wwPDB EM Validation Summary Report (i)

Sep 16, 2026 – 01:23 PM JST

PDB ID	:	7Y7D / pdb_00007y7d
EMDB ID	:	EMD-33661
Title	:	Structure of the Bacterial Ribosome with human tRNA Asp(Q34) and mRNA(GAU)
Authors	:	Ishiguro, K.; Yokoyama, T.; Shirouzu, M.; Suzuki, T.
Deposited on	:	2022-06-22
Resolution	:	2.58 Å(reported)
Based on initial model	:	7K00

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

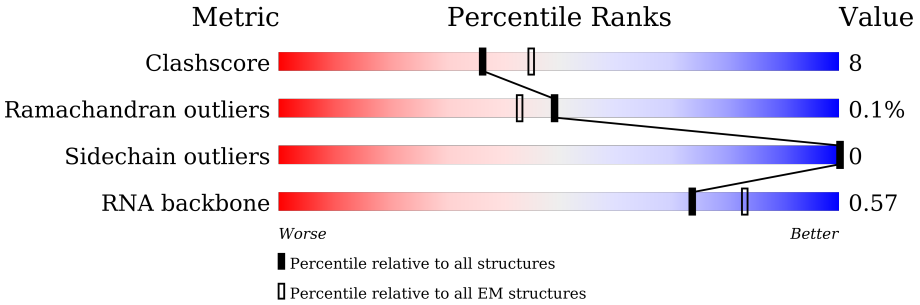
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

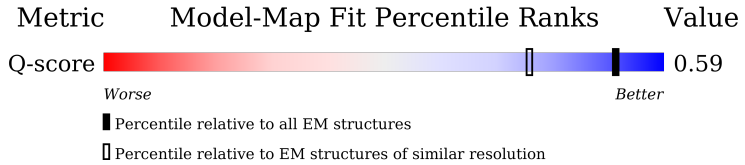
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.58 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	7675 (2.08 - 3.08)

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	A	1542	31% 57% 36% 5% •
2	B	241	93% 65% 28% 7%
3	C	233	55% 74% 14% 12%

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Mol	Chain	Length	Quality of chain
4	D	206	92% 68% 32%
5	E	167	40% 69% 25% 7%
6	F	135	67% 41% 35% 24%
7	G	179	72% 62% 23% 15%
8	H	130	60% 78% 21%
9	I	130	68% 71% 27%
10	J	103	74% 68% 27% 5%
11	K	129	53% 62% 29% 9%
12	L	124	37% 84% 15%
13	M	118	77% 69% 26%
14	N	101	59% 71% 28%
15	O	89	60% 73% 26%
16	P	82	88% 65% 34%
17	Q	84	71% 64% 30% 6%
18	R	75	59% 59% 29% 12%
19	S	92	65% 73% 18% 9%
20	T	87	93% 82% 17%
21	U	71	94% 80% 18%
22	a	2904	13% 62% 30% 5%
23	b	120	37% 67% 31%
24	c	273	14% 84% 16%
25	d	209	29% 83% 17%
26	e	201	49% 82% 18%
27	f	179	84% 73% 26%
28	g	177	94% 65% 34%

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Mol	Chain	Length	Quality of chain
29	h	149	26% 19% 9% 72%
30	i	142	23% 85% 15%
31	j	123	23% 83% 17%
32	k	144	34% 77% 23%
33	l	136	15% 78% 22%
34	m	127	9% 75% 18% 7%
35	n	117	74% 79% 21%
36	o	115	37% 83% 17%
37	p	118	19% 81% 19%
38	q	103	45% 82% 18%
39	r	110	12% 91% 9%
40	s	100	45% 64% 29% 7%
41	t	104	64% 77% 21%
42	u	94	66% 69% 31%
43	v	85	24% 86% 13%
44	w	78	31% 79% 19%
45	x	63	84% 83% 16%
46	y	59	32% 76% 22%
47	z	57	33% 77% 21%
48	0	55	35% 76% 16% 7%
49	1	46	9% 96%
50	2	65	5% 82% 14%
51	3	38	24% 71% 29%
52	4	70	83% 57% 29% 14%
53	X	35	17% 37% 63%

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Mol	Chain	Length	Quality of chain
54	Z	77	47% 52% 36% 10% •
55	V	75	44% 48% 39% 9% •

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 141917 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1520	32634	14562	5991	10561	1520	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	224	1753	1109	315	321	8	0	0

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	156	1152	717	217	212	6	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	103	839	530	151	151	7	0	0

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	153	1203	750	231	218	4	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	117	877	540	173	161	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	123	957	591	196	165	5	0	0

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	115	891	552	179	157	3	0	0

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	100	805	499	164	139	3	0	0

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	88	714	439	144	130	1	0	0

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	81	643	403	127	112	1	0	0

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	79	641	406	120	112	3	0	0

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	66	544	345	102	96	1	0	0

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	84	668	427	127	112	2	0	0

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	86	670	414	138	115	3	0	0

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	70	589	366	125	97	1	0	0

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	a	2753	59130	26384	10897	19096	2753	0	0

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
23	b	119	2549	1135	466	829	119	0	0

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	d	209	1566	980	288	294	4	0	0

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	h	41	303	194	54	54	1	0	0

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	j	123	946	593	181	166	6	0	0

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	k	144	1053	654	207	190	2	0	0

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	l	136	1075	686	205	177	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	m	118	945	585	194	161	5	0	0

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	s	93	738	466	139	131	2	0	0

- Molecule 41 is a protein called 50S ribosomal protein L24.

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

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	v	84	628	388	126	113	1	0	0

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	x	62	501	308	98	94	1	0	0

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	0	51	417	269	76	72	0	0

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	1	46	377	228	90	57	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	2	64	504	323	105	74	2	0	0

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	3	38	302	185	65	48	4	0	0

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	4	60	480	299	90	85	6	0	0

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	X	13	279	125	52	89	13	0	0

- Molecule 54 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
54	Z	77	1645	734	297	536	77	1	0	0

- Molecule 55 is a RNA chain called A-site tRNA-Asp.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
55	V	75	1612	726	283	529	74	0	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

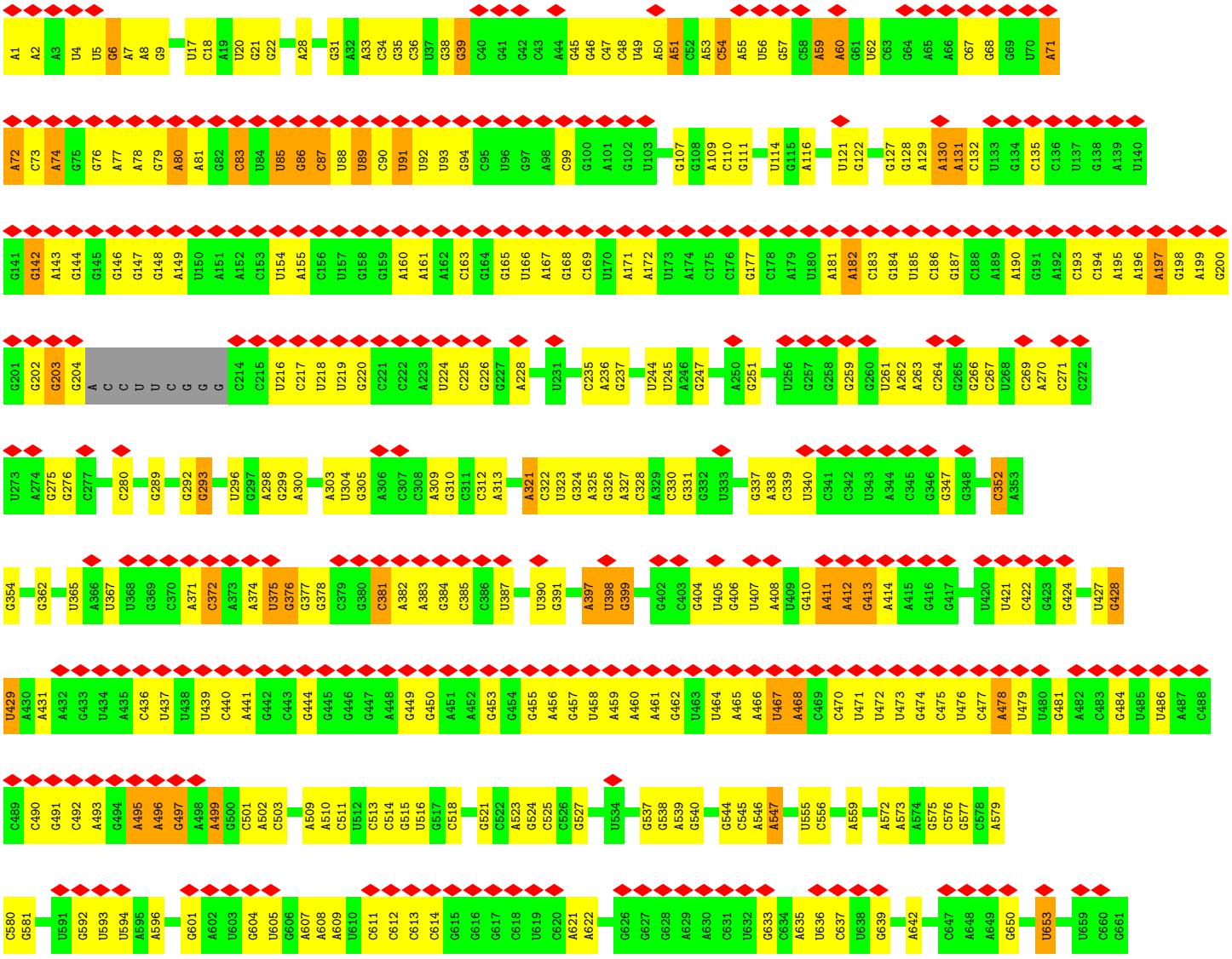
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
56	A	58	58	58	0
56	I	1	1	1	0
56	a	191	191	191	0
56	b	2	2	2	0
56	c	1	1	1	0
56	z	1	1	1	0
56	Z	2	2	2	0
56	V	2	2	2	0

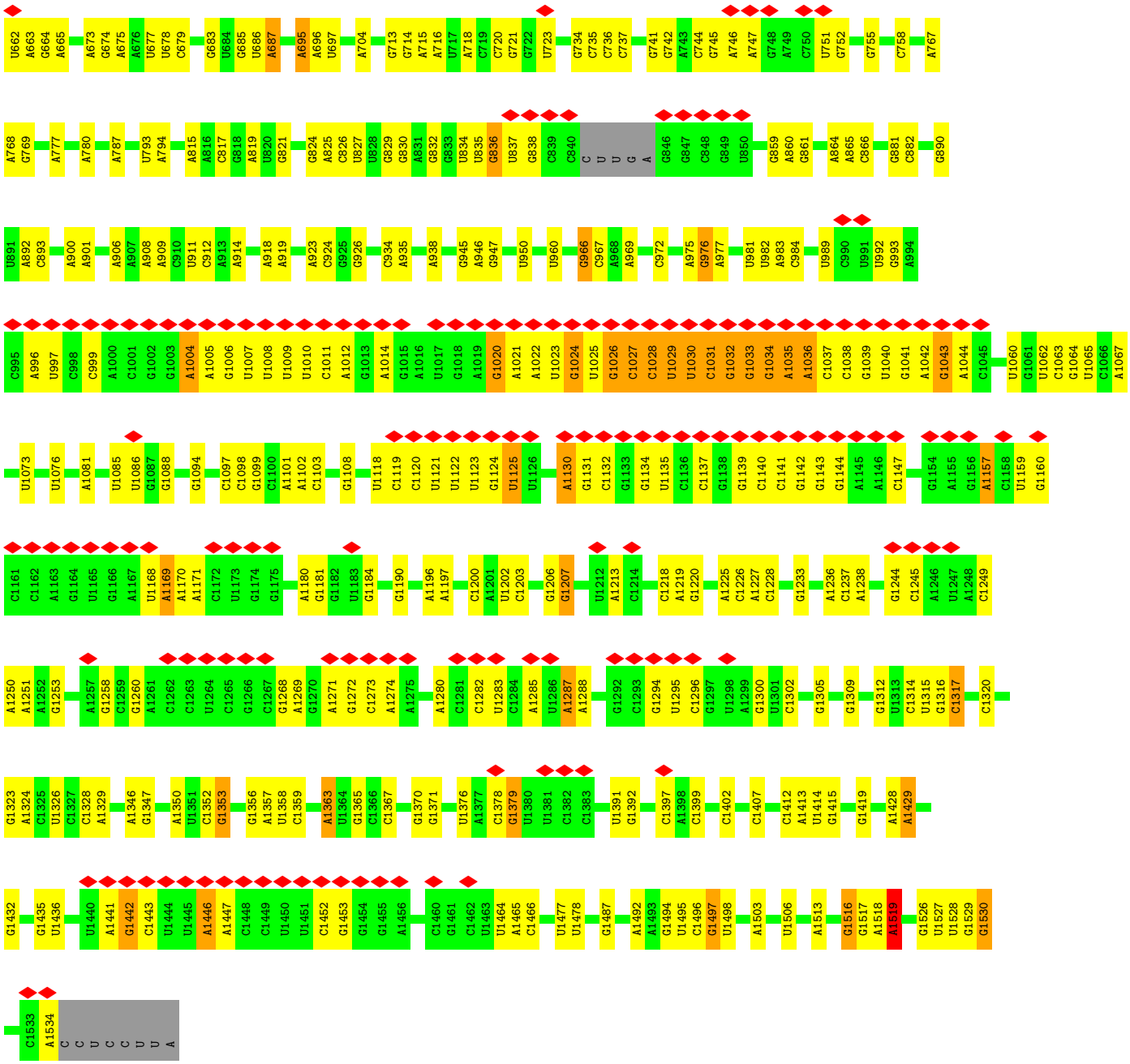
3 Residue-property plots (i)

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: 16S rRNA

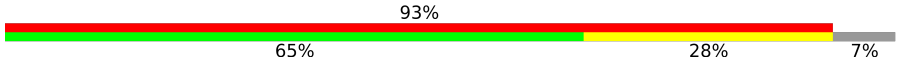
Chain A: 31% 57% 36% 5%

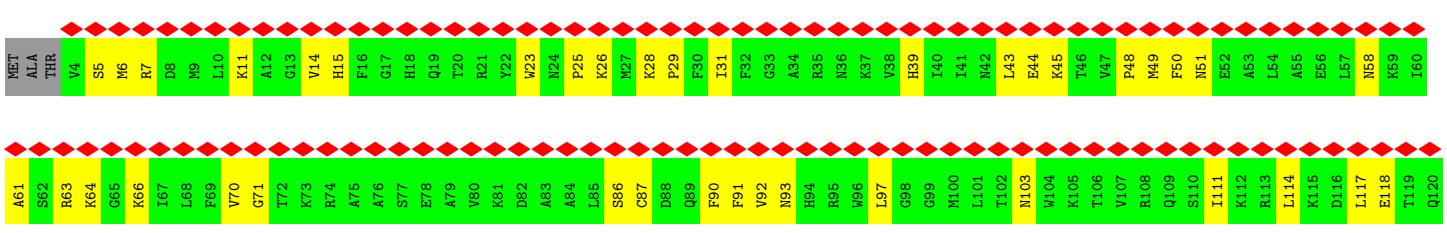




- Molecule 2: 30S ribosomal protein S2

Chain B:





S121 Q122 D123 G124 T125 F126 D127 K128 L129 T130 K131 K132 E133 A134 L135 M136 R137 T138 R139 E140 L141 E142 K143 L144 E145 N146 S147 L148 G149 G150 I151 K152 D153 M154 G155 G156 L157 P158 D159 A160 L161 F162 V163 I164 D165 A166 D167 H168 E169 H170 I171 A172 I173 K174 E175 A176 N177 N178 L179 G180

I181 P182 V183 F184 A185 I186 V187 D188 T189 N190 S191 D192 P193 D194 G195 V196 D197 F198 V199 I200 P201 G202 N203 D204 D205 A206 I207 R208 A209 V210 T211 L212 Y213 L214 G215 A216 V217 A218 A219 T220 V221 R222 E223 G224 R225 S226 Q227 ASP LEU ALA SER GLN ALA GLU GLU SER PHE VAL GLU ALA

GLU

- Molecule 3: 30S ribosomal protein S3

Chain C: 55% 74% 14% 12%

MET G2 V5 G9 I10 R11 I14 V15 K16 P17 W18 N19 S20 T21 W22 F23 A24 N25 T26 K27 E28 F29 A30 D31 D34 S35 D36 F37 K38 V39 R40 Q41 Y42 L43 T44 K45 E46 L47 A48 K49 A50 S51 V52 S53 R54 I55 V56 I57 E58 R59 P60 A61 K62 S63 I64 R65

V66 T67 I68 H69 T70 A71 R72 P73 G74 I75 V76 I77 G78 K79 K80 G81 E82 D83 V84 E85 K86 L87 R88 K89 V90 V91 A92 D93 I94 A95 G96 V97 P98 A99 Q100 I101 N102 I103 A104 E105 V106 R107 K108 P109 E110 L111 D112 A113 D118 L124 E125 R126 R127 V128 M129 F130 R131 R132

A133 M134 K135 R136 A137 V138 Q139 N140 A141 M142 R143 L144 G145 A146 E152 G158 E161 I162 T165 E166 W167 Y168 R169 R172 V173 P174 L175 H176 T177 L178 R179 A180 D181 I182 D183 E188 A189 H190 K199 K204 G205 E206 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 4: 30S ribosomal protein S4

Chain D: 92% 68% 32%

MET A2 R3 Y4 L5 K8 L9 K10 L11 S12 R13 R14 E15 G16 T17 D18 L19 F20 L21 K22 S23 G24 V25 R26 A27 I28 D29 T30 K31 C32 K33 I34 E35 Q36 A37 P38 G39 Q40 H41 G42 A43 R44 K45 P46 R47 L48 S49 D50 V53 Q54 L55 R56 E57 K58 Q59 K60 V61 R62

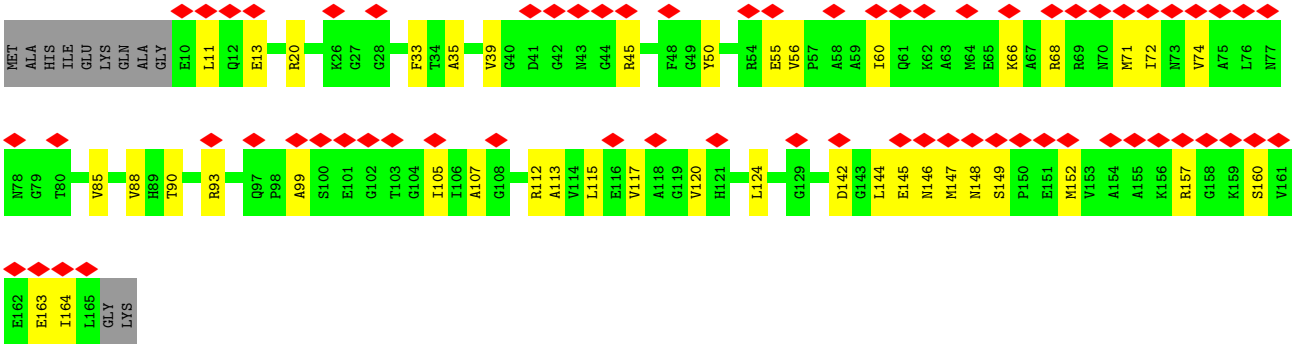
R63 I64 Y65 G66 V67 L68 E69 R70 Q71 F72 R73 N74 Y75 Y76 K77 E78 R81 L82 K83 G84 N85 T86 G87 E88 N89 L90 L91 A92 L93 L94 E95 G96 R97 L98 D99 N100 V101 V102 Y103 R104 M105 G106 F107 G108 A109 T110 R111 A112 E113 A114 R115 Q116 L117 V118 S119 H120 K121 A122 I123

M124 V125 N126 G127 R128 V129 V130 N131 I132 A133 S134 Y135 Q136 V137 S138 P139 N140 D141 V142 V143 S144 I145 R146 E147 K148 A149 K150 K151 Q152 S153 R154 V155 K156 A157 A158 L159 E160 L161 A162 E163 Q164 R165 E166 K167 P168 T169 W170 L171 E172 V173 D174 A175 G176 K177 M178 E179 G180 T181 F182 K183

R184 K185 P186 E187 R188 S189 D190 L191 S192 A193 D194 I195 N196 E197 H198 L199 I200 V201 E202 L203 Y204 S205 K206

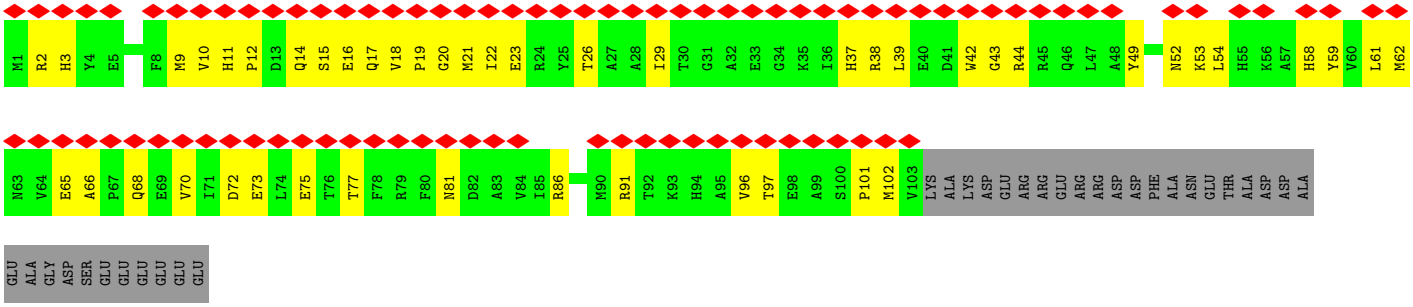
- Molecule 5: 30S ribosomal protein S5

Chain E: 40% 69% 25% 7%



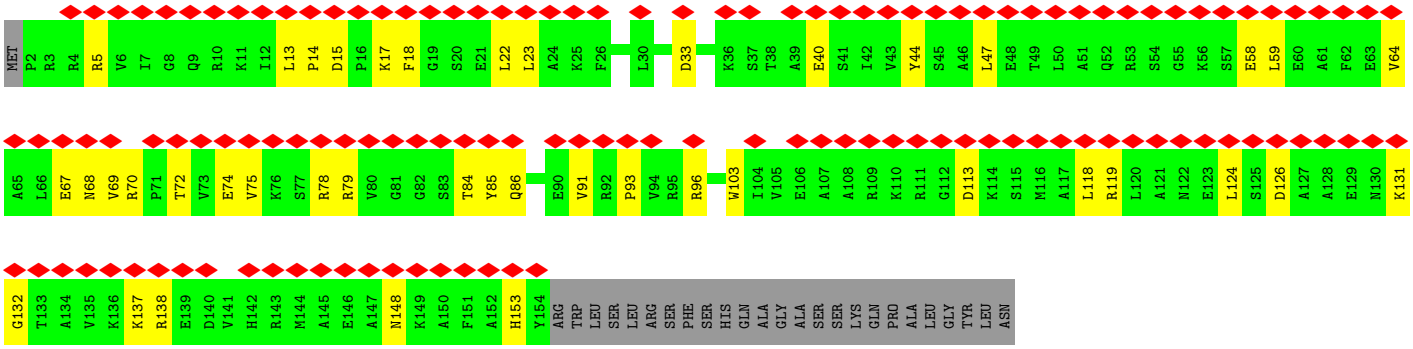
- Molecule 6: 30S ribosomal protein S6, fully modified isoform

Chain F:



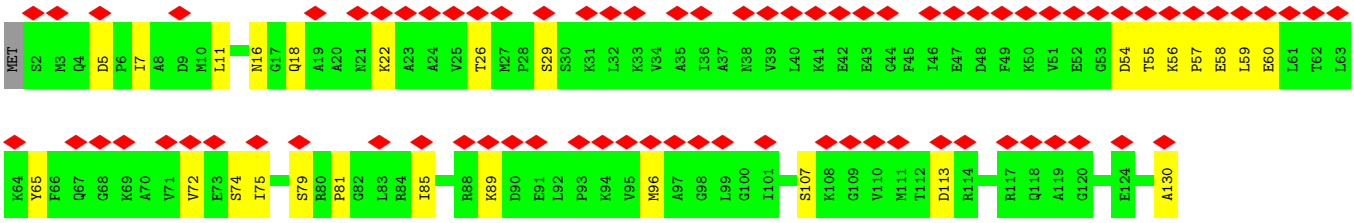
- Molecule 7: 30S ribosomal protein S7

Chain G:



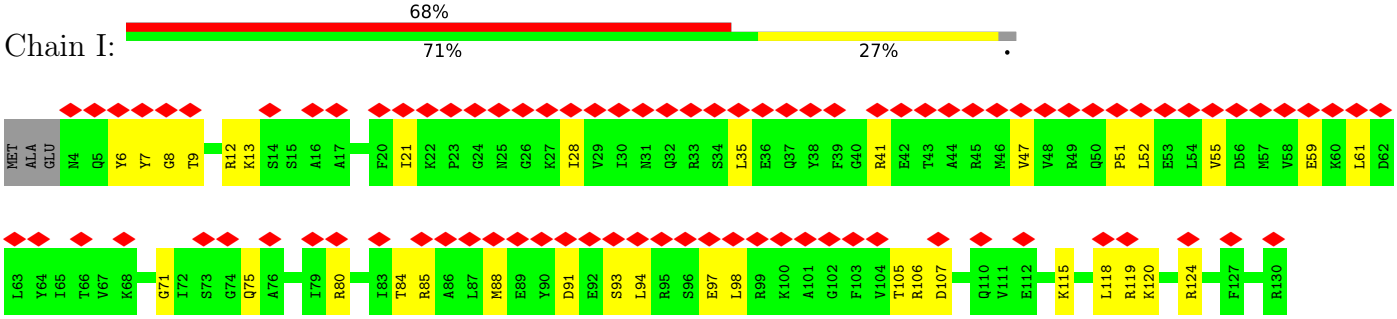
- Molecule 8: 30S ribosomal protein S8

Chain H:



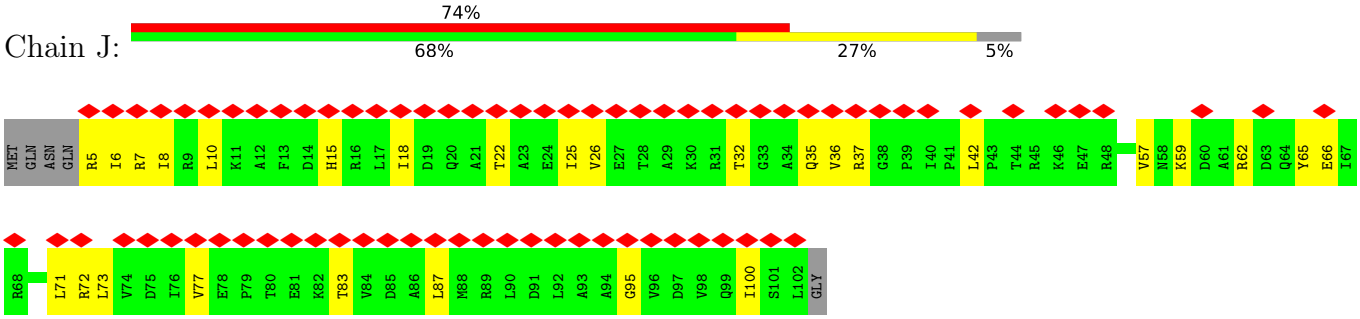
- Molecule 9: 30S ribosomal protein S9

Chain I:



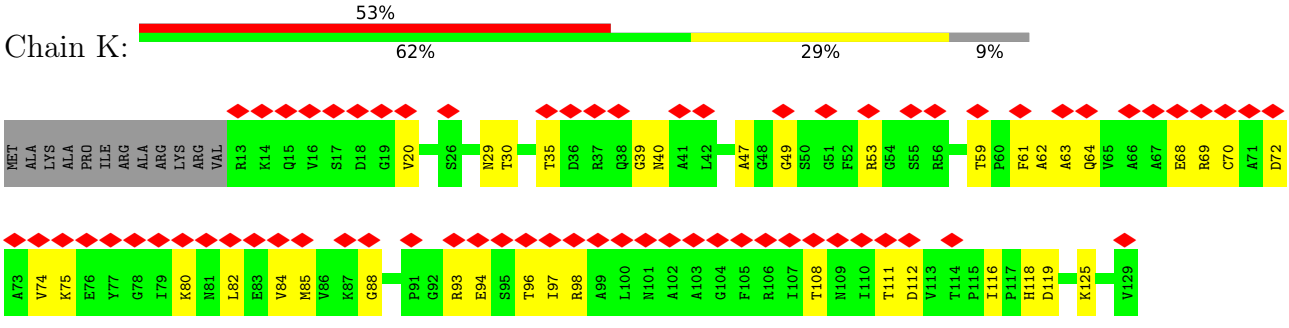
- Molecule 10: 30S ribosomal protein S10

Chain J:



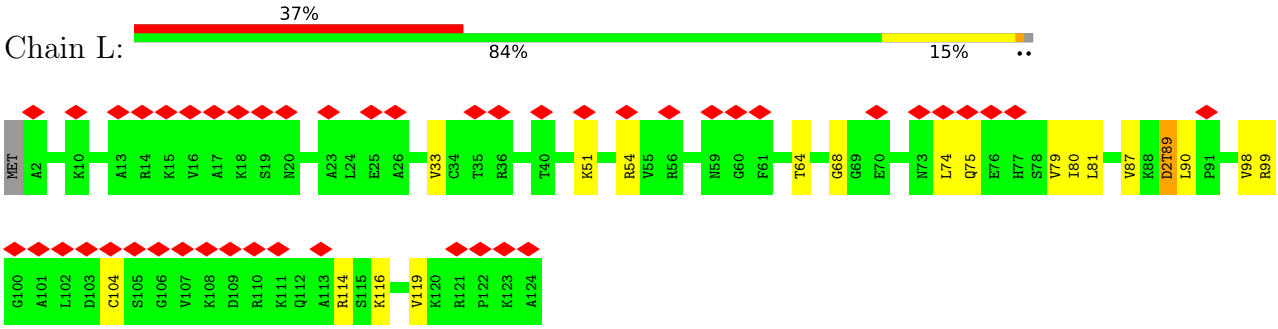
- Molecule 11: 30S ribosomal protein S11

Chain K:



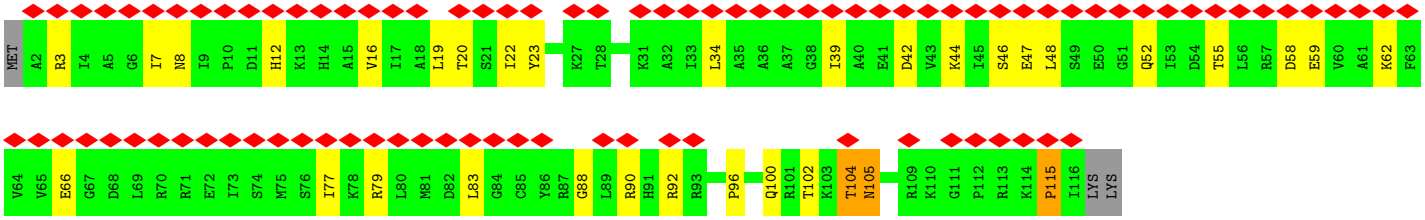
- Molecule 12: 30S ribosomal protein S12

Chain L:



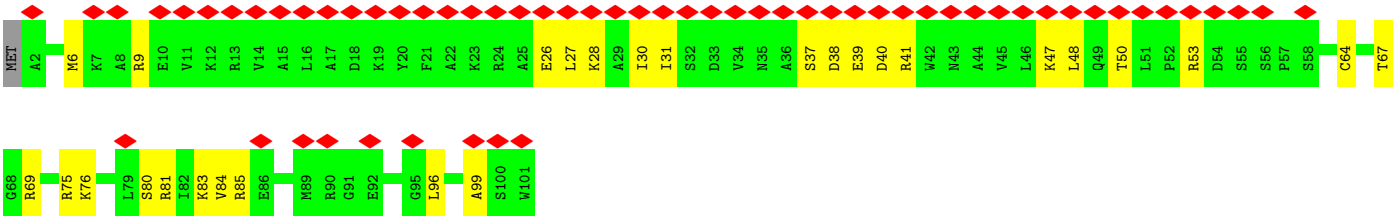
- Molecule 13: 30S ribosomal protein S13

Chain M:



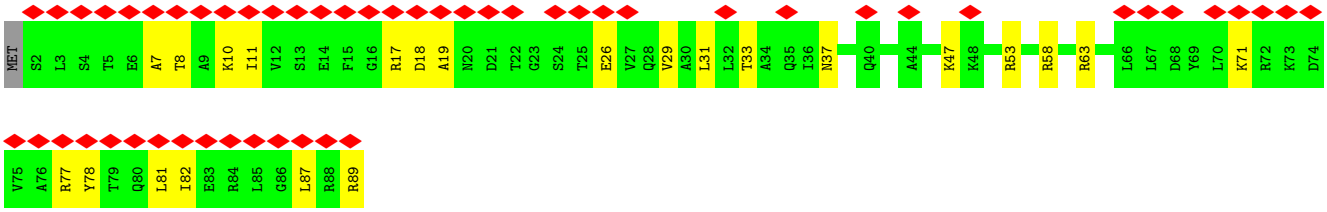
- Molecule 14: 30S ribosomal protein S14

Chain N:



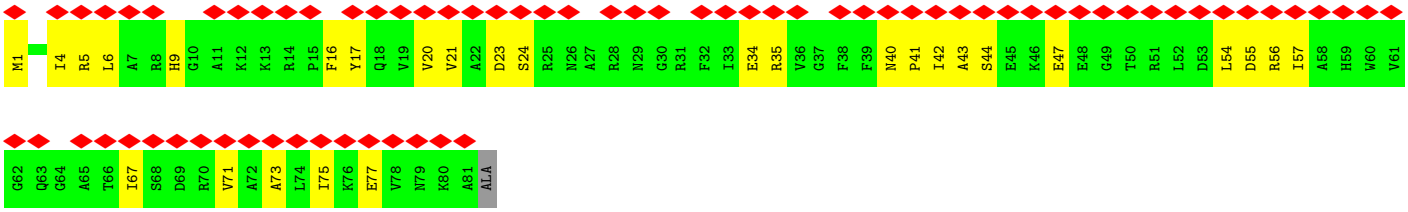
- Molecule 15: 30S ribosomal protein S15

Chain O:



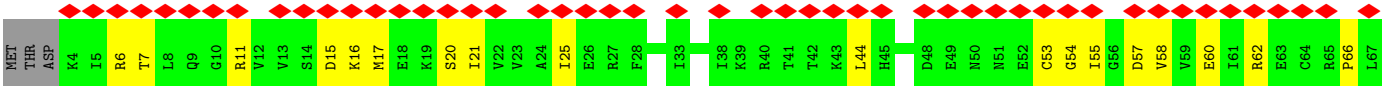
- Molecule 16: 30S ribosomal protein S16

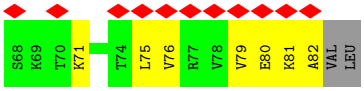
Chain P:



- Molecule 17: 30S ribosomal protein S17

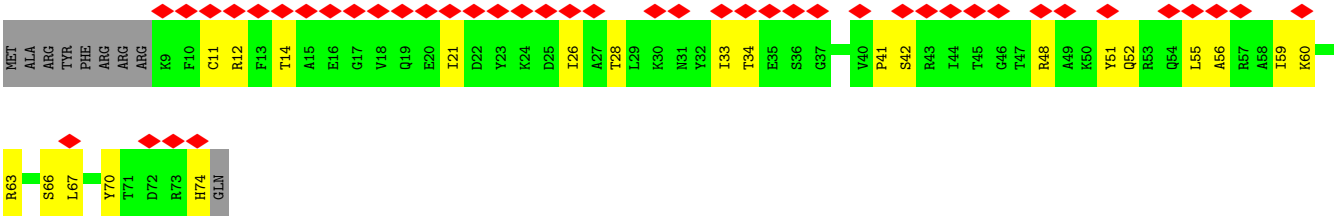
Chain Q:





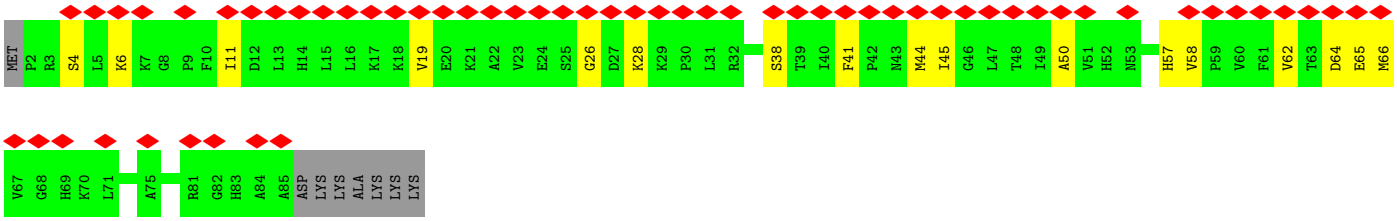
- Molecule 18: 30S ribosomal protein S18

Chain R:



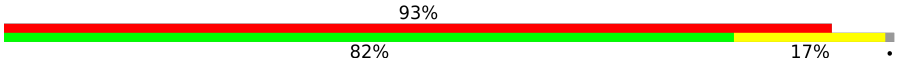
- Molecule 19: 30S ribosomal protein S19

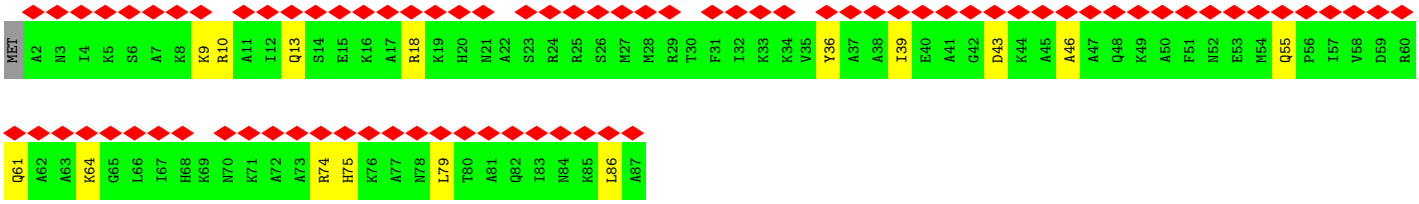
Chain S:



- Molecule 20: 30S ribosomal protein S20

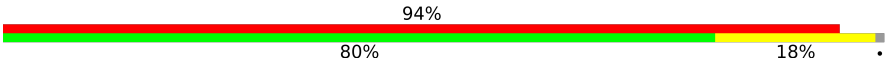
Chain T:

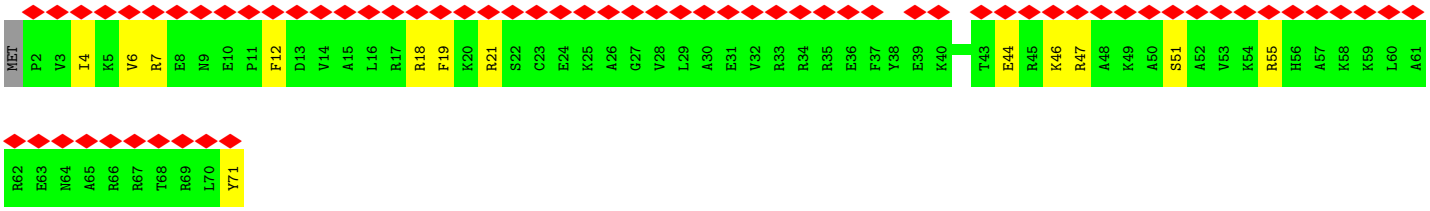




- Molecule 21: 30S ribosomal protein S21

Chain U:

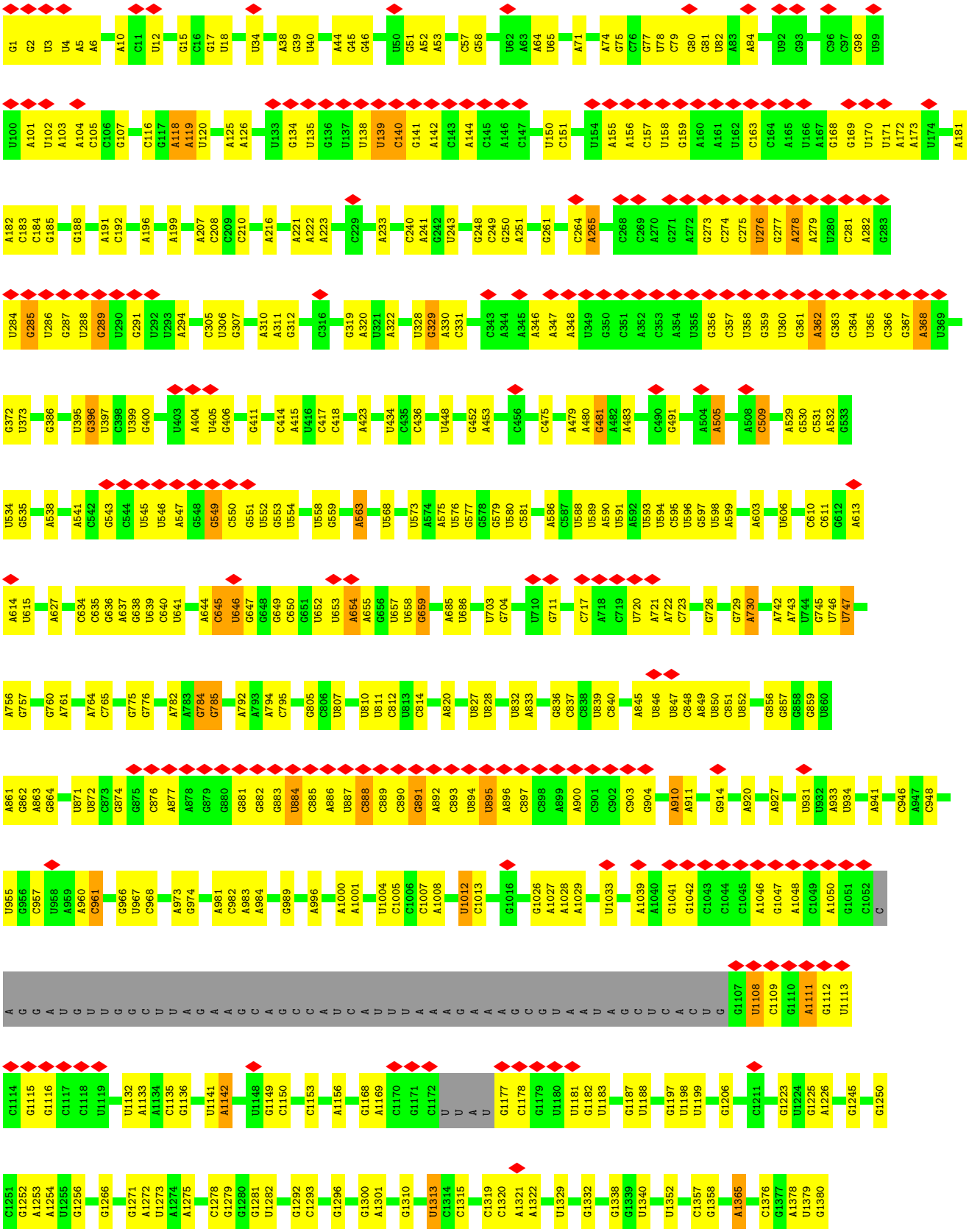


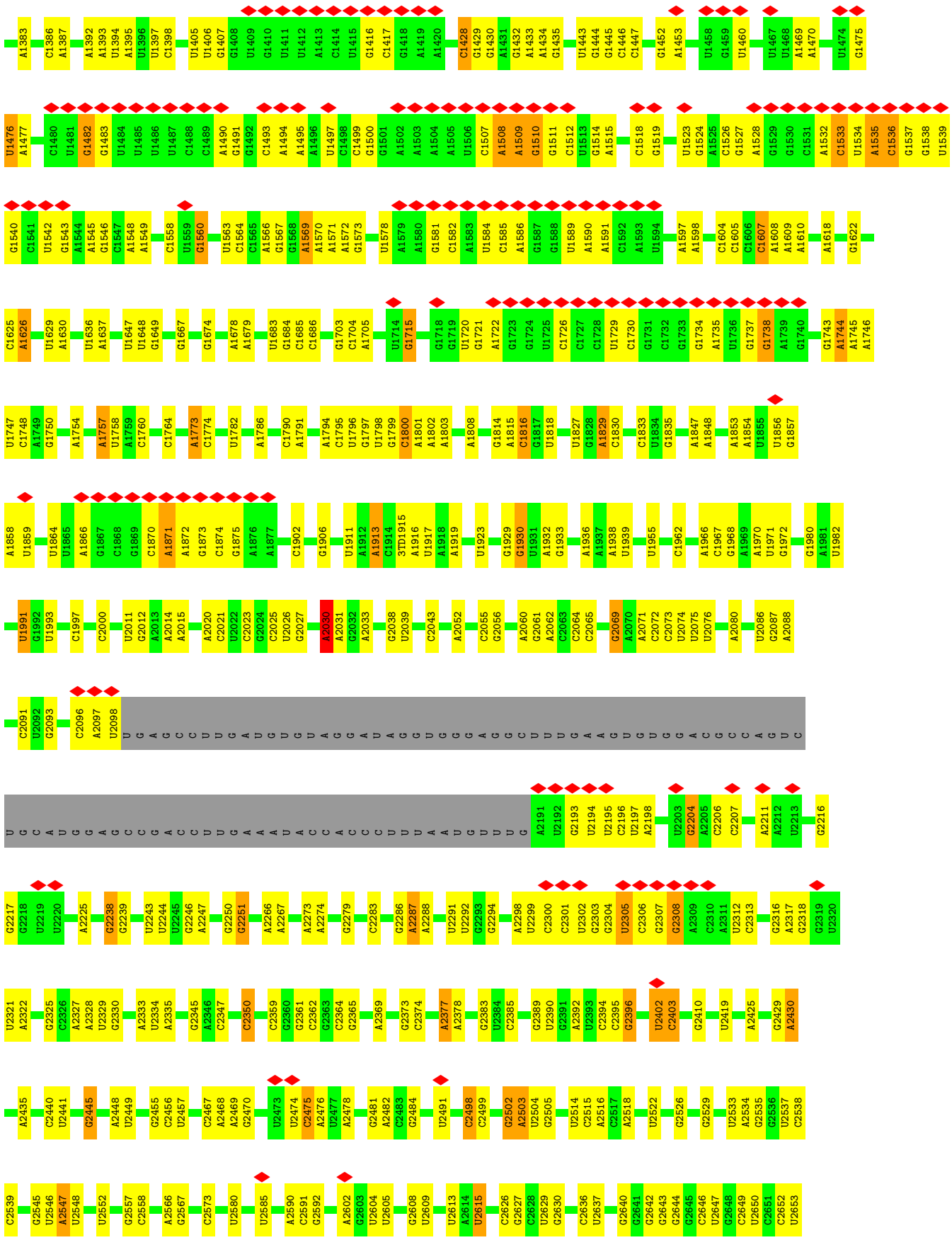


- Molecule 22: 23S rRNA

Chain a:

13%
62%
30%
5%


G1 G2 U3 U4 A5 A6 A10 C11 U12 G15 C16 G17 U18 U34 A38 G39 U40 A44 G45 G46 U50 G51 A52 A53 C57 G58 U62 A63 A64 U65 A71 A74 G75 G76 G77 U78 C79 G80 C81 U82 A83 A84 U92 G93 C96 C97 G98 U99
U100 A101 U102 A103 A104 C105 C106 G107 C116 G117 A118 A119 U120 A125 A126 U133 G134 U135 G136 U137 U138 U139 C140 G141 A142 C143 A144 C145 A146 C147 U150 C151 U154 A155 A156 C157 U158 G159 A160 A161 U162 C163 C164 A165 U166 A167 G168 G169 U170 U171 A172 A173 U174 A181
A182 C183 C184 G185 G188 A191 C192 A196 A199 A207 C208 C209 C210 A216 A221 A222 A223 C229 A233 C240 A241 G242 U243 G248 C249 G250 A251 G261 C264 A265 C268 C269 A270 G271 A272 G273 C274 C275 U276 G277 A278 A279 U280 C281 A282 G283
U284 G285 U286 G287 U288 G289 U290 G291 U292 U293 A294 C305 U306 G307 A310 A311 G312 C316 G319 A320 U321 A322 U328 G329 A330 C331 C343 A344 A345 A346 A347 A348 U349 G350 C351 A352 C353 A354 U355 G356 C357 U358 G359 U360 G361 A362 G363 C364 U365 C366 G367 A368 U369
G372 U373 G386 U395 G396 U397 G398 U399 G400 U403 A404 U405 G406 G411 C414 A415 U416 C417 C418 A423 U434 C435 C436 U448 G452 A453 C456 C475 A479 A480 G481 A482 A483 C490 G491 A504 A505 A508 C509 G529 G530 C531 A532 G533
U534 G535 A538 A541 C542 G543 C544 U545 U546 A547 G548 G549 C550 G551 U552 G553 U554 U558 G559 A563 U568 U573 A574 A575 U576 G577 G578 G579 U580 C581 A586 C587 U588 U589 A590 U591 A592 U593 U594 C595 U596 G597 U598 A599 A603 U606 C610 C611 G612 A613
A614 U615 A627 C634 C635 G636 A637 G638 U639 C640 U641 A644 C645 U646 G647 G648 G649 C650 G651 U652 U653 A654 A655 G656 U657 U658 G659 A685 U686 U703 G704 U710 G711 C717 A718 C719 U720 A721 A722 C723 G726 G729 A730 A742 A743 U744 G745 U746 U747
A756 G757 G760 A761 A764 C765 G775 G776 A782 A783 G784 G785 A792 A793 A794 C795 G805 C806 U807 U810 U811 C812 U813 C814 A820 U827 U828 U832 A833 G836 C837 C838 U839 C840 A845 U846 U847 C848 A849 U850 C851 U852 G856 G857 G858 G859 U860
A861 G862 A863 G864 U871 U872 C873 G874 G875 C876 A877 A878 G879 G880 G881 G882 G883 U884 C885 A886 U887 C888 C889 C890 G891 A892 C893 U894 U895 A896 C897 C898 A899 A900 C901 C902 C903 G904 A910 A911 G914 A920 A927 U931 U932 A933 U934 A941 C946 A947 C948
U955 G956 C957 U958 A959 A960 C961 G966 U967 C968 A973 G974 A981 C982 A983 A984 G989 A996 A1000 A1001 U1004 C1005 C1006 C1007 A1008 U1012 C1013 G1016 G1026 A1027 A1028 A1029 U1033 A1039 A1040 G1041 G1042 C1043 C1044 C1045 A1046 G1047 A1048 C1049 A1050 C1051 C1052 C
A G G A U G U U G G C U U A G A A G C A G C C A U C A U U U A A G A A A A G C A G C U U C A C U G G1107 U1108 C1109 G1110 A1111 G1112 U1113
C1114 G1115 G1116 C1117 C1118 U1119 U1132 A1133 A1134 C1135 G1136 U1141 A1142 U1148 G1149 C1150 C1153 A1156 G1168 A1169 C1170 G1171 C1172 U U A U G1177 C1178 G1179 U1180 U1181 G1182 U1183 G1187 U1188 G1197 U1198 U1199 G1206 C1211 G1223 U1224 G1225 A1226 G1245 G1250
C1251 G1252 A1253 A1254 U1255 G1256 G1266 G1271 A1272 U1273 A1274 A1275 C1278 G1279 G1280 G1281 U1282 G1292 C1293 G1296 G1300 A1301 G1310 U1313 C1314 C1315 C1319 C1320 A1321 A1322 U1329 G1332 G1338 G1339 U1340 U1352 C1357 G1358 A1385 C1376 G1377 A1378 U1379 G1380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U1476 A1477 C1480 U1481 G1482 G1483 U1484 U1485 U1486 U1487 C1488 C1489 A1490 G1491 G1492 C1493 A1494 A1495 A1496 U1497 C1498 C1499 G1500 G1501 A1502 A1503 A1504 A1505 U1506 C1507 A1508 A1509 G1510 G1511 C1512 U1513 G1514 A1515 C1518 G1519 U1523 G1524 A1525 C1526 G1527 A1528 G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1538 U1539
G1540 C1541 U1542 G1543 A1544 A1545 G1546 C1547 A1548 A1549 C1558 U1559 G1560 U1563 C1564 C1565 A1566 G1567 G1568 A1569 A1570 A1571 A1572 G1573 U1578 A1579 A1580 G1581 C1582 A1583 U1584 C1585 A1586 G1587 G1588 U1589 A1590 A1591 C1592 A1593 U1594 A1597 A1598 C1604 C1605 C1606 C1607 A1608 A1609 A1610 A1618 G1622
C1625 A1626 U1629 A1630 U1636 A1637 U1647 U1648 G1649 G1667 G1674 A1678 A1679 U1683 G1684 C1685 C1686 G1703 C1704 A1705 U1714 G1715 G1718 G1719 U1720 G1721 A1722 G1723 G1724 U1725 C1726 C1727 C1728 U1729 C1730 G1731 C1732 G1733 G1734 A1735 U1736 G1737 G1738 A1739 G1740 G1743 A1744 A1745 A1746
U1747 C1748 A1749 G1750 A1754 A1757 U1758 A1759 C1760 C1764 A1773 C1774 U1782 A1786 C1790 A1791 A1794 C1795 U1796 G1797 U1798 G1799 C1800 A1801 A1802 A1803 A1808 G1814 A1815 C1816 G1817 U1818 U1827 G1828 A1829 C1830 C1833 U1834 G1835 A1847 A1848 A1853 A1854 U1855 U1856 G1857
A1858 U1859 U1864 U1865 A1866 G1867 C1868 G1869 C1870 A1871 A1872 G1873 C1874 G1875 A1876 A1877 C1902 G1906 U1911 A1912 A1913 C1914 3TD1915 A1916 U1917 A1918 A1919 U1923 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 U1955 C1962 A1966 C1967 G1968 A1969 A1970 U1971 G1972 G1980 A1981 U1982
U1991 G1992 U1993 C1997 C2000 U2011 G2012 A2013 A2014 A2015 A2020 C2021 U2022 C2023 G2024 C2025 U2026 G2027 A2030 A2031 G2032 A2033 G2038 U2039 C2043 A2052 C2055 G2056 A2060 G2061 A2062 C2063 C2064 C2065 G2069 A2070 A2071 C2072 C2073 U2074 U2075 U2076 A2080 U2086 G2087 A2088
C2091 U2092 G2093 C2096 A2097 U2098 U G A G C C U U G A U G U G U A G G A U A G G U G G G A G G C U U U G A A G U G U G G A C G C C A G U C
U G C A U G G A G C C G A C C U U G A A U A C C A C C C U U U A A U G U U U G A2191 U2192 G2193 U2194 U2195 C2196 U2197 A2198 U2203 G2204 A2205 C2206 C2207 A2211 A2212 U2213 G2216
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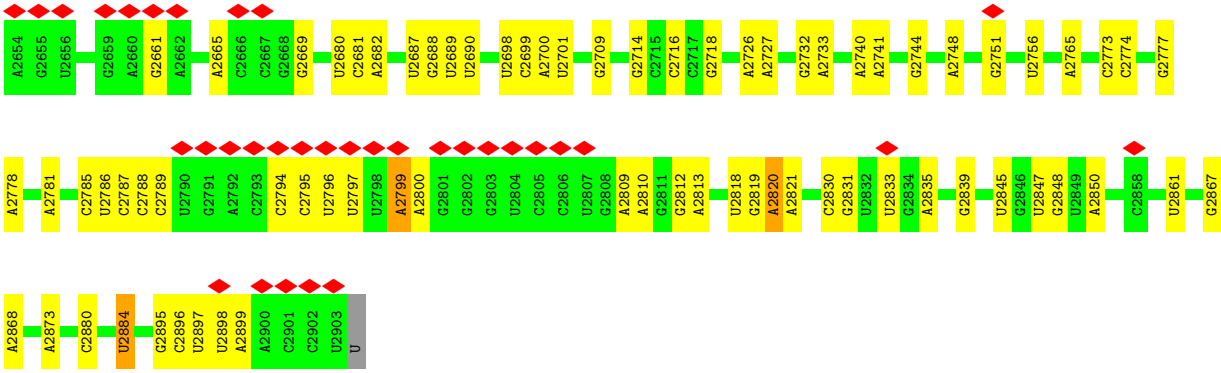
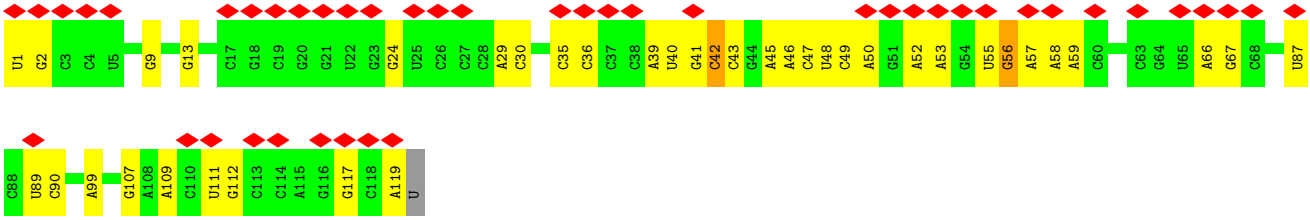


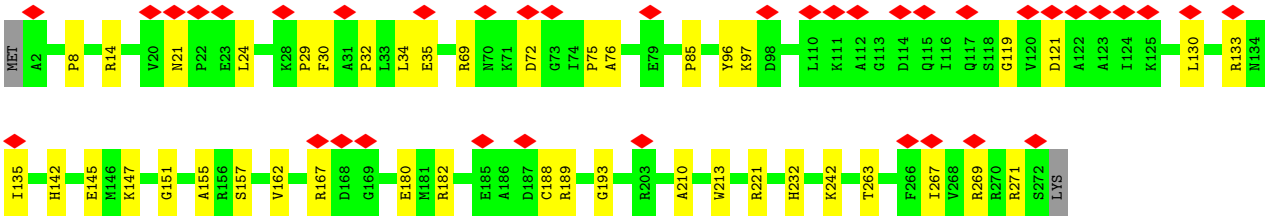
- Molecule 23: 5S rRNA

Chain b:



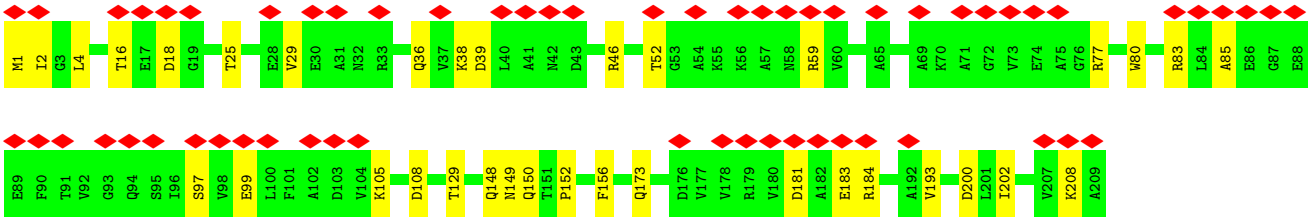
- Molecule 24: 50S ribosomal protein L2

Chain c:



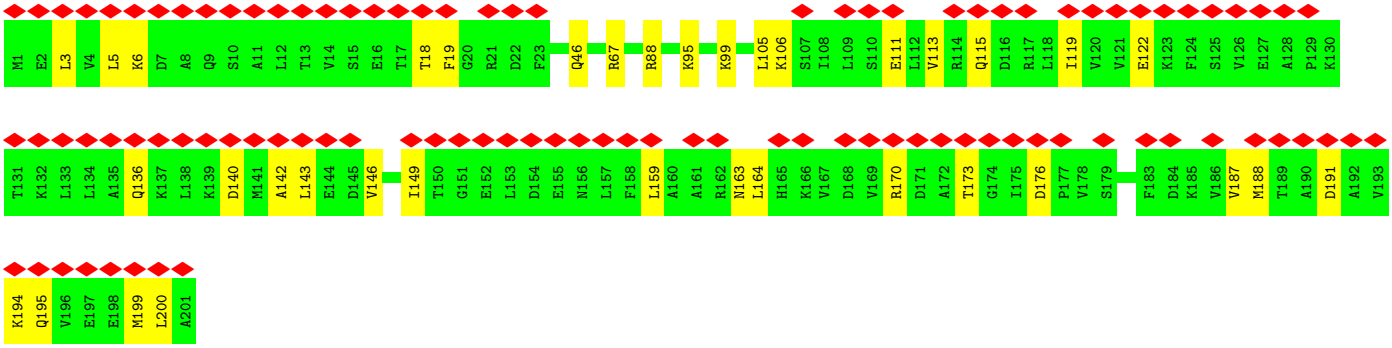
- Molecule 25: 50S ribosomal protein L3

Chain d:



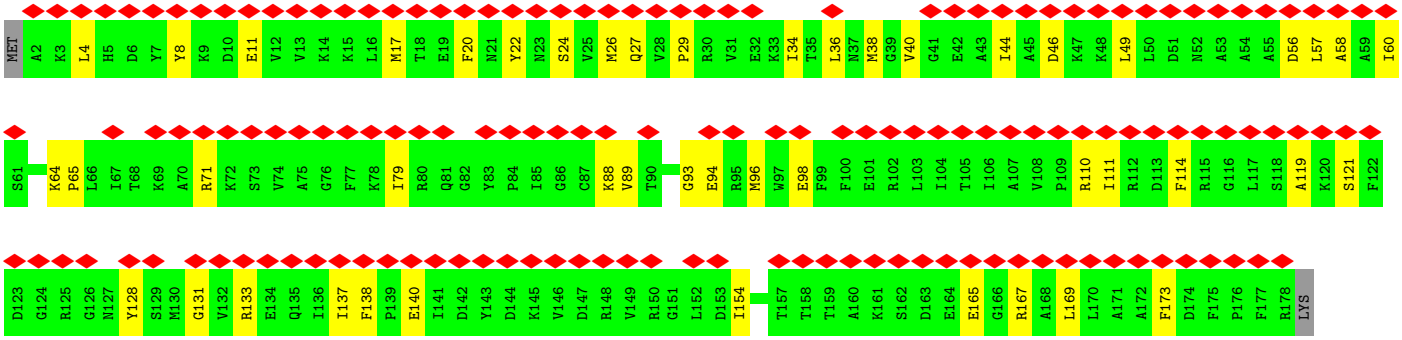
- Molecule 26: 50S ribosomal protein L4

Chain e:



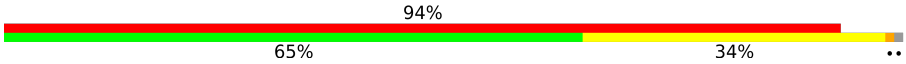
- Molecule 27: 50S ribosomal protein L5

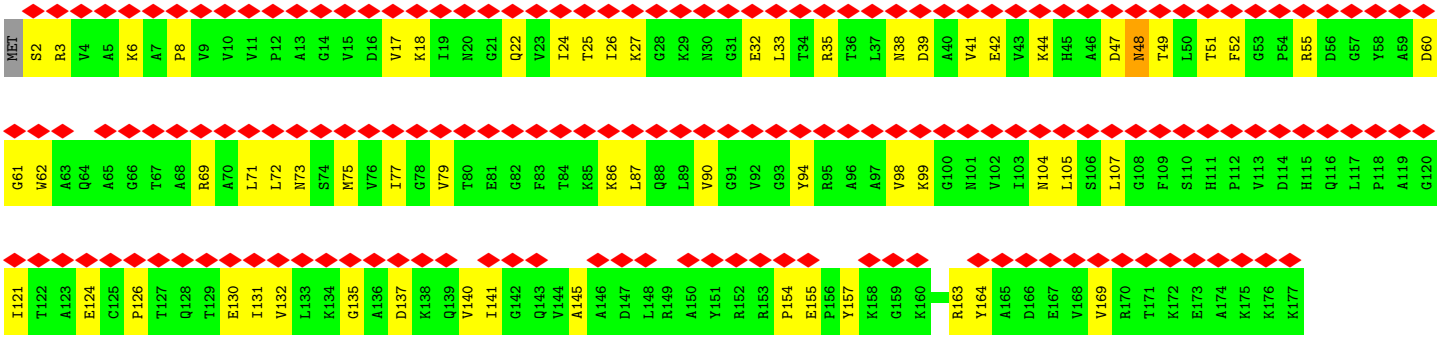
Chain f:



- Molecule 28: 50S ribosomal protein L6

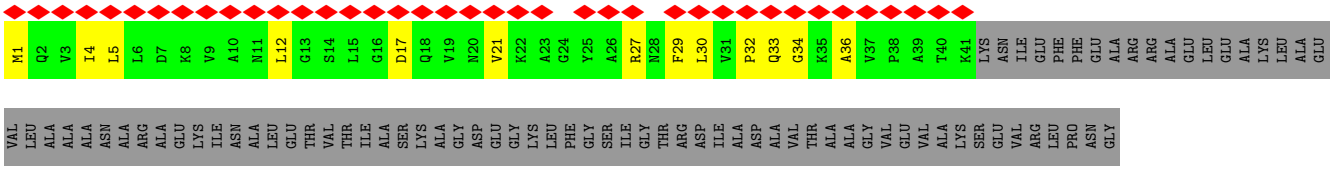
Chain g:





- Molecule 29: 50S ribosomal protein L9

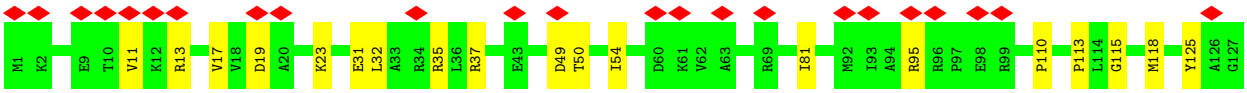
Chain h:

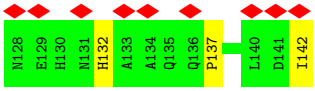


VAL LEU ARG THR THR GLY GLU HIS GLU VAL SER PHE GLN VAL HIS SER GLU VAL PHE ALA LYS VAL ILE VAL ASN VAL VAL ALA GLU

- Molecule 30: 50S ribosomal protein L13

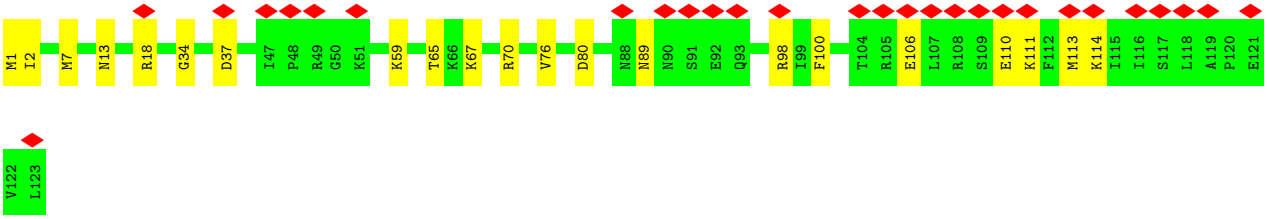
Chain i:





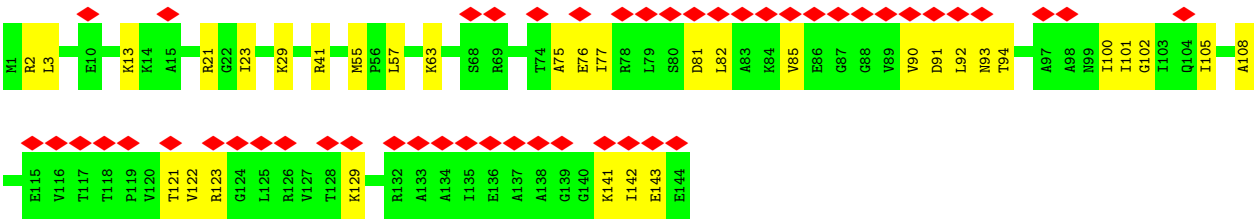
- Molecule 31: 50S ribosomal protein L14

Chain j:



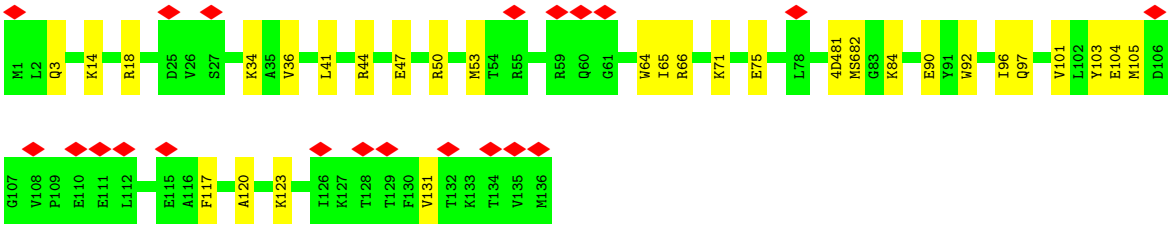
- Molecule 32: 50S ribosomal protein L15

Chain k:



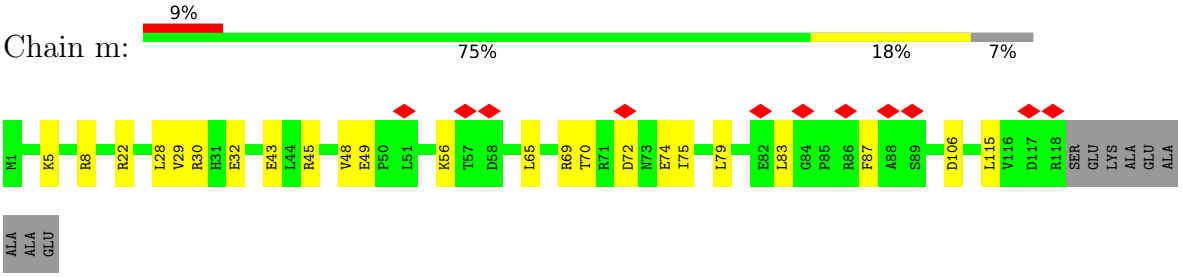
- Molecule 33: 50S ribosomal protein L16

Chain l:



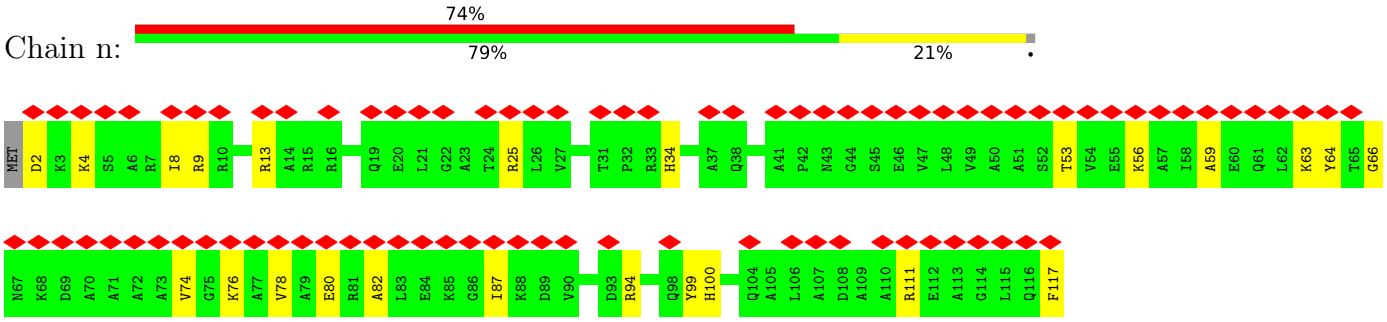
- Molecule 34: 50S ribosomal protein L17

Chain m:



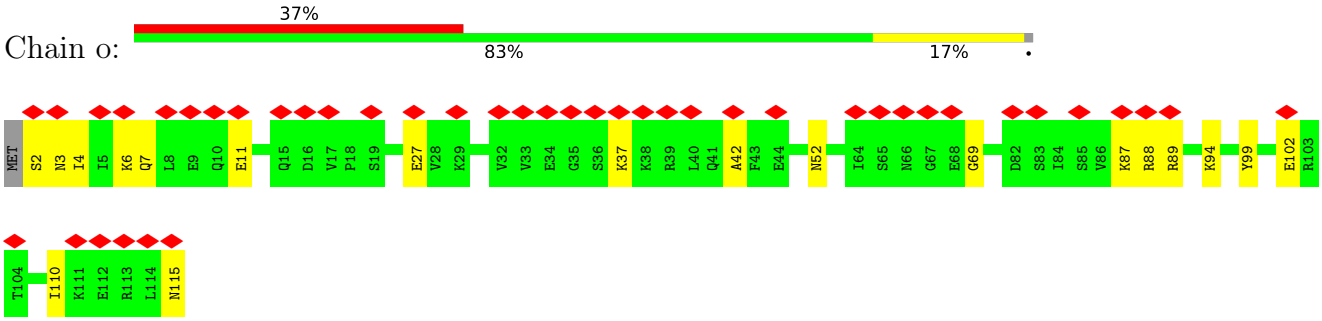
- Molecule 35: 50S ribosomal protein L18

Chain n:



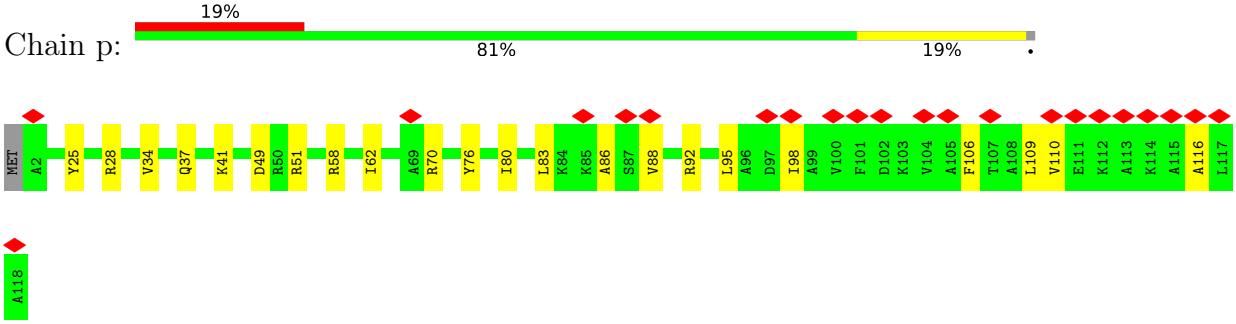
- Molecule 36: 50S ribosomal protein L19

Chain o:



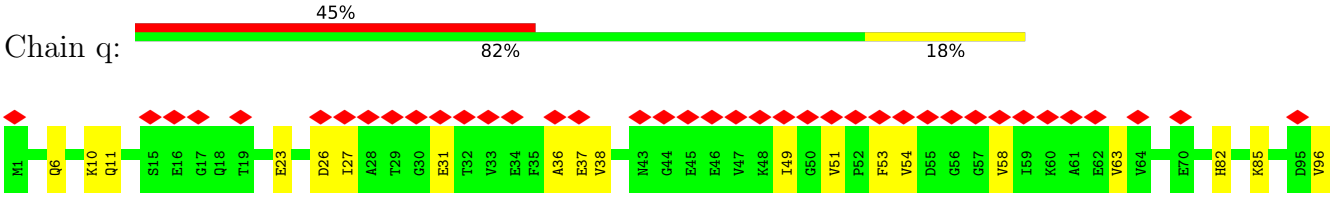
- Molecule 37: 50S ribosomal protein L20

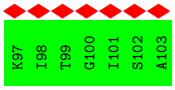
Chain p:



- Molecule 38: 50S ribosomal protein L21

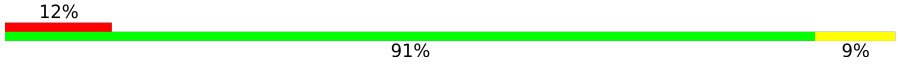
Chain q:

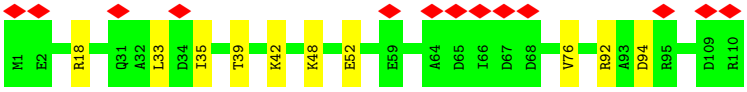




• Molecule 39: 50S ribosomal protein L22

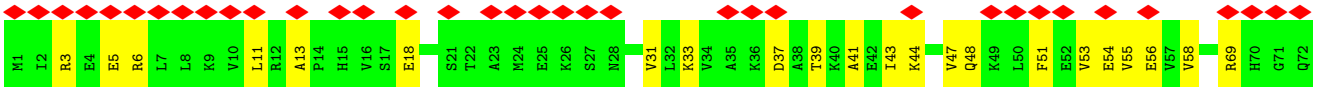
Chain r:

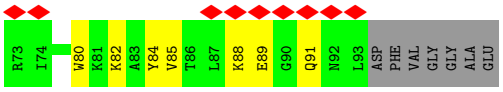




• Molecule 40: 50S ribosomal protein L23

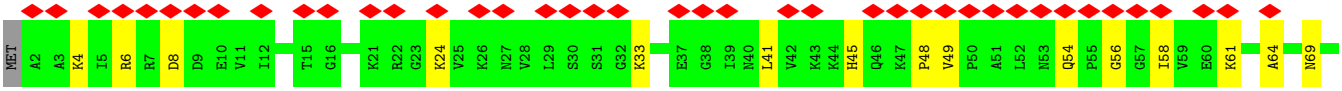
Chain s:

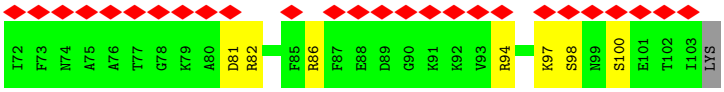




• Molecule 41: 50S ribosomal protein L24

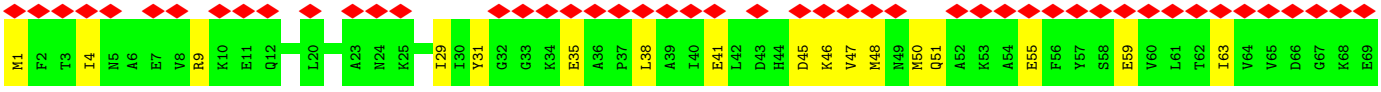
Chain t:

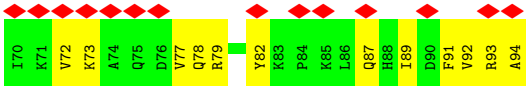




• Molecule 42: 50S ribosomal protein L25

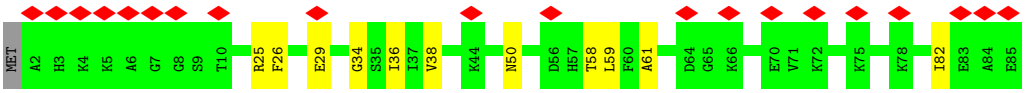
Chain u:





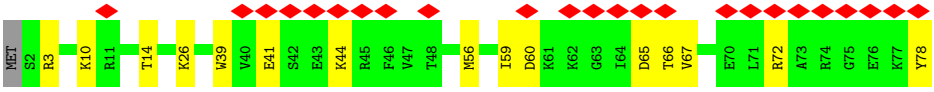
• Molecule 43: 50S ribosomal protein L27

Chain v:



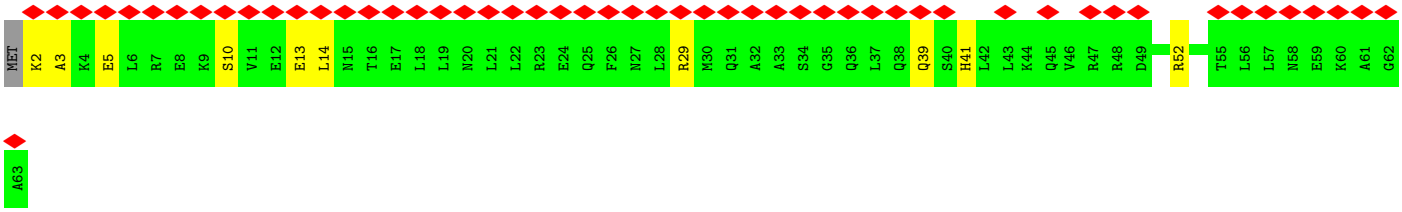
• Molecule 44: 50S ribosomal protein L28

Chain w:



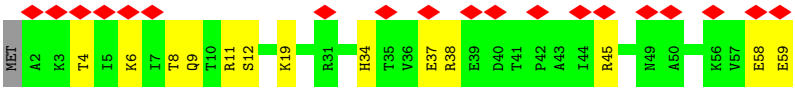
• Molecule 45: 50S ribosomal protein L29

Chain x:



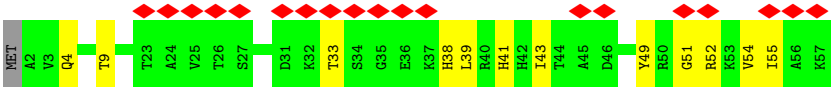
• Molecule 46: 50S ribosomal protein L30

Chain y:



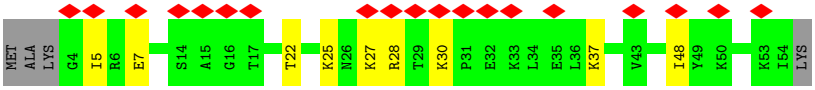
• Molecule 47: 50S ribosomal protein L32

Chain z:



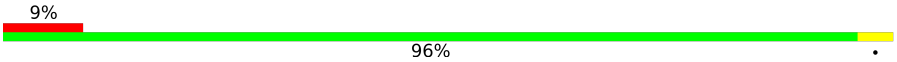
• Molecule 48: 50S ribosomal protein L33

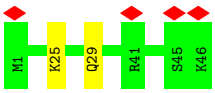
Chain 0:



• Molecule 49: 50S ribosomal protein L34

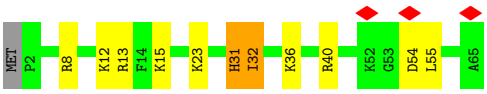
Chain 1:





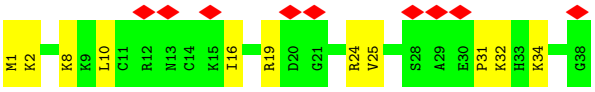
• Molecule 50: 50S ribosomal protein L35

Chain 2:



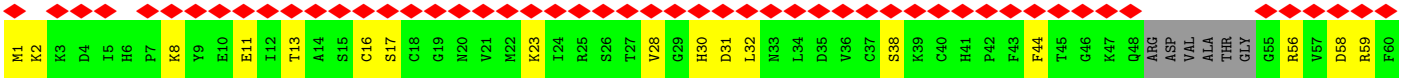
• Molecule 51: 50S ribosomal protein L36

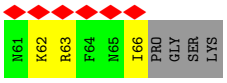
Chain 3:



• Molecule 52: 50S ribosomal protein L31

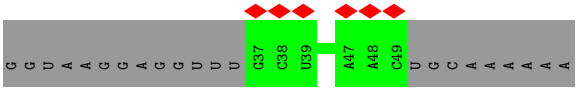
Chain 4:





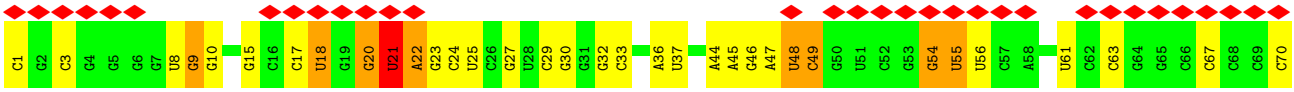
• Molecule 53: mRNA

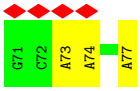
Chain X:



• Molecule 54: P-site tRNA-fMet

Chain Z:

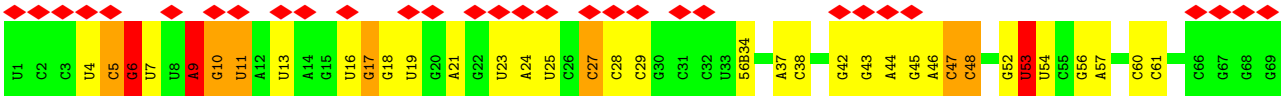


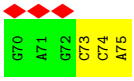


• Molecule 55: A-site tRNA-Asp

Chain V:

44%
48%
39%
9%


U1 C2 C3 U4 C5 G6 U7 U8 A9 G10 U11 A12 U13 A14 G15 U16 G17 G18 U19 G20 A21 G22 U23 A24 U25 C26 C27 C28 C29 G30 C31 C32 U33 56B34 A37 C38 G42 G43 A44 G45 A46 C47 C48 G52 U53 U54 C55 G56 A57 C60 C61 C66 G67 G68 G69


G70 A71 G72 C73 C74 A75

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	946282	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.267	Depositor
Minimum map value	-0.121	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	439.10498, 439.10498, 439.10498	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8285, 0.8285, 0.8285	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: 6MZ, UR3, D2T, 4D4, OMC, 3TD, 5MC, PSU, 4SU, MEQ, 56B, MA6, 5MU, 4OC, 2MG, MS6, MG, OMG, OMU, 1MA, G7M, H2U, 1MG, IAS, 2MA

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	A	0.49	0/36261	0.34	0/56559
2	B	0.24	0/1784	0.48	0/2403
3	C	0.42	0/1651	0.50	0/2225
4	D	0.33	0/1665	0.48	0/2227
5	E	0.44	0/1165	0.51	0/1568
6	F	0.39	0/858	0.62	0/1160
7	G	0.37	0/1219	0.55	0/1635
8	H	0.46	0/989	0.46	0/1326
9	I	0.39	0/1034	0.53	0/1375
10	J	0.41	0/796	0.55	1/1077 (0.1%)
11	K	0.40	0/884	0.48	0/1191
12	L	0.45	0/960	0.48	0/1286
13	M	0.40	0/900	0.62	1/1204 (0.1%)
14	N	0.41	0/817	0.52	0/1088
15	O	0.42	0/722	0.54	0/964
16	P	0.33	0/653	0.50	0/877
17	Q	0.39	0/650	0.53	0/871
18	R	0.41	0/553	0.45	0/742
19	S	0.37	0/685	0.45	0/922
20	T	0.33	0/676	0.44	0/895
21	U	0.24	0/597	0.44	0/792
22	a	0.58	0/65651	0.37	0/102413
23	b	0.44	0/2850	0.30	0/4444
24	c	0.53	0/2121	0.47	0/2852
25	d	0.50	0/1576	0.44	0/2119
26	e	0.45	0/1571	0.45	0/2113
27	f	0.38	0/1434	0.48	0/1926
28	g	0.35	0/1343	0.51	2/1816 (0.1%)
29	h	0.30	0/306	0.60	0/413
30	i	0.48	0/1152	0.43	0/1551
31	j	0.49	0/955	0.45	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	k	0.49	0/1062	0.52	0/1413
33	l	0.49	0/1073	0.49	0/1433
34	m	0.50	0/958	0.49	0/1281
35	n	0.39	0/902	0.61	2/1209 (0.2%)
36	o	0.46	0/929	0.45	0/1242
37	p	0.57	0/960	0.50	0/1278
38	q	0.51	0/829	0.51	0/1107
39	r	0.51	0/864	0.47	0/1156
40	s	0.41	0/744	0.56	0/994
41	t	0.40	0/787	0.51	0/1051
42	u	0.40	0/766	0.45	0/1025
43	v	0.50	0/636	0.49	0/841
44	w	0.48	0/635	0.50	0/848
45	x	0.35	0/502	0.47	0/667
46	y	0.46	0/453	0.56	0/605
47	z	0.51	0/450	0.49	0/599
48	0	0.46	0/424	0.51	0/565
49	1	0.57	0/380	0.53	0/498
50	2	0.52	0/513	0.48	0/676
51	3	0.49	0/303	0.50	0/397
52	4	0.31	0/488	0.57	0/649
53	X	0.47	0/312	0.34	0/484
54	Z	0.42	0/1725	0.32	0/2687
55	V	0.40	0/1525	0.37	0/2375
All	All	0.51	0/152698	0.40	6/228393 (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
13	M	0	1
28	g	0	1
50	2	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	M	115	PRO	CA-N-CD	-7.38	101.67	112.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	n	59	ALA	CA-C-N	-5.68	110.95	122.31
35	n	59	ALA	C-N-CA	-5.68	110.95	122.31
28	g	154	PRO	CA-C-N	5.43	128.20	120.49
28	g	154	PRO	C-N-CA	5.43	128.20	120.49

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	2	31	HIS	Peptide
13	M	104	THR	Peptide
28	g	47	ASP	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	A	32634	0	16443	413	0
2	B	1753	0	1780	52	0
3	C	1624	0	1696	25	0
4	D	1643	0	1707	51	0
5	E	1152	0	1196	29	0
6	F	839	0	833	36	0
7	G	1203	0	1254	35	0
8	H	979	0	1031	21	0
9	I	1022	0	1070	35	0
10	J	786	0	828	28	0
11	K	877	0	884	27	0
12	L	957	0	1017	14	0
13	M	891	0	952	32	0
14	N	805	0	844	25	0
15	O	714	0	734	16	0
16	P	643	0	661	18	0
17	Q	641	0	682	22	0
18	R	544	0	565	18	0
19	S	668	0	693	14	0
20	T	670	0	719	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	U	589	0	629	9	0
22	a	59130	0	29765	523	0
23	b	2549	0	1291	25	0
24	c	2082	0	2154	30	0
25	d	1566	0	1618	26	0
26	e	1552	0	1619	26	0
27	f	1410	0	1444	39	0
28	g	1323	0	1371	41	0
29	h	303	0	327	9	0
30	i	1129	0	1162	18	0
31	j	946	0	1023	15	0
32	k	1053	0	1129	29	0
33	l	1075	0	1144	19	0
34	m	945	0	989	15	0
35	n	892	0	923	18	0
36	o	917	0	962	15	0
37	p	947	0	1019	15	0
38	q	816	0	839	15	0
39	r	857	0	922	7	0
40	s	738	0	807	24	0
41	t	779	0	831	18	0
42	u	753	0	780	22	0
43	v	628	0	642	6	0
44	w	625	0	652	12	0
45	x	501	0	531	6	0
46	y	449	0	488	11	0
47	z	444	0	458	8	0
48	0	417	0	451	8	0
49	1	377	0	418	2	0
50	2	504	0	572	11	0
51	3	302	0	343	9	0
52	4	480	0	482	22	0
53	X	279	0	141	0	0
54	Z	1645	0	842	19	0
55	V	1612	0	813	22	0
56	A	58	0	0	0	0
56	I	1	0	0	0	0
56	V	2	0	0	0	0
56	Z	2	0	0	0	0
56	a	191	0	0	0	0
56	b	2	0	0	0	0
56	c	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	z	1	0	0	0	0
All	All	141917	0	95170	1791	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 8.

The worst 5 of 1791 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)
22:a:882:G:H1	22:a:894:U:H3	1.04	0.93
1:A:458:U:H3	1:A:474:G:H1	1.12	0.92
1:A:664:G:H22	1:A:741:G:H1	1.21	0.89
46:y:6:LYS:NZ	46:y:37:GLU:OE2	2.06	0.88
22:a:2796:U:H3	22:a:2799:A:H61	1.14	0.88

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	210 (95%)	12 (5%)	0	100	100
3	C	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
4	D	203/206 (98%)	199 (98%)	4 (2%)	0	100	100
5	E	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
6	F	101/135 (75%)	94 (93%)	7 (7%)	0	100	100
7	G	151/179 (84%)	140 (93%)	11 (7%)	0	100	100
8	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
9	I	125/130 (96%)	119 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	96/103 (93%)	88 (92%)	7 (7%)	1 (1%)	12	26
11	K	113/129 (88%)	107 (95%)	6 (5%)	0	100	100
12	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
13	M	113/118 (96%)	104 (92%)	8 (7%)	1 (1%)	14	29
14	N	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
15	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	P	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
17	Q	77/84 (92%)	76 (99%)	1 (1%)	0	100	100
18	R	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
19	S	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
20	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
21	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
24	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
25	d	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	24	44
26	e	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
27	f	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
28	g	174/177 (98%)	161 (92%)	12 (7%)	1 (1%)	21	39
29	h	39/149 (26%)	32 (82%)	7 (18%)	0	100	100
30	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
31	j	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
32	k	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
33	l	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
34	m	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
35	n	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
36	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
37	p	115/118 (98%)	115 (100%)	0	0	100	100
38	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
39	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
40	s	91/100 (91%)	86 (94%)	5 (6%)	0	100	100
41	t	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
42	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	v	82/85 (96%)	80 (98%)	2 (2%)	0	100	100
44	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
45	x	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	y	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
48	0	49/55 (89%)	47 (96%)	2 (4%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	7	15
51	3	36/38 (95%)	36 (100%)	0	0	100	100
52	4	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
All	All	5487/5913 (93%)	5262 (96%)	220 (4%)	5 (0%)	49	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	57	VAL
25	d	149	ASN
50	2	32	ILE
13	M	105	ASN
28	g	48	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	B	186/199 (94%)	186 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	172 (100%)	0	100	100
5	E	119/126 (94%)	119 (100%)	0	100	100
6	F	90/116 (78%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	126/147 (86%)	126 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	102 (100%)	0	100	100
13	M	93/96 (97%)	93 (100%)	0	100	100
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	65 (100%)	0	100	100
17	Q	73/78 (94%)	73 (100%)	0	100	100
18	R	57/65 (88%)	57 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	60 (100%)	0	100	100
24	c	216/218 (99%)	216 (100%)	0	100	100
25	d	163/163 (100%)	163 (100%)	0	100	100
26	e	165/165 (100%)	165 (100%)	0	100	100
27	f	148/150 (99%)	148 (100%)	0	100	100
28	g	137/138 (99%)	137 (100%)	0	100	100
29	h	32/114 (28%)	32 (100%)	0	100	100
30	i	116/116 (100%)	116 (100%)	0	100	100
31	j	104/104 (100%)	104 (100%)	0	100	100
32	k	103/103 (100%)	103 (100%)	0	100	100
33	l	107/107 (100%)	107 (100%)	0	100	100
34	m	98/103 (95%)	98 (100%)	0	100	100
35	n	86/87 (99%)	86 (100%)	0	100	100
36	o	99/100 (99%)	99 (100%)	0	100	100
37	p	89/90 (99%)	89 (100%)	0	100	100
38	q	84/84 (100%)	84 (100%)	0	100	100
39	r	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	s	80/84 (95%)	80 (100%)	0	100	100
41	t	83/85 (98%)	83 (100%)	0	100	100
42	u	78/78 (100%)	78 (100%)	0	100	100
43	v	61/63 (97%)	61 (100%)	0	100	100
44	w	67/68 (98%)	67 (100%)	0	100	100
45	x	54/55 (98%)	54 (100%)	0	100	100
46	y	48/49 (98%)	48 (100%)	0	100	100
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	46 (100%)	0	100	100
49	1	38/38 (100%)	38 (100%)	0	100	100
50	2	51/52 (98%)	51 (100%)	0	100	100
51	3	34/34 (100%)	34 (100%)	0	100	100
52	4	55/62 (89%)	55 (100%)	0	100	100
All	All	4575/4825 (95%)	4575 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
40	s	70	HIS
52	4	20	ASN
42	u	51	GLN
44	w	36	HIS
26	e	41	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1517/1542 (98%)	218 (14%)	5 (0%)
22	a	2749/2904 (94%)	319 (11%)	0
23	b	118/120 (98%)	15 (12%)	0
53	X	12/35 (34%)	0	0
54	Z	76/77 (98%)	15 (19%)	1 (1%)
55	V	74/75 (98%)	15 (20%)	3 (4%)
All	All	4546/4753 (95%)	582 (12%)	9 (0%)

5 of 582 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	9	G
1	A	22	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	V	6	2MG
55	V	10	G
1	A	1033	G
1	A	1035	A
54	Z	20	G

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

56 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	2MG	A	1516	1	23,26,27	2.46	7 (30%)	32,38,41	2.22	11 (34%)
12	D2T	L	89	12	7,9,10	1.32	0	6,11,13	2.38	3 (50%)
55	PSU	V	13	55	18,21,22	0.99	1 (5%)	22,30,33	1.88	5 (22%)
22	PSU	a	2504	22	18,21,22	1.09	2 (11%)	22,30,33	1.83	3 (13%)
55	5MC	V	47	55	18,22,23	3.58	8 (44%)	26,32,35	1.10	2 (7%)
54	OMC	Z	33	54	19,22,23	2.78	8 (42%)	26,31,34	0.75	0
1	MA6	A	1518	1	23,26,27	1.56	5 (21%)	34,38,41	2.29	12 (35%)
55	1MA	V	9	55	21,25,26	0.70	0	31,37,40	0.82	1 (3%)
22	1MG	a	745	22	22,26,27	2.53	8 (36%)	33,39,42	1.72	7 (21%)
22	2MG	a	1835	22	23,26,27	2.46	7 (30%)	32,38,41	2.16	9 (28%)
1	UR3	A	1498	1	19,22,23	2.45	6 (31%)	26,32,35	1.34	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
22	PSU	a	2580	22	18,21,22	1.21	2 (11%)	22,30,33	2.17	6 (27%)
25	MEQ	d	150	25	8,9,10	1.36	1 (12%)	5,10,12	1.50	2 (40%)
22	PSU	a	746	22,56	18,21,22	1.07	2 (11%)	22,30,33	1.78	4 (18%)
22	5MC	a	1962	22	18,22,23	3.36	7 (38%)	26,32,35	1.24	3 (11%)
33	MS6	l	82	33	5,7,8	1.05	1 (20%)	2,7,9	2.07	1 (50%)
55	PSU	V	54	55	18,21,22	1.04	2 (11%)	22,30,33	1.99	5 (22%)
22	2MG	a	2445	22	23,26,27	2.46	7 (30%)	32,38,41	2.32	10 (31%)
1	PSU	A	516	1,56	18,21,22	1.01	3 (16%)	22,30,33	1.67	5 (22%)
1	2MG	A	966	1	23,26,27	2.56	6 (26%)	32,38,41	2.25	10 (31%)
22	PSU	a	2457	22	18,21,22	1.15	3 (16%)	22,30,33	2.11	5 (22%)
22	PSU	a	2605	22	18,21,22	1.07	1 (5%)	22,30,33	1.84	2 (9%)
55	56B	V	34	55	29,35,36	2.91	11 (37%)	36,52,55	1.92	8 (22%)
55	2MG	V	6	55	23,26,27	2.57	7 (30%)	32,38,41	2.21	10 (31%)
22	6MZ	a	1618	22	22,25,26	2.67	4 (18%)	30,36,39	2.49	10 (33%)
1	2MG	A	1207	1	23,26,27	2.51	7 (30%)	32,38,41	2.16	10 (31%)
22	PSU	a	2604	22	18,21,22	1.07	2 (11%)	22,30,33	1.85	4 (18%)
1	5MC	A	967	1	18,22,23	3.58	8 (44%)	26,32,35	1.08	2 (7%)
54	PSU	Z	56	54	18,21,22	1.01	1 (5%)	22,30,33	1.81	3 (13%)
22	PSU	a	955	22	18,21,22	1.13	3 (16%)	22,30,33	1.91	4 (18%)
55	5MU	V	53	55	19,22,23	4.39	7 (36%)	28,32,35	3.69	9 (32%)
55	H2U	V	19	55	18,21,22	1.24	3 (16%)	21,30,33	0.85	0
22	G7M	a	2069	22	23,26,27	2.66	9 (39%)	35,39,42	1.73	9 (25%)
22	H2U	a	2449	22	18,21,22	1.41	3 (16%)	21,30,33	1.19	3 (14%)
55	5MC	V	48	55	18,22,23	3.53	7 (38%)	26,32,35	1.13	2 (7%)
22	OMC	a	2498	22,56	19,22,23	2.64	7 (36%)	26,31,34	0.88	0
22	PSU	a	1917	22	18,21,22	1.07	2 (11%)	22,30,33	1.95	4 (18%)
22	2MA	a	2503	22,56	22,25,26	3.68	9 (40%)	33,37,40	2.87	10 (30%)
22	3TD	a	1915	22	18,22,23	3.88	7 (38%)	22,32,35	1.90	3 (13%)
1	4OC	A	1402	1	20,23,24	2.80	8 (40%)	26,32,35	1.05	3 (11%)
22	OMG	a	2251	54,22	23,26,27	2.51	8 (34%)	33,38,41	2.02	9 (27%)
33	4D4	l	81	33	9,11,12	1.71	1 (11%)	8,13,15	2.03	3 (37%)
55	1MA	V	57	55	21,25,26	0.76	0	31,37,40	0.81	1 (3%)
1	MA6	A	1519	1	23,26,27	1.56	5 (21%)	34,38,41	2.31	12 (35%)
22	PSU	a	1911	22	18,21,22	1.06	1 (5%)	22,30,33	1.90	4 (18%)
22	OMU	a	2552	22	19,22,23	2.61	6 (31%)	26,31,34	1.88	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
54	5MU	Z	55	54	19,22,23	4.56	6 (31%)	28,32,35	3.78	9 (32%)
22	5MU	a	747	22	19,22,23	4.40	7 (36%)	28,32,35	3.94	9 (32%)
1	G7M	A	527	1	23,26,27	2.74	9 (39%)	35,39,42	1.66	8 (22%)
22	5MU	a	1939	22	19,22,23	4.40	7 (36%)	28,32,35	3.93	10 (35%)
54	4SU	Z	8	54	18,21,22	3.99	8 (44%)	26,30,33	2.32	5 (19%)
55	5MC	V	38	55	18,22,23	3.52	8 (44%)	26,32,35	1.16	2 (7%)
1	5MC	A	1407	1	18,22,23	3.33	7 (38%)	26,32,35	1.15	2 (7%)
11	IAS	K	119	11	6,7,8	1.00	0	6,8,10	1.22	1 (16%)
54	H2U	Z	21	54	18,21,22	1.01	2 (11%)	21,30,33	0.76	1 (4%)
22	6MZ	a	2030	22	22,25,26	2.70	5 (22%)	30,36,39	2.48	12 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
12	D2T	L	89	12	-	1/7/12/14	-
55	PSU	V	13	55	-	0/7/25/26	0/2/2/2
22	PSU	a	2504	22	-	2/7/25/26	0/2/2/2
55	5MC	V	47	55	-	2/7/25/26	0/2/2/2
54	OMC	Z	33	54	-	0/9/27/28	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
55	1MA	V	9	55	-	3/7/25/26	0/3/3/3
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
25	MEQ	d	150	25	-	2/8/9/11	-
22	PSU	a	746	22,56	-	1/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
33	MS6	l	82	33	-	1/4/6/8	-
55	PSU	V	54	55	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	2/9/27/28	0/3/3/3
1	PSU	A	516	1,56	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	2/9/27/28	0/3/3/3
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	56B	V	34	55	-	2/12/43/44	0/4/4/4
55	2MG	V	6	55	-	3/9/27/28	0/3/3/3
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
54	PSU	Z	56	54	-	0/7/25/26	0/2/2/2
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
55	5MU	V	53	55	-	0/7/25/26	0/2/2/2
55	H2U	V	19	55	-	0/7/38/39	0/2/2/2
22	G7M	a	2069	22	-	1/7/25/26	0/3/3/3
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2
55	5MC	V	48	55	-	2/7/25/26	0/2/2/2
22	OMC	a	2498	22,56	-	0/9/27/28	0/2/2/2
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
22	2MA	a	2503	22,56	-	1/7/25/26	0/3/3/3
22	3TD	a	1915	22	-	0/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
22	OMG	a	2251	54,22	-	1/9/27/28	0/3/3/3
33	4D4	l	81	33	-	1/11/12/14	-
55	1MA	V	57	55	-	0/7/25/26	0/3/3/3
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
54	5MU	Z	55	54	-	0/7/25/26	0/2/2/2
22	5MU	a	747	22	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
54	4SU	Z	8	54	-	0/7/25/26	0/2/2/2
55	5MC	V	38	55	-	0/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
54	H2U	Z	21	54	-	7/7/38/39	0/2/2/2
22	6MZ	a	2030	22	-	2/9/27/28	0/3/3/3

The worst 5 of 272 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	11.69	1.48	1.35
22	a	2503	2MA	C4-N3	11.25	1.48	1.34
22	a	2030	6MZ	C6-N6	10.78	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1618	6MZ	C6-N6	10.71	1.45	1.34
54	Z	55	5MU	C6-N1	10.42	1.55	1.38

The worst 5 of 294 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	a	747	5MU	C5-C4-N3	13.09	126.48	115.31
22	a	1939	5MU	C5-C4-N3	13.00	126.41	115.31
54	Z	55	5MU	C5-C4-N3	12.69	126.15	115.31
55	V	53	5MU	C5-C4-N3	12.10	125.64	115.31
22	a	1939	5MU	C5-C6-N1	-11.31	111.71	123.34

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1519	MA6	O4'-C4'-C5'-O5'
54	Z	21	H2U	O4'-C1'-N1-C6
54	Z	21	H2U	C2'-C1'-N1-C2
54	Z	21	H2U	C2'-C1'-N1-C6
22	a	2030	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1516	2MG	1	0
12	L	89	D2T	2	0
55	V	9	1MA	1	0
55	V	6	2MG	2	0
1	A	1207	2MG	1	0
55	V	53	5MU	4	0
22	a	2503	2MA	1	0
22	a	2251	OMG	1	0
1	A	1519	MA6	1	0
54	Z	55	5MU	1	0
54	Z	21	H2U	1	0
22	a	2030	6MZ	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 258 ligands modelled in this entry, 258 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	119:IAS	CG	120:GLY	N	1.20

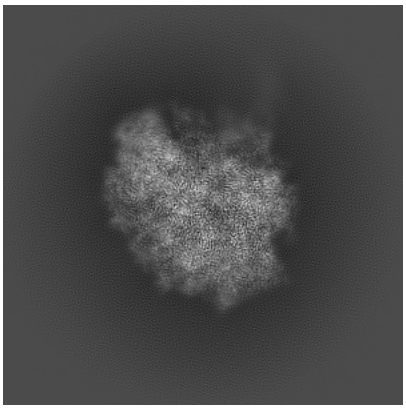
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-33661. These allow visual inspection of the internal detail of the map and identification of artifacts.

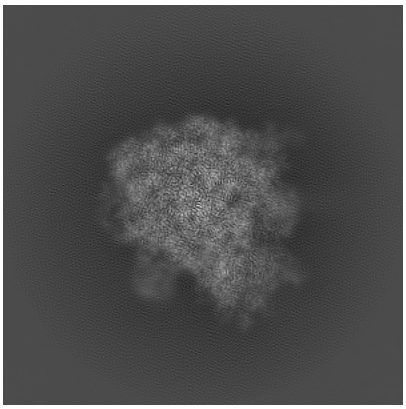
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

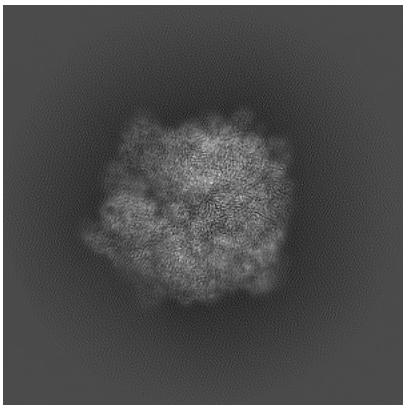
6.1.1 Primary map



X

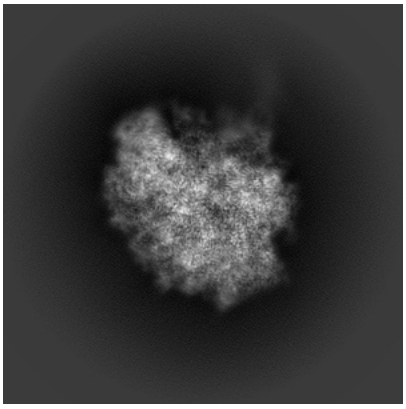


Y

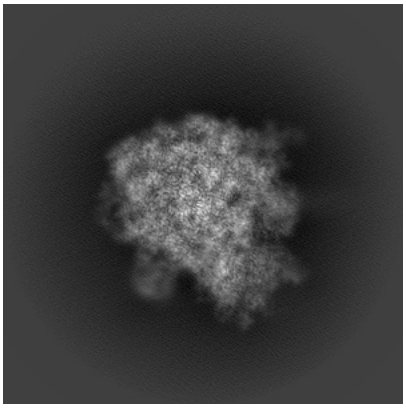


Z

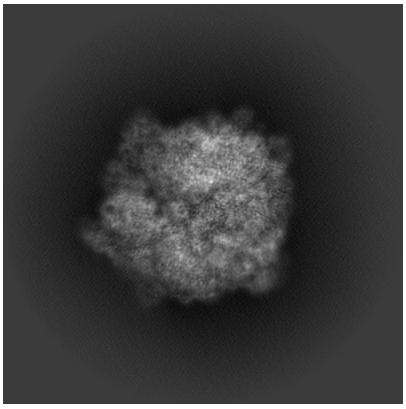
6.1.2 Raw map



X



Y

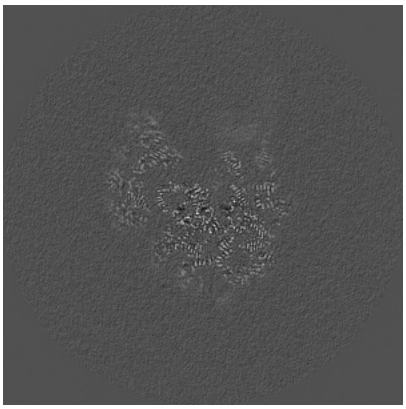


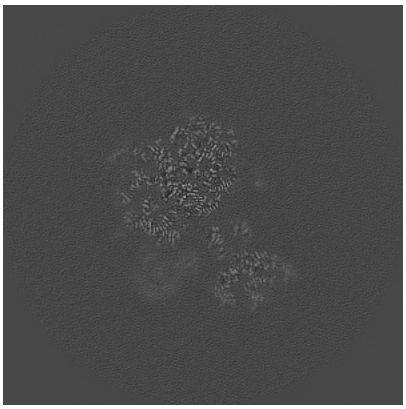
Z

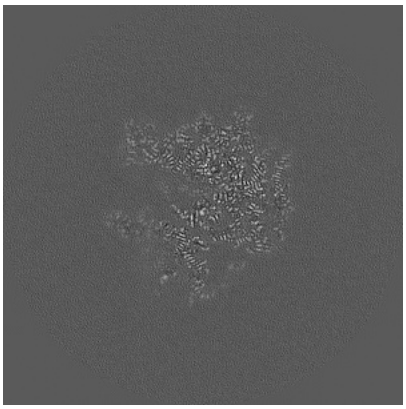
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

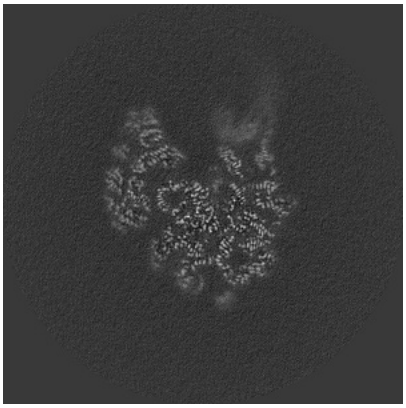
6.2.1 Primary map

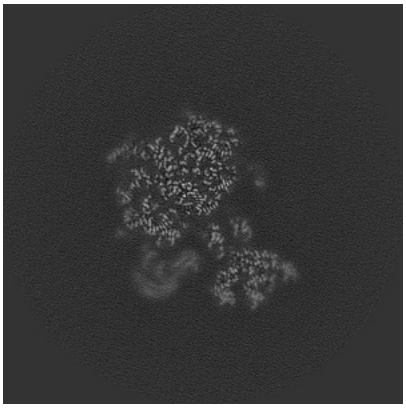

X Index: 265

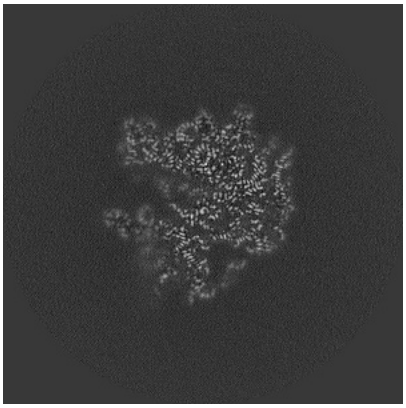

Y Index: 265


Z Index: 265

6.2.2 Raw map


X Index: 265

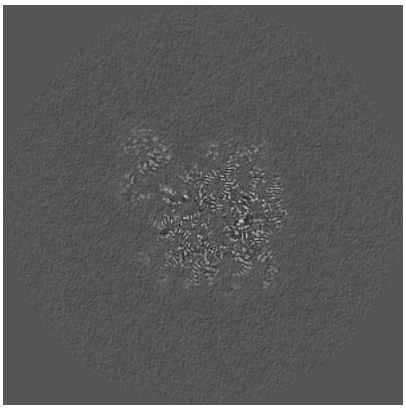

Y Index: 265

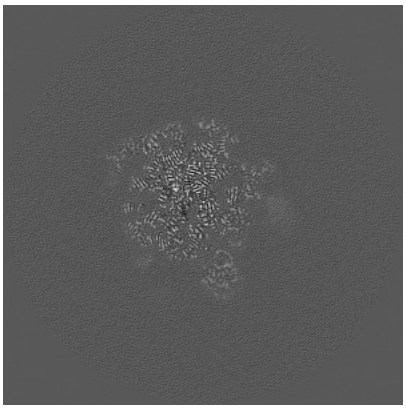

Z Index: 265

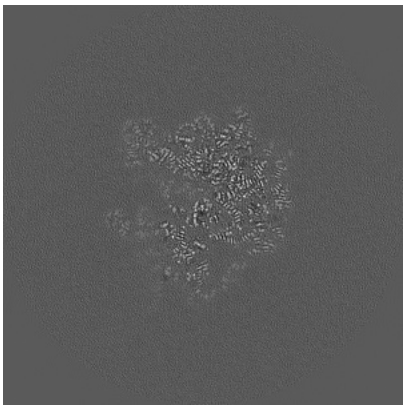
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

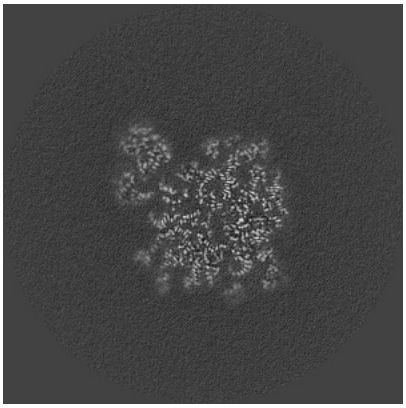
6.3.1 Primary map

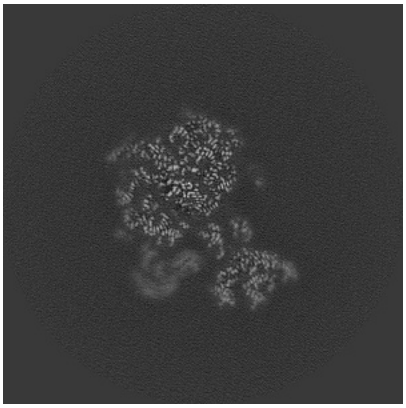

X Index: 297

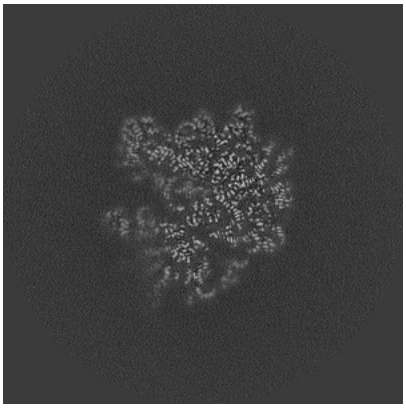

Y Index: 318


Z Index: 267

6.3.2 Raw map


X Index: 297

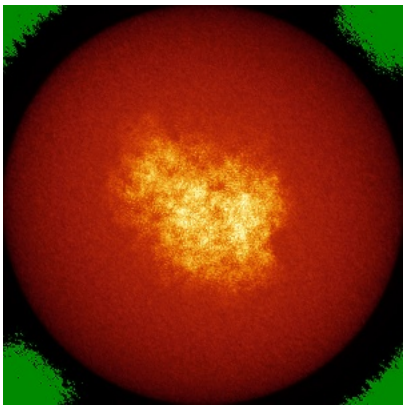

Y Index: 264

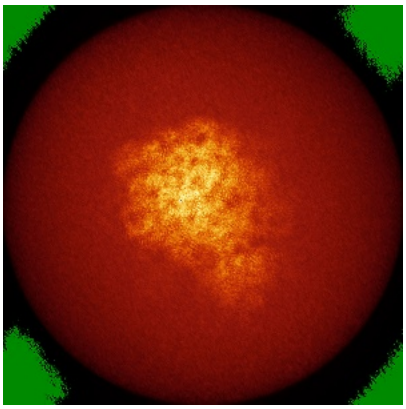

Z Index: 268

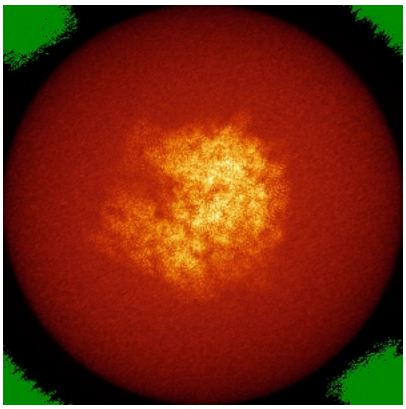
The images above show the largest variance slices of the map in three orthogonal directions.

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

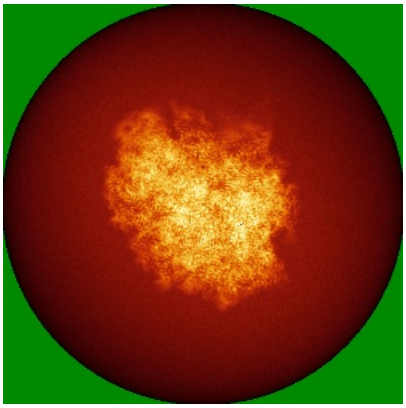
6.4.1 Primary map

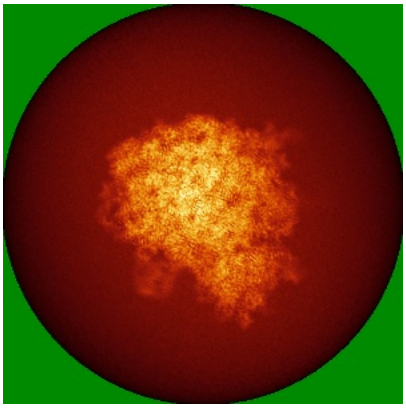

X

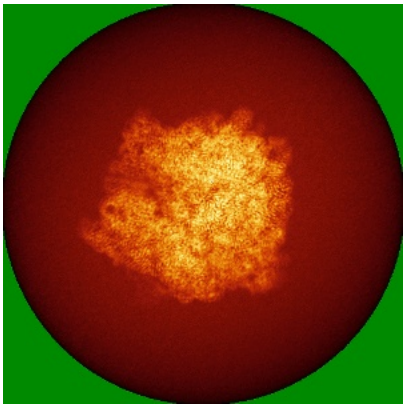

Y


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 0.035. 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.

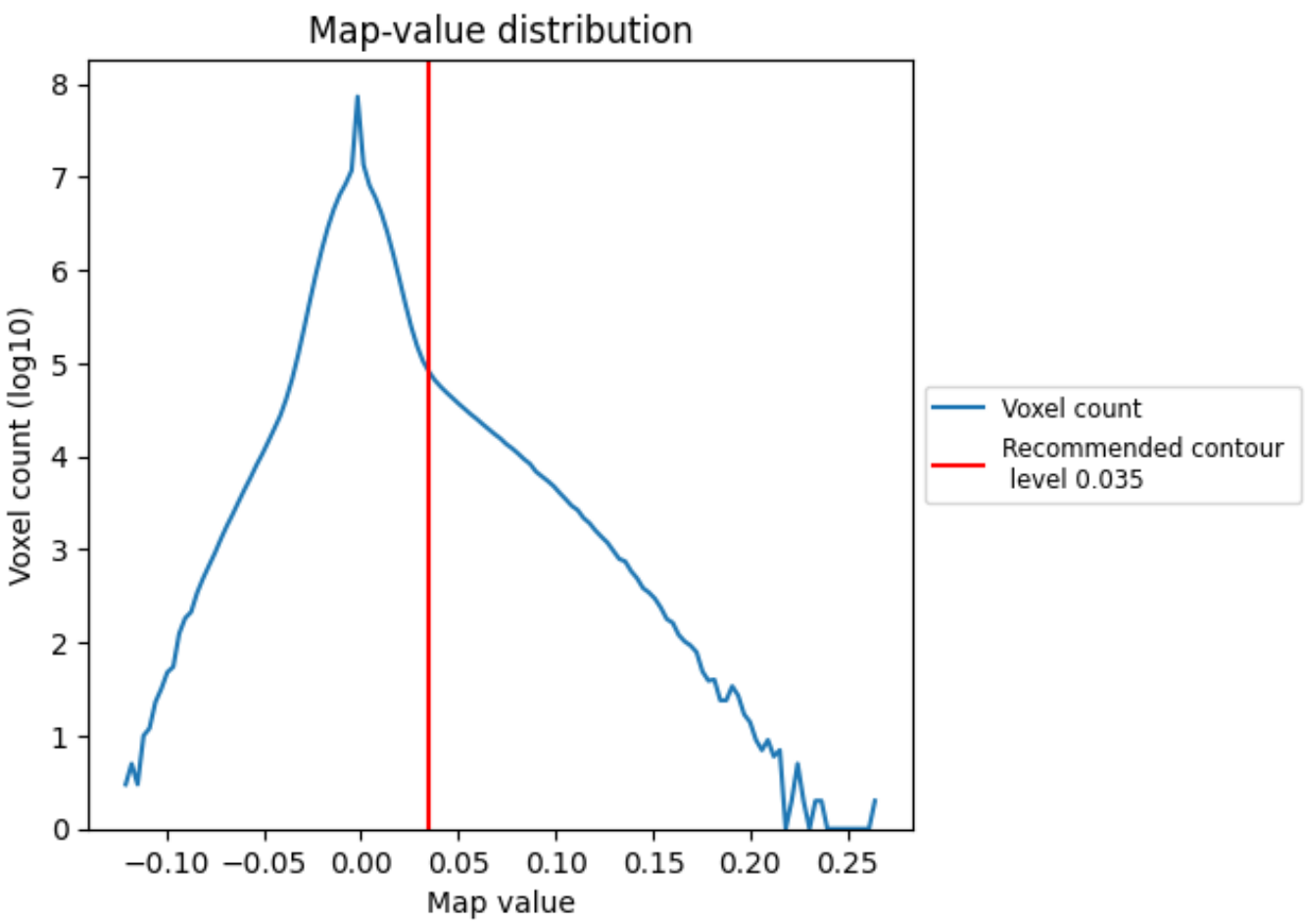
6.6 Mask visualisation (i)

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

7 Map analysis (i)

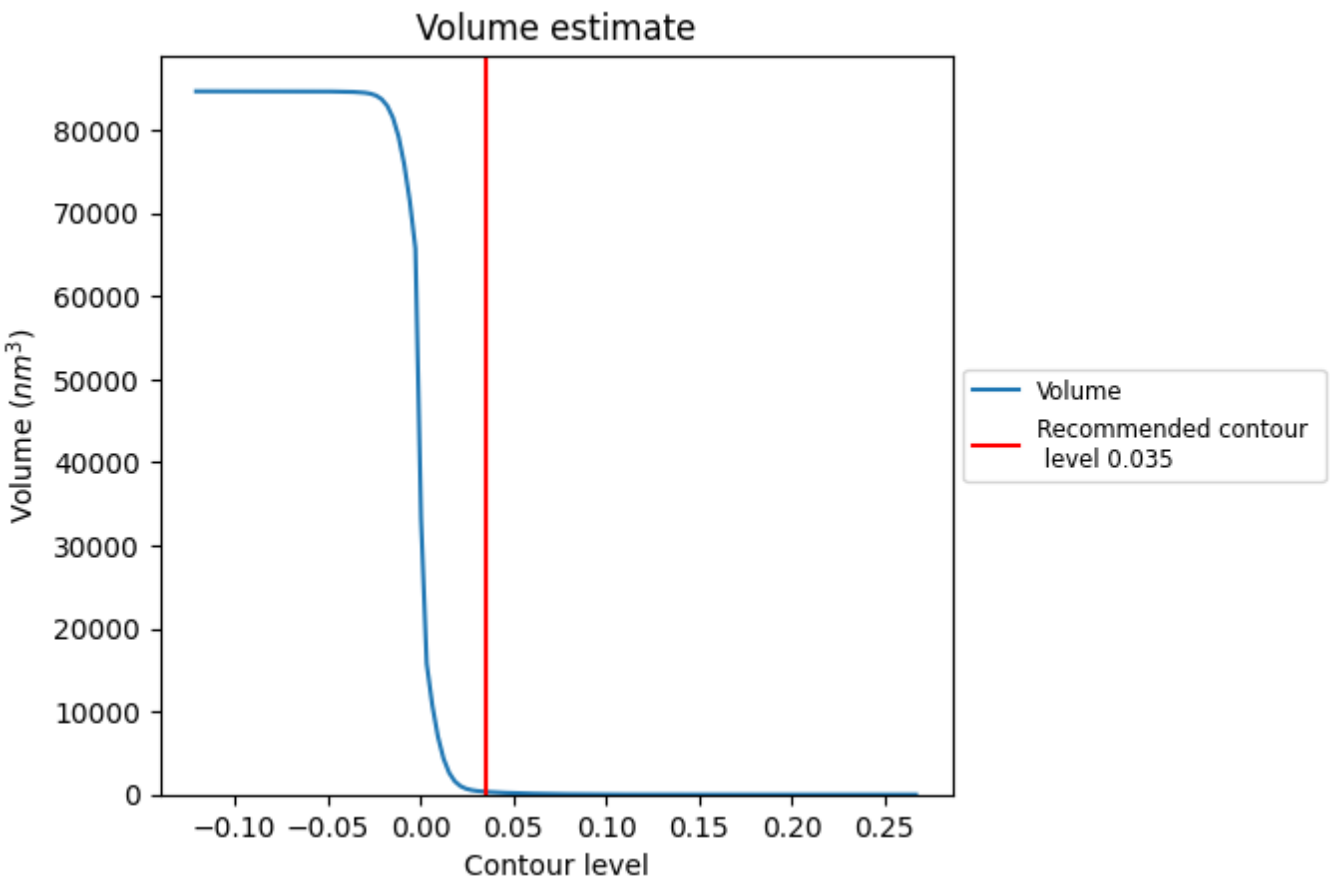
This section contains the results of statistical analysis of the map.

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.

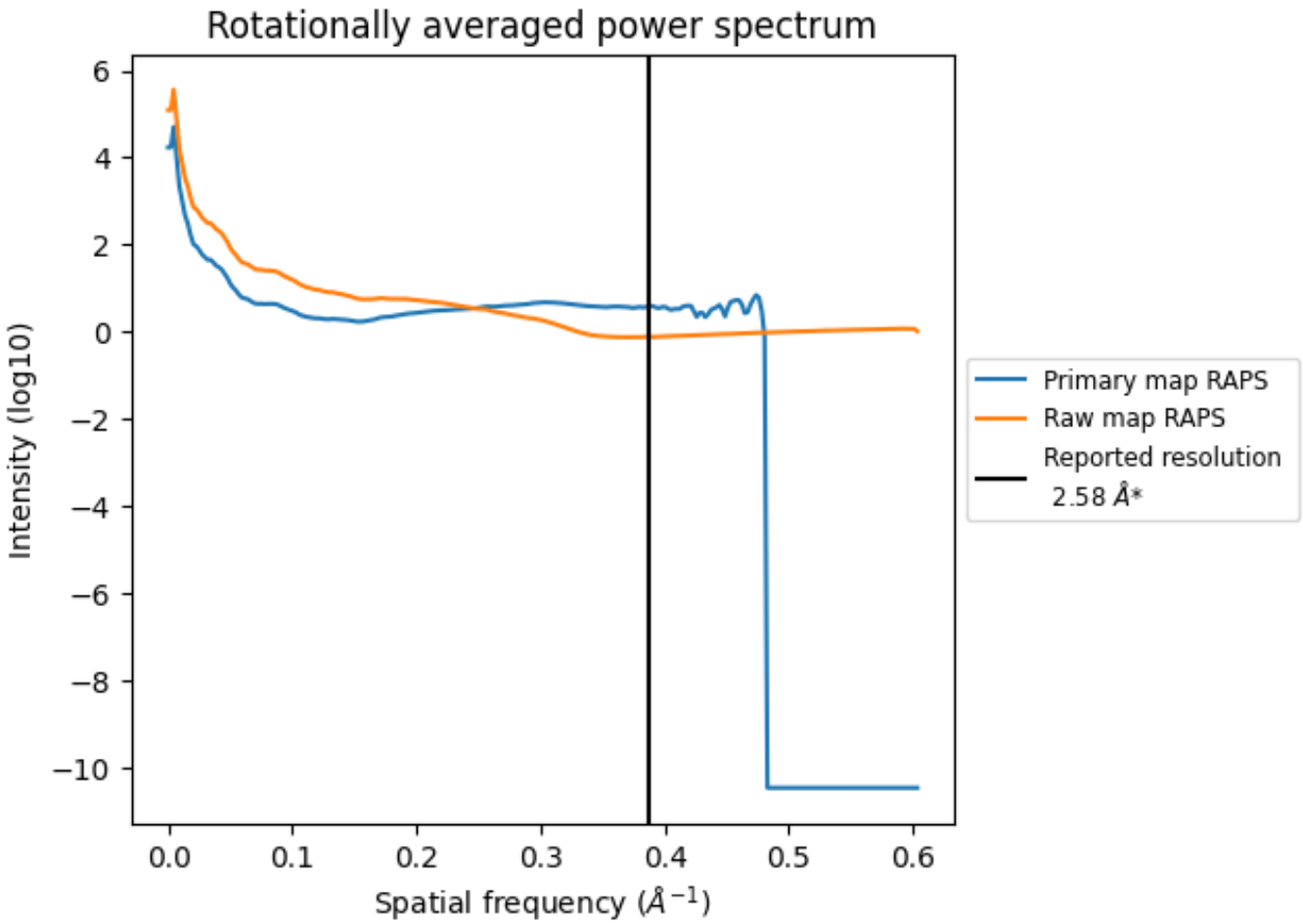
7.2 Volume estimate (i)



The volume at the recommended contour level is 339 nm^3; this corresponds to an approximate mass of 306 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)

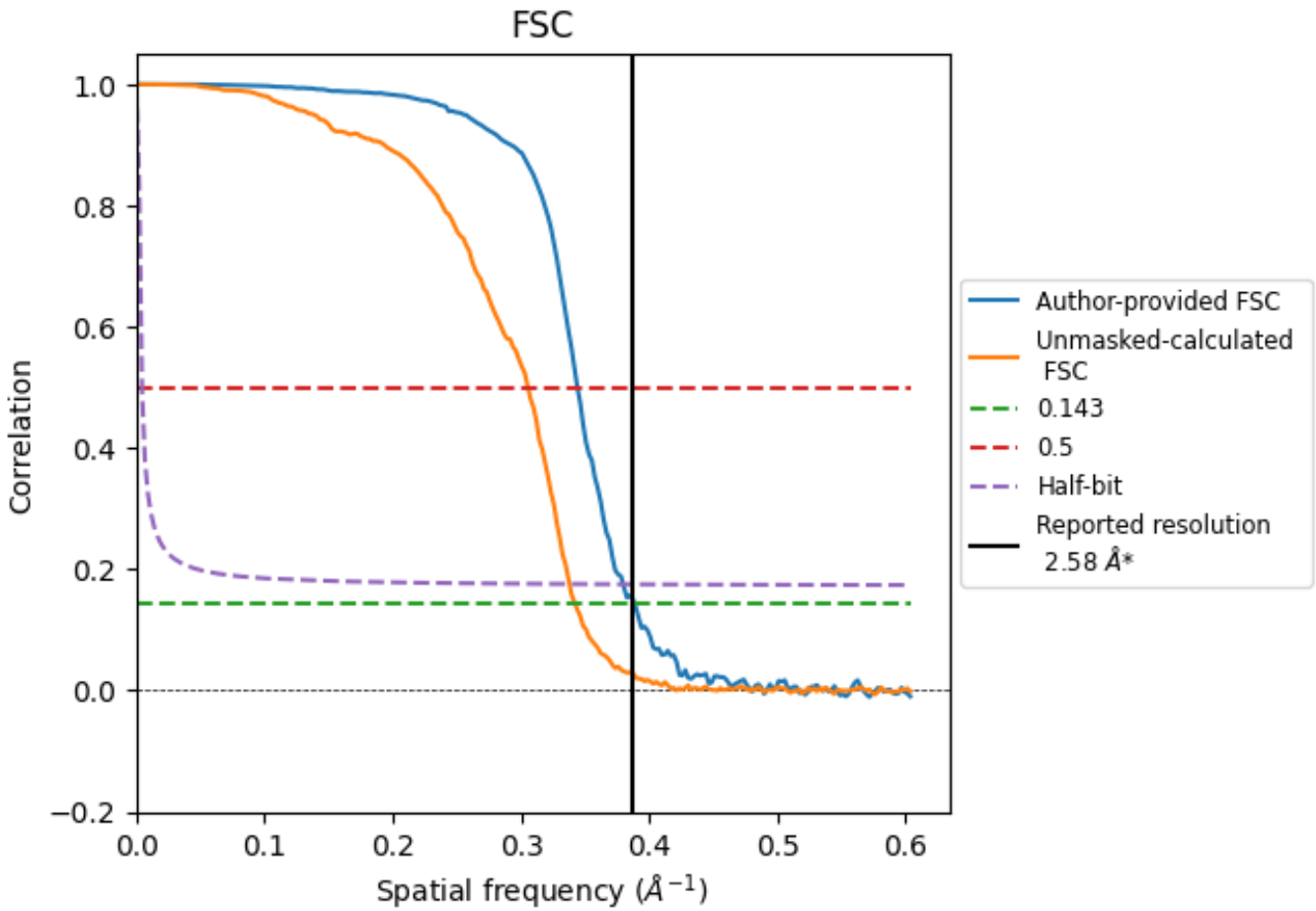


*Reported resolution corresponds to spatial frequency of 0.388 Å^{-1}

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 0.388 Å^{-1}

8.2 Resolution estimates (i)

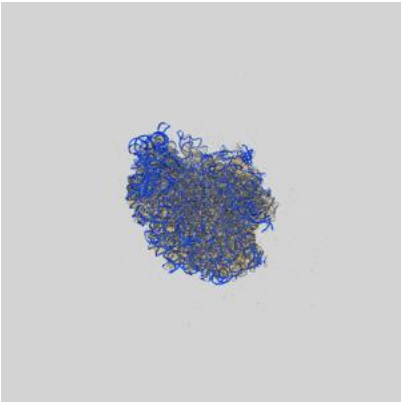
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.58	-	-
Author-provided FSC curve	2.57	2.91	2.63
Unmasked-calculated*	2.92	3.27	2.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.92 differs from the reported value 2.58 by more than 10 %

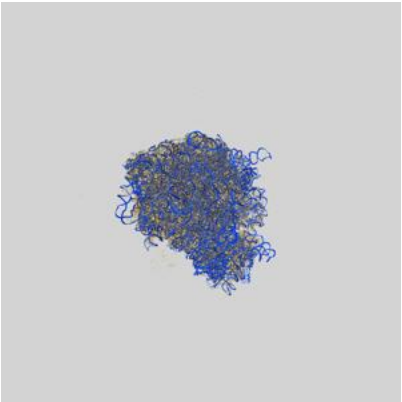
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-33661 and PDB model 7Y7D. Per-residue inclusion information can be found in section 3 on page 15.

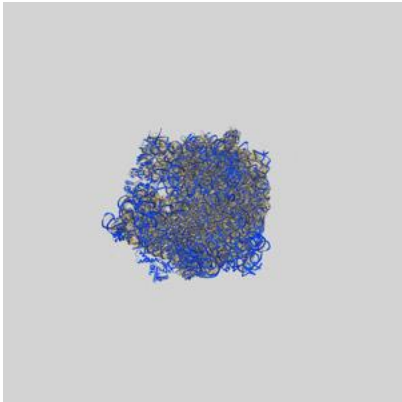
9.1 Map-model overlay (i)



X



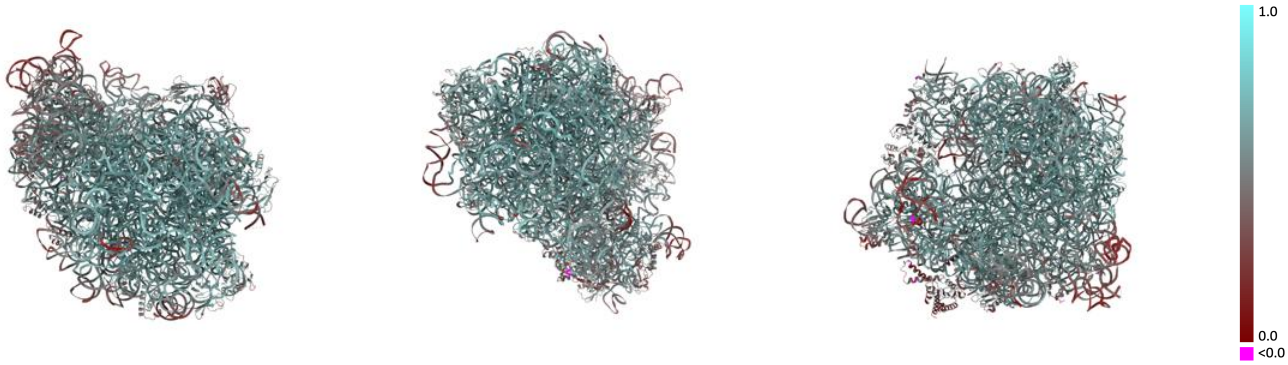
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035 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.

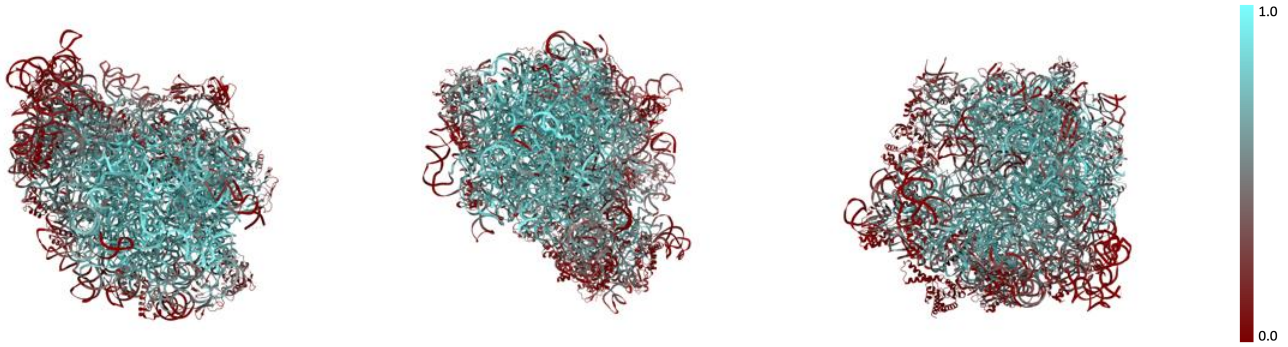
9.2 Q-score mapped to coordinate model (i)



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.

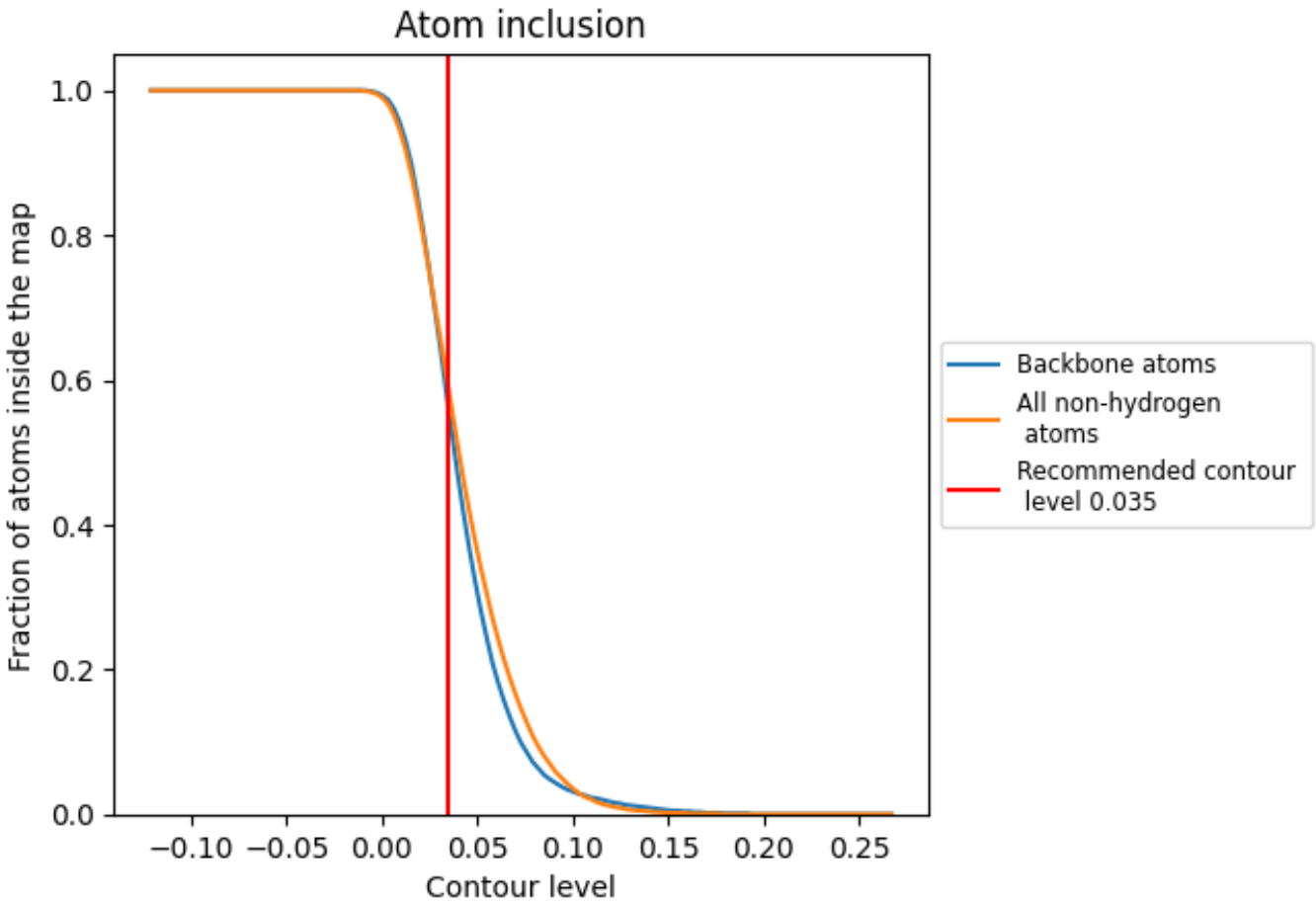
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.035).

9.4 Atom inclusion (i)



At the recommended contour level, 56% of all backbone atoms, 59% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5880	0.5900
0	0.5090	0.5840
1	0.8370	0.6700
2	0.8000	0.6790
3	0.5930	0.6020
4	0.0660	0.4020
A	0.5610	0.5710
B	0.0070	0.3300
C	0.3430	0.5440
D	0.1160	0.4540
E	0.4660	0.5750
F	0.1660	0.4490
G	0.1980	0.4870
H	0.3760	0.5680
I	0.2750	0.5300
J	0.2310	0.4540
K	0.3590	0.5520
L	0.4850	0.5960
M	0.2490	0.5110
N	0.3620	0.5520
O	0.3800	0.5530
P	0.1800	0.4710
Q	0.2740	0.5210
R	0.3120	0.5140
S	0.2790	0.5140
T	0.1470	0.4880
U	0.0970	0.3950
V	0.4710	0.5630
X	0.5560	0.5710
Z	0.4620	0.5330
a	0.7480	0.6330
b	0.4990	0.5700
c	0.7300	0.6640
d	0.6310	0.6360
e	0.4630	0.5730

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Chain	Atom inclusion	Q-score
f	0.1850	0.5010
g	0.1140	0.4500
h	0.0830	0.4330
i	0.6440	0.6280
j	0.6350	0.6390
k	0.5530	0.5990
l	0.6750	0.6500
m	0.7550	0.6710
n	0.2710	0.5250
o	0.5380	0.6080
p	0.7390	0.6600
q	0.4990	0.5830
r	0.6950	0.6330
s	0.4180	0.5420
t	0.2880	0.5210
u	0.3540	0.5450
v	0.6350	0.6340
w	0.5620	0.6120
x	0.2210	0.4960
y	0.5720	0.6000
z	0.6570	0.6170