wwPDB EM Validation Summary Report

Nov 11, 2026 – 10:39 AM JST

PDB ID	:	24NN / pdb_000024nn
EMDB ID	:	EMD-69698
Title	:	E/E-tRNA bound M. smegmatis 70S ribosome in complex with RRF (RRI II)
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 ⓘ 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:

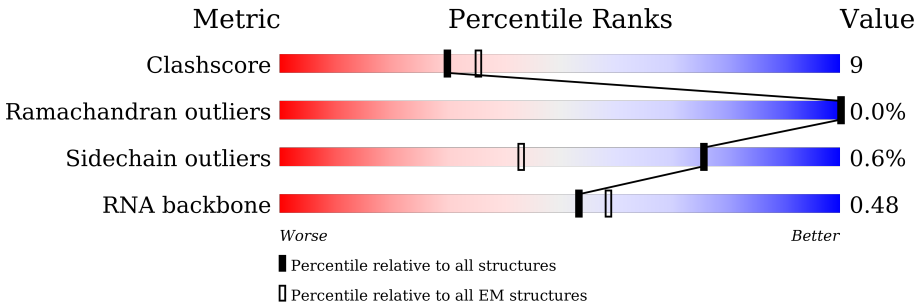
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

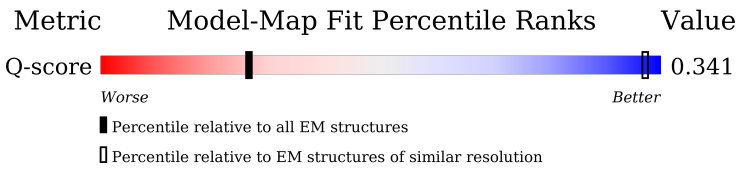
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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.





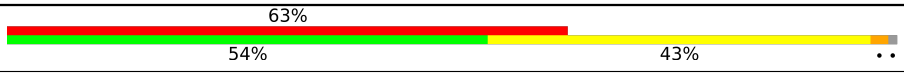
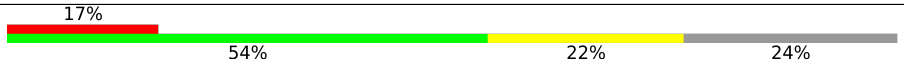
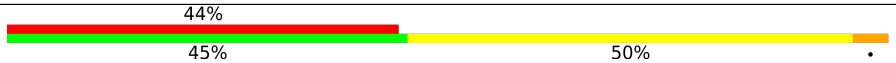
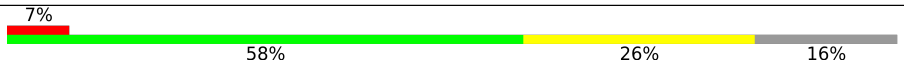
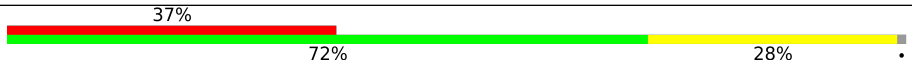
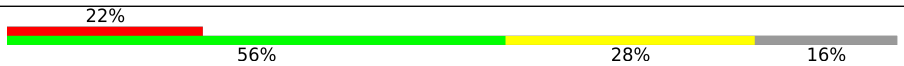
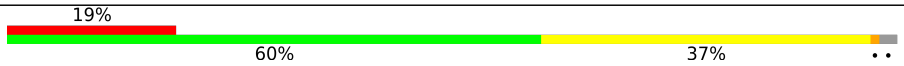
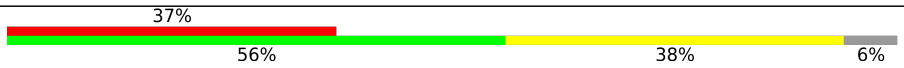
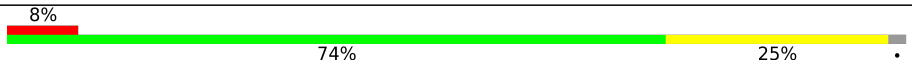
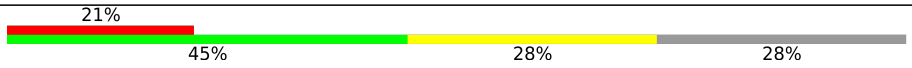
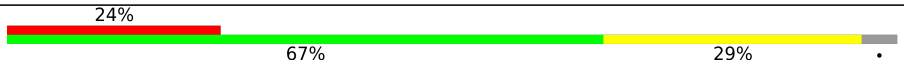
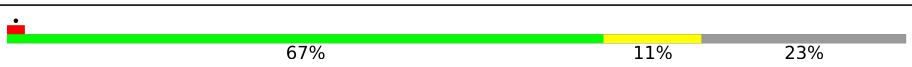
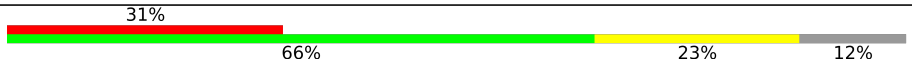
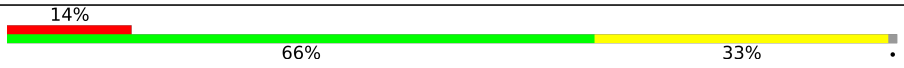
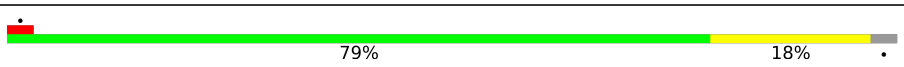
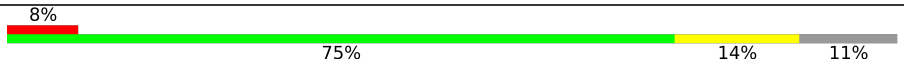
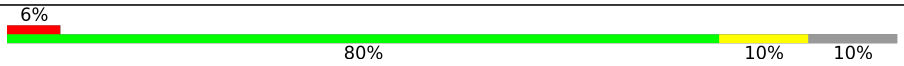
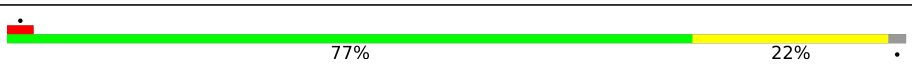
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

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	9% 35% 47% 18%
2	3	24	17% 88% 8%
3	4	3	100%

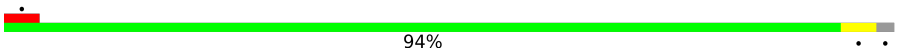
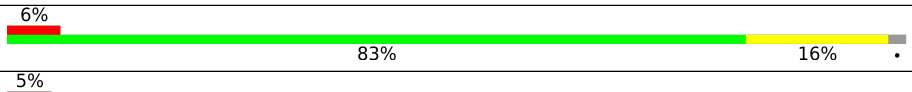
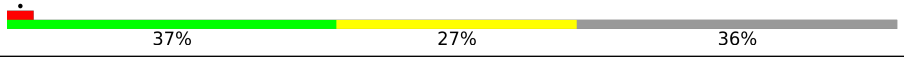
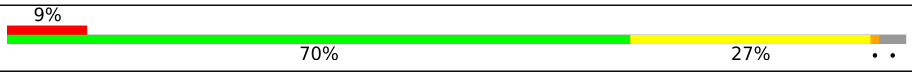
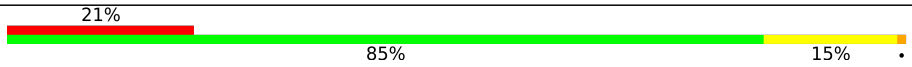
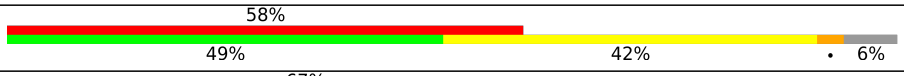
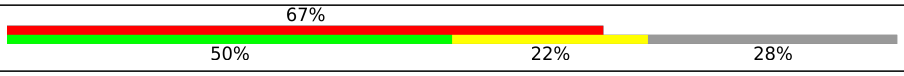
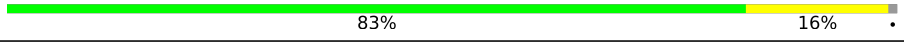
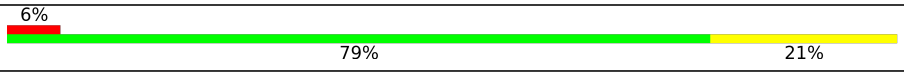
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Mol	Chain	Length	Quality of chain
4	6	235	
5	A	1528	
6	B	118	
7	C	275	
8	D	201	
9	E	214	
10	F	96	
11	G	156	
12	H	132	
13	I	150	
14	J	101	
15	K	138	
16	L	124	
17	M	124	
18	N	61	
19	O	89	
20	P	156	
21	Q	98	
22	R	84	
23	S	93	
24	T	86	
25	U	100	
26	W	215	
27	X	88	
28	Y	64	

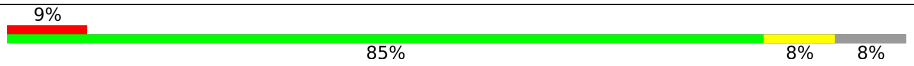
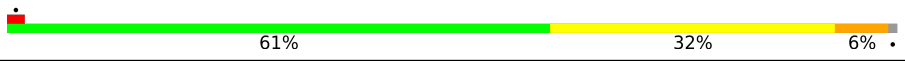
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Mol	Chain	Length	Quality of chain
29	Z	77	
30	a	61	
31	b	57	
32	c	55	
33	d	47	
34	e	64	
35	f	37	
36	g	75	
37	i	278	
38	j	217	
39	k	215	
40	l	187	
41	m	179	
42	n	151	
43	o	142	
44	p	175	
45	q	147	
46	r	122	
47	s	147	
48	t	138	
49	u	199	
50	v	127	
51	w	113	
52	x	129	
53	y	103	

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Mol	Chain	Length	Quality of chain
54	z	153	
55	5	185	
56	1	105	
57	h	3120	

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 151085 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 Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	6	232	1736	1084	313	336	3	0	0

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

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

- Molecule 6 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 7 is a protein called 30S ribosomal protein S3.

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

- Molecule 8 is a protein called 30S ribosomal protein S4.

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

- 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 748	C 469	N 142	O 135	S 2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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 Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	185	Total 1458	C 894	N 265	O 294	S 5	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	

Continued on next page...

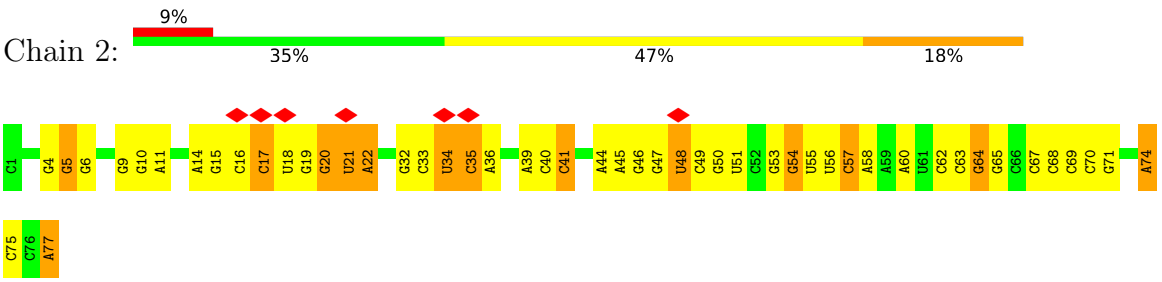
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Mol	Chain	Residues	Atoms	AltConf
59	f	1	Total Zn 1 1	0
59	g	1	Total Zn 1 1	0

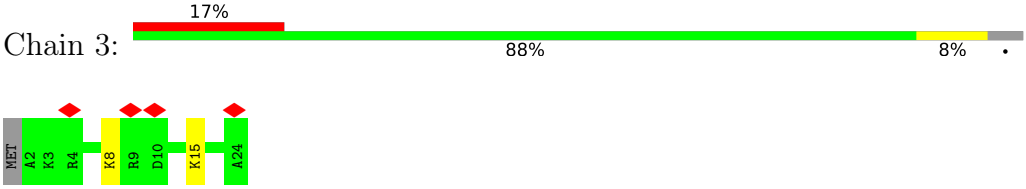
3 Residue-property plots (i)

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



• Molecule 2: 50S ribosomal protein bL37

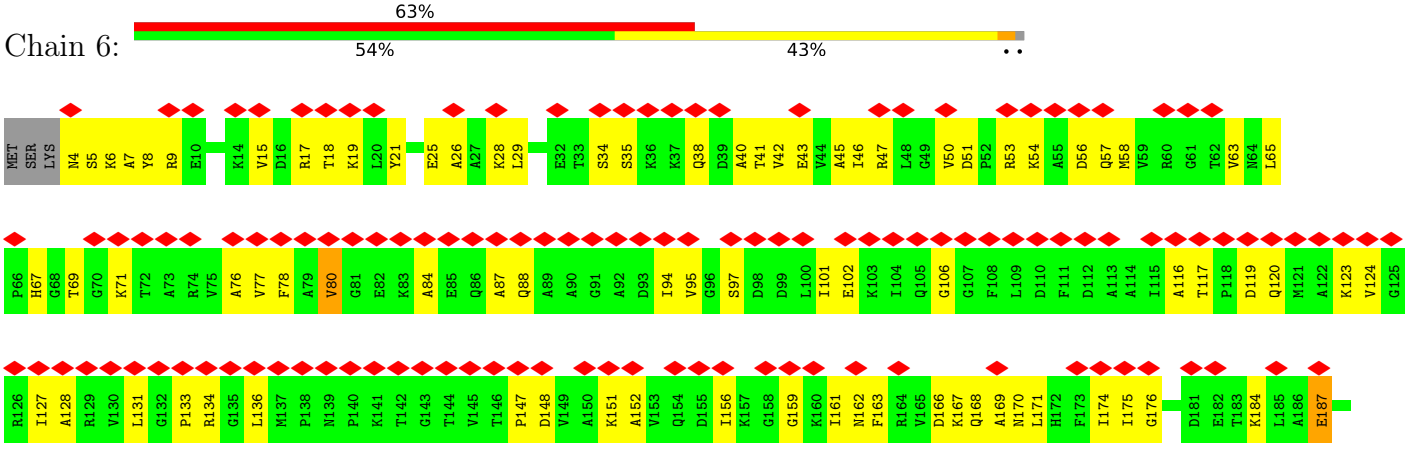


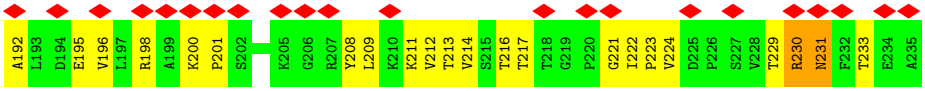
• Molecule 3: mRNA fragment



There are no outlier residues recorded for this chain.

• Molecule 4: Large ribosomal subunit protein uL1

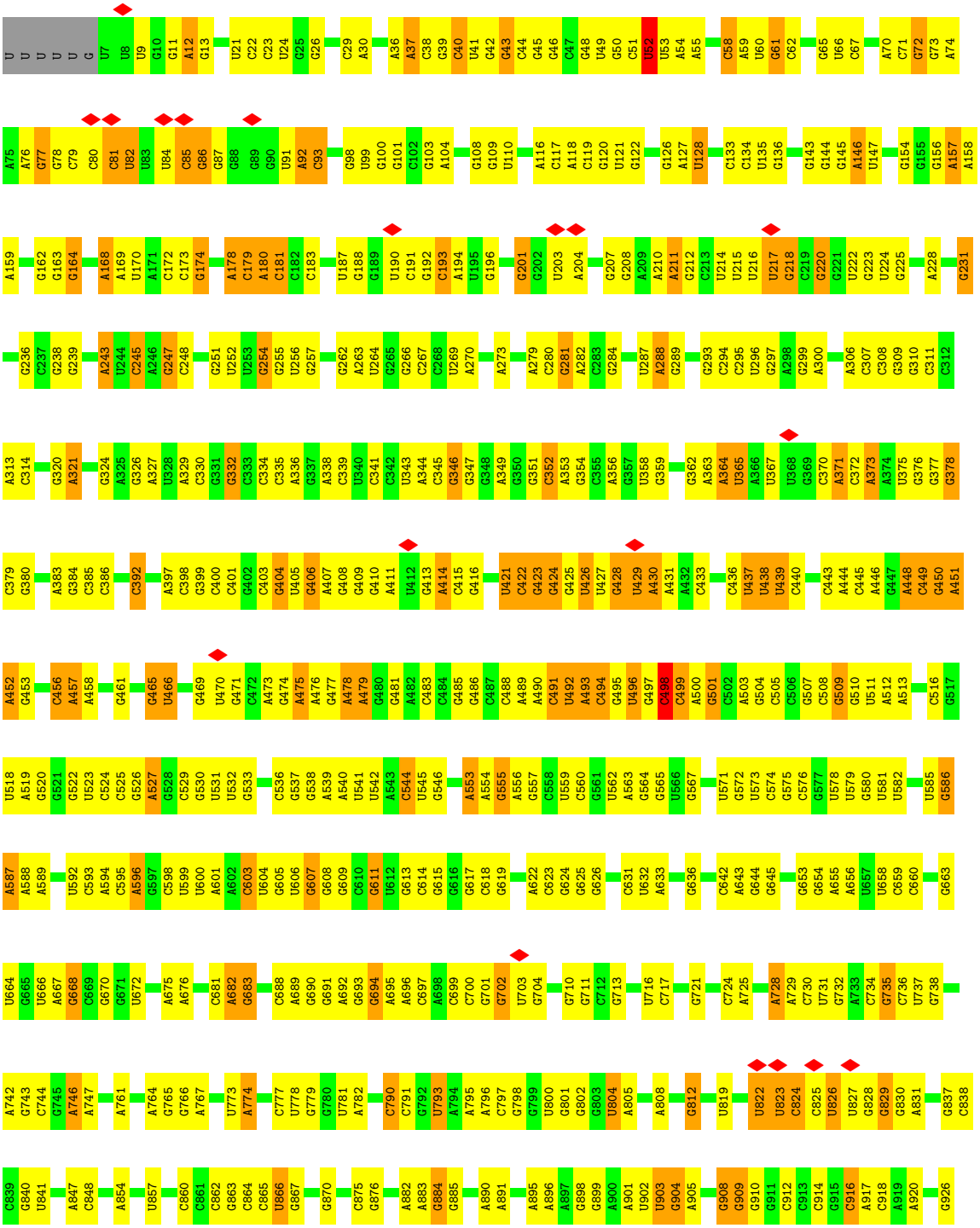


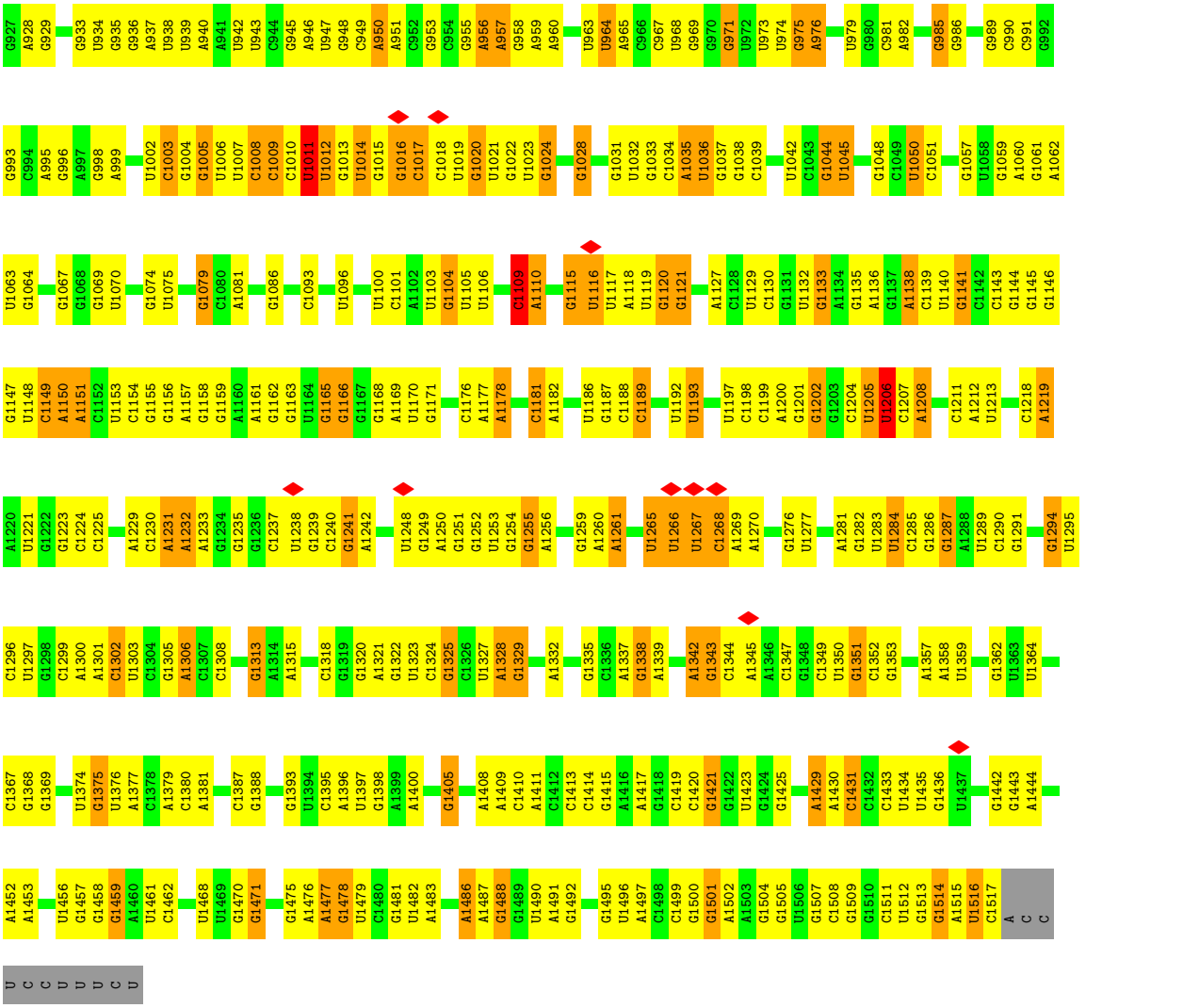


• Molecule 5: 16S ribosomal RNA

Chain A:



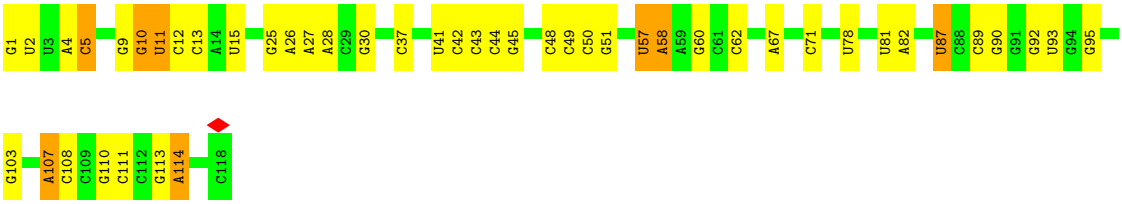




• Molecule 6: 5S ribosomal RNA

Chain B:

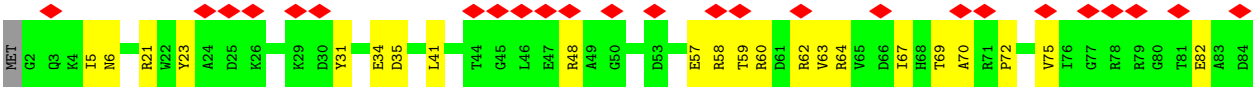


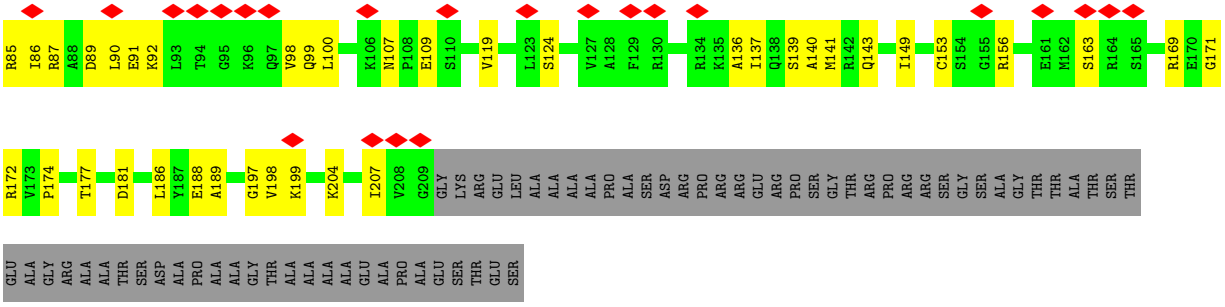


• Molecule 7: 30S ribosomal protein S3

Chain C:







• Molecule 8: 30S ribosomal protein S4

Chain D:

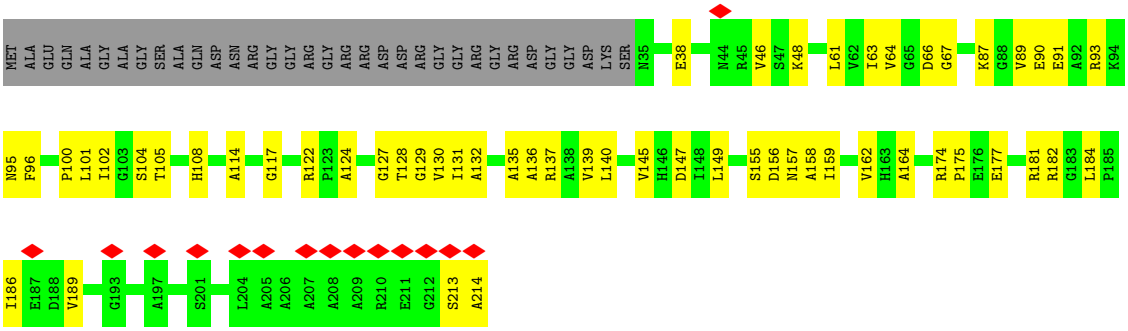




• Molecule 9: 30S ribosomal protein S5

Chain E:

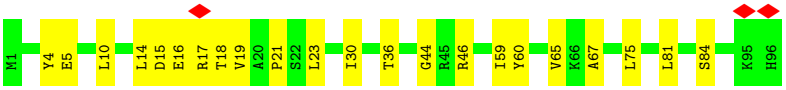




• Molecule 10: Small ribosomal subunit protein bS6

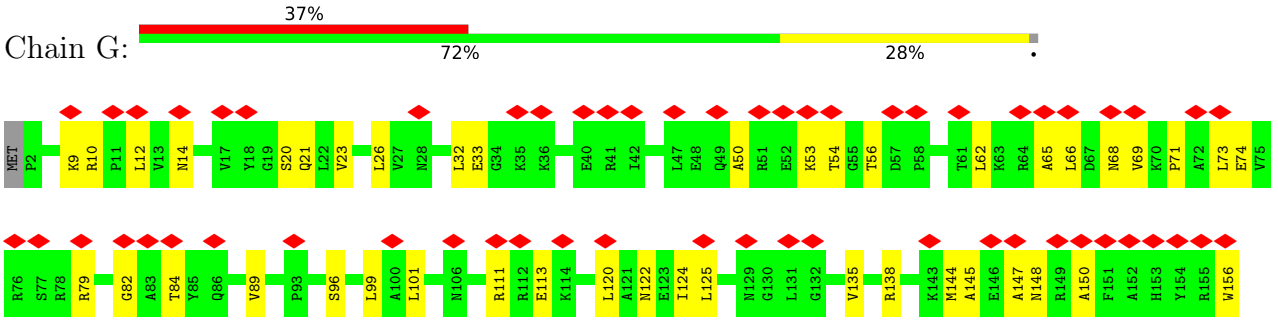
Chain F:





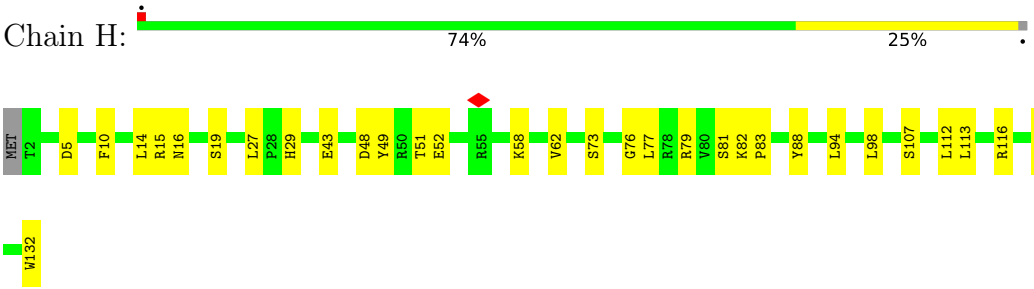
• Molecule 11: 30S ribosomal protein S7

Chain G:



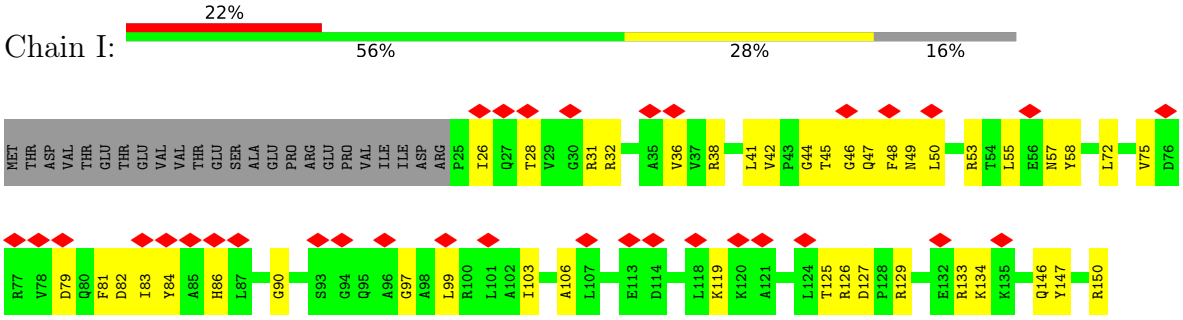
• Molecule 12: 30S ribosomal protein S8

Chain H:



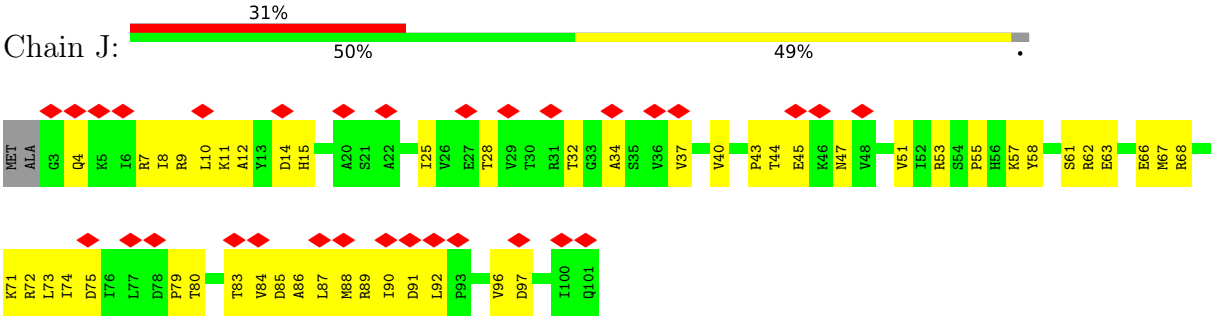
• Molecule 13: 30S ribosomal protein S9

Chain I:



• Molecule 14: 30S ribosomal protein S10

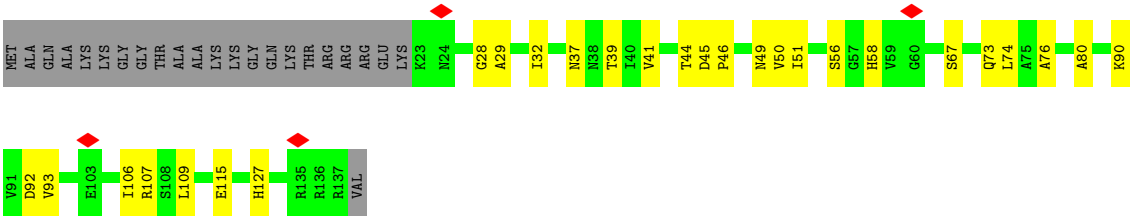
Chain J:



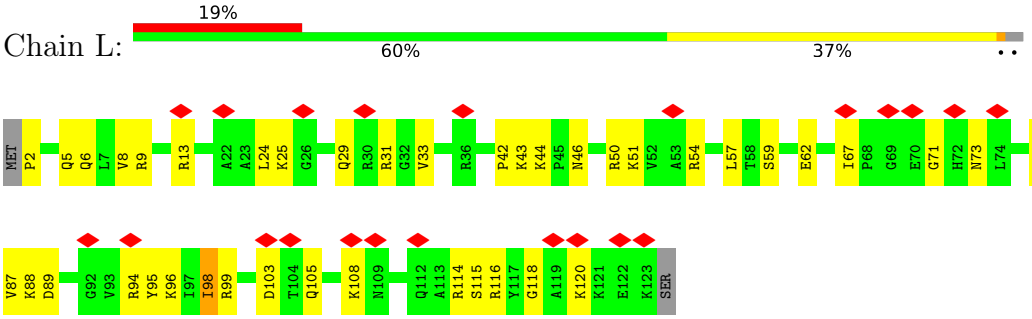
• Molecule 15: 30S ribosomal protein S11

Chain K:

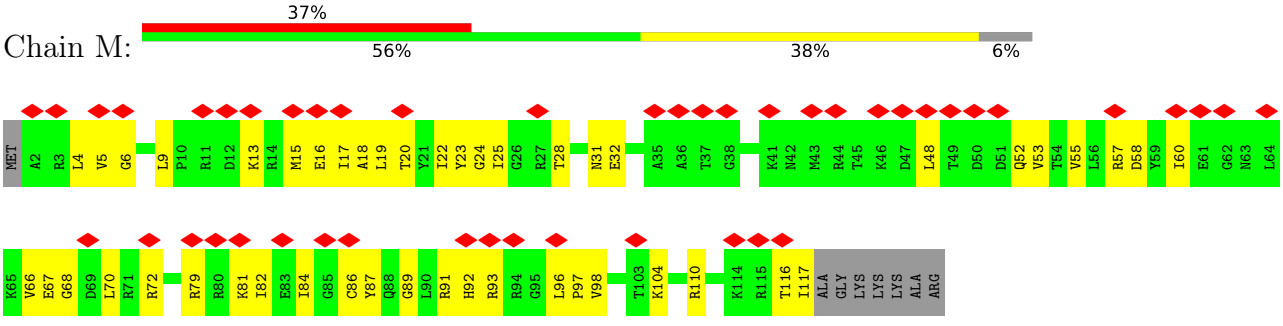




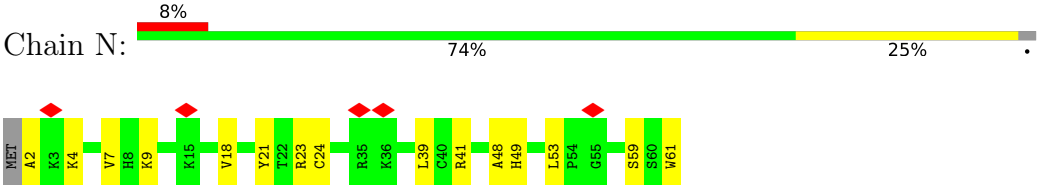
• Molecule 16: 30S ribosomal protein S12



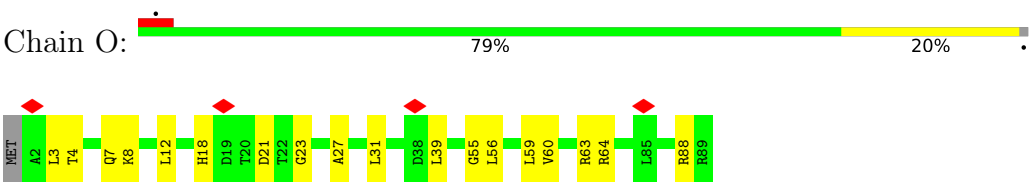
• Molecule 17: 30S ribosomal protein S13



• Molecule 18: 30S ribosomal protein S14 type Z

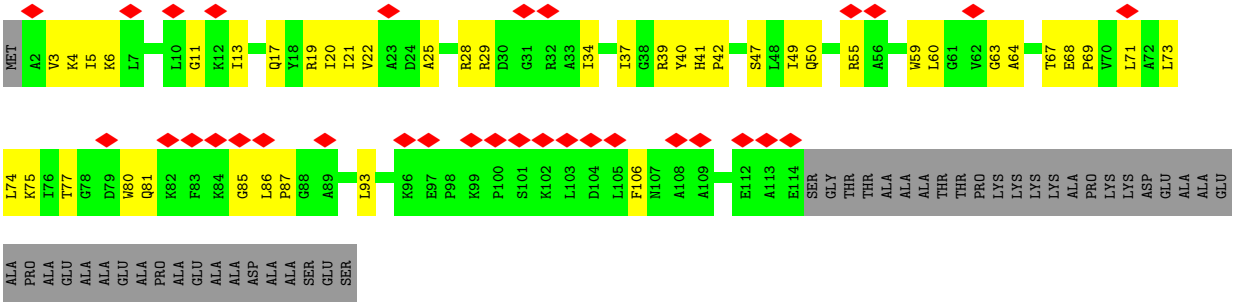


• Molecule 19: 30S ribosomal protein S15



• Molecule 20: 30S ribosomal protein S16

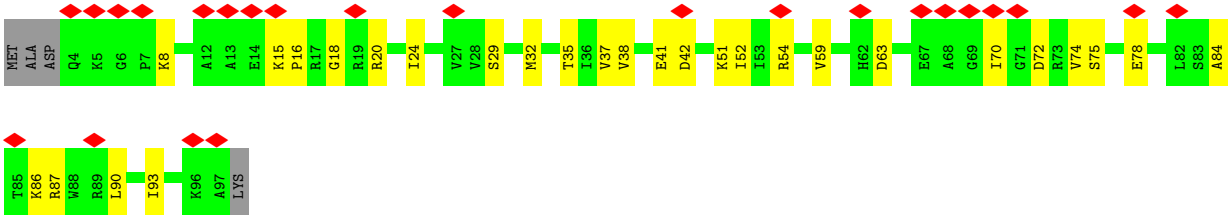




• Molecule 21: 30S ribosomal protein S17

Chain Q:

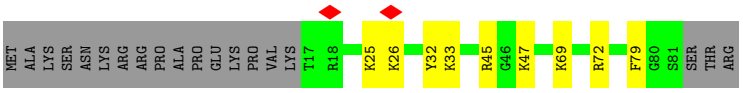




• Molecule 22: 30S ribosomal protein S18 2

Chain R:

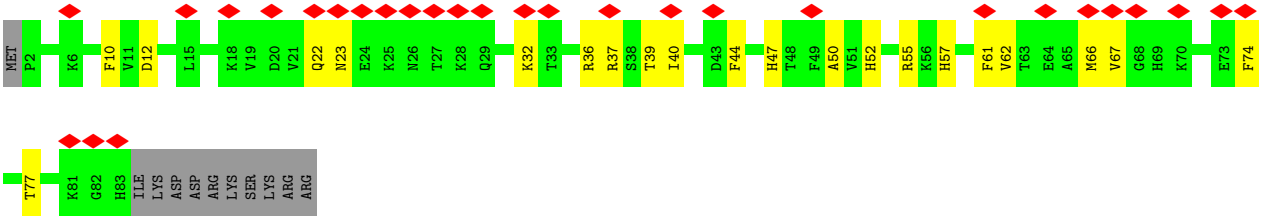




• Molecule 23: 30S ribosomal protein S19

Chain S:

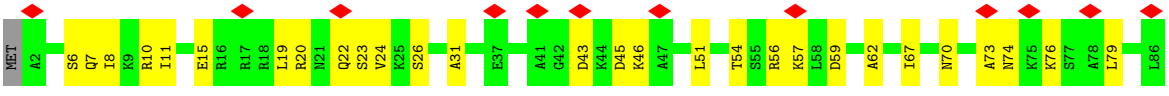




• Molecule 24: 30S ribosomal protein S20

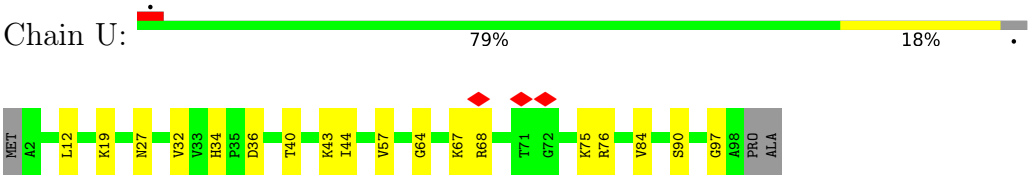
Chain T:





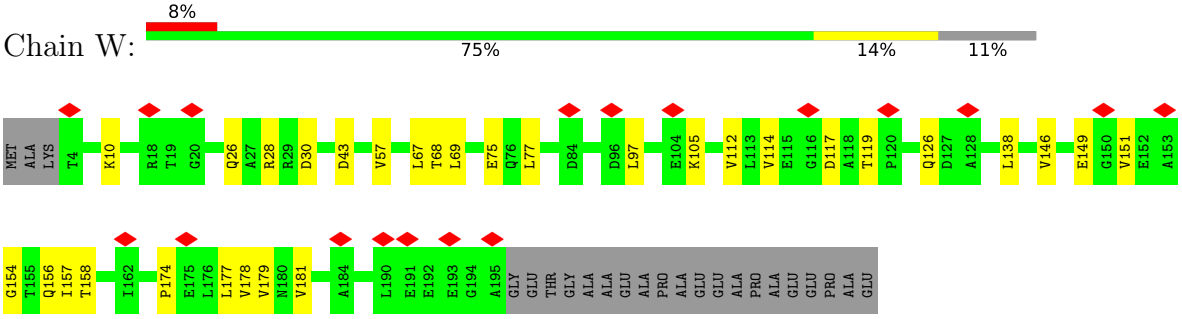
• Molecule 25: 50S ribosomal protein L23

Chain U:



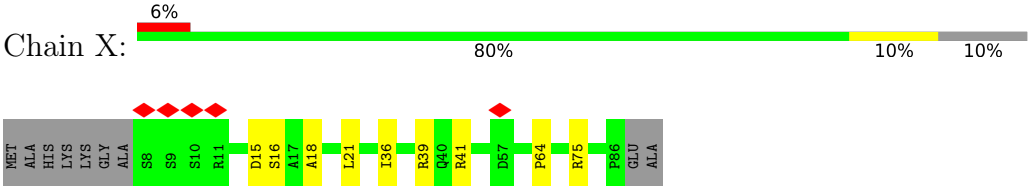
• Molecule 26: 50S ribosomal protein L25

Chain W:



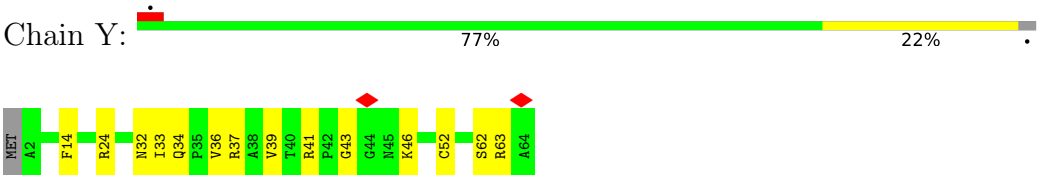
• Molecule 27: 50S ribosomal protein L27

Chain X:



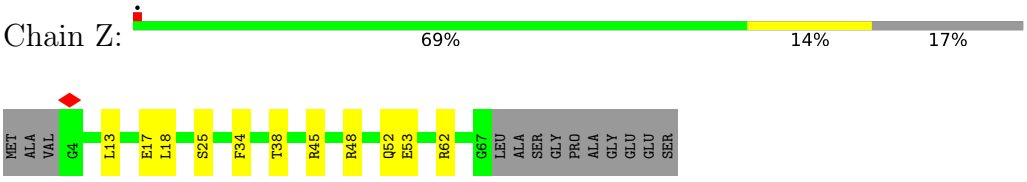
• Molecule 28: 50S ribosomal protein L28

Chain Y:



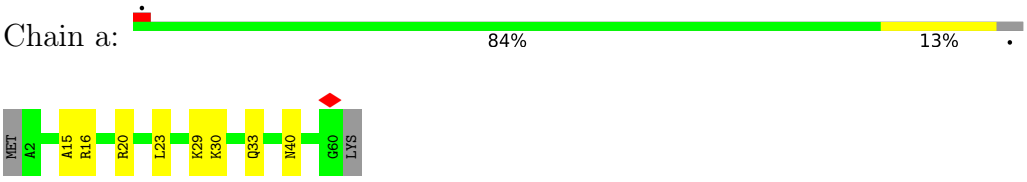
• Molecule 29: 50S ribosomal protein L29

Chain Z:



• Molecule 30: 50S ribosomal protein L30

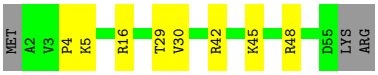
Chain a:



• Molecule 31: 50S ribosomal protein L32

Chain b:

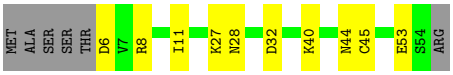




• Molecule 32: 50S ribosomal protein L33 1

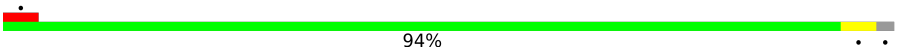
Chain c:

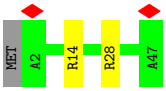




• Molecule 33: 50S ribosomal protein L34

Chain d:

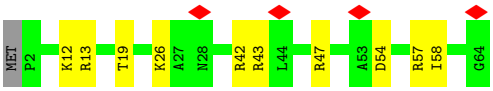




• Molecule 34: 50S ribosomal protein L35

Chain e:

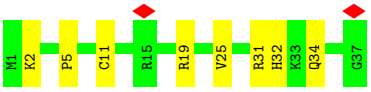




• Molecule 35: 50S ribosomal protein L36

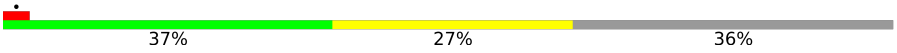
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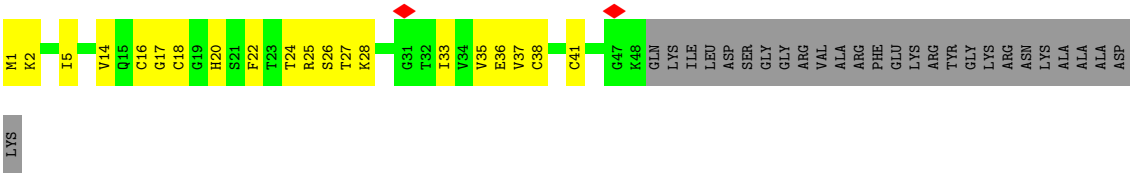




• Molecule 36: 50S ribosomal protein L31

Chain g:

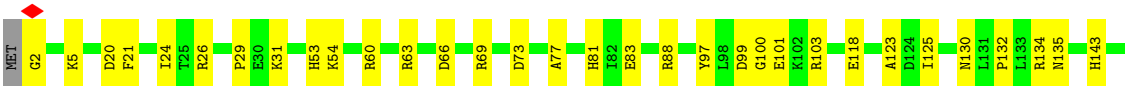


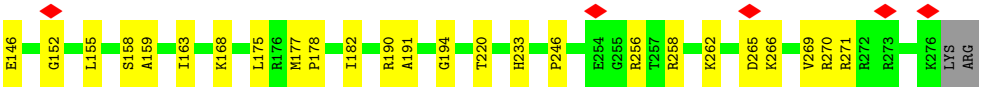


• Molecule 37: 50S ribosomal protein L2

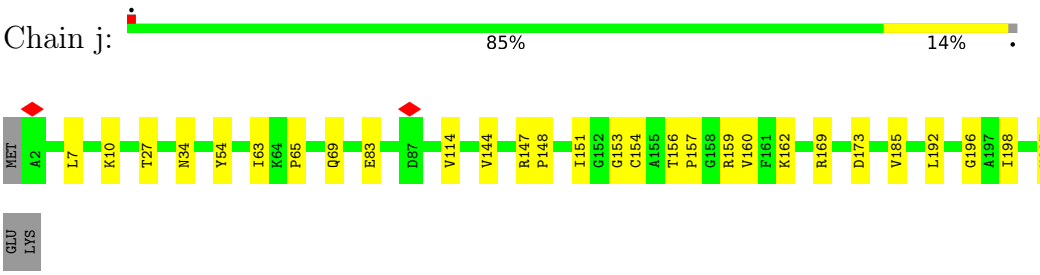
Chain i:



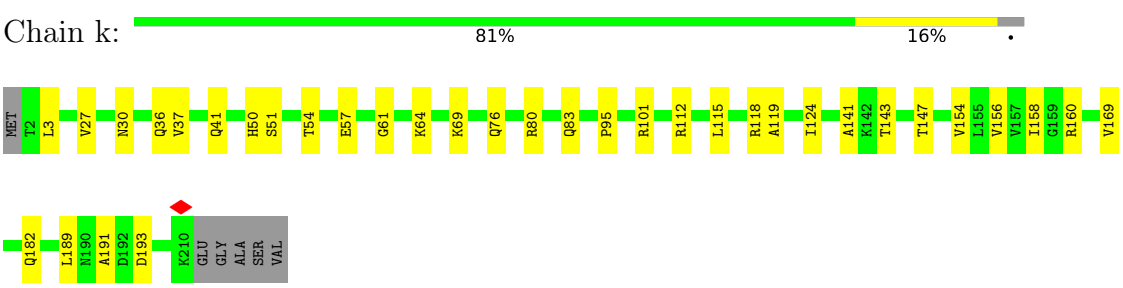




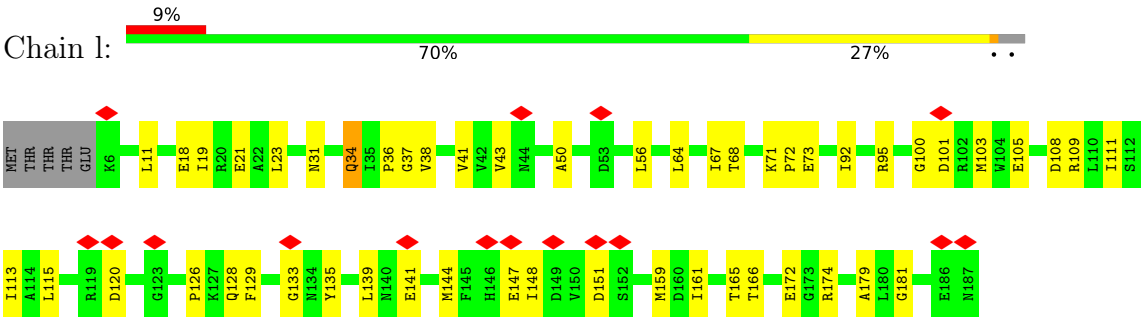
• Molecule 38: 50S ribosomal protein L3



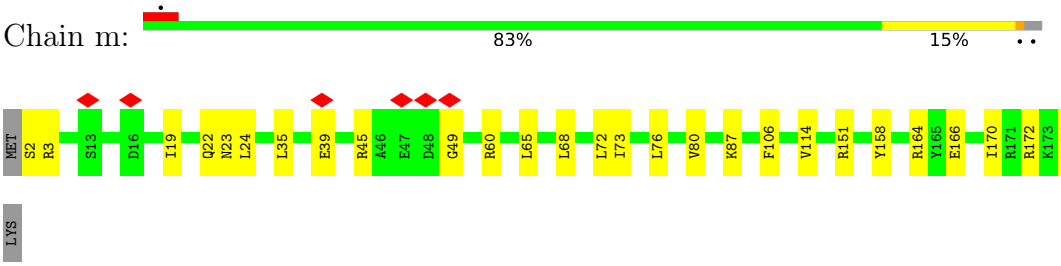
• Molecule 39: 50S ribosomal protein L4



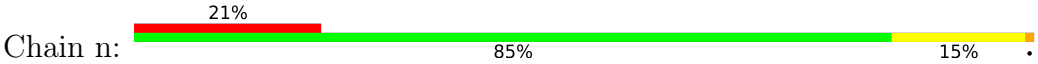
• Molecule 40: 50S ribosomal protein L5

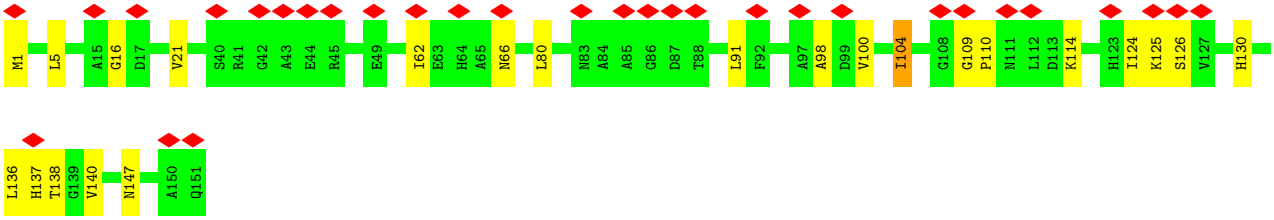


• Molecule 41: 50S ribosomal protein L6



• Molecule 42: 50S ribosomal protein L9

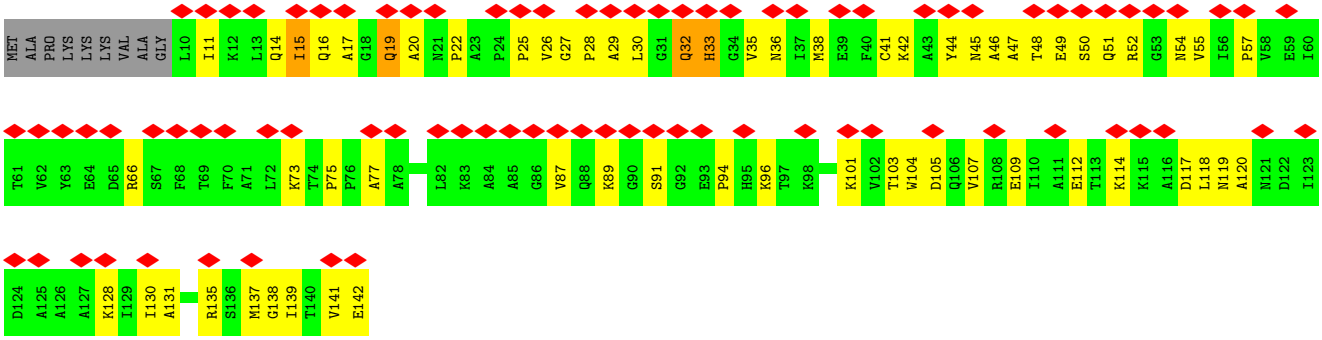




• Molecule 43: 50S ribosomal protein L11

Chain o:

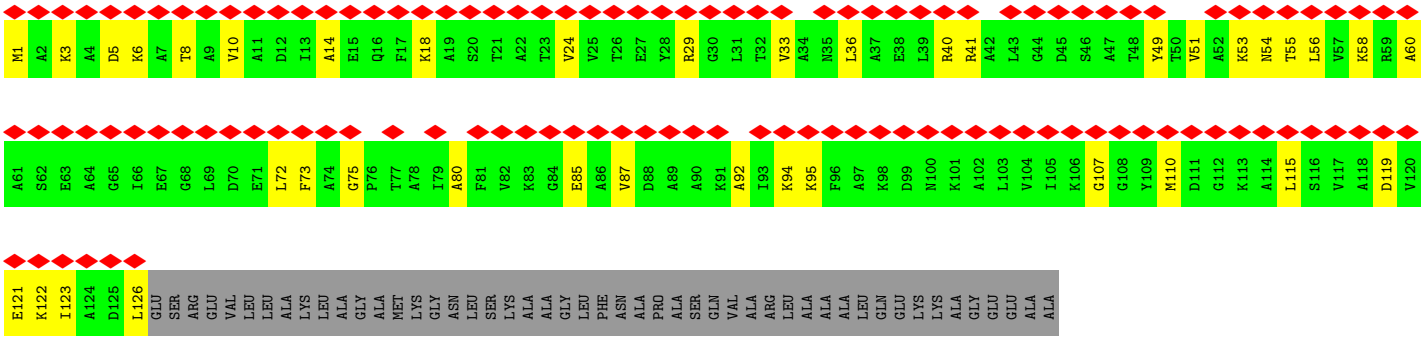




• Molecule 44: 50S ribosomal protein L10

Chain p:

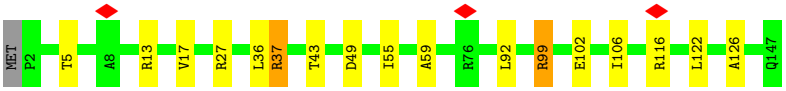




• Molecule 45: 50S ribosomal protein L13

Chain q:

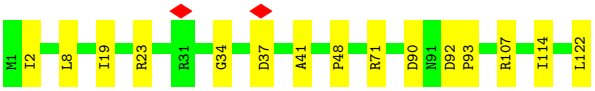




• Molecule 46: 50S ribosomal protein L14

Chain r:

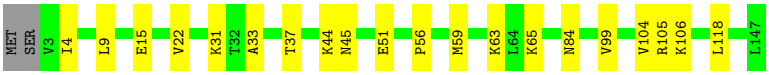




• Molecule 47: 50S ribosomal protein L15

Chain s:

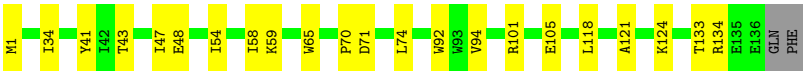




• Molecule 48: 50S ribosomal protein L16

Chain t:

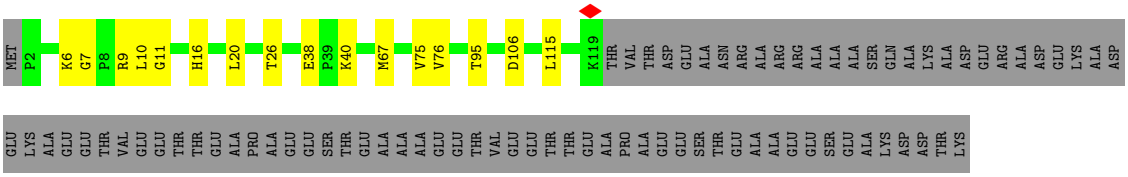




• Molecule 49: 50S ribosomal protein L17

Chain u:





• Molecule 50: 50S ribosomal protein L18

Chain v:

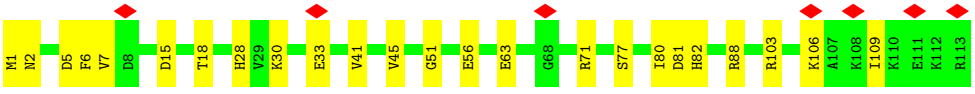




• Molecule 51: 50S ribosomal protein L19

Chain w:

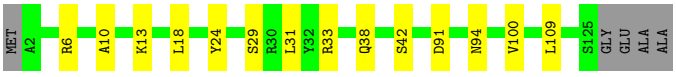




• Molecule 52: 50S ribosomal protein L20

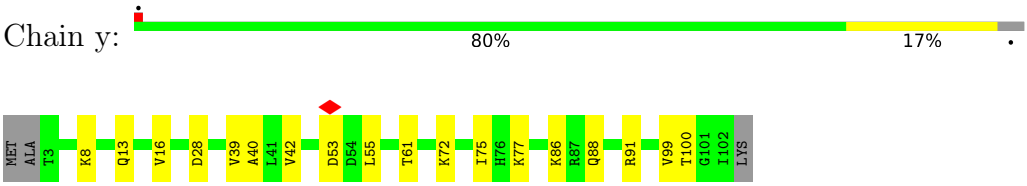
Chain x:





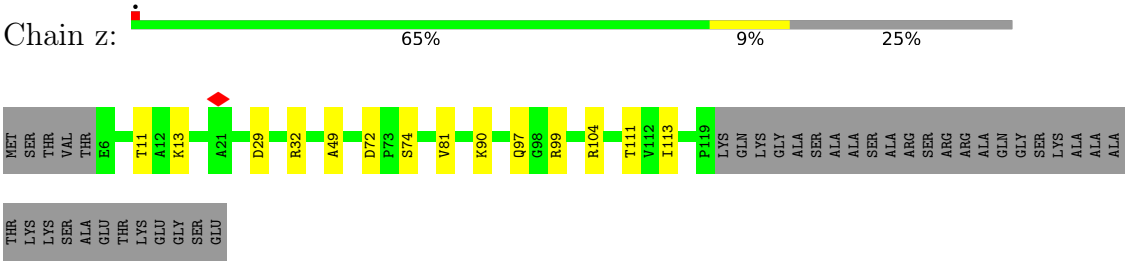
• Molecule 53: 50S ribosomal protein L21

Chain y:



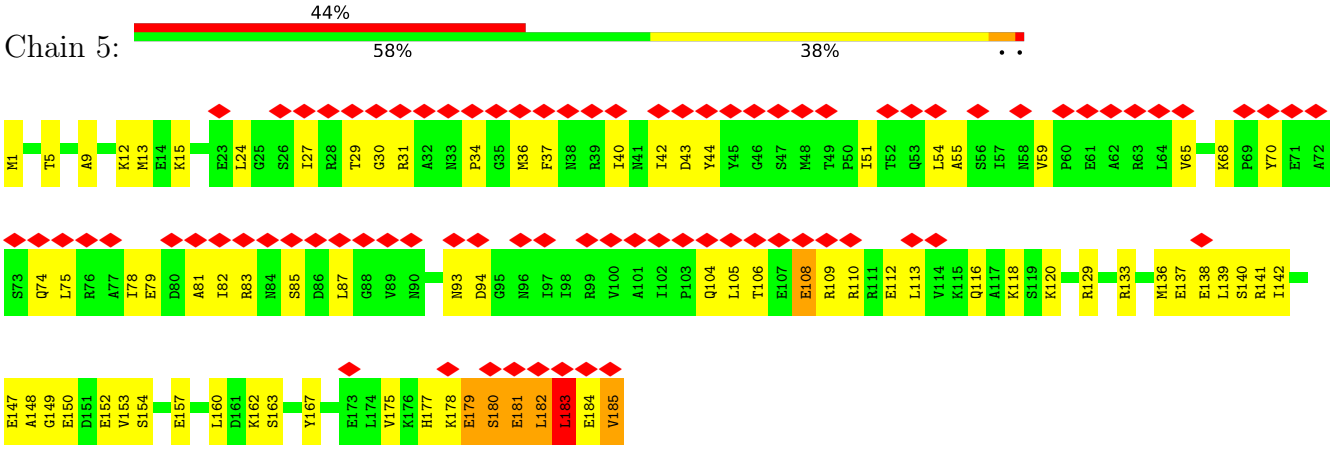
• Molecule 54: 50S ribosomal protein L22

Chain z:



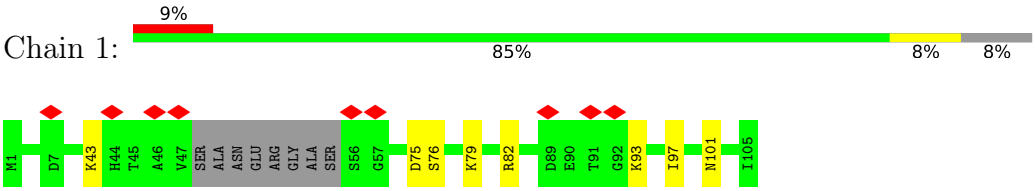
• Molecule 55: Ribosome-recycling factor

Chain 5:



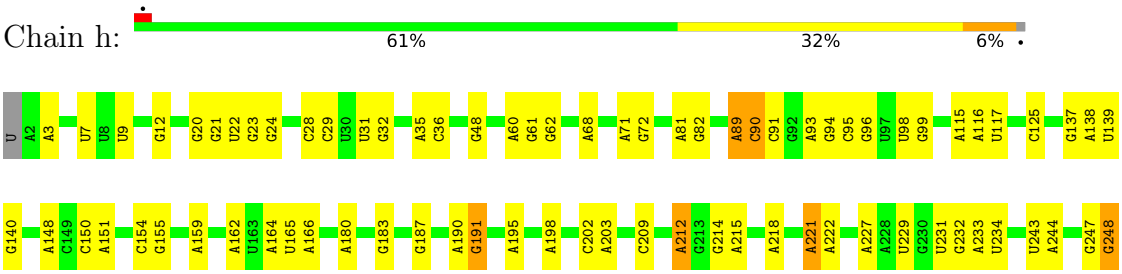
• Molecule 56: Large ribosomal subunit protein uL24

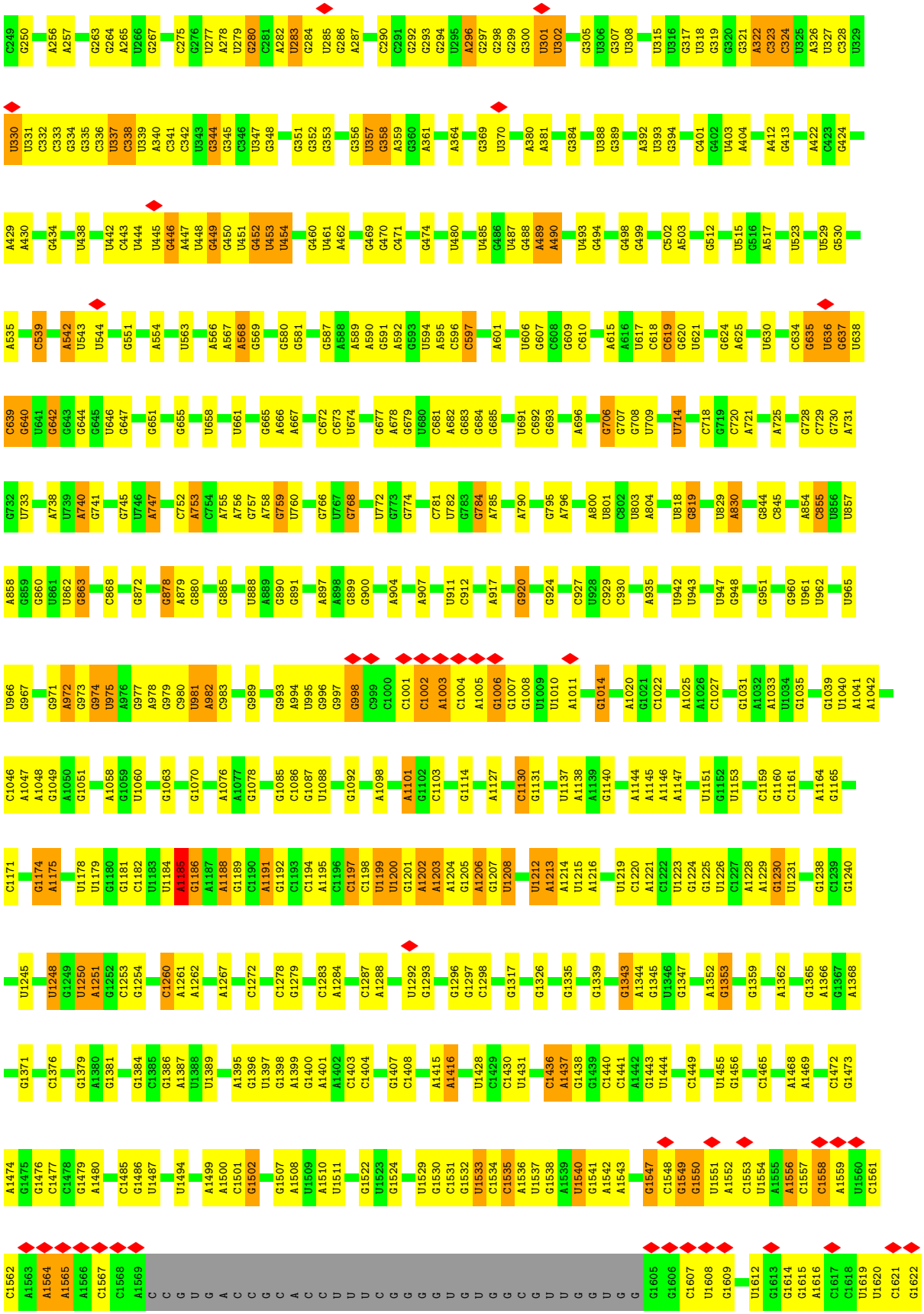
Chain 1:

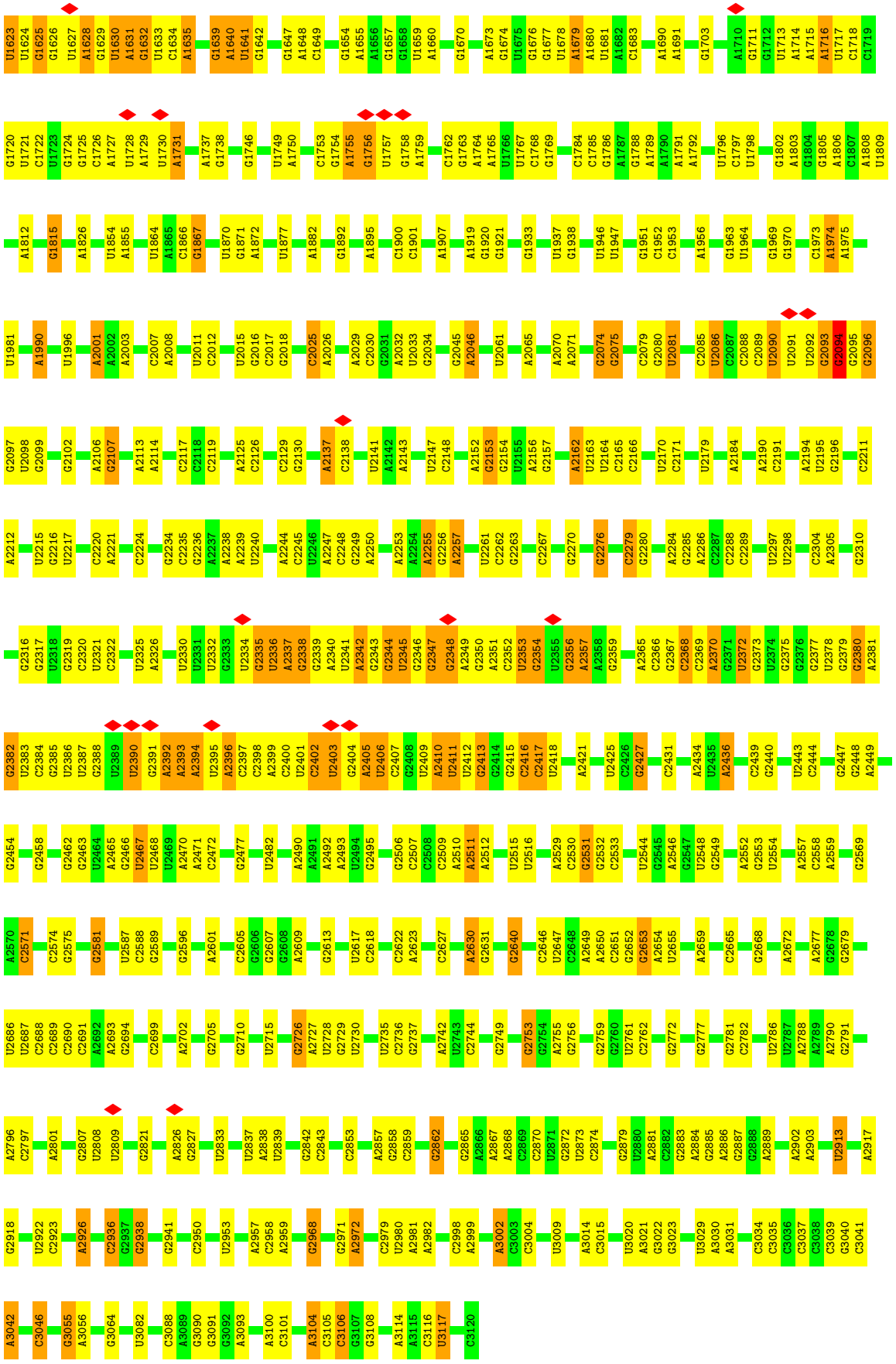


• Molecule 57: 23S ribosomal RNA

Chain h:




C249 G250 A256 A257 G263 G264 A265 U266 G267 C275 G276 U277 A278 U279 G280 C281 A282 U283 G284 U285 G286 A287 C290 C291 G292 G293 G294 U295 A296 G297 G298 G299 G300 U301 U302 G305 U306 G307 U308 U315 U316 G317 U318 G319 G320 G321 A322 C323 C324 U325 A326 U327 C328 U329
U330 U331 C332 C333 G334 G335 C336 U337 C338 U339 A340 C341 C342 U343 G344 G345 C346 U347 G348 G351 G352 G353 G356 U357 G358 A359 G360 A361 A364 G369 U370 A380 A381 G384 U388 G389 A392 U393 G394 C401 G402 U403 A404 A412 G413 A422 C423 G424
A429 A430 G434 U438 U442 C443 U444 U445 G446 A447 U448 G449 G450 U451 G452 U453 U454 G460 U461 A462 G469 G470 C471 G474 U480 U485 G486 U487 G488 A489 A490 U493 G494 G498 G499 C502 A503 G512 U515 G516 A517 U523 U529 G530
A535 C539 A542 U543 U544 G551 A554 U563 A566 A567 A568 G569 G580 G581 G587 A588 A589 A590 G591 A592 G593 U594 A595 C596 C597 A601 U606 G607 C608 G609 C610 A615 A616 U617 C618 C619 G620 U621 G624 A625 U630 C634 G635 U636 G637 U638
C639 G640 U641 G642 G643 G644 G645 U646 G647 G651 G655 U658 U661 G665 A666 A667 C672 C673 U674 G677 A678 G679 U680 C681 A682 G683 G684 G685 U691 C692 G693 A696 G706 G707 G708 U709 U714 C718 G719 C720 A721 A725 G728 C729 G730 A731
G732 U733 A738 U739 A740 G741 G745 U746 A747 C752 A753 C754 A755 A756 G757 A758 G759 U760 G766 U767 G768 U772 G773 G774 C781 U782 G783 G784 A785 A790 G795 A796 A800 U801 C802 U803 A804 U818 G819 U829 A830 G844 C845 A854 C855 U856 U857
A858 G859 G860 U861 U862 G863 C868 G872 G878 A879 G880 G885 U888 A889 G890 G891 A897 A898 G899 G900 A904 A907 U911 C912 A917 G920 G924 C927 U928 C929 C930 A935 U942 U943 U947 G948 G951 G960 U961 U962 U965
U966 C967 G971 A972 G973 G974 U975 A976 G977 A978 C979 C980 U981 A982 C983 G989 G993 A994 U995 G996 G997 G998 C999 C1000 C1001 C1002 A1003 C1004 A1005 G1006 G1007 G1008 U1009 U1010 A1011 G1014 A1020 G1021 C1022 A1025 A1026 C1027 G1031 A1032 A1033 U1034 G1035 G1039 U1040 A1041 A1042
C1046 A1047 A1048 G1049 A1050 G1051 A1058 G1059 U1060 G1063 G1070 A1076 A1077 G1078 G1085 C1086 G1087 U1088 G1092 A1098 A1101 G1102 C1103 G1114 A1127 C1130 G1131 U1137 A1138 A1139 G1140 A1144 A1145 A1146 A1147 U1151 G1152 U1153 C1159 G1160 C1161 A1164 G1165
C1171 G1174 A1175 U1178 U1179 G1180 G1181 C1182 U1183 U1184 A1185 G1186 A1187 A1188 G1189 C1190 A1191 G1192 C1193 C1194 A1195 C1196 C1197 C1198 U1199 U1200 G1201 A1202 A1203 A1204 G1205 A1206 G1207 U1208 U1212 A1213 A1214 U1215 A1216 U1219 C1220 A1221 C1222 U1223 G1224 G1225 U1226 C1227 A1228 A1229 G1230 U1231 G1238 C1239 G1240
U1245 U1248 G1249 U1250 A1251 G1252 C1253 G1254 C1260 A1261 A1262 A1267 C1272 C1278 G1279 C1283 A1284 C1287 A1288 U1292 G1293 G1296 G1297 C1298 G1317 G1326 G1335 G1339 G1343 A1344 G1345 U1346 G1347 A1352 G1353 G1359 A1362 G1365 A1366 G1367 A1368
G1371 C1376 G1379 A1380 G1381 G1384 C1385 G1386 A1387 U1388 U1389 A1395 G1396 U1397 G1398 A1399 G1400 A1401 A1402 C1403 C1404 G1407 C1408 A1415 A1416 U1428 C1429 C1430 U1431 C1436 A1437 G1438 G1439 C1440 C1441 A1442 G1443 U1444 C1449 U1455 G1456 C1465 A1468 A1469 C1472 G1473
A1474 G1475 G1476 C1477 C1478 G1479 A1480 C1485 G1486 U1487 U1494 A1499 A1500 C1501 G1502 G1507 A1508 U1509 A1510 U1511 G1522 U1523 G1524 U1529 G1530 C1531 G1532 U1533 C1534 C1535 A1536 U1537 G1538 A1539 U1540 G1541 A1542 A1543 G1547 C1548 G1549 G1550 U1551 A1552 C1553 U1554 A1555 A1556 C1557 C1558 A1559 U1560 C1561
C1562 A1563 A1564 A1565 A1566 C1567 C1568 A1569 C C G U G A C C G C A C C U U U C G G G G G U G U G C G G U U G G U G G C1605 G1606 C1607 U1608 G1609 U1612 G1613 G1614 G1615 A1616 C1617 C1618 U1619 U1620 C1621 G1622



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18050	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	0.178	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	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	0.50	0/1836	0.85	0/2859
2	3	0.16	0/191	0.37	0/247
3	4	1.07	0/65	0.99	0/98
4	6	0.40	2/1760 (0.1%)	0.91	4/2375 (0.2%)
5	A	0.58	0/36309	0.88	25/56657 (0.0%)
6	B	0.34	0/2821	0.76	0/4396
7	C	0.17	0/1684	0.36	0/2261
8	D	3.92	10/1672 (0.6%)	3.35	12/2251 (0.5%)
9	E	0.20	0/1312	0.39	0/1772
10	F	0.17	0/782	0.36	0/1059
11	G	0.16	0/1252	0.37	0/1690
12	H	0.20	0/1025	0.38	0/1385
13	I	0.17	0/1012	0.39	0/1362
14	J	0.19	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	0.21	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	0.32	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	0.17	0/534	0.26	0/713
30	a	0.20	0/477	0.28	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	0.14	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	0.18	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	0.20	0/945	0.36	0/1267
50	v	0.16	0/966	0.29	0/1298
51	w	0.19	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	5	0.49	1/1471 (0.1%)	0.68	5/1976 (0.3%)
56	1	0.17	0/738	0.32	0/987
57	h	0.49	0/74164	0.80	30/115718 (0.0%)
All	All	0.66	19/164063 (0.0%)	0.83	85/245481 (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
4	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)
8	D	115	HIS	ND1-CE1	87.28	2.19	1.32
8	D	117	HIS	ND1-CE1	87.19	2.19	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	o	33	HIS	ND1-CE1	87.09	2.19	1.32
8	D	115	HIS	CD2-NE2	69.92	2.14	1.37
43	o	33	HIS	CD2-NE2	69.80	2.14	1.37

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	D	115	HIS	CE1-NE2-CD2	-73.21	35.79	109.00
43	o	33	HIS	CE1-NE2-CD2	-73.19	35.81	109.00
8	D	117	HIS	CE1-NE2-CD2	-73.17	35.84	109.00
8	D	117	HIS	ND1-CE1-NE2	-72.15	36.25	108.40
8	D	115	HIS	ND1-CE1-NE2	-72.06	36.34	108.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	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	6	1736	0	1788	91	0
5	A	32439	0	16321	651	0
6	B	2522	0	1285	32	0
7	C	1660	0	1707	43	0
8	D	1641	0	1668	135	0
9	E	1296	0	1360	36	0
10	F	771	0	797	16	0
11	G	1232	0	1282	31	0
12	H	1010	0	1046	24	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	58	0
17	M	935	0	986	37	0
18	N	477	0	499	15	0
19	O	720	0	760	16	0
20	P	891	0	935	40	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	8	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	39	0
38	j	1587	0	1630	24	0
39	k	1569	0	1607	25	0
40	l	1445	0	1476	41	0
41	m	1348	0	1399	19	0
42	n	1018	0	988	14	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	15	0
48	t	1092	0	1128	14	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	12	0
53	y	754	0	802	12	0
54	z	873	0	909	9	0
55	5	1458	0	1478	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1	732	0	782	7	0
57	h	66232	0	33325	582	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	151085	0	101789	2240	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 2240 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)
55:5:42:ILE:HD13	55:5:51:ILE:HG22	1.38	1.04
55:5:36:MET:HB3	55:5:87:LEU:HD22	1.42	1.02
55:5:43:ASP:O	55:5:74:GLN:NE2	1.91	1.02
5:A:532:U:H4'	16:L:84:GLY:O	1.64	0.96
55:5:105:LEU:H	55:5:110:ARG:HE	1.13	0.95

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
4	6	230/235 (98%)	216 (94%)	13 (6%)	1 (0%)	30	67
7	C	206/275 (75%)	195 (95%)	11 (5%)	0	100	100
8	D	198/201 (98%)	182 (92%)	16 (8%)	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%)	151 (99%)	2 (1%)	0	100	100
12	H	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
13	I	124/150 (83%)	114 (92%)	10 (8%)	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%)	184 (97%)	6 (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	5	183/185 (99%)	172 (94%)	9 (5%)	2 (1%)	11	45
56	1	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
All	All	6127/6789 (90%)	5872 (96%)	252 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	5	183	LEU
55	5	180	SER
4	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	6	181/184 (98%)	178 (98%)	3 (2%)	53	68
7	C	170/212 (80%)	170 (100%)	0	100	100
8	D	175/176 (99%)	167 (95%)	8 (5%)	24	45
9	E	127/147 (86%)	126 (99%)	1 (1%)	73	78
10	F	85/85 (100%)	85 (100%)	0	100	100
11	G	131/132 (99%)	130 (99%)	1 (1%)	73	78
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	74
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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
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 82
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 80
41	m	148/150 (99%)	147 (99%)	1 (1%)	76 80
42	n	90/116 (78%)	89 (99%)	1 (1%)	65 74
43	o	102/108 (94%)	101 (99%)	1 (1%)	68 77
44	p	89/120 (74%)	89 (100%)	0	100 100
45	q	119/120 (99%)	117 (98%)	2 (2%)	53 68
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	5	160/160 (100%)	153 (96%)	7 (4%)	25 46
56	1	81/86 (94%)	81 (100%)	0	100 100
All	All	5050/5470 (92%)	5020 (99%)	30 (1%)	76 82

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	L	33	VAL
55	5	183	LEU

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Mol	Chain	Res	Type
40	l	34	GLN
55	5	185	VAL
55	5	179	GLU

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

Mol	Chain	Res	Type
39	k	91	HIS
55	5	84	ASN
43	o	21	ASN
55	5	41	ASN
55	5	177	HIS

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
5	A	1510/1528 (98%)	383 (25%)	20 (1%)
57	h	3082/3120 (98%)	603 (19%)	0
6	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
5	A	1109	C
5	A	1435	U
6	B	10	G
5	A	1477	A
5	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 (i)

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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

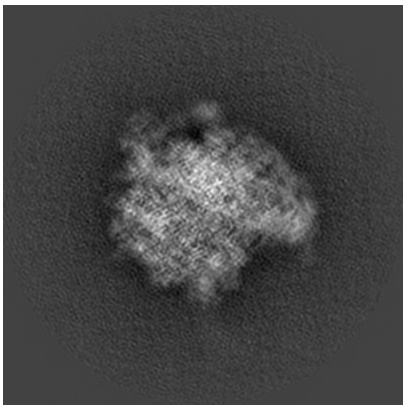
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-69698. These allow visual inspection of the internal detail of the map and identification of artifacts.

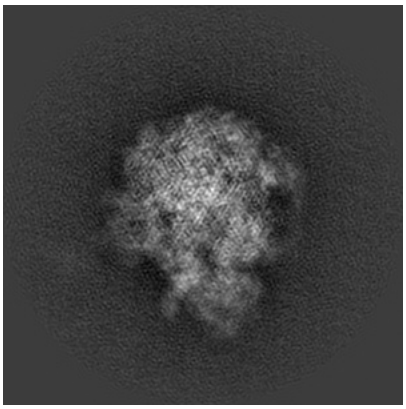
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

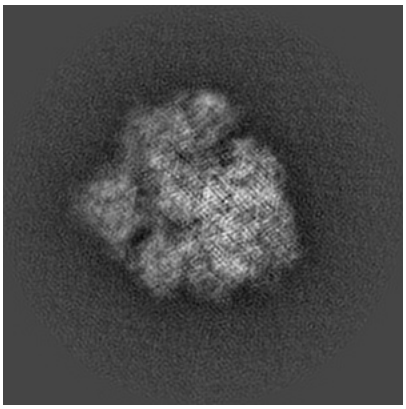
6.1.1 Primary map



X

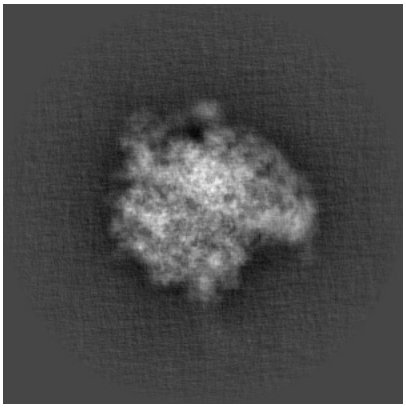


Y

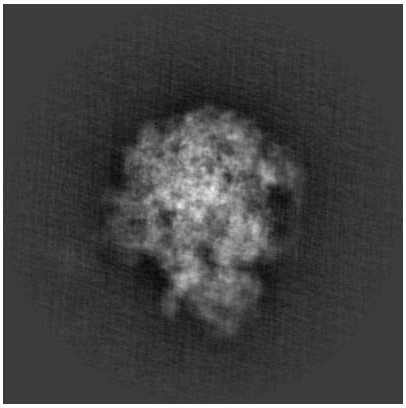


Z

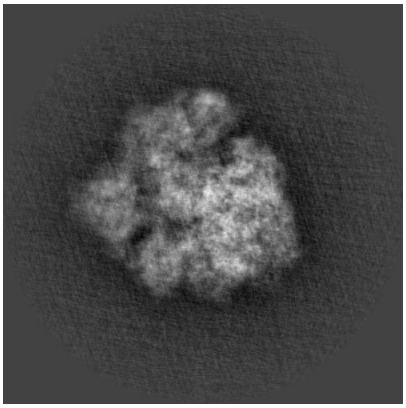
6.1.2 Raw map



X



Y

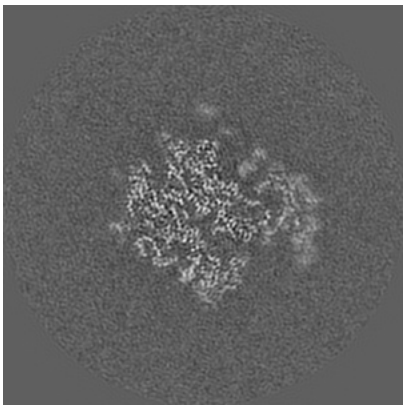


Z

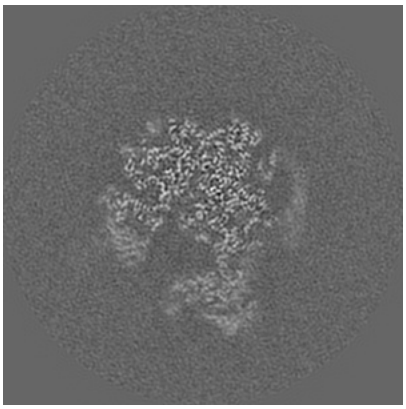
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

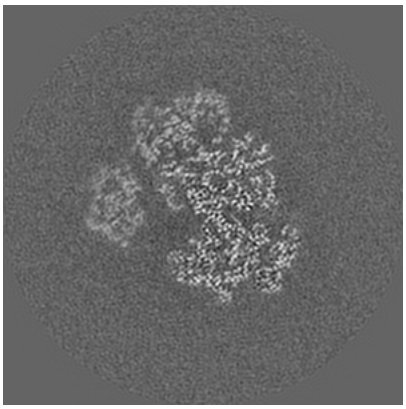
6.2.1 Primary map



X Index: 210

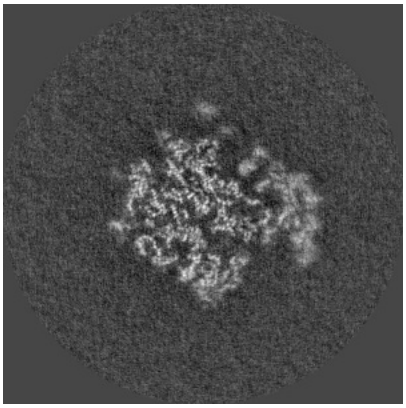


Y Index: 210

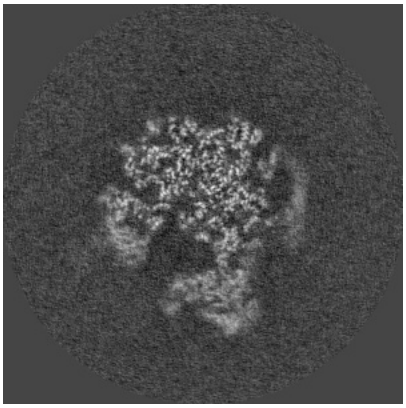


Z Index: 210

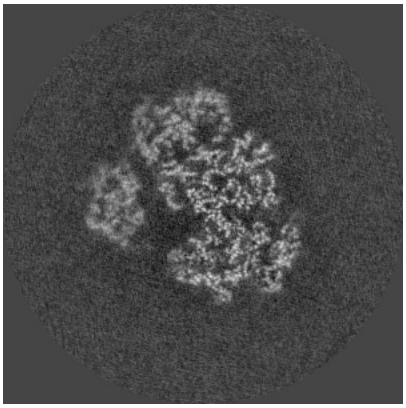
6.2.2 Raw map



X Index: 210



Y Index: 210

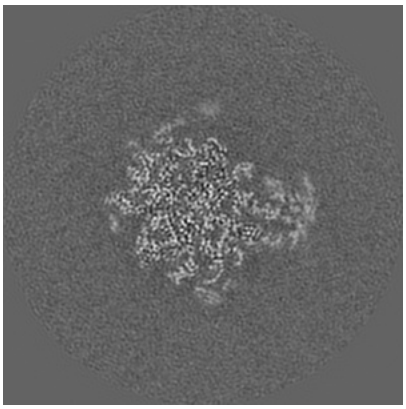


Z Index: 210

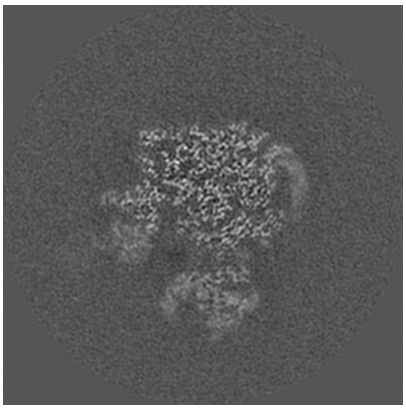
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

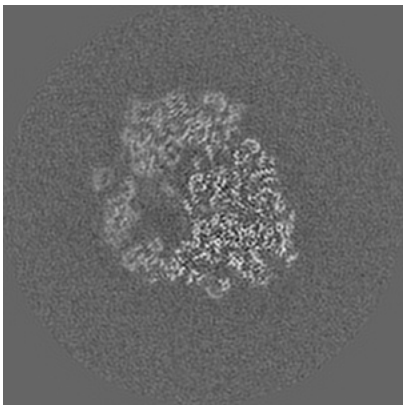
6.3.1 Primary map



X Index: 222

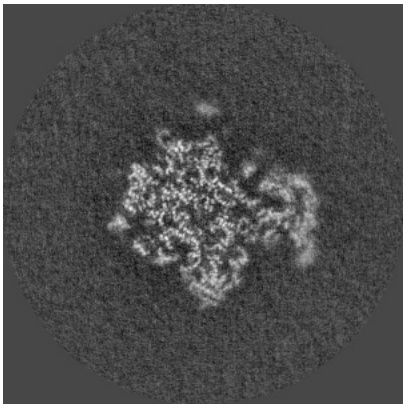


Y Index: 220

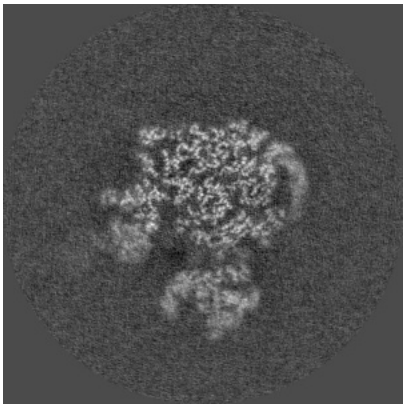


Z Index: 198

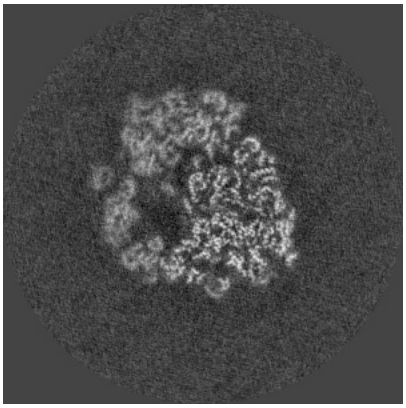
6.3.2 Raw map



X Index: 213



Y Index: 220

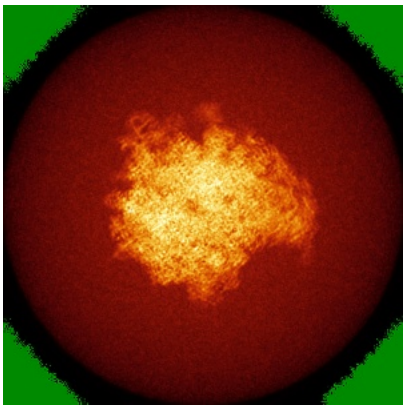


Z Index: 198

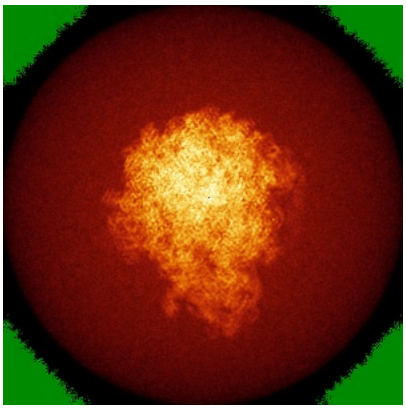
The images above show the largest variance slices of the map in three orthogonal directions.

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

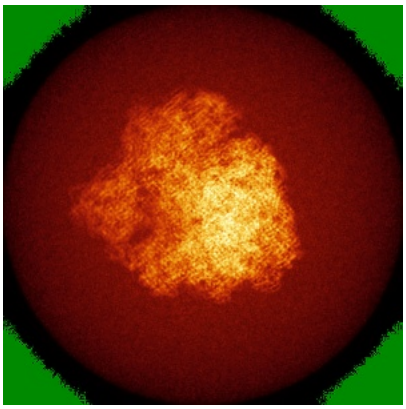
6.4.1 Primary map



X

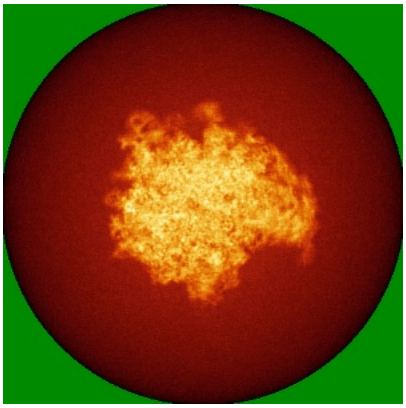


Y

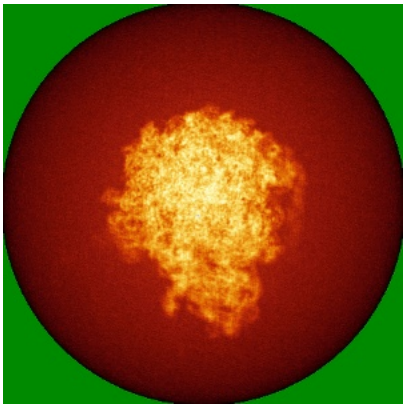


Z

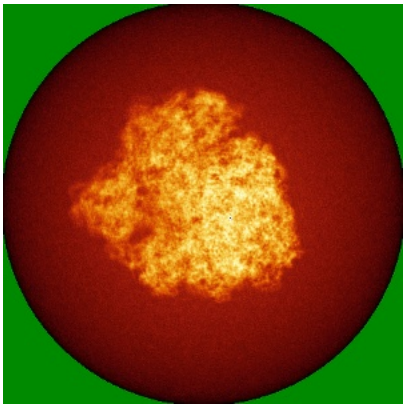
6.4.2 Raw map



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.

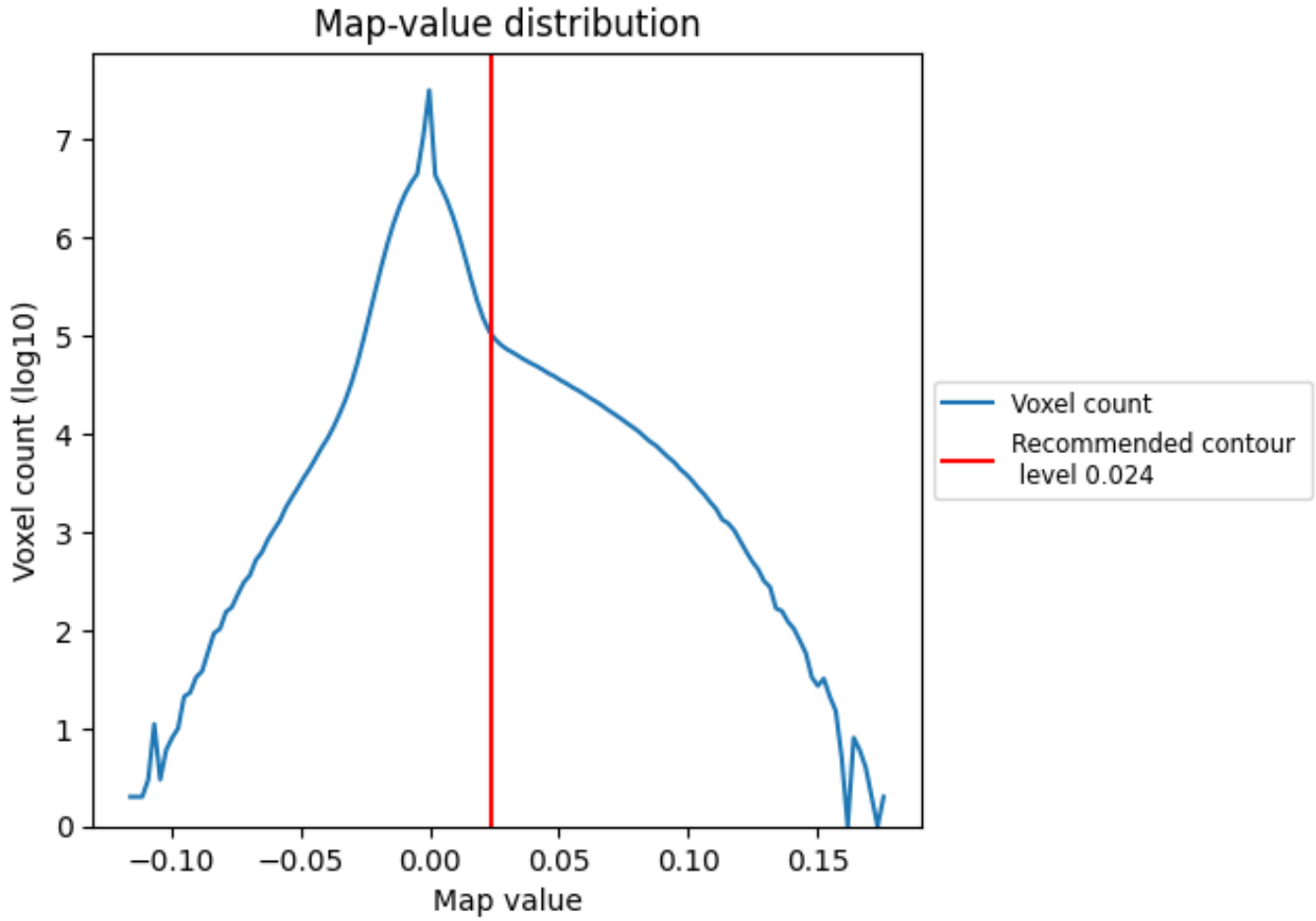
6.6 Mask visualisation (i)

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

7 Map analysis

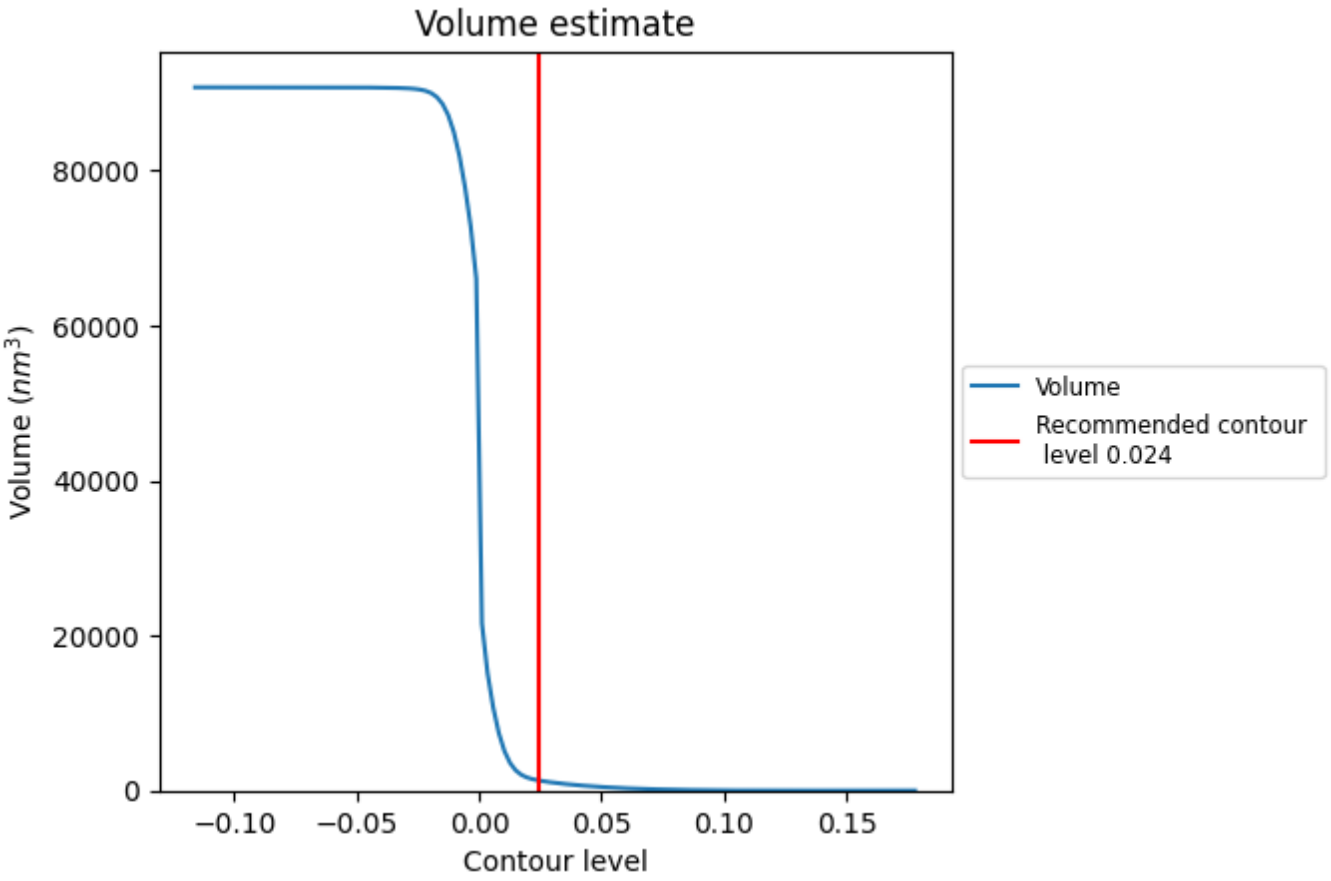
This section contains the results of statistical analysis of the map.

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.

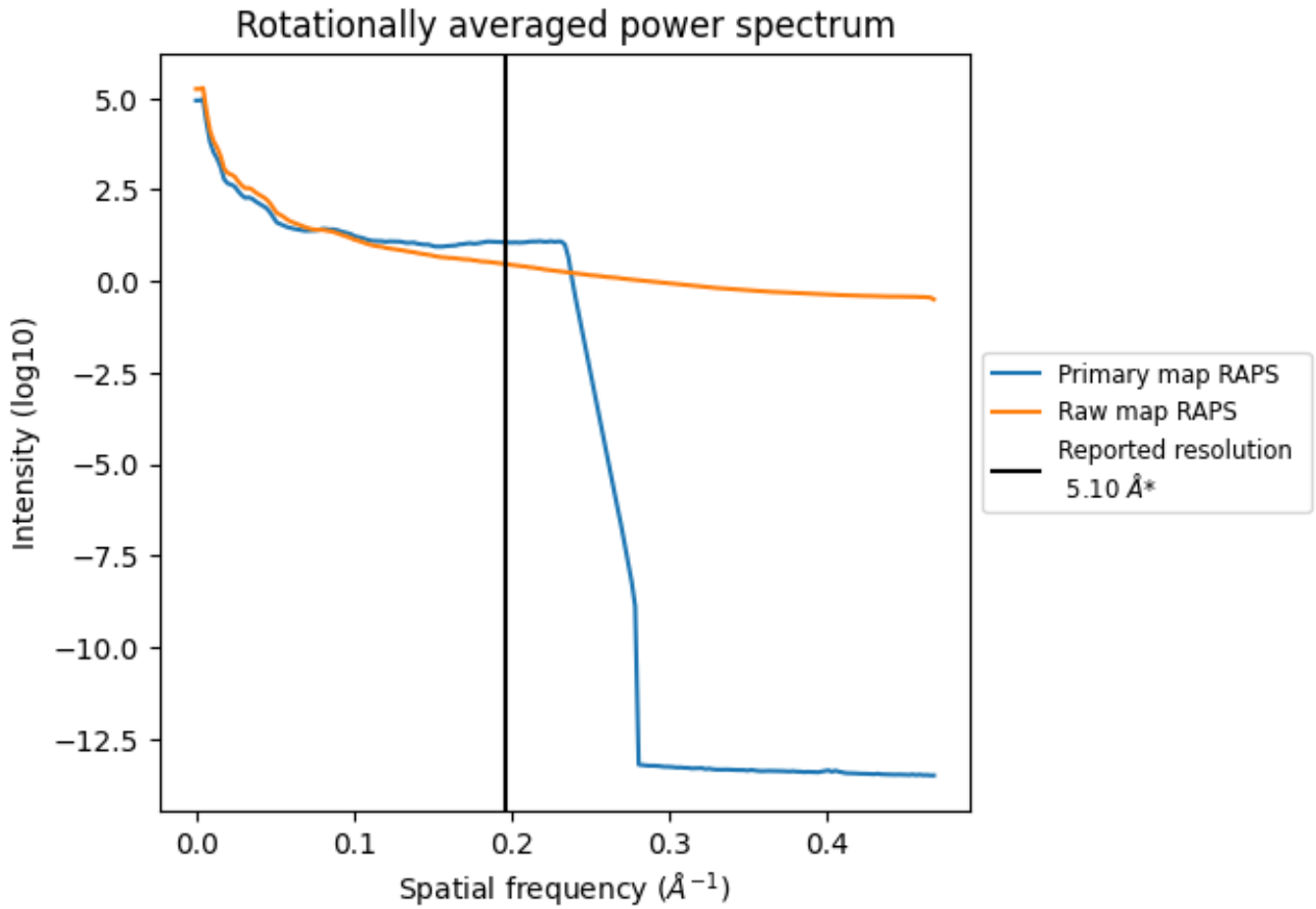
7.2 Volume estimate (i)



The volume at the recommended contour level is 1325 nm^3; this corresponds to an approximate mass of 1197 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)

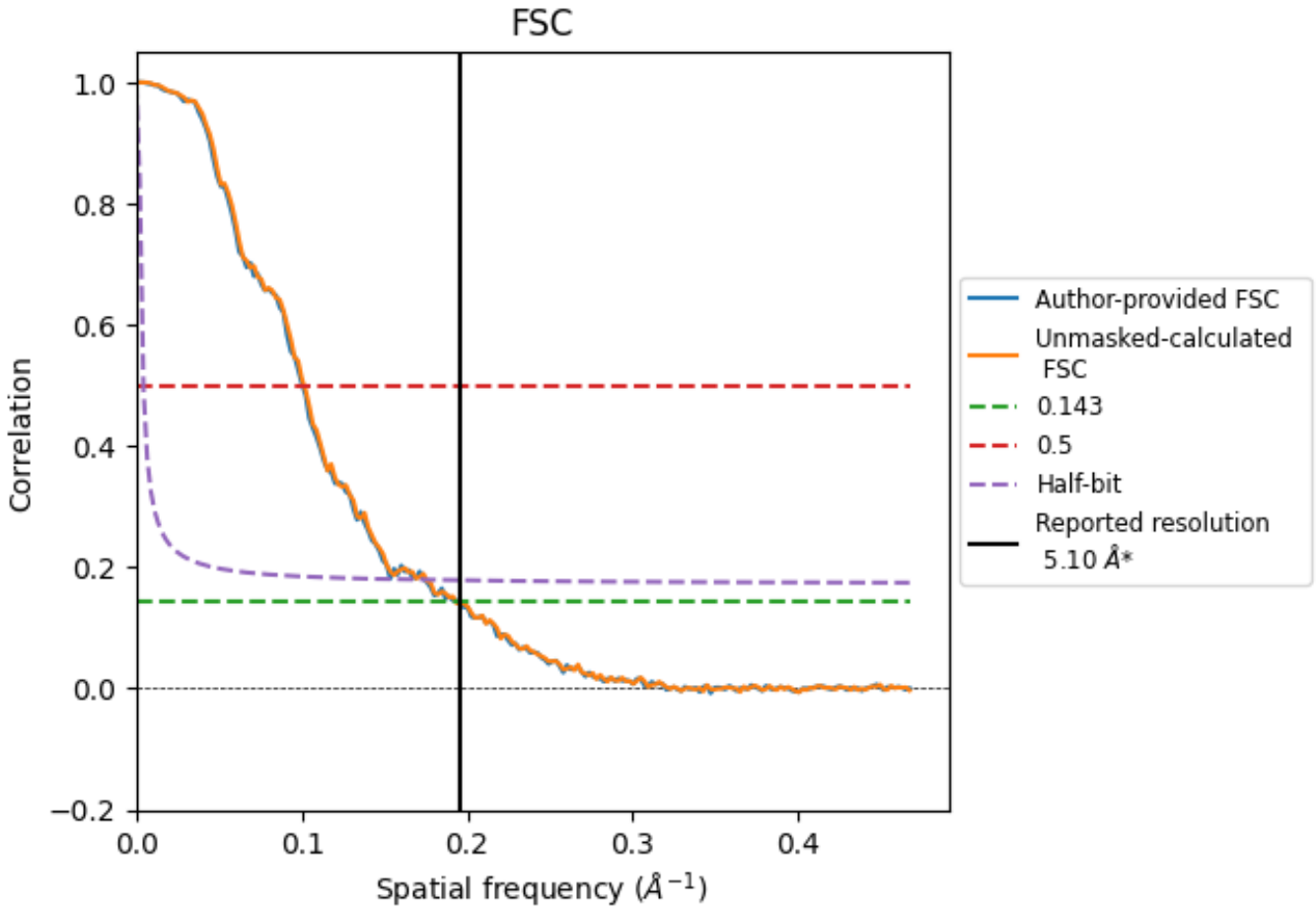


*Reported resolution corresponds to spatial frequency of 0.196 $Å^{-1}$

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)

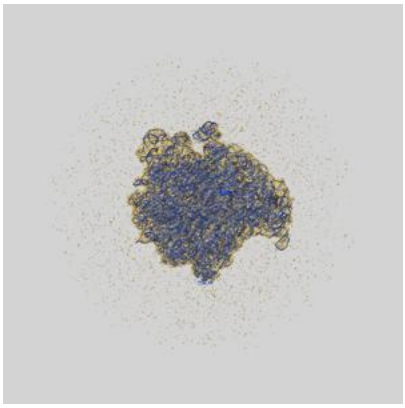
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.15	9.95	5.73
Unmasked-calculated*	5.18	9.86	5.70

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

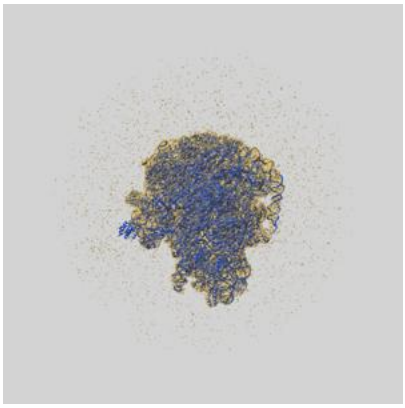
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-69698 and PDB model 24NN. Per-residue inclusion information can be found in section 3 on page 16.

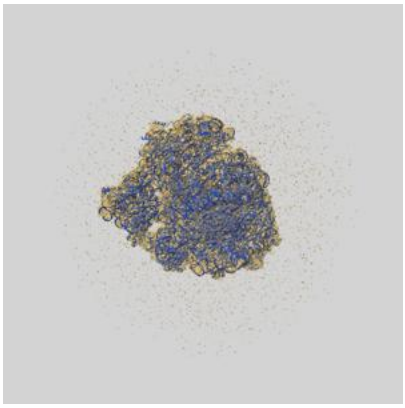
9.1 Map-model overlay



X



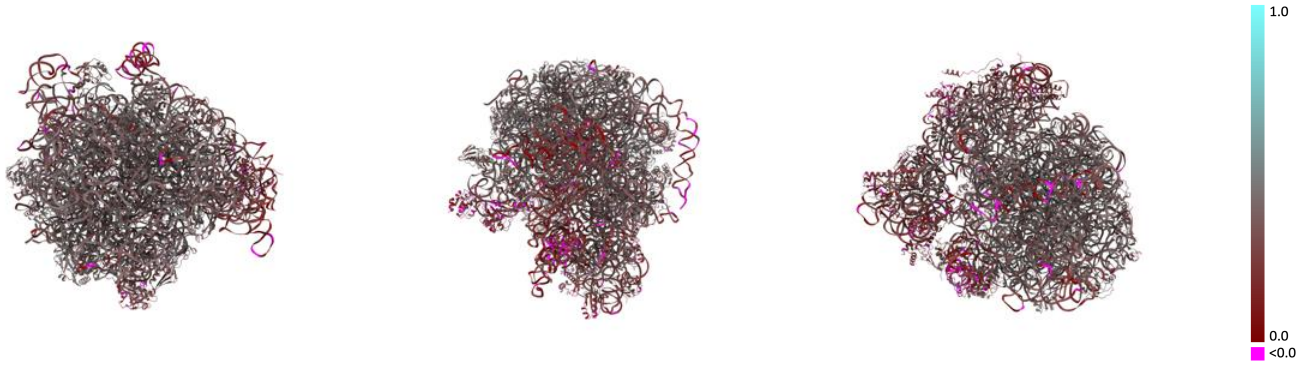
Y



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.

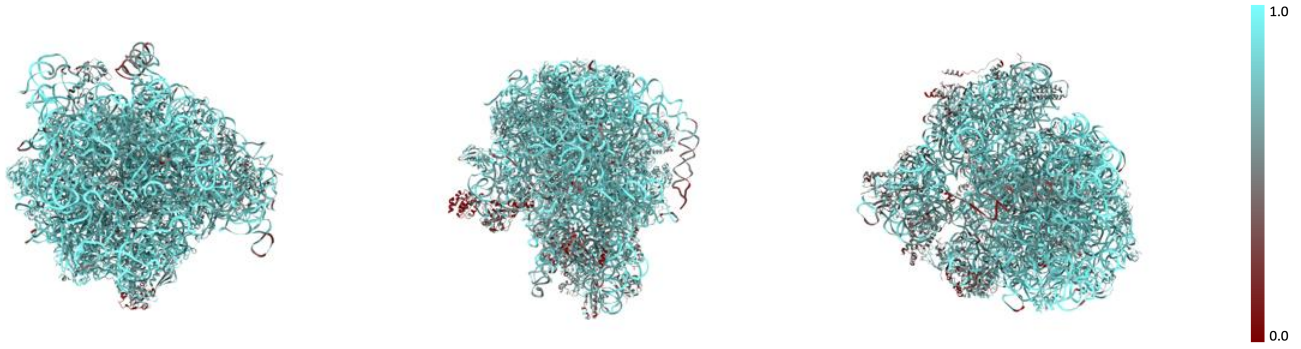
9.2 Q-score mapped to coordinate model



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.

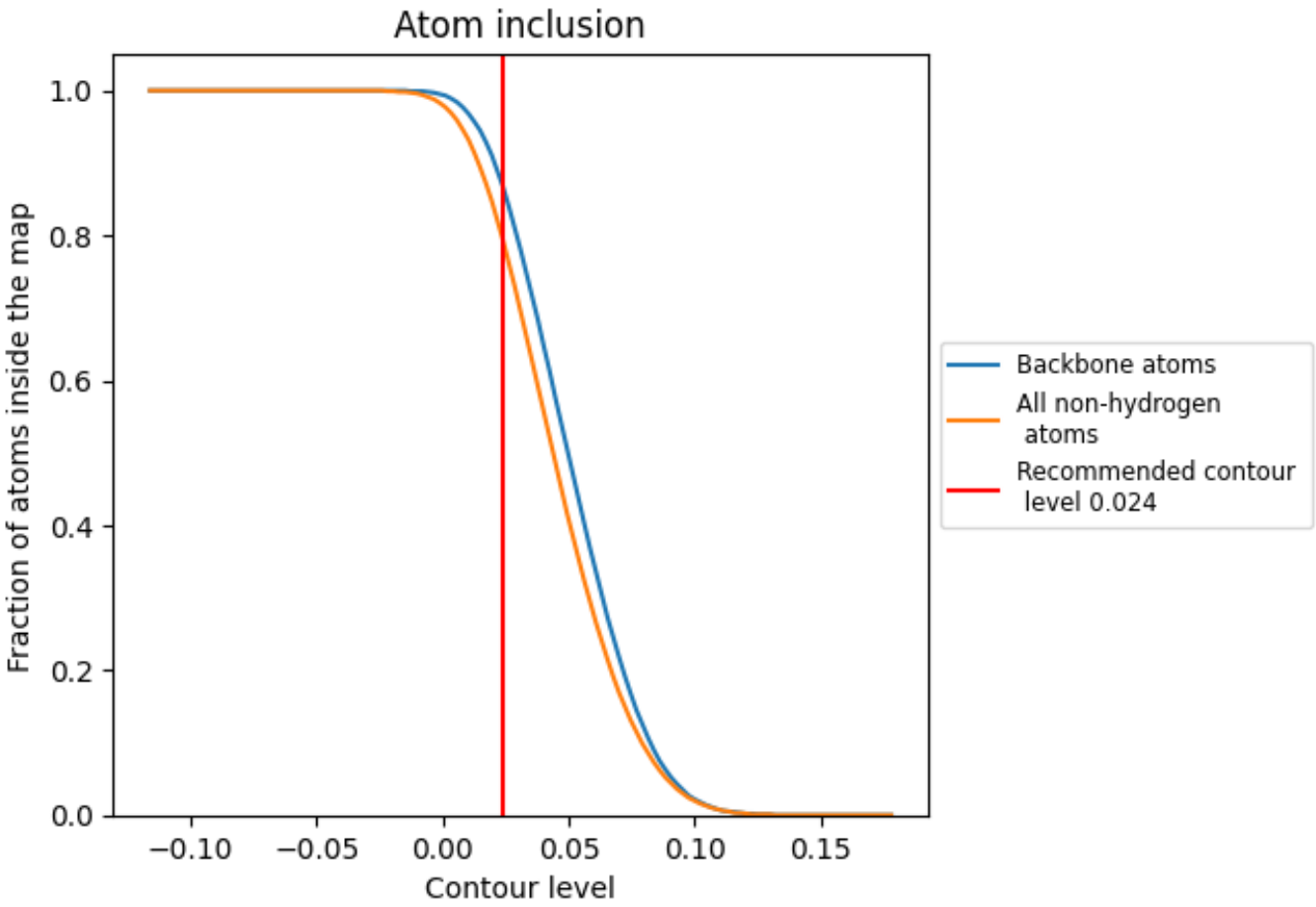
9.3 Atom inclusion mapped to coordinate model



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, 87% of all backbone atoms, 79% 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	0.7940	0.3410
1	0.7150	0.3830
2	0.7120	0.3000
3	0.6650	0.3870
4	0.8500	0.4050
5	0.4120	0.2170
6	0.3080	0.1330
A	0.8340	0.3040
B	0.9150	0.3790
C	0.5790	0.2710
D	0.4540	0.1360
E	0.6850	0.3370
F	0.7160	0.3720
G	0.4700	0.1930
H	0.7620	0.3780
I	0.5690	0.2710
J	0.5110	0.2500
K	0.7160	0.3850
L	0.5710	0.2740
M	0.4760	0.1930
N	0.6460	0.3070
O	0.7400	0.3610
P	0.5450	0.2350
Q	0.5790	0.2610
R	0.7520	0.3700
S	0.4790	0.2020
T	0.6060	0.1940
U	0.7390	0.3920
W	0.6870	0.3660
X	0.7430	0.4010
Y	0.7880	0.4210
Z	0.7690	0.3650
a	0.7820	0.4160
b	0.7660	0.3870
c	0.8050	0.3950



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Chain	Atom inclusion	Q-score
d	0.8110	0.4100
e	0.7540	0.4210
f	0.7400	0.3970
g	0.6980	0.3110
h	0.8730	0.3690
i	0.7830	0.4230
j	0.7920	0.4160
k	0.8000	0.4130
l	0.6980	0.3360
m	0.7350	0.3600
n	0.5920	0.3280
o	0.3250	0.1520
p	0.0880	0.1300
q	0.7790	0.4080
r	0.7460	0.4150
s	0.8020	0.4160
t	0.7460	0.4170
u	0.8010	0.4100
v	0.7850	0.3670
w	0.7210	0.3950
x	0.8080	0.3970
y	0.8070	0.4240
z	0.7980	0.4180