



wwPDB EM Validation Summary Report ⓘ

Sep 18, 2025 – 05:06 PM EDT

PDB ID : 9O17 / pdb_00009o17
EMDB ID : EMD-49998
Title : Cryo-EM structure of Methanosarcina acetivorans 70S ribosome
Authors : Ghosh, A.; Fordjour, G.N.R.; Armache, J.-P.; Ferry, J.G.; Murakami, K.S.;
Bevilacqua, P.C.
Deposited on : 2025-04-03
Resolution : 2.92 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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.45.1

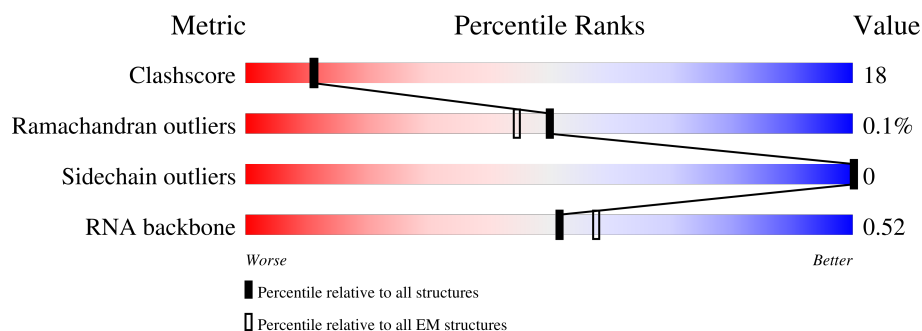
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.92 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	AA	1478	
2	AB	247	
3	AC	318	
4	AD	203	
5	AE	218	
6	AF	235	
7	AG	209	

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Mol	Chain	Length	Quality of chain
8	AI	189	
9	AJ	130	
10	AK	125	
11	AL	134	
12	AN	126	
13	AO	142	
14	AP	182	
15	AR	50	
16	AQ	152	
17	AS	109	
18	AU	136	
19	AV	149	
20	AW	101	
21	AX	62	
22	AY	76	
23	AH	136	
24	AM	102	
25	AT	64	
26	BA	2899	
27	BB	129	
28	BC	238	
29	BD	337	
30	BE	253	
31	BF	165	
32	BG	176	

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Mol	Chain	Length	Quality of chain
33	BH	120	
34	BI	173	
35	BJ	143	
36	BK	132	
37	BL	140	
38	BM	196	
39	BN	174	
40	BO	126	
41	BP	151	
42	BQ	61	
43	BR	97	
44	BS	151	
45	BT	82	
46	BU	119	
47	BV	62	
48	BW	67	
49	BX	153	
50	BY	99	
51	BZ	89	
52	Ba	161	
53	Bb	94	
54	Bc	56	
55	Bd	51	
56	Be	52	
57	Bf	92	

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Mol	Chain	Length	Quality of chain
58	AZ	56	<div><div></div><div>89%</div><div>48%</div><div>41%</div><div>11%</div></div>

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 179267 atoms, of which 29860 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
1	AA	1462	Total	C	N	O	P	0	0
			31324	13965	5707	10190	1462		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	190	Total	C	N	O	S	0	0
			1492	944	262	281	5		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	186	Total	C	N	O	S	0	0
			1425	898	256	262	9		

- Molecule 4 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	182	Total	C	N	O	S	0	0
			1454	912	262	272	8		

- Molecule 5 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	167	Total	C	N	O	S	0	0
			1351	851	253	242	5		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	234	Total	C	N	O	S	0	0
			1837	1154	333	345	5		

- Molecule 7 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	198	Total	C	N	O	S	0	0
			1506	954	269	276	7		

- Molecule 8 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	189	Total	C	N	O	S	0	0
			1479	928	274	273	4		

- Molecule 9 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	129	Total	C	N	O	S	0	0
			981	628	166	183	4		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	125	Total	C	N	O	S	0	0
			964	587	196	177	4		

- Molecule 11 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	132	Total	C	N	O	S	0	0
			993	617	185	187	4		

- Molecule 12 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AN	123	Total	C	N	O	S	0	0
			911	560	180	167	4		

- Molecule 13 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AO	142	Total	C	N	O	S	0	0
			1088	679	211	192	6		

- Molecule 14 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AP	132	Total	C	N	O	S	0	0
			1033	649	198	184	2		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	-19	MET	-	initiating methionine	UNP Q8TRR2
AP	-18	ARG	-	expression tag	UNP Q8TRR2
AP	-17	ALA	-	expression tag	UNP Q8TRR2
AP	-16	ALA	-	expression tag	UNP Q8TRR2
AP	-15	PRO	-	expression tag	UNP Q8TRR2
AP	-14	GLU	-	expression tag	UNP Q8TRR2
AP	-13	PHE	-	expression tag	UNP Q8TRR2
AP	-12	SER	-	expression tag	UNP Q8TRR2
AP	-11	ALA	-	expression tag	UNP Q8TRR2
AP	-10	TYR	-	expression tag	UNP Q8TRR2
AP	-9	SER	-	expression tag	UNP Q8TRR2
AP	-8	LEU	-	expression tag	UNP Q8TRR2
AP	-7	ARG	-	expression tag	UNP Q8TRR2
AP	-6	VAL	-	expression tag	UNP Q8TRR2
AP	-5	PHE	-	expression tag	UNP Q8TRR2
AP	-4	ASP	-	expression tag	UNP Q8TRR2
AP	-3	ARG	-	expression tag	UNP Q8TRR2
AP	-2	GLY	-	expression tag	UNP Q8TRR2
AP	-1	TYR	-	expression tag	UNP Q8TRR2
AP	0	ARG	-	expression tag	UNP Q8TRR2

- Molecule 15 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AR	44	Total	C	N	O	S	0	0
			366	226	73	62	5		

- Molecule 16 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	152	Total	C	N	O	S	0	0
			1226	777	223	220	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	109	Total	C	N	O	S	0	0
			849	533	152	156	8		

- Molecule 18 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AU	95	Total	C	N	O	S	0	0
			775	491	142	139	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AV	149	Total	C	N	O	S	0	0
			1163	739	204	215	5		

- Molecule 20 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AW	95	Total	C	N	O	S	0	0
			766	481	136	145	4		

- Molecule 21 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AX	60	Total	C	N	O	S	0	0
			468	288	85	91	4		

- Molecule 22 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	63	Total	C	N	O	S	0	0
			471	289	90	88	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AH	124	Total	C	N	O	S	0	0
			930	591	168	167	4		

- Molecule 24 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AM	102	Total	C	N	O	S	0	0
			796	497	150	145	4		

- Molecule 25 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	58	Total	C	N	O	S	0	0
			477	302	87	87	1		

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	BA	2776	Total	C	H	N	O	P	0	0
			89273	26520	29860	10811	19307	2775		

- Molecule 27 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BB	128	Total	C	N	O	P	0	0
			2720	1214	481	897	128		

- Molecule 28 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BC	238	Total	C	N	O	S	0	0
			1808	1129	350	321	8		

- Molecule 29 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BD	337	Total	C	N	O	S	0	0
			2597	1639	474	476	8		

- Molecule 30 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BE	252	Total	C	N	O	S	0	0
			1930	1208	368	353	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BF	165	Total	C	N	O	S	0	0
			1289	812	234	235	8		

- Molecule 32 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BG	176	Total	C	N	O	S	0	0
			1371	876	235	254	6		

- Molecule 33 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BH	115	Total	C	N	O	S	0	0
			857	541	144	170	2		

- Molecule 34 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BI	159	Total	C	N	O	S	0	0
			1261	794	240	218	9		

- Molecule 35 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BJ	138	Total	C	N	O	S	0	0
			1086	683	200	199	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BK	132	Total	C	N	O	S	0	0
			999	623	185	182	9		

- Molecule 37 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	140	Total	C	N	O	S	0	0
			1058	643	204	205	6		

- Molecule 38 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BM	196	Total	C	N	O	S	0	0
			1593	986	329	273	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BN	174	Total	C	N	O	S	0	0
			1356	853	242	259	2		

- Molecule 40 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BO	126	Total	C	N	O	S	0	0
			962	608	173	178	3		

- Molecule 41 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	151	Total	C	N	O	S	0	0
			1195	739	242	210	4		

- Molecule 42 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BQ	57	Total	C	N	O	0	0
			457	289	79	89		

- Molecule 43 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	96	Total	C	N	O	S	0	0
			766	475	146	141	4		

- Molecule 44 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	151	Total	C	N	O	S	0	0
			1169	729	218	212	10		

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	82	Total	C	N	O	S	0	0
			656	418	108	122	8		

- Molecule 46 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BU	119	Total	C	N	O	S	0	0
			910	564	170	169	7		

- Molecule 47 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BV	62	Total	C	N	O	S	0	0
			499	316	88	87	8		

- Molecule 48 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BW	67	Total	C	N	O	S	0	0
			532	321	103	106	2		

- Molecule 49 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BX	153	Total	C	N	O	S	0	0
			1237	779	230	222	6		

- Molecule 50 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BY	92	Total	C	N	O	S	0	0
			658	415	108	131	4		

- Molecule 51 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BZ	86	Total	C	N	O	S	0	0
			703	446	131	123	3		

- Molecule 52 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ba	132	Total	C	N	O	S	0	0
			1028	645	197	184	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ba	-2	MET	-	initiating methionine	UNP A0A832W8Z7
Ba	-1	ILE	-	expression tag	UNP A0A832W8Z7
Ba	0	MET	-	expression tag	UNP A0A832W8Z7

- Molecule 53 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Bb	94	Total	C	N	O	S	0	0
			736	459	145	125	7		

- Molecule 54 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bc	56	Total	C	N	O	S	0	0
			445	269	92	76	8		

- Molecule 55 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bd	51	Total	C	N	O	S	0	0
			439	272	101	64	2		

- Molecule 56 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Be	44	Total	C	N	O	S	0	0
			353	215	74	59	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Be	-2	MET	-	initiating methionine	UNP Q8TJ19
Be	-1	THR	-	expression tag	UNP Q8TJ19
Be	0	LYS	-	expression tag	UNP Q8TJ19

- Molecule 57 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Bf	92	Total	C	N	O	S	0	0
			760	480	151	122	7		

- Molecule 58 is a protein called Putative zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AZ	50	Total	C	N	O	S	0	0
			379	236	67	68	8		

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	AA	6	Total	Mg	0
			6	6	
59	AN	1	Total	Mg	0
			1	1	
59	AS	1	Total	Mg	0
			1	1	
59	BA	42	Total	Mg	0
			42	42	
59	Bc	1	Total	Mg	0
			1	1	

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	AG	1	Total	Zn	0
			1	1	
60	AR	1	Total	Zn	0
			1	1	
60	AS	1	Total	Zn	0
			1	1	
60	AX	1	Total	Zn	0
			1	1	
60	BV	1	Total	Zn	0
			1	1	
60	Bb	1	Total	Zn	0
			1	1	
60	Bc	1	Total	Zn	0
			1	1	
60	Be	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
60	Bf	1	1	1	0

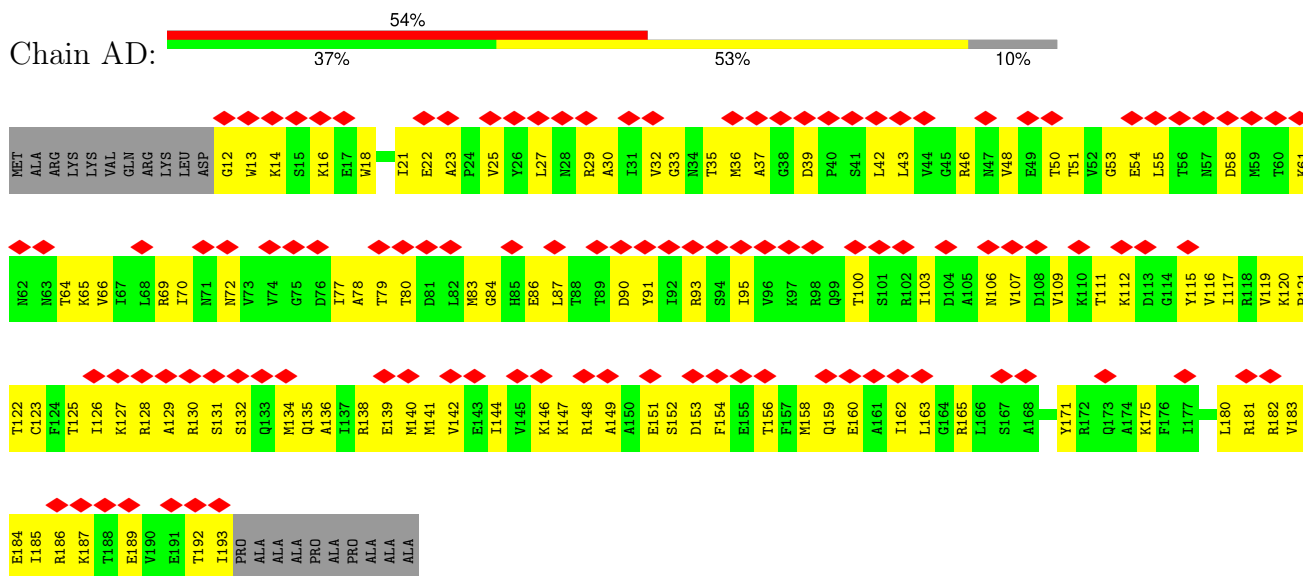
3 Residue-property plots

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.

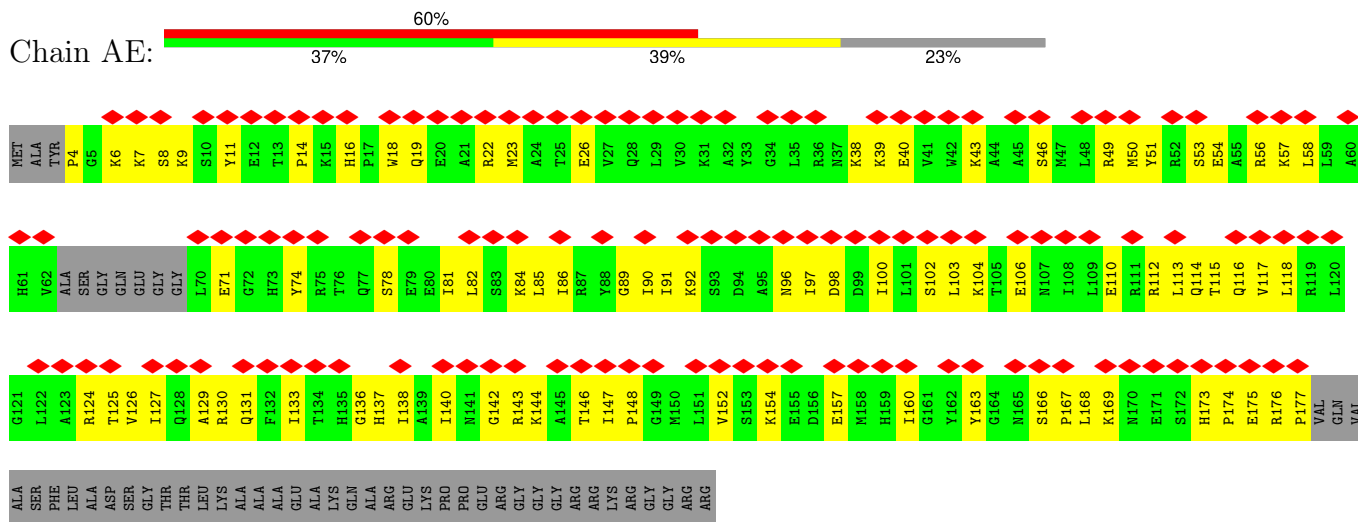
• Molecule 1: 16S rRNA



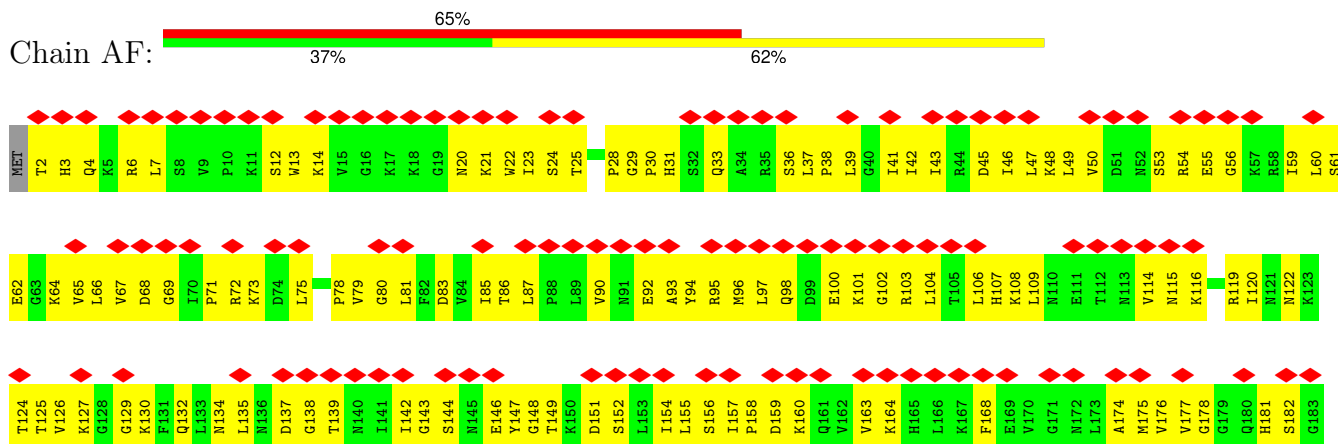




- Molecule 5: Small ribosomal subunit protein uS4

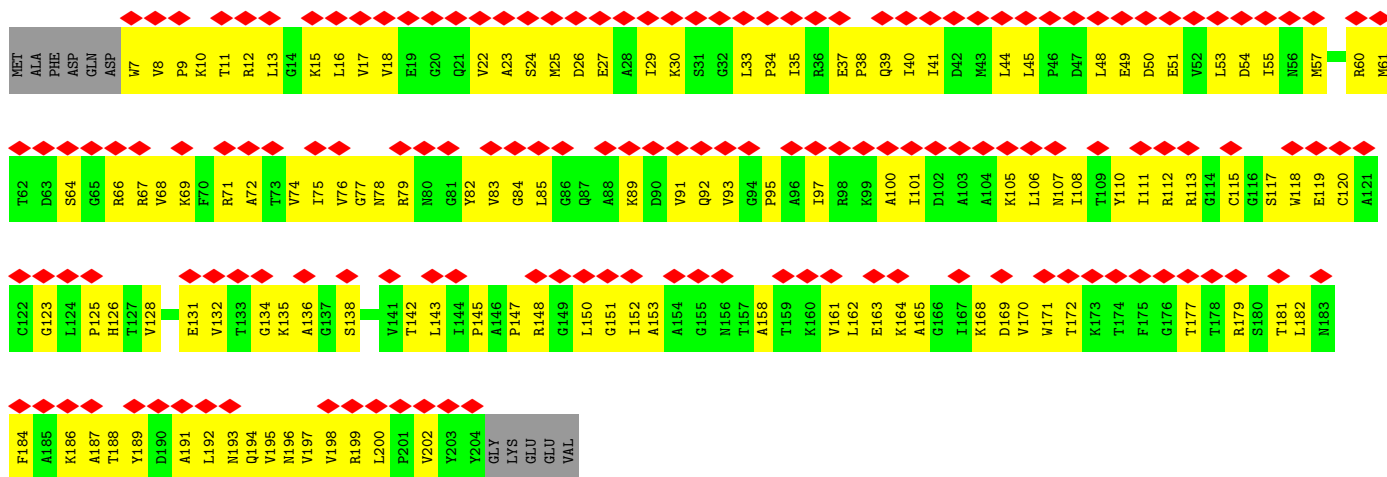
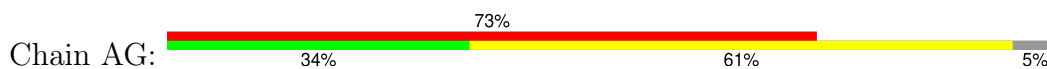


- Molecule 6: Small ribosomal subunit protein eS4

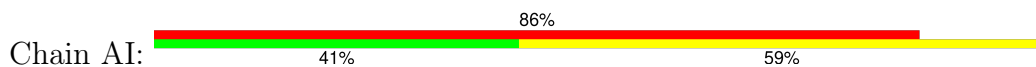




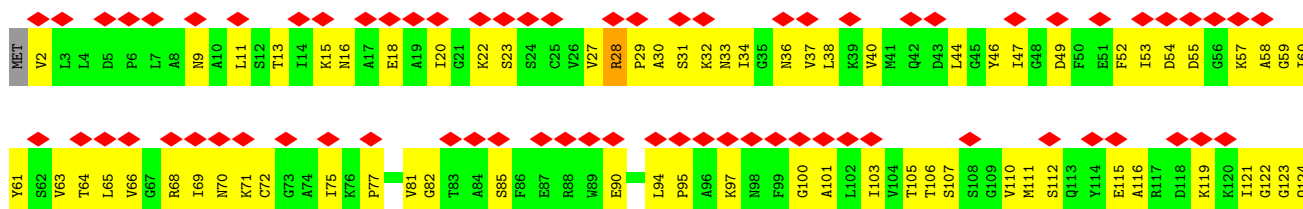
• Molecule 7: Small ribosomal subunit protein uS5

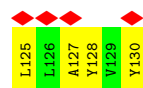


• Molecule 8: Small ribosomal subunit protein uS7

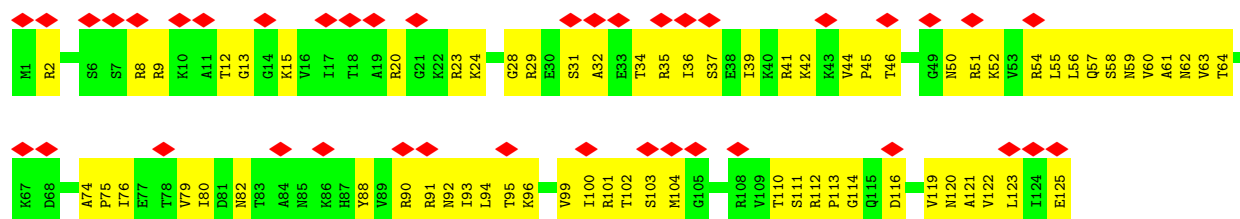


• Molecule 9: Small ribosomal subunit protein uS8

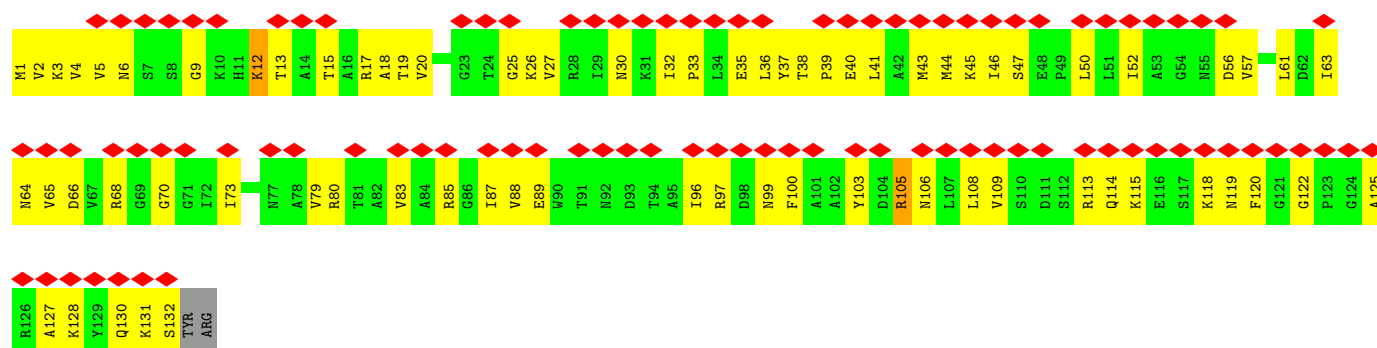
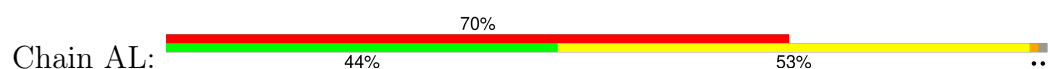




- Molecule 10: Small ribosomal subunit protein eS8



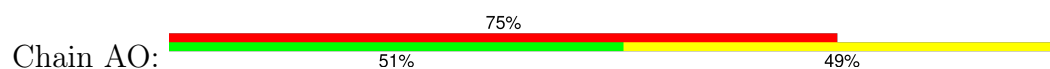
- Molecule 11: Small ribosomal subunit protein uS9

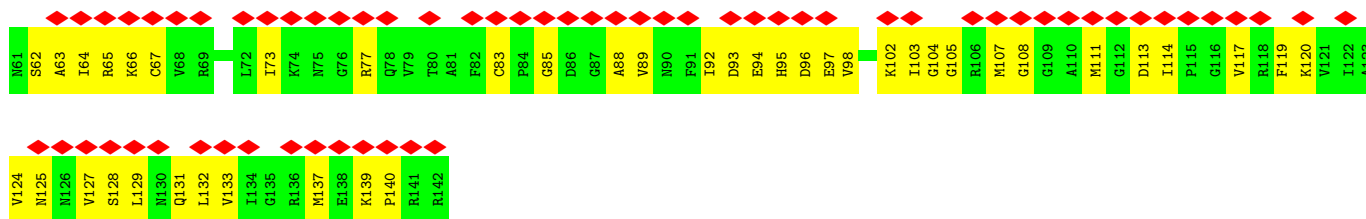


- Molecule 12: Small ribosomal subunit protein uS11

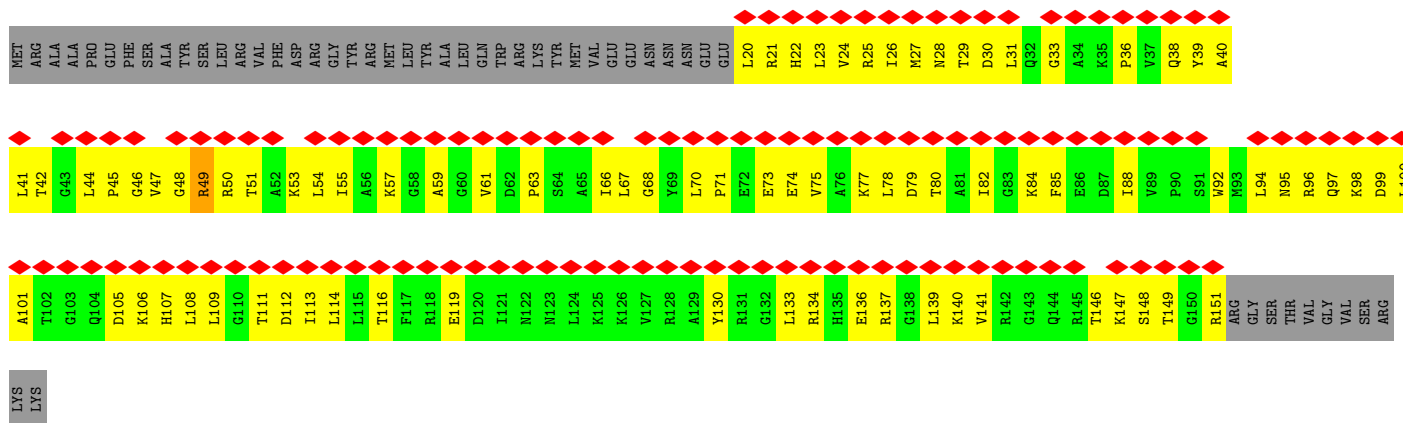


- Molecule 13: Small ribosomal subunit protein uS12

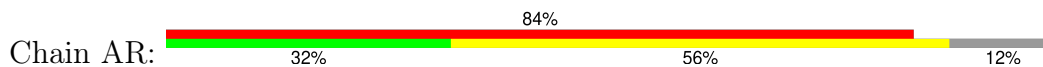




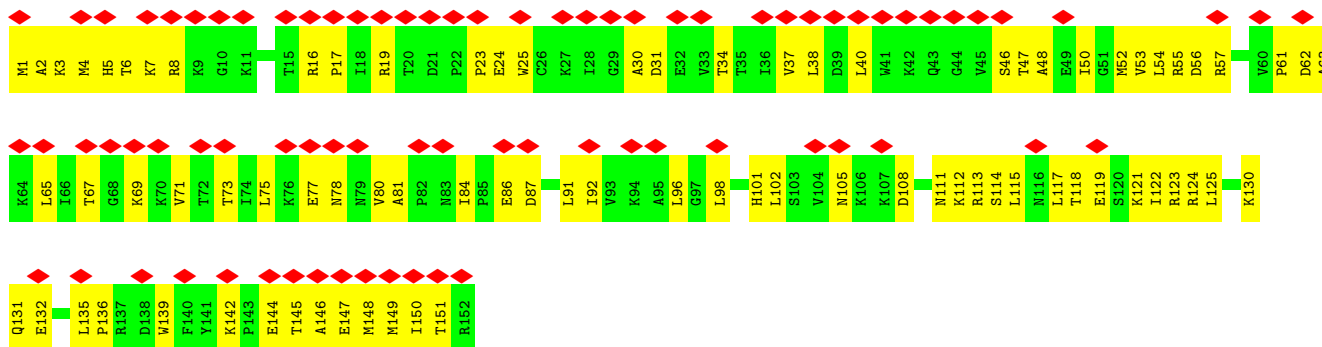
• Molecule 14: Small ribosomal subunit protein uS13



• Molecule 15: Small ribosomal subunit protein uS14

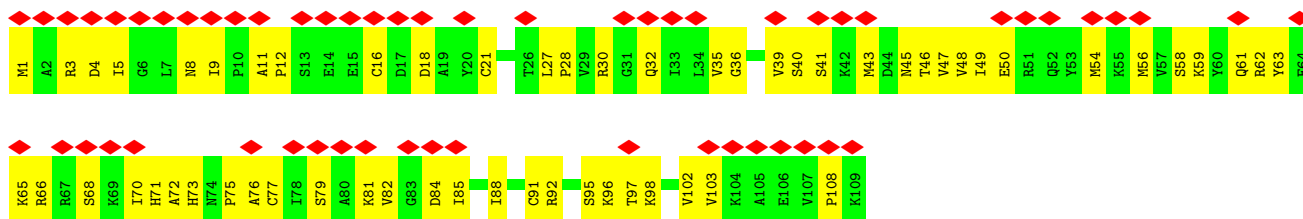


• Molecule 16: Small ribosomal subunit protein uS15

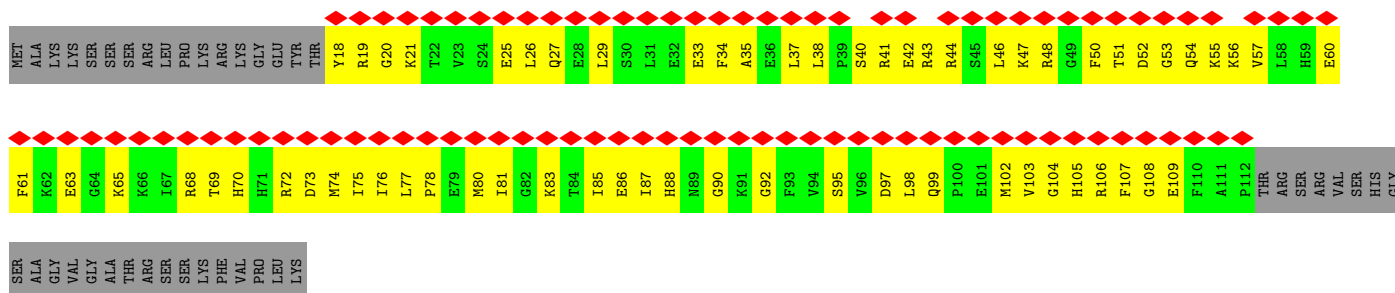


• Molecule 17: Small ribosomal subunit protein uS17A

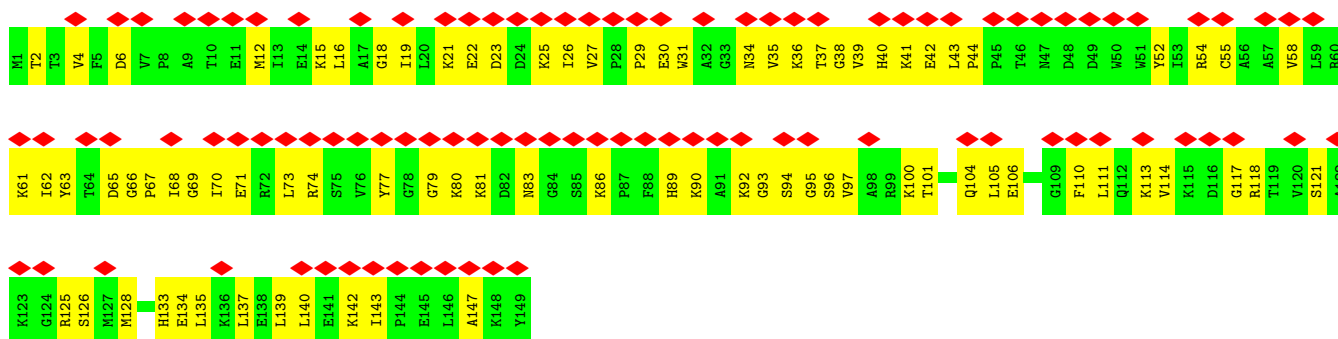




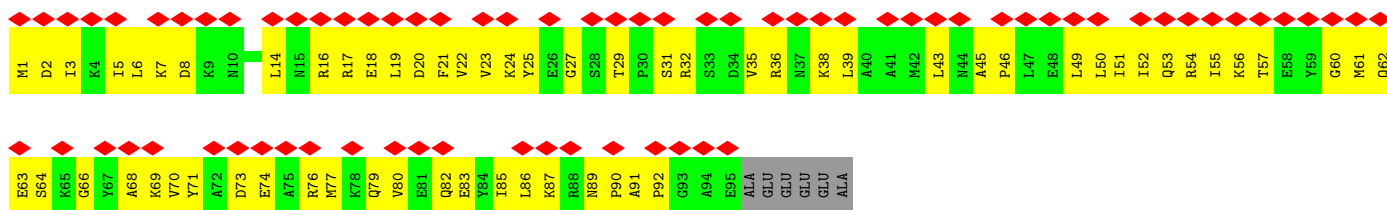
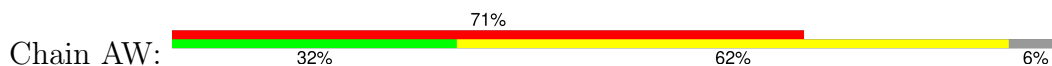
• Molecule 18: Small ribosomal subunit protein uS19



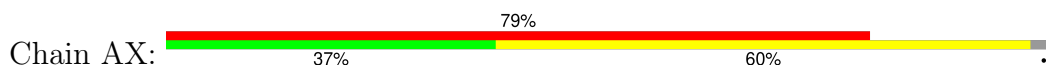
• Molecule 19: Small ribosomal subunit protein eS19

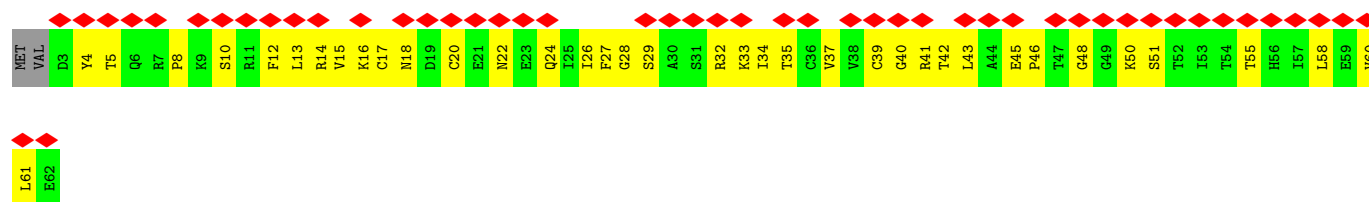


• Molecule 20: Small ribosomal subunit protein eS24

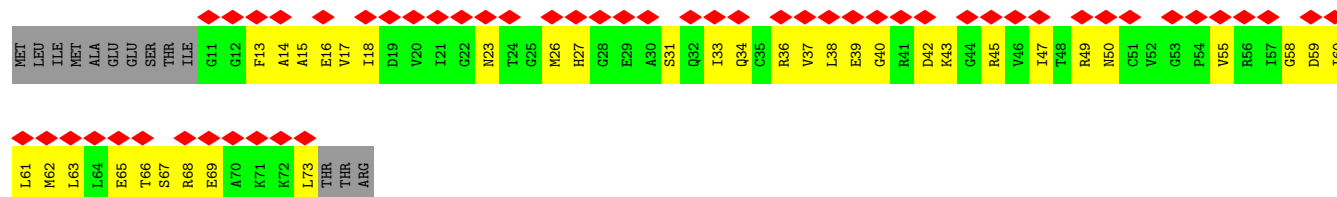


• Molecule 21: Small ribosomal subunit protein eS27

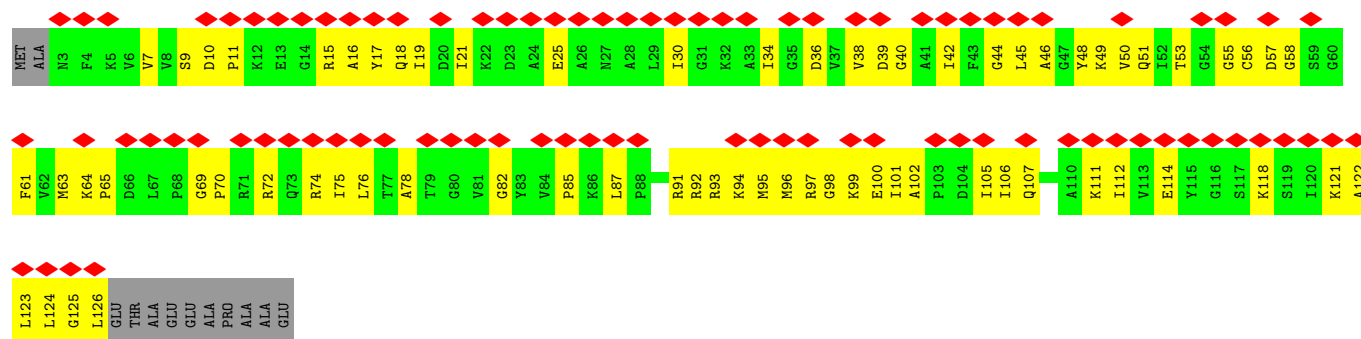




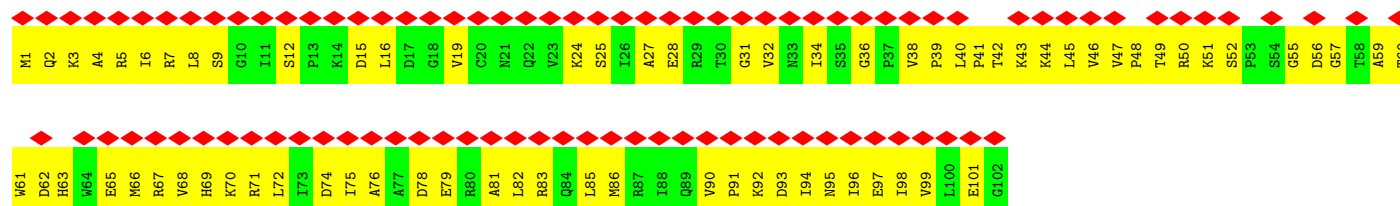
- Molecule 22: Small ribosomal subunit protein eS28



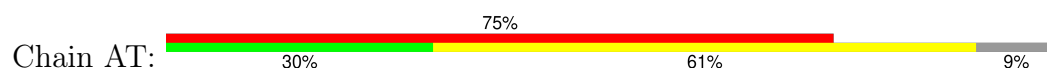
- Molecule 23: Small ribosomal subunit protein eS6



- Molecule 24: Small ribosomal subunit protein uS10

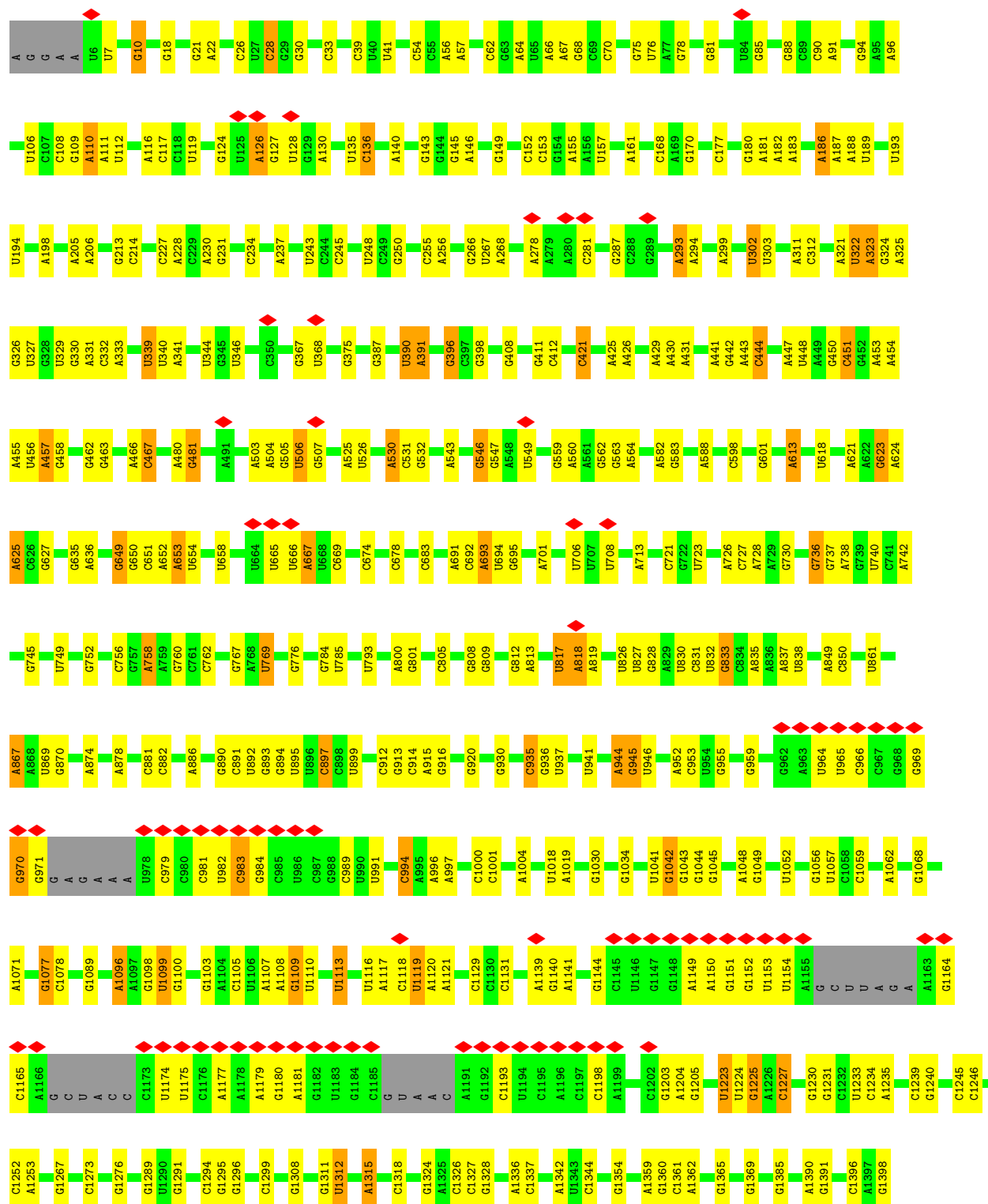


- Molecule 25: Small ribosomal subunit protein eS17

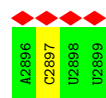




• Molecule 26: 23S rRNA

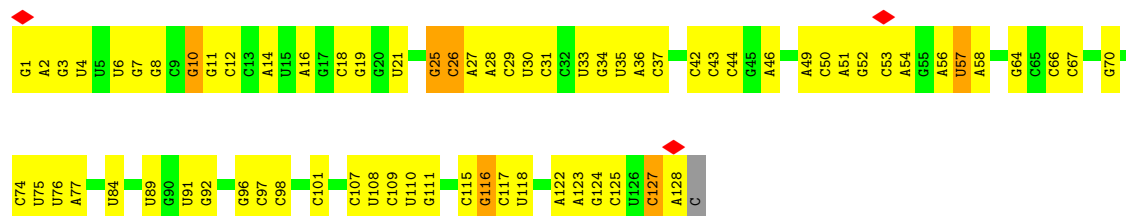






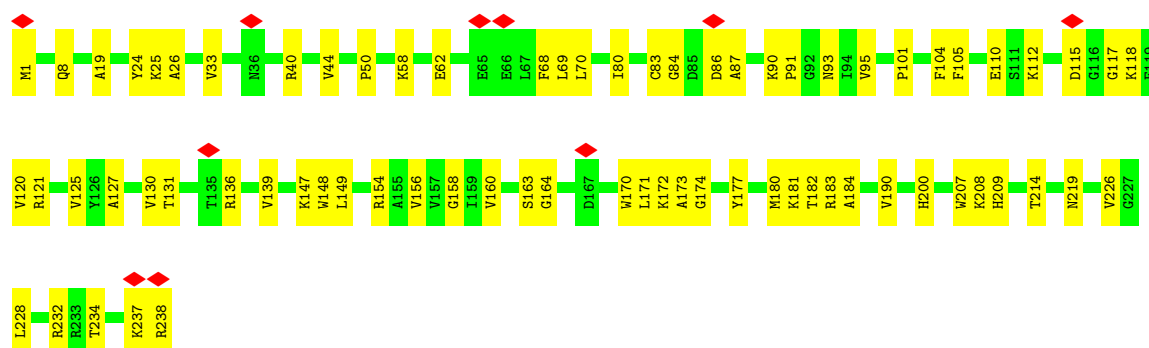
• Molecule 27: 5S rRNA

Chain BB: 44% 50% 5%



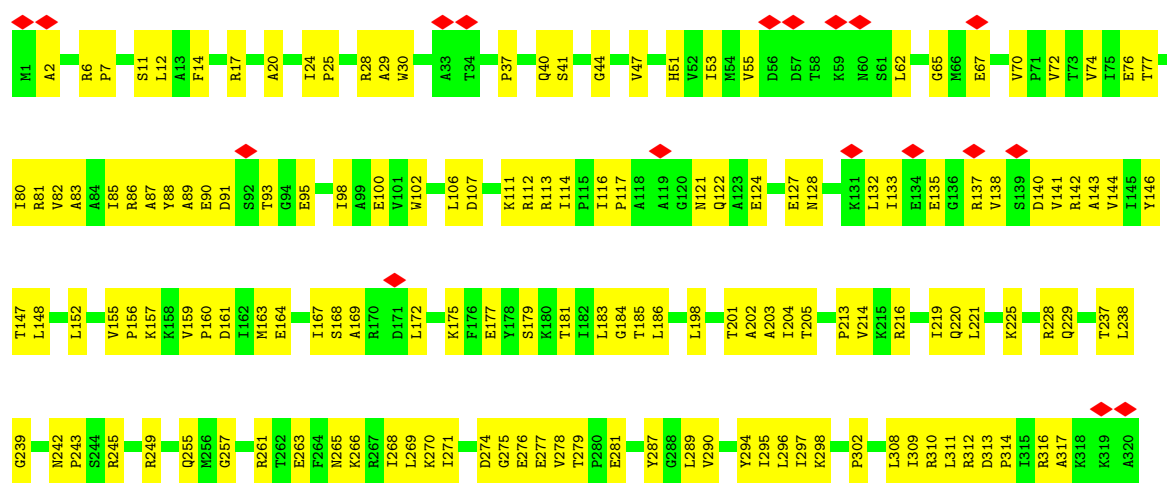
• Molecule 28: Large ribosomal subunit protein uL2

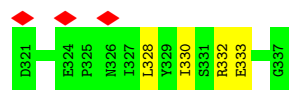
Chain BC: 69% 31%



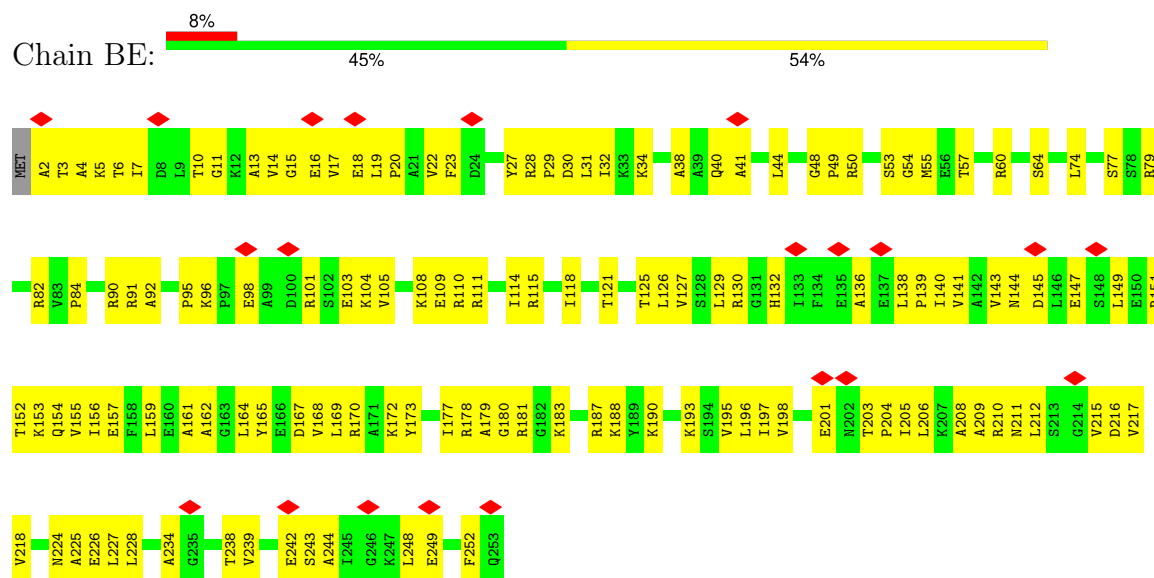
• Molecule 29: Large ribosomal subunit protein uL3

Chain BD: 6% 55% 45%

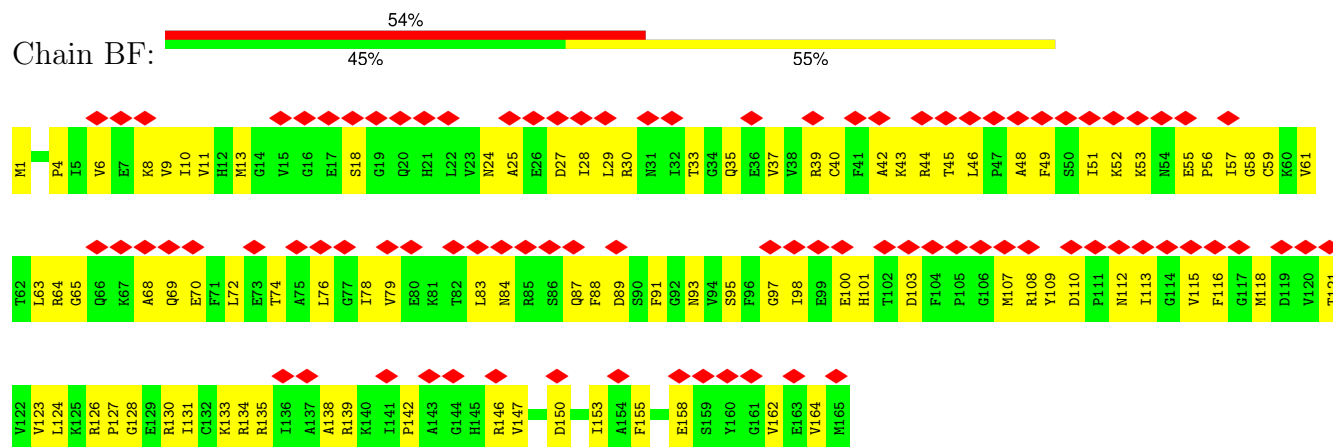




• Molecule 30: Large ribosomal subunit protein uL4

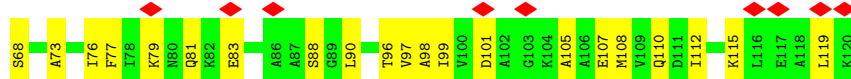


• Molecule 31: Large ribosomal subunit protein uL5

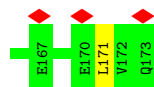
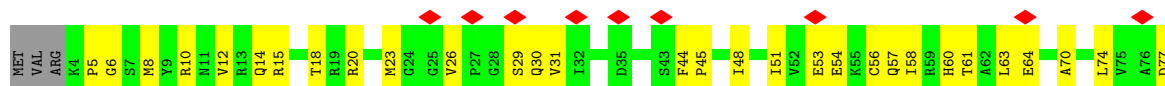




- Molecule 33: Large ribosomal subunit protein eL8



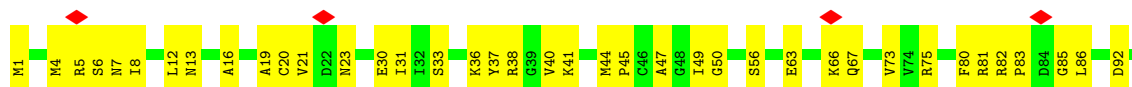
- Molecule 34: Large ribosomal subunit protein uL16

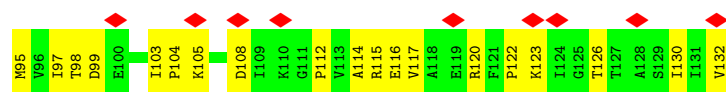


- Molecule 35: Large ribosomal subunit protein uL13

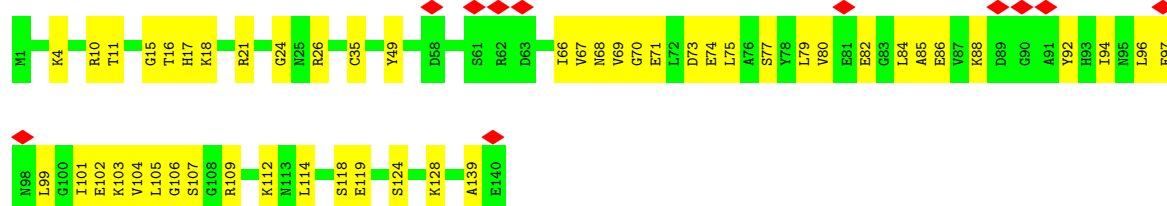


- Molecule 36: Large ribosomal subunit protein uL14

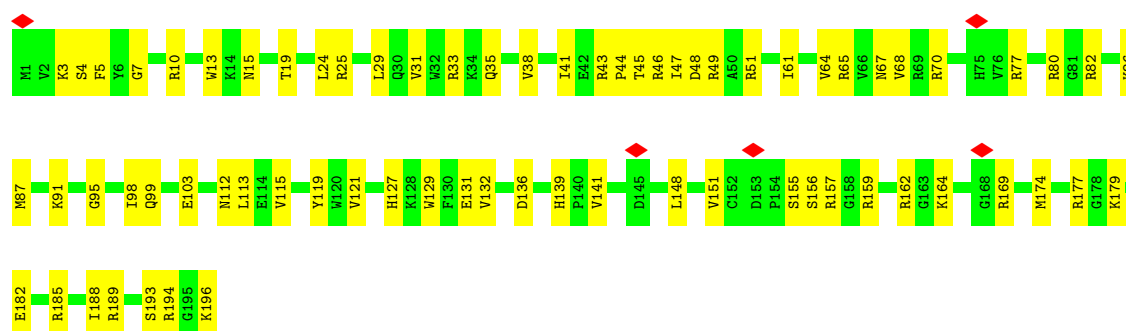




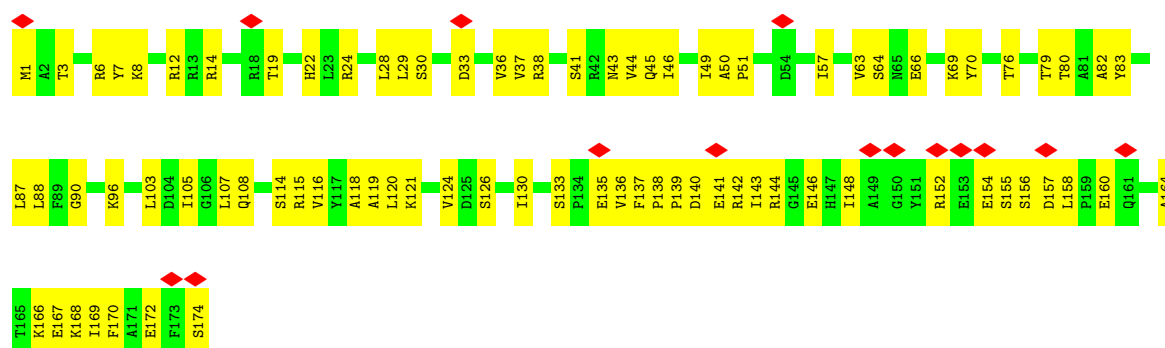
- Molecule 37: Large ribosomal subunit protein uL15



- Molecule 38: Large ribosomal subunit protein eL15

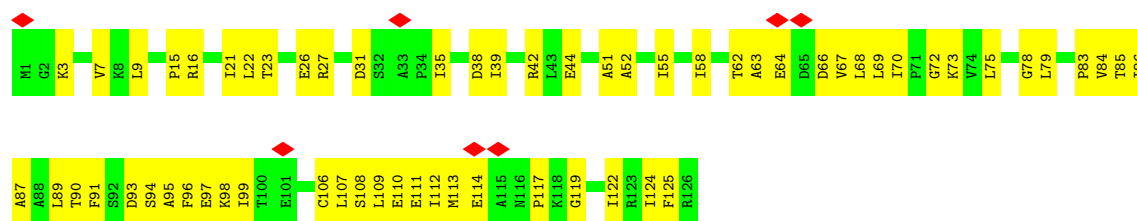


- Molecule 39: Large ribosomal subunit protein uL18



- Molecule 40: Large ribosomal subunit protein eL18

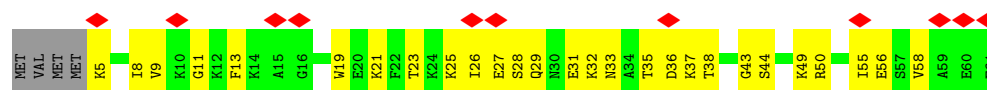




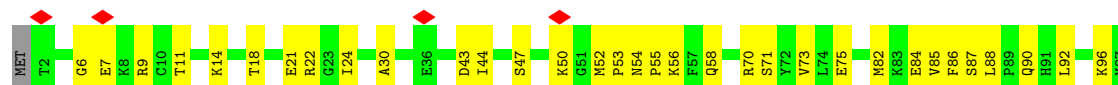
- Molecule 41: Large ribosomal subunit protein eL19



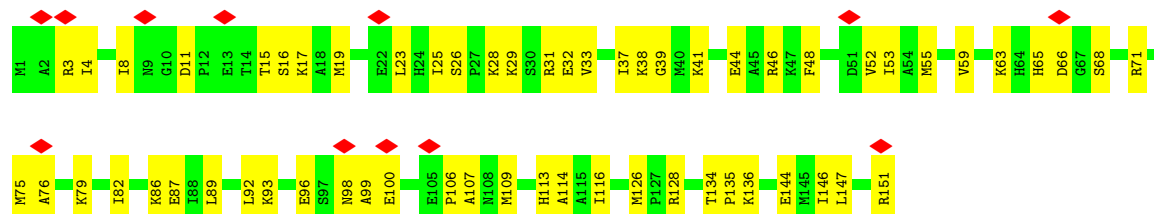
- Molecule 42: Large ribosomal subunit protein eL20



- Molecule 43: Large ribosomal subunit protein eL21

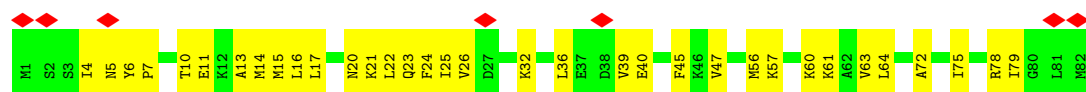


- Molecule 44: Large ribosomal subunit protein uL22

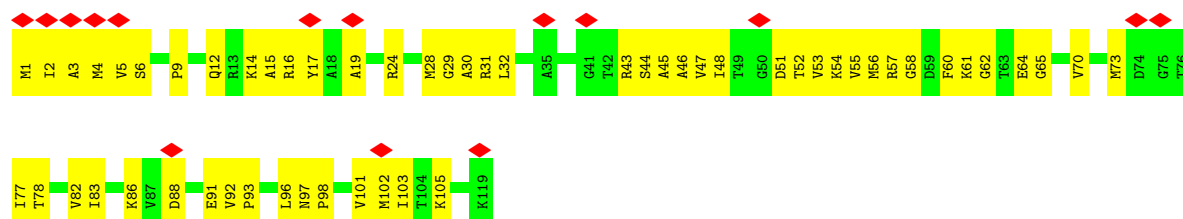


- Molecule 45: Large ribosomal subunit protein uL23

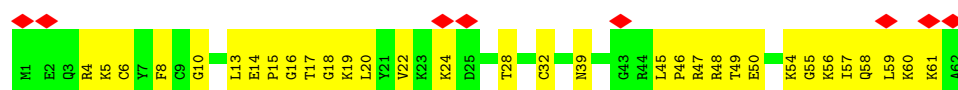




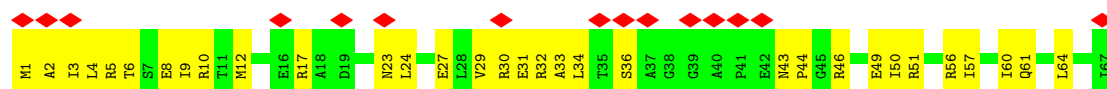
- Molecule 46: Large ribosomal subunit protein uL24



- Molecule 47: Large ribosomal subunit protein eL24



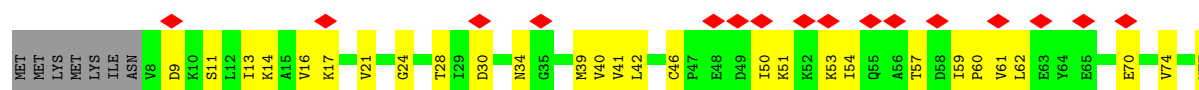
- Molecule 48: Large ribosomal subunit protein uL29

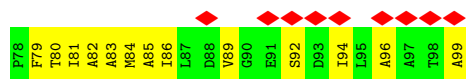


- Molecule 49: Large ribosomal subunit protein uL30



- Molecule 50: Large ribosomal subunit protein eL30

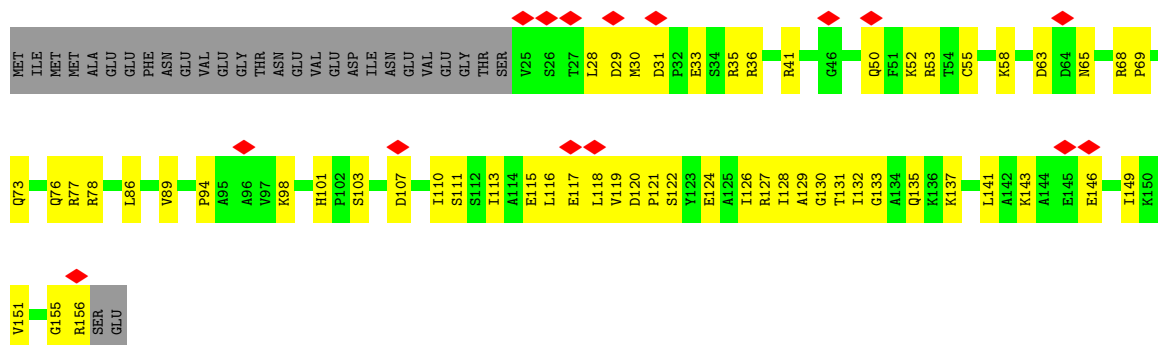




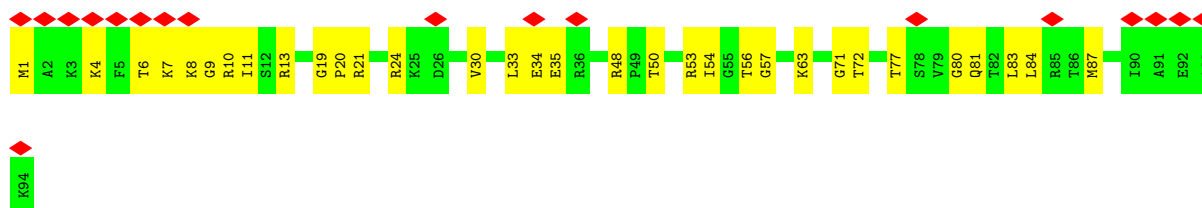
- Molecule 51: Large ribosomal subunit protein eL31



- Molecule 52: Large ribosomal subunit protein eL32



- Molecule 53: Large ribosomal subunit protein eL43

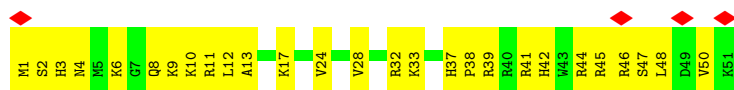


- Molecule 54: Large ribosomal subunit protein eL37



- Molecule 55: Large ribosomal subunit protein eL39

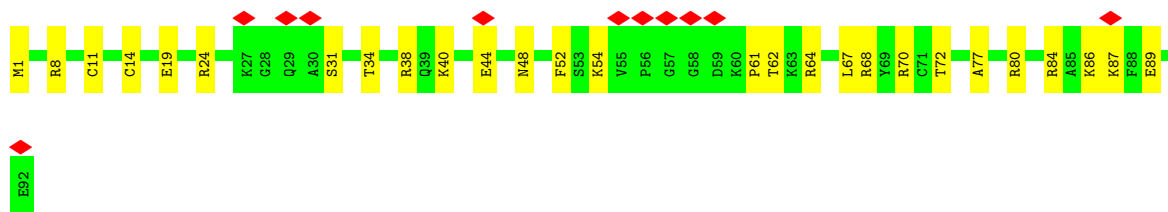




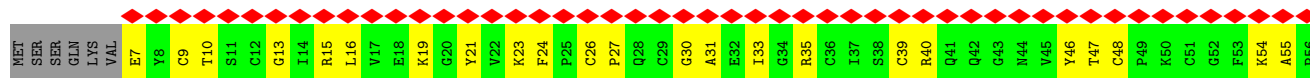
- Molecule 56: Large ribosomal subunit protein eL40



- Molecule 57: Large ribosomal subunit protein eL42



- Molecule 58: Putative zinc finger domain-containing protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91385	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.256	Depositor
Minimum map value	-0.151	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.046	Depositor
Map size (Å)	351.84, 351.84, 351.84	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.733, 0.733, 0.733	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.15	0/35052	0.25	0/54669
2	AB	0.13	0/1521	0.32	0/2068
3	AC	0.14	0/1447	0.35	0/1945
4	AD	0.15	0/1472	0.36	0/1985
5	AE	0.13	0/1375	0.33	0/1845
6	AF	0.14	0/1863	0.34	0/2504
7	AG	0.13	0/1531	0.32	0/2078
8	AI	0.16	0/1499	0.39	0/2017
9	AJ	0.16	0/997	0.38	0/1343
10	AK	0.17	0/972	0.35	0/1300
11	AL	0.19	0/1004	0.49	0/1352
12	AN	0.15	0/925	0.33	0/1244
13	AO	0.16	0/1102	0.34	0/1476
14	AP	0.14	0/1047	0.36	0/1407
15	AR	0.12	0/372	0.34	0/488
16	AQ	0.16	0/1247	0.31	0/1678
17	AS	0.16	0/864	0.35	0/1165
18	AU	0.12	0/790	0.33	0/1053
19	AV	0.13	0/1186	0.35	0/1596
20	AW	0.13	0/775	0.32	0/1038
21	AX	0.14	0/473	0.40	0/635
22	AY	0.13	0/473	0.32	0/632
23	AH	0.13	0/943	0.29	0/1266
24	AM	0.11	0/808	0.28	0/1090
25	AT	0.12	0/482	0.27	0/645
26	BA	0.29	0/66494	0.42	0/103680
27	BB	0.19	0/3037	0.29	0/4728
28	BC	0.26	0/1850	0.33	0/2497
29	BD	0.24	0/2646	0.33	0/3569
30	BE	0.22	0/1964	0.34	0/2654
31	BF	0.14	0/1310	0.30	0/1762
32	BG	0.16	0/1392	0.28	0/1870

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BH	0.15	0/864	0.30	0/1161
34	BI	0.21	0/1284	0.30	0/1719
35	BJ	0.23	0/1101	0.34	0/1474
36	BK	0.23	0/1010	0.33	0/1355
37	BL	0.22	0/1071	0.35	0/1425
38	BM	0.26	0/1625	0.34	0/2176
39	BN	0.18	0/1382	0.31	0/1863
40	BO	0.19	0/975	0.33	0/1312
41	BP	0.22	0/1209	0.32	0/1602
42	BQ	0.18	0/464	0.34	0/614
43	BR	0.23	0/780	0.28	0/1042
44	BS	0.21	0/1189	0.35	0/1588
45	BT	0.18	0/664	0.32	0/884
46	BU	0.18	0/919	0.36	0/1227
47	BV	0.20	0/508	0.26	0/670
48	BW	0.17	0/534	0.31	0/716
49	BX	0.22	0/1259	0.30	0/1692
50	BY	0.15	0/663	0.28	0/897
51	BZ	0.22	0/715	0.30	0/960
52	Ba	0.23	0/1044	0.33	0/1397
53	Bb	0.21	0/749	0.35	0/997
54	Bc	0.31	0/452	0.38	0/593
55	Bd	0.25	0/448	0.37	0/595
56	Be	0.18	0/355	0.27	0/468
57	Bf	0.23	0/777	0.34	0/1029
58	AZ	0.11	0/387	0.29	0/518
All	All	0.23	0/161341	0.35	0/239253

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
9	AJ	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	AJ	28	ARG	Peptide

5.2 Too-close contacts

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	AA	31324	0	15792	1066	0
2	AB	1492	0	1500	109	0
3	AC	1425	0	1460	119	0
4	AD	1454	0	1504	114	0
5	AE	1351	0	1397	103	0
6	AF	1837	0	1912	170	0
7	AG	1506	0	1561	160	0
8	AI	1479	0	1548	126	0
9	AJ	981	0	1008	84	0
10	AK	964	0	1028	85	0
11	AL	993	0	1033	80	0
12	AN	911	0	937	61	0
13	AO	1088	0	1142	78	0
14	AP	1033	0	1089	107	0
15	AR	366	0	362	44	0
16	AQ	1226	0	1305	101	0
17	AS	849	0	877	60	0
18	AU	775	0	787	85	0
19	AV	1163	0	1197	85	0
20	AW	766	0	795	86	0
21	AX	468	0	472	56	0
22	AY	471	0	490	53	0
23	AH	930	0	983	69	0
24	AM	796	0	841	91	0
25	AT	477	0	501	44	0
26	BA	59413	29860	29955	448	0
27	BB	2720	0	1382	62	0
28	BC	1808	0	1842	73	0
29	BD	2597	0	2692	121	0
30	BE	1930	0	1989	117	0
31	BF	1289	0	1317	79	0
32	BG	1371	0	1426	57	0
33	BH	857	0	898	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	BI	1261	0	1300	45	0
35	BJ	1086	0	1135	47	0
36	BK	999	0	1059	55	0
37	BL	1058	0	1044	41	0
38	BM	1593	0	1637	56	0
39	BN	1356	0	1358	75	0
40	BO	962	0	1021	52	0
41	BP	1195	0	1277	56	0
42	BQ	457	0	463	23	0
43	BR	766	0	777	25	0
44	BS	1169	0	1211	56	0
45	BT	656	0	688	27	0
46	BU	910	0	972	58	0
47	BV	499	0	515	34	0
48	BW	532	0	547	31	0
49	BX	1237	0	1269	49	0
50	BY	658	0	696	41	0
51	BZ	703	0	735	19	0
52	Ba	1028	0	1079	54	0
53	Bb	736	0	771	34	0
54	Bc	445	0	455	21	0
55	Bd	439	0	479	26	0
56	Be	353	0	374	13	0
57	Bf	760	0	797	24	0
58	AZ	379	0	374	32	0
59	AA	6	0	0	0	0
59	AN	1	0	0	0	0
59	AS	1	0	0	0	0
59	BA	42	0	0	0	0
59	Bc	1	0	0	0	0
60	AG	1	0	0	0	0
60	AR	1	0	0	0	0
60	AS	1	0	0	0	0
60	AX	1	0	0	0	0
60	BV	1	0	0	0	0
60	Bb	1	0	0	0	0
60	Bc	1	0	0	0	0
60	Be	1	0	0	0	0
60	Bf	1	0	0	0	0
All	All	149407	29860	105055	4401	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 18.

The worst 5 of 4401 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:120:CYS:HB2	7:AG:147:PRO:HA	1.45	0.97
21:AX:20:CYS:HB3	21:AX:39:CYS:SG	2.05	0.97
9:AJ:27:VAL:HB	9:AJ:61:TYR:HB2	1.47	0.96
1:AA:1343:A:H4'	1:AA:1344:C:H5''	1.49	0.94
29:BD:25:PRO:HG2	29:BD:310:ARG:HG3	1.51	0.93

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	AB	188/247 (76%)	183 (97%)	5 (3%)	0	100	100
3	AC	184/318 (58%)	167 (91%)	17 (9%)	0	100	100
4	AD	180/203 (89%)	174 (97%)	6 (3%)	0	100	100
5	AE	163/218 (75%)	154 (94%)	9 (6%)	0	100	100
6	AF	232/235 (99%)	205 (88%)	27 (12%)	0	100	100
7	AG	196/209 (94%)	184 (94%)	12 (6%)	0	100	100
8	AI	187/189 (99%)	168 (90%)	19 (10%)	0	100	100
9	AJ	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
10	AK	123/125 (98%)	109 (89%)	14 (11%)	0	100	100
11	AL	130/134 (97%)	110 (85%)	18 (14%)	2 (2%)	8	28
12	AN	121/126 (96%)	111 (92%)	9 (7%)	1 (1%)	16	44
13	AO	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
14	AP	130/182 (71%)	120 (92%)	9 (7%)	1 (1%)	16	44
15	AR	42/50 (84%)	38 (90%)	4 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AQ	150/152 (99%)	143 (95%)	7 (5%)	0	100	100
17	AS	107/109 (98%)	93 (87%)	14 (13%)	0	100	100
18	AU	93/136 (68%)	86 (92%)	7 (8%)	0	100	100
19	AV	147/149 (99%)	132 (90%)	14 (10%)	1 (1%)	19	47
20	AW	93/101 (92%)	84 (90%)	9 (10%)	0	100	100
21	AX	58/62 (94%)	52 (90%)	6 (10%)	0	100	100
22	AY	61/76 (80%)	52 (85%)	9 (15%)	0	100	100
23	AH	122/136 (90%)	114 (93%)	8 (7%)	0	100	100
24	AM	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
25	AT	56/64 (88%)	54 (96%)	2 (4%)	0	100	100
28	BC	236/238 (99%)	228 (97%)	8 (3%)	0	100	100
29	BD	335/337 (99%)	318 (95%)	17 (5%)	0	100	100
30	BE	250/253 (99%)	234 (94%)	16 (6%)	0	100	100
31	BF	163/165 (99%)	157 (96%)	6 (4%)	0	100	100
32	BG	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
33	BH	113/120 (94%)	111 (98%)	2 (2%)	0	100	100
34	BI	155/173 (90%)	148 (96%)	7 (4%)	0	100	100
35	BJ	136/143 (95%)	127 (93%)	9 (7%)	0	100	100
36	BK	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
37	BL	138/140 (99%)	130 (94%)	8 (6%)	0	100	100
38	BM	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
39	BN	172/174 (99%)	168 (98%)	4 (2%)	0	100	100
40	BO	124/126 (98%)	119 (96%)	5 (4%)	0	100	100
41	BP	149/151 (99%)	146 (98%)	3 (2%)	0	100	100
42	BQ	55/61 (90%)	53 (96%)	2 (4%)	0	100	100
43	BR	94/97 (97%)	90 (96%)	4 (4%)	0	100	100
44	BS	149/151 (99%)	140 (94%)	9 (6%)	0	100	100
45	BT	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
46	BU	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
47	BV	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
48	BW	65/67 (97%)	63 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	BX	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
50	BY	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
51	BZ	84/89 (94%)	83 (99%)	1 (1%)	0	100	100
52	Ba	130/161 (81%)	126 (97%)	4 (3%)	0	100	100
53	Bb	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
54	Bc	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
55	Bd	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
56	Be	42/52 (81%)	38 (90%)	4 (10%)	0	100	100
57	Bf	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
58	AZ	48/56 (86%)	46 (96%)	2 (4%)	0	100	100
All	All	7049/7661 (92%)	6635 (94%)	409 (6%)	5 (0%)	50	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	AL	105	ARG
19	AV	30	GLU
11	AL	12	LYS
14	AP	49	ARG
12	AN	124	ARG

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	
2	AB	166/212 (78%)	166 (100%)	0	100	100
3	AC	149/250 (60%)	149 (100%)	0	100	100
4	AD	160/173 (92%)	160 (100%)	0	100	100
5	AE	145/178 (82%)	145 (100%)	0	100	100
6	AF	208/209 (100%)	208 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	AG	161/170 (95%)	161 (100%)	0	100	100
8	AI	159/159 (100%)	159 (100%)	0	100	100
9	AJ	104/105 (99%)	104 (100%)	0	100	100
10	AK	105/105 (100%)	105 (100%)	0	100	100
11	AL	105/107 (98%)	105 (100%)	0	100	100
12	AN	92/94 (98%)	92 (100%)	0	100	100
13	AO	112/112 (100%)	112 (100%)	0	100	100
14	AP	108/151 (72%)	108 (100%)	0	100	100
15	AR	38/44 (86%)	38 (100%)	0	100	100
16	AQ	138/138 (100%)	138 (100%)	0	100	100
17	AS	96/96 (100%)	96 (100%)	0	100	100
18	AU	84/118 (71%)	84 (100%)	0	100	100
19	AV	123/123 (100%)	123 (100%)	0	100	100
20	AW	83/87 (95%)	83 (100%)	0	100	100
21	AX	54/56 (96%)	54 (100%)	0	100	100
22	AY	50/62 (81%)	50 (100%)	0	100	100
23	AH	96/103 (93%)	96 (100%)	0	100	100
24	AM	89/89 (100%)	89 (100%)	0	100	100
25	AT	52/57 (91%)	52 (100%)	0	100	100
28	BC	188/188 (100%)	188 (100%)	0	100	100
29	BD	277/277 (100%)	277 (100%)	0	100	100
30	BE	197/198 (100%)	197 (100%)	0	100	100
31	BF	140/140 (100%)	140 (100%)	0	100	100
32	BG	148/148 (100%)	148 (100%)	0	100	100
33	BH	88/91 (97%)	88 (100%)	0	100	100
34	BI	132/141 (94%)	132 (100%)	0	100	100
35	BJ	114/119 (96%)	114 (100%)	0	100	100
36	BK	109/109 (100%)	109 (100%)	0	100	100
37	BL	108/108 (100%)	108 (100%)	0	100	100
38	BM	166/166 (100%)	166 (100%)	0	100	100
39	BN	143/143 (100%)	143 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	BO	104/104 (100%)	104 (100%)	0	100	100
41	BP	123/123 (100%)	123 (100%)	0	100	100
42	BQ	50/54 (93%)	50 (100%)	0	100	100
43	BR	85/86 (99%)	85 (100%)	0	100	100
44	BS	124/124 (100%)	124 (100%)	0	100	100
45	BT	73/73 (100%)	73 (100%)	0	100	100
46	BU	100/100 (100%)	100 (100%)	0	100	100
47	BV	54/54 (100%)	54 (100%)	0	100	100
48	BW	57/57 (100%)	57 (100%)	0	100	100
49	BX	134/134 (100%)	134 (100%)	0	100	100
50	BY	71/78 (91%)	71 (100%)	0	100	100
51	BZ	76/78 (97%)	76 (100%)	0	100	100
52	Ba	109/135 (81%)	109 (100%)	0	100	100
53	Bb	76/76 (100%)	76 (100%)	0	100	100
54	Bc	49/49 (100%)	49 (100%)	0	100	100
55	Bd	48/48 (100%)	48 (100%)	0	100	100
56	Be	37/43 (86%)	37 (100%)	0	100	100
57	Bf	82/82 (100%)	82 (100%)	0	100	100
58	AZ	42/48 (88%)	42 (100%)	0	100	100
All	All	5981/6372 (94%)	5981 (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 27 such sidechains are listed below:

Mol	Chain	Res	Type
34	BI	33	HIS
38	BM	138	HIS
52	Ba	44	GLN
38	BM	127	HIS
39	BN	108	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1459/1478 (98%)	304 (20%)	4 (0%)
26	BA	2769/2899 (95%)	424 (15%)	6 (0%)
27	BB	127/129 (98%)	13 (10%)	0
All	All	4355/4506 (96%)	741 (17%)	10 (0%)

5 of 741 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	U
1	AA	4	C
1	AA	8	U
1	AA	17	C
1	AA	33	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BA	869	U
26	BA	1932	U
26	BA	1984	U
1	AA	1187	U
26	BA	817	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 60 ligands modelled in this entry, 60 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

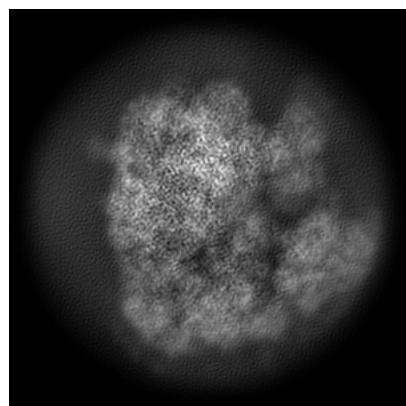
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49998. These allow visual inspection of the internal detail of the map and identification of artifacts.

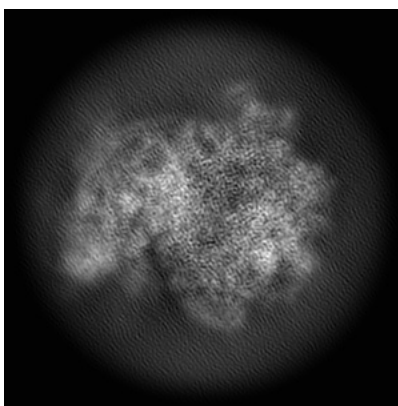
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

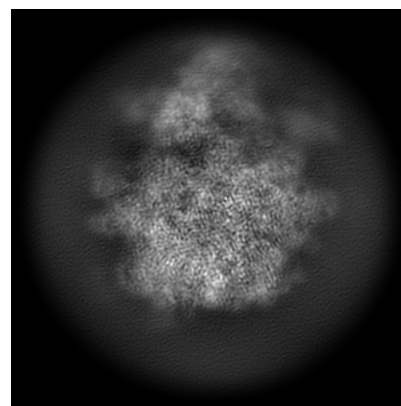
6.1.1 Primary map



X

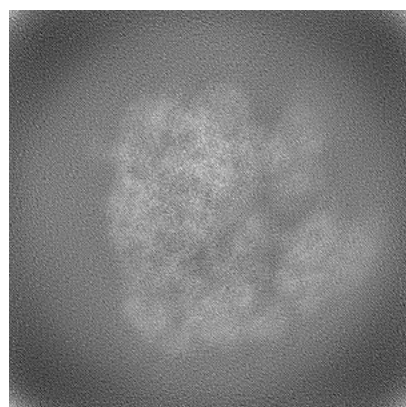


Y

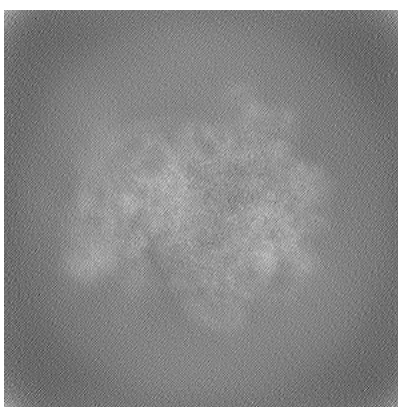


Z

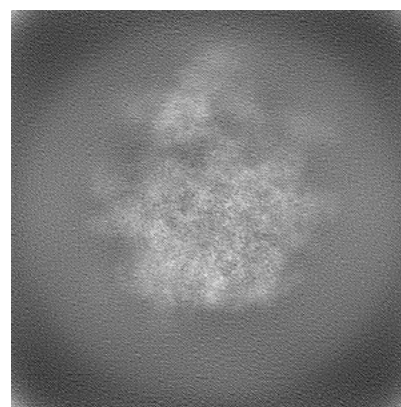
6.1.2 Raw map



X



Y

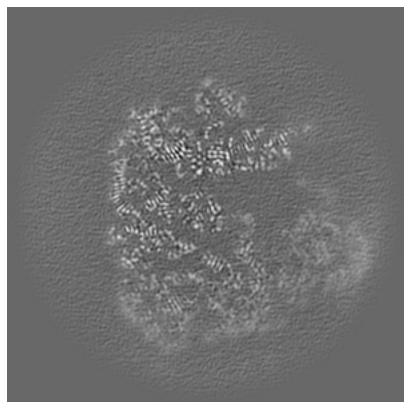


Z

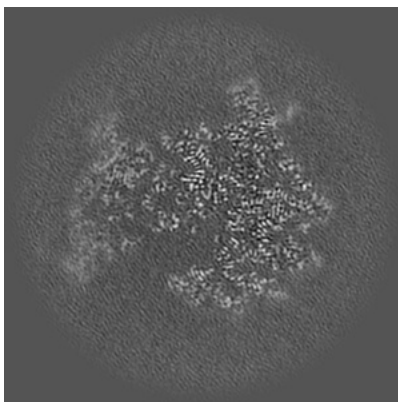
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

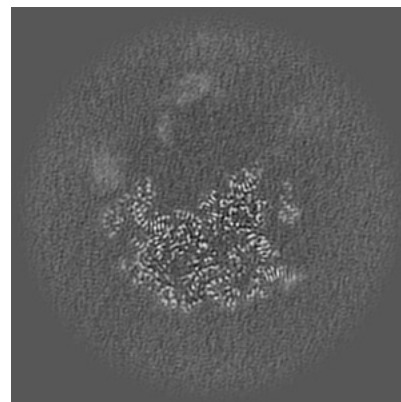
6.2.1 Primary map



X Index: 240

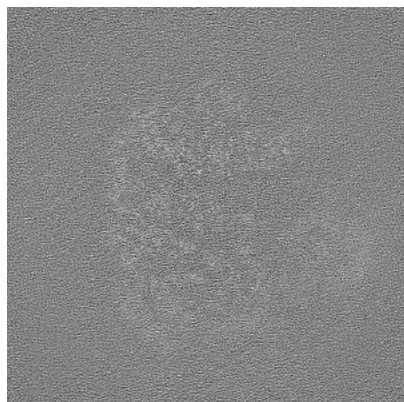


Y Index: 240

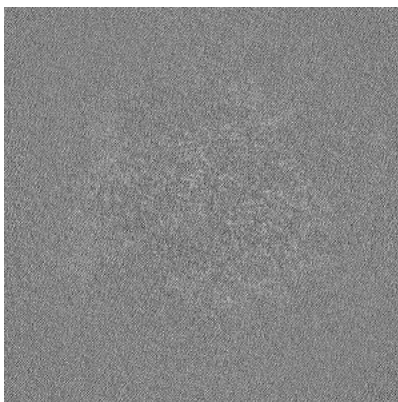


Z Index: 240

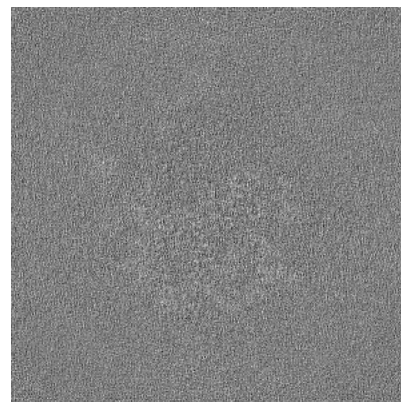
6.2.2 Raw map



X Index: 240



Y Index: 240

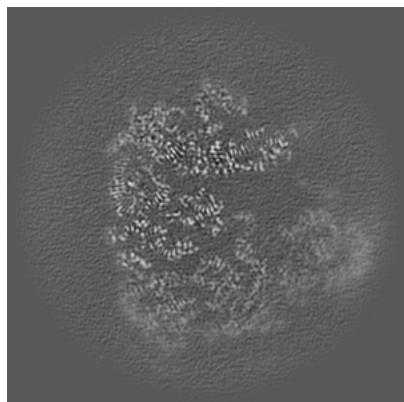


Z Index: 240

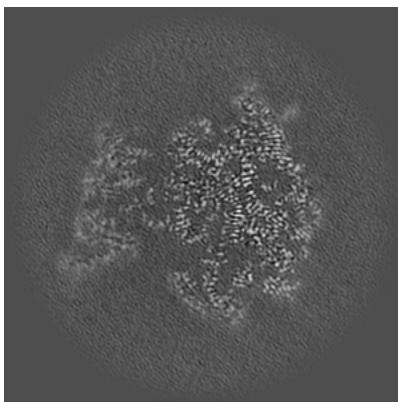
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

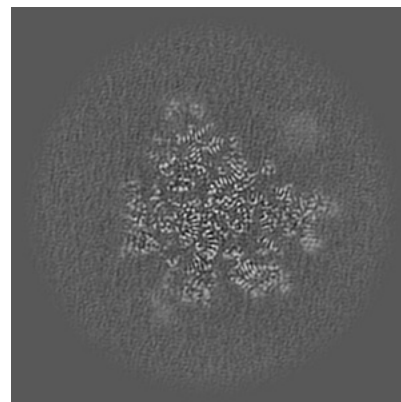
6.3.1 Primary map



X Index: 242

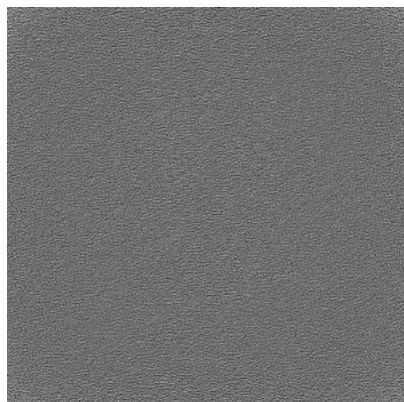


Y Index: 231

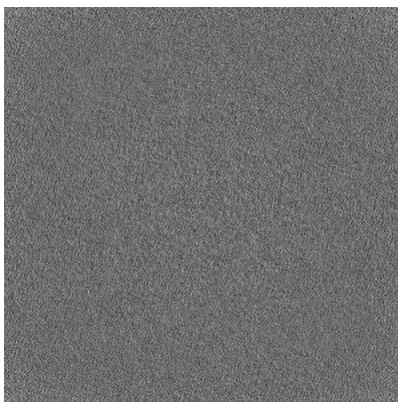


Z Index: 299

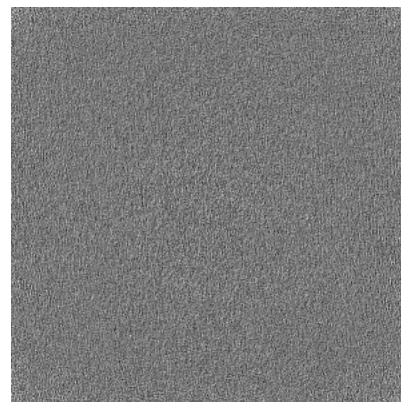
6.3.2 Raw map



X Index: 0



Y Index: 0

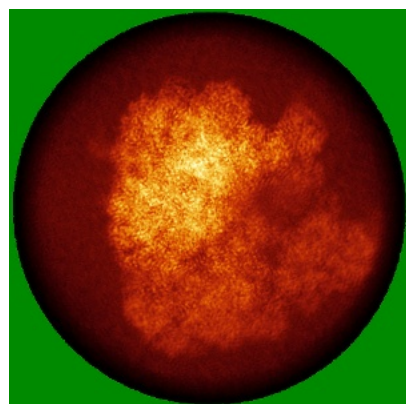


Z Index: 0

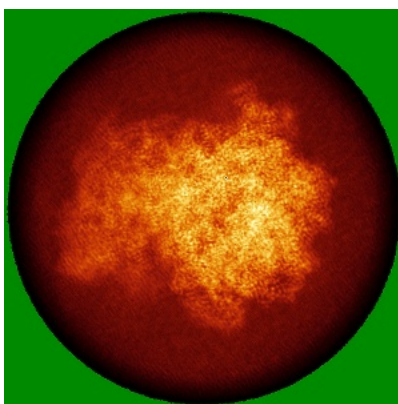
The images above show the largest variance slices of the map in three orthogonal directions.

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

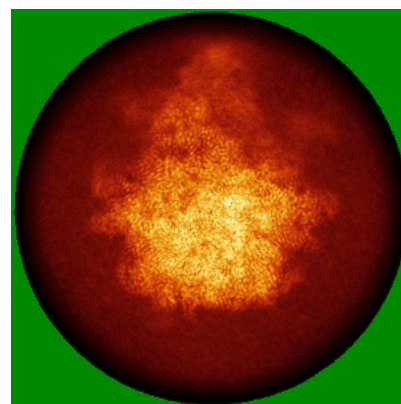
6.4.1 Primary map



X

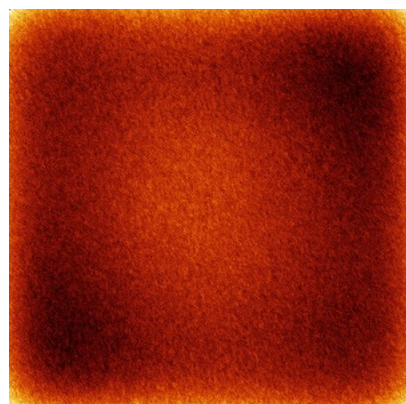


Y

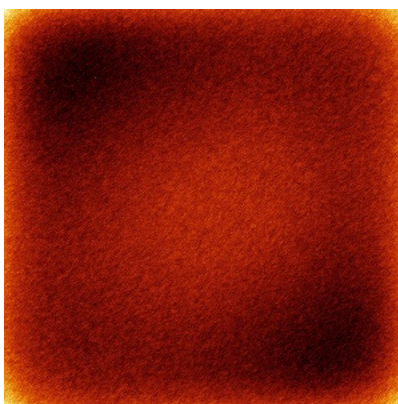


Z

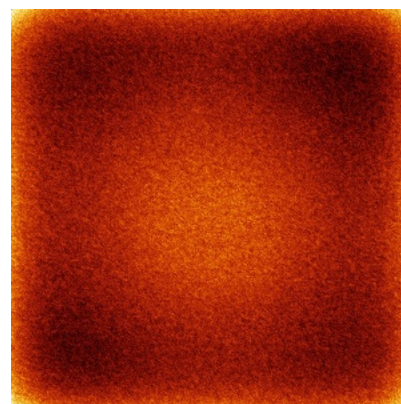
6.4.2 Raw map



X



Y

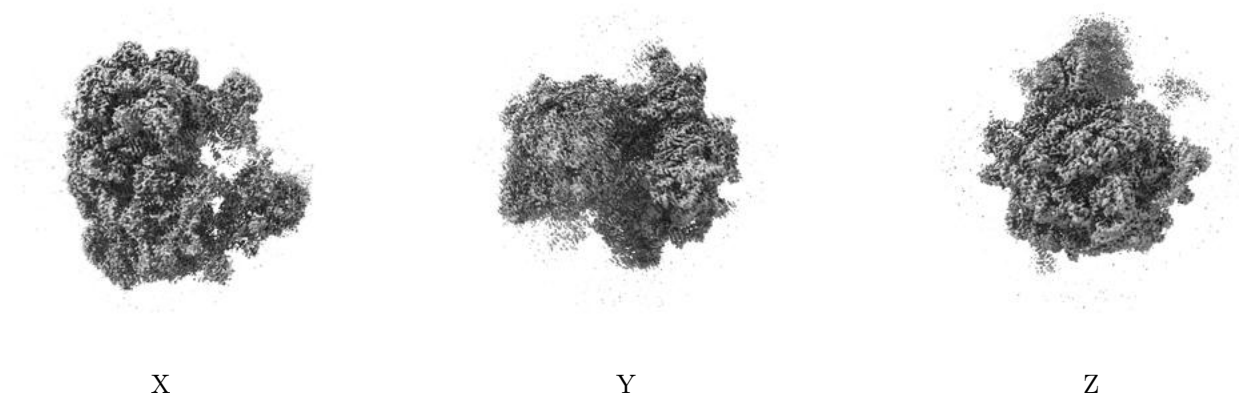


Z

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.

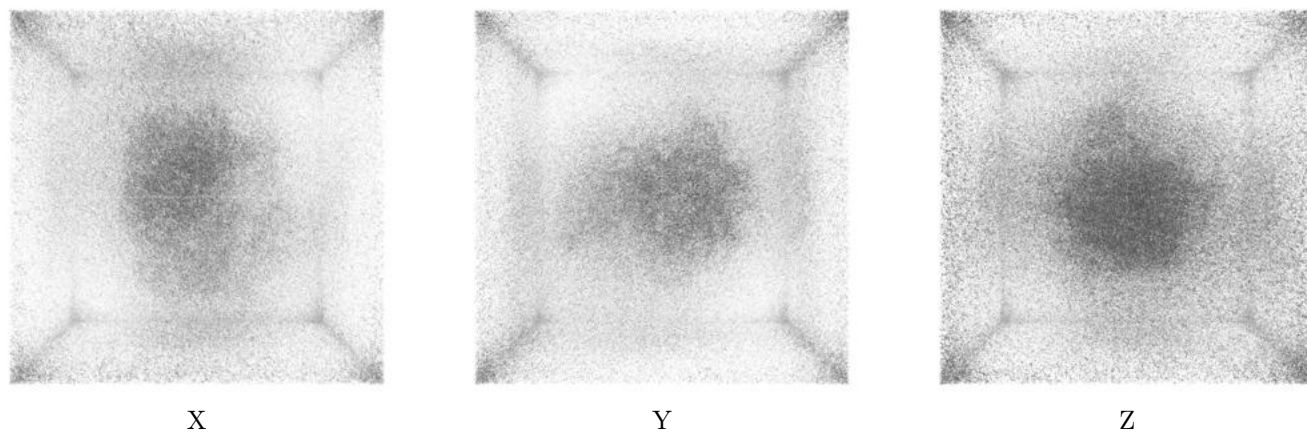
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.046. 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



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.

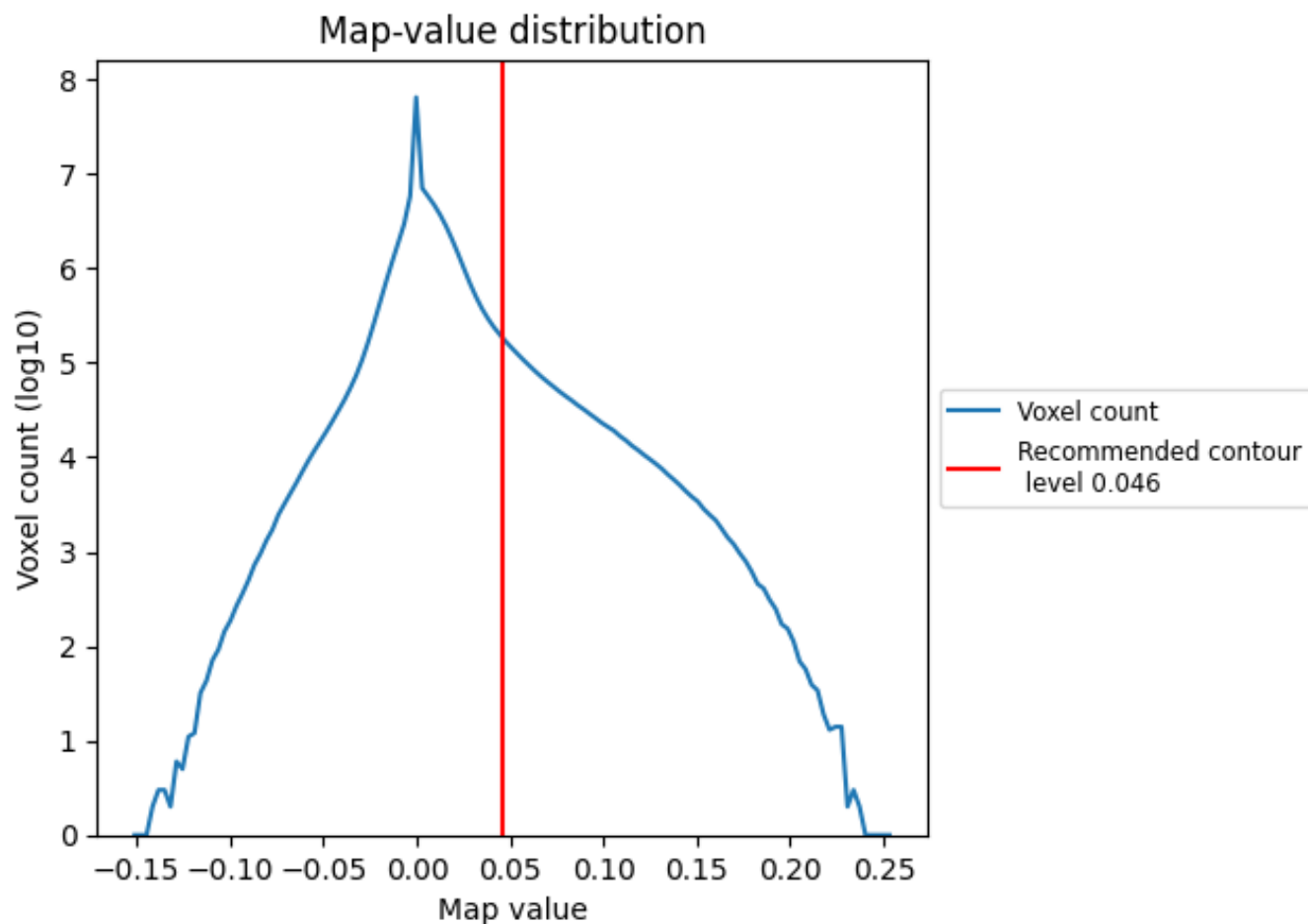
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

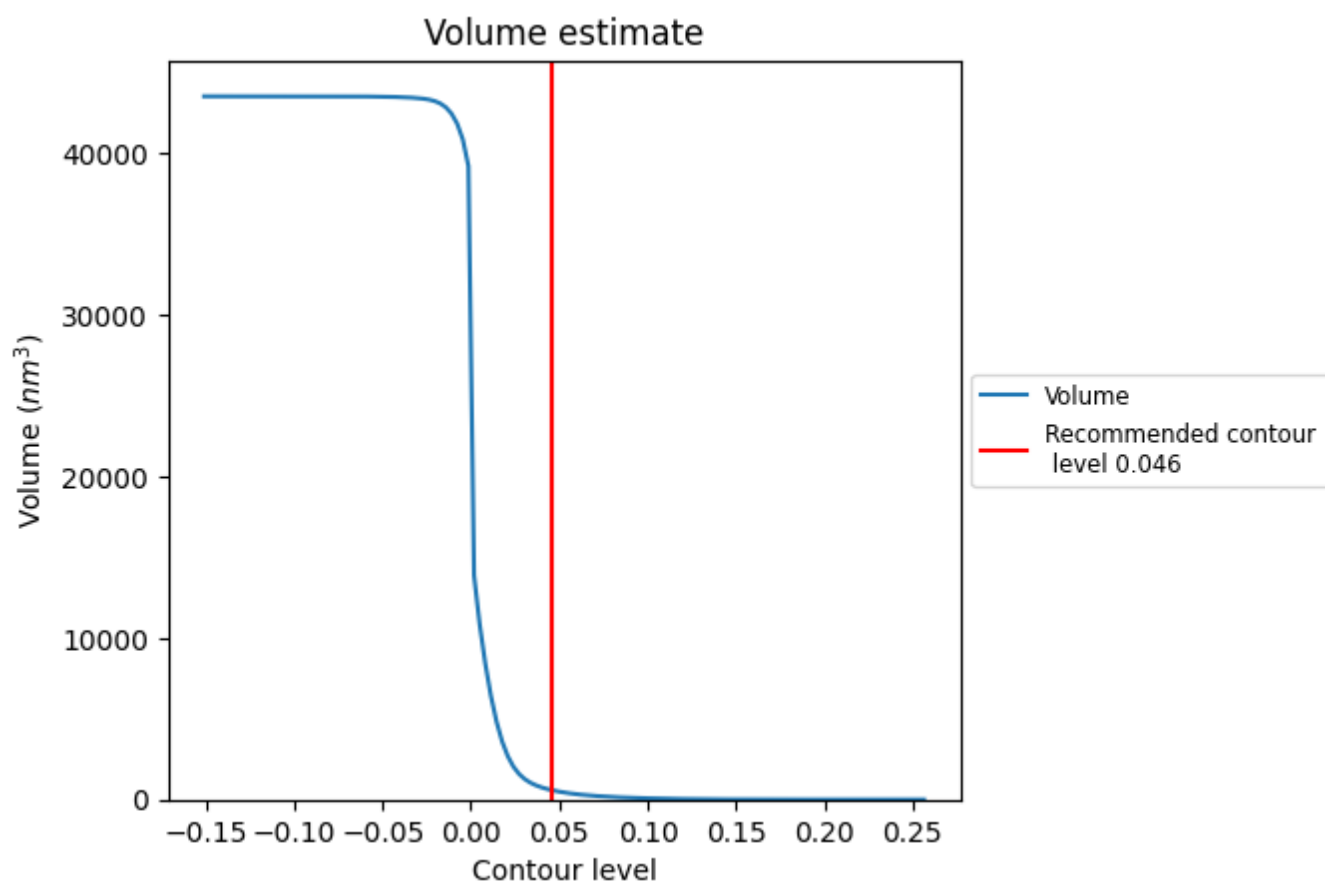
This section contains the results of statistical analysis of the map.

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.

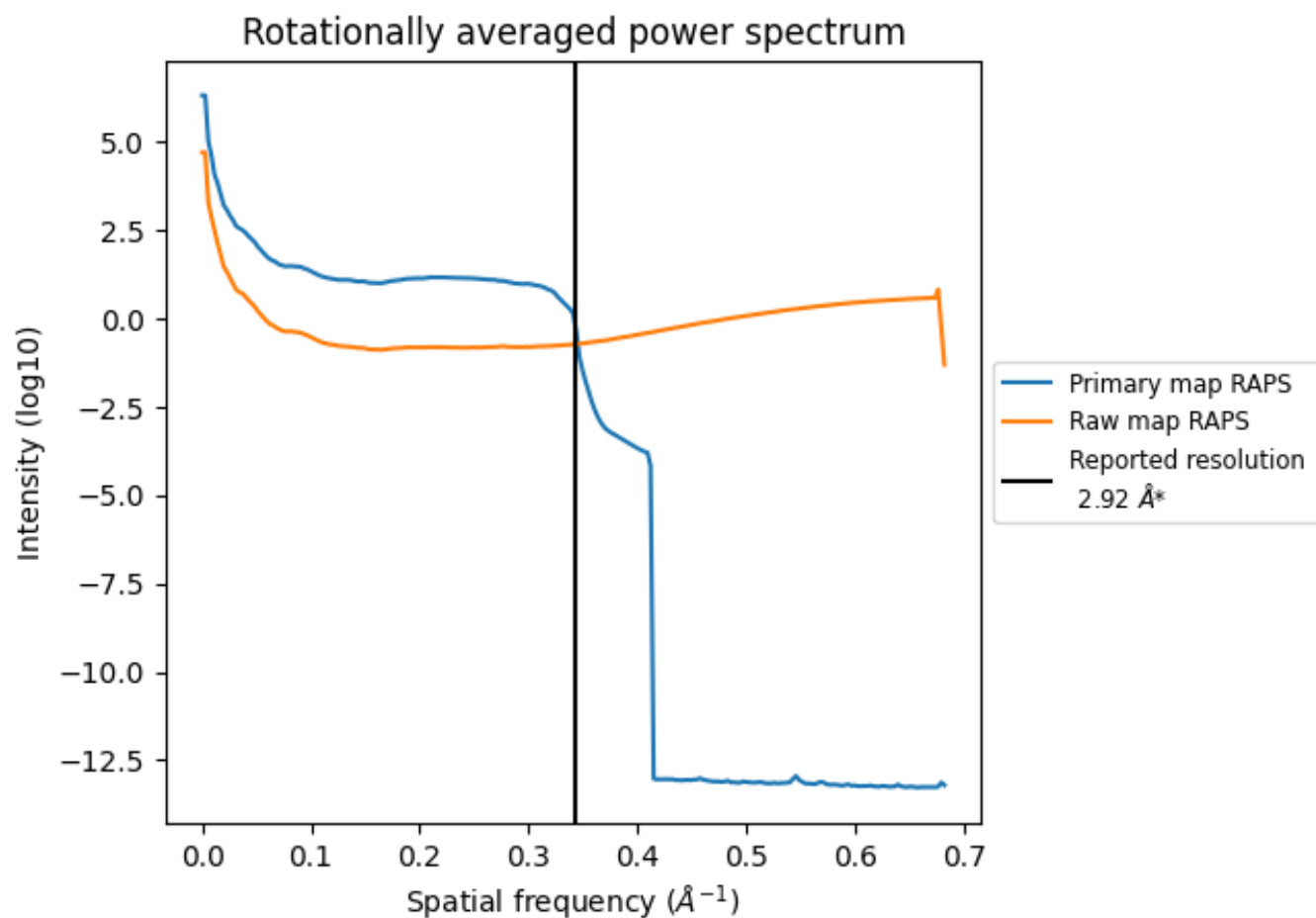
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 578 nm³; this corresponds to an approximate mass of 522 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 ⓘ

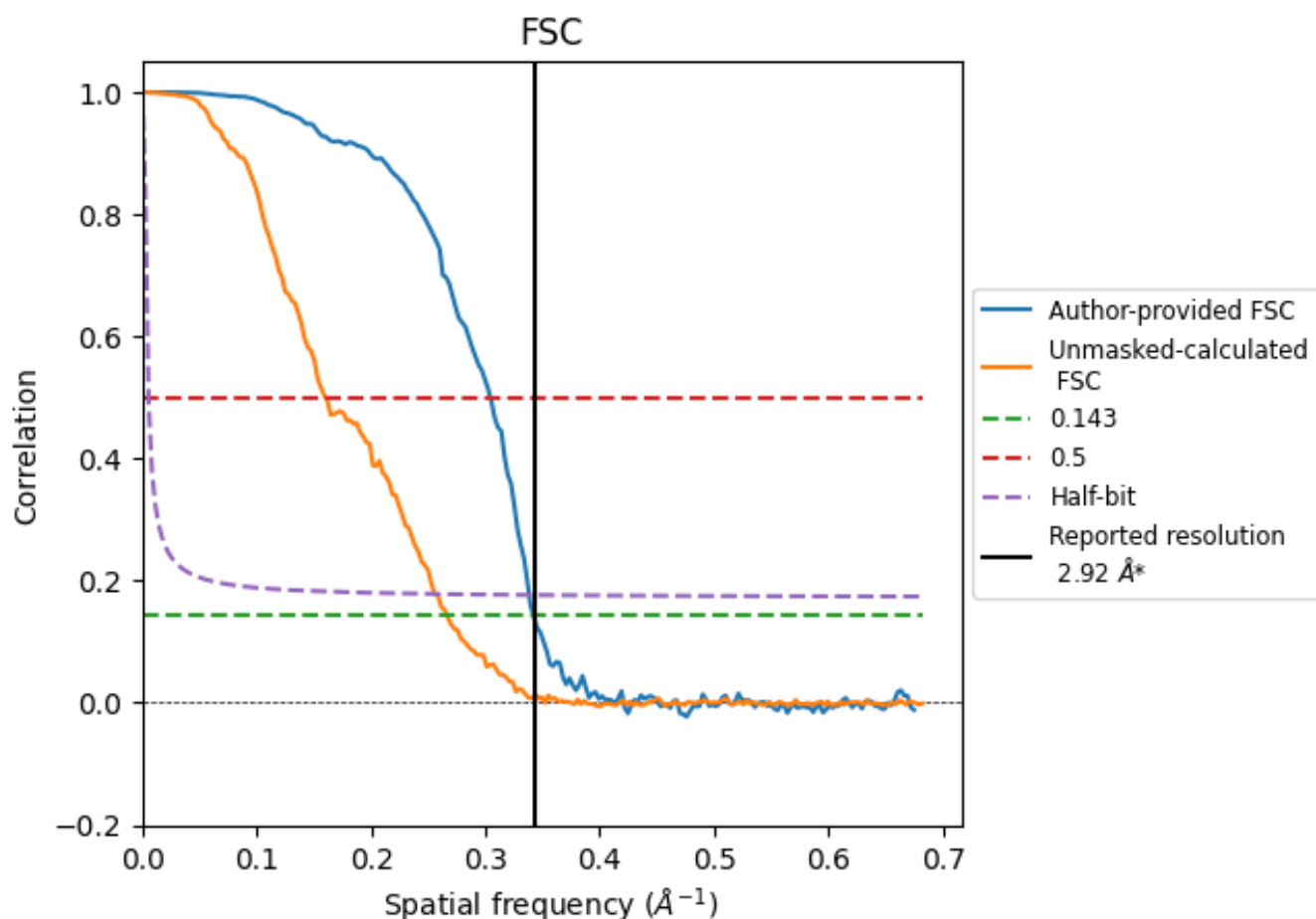


*Reported resolution corresponds to spatial frequency of 0.342 \AA^{-1}

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 0.342 \AA^{-1}

8.2 Resolution estimates [i](#)

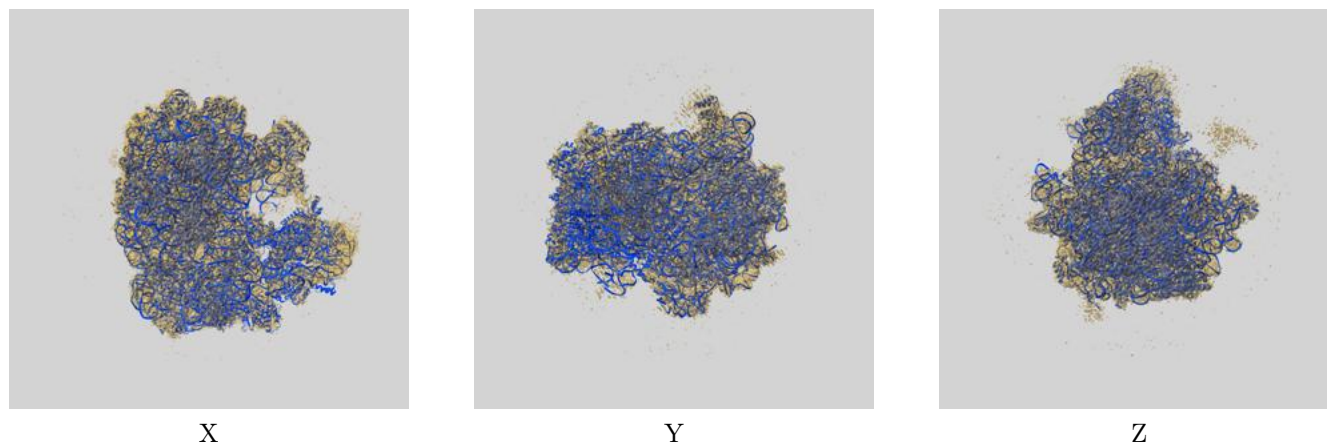
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.92	-	-
Author-provided FSC curve	2.92	3.28	2.95
Unmasked-calculated*	3.75	6.24	3.91

*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 3.75 differs from the reported value 2.92 by more than 10 %

9 Map-model fit [i](#)

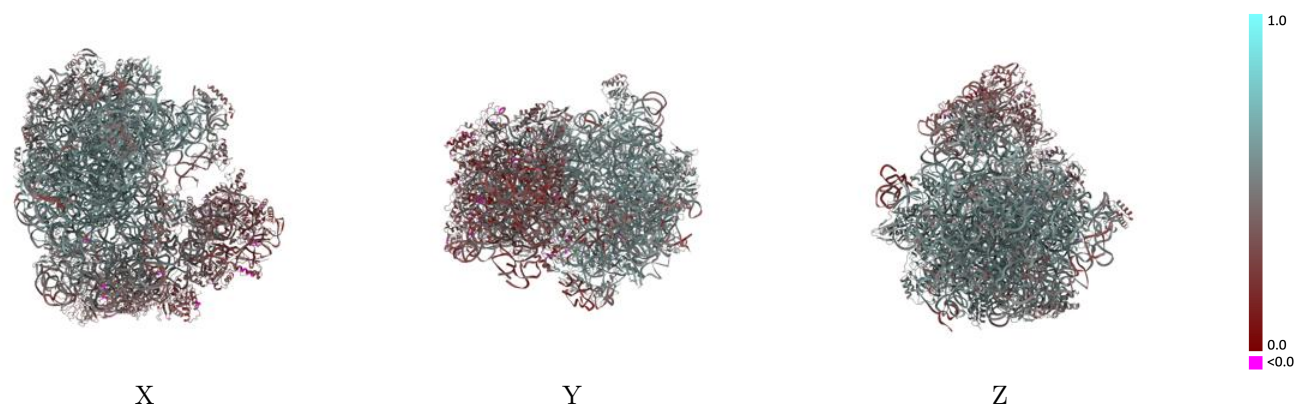
This section contains information regarding the fit between EMDB map EMD-49998 and PDB model 9O17. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



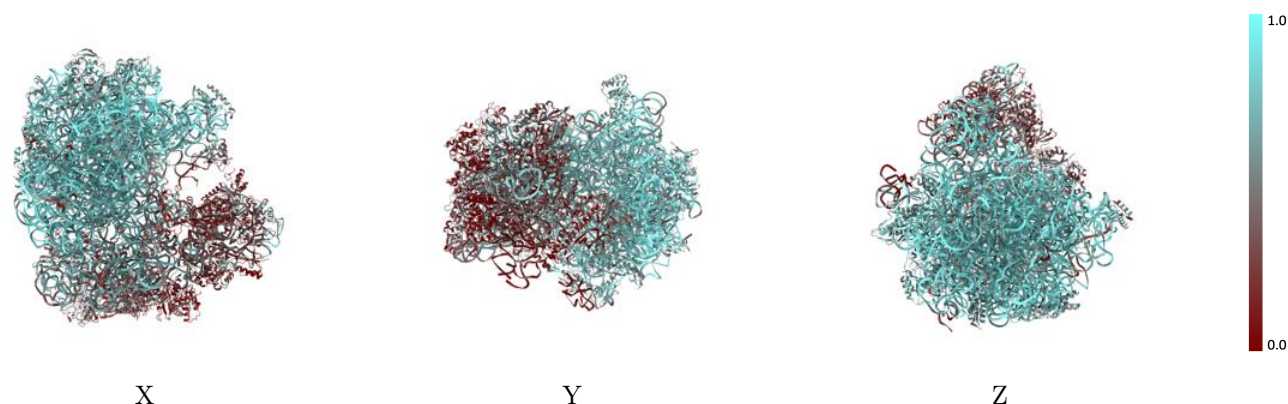
The images above show the 3D surface view of the map at the recommended contour level 0.046 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



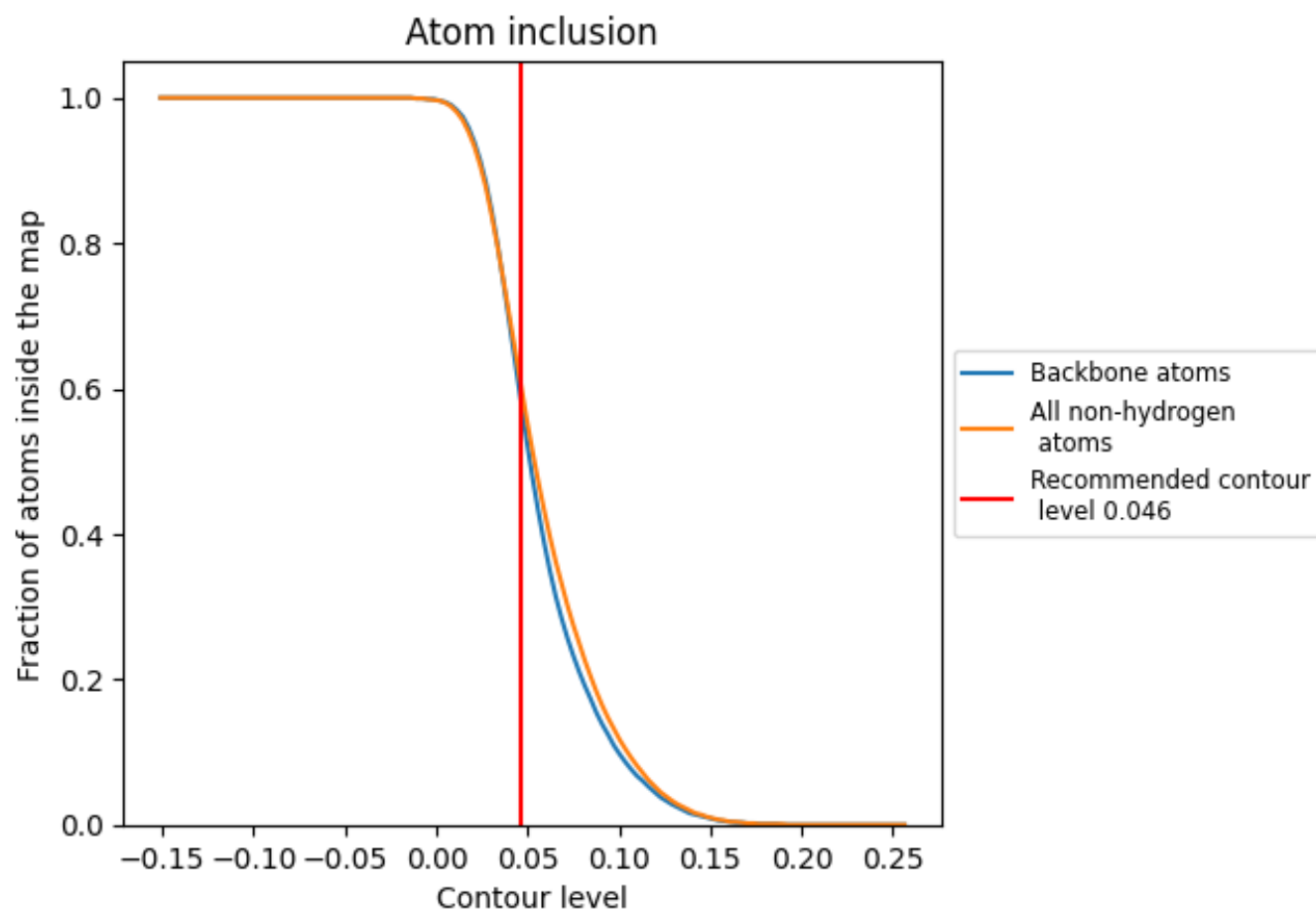
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.046).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 61% 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 (0.046) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6090	 0.4870
AA	 0.5390	 0.4340
AB	 0.1810	 0.3070
AC	 0.0270	 0.2910
AD	 0.3400	 0.4010
AE	 0.2570	 0.3420
AF	 0.3430	 0.3760
AG	 0.2750	 0.3640
AH	 0.2990	 0.4110
AI	 0.2170	 0.3360
AJ	 0.3830	 0.3900
AK	 0.4860	 0.4770
AL	 0.2690	 0.2830
AM	 0.0800	 0.2550
AN	 0.3680	 0.4470
AO	 0.2740	 0.4550
AP	 0.1400	 0.3260
AQ	 0.3890	 0.4190
AR	 0.0910	 0.3490
AS	 0.4110	 0.4610
AT	 0.2080	 0.3030
AU	 0.0780	 0.2530
AV	 0.3450	 0.2710
AW	 0.2640	 0.3030
AX	 0.2530	 0.3590
AY	 0.2030	 0.3460
AZ	 0.0510	 0.2900
BA	 0.8310	 0.5490
BB	 0.8250	 0.4990
BC	 0.7420	 0.5760
BD	 0.7510	 0.5630
BE	 0.7060	 0.5040
BF	 0.4010	 0.4120
BG	 0.6260	 0.5050
BH	 0.6070	 0.4680



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Chain	Atom inclusion	Q-score
BI	 0.6580	 0.5550
BJ	 0.7300	 0.5460
BK	 0.6390	 0.5630
BL	 0.7140	 0.5410
BM	 0.7560	 0.5700
BN	 0.7020	 0.4900
BO	 0.7040	 0.5120
BP	 0.7110	 0.5430
BQ	 0.6050	 0.5410
BR	 0.7430	 0.5680
BS	 0.6700	 0.5280
BT	 0.6770	 0.5120
BU	 0.6380	 0.4530
BV	 0.6370	 0.5560
BW	 0.5540	 0.4290
BX	 0.7340	 0.5350
BY	 0.5530	 0.4610
BZ	 0.7340	 0.5530
Ba	 0.7070	 0.5170
Bb	 0.6260	 0.5310
Bc	 0.8120	 0.5750
Bd	 0.7470	 0.5500
Be	 0.6310	 0.5440
Bf	 0.7090	 0.5730