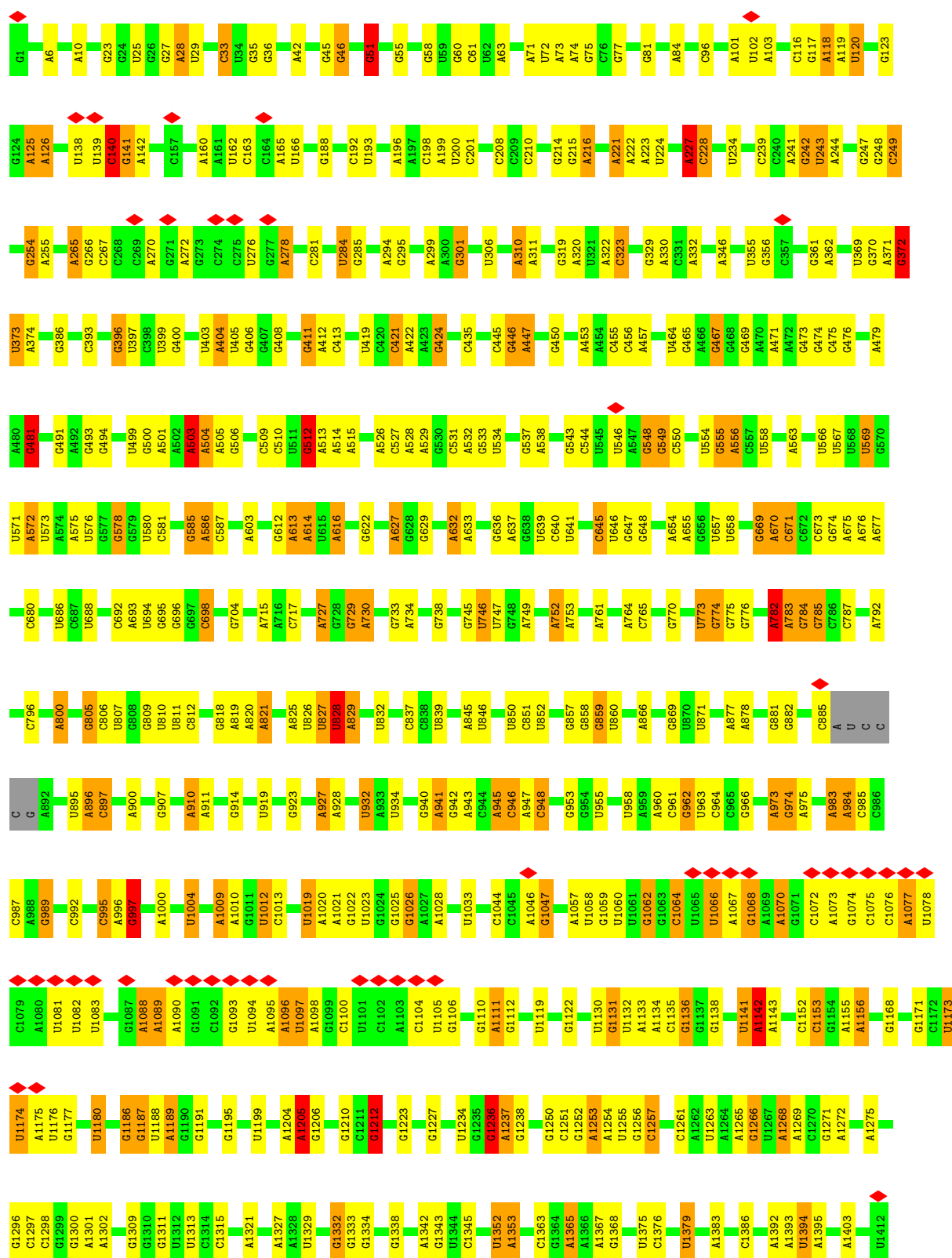


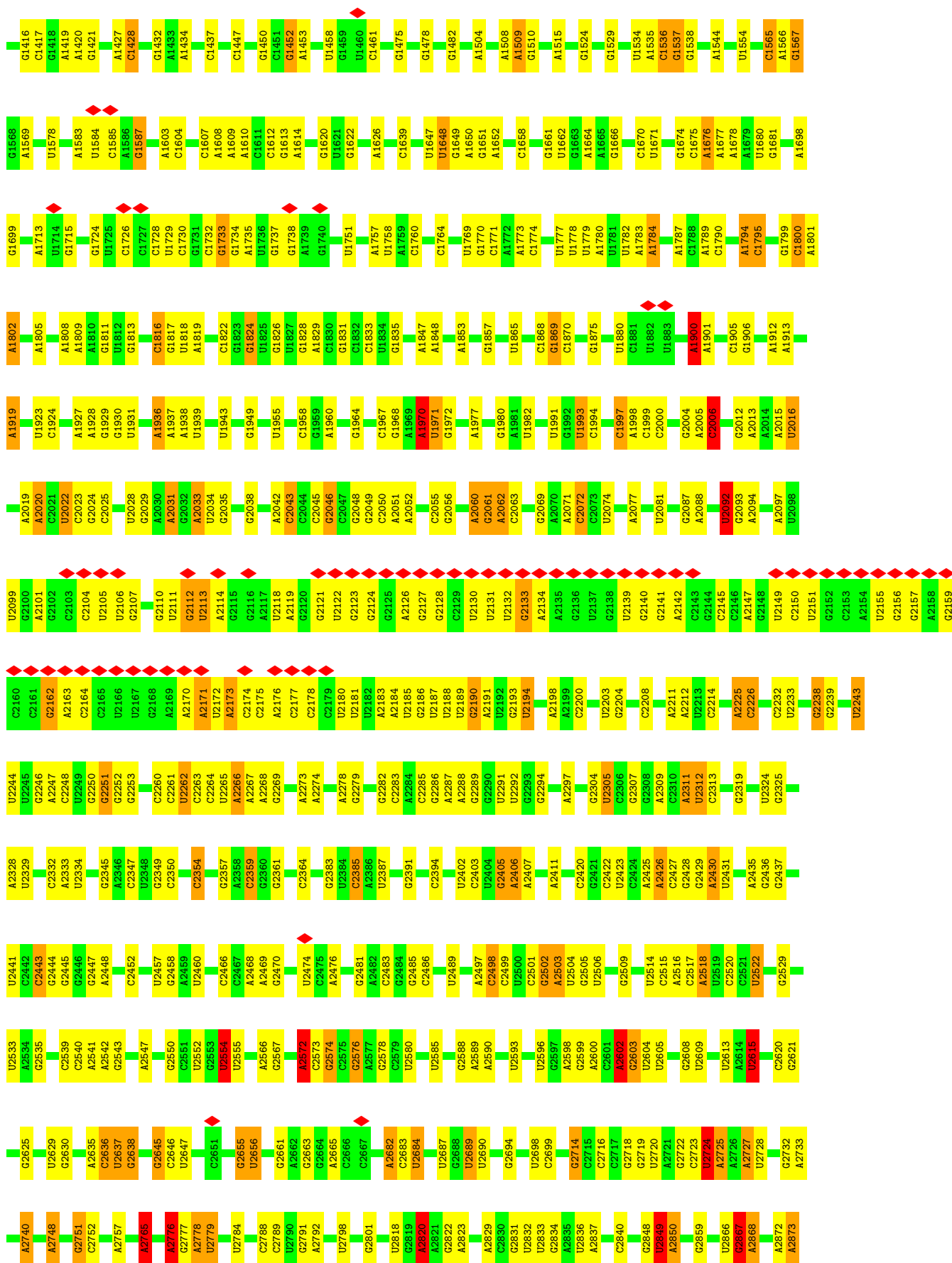
- Molecule 29: 50S ribosomal protein L36

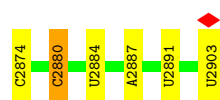


- Molecule 30: 23S rRNA

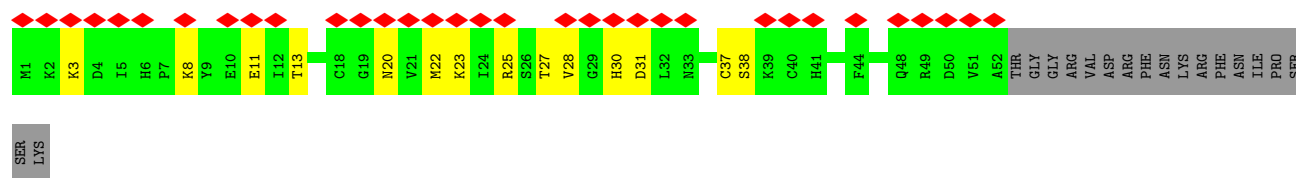
Chain N:  64% 28% 7%



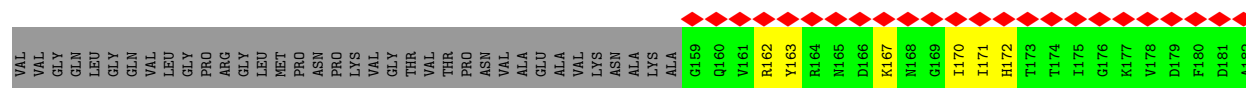
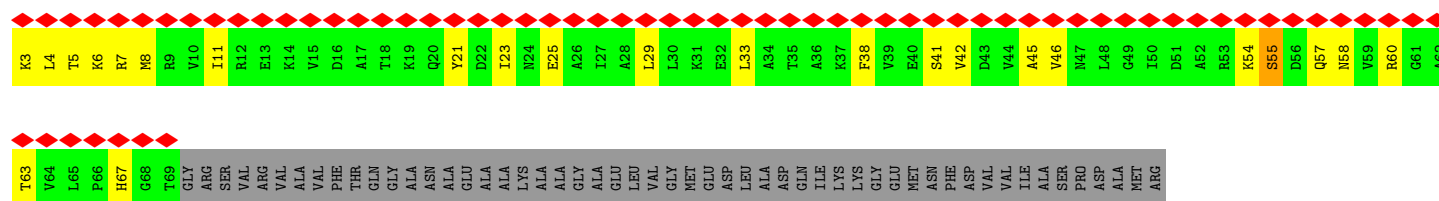




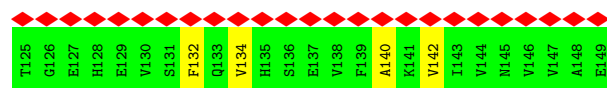
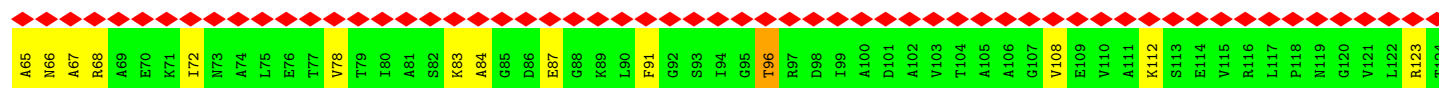
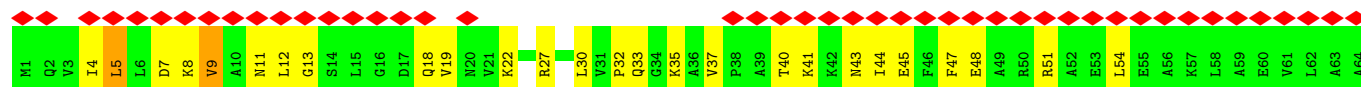
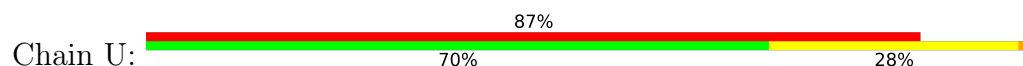
• Molecule 31: 50S ribosomal protein L31



• Molecule 32: 50S ribosomal protein L1

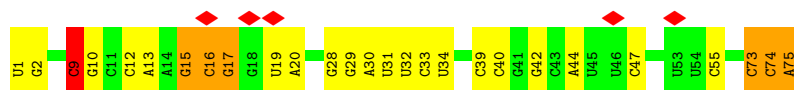


• Molecule 33: 50S ribosomal protein L9



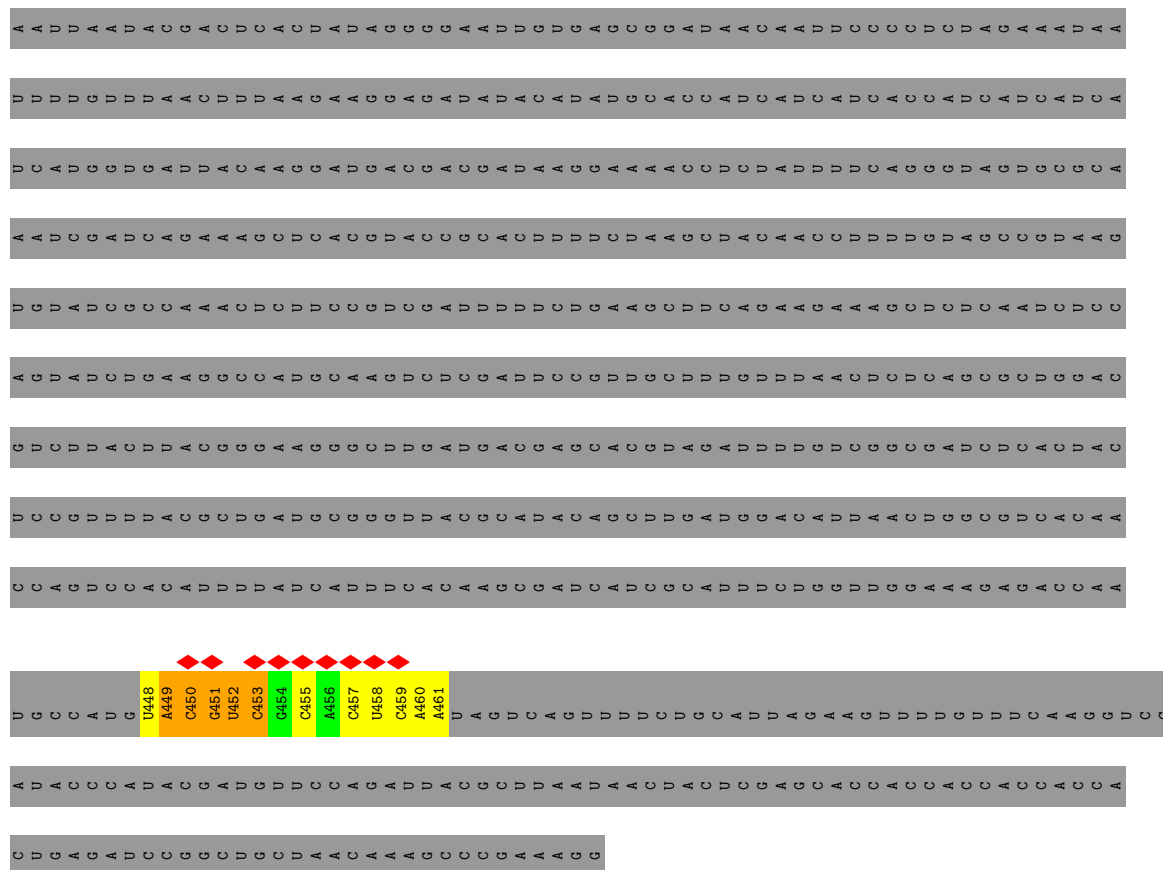
• Molecule 34: P-site tRNA





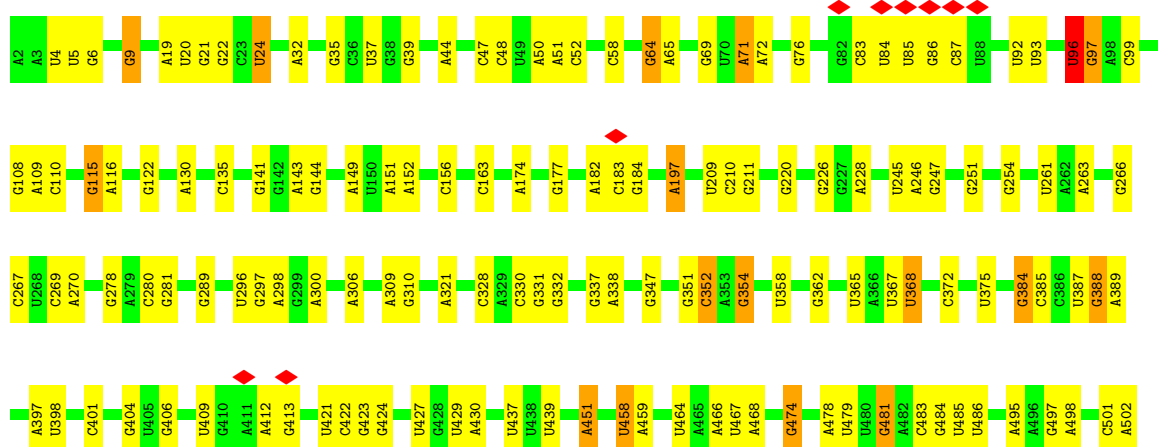
• Molecule 35: mRNA

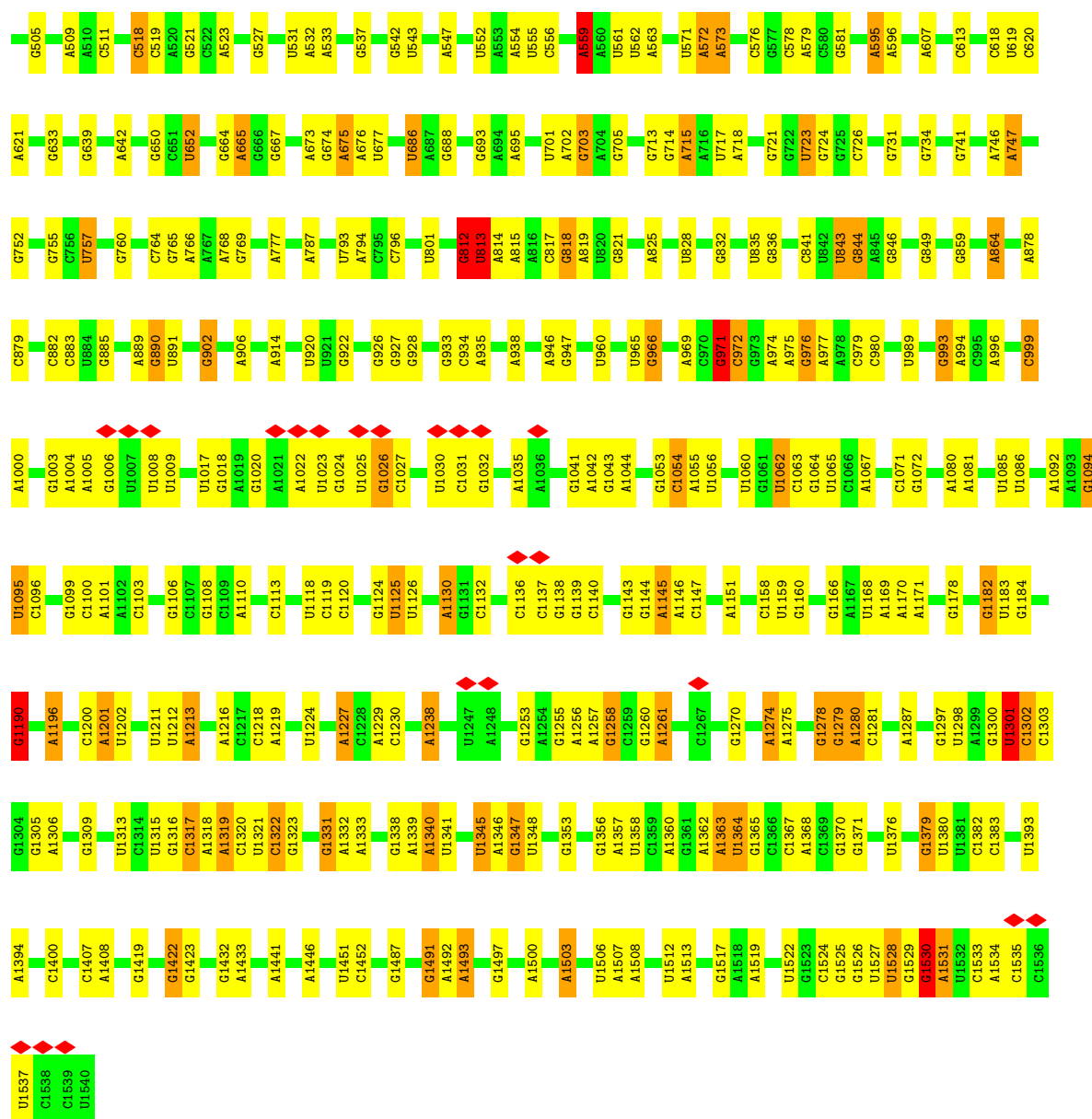
Chain x: 98%



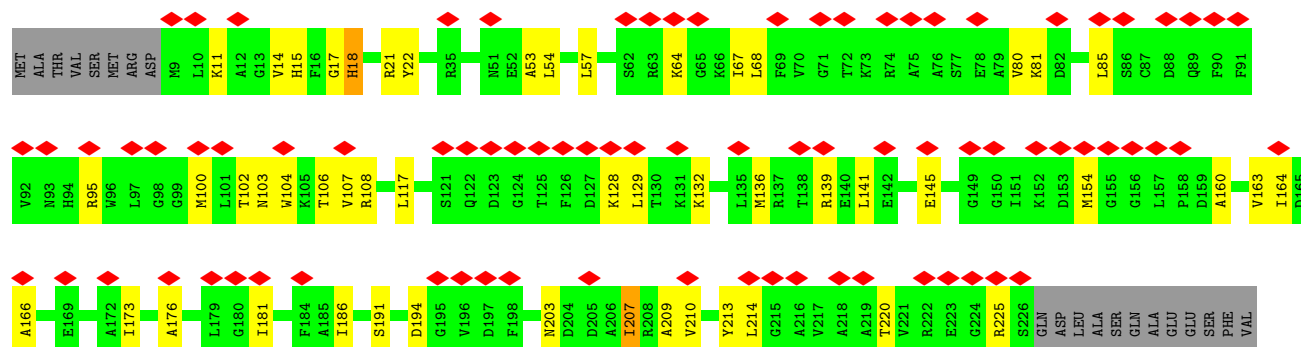
• Molecule 36: 16S rRNA

Chain 0: 68% 27% 5%



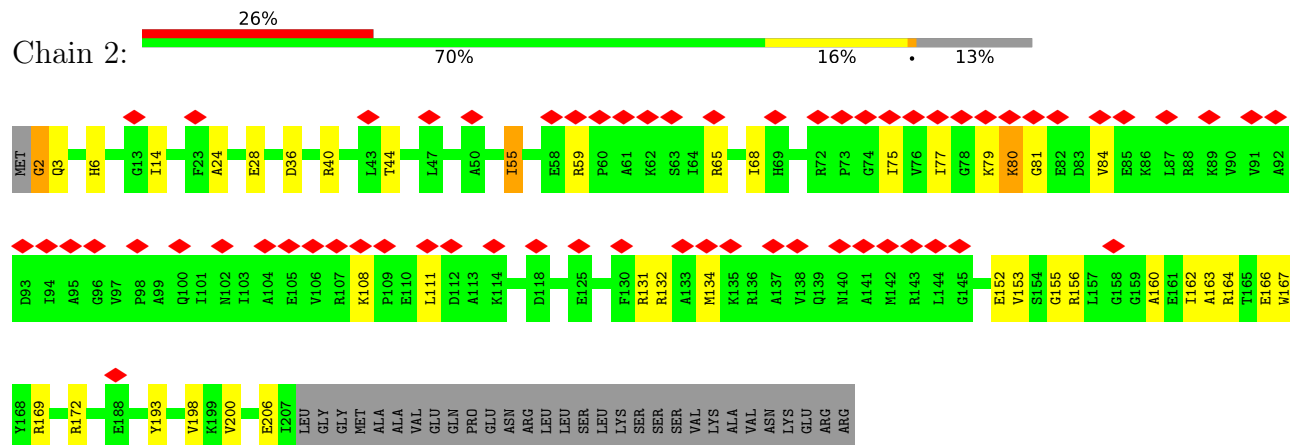


• Molecule 37: 30S ribosomal protein S2

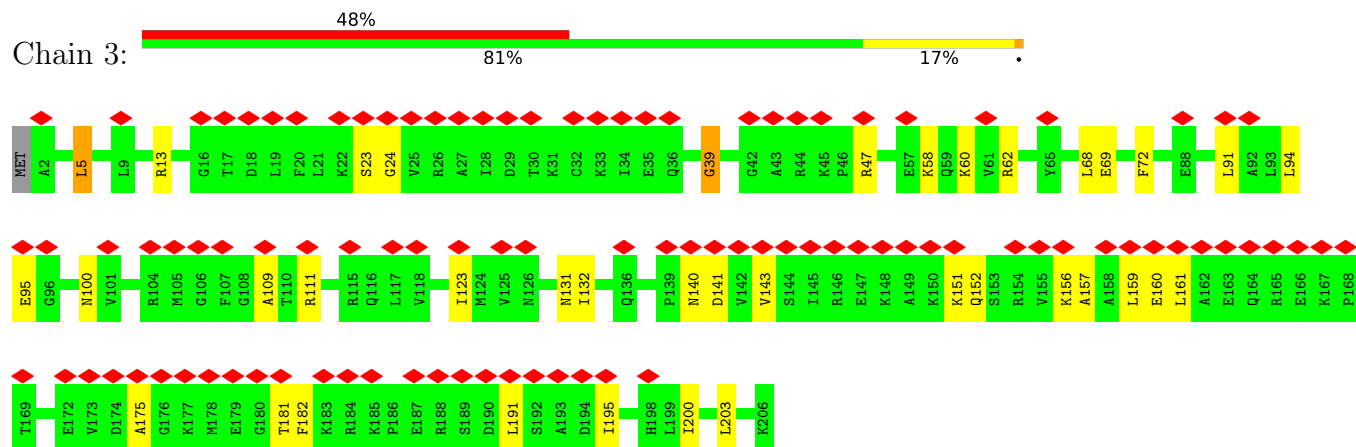


GLU
LEU
SER
ASN
LYS
ALA

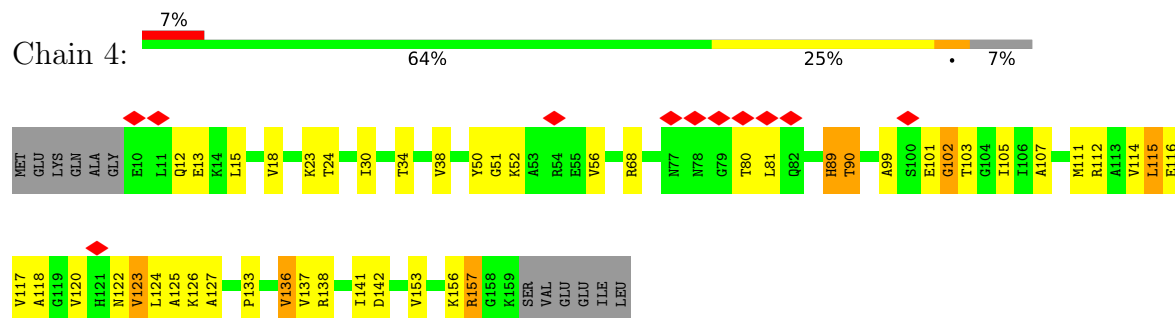
• Molecule 38: 30S ribosomal protein S3



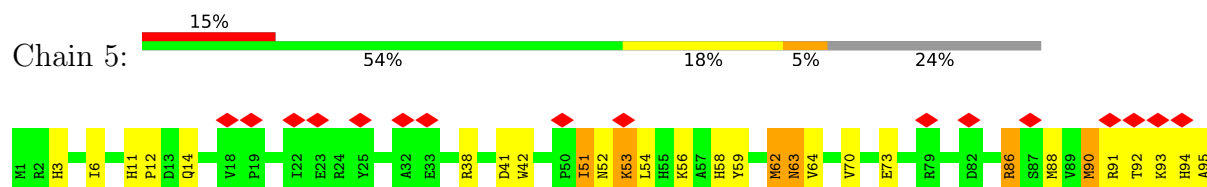
• Molecule 39: 30S ribosomal protein S4

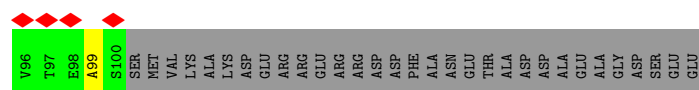


• Molecule 40: 30S ribosomal protein S5

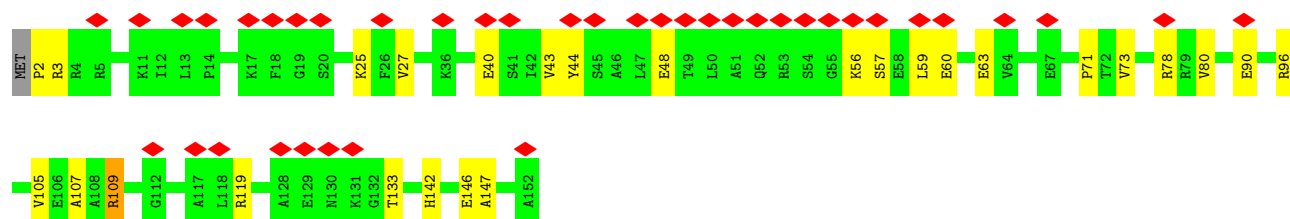
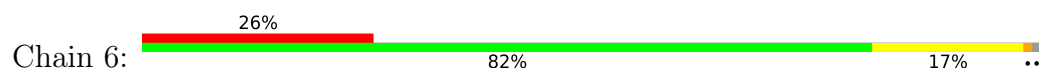


• Molecule 41: 30S ribosomal protein S6, non-modified isoform

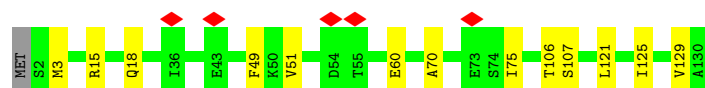
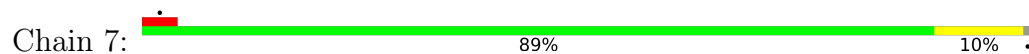




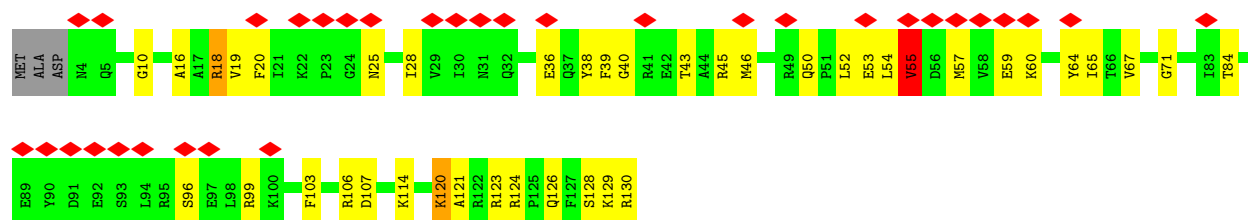
• Molecule 42: 30S ribosomal protein S7



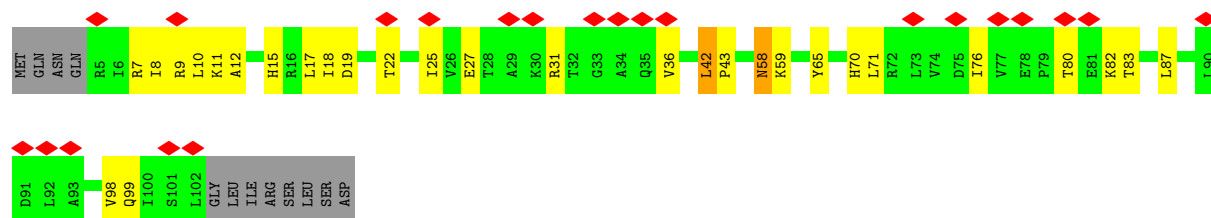
• Molecule 43: 30S ribosomal protein S8



• Molecule 44: 30S ribosomal protein S9

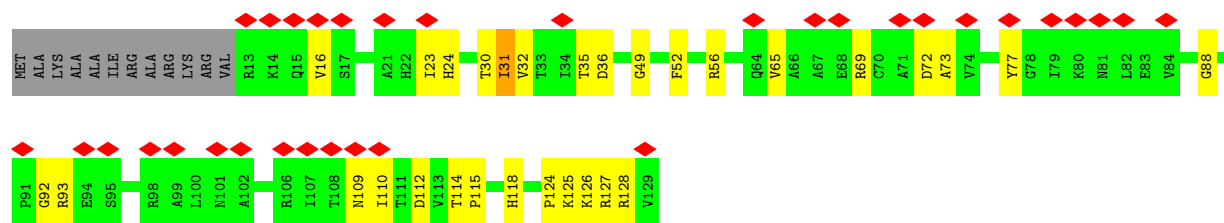


• Molecule 45: 30S ribosomal protein S10

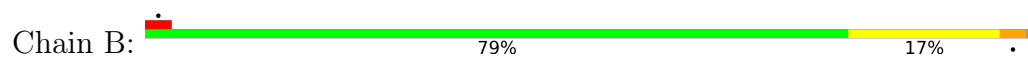


• Molecule 46: 30S ribosomal protein S11

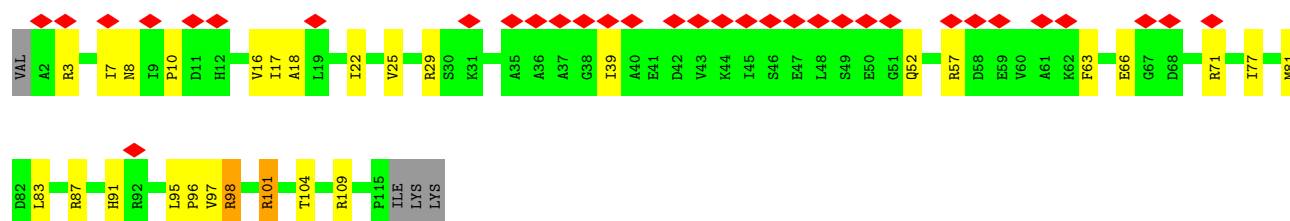
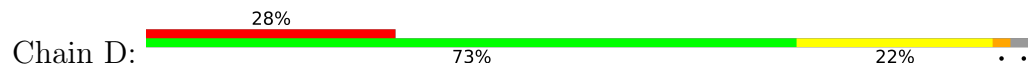




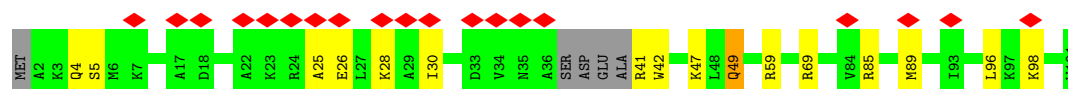
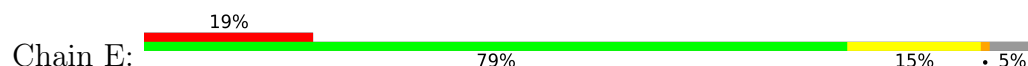
- Molecule 47: 30S ribosomal protein S12



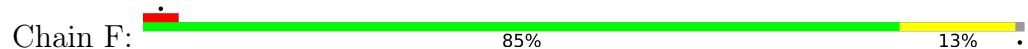
- Molecule 48: 30S ribosomal protein S13



- Molecule 49: 30S ribosomal protein S14



- Molecule 50: 30S ribosomal protein S15



- Molecule 51: 30S ribosomal protein S16



- Molecule 52: 30S ribosomal protein S17

Chain H:  80% 13% .. 5%



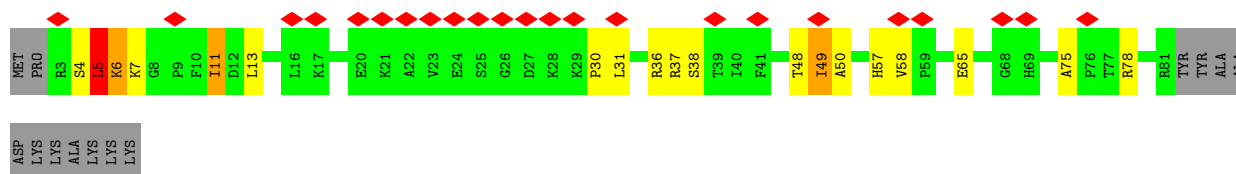
- Molecule 53: 30S ribosomal protein S18

Chain I:  45% 27% . 27%



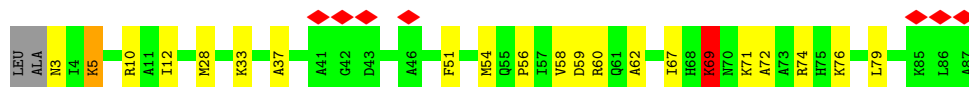
- Molecule 54: 30S ribosomal protein S19

Chain J:  25% 65% 16% . . 14%

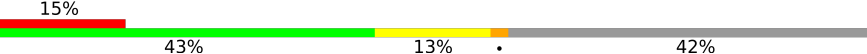


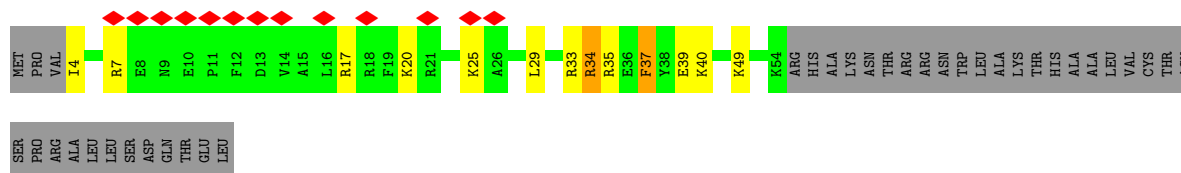
- Molecule 55: 30S ribosomal protein S20

Chain K:  8% 74% 22% . . .



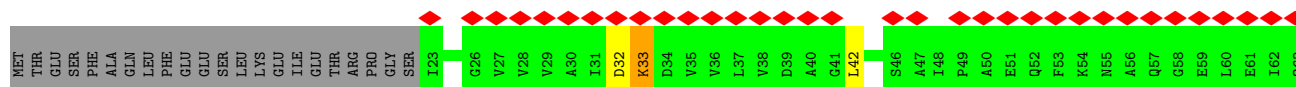
- Molecule 56: 30S ribosomal protein S21

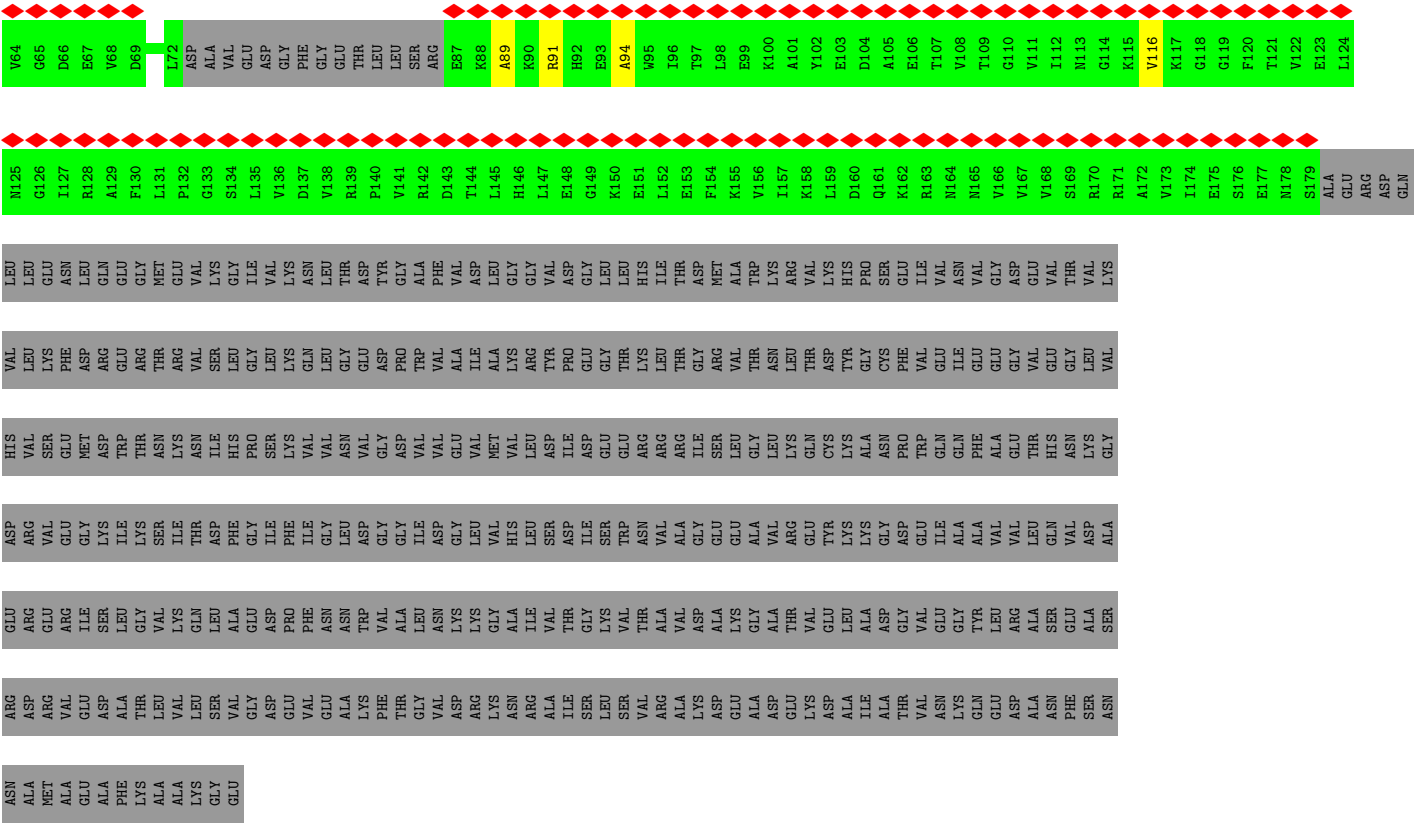
Chain s:  15% 43% 13% . 42%



- Molecule 57: 30S ribosomal protein S1

Chain t:  24% 24% . 74%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75081	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.366	Depositor
Minimum map value	-0.728	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.144	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	654.0, 654.0, 654.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	O	0.65	1/2828 (0.0%)	0.83	7/4410 (0.2%)
2	P	1.71	40/2121 (1.9%)	1.42	17/2852 (0.6%)
3	Q	1.54	14/1585 (0.9%)	1.29	10/2134 (0.5%)
4	R	1.21	8/1571 (0.5%)	1.09	5/2113 (0.2%)
5	S	0.84	0/1434	0.89	0/1926
6	T	0.83	0/1342	0.87	0/1816
7	V	0.77	0/1045	0.74	0/1410
8	W	1.42	10/1151 (0.9%)	1.10	0/1551
9	X	1.53	8/947 (0.8%)	1.27	4/1268 (0.3%)
10	Y	1.65	14/1053 (1.3%)	1.44	7/1403 (0.5%)
11	Z	1.42	4/1092 (0.4%)	1.20	2/1460 (0.1%)
12	a	1.65	10/973 (1.0%)	1.35	5/1301 (0.4%)
13	b	1.05	1/901 (0.1%)	1.04	5/1209 (0.4%)
14	c	1.38	4/927 (0.4%)	1.21	4/1240 (0.3%)
15	d	1.57	7/959 (0.7%)	1.33	8/1278 (0.6%)
16	e	1.40	6/828 (0.7%)	1.21	1/1107 (0.1%)
17	f	1.33	2/864 (0.2%)	1.14	1/1156 (0.1%)
18	g	1.22	0/744	1.11	0/994
19	h	1.01	1/787 (0.1%)	1.06	0/1051
20	i	0.96	0/765	0.90	0/1025
21	j	1.50	5/575 (0.9%)	1.38	6/762 (0.8%)
22	k	1.35	1/634 (0.2%)	1.16	2/848 (0.2%)
23	l	0.90	0/509	1.00	0/677
24	m	1.18	0/452	1.15	1/605 (0.2%)
25	n	1.48	2/449 (0.4%)	1.40	6/599 (1.0%)
26	o	1.44	5/416 (1.2%)	1.02	0/554
27	p	1.73	5/379 (1.3%)	1.61	5/498 (1.0%)
28	q	1.50	0/512	1.35	2/676 (0.3%)
29	r	1.43	3/302 (1.0%)	1.34	3/397 (0.8%)
30	N	0.95	272/69681 (0.4%)	0.95	167/108706 (0.2%)
31	L	0.74	0/411	0.84	0/550
32	C	0.32	0/1034	0.81	1/1387 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	U	0.33	0/1122	0.96	4/1515 (0.3%)
34	M	0.51	0/1779	0.77	3/2768 (0.1%)
35	x	0.41	0/327	0.69	0/506
36	0	0.76	33/36966 (0.1%)	0.85	49/57666 (0.1%)
37	1	1.00	1/1735 (0.1%)	0.98	2/2338 (0.1%)
38	2	1.08	4/1651 (0.2%)	0.97	3/2225 (0.1%)
39	3	0.97	2/1664 (0.1%)	1.03	2/2227 (0.1%)
40	4	1.53	6/1118 (0.5%)	1.35	7/1504 (0.5%)
41	5	1.16	5/835 (0.6%)	1.14	3/1128 (0.3%)
42	6	0.83	0/1195	0.86	1/1602 (0.1%)
43	7	1.15	1/988 (0.1%)	1.05	0/1326
44	8	1.09	1/1033 (0.1%)	1.13	2/1375 (0.1%)
45	9	0.95	1/796 (0.1%)	1.02	2/1077 (0.2%)
46	A	1.11	0/892	1.12	3/1205 (0.2%)
47	B	1.37	5/968 (0.5%)	1.24	3/1300 (0.2%)
48	D	1.09	1/892 (0.1%)	1.07	0/1193
49	E	1.10	0/784	1.14	1/1043 (0.1%)
50	F	1.20	2/717 (0.3%)	1.03	1/959 (0.1%)
51	G	1.18	3/658 (0.5%)	1.19	5/884 (0.6%)
52	H	1.08	1/657 (0.2%)	1.06	1/881 (0.1%)
53	I	1.20	0/462	1.15	1/621 (0.2%)
54	J	1.02	1/652 (0.2%)	1.00	1/877 (0.1%)
55	K	1.19	2/670 (0.3%)	1.20	2/888 (0.2%)
56	s	1.32	5/430 (1.2%)	1.22	1/570 (0.2%)
57	t	0.59	0/702	0.91	0/973
58	u	0.51	0/1744	0.72	0/2716
All	All	0.99	497/160708 (0.3%)	0.97	366/240330 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	P	0	3
3	Q	0	1
5	S	0	2
10	Y	0	2
11	Z	0	2
19	h	0	1
28	q	0	1
30	N	0	6

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
36	0	0	5
37	1	0	2
38	2	0	2
40	4	0	5
41	5	0	2
44	8	0	4
46	A	0	1
47	B	0	2
52	H	0	2
54	J	0	1
55	K	0	1
56	s	0	1
All	All	0	46

The worst 5 of 497 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	N	2502	G	P-OP2	14.13	1.77	1.49
30	N	1156	A	P-OP2	12.90	1.74	1.49
30	N	1333	G	P-OP2	10.90	1.70	1.49
30	N	783	A	P-OP2	10.79	1.70	1.49
40	4	127	ALA	C-O	-10.54	1.10	1.23

The worst 5 of 366 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	M	73	C	O3'-P-O5'	18.22	131.33	104.00
3	Q	151	THR	CA-C-N	12.71	134.22	119.47
3	Q	151	THR	C-N-CA	12.71	134.22	119.47
30	N	1936	A	C4'-C3'-O3'	-11.05	96.43	113.00
30	N	2725	A	C3'-C2'-O2'	-10.61	94.78	110.70

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	P	195	VAL	Peptide
2	P	234	GLY	Peptide
2	P	238	ARG	Peptide
3	Q	151	THR	Peptide
5	S	174	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	2529	0	1281	11	0
2	P	2082	0	2154	55	0
3	Q	1564	0	1616	24	0
4	R	1552	0	1619	18	0
5	S	1410	0	1443	33	0
6	T	1322	0	1371	14	0
7	V	1031	0	1085	21	0
8	W	1128	0	1162	15	0
9	X	938	0	1012	19	0
10	Y	1044	0	1117	18	0
11	Z	1073	0	1157	17	0
12	a	960	0	1000	15	0
13	b	891	0	923	9	0
14	c	915	0	958	14	0
15	d	946	0	1019	21	0
16	e	815	0	839	19	0
17	f	857	0	922	10	0
18	g	738	0	807	5	0
19	h	779	0	831	11	0
20	i	752	0	780	9	0
21	j	568	0	581	10	0
22	k	624	0	652	15	0
23	l	508	0	543	7	0
24	m	448	0	488	2	0
25	n	443	0	458	13	0
26	o	409	0	440	6	0
27	p	376	0	418	16	0
28	q	503	0	572	12	0
29	r	301	0	341	7	0
30	N	62215	0	31274	421	0
31	L	404	0	405	11	0
32	C	1027	0	1091	43	0
33	U	1111	0	1148	52	0
34	M	1594	0	809	110	0
35	x	294	0	150	38	0
36	0	33015	0	16607	244	0
37	1	1704	0	1731	39	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	2	1624	0	1696	48	0
39	3	1642	0	1704	31	0
40	4	1105	0	1148	21	0
41	5	817	0	808	17	0
42	6	1181	0	1238	17	0
43	7	978	0	1031	6	0
44	8	1021	0	1070	36	0
45	9	786	0	828	19	0
46	A	876	0	887	23	0
47	B	954	0	1016	18	0
48	D	883	0	939	24	0
49	E	773	0	824	12	0
50	F	709	0	728	16	0
51	G	648	0	666	9	0
52	H	648	0	691	6	0
53	I	455	0	478	13	0
54	J	637	0	665	10	0
55	K	664	0	714	17	0
56	s	425	0	449	13	0
57	t	704	0	327	3	0
58	u	1561	0	785	44	0
59	u	2	0	0	0	0
60	u	1	0	0	0	0
61	u	9	0	0	0	0
All	All	147973	0	99496	1314	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 6.

The worst 5 of 1314 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)
35:x:448:U:C6	38:2:162:ILE:HD11	1.46	1.47
30:N:306:U:H3	30:N:310:A:N6	1.15	1.41
35:x:451:G:N3	39:3:47:ARG:HD3	1.35	1.39
2:P:133:ARG:CD	33:U:123:ARG:NH1	1.86	1.37
35:x:448:U:C5	38:2:162:ILE:HD11	1.60	1.37

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	
2	P	269/275 (98%)	247 (92%)	18 (7%)	4 (2%)	8	38
3	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	24	63
4	R	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
5	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	21	59
6	T	174/177 (98%)	164 (94%)	10 (6%)	0	100	100
7	V	139/142 (98%)	112 (81%)	27 (19%)	0	100	100
8	W	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
9	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	7	35
10	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	4	24
11	Z	134/137 (98%)	118 (88%)	11 (8%)	5 (4%)	2	20
12	a	118/127 (93%)	103 (87%)	13 (11%)	2 (2%)	7	35
13	b	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
14	c	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
15	d	115/118 (98%)	115 (100%)	0	0	100	100
16	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12	47
17	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	50
18	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	5	29
19	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	6	31
20	i	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
21	j	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
22	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	9	41
23	l	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
24	m	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
25	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
26	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	p	44/47 (94%)	40 (91%)	4 (9%)	0	100	100
28	q	62/67 (92%)	56 (90%)	5 (8%)	1 (2%)	7	37
29	r	36/55 (66%)	35 (97%)	1 (3%)	0	100	100
31	L	50/70 (71%)	44 (88%)	5 (10%)	1 (2%)	6	31
32	C	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
33	U	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	9	39
37	1	216/244 (88%)	188 (87%)	27 (12%)	1 (0%)	24	63
38	2	204/237 (86%)	186 (91%)	16 (8%)	2 (1%)	12	47
39	3	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
40	4	148/162 (91%)	116 (78%)	30 (20%)	2 (1%)	9	39
41	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1	13
42	6	149/152 (98%)	139 (93%)	10 (7%)	0	100	100
43	7	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
44	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	7	37
45	9	96/110 (87%)	84 (88%)	9 (9%)	3 (3%)	3	22
46	A	115/129 (89%)	102 (89%)	13 (11%)	0	100	100
47	B	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	7	35
48	D	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	14	50
49	E	92/101 (91%)	78 (85%)	13 (14%)	1 (1%)	11	45
50	F	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
51	G	80/100 (80%)	69 (86%)	10 (12%)	1 (1%)	9	41
52	H	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	2	19
53	I	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	6	32
54	J	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
55	K	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	43
56	s	49/88 (56%)	40 (82%)	9 (18%)	0	100	100
57	t	139/557 (25%)	115 (83%)	21 (15%)	3 (2%)	5	29
All	All	5936/6871 (86%)	5354 (90%)	522 (9%)	60 (1%)	15	47

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	239	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	Y	36	LYS
11	Z	58	LYS
16	e	53	PHE
25	n	55	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	216/220 (98%)	213 (99%)	3 (1%)	59	71
3	Q	164/164 (100%)	159 (97%)	5 (3%)	36	56
4	R	165/165 (100%)	162 (98%)	3 (2%)	51	66
5	S	148/150 (99%)	147 (99%)	1 (1%)	76	79
6	T	137/138 (99%)	137 (100%)	0	100	100
7	V	109/110 (99%)	109 (100%)	0	100	100
8	W	116/116 (100%)	115 (99%)	1 (1%)	70	76
9	X	103/104 (99%)	101 (98%)	2 (2%)	50	66
10	Y	102/103 (99%)	100 (98%)	2 (2%)	48	65
11	Z	109/110 (99%)	108 (99%)	1 (1%)	70	76
12	a	100/102 (98%)	98 (98%)	2 (2%)	48	65
13	b	86/87 (99%)	85 (99%)	1 (1%)	63	73
14	c	98/100 (98%)	95 (97%)	3 (3%)	35	56
15	d	89/90 (99%)	87 (98%)	2 (2%)	45	64
16	e	84/84 (100%)	83 (99%)	1 (1%)	63	73
17	f	93/93 (100%)	93 (100%)	0	100	100
18	g	80/85 (94%)	79 (99%)	1 (1%)	61	72
19	h	83/85 (98%)	81 (98%)	2 (2%)	43	63
20	i	78/78 (100%)	77 (99%)	1 (1%)	61	72
21	j	56/62 (90%)	55 (98%)	1 (2%)	51	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	k	67/68 (98%)	67 (100%)	0	100	100
23	l	55/55 (100%)	54 (98%)	1 (2%)	51	66
24	m	48/49 (98%)	48 (100%)	0	100	100
25	n	47/48 (98%)	46 (98%)	1 (2%)	47	65
26	o	45/49 (92%)	45 (100%)	0	100	100
27	p	38/39 (97%)	38 (100%)	0	100	100
28	q	51/54 (94%)	49 (96%)	2 (4%)	28	50
29	r	34/50 (68%)	33 (97%)	1 (3%)	37	57
31	L	47/63 (75%)	47 (100%)	0	100	100
32	C	110/174 (63%)	109 (99%)	1 (1%)	70	76
33	U	114/114 (100%)	114 (100%)	0	100	100
37	1	180/202 (89%)	178 (99%)	2 (1%)	65	74
38	2	170/196 (87%)	167 (98%)	3 (2%)	51	66
39	3	172/173 (99%)	170 (99%)	2 (1%)	63	73
40	4	113/123 (92%)	107 (95%)	6 (5%)	20	42
41	5	87/112 (78%)	87 (100%)	0	100	100
42	6	124/125 (99%)	123 (99%)	1 (1%)	73	77
43	7	104/105 (99%)	101 (97%)	3 (3%)	37	57
44	8	105/107 (98%)	104 (99%)	1 (1%)	68	76
45	9	86/97 (89%)	85 (99%)	1 (1%)	63	73
46	A	90/98 (92%)	89 (99%)	1 (1%)	65	74
47	B	103/104 (99%)	103 (100%)	0	100	100
48	D	92/96 (96%)	90 (98%)	2 (2%)	45	64
49	E	79/83 (95%)	79 (100%)	0	100	100
50	F	75/77 (97%)	75 (100%)	0	100	100
51	G	65/80 (81%)	64 (98%)	1 (2%)	57	70
52	H	74/77 (96%)	73 (99%)	1 (1%)	59	71
53	I	48/66 (73%)	47 (98%)	1 (2%)	47	65
54	J	70/80 (88%)	66 (94%)	4 (6%)	18	41
55	K	65/66 (98%)	65 (100%)	0	100	100
56	s	44/76 (58%)	43 (98%)	1 (2%)	44	63

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4818/5152 (94%)	4750 (99%)	68 (1%)	57 71

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	A	31	ILE
48	D	98	ARG
54	J	49	ILE
15	d	16	LYS
14	c	73	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
50	F	37	ASN
52	H	31	HIS
55	K	78	ASN
17	f	15	GLN
15	d	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	O	117/120 (97%)	21 (17%)	1 (0%)
30	N	2894/2903 (99%)	521 (18%)	34 (1%)
34	M	74/75 (98%)	11 (14%)	0
35	x	13/692 (1%)	11 (84%)	0
36	0	1538/1539 (99%)	283 (18%)	21 (1%)
58	u	72/73 (98%)	20 (27%)	0
All	All	4708/5402 (87%)	867 (18%)	56 (1%)

5 of 867 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	O	13	G
1	O	25	U
1	O	31	C
1	O	35	C
1	O	41	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	N	2286	G
36	0	1528	U
36	0	64	G
36	0	1491	G
36	0	1190	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

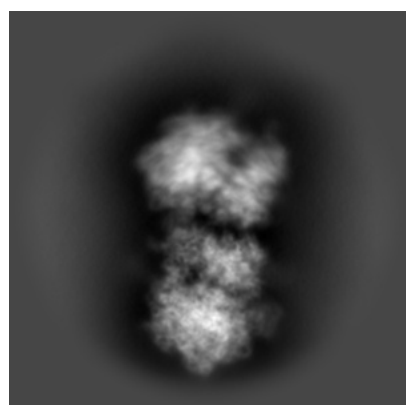
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13955. These allow visual inspection of the internal detail of the map and identification of artifacts.

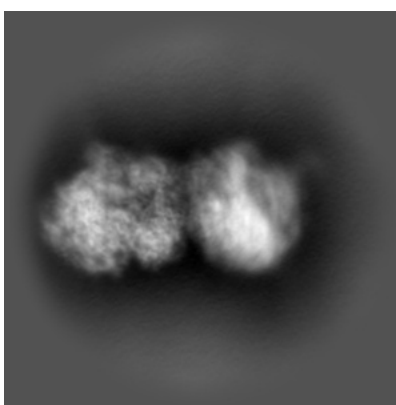
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

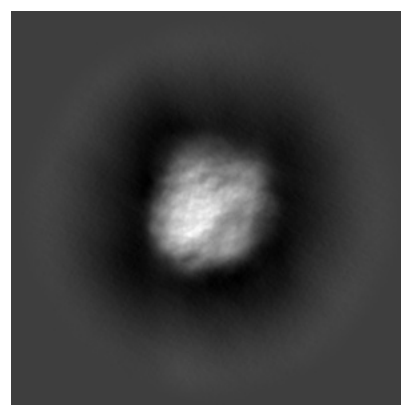
6.1.1 Primary map



X



Y

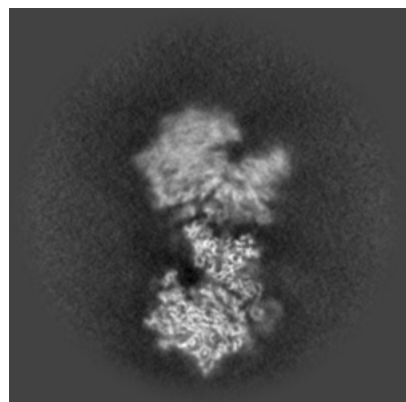


Z

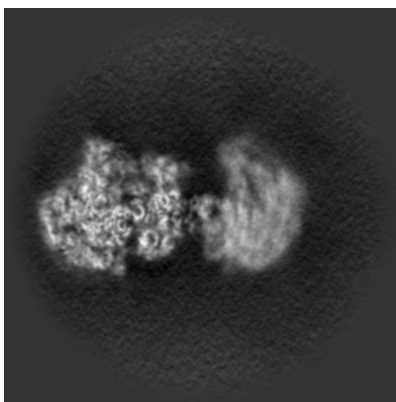
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

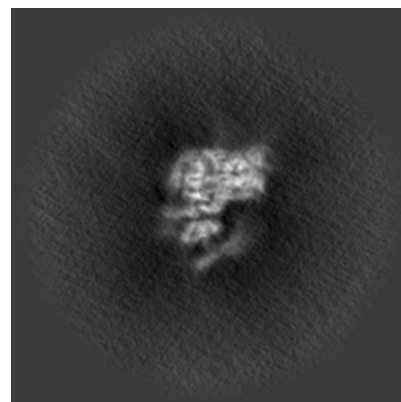
6.2.1 Primary map



X Index: 300



Y Index: 300

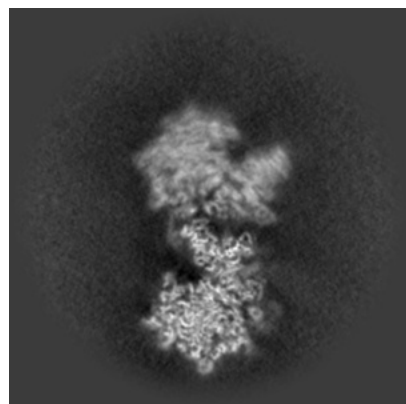


Z Index: 300

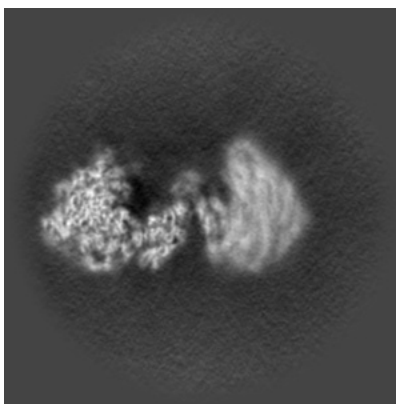
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

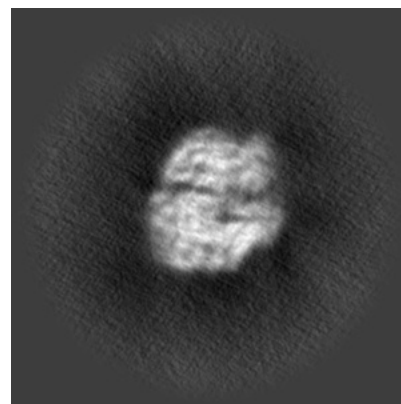
6.3.1 Primary map



X Index: 294



Y Index: 273

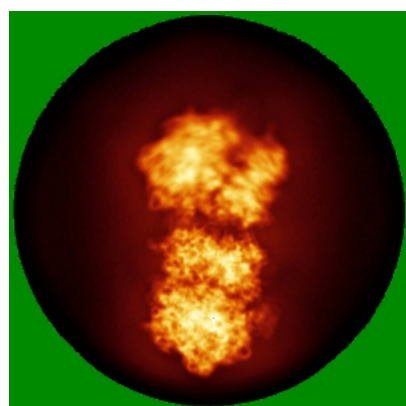


Z Index: 348

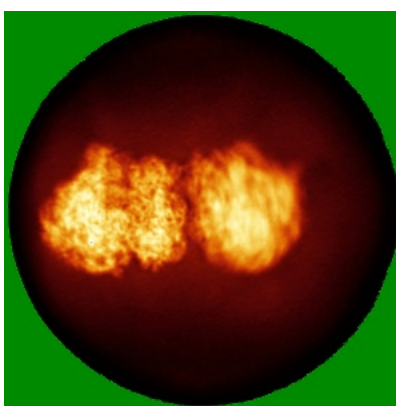
The images above show the largest variance slices of the map in three orthogonal directions.

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

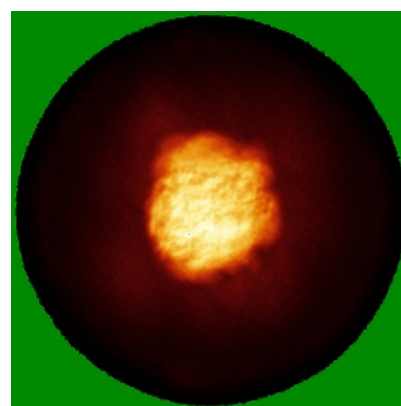
6.4.1 Primary map



X



Y



Z

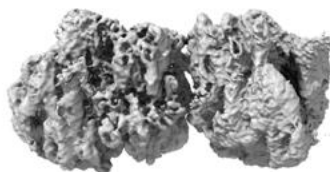
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

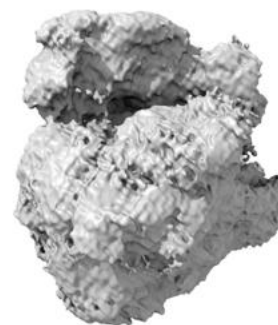
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

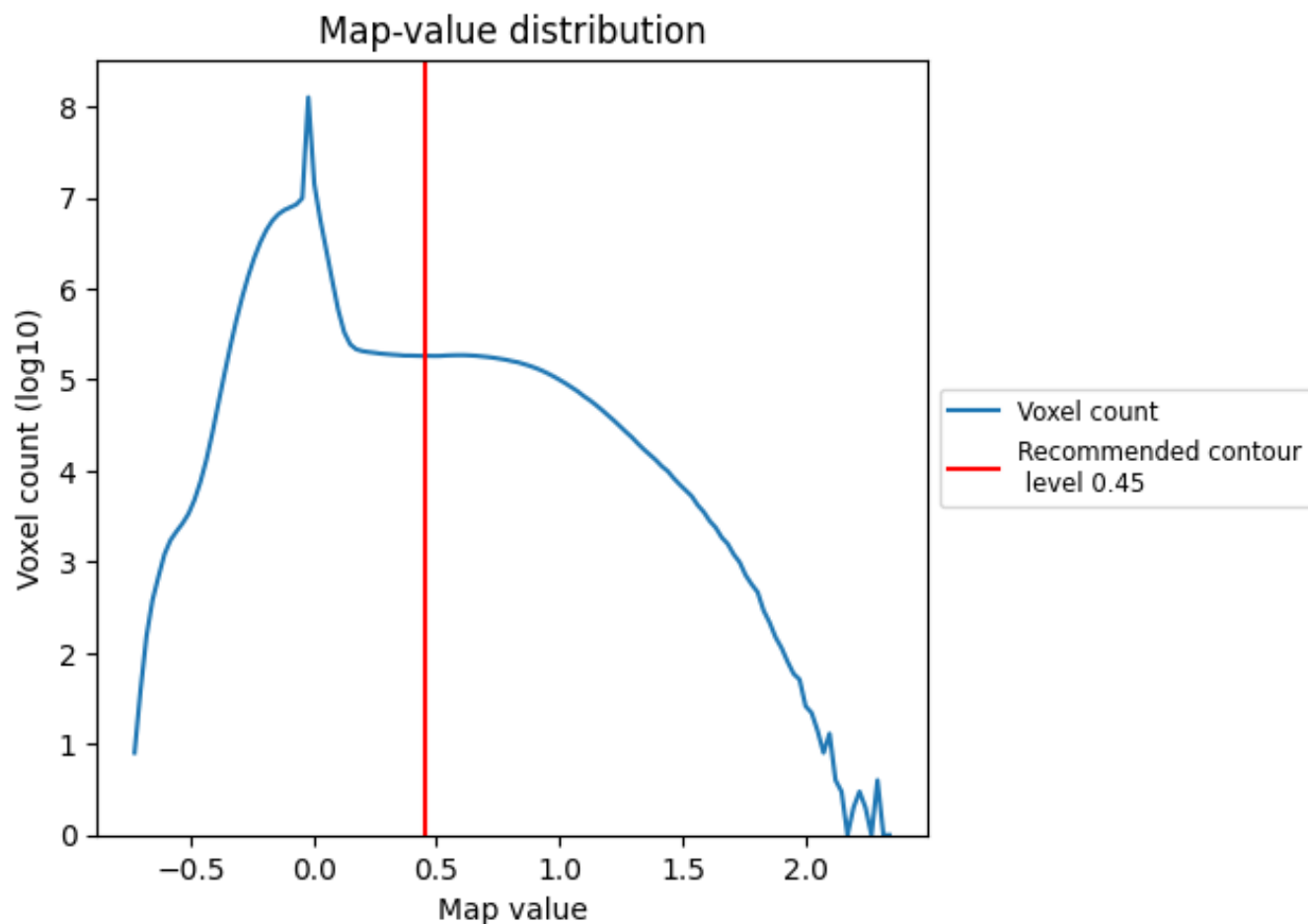
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

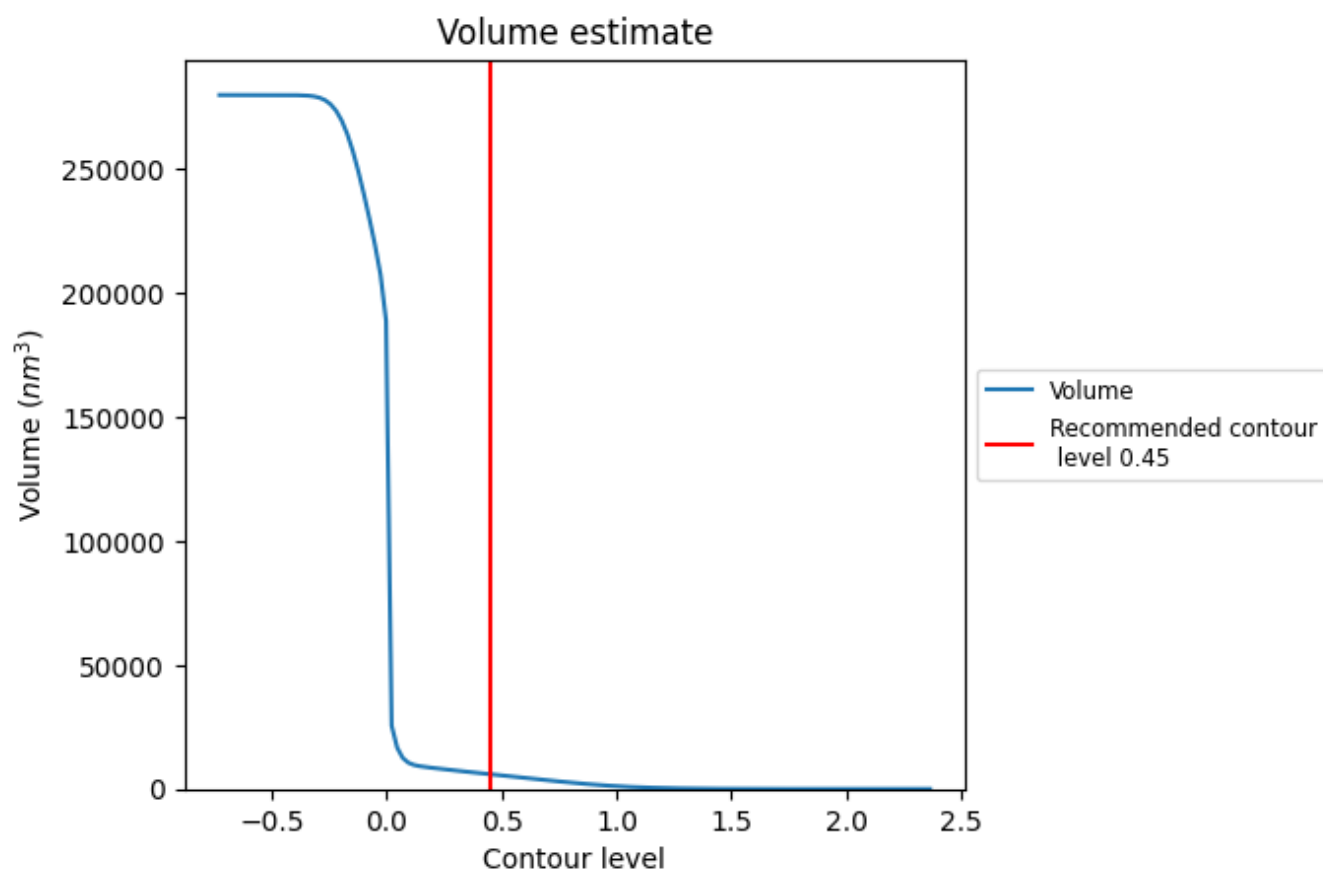
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

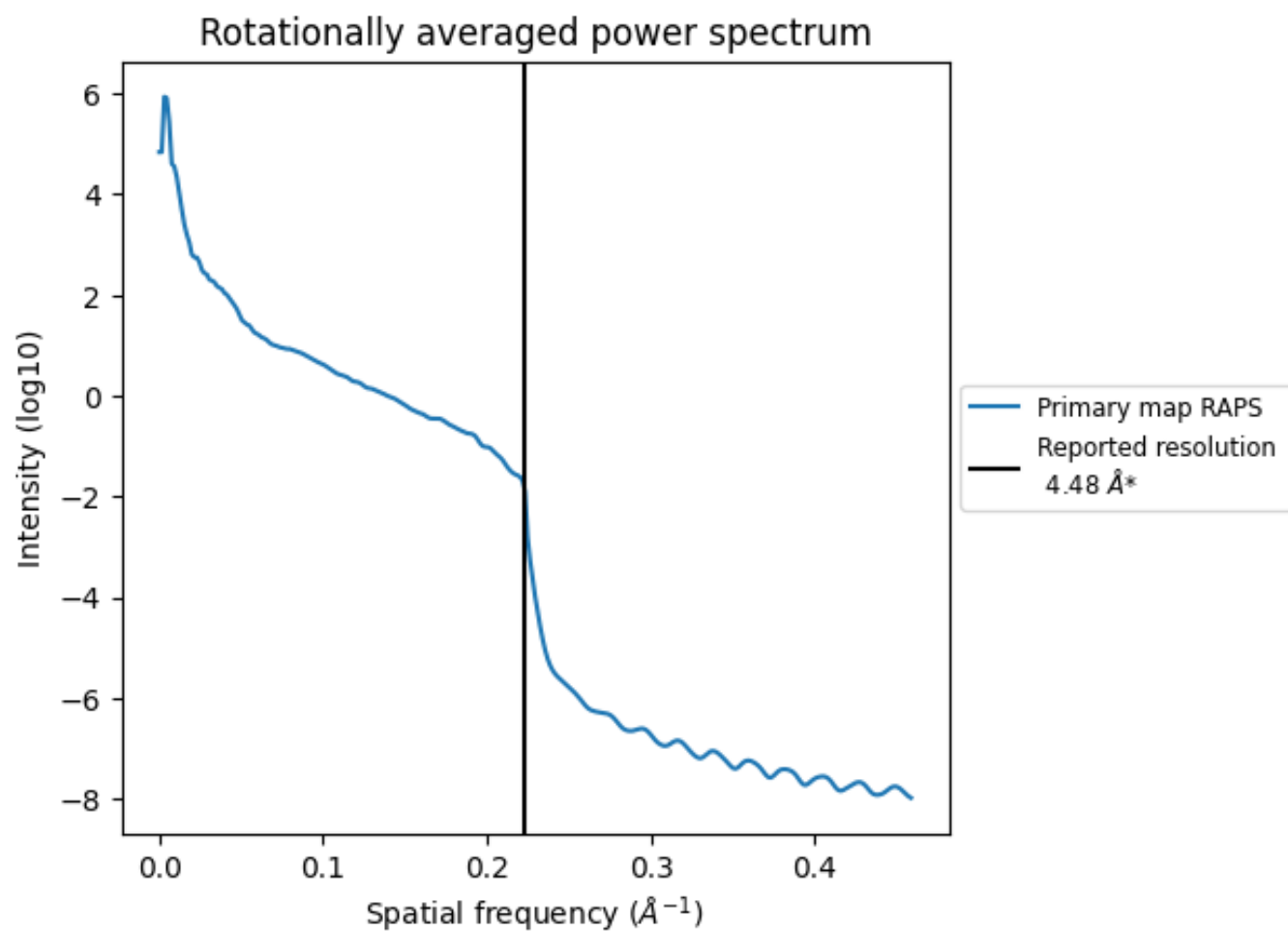
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5945 nm³; this corresponds to an approximate mass of 5371 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 0.223 Å⁻¹

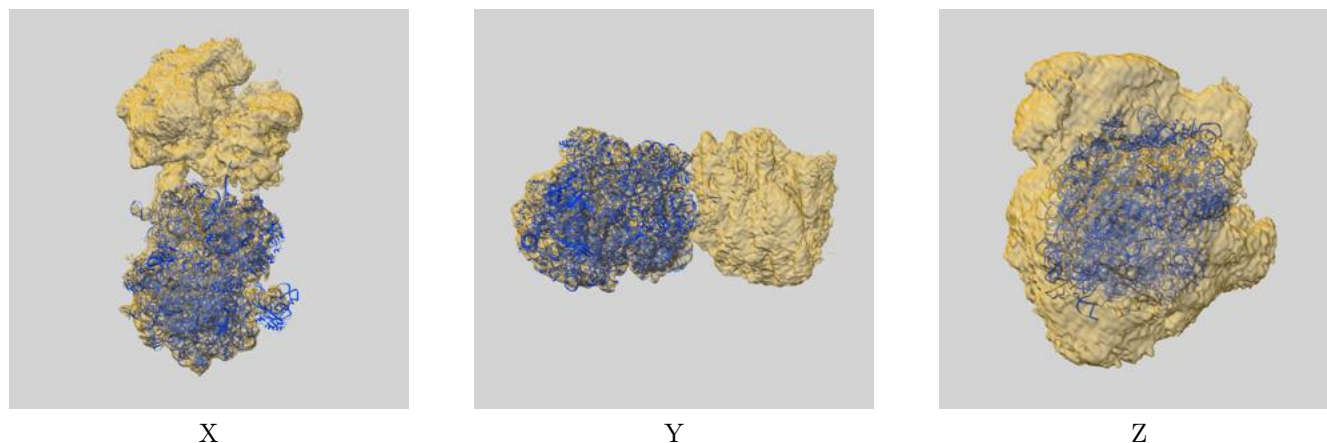
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

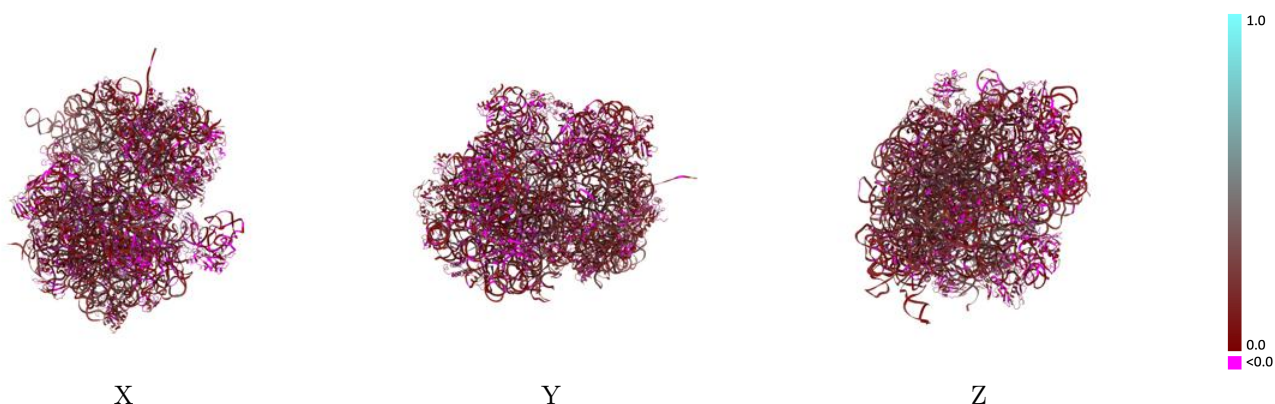
This section contains information regarding the fit between EMDB map EMD-13955 and PDB model 7QGH. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



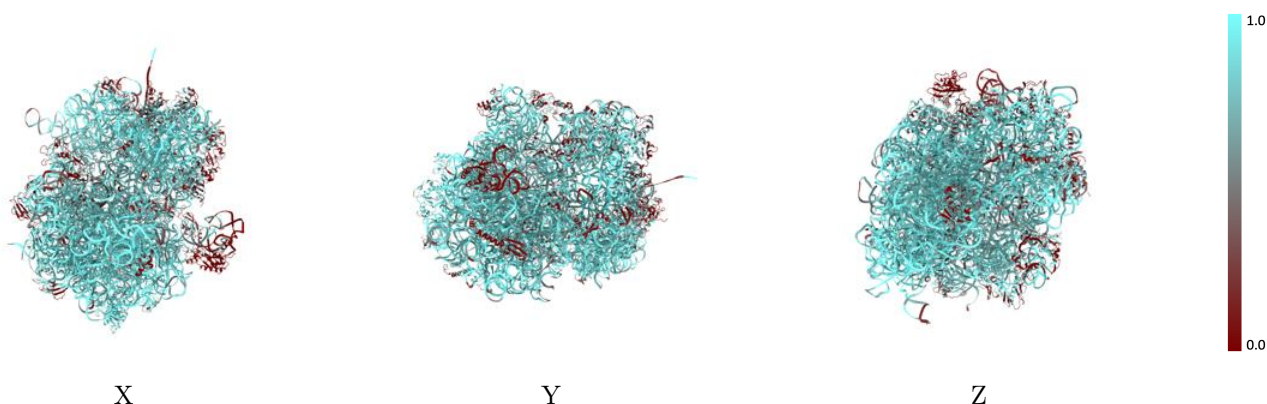
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



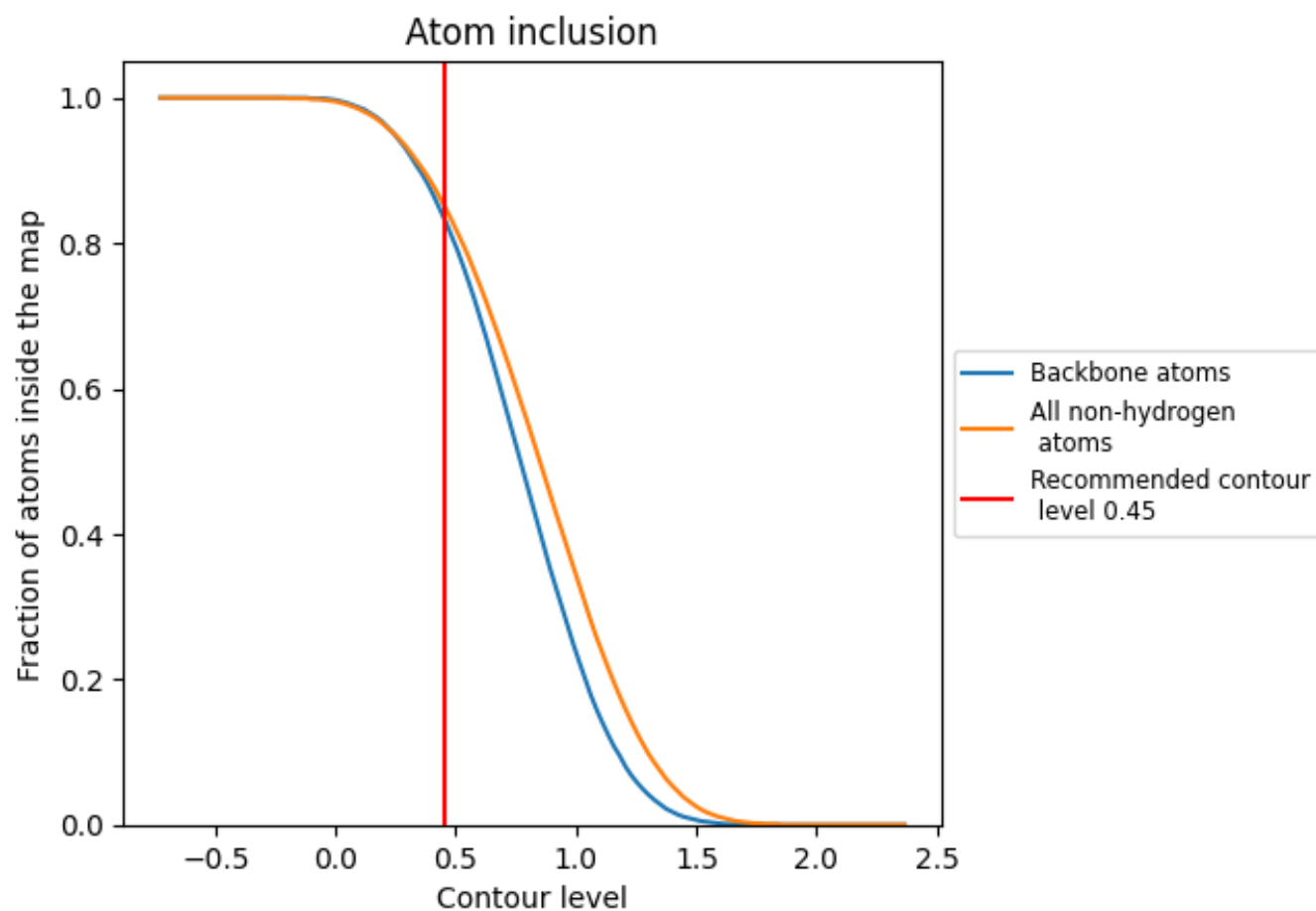
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 85% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.1260
0	 0.9470	 0.1750
1	 0.5300	 0.1370
2	 0.5970	 0.1260
3	 0.4370	 0.1170
4	 0.7880	 0.1780
5	 0.6680	 0.1140
6	 0.6370	 0.1040
7	 0.8380	 0.1220
8	 0.6570	 0.0640
9	 0.6870	 0.0780
A	 0.6270	 0.1110
B	 0.8960	 0.1470
C	 0.0020	 0.0400
D	 0.6710	 0.0590
E	 0.7250	 0.0510
F	 0.8700	 0.1310
G	 0.8510	 0.1410
H	 0.8840	 0.1200
I	 0.8530	 0.1100
J	 0.6140	 0.0190
K	 0.8520	 0.1010
L	 0.3380	 0.0890
M	 0.8590	 0.1080
N	 0.9270	 0.1290
O	 0.9350	 0.1110
P	 0.7520	 0.0440
Q	 0.7160	 0.0520
R	 0.9240	 0.1200
S	 0.7110	 0.0620
T	 0.4970	 0.0780
U	 0.1410	 0.0450
V	 0.3040	 0.0550
W	 0.9390	 0.0820
X	 0.6060	 0.0450



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Y	 0.9340	 0.0880
Z	 0.7980	 0.0800
a	 0.9430	 0.0940
b	 0.6200	 0.0510
c	 0.7010	 0.0640
d	 0.8750	 0.0840
e	 0.6420	 0.0980
f	 0.8530	 0.1010
g	 0.9090	 0.1010
h	 0.8460	 0.1170
i	 0.7480	 0.0790
j	 0.9530	 0.0720
k	 0.9550	 0.0540
l	 0.6830	 0.1010
m	 0.8900	 0.1020
n	 0.9130	 0.1070
o	 0.5640	 0.0540
p	 0.8360	 0.0530
q	 0.9760	 0.0870
r	 0.7220	 0.0730
s	 0.6380	 0.1440
t	 0.0670	 0.0660
u	 0.6700	 0.0970
x	 0.3500	 0.0950