



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:23 PM UTC

PDB ID : 7O5B / pdb_00007o5b
EMDB ID : EMD-12734
Title : Cryo-EM structure of a Bacillus subtilis MifM-stalled ribosome-nascent chain complex with (p)ppGpp-SRP bound
Authors : Kratzat, H.; Czech, L.; Berninghausen, O.; Bange, G.; Beckmann, R.
Deposited on : 2021-04-08
Resolution : 3.33 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:

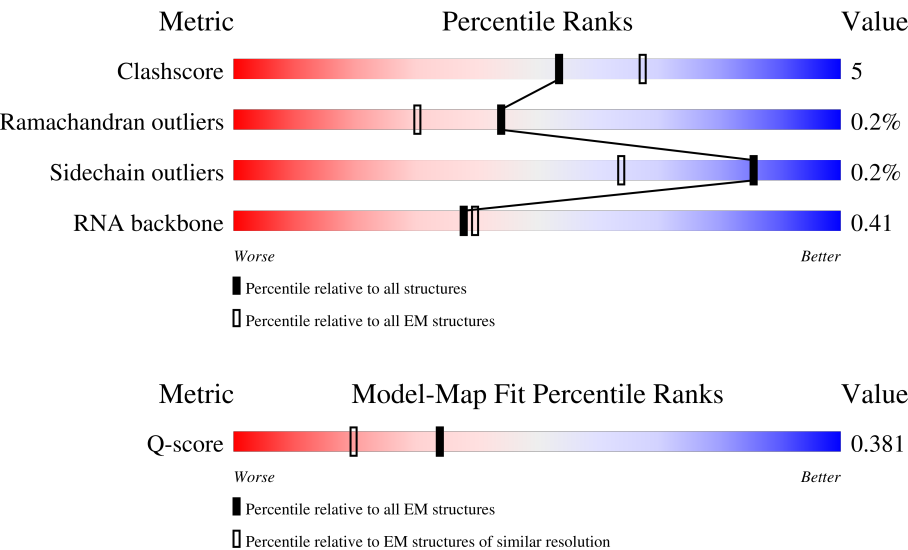
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.33 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	14484 (2.83 - 3.83)

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	U	77	
2	V	8	
3	W	266	

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Mol	Chain	Length	Quality of chain
4	g	447	
5	h	96	
6	p	166	
7	q	141	
8	X	2887	
9	Y	112	
10	Z	277	
11	a	208	
12	b	207	
13	c	179	
14	d	179	
15	e	145	
16	f	122	
17	i	146	
18	j	144	
19	k	120	
20	l	120	
21	m	115	
22	n	119	
23	o	102	
24	r	113	
25	s	95	
26	t	103	
27	u	94	
28	v	62	

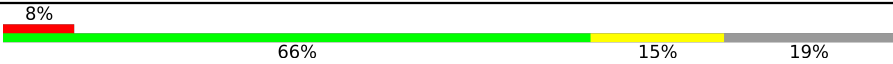
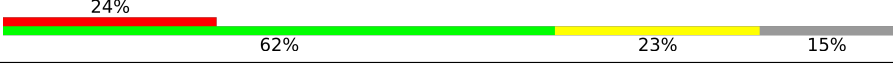
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Mol	Chain	Length	Quality of chain
29	w	66	
30	x	59	
31	0	59	
32	1	49	
33	2	44	
34	3	66	
35	4	37	
36	6	66	
37	A	1533	
38	B	246	
39	C	218	
40	D	200	
41	E	166	
42	F	95	
43	G	156	
44	H	132	
45	I	130	
46	J	102	
47	K	131	
48	L	138	
49	M	121	
50	N	61	
51	O	89	
52	P	90	
53	Q	87	

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Mol	Chain	Length	Quality of chain
54	R	79	
55	S	92	
56	T	88	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150422 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 tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	8	Total	C	N	O	P	0	0
			177	79	38	52	8		

- Molecule 3 is a RNA chain called SRP RNA (266-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	266	Total	C	N	O	P	0	0
			5685	2535	1018	1866	266		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	?	-	U	deletion	GB 1837880844

- Molecule 4 is a protein called Signal recognition particle protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	g	403	Total	C	N	O	0	0
			1911	1097	410	404		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	-2	HIS	-	expression tag	UNP P37105
g	-1	MET	-	expression tag	UNP P37105
g	0	GLY	-	expression tag	UNP P37105

- Molecule 5 is a protein called MifM-stalling construct.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	h	43	Total	C	N	O	0	0
			189	114	43	32		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	p	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	154	THR	ALA	conflict	UNP P42923

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	q	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 8 is a RNA chain called 23S rRNA (2887-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	X	2887	Total	C	N	O	P	0	0
			61997	27661	11460	19992	2884		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	243	G	A	conflict	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	G	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	C	deletion	GB 1491848961
X	?	-	G	deletion	GB 1491848961
X	?	-	G	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961

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Chain	Residue	Modelled	Actual	Comment	Reference
X	?	-	C	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	C	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	C	deletion	GB 1491848961
X	?	-	C	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	640	U	C	conflict	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	C	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	G	deletion	GB 1491848961
X	?	-	U	deletion	GB 1491848961
X	?	-	A	deletion	GB 1491848961
X	?	-	G	deletion	GB 1491848961

- Molecule 9 is a RNA chain called 5S rRNA (112-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Y	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	k	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	m	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	n	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	o	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	r	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	s	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	u	82	Total	C	N	O	S	0	0
			630	390	123	117			

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	v	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	x	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 31 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	0	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 32 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 33 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 34 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 35 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 36 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	6	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

- Molecule 37 is a RNA chain called 16S rRNA (1533-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	B	218	Total	C	N	O	S	0	0
			1757	1119	309	323	6		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	C	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	213	THR	ASN	conflict	UNP P21465

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	D	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	E	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	F	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	149	Total	C	N	O	S	0	0
			1181	740	220	215	6		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	H	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	I	125	Total	C	N	O	S	0	0
			966	599	191	175	1		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	J	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	K	114	Total	C	N	O	S	0	0
			838	516	164	156	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	7	GLN	SER	conflict	UNP P04969

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	M	108	Total	C	N	O	S	0	0
			868	534	176	158			

- Molecule 50 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

- Molecule 51 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	O	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	P	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	R	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

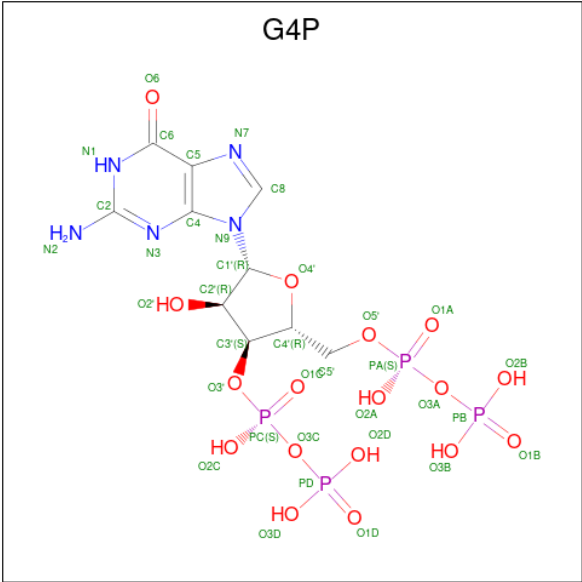
- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S	78	Total	C	N	O	S	0	0
			633	409	112	110	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	T	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 57 is GUANOSINE-5',3'-TETRAPHOSPHATE (CCD ID: G4P) (formula: C₁₀H₁₇N₅O₁₇P₄).

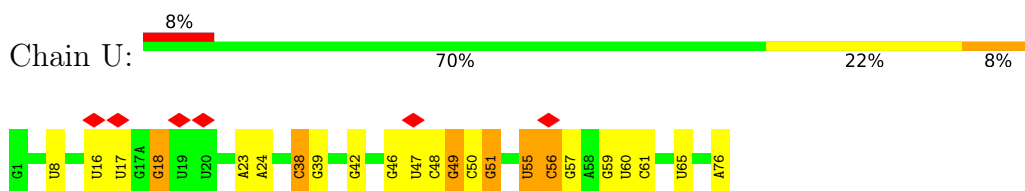


Mol	Chain	Residues	Atoms					AltConf
57	g	1	Total	C	N	O	P	0
			36	10	5	17	4	

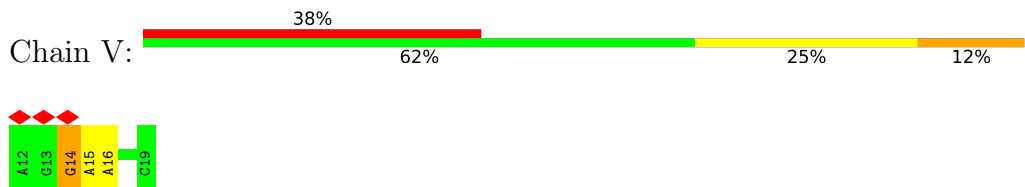
3 Residue-property plots [i](#)

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.

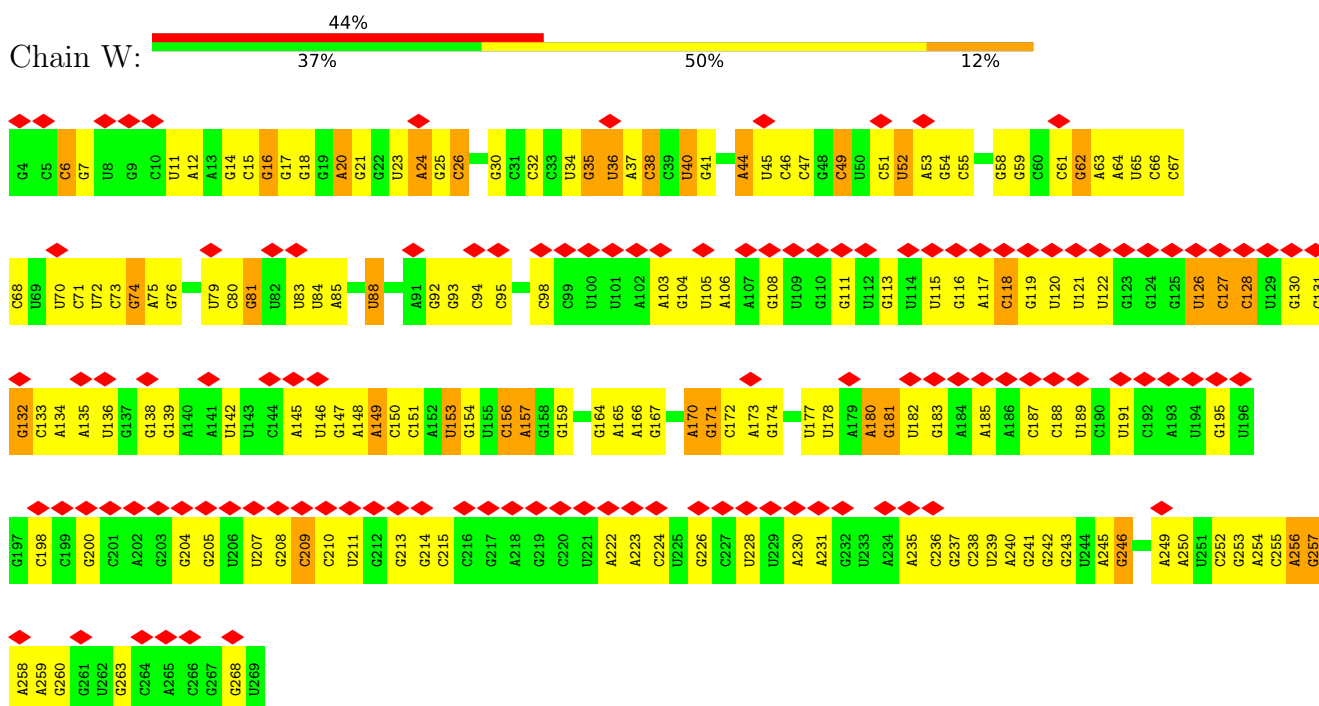
- Molecule 1: tRNA



- Molecule 2: mRNA



- Molecule 3: SRP RNA (266-MER)



- Molecule 4: Signal recognition particle protein

Chain g:

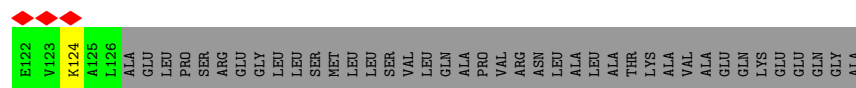
- Molecule 5: MifM-stalling construct

Chain h:

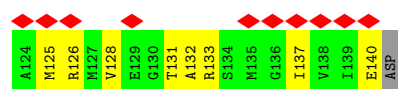
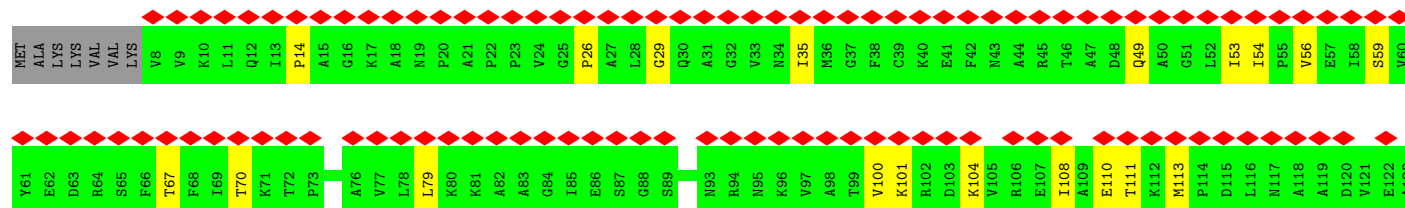
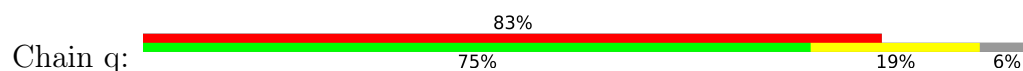
- Molecule 6: 50S ribosomal protein L10

Chain p:

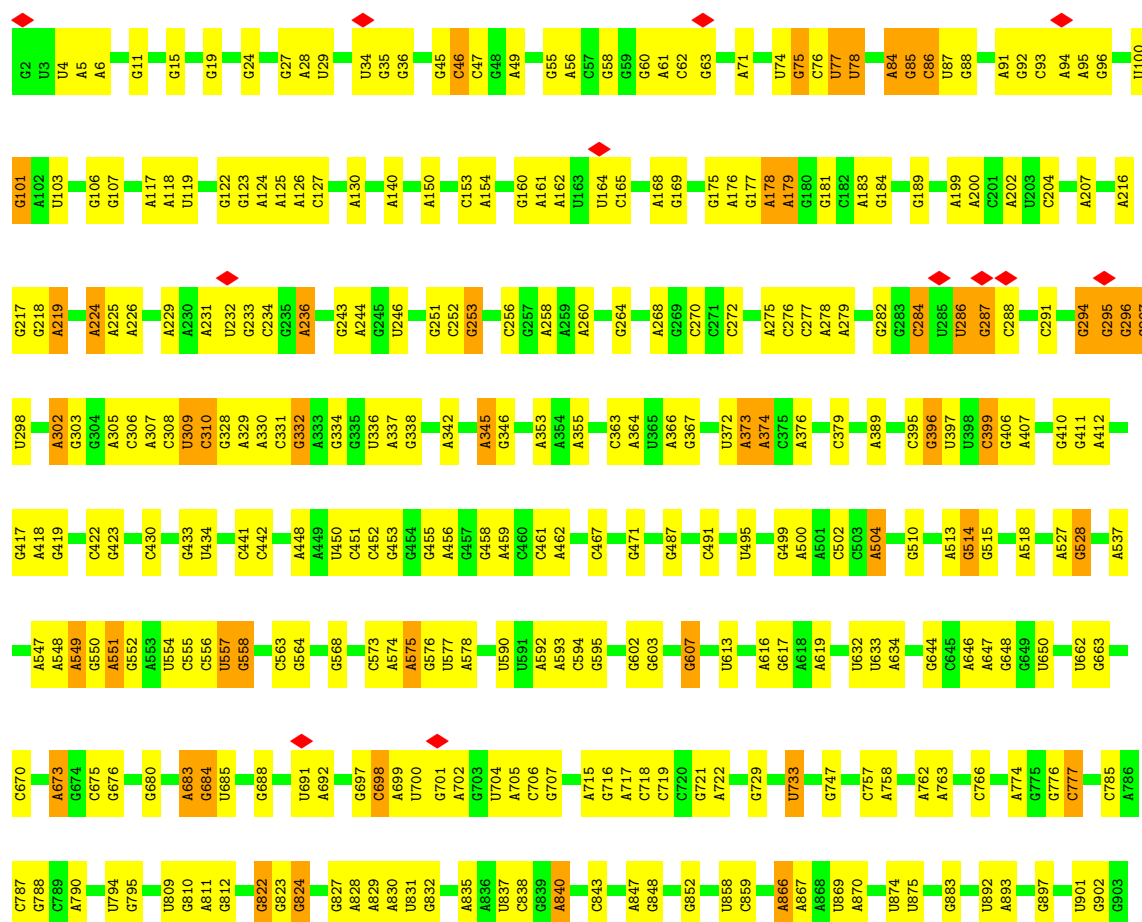




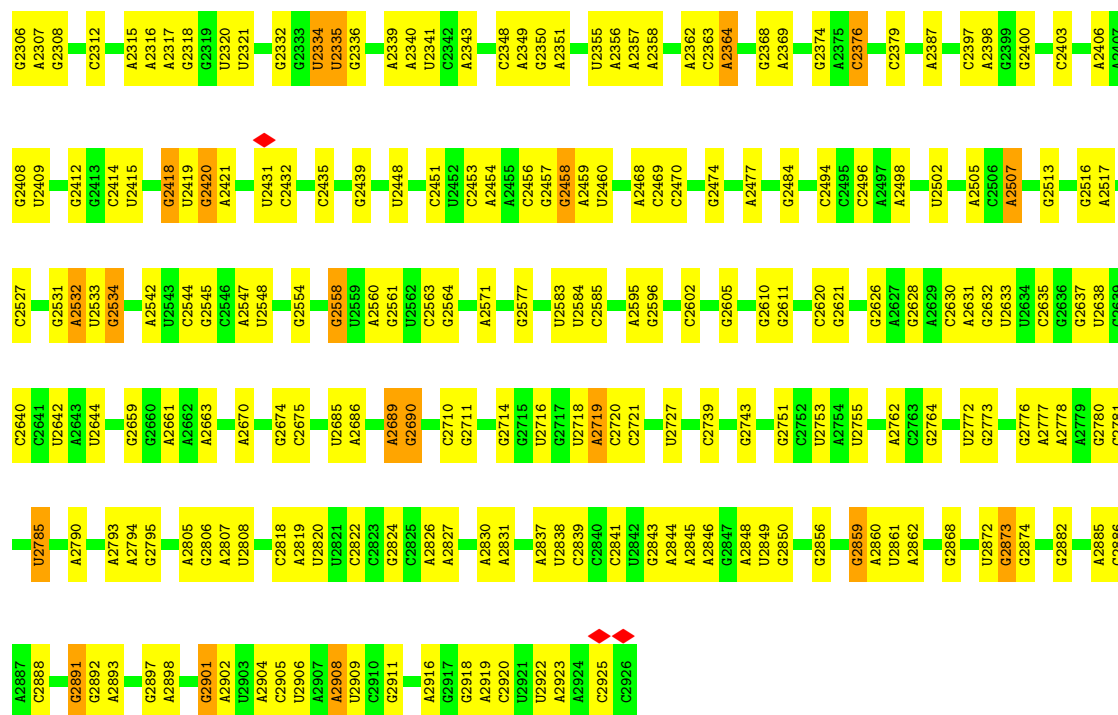
• Molecule 7: 50S ribosomal protein L11



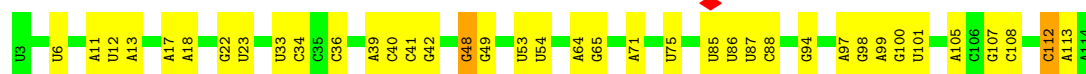
• Molecule 8: 23S rRNA (2887-MER)



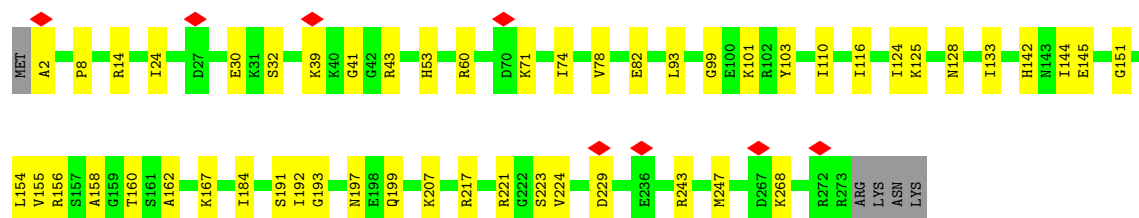
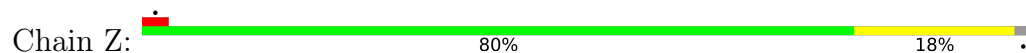




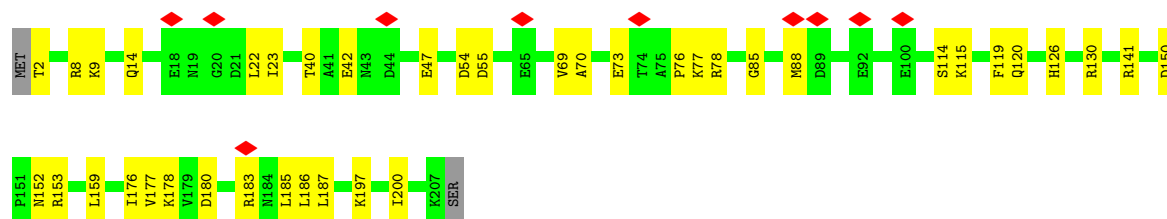
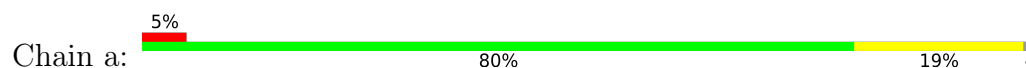
• Molecule 9: 5S rRNA (112-MER)



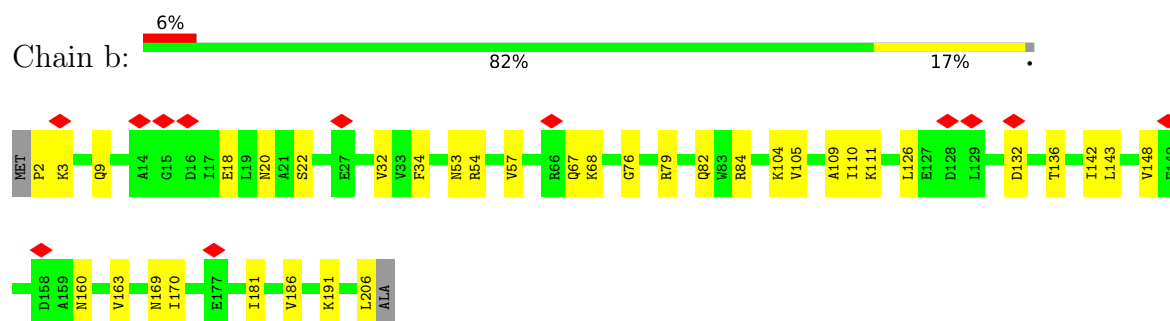
• Molecule 10: 50S ribosomal protein L2



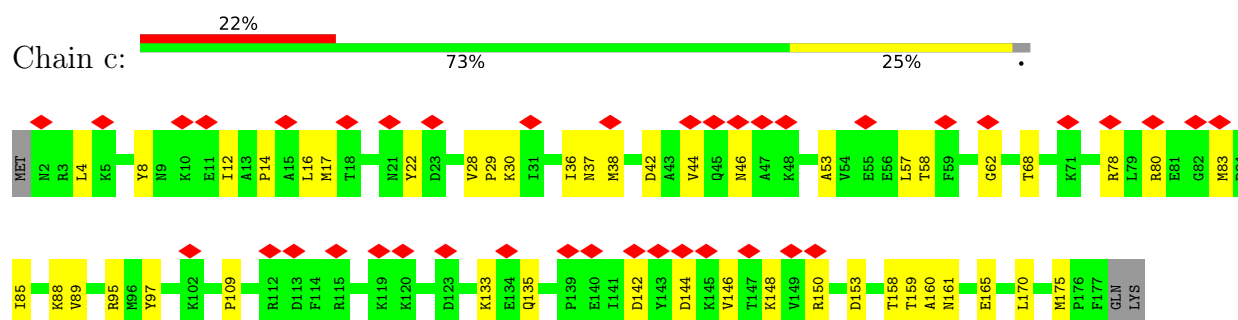
• Molecule 11: 50S ribosomal protein L3



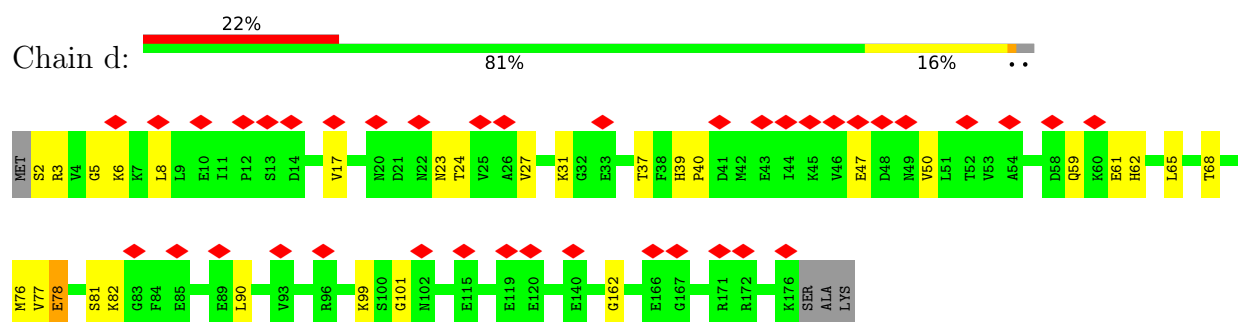
- Molecule 12: 50S ribosomal protein L4



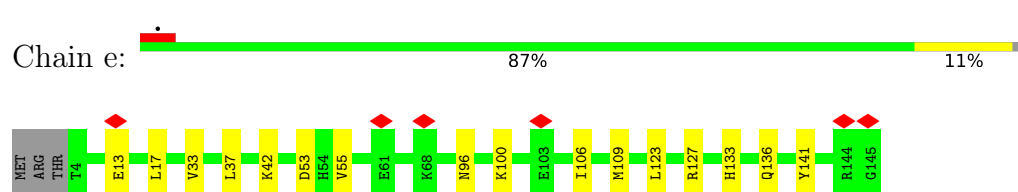
- Molecule 13: 50S ribosomal protein L5



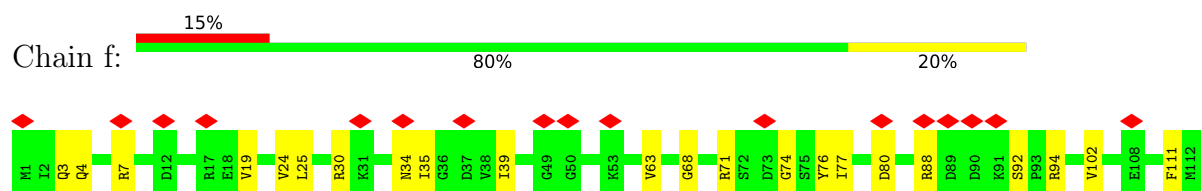
- Molecule 14: 50S ribosomal protein L6

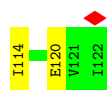


- Molecule 15: 50S ribosomal protein L13

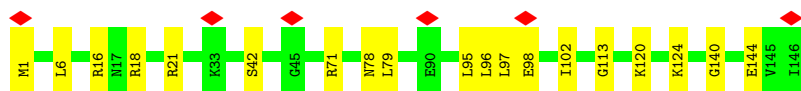
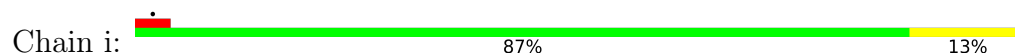


- Molecule 16: 50S ribosomal protein L14

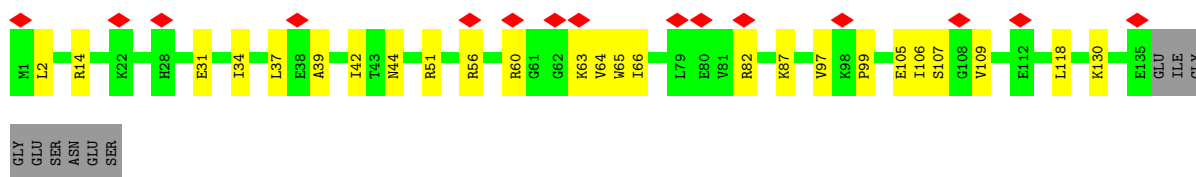
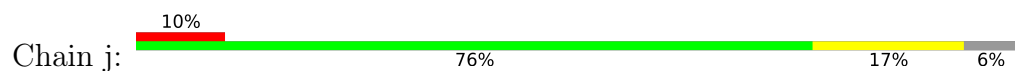




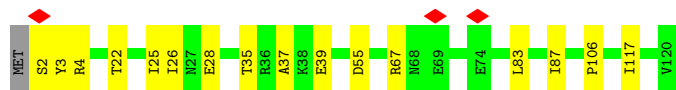
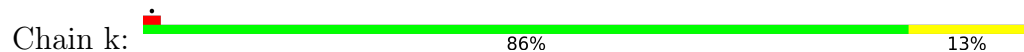
- Molecule 17: 50S ribosomal protein L15



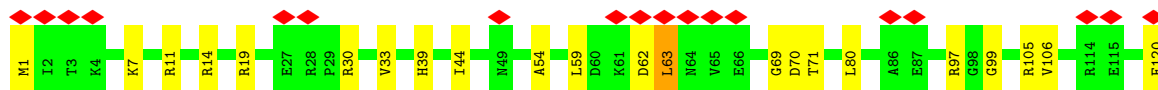
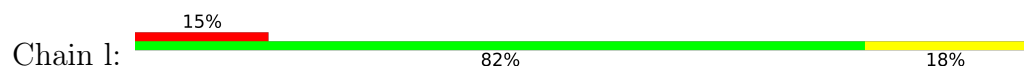
- Molecule 18: 50S ribosomal protein L16



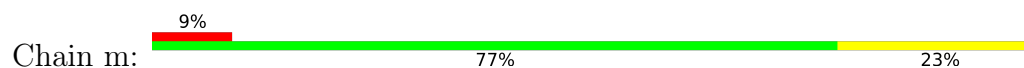
- Molecule 19: 50S ribosomal protein L17



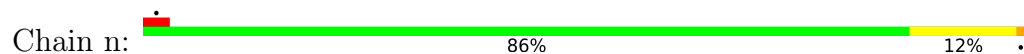
- Molecule 20: 50S ribosomal protein L18

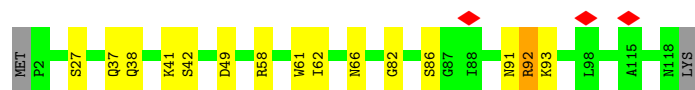


- Molecule 21: 50S ribosomal protein L19

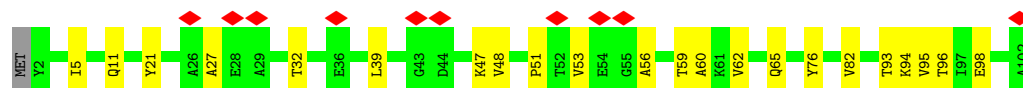
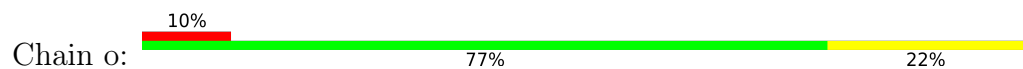


- Molecule 22: 50S ribosomal protein L20

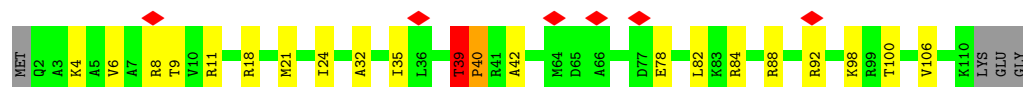
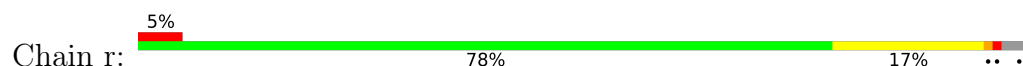




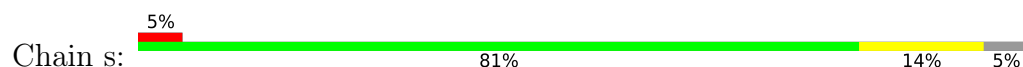
- Molecule 23: 50S ribosomal protein L21



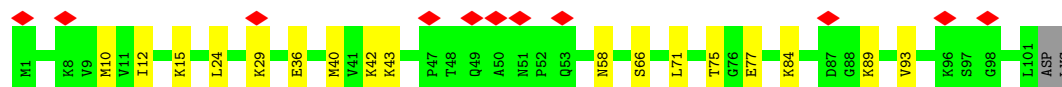
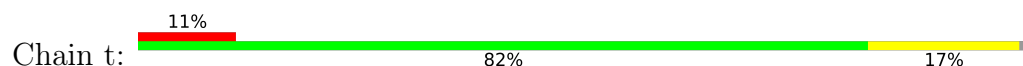
- Molecule 24: 50S ribosomal protein L22



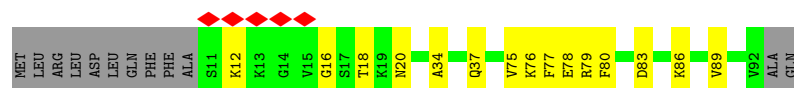
- Molecule 25: 50S ribosomal protein L23



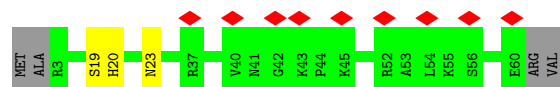
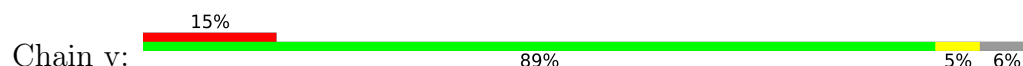
- Molecule 26: 50S ribosomal protein L24



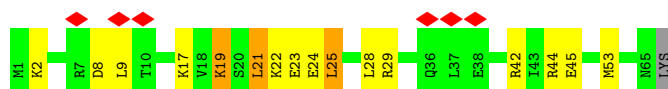
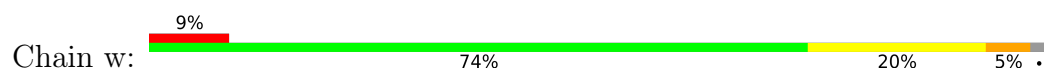
- Molecule 27: 50S ribosomal protein L27



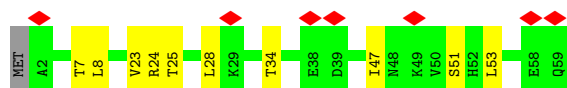
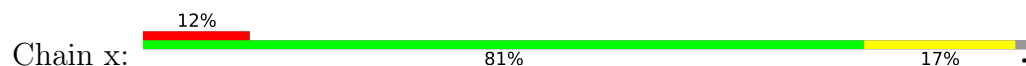
- Molecule 28: 50S ribosomal protein L28



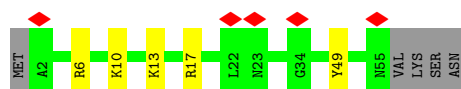
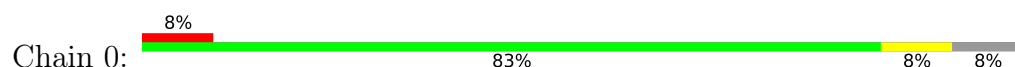
- Molecule 29: 50S ribosomal protein L29



- Molecule 30: 50S ribosomal protein L30



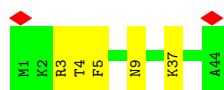
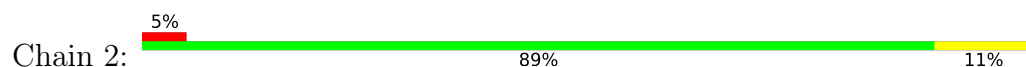
- Molecule 31: 50S ribosomal protein L32



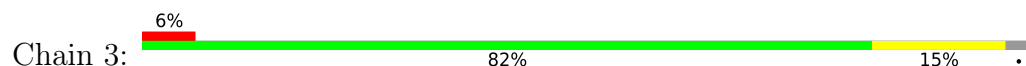
- Molecule 32: 50S ribosomal protein L33 1



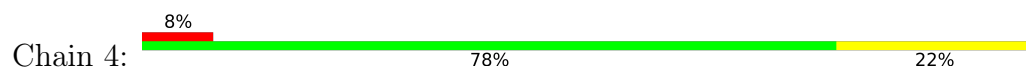
- Molecule 33: 50S ribosomal protein L34



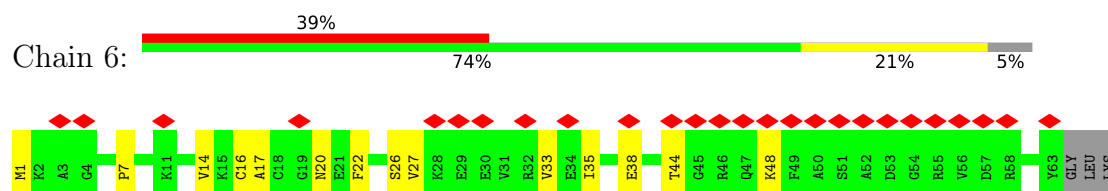
- Molecule 34: 50S ribosomal protein L35



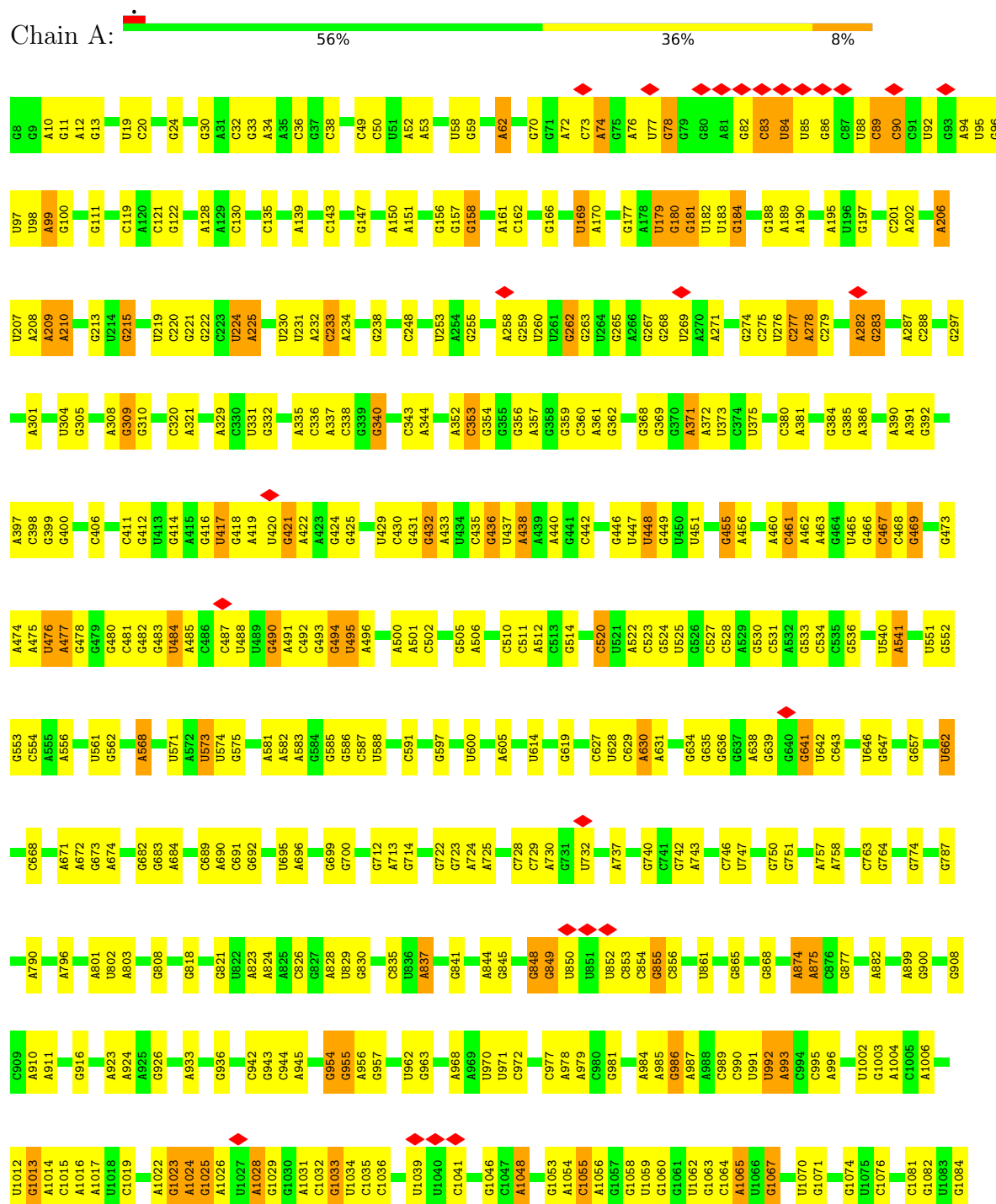
- Molecule 35: 50S ribosomal protein L36

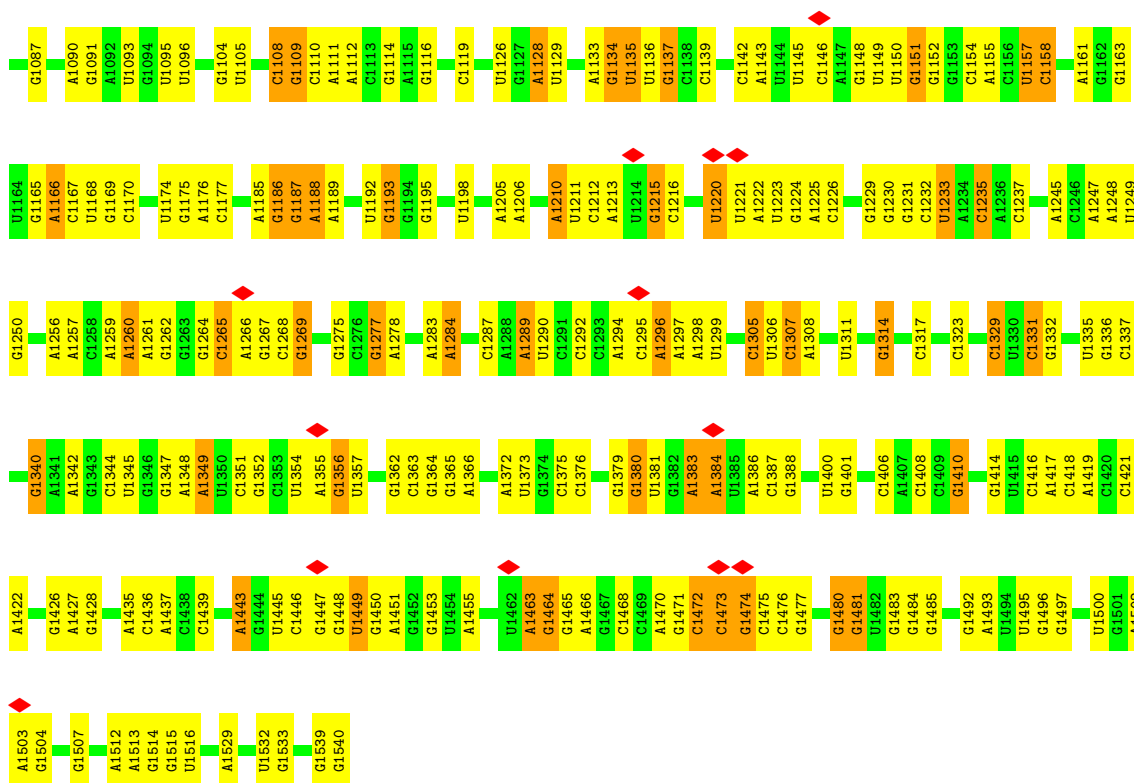


- Molecule 36: 50S ribosomal protein L31

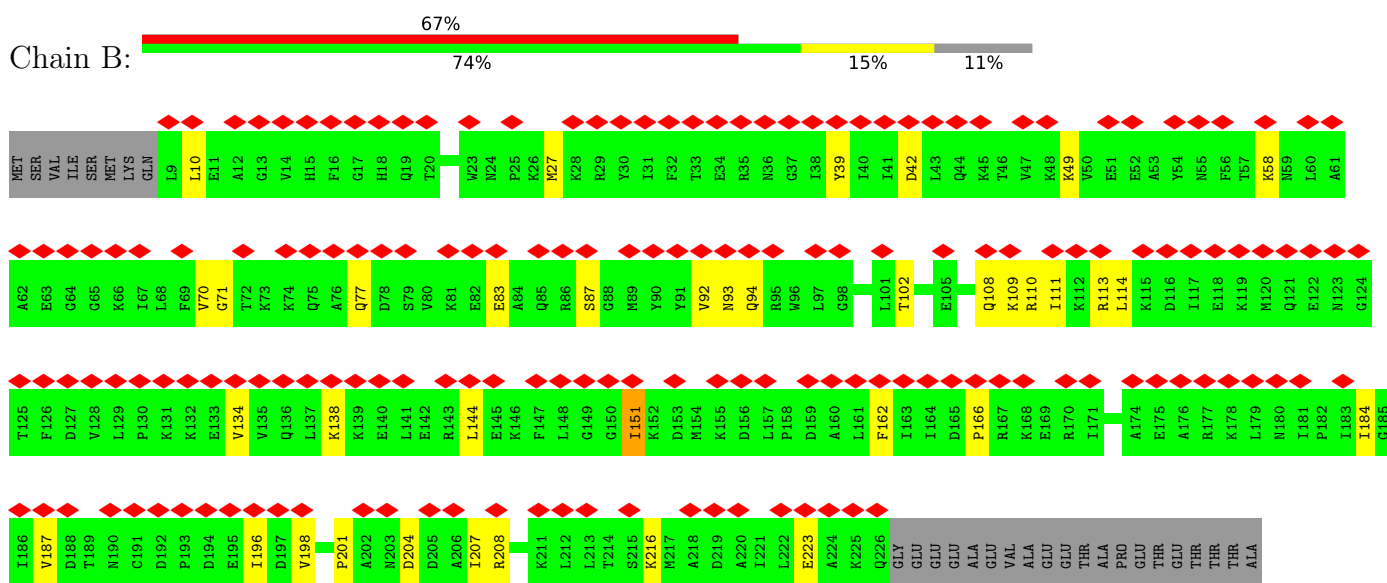


- Molecule 37: 16S rRNA (1533-MER)

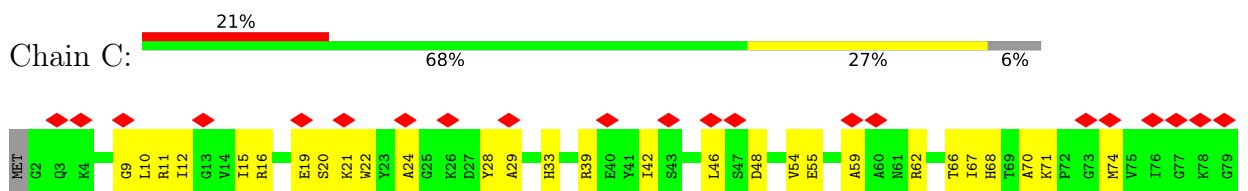


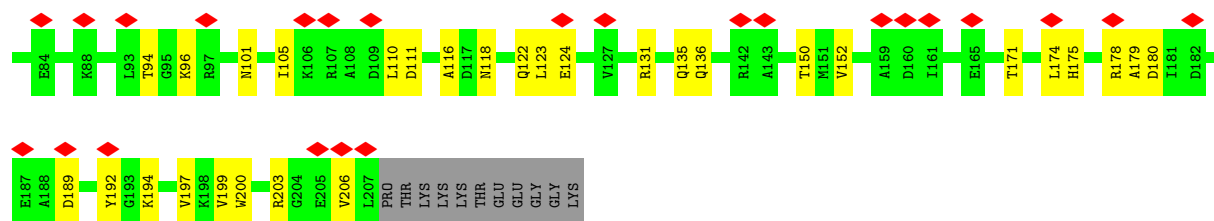


• Molecule 38: 30S ribosomal protein S2

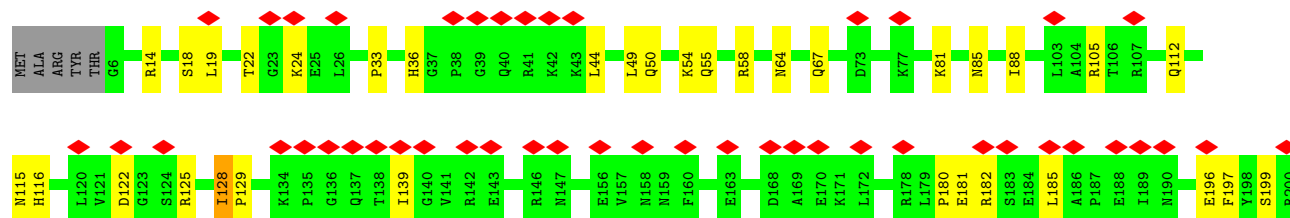
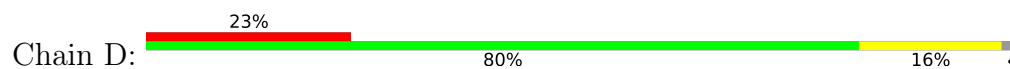


• Molecule 39: 30S ribosomal protein S3

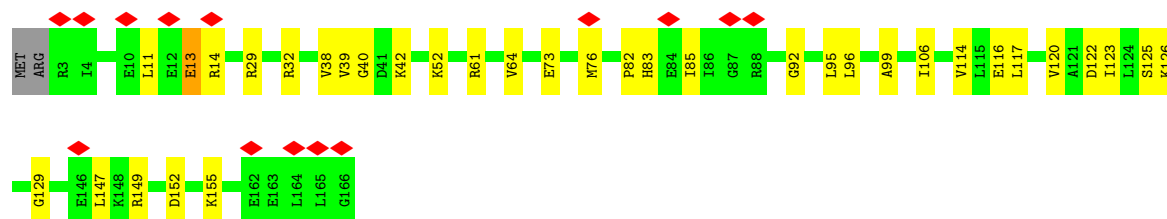
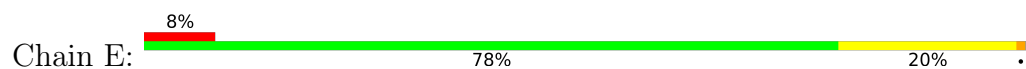




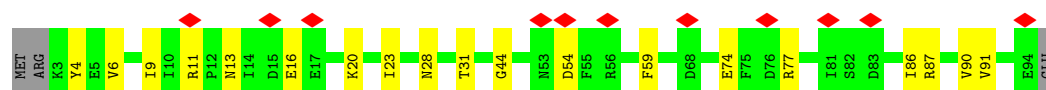
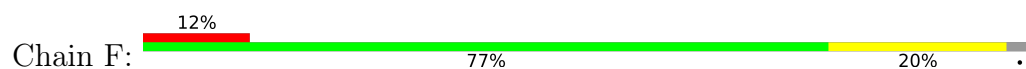
• Molecule 40: 30S ribosomal protein S4



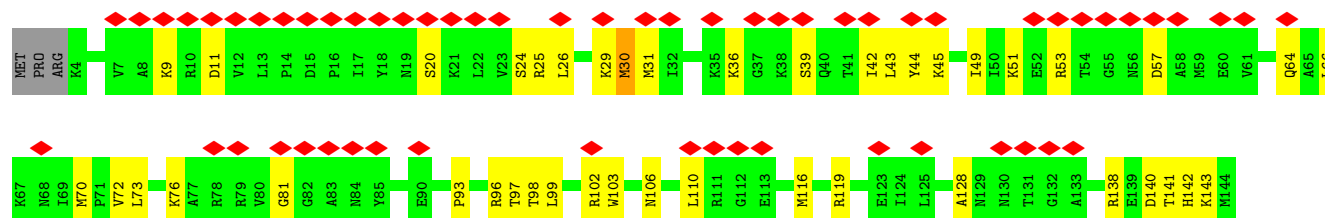
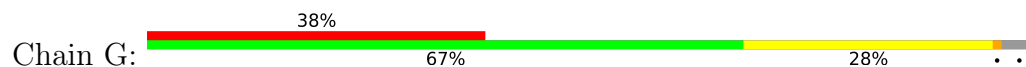
• Molecule 41: 30S ribosomal protein S5

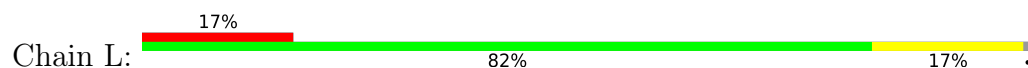


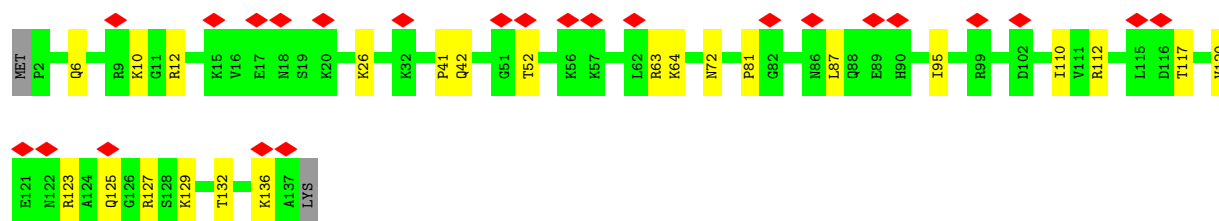
• Molecule 42: 30S ribosomal protein S6



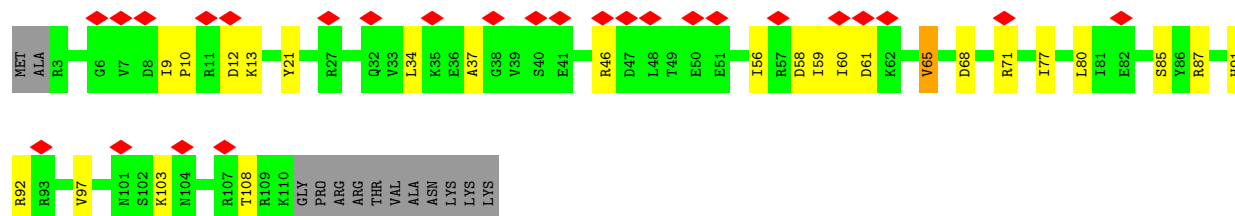
• Molecule 43: 30S ribosomal protein S7



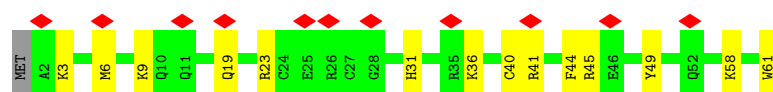
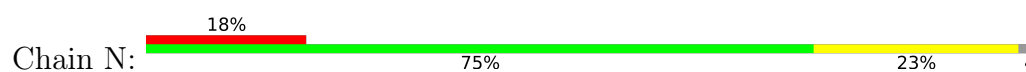




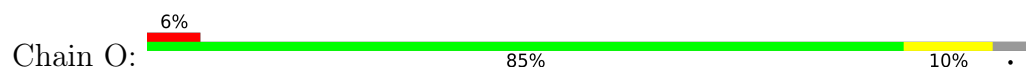
- Molecule 49: 30S ribosomal protein S13



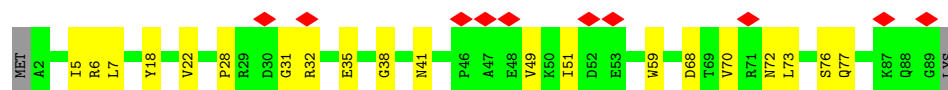
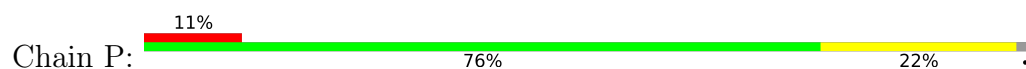
- Molecule 50: 30S ribosomal protein S14



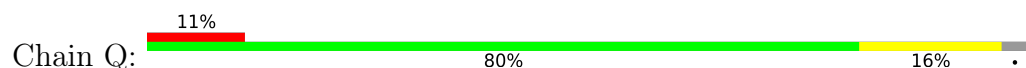
- Molecule 51: 30S ribosomal protein S15



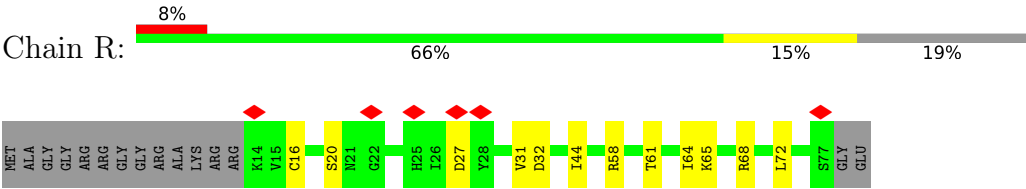
- Molecule 52: 30S ribosomal protein S16



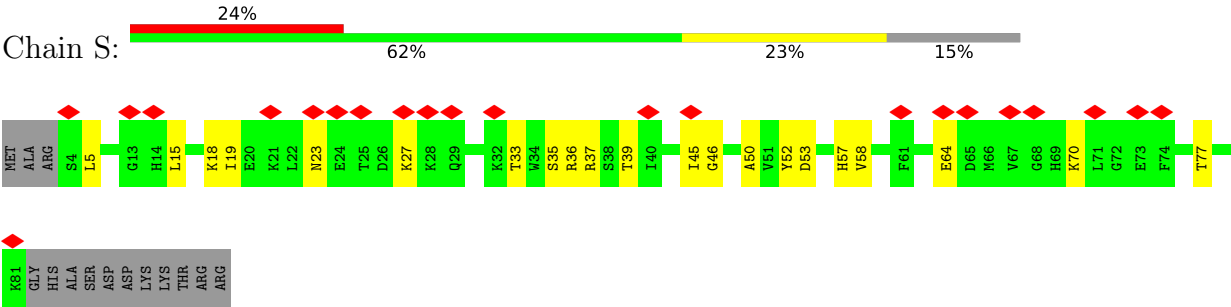
- Molecule 53: 30S ribosomal protein S17



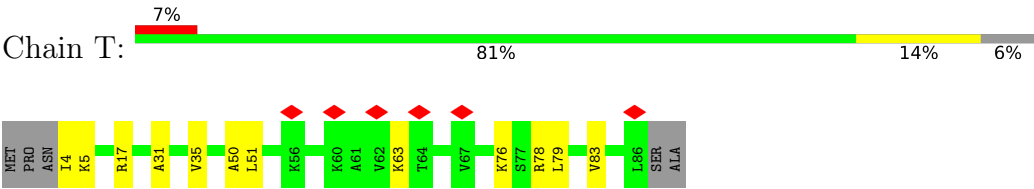
- Molecule 54: 30S ribosomal protein S18



• Molecule 55: 30S ribosomal protein S19



• Molecule 56: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21229	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.675	Depositor
Minimum map value	-0.494	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.127	Depositor
Recommended contour level	0.479	Depositor
Map size ($\text{\AA}$)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G4P

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	U	0.19	0/1834	0.34	0/2858
2	V	0.21	0/199	0.36	0/309
3	W	0.14	0/6357	0.32	0/9911
4	g	0.30	0/1909	0.65	2/2593 (0.1%)
5	h	0.27	0/187	0.86	0/236
6	p	0.25	0/963	0.73	5/1298 (0.4%)
7	q	0.21	0/995	0.52	0/1346
8	X	0.37	0/69443	0.43	1/108331 (0.0%)
9	Y	0.23	0/2675	0.40	1/4170 (0.0%)
10	Z	0.42	0/2120	0.60	0/2845
11	a	0.42	0/1591	0.70	0/2132
12	b	0.37	0/1580	0.63	1/2132 (0.0%)
13	c	0.29	0/1405	0.76	1/1887 (0.1%)
14	d	0.25	0/1360	0.68	3/1832 (0.2%)
15	e	0.32	0/1146	0.62	1/1542 (0.1%)
16	f	0.38	0/927	0.67	0/1245
17	i	0.34	0/1093	0.57	0/1457
18	j	0.33	0/1099	0.63	0/1468
19	k	0.41	0/960	0.68	1/1284 (0.1%)
20	l	0.28	0/921	0.73	1/1236 (0.1%)
21	m	0.33	0/957	0.59	0/1279
22	n	0.38	0/952	0.66	2/1266 (0.2%)
23	o	0.38	0/797	0.74	0/1070
24	r	0.40	0/851	0.71	1/1146 (0.1%)
25	s	0.38	0/731	0.62	0/974
26	t	0.35	0/772	0.72	0/1032
27	u	0.36	0/638	0.88	4/847 (0.5%)
28	v	0.36	0/448	0.74	0/596
29	w	0.60	2/531 (0.4%)	0.75	0/707
30	x	0.34	0/457	0.77	0/613
31	0	0.36	0/433	0.73	0/574
32	1	0.28	0/406	0.63	0/540

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	2	0.45	0/370	0.60	0/483
34	3	0.33	0/519	0.58	0/680
35	4	0.30	0/299	0.68	0/393
36	6	0.20	0/509	0.51	0/678
37	A	0.28	0/36826	0.40	2/57450 (0.0%)
38	B	0.25	0/1782	0.68	1/2392 (0.0%)
39	C	0.29	0/1641	0.72	3/2208 (0.1%)
40	D	0.27	0/1598	0.69	0/2147
41	E	0.33	0/1230	0.74	1/1655 (0.1%)
42	F	0.31	0/766	0.71	0/1031
43	G	0.29	0/1196	0.79	2/1604 (0.1%)
44	H	0.33	0/1048	0.73	0/1407
45	I	0.27	0/979	0.74	0/1315
46	J	0.29	0/773	0.71	0/1044
47	K	0.27	0/852	0.66	0/1153
48	L	0.31	0/1069	0.60	0/1435
49	M	0.29	0/873	0.79	0/1166
50	N	0.35	0/507	0.91	3/672 (0.4%)
51	O	0.35	0/718	0.71	0/960
52	P	0.31	0/708	0.73	0/950
53	Q	0.28	0/699	0.62	0/933
54	R	0.29	0/526	0.56	0/705
55	S	0.21	0/649	0.61	0/872
56	T	0.30	0/639	0.69	0/852
All	All	0.33	2/163513 (0.0%)	0.50	36/244941 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	a	0	1
13	c	0	1
21	m	0	1
24	r	0	1
27	u	0	1
40	D	0	1
43	G	0	1
47	K	0	2
49	M	0	1
54	R	0	1
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	w	29	ARG	C-O	-8.55	1.14	1.24
29	w	29	ARG	CA-C	-5.66	1.45	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	u	77	PHE	CA-C-N	-9.38	111.27	122.44
27	u	77	PHE	C-N-CA	-9.38	111.27	122.44
14	d	78	GLU	N-CA-CB	6.87	121.59	110.40
6	p	89	VAL	CA-C-N	6.78	134.17	121.97
6	p	89	VAL	C-N-CA	6.78	134.17	121.97

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	a	120	GLN	Peptide
13	c	53	ALA	Peptide
21	m	106	LYS	Peptide
24	r	39	THR	Peptide
27	u	79	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	U	1643	0	831	8	0
2	V	177	0	89	2	0
3	W	5685	0	2865	55	0
4	g	1911	0	845	6	0
5	h	189	0	79	0	0
6	p	955	0	990	17	0
7	q	981	0	1020	18	0
8	X	61997	0	31209	348	0
9	Y	2392	0	1213	4	0
10	Z	2083	0	2168	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	a	1569	0	1637	26	0
12	b	1561	0	1647	25	0
13	c	1386	0	1446	29	0
14	d	1342	0	1388	22	0
15	e	1123	0	1162	10	0
16	f	920	0	977	17	0
17	i	1081	0	1132	17	0
18	j	1076	0	1145	16	0
19	k	953	0	983	11	0
20	l	912	0	947	15	0
21	m	944	0	1020	19	0
22	n	940	0	1005	12	0
23	o	786	0	826	13	0
24	r	842	0	899	14	0
25	s	725	0	770	16	0
26	t	762	0	821	13	0
27	u	630	0	644	9	0
28	v	444	0	487	2	0
29	w	530	0	568	18	0
30	x	455	0	491	6	0
31	0	426	0	445	5	0
32	1	401	0	413	10	0
33	2	367	0	410	5	0
34	3	512	0	564	8	0
35	4	296	0	342	7	0
36	6	499	0	491	9	0
37	A	32891	0	16559	278	0
38	B	1757	0	1830	22	0
39	C	1619	0	1658	35	0
40	D	1568	0	1604	25	0
41	E	1218	0	1300	22	0
42	F	755	0	746	11	0
43	G	1181	0	1235	26	0
44	H	1036	0	1095	17	0
45	I	966	0	1005	32	0
46	J	761	0	795	14	0
47	K	838	0	854	15	0
48	L	1052	0	1112	18	0
49	M	868	0	925	16	0
50	N	497	0	531	11	0
51	O	710	0	735	5	0
52	P	695	0	721	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Q	691	0	728	11	0
54	R	518	0	555	8	0
55	S	633	0	649	14	0
56	T	637	0	696	13	0
57	g	36	0	11	0	0
All	All	150422	0	99313	1233	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 5.

The worst 5 of 1233 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:s:5:ARG:NH2	29:w:23:GLU:HG3	1.65	1.11
8:X:47:C:C2	8:X:181:G:N2	2.27	1.00
37:A:1126:U:H3	37:A:1193:G:H1	1.02	0.98
25:s:5:ARG:CZ	29:w:23:GLU:HG3	1.93	0.98
37:A:1129:U:H3	37:A:1163:G:H1	0.96	0.96

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	g	399/447 (89%)	388 (97%)	10 (2%)	1 (0%)	36	65
5	h	39/96 (41%)	35 (90%)	2 (5%)	2 (5%)	1	11
6	p	121/166 (73%)	112 (93%)	6 (5%)	3 (2%)	4	24
7	q	131/141 (93%)	130 (99%)	1 (1%)	0	100	100
10	Z	270/277 (98%)	267 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	a	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
12	b	203/207 (98%)	199 (98%)	4 (2%)	0	100	100
13	c	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
14	d	173/179 (97%)	170 (98%)	3 (2%)	0	100	100
15	e	140/145 (97%)	137 (98%)	3 (2%)	0	100	100
16	f	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
17	i	144/146 (99%)	143 (99%)	1 (1%)	0	100	100
18	j	133/144 (92%)	130 (98%)	3 (2%)	0	100	100
19	k	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
20	l	118/120 (98%)	118 (100%)	0	0	100	100
21	m	113/115 (98%)	113 (100%)	0	0	100	100
22	n	115/119 (97%)	112 (97%)	2 (2%)	1 (1%)	14	43
23	o	99/102 (97%)	95 (96%)	4 (4%)	0	100	100
24	r	107/113 (95%)	101 (94%)	5 (5%)	1 (1%)	14	43
25	s	88/95 (93%)	88 (100%)	0	0	100	100
26	t	99/103 (96%)	95 (96%)	4 (4%)	0	100	100
27	u	80/94 (85%)	76 (95%)	4 (5%)	0	100	100
28	v	56/62 (90%)	54 (96%)	2 (4%)	0	100	100
29	w	63/66 (96%)	63 (100%)	0	0	100	100
30	x	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
32	1	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
33	2	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
34	3	62/66 (94%)	61 (98%)	1 (2%)	0	100	100
35	4	35/37 (95%)	35 (100%)	0	0	100	100
36	6	61/66 (92%)	60 (98%)	1 (2%)	0	100	100
38	B	216/246 (88%)	210 (97%)	6 (3%)	0	100	100
39	C	204/218 (94%)	202 (99%)	2 (1%)	0	100	100
40	D	193/200 (96%)	190 (98%)	3 (2%)	0	100	100
41	E	162/166 (98%)	160 (99%)	2 (1%)	0	100	100
42	F	90/95 (95%)	88 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	G	147/156 (94%)	145 (99%)	2 (1%)	0	100	100
44	H	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	46
45	I	123/130 (95%)	119 (97%)	4 (3%)	0	100	100
46	J	93/102 (91%)	90 (97%)	3 (3%)	0	100	100
47	K	112/131 (86%)	110 (98%)	2 (2%)	0	100	100
48	L	134/138 (97%)	132 (98%)	2 (2%)	0	100	100
49	M	106/121 (88%)	102 (96%)	4 (4%)	0	100	100
50	N	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
51	O	83/89 (93%)	80 (96%)	3 (4%)	0	100	100
52	P	86/90 (96%)	85 (99%)	1 (1%)	0	100	100
53	Q	82/87 (94%)	82 (100%)	0	0	100	100
54	R	62/79 (78%)	59 (95%)	3 (5%)	0	100	100
55	S	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
56	T	81/88 (92%)	81 (100%)	0	0	100	100
All	All	5897/6367 (93%)	5764 (98%)	124 (2%)	9 (0%)	44	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	g	347	LEU
5	h	83	PRO
5	h	87	GLU
6	p	108	ILE
24	r	40	PRO

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	
4	g	4/381 (1%)	4 (100%)	0	100	100
5	h	3/85 (4%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	p	105/139 (76%)	105 (100%)	0	100	100
7	q	103/110 (94%)	103 (100%)	0	100	100
10	Z	220/225 (98%)	220 (100%)	0	100	100
11	a	167/169 (99%)	167 (100%)	0	100	100
12	b	169/170 (99%)	168 (99%)	1 (1%)	78	81
13	c	151/154 (98%)	151 (100%)	0	100	100
14	d	148/151 (98%)	148 (100%)	0	100	100
15	e	120/123 (98%)	120 (100%)	0	100	100
16	f	101/101 (100%)	101 (100%)	0	100	100
17	i	110/110 (100%)	110 (100%)	0	100	100
18	j	109/116 (94%)	109 (100%)	0	100	100
19	k	99/100 (99%)	99 (100%)	0	100	100
20	l	93/93 (100%)	93 (100%)	0	100	100
21	m	100/100 (100%)	100 (100%)	0	100	100
22	n	96/98 (98%)	96 (100%)	0	100	100
23	o	83/84 (99%)	83 (100%)	0	100	100
24	r	90/93 (97%)	90 (100%)	0	100	100
25	s	81/85 (95%)	81 (100%)	0	100	100
26	t	85/87 (98%)	85 (100%)	0	100	100
27	u	64/74 (86%)	64 (100%)	0	100	100
28	v	47/50 (94%)	47 (100%)	0	100	100
29	w	56/57 (98%)	50 (89%)	6 (11%)	6	25
30	x	52/53 (98%)	52 (100%)	0	100	100
31	0	48/53 (91%)	48 (100%)	0	100	100
32	1	46/47 (98%)	46 (100%)	0	100	100
33	2	39/39 (100%)	39 (100%)	0	100	100
34	3	54/56 (96%)	54 (100%)	0	100	100
35	4	35/35 (100%)	35 (100%)	0	100	100
36	6	53/55 (96%)	53 (100%)	0	100	100
38	B	189/212 (89%)	189 (100%)	0	100	100
39	C	168/178 (94%)	168 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	D	169/173 (98%)	169 (100%)	0	100	100
41	E	128/130 (98%)	128 (100%)	0	100	100
42	F	81/84 (96%)	81 (100%)	0	100	100
43	G	125/132 (95%)	125 (100%)	0	100	100
44	H	111/112 (99%)	111 (100%)	0	100	100
45	I	98/102 (96%)	98 (100%)	0	100	100
46	J	86/92 (94%)	86 (100%)	0	100	100
47	K	86/100 (86%)	86 (100%)	0	100	100
48	L	114/116 (98%)	114 (100%)	0	100	100
49	M	94/104 (90%)	94 (100%)	0	100	100
50	N	53/54 (98%)	53 (100%)	0	100	100
51	O	80/83 (96%)	80 (100%)	0	100	100
52	P	74/76 (97%)	74 (100%)	0	100	100
53	Q	77/80 (96%)	77 (100%)	0	100	100
54	R	56/64 (88%)	56 (100%)	0	100	100
55	S	70/81 (86%)	70 (100%)	0	100	100
56	T	66/70 (94%)	66 (100%)	0	100	100
All	All	4656/5336 (87%)	4649 (100%)	7 (0%)	85	87

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	w	22	LYS
29	w	24	GLU
29	w	28	LEU
29	w	25	LEU
29	w	21	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
42	F	33	ASN
51	O	18	HIS
43	G	19	ASN
46	J	56	HIS

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Mol	Chain	Res	Type
55	S	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	U	76/77 (98%)	18 (23%)	0
2	V	7/8 (87%)	2 (28%)	0
3	W	265/266 (99%)	127 (47%)	2 (0%)
37	A	1532/1533 (99%)	433 (28%)	11 (0%)
8	X	2881/2887 (99%)	741 (25%)	25 (0%)
9	Y	111/112 (99%)	31 (27%)	2 (1%)
All	All	4872/4883 (99%)	1352 (27%)	40 (0%)

5 of 1352 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	U	8	U
1	U	16	U
1	U	17	U
1	U	18	G
1	U	38	C

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	Y	48	G
37	A	848	G
37	A	260	U
37	A	455	G
37	A	1157	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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$
57	G4P	g	501	-	36,38,38	3.12	16 (44%)	56,61,61	1.57	12 (21%)

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	G4P	g	501	-	-	2/27/43/43	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	g	501	G4P	O4'-C1'	8.91	1.62	1.42
57	g	501	G4P	C2'-C1'	-7.08	1.31	1.53
57	g	501	G4P	C4-N3	6.41	1.48	1.34
57	g	501	G4P	O4'-C4'	-5.84	1.32	1.45
57	g	501	G4P	C2-N3	5.09	1.45	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	g	501	G4P	C5-C4-N3	-5.23	120.06	128.39
57	g	501	G4P	C2-N3-C4	4.71	120.42	112.30
57	g	501	G4P	N9-C8-N7	-2.75	108.31	113.40
57	g	501	G4P	N9-C4-N3	2.58	131.11	125.95
57	g	501	G4P	C2-N1-C6	-2.44	120.68	125.11

There are no chirality outliers.

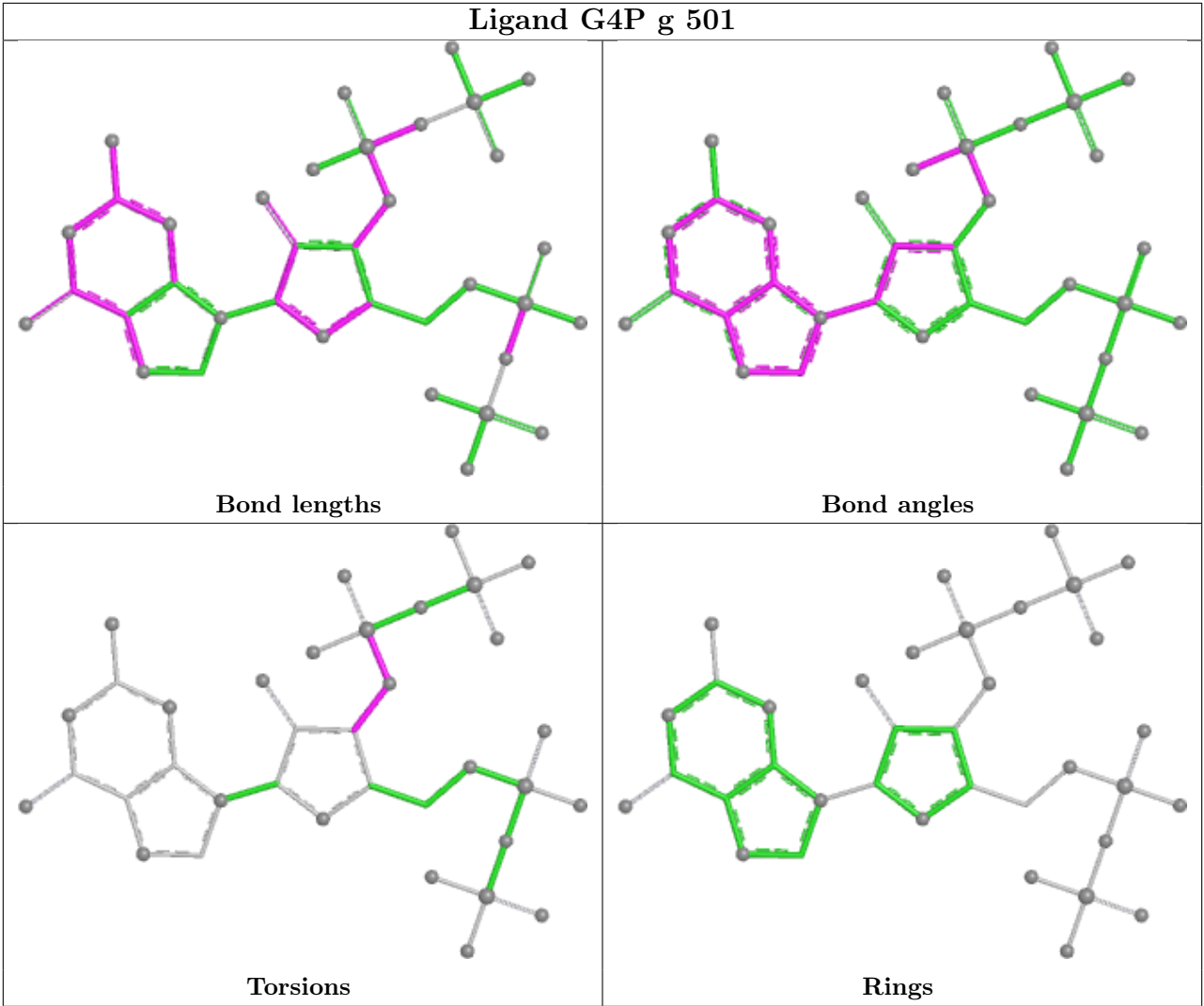
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	g	501	G4P	C4'-C3'-O3'-PC
57	g	501	G4P	C3'-O3'-PC-O2C

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	X	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	399:C	O3'	406:G	P	23.95

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	1577:C	O3'	1589:G	P	17.01
1	X	1553:A	O3'	1555:A	P	7.39

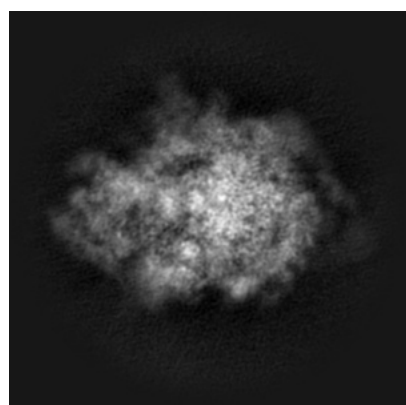
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12734. These allow visual inspection of the internal detail of the map and identification of artifacts.

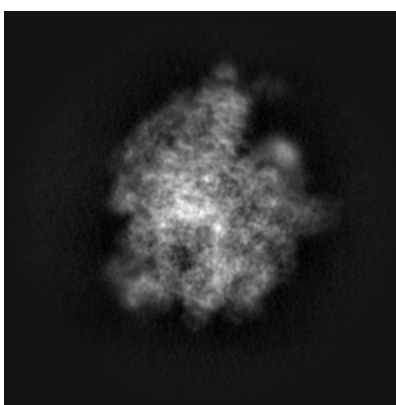
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

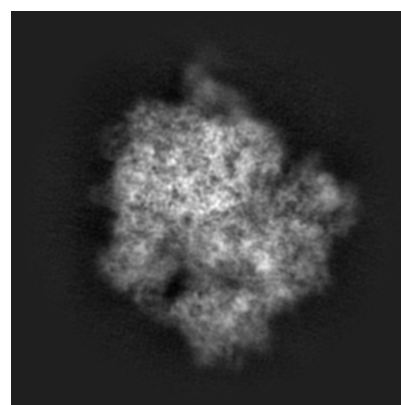
6.1.1 Primary map



X



Y

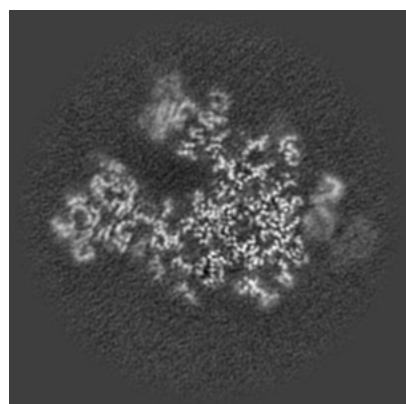


Z

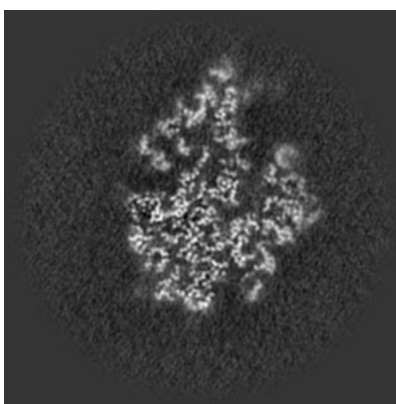
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

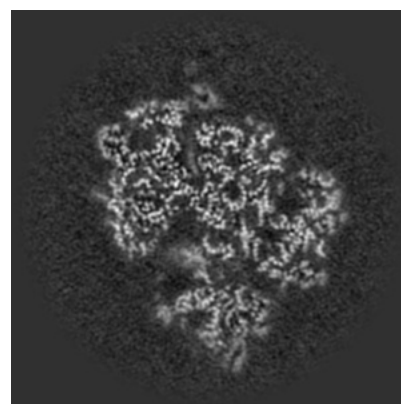
6.2.1 Primary map



X Index: 180



Y Index: 180

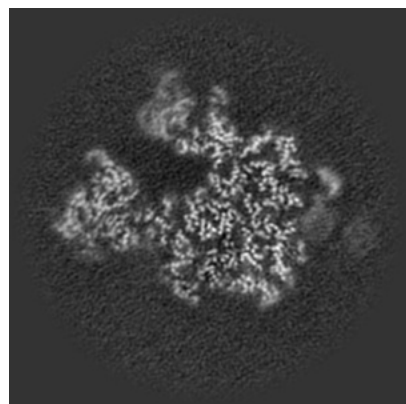


Z Index: 180

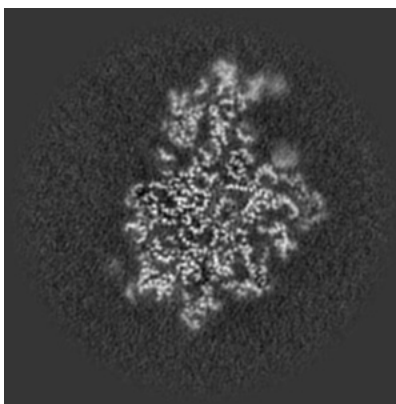
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

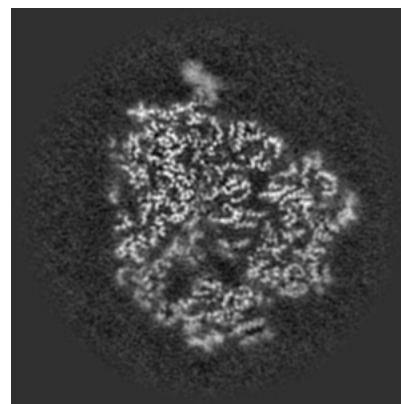
6.3.1 Primary map



X Index: 185



Y Index: 189

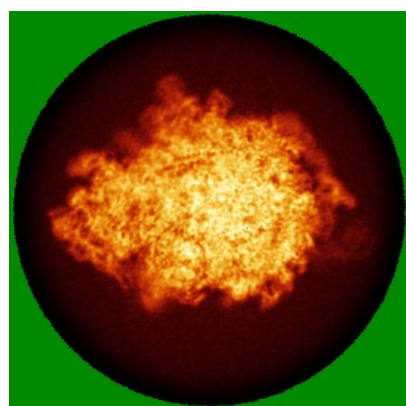


Z Index: 191

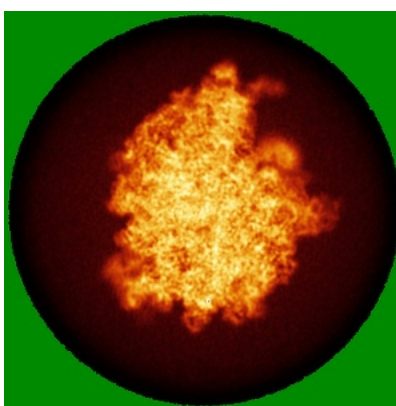
The images above show the largest variance slices of the map in three orthogonal directions.

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

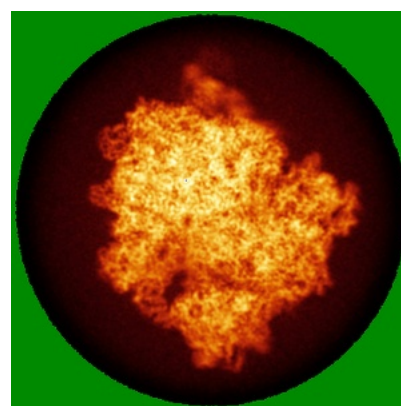
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.479. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

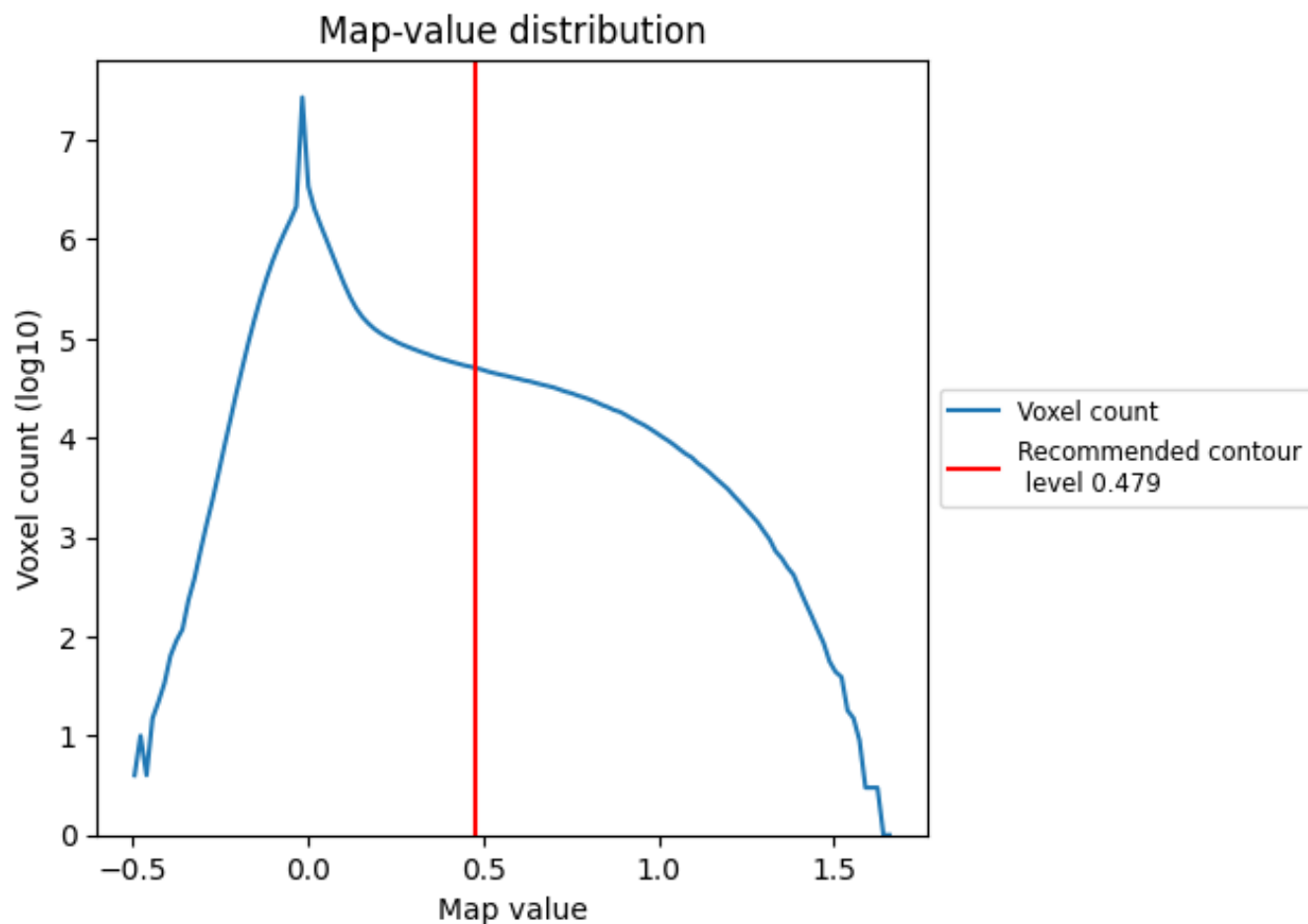
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

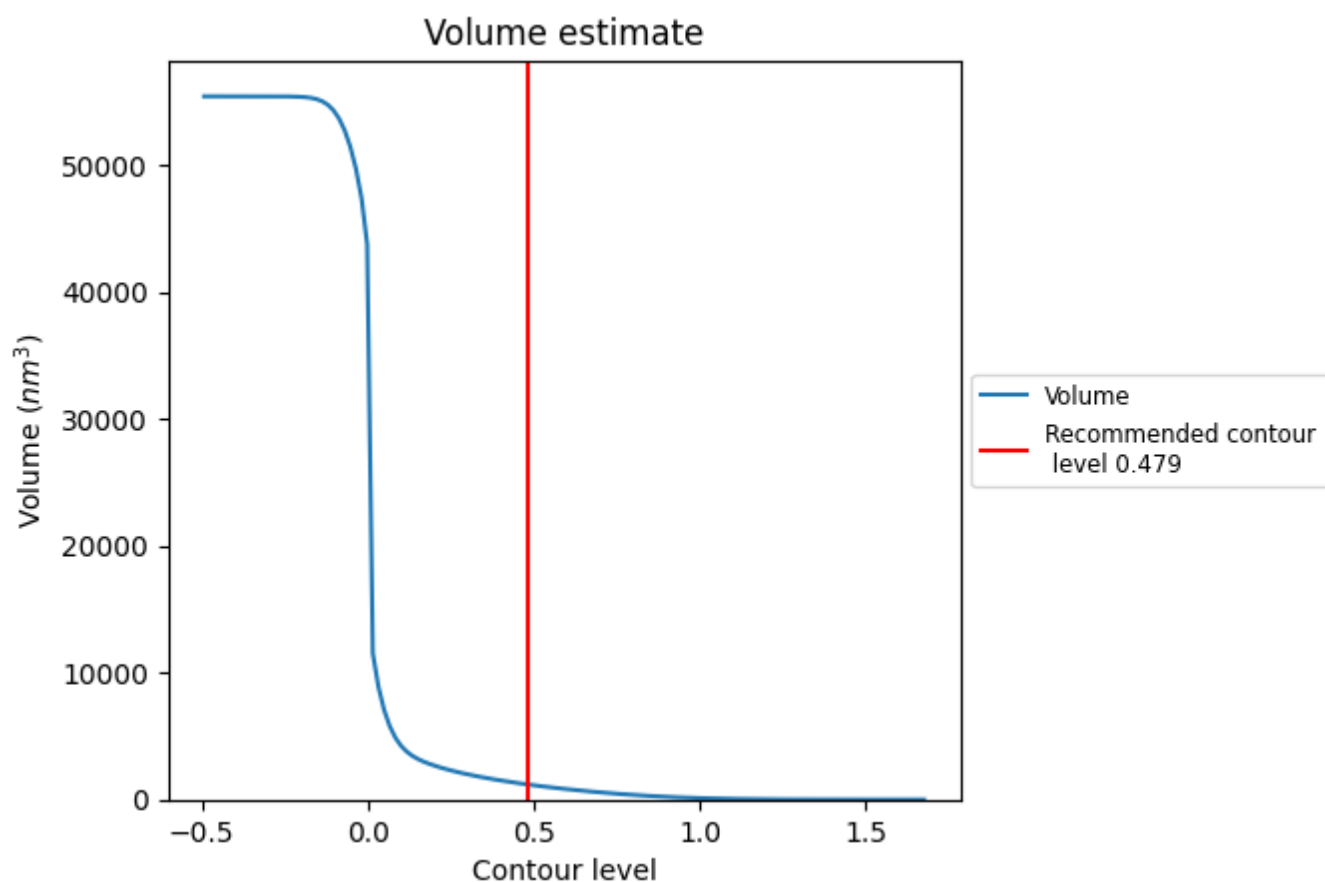
This section contains the results of statistical analysis of the map.

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.

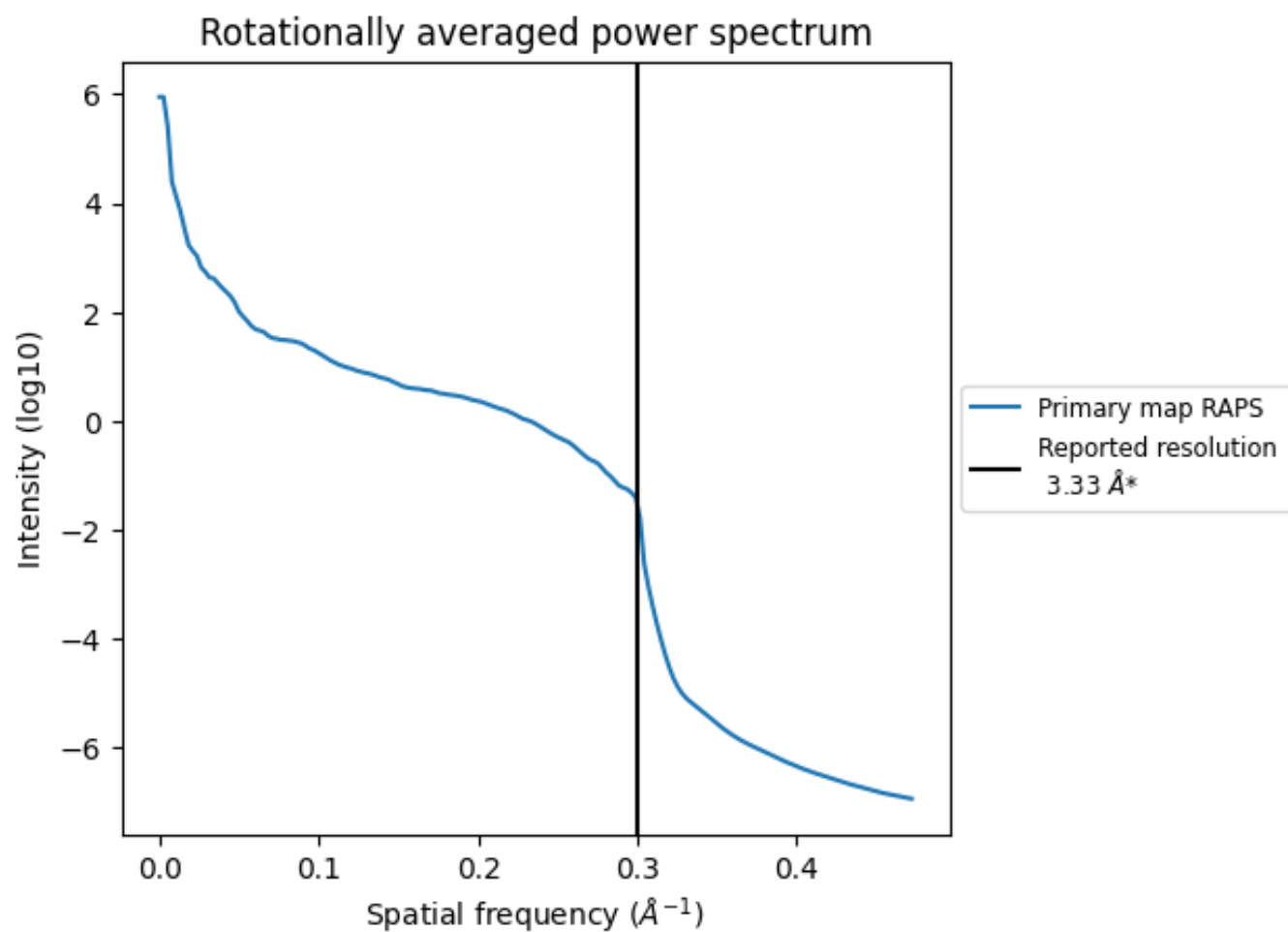
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1198 nm³; this corresponds to an approximate mass of 1082 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 0.300 Å⁻¹

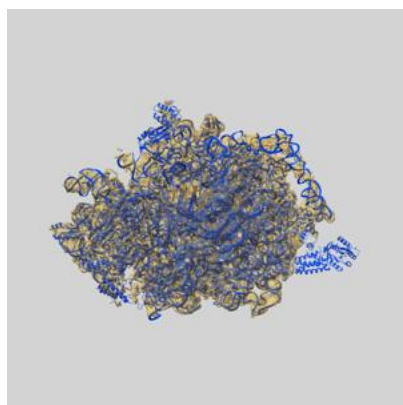
8 Fourier-Shell correlation ⓘ

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

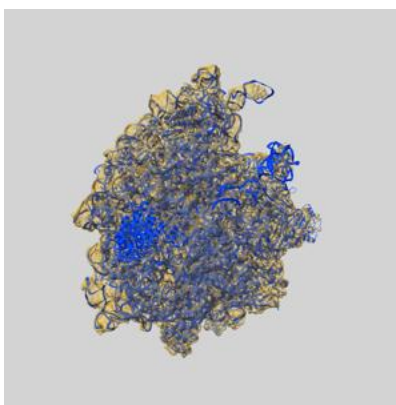
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12734 and PDB model 7O5B. Per-residue inclusion information can be found in section [3](#) on page [17](#).

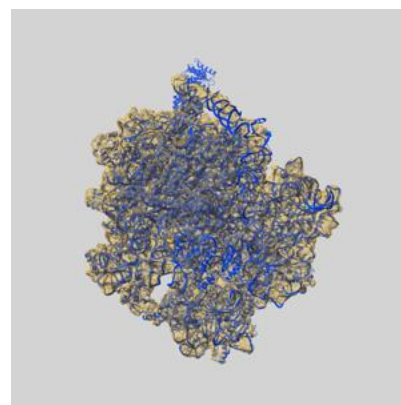
9.1 Map-model overlay [i](#)



X



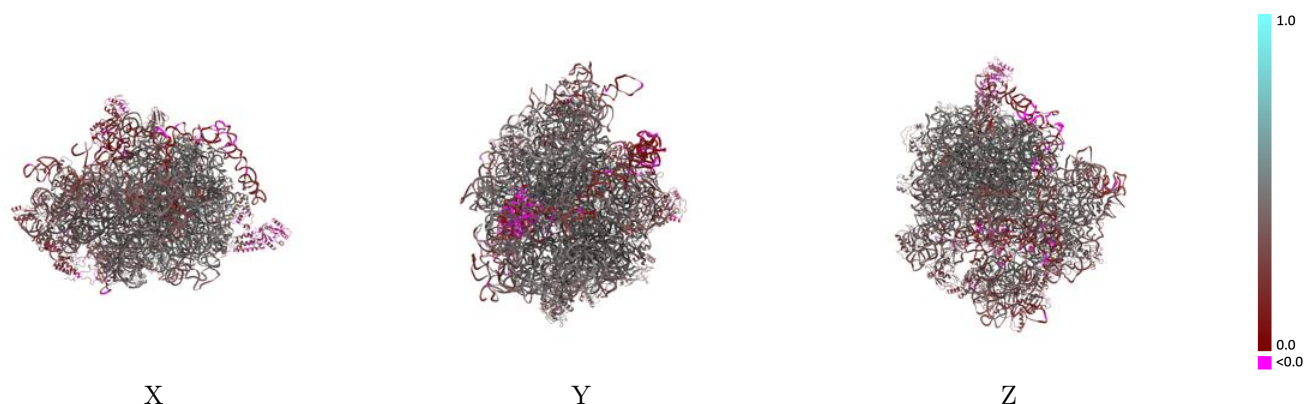
Y



Z

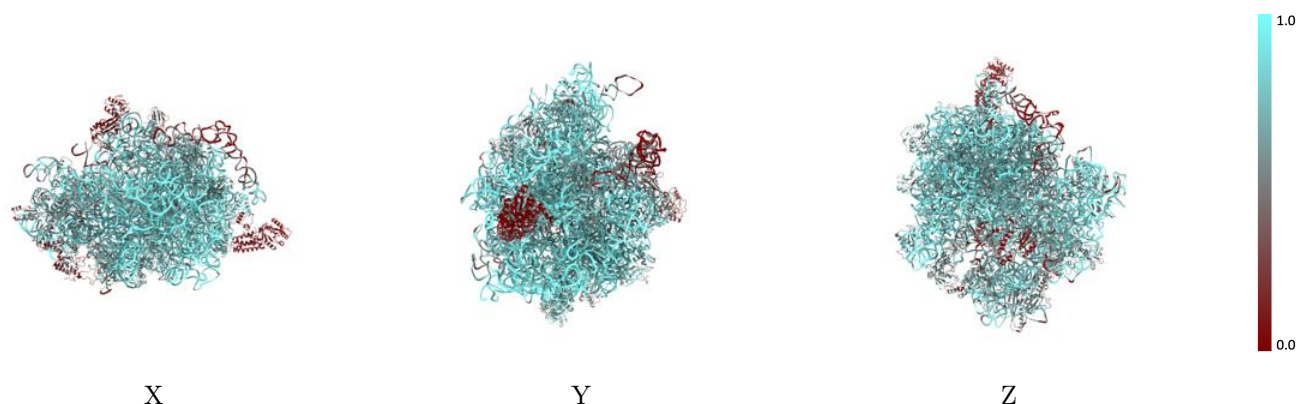
The images above show the 3D surface view of the map at the recommended contour level 0.479 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



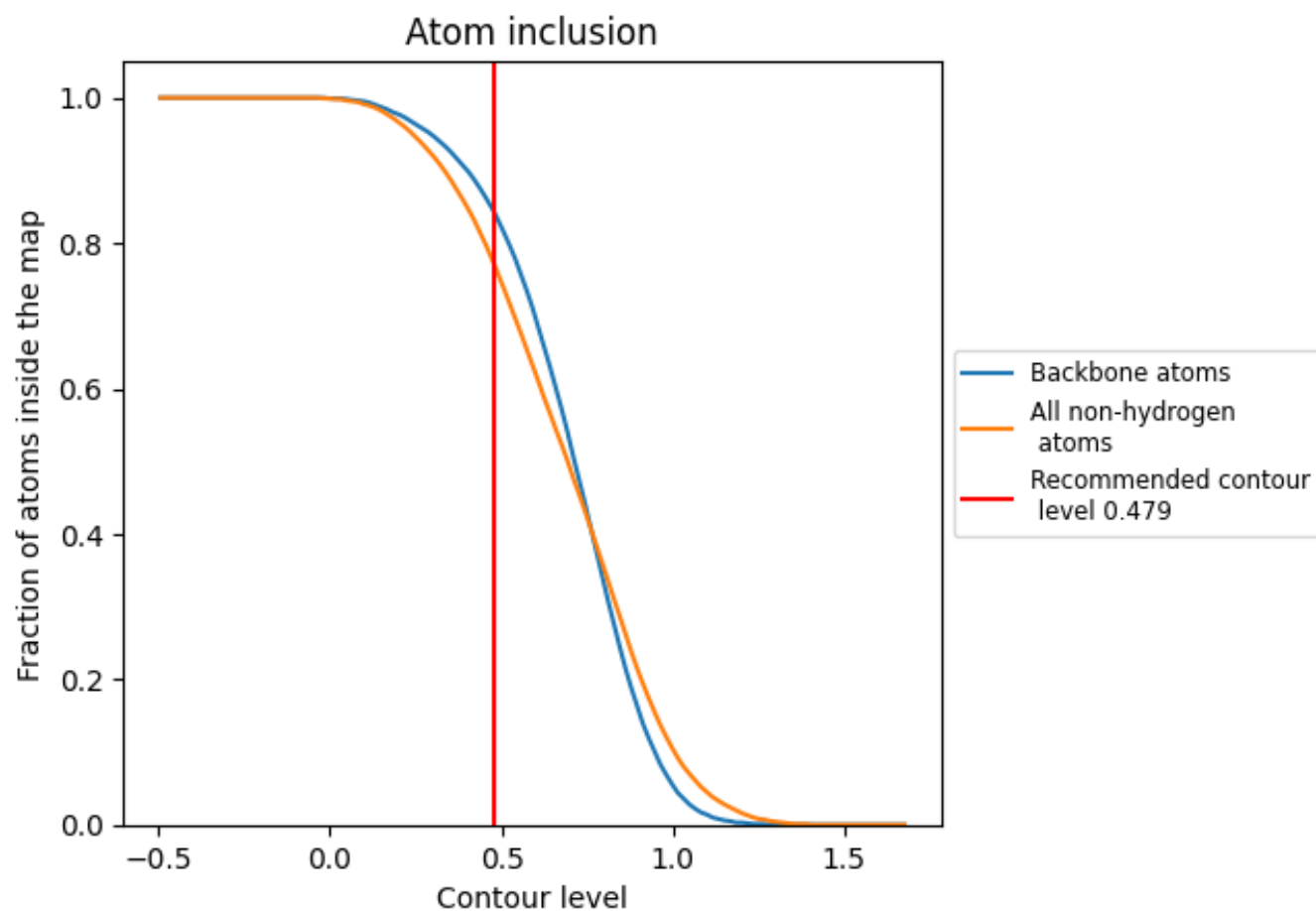
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.479).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 77% 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 (0.479) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7710	 0.3810
0	 0.6710	 0.4440
1	 0.6360	 0.4280
2	 0.7420	 0.4780
3	 0.6290	 0.4670
4	 0.6280	 0.4410
6	 0.4760	 0.2500
A	 0.8830	 0.3860
B	 0.2370	 0.2130
C	 0.5480	 0.3360
D	 0.5540	 0.3150
E	 0.6060	 0.3980
F	 0.6290	 0.4070
G	 0.4570	 0.2340
H	 0.6380	 0.4010
I	 0.5310	 0.2700
J	 0.4920	 0.3060
K	 0.6050	 0.3750
L	 0.5730	 0.4190
M	 0.5410	 0.2990
N	 0.5980	 0.3800
O	 0.6530	 0.3940
P	 0.6560	 0.3750
Q	 0.5970	 0.4190
R	 0.6370	 0.4000
S	 0.5470	 0.3170
T	 0.6160	 0.3200
U	 0.7290	 0.3300
V	 0.5250	 0.3330
W	 0.4540	 0.1290
X	 0.8930	 0.4180
Y	 0.9030	 0.3790
Z	 0.6960	 0.4740
a	 0.6500	 0.4500
b	 0.6680	 0.4290



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Chain	Atom inclusion	Q-score
c	 0.5350	 0.3080
d	 0.5370	 0.3330
e	 0.6780	 0.4300
f	 0.5850	 0.4480
g	 0.1410	 0.1360
h	 0.0900	 0.1950
i	 0.6850	 0.4380
j	 0.6140	 0.4280
k	 0.6950	 0.4450
l	 0.6230	 0.3490
m	 0.6170	 0.4320
n	 0.7050	 0.4030
o	 0.6510	 0.4210
p	 0.1600	 0.1280
q	 0.1120	 0.1560
r	 0.6450	 0.4460
s	 0.6530	 0.4480
t	 0.6360	 0.4220
u	 0.6550	 0.4320
v	 0.5230	 0.4400
w	 0.6340	 0.3690
x	 0.6160	 0.4180