wwPDB EM Validation Summary Report (i)

Sep 19, 2026 – 11:36 AM JST

PDB ID	:	7D80 / pdb_00007d80
EMDB ID	:	EMD-30611
Title	:	Molecular model of the cryo-EM structure of 70S ribosome in complex with peptide deformylase, trigger factor, and methionine aminopeptidase
Authors	:	Akbar, S.; Bhakta, S.; Sengupta, J.
Deposited on	:	2020-10-06
Resolution	:	4.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

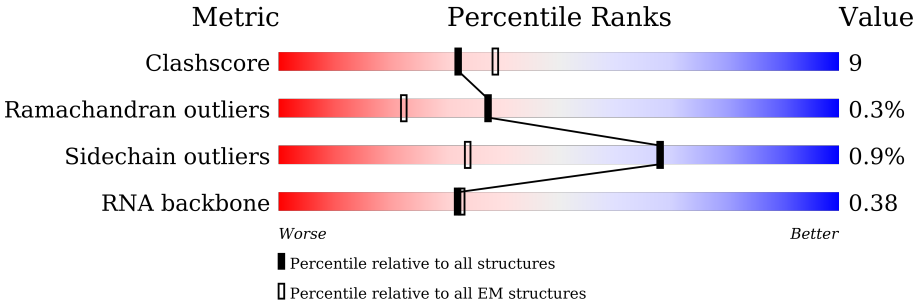
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

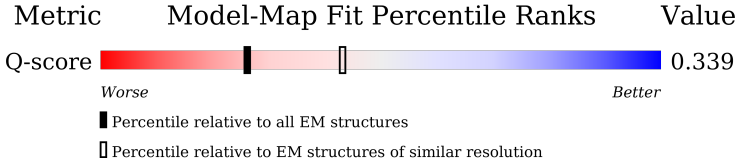
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	0	46	78% 22%
2	1	65	75% 18% • • •
3	2	38	61% 37% •

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Mol	Chain	Length	Quality of chain
4	3	169	71% 28%
5	5	432	28% 88% 12%
6	6	57	84% 14%
7	A	2903	56% 37% 7%
8	B	1539	49% 41% 9%
9	C	241	75% 16% 10%
10	D	233	65% 22% 12%
11	E	206	63% 37%
12	F	167	66% 24% 10%
13	G	135	54% 20% 26%
14	H	179	60% 24% 16%
15	I	130	66% 33%
16	J	130	65% 32%
17	K	103	68% 26% 5%
18	L	129	69% 22% 9%
19	M	124	73% 26%
20	N	118	67% 28%
21	O	101	57% 38% 5%
22	P	89	78% 21%
23	Q	82	72% 27%
24	R	84	52% 42% 5%
25	S	75	52% 21% 27%
26	T	92	67% 18% 14%
27	U	87	64% 31%
28	V	71	54% 17% 28%

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Mol	Chain	Length	Quality of chain
29	W	100	72% 22%
30	X	73	29% 36% 25% 11%
31	Z	76	32% 42% 34% 11% 13%
32	a	118	64% 35%
33	b	273	71% 27%
34	c	209	78% 21%
35	d	201	84% 16%
36	e	179	63% 36%
37	f	177	81% 17%
38	g	149	26% 6% 68%
39	h	142	10% 77% 22%
40	i	142	81% 18%
41	j	123	72% 27%
42	k	144	83% 15%
43	l	136	81% 18%
44	m	127	76% 19% 6%
45	n	117	83% 16%
46	o	115	77% 23%
47	p	118	78% 21%
48	q	103	83% 17%
49	r	110	81% 18%
50	s	104	78% 17%
51	t	94	86% 13%
52	u	85	81% 7% 12%
53	v	78	74% 24%

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Mol	Chain	Length	Quality of chain
54	w	63	78% 22%
55	x	59	85% 14%
56	y	77	45% 39% 6% 9%
57	z	55	73% 18% 9%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 150808 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	46	377	228	90	57	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	64	504	323	105	74	2	0	0

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	38	302	185	65	48	4	0	0

- Molecule 4 is a protein called Peptide deformylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	168	1346	844	241	255	6	0	0

- Molecule 5 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	432	3386	2119	582	674	11	0	0

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	56	444	269	94	80	1	0	0

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	A	2903	62317	27801	11467	20147	2902	0	0

- Molecule 8 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 9 is a protein called 30S ribosomal protein S2.

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

- Molecule 10 is a protein called 30S ribosomal protein S3.

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

- Molecule 11 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	205	1643	1026	315	298	4	0	0

- Molecule 12 is a protein called 30S ribosomal protein S5.

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

- Molecule 13 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 14 is a protein called 30S ribosomal protein S7.

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

- Molecule 15 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	I	129	979	616	173	184	6	0	0

- Molecule 16 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	J	127	1022	634	206	179	3	0	0

- Molecule 17 is a protein called 30S ribosomal protein S10.

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

- Molecule 18 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L	117	877	540	174	160	3	0	0

- Molecule 19 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	M	123	955	590	196	165	4	0	0

- Molecule 20 is a protein called 30S ribosomal protein S13.

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

- Molecule 21 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	O	96	774	483	160	128	3	0	0

- Molecule 22 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	P	88	710	437	143	129	1	0	0

- Molecule 23 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Q	82	649	406	128	114	1	0	0

- Molecule 24 is a protein called 30S ribosomal protein S17.

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

- Molecule 25 is a protein called 30S ribosomal protein S18.

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

- Molecule 26 is a protein called 30S ribosomal protein S19.

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

- Molecule 27 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	U	85	665	411	137	114	3	0	0

- Molecule 28 is a protein called 30S ribosomal protein S21.

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

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	W	96	764	484	142	136	2	0	0

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
30	X	65	1392	621	258	449	64	0	0

- Molecule 31 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
31	Z	66	1406	629	255	457	65	0	0

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 33 is a protein called 50S ribosomal protein L2.

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

- Molecule 34 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	c	209	1565	979	288	294	4	0	0

- Molecule 35 is a protein called 50S ribosomal protein L4.

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

- Molecule 36 is a protein called 50S ribosomal protein L5.

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

- Molecule 37 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	f	176	1323	832	243	246	2	0	0

- Molecule 38 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	g	47	359	233	62	63	1	0	0

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	h	141	1032	651	179	196	6	0	0

- Molecule 40 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	i	142	1129	714	212	199	4	0	0

- Molecule 41 is a protein called 50S ribosomal protein L14.

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

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	k	143	1045	649	206	189	1	0	0

- Molecule 43 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	l	136	1074	686	205	177	6	0	0

- Molecule 44 is a protein called 50S ribosomal protein L17.

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

- Molecule 45 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	n	116	892	552	178	162	0	0

- Molecule 46 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	o	114	917	574	179	163	1	0	0

- Molecule 47 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	p	117	947	604	192	151	0	0

- Molecule 48 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	q	103	816	516	153	145	2	0	0

- Molecule 49 is a protein called 50S ribosomal protein L22.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	t	94	753	479	137	134	3	0	0

- Molecule 52 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	u	75	569	353	113	102	1	0	0

- Molecule 53 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	v	77	625	388	129	106	2	0	0

- Molecule 54 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	w	63	509	313	99	95	2	0	0

- Molecule 55 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	x	58	449	281	87	79	2	0	0

- Molecule 56 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	y	70	1496	665	267	494	70	0	0

- Molecule 57 is a protein called 50S ribosomal protein L33.

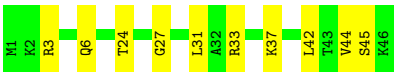
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	z	50	409	263	75	71	0	0

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.

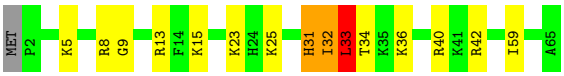
- Molecule 1: 50S ribosomal protein L34

Chain 0:



- Molecule 2: 50S ribosomal protein L35

Chain 1:

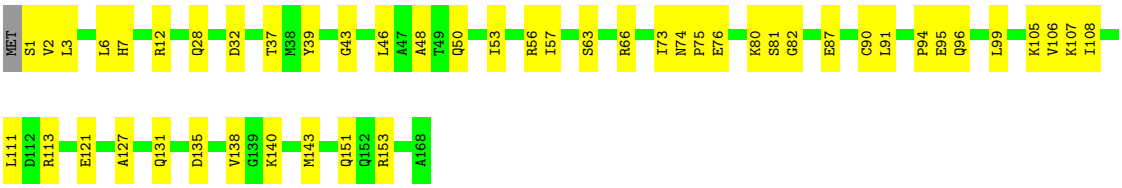


- Molecule 3: 50S ribosomal protein L36

Chain 2:

- Molecule 4: Peptide deformylase

Chain 3:



- Molecule 5: Trigger factor

Chain 5:

M1 S4 T16 V28 K29 S30 E31 N34 K37 R40 I41 D42 R63 L67 L70 R73 D77 P113 E114 V115 E116 L117 Q118 G119 L120 E121 A122 I123 E124 V125 E126 K127 P128 D134 A135 A149 K152 E153 K154 D155 G156 A157 V158 E159 A160

T165 T169 G170 S171 V172 D173 G174 E175 E176 F177 E178 G179 G180 K181 A182 S183 D184 F185 V186 L187 A188 G192 R193 M194 T195 P196 G197 F198 E199 D200 G201 I202 K203 G204 H205 K206 A207 G208 E209 E210 F211 T212 I213 D214 V215 T216 E219 E220 Y221 H222 A223 E224 N225 L226 K227 G228

K229 A230 A231 K232 F233 A234 I235 N236 L237 K238 K239 E244 L245 P246 E247 L248 I253 K254 G257 D260 G261 S262 V263 E264 R271 K272 N273 M274 E275 L278 K279 S280 R283 N284 R285 L294 V295 K296 A297 A304 I307 D308 R315 A318 A319 Q320 R321 F322

G323 G324 N325 E326 K327 Q328 A329 L330 E331 L332 P333 R334 E335 L336 Q340 V345 V354 E359 E365 S376 D380 P381 K382 E383 V384 M395 E405 Q406 A407 V411 K414 T418 E419 K420 E421 L427 Q431 A432

- Molecule 6: 50S ribosomal protein L32

Chain 6: 84% 14% •

MET A2 V3 Q4 R13 R16 V25 H38 T44 I55 A56 K57

- Molecule 7: 23S ribosomal RNA

Chain A: 56% 37% 7%

G1 A5 A6 A10 C11 U12 A13 A14 U18 A19 C20 G23 G26 G27 A28 U29 G30 U34 G35 A42 G45 G46 G51 G54 G58 U62 A63 C66 C69 G70 A71 U72 A73 A74 G75 U78 C79 G80 A83 A84 G85 G86 C96

U100 A101 U102 A103 A104 G107 G108 U112 U113 A118 A119 U120 A126 A127 C128 C129 U138 U139 C140 G141 A142 A149 U150 C151 A152 A155 A156 U162 C163 A172 A173 G178 G186 G187 A190 A191 A196 A199 U200 A204 G215 A216

A222 A223 U224 C225 A226 A227 C228 C229 G242 U243 A244 G245 C246 G247 G248 C253 G254 A255 A265 G266 G271 A272 C275 U276 G277 A278 A279 U280 C281 A282 G283 U284 U296 G297 G298 C302 G307 G308 A309 A310 A311 G315 G319 A320 U321 A322 C323 A324 G325 G326

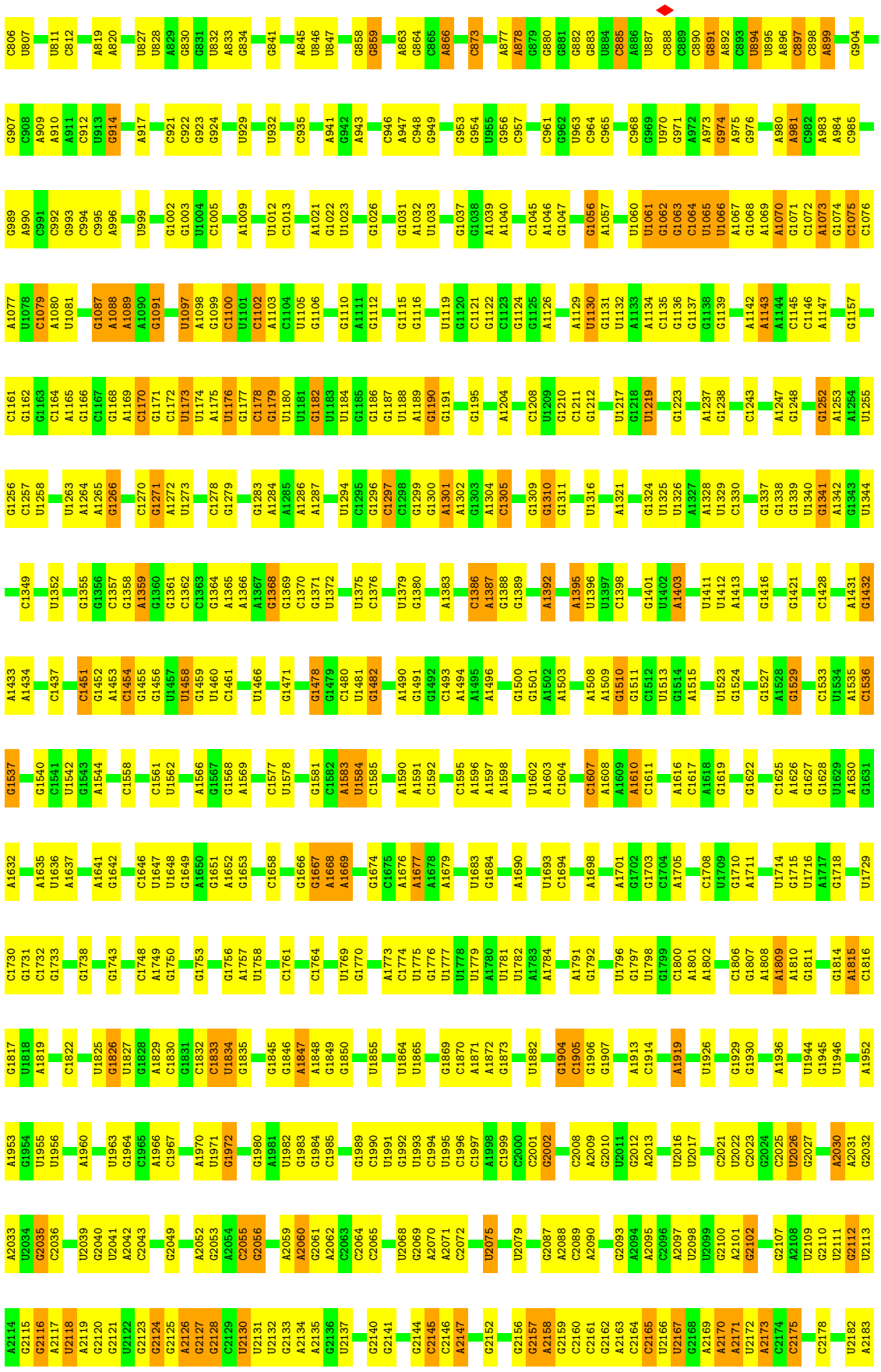
G327 U328 G329 A330 C331 C335 G338 C351 A352 C353 A354 U355 G356 C357 U358 G359 U360 G361 A362 G363 G370 A371 G372 G379 G380 G381 C385 G386 A391 U392 C393 U399 G400 A404 U405 G406 G407 G410 G411 A412 C413 C414 A415 C418 U419 C420 G424

A428 C445 G446 A447 U448 A454 C455 C456 A457 G458 U459 A460 U464 G465 A466 G467 G468 G469 A470 G473 A477 A478 A479 A480 G481 A482 A483 C484 G489 C490 G491 G494 G495 G496 U499 G500 A501 A502 A503 A504 A505 G506 A507 A508 C509 C510 U511 G512 C517 G518

C523 G524 U525 A526 C527 A528 A529 G530 C531 A532 G536 G537 C540 A541 C542 G543 C544 U545 U546 A547 G548 G549 C550 U554 G555 G559 C560 A563 U567 U568 U569 G570 U571 A572 U573 A574 A575 U576 G577 G578 G579 U580 C581 A582 A586 C587 G597 U598 A599 A603 G604

G605 A614 U615 A616 G619 G620 A621 G622 A626 A627 G628 G629 G630 A631 A632 A633 C634 C635 G636 A637 G638 U639 C640 U641 U642 A643 A644 C645 U646 G647 G648 A654 A655 G656 U657 U658 G659 C660 A661 G664 A668 G669 A670 C671 A675 A676 A677 C680 G681 U686

G690 G695 G713 U714 A718 C719 U720 A721 G728 G729 A730 C736 C737 G738 U747 G748 A749 A752 U762 G763 A764 C765 U766 U773 G774 G775 G776 G777 G778 U779 G780 A781 A782 A783 G784 G785 A789 A792 A793 C796 G797 G798 G799 A800 U803 A804 G805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C1730 G1731 C1732 G1733 G1738 G1743 C1748 A1749 G1750 G1753 G1756 A1757 U1758 C1761 C1764 U1769 G1770 A1773 C1774 U1775 G1776 U1777 U1778 U1779 A1780 U1781 U1782 A1783 A1784 A1791 G1792 U1796 G1797 U1798 G1799 C1800 A1801 A1802 C1806 G1807 A1808 A1809 A1810 G1811 G1814 A1815 C1816
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G1256 C1257 U1258 U1263 A1264 A1265 G1266 C1270 G1271 A1272 U1273 C1278 G1279 G1283 A1284 A1285 A1286 A1287 U1294 C1295 G1296 C1297 C1298 G1299 G1300 A1301 A1302 C1303 A1304 C1305 G1309 G1310 G1311 U1316 A1321 G1324 U1325 U1326 A1327 A1328 U1329 C1330 G1337 G1338 G1339 U1340 G1341 A1342 G1343 U1344
C1161 G1162 G1163 C1164 A1165 G1166 C1167 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 U1180 U1181 G1182 U1183 U1184 G1185 G1186 G1187 U1188 A1189 G1190 G1191 G1195 A1204 C1208 U1209 G1210 C1211 G1212 U1217 G1218 U1219 G1223 A1237 G1238 C1243 A1247 G1248 G1252 A1253 A1254 U1255
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G907 C908 A909 A910 A911 C912 U913 G914 A917 C921 C922 G923 G924 U929 U932 C935 A941 G942 A943 C946 A947 C948 G949 G953 G954 U955 G956 C957 C961 G962 U963 C964 C965 C968 G969 U970 G971 A972 A973 G974 A975 G976 A980 A981 C982 A983 A984 C985
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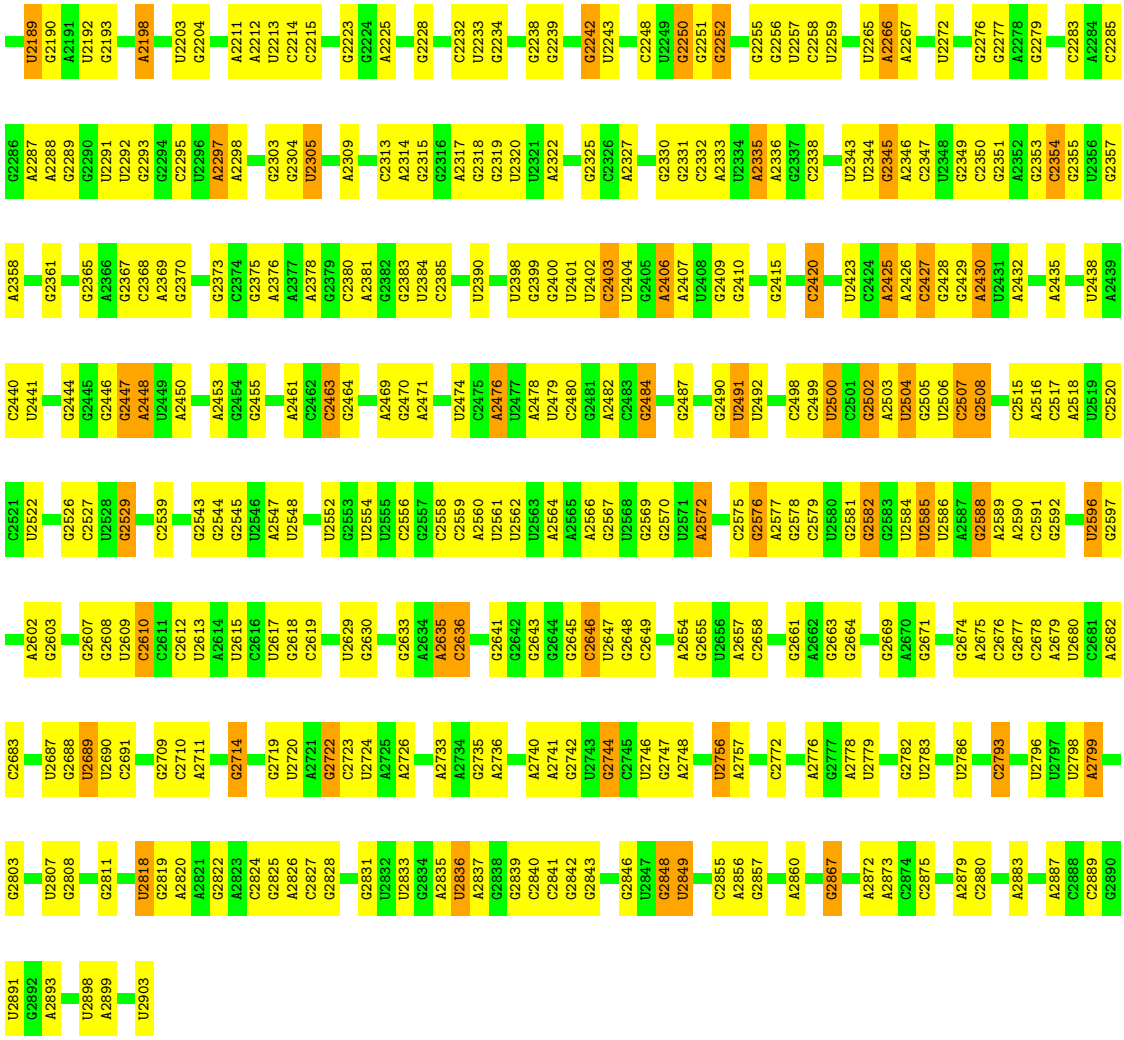
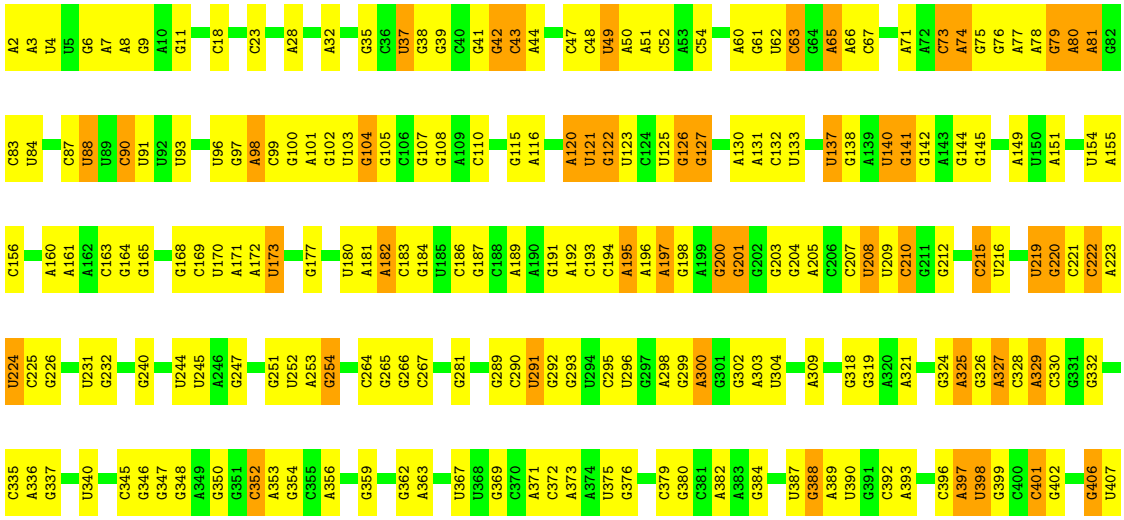
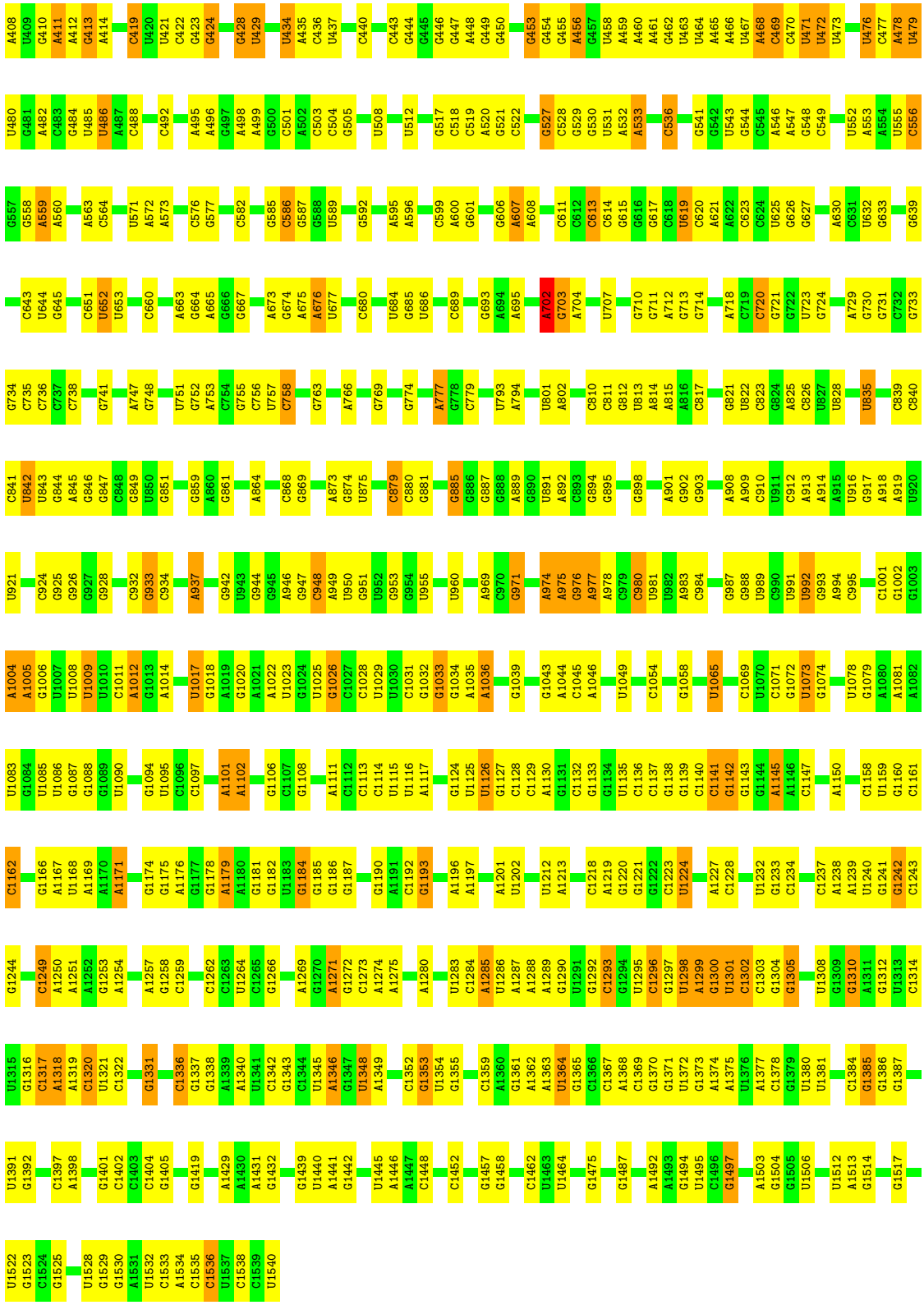


- Molecule 8: 16S ribosomal RNA

Chain B:





- Molecule 9: 30S ribosomal protein S2

Chain C: 75% 16% 10%

MET ALA THR VAL SER MET ARG ASP M9 T20 V38 N42 K45 A53 L57 K64 G65 K66 G71 V80 K81 D82 A83 A84 L85 S86 C87 D88 Q89 L97 K115 T130 K131 K132 E133 A134 T138 L141 E142 S147 L148 K152 V163

I173 D205 R208 L212 Y213 L214 V217 R222 R225 S226 GLN ASP LEU ALA SER GLN ALA GLU GLU SER PHE VAL GLU ALA GLU

- Molecule 10: 30S ribosomal protein S3

Chain D: 65% 22% • 12%

MET G2 V5 I10 R11 L12 V15 K16 N19 W22 F23 A24 E28 F29 A30 D31 N32 S35 K38 V39 R40 L47 A48 K49 R54 E58 R59 S63 I64 P73 V76 R88 V97 P98 A99 E105 K108 A113 V116 A117

D118 S119 I120 T121 S122 Q123 V138 Q139 R143 L144 I149 G155 R156 L157 A163 R164 W167 Y168 R169 H176 T177 N185 A189 H190 T191 T192 Y193 I196 I207 LEU GLY GLY MET ALA ALA VAL GLU GLN PRO GLU LYS PRO ALA ALA GLN PRO LYS LYS GLN

GLN ARG LYS GLY ARG LYS

- Molecule 11: 30S ribosomal protein S4

Chain E: 63% 37%

MET A2 R3 L9 K10 R13 R14 D18 L19 F20 K31 C32 K33 I34 R44 K45 P46 R47 Y51 L55 K58 R62 R63 I64 Y65 G66 V67 L68 E69 R70 R73 N74 Y75 Y76 K77 R81 L82 K83 G84 N85 E88 N89 E95 G96 R97 N100

V101 V102 Y103 R104 M105 R111 A112 E113 A114 R115 Q116 L117 V118 S119 H120 I123 N126 V129 V130 N131 S134 P139 N140 D141 S144 I145 K150 K151 Q152 S153 R154 V155 K156 L161 R165 L171 E172 V173 D174 A175 G176 K177 M178 F182 E187 R188 S189

D194 H198 L203 K206

- Molecule 12: 30S ribosomal protein S5

Chain F: 66% 24% 10%

MET ALA HIS ILE GLU LYS GLN ALA GLY E10 L15 K23 S32 F33 T37 V38 D41 R45 F48 A53 K62 M71 I72 N73 V74 N77 L81 Q82 S92 Q97 P98 A99 G102 T103 G104 I105 I106 A107 M111 V114 V120 H121

N122 V123 L124 A127 N132 P133 I134 N135 V136 V137 R138 A139 T140 L144 M147 K156 R157 G158 K159 SER VAL GLU GLU ILE LEU GLY LYS

- Molecule 13: 30S ribosomal protein S6, fully modified isoform

Chain G: 54% 20% 26%

M1 R2 H3 V10 V18 P19 G20 M21 I22 E23 R24 E40 D41 W42 G43 R44 L47 A48 Y49 P50 I51 N52 K53 K56 A57 H58 M62 N63 V64 E65 A66 R86 R91 T92 A95 V96 S100 PRO MET VAL LYS ALA LYS ASP GLU ARG ARG GLU ARG ARG

ASP ASP PHE ALA ASN GLU THR ALA ASP ASP ALA GLU ALA GLY ASP SER GLU GLU GLU GLU GLU GLU

• Molecule 14: 30S ribosomal protein S7

Chain H: 60% 24% 16%

MET P2 R3 R4 R5 V6 I7 P16 E21 A24 K25 F26 V27 N28 M31 K35 V43 L47 A51 S57 E58 A65 N68 V69 R70 P71 K76 R79 V89 R96 N97 A108 R111 G112 D113 K114 S115 M116 A117 L118 R119 L120 A121

N122 E123 D126 A127 A128 E129 N130 D140 R143 A152 HIS TYR ARG TRP LEU SER LEU ARG SER PHE SER HIS GLN ALA GLY ALA SER SER LYS GLN PRO ALA LEU GLY TYR LEU ASN

• Molecule 15: 30S ribosomal protein S8

Chain I: 66% 33%

MET S2 M3 Q4 D5 P6 I7 A8 D9 M10 L11 I14 R15 N16 M27 P28 S29 S30 K31 L32 K33 V34 K41 F45 F49 L59 K64 Q67 G68 K69 A70 V71 S74 I75 Q76 R77 R84 K87 R88 A102 V103 V104 S105 D113 R117

E124 I125 I126 C127 Y128 V129 A130

• Molecule 16: 30S ribosomal protein S9

Chain J: 65% 32%

MET ALA GLU N4 Q5 Y6 T9 R12 K13 R18 V19 K22 P23 G24 N25 G26 K27 I28 V29 I30 R45 R49 L52 E53 L54 V55 D56 M57 V58 E59 K60 L61 D62 L63 Y64 I65 T66 G74 I83 T84 R85 E89 Y90 D91 R95 L98 G102

R106 D107 K120 A121 R122 R123 R124 P125 Q126 F127 S128 K129 R130

• Molecule 17: 30S ribosomal protein S10

Chain K: 68% 26% 5%

MET GLN ASN GLN R5 I6 R7 A12 F13 D14 H15 I18 P41 L42 P43 T44 R45 K46 E47 S54 P55 H56 V57 N58 R62 D63 Q64 Y65 E66 T69 H70 L71 R72 T80 T83 V84 D85 M88 R89 L102 GLY

• Molecule 18: 30S ribosomal protein S11

Chain L: 69% 22% 9%

MET ALA LYS ALA PRO ILE ARG ALA ARG LYS ARG VAL R13 S17 V20 A21 H22 I23 V32 T33 N40 W44 R53 G54 S55 S58 E76 I79 E83 V84 M85 V86 K87 R93 N101 R106 I107 D112 V113 P117 R122 K126 R127

R128 V129

• Molecule 19: 30S ribosomal protein S12

Chain M: 73% 26%

MET A2 N5 R12 A23 L24 C27 P28 Q29 K30 R36 V37 N46 R50 K51 V52 Y66 I67 E70 G71 E76 H77 L81 I82 R83 R86 Y95 H96 T97 V98 R99 G106 V107 K108 D109 R110 S115 V119 A124

• Molecule 20: 30S ribosomal protein S13

Chain N: 67% 28%

MET A2 R3 I4 N8 D11 H12 A15 V16 I17 A18 L19 I22 Y23 S30 L34 D42 I45 E50 I53 V65 E66 G67 D68 L69 E72 S76 R79 L80 M81 R87 G88 L89 R90 H91 R92 R93 V97 N105 R109 P115

ILE LYS LYS

• Molecule 21: 30S ribosomal protein S14

Chain O: 57% 38% 5%

MET A2 K3 Q4 S5 M6 K7 A8 R9 R13 L16 A17 D18 K19 Y20 K23 R24 L27 K28 A29 I30 I31 S32 D33 V34 N35 A36 SER ASP GLU ASP R41 L51 P52 R53 D54 S55 S56 R59 Q60 R61 N62 R63 C64 R65 R69 R75 K76 F77 R81

L96 K97 K98 A99 S100 W101

• Molecule 22: 30S ribosomal protein S15

Chain P: 78% 21%

MET S2 L3 S4 T8 A9 K10 S13 R17 D18 A19 S24 T25 E26 L32 I36 K47 K48 D49 S61 K65 L66 L67 D74 R77 L87 R88 R89

• Molecule 23: 30S ribosomal protein S16

Chain Q: 72% 27%

M1 V2 T3 I4 R5 L6 G10 P15 Q18 V21 A22 D23 S24 R28 R35 V36 G37 F38 I42 K46 I67 R70 V71 I75 K76 E77 K80 A81 A82

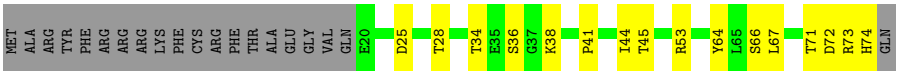
• Molecule 24: 30S ribosomal protein S17

Chain R: 52% 42% 5%

MET THR ASP K4 I5 R6 T7 L8 R11 V12 V13 S14 D15 K16 M17 E18 K19 V22 H31 P32 I33 K36 H45 V46 H47 D48 E49 E52 G56 D57 V58 I61 R62 E63 P66 L67 S68 K69 T70 K71 S72 V76 R77 V78 V79 E80 K81 A82 V83 LEU

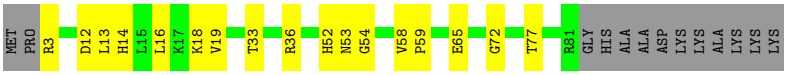
• Molecule 25: 30S ribosomal protein S18

Chain S: 52% 21% 27%



• Molecule 26: 30S ribosomal protein S19

Chain T:



• Molecule 27: 30S ribosomal protein S20

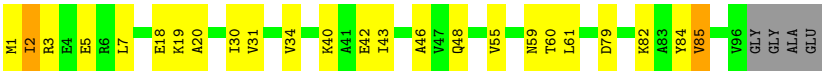
Chain U:

• Molecule 28: 30S ribosomal protein S21

Chain V:

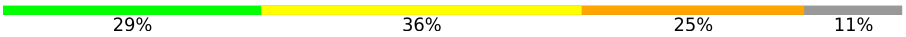
• Molecule 29: 50S ribosomal protein L23

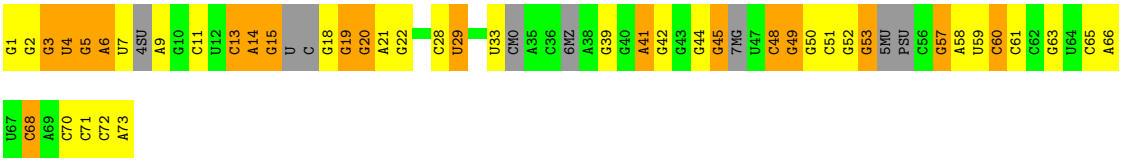
Chain W:



• Molecule 30: E-site tRNA

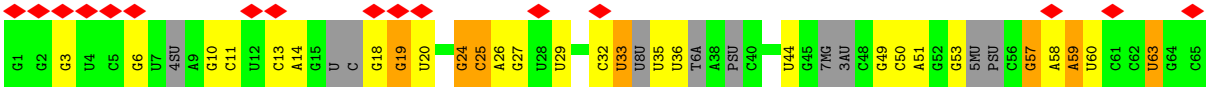
Chain X:

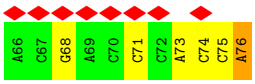




• Molecule 31: A-site tRNA

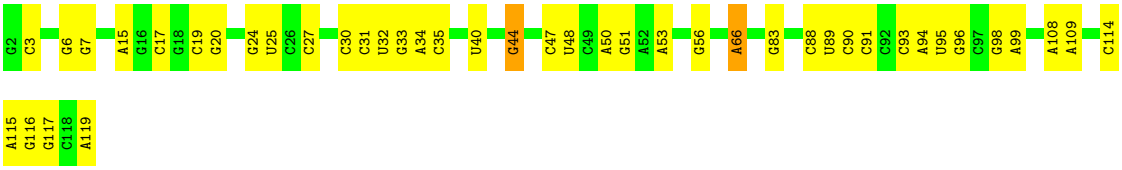
Chain Z:





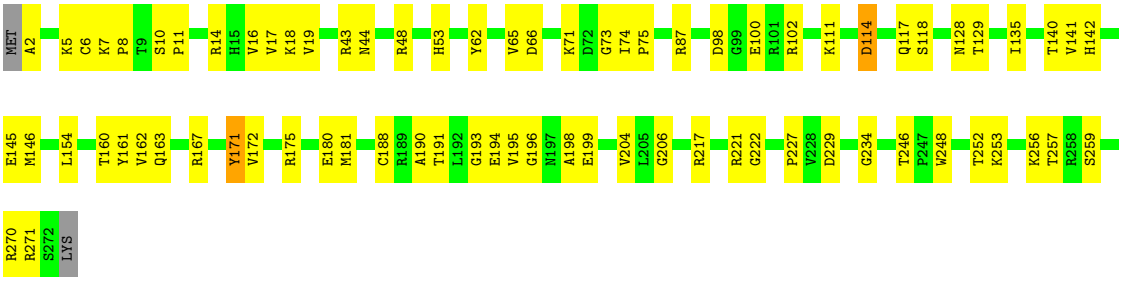
• Molecule 32: 5S ribosomal RNA

Chain a:



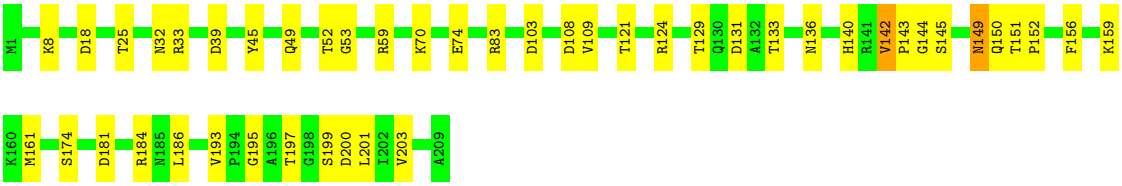
• Molecule 33: 50S ribosomal protein L2

Chain b:



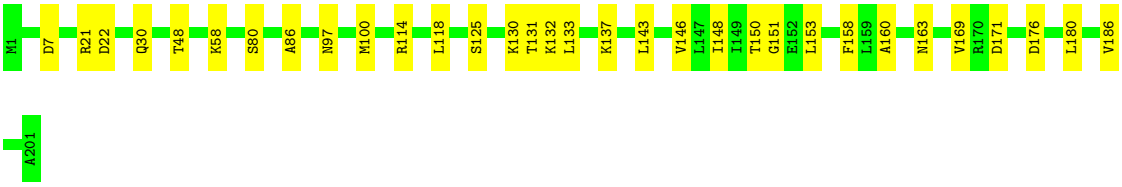
• Molecule 34: 50S ribosomal protein L3

Chain c:



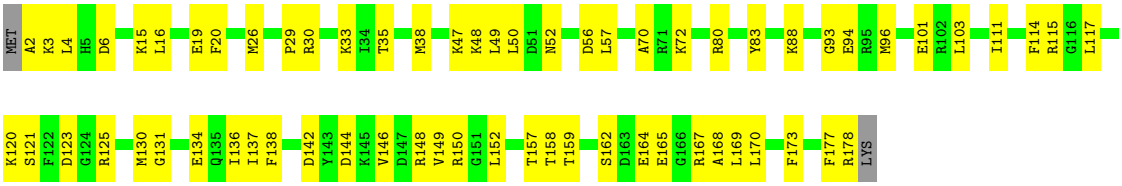
• Molecule 35: 50S ribosomal protein L4

Chain d:



• Molecule 36: 50S ribosomal protein L5

Chain e:

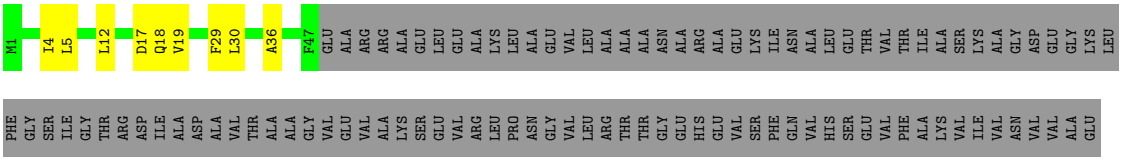


• Molecule 37: 50S ribosomal protein L6

Chain f:

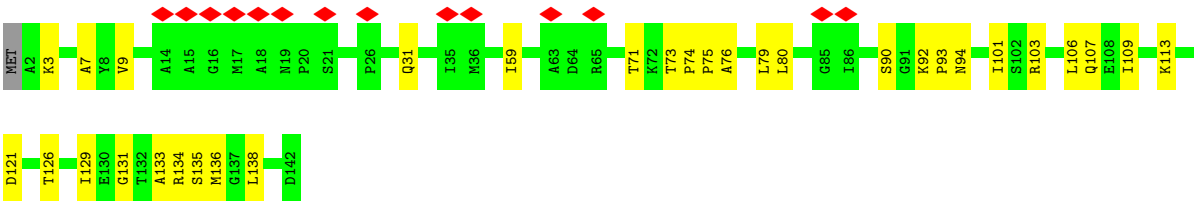
• Molecule 38: 50S ribosomal protein L9

Chain g:



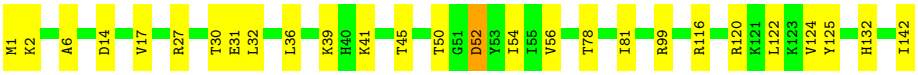
• Molecule 39: 50S ribosomal protein L11

Chain h:



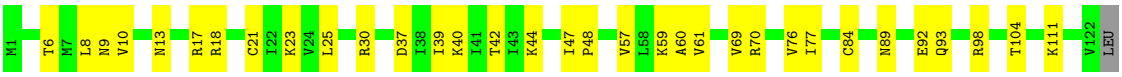
• Molecule 40: 50S ribosomal protein L13

Chain i:



• Molecule 41: 50S ribosomal protein L14

Chain j:

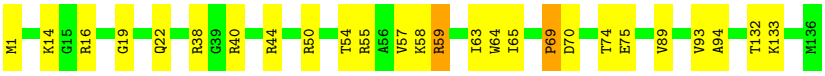


• Molecule 42: 50S ribosomal protein L15

Chain k:

• Molecule 43: 50S ribosomal protein L16

Chain l:

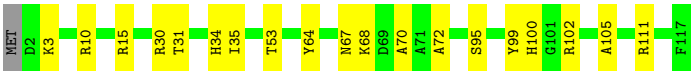


• Molecule 44: 50S ribosomal protein L17

Chain m:

• Molecule 45: 50S ribosomal protein L18

Chain n:



• Molecule 46: 50S ribosomal protein L19

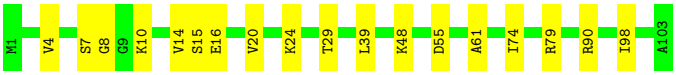
Chain o:

• Molecule 47: 50S ribosomal protein L20

Chain p:

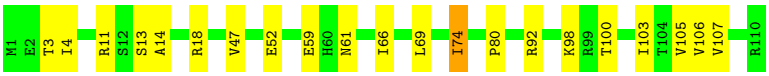
• Molecule 48: 50S ribosomal protein L21

Chain q:



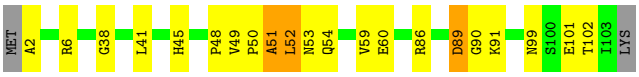
• Molecule 49: 50S ribosomal protein L22

Chain r:



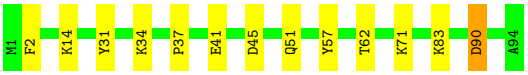
• Molecule 50: 50S ribosomal protein L24

Chain s:



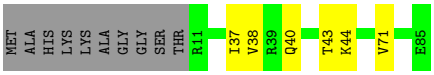
• Molecule 51: 50S ribosomal protein L25

Chain t:



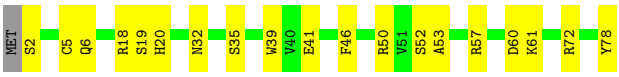
• Molecule 52: 50S ribosomal protein L27

Chain u:



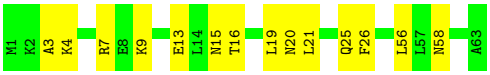
• Molecule 53: 50S ribosomal protein L28

Chain v:



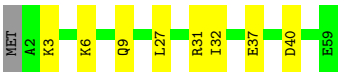
• Molecule 54: 50S ribosomal protein L29

Chain w:



• Molecule 55: 50S ribosomal protein L30

Chain x:



• Molecule 56: P-site tRNA

Chain y: 45% 39% 6% 9%

G1 G2 A3 G7 4SU A9 G10 C13 U16 C17 G17A G18 U19 U20 A21 G22 A26 U29 G30 U33 QUO U35 C36 2MA C38 G39 G45 7MG U47 C48 G49 C50 G51 G52 G53 5MU PSU C56 G57 G64 PSU C66 C67 G68 U69 U70 C71 C72 G73 C74 C75 A76

- Molecule 57: 50S ribosomal protein L33

Chain z: 73% 18% 9%

MET ALA LYS G4 I5 R6 K10 T17 G18 T22 K33 L34 R44 E51 A52 R53 ILE LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54875	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	32.57	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0	0.79	0/380	0.76	0/498
2	1	0.66	0/513	0.86	1/676 (0.1%)
3	2	0.57	0/303	0.66	0/397
4	3	0.25	0/1361	0.58	0/1830
5	5	0.21	0/3426	0.52	0/4605
6	6	0.66	0/450	0.76	0/599
7	A	0.72	0/69796	0.52	0/108888
8	B	0.36	0/36966	0.40	1/57666 (0.0%)
9	C	0.32	0/1735	0.57	0/2338
10	D	0.27	0/1651	0.57	0/2225
11	E	0.27	0/1665	0.61	0/2227
12	F	0.36	0/1118	0.71	2/1504 (0.1%)
13	G	0.29	0/835	0.66	0/1128
14	H	0.24	0/1195	0.54	0/1602
15	I	0.33	0/989	0.55	0/1326
16	J	0.24	0/1034	0.60	0/1375
17	K	0.26	0/796	0.64	0/1077
18	L	0.31	0/893	0.60	0/1205
19	M	0.35	0/969	0.65	0/1300
20	N	0.25	0/892	0.62	1/1193 (0.1%)
21	O	0.25	0/785	0.58	0/1043
22	P	0.34	0/718	0.61	0/959
23	Q	0.30	0/659	0.59	0/884
24	R	0.33	0/657	0.66	0/881
25	S	0.30	0/462	0.64	2/621 (0.3%)
26	T	0.23	0/652	0.50	0/877
27	U	0.31	0/671	0.61	0/888
28	V	0.35	0/430	0.87	0/570
29	W	0.63	0/771	0.76	0/1031
30	X	0.20	0/1551	0.38	0/2404
31	Z	0.23	0/1565	0.37	0/2421
32	a	0.51	0/2828	0.40	0/4410
33	b	0.70	0/2121	0.72	0/2852
34	c	0.67	0/1586	0.69	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	d	0.69	0/1571	0.65	0/2113
36	e	0.31	0/1434	0.56	0/1926
37	f	0.43	0/1343	0.56	0/1816
38	g	0.41	0/364	0.74	0/490
39	h	0.28	0/1046	0.65	1/1410 (0.1%)
40	i	0.71	0/1152	0.68	2/1551 (0.1%)
41	j	0.65	0/947	0.77	0/1268
42	k	0.66	0/1054	0.82	0/1403
43	l	0.63	0/1093	0.73	0/1460
44	m	0.71	0/973	0.86	0/1301
45	n	0.45	0/902	0.58	0/1209
46	o	0.61	0/929	0.69	0/1242
47	p	0.78	0/960	0.71	0/1278
48	q	0.64	0/829	0.68	0/1107
49	r	0.71	0/864	0.70	0/1156
50	s	0.56	0/787	0.69	0/1051
51	t	0.53	0/766	0.54	0/1025
52	u	0.63	0/576	0.61	0/762
53	v	0.67	0/635	0.66	0/848
54	w	0.56	0/510	0.65	0/677
55	x	0.65	0/453	0.71	0/605
56	y	0.21	0/1664	0.35	0/2577
57	z	0.41	0/416	0.57	0/554
All	All	0.57	0/163691	0.53	10/244463 (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
2	1	0	1
3	2	0	1
9	C	0	1
11	E	0	2
12	F	0	2
13	G	0	1
16	J	0	2
17	K	0	1
19	M	0	1
20	N	0	1
23	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	R	0	2
28	V	0	2
29	W	0	1
34	c	0	1
37	f	0	2
41	j	0	1
42	k	0	1
43	l	0	1
50	s	0	3
All	All	0	28

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	S	67	LEU	CA-C-N	7.08	138.87	122.31
25	S	67	LEU	C-N-CA	7.08	138.87	122.31
39	h	109	ILE	N-CA-C	-6.89	105.78	111.91
2	1	32	ILE	N-CA-C	6.32	122.49	109.34
12	F	77	ASN	CA-C-N	5.89	132.78	121.54

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	31	HIS	Peptide
3	2	20	ASP	Peptide
9	C	84	ALA	Peptide
11	E	173	VAL	Peptide
11	E	20	PHE	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	377	0	418	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1	504	0	572	13	0
3	2	302	0	343	13	0
4	3	1346	0	1394	31	0
5	5	3386	0	3403	34	0
6	6	444	0	458	7	0
7	A	62317	0	31343	644	0
8	B	33015	0	16617	383	0
9	C	1704	0	1732	26	0
10	D	1624	0	1696	34	0
11	E	1643	0	1707	59	0
12	F	1105	0	1148	29	0
13	G	817	0	808	18	0
14	H	1181	0	1238	34	0
15	I	979	0	1031	33	0
16	J	1022	0	1070	33	0
17	K	786	0	828	22	0
18	L	877	0	887	22	0
19	M	955	0	1016	23	0
20	N	883	0	941	26	0
21	O	774	0	824	33	0
22	P	710	0	728	13	0
23	Q	649	0	666	18	0
24	R	648	0	691	25	0
25	S	455	0	478	15	0
26	T	637	0	665	13	0
27	U	665	0	714	17	0
28	V	425	0	449	9	0
29	W	764	0	829	19	0
30	X	1392	0	714	24	0
31	Z	1406	0	722	25	0
32	a	2529	0	1281	17	0
33	b	2082	0	2154	50	0
34	c	1565	0	1616	33	0
35	d	1552	0	1619	21	0
36	e	1410	0	1444	47	0
37	f	1323	0	1371	18	0
38	g	359	0	381	6	0
39	h	1032	0	1085	22	0
40	i	1129	0	1162	18	0
41	j	938	0	1012	22	0
42	k	1045	0	1117	18	0
43	l	1074	0	1157	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	m	960	0	1000	18	0
45	n	892	0	923	16	0
46	o	917	0	962	21	0
47	p	947	0	1019	19	0
48	q	816	0	839	14	0
49	r	857	0	922	14	0
50	s	779	0	831	12	0
51	t	753	0	780	10	0
52	u	569	0	581	3	0
53	v	625	0	652	14	0
54	w	509	0	543	13	0
55	x	449	0	488	5	0
56	y	1496	0	764	14	0
57	z	409	0	440	7	0
All	All	150808	0	102273	1872	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 1872 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)
7:A:2506:U:O2'	7:A:2507:C:O4'	1.56	1.19
8:B:98:A:H2'	8:B:99:C:C6	1.85	1.11
7:A:2572:A:N6	34:c:150:GLN:OE1	1.93	1.02
7:A:2508:G:OP1	31:Z:76:A:O5'	1.82	0.95
7:A:2507:C:O2'	31:Z:76:A:C1'	2.14	0.95

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	
1	0	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
2	1	62/65 (95%)	51 (82%)	9 (14%)	2 (3%)	3	24
3	2	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
4	3	166/169 (98%)	145 (87%)	21 (13%)	0	100	100
5	5	430/432 (100%)	387 (90%)	43 (10%)	0	100	100
6	6	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	6	34
9	C	216/241 (90%)	178 (82%)	38 (18%)	0	100	100
10	D	204/233 (88%)	176 (86%)	28 (14%)	0	100	100
11	E	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
12	F	148/167 (89%)	114 (77%)	34 (23%)	0	100	100
13	G	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
14	H	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
15	I	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
16	J	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
17	K	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
18	L	115/129 (89%)	92 (80%)	23 (20%)	0	100	100
19	M	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
20	N	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	35
21	O	92/101 (91%)	81 (88%)	11 (12%)	0	100	100
22	P	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
23	Q	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
24	R	78/84 (93%)	58 (74%)	19 (24%)	1 (1%)	9	41
25	S	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
26	T	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
27	U	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	42
28	V	49/71 (69%)	37 (76%)	12 (24%)	0	100	100
29	W	94/100 (94%)	80 (85%)	14 (15%)	0	100	100
33	b	269/273 (98%)	230 (86%)	39 (14%)	0	100	100
34	c	207/209 (99%)	187 (90%)	18 (9%)	2 (1%)	12	46
35	d	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
36	e	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
37	f	174/177 (98%)	159 (91%)	13 (8%)	2 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	g	45/149 (30%)	34 (76%)	11 (24%)	0	100	100
39	h	139/142 (98%)	115 (83%)	24 (17%)	0	100	100
40	i	140/142 (99%)	126 (90%)	14 (10%)	0	100	100
41	j	120/123 (98%)	89 (74%)	30 (25%)	1 (1%)	16	52
42	k	141/144 (98%)	121 (86%)	19 (14%)	1 (1%)	18	55
43	l	134/136 (98%)	118 (88%)	13 (10%)	3 (2%)	5	31
44	m	118/127 (93%)	99 (84%)	17 (14%)	2 (2%)	7	36
45	n	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
46	o	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
47	p	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
48	q	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
49	r	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
50	s	100/104 (96%)	81 (81%)	17 (17%)	2 (2%)	6	33
51	t	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
52	u	73/85 (86%)	62 (85%)	11 (15%)	0	100	100
53	v	75/78 (96%)	64 (85%)	11 (15%)	0	100	100
54	w	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
55	x	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
57	z	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
All	All	6114/6586 (93%)	5314 (87%)	779 (13%)	21 (0%)	37	70

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	32	ILE
20	N	67	GLY
37	f	48	ASN
2	1	33	LEU
3	2	21	GLY

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	
1	0	38/38 (100%)	37 (97%)	1 (3%)	40	61
2	1	51/52 (98%)	50 (98%)	1 (2%)	48	66
3	2	34/34 (100%)	34 (100%)	0	100	100
4	3	148/149 (99%)	148 (100%)	0	100	100
5	5	359/359 (100%)	359 (100%)	0	100	100
6	6	47/48 (98%)	46 (98%)	1 (2%)	47	65
9	C	180/199 (90%)	180 (100%)	0	100	100
10	D	170/190 (90%)	166 (98%)	4 (2%)	43	63
11	E	172/173 (99%)	171 (99%)	1 (1%)	78	80
12	F	113/126 (90%)	113 (100%)	0	100	100
13	G	87/116 (75%)	86 (99%)	1 (1%)	65	74
14	H	124/147 (84%)	124 (100%)	0	100	100
15	I	104/105 (99%)	103 (99%)	1 (1%)	68	76
16	J	105/107 (98%)	105 (100%)	0	100	100
17	K	86/90 (96%)	85 (99%)	1 (1%)	63	73
18	L	90/99 (91%)	90 (100%)	0	100	100
19	M	103/104 (99%)	103 (100%)	0	100	100
20	N	92/96 (96%)	90 (98%)	2 (2%)	45	64
21	O	79/84 (94%)	79 (100%)	0	100	100
22	P	75/77 (97%)	75 (100%)	0	100	100
23	Q	65/65 (100%)	65 (100%)	0	100	100
24	R	74/78 (95%)	74 (100%)	0	100	100
25	S	48/65 (74%)	48 (100%)	0	100	100
26	T	70/79 (89%)	70 (100%)	0	100	100
27	U	65/66 (98%)	64 (98%)	1 (2%)	57	70
28	V	44/61 (72%)	43 (98%)	1 (2%)	44	64
29	W	83/84 (99%)	82 (99%)	1 (1%)	63	73
33	b	216/218 (99%)	210 (97%)	6 (3%)	38	59
34	c	164/164 (100%)	160 (98%)	4 (2%)	43	63
35	d	165/165 (100%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	e	148/150 (99%)	146 (99%)	2 (1%)	59	71
37	f	137/138 (99%)	136 (99%)	1 (1%)	76	79
38	g	38/114 (33%)	38 (100%)	0	100	100
39	h	109/110 (99%)	108 (99%)	1 (1%)	70	76
40	i	116/116 (100%)	113 (97%)	3 (3%)	40	61
41	j	103/104 (99%)	101 (98%)	2 (2%)	50	67
42	k	102/103 (99%)	100 (98%)	2 (2%)	48	66
43	l	109/109 (100%)	108 (99%)	1 (1%)	70	76
44	m	100/103 (97%)	98 (98%)	2 (2%)	48	66
45	n	86/87 (99%)	86 (100%)	0	100	100
46	o	99/100 (99%)	99 (100%)	0	100	100
47	p	89/90 (99%)	88 (99%)	1 (1%)	65	74
48	q	84/84 (100%)	84 (100%)	0	100	100
49	r	93/93 (100%)	92 (99%)	1 (1%)	65	74
50	s	83/85 (98%)	82 (99%)	1 (1%)	63	73
51	t	78/78 (100%)	77 (99%)	1 (1%)	61	72
52	u	56/63 (89%)	55 (98%)	1 (2%)	51	67
53	v	67/68 (98%)	67 (100%)	0	100	100
54	w	55/55 (100%)	55 (100%)	0	100	100
55	x	48/49 (98%)	48 (100%)	0	100	100
57	z	45/49 (92%)	45 (100%)	0	100	100
All	All	5096/5386 (95%)	5051 (99%)	45 (1%)	68	76

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	f	98	VAL
42	k	89	VAL
39	h	71	THR
40	i	52	ASP
43	l	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
37	f	143	GLN
45	n	43	ASN
39	h	31	GLN
42	k	35	HIS
49	r	7	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	58/73 (79%)	30 (51%)	0
31	Z	58/76 (76%)	24 (41%)	1 (1%)
32	a	117/118 (99%)	21 (17%)	0
56	y	63/77 (81%)	19 (30%)	0
7	A	2902/2903 (99%)	740 (25%)	13 (0%)
8	B	1538/1539 (99%)	427 (27%)	3 (0%)
All	All	4736/4786 (98%)	1261 (26%)	17 (0%)

5 of 1261 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	10	A
7	A	14	A
7	A	23	G
7	A	34	U
7	A	42	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	B	428	G
31	Z	13	C
7	A	1730	C
7	A	1904	G
7	A	1913	A

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)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

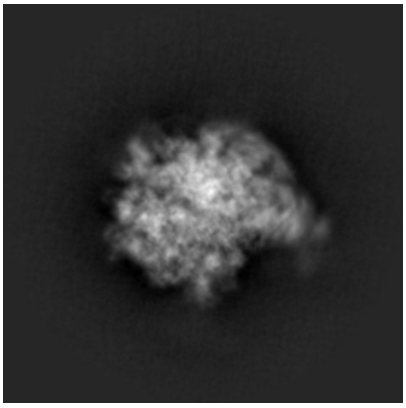
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-30611. These allow visual inspection of the internal detail of the map and identification of artifacts.

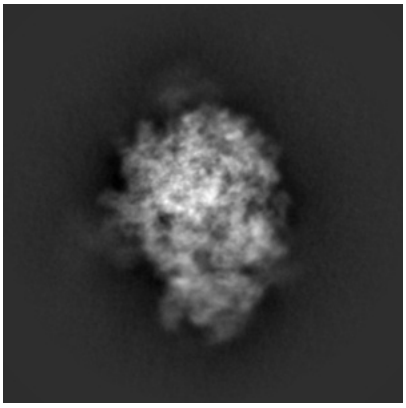
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

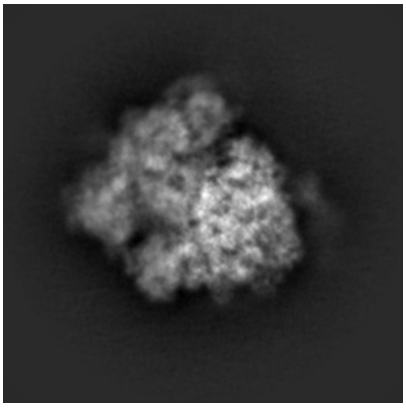
6.1.1 Primary map



X



Y

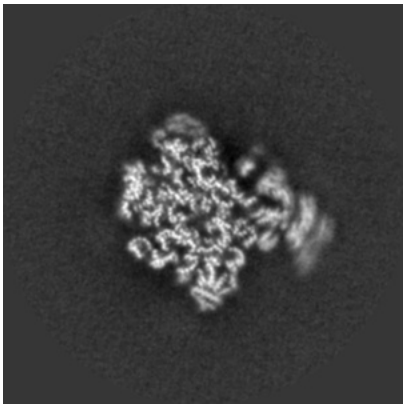


Z

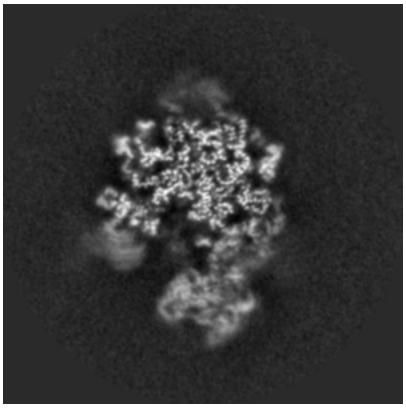
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

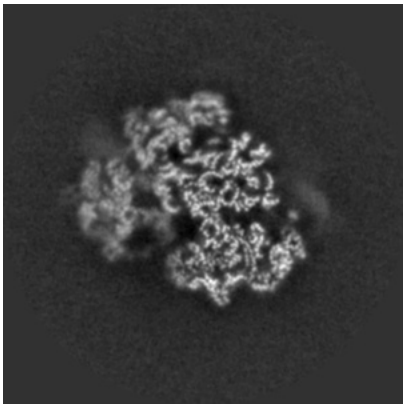
6.2.1 Primary map



X Index: 160



Y Index: 160

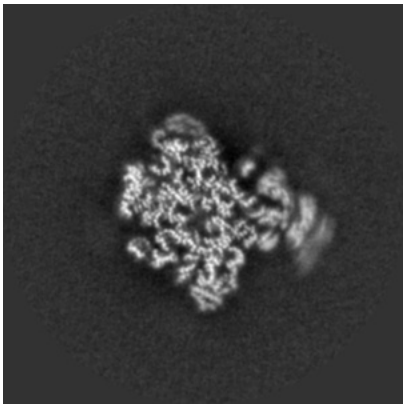


Z Index: 160

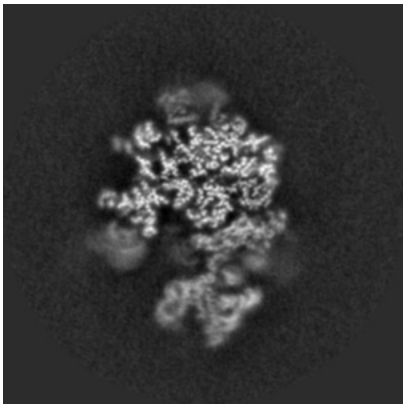
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

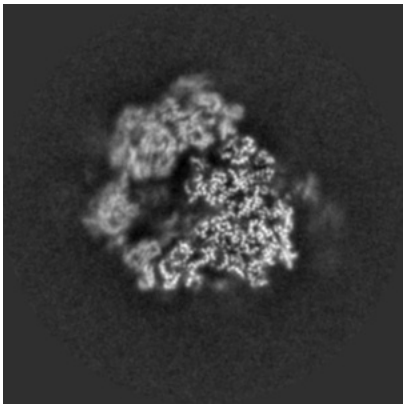
6.3.1 Primary map



X Index: 161



Y Index: 165

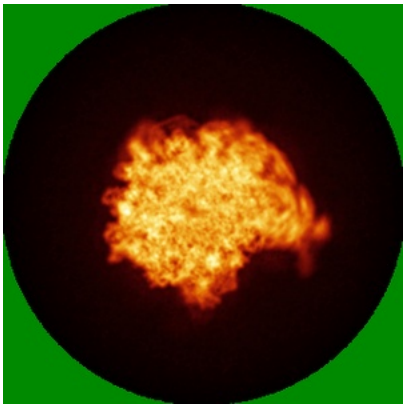


Z Index: 147

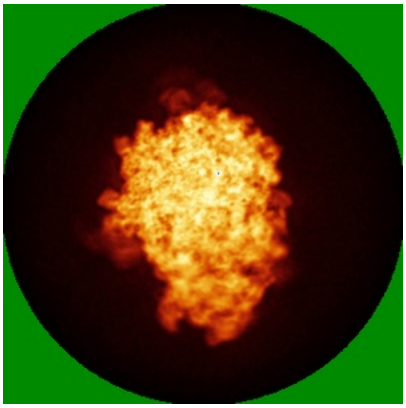
The images above show the largest variance slices of the map in three orthogonal directions.

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

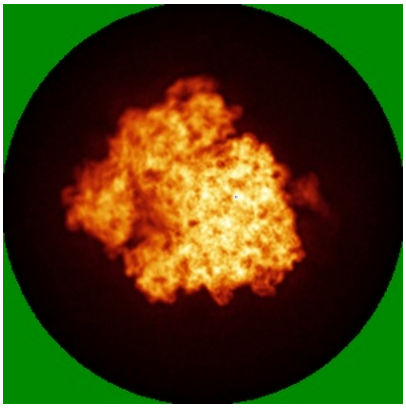
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

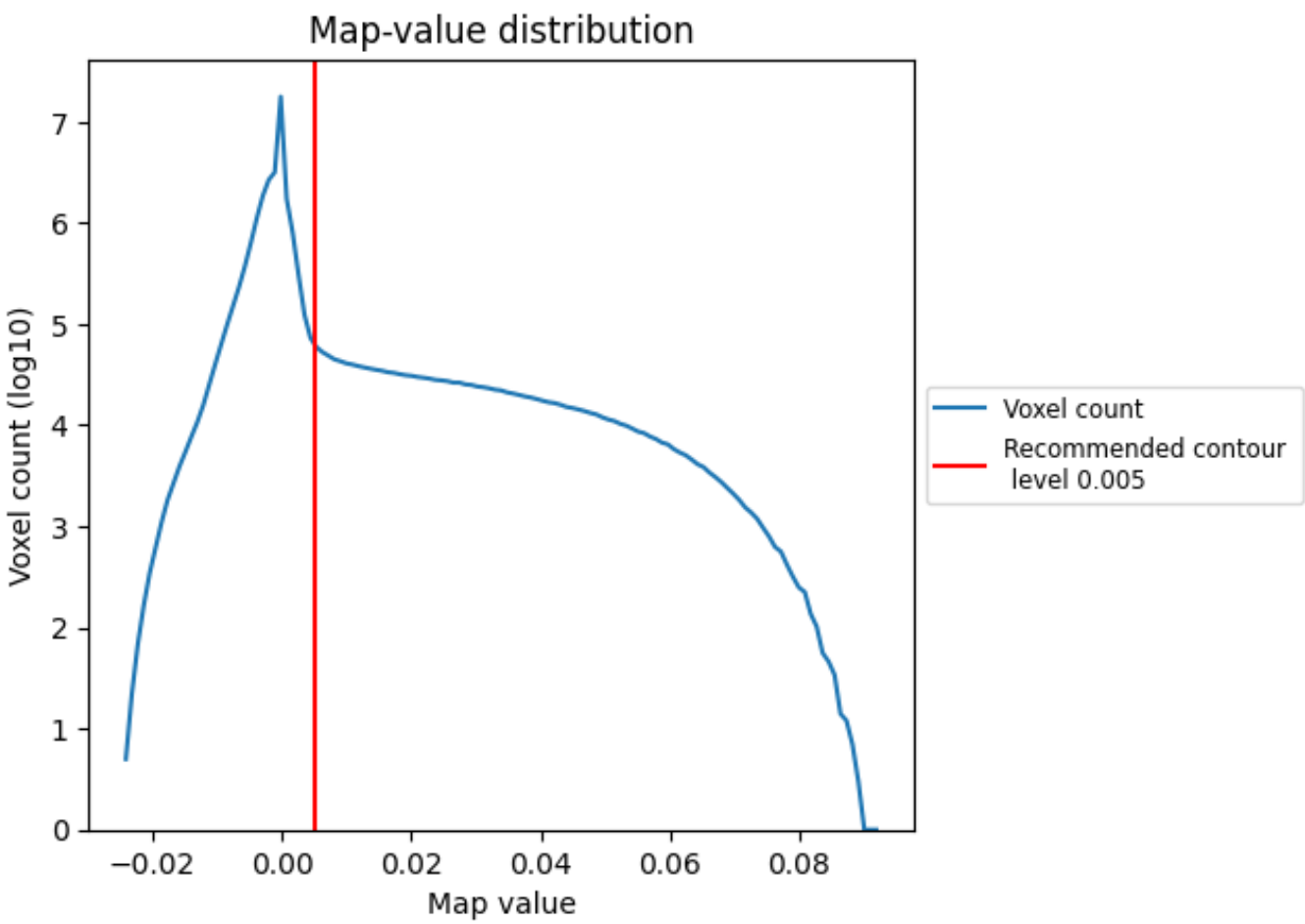
6.6 Mask visualisation (i)

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

7 Map analysis (i)

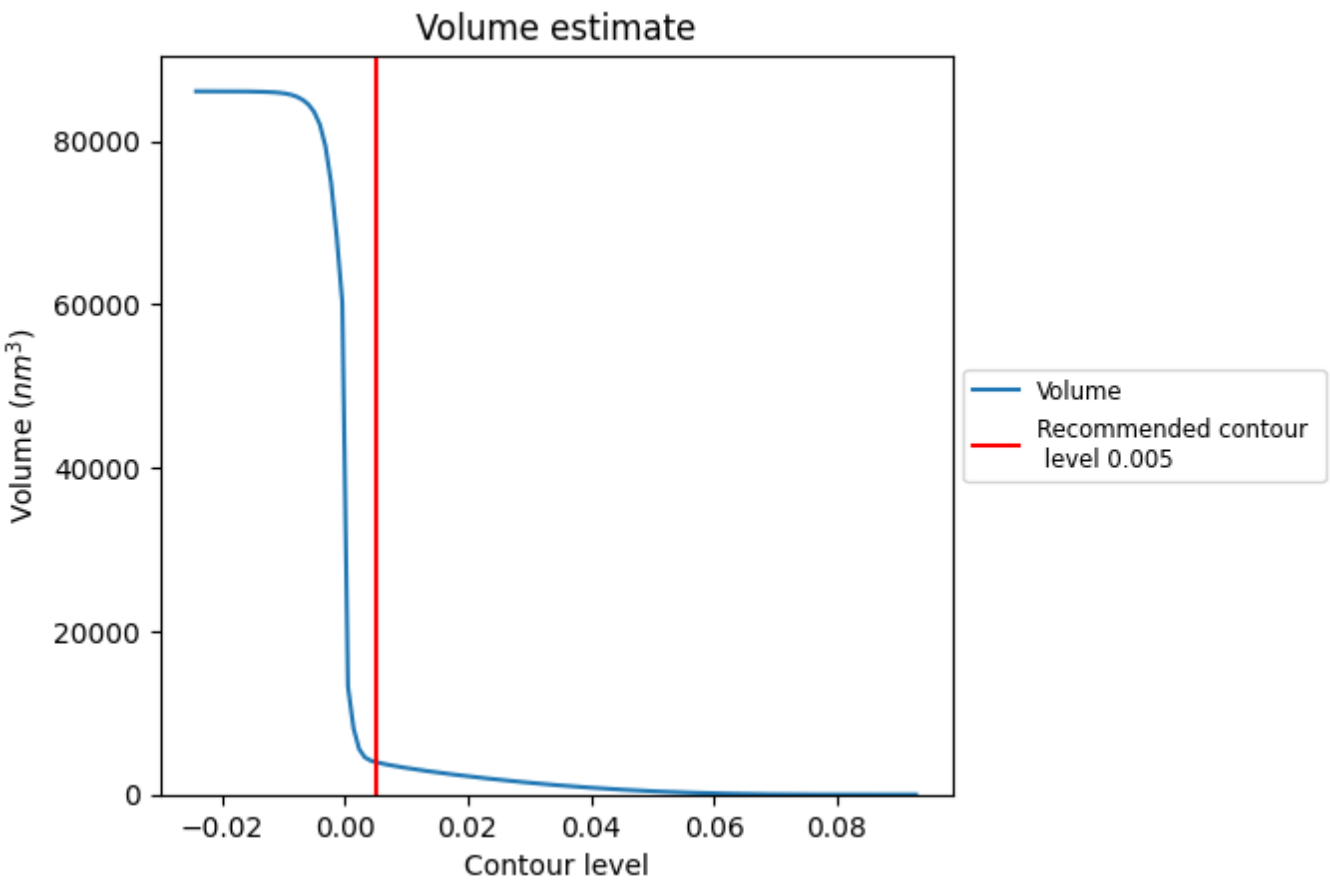
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

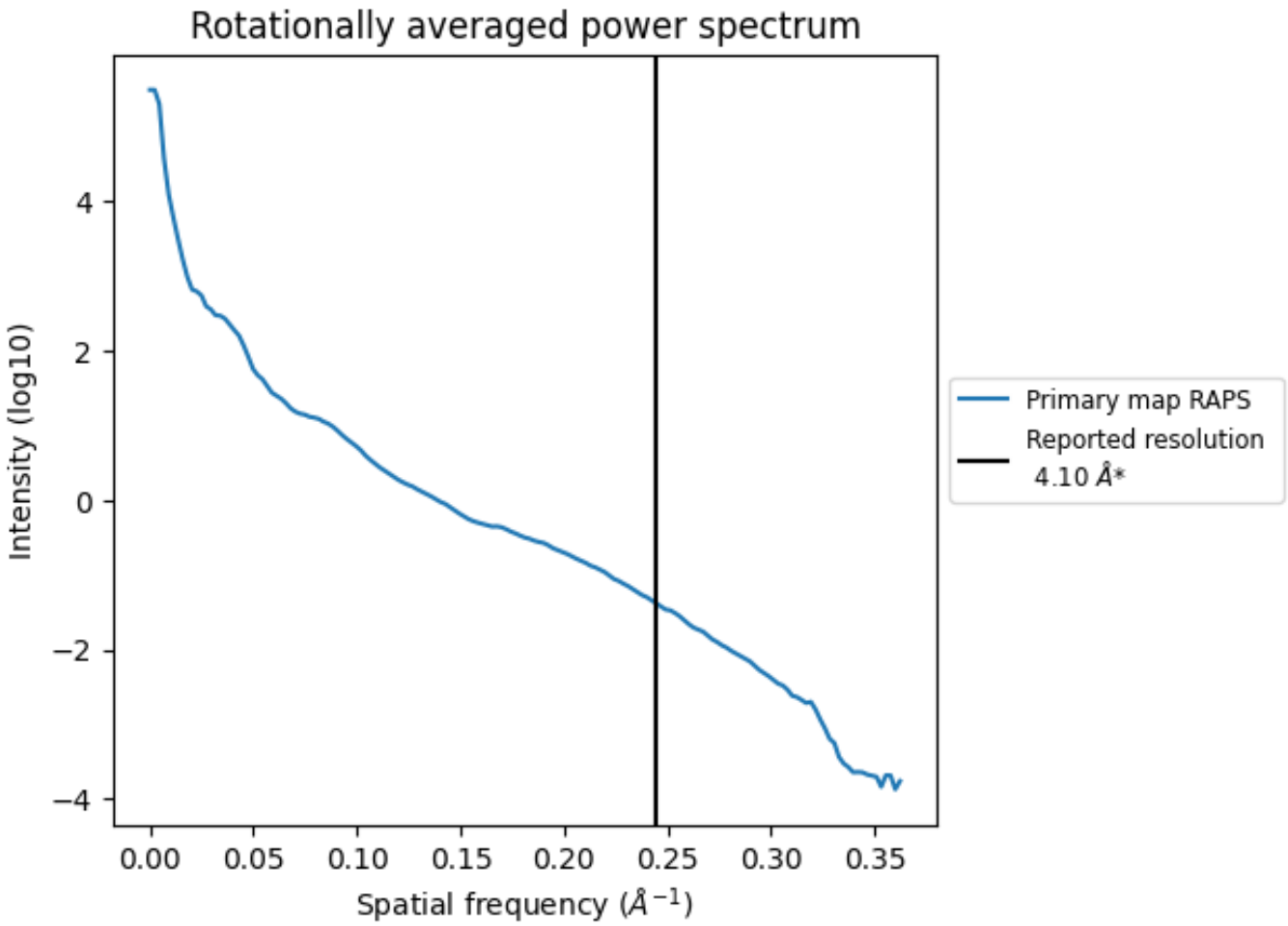
7.2 Volume estimate (i)



The volume at the recommended contour level is 3991 nm^3; this corresponds to an approximate mass of 3605 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)

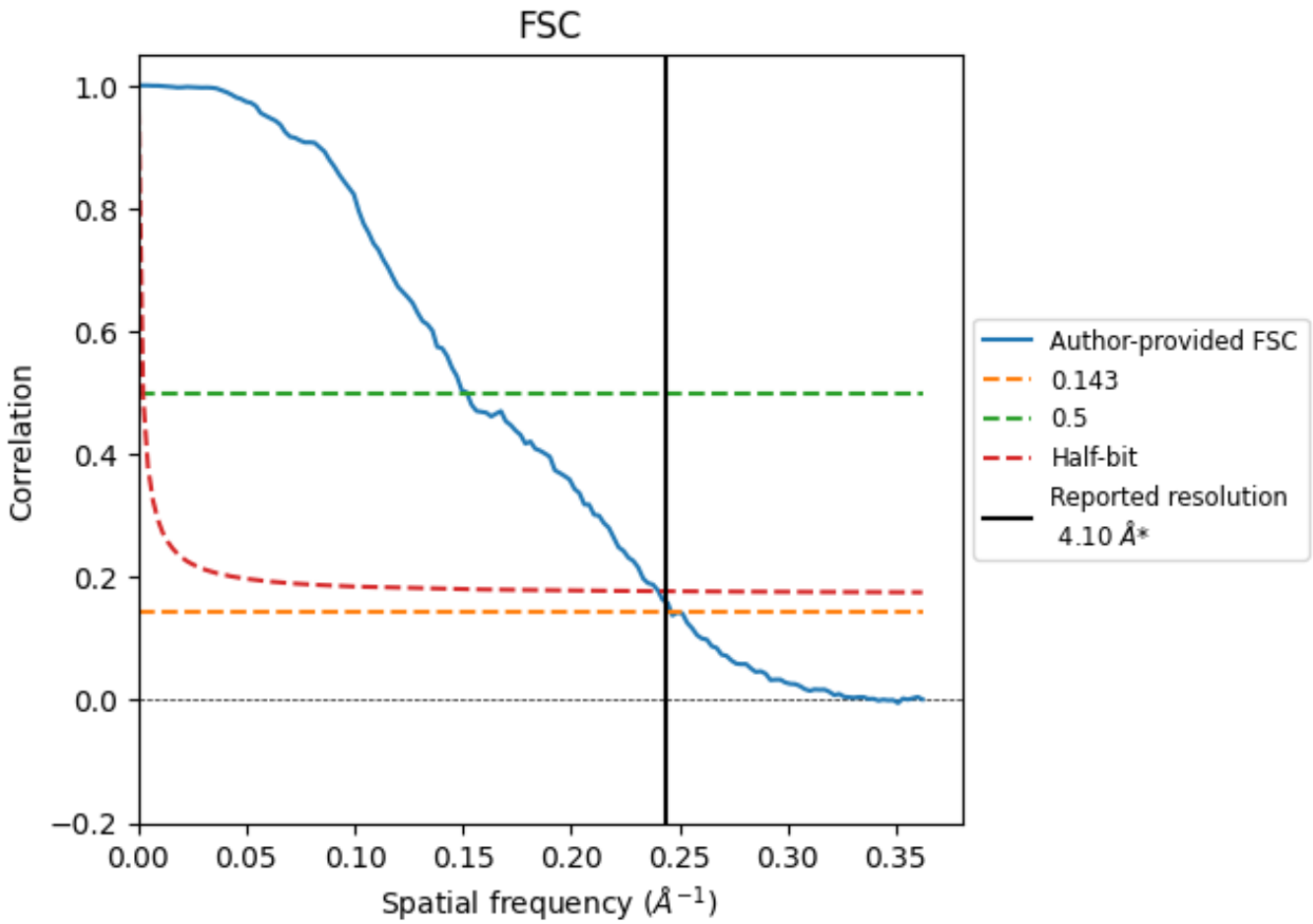


*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8 Fourier-Shell correlation (i)

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 (i)



*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8.2 Resolution estimates (i)

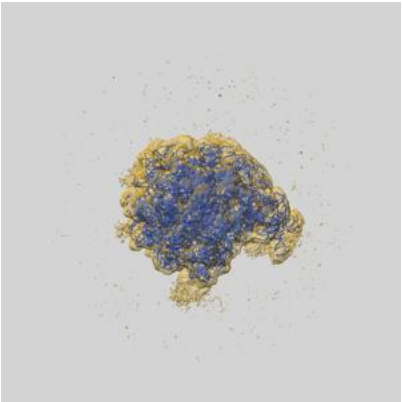
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.06	6.59	4.16
Unmasked-calculated*	-	-	-

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

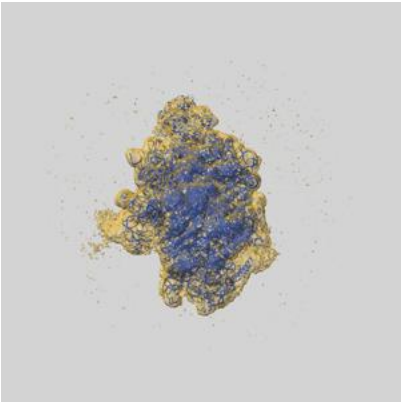
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-30611 and PDB model 7D80. Per-residue inclusion information can be found in section 3 on page 15.

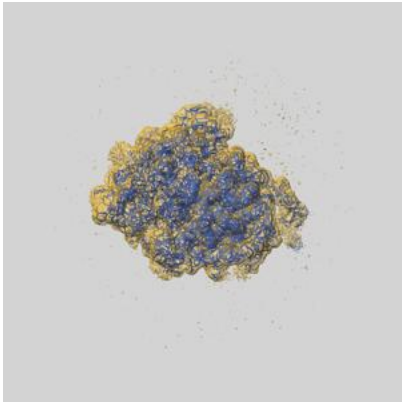
9.1 Map-model overlay (i)



X



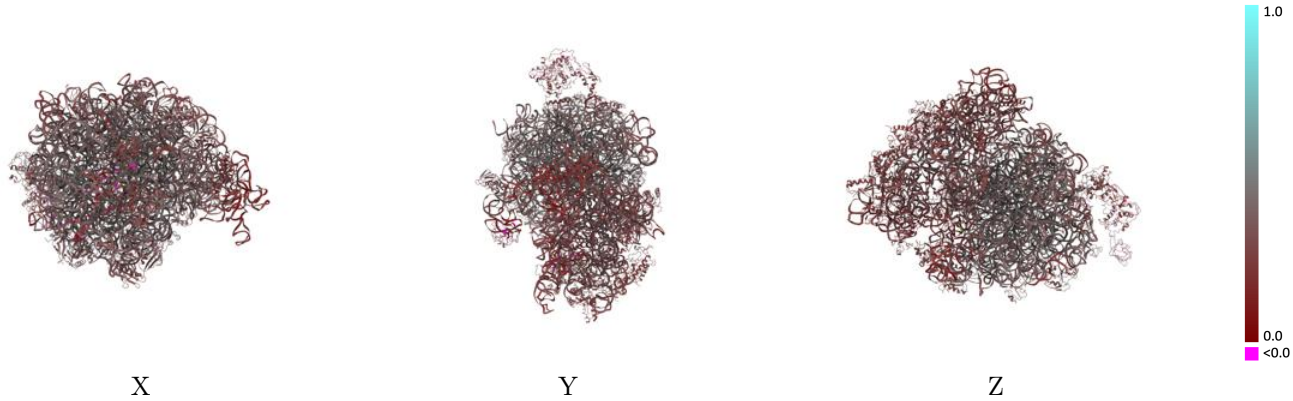
Y



Z

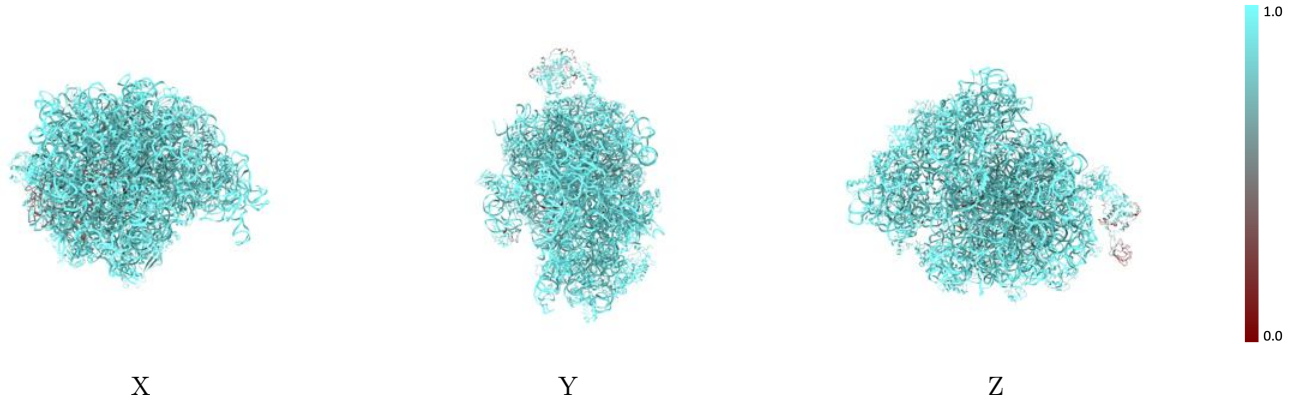
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



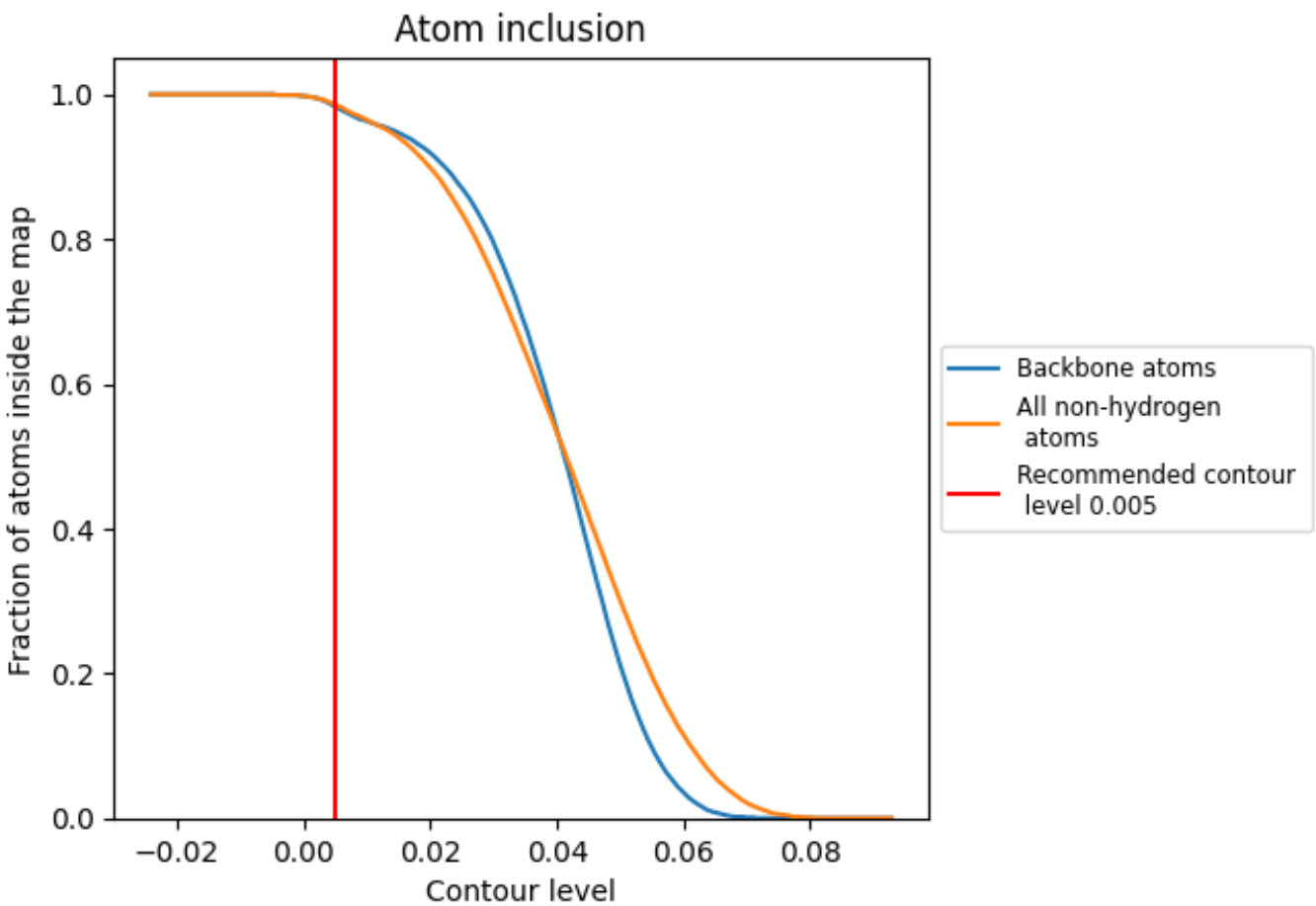
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9860	0.3390
0	0.9750	0.3790
1	0.9940	0.3960
2	1.0000	0.3610
3	0.9890	0.2710
5	0.6750	0.2400
6	1.0000	0.3920
A	0.9990	0.3870
B	1.0000	0.3000
C	1.0000	0.2690
D	0.9980	0.2850
E	1.0000	0.2120
F	0.9980	0.3040
G	0.9940	0.2860
H	0.9990	0.2410
I	0.9990	0.2790
J	1.0000	0.2260
K	0.9970	0.2560
L	0.9970	0.2910
M	0.9940	0.2620
N	0.9980	0.2210
O	1.0000	0.2350
P	0.9960	0.2560
Q	0.9980	0.2510
R	1.0000	0.2680
S	1.0000	0.3140
T	0.9980	0.2050
U	0.9970	0.2250
V	0.9930	0.2600
W	0.9950	0.3610
X	0.9980	0.2180
Z	0.5280	0.2640
a	1.0000	0.3520
b	0.9910	0.4030
c	0.9940	0.4000

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Chain	Atom inclusion	Q-score
d	0.9970	0.3740
e	0.9990	0.2550
f	1.0000	0.3330
g	1.0000	0.3360
h	0.8800	0.1720
i	0.9960	0.3910
j	0.9910	0.4010
k	0.9950	0.3920
l	0.9970	0.3940
m	0.9980	0.3800
n	1.0000	0.3220
o	0.9930	0.3830
p	0.9990	0.3670
q	0.9960	0.4020
r	0.9920	0.3850
s	0.9960	0.3580
t	1.0000	0.3620
u	0.9980	0.4010
v	0.9970	0.3730
w	1.0000	0.2840
x	0.9950	0.3850
y	0.9700	0.2890
z	0.9880	0.3580