wwPDB EM Validation Summary Report (i)

Nov 11, 2026 – 11:15 AM JST

PDB ID	:	24NW / pdb_000024nw
EMDB ID	:	EMD-69709
Title	:	tRNA bound M. smegmatis 70S ribosome in complex with EF-G1.
Authors	:	Sengupta, J.; Dhur, A.; Baid, P.; Srinivasan, K.
Deposited on	:	2026-03-12
Resolution	:	5.10 Å(reported)
Based on initial model	:	5O61

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 (i) 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 (i)) were used in the production of this report:

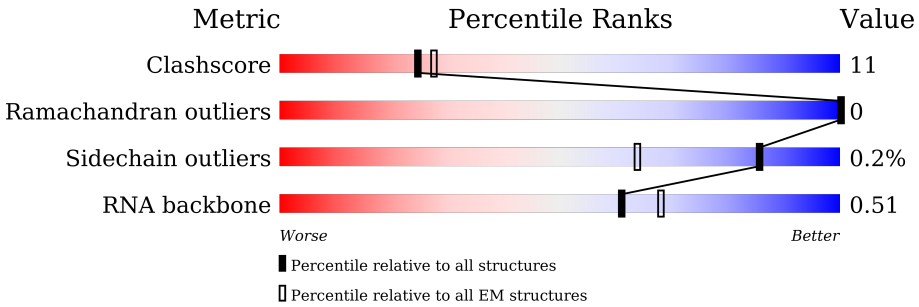
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.51

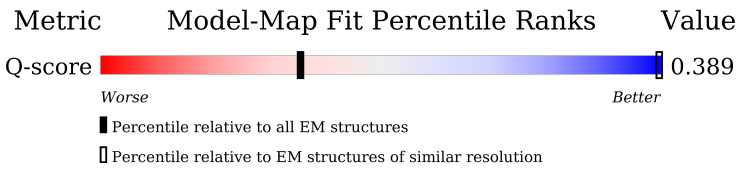
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	2	77	8% 34% 53% 13%
2	3	24	8% 79% 17%
3	4	3	100%

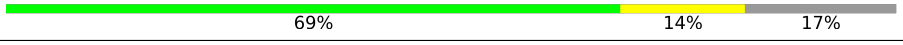
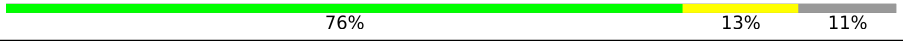
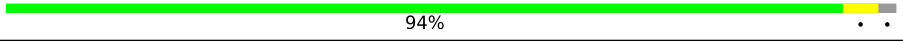
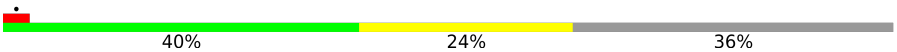
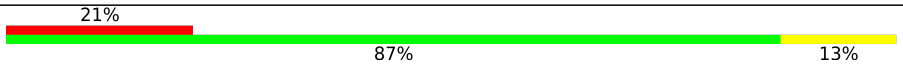
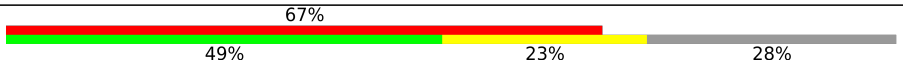
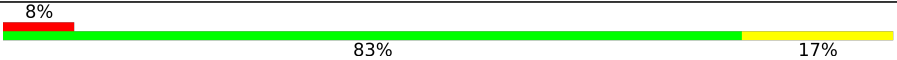
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Mol	Chain	Length	Quality of chain
4	5	701	42% 65% 35%
5	6	235	51% 61% 38%
6	A	1528	37% 50% 11%
7	B	118	52% 41% 8%
8	C	275	8% 55% 20% 24%
9	D	201	24% 65% 34%
10	E	214	8% 59% 25% 16%
11	F	96	72% 28%
12	G	156	26% 72% 27%
13	H	132	78% 21%
14	I	150	11% 57% 27% 16%
15	J	101	20% 57% 40%
16	K	138	64% 19% 17%
17	L	124	10% 73% 25%
18	M	124	22% 58% 35% 6%
19	N	61	72% 26%
20	O	89	78% 21%
21	P	156	14% 47% 26% 28%
22	Q	98	9% 64% 32%
23	R	84	67% 11% 23%
24	S	93	17% 72% 16% 12%
25	T	86	5% 67% 31%
26	U	100	79% 18%
27	W	215	7% 75% 14% 11%
28	X	88	81% 9% 10%

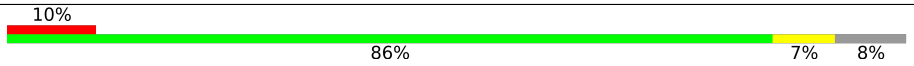
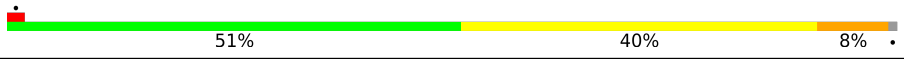
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Mol	Chain	Length	Quality of chain
29	Y	64	
30	Z	77	
31	a	61	
32	b	57	
33	c	55	
34	d	47	
35	e	64	
36	f	37	
37	g	75	
38	i	278	
39	j	217	
40	k	215	
41	l	187	
42	m	179	
43	n	151	
44	o	142	
45	p	175	
46	q	147	
47	r	122	
48	s	147	
49	t	138	
50	u	199	
51	v	127	
52	w	113	
53	x	129	

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Mol	Chain	Length	Quality of chain
54	y	103	
55	z	153	
56	1	105	
57	h	3120	

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 155100 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
			Total	C	N	O	P		
1	2	77	1644	732	297	538	77	0	0

- Molecule 2 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	3	23	189	111	50	28	0	0

- Molecule 3 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	3	60	27	7	23	3	0	0

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	701	5441	3433	916	1071	21	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	6	232	1736	1084	313	336	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	A	1511	32439	14448	5930	10550	1511	0	0

- Molecule 7 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 13 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 14 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	126	Total 994	C 630	N 194	O 170	0	0

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	99	Total 788	C 495	N 146	O 144	S 3	0	0

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	115	Total 855	C 528	N 170	O 156	S 1	0	0

- Molecule 17 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total 958	C 594	N 197	O 165	S 2	0	0

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	116	Total 935	C 572	N 191	O 169	S 3	0	0

- Molecule 19 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	60	Total 477	C 302	N 97	O 73	S 5	0	0

- Molecule 20 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	O	88	Total 720	C 449	N 147	O 124	0	0

- Molecule 21 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	113	Total 891	C 570	N 162	O 159	0	0

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	94	Total 748	C 469	N 142	O 135	S 2	0	0

- Molecule 23 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	65	Total 513	C 318	N 102	O 90	S 3	0	0

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	82	Total 662	C 425	N 124	O 112	S 1	0	0

- Molecule 25 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	85	Total 660	C 402	N 139	O 119	0	0

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	97	Total 756	C 479	N 138	O 139	0	0

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	W	192	Total 1428	C 881	N 255	O 292	0	0

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 32 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 33 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 34 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 35 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 36 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 37 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 38 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 39 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 40 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 41 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 42 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 43 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 44 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 45 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 46 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 47 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 48 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 49 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 51 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	v	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 52 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 53 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	x	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 54 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	y	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 55 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	z	114	Total	C	N	O	0	0
			873	543	171	159		

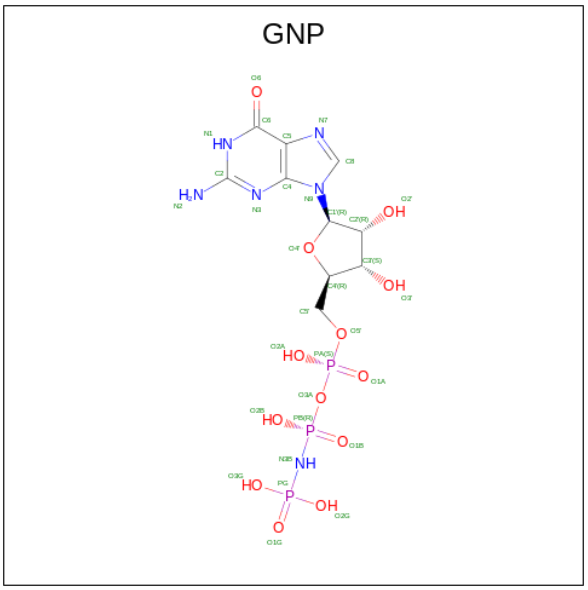
- Molecule 56 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	1	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 57 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	h	3084	Total	C	N	O	P	0	0
			66232	29522	12183	21443	3084		

- Molecule 58 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
59	F	1	Total	Mg	0
			1	1	
59	R	1	Total	Mg	0
			1	1	
59	X	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
59	i	4	Total Mg 4 4	0
59	l	1	Total Mg 1 1	0
59	t	1	Total Mg 1 1	0
59	z	1	Total Mg 1 1	0
59	h	2	Total Mg 2 2	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
60	N	1	Total Zn 1 1	0
60	R	1	Total Zn 1 1	0
60	Y	1	Total Zn 1 1	0
60	c	1	Total Zn 1 1	0
60	f	1	Total Zn 1 1	0
60	g	1	Total Zn 1 1	0

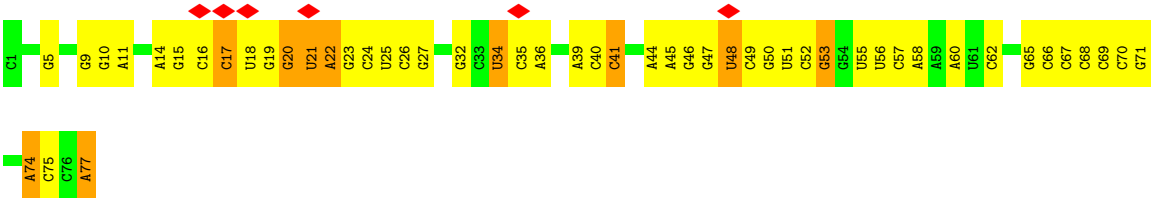
3 Residue-property plots (i)

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

- Molecule 1: tRNA

Chain 2:

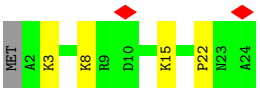




- Molecule 2: 50S ribosomal protein bL37

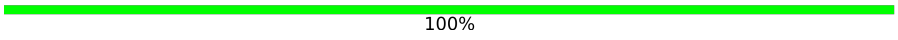
Chain 3:





- Molecule 3: mRNA fragment

Chain 4:

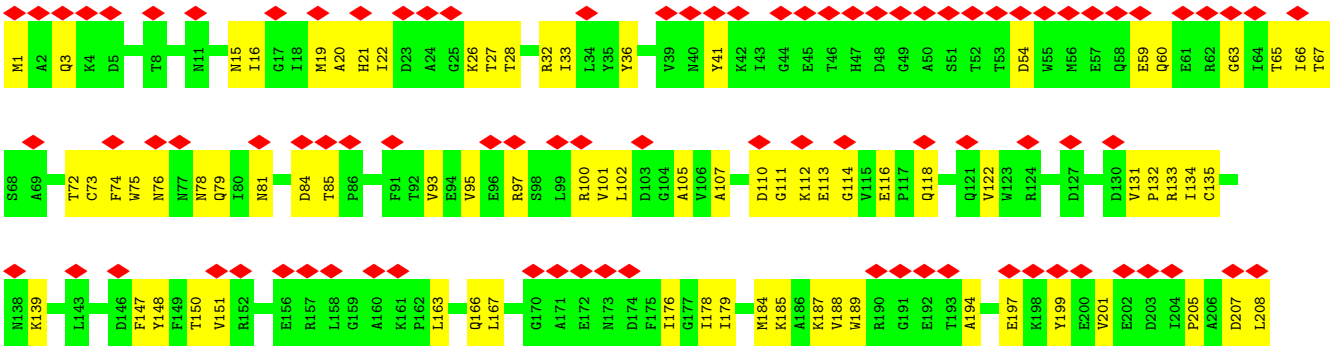


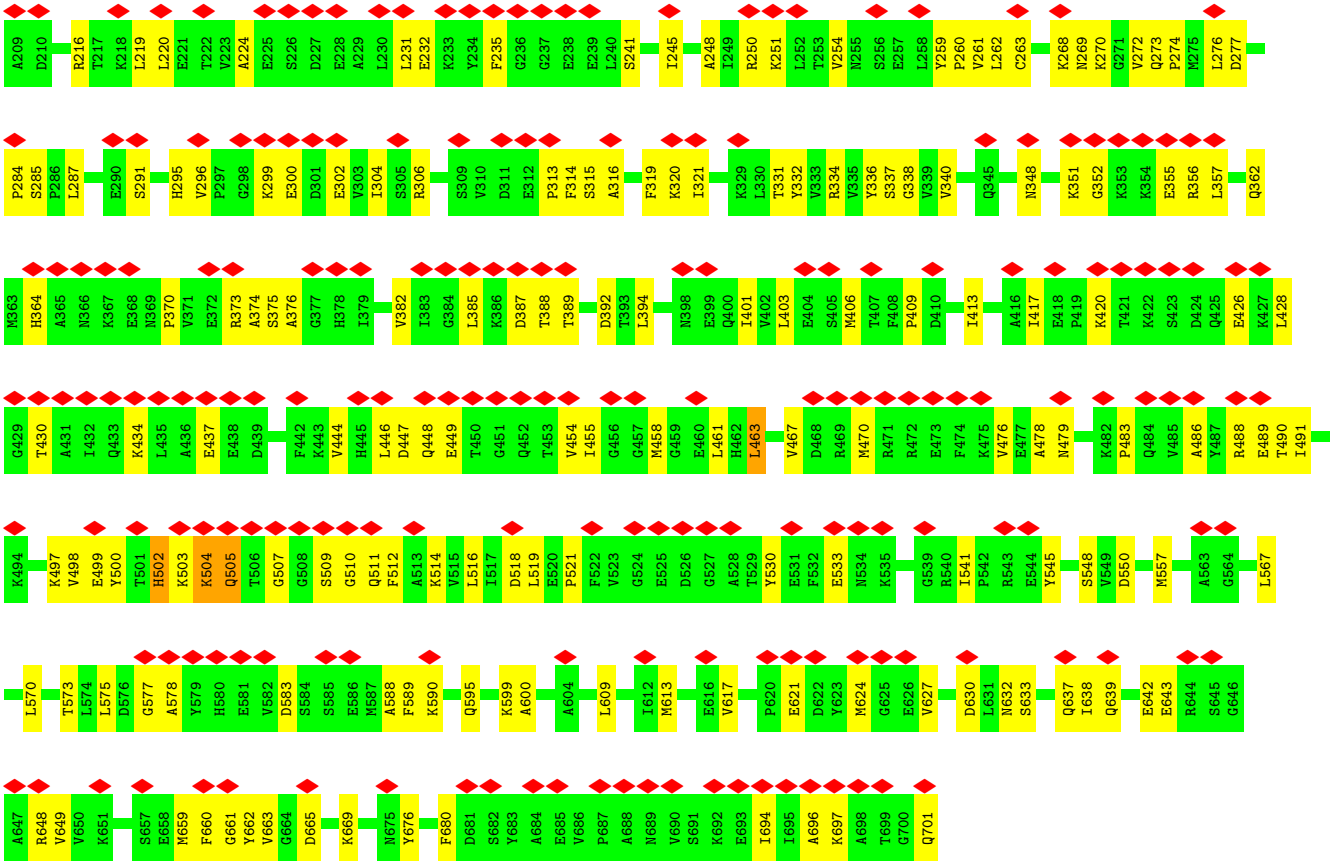
There are no outlier residues recorded for this chain.

- Molecule 4: Elongation factor G

Chain 5:

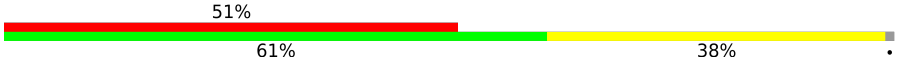


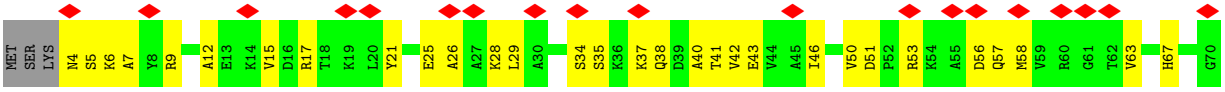


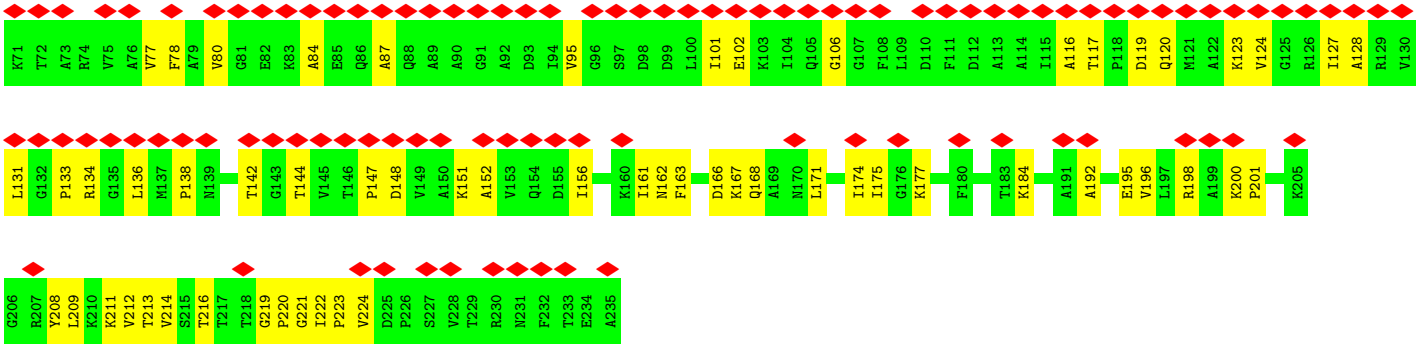


• Molecule 5: Large ribosomal subunit protein uL1

Chain 6:



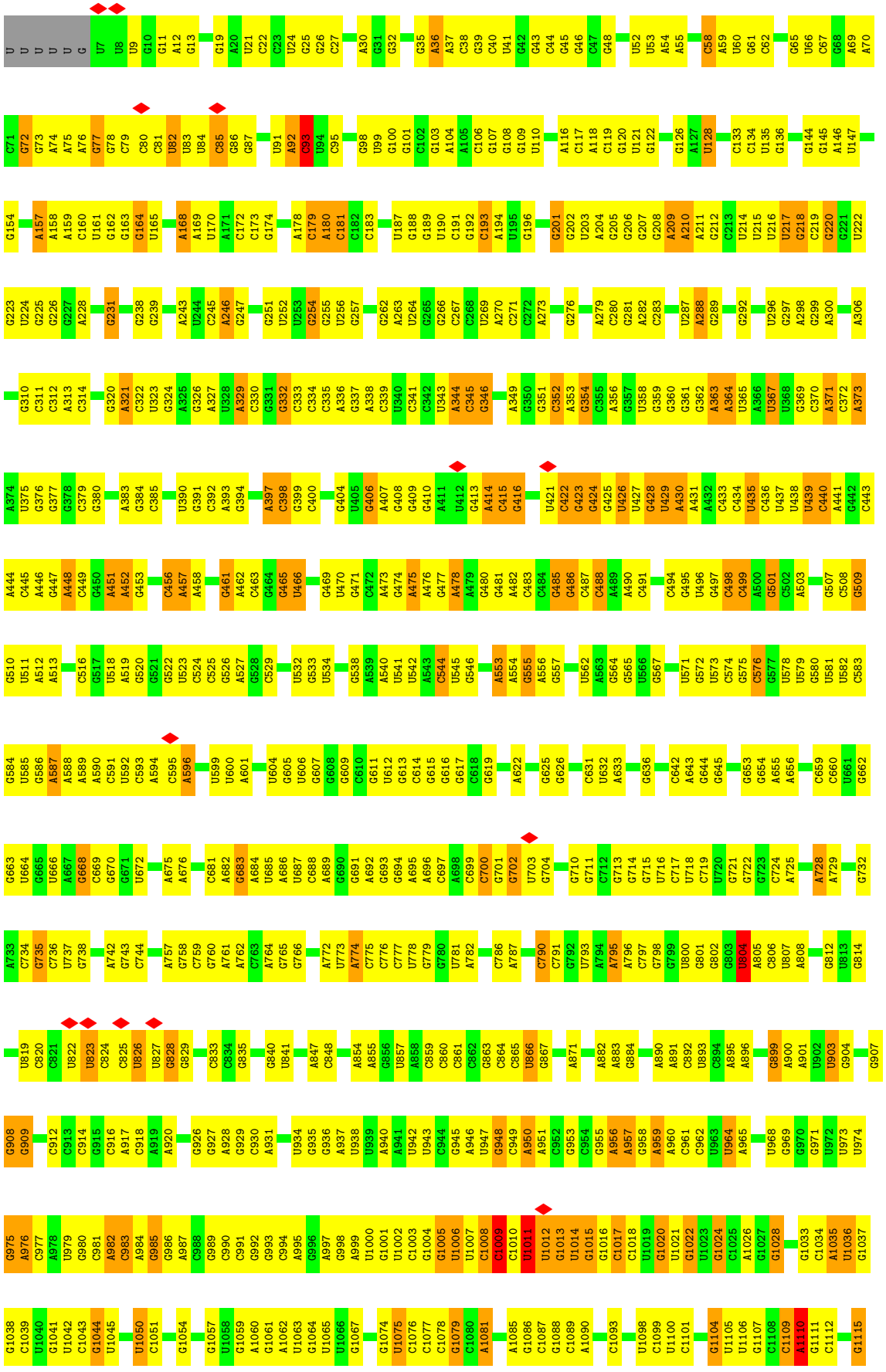


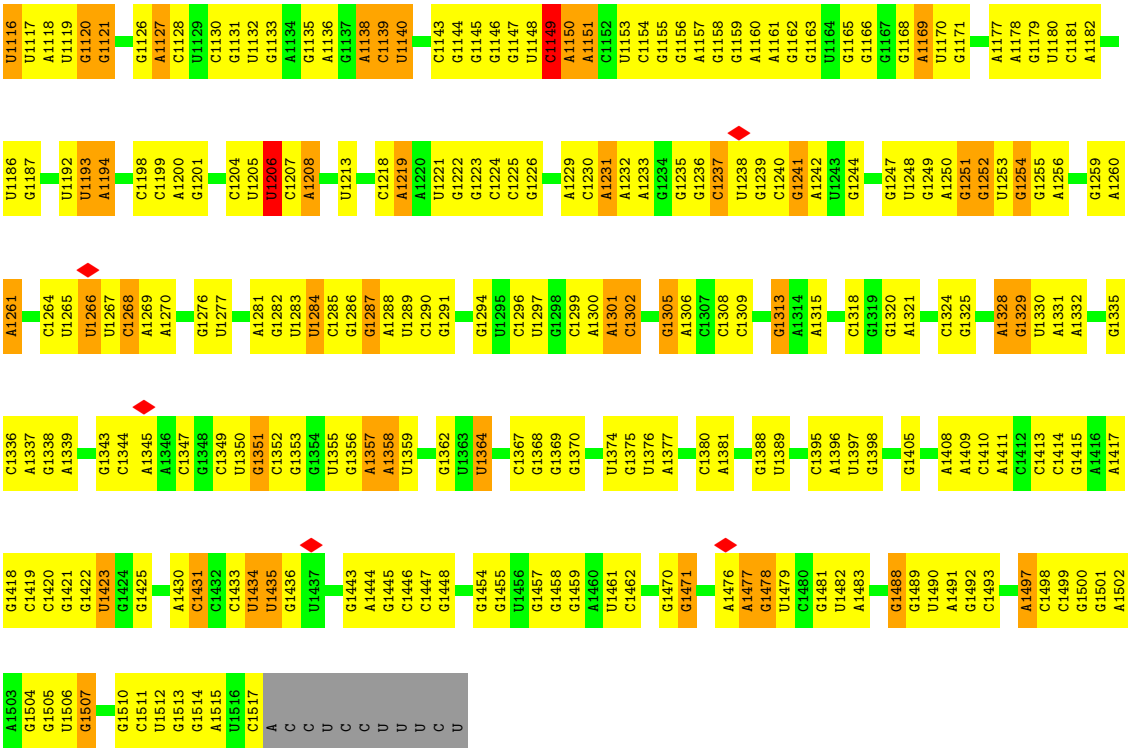


• Molecule 6: 16S ribosomal RNA

Chain A:

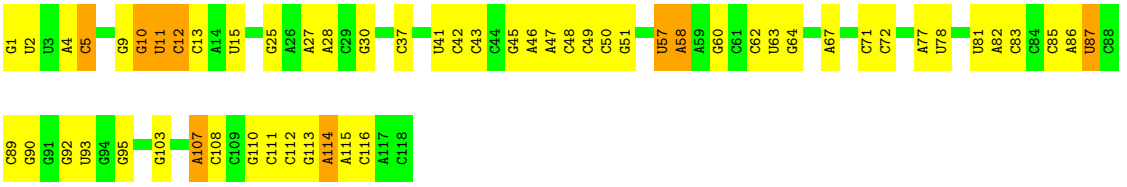






• Molecule 7: 5S ribosomal RNA

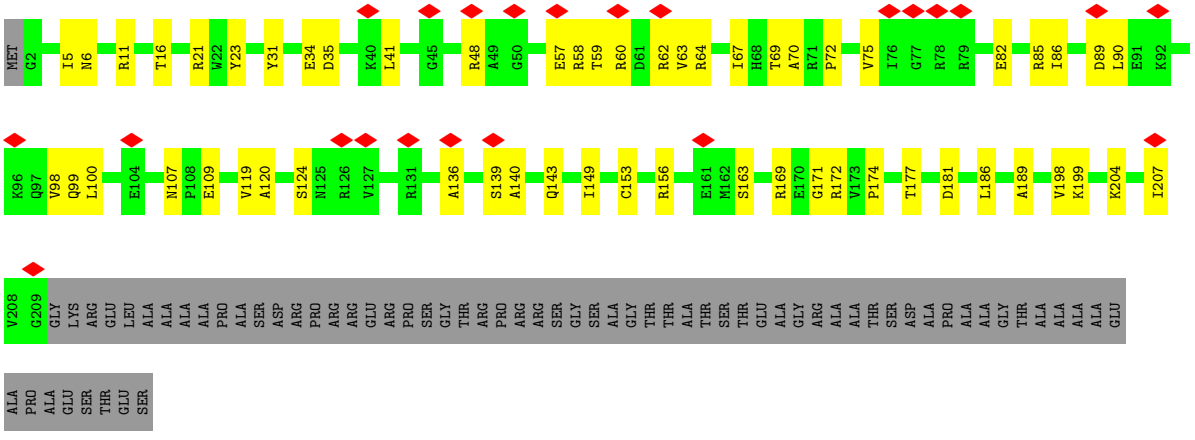
Chain B:



• Molecule 8: 30S ribosomal protein S3

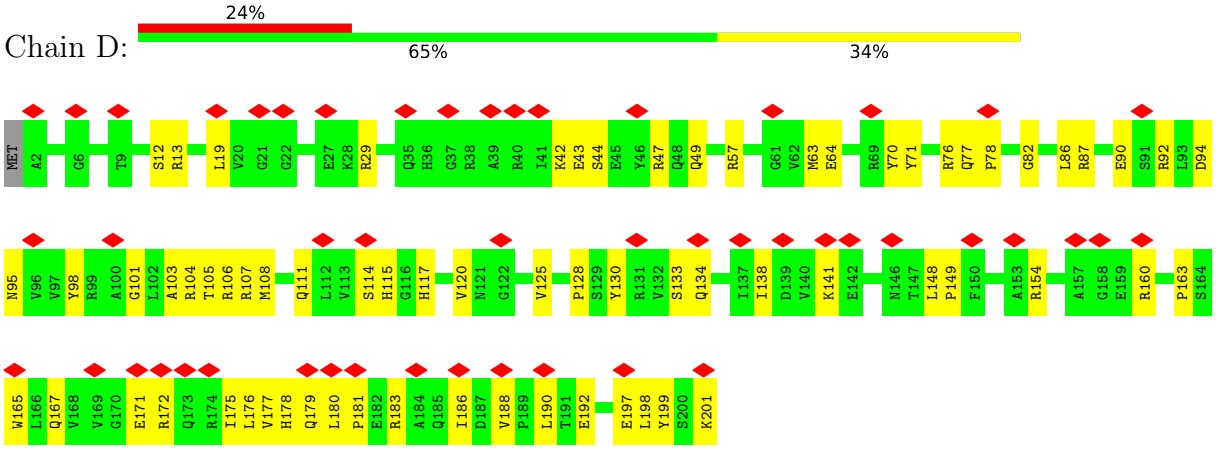
Chain C:





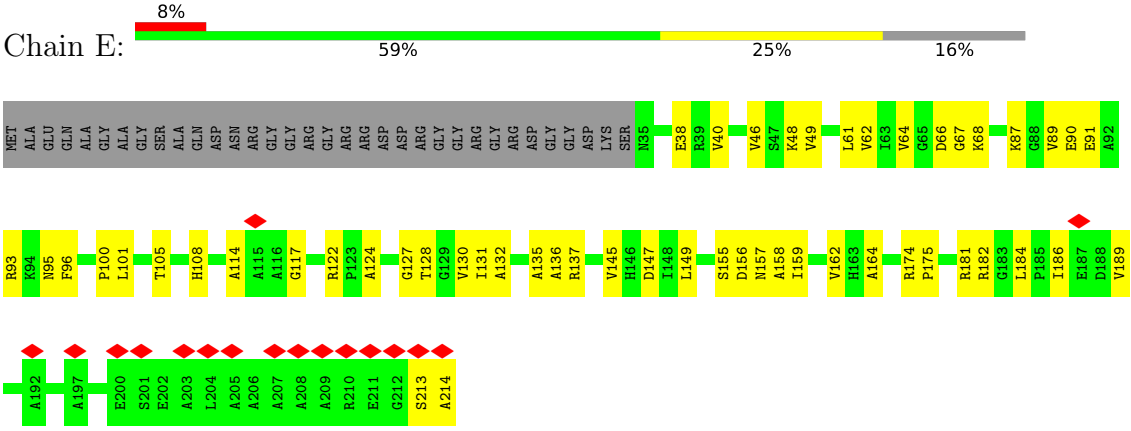
• Molecule 9: 30S ribosomal protein S4

Chain D:



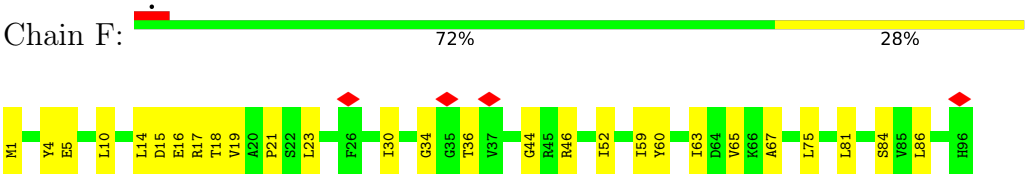
• Molecule 10: 30S ribosomal protein S5

Chain E:



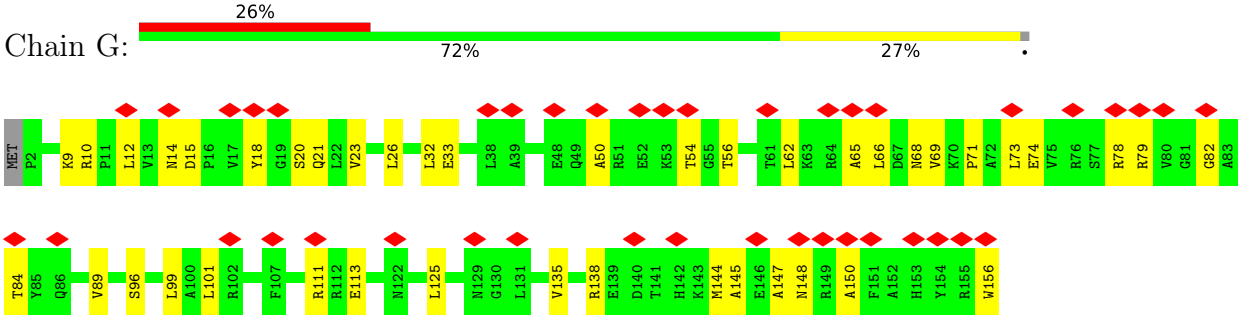
• Molecule 11: Small ribosomal subunit protein bS6

Chain F:



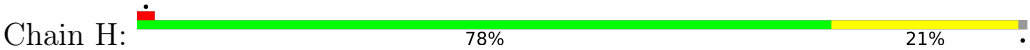
• Molecule 12: 30S ribosomal protein S7

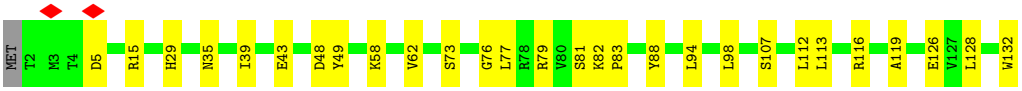
Chain G:



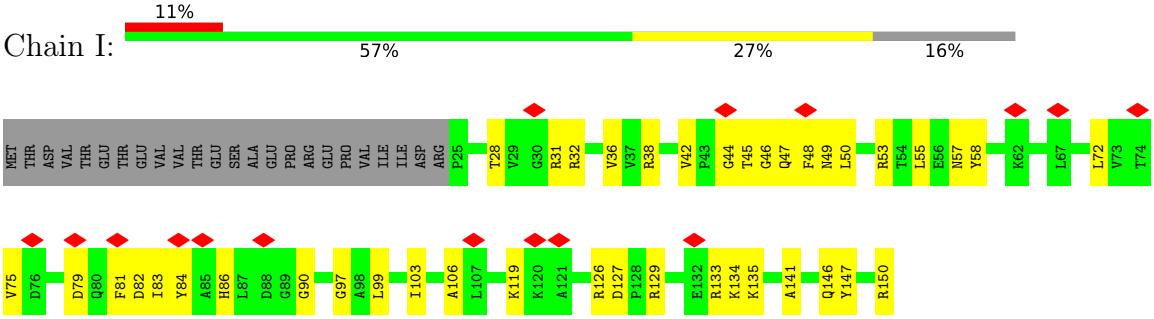
• Molecule 13: 30S ribosomal protein S8

Chain H:

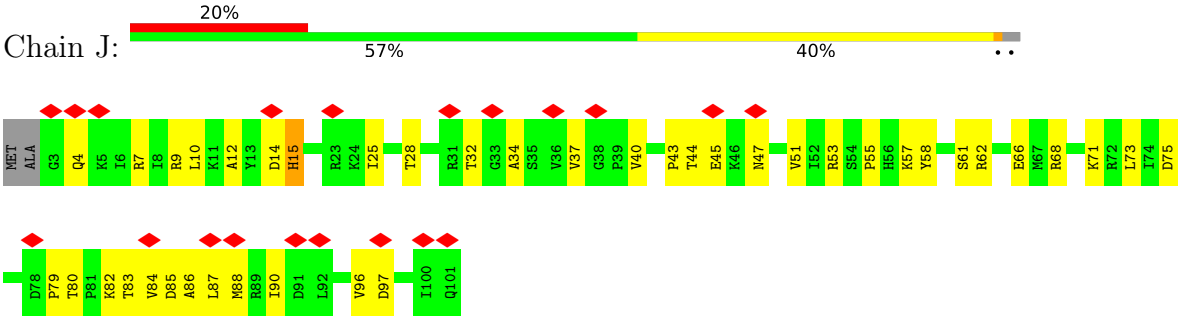




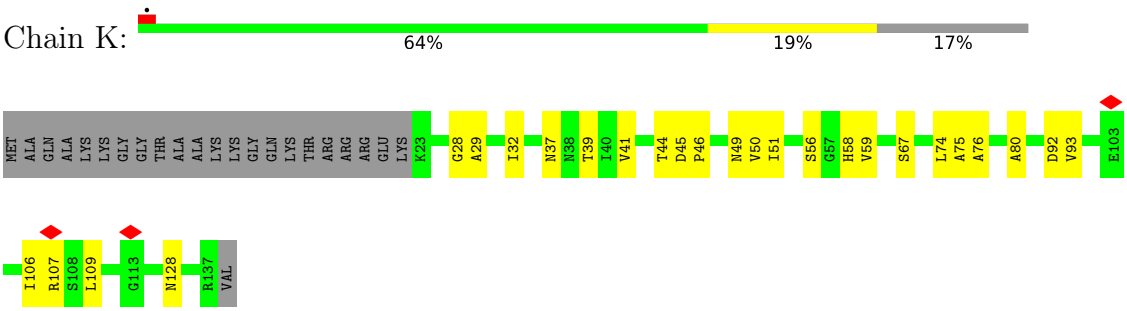
• Molecule 14: 30S ribosomal protein S9



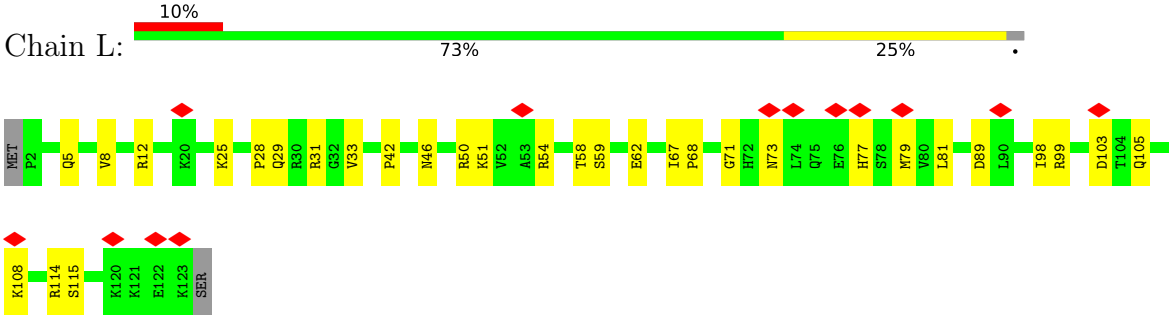
• Molecule 15: 30S ribosomal protein S10



• Molecule 16: 30S ribosomal protein S11

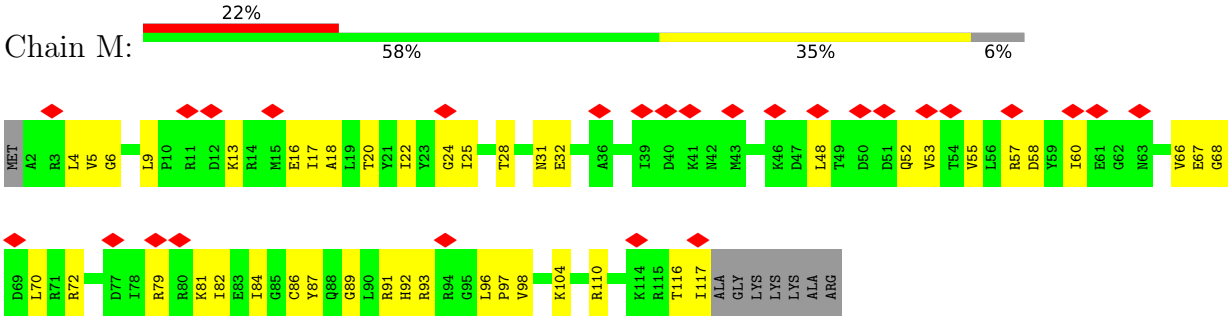


• Molecule 17: 30S ribosomal protein S12



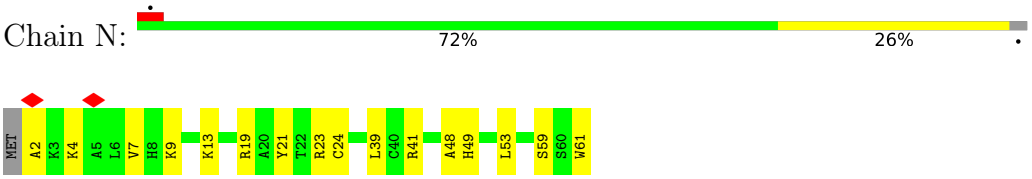
• Molecule 18: 30S ribosomal protein S13

Chain M:



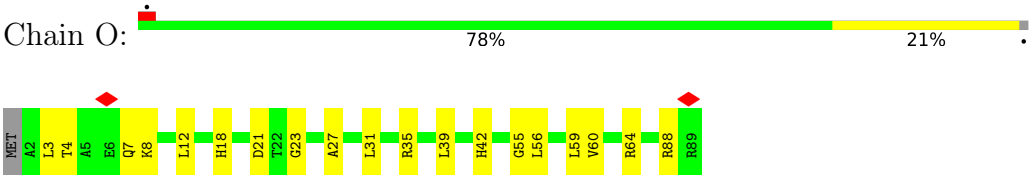
• Molecule 19: 30S ribosomal protein S14 type Z

Chain N:



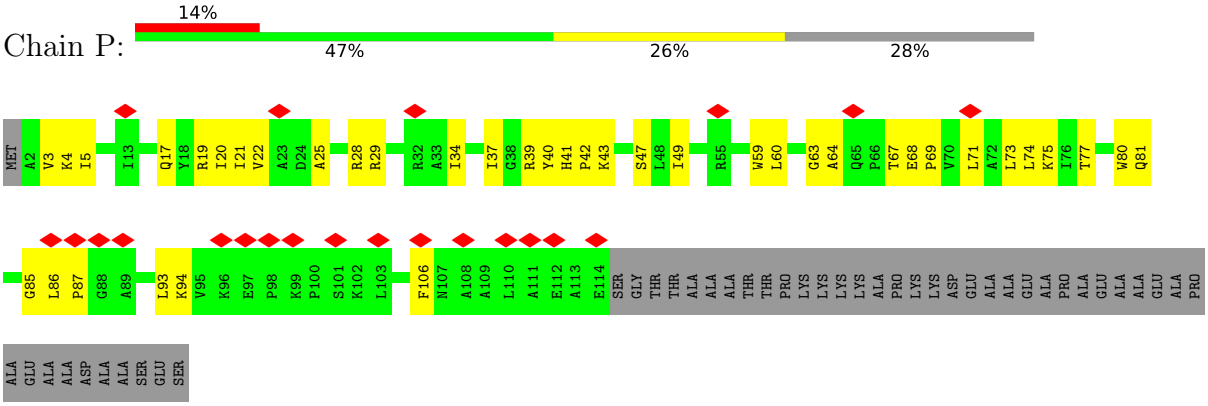
• Molecule 20: 30S ribosomal protein S15

Chain O:



• Molecule 21: 30S ribosomal protein S16

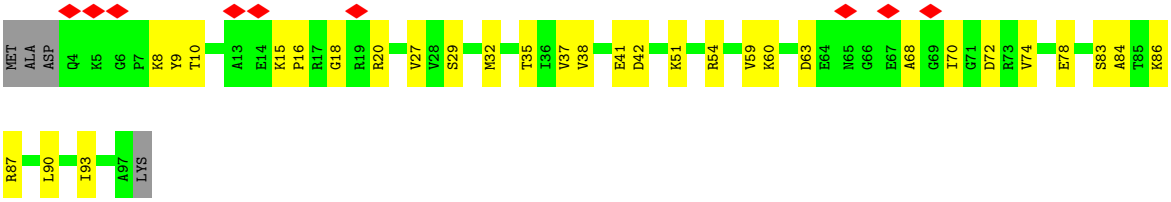
Chain P:



• Molecule 22: 30S ribosomal protein S17

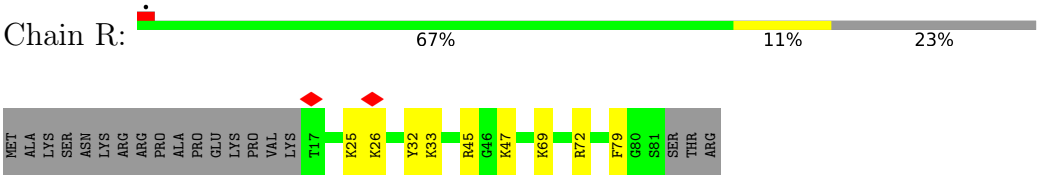
Chain Q:





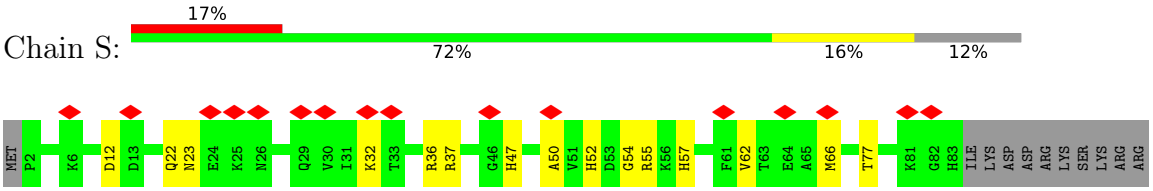
• Molecule 23: 30S ribosomal protein S18 2

Chain R:



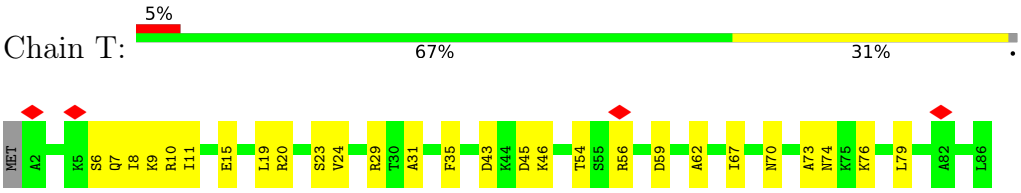
• Molecule 24: 30S ribosomal protein S19

Chain S:



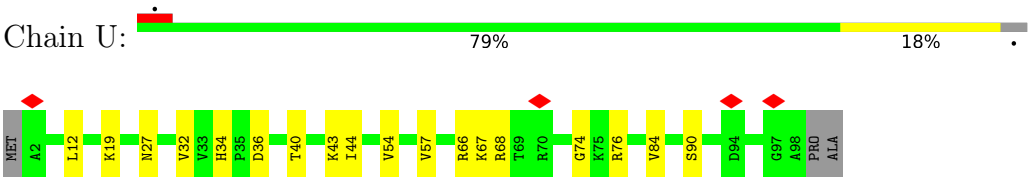
• Molecule 25: 30S ribosomal protein S20

Chain T:



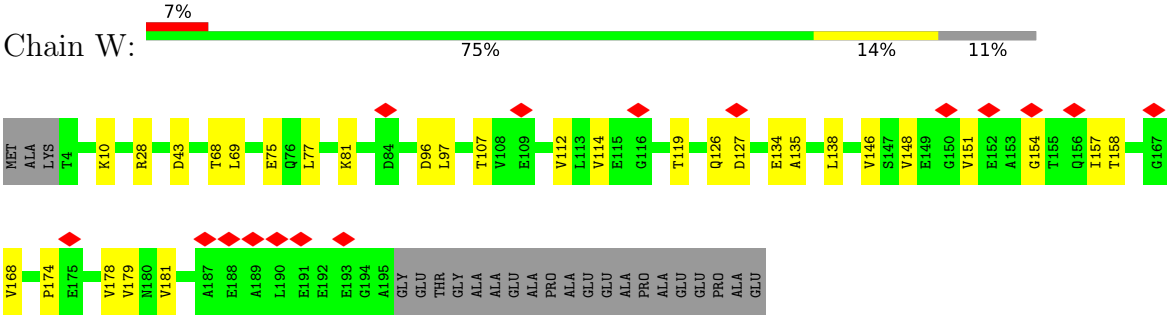
• Molecule 26: 50S ribosomal protein L23

Chain U:



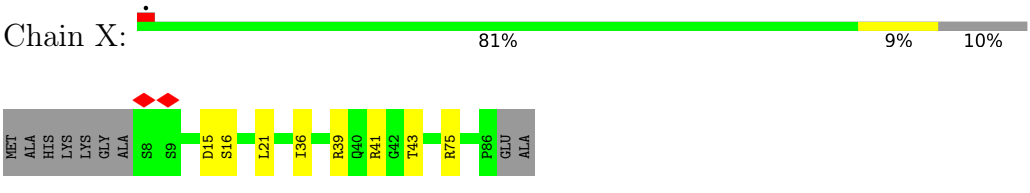
• Molecule 27: 50S ribosomal protein L25

Chain W:



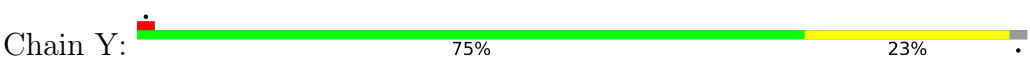
• Molecule 28: 50S ribosomal protein L27

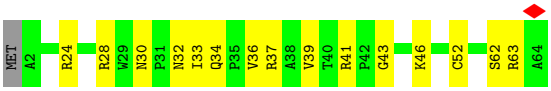
Chain X:



• Molecule 29: 50S ribosomal protein L28

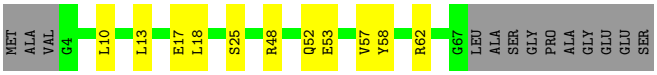
Chain Y:



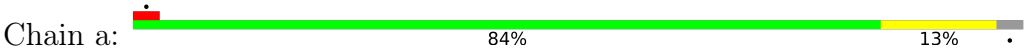


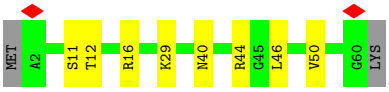
• Molecule 30: 50S ribosomal protein L29



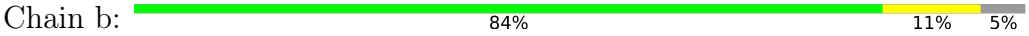


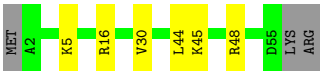
• Molecule 31: 50S ribosomal protein L30





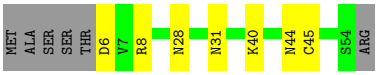
• Molecule 32: 50S ribosomal protein L32





• Molecule 33: 50S ribosomal protein L33 1





• Molecule 34: 50S ribosomal protein L34



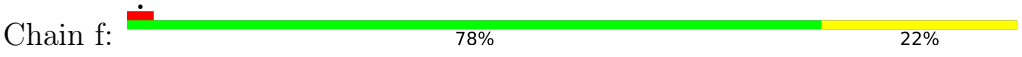


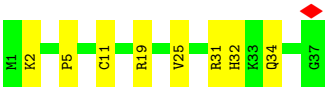
• Molecule 35: 50S ribosomal protein L35





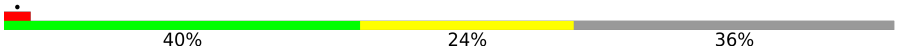
• Molecule 36: 50S ribosomal protein L36

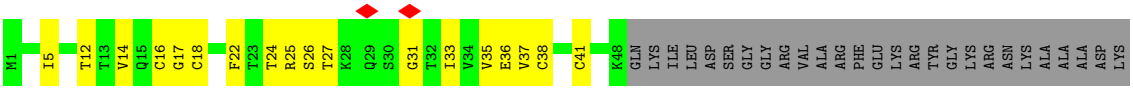




• Molecule 37: 50S ribosomal protein L31

Chain g:

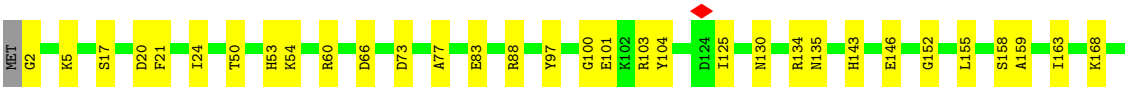




• Molecule 38: 50S ribosomal protein L2

Chain i:

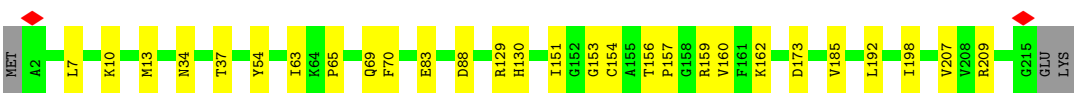




• Molecule 39: 50S ribosomal protein L3

Chain j:

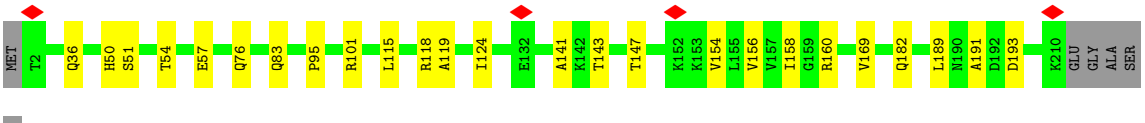




• Molecule 40: 50S ribosomal protein L4

Chain k:

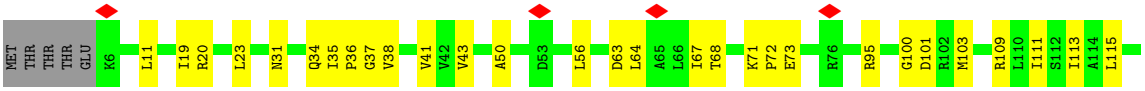


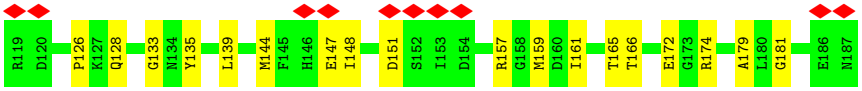


• Molecule 41: 50S ribosomal protein L5

Chain l:



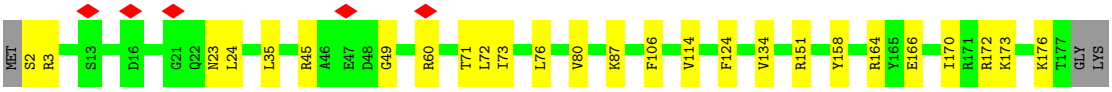




• Molecule 42: 50S ribosomal protein L6

Chain m:

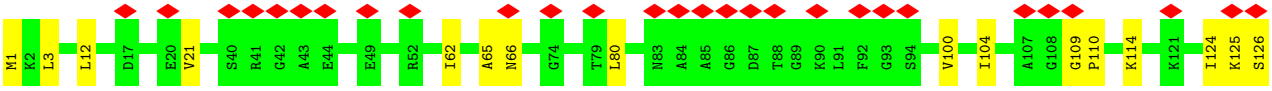


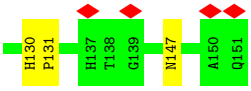


• Molecule 43: 50S ribosomal protein L9

Chain n:



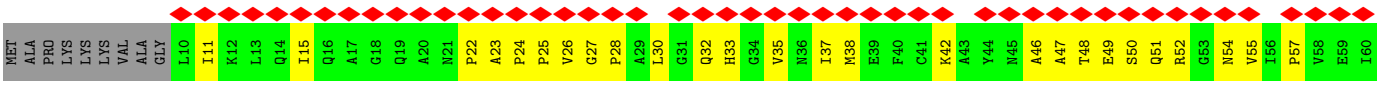


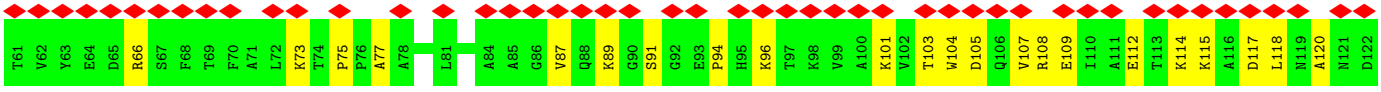


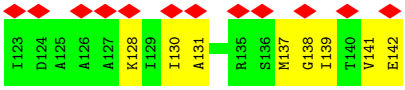
• Molecule 44: 50S ribosomal protein L11

Chain o:





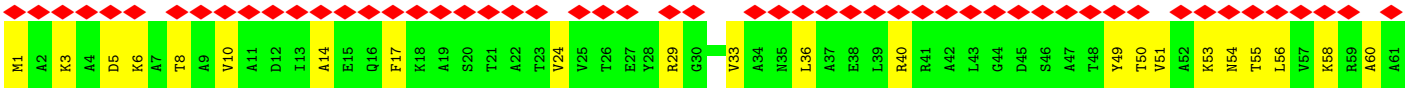


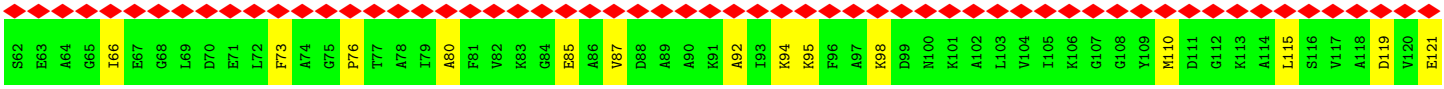


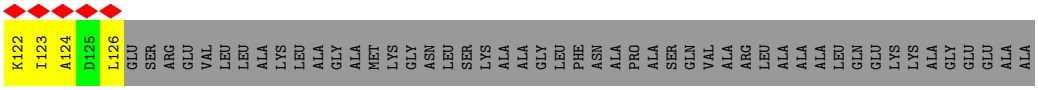
• Molecule 45: 50S ribosomal protein L10

Chain p:

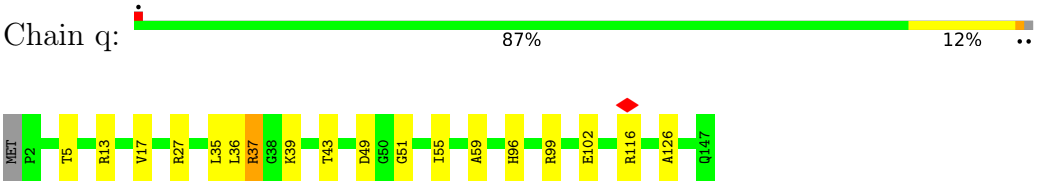




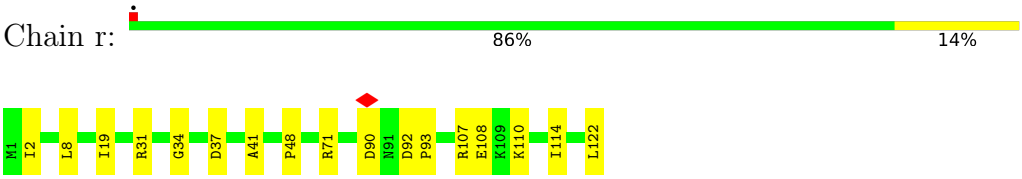




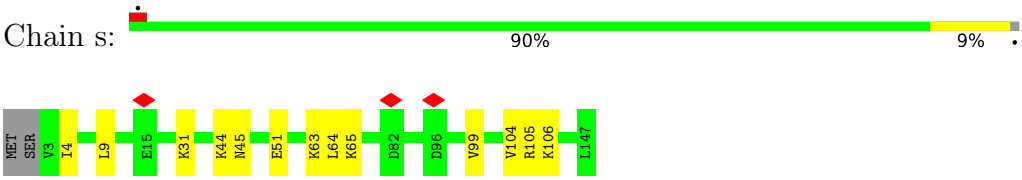
• Molecule 46: 50S ribosomal protein L13



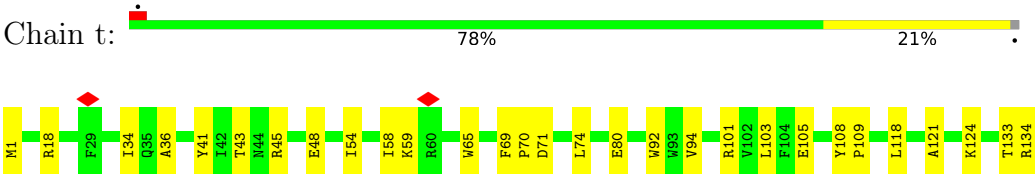
• Molecule 47: 50S ribosomal protein L14



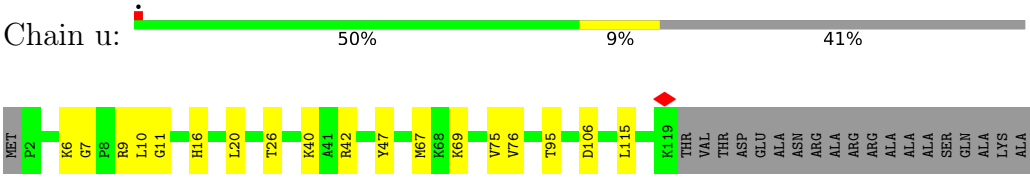
• Molecule 48: 50S ribosomal protein L15



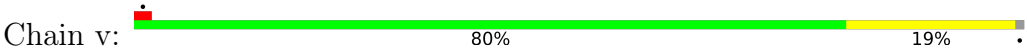
• Molecule 49: 50S ribosomal protein L16

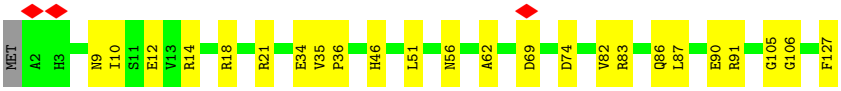


• Molecule 50: 50S ribosomal protein L17



• Molecule 51: 50S ribosomal protein L18





• Molecule 52: 50S ribosomal protein L19

Chain w:

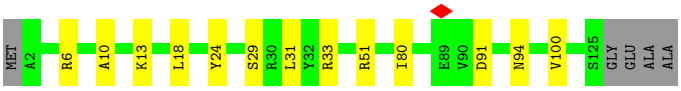




• Molecule 53: 50S ribosomal protein L20

Chain x:

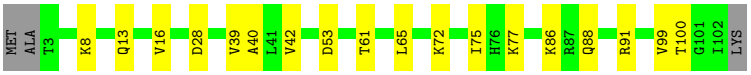




• Molecule 54: 50S ribosomal protein L21

Chain y:

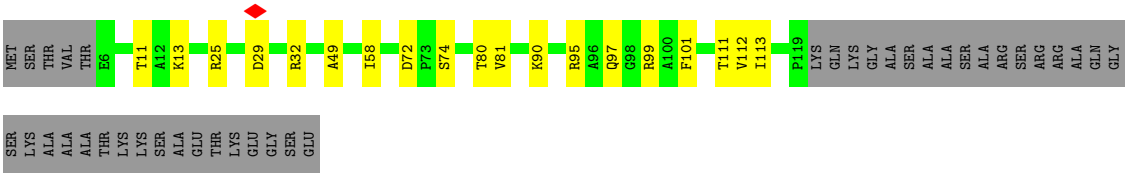




• Molecule 55: 50S ribosomal protein L22

Chain z:

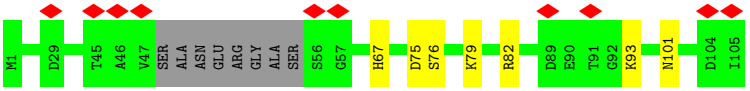




• Molecule 56: Large ribosomal subunit protein uL24

Chain 1:

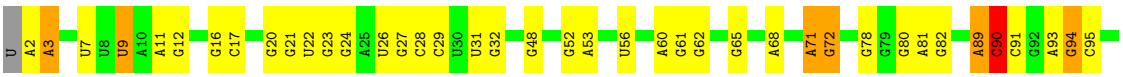


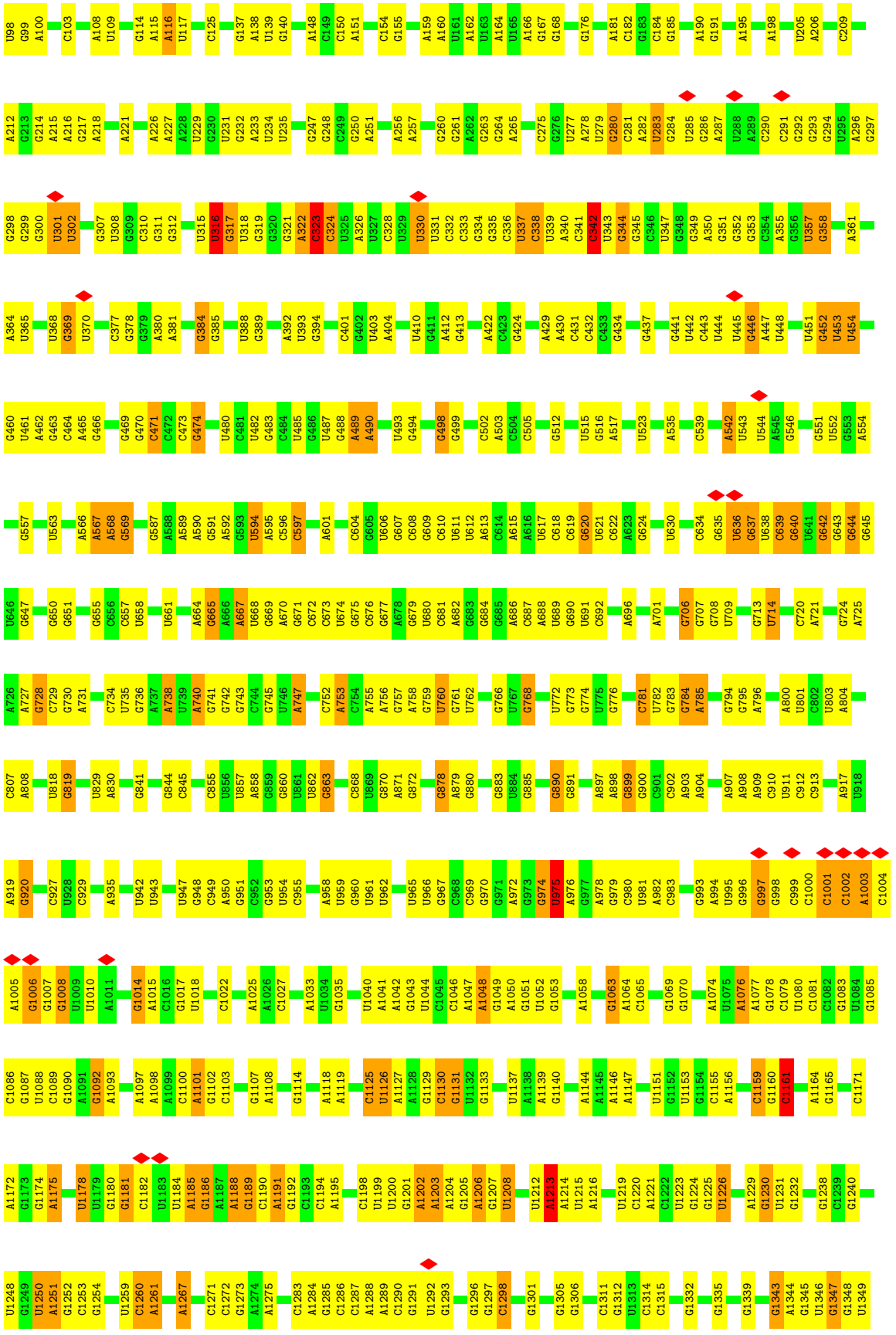


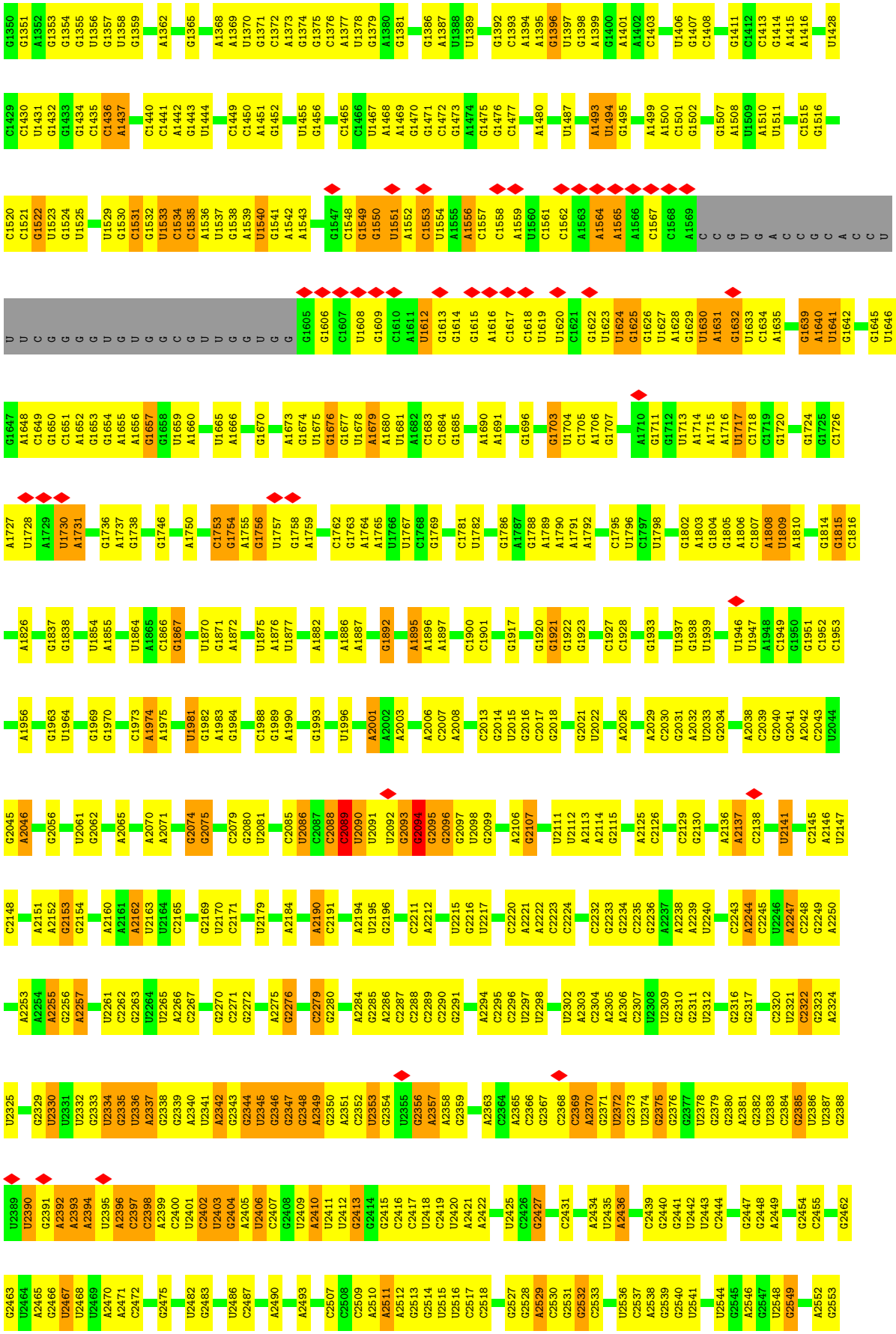
• Molecule 57: 23S ribosomal RNA

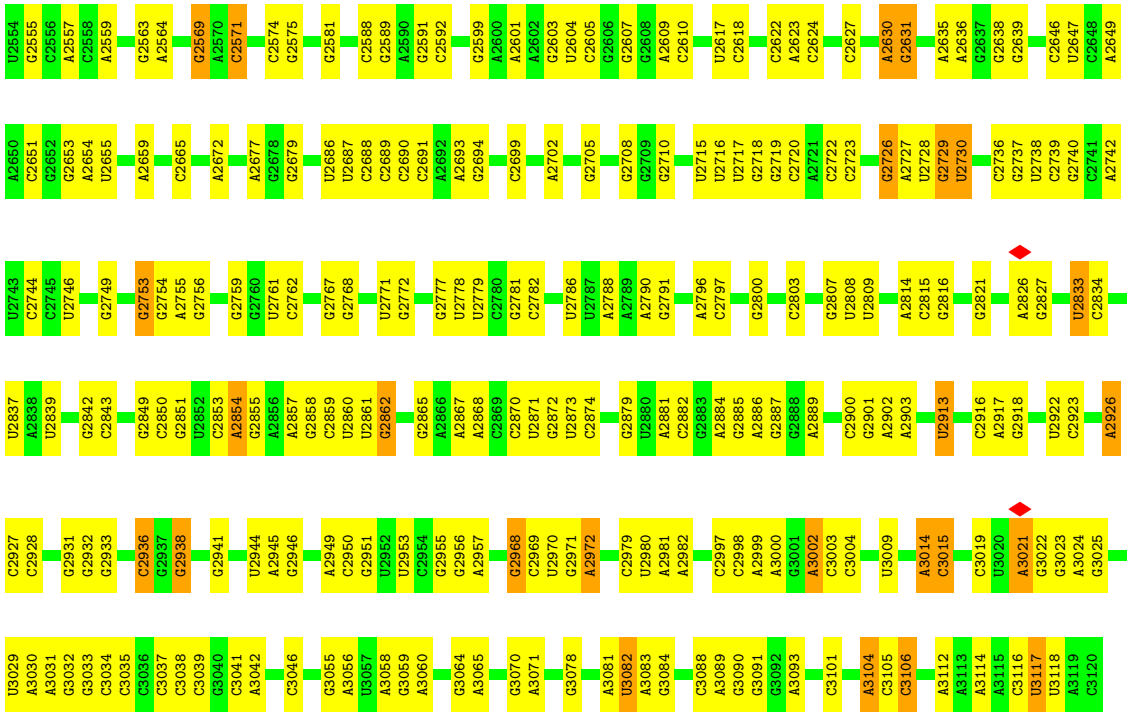
Chain h:










U2554 G2555 C2556 A2557 C2558 A2559 G2563 A2564 G2569 A2570 C2571 C2574 G2575 G2581 C2588 G2589 A2590 G2591 C2592 G2599 A2600 A2601 A2602 G2603 U2604 C2605 G2606 G2607 G2608 A2609 C2610 U2617 C2618 C2622 A2623 C2624 C2627 A2630 G2631 A2635 A2636 G2637 G2638 G2639 C2646 U2647 C2648 A2649
A2650 C2651 G2652 G2653 A2654 U2655 A2659 C2665 A2672 A2677 G2678 G2679 U2686 U2687 C2688 C2689 C2690 C2691 A2692 A2693 G2694 C2699 A2702 G2705 G2708 G2709 G2710 U2715 U2716 U2717 G2718 G2719 C2720 A2721 C2722 C2723 G2726 A2727 U2728 G2729 U2730 C2736 G2737 U2738 C2739 G2740 C2741 A2742
U2743 C2744 C2745 U2746 G2749 G2753 G2754 A2755 G2756 G2759 G2760 U2761 C2762 G2767 G2768 U2771 G2772 G2777 U2778 U2779 C2780 G2781 C2782 U2786 U2787 A2788 A2789 A2790 G2791 A2796 C2797 G2800 C2803 G2807 U2808 U2809 A2814 C2815 G2816 G2821 A2826 G2827 U2833 C2834
U2837 A2838 U2839 G2842 C2843 G2849 C2850 G2851 U2852 C2853 A2854 G2855 A2856 A2857 G2858 C2859 U2860 U2861 G2862 G2865 A2866 A2867 A2868 C2869 C2870 U2871 G2872 U2873 C2874 G2879 U2880 A2881 C2882 G2883 A2884 G2885 A2886 G2887 G2888 A2889 C2900 G2901 A2902 A2903 U2913 C2916 A2917 G2918 U2922 C2923 A2926
C2927 C2928 G2931 G2932 G2933 C2936 G2937 G2938 G2941 U2944 A2945 G2946 A2949 C2950 G2951 U2952 U2953 C2954 G2955 G2956 A2957 G2968 C2969 U2970 G2971 A2972 C2979 U2980 A2981 A2982 C2997 C2998 A2999 A3000 G3001 A3002 C3003 C3004 U3009 A3014 C3015 C3019 U3020 A3021 G3022 G3023 A3024 G3025
U3029 A3030 A3031 G3032 G3033 C3034 C3035 C3036 C3037 C3038 C3039 G3040 C3041 A3042 C3046 G3055 A3056 U3057 A3058 G3059 A3060 G3064 A3065 G3070 A3071 G3078 A3081 U3082 A3083 G3084 C3088 A3089 G3090 G3091 G3092 A3093 C3101 A3104 C3105 C3106 A3112 A3113 A3114 A3115 C3116 U3117 U3118 A3119 C3120

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13826	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20.82	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.190	Depositor
Minimum map value	-0.123	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0254	Depositor
Map size (Å)	449.40002, 449.40002, 449.40002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: GNP, ZN, 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	2	0.39	0/1836	0.97	12/2859 (0.4%)
2	3	0.15	0/191	0.34	0/247
3	4	0.38	0/65	0.73	0/98
4	5	0.18	0/5536	0.35	0/7489
5	6	0.24	0/1760	0.47	1/2375 (0.0%)
6	A	0.34	0/36309	0.81	25/56657 (0.0%)
7	B	0.31	0/2821	0.75	0/4396
8	C	0.12	0/1684	0.29	0/2261
9	D	0.15	0/1672	0.34	0/2251
10	E	0.13	0/1312	0.28	0/1772
11	F	0.11	0/782	0.25	0/1059
12	G	0.11	0/1252	0.30	0/1690
13	H	0.13	0/1025	0.28	0/1385
14	I	0.13	0/1012	0.33	0/1362
15	J	0.13	0/802	0.30	0/1086
16	K	0.14	0/873	0.31	0/1180
17	L	0.14	0/969	0.32	0/1294
18	M	0.11	0/942	0.33	0/1260
19	N	0.13	0/488	0.32	0/650
20	O	0.13	0/729	0.27	0/977
21	P	0.14	0/908	0.34	0/1226
22	Q	0.13	0/759	0.33	0/1016
23	R	0.12	0/518	0.24	0/693
24	S	0.10	0/680	0.27	0/915
25	T	0.16	0/663	0.32	0/882
26	U	0.17	0/766	0.28	0/1030
27	W	0.13	0/1443	0.25	0/1970
28	X	0.17	0/595	0.33	0/798
29	Y	0.17	0/478	0.28	0/641
30	Z	0.14	0/534	0.23	0/713
31	a	0.16	0/477	0.24	0/640
32	b	0.16	0/427	0.24	0/572

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c	0.15	0/413	0.24	0/553
34	d	0.17	0/380	0.26	0/500
35	e	0.17	0/507	0.29	0/672
36	f	0.16	0/303	0.27	0/401
37	g	0.11	0/372	0.23	0/503
38	i	0.19	0/2153	0.29	0/2895
39	j	0.17	0/1609	0.32	0/2165
40	k	0.16	0/1592	0.28	0/2153
41	l	0.14	0/1467	0.30	0/1973
42	m	0.15	0/1369	0.29	0/1848
43	n	0.14	0/1027	0.34	0/1398
44	o	0.30	0/1006	0.44	0/1364
45	p	0.09	0/925	0.27	0/1246
46	q	0.19	0/1157	0.31	0/1567
47	r	0.18	0/946	0.28	0/1268
48	s	0.17	0/1091	0.34	0/1457
49	t	0.17	0/1118	0.33	0/1506
50	u	0.17	0/945	0.30	0/1267
51	v	0.13	0/966	0.25	0/1298
52	w	0.17	0/921	0.32	0/1236
53	x	0.18	0/1000	0.27	0/1341
54	y	0.17	0/764	0.29	0/1030
55	z	0.19	0/887	0.29	0/1204
56	1	0.14	0/738	0.26	0/987
57	h	0.38	0/74164	0.79	39/115718 (0.0%)
All	All	0.32	0/168128	0.70	77/250994 (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
46	q	0	1

There are no bond length outliers.

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	67	C	C6-N1-C2	-10.00	116.30	120.30
1	2	66	C	N1-C2-O2	9.48	124.59	118.90
6	A	179	C	C2-N1-C1'	8.70	128.37	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	67	C	N1-C2-N3	8.27	124.99	119.20
6	A	179	C	N1-C2-O2	8.11	123.77	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	q	37	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	1644	0	836	30	0
2	3	189	0	205	4	0
3	4	60	0	32	0	0
4	5	5441	0	5422	182	0
5	6	1736	0	1788	70	0
6	A	32439	0	16321	742	0
7	B	2522	0	1285	44	0
8	C	1660	0	1707	39	0
9	D	1641	0	1668	58	0
10	E	1296	0	1360	35	0
11	F	771	0	797	18	0
12	G	1232	0	1282	27	0
13	H	1010	0	1046	21	0
14	I	994	0	1050	37	0
15	J	788	0	819	32	0
16	K	855	0	863	25	0
17	L	958	0	1045	26	0
18	M	935	0	986	34	0
19	N	477	0	499	15	0
20	O	720	0	760	13	0
21	P	891	0	935	36	0
22	Q	748	0	795	21	0
23	R	513	0	537	9	0
24	S	662	0	677	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	T	660	0	712	21	0
26	U	756	0	802	11	0
27	W	1428	0	1443	19	0
28	X	586	0	601	7	0
29	Y	470	0	480	9	0
30	Z	531	0	541	6	0
31	a	474	0	500	6	0
32	b	423	0	463	7	0
33	c	405	0	407	6	0
34	d	377	0	411	2	0
35	e	502	0	541	10	0
36	f	299	0	321	7	0
37	g	364	0	348	14	0
38	i	2110	0	2165	36	0
39	j	1587	0	1630	22	0
40	k	1569	0	1607	18	0
41	l	1445	0	1476	38	0
42	m	1348	0	1399	19	0
43	n	1018	0	988	13	0
44	o	990	0	1021	44	0
45	p	918	0	959	31	0
46	q	1130	0	1167	20	0
47	r	938	0	1000	13	0
48	s	1078	0	1151	11	0
49	t	1092	0	1128	20	0
50	u	928	0	972	12	0
51	v	956	0	991	19	0
52	w	907	0	938	14	0
53	x	988	0	1038	12	0
54	y	754	0	802	12	0
55	z	873	0	909	12	0
56	1	732	0	782	6	0
57	h	66232	0	33325	997	0
58	5	32	0	13	2	0
59	F	1	0	0	0	0
59	R	1	0	0	0	0
59	X	1	0	0	0	0
59	h	2	0	0	0	0
59	i	4	0	0	0	0
59	l	1	0	0	0	0
59	t	1	0	0	0	0
59	z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	N	1	0	0	0	0
60	R	1	0	0	0	0
60	Y	1	0	0	0	0
60	c	1	0	0	0	0
60	f	1	0	0	0	0
60	g	1	0	0	0	0
All	All	155100	0	105746	2721	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 11.

The worst 5 of 2721 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:507:GLY:HA3	6:A:1479:U:OP1	1.38	1.23
4:5:669:LYS:HE2	42:m:176:LYS:HE3	1.42	0.97
4:5:507:GLY:CA	6:A:1479:U:OP1	2.18	0.91
6:A:22:C:H1'	6:A:1059:G:H21	1.41	0.85
57:h:929:C:H1'	57:h:1339:G:H21	1.40	0.85

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
4	5	699/701 (100%)	669 (96%)	30 (4%)	0	100	100
5	6	230/235 (98%)	218 (95%)	12 (5%)	0	100	100
8	C	206/275 (75%)	194 (94%)	12 (6%)	0	100	100
9	D	198/201 (98%)	183 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	E	178/214 (83%)	167 (94%)	11 (6%)	0	100	100
11	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
12	G	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
13	H	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
14	I	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
15	J	97/101 (96%)	91 (94%)	6 (6%)	0	100	100
16	K	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
17	L	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
18	M	114/124 (92%)	108 (95%)	6 (5%)	0	100	100
19	N	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
20	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
21	P	111/156 (71%)	101 (91%)	10 (9%)	0	100	100
22	Q	92/98 (94%)	90 (98%)	2 (2%)	0	100	100
23	R	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
24	S	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
25	T	83/86 (96%)	83 (100%)	0	0	100	100
26	U	95/100 (95%)	92 (97%)	3 (3%)	0	100	100
27	W	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
28	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
29	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
30	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
31	a	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
32	b	52/57 (91%)	52 (100%)	0	0	100	100
33	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
34	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
35	e	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
36	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
37	g	46/75 (61%)	44 (96%)	2 (4%)	0	100	100
38	i	273/278 (98%)	260 (95%)	13 (5%)	0	100	100
39	j	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
40	k	207/215 (96%)	202 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	l	180/187 (96%)	176 (98%)	4 (2%)	0	100	100
42	m	174/179 (97%)	171 (98%)	3 (2%)	0	100	100
43	n	149/151 (99%)	141 (95%)	8 (5%)	0	100	100
44	o	131/142 (92%)	125 (95%)	6 (5%)	0	100	100
45	p	124/175 (71%)	121 (98%)	3 (2%)	0	100	100
46	q	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
47	r	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
48	s	143/147 (97%)	130 (91%)	13 (9%)	0	100	100
49	t	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
50	u	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
51	v	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
52	w	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
53	x	122/129 (95%)	122 (100%)	0	0	100	100
54	y	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
55	z	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
56	1	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
All	All	6643/7305 (91%)	6357 (96%)	286 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	3	18/19 (95%)	18 (100%)	0	100	100
4	5	587/587 (100%)	581 (99%)	6 (1%)	68	77
5	6	181/184 (98%)	181 (100%)	0	100	100
8	C	170/212 (80%)	170 (100%)	0	100	100
9	D	175/176 (99%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	E	127/147 (86%)	127 (100%)	0	100	100
11	F	85/85 (100%)	85 (100%)	0	100	100
12	G	131/132 (99%)	130 (99%)	1 (1%)	73	78
13	H	107/108 (99%)	107 (100%)	0	100	100
14	I	102/125 (82%)	102 (100%)	0	100	100
15	J	89/90 (99%)	88 (99%)	1 (1%)	65	74
16	K	89/105 (85%)	89 (100%)	0	100	100
17	L	103/105 (98%)	103 (100%)	0	100	100
18	M	99/104 (95%)	99 (100%)	0	100	100
19	N	49/50 (98%)	49 (100%)	0	100	100
20	O	76/77 (99%)	76 (100%)	0	100	100
21	P	92/118 (78%)	92 (100%)	0	100	100
22	Q	80/83 (96%)	79 (99%)	1 (1%)	61	73
23	R	55/72 (76%)	55 (100%)	0	100	100
24	S	73/84 (87%)	73 (100%)	0	100	100
25	T	69/70 (99%)	69 (100%)	0	100	100
26	U	83/85 (98%)	82 (99%)	1 (1%)	63	74
27	W	155/168 (92%)	155 (100%)	0	100	100
28	X	58/63 (92%)	58 (100%)	0	100	100
29	Y	50/51 (98%)	50 (100%)	0	100	100
30	Z	58/66 (88%)	57 (98%)	1 (2%)	53	68
31	a	52/54 (96%)	52 (100%)	0	100	100
32	b	43/46 (94%)	43 (100%)	0	100	100
33	c	47/52 (90%)	47 (100%)	0	100	100
34	d	35/36 (97%)	35 (100%)	0	100	100
35	e	53/54 (98%)	53 (100%)	0	100	100
36	f	35/35 (100%)	35 (100%)	0	100	100
37	g	43/63 (68%)	43 (100%)	0	100	100
38	i	215/218 (99%)	213 (99%)	2 (1%)	70	77
39	j	160/163 (98%)	160 (100%)	0	100	100
40	k	169/173 (98%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	l	151/156 (97%)	151 (100%)	0	100	100
42	m	148/150 (99%)	148 (100%)	0	100	100
43	n	90/116 (78%)	90 (100%)	0	100	100
44	o	102/108 (94%)	102 (100%)	0	100	100
45	p	89/120 (74%)	89 (100%)	0	100	100
46	q	119/120 (99%)	119 (100%)	0	100	100
47	r	100/100 (100%)	100 (100%)	0	100	100
48	s	112/114 (98%)	112 (100%)	0	100	100
49	t	114/116 (98%)	114 (100%)	0	100	100
50	u	97/158 (61%)	97 (100%)	0	100	100
51	v	93/94 (99%)	93 (100%)	0	100	100
52	w	100/100 (100%)	100 (100%)	0	100	100
53	x	97/99 (98%)	97 (100%)	0	100	100
54	y	81/83 (98%)	81 (100%)	0	100	100
55	z	90/117 (77%)	90 (100%)	0	100	100
56	1	81/86 (94%)	81 (100%)	0	100	100
All	All	5477/5897 (93%)	5464 (100%)	13 (0%)	85	86

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	J	15	HIS
22	Q	9	TYR
38	i	198	ASN
30	Z	58	TYR
38	i	73	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
40	k	41	GLN
45	p	35	ASN
40	k	91	HIS
42	m	86	GLN
46	q	58	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	76/77 (98%)	19 (25%)	0
3	4	2/3 (66%)	0	0
57	h	3082/3120 (98%)	583 (18%)	0
6	A	1510/1528 (98%)	333 (22%)	14 (0%)
7	B	117/118 (99%)	17 (14%)	1 (0%)
All	All	4787/4846 (98%)	952 (19%)	15 (0%)

5 of 952 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	5	G
1	2	17	C
1	2	19	G
1	2	20	G
1	2	21	U

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	895	A
6	A	1482	U
6	A	1011	U
7	B	10	G
6	A	1435	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

Of 19 ligands modelled in this entry, 18 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
58	GNP	5	801	-	33,34,34	1.32	5 (15%)	46,54,54	0.68	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	GNP	5	801	-	-	4/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	5	801	GNP	PB-O3A	4.71	1.65	1.59
58	5	801	GNP	PB-O1B	3.11	1.51	1.46
58	5	801	GNP	PG-N3B	2.90	1.70	1.63
58	5	801	GNP	PG-O1G	2.58	1.50	1.46
58	5	801	GNP	PB-O2B	-2.14	1.51	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
58	5	801	GNP	PB-O3A-PA	-2.03	125.47	132.62

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	5	801	GNP	PB-N3B-PG-O1G
58	5	801	GNP	PA-O3A-PB-O1B
58	5	801	GNP	PA-O3A-PB-O2B
58	5	801	GNP	O4'-C4'-C5'-O5'

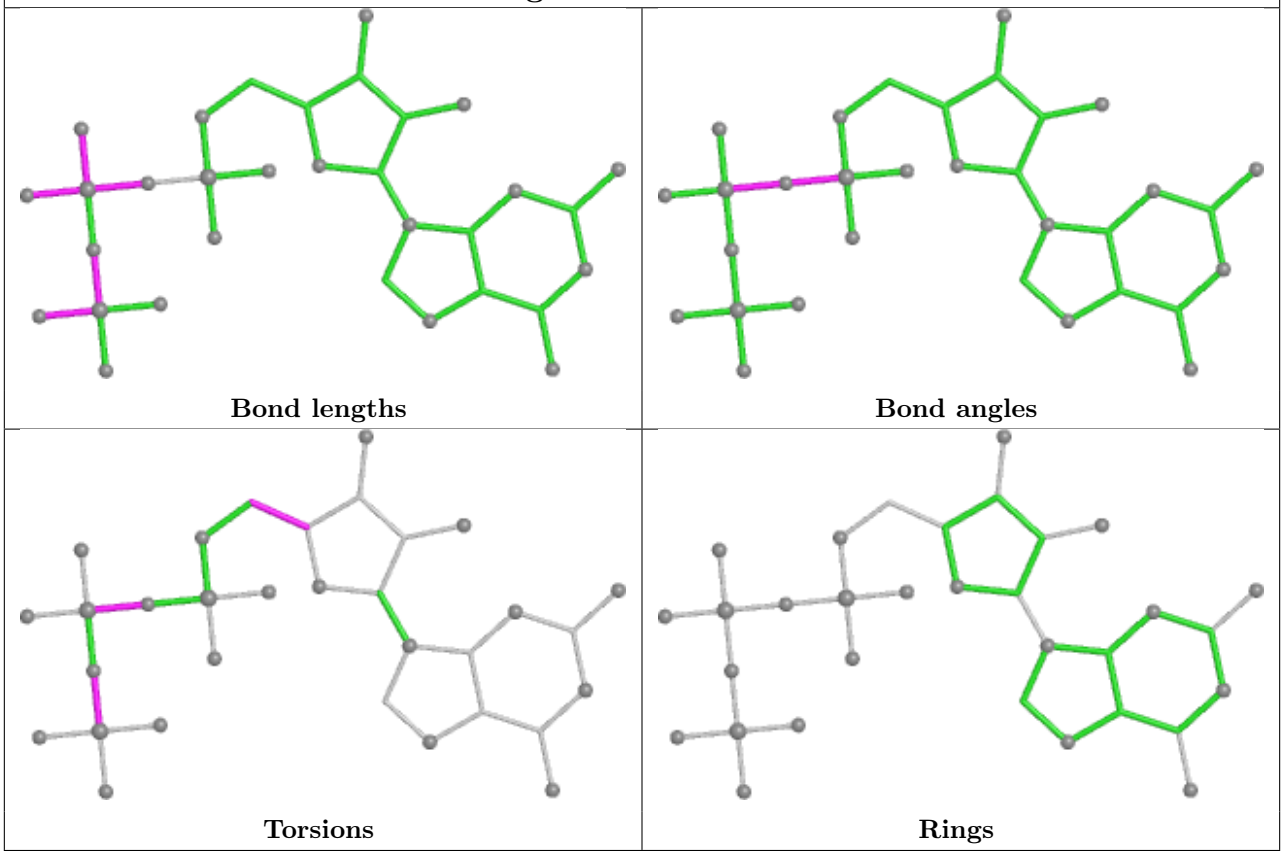
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	5	801	GNP	2	0

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 then 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.

Ligand GNP 5 801



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.

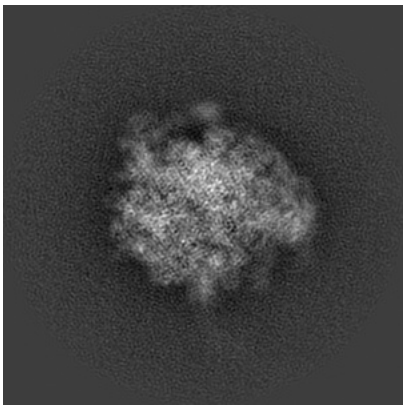
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-69709. These allow visual inspection of the internal detail of the map and identification of artifacts.

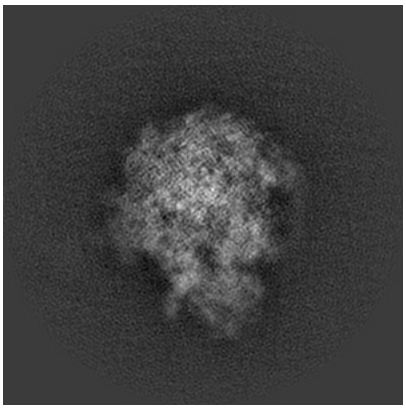
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

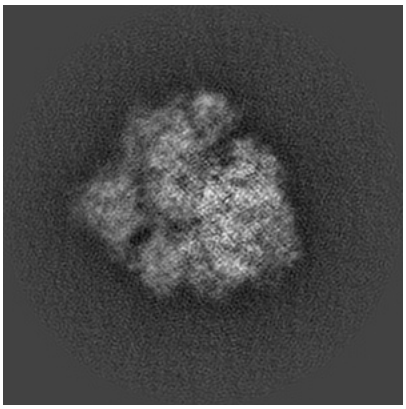
6.1.1 Primary map



X

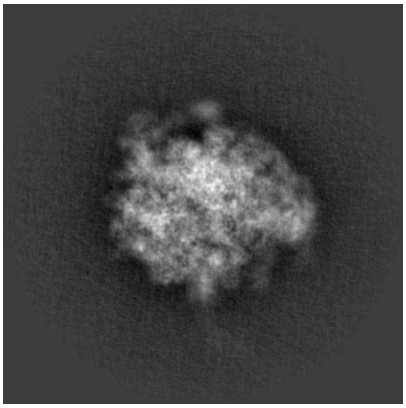


Y

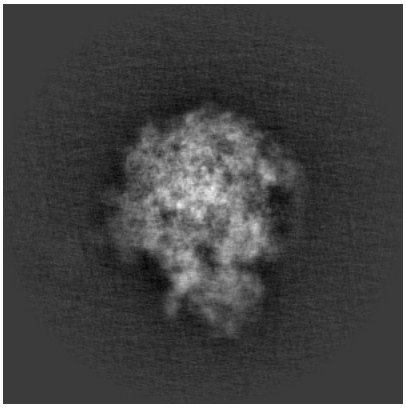


Z

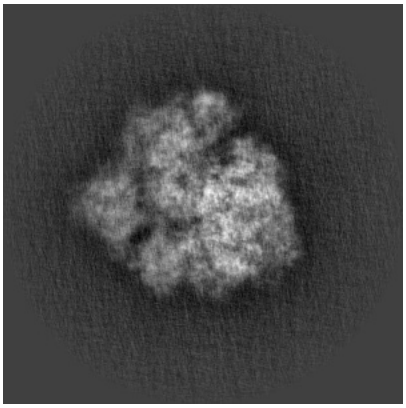
6.1.2 Raw map



X



Y

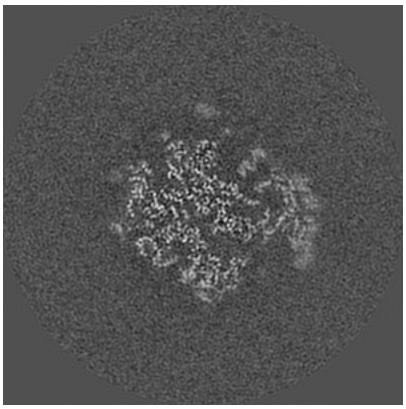


Z

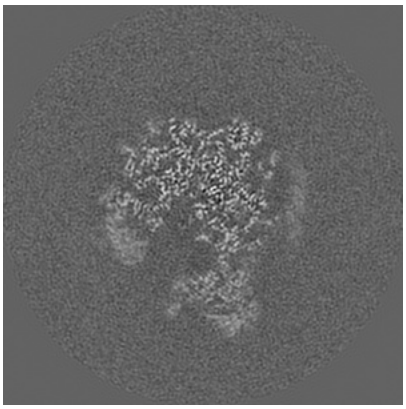
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

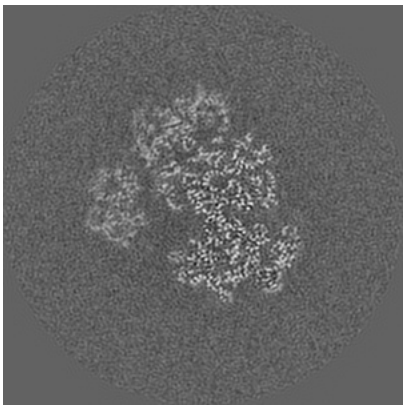
6.2.1 Primary map



X Index: 210

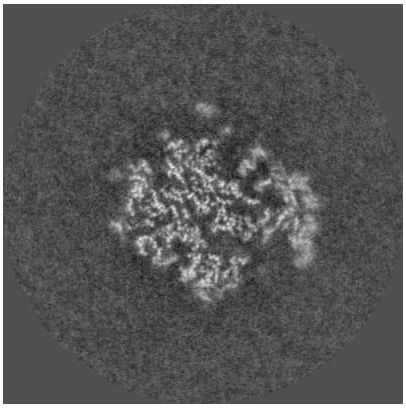


Y Index: 210

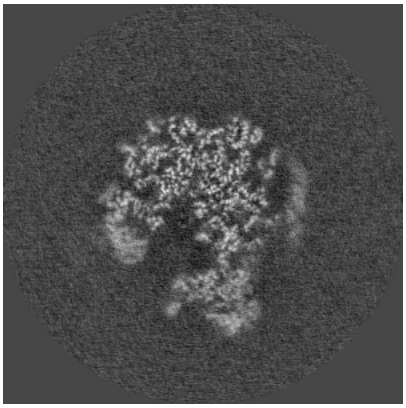


Z Index: 210

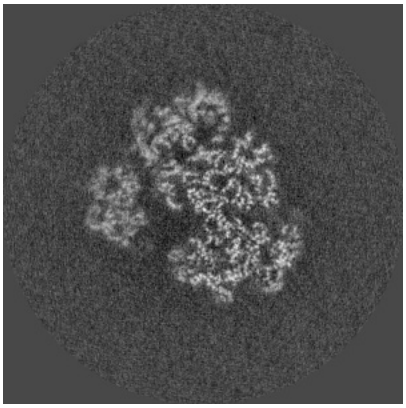
6.2.2 Raw map



X Index: 210



Y Index: 210

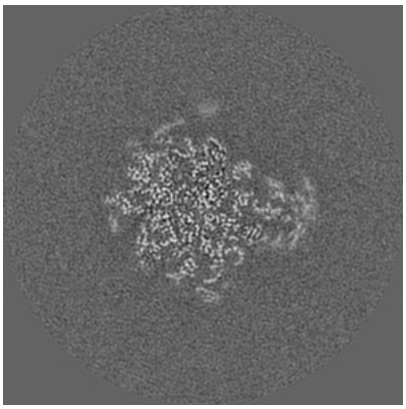


Z Index: 210

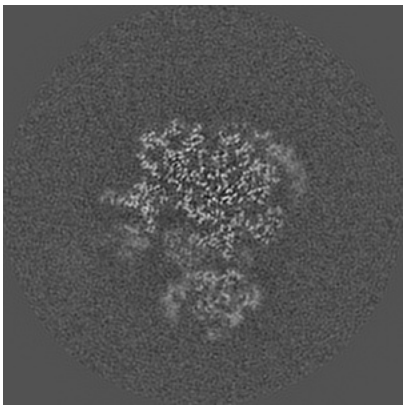
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

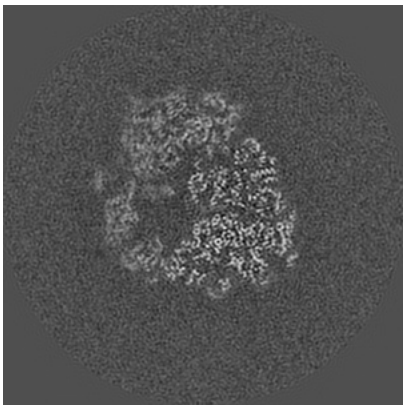
6.3.1 Primary map



X Index: 223

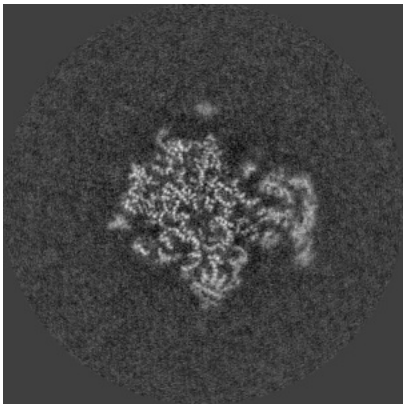


Y Index: 224

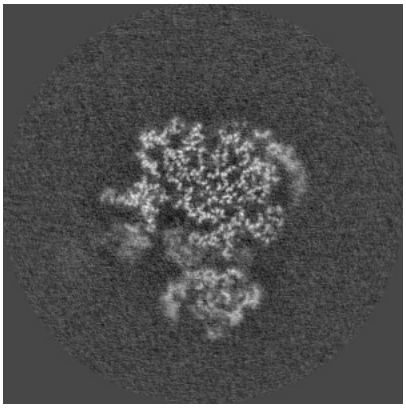


Z Index: 198

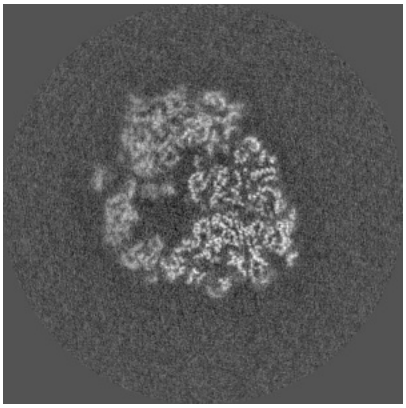
6.3.2 Raw map



X Index: 214



Y Index: 224

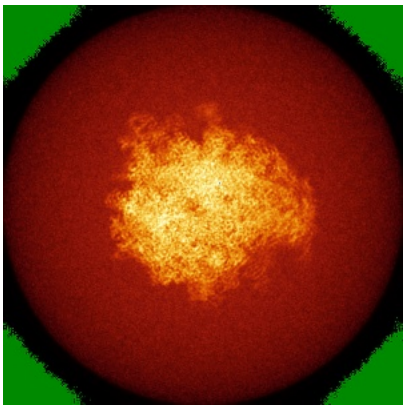


Z Index: 198

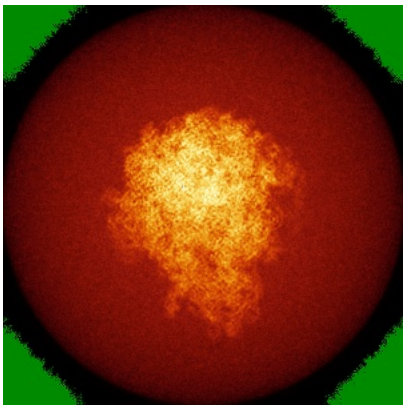
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

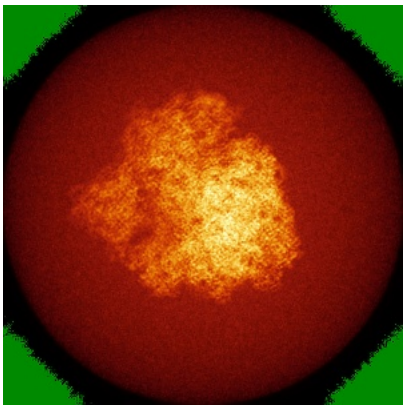
6.4.1 Primary map



X

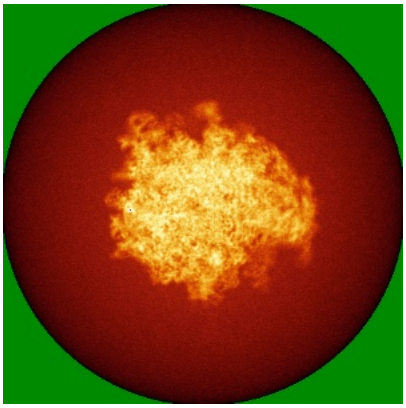


Y

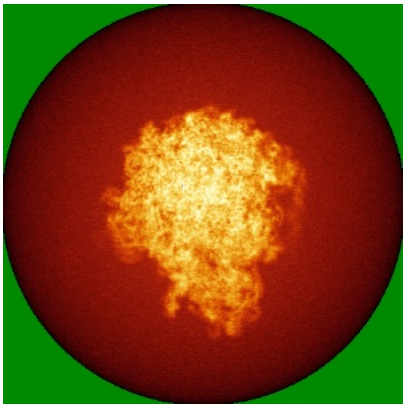


Z

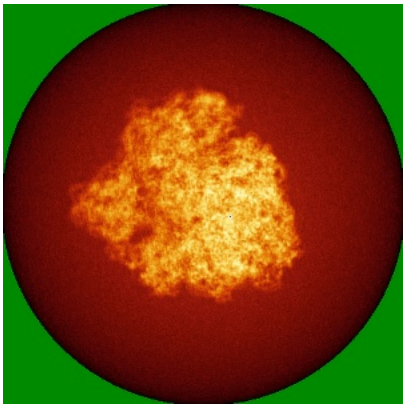
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0254. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

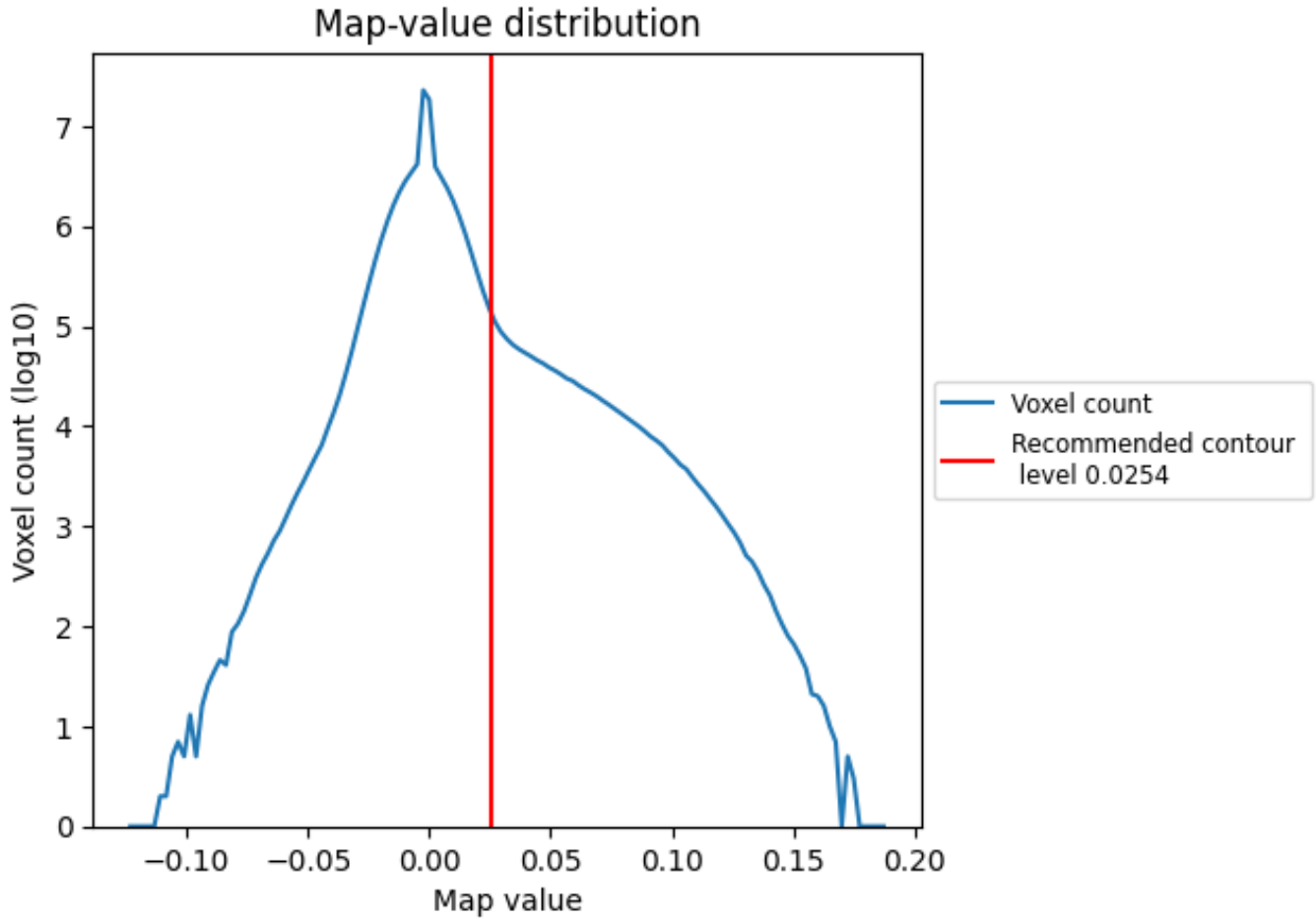
6.6 Mask visualisation (i)

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

7 Map analysis

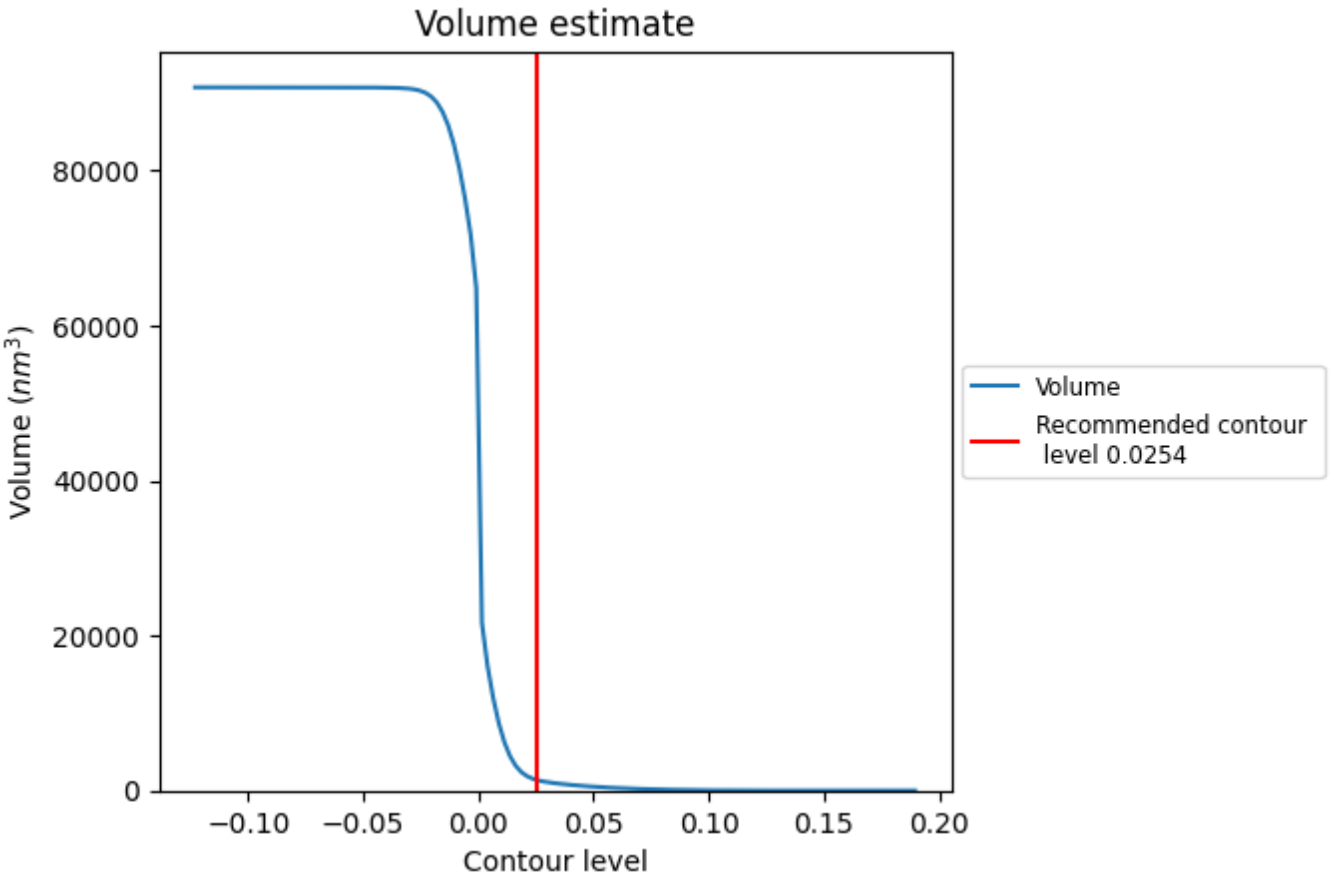
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

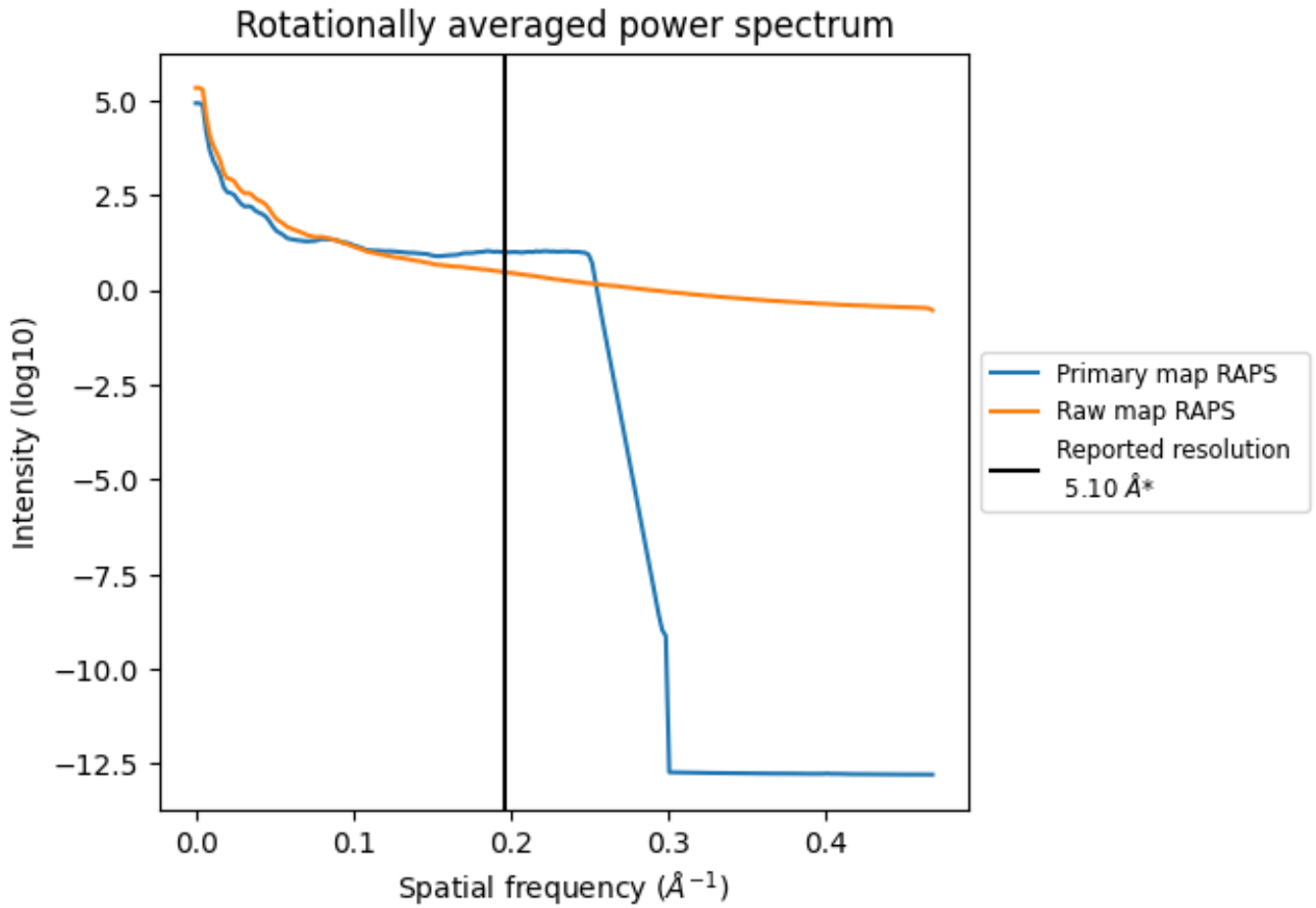
7.2 Volume estimate (i)



The volume at the recommended contour level is 1362 nm^3; this corresponds to an approximate mass of 1231 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 (i)

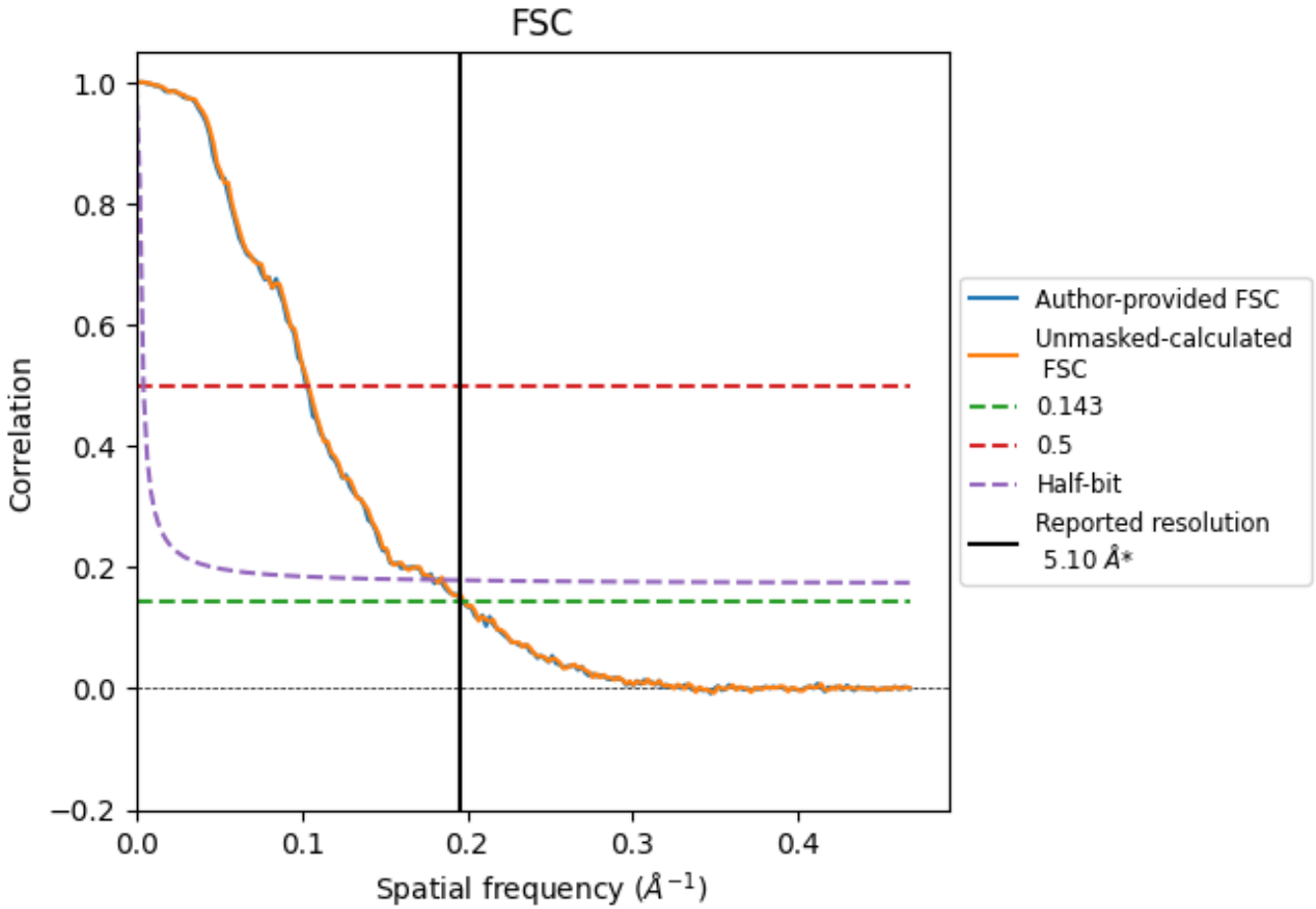


*Reported resolution corresponds to spatial frequency of 0.196 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.196 Å^{-1}

8.2 Resolution estimates (i)

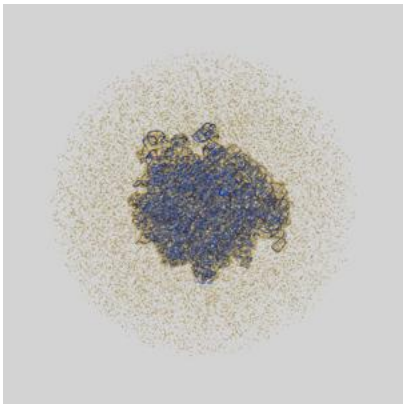
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.07	9.72	5.57
Unmasked-calculated*	5.05	9.62	5.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

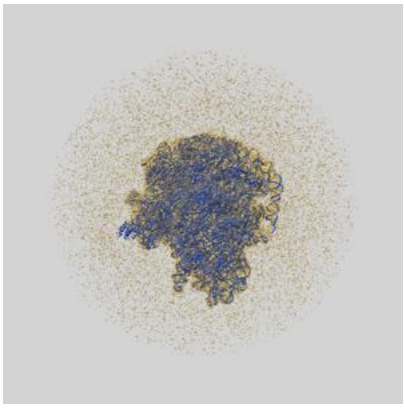
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-69709 and PDB model 24NW. Per-residue inclusion information can be found in section 3 on page 16.

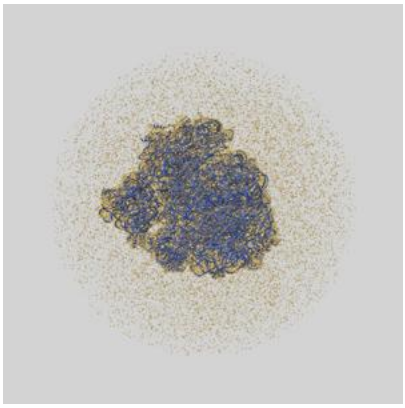
9.1 Map-model overlay



X



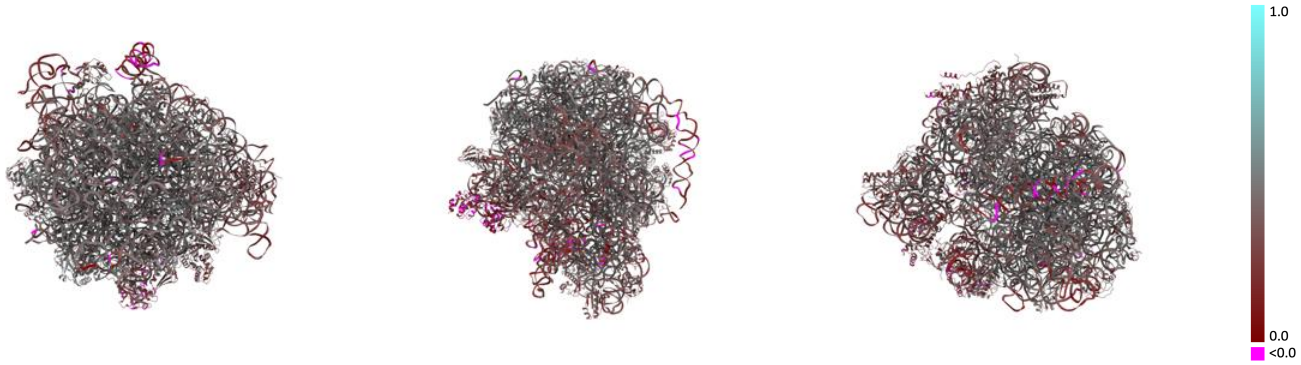
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0254 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.

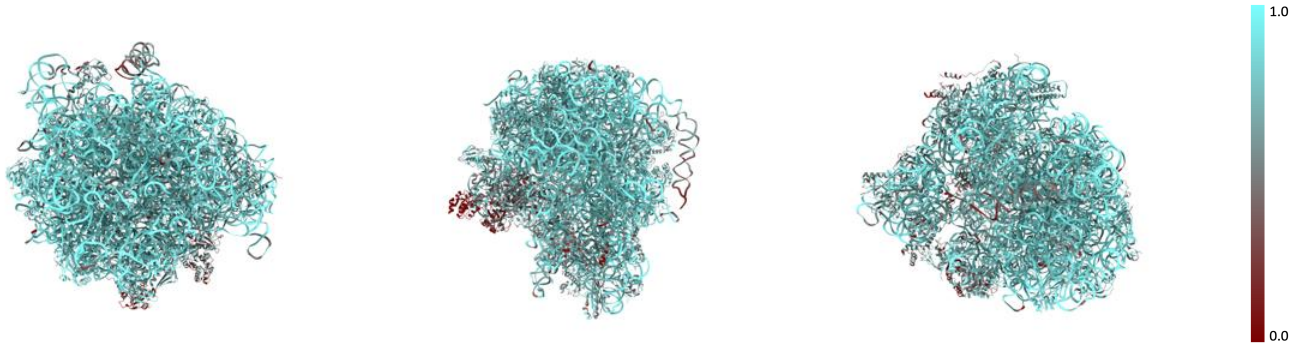
9.2 Q-score mapped to coordinate model



X Y Z

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.

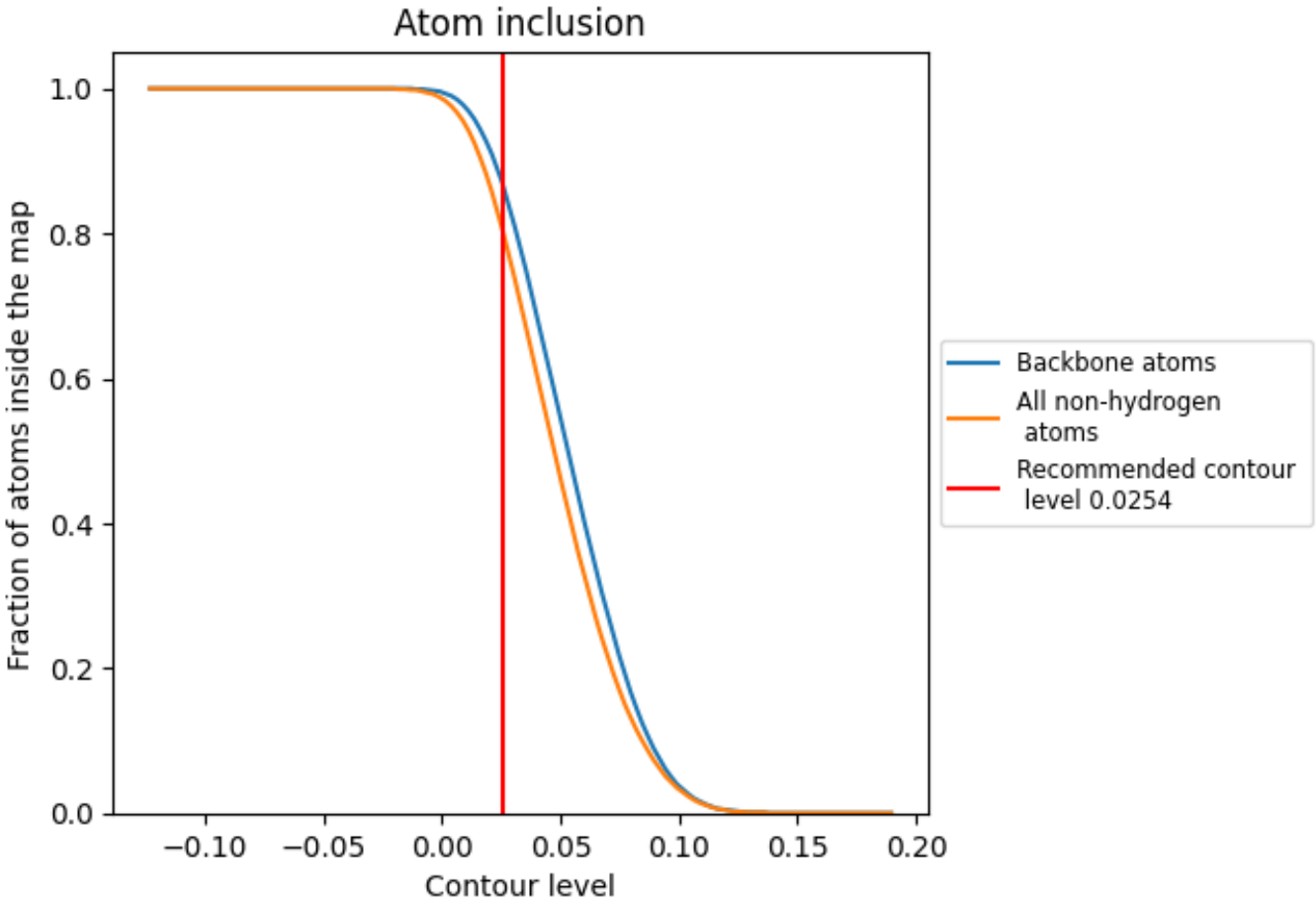
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.0254).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 81% 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 (0.0254) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8080	0.3890
1	0.7080	0.4050
2	0.7510	0.3470
3	0.6700	0.4300
4	0.9000	0.4340
5	0.4480	0.3280
6	0.3900	0.2660
A	0.8690	0.3720
B	0.9130	0.3990
C	0.6590	0.3800
D	0.5650	0.2730
E	0.7180	0.4030
F	0.7450	0.4340
G	0.5450	0.2870
H	0.8010	0.4400
I	0.6580	0.3340
J	0.6210	0.3520
K	0.7620	0.4470
L	0.6310	0.4180
M	0.5690	0.2860
N	0.7600	0.4190
O	0.8020	0.4430
P	0.6200	0.3310
Q	0.6820	0.4010
R	0.7670	0.4390
S	0.6240	0.3370
T	0.6910	0.3420
U	0.7580	0.4300
W	0.6770	0.3910
X	0.8060	0.4630
Y	0.8190	0.4660
Z	0.8020	0.4060
a	0.7890	0.4560
b	0.8110	0.4490
c	0.8150	0.4420



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Chain	Atom inclusion	Q-score
d	0.8450	0.4690
e	0.8100	0.4910
f	0.7600	0.4470
g	0.6980	0.2820
h	0.8820	0.4040
i	0.8060	0.4670
j	0.8220	0.4620
k	0.8140	0.4530
l	0.7140	0.3460
m	0.7400	0.3730
n	0.6060	0.3490
o	0.2130	0.1090
p	0.0860	0.0960
q	0.8120	0.4540
r	0.7590	0.4530
s	0.7990	0.4500
t	0.7680	0.4510
u	0.8060	0.4510
v	0.8030	0.4070
w	0.7300	0.4200
x	0.8220	0.4450
y	0.8360	0.4790
z	0.8130	0.4650