wwPDB EM Validation Summary Report

Nov 11, 2026 – 10:44 AM JST

PDB ID	:	24NP / pdb_000024np
EMDB ID	:	EMD-69703
Title	:	E/E-tRNA bound M. smegmatis 70S ribosome in complex with RRF (RRI III)
Authors	:	Sengupta, J.; Dhur, A.; Baid, P.; Srinivasan, K.
Deposited on	:	2026-03-12
Resolution	:	4.20 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 ⓘ 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:

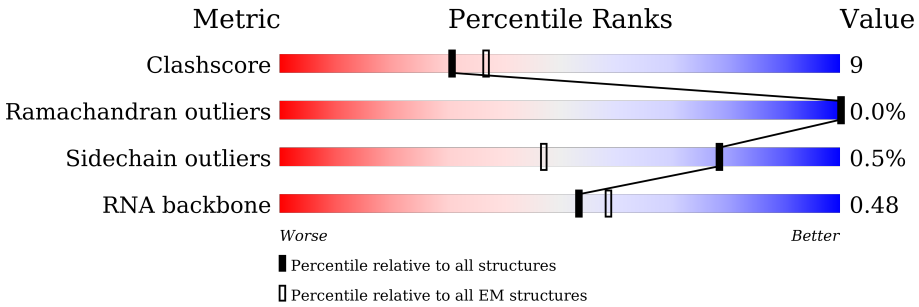
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

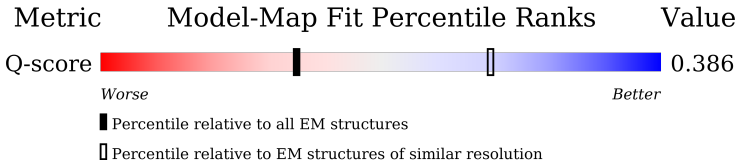
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	6%, 35%, 47%, 18%
2	3	24	·, 88%, 8%, ·
3	4	3	100%

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Mol	Chain	Length	Quality of chain
4	5	185	42% 75% 25%
5	6	235	57% 54% 43%
6	A	1528	40% 46% 13%
7	B	118	62% 31% 7%
8	C	275	11% 54% 21% 24%
9	E	214	6% 59% 25% 16%
10	F	96	76% 24%
11	G	156	26% 72% 28%
12	H	132	76% 23%
13	I	150	12% 56% 28% 16%
14	J	101	23% 50% 49%
15	K	138	64% 20% 17%
16	L	124	14% 61% 36%
17	M	124	27% 55% 39% 6%
18	N	61	74% 25%
19	O	89	79% 20%
20	P	156	22% 43% 29% 28%
21	Q	98	16% 67% 29%
22	R	84	67% 11% 23%
23	S	93	14% 66% 23% 12%
24	T	86	14% 66% 33%
25	U	100	79% 18%
26	W	215	75% 14% 11%
27	X	88	80% 10% 10%
28	Y	64	77% 22%

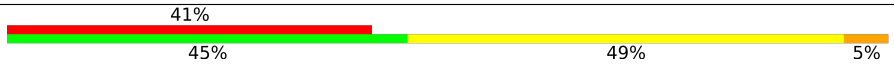
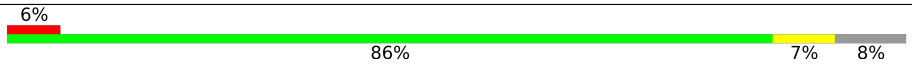
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Mol	Chain	Length	Quality of chain
29	Z	77	69% 14% 17%
30	a	61	84% 13%
31	b	57	81% 14% 5%
32	c	55	71% 18% 11%
33	d	47	94%
34	e	64	83% 16%
35	f	37	78% 22%
36	g	75	37% 27% 36%
37	i	278	79% 19%
38	j	217	85% 13%
39	k	215	81% 16%
40	l	187	70% 27%
41	m	179	83% 15%
42	n	151	10% 84% 15%
43	o	142	56% 49% 42% 6%
44	p	175	68% 50% 22% 28%
45	q	147	88% 10%
46	r	122	88% 12%
47	s	147	84% 14%
48	t	138	83% 15%
49	u	199	51% 8% 41%
50	v	127	80% 20%
51	w	113	79% 21%
52	x	129	86% 10%
53	y	103	80% 17%

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Mol	Chain	Length	Quality of chain
54	z	153	
55	D	201	
56	1	105	
57	h	3120	

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 151086 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 E/E-site 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 Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	185	1459	894	265	295	5	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 S5.

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

- Molecule 10 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 11 is a protein called 30S ribosomal protein S7.

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

- Molecule 12 is a protein called 30S ribosomal protein S8.

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

- Molecule 13 is a protein called 30S ribosomal protein S9.

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

- Molecule 14 is a protein called 30S ribosomal protein S10.

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

- Molecule 15 is a protein called 30S ribosomal protein S11.

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

- Molecule 16 is a protein called 30S ribosomal protein S12.

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

- Molecule 17 is a protein called 30S ribosomal protein S13.

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

- Molecule 18 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 19 is a protein called 30S ribosomal protein S15.

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

- Molecule 20 is a protein called 30S ribosomal protein S16.

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

- Molecule 21 is a protein called 30S ribosomal protein S17.

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

- Molecule 22 is a protein called 30S ribosomal protein S18 2.

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

- Molecule 23 is a protein called 30S ribosomal protein S19.

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

- Molecule 24 is a protein called 30S ribosomal protein S20.

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

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

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

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 37 is a protein called 50S ribosomal protein L2.

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

- Molecule 38 is a protein called 50S ribosomal protein L3.

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

- Molecule 39 is a protein called 50S ribosomal protein L4.

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

- Molecule 40 is a protein called 50S ribosomal protein L5.

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

- Molecule 41 is a protein called 50S ribosomal protein L6.

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

- Molecule 42 is a protein called 50S ribosomal protein L9.

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

- Molecule 43 is a protein called 50S ribosomal protein L11.

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

- Molecule 44 is a protein called 50S ribosomal protein L10.

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

- Molecule 45 is a protein called 50S ribosomal protein L13.

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

- Molecule 46 is a protein called 50S ribosomal protein L14.

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

- Molecule 47 is a protein called 50S ribosomal protein L15.

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

- Molecule 48 is a protein called 50S ribosomal protein L16.

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

- Molecule 49 is a protein called 50S ribosomal protein L17.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L19.

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

- Molecule 52 is a protein called 50S ribosomal protein L20.

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

- Molecule 53 is a protein called 50S ribosomal protein L21.

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

- Molecule 54 is a protein called 50S ribosomal protein L22.

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

- Molecule 55 is a protein called 30S ribosomal protein S4.

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

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

Mol	Chain	Residues	Atoms		AltConf
58	F	1	Total	Mg	0
			1	1	
58	R	1	Total	Mg	0
			1	1	
58	X	1	Total	Mg	0
			1	1	
58	i	4	Total	Mg	0
			4	4	
58	l	1	Total	Mg	0
			1	1	
58	t	1	Total	Mg	0
			1	1	
58	z	1	Total	Mg	0
			1	1	
58	h	2	Total	Mg	0
			2	2	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
59	N	1	Total	Zn	0
			1	1	
59	R	1	Total	Zn	0
			1	1	
59	Y	1	Total	Zn	0
			1	1	
59	c	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
59	f	1	Total Zn 1 1	0
59	g	1	Total Zn 1 1	0

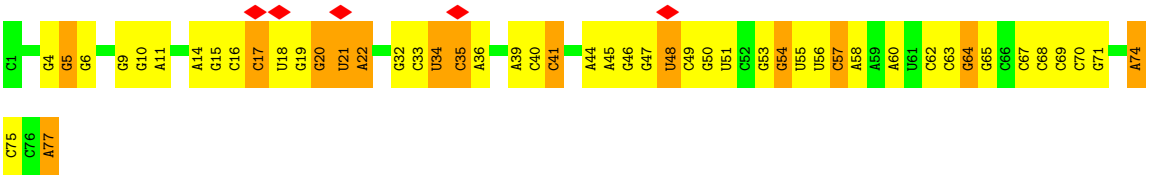
3 Residue-property plots (i)

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: E/E-site tRNA

Chain 2:

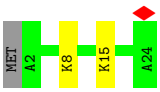




• Molecule 2: 50S ribosomal protein bL37

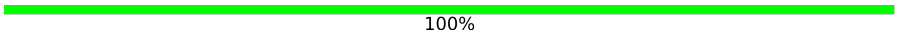
Chain 3:





• Molecule 3: mRNA fragment

Chain 4:

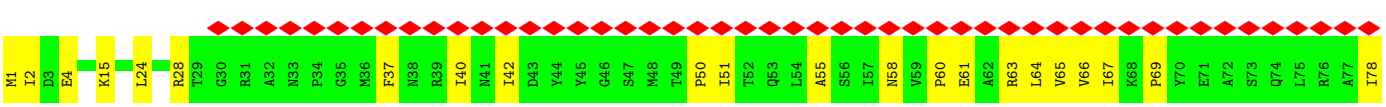


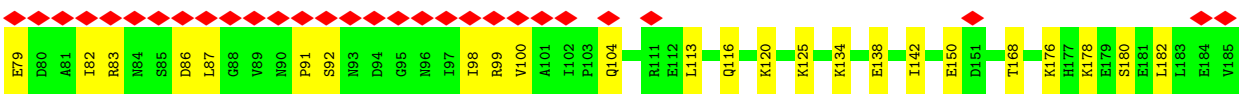
There are no outlier residues recorded for this chain.

• Molecule 4: Ribosome-recycling factor

Chain 5:



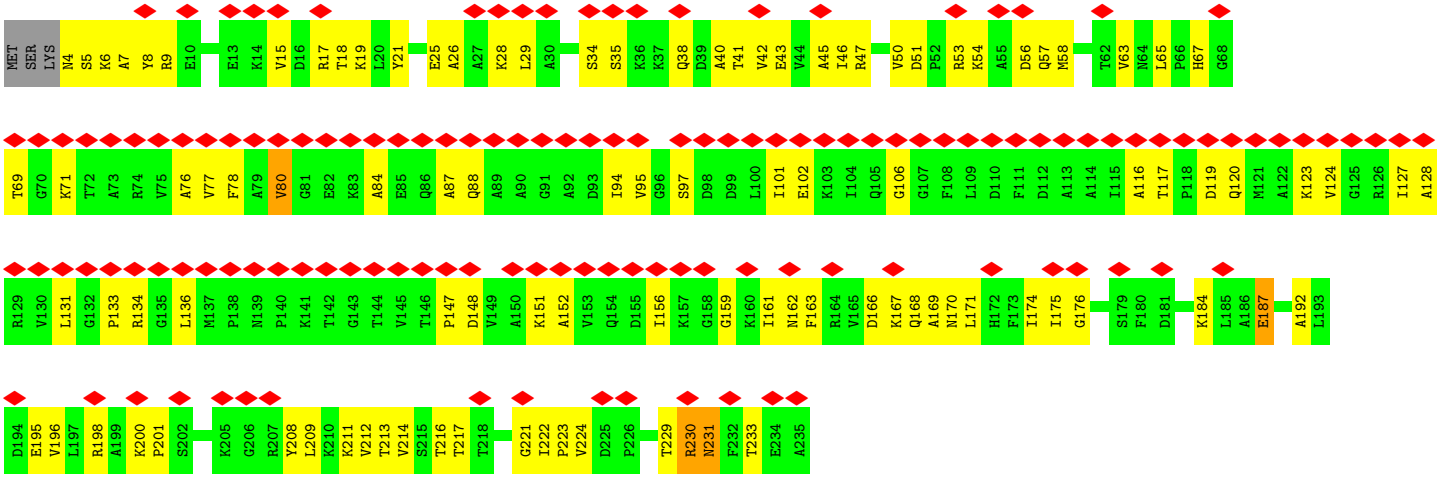


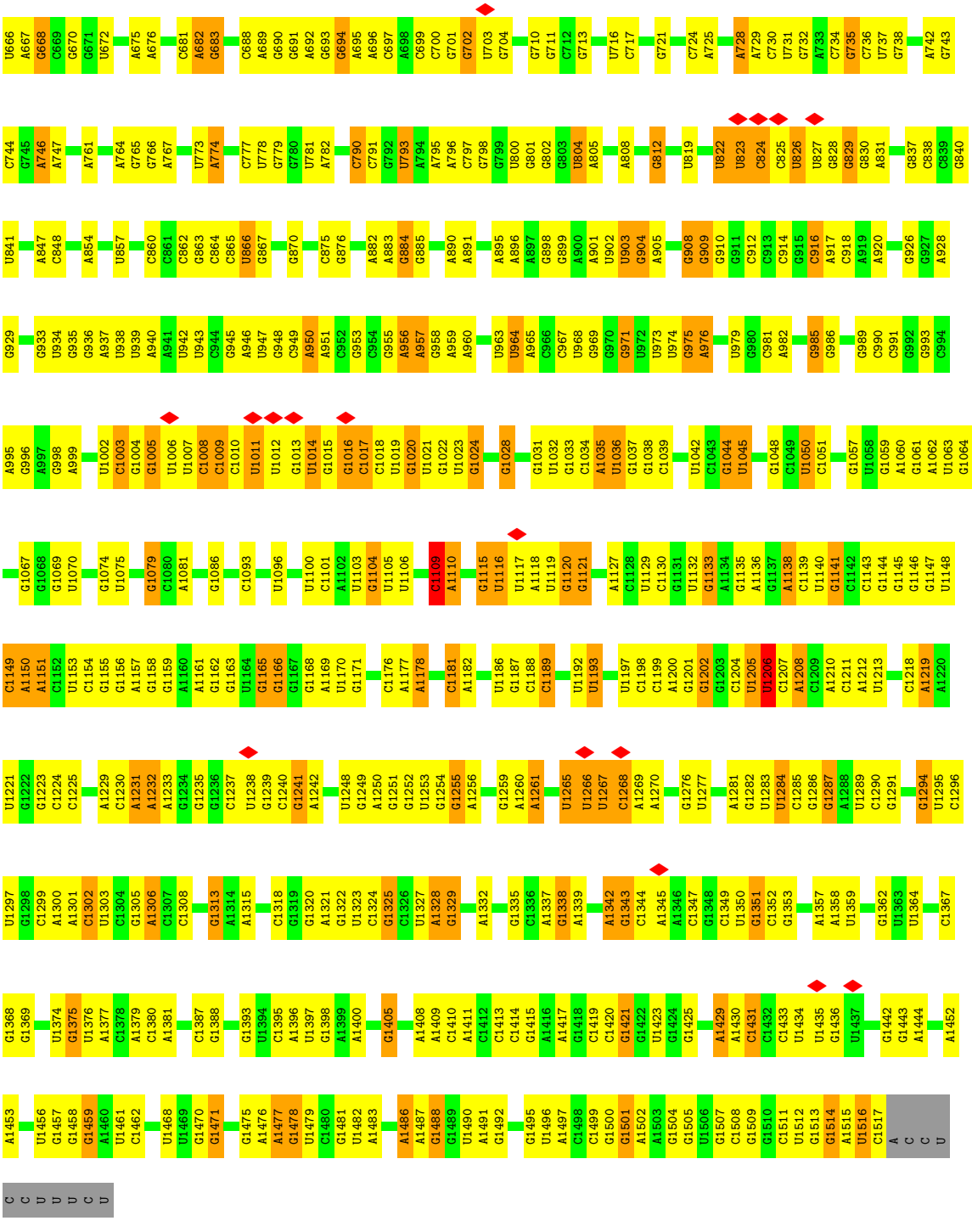


• Molecule 5: Large ribosomal subunit protein uL1

Chain 6:





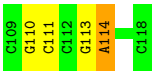


• Molecule 7: 5S ribosomal RNA

Chain B:



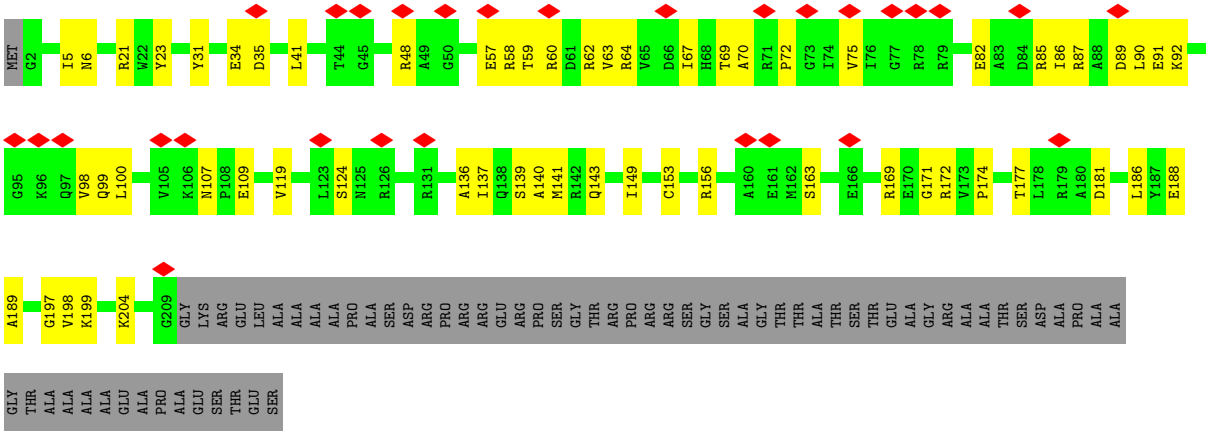




• Molecule 8: 30S ribosomal protein S3

Chain C:

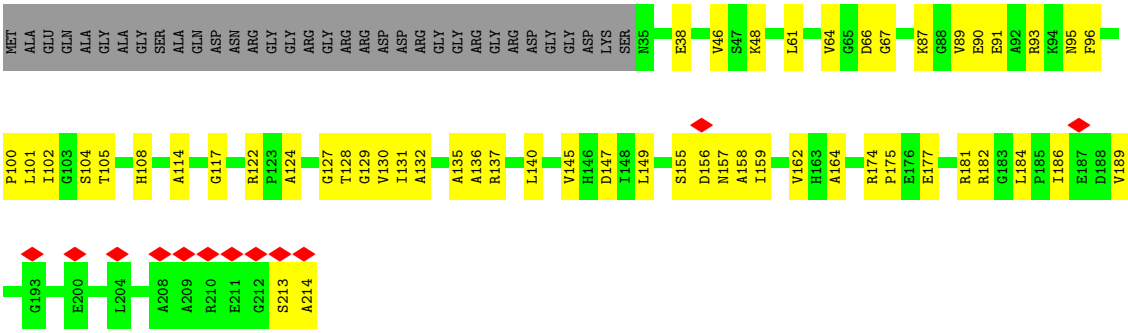




• Molecule 9: 30S ribosomal protein S5

Chain E:

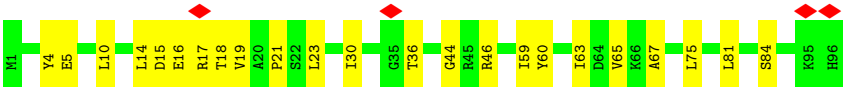




• Molecule 10: Small ribosomal subunit protein bS6

Chain F:

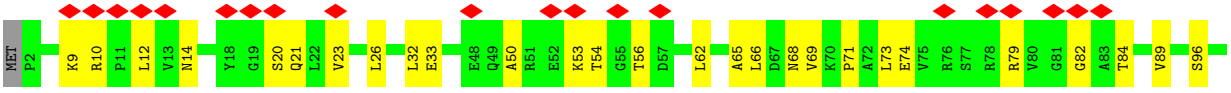


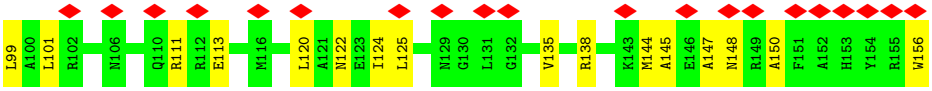


• Molecule 11: 30S ribosomal protein S7

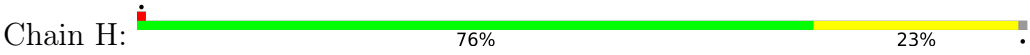
Chain G:

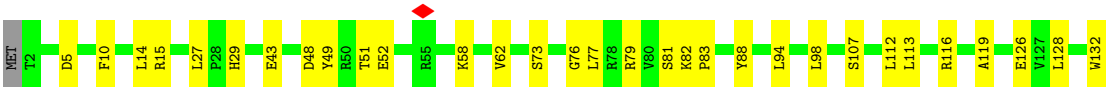






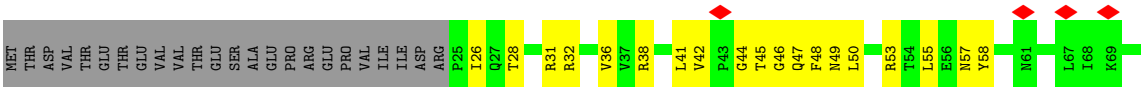
• Molecule 12: 30S ribosomal protein S8

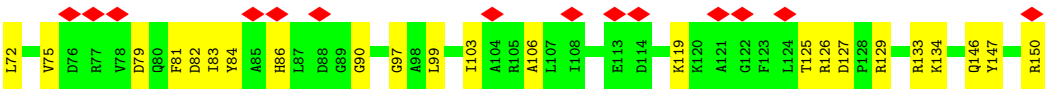




• Molecule 13: 30S ribosomal protein S9

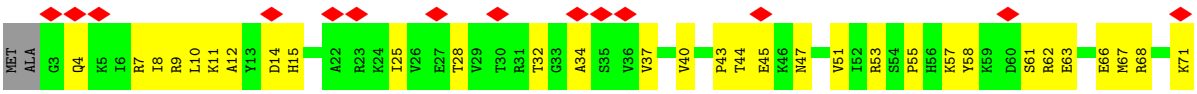


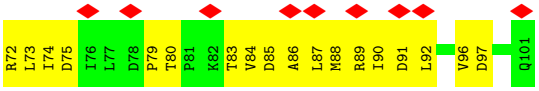




• Molecule 14: 30S ribosomal protein S10

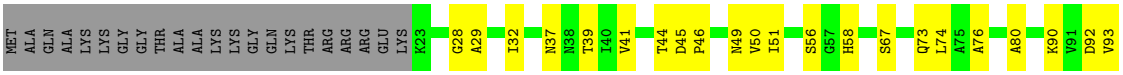






• Molecule 15: 30S ribosomal protein S11

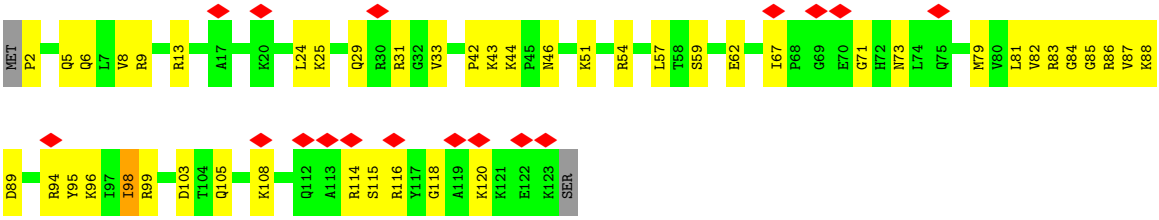






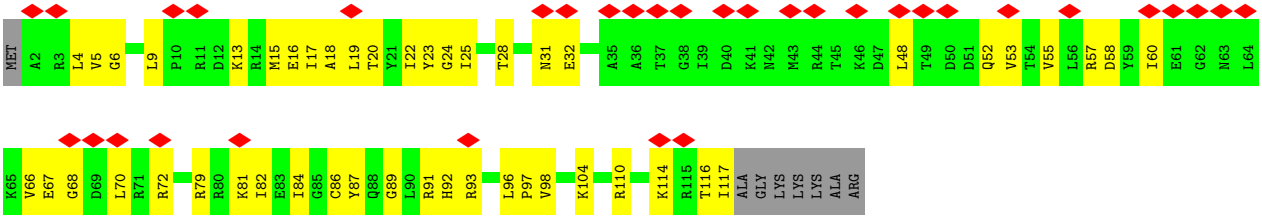
• Molecule 16: 30S ribosomal protein S12





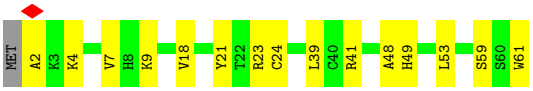
• Molecule 17: 30S ribosomal protein S13



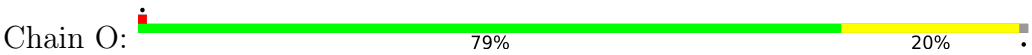


• Molecule 18: 30S ribosomal protein S14 type Z





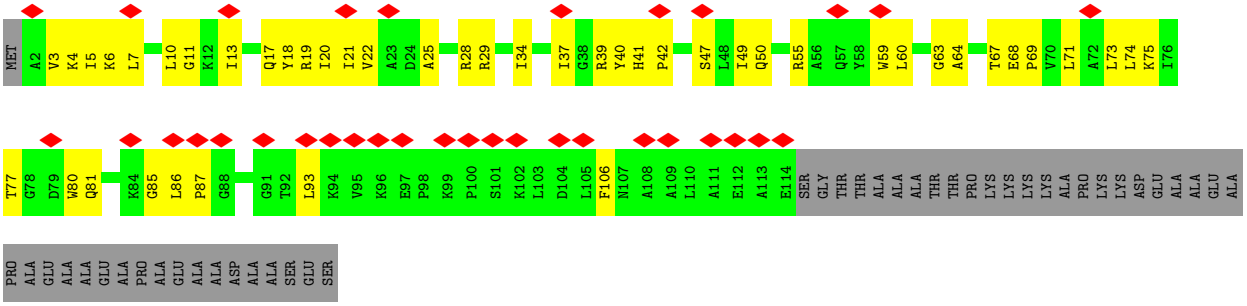
• Molecule 19: 30S ribosomal protein S15





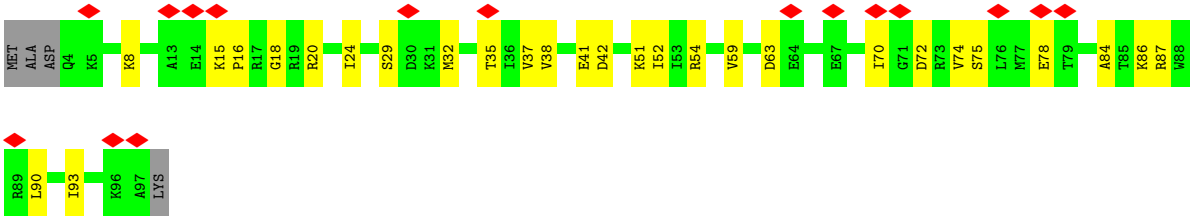
• Molecule 20: 30S ribosomal protein S16



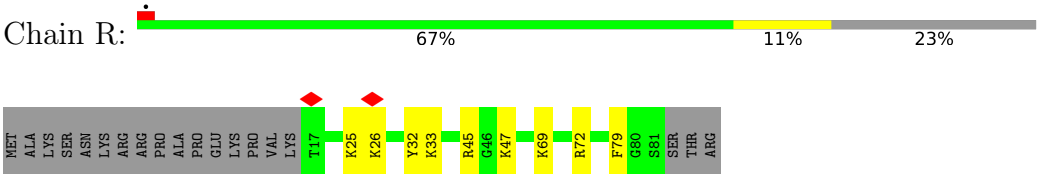


• Molecule 21: 30S ribosomal protein S17

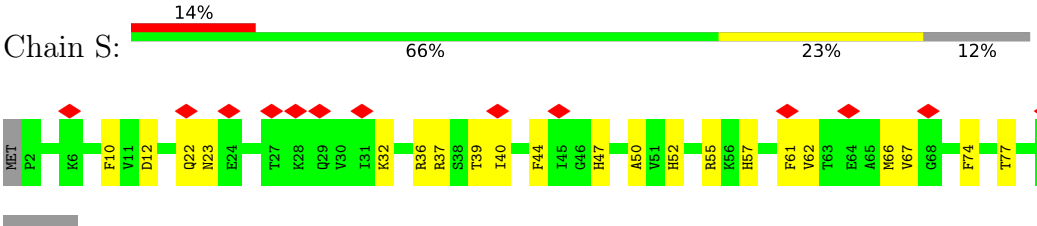




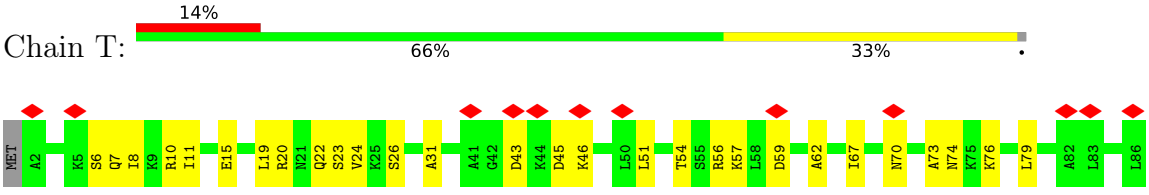
• Molecule 22: 30S ribosomal protein S18 2



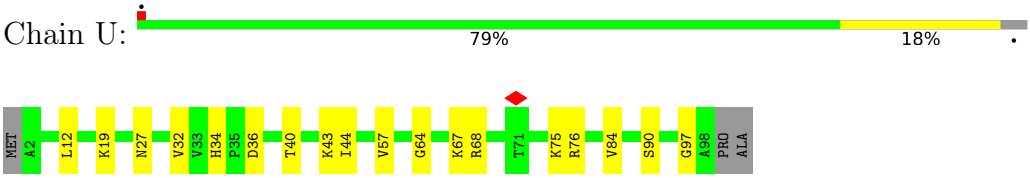
• Molecule 23: 30S ribosomal protein S19



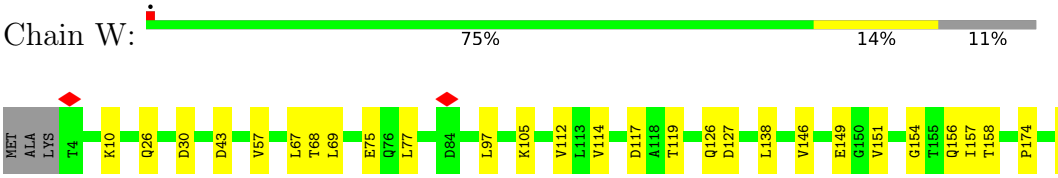
• Molecule 24: 30S ribosomal protein S20



• Molecule 25: 50S ribosomal protein L23



• Molecule 26: 50S ribosomal protein L25



• Molecule 27: 50S ribosomal protein L27

Chain X:

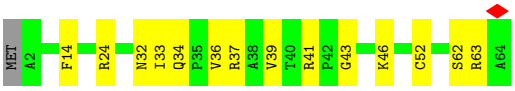




• Molecule 28: 50S ribosomal protein L28

Chain Y:

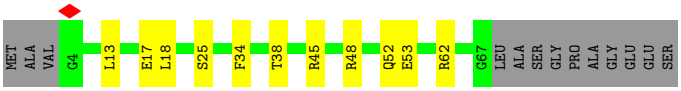




• Molecule 29: 50S ribosomal protein L29

Chain Z:

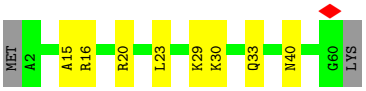




• Molecule 30: 50S ribosomal protein L30

Chain a:

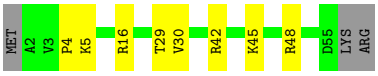




• Molecule 31: 50S ribosomal protein L32

Chain b:

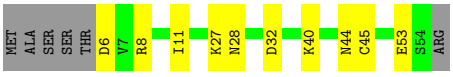




• Molecule 32: 50S ribosomal protein L33 1

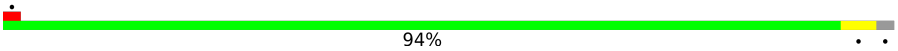
Chain c:

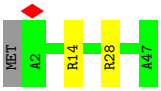




• Molecule 33: 50S ribosomal protein L34

Chain d:





• Molecule 34: 50S ribosomal protein L35

Chain e:





• Molecule 35: 50S ribosomal protein L36

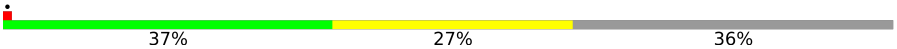
Chain f:

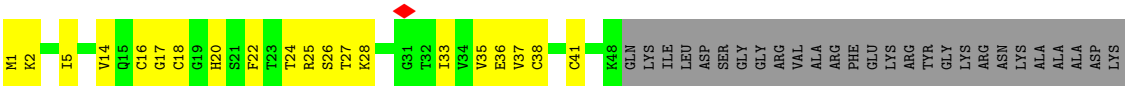




• Molecule 36: 50S ribosomal protein L31

Chain g:



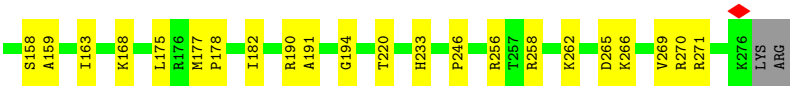


• Molecule 37: 50S ribosomal protein L2

Chain i:



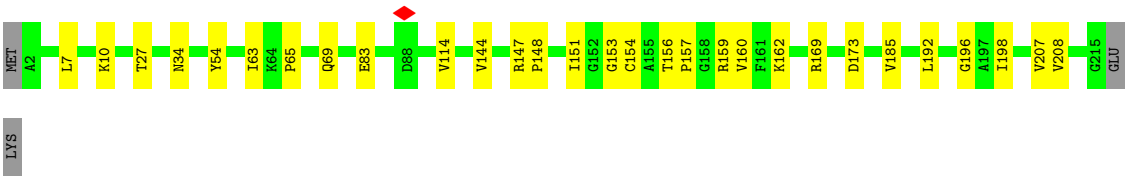




• Molecule 38: 50S ribosomal protein L3

Chain j:

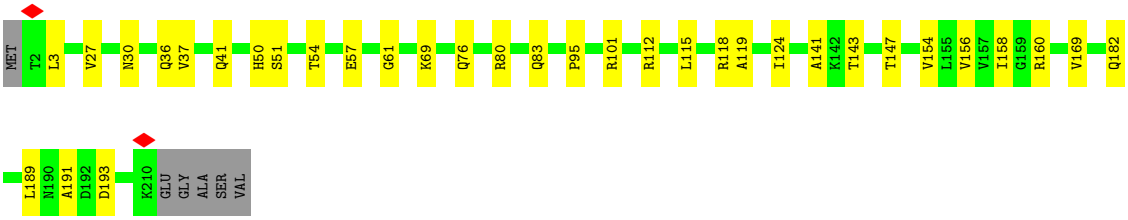




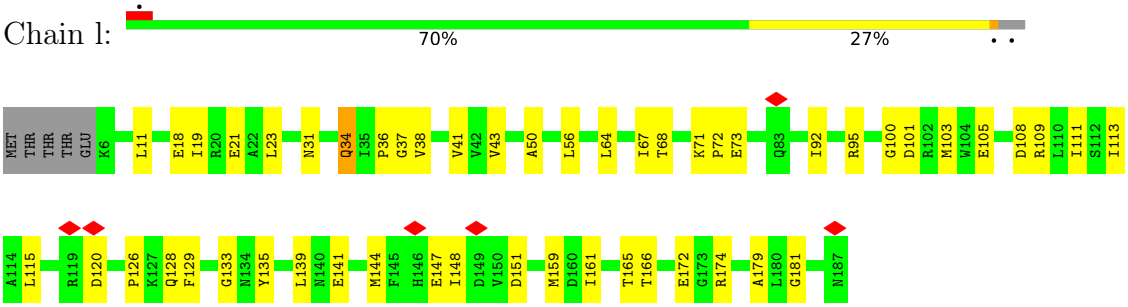
• Molecule 39: 50S ribosomal protein L4

Chain k:

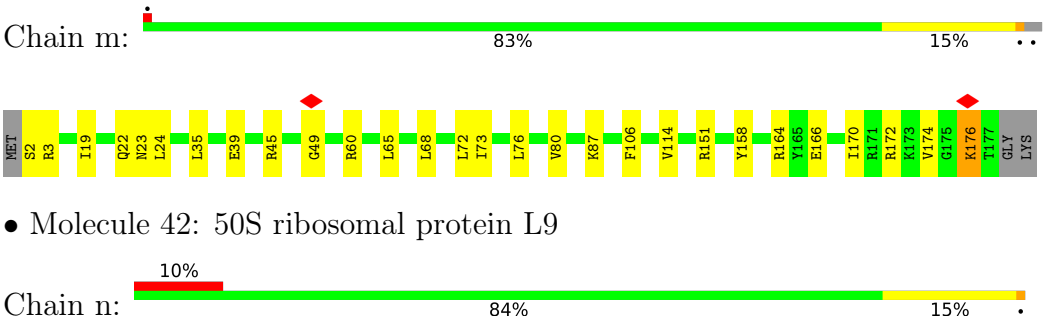




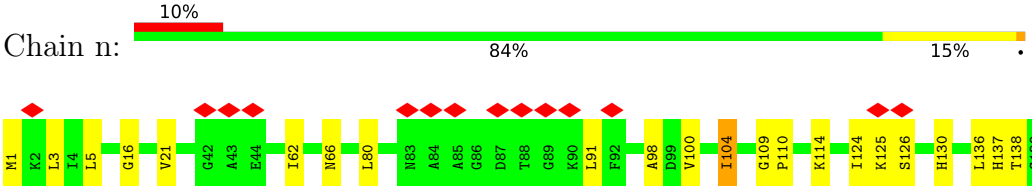
• Molecule 40: 50S ribosomal protein L5



• Molecule 41: 50S ribosomal protein L6

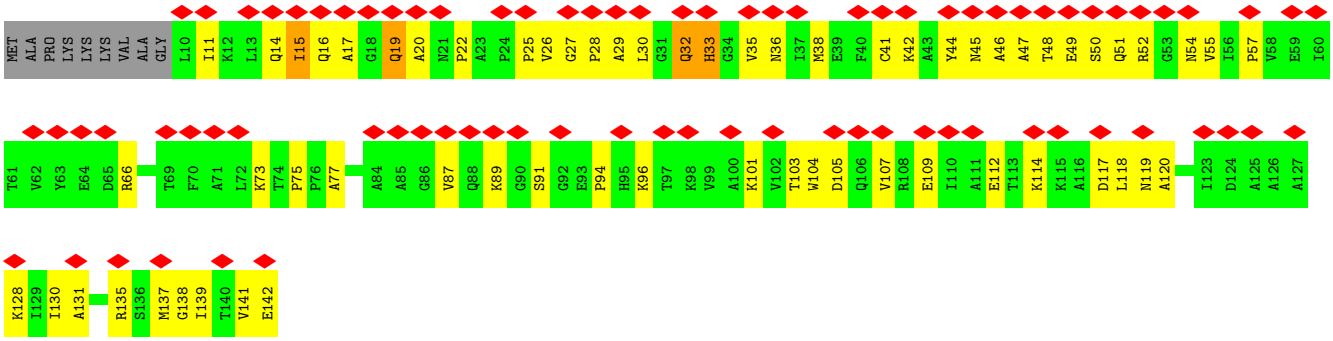


• Molecule 42: 50S ribosomal protein L9



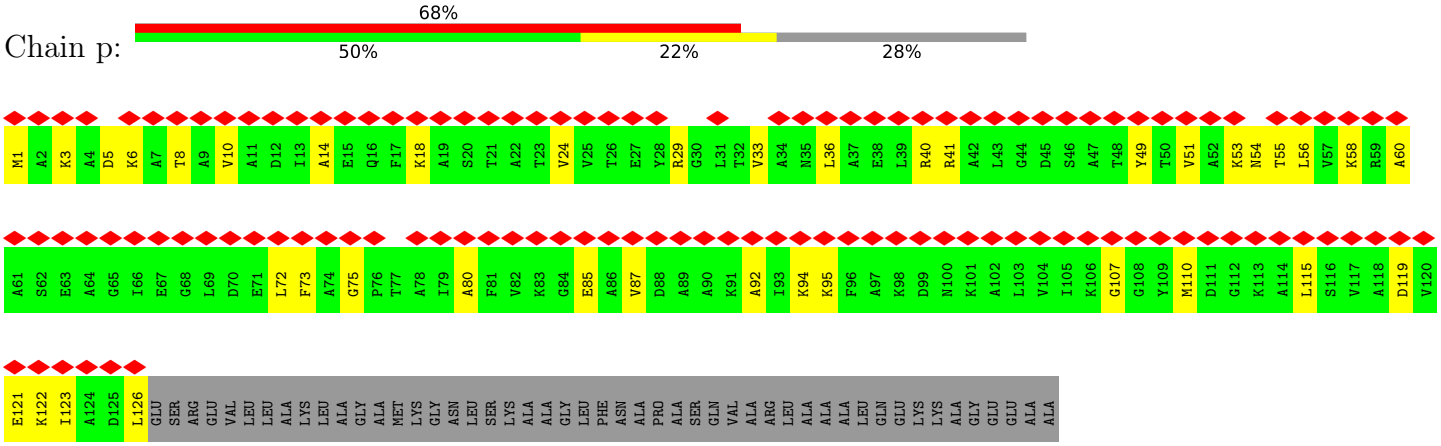
• Molecule 43: 50S ribosomal protein L11





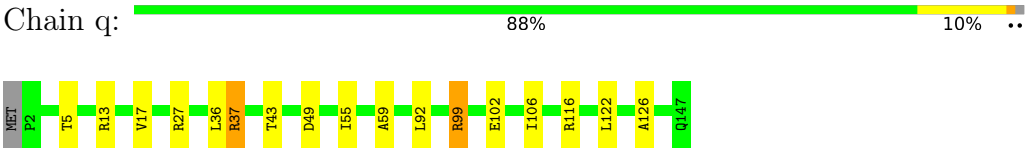
• Molecule 44: 50S ribosomal protein L10

Chain p:



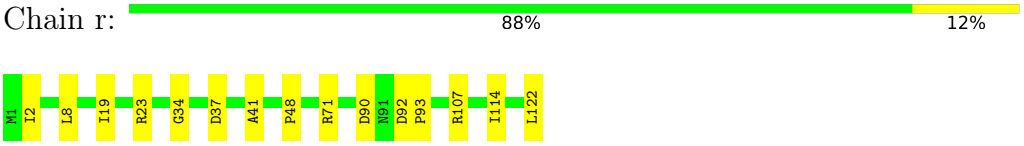
• Molecule 45: 50S ribosomal protein L13

Chain q:



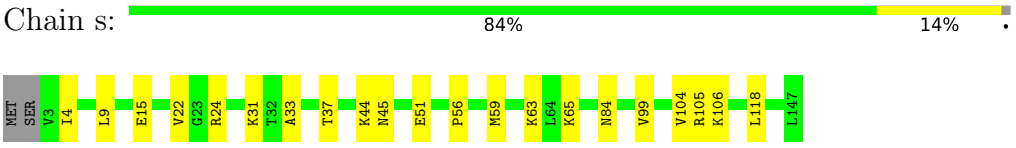
• Molecule 46: 50S ribosomal protein L14

Chain r:



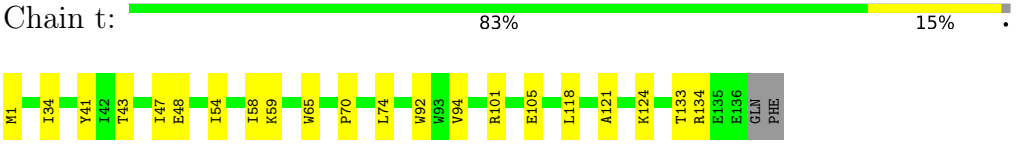
• Molecule 47: 50S ribosomal protein L15

Chain s:



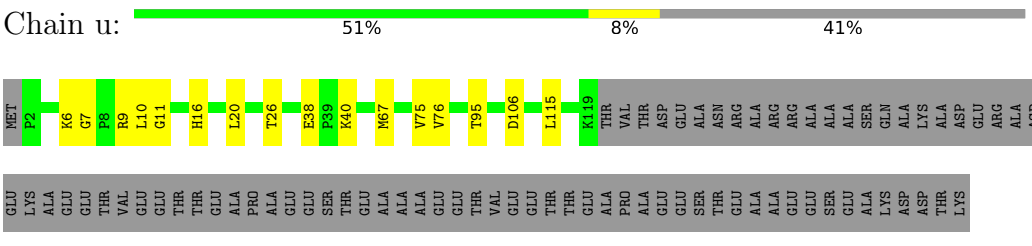
• Molecule 48: 50S ribosomal protein L16

Chain t:



• Molecule 49: 50S ribosomal protein L17

Chain u:



• Molecule 50: 50S ribosomal protein L18

Chain v:





• Molecule 51: 50S ribosomal protein L19

Chain w:





• Molecule 52: 50S ribosomal protein L20

Chain x:

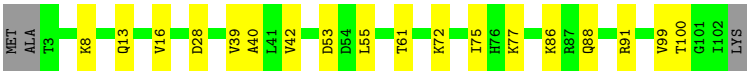




• Molecule 53: 50S ribosomal protein L21

Chain y:





• Molecule 54: 50S ribosomal protein L22

Chain z:

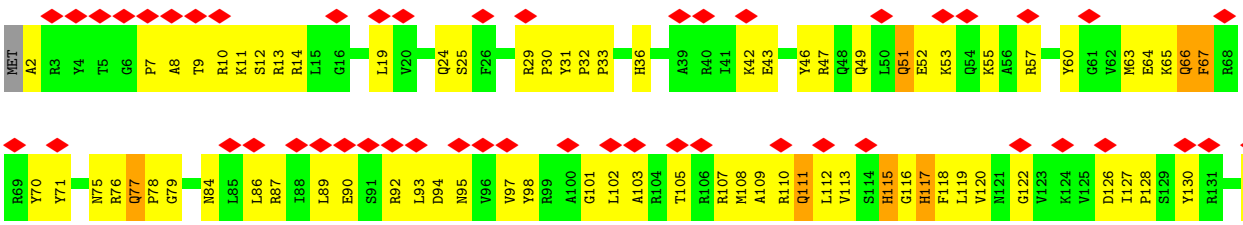


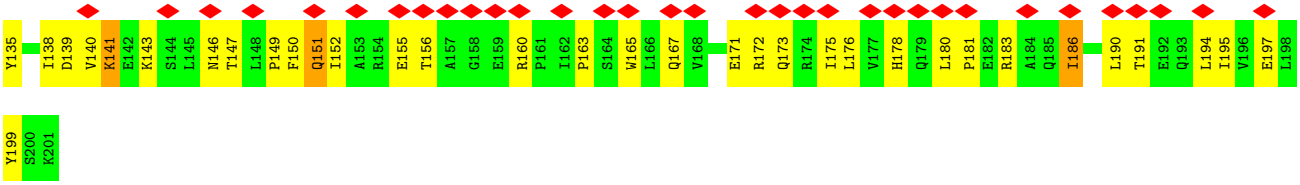


• Molecule 55: 30S ribosomal protein S4

Chain D:



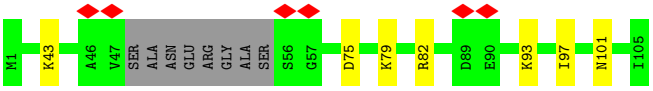




• Molecule 56: Large ribosomal subunit protein uL24

Chain 1:

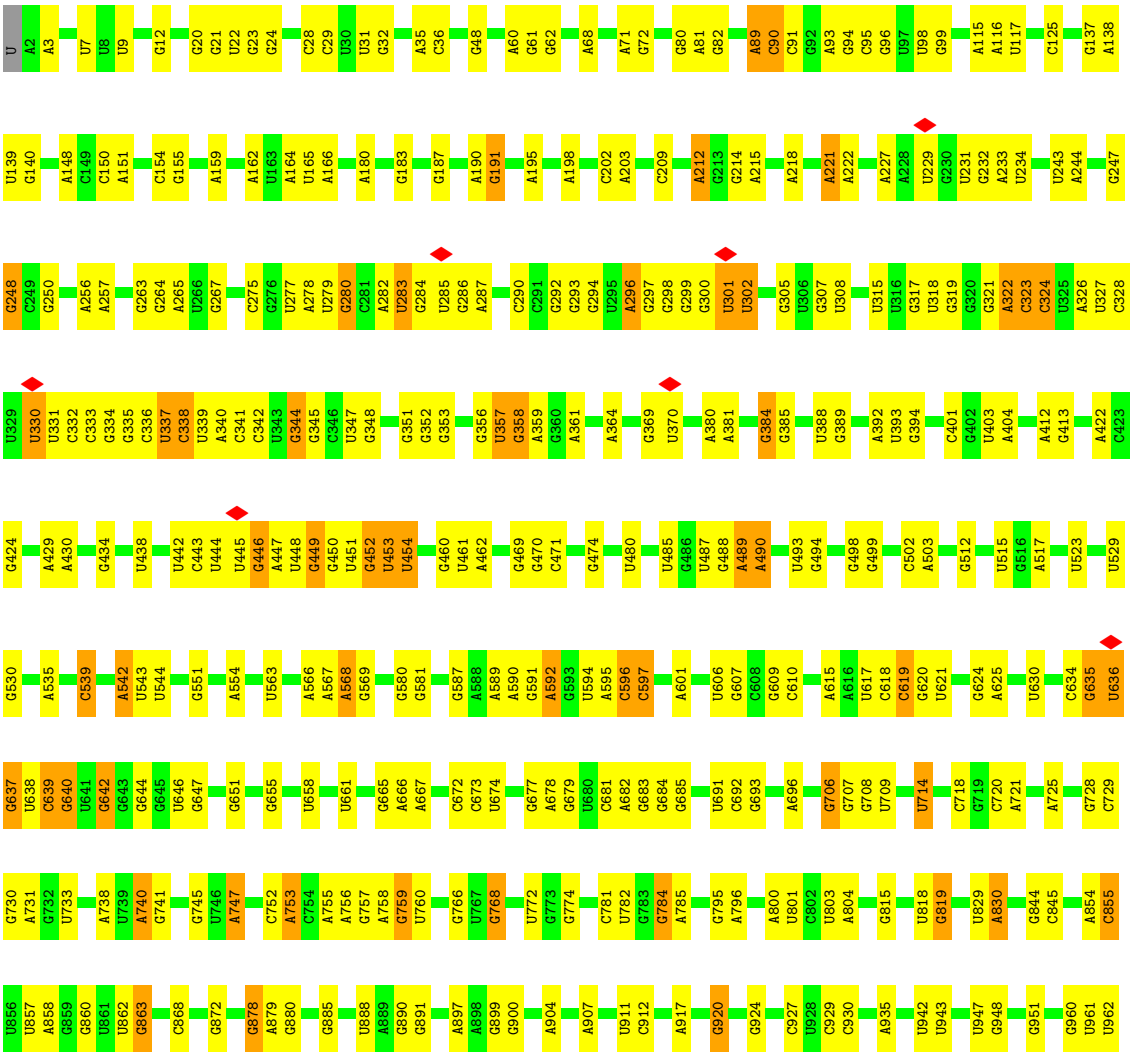


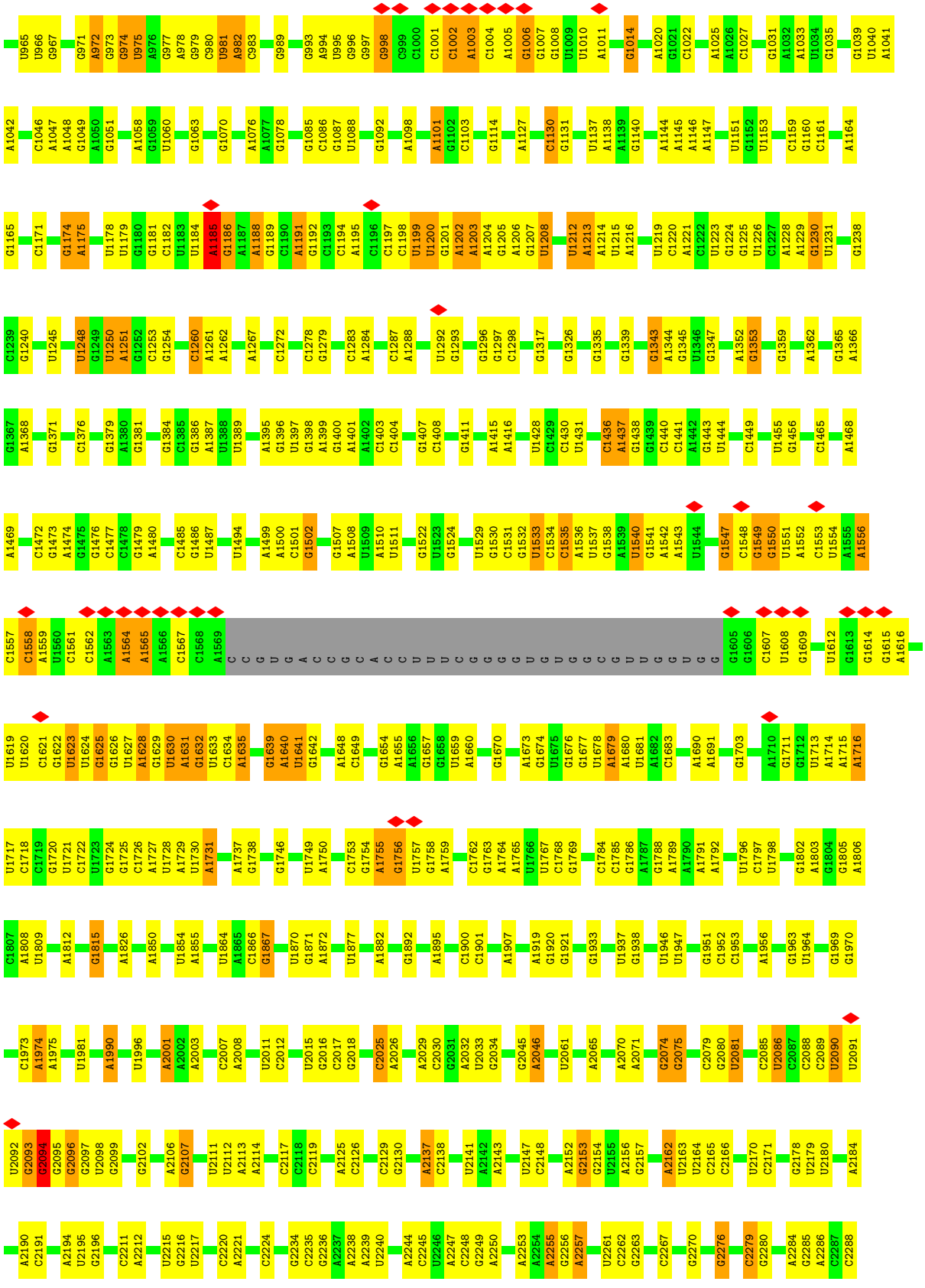


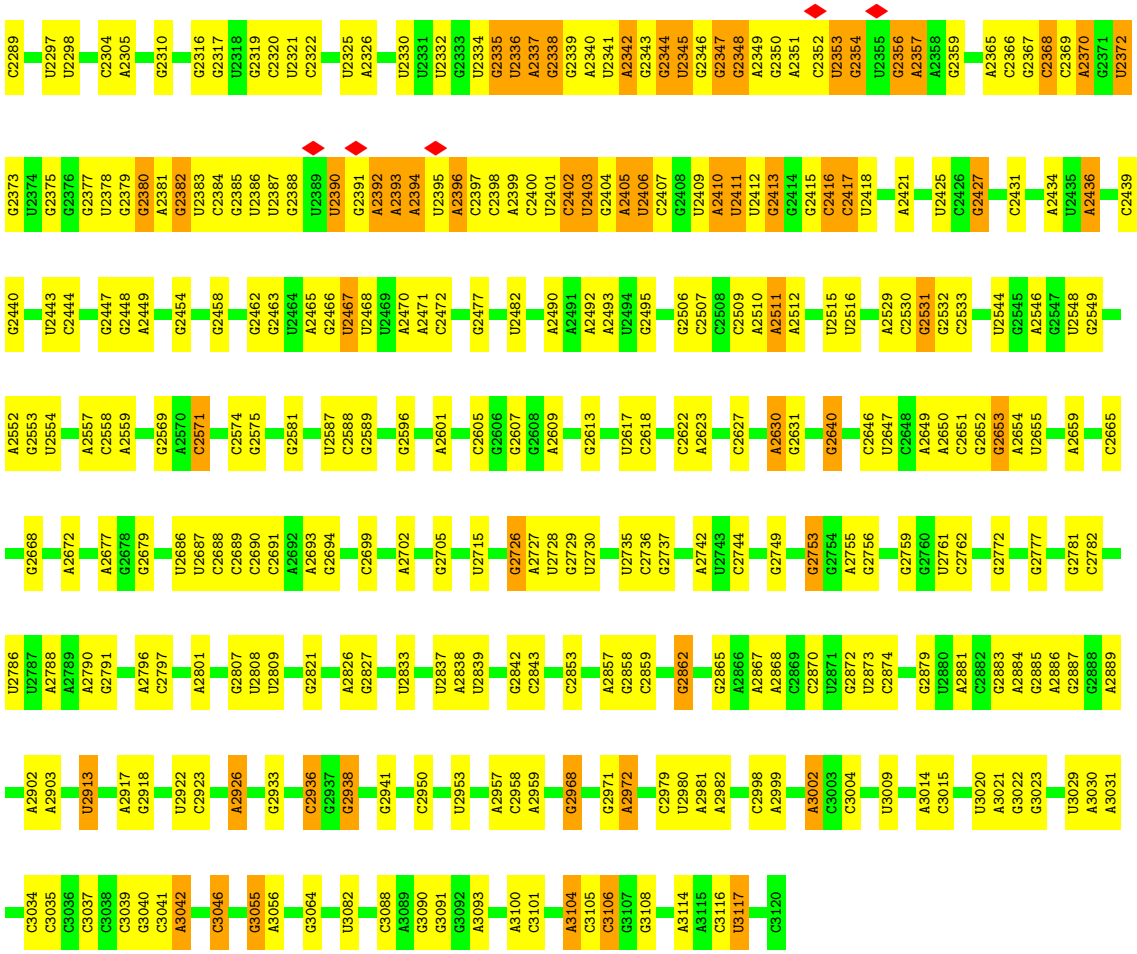
• Molecule 57: 23S ribosomal RNA

Chain h:








C2289 U2297 U2298 C2304 A2305 G2310 G2316 G2317 U2318 G2319 C2320 U2321 C2322 U2325 A2326 U2330 U2331 U2332 G2333 U2334 G2335 U2336 A2337 G2338 G2339 A2340 U2341 A2342 G2343 G2344 U2345 G2346 G2347 G2348 A2349 G2350 A2351 C2352 U2353 G2354 U2355 G2356 A2357 A2358 G2359 A2365 C2366 G2367 C2368 C2369 A2370 G2371 U2372
G2373 U2374 G2375 G2376 G2377 U2378 G2379 G2380 A2381 G2382 U2383 C2384 G2385 U2386 U2387 G2388 U2389 U2390 G2391 A2392 A2393 A2394 U2395 A2396 C2397 C2398 A2399 C2400 U2401 C2402 U2403 G2404 A2405 U2406 C2407 G2408 U2409 A2410 U2411 U2412 G2413 G2414 G2415 C2416 C2417 U2418 A2421 U2425 G2426 G2427 C2431 A2434 U2435 A2436 C2439
G2440 U2443 C2444 G2447 G2448 A2449 G2454 G2458 G2462 G2463 U2464 A2465 G2466 U2467 U2468 U2469 A2470 A2471 C2472 G2477 U2482 A2490 A2491 A2492 A2493 U2494 G2495 G2506 C2507 C2508 C2509 A2510 A2511 A2512 U2515 U2516 A2529 C2530 G2531 G2532 C2533 U2544 G2545 A2546 G2547 U2548 G2549
A2552 G2553 U2554 A2557 C2558 A2559 G2569 A2570 C2571 C2574 G2575 G2581 U2587 C2588 G2589 G2596 A2601 C2605 G2606 G2607 G2608 A2609 G2613 U2617 C2618 C2622 A2623 C2627 A2630 G2631 G2640 C2646 U2647 C2648 A2649 A2650 C2651 G2652 G2653 A2654 U2655 A2659 C2665
G2668 A2672 A2677 G2678 G2679 U2686 U2687 C2688 C2689 C2690 C2691 A2692 A2693 G2694 C2699 A2702 G2705 U2715 G2726 A2727 U2728 G2729 U2730 U2735 C2736 G2737 A2742 U2743 C2744 G2749 G2753 G2754 A2755 G2756 G2759 G2760 U2761 C2762 G2772 G2777 G2781 C2782
U2786 U2787 A2788 A2789 A2790 G2791 A2796 C2797 A2801 G2807 U2808 U2809 G2821 A2826 G2827 U2833 U2837 A2838 U2839 G2842 C2843 C2853 A2857 G2858 C2859 G2862 G2865 A2866 A2867 A2868 C2869 C2870 U2871 G2872 U2873 C2874 G2879 U2880 A2881 C2882 G2883 A2884 G2885 A2886 G2887 G2888 A2889
A2902 A2903 U2913 A2917 G2918 U2922 C2923 A2926 G2933 C2936 G2937 G2938 G2941 C2950 U2953 A2957 C2958 A2959 G2968 G2971 A2972 C2979 U2980 A2981 A2982 C2998 A2999 A3002 C3003 C3004 U3009 A3014 C3015 U3020 A3021 G3022 G3023 U3029 A3030 A3031
C3034 C3035 C3036 C3037 C3038 C3039 G3040 C3041 A3042 C3046 G3055 A3056 G3064 U3082 C3088 A3089 G3090 G3091 G3092 A3093 A3100 C3101 A3104 C3105 C3106 G3107 G3108 A3114 A3115 C3116 U3117 C3120

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32720	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	0.257	Depositor
Minimum map value	-0.164	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.024	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: 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	0.49	0/1836	0.85	0/2859
2	3	0.16	0/191	0.37	0/247
3	4	1.06	0/65	0.99	0/98
4	5	0.20	0/1472	0.43	2/1976 (0.1%)
5	6	0.40	2/1760 (0.1%)	0.91	4/2375 (0.2%)
6	A	0.58	0/36309	0.88	25/56657 (0.0%)
7	B	0.34	0/2821	0.76	0/4396
8	C	0.17	0/1684	0.36	0/2261
9	E	0.20	0/1312	0.39	0/1772
10	F	0.17	0/782	0.35	0/1059
11	G	0.16	0/1252	0.37	0/1690
12	H	0.19	0/1025	0.38	0/1385
13	I	0.17	0/1012	0.39	0/1362
14	J	0.18	0/802	0.41	0/1086
15	K	0.21	0/873	0.40	0/1180
16	L	0.33	0/969	0.53	0/1294
17	M	0.16	0/942	0.39	0/1260
18	N	0.20	0/488	0.41	0/650
19	O	0.18	0/729	0.32	0/977
20	P	0.19	0/908	0.42	0/1226
21	Q	0.19	0/759	0.42	0/1016
22	R	0.17	0/518	0.32	0/693
23	S	0.15	0/680	0.36	0/915
24	T	0.20	0/663	0.37	0/882
25	U	0.19	0/766	0.31	0/1030
26	W	0.16	0/1443	0.31	0/1970
27	X	0.21	0/595	0.37	0/798
28	Y	0.20	0/478	0.34	0/641
29	Z	0.16	0/534	0.26	0/713
30	a	0.20	0/477	0.27	0/640
31	b	0.19	0/427	0.29	0/572
32	c	0.17	0/413	0.29	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	d	0.21	0/380	0.29	0/500
34	e	0.19	0/507	0.34	0/672
35	f	0.20	0/303	0.29	0/401
36	g	0.13	0/372	0.31	0/503
37	i	0.21	0/2153	0.35	0/2895
38	j	0.21	0/1609	0.38	0/2165
39	k	0.18	0/1592	0.32	0/2153
40	l	0.15	0/1467	0.33	0/1973
41	m	0.17	0/1369	0.34	0/1848
42	n	0.14	0/1027	0.37	0/1398
43	o	3.56	6/1006 (0.6%)	3.09	9/1364 (0.7%)
44	p	0.11	0/925	0.29	0/1246
45	q	0.21	0/1157	0.33	0/1567
46	r	0.21	0/946	0.32	0/1268
47	s	0.20	0/1091	0.38	0/1457
48	t	0.20	0/1118	0.38	0/1506
49	u	0.19	0/945	0.36	0/1267
50	v	0.16	0/966	0.29	0/1298
51	w	0.18	0/921	0.35	0/1236
52	x	0.20	0/1000	0.27	0/1341
53	y	0.18	0/764	0.30	0/1030
54	z	0.22	0/887	0.32	0/1204
55	D	3.91	11/1672 (0.7%)	3.35	12/2251 (0.5%)
56	1	0.17	0/738	0.32	0/987
57	h	0.49	0/74164	0.80	29/115718 (0.0%)
All	All	0.66	19/164064 (0.0%)	0.83	81/245481 (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
5	6	0	1
45	q	0	1
All	All	0	2

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	D	115	HIS	ND1-CE1	87.21	2.19	1.32
55	D	117	HIS	ND1-CE1	87.18	2.19	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	o	33	HIS	ND1-CE1	87.14	2.19	1.32
55	D	115	HIS	CD2-NE2	69.88	2.14	1.37
43	o	33	HIS	CD2-NE2	69.78	2.14	1.37

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	D	115	HIS	CE1-NE2-CD2	-73.19	35.81	109.00
43	o	33	HIS	CE1-NE2-CD2	-73.17	35.83	109.00
55	D	117	HIS	CE1-NE2-CD2	-73.17	35.83	109.00
55	D	117	HIS	ND1-CE1-NE2	-72.13	36.27	108.40
43	o	33	HIS	ND1-CE1-NE2	-72.09	36.31	108.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	6	230	ARG	Sidechain
45	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	45	0
2	3	189	0	205	2	0
3	4	60	0	32	0	0
4	5	1459	0	1477	33	0
5	6	1736	0	1788	92	0
6	A	32439	0	16321	651	0
7	B	2522	0	1285	30	0
8	C	1660	0	1707	42	0
9	E	1296	0	1360	35	0
10	F	771	0	797	17	0
11	G	1232	0	1282	31	0
12	H	1010	0	1046	23	0
13	I	994	0	1050	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	J	788	0	819	39	0
15	K	855	0	863	23	0
16	L	958	0	1045	56	0
17	M	935	0	986	38	0
18	N	477	0	499	15	0
19	O	720	0	760	16	0
20	P	891	0	935	43	0
21	Q	748	0	795	19	0
22	R	513	0	537	8	0
23	S	662	0	677	18	0
24	T	660	0	712	23	0
25	U	756	0	802	12	0
26	W	1428	0	1443	18	0
27	X	586	0	601	8	0
28	Y	470	0	480	8	0
29	Z	531	0	541	9	0
30	a	474	0	500	6	0
31	b	423	0	463	9	0
32	c	405	0	407	7	0
33	d	377	0	411	2	0
34	e	502	0	541	10	0
35	f	299	0	321	8	0
36	g	364	0	348	18	0
37	i	2110	0	2165	36	0
38	j	1587	0	1630	23	0
39	k	1569	0	1607	24	0
40	l	1445	0	1476	41	0
41	m	1348	0	1399	19	0
42	n	1018	0	988	15	0
43	o	990	0	1021	55	0
44	p	918	0	959	32	0
45	q	1130	0	1167	14	0
46	r	938	0	1000	11	0
47	s	1078	0	1151	16	0
48	t	1092	0	1128	13	0
49	u	928	0	972	10	0
50	v	956	0	991	21	0
51	w	907	0	938	17	0
52	x	988	0	1038	11	0
53	y	754	0	802	12	0
54	z	873	0	909	9	0
55	D	1641	0	1668	137	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1	732	0	782	6	0
57	h	66232	0	33324	586	0
58	F	1	0	0	0	0
58	R	1	0	0	0	0
58	X	1	0	0	0	0
58	h	2	0	0	0	0
58	i	4	0	0	0	0
58	l	1	0	0	0	0
58	t	1	0	0	0	0
58	z	1	0	0	0	0
59	N	1	0	0	0	0
59	R	1	0	0	0	0
59	Y	1	0	0	0	0
59	c	1	0	0	0	0
59	f	1	0	0	0	0
59	g	1	0	0	0	0
All	All	151086	0	101787	2197	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 9.

The worst 5 of 2197 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)
6:A:532:U:H4'	16:L:84:GLY:O	1.64	0.96
43:o:35:VAL:HA	43:o:66:ARG:NH1	1.85	0.91
43:o:35:VAL:HA	43:o:66:ARG:HH12	1.37	0.90
55:D:93:LEU:HG	55:D:113:VAL:CG2	2.02	0.88
55:D:93:LEU:HD23	55:D:113:VAL:HG13	1.55	0.87

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	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
5	6	230/235 (98%)	216 (94%)	13 (6%)	1 (0%)	30	66
8	C	206/275 (75%)	195 (95%)	11 (5%)	0	100	100
9	E	178/214 (83%)	167 (94%)	11 (6%)	0	100	100
10	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
11	G	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
12	H	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
13	I	124/150 (83%)	113 (91%)	11 (9%)	0	100	100
14	J	97/101 (96%)	92 (95%)	5 (5%)	0	100	100
15	K	113/138 (82%)	108 (96%)	5 (4%)	0	100	100
16	L	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
17	M	114/124 (92%)	108 (95%)	6 (5%)	0	100	100
18	N	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
19	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
20	P	111/156 (71%)	103 (93%)	8 (7%)	0	100	100
21	Q	92/98 (94%)	90 (98%)	2 (2%)	0	100	100
22	R	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
23	S	80/93 (86%)	79 (99%)	1 (1%)	0	100	100
24	T	83/86 (96%)	83 (100%)	0	0	100	100
25	U	95/100 (95%)	92 (97%)	3 (3%)	0	100	100
26	W	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
27	X	77/88 (88%)	72 (94%)	5 (6%)	0	100	100
28	Y	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
29	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
30	a	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
31	b	52/57 (91%)	52 (100%)	0	0	100	100
32	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
33	d	44/47 (94%)	44 (100%)	0	0	100	100
34	e	61/64 (95%)	61 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
36	g	46/75 (61%)	42 (91%)	4 (9%)	0	100	100
37	i	273/278 (98%)	262 (96%)	11 (4%)	0	100	100
38	j	212/217 (98%)	201 (95%)	11 (5%)	0	100	100
39	k	207/215 (96%)	201 (97%)	6 (3%)	0	100	100
40	l	180/187 (96%)	176 (98%)	4 (2%)	0	100	100
41	m	174/179 (97%)	172 (99%)	2 (1%)	0	100	100
42	n	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
43	o	131/142 (92%)	123 (94%)	8 (6%)	0	100	100
44	p	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
45	q	144/147 (98%)	142 (99%)	2 (1%)	0	100	100
46	r	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
47	s	143/147 (97%)	132 (92%)	11 (8%)	0	100	100
48	t	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
49	u	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
50	v	124/127 (98%)	124 (100%)	0	0	100	100
51	w	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
52	x	122/129 (95%)	122 (100%)	0	0	100	100
53	y	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
54	z	112/153 (73%)	108 (96%)	4 (4%)	0	100	100
55	D	198/201 (98%)	182 (92%)	16 (8%)	0	100	100
56	1	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
All	All	6127/6789 (90%)	5878 (96%)	248 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	6	231	ASN

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	160/160 (100%)	160 (100%)	0	100	100
5	6	181/184 (98%)	178 (98%)	3 (2%)	53	67
8	C	170/212 (80%)	170 (100%)	0	100	100
9	E	127/147 (86%)	126 (99%)	1 (1%)	73	77
10	F	85/85 (100%)	85 (100%)	0	100	100
11	G	131/132 (99%)	130 (99%)	1 (1%)	73	77
12	H	107/108 (99%)	107 (100%)	0	100	100
13	I	102/125 (82%)	102 (100%)	0	100	100
14	J	89/90 (99%)	89 (100%)	0	100	100
15	K	89/105 (85%)	88 (99%)	1 (1%)	65	73
16	L	103/105 (98%)	101 (98%)	2 (2%)	50	66
17	M	99/104 (95%)	99 (100%)	0	100	100
18	N	49/50 (98%)	49 (100%)	0	100	100
19	O	76/77 (99%)	76 (100%)	0	100	100
20	P	92/118 (78%)	92 (100%)	0	100	100
21	Q	80/83 (96%)	80 (100%)	0	100	100
22	R	55/72 (76%)	55 (100%)	0	100	100
23	S	73/84 (87%)	73 (100%)	0	100	100
24	T	69/70 (99%)	69 (100%)	0	100	100
25	U	83/85 (98%)	83 (100%)	0	100	100
26	W	155/168 (92%)	155 (100%)	0	100	100
27	X	58/63 (92%)	58 (100%)	0	100	100
28	Y	50/51 (98%)	50 (100%)	0	100	100
29	Z	58/66 (88%)	58 (100%)	0	100	100
30	a	52/54 (96%)	52 (100%)	0	100	100
31	b	43/46 (94%)	43 (100%)	0	100	100
32	c	47/52 (90%)	47 (100%)	0	100	100
33	d	35/36 (97%)	35 (100%)	0	100	100
34	e	53/54 (98%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
35	f	35/35 (100%)	35 (100%)	0	100 100
36	g	43/63 (68%)	43 (100%)	0	100 100
37	i	215/218 (99%)	214 (100%)	1 (0%)	81 81
38	j	160/163 (98%)	160 (100%)	0	100 100
39	k	169/173 (98%)	169 (100%)	0	100 100
40	l	151/156 (97%)	150 (99%)	1 (1%)	76 78
41	m	148/150 (99%)	147 (99%)	1 (1%)	76 78
42	n	90/116 (78%)	89 (99%)	1 (1%)	65 73
43	o	102/108 (94%)	101 (99%)	1 (1%)	68 75
44	p	89/120 (74%)	89 (100%)	0	100 100
45	q	119/120 (99%)	117 (98%)	2 (2%)	53 67
46	r	100/100 (100%)	100 (100%)	0	100 100
47	s	112/114 (98%)	112 (100%)	0	100 100
48	t	114/116 (98%)	114 (100%)	0	100 100
49	u	97/158 (61%)	97 (100%)	0	100 100
50	v	93/94 (99%)	93 (100%)	0	100 100
51	w	100/100 (100%)	100 (100%)	0	100 100
52	x	97/99 (98%)	97 (100%)	0	100 100
53	y	81/83 (98%)	81 (100%)	0	100 100
54	z	90/117 (77%)	90 (100%)	0	100 100
55	D	175/176 (99%)	167 (95%)	8 (5%)	24 46
56	1	81/86 (94%)	81 (100%)	0	100 100
All	All	5050/5470 (92%)	5027 (100%)	23 (0%)	78 81

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	q	99	ARG
55	D	66	GLN
55	D	51	GLN
55	D	67	PHE
16	L	33	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
43	o	21	ASN
55	D	134	GLN
44	p	100	ASN
55	D	111	GLN
55	D	48	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	76/77 (98%)	23 (30%)	0
3	4	2/3 (66%)	0	0
57	h	3082/3120 (98%)	602 (19%)	0
6	A	1510/1528 (98%)	384 (25%)	20 (1%)
7	B	117/118 (99%)	17 (14%)	1 (0%)
All	All	4787/4846 (98%)	1026 (21%)	21 (0%)

5 of 1026 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	G
1	2	5	G
1	2	17	C
1	2	19	G
1	2	20	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	1109	C
6	A	1435	U
7	B	10	G
6	A	1477	A
6	A	1149	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

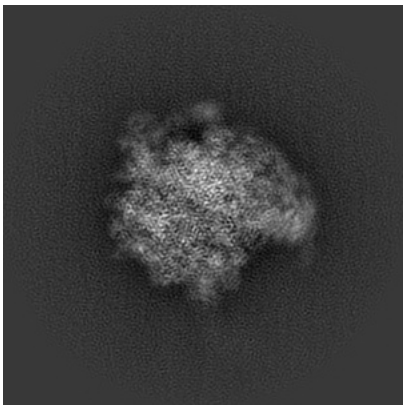
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-69703. These allow visual inspection of the internal detail of the map and identification of artifacts.

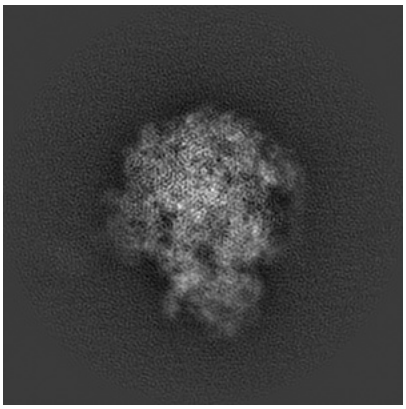
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

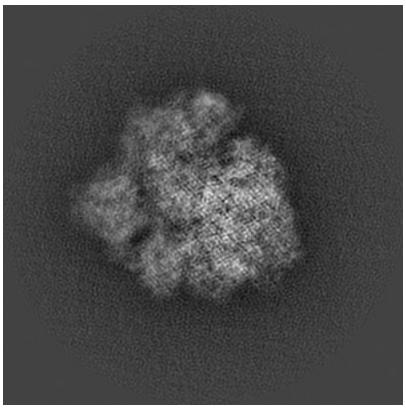
6.1.1 Primary map



X

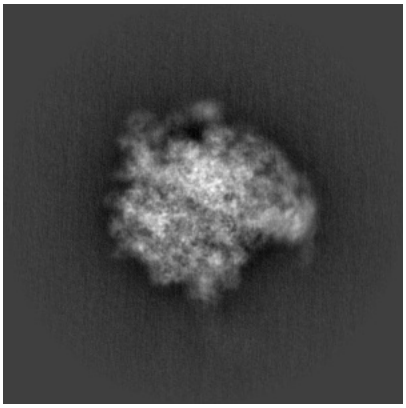


Y

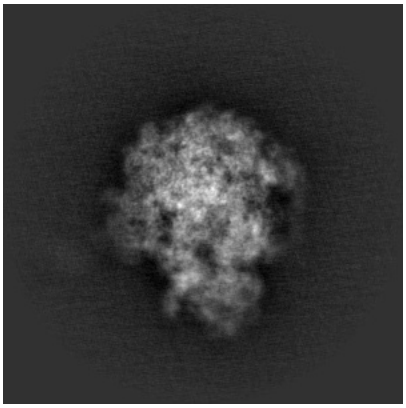


Z

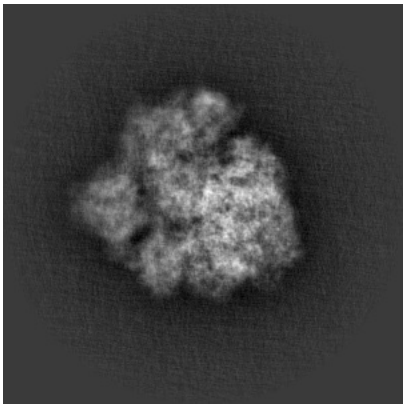
6.1.2 Raw map



X



Y

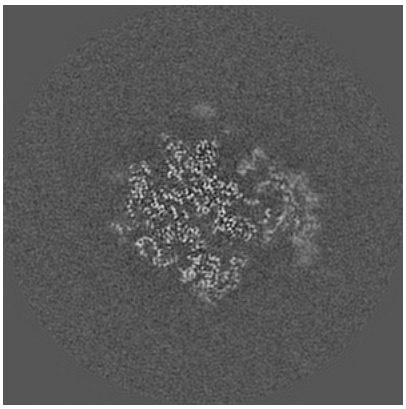


Z

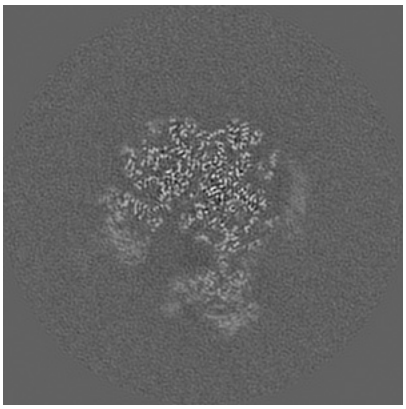
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

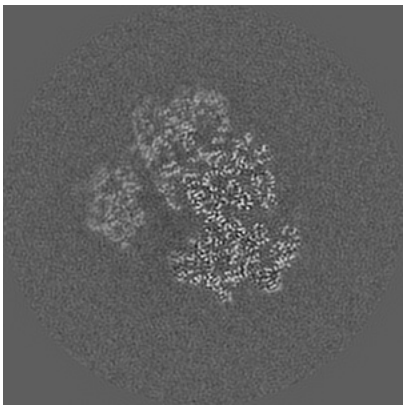
6.2.1 Primary map



X Index: 210

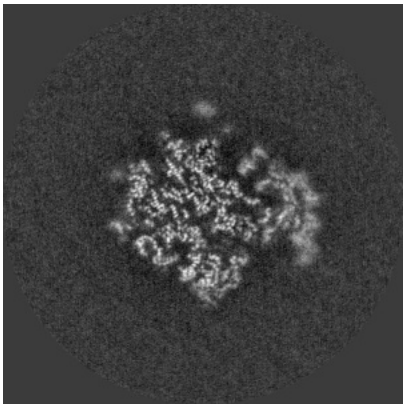


Y Index: 210

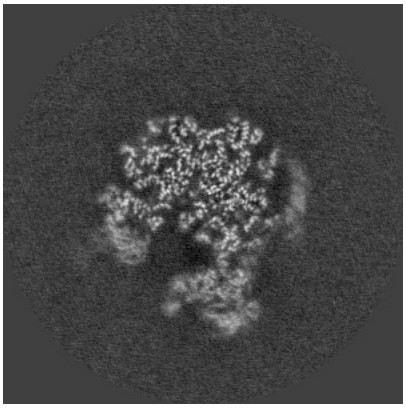


Z Index: 210

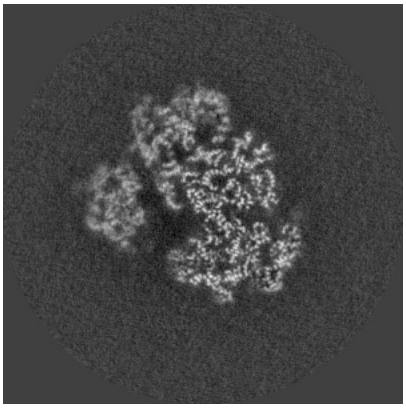
6.2.2 Raw map



X Index: 210



Y Index: 210

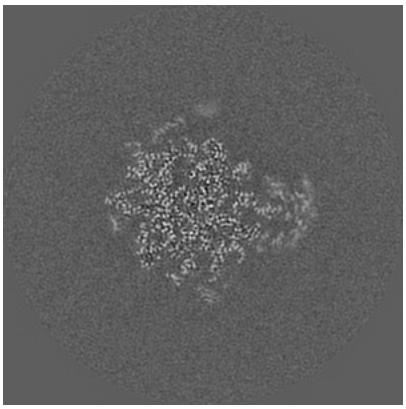


Z Index: 210

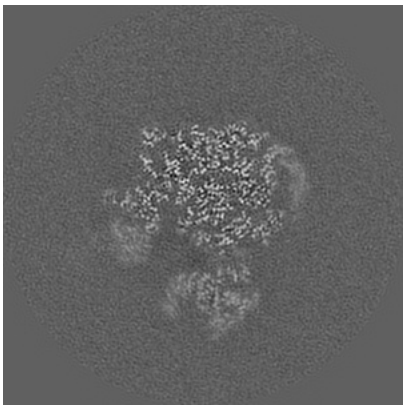
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

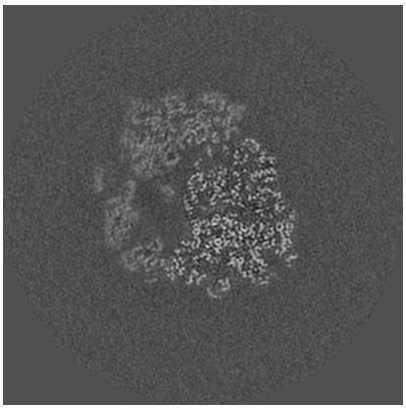
6.3.1 Primary map



X Index: 224

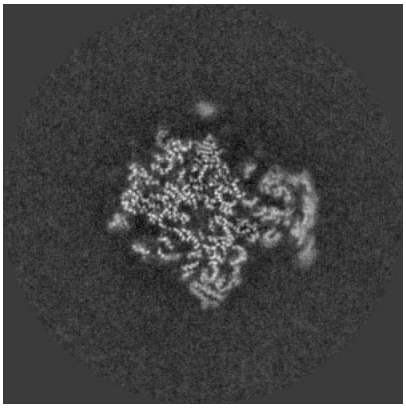


Y Index: 219

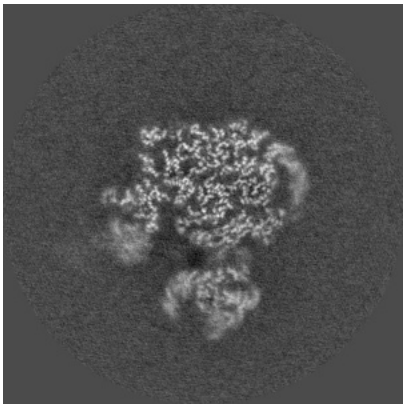


Z Index: 198

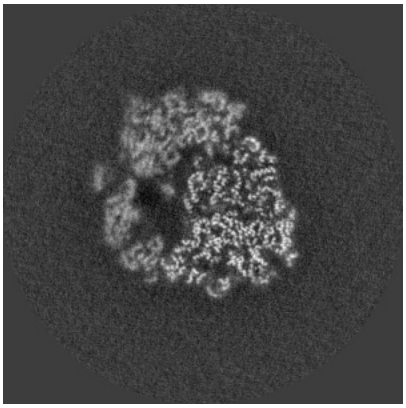
6.3.2 Raw map



X Index: 215



Y Index: 220

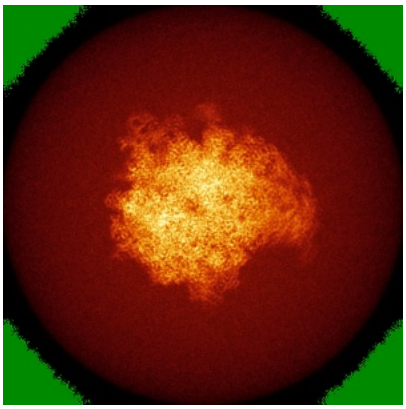


Z Index: 198

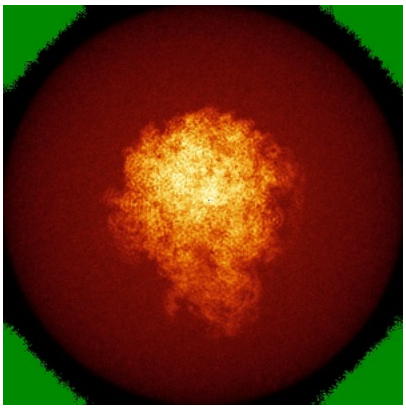
The images above show the largest variance slices of the map in three orthogonal directions.

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

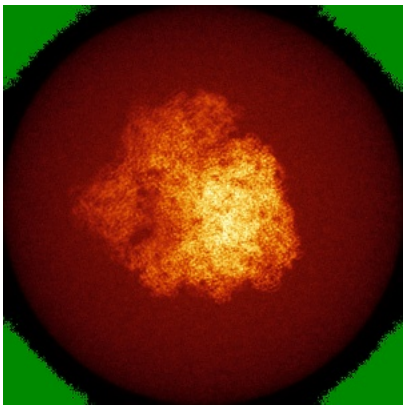
6.4.1 Primary map



X

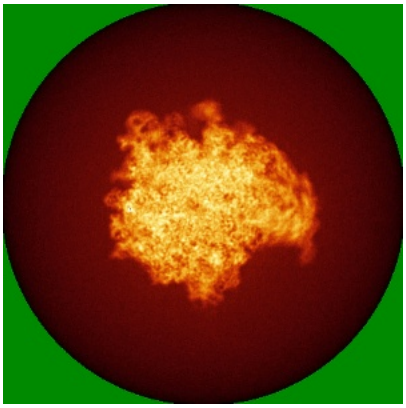


Y

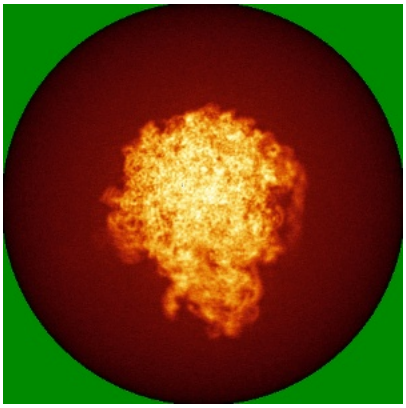


Z

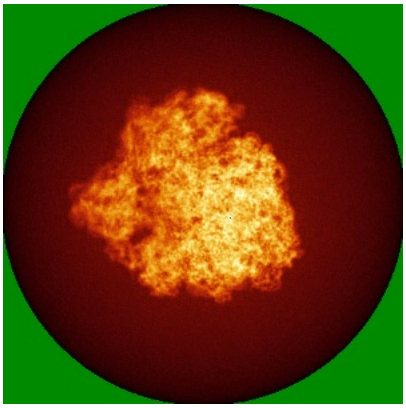
6.4.2 Raw map



X



Y

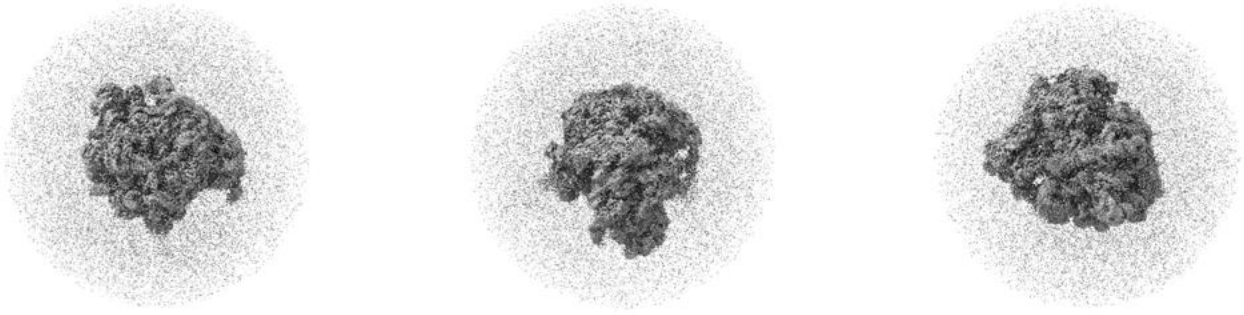


Z

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 0.024. 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.

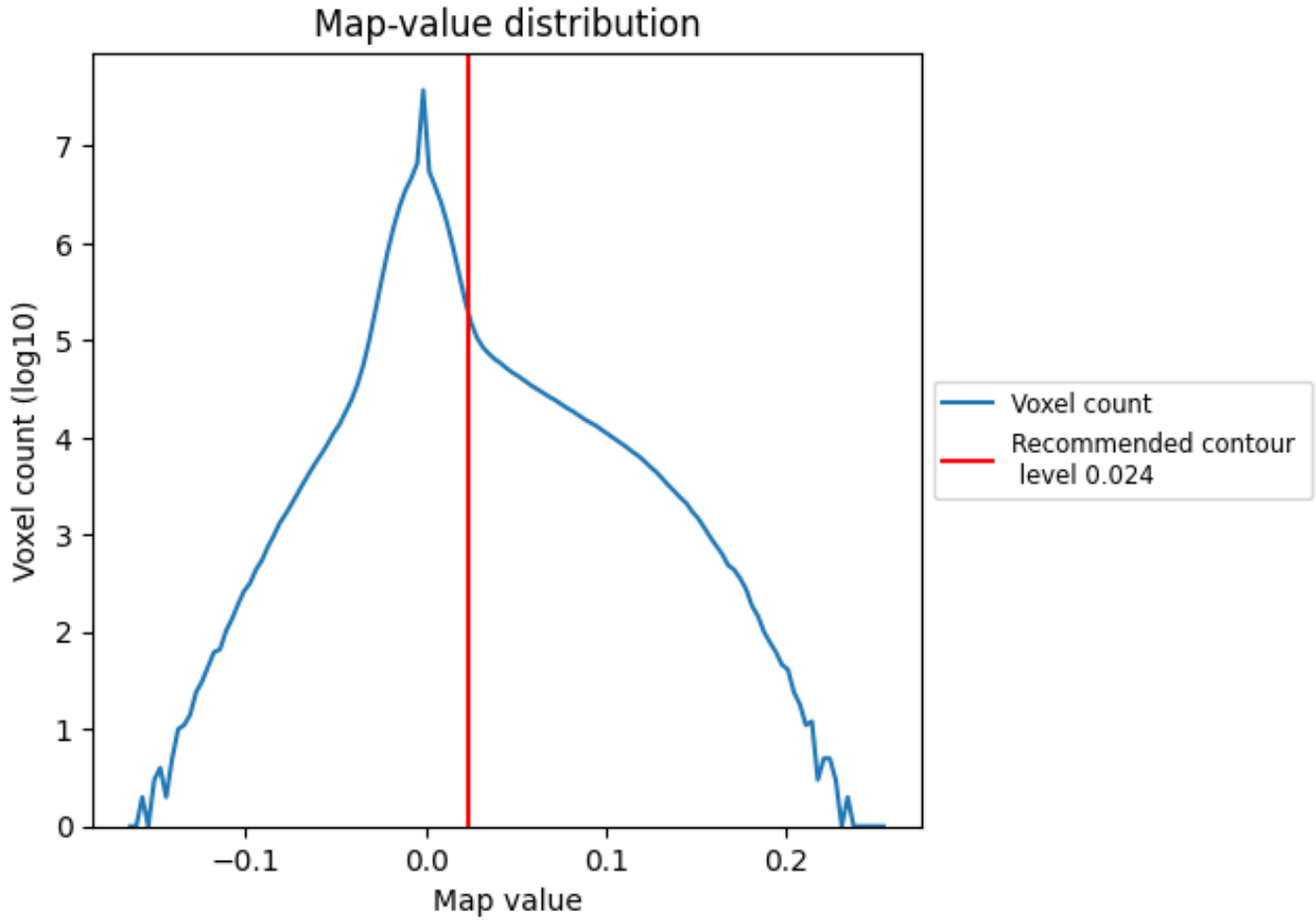
6.6 Mask visualisation (i)

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

7 Map analysis

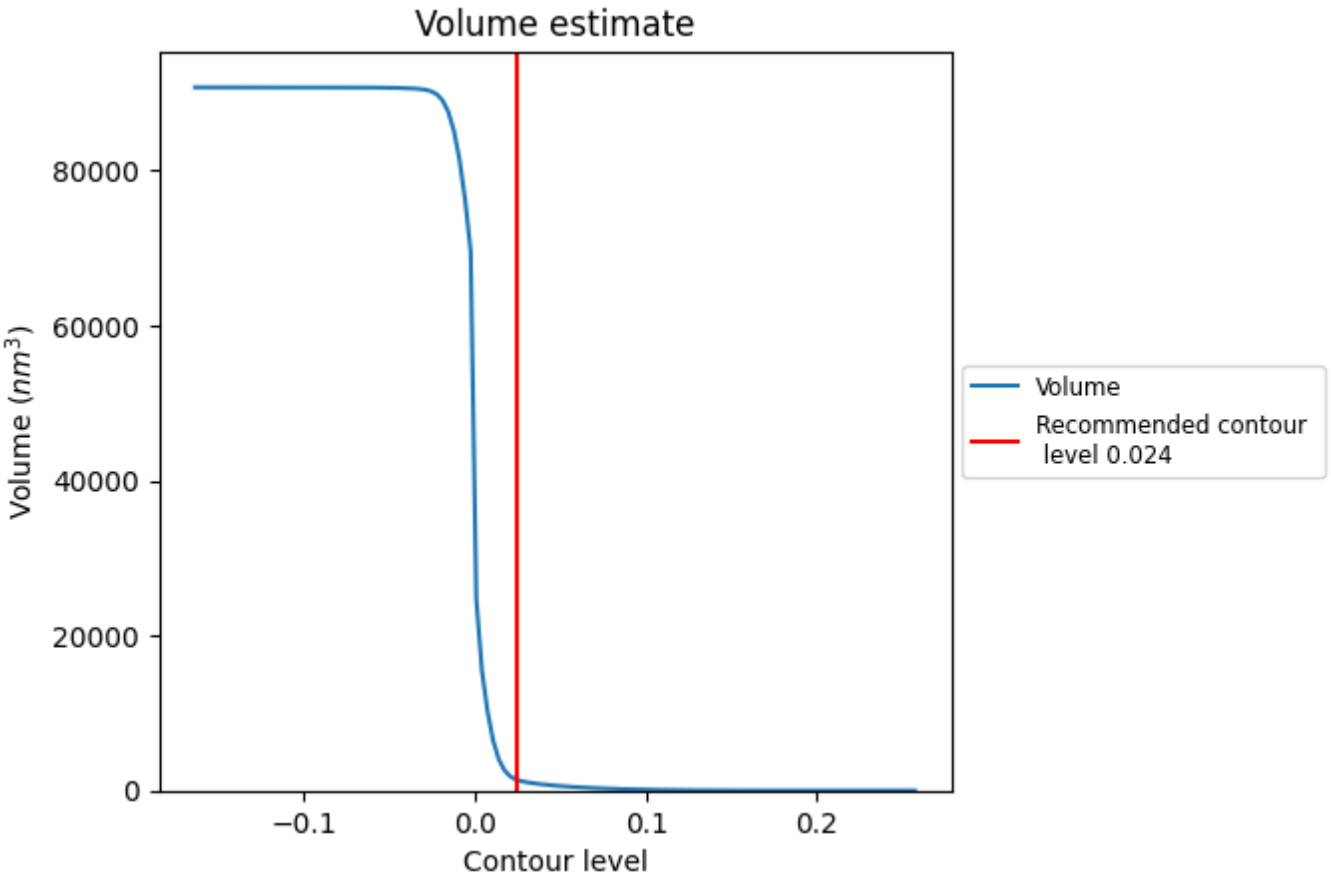
This section contains the results of statistical analysis of the map.

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.

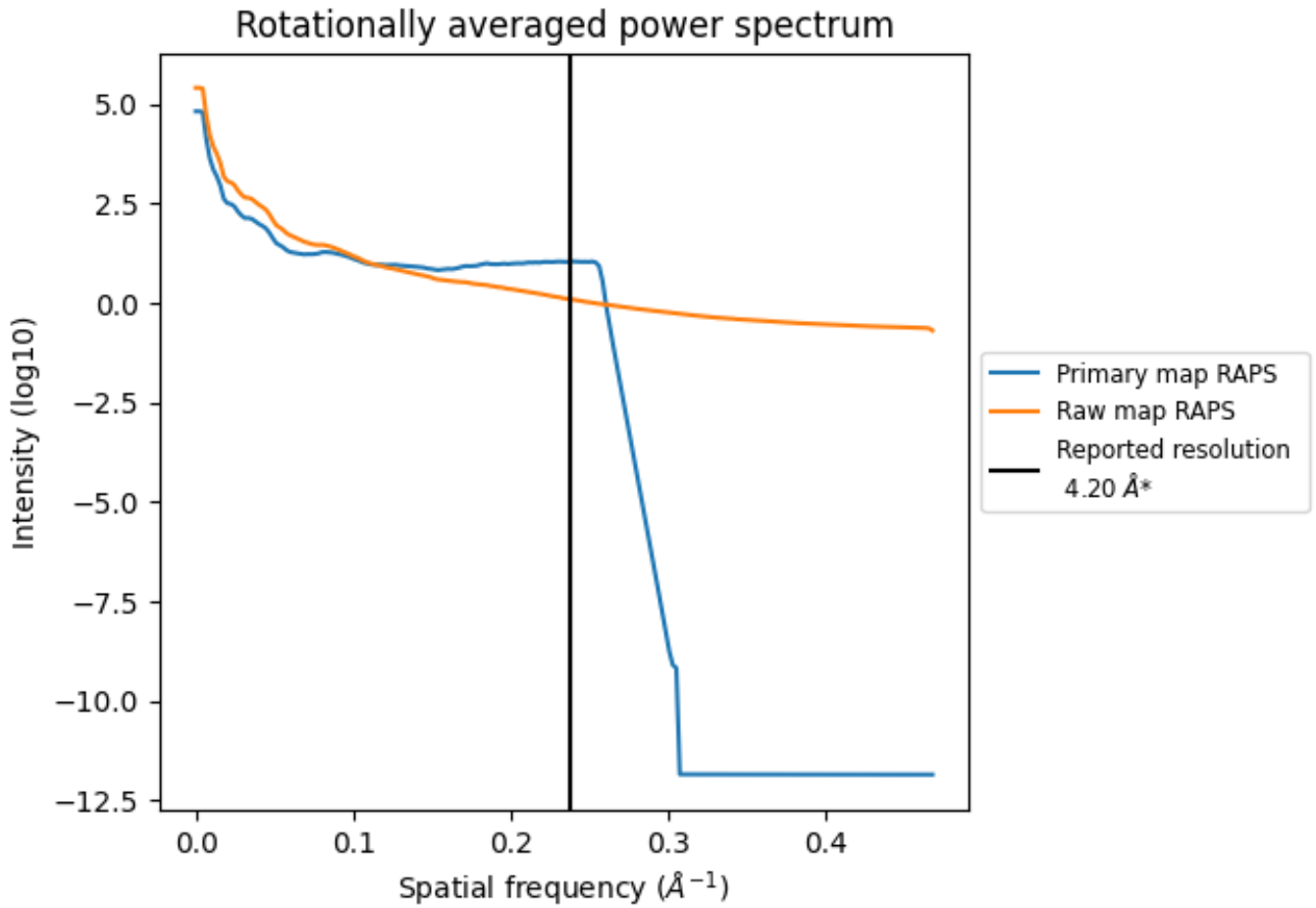
7.2 Volume estimate (i)



The volume at the recommended contour level is 1429 nm^3; this corresponds to an approximate mass of 1291 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)

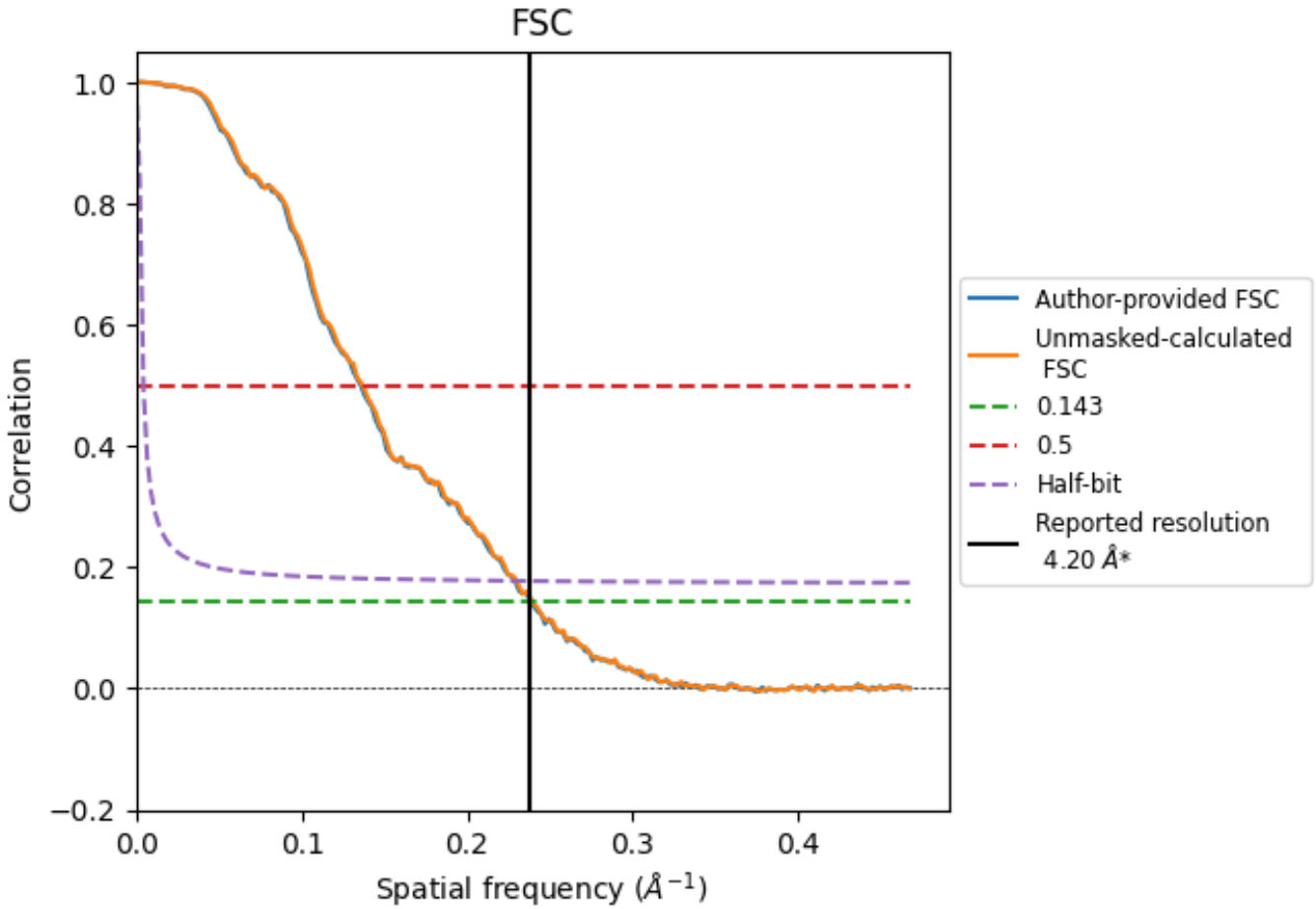


*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

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 0.238 Å^{-1}

8.2 Resolution estimates (i)

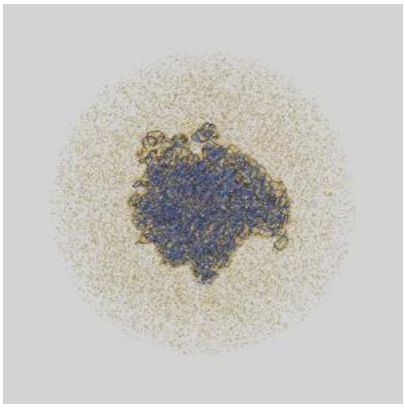
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.19	7.36	4.37
Unmasked-calculated*	4.17	7.32	4.35

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

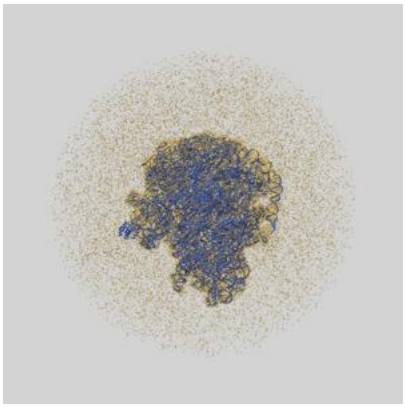
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-69703 and PDB model 24NP. Per-residue inclusion information can be found in section 3 on page 16.

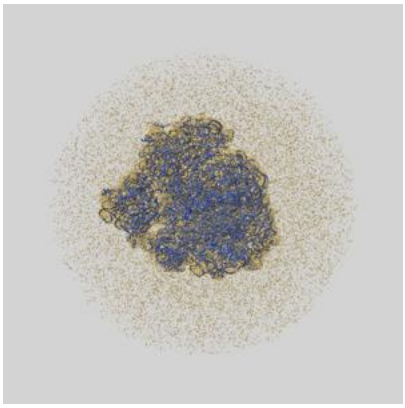
9.1 Map-model overlay



X



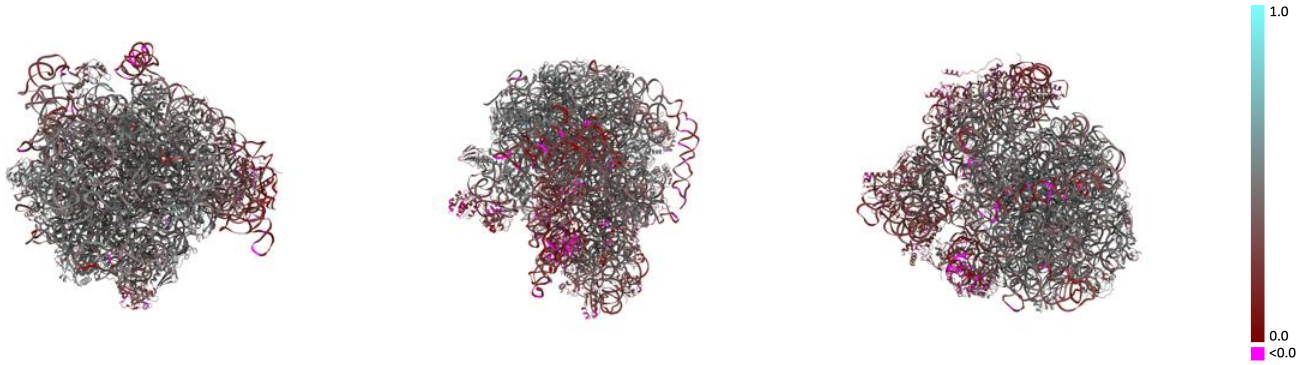
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.024 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.

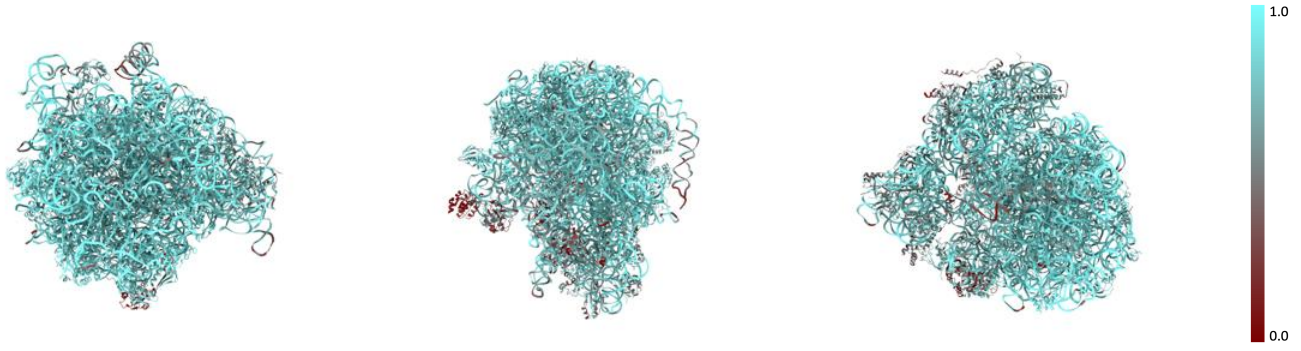
9.2 Q-score mapped to coordinate model



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.

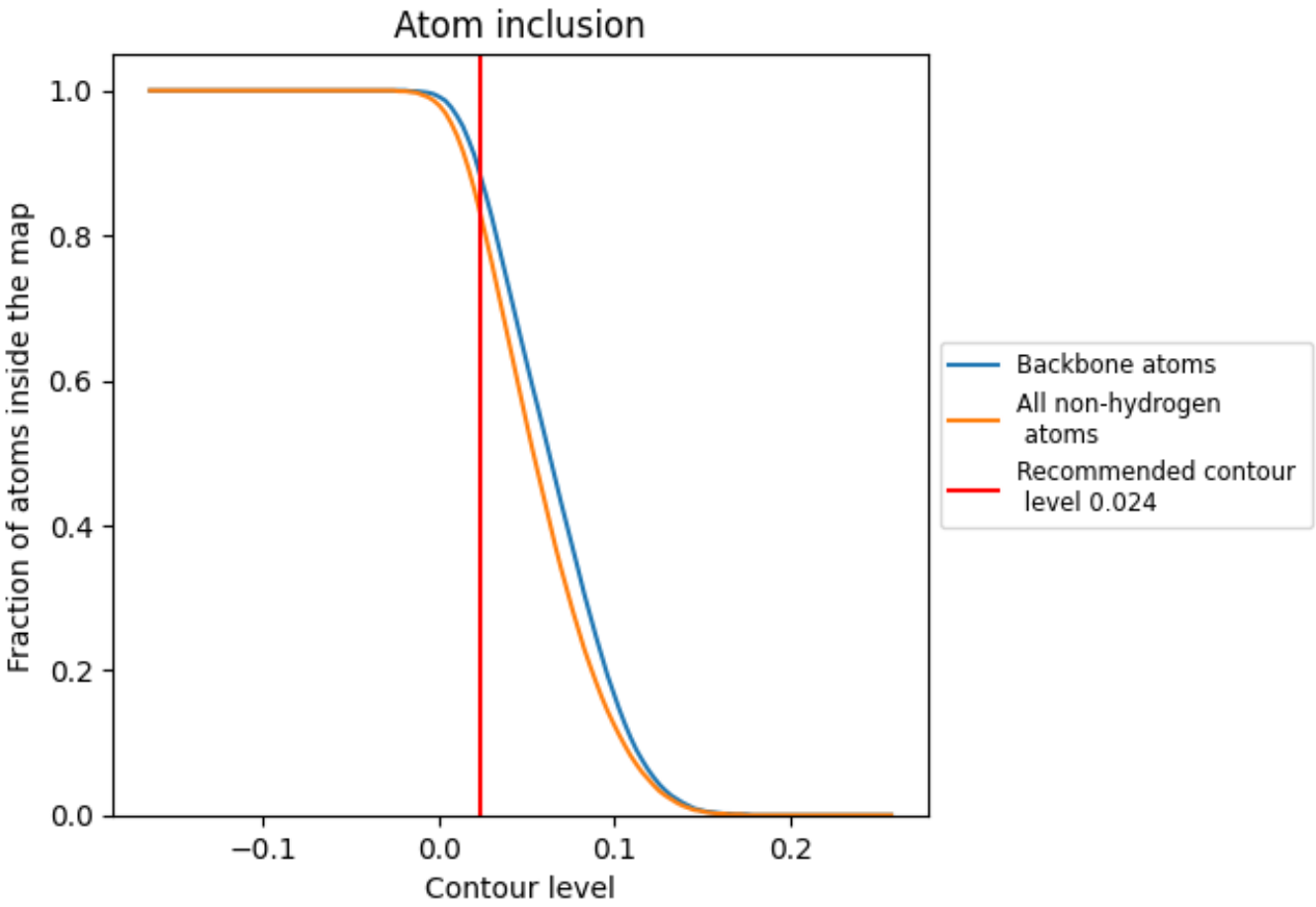
9.3 Atom inclusion mapped to coordinate model



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 (0.024).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8290	0.3860
1	0.7970	0.4430
2	0.7630	0.3290
3	0.7710	0.4690
4	0.8670	0.4260
5	0.4510	0.2450
6	0.3470	0.1480
A	0.8500	0.3290
B	0.9250	0.4240
C	0.6470	0.3280
D	0.4740	0.1490
E	0.7410	0.3900
F	0.7610	0.4210
G	0.5530	0.2310
H	0.8250	0.4280
I	0.6430	0.2770
J	0.5800	0.2820
K	0.7960	0.4350
L	0.6160	0.2870
M	0.5410	0.2250
N	0.7670	0.3880
O	0.8250	0.4440
P	0.5560	0.2290
Q	0.6350	0.2680
R	0.8010	0.4300
S	0.5990	0.2670
T	0.6580	0.2440
U	0.8120	0.4610
W	0.7570	0.4210
X	0.8310	0.4840
Y	0.8590	0.4850
Z	0.8240	0.4380
a	0.8240	0.4730
b	0.8710	0.4740
c	0.8460	0.4610



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
d	0.8570	0.4940
e	0.8480	0.5040
f	0.8230	0.4850
g	0.7560	0.3200
h	0.8970	0.4210
i	0.8600	0.4910
j	0.8670	0.4860
k	0.8580	0.4800
l	0.7720	0.3910
m	0.8160	0.4140
n	0.6840	0.3840
o	0.3360	0.1630
p	0.1210	0.1260
q	0.8670	0.4810
r	0.8180	0.4770
s	0.8560	0.4820
t	0.8500	0.4890
u	0.8630	0.4870
v	0.8360	0.4370
w	0.8190	0.4650
x	0.8710	0.4840
y	0.8830	0.5020
z	0.8680	0.4920