



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 06:56 AM EDT

PDB ID : 9ZNF / pdb_00009znf
EMDB ID : EMD-74446
Title : Cryo-EM structure of the Methanosarcina acetivorans 70S ribosome in complex with SriA and SriB
Authors : Nissley, A.J.; Cate, J.H.D.
Deposited on : 2025-12-12
Resolution : 2.03 Å(reported)
Based on initial model : .

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:

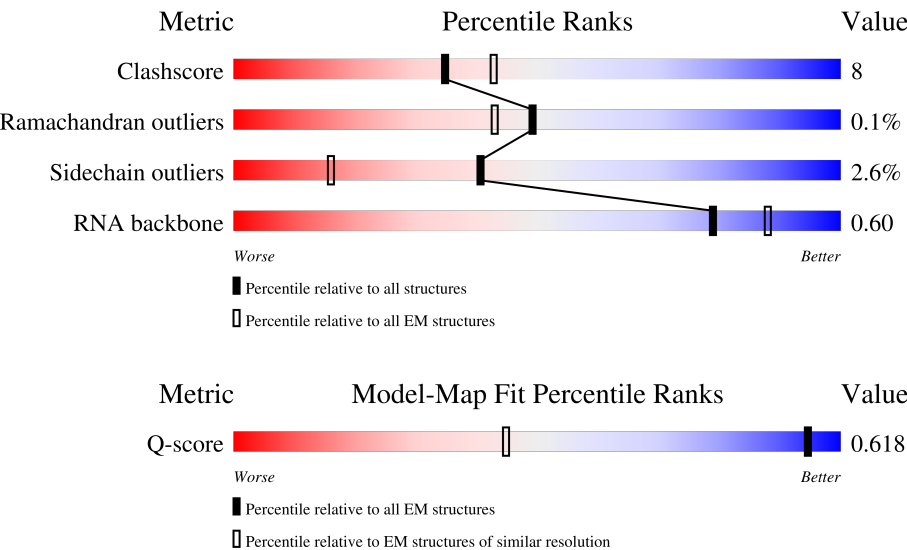
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.03 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1771 (1.55 - 2.53)

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	1	2904	
2	2	133	
3	3	1478	

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Mol	Chain	Length	Quality of chain
4	5	339	
5	4	270	
6	8	75	
7	AA	238	
8	AB	337	
9	AC	253	
10	AD	165	
11	AE	176	
12	AF	120	
13	AG	143	
14	AH	132	
15	AI	140	
16	AJ	196	
17	AK	173	
18	AL	174	
19	AM	126	
20	AN	151	
21	AO	61	
22	AP	97	
23	AQ	151	
24	AR	82	
25	AS	119	
26	AT	62	
27	AU	67	
28	AV	153	

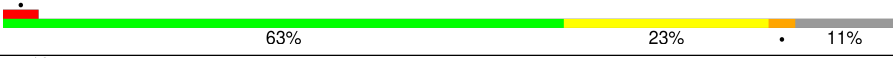
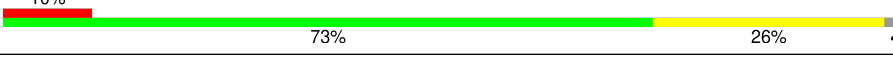
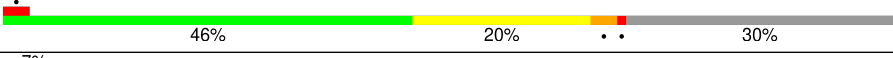
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Mol	Chain	Length	Quality of chain
29	AW	99	
30	AX	89	
31	AY	129	
32	AZ	56	
33	Aa	51	
34	Ab	49	
35	Ac	92	
36	Ad	94	
37	BA	203	
38	BB	225	
39	BC	318	
40	BD	218	
41	BE	235	
42	BF	209	
43	BG	136	
44	BH	189	
45	BI	130	
46	BJ	134	
47	BK	125	
48	BL	102	
49	BM	126	
50	BN	142	
51	BO	162	
52	BP	50	
53	BQ	152	

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Mol	Chain	Length	Quality of chain
54	BR	109	
55	BS	64	
56	BT	136	
57	BU	149	
58	BV	56	
59	BW	101	
60	BX	62	
61	BY	76	
62	BZ	57	

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 157707 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2716	Total	C	N	O	P	0	0
			58152	25958	10598	18880	2716		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1	A	-	insertion	GB 470469544
1	2	A	-	insertion	GB 470469544
1	3	U	-	insertion	GB 470469544
1	4	U	-	insertion	GB 470469544
1	403	G	U	conflict	GB 470469544
1	408	U	C	conflict	GB 470469544
1	2716	U	C	conflict	GB 470469544
1	2721	A	G	conflict	GB 470469544
1	2904	A	-	insertion	GB 470469544

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	127	Total	C	N	O	P	0	0
			2697	1204	476	890	127		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	1425	Total	C	N	O	P	0	0
			30541	13619	5564	9933	1425		

- Molecule 4 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	47	Total	C	N	O	S	0	0
			364	226	69	66	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	334	HIS	-	insertion	UNP A0A832S9K2
5	335	HIS	-	insertion	UNP A0A832S9K2
5	336	HIS	-	insertion	UNP A0A832S9K2
5	337	HIS	-	insertion	UNP A0A832S9K2
5	338	HIS	-	insertion	UNP A0A832S9K2
5	339	HIS	-	insertion	UNP A0A832S9K2

- Molecule 5 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	263	Total	C	N	O	S	0	0
			2041	1264	364	397	16		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	265	HIS	-	insertion	UNP A0A832SJD6
4	266	HIS	-	insertion	UNP A0A832SJD6
4	267	HIS	-	insertion	UNP A0A832SJD6
4	268	HIS	-	insertion	UNP A0A832SJD6
4	269	HIS	-	insertion	UNP A0A832SJD6
4	270	HIS	-	insertion	UNP A0A832SJD6

- Molecule 6 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	18	Total	C	N	O	P	0	0
			381	171	70	123	17		

- Molecule 7 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AA	235	Total	C	N	O	S	0	0
			1779	1112	343	317	7		

- Molecule 8 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AB	335	Total	C	N	O	S	0	0
			2583	1631	472	473	7		

- Molecule 9 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AC	252	Total	C	N	O	S	0	0
			1929	1208	368	352	1		

- Molecule 10 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AD	159	Total	C	N	O	S	0	0
			1241	781	228	225	7		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AE	171	Total	C	N	O	S	0	0
			1329	849	229	246	5		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AF	106	Total	C	N	O	S	0	0
			779	490	133	154	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AG	139	Total	C	N	O	S	0	0
			1092	687	201	200	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AH	132	Total	C	N	O	S	0	0
			998	623	185	181	9		

- Molecule 15 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AI	139	Total	C	N	O	S	0	0
			1048	638	203	201	6		

- Molecule 16 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AJ	195	Total	C	N	O	S	0	0
			1584	981	328	271	4		

- Molecule 17 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AK	170	Total	C	N	O	S	0	0
			1333	835	257	232	9		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL	172	Total	C	N	O	S	0	0
			1341	845	240	255	1		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AM	125	Total	C	N	O	S	0	0
			953	603	172	176	2		

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AN	147	Total	C	N	O	S	0	0
			1159	717	236	203	3		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AO	56	Total	C	N	O	0	0
			447	284	78	85		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AP	96	Total	C	N	O	S	0	0
			765	475	146	140	4		

- Molecule 23 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AQ	149	Total	C	N	O	S	0	0
			1149	718	213	209	9		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AR	80	Total	C	N	O	S	0	0
			639	408	106	119	6		

- Molecule 25 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AS	115	Total	C	N	O	S	0	0
			880	545	166	164	5		

- Molecule 26 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AT	60	Total	C	N	O	S	0	0
			484	307	85	84	8		

- Molecule 27 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AU	65	Total	C	N	O	S	0	0
			515	310	101	103	1		

- Molecule 28 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AV	153	Total	C	N	O	S	0	0
			1236	779	230	221	6		

- Molecule 29 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AW	87	Total	C	N	O	S	0	0
			627	396	103	124	4		

- Molecule 30 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AX	84	Total	C	N	O	S	0	0
			685	437	128	117	3		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AY	126	Total	C	N	O	S	0	0
			981	617	188	174	2		

- Molecule 32 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AZ	55	Total	C	N	O	S	0	0
			436	264	91	74	7		

- Molecule 33 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Aa	50	Total	C	N	O	S	0	0
			430	267	100	62	1		

- Molecule 34 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ab	43	Total	C	N	O	S	0	0
			348	212	73	58	5		

- Molecule 35 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ac	91	Total	C	N	O	S	0	0
			750	475	150	118	7		

- Molecule 36 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ad	89	Total	C	N	O	S	0	0
			699	437	139	117	6		

- Molecule 37 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BA	179	Total	C	N	O	S	0	0
			1435	900	259	268	8		

- Molecule 38 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BB	188	Total	C	N	O	S	0	0
			1476	933	260	278	5		

- Molecule 39 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BC	109	Total	C	N	O	S	0	0
			826	522	152	147	5		

- Molecule 40 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BD	162	Total	C	N	O	S	0	0
			1303	824	241	233	5		

- Molecule 41 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BE	228	Total	C	N	O	S	0	0
			1796	1131	327	333	5		

- Molecule 42 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BF	201	Total	C	N	O	S	0	0
			1527	966	273	281	7		

- Molecule 43 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BG	125	Total	C	N	O	S	0	0
			935	594	169	168	4		

- Molecule 44 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BH	175	Total	C	N	O	S	0	0
			1363	851	253	256	3		

- Molecule 45 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BI	129	Total	C	N	O	S	0	0
			980	628	166	182	4		

- Molecule 46 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BJ	132	Total	C	N	O	S	0	0
			1001	622	188	188	3		

- Molecule 47 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BK	124	Total	C	N	O	S	0	0
			954	582	195	173	4		

- Molecule 48 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BL	39	Total	C	N	O	S	0	0
			308	197	58	52	1		

- Molecule 49 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BM	123	Total	C	N	O	S	0	0
			910	560	180	166	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	116	IAS	ASP	conflict	UNP Q8TRR0

- Molecule 50 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BN	139	Total	C	N	O	S	0	0
			1057	662	202	188	5		

- Molecule 51 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BO	131	Total	C	N	O	S	0	0
			1025	643	197	183	2		

- Molecule 52 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BP	46	Total	C	N	O	S	0	0
			382	238	76	63	5		

- Molecule 53 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BQ	150	Total	C	N	O	S	0	0
			1206	766	218	217	5		

- Molecule 54 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BR	107	Total	C	N	O	S	0	0
			831	522	149	153	7		

- Molecule 55 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BS	58	Total	C	N	O	S	0	0
			476	302	86	87	1		

- Molecule 56 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BT	105	Total	C	N	O	S	0	0
			861	542	160	156	3		

- Molecule 57 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BU	148	Total	C	N	O	S	0	0
			1154	734	203	213	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BV	52	Total	C	N	O	S	0	0
			394	247	70	69	8		

- Molecule 59 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BW	90	Total	C	N	O	S	0	0
			736	463	131	138	4		

- Molecule 60 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BX	61	Total	C	N	O	S	0	0
			474	293	86	91	4		

- Molecule 61 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BY	53	Total	C	N	O	S	0	0
			394	241	75	74	4		

- Molecule 62 is a protein called DUF5350 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BZ	57	Total	C	N	O	S	0	0
			452	283	97	71	1		

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	1	244	Total	Mg	0
			244	244	
63	2	2	Total	Mg	0
			2	2	
63	3	45	Total	Mg	0
			45	45	

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Mol	Chain	Residues	Atoms		AltConf
63	4	2	Total 2	Mg 2	0
63	AA	2	Total 2	Mg 2	0
63	AB	2	Total 2	Mg 2	0
63	AH	1	Total 1	Mg 1	0
63	AI	1	Total 1	Mg 1	0
63	AK	1	Total 1	Mg 1	0
63	AN	1	Total 1	Mg 1	0
63	AQ	1	Total 1	Mg 1	0
63	AZ	2	Total 2	Mg 2	0
63	BM	1	Total 1	Mg 1	0

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
64	AT	1	Total 1	Zn 1	0
64	AZ	1	Total 1	Zn 1	0
64	Ab	1	Total 1	Zn 1	0
64	Ac	1	Total 1	Zn 1	0
64	Ad	1	Total 1	Zn 1	0
64	BF	1	Total 1	Zn 1	0
64	BP	1	Total 1	Zn 1	0
64	BR	1	Total 1	Zn 1	0
64	BV	2	Total 2	Zn 2	0

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Mol	Chain	Residues	Atoms		AltConf
64	BX	1	Total	Zn	0
			1	1	

- Molecule 65 is water.

Mol	Chain	Residues	Atoms		AltConf
65	1	5513	Total	O	0
			5513	5513	
65	2	92	Total	O	0
			92	92	
65	3	1723	Total	O	0
			1723	1723	
65	5	14	Total	O	0
			14	14	
65	4	20	Total	O	0
			20	20	
65	8	12	Total	O	0
			12	12	
65	AA	76	Total	O	0
			76	76	
65	AB	85	Total	O	0
			85	85	
65	AC	78	Total	O	0
			78	78	
65	AD	6	Total	O	0
			6	6	
65	AE	13	Total	O	0
			13	13	
65	AF	6	Total	O	0
			6	6	
65	AG	42	Total	O	0
			42	42	
65	AH	28	Total	O	0
			28	28	
65	AI	55	Total	O	0
			55	55	
65	AJ	66	Total	O	0
			66	66	
65	AK	43	Total	O	0
			43	43	
65	AL	10	Total	O	0
			10	10	

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Mol	Chain	Residues	Atoms		AltConf
65	AM	20	Total 20	O 20	0
65	AN	48	Total 48	O 48	0
65	AO	6	Total 6	O 6	0
65	AP	38	Total 38	O 38	0
65	AQ	35	Total 35	O 35	0
65	AR	22	Total 22	O 22	0
65	AS	23	Total 23	O 23	0
65	AT	16	Total 16	O 16	0
65	AU	4	Total 4	O 4	0
65	AV	24	Total 24	O 24	0
65	AW	5	Total 5	O 5	0
65	AX	21	Total 21	O 21	0
65	AY	53	Total 53	O 53	0
65	AZ	25	Total 25	O 25	0
65	Aa	20	Total 20	O 20	0
65	Ab	9	Total 9	O 9	0
65	Ac	25	Total 25	O 25	0
65	Ad	19	Total 19	O 19	0
65	BA	10	Total 10	O 10	0
65	BB	11	Total 11	O 11	0
65	BC	1	Total 1	O 1	0

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Mol	Chain	Residues	Atoms		AltConf
65	BD	29	Total 29	O 29	0
65	BE	52	Total 52	O 52	0
65	BF	25	Total 25	O 25	0
65	BG	14	Total 14	O 14	0
65	BH	18	Total 18	O 18	0
65	BI	36	Total 36	O 36	0
65	BJ	21	Total 21	O 21	0
65	BK	42	Total 42	O 42	0
65	BL	3	Total 3	O 3	0
65	BM	17	Total 17	O 17	0
65	BN	28	Total 28	O 28	0
65	BO	12	Total 12	O 12	0
65	BP	3	Total 3	O 3	0
65	BQ	36	Total 36	O 36	0
65	BR	25	Total 25	O 25	0
65	BS	4	Total 4	O 4	0
65	BT	6	Total 6	O 6	0
65	BU	18	Total 18	O 18	0
65	BV	2	Total 2	O 2	0
65	BW	6	Total 6	O 6	0
65	BX	6	Total 6	O 6	0

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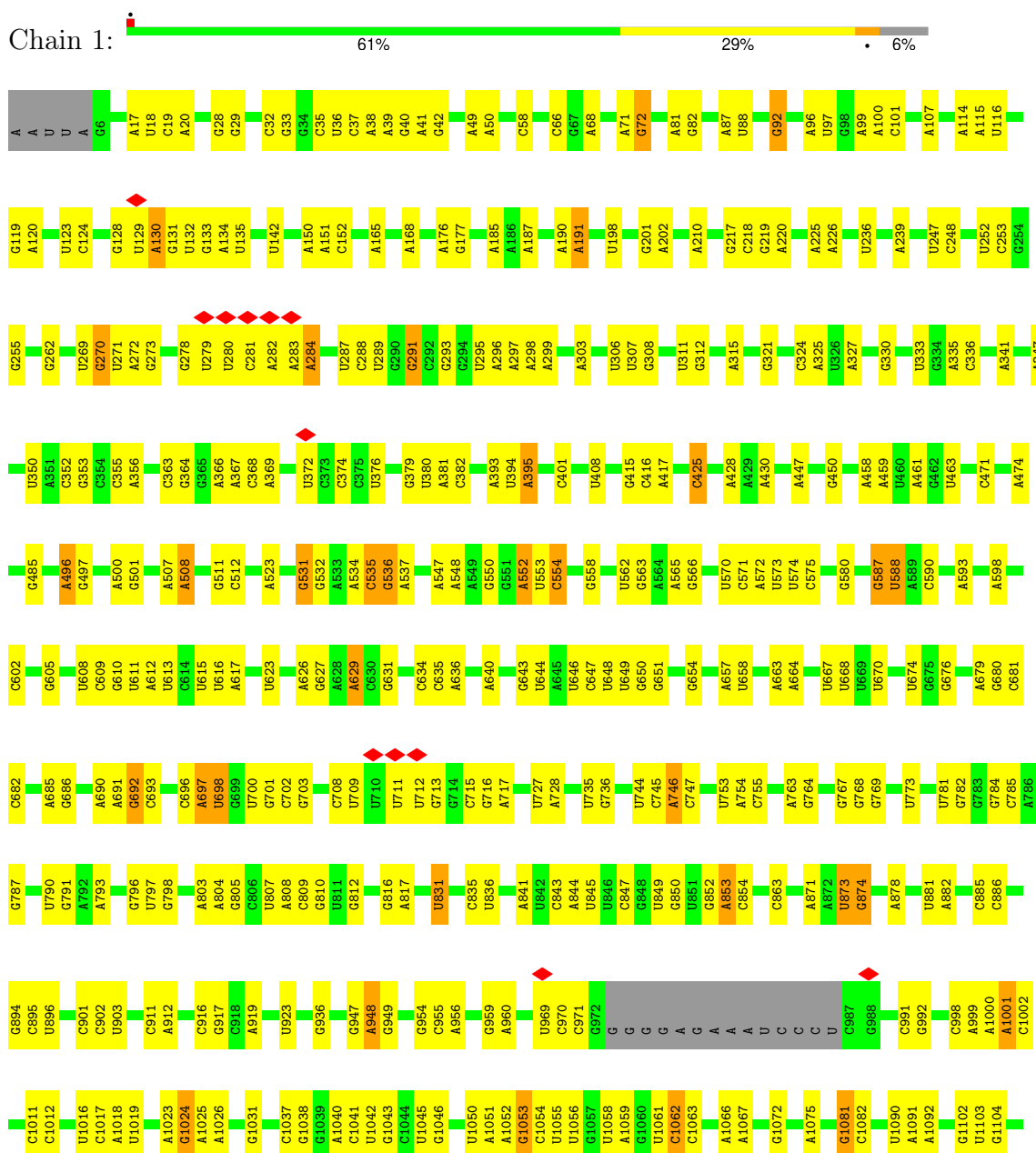
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Mol	Chain	Residues	Atoms		AltConf
65	BY	4	Total 4	O 4	0
65	BZ	16	Total 16	O 16	0

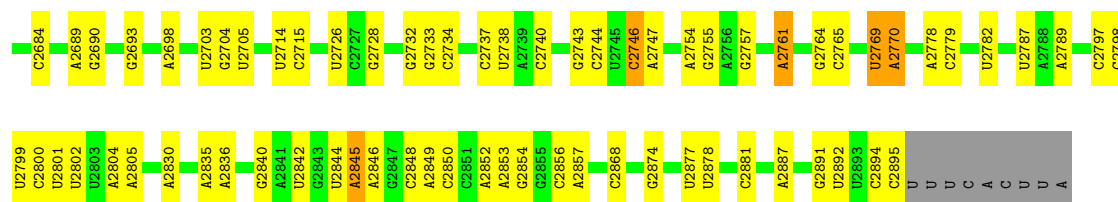
3 Residue-property plots

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.

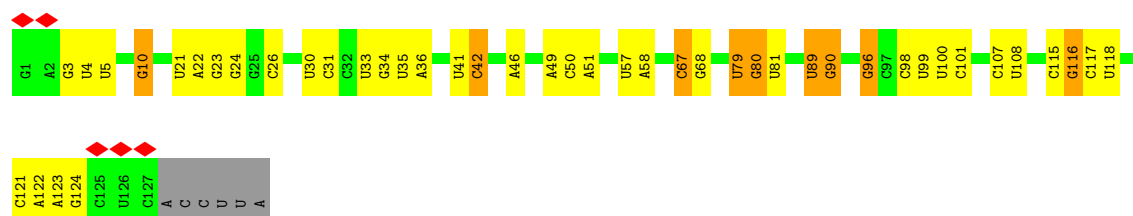
• Molecule 1: 23S rRNA



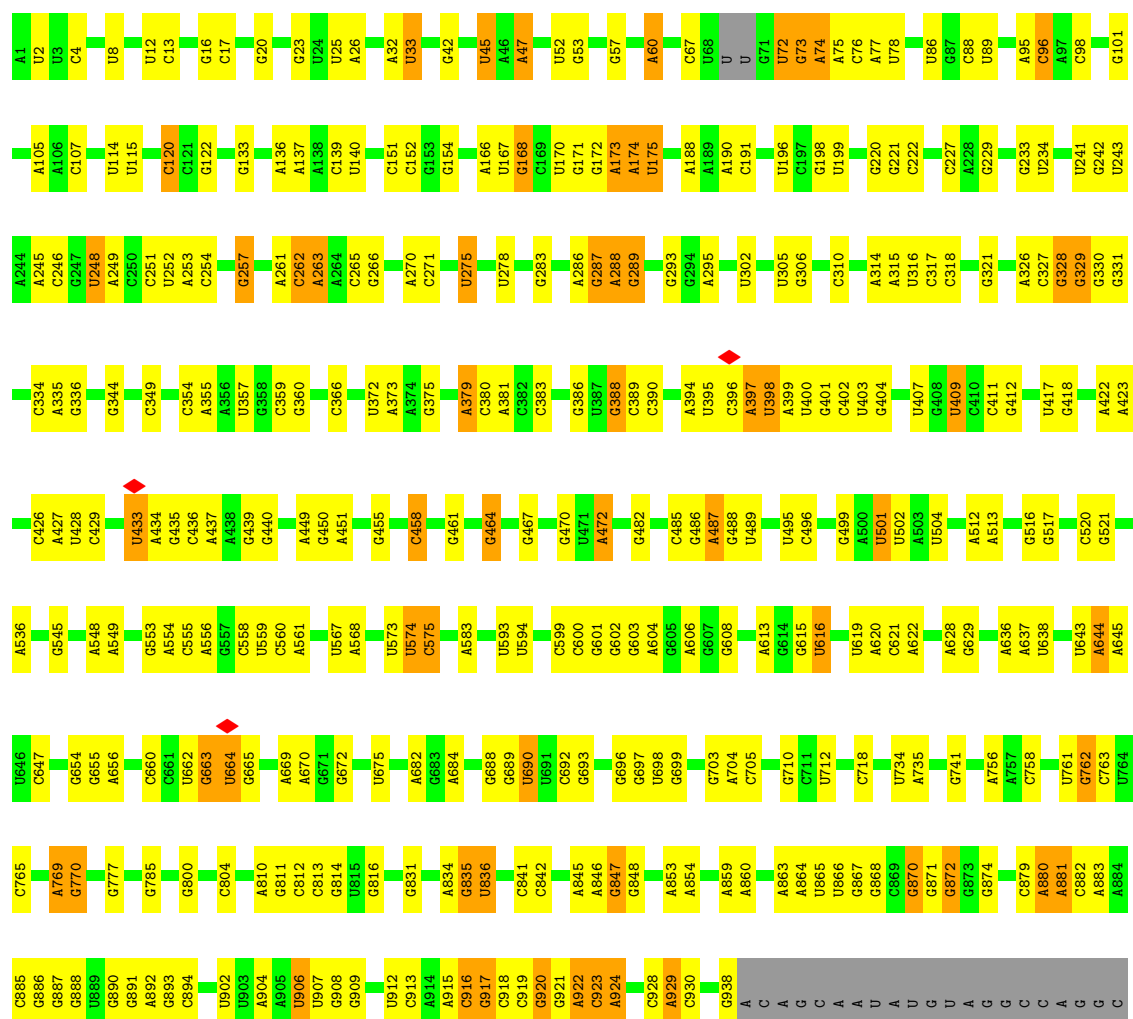
A2566	A2437	G2317	C	G2074	G1963	A1856	U1747	C1615	C1507	A1394	C1265	A	A1108
U2566	U2441	G2318	G	G2075	C1967	A1861	U1751	A1616	G	G1395	A1269	G	A1111
U2567	G2442	G2319	G	G2076	A1862	A1862	U1752	A1617	U	A1400	A1270	G	A1118
U2568		G2320	A	A2080	U1971	C1866	C1753	A1618	U	A1401	G1271	C	A1124
U2570	A2447	G2321	C	A2084	C1972	A1869	C1754	A1642	A	U1409	U1275	U	A1126
A2448	A2448	A2322	C	A2085	U1979	A1870	G1759	A1643	G1513	A1424	U1276	A	A1125
A2450	A2450	A2323	U	A2086	U1980	U1871	A1763	A1644	U1514	A1402	C1277	A	A1132
G2571		A2324	A	A2087	G1981	A1879	A1764	A1645	C1519	U1278	U1278	C	C1130
U2577	U2453	A2325	G	C2088	U1981	A1884	A1772	G1646	G1520	A1425	G1280	A	G1131
A2581	A2456	A2326	A	C2089	G1984	A1884	U1773	A	U1521	G1426	U1280	C	U1132
G2582		A2327	G	C2090		G1884	G1774	G	G1528	G1288	G1288	U	C1133
G2583	G2460	A2328	C	C2091	U1988	G1885	G1775	A1652	A1529	G1431	U1291	C	A1136
C2588	G2462	A2329	G	U2093	G1886	U1887	U1776	U1653	A1530	C1443	U1292	C	A1137
A2463	A2463	G2334	G	G2094	U1887	U1887	G1777	A1654	G1535	U1444	U1293	C	
		A2335	G	G2095	U1992	A1893	U1780	A1655	G1536	U1445	U1294	A	
G2593	G2474	A2336	U	A2096	G1993	A1894	A1781	U1656	G1545	A1446	G1295	G	
G2597	U2475	A2341	G	C2097	U1994	U1903	G1782	G1658	C1549	A1448	G1299	U	
U2601	U2476	A2342	G	U2099	A1995	U1904	A1783	C1680	G1550	U1451	G1300	C	
	G2477	G2343	C	U2100	G1997	A1905	C1787	C1681	C1549	G1450	G1304	G	
C2606	C2478	A2349	A	U2104	G1998	A1906	U1788	C1682	G1550	U1451	G1305	U	
G2607	U2479		G	G2105	A1999	U2000		U1683	U1554	A1452	U1306	C	
G2614	A2483	U2352	C	U2111	A2006	A1914	C1801	A1664	U1554	C1453	G1312		
A2615		C2353	C	G2112	G2007	A1915	A1802	A1665	A1557	A1458	U1316		
A2616	A2489	G2359	U	U2117	C2012	A1926	G1803	C1686	A1558	U1459	G1217		
A2617	U2492	A2360	U	U2118	C2012	C1927	G1804	C1687	G1559		G1218		
G2618	A2493	C2361	C	G2119	U2016	A1928	G1807	A1671	C1560	U1459	G1219		
		U2366	U	G2119	G2017	U1932	U1811		A1561	G1462	G1319		
U2624	G2502	U2367	G	U2122	U2018	G1932	A1812	A1679	G1562	A1463	G1320		
U2625		C2368	G	G2123	G2019	G1934	A1813		C1563	A1223	U1321		
U2628			A	U	C2020	G1935		G1683	C1570	A1224	A1225		
A2629			C	G	C2021	U1936	G1816	C1684	G1571	A1226	U1227		
U2630		G2384	C	U	U2022	A1937		C1685	A1575	U1227	U1231		
G2640		A2385	C	U	U2026	A1938	A1820		G1576	C1231			
A2645		G2389	U	U	C2027	C	A1821	A1694	A1577	G1236			
G2646		C2391	C	U	U2048	U1941	U1822		G1578	G1236			
C2654		A2394	U	G	U2049	U1942	A1823	A1702	C1579	U1237			
G2655		G2395	U	A	U2050	G1943	U1830	C1706	C1580	A1482			
U2658		U2397	G	U	A2051	C1944	A1831	G1707	G1581	A1488			
			G	U		C1945	A1834	U1708	U1582	U1489			
A2660			A	U		U1948	A1835	G1709	A1584	A1490			
G2661		G2400	C	U	C2055	U1949	G1835	U1710	U1585	C1348			
A2664		U2412	C	A	A2056	C1949	A1836	C1711	U1586	A1367			
C2665		U2413	C	C	C2057	U1950	U1837		G1587	A1368			
G2671		U2414	U	G	A2058	U1951	U1838	A1717	C1588	U1495			
U2672		A2417	C	U	G2066	A1952	C1840	A1718	G1599	C1500			
A2678		G2418	C	U	A2067	G1954		G1730	G1600	A1501			
G2679		C2419	C	A	C2068	C2068	A1849	G1737	U1603	U1502			
G2680		A2436	U	G	C2069	U2070	A1850	C1738	U1603	U1503			
			U	G	C2071	G1958	G1852		G1611	U1504			
			C	U		A1962		C1746		A1506			

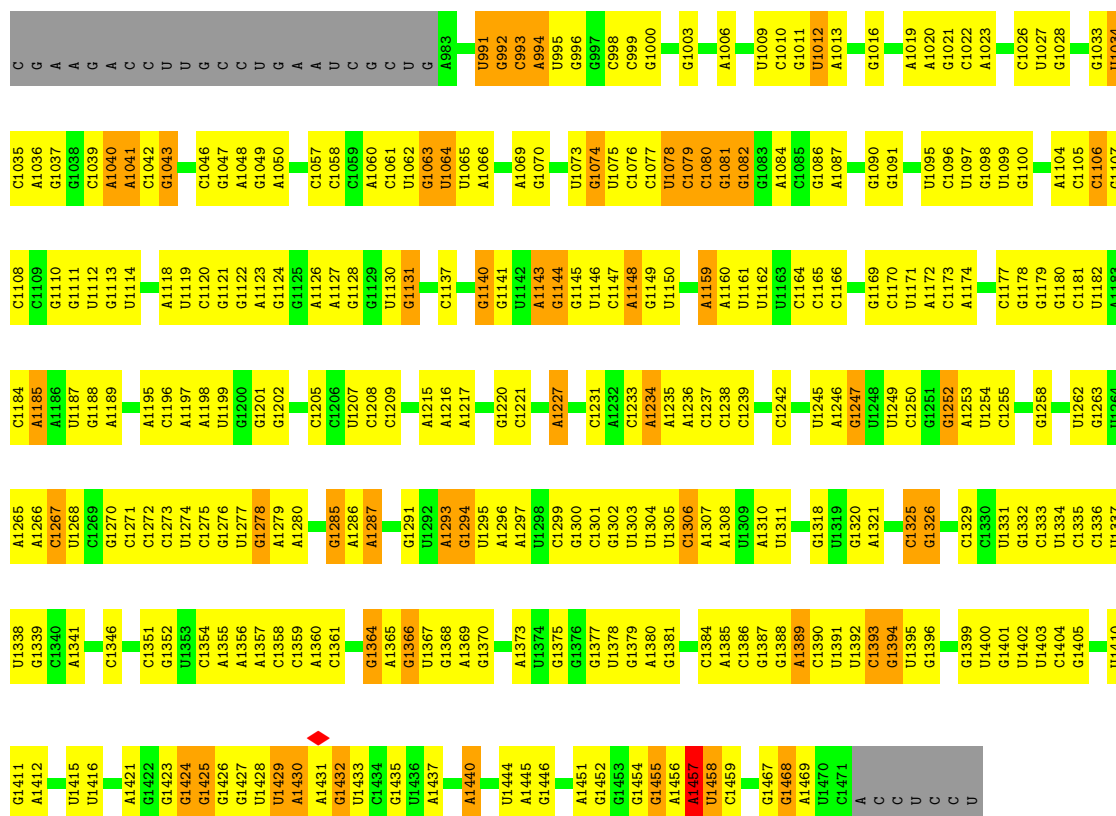


• Molecule 2: 5S rRNA

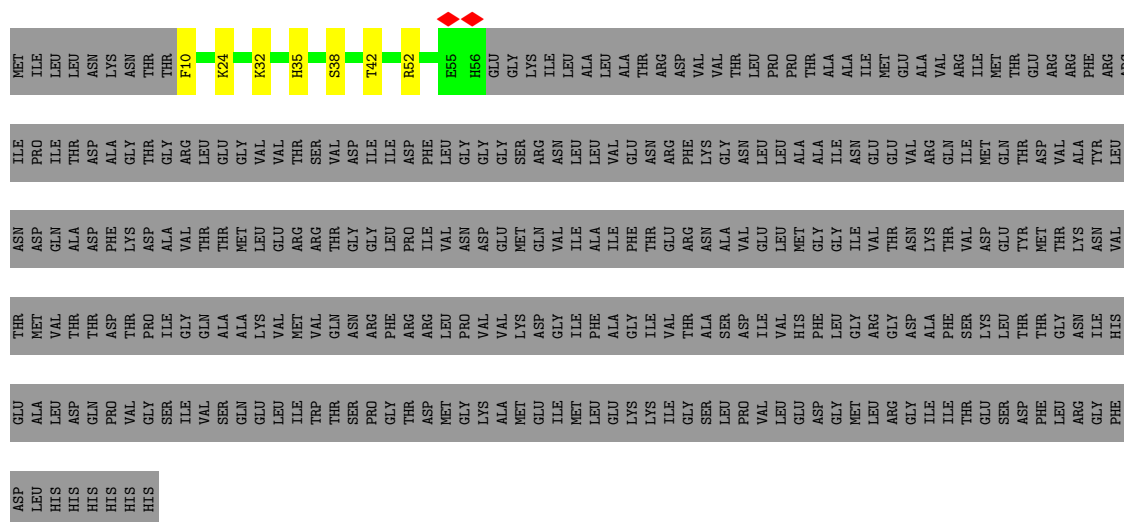


• Molecule 3: 16S rRNA



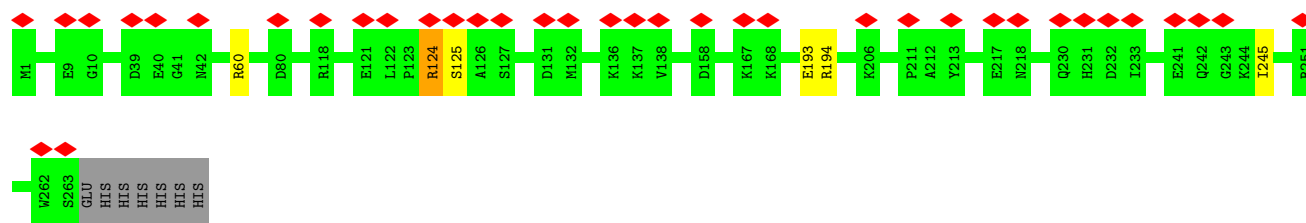


● Molecule 4: CBS domain-containing protein



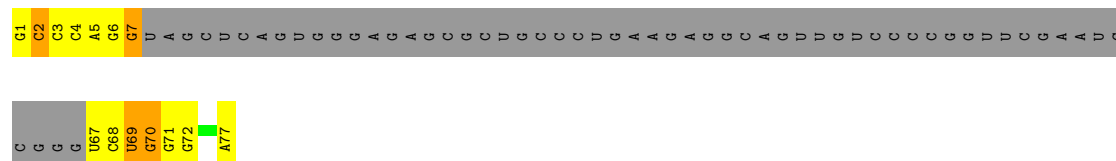
● Molecule 5: CBS domain-containing protein





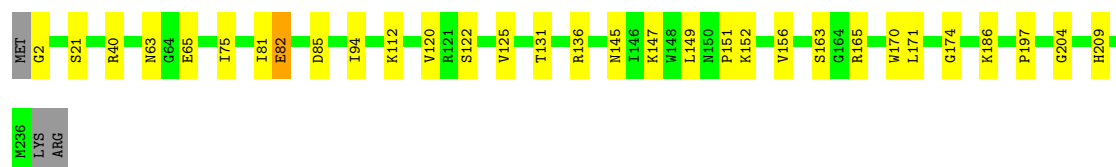
- Molecule 6: E-site tRNA

Chain 8: 5% 13% 5% 76%



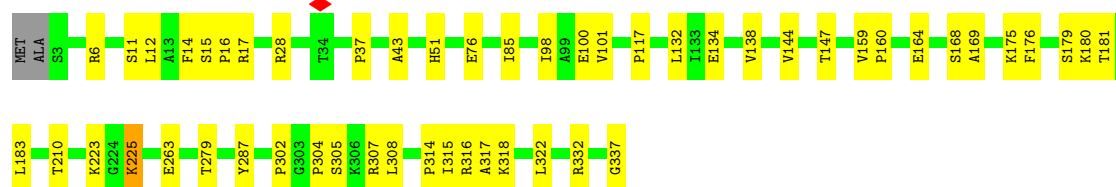
- Molecule 7: Large ribosomal subunit protein uL2

Chain AA: 86% 13%



- Molecule 8: Large ribosomal subunit protein uL3

Chain AB: 84% 15%



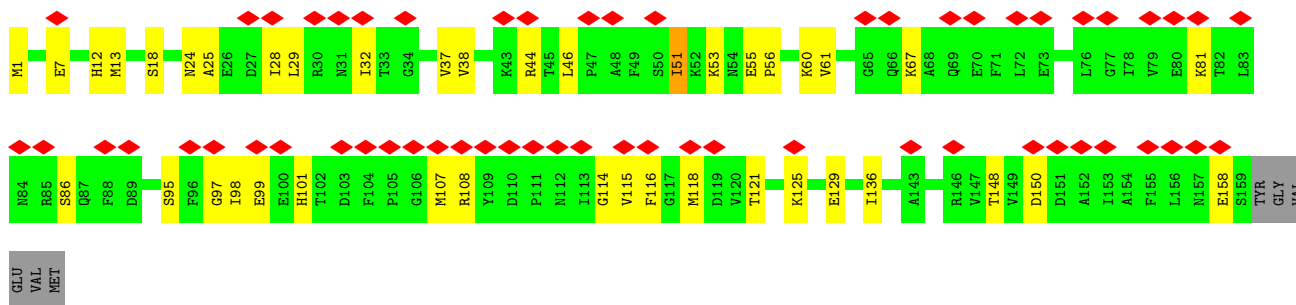
- Molecule 9: Large ribosomal subunit protein uL4

Chain AC: 91% 9%

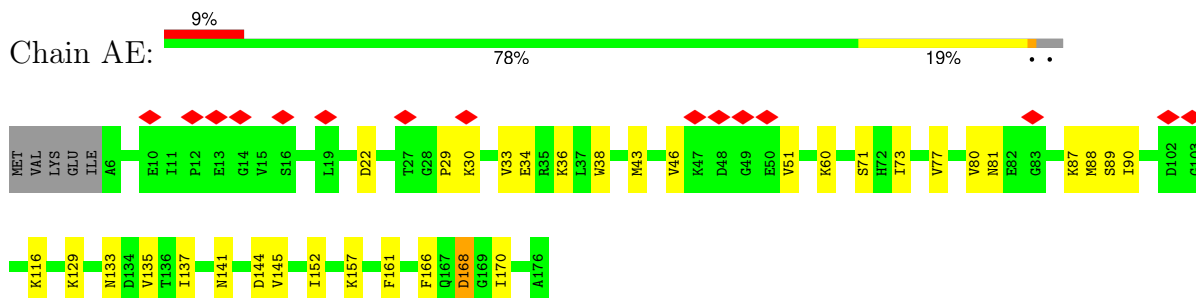


- Molecule 10: Large ribosomal subunit protein uL5

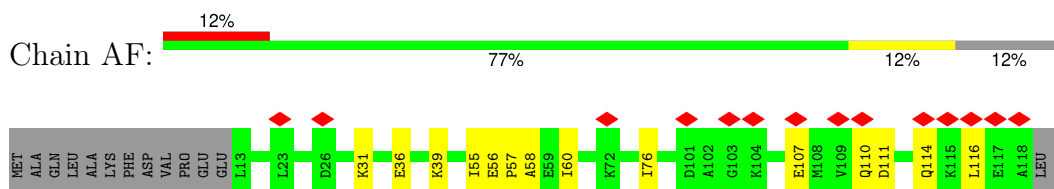
Chain AD: 35% 72% 24%



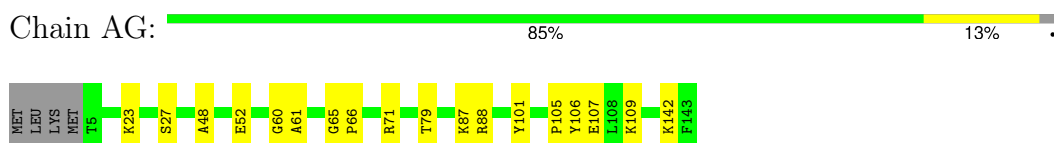
- Molecule 11: Large ribosomal subunit protein uL6



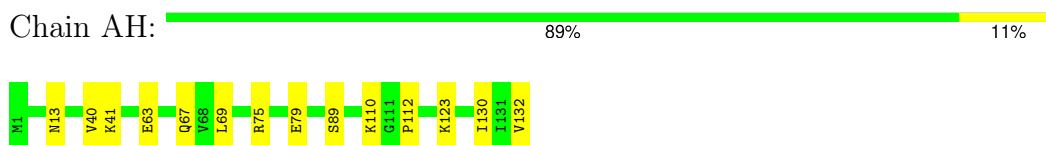
- Molecule 12: Large ribosomal subunit protein eL8



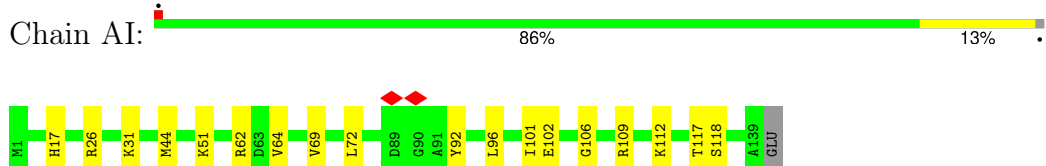
- Molecule 13: Large ribosomal subunit protein uL13



- Molecule 14: Large ribosomal subunit protein uL14



- Molecule 15: Large ribosomal subunit protein uL15



- Molecule 16: Large ribosomal subunit protein eL15

Chain AJ:  90% 9% ..



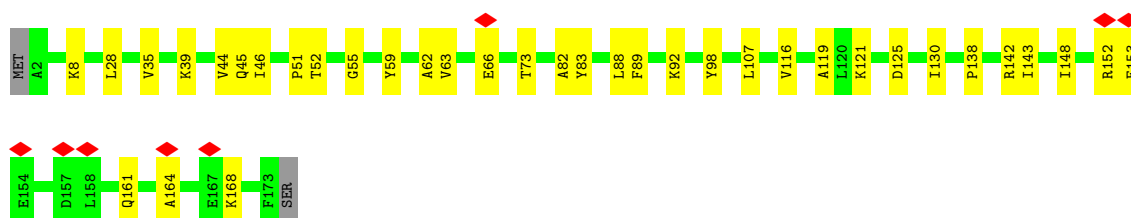
- Molecule 17: Large ribosomal subunit protein uL16

Chain AK:  82% 16% ..



- Molecule 18: Large ribosomal subunit protein uL18

Chain AL:  5% 78% 21% .



- Molecule 19: Large ribosomal subunit protein eL18

Chain AM:  87% 12% .



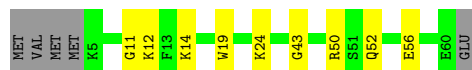
- Molecule 20: Large ribosomal subunit protein eL19

Chain AN:  93% 5% .



- Molecule 21: Large ribosomal subunit protein eL20

Chain AO:  77% 15% 8%



- Molecule 22: Large ribosomal subunit protein eL21

Chain AP:  88% 11% .



- Molecule 23: Large ribosomal subunit protein uL22

Chain AQ: 87% 12%



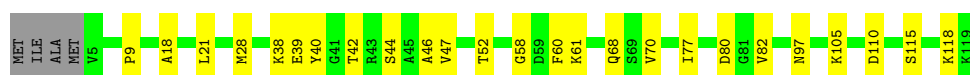
- Molecule 24: Large ribosomal subunit protein uL23

Chain AR: 83% 15%



- Molecule 25: Large ribosomal subunit protein uL24

Chain AS: 76% 21%



- Molecule 26: Large ribosomal subunit protein eL24

Chain AT: 73% 24%



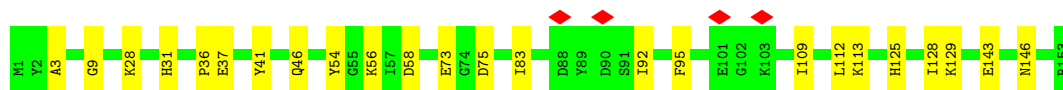
- Molecule 27: Large ribosomal subunit protein uL29

Chain AU: 79% 18%



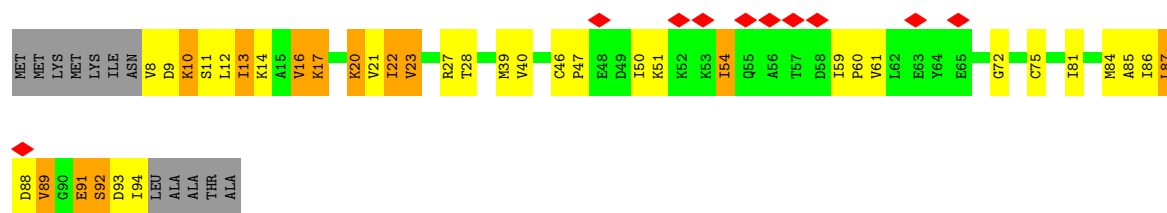
- Molecule 28: Large ribosomal subunit protein uL30

Chain AV: 84% 16%



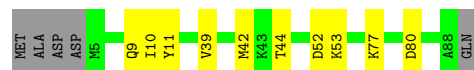
- Molecule 29: Large ribosomal subunit protein eL30

Chain AW: 10% 49% 26% 12% 12%



- Molecule 30: Large ribosomal subunit protein eL31

Chain AX: 83% 11% 6%



- Molecule 31: Large ribosomal subunit protein eL32

Chain AY: 86% 12% .



- Molecule 32: Large ribosomal subunit protein eL37

Chain AZ: 86% 12% .



- Molecule 33: Large ribosomal subunit protein eL39

Chain Aa: 84% 14% .



- Molecule 34: Large ribosomal subunit protein eL40

Chain Ab: 73% 14% 12%



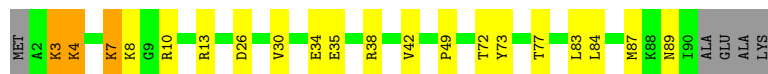
- Molecule 35: Large ribosomal subunit protein eL42

Chain Ac: 93% 5% .



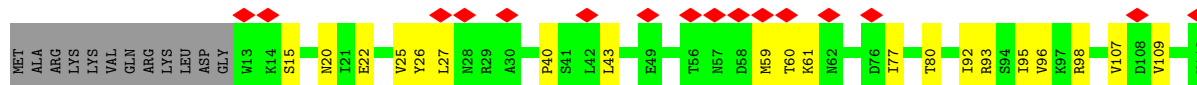
- Molecule 36: Large ribosomal subunit protein eL43

Chain Ad:  73% 18% 5%



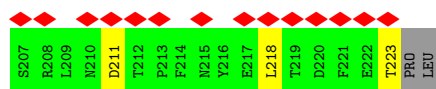
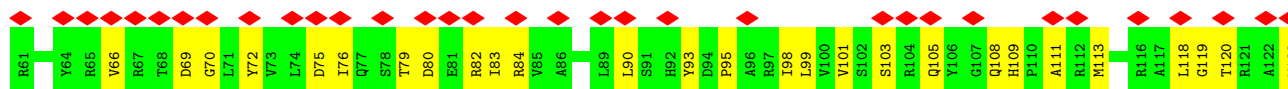
- Molecule 37: Small ribosomal subunit protein eS1

Chain BA:  8% 67% 20% 12%



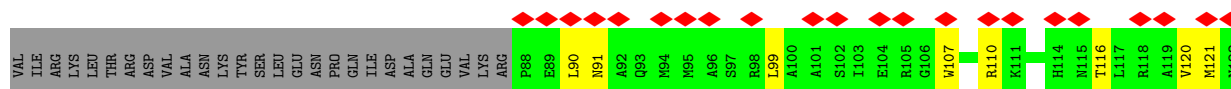
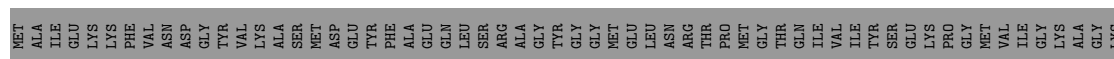
- Molecule 38: Small ribosomal subunit protein uS2

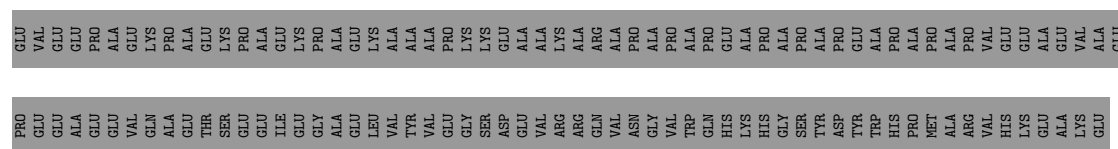
Chain BB:  40% 54% 29% 16%



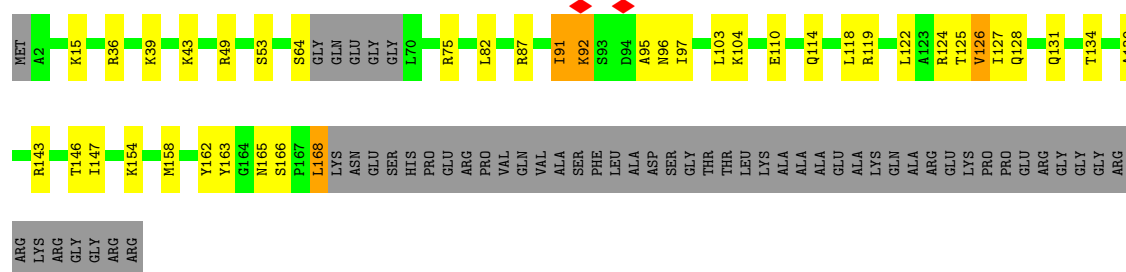
- Molecule 39: Small ribosomal subunit protein uS3

Chain BC:  12% 23% 11% 66%

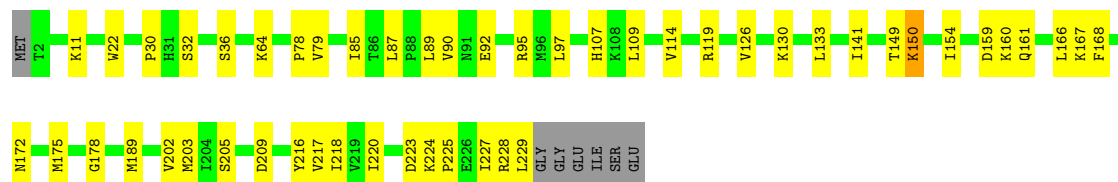
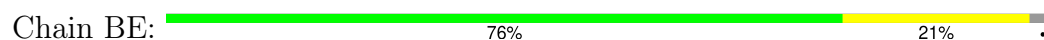




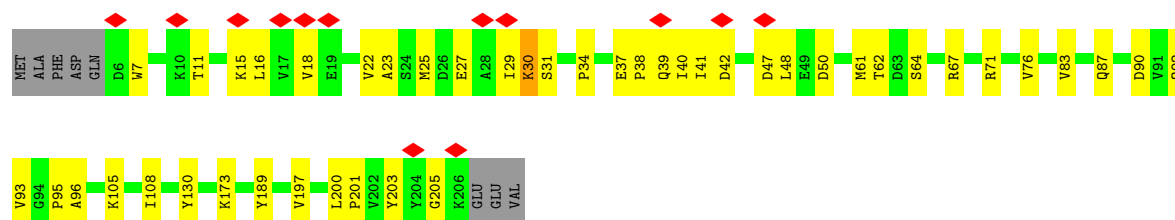
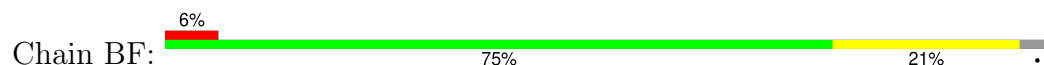
• Molecule 40: Small ribosomal subunit protein uS4



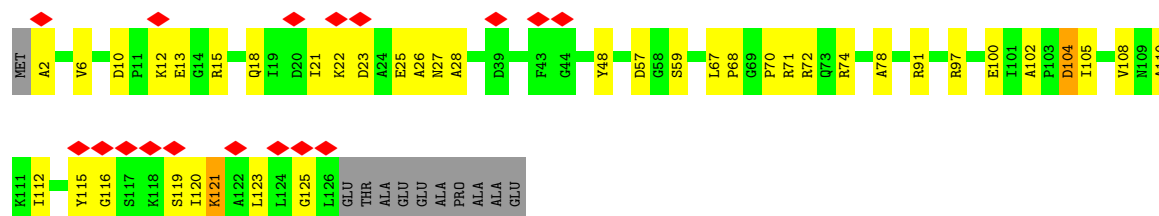
• Molecule 41: Small ribosomal subunit protein eS4



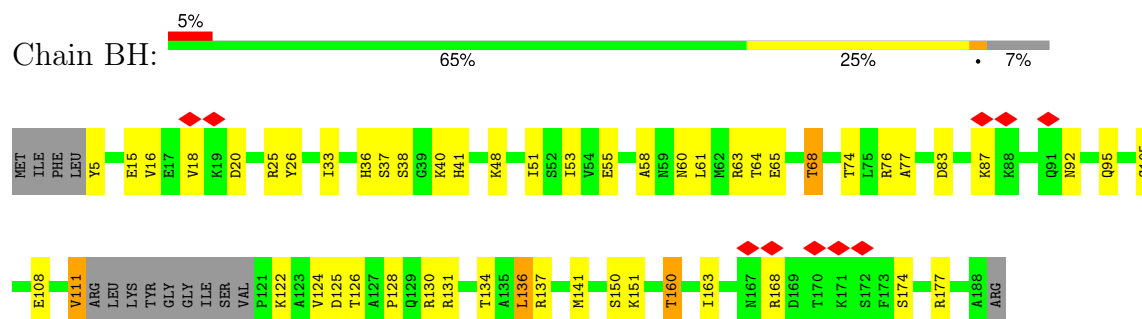
• Molecule 42: Small ribosomal subunit protein uS5



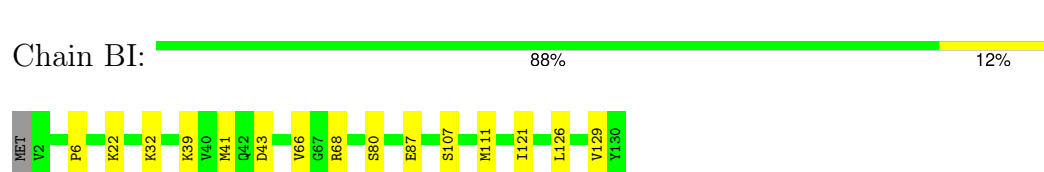
• Molecule 43: Small ribosomal subunit protein eS6



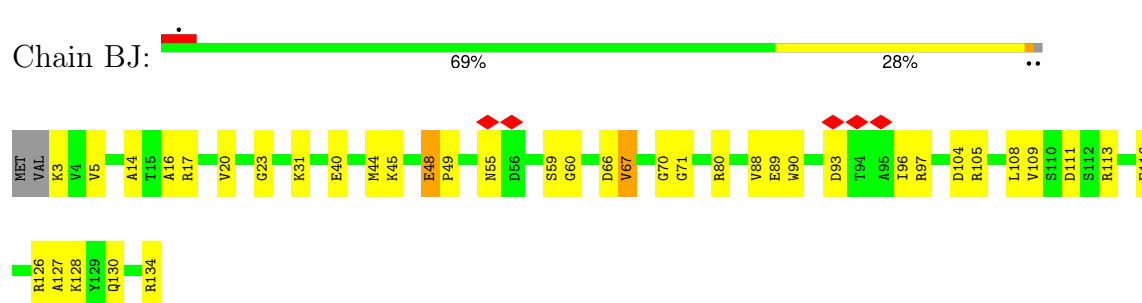
- Molecule 44: Small ribosomal subunit protein uS7



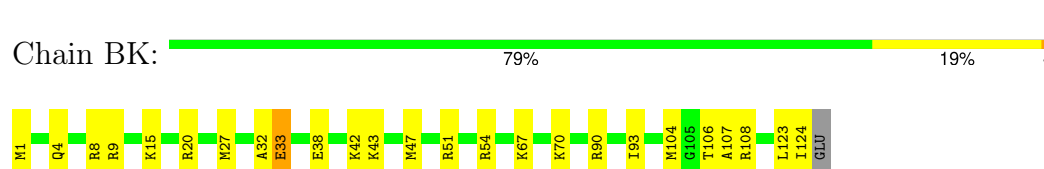
- Molecule 45: Small ribosomal subunit protein uS8



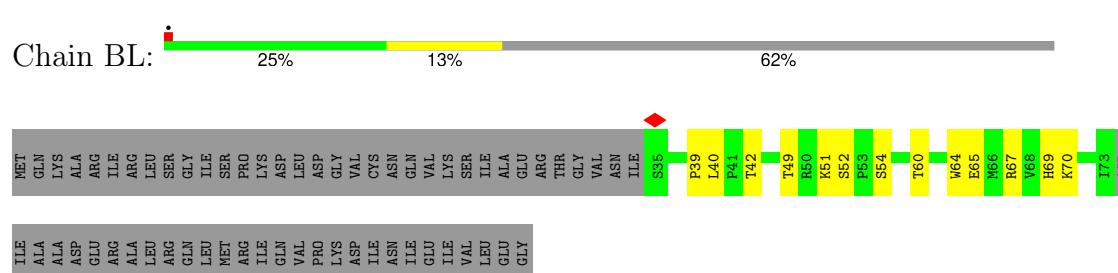
- Molecule 46: Small ribosomal subunit protein uS9



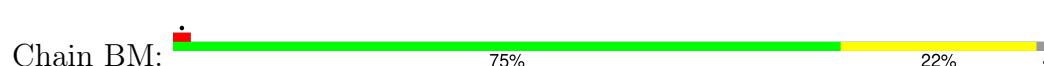
- Molecule 47: Small ribosomal subunit protein eS8

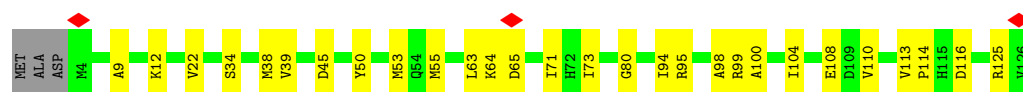


- Molecule 48: Small ribosomal subunit protein uS10



- Molecule 49: Small ribosomal subunit protein uS11

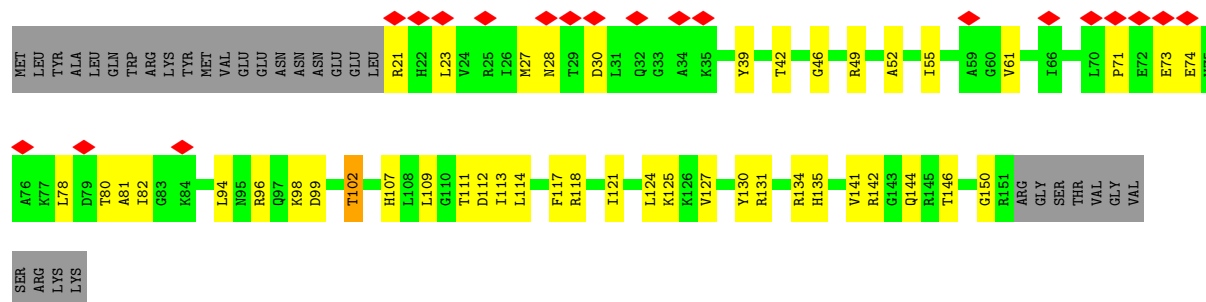




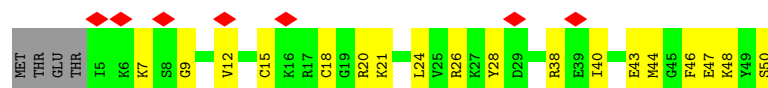
- Molecule 50: Small ribosomal subunit protein uS12



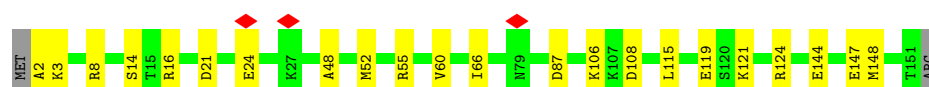
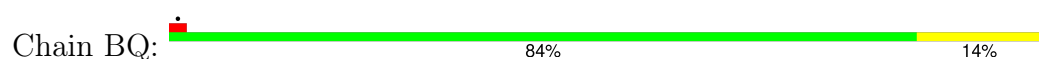
- Molecule 51: Small ribosomal subunit protein uS13



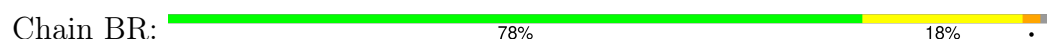
- Molecule 52: Small ribosomal subunit protein uS14



- Molecule 53: Small ribosomal subunit protein uS15

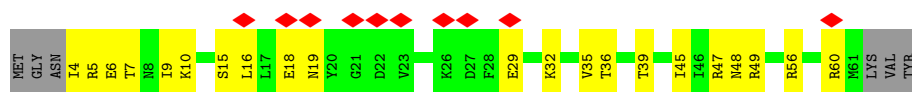


- Molecule 54: Small ribosomal subunit protein uS17A



- Molecule 55: Small ribosomal subunit protein eS17

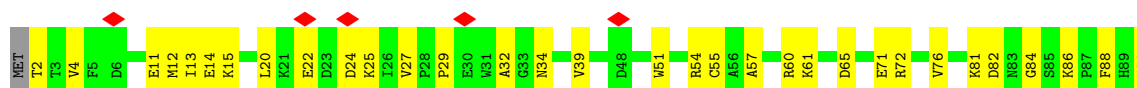




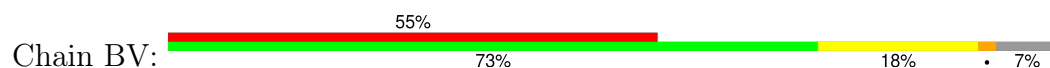
- Molecule 56: Small ribosomal subunit protein uS19



- Molecule 57: Small ribosomal subunit protein eS19



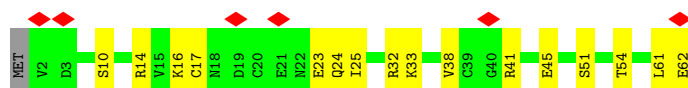
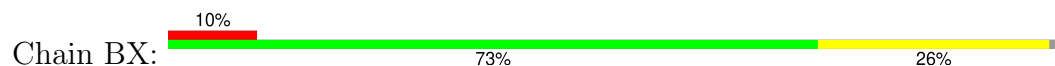
- Molecule 58: Putative zinc finger domain-containing protein



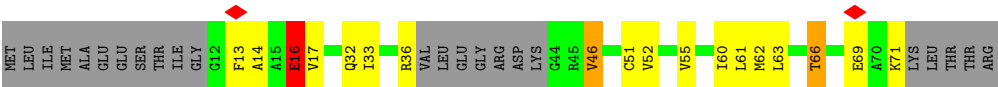
- Molecule 59: Small ribosomal subunit protein eS24



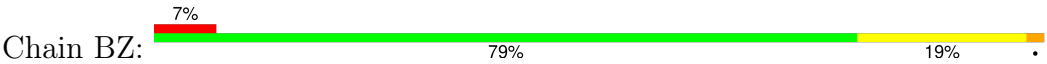
- Molecule 60: Small ribosomal subunit protein eS27



- Molecule 61: Small ribosomal subunit protein eS28



● Molecule 62: DUF5350 family protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95430	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.856	Depositor
Minimum map value	-0.146	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.138	Depositor
Map size ($\text{\AA}$)	423.1168, 423.1168, 423.1168	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8264, 0.8264, 0.8264	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, OMG, 5MC, 6MZ, 5MU, MG, OMU, MA6, IAS

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	1	0.26	0/64989	0.33	0/101333
2	2	0.20	0/3011	0.30	0/4689
3	3	0.34	0/34071	0.35	0/53137
4	5	0.24	0/371	0.34	0/495
5	4	0.78	0/2067	1.29	0/2793
6	8	0.51	0/424	0.68	0/657
7	AA	0.21	0/1821	0.36	0/2462
8	AB	0.27	0/2632	0.41	0/3552
9	AC	0.25	0/1963	0.34	0/2654
10	AD	0.18	0/1261	0.39	0/1697
11	AE	0.27	0/1350	0.38	0/1816
12	AF	0.16	0/784	0.31	0/1055
13	AG	0.22	0/1107	0.31	0/1484
14	AH	0.19	0/1009	0.30	0/1355
15	AI	0.26	0/1061	0.37	0/1413
16	AJ	0.25	0/1616	0.38	0/2166
17	AK	0.19	0/1357	0.31	0/1820
18	AL	0.18	0/1367	0.33	0/1845
19	AM	0.20	0/966	0.32	0/1302
20	AN	0.19	0/1173	0.29	0/1558
21	AO	0.17	0/454	0.24	0/602
22	AP	0.23	0/779	0.33	0/1042
23	AQ	0.20	0/1169	0.32	0/1564
24	AR	0.17	0/647	0.32	0/864
25	AS	0.19	0/889	0.29	0/1189
26	AT	0.20	0/493	0.28	0/652
27	AU	0.16	0/517	0.25	0/695
28	AV	0.20	0/1258	0.33	0/1692
29	AW	0.55	0/632	0.67	0/855
30	AX	0.19	0/697	0.28	0/937
31	AY	0.20	0/997	0.33	0/1333
32	AZ	0.22	0/443	0.34	0/583

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Aa	0.20	0/439	0.30	0/585
34	Ab	0.17	0/350	0.29	0/461
35	Ac	0.21	0/767	0.35	0/1017
36	Ad	0.32	0/712	0.45	0/950
37	BA	0.22	0/1453	0.30	0/1959
38	BB	0.23	0/1504	0.38	0/2045
39	BC	0.20	0/839	0.34	0/1128
40	BD	0.33	0/1325	0.40	0/1779
41	BE	0.29	0/1822	0.35	0/2451
42	BF	0.24	0/1552	0.36	0/2105
43	BG	0.47	1/948 (0.1%)	0.58	0/1273
44	BH	0.16	0/1380	0.33	0/1858
45	BI	0.45	1/996 (0.1%)	0.41	0/1343
46	BJ	0.14	0/1013	0.33	0/1364
47	BK	0.30	0/962	0.33	0/1288
48	BL	0.14	0/318	0.27	0/433
49	BM	0.24	0/915	0.32	0/1230
50	BN	0.28	0/1071	0.32	0/1438
51	BO	0.34	0/1039	0.44	0/1396
52	BP	0.14	0/388	0.35	0/510
53	BQ	0.30	0/1227	0.31	0/1654
54	BR	0.28	0/846	0.39	0/1144
55	BS	0.15	0/481	0.36	0/645
56	BT	0.19	0/878	0.33	0/1172
57	BU	0.17	0/1177	0.29	0/1586
58	BV	0.32	0/402	0.41	0/539
59	BW	0.31	0/744	0.39	0/995
60	BX	0.21	0/479	0.28	0/645
61	BY	0.33	0/395	0.52	0/528
62	BZ	0.24	0/459	0.31	0/603
All	All	0.29	2/160256 (0.0%)	0.37	0/237415

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
5	4	0	1
59	BW	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	BG	110	ALA	C-N	9.50	1.47	1.33
45	BI	80	SER	C-N	8.39	1.43	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	4	124	ARG	Sidechain
59	BW	88	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	58152	0	29316	556	0
2	2	2697	0	1371	34	0
3	3	30541	0	15403	496	0
4	5	364	0	373	7	0
5	4	2041	0	2096	2	0
6	8	381	0	199	17	0
7	AA	1779	0	1803	26	0
8	AB	2583	0	2674	32	0
9	AC	1929	0	1989	21	0
10	AD	1241	0	1272	39	0
11	AE	1329	0	1375	21	0
12	AF	779	0	820	10	0
13	AG	1092	0	1142	15	0
14	AH	998	0	1059	10	0
15	AI	1048	0	1037	14	0
16	AJ	1584	0	1625	17	0
17	AK	1333	0	1373	18	0
18	AL	1341	0	1341	22	0
19	AM	953	0	1009	9	0
20	AN	1159	0	1233	5	0
21	AO	447	0	457	6	0
22	AP	765	0	777	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AQ	1149	0	1186	11	0
24	AR	639	0	667	8	0
25	AS	880	0	935	16	0
26	AT	484	0	497	15	0
27	AU	515	0	524	7	0
28	AV	1236	0	1269	15	0
29	AW	627	0	663	32	0
30	AX	685	0	723	6	0
31	AY	981	0	1033	10	0
32	AZ	436	0	443	4	0
33	Aa	430	0	467	6	0
34	Ab	348	0	369	6	0
35	Ac	750	0	791	4	0
36	Ad	699	0	730	21	0
37	BA	1435	0	1483	34	0
38	BB	1476	0	1482	77	0
39	BC	826	0	856	24	0
40	BD	1303	0	1350	37	0
41	BE	1796	0	1878	41	0
42	BF	1527	0	1581	35	0
43	BG	935	0	988	34	0
44	BH	1363	0	1415	39	0
45	BI	980	0	1008	11	0
46	BJ	1001	0	1034	35	0
47	BK	954	0	1022	35	0
48	BL	308	0	319	9	0
49	BM	910	0	936	19	0
50	BN	1057	0	1104	14	0
51	BO	1025	0	1078	52	0
52	BP	382	0	384	19	0
53	BQ	1206	0	1280	22	0
54	BR	831	0	852	18	0
55	BS	476	0	499	24	0
56	BT	861	0	868	39	0
57	BU	1154	0	1185	38	0
58	BV	394	0	388	7	0
59	BW	736	0	769	22	0
60	BX	474	0	481	10	0
61	BY	394	0	403	18	0
62	BZ	452	0	502	10	0
63	1	244	0	0	0	0
63	2	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	3	45	0	0	0	0
63	4	2	0	0	0	0
63	AA	2	0	0	0	0
63	AB	2	0	0	0	0
63	AH	1	0	0	0	0
63	AI	1	0	0	0	0
63	AK	1	0	0	0	0
63	AN	1	0	0	0	0
63	AQ	1	0	0	0	0
63	AZ	2	0	0	0	0
63	BM	1	0	0	0	0
64	AT	1	0	0	0	0
64	AZ	1	0	0	0	0
64	Ab	1	0	0	0	0
64	Ac	1	0	0	0	0
64	Ad	1	0	0	0	0
64	BF	1	0	0	0	0
64	BP	1	0	0	0	0
64	BR	1	0	0	0	0
64	BV	2	0	0	0	0
64	BX	1	0	0	0	0
65	1	5513	0	0	68	0
65	2	92	0	0	7	0
65	3	1723	0	0	63	0
65	4	20	0	0	0	0
65	5	14	0	0	1	0
65	8	12	0	0	0	0
65	AA	76	0	0	1	0
65	AB	85	0	0	3	0
65	AC	78	0	0	3	0
65	AD	6	0	0	8	0
65	AE	13	0	0	3	0
65	AF	6	0	0	2	0
65	AG	42	0	0	0	0
65	AH	28	0	0	1	0
65	AI	55	0	0	0	0
65	AJ	66	0	0	3	0
65	AK	43	0	0	1	0
65	AL	10	0	0	0	0
65	AM	20	0	0	1	0
65	AN	48	0	0	1	0
65	AO	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	AP	38	0	0	1	0
65	AQ	35	0	0	1	0
65	AR	22	0	0	2	0
65	AS	23	0	0	2	0
65	AT	16	0	0	0	0
65	AU	4	0	0	0	0
65	AV	24	0	0	1	0
65	AW	5	0	0	11	0
65	AX	21	0	0	0	0
65	AY	53	0	0	1	0
65	AZ	25	0	0	0	0
65	Aa	20	0	0	1	0
65	Ab	9	0	0	2	0
65	Ac	25	0	0	0	0
65	Ad	19	0	0	2	0
65	BA	10	0	0	1	0
65	BB	11	0	0	4	0
65	BC	1	0	0	0	0
65	BD	29	0	0	3	0
65	BE	52	0	0	12	0
65	BF	25	0	0	4	0
65	BG	14	0	0	5	0
65	BH	18	0	0	4	0
65	BI	36	0	0	3	0
65	BJ	21	0	0	2	0
65	BK	42	0	0	2	0
65	BL	3	0	0	0	0
65	BM	17	0	0	1	0
65	BN	28	0	0	4	0
65	BO	12	0	0	11	0
65	BP	3	0	0	0	0
65	BQ	36	0	0	2	0
65	BR	25	0	0	3	0
65	BS	4	0	0	3	0
65	BT	6	0	0	0	0
65	BU	18	0	0	8	0
65	BV	2	0	0	1	0
65	BW	6	0	0	1	0
65	BX	6	0	0	0	0
65	BY	4	0	0	4	0
65	BZ	16	0	0	0	0
All	All	157707	0	105186	2017	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2017 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)
2:2:3:G:H5''	65:2:362:HOH:O	1.38	1.23
51:BO:27:MET:HE1	65:BO:208:HOH:O	1.43	1.18
3:3:433:U:H2'	65:3:3054:HOH:O	1.51	1.11
3:3:1302:G:H5''	65:3:2034:HOH:O	1.53	1.08
10:AD:81:LYS:HD2	65:AD:201:HOH:O	1.54	1.07

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	
4	5	45/339 (13%)	45 (100%)	0	0	100	100
5	4	261/270 (97%)	257 (98%)	3 (1%)	1 (0%)	30	22
7	AA	233/238 (98%)	228 (98%)	4 (2%)	1 (0%)	30	22
8	AB	333/337 (99%)	330 (99%)	3 (1%)	0	100	100
9	AC	250/253 (99%)	246 (98%)	4 (2%)	0	100	100
10	AD	157/165 (95%)	154 (98%)	3 (2%)	0	100	100
11	AE	169/176 (96%)	164 (97%)	5 (3%)	0	100	100
12	AF	104/120 (87%)	101 (97%)	3 (3%)	0	100	100
13	AG	137/143 (96%)	136 (99%)	1 (1%)	0	100	100
14	AH	130/132 (98%)	128 (98%)	2 (2%)	0	100	100
15	AI	137/140 (98%)	134 (98%)	3 (2%)	0	100	100
16	AJ	193/196 (98%)	190 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AK	168/173 (97%)	163 (97%)	5 (3%)	0	100	100
18	AL	170/174 (98%)	170 (100%)	0	0	100	100
19	AM	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
20	AN	145/151 (96%)	143 (99%)	2 (1%)	0	100	100
21	AO	54/61 (88%)	52 (96%)	2 (4%)	0	100	100
22	AP	94/97 (97%)	93 (99%)	1 (1%)	0	100	100
23	AQ	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
24	AR	78/82 (95%)	78 (100%)	0	0	100	100
25	AS	113/119 (95%)	112 (99%)	1 (1%)	0	100	100
26	AT	58/62 (94%)	58 (100%)	0	0	100	100
27	AU	63/67 (94%)	63 (100%)	0	0	100	100
28	AV	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
29	AW	85/99 (86%)	79 (93%)	4 (5%)	2 (2%)	4	1
30	AX	82/89 (92%)	81 (99%)	1 (1%)	0	100	100
31	AY	124/129 (96%)	120 (97%)	3 (2%)	1 (1%)	16	8
32	AZ	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
33	Aa	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
34	Ab	41/49 (84%)	41 (100%)	0	0	100	100
35	Ac	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
36	Ad	87/94 (93%)	81 (93%)	6 (7%)	0	100	100
37	BA	177/203 (87%)	169 (96%)	8 (4%)	0	100	100
38	BB	186/225 (83%)	184 (99%)	2 (1%)	0	100	100
39	BC	107/318 (34%)	106 (99%)	1 (1%)	0	100	100
40	BD	158/218 (72%)	152 (96%)	6 (4%)	0	100	100
41	BE	226/235 (96%)	218 (96%)	8 (4%)	0	100	100
42	BF	199/209 (95%)	182 (92%)	17 (8%)	0	100	100
43	BG	123/136 (90%)	117 (95%)	5 (4%)	1 (1%)	16	8
44	BH	171/189 (90%)	167 (98%)	4 (2%)	0	100	100
45	BI	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
46	BJ	130/134 (97%)	126 (97%)	4 (3%)	0	100	100
47	BK	122/125 (98%)	118 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	BL	37/102 (36%)	35 (95%)	2 (5%)	0	100	100
49	BM	119/126 (94%)	117 (98%)	2 (2%)	0	100	100
50	BN	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
51	BO	129/162 (80%)	121 (94%)	8 (6%)	0	100	100
52	BP	44/50 (88%)	40 (91%)	4 (9%)	0	100	100
53	BQ	148/152 (97%)	147 (99%)	1 (1%)	0	100	100
54	BR	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
55	BS	56/64 (88%)	55 (98%)	1 (2%)	0	100	100
56	BT	103/136 (76%)	103 (100%)	0	0	100	100
57	BU	146/149 (98%)	144 (99%)	2 (1%)	0	100	100
58	BV	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
59	BW	88/101 (87%)	85 (97%)	3 (3%)	0	100	100
60	BX	59/62 (95%)	56 (95%)	3 (5%)	0	100	100
61	BY	49/76 (64%)	43 (88%)	4 (8%)	2 (4%)	2	0
62	BZ	55/57 (96%)	50 (91%)	5 (9%)	0	100	100
All	All	7173/8250 (87%)	6985 (97%)	180 (2%)	8 (0%)	49	45

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	BG	28	ALA
5	4	125	SER
29	AW	92	SER
31	AY	4	GLU
61	BY	16	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	
4	5	42/289 (14%)	41 (98%)	1 (2%)	43	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	236/243 (97%)	233 (99%)	3 (1%)	61	63
7	AA	185/188 (98%)	183 (99%)	2 (1%)	65	68
8	AB	276/277 (100%)	269 (98%)	7 (2%)	42	40
9	AC	197/198 (100%)	195 (99%)	2 (1%)	68	71
10	AD	135/140 (96%)	131 (97%)	4 (3%)	36	32
11	AE	143/148 (97%)	136 (95%)	7 (5%)	22	15
12	AF	79/91 (87%)	79 (100%)	0	100	100
13	AG	115/119 (97%)	115 (100%)	0	100	100
14	AH	109/109 (100%)	107 (98%)	2 (2%)	51	52
15	AI	107/108 (99%)	104 (97%)	3 (3%)	38	35
16	AJ	165/166 (99%)	163 (99%)	2 (1%)	63	65
17	AK	138/141 (98%)	136 (99%)	2 (1%)	59	61
18	AL	141/143 (99%)	140 (99%)	1 (1%)	76	77
19	AM	103/104 (99%)	101 (98%)	2 (2%)	50	50
20	AN	119/123 (97%)	117 (98%)	2 (2%)	53	53
21	AO	49/54 (91%)	49 (100%)	0	100	100
22	AP	85/86 (99%)	84 (99%)	1 (1%)	63	65
23	AQ	122/124 (98%)	122 (100%)	0	100	100
24	AR	71/73 (97%)	69 (97%)	2 (3%)	38	35
25	AS	97/100 (97%)	96 (99%)	1 (1%)	68	71
26	AT	53/54 (98%)	53 (100%)	0	100	100
27	AU	55/57 (96%)	55 (100%)	0	100	100
28	AV	134/134 (100%)	132 (98%)	2 (2%)	57	59
29	AW	69/78 (88%)	57 (83%)	12 (17%)	2	0
30	AX	74/78 (95%)	74 (100%)	0	100	100
31	AY	103/106 (97%)	103 (100%)	0	100	100
32	AZ	48/49 (98%)	46 (96%)	2 (4%)	26	20
33	Aa	47/48 (98%)	45 (96%)	2 (4%)	26	19
34	Ab	37/40 (92%)	36 (97%)	1 (3%)	39	37
35	Ac	81/82 (99%)	79 (98%)	2 (2%)	42	40
36	Ad	73/76 (96%)	69 (94%)	4 (6%)	19	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BA	158/173 (91%)	154 (98%)	4 (2%)	42	40
38	BB	164/193 (85%)	160 (98%)	4 (2%)	43	41
39	BC	86/250 (34%)	80 (93%)	6 (7%)	14	7
40	BD	138/178 (78%)	131 (95%)	7 (5%)	21	14
41	BE	204/209 (98%)	203 (100%)	1 (0%)	81	81
42	BF	163/170 (96%)	158 (97%)	5 (3%)	35	31
43	BG	96/103 (93%)	93 (97%)	3 (3%)	35	31
44	BH	147/159 (92%)	133 (90%)	14 (10%)	8	3
45	BI	104/105 (99%)	104 (100%)	0	100	100
46	BJ	105/107 (98%)	103 (98%)	2 (2%)	50	50
47	BK	104/105 (99%)	103 (99%)	1 (1%)	68	71
48	BL	35/89 (39%)	35 (100%)	0	100	100
49	BM	91/93 (98%)	89 (98%)	2 (2%)	45	45
50	BN	109/112 (97%)	108 (99%)	1 (1%)	70	73
51	BO	107/135 (79%)	100 (94%)	7 (6%)	15	9
52	BP	40/44 (91%)	40 (100%)	0	100	100
53	BQ	136/138 (99%)	135 (99%)	1 (1%)	76	77
54	BR	94/96 (98%)	92 (98%)	2 (2%)	47	47
55	BS	52/57 (91%)	51 (98%)	1 (2%)	50	50
56	BT	94/118 (80%)	92 (98%)	2 (2%)	47	47
57	BU	122/123 (99%)	118 (97%)	4 (3%)	33	29
58	BV	44/48 (92%)	41 (93%)	3 (7%)	14	8
59	BW	81/87 (93%)	74 (91%)	7 (9%)	10	4
60	BX	55/56 (98%)	53 (96%)	2 (4%)	31	26
61	BY	42/62 (68%)	37 (88%)	5 (12%)	5	1
62	BZ	47/47 (100%)	44 (94%)	3 (6%)	16	8
All	All	6106/6883 (89%)	5950 (97%)	156 (3%)	41	38

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	BK	33	GLU
59	BW	79	GLN

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Mol	Chain	Res	Type
51	BO	21	ARG
56	BT	45	SER
61	BY	33	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
40	BD	141	ASN
46	BJ	114	GLN
41	BE	91	ASN
44	BH	44	GLN
49	BM	54	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2710/2904 (93%)	347 (12%)	18 (0%)
2	2	126/133 (94%)	18 (14%)	3 (2%)
3	3	1422/1478 (96%)	236 (16%)	18 (1%)
6	8	16/75 (21%)	5 (31%)	0
All	All	4274/4590 (93%)	606 (14%)	39 (0%)

5 of 606 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	32	C
1	1	40	G
1	1	58	C
1	1	68	A
1	1	71	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	3	835	G
3	3	1148	A
3	3	916	C
3	3	993	C
3	3	1393	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	1	2514	63,1	19,22,23	0.83	1 (5%)	26,32,35	0.52	0
3	MA6	3	1456	3	23,26,27	0.28	0	33,38,41	0.72	1 (3%)
1	5MC	1	2516	1	19,22,23	0.96	1 (5%)	26,32,35	0.68	1 (3%)
3	5MU	3	1222	3	19,22,23	0.26	0	27,32,35	0.39	0
3	MA6	3	1457	3	23,26,27	0.27	0	33,38,41	0.73	1 (3%)
1	OMG	1	2568	1	23,26,27	0.31	0	32,38,41	0.46	0
3	6MZ	3	1438	63,3	22,25,26	0.42	0	29,36,39	0.70	0
1	OMU	1	2567	63,1	19,22,23	0.22	0	25,31,34	0.50	0
49	IAS	BM	116	49	6,7,8	1.35	1 (16%)	3,8,10	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	1	2514	63,1	-	0/7/25/26	0/2/2/2
3	MA6	3	1456	3	-	0/11/29/30	0/3/3/3
1	5MC	1	2516	1	-	3/7/25/26	0/2/2/2
3	5MU	3	1222	3	-	0/7/25/26	0/2/2/2
3	MA6	3	1457	3	-	2/11/29/30	0/3/3/3
1	OMG	1	2568	1	-	1/9/27/28	0/3/3/3
3	6MZ	3	1438	63,3	-	0/9/27/28	0/3/3/3
1	OMU	1	2567	63,1	-	0/9/27/28	0/2/2/2
49	IAS	BM	116	49	-	0/7/7/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2516	5MC	C5-C4	-3.83	1.41	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2514	5MC	C5-C4	-3.36	1.41	1.44
49	BM	116	IAS	CB-CG	2.29	1.56	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	1456	MA6	C2-N1-C6	2.90	118.92	111.83
3	3	1457	MA6	C2-N1-C6	2.83	118.74	111.83
1	1	2516	5MC	C5-C6-N1	-2.28	120.84	123.31

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	3	1457	MA6	O4'-C4'-C5'-O5'
3	3	1457	MA6	C3'-C4'-C5'-O5'
1	1	2516	5MC	C2'-C1'-N1-C6
1	1	2568	OMG	C3'-C2'-O2'-CM2
1	1	2516	5MC	O4'-C1'-N1-C6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2514	5MC	1	0
1	1	2516	5MC	2	0
3	3	1457	MA6	1	0
1	1	2568	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 316 ligands modelled in this entry, 316 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

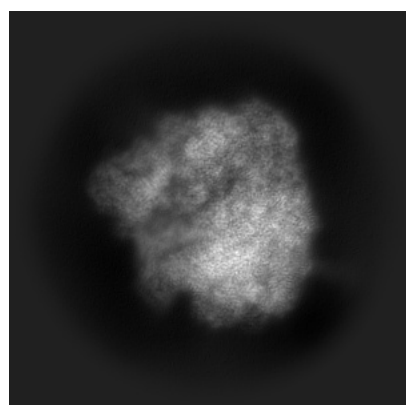
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74446. These allow visual inspection of the internal detail of the map and identification of artifacts.

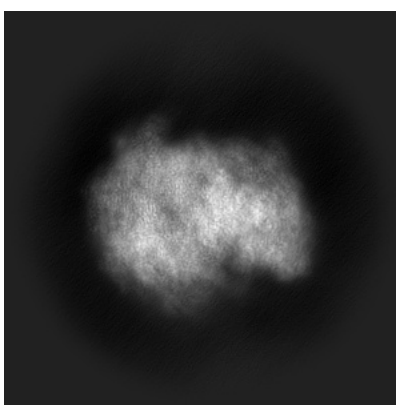
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

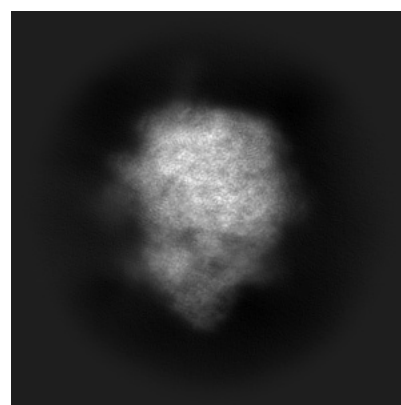
6.1.1 Primary map



X



Y

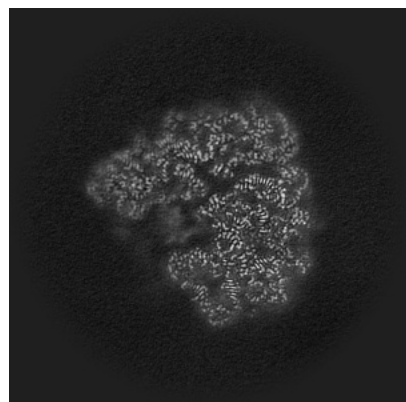


Z

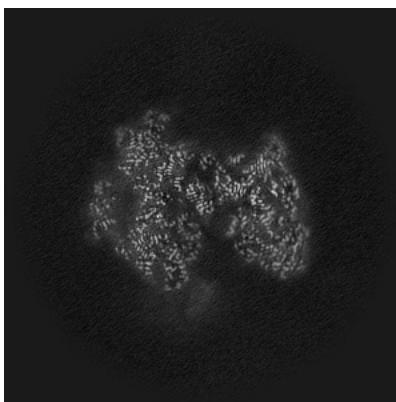
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

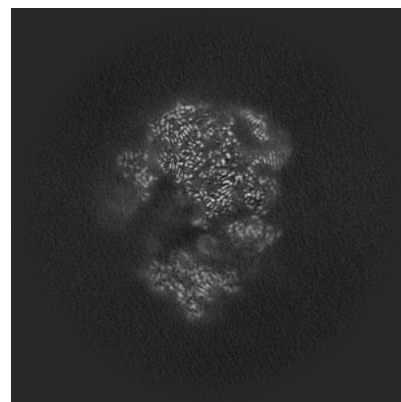
6.2.1 Primary map



X Index: 256



Y Index: 256

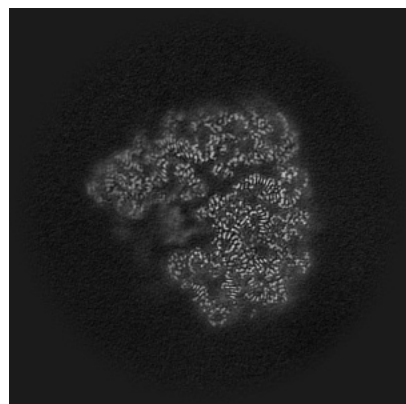


Z Index: 256

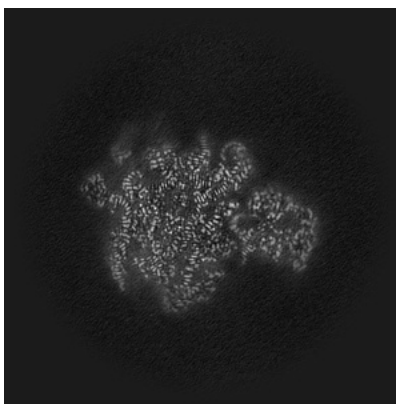
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

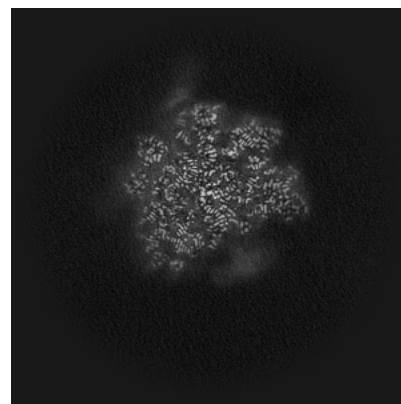
6.3.1 Primary map



X Index: 257



Y Index: 315

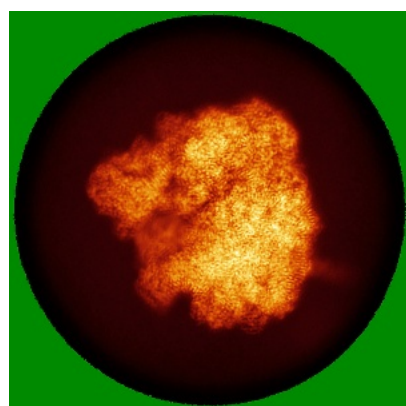


Z Index: 188

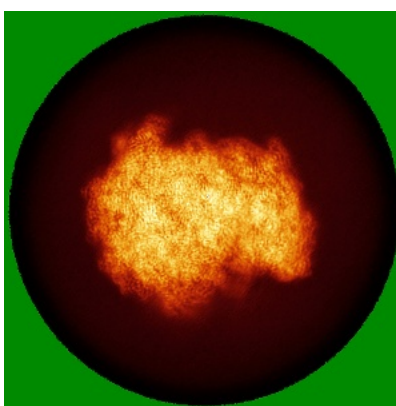
The images above show the largest variance slices of the map in three orthogonal directions.

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

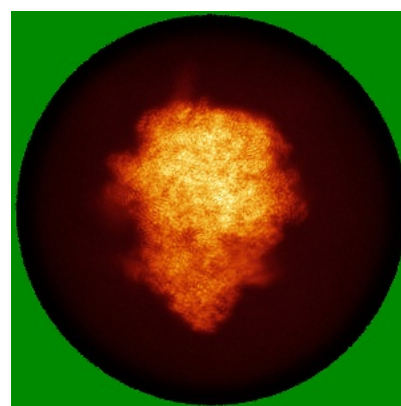
6.4.1 Primary map



X



Y

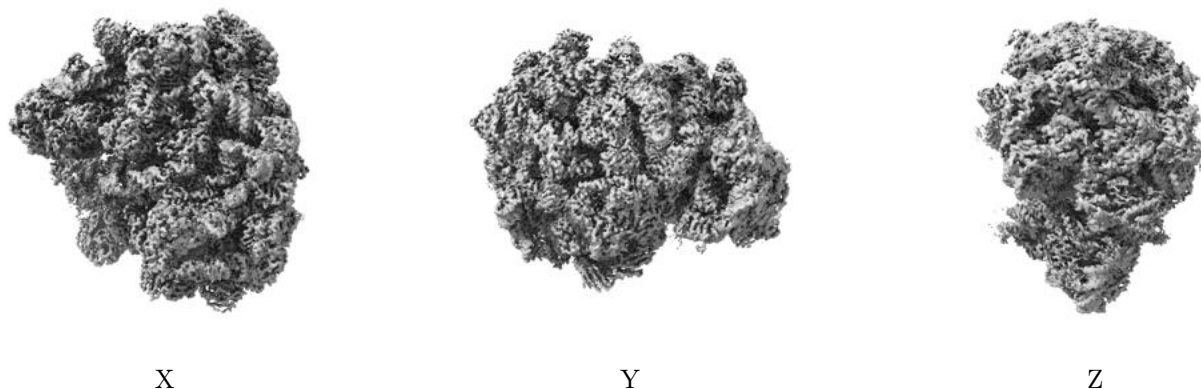


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.138. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

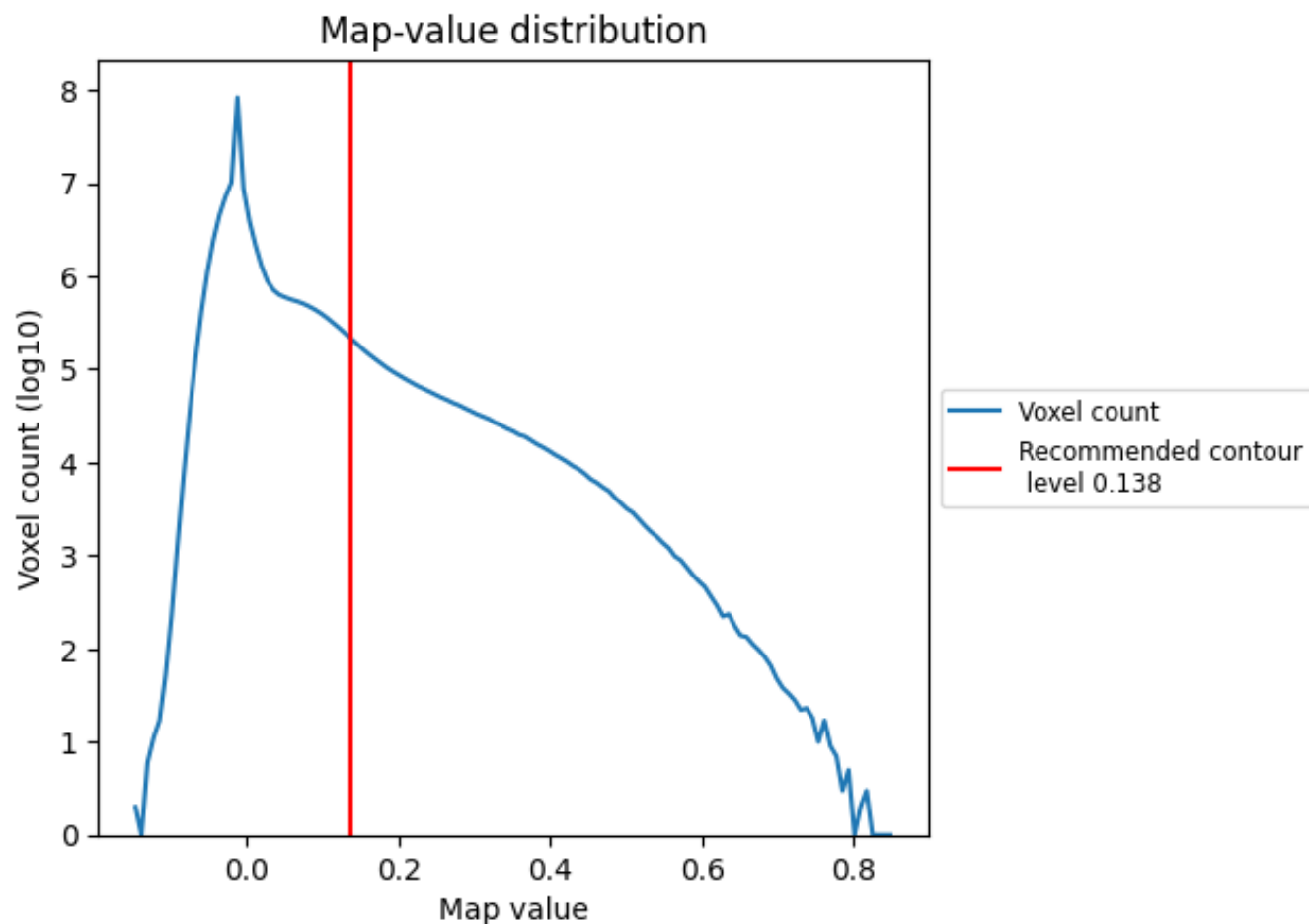
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

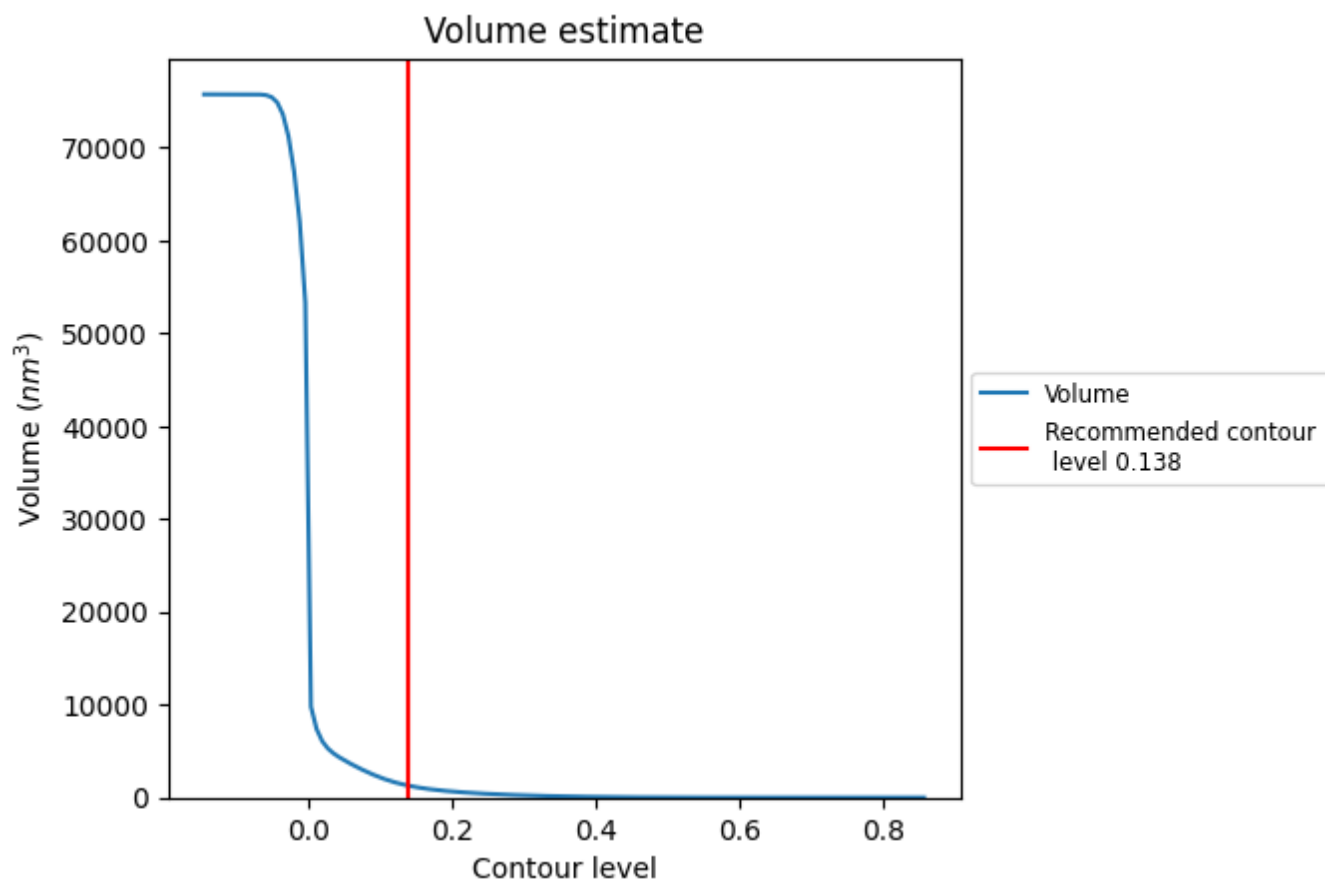
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

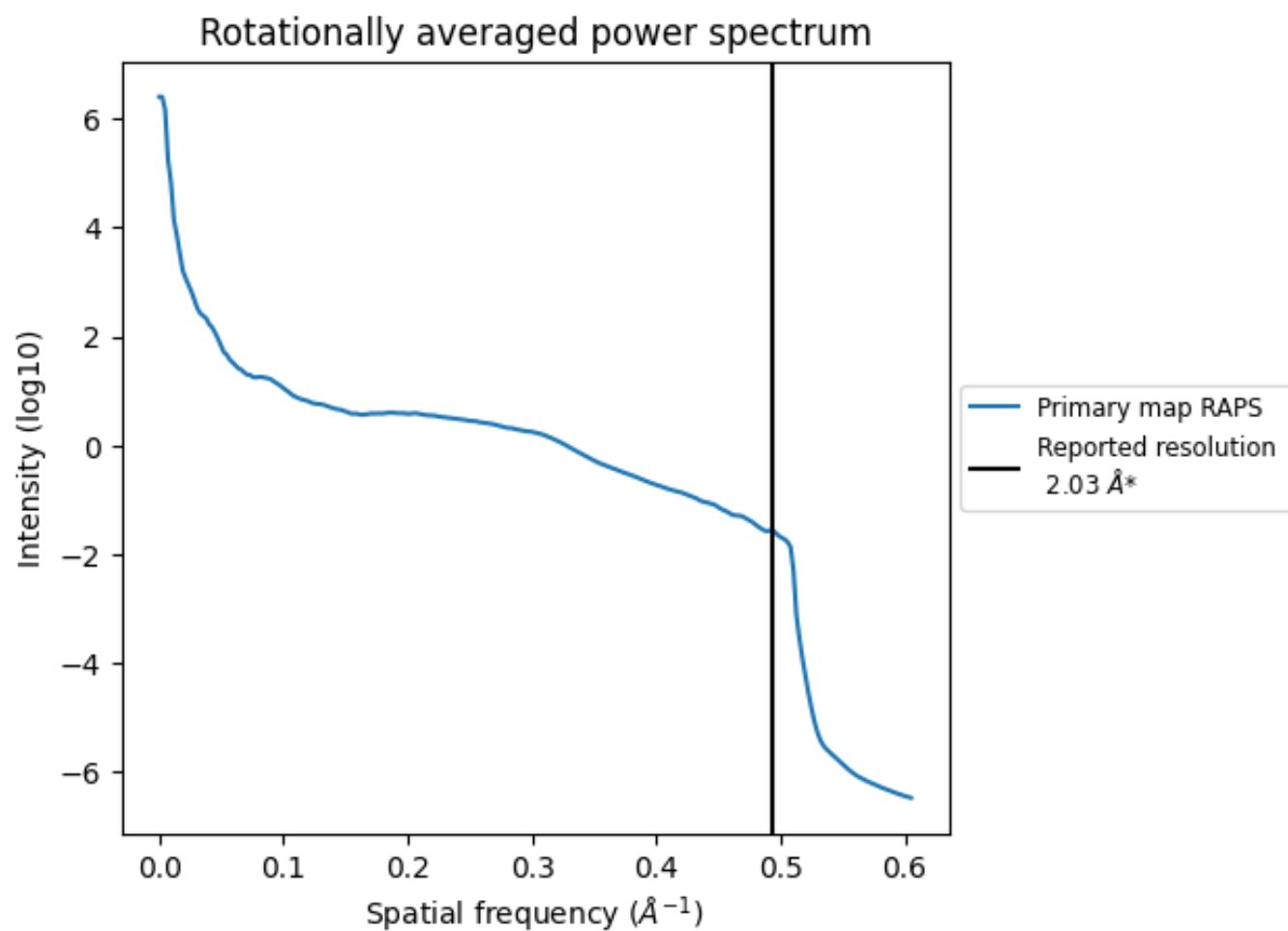
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1288 nm³; this corresponds to an approximate mass of 1163 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 0.493 Å⁻¹

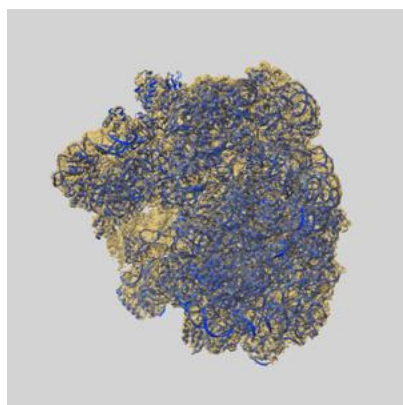
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

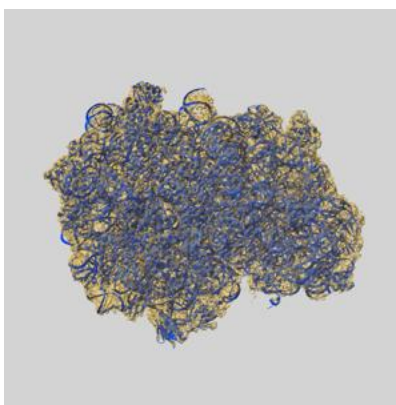
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74446 and PDB model 9ZNF. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

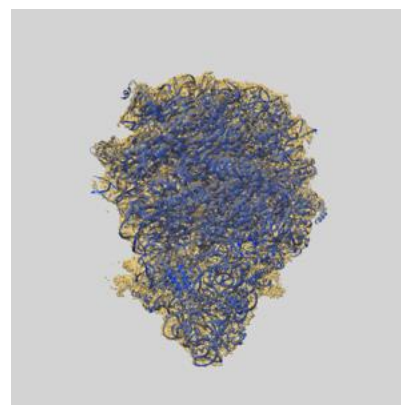
9.1 Map-model overlay [i](#)



X



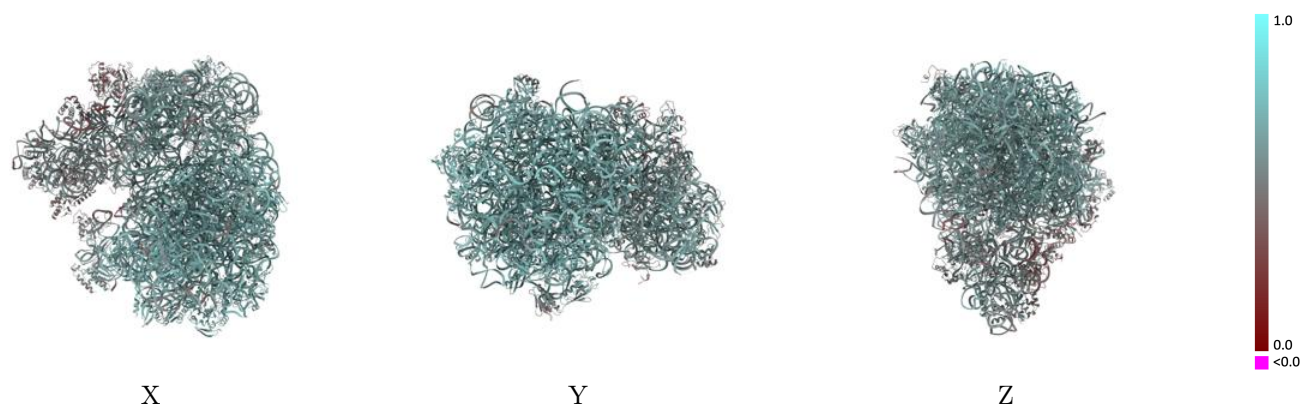
Y



Z

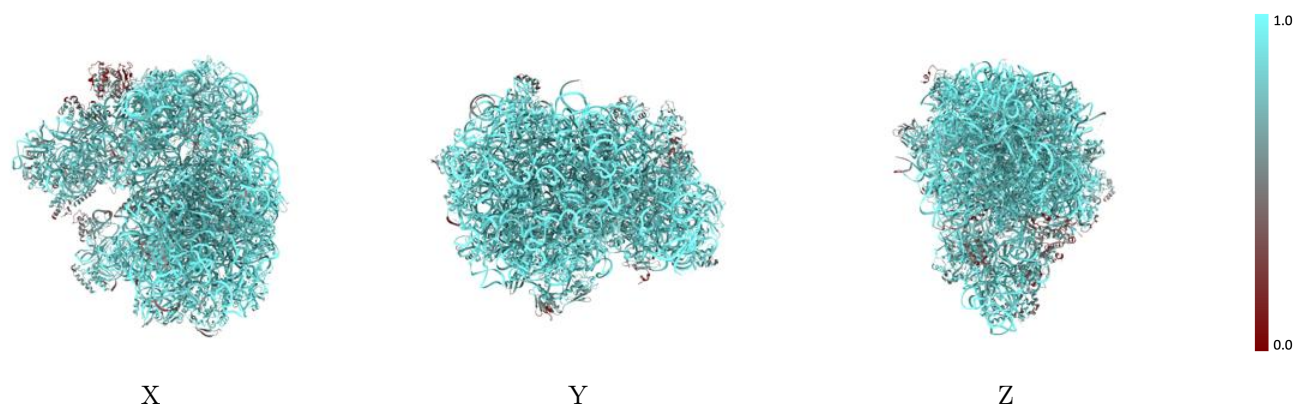
The images above show the 3D surface view of the map at the recommended contour level 0.138 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



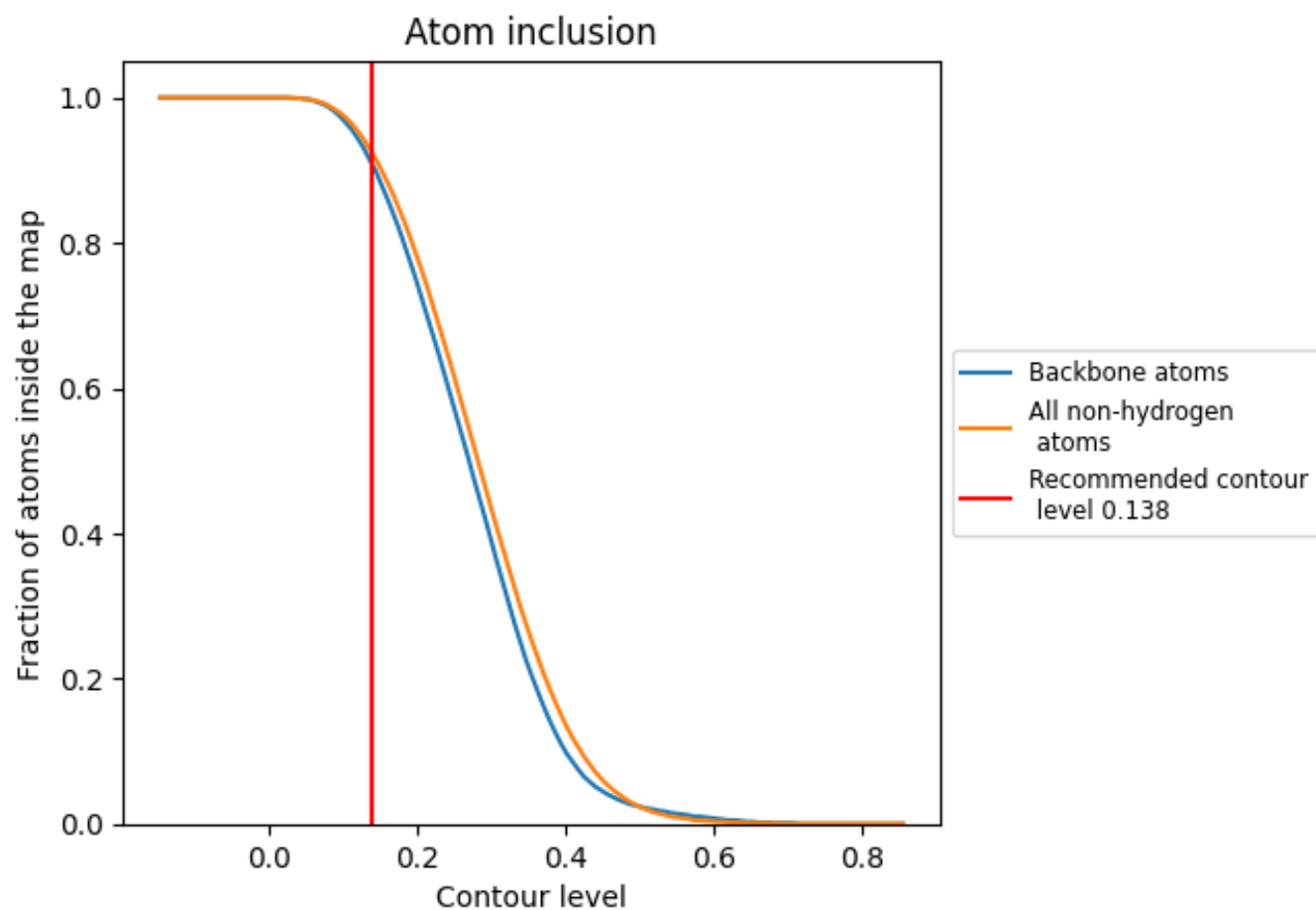
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.138).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 93% 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 (0.138) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.6180
1	 0.9820	 0.6630
2	 0.9200	 0.5940
3	 0.9740	 0.5810
4	 0.6910	 0.5600
5	 0.8780	 0.6540
8	 0.8790	 0.5580
AA	 0.9460	 0.6760
AB	 0.9520	 0.6740
AC	 0.9080	 0.6720
AD	 0.5370	 0.4850
AE	 0.7660	 0.5850
AF	 0.7310	 0.5920
AG	 0.9580	 0.6740
AH	 0.9330	 0.6680
AI	 0.8950	 0.6570
AJ	 0.9820	 0.6900
AK	 0.9260	 0.6640
AL	 0.8760	 0.6070
AM	 0.9380	 0.6570
AN	 0.9550	 0.6550
AO	 0.8560	 0.6300
AP	 0.9720	 0.6790
AQ	 0.9650	 0.6710
AR	 0.9140	 0.6490
AS	 0.9460	 0.6490
AT	 0.9580	 0.6730
AU	 0.8830	 0.6050
AV	 0.9070	 0.6590
AW	 0.7160	 0.4980
AX	 0.9520	 0.6740
AY	 0.9670	 0.6670
AZ	 1.0000	 0.7070
Aa	 0.9880	 0.6810
Ab	 0.8590	 0.6340



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Chain	Atom inclusion	Q-score
Ac	 0.9450	 0.6760
Ad	 0.9140	 0.6510
BA	 0.7500	 0.5130
BB	 0.4280	 0.4210
BC	 0.5510	 0.4810
BD	 0.9050	 0.5560
BE	 0.9320	 0.5790
BF	 0.8230	 0.5300
BG	 0.7270	 0.5220
BH	 0.7790	 0.4860
BI	 0.9670	 0.6020
BJ	 0.8330	 0.5290
BK	 0.9340	 0.5840
BL	 0.8370	 0.5640
BM	 0.8400	 0.5480
BN	 0.8540	 0.5810
BO	 0.7150	 0.4520
BP	 0.7470	 0.5390
BQ	 0.8770	 0.5740
BR	 0.9310	 0.5680
BS	 0.6460	 0.4520
BT	 0.8020	 0.4910
BU	 0.8280	 0.5270
BV	 0.3130	 0.4690
BW	 0.7940	 0.5440
BX	 0.7870	 0.5200
BY	 0.8120	 0.4690
BZ	 0.7780	 0.5420