



wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 11:22 AM EDT

PDB ID : 5KPW
EMDB ID : EMD-8281
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure III)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-07-05
Resolution : 3.90 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

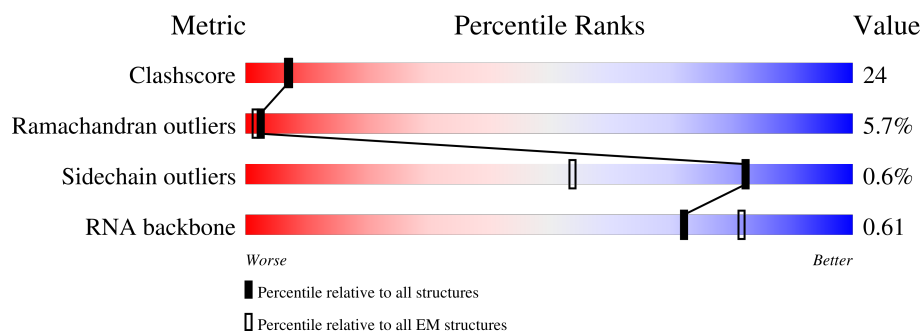
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 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.








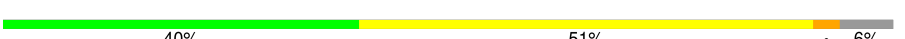


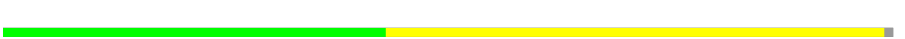
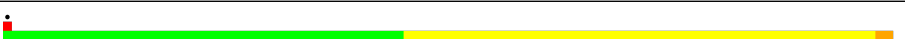

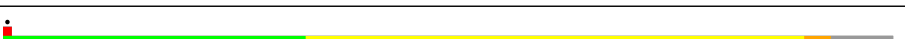


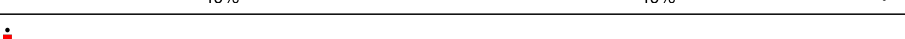
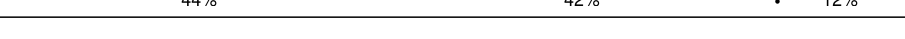
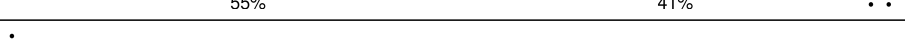
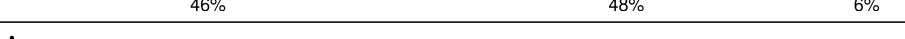
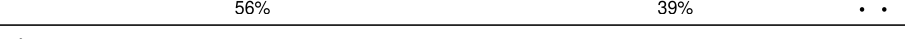

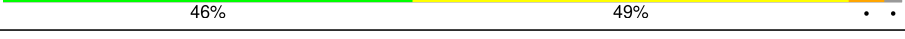

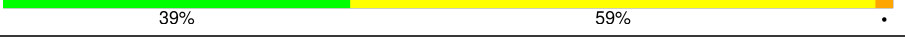


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 $\leq 5\%$. 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	273	<div> <div>58%</div> <div>40%</div> <div>..</div> </div>
2	B	209	<div> <div>46%</div> <div>50%</div> <div>.</div> </div>
3	C	201	<div> <div>48%</div> <div>49%</div> <div>.</div> </div>
4	D	179	<div> <div>41%</div> <div>54%</div> <div>..</div> </div>
5	E	177	<div> <div>50%</div> <div>48%</div> <div>..</div> </div>
6	F	149	<div> <div>17%</div> <div>40%</div> <div>54%</div> <div>5%</div> <div>.</div> </div>
7	G	165	<div> <div>18%</div> <div>17%</div> <div>52%</div> <div>10%</div> <div>21%</div> </div>


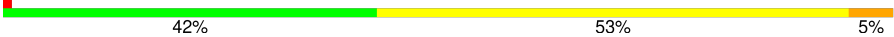

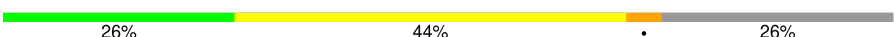


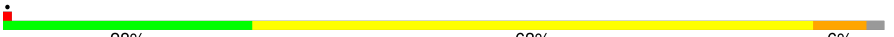
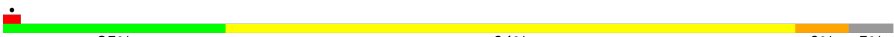
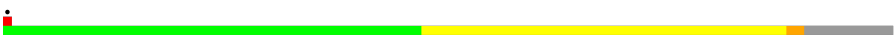

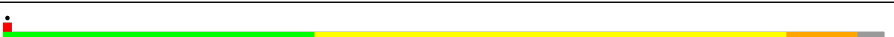
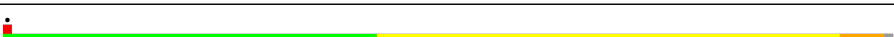

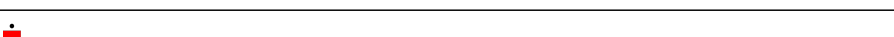
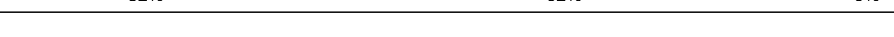
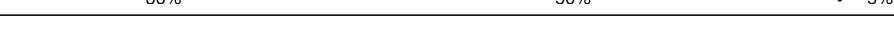



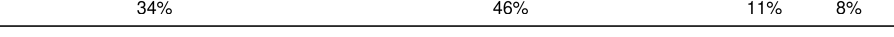


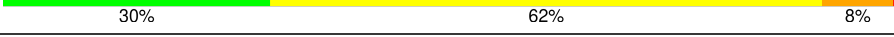

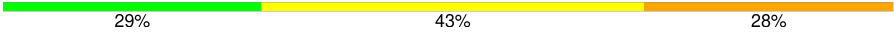
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Mol	Chain	Length	Quality of chain
8	H	142	
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4	65	
31	5	38	
32	6	241	

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Mol	Chain	Length	Quality of chain
33	7	233	
34	8	206	
35	9	167	
36	10	135	
37	11	179	
38	12	130	
39	13	130	
40	14	103	
41	15	129	
42	16	124	
43	17	118	
44	18	101	
45	19	89	
46	20	82	
47	21	84	
48	22	75	
49	23	92	
50	24	87	
51	25	71	
52	26	1539	
53	27	2903	
54	28	120	
55	29	20	
56	30	76	
57	31	77	

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Mol	Chain	Length	Quality of chain
58	32	77	<div><div></div><div>22%</div><div>56%</div><div>22%</div></div>
59	33	750	<div><div></div><div>48%</div><div>38%</div><div>45%</div><div>6%</div><div>10%</div></div>

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 154603 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 L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

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

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

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

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	2	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	10	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	11	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	12	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	13	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	14	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	15	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	16	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	17	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	18	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	19	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	20	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	21	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	22	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	23	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	24	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	25	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	26	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	27	2903	Total	C	N	O	P	0	0
			62322	27801	11468	20150	2903		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
27	747	C	U	conflict	GB 802133627
27	1847	G	A	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	28	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
28	120	A	-	conflict	GB 1028475309

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	29	20	Total	C	N	O	P	0	0
			432	195	86	132	19		

- Molecule 56 is a RNA chain called A-site tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	30	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 57 is a RNA chain called P-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	31	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 58 is a RNA chain called E-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	32	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 59 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	33	675	Total	C	N	O	S	0	0
			4911	3070	904	915	22		

There are 7 discrepancies between the modelled and reference sequences:

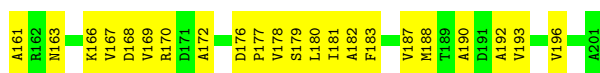
Chain	Residue	Modelled	Actual	Comment	Reference
33	-5	MET	-	expression tag	UNP P0AG20
33	-4	HIS	-	expression tag	UNP P0AG20
33	-3	HIS	-	expression tag	UNP P0AG20
33	-2	HIS	-	expression tag	UNP P0AG20
33	-1	HIS	-	expression tag	UNP P0AG20
33	0	HIS	-	expression tag	UNP P0AG20
33	1	HIS	-	expression tag	UNP P0AG20

3 Residue-property plots

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 L2





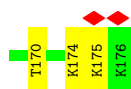
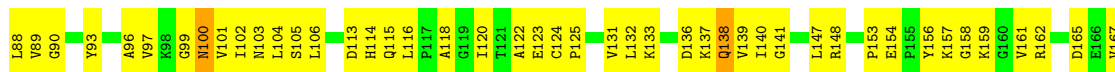
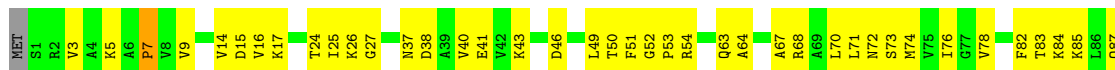
• Molecule 4: 50S ribosomal protein L5

Chain D: 41% 54% ..



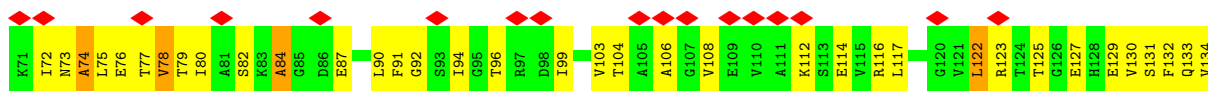
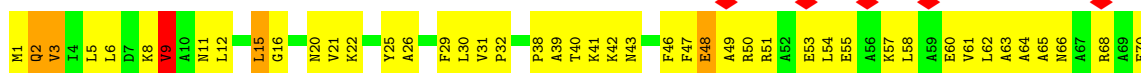
• Molecule 5: 50S ribosomal protein L6

Chain E: 50% 48% ..



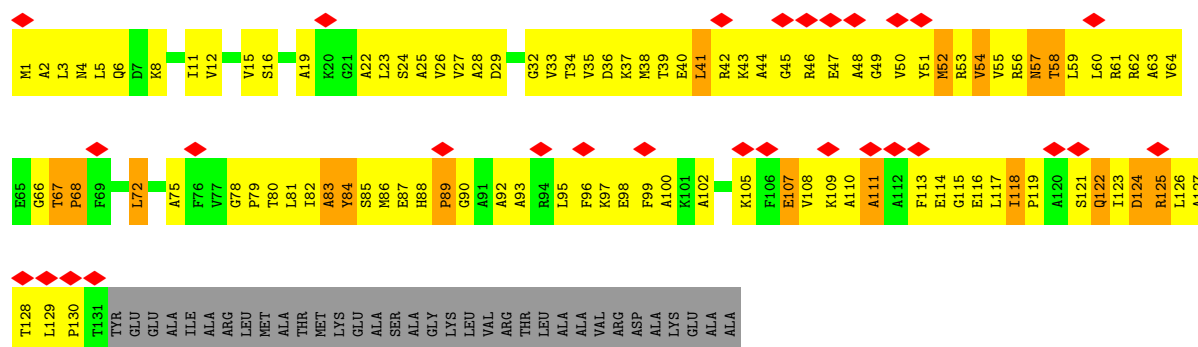
• Molecule 6: 50S ribosomal protein L9

Chain F: 17% 40% 54% 5% ..



• Molecule 7: 50S ribosomal protein L10

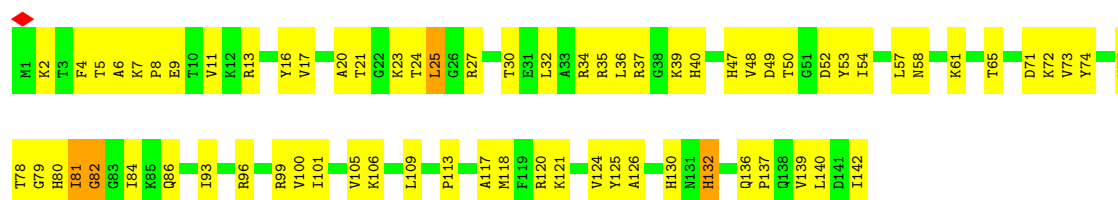
Chain G: 18% 17% 52% 10% 21%



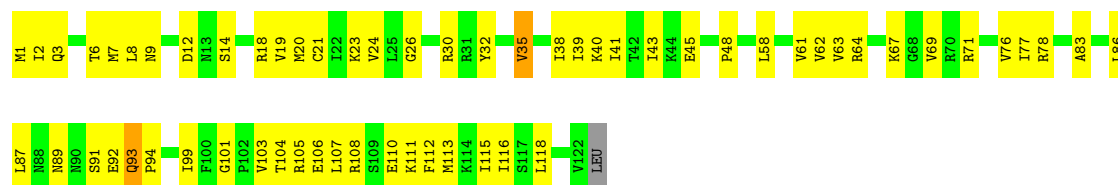
• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15





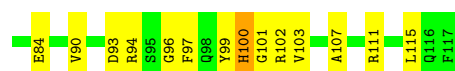
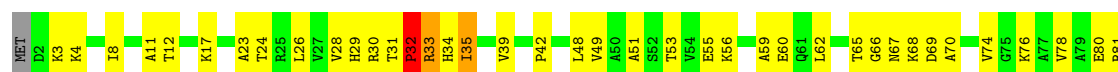
• Molecule 12: 50S ribosomal protein L16



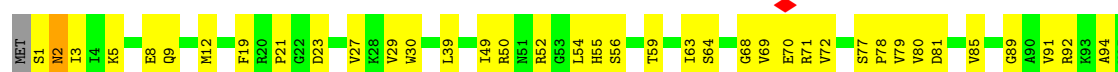
• Molecule 13: 50S ribosomal protein L17



• Molecule 14: 50S ribosomal protein L18

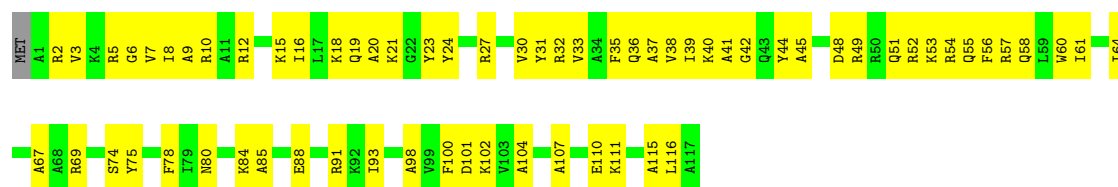


• Molecule 15: 50S ribosomal protein L19



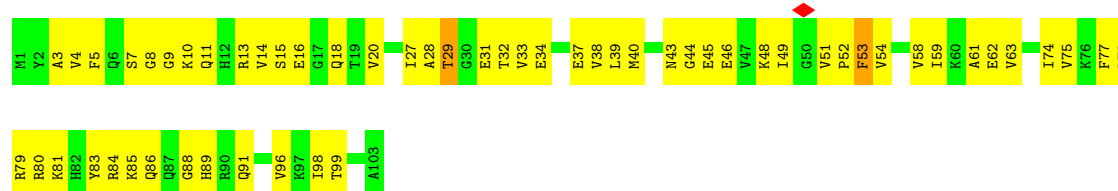
• Molecule 16: 50S ribosomal protein L20

Chain P: 



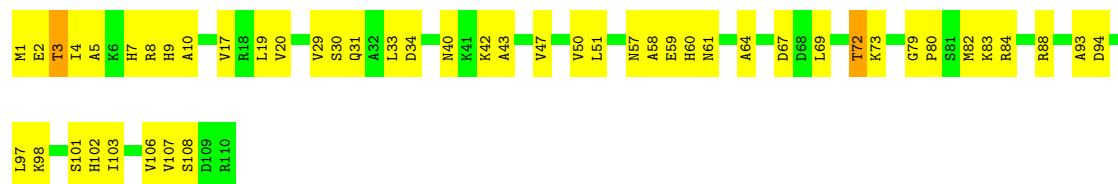
- Molecule 17: 50S ribosomal protein L21

Chain Q: 



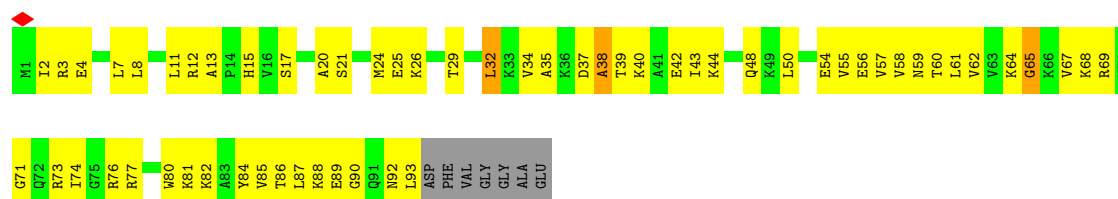
- Molecule 18: 50S ribosomal protein L22

Chain R: 



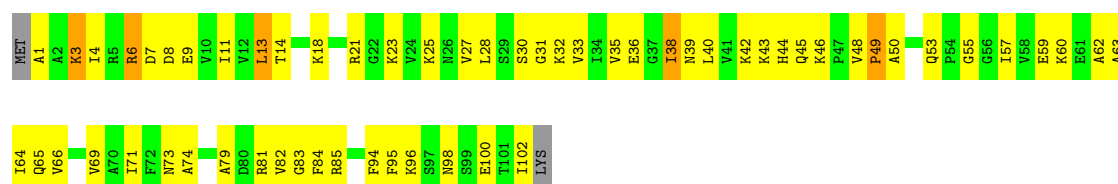
- Molecule 19: 50S ribosomal protein L23

Chain S: 

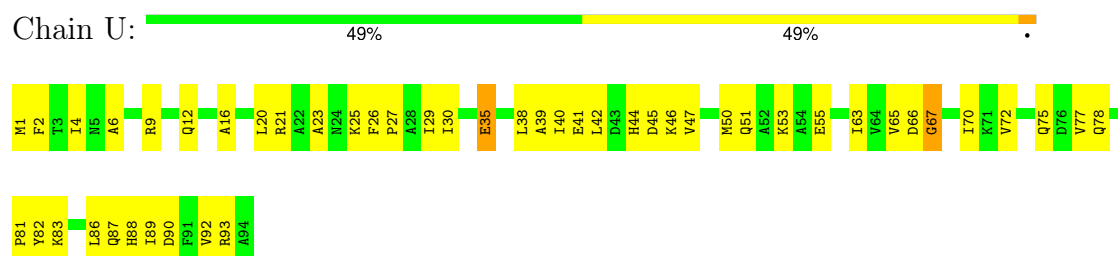


- Molecule 20: 50S ribosomal protein L24

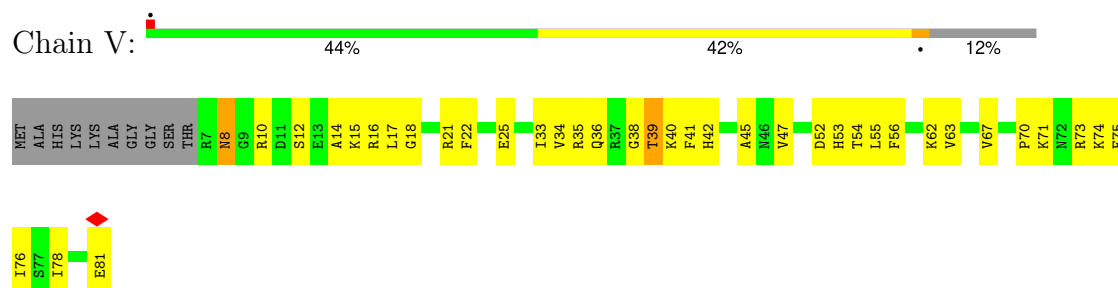
Chain T: 



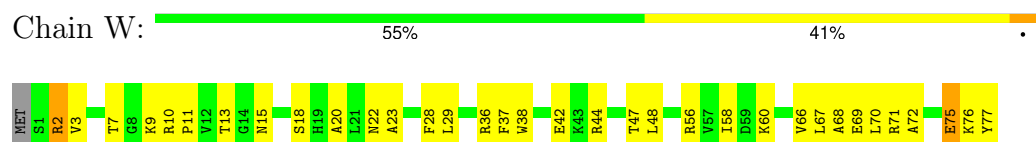
- Molecule 21: 50S ribosomal protein L25



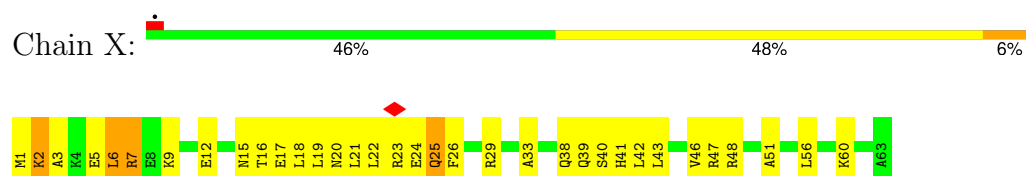
- Molecule 22: 50S ribosomal protein L27



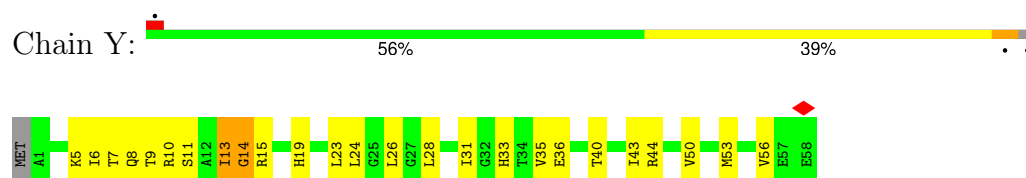
- Molecule 23: 50S ribosomal protein L28



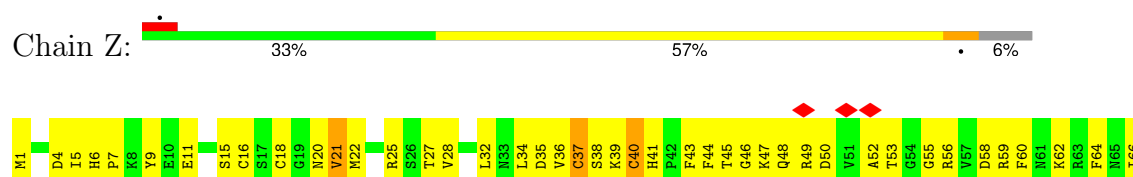
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L31



PRO
GLY
SER
LYS

- Molecule 27: 50S ribosomal protein L32

Chain 1: 

MET A1 V2 Q3 Q4 N5 T8 R12 R16 S17 H18 D19 A23 V24 T25 S26 L27 V29 D30 S33 G34 E35 L38 R39 H40 H41 T42 T43 G46 Y47 R51 K52 V53 I54 A55 K56

- Molecule 28: 50S ribosomal protein L33

Chain 2: 

MET ALA LYS G3 T4 R5 E6 K9 S13 A14 G15 T16 F19 Y20 N25 K26 K29 E34 F38 V41 V42 H45 V46 I47 Y48 K49 E50 A51 K52 ILE LYS

- Molecule 29: 50S ribosomal protein L34

Chain 3: 

H1 K2 R3 T4 R5 G6 P7 S8 V9 L10 K11 N12 R13 R14 G17 F18 R19 A20 N21 M22 A23 T24 K25 N26 G27 R28 V30 R33 R34 R35 R39 L42 T43 V44 K45

- Molecule 30: 50S ribosomal protein L35

Chain 4: 

MET F1 K2 I3 R4 A5 T5 V6 R7 G8 A9 R12 R13 K14 K15 K18 F19 G19 G20 F21 K22 H23 A23 K24 H25 A26 N27 R28 R29 R30 K31 L32 L33 K34 K35 K38 R39 K40 R41 R42 L43 R44 P45 M48 K51 L54 G55 L56 L61 P62 Y63 A64

- Molecule 31: 50S ribosomal protein L36

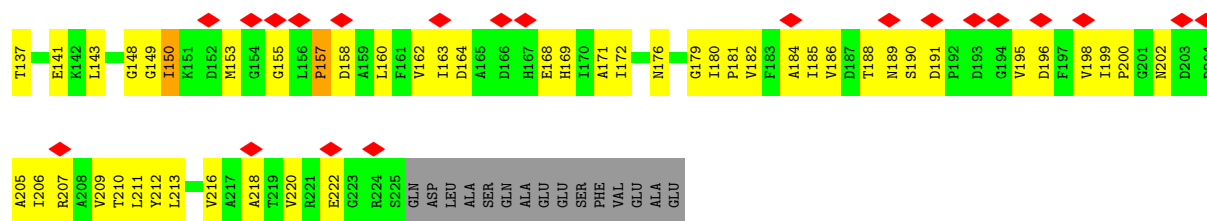
Chain 5: 

M1 K2 V3 R4 A5 S6 V7 C11 R12 N13 C14 V22 I23 R24 V25 I26 C27 S28 A29 P31 K32 H33 K34 Q35 R36 Q37 G38

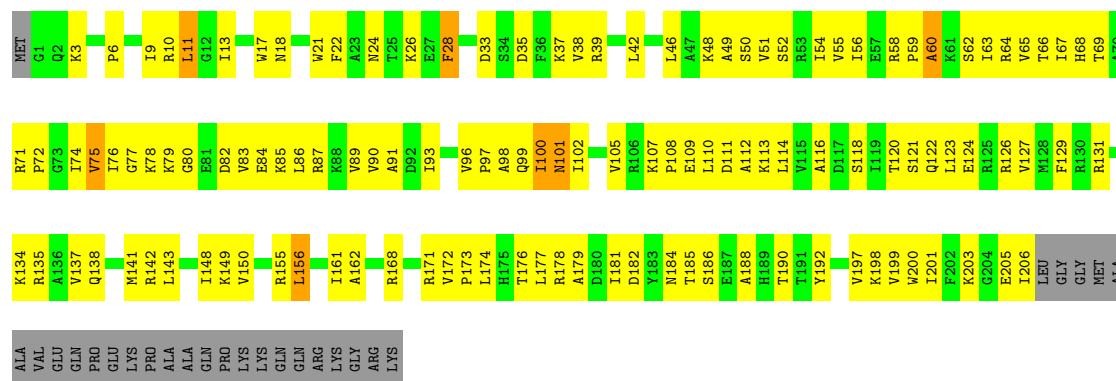
- Molecule 32: 30S ribosomal protein S2

Chain 6: 

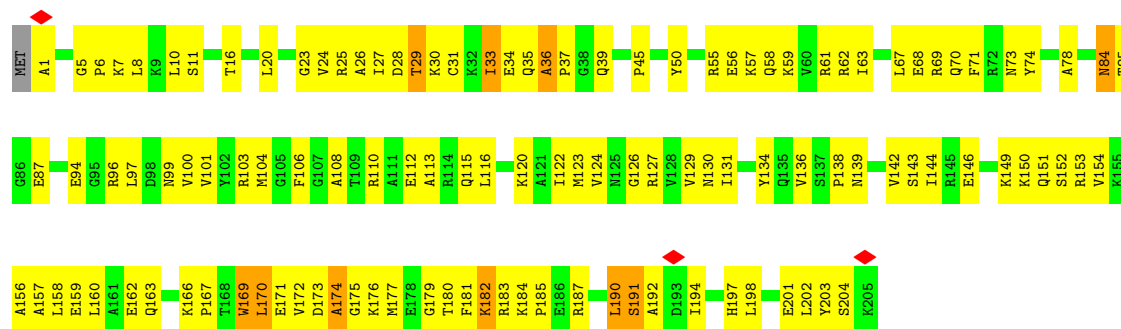
MET ALA THR VAL SER MET ARG ASP M8 L9 K10 A11 G12 V13 H14 F15 G16 H17 Q18 T19 R20 Y21 W22 N23 P24 K25 M26 K27 P28 F29 I30 I31 G32 T105 A33 R34 N35 K36 V37 H38 I39 I40 N41 L42 E43 K44 T45 V46 P47 Q48 F49 N50 E51 A52 L53 A54 E55 L56 N57 K58 I59 K63 G64 K65 I66 L67 K72 R73 A74 A75 V79 A82 A83 L84 S85 F90 H93 R94 N95 N99 L100 T101 N102 V103 K104 T105 V106 R107 I110 K111 R112 L113 K114 D115 L116 E117 T118 Q119 S120 Q121 D122 G123 T124 D125 D126 K127 L128 T129 K130 K131 E132 A133



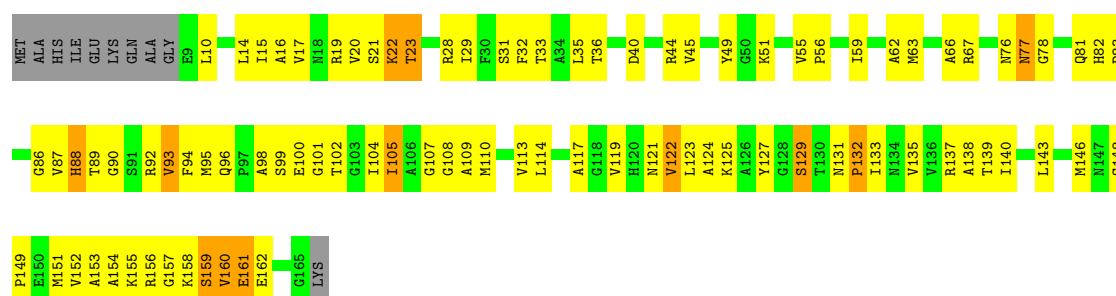
• Molecule 33: 30S ribosomal protein S3



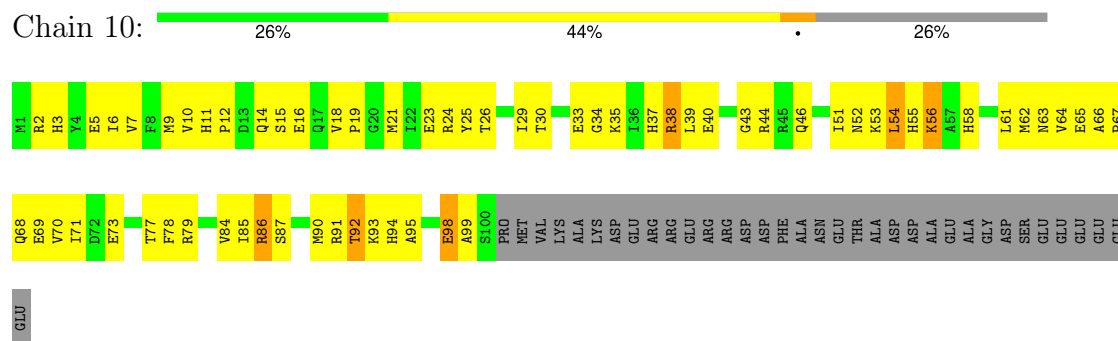
• Molecule 34: 30S ribosomal protein S4



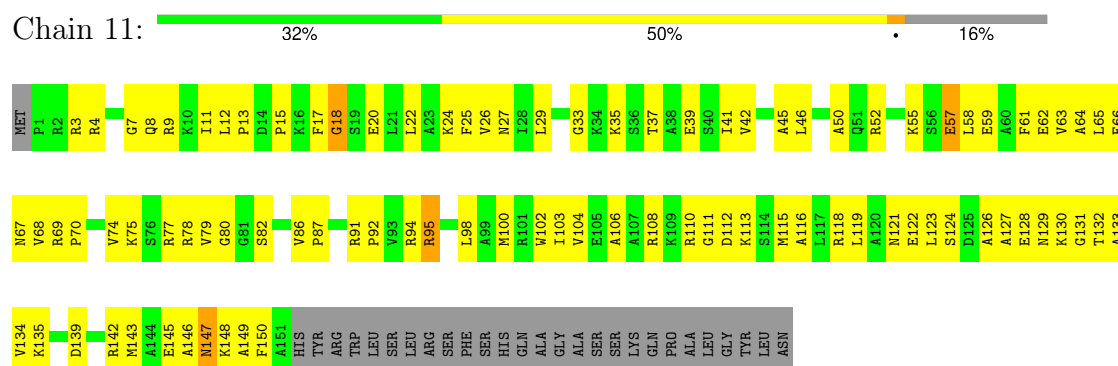
• Molecule 35: 30S ribosomal protein S5



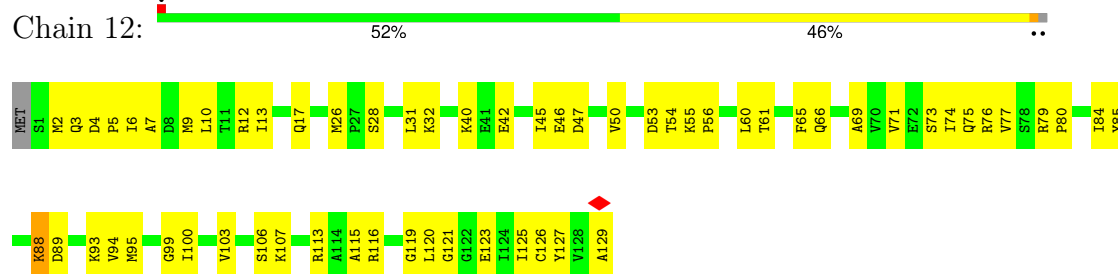
- Molecule 36: 30S ribosomal protein S6



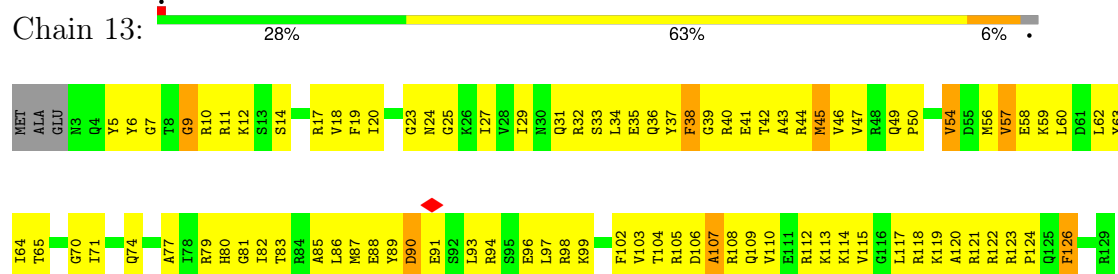
- Molecule 37: 30S ribosomal protein S7



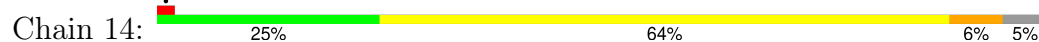
- Molecule 38: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S9



- Molecule 40: 30S ribosomal protein S10

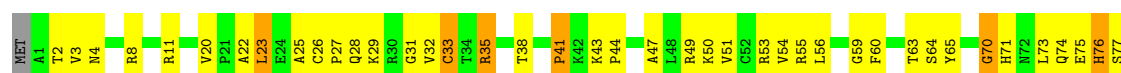




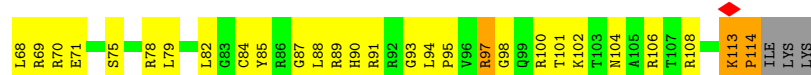
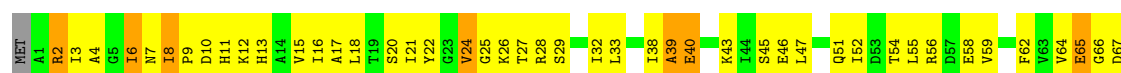
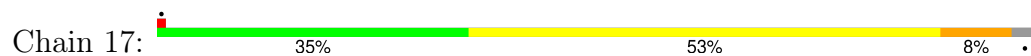
• Molecule 41: 30S ribosomal protein S11



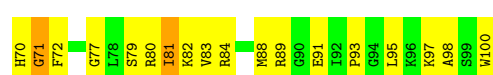
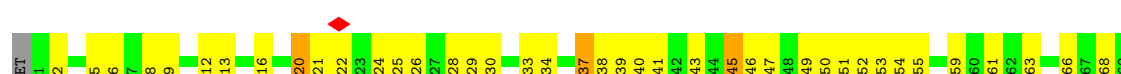
• Molecule 42: 30S ribosomal protein S12



• Molecule 43: 30S ribosomal protein S13



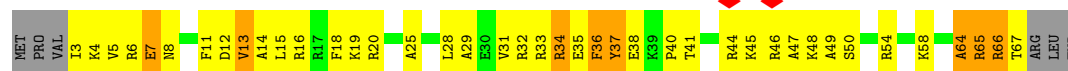
• Molecule 44: 30S ribosomal protein S14



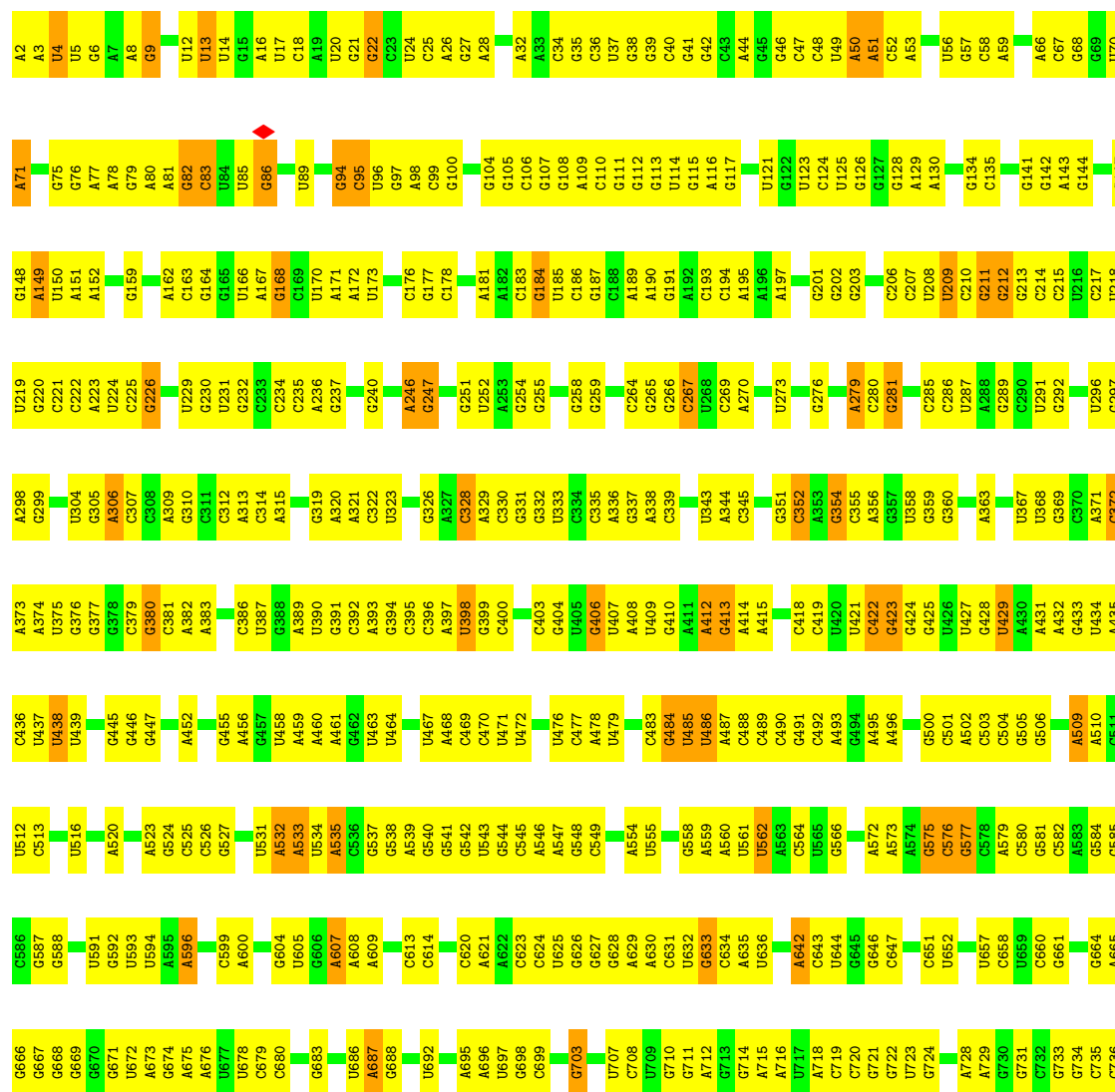
- Chain 24:  51% 46% ..

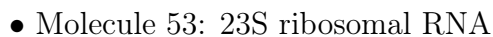


- Molecule 51: 30S ribosomal protein S21



- Molecule 52: 16S ribosomal RNA

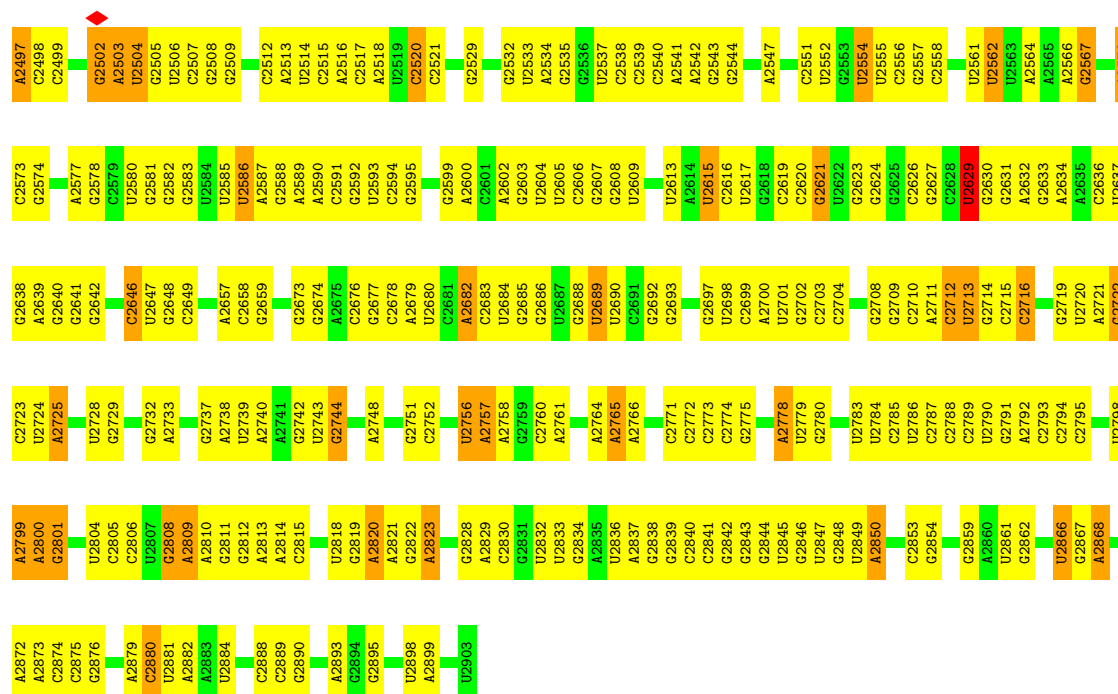




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A156	C79	U4
A157	G80	A5
A158	G81	A6
A159	U82	G7
A160	A83	C8
A161	G84	G9
U162	G85	A10
C163	U92	C11
C164	A95	U12
A165	C96	A13
A166	U100	A14
A167	A101	G15
G168	U102	C16
A172	A103	G17
A173	A104	A18
U174	C105	A19
G175	G106	C20
A176	G107	A21
G177	U112	G24
G178	U113	U25
G179	U114	U26
G180	C115	G27
A181	C116	A28
C184	G117	U29
G185	A118	U34
G186	A119	G35
G187	U120	U40
G188	C121	C41
G189	G122	A44
A190	G123	C45
C192	A127	G46
C193	C128	A49
G194	U131	U50
A195	G132	G51
A196	U133	A52
A197	G134	A53
C198	U139	G54
A199	C140	G55
C200	A141	A56
U202	G142	C57
G205	C143	G58
U206	A144	C61
C208	U145	U62
C209	C146	A63
C210	A149	A64
C211	U150	U65
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G215	U154	C75
G216		
A217		
C218		

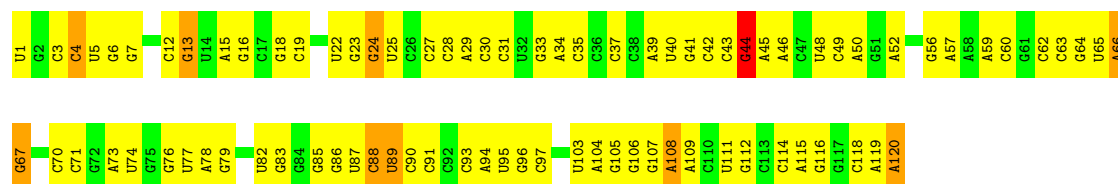
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C1145	C1146	U1147	U1148	G1149	C1150	A1151	C1152	C1153	G1154	A1155	A1156	G1157	C1158	U1159	G1160	C1161	G1162	G1163	C1164	A1165	G1166	G1171	C1172	U1173	U1174	A1175	U1176	G1177	C1178	U1179	U1180	U1181	G1182	U1183	U1184	G1185	G1186	G1187	U1188	A1189	G1190	G1197	U1198	U1199	C1200	U1203	A1204	A1205	G1206	G1210	C1211	G1212	A1213	A1214	G1215
G1225	C1229	A1230	C1233	U1234	G1235	G1236	G1239	U1240	C1243	A1244	G1245	U1248	G1249	G1250	C1251	G1252	A1253	U1254	U1255	G1256	U1257	U1258	G1259	C1260	A1261	A1262	U1263	A1264	G1265	G1266	C1270	G1271	A1272	G1278	G1279	G1280	G1281	U1282	G1283	U1284	A1285	A1286	A1287	G1288	C1289	C1295	G1296	C1297	C1298	G1299					
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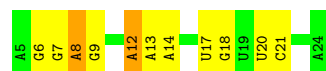
• Molecule 54: 5S ribosomal RNA

Chain 28: 30% 62% 8%



• Molecule 55: mRNA

Chain 29: 45% 45% 10%



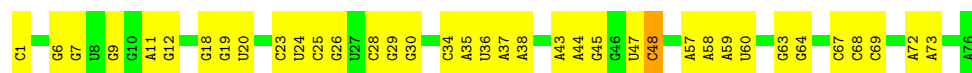
• Molecule 56: A-site tRNA^{Phe}

Chain 30: 29% 43% 28%

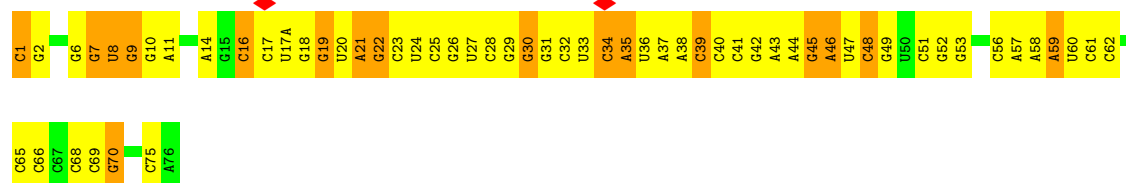


• Molecule 57: P-site tRNA^{fMet}

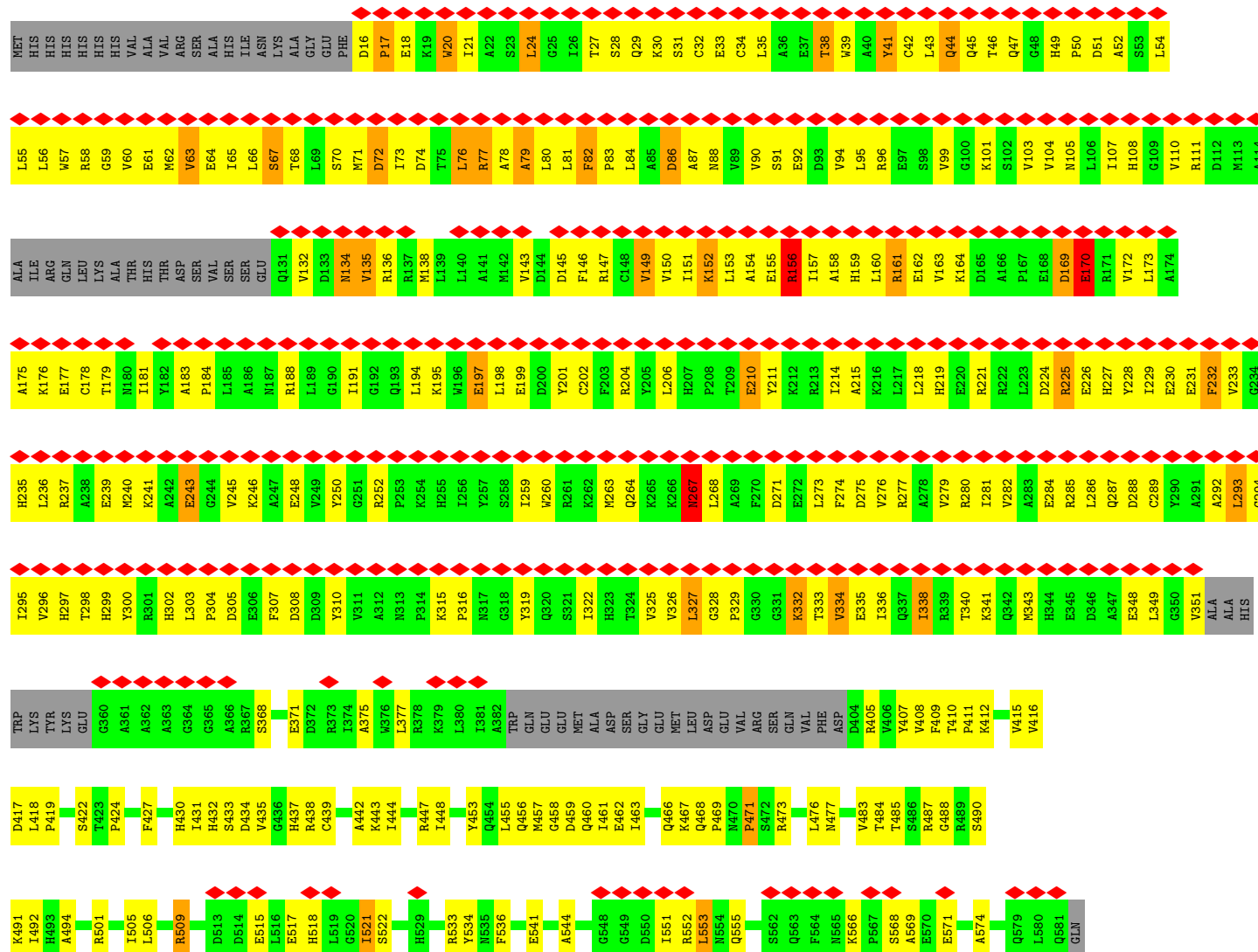
Chain 31: 52% 47% 1%

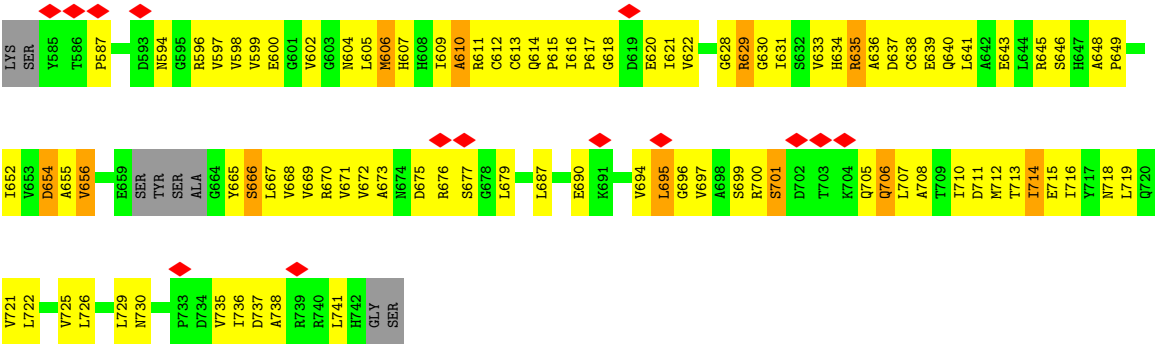


• Molecule 58: E-site tRNA^{fMet}



• Molecule 59: GTP pyrophosphokinase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77862	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 ($e^-/\text{\AA}^2$)	1.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.469	Depositor
Minimum map value	-0.137	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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	0.29	0/2121	0.64	0/2852
2	B	0.33	0/1586	0.62	0/2134
3	C	0.34	0/1571	0.62	0/2113
4	D	0.34	0/1434	0.58	0/1926
5	E	0.30	0/1343	0.62	0/1816
6	F	0.36	0/1122	0.68	0/1515
7	G	0.41	0/1001	0.74	1/1350 (0.1%)
8	H	0.38	0/1046	0.72	1/1410 (0.1%)
9	I	0.30	0/1152	0.61	0/1551
10	J	0.30	0/947	0.63	0/1268
11	K	0.30	0/1054	0.66	0/1403
12	L	0.33	0/1093	0.59	0/1460
13	M	0.32	0/973	0.63	0/1301
14	N	0.28	0/902	0.57	0/1209
15	O	0.32	0/929	0.61	0/1242
16	P	0.32	0/960	0.56	0/1278
17	Q	0.35	0/829	0.67	1/1107 (0.1%)
18	R	0.27	0/864	0.65	0/1156
19	S	0.30	0/744	0.61	0/994
20	T	0.35	0/787	0.69	0/1051
21	U	0.32	0/766	0.58	0/1025
22	V	0.34	0/582	0.60	0/769
23	W	0.34	0/635	0.63	0/848
24	X	0.31	0/510	0.59	0/677
25	Y	0.30	0/453	0.55	0/605
26	Z	0.37	0/531	0.91	3/709 (0.4%)
27	1	0.28	0/450	0.56	0/599
28	2	0.32	0/416	0.57	0/554
29	3	0.35	0/380	0.58	0/498
30	4	0.32	0/513	0.61	0/676
31	5	0.29	0/303	0.63	0/397
32	6	0.37	0/1735	0.60	0/2338
33	7	0.32	0/1651	0.60	0/2225
34	8	0.32	0/1665	0.60	0/2227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	9	0.31	0/1169	0.70	1/1573 (0.1%)
36	10	0.34	0/835	0.64	0/1128
37	11	0.29	0/1195	0.60	0/1602
38	12	0.31	0/989	0.60	0/1326
39	13	0.33	0/1034	0.66	0/1375
40	14	0.31	0/796	0.62	0/1077
41	15	0.33	0/885	0.68	0/1195
42	16	0.33	0/969	0.73	0/1300
43	17	0.28	0/892	0.63	0/1193
44	18	0.40	0/817	0.58	0/1088
45	19	0.28	0/722	0.55	0/964
46	20	0.35	0/659	0.64	1/884 (0.1%)
47	21	0.33	0/657	0.66	0/881
48	22	0.34	0/544	0.67	0/731
49	23	0.33	0/652	0.62	0/877
50	24	0.29	0/671	0.55	0/888
51	25	0.38	0/550	0.73	0/728
52	26	0.38	1/36967 (0.0%)	0.70	5/57666 (0.0%)
53	27	0.39	1/69801 (0.0%)	0.70	5/108894 (0.0%)
54	28	0.36	1/2876 (0.0%)	0.70	1/4483 (0.0%)
55	29	0.84	0/486	0.70	0/757
56	30	0.50	1/1813 (0.1%)	0.74	0/2823
57	31	0.37	1/1836 (0.1%)	0.68	0/2859
58	32	0.80	2/1835 (0.1%)	0.74	1/2857 (0.0%)
59	33	0.66	6/4985 (0.1%)	1.08	38/6770 (0.6%)
All	All	0.39	13/167683 (0.0%)	0.70	58/250202 (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
52	26	0	9
53	27	0	22
56	30	0	1
59	33	0	2
All	All	0	34

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.64	1.19	1.33
59	33	152	LYS	CD-CE	-7.75	1.31	1.51
59	33	17	PRO	CA-CB	-7.24	1.39	1.53
52	26	2	A	OP3-P	-7.10	1.52	1.61
58	32	1	C	OP3-P	-7.09	1.52	1.61

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.60	130.10	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.76	104.26	119.40
59	33	17	PRO	N-CA-CB	-11.19	89.87	103.30
59	33	17	PRO	CA-CB-CG	10.30	124.37	104.80
59	33	63	VAL	CG1-CB-CG2	-9.24	96.11	110.90

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	159	G	Sidechain
52	26	380	G	Sidechain
52	26	820	U	Sidechain
52	26	898	G	Sidechain
52	26	938	A	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2082	0	2157	111	0
2	B	1565	0	1616	100	0
3	C	1552	0	1619	102	0
4	D	1410	0	1447	120	0
5	E	1323	0	1374	77	0
6	F	1111	0	1148	93	0
7	G	988	0	1025	135	0
8	H	1032	0	1088	109	0
9	I	1129	0	1162	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	64	0
11	K	1045	0	1117	88	0
12	L	1074	0	1157	62	0
13	M	960	0	1000	65	0
14	N	892	0	923	51	0
15	O	917	0	965	61	0
16	P	947	0	1022	72	0
17	Q	816	0	839	54	0
18	R	857	0	922	45	0
19	S	738	0	807	51	0
20	T	779	0	834	55	0
21	U	753	0	780	37	0
22	V	575	0	592	31	0
23	W	625	0	655	32	0
24	X	509	0	543	40	0
25	Y	449	0	491	25	0
26	Z	522	0	521	41	0
27	1	444	0	461	36	0
28	2	409	0	440	17	0
29	3	377	0	418	35	0
30	4	504	0	574	32	0
31	5	302	0	343	28	0
32	6	1704	0	1732	100	0
33	7	1624	0	1699	126	0
34	8	1643	0	1710	136	0
35	9	1156	0	1199	80	0
36	10	817	0	808	68	0
37	11	1181	0	1240	65	0
38	12	979	0	1034	59	0
39	13	1022	0	1070	118	0
40	14	786	0	828	83	0
41	15	869	0	878	65	0
42	16	955	0	1019	65	0
43	17	883	0	944	85	0
44	18	805	0	847	62	0
45	19	714	0	737	26	0
46	20	649	0	666	62	0
47	21	648	0	691	50	0
48	22	535	0	552	40	0
49	23	637	0	665	52	0
50	24	665	0	714	42	0
51	25	544	0	579	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	892	0
53	27	62322	0	31345	1639	0
54	28	2572	0	1302	90	0
55	29	432	0	218	13	0
56	30	1623	0	821	66	0
57	31	1644	0	836	26	0
58	32	1643	0	836	76	0
59	33	4911	0	4550	616	0
All	All	154603	0	105189	6144	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 24.

The worst 5 of 6144 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)
52:26:484:G:H4'	52:26:485:U:H5'	1.23	1.18
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.18
51:25:20:ARG:HH22	52:26:1538:C:H1'	1.05	1.13
59:33:65:ILE:HG21	59:33:157:ILE:HD11	1.31	1.11
59:33:188:ARG:HH12	59:33:377:LEU:HA	1.08	1.11

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	A	269/273 (98%)	226 (84%)	34 (13%)	9 (3%)	3	25
2	B	207/209 (99%)	165 (80%)	29 (14%)	13 (6%)	1	16
3	C	199/201 (99%)	164 (82%)	23 (12%)	12 (6%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	140 (80%)	27 (15%)	8 (5%)	2	20
5	E	174/177 (98%)	145 (83%)	22 (13%)	7 (4%)	2	22
6	F	147/149 (99%)	119 (81%)	16 (11%)	12 (8%)	1	11
7	G	129/165 (78%)	92 (71%)	17 (13%)	20 (16%)	0	3
8	H	139/142 (98%)	106 (76%)	27 (19%)	6 (4%)	2	21
9	I	140/142 (99%)	127 (91%)	7 (5%)	6 (4%)	2	21
10	J	120/123 (98%)	101 (84%)	14 (12%)	5 (4%)	2	21
11	K	141/144 (98%)	116 (82%)	16 (11%)	9 (6%)	1	15
12	L	134/136 (98%)	110 (82%)	20 (15%)	4 (3%)	3	27
13	M	118/127 (93%)	99 (84%)	14 (12%)	5 (4%)	2	21
14	N	114/117 (97%)	92 (81%)	16 (14%)	6 (5%)	1	18
15	O	112/115 (97%)	88 (79%)	20 (18%)	4 (4%)	3	24
16	P	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	7	36
17	Q	101/103 (98%)	82 (81%)	16 (16%)	3 (3%)	3	27
18	R	108/110 (98%)	85 (79%)	19 (18%)	4 (4%)	2	23
19	S	91/100 (91%)	73 (80%)	13 (14%)	5 (6%)	1	18
20	T	100/104 (96%)	80 (80%)	13 (13%)	7 (7%)	1	14
21	U	92/94 (98%)	76 (83%)	13 (14%)	3 (3%)	3	25
22	V	73/85 (86%)	64 (88%)	7 (10%)	2 (3%)	4	29
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	4	29
24	X	61/63 (97%)	52 (85%)	5 (8%)	4 (7%)	1	15
25	Y	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	3	24
26	Z	64/70 (91%)	50 (78%)	9 (14%)	5 (8%)	1	12
27	1	54/57 (95%)	42 (78%)	6 (11%)	6 (11%)	0	6
28	2	48/55 (87%)	41 (85%)	6 (12%)	1 (2%)	5	33
29	3	44/46 (96%)	35 (80%)	7 (16%)	2 (4%)	2	20
30	4	62/65 (95%)	51 (82%)	6 (10%)	5 (8%)	1	11
31	5	36/38 (95%)	26 (72%)	6 (17%)	4 (11%)	0	6
32	6	216/241 (90%)	177 (82%)	31 (14%)	8 (4%)	2	23
33	7	204/233 (88%)	172 (84%)	26 (13%)	6 (3%)	3	27
34	8	203/206 (98%)	158 (78%)	30 (15%)	15 (7%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	116 (75%)	25 (16%)	14 (9%)	0	10
36	10	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	14
37	11	149/179 (83%)	123 (83%)	17 (11%)	9 (6%)	1	16
38	12	127/130 (98%)	112 (88%)	13 (10%)	2 (2%)	8	37
39	13	125/130 (96%)	98 (78%)	17 (14%)	10 (8%)	1	12
40	14	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	0	11
41	15	114/129 (88%)	92 (81%)	18 (16%)	4 (4%)	3	24
42	16	121/124 (98%)	98 (81%)	11 (9%)	12 (10%)	0	8
43	17	112/118 (95%)	90 (80%)	11 (10%)	11 (10%)	0	8
44	18	98/101 (97%)	71 (72%)	20 (20%)	7 (7%)	1	14
45	19	86/89 (97%)	73 (85%)	8 (9%)	5 (6%)	1	16
46	20	80/82 (98%)	64 (80%)	12 (15%)	4 (5%)	1	19
47	21	78/84 (93%)	53 (68%)	19 (24%)	6 (8%)	1	12
48	22	63/75 (84%)	48 (76%)	9 (14%)	6 (10%)	0	9
49	23	77/92 (84%)	60 (78%)	13 (17%)	4 (5%)	1	18
50	24	83/87 (95%)	75 (90%)	5 (6%)	3 (4%)	3	24
51	25	63/71 (89%)	44 (70%)	9 (14%)	10 (16%)	0	3
59	33	663/750 (88%)	550 (83%)	78 (12%)	35 (5%)	1	18
All	All	6509/6970 (93%)	5299 (81%)	841 (13%)	369 (6%)	2	17

5 of 369 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	18	ASP
2	B	181	ASP
2	B	188	LEU
3	C	55	SER
3	C	127	GLU

5.3.2 Protein sidechains ⓘ

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	A	216/218 (99%)	215 (100%)	1 (0%)	86	90
2	B	164/164 (100%)	163 (99%)	1 (1%)	84	88
3	C	165/165 (100%)	164 (99%)	1 (1%)	84	88
4	D	148/150 (99%)	146 (99%)	2 (1%)	62	75
5	E	137/138 (99%)	136 (99%)	1 (1%)	81	86
6	F	114/114 (100%)	113 (99%)	1 (1%)	75	83
7	G	100/123 (81%)	99 (99%)	1 (1%)	73	81
8	H	109/110 (99%)	109 (100%)	0	100	100
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	103 (100%)	0	100	100
11	K	102/103 (99%)	102 (100%)	0	100	100
12	L	109/109 (100%)	109 (100%)	0	100	100
13	M	100/103 (97%)	99 (99%)	1 (1%)	73	81
14	N	86/87 (99%)	84 (98%)	2 (2%)	45	64
15	O	99/100 (99%)	99 (100%)	0	100	100
16	P	89/90 (99%)	89 (100%)	0	100	100
17	Q	84/84 (100%)	84 (100%)	0	100	100
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	79 (99%)	1 (1%)	65	76
20	T	83/85 (98%)	82 (99%)	1 (1%)	67	78
21	U	78/78 (100%)	78 (100%)	0	100	100
22	V	57/63 (90%)	57 (100%)	0	100	100
23	W	67/68 (98%)	67 (100%)	0	100	100
24	X	55/55 (100%)	55 (100%)	0	100	100
25	Y	48/49 (98%)	48 (100%)	0	100	100
26	Z	59/62 (95%)	58 (98%)	1 (2%)	56	72
27	1	47/48 (98%)	47 (100%)	0	100	100
28	2	45/49 (92%)	45 (100%)	0	100	100
29	3	38/38 (100%)	38 (100%)	0	100	100
30	4	51/52 (98%)	51 (100%)	0	100	100
31	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	179 (99%)	1 (1%)	84	88
33	7	170/190 (90%)	168 (99%)	2 (1%)	67	78
34	8	172/173 (99%)	171 (99%)	1 (1%)	84	88
35	9	119/126 (94%)	117 (98%)	2 (2%)	56	72
36	10	87/116 (75%)	86 (99%)	1 (1%)	70	79
37	11	124/147 (84%)	124 (100%)	0	100	100
38	12	104/105 (99%)	104 (100%)	0	100	100
39	13	105/107 (98%)	103 (98%)	2 (2%)	52	70
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	89 (100%)	0	100	100
42	16	103/104 (99%)	103 (100%)	0	100	100
43	17	92/96 (96%)	91 (99%)	1 (1%)	70	79
44	18	83/84 (99%)	81 (98%)	2 (2%)	44	63
45	19	76/77 (99%)	76 (100%)	0	100	100
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	74 (100%)	0	100	100
48	22	56/65 (86%)	55 (98%)	1 (2%)	54	71
49	23	70/79 (89%)	70 (100%)	0	100	100
50	24	65/66 (98%)	65 (100%)	0	100	100
51	25	55/61 (90%)	55 (100%)	0	100	100
59	33	452/635 (71%)	449 (99%)	3 (1%)	81	86
All	All	5303/5698 (93%)	5273 (99%)	30 (1%)	82	88

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

Mol	Chain	Res	Type
32	6	22	TRP
59	33	267	ASN
34	8	170	LEU
59	33	714	ILE
44	18	45	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
36	10	37	HIS
46	20	9	HIS
37	11	121	ASN
39	13	109	GLN
46	20	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	178 (11%)	5 (0%)
53	27	2902/2903 (99%)	379 (13%)	17 (0%)
54	28	119/120 (99%)	15 (12%)	1 (0%)
55	29	19/20 (95%)	3 (15%)	0
56	30	75/76 (98%)	22 (29%)	1 (1%)
57	31	76/77 (98%)	5 (6%)	0
58	32	76/77 (98%)	16 (21%)	0
All	All	4805/4812 (99%)	618 (12%)	24 (0%)

5 of 618 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	4	U
52	26	9	G
52	26	13	U
52	26	22	G
52	26	32	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	1730	C
53	27	2296	U
53	27	2286	G
53	27	2326	C
53	27	421	C

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

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

5.5 Carbohydrates [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.

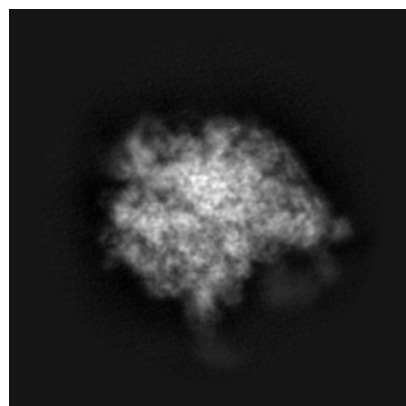
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8281. These allow visual inspection of the internal detail of the map and identification of artifacts.

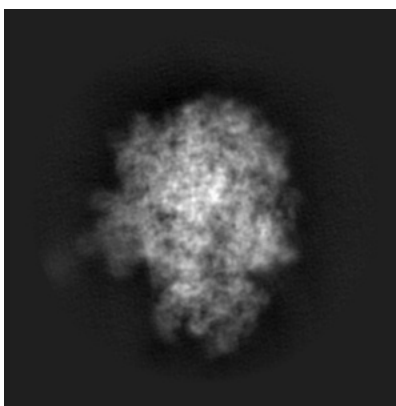
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

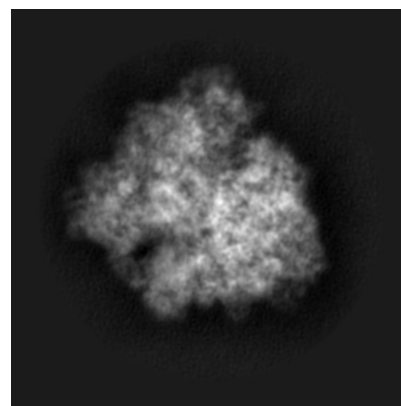
6.1.1 Primary map



X

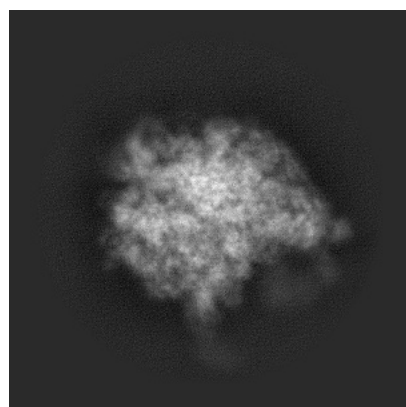


Y

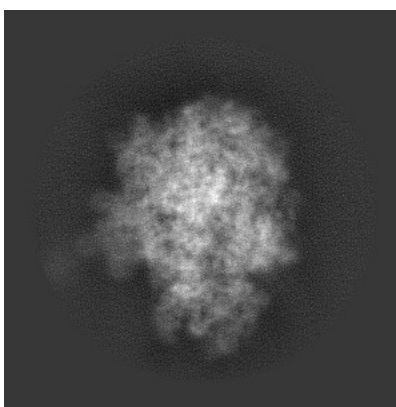


Z

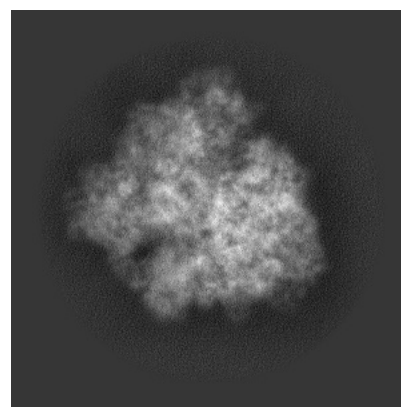
6.1.2 Raw map



X



Y

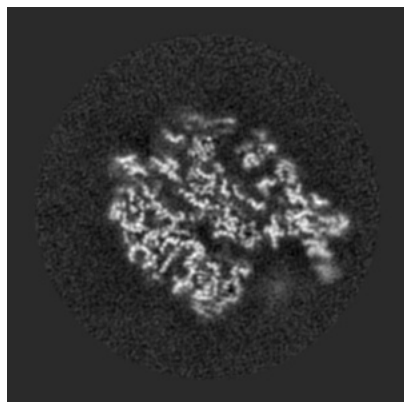


Z

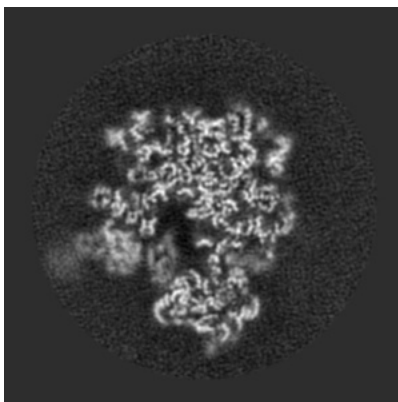
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

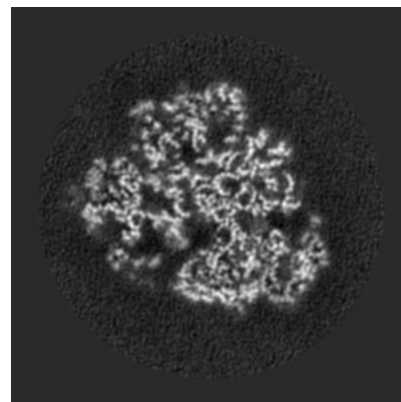
6.2.1 Primary map



X Index: 240

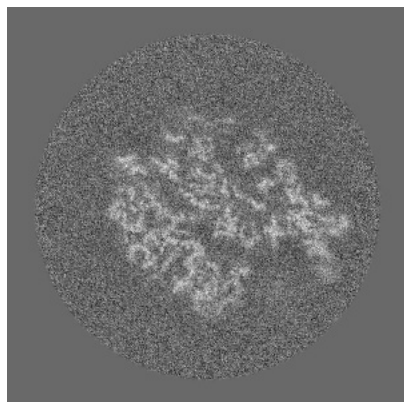


Y Index: 240

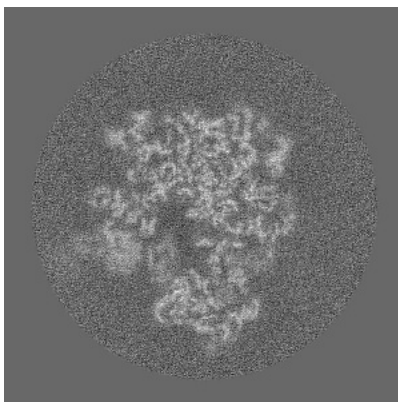


Z Index: 240

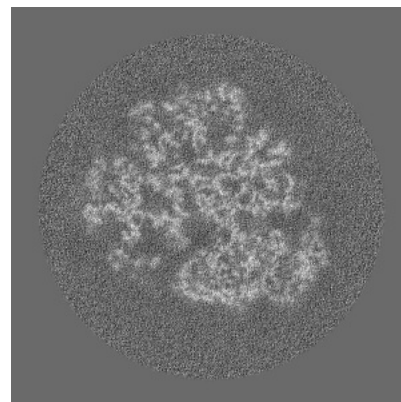
6.2.2 Raw map



X Index: 240



Y Index: 240

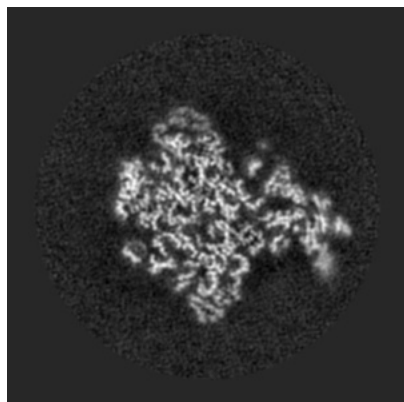


Z Index: 240

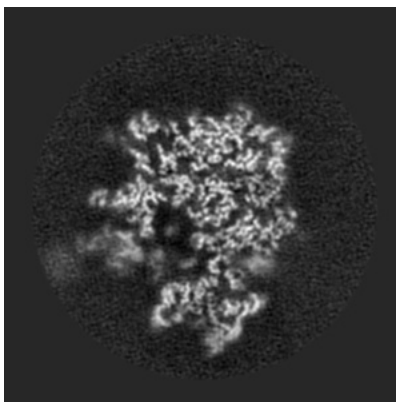
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

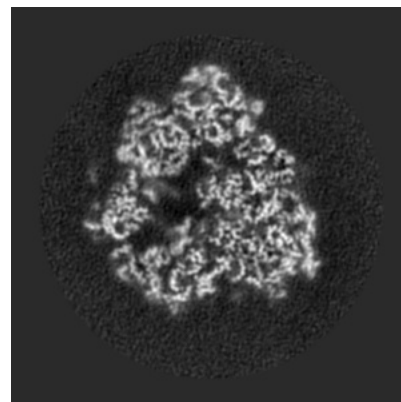
6.3.1 Primary map



X Index: 249

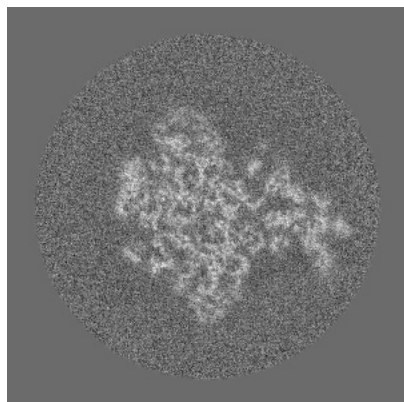


Y Index: 247

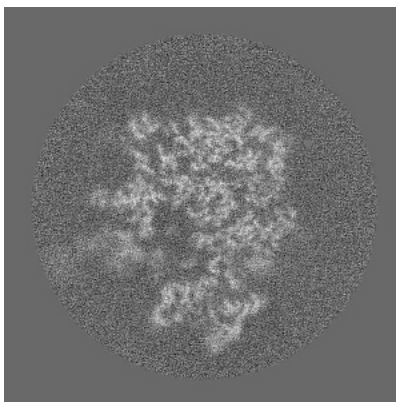


Z Index: 220

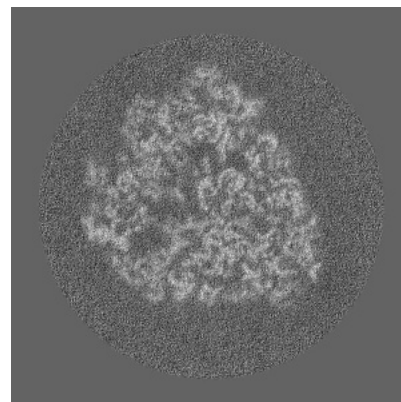
6.3.2 Raw map



X Index: 249



Y Index: 247

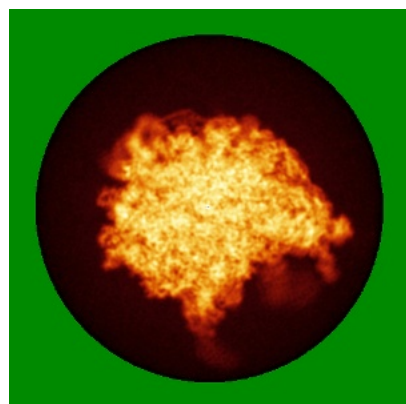


Z Index: 227

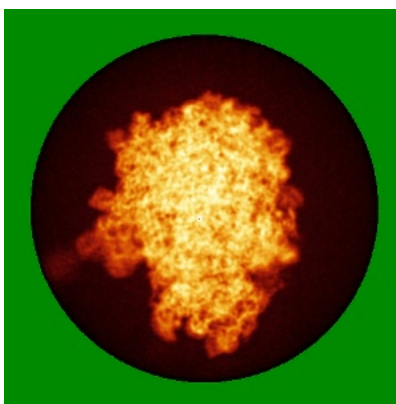
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

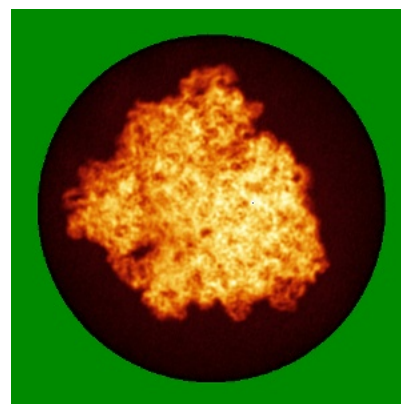
6.4.1 Primary map



X

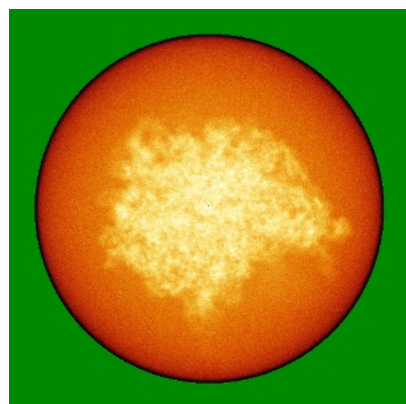


Y

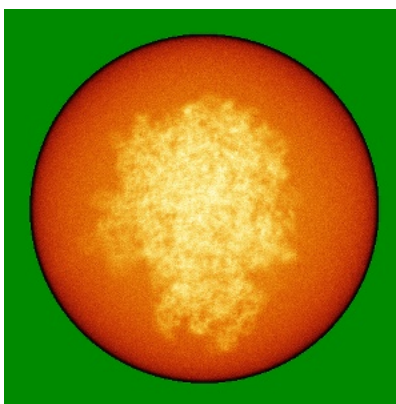


Z

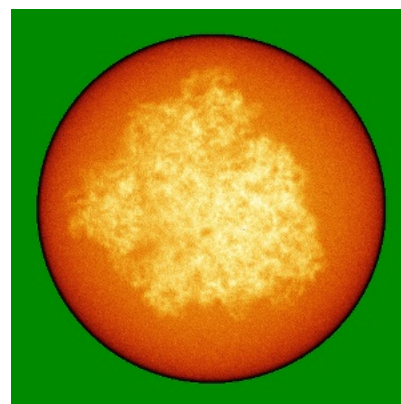
6.4.2 Raw map



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](#)

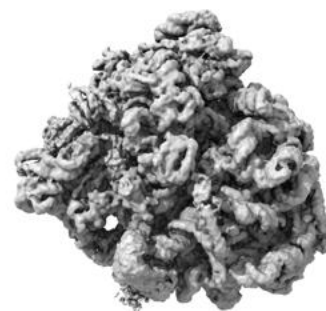
6.5.1 Primary map



X



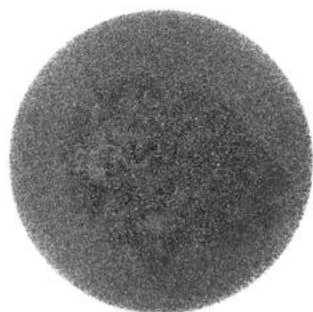
Y



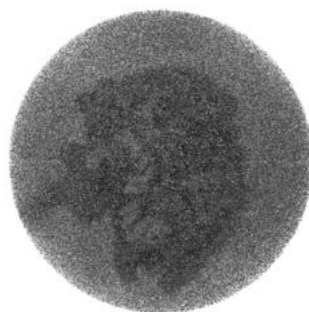
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

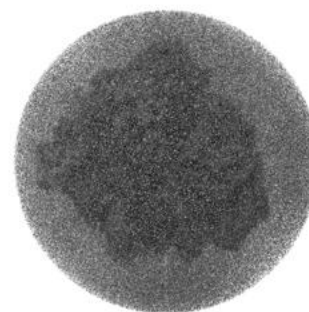
6.5.2 Raw map



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.

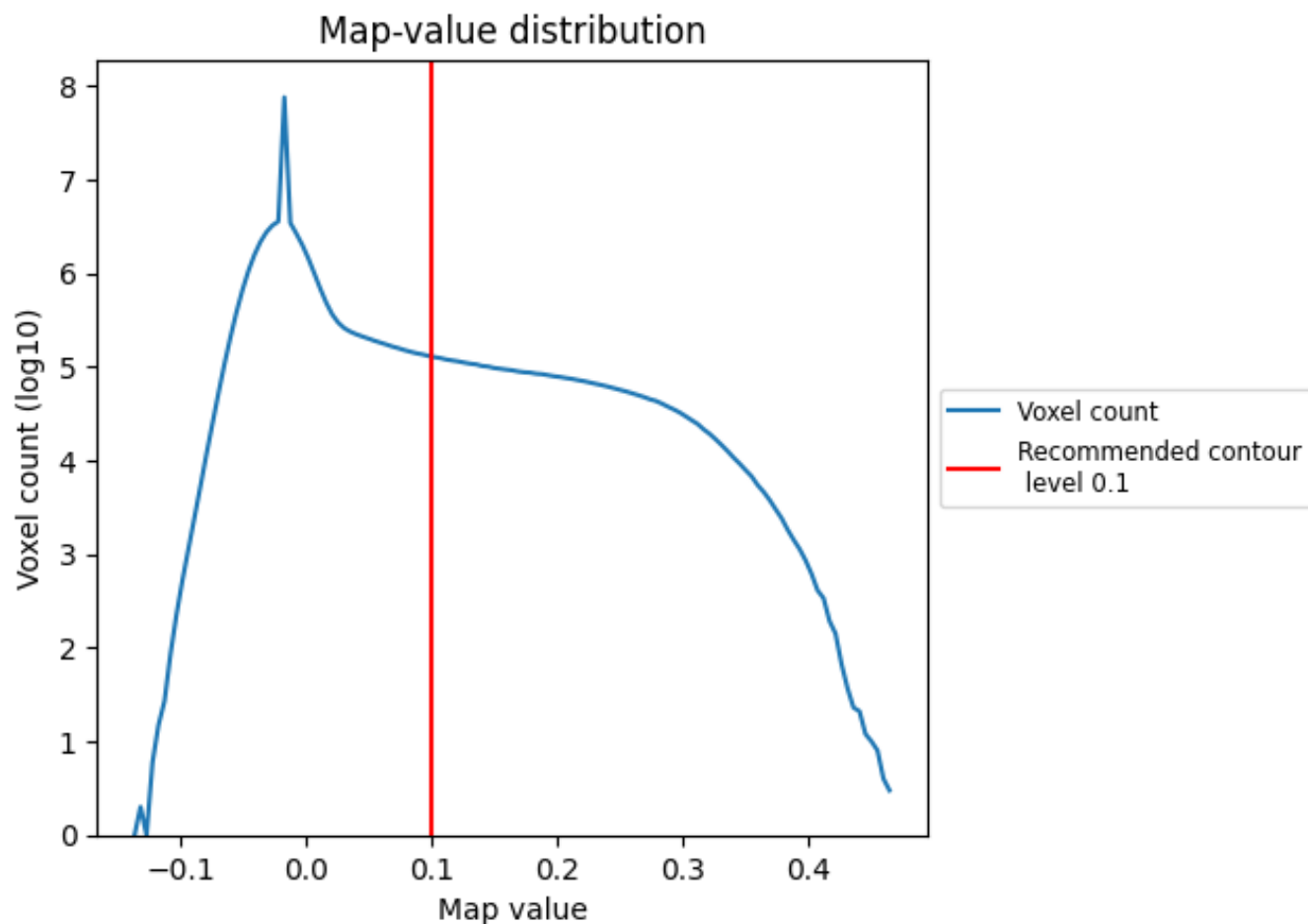
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

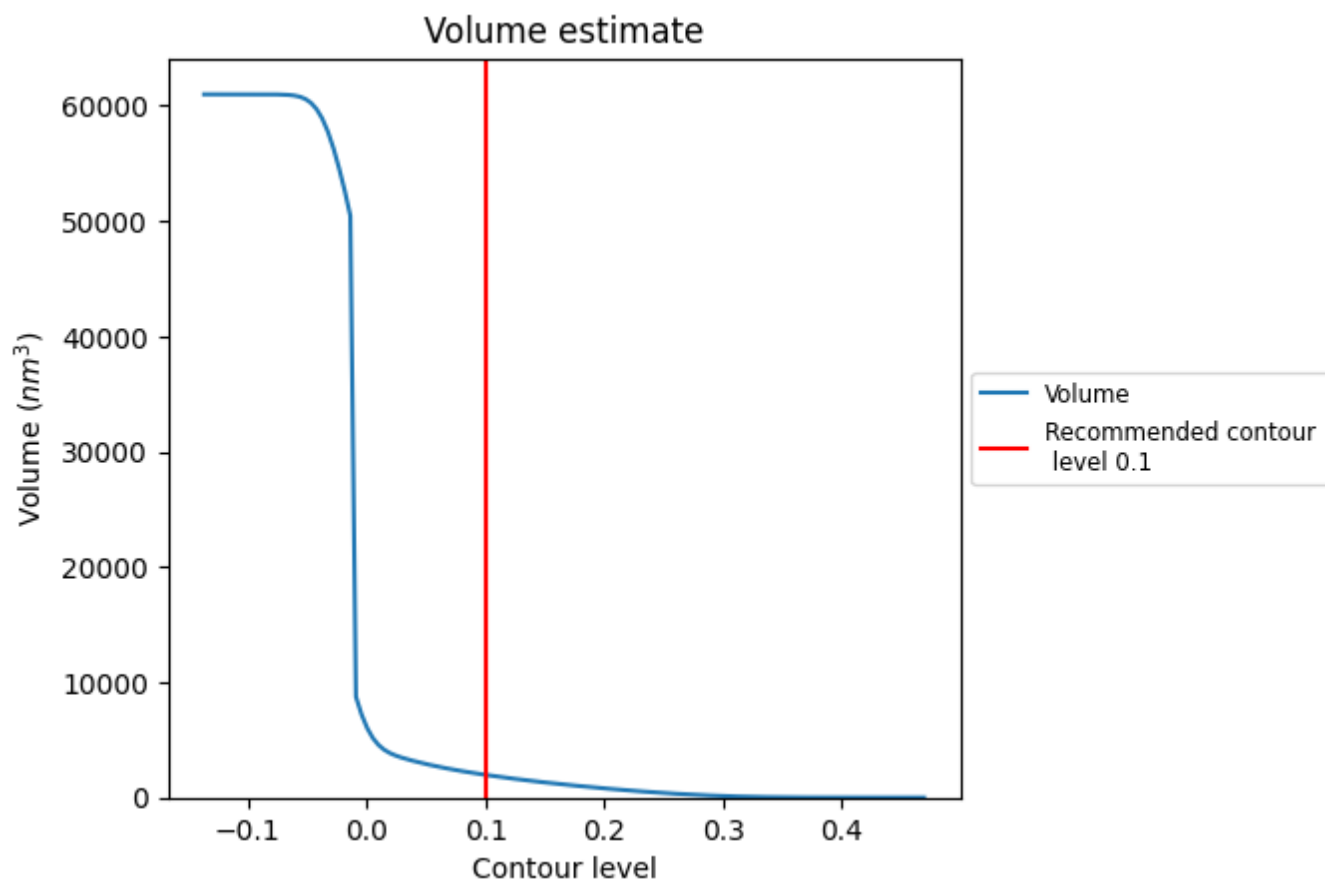
This section contains the results of statistical analysis of the map.

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.

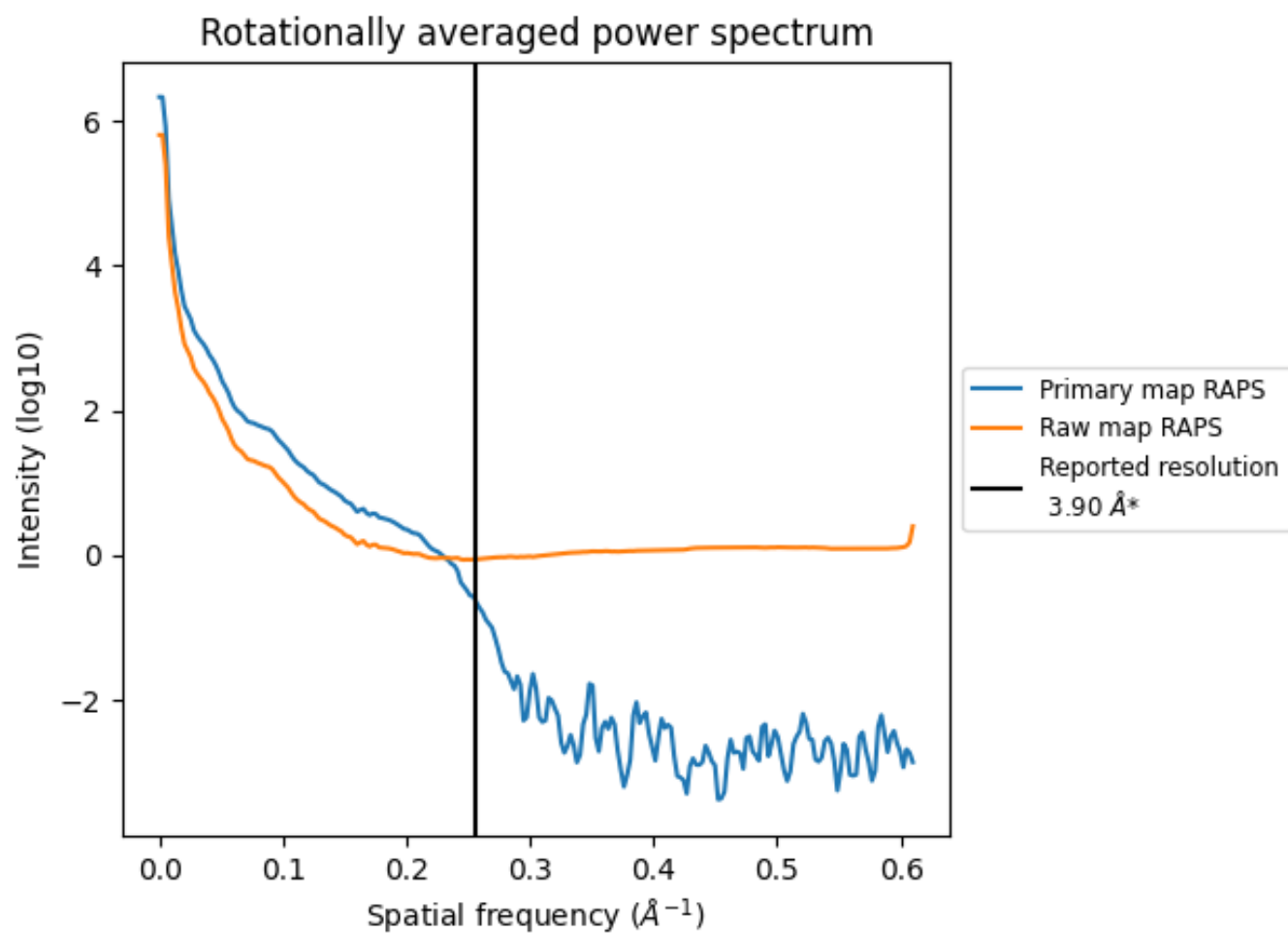
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1970 nm³; this corresponds to an approximate mass of 1779 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 ⓘ

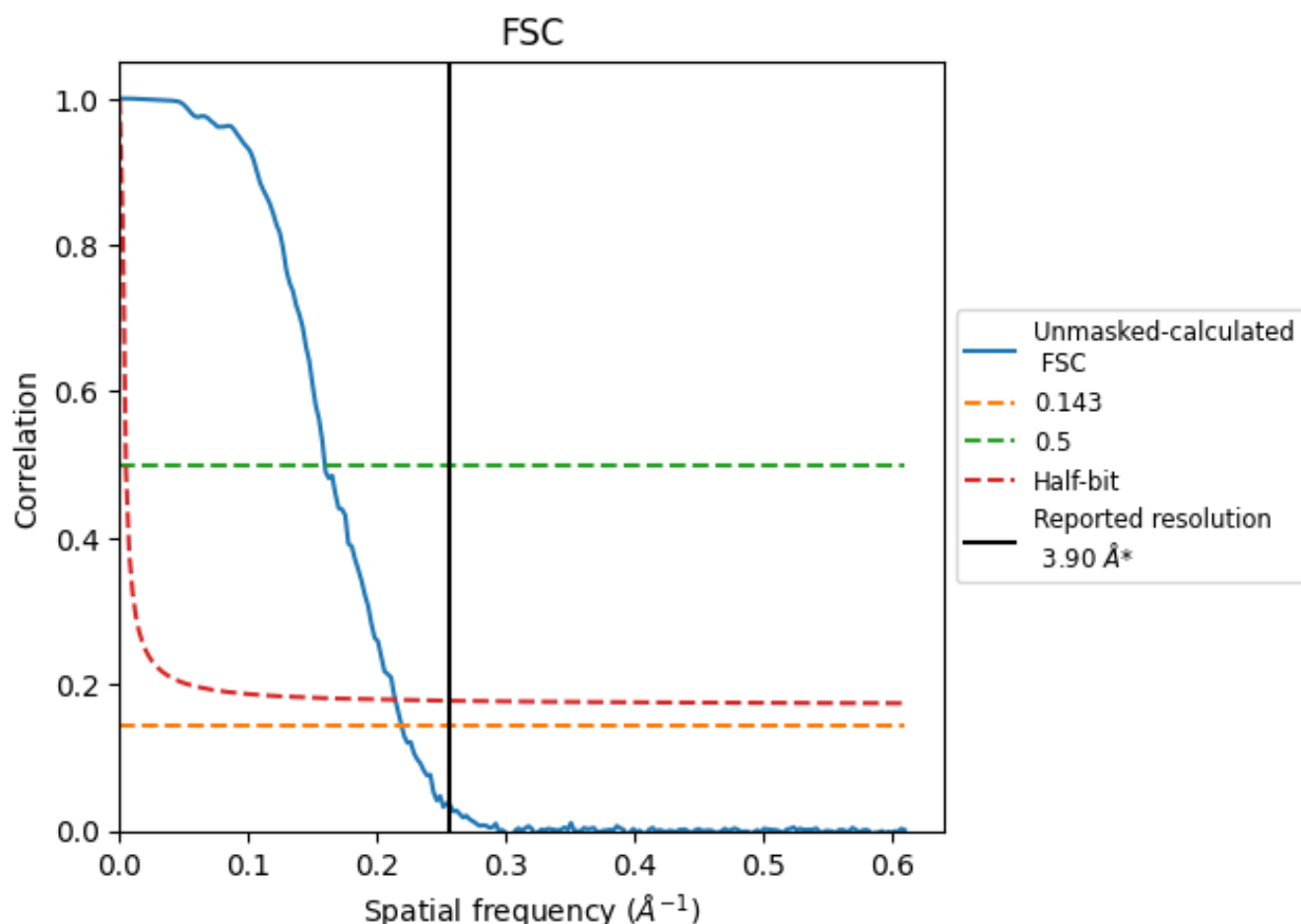


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

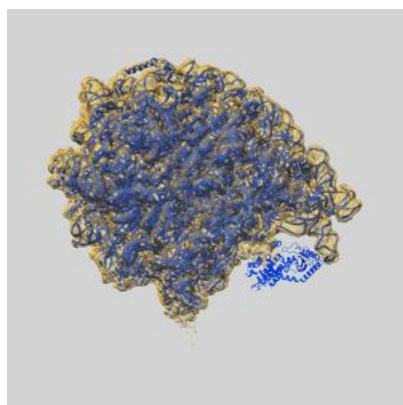
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.57	6.27	4.67

*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 4.57 differs from the reported value 3.9 by more than 10 %

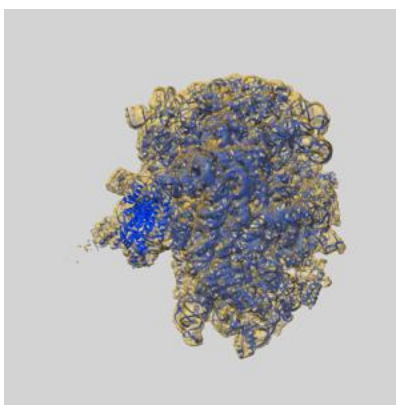
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8281 and PDB model 5KPW. Per-residue inclusion information can be found in section [3](#) on page [15](#).

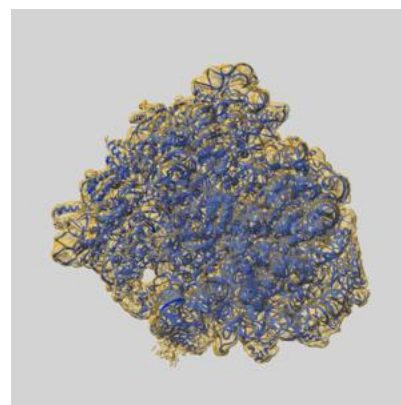
9.1 Map-model overlay [i](#)



X



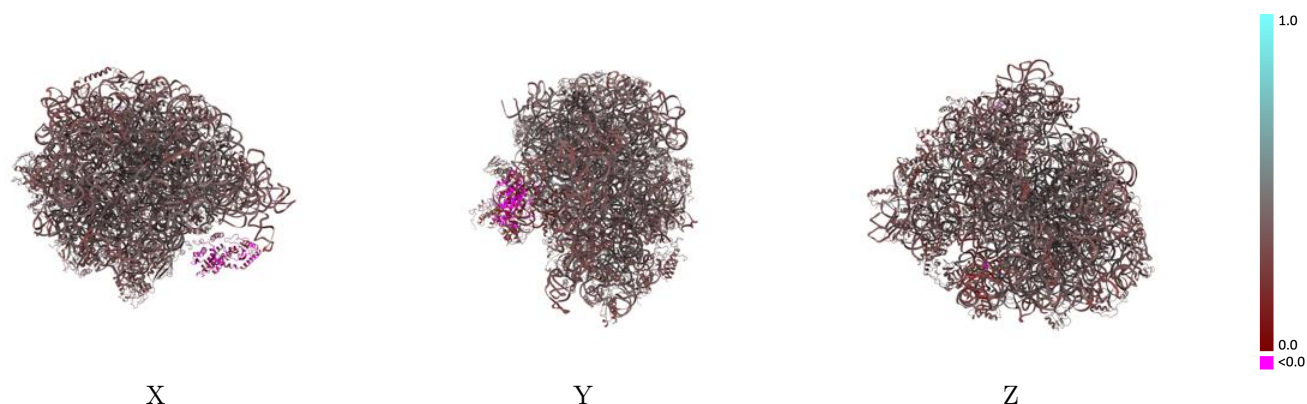
Y



Z

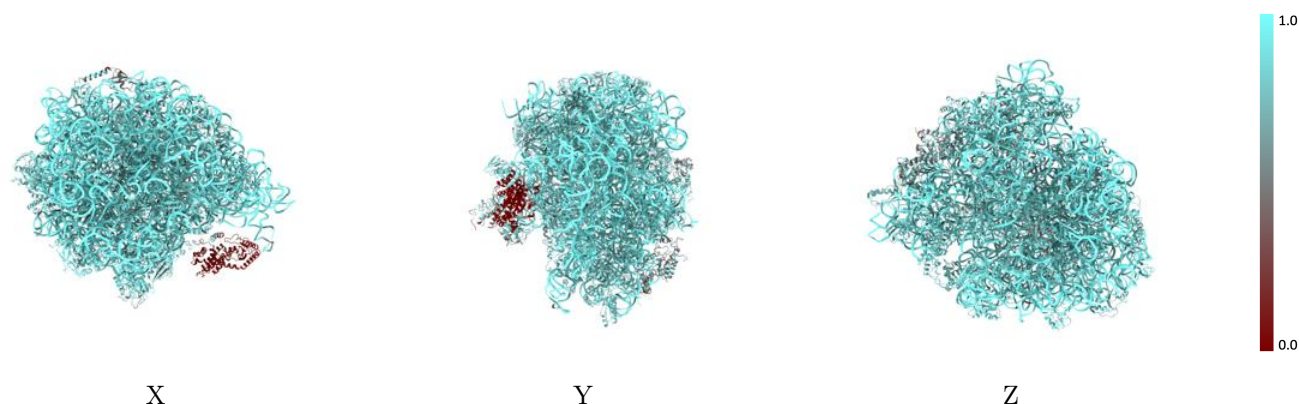
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



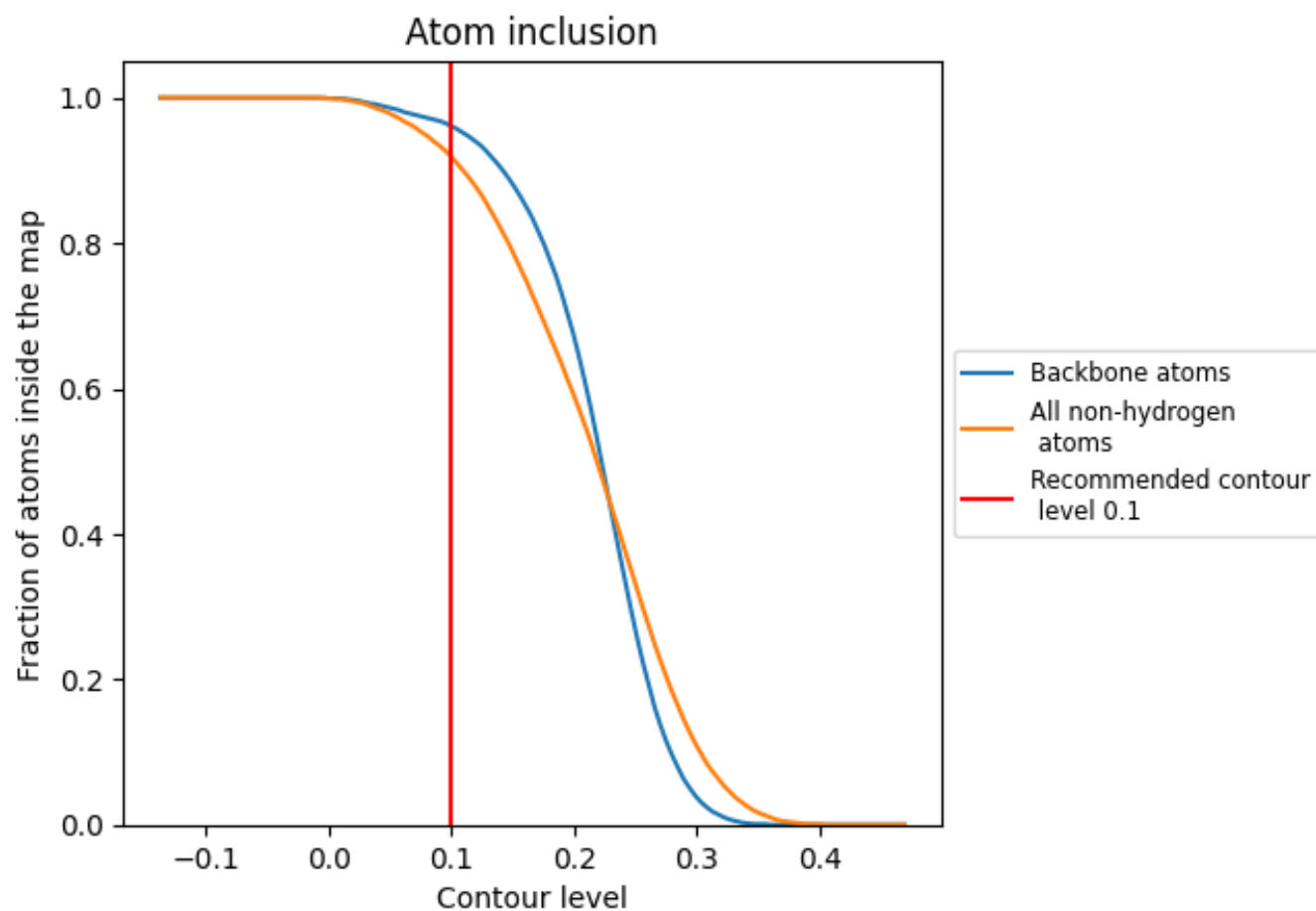
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ



















































The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.3600
1	 0.8440	 0.3830
10	 0.8520	 0.3570
11	 0.8530	 0.3410
12	 0.8480	 0.3770
13	 0.8630	 0.3510
14	 0.7740	 0.3480
15	 0.8750	 0.3720
16	 0.7990	 0.3750
17	 0.8680	 0.3440
18	 0.8460	 0.3530
19	 0.8750	 0.3420
2	 0.7780	 0.3950
20	 0.8630	 0.3510
21	 0.8430	 0.3880
22	 0.8850	 0.3700
23	 0.8550	 0.3630
24	 0.8510	 0.3280
25	 0.7660	 0.3170
26	 0.9890	 0.3690
27	 0.9910	 0.3740
28	 0.9910	 0.3710
29	 0.9190	 0.3190
3	 0.8560	 0.3660
30	 0.9530	 0.2700
31	 0.9640	 0.3630
32	 0.9030	 0.2480
33	 0.3880	 0.1660
4	 0.8210	 0.3880
5	 0.8390	 0.4000
6	 0.5300	 0.3380
7	 0.8090	 0.3710
8	 0.8180	 0.3340
9	 0.8630	 0.3840
A	 0.8620	 0.4020



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Chain	Atom inclusion	Q-score
B	 0.8370	 0.4050
C	 0.7890	 0.3530
D	 0.8470	 0.3540
E	 0.8740	 0.3750
F	 0.6540	 0.3290
G	 0.6510	 0.2630
H	 0.7020	 0.2650
I	 0.8520	 0.3730
J	 0.7790	 0.4090
K	 0.8600	 0.3860
L	 0.8130	 0.3990
M	 0.8830	 0.3800
N	 0.8880	 0.3660
O	 0.8370	 0.3940
P	 0.8620	 0.3550
Q	 0.8600	 0.3920
R	 0.8060	 0.3840
S	 0.8500	 0.3670
T	 0.8580	 0.3600
U	 0.8470	 0.3850
V	 0.8300	 0.3930
W	 0.8590	 0.3700
X	 0.8290	 0.3120
Y	 0.8470	 0.3870
Z	 0.8530	 0.3420