



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 11:00 AM EDT

PDB ID : 9ZNG / pdb_00009zng
EMDB ID : EMD-74447
Title : Cryo-EM structure of the Methanosarcina acetivorans 70S ribosome in complex with SriD
Authors : Nissley, A.J.; Cate, J.H.D.
Deposited on : 2025-12-12
Resolution : 2.06 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:

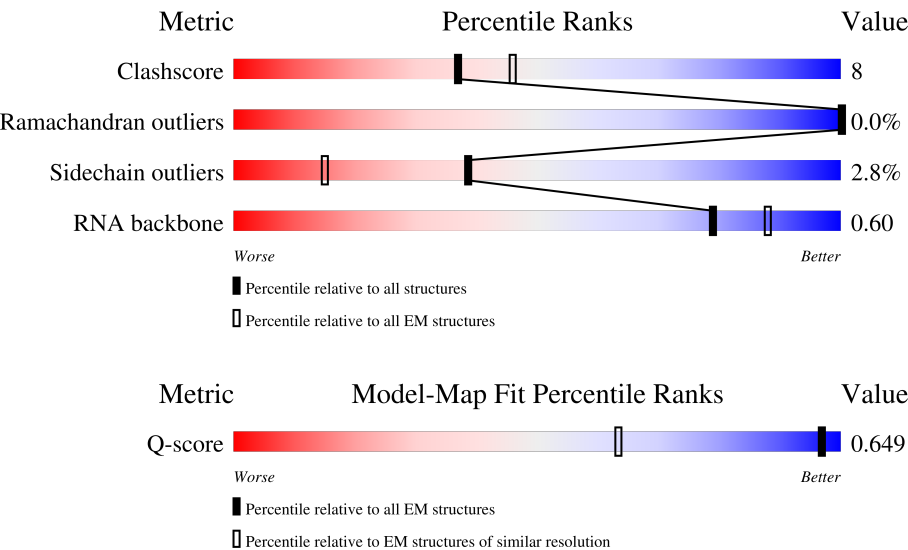
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.06 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	1895 (1.56 - 2.56)

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	61%29%7%
2	2	133	58%30%8%5%
3	3	1478	59%32%5%

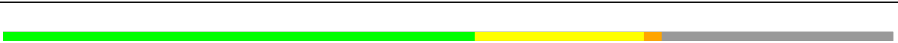
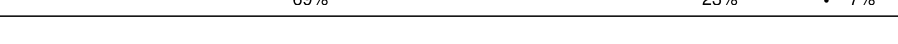
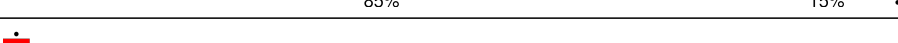
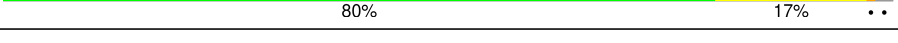
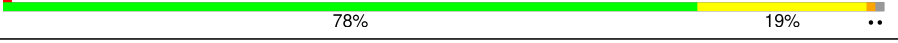
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Mol	Chain	Length	Quality of chain
4	7	280	
5	8	75	
6	AA	238	
7	AB	337	
8	AC	253	
9	AD	165	
10	AE	176	
11	AF	120	
12	AG	143	
13	AH	132	
14	AI	140	
15	AJ	196	
16	AK	173	
17	AL	174	
18	AM	126	
19	AN	151	
20	AO	61	
21	AP	97	
22	AQ	151	
23	AR	82	
24	AS	119	
25	AT	62	
26	AU	67	
27	AV	153	
28	AW	99	

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Mol	Chain	Length	Quality of chain
29	AX	89	
30	AY	129	
31	AZ	56	
32	Aa	51	
33	Ab	49	
34	Ac	92	
35	Ad	94	
36	BA	203	
37	BB	225	
38	BC	318	
39	BD	218	
40	BE	235	
41	BF	209	
42	BG	136	
43	BH	189	
44	BI	130	
45	BJ	134	
46	BK	125	
47	BL	102	
48	BM	126	
49	BN	142	
50	BO	162	
51	BP	50	
52	BQ	152	
53	BR	109	

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

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 159419 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	2711	Total	C	N	O	P	0	0
			58043	25909	10576	18847	2711		

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	7	257	Total	C	N	O	S	0	0
			1995	1250	353	382	10		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	275	HIS	-	insertion	UNP Q8TH71
7	276	HIS	-	insertion	UNP Q8TH71
7	277	HIS	-	insertion	UNP Q8TH71
7	278	HIS	-	insertion	UNP Q8TH71
7	279	HIS	-	insertion	UNP Q8TH71
7	280	HIS	-	insertion	UNP Q8TH71

- Molecule 5 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	18	Total	C	N	O	P	0	0
			381	171	70	123	17		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 15 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	161	Total	C	N	O	S	0	0
			1277	803	245	220	9		

- Molecule 17 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 18 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 19 is a protein called Large ribosomal subunit protein eL19.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 21 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 22 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	84	Total	C	N	O	S	0	0
			605	383	100	118	4		

- Molecule 29 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 36 is a protein called Small ribosomal subunit protein eS1.

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

- Molecule 37 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 38 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BC	142	Total	C	N	O	S	0	0
			1085	686	193	199	7		

- Molecule 39 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 40 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 41 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 42 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 43 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 46 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 47 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BL	70	Total	C	N	O	S	0	0
			538	337	103	96	2		

- Molecule 48 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	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 49 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS17A.

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

- Molecule 54 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BT	116	Total	C	N	O	S	0	0
			941	593	175	170	3		

- Molecule 56 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 57 is a protein called Putative zinc finger domain-containing protein.

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

- Molecule 58 is a protein called Small ribosomal subunit protein eS24.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BY	52	Total	C	N	O	S	0	0
			389	238	74	73	4		

- Molecule 61 is a protein called DUF5350 family protein.

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

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	1	236	Total	Mg	0
			236	236	
62	2	2	Total	Mg	0
			2	2	
62	3	64	Total	Mg	0
			64	64	
62	7	1	Total	Mg	0
			1	1	
62	AA	2	Total	Mg	0
			2	2	
62	AB	2	Total	Mg	0
			2	2	
62	AH	1	Total	Mg	0
			1	1	
62	AI	2	Total	Mg	0
			2	2	
62	AN	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
62	AZ	1	Total 1	Mg 1	0
62	BF	1	Total 1	Mg 1	0
62	BM	1	Total 1	Mg 1	0

- Molecule 63 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	1	6124	Total 6124	O 6124	0
64	2	109	Total 109	O 109	0
64	3	2579	Total 2579	O 2579	0
64	7	22	Total 22	O 22	0

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Mol	Chain	Residues	Atoms		AltConf
64	8	5	Total 5	O 5	0
64	AA	80	Total 80	O 80	0
64	AB	101	Total 101	O 101	0
64	AC	100	Total 100	O 100	0
64	AD	11	Total 11	O 11	0
64	AE	20	Total 20	O 20	0
64	AF	11	Total 11	O 11	0
64	AG	55	Total 55	O 55	0
64	AH	27	Total 27	O 27	0
64	AI	54	Total 54	O 54	0
64	AJ	77	Total 77	O 77	0
64	AK	42	Total 42	O 42	0
64	AL	24	Total 24	O 24	0
64	AM	27	Total 27	O 27	0
64	AN	57	Total 57	O 57	0
64	AO	6	Total 6	O 6	0
64	AP	41	Total 41	O 41	0
64	AQ	31	Total 31	O 31	0
64	AR	30	Total 30	O 30	0
64	AS	28	Total 28	O 28	0
64	AT	16	Total 16	O 16	0

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Mol	Chain	Residues	Atoms		AltConf
64	AU	13	Total 13	O 13	0
64	AV	36	Total 36	O 36	0
64	AW	9	Total 9	O 9	0
64	AX	27	Total 27	O 27	0
64	AY	34	Total 34	O 34	0
64	AZ	27	Total 27	O 27	0
64	Aa	23	Total 23	O 23	0
64	Ab	7	Total 7	O 7	0
64	Ac	36	Total 36	O 36	0
64	Ad	24	Total 24	O 24	0
64	BA	22	Total 22	O 22	0
64	BB	8	Total 8	O 8	0
64	BC	14	Total 14	O 14	0
64	BD	36	Total 36	O 36	0
64	BE	56	Total 56	O 56	0
64	BF	38	Total 38	O 38	0
64	BG	14	Total 14	O 14	0
64	BH	22	Total 22	O 22	0
64	BI	42	Total 42	O 42	0
64	BJ	20	Total 20	O 20	0
64	BK	29	Total 29	O 29	0

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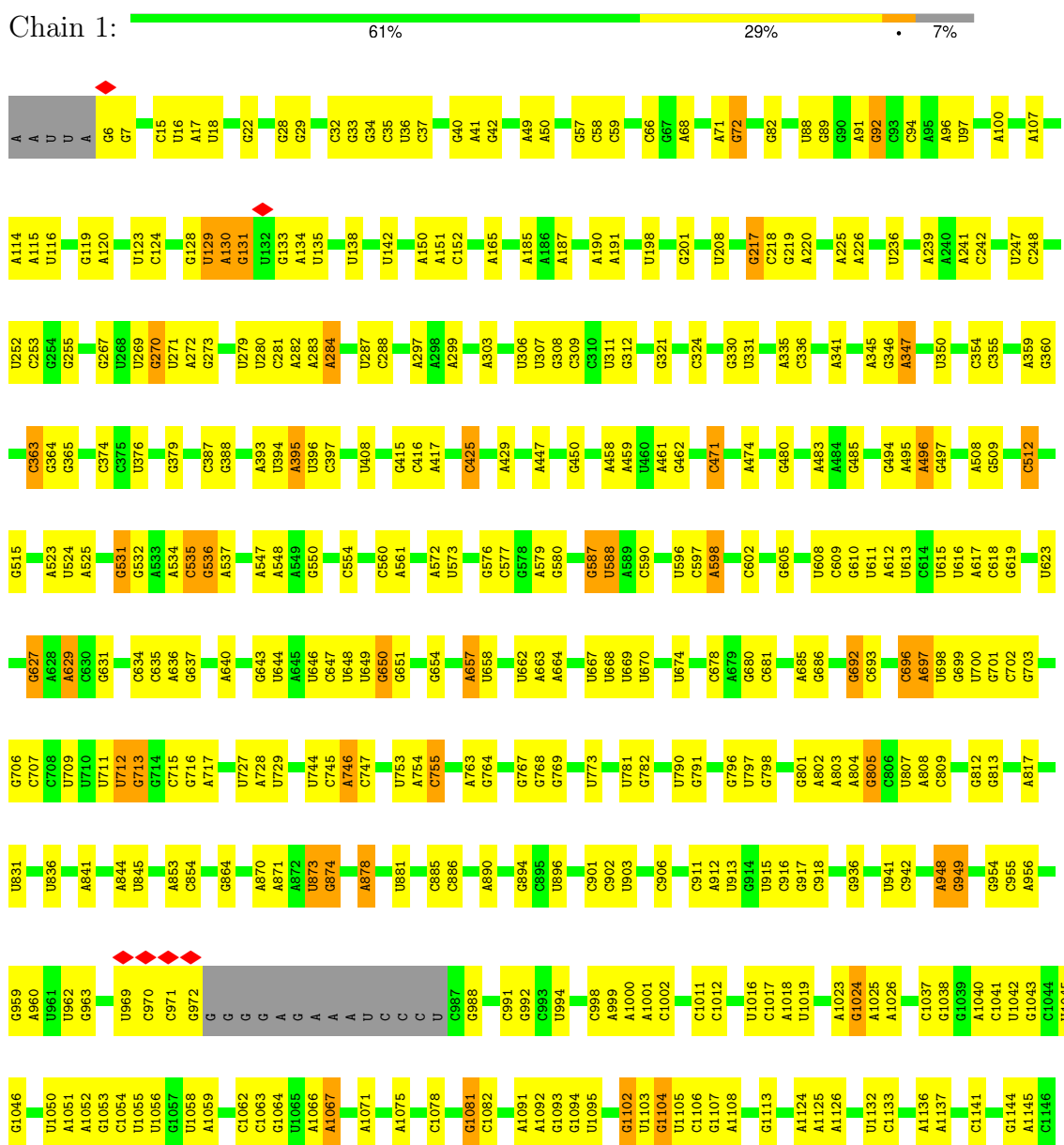
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Mol	Chain	Residues	Atoms		AltConf
64	BL	12	Total 12	O 12	0
64	BM	27	Total 27	O 27	0
64	BN	42	Total 42	O 42	0
64	BO	19	Total 19	O 19	0
64	BP	12	Total 12	O 12	0
64	BQ	31	Total 31	O 31	0
64	BR	36	Total 36	O 36	0
64	BS	3	Total 3	O 3	0
64	BT	22	Total 22	O 22	0
64	BU	23	Total 23	O 23	0
64	BV	9	Total 9	O 9	0
64	BW	7	Total 7	O 7	0
64	BX	7	Total 7	O 7	0
64	BY	4	Total 4	O 4	0
64	BZ	8	Total 8	O 8	0

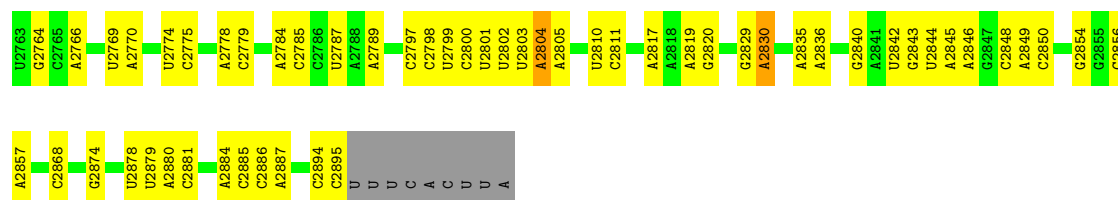
3 Residue-property plots

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.

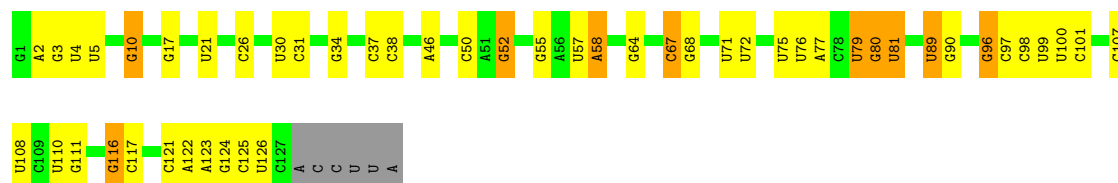
• Molecule 1: 23S rRNA



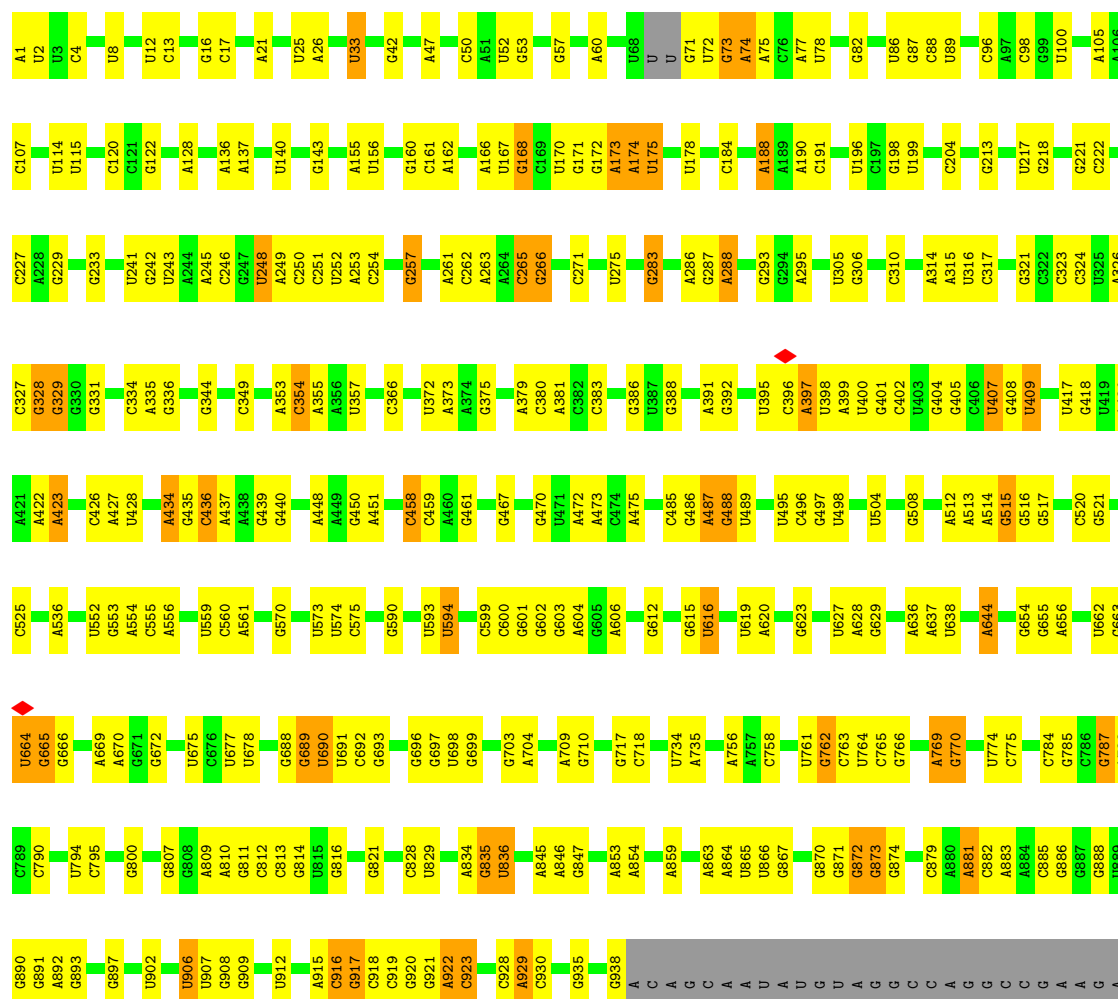
C2654	U2526	U2412	G2293	A	C	C2057	U1950	G	C1885	U1554	G1450	G1315	G1207	A1147
G2655	U2529	U2413	C2297	C	A	A2058	U1951	A1849	C1886	A1557	G1451	U1316	A1208	G
A2660	U2530	U2414	G2297	U	U	G2066	A1952	A1850	A1703	A1558	A1458	G1317	G1209	C
G2661	C2531	A2300	A2301	C	G	C2067	G1954	G1851	U1706	C1562	U1459	A1318	G1210	U
C2662	A2532	G2418	U2302	C	U	C2068	G1955	A1861	C1707	C1563	G1462	G1320	G1215	G
U2663	U2534	C2419	C2303	C	A	C2069	U1956	A1862	U1708	G1574	A1463	U1321	G1216	A
C2664	A2436	A2437	G2304	U	G	U2070	A1957	A1866	G1709	G1575	G1468	C1322	G1217	A
C2665	U2441	U2305	U2306	C	U	G2071	G1958	C1866	C1711	G1576	U1324	U1323	G1218	G
G2671	U2442	G2307	G2307	C	A	G2074	A1962	A1869	A1718	A1577	G1475	A1223	A1223	U
U2672	G2442	A2408	C2309	G	C	G2075	G1963	A1870	U1737	G1578	C1330	A1224	A1224	U
A2673	A2445	C2310	U2311	G	A	G2076	G1970	U1871	U1744	C1579	G1477	A1225	A1225	A
C2677	G2446	C2311	C2312	C	G	A2080	C1972	C1872	U1745	G1580	A1478	A1226	A1226	G
U2678	A2447	A2448	A2313	U	C	G2083	A1962	U1877	G1746	G1581	A1479	A1230	A1230	C
G2679	U2452	U2453	G2317	A	C	G2084	U1979	G1882	U1747	G1582	A1480	C1231	C1231	U
G2680	U2454	C2455	U2318	C	U	A2085	U1980	C1883	U1748	U1583	A1481	A1235	A1235	A
A2681	U2455	C2456	U2319	C	A	C2086	G1981	C1884	G1759	U1584	A1482	A1239	A1239	A
C2684	U2456	C2457	G2320	C	G	C2087	U1982	G1885	U1762	G1585	U1489	A1348	A1348	A
A2689	G2460	U2467	G2321	C	G	C2088	A1991	G1886	U1763	U1586	A1490	A1355	A1355	G
G2690	G2461	U2476	G2322	C	C	C2091	U2000	U1887	G1775	G1600	U1495	A1366	A1366	A
G2693	A2462	U2483	A2323	G	G	G2092	A2006	G1888	U1776	U1603	G1496	A1367	A1367	G
G2701	A2463	G2485	A2324	G	G	U2093	G2007	A1894	G1777	A1610	A1500	A1368	A1368	C
G2702	U2467	U2489	G2325	U	U	G2094	U2016	A1895	U1780	U1614	A1501	A1252	A1252	A
U2703	U2476	U2496	C2326	C	C	A2095	G2017	U1896	U1781	G1618	U1502	U1253	U1253	C
G2704	U2483	A2484	U2331	C	C	C2097	U2018	G1897	G1782	U1505	U1504	G1389	A1257	C
U2705	A2485	G2495	A2334	C	C	C2098	C2021	U1902	A1783	A1506	A1506	A1393	C1258	C
C2714	G2498	U2507	A2335	C	C	U2100	U2022	U1903	C1787	G1507	G1507	A1394	U1263	U
C2715	C2499	U2508	G2336	A	A	G2105	G2026	C1904	A1788	U	U	G1395	A1264	C
U2716	U2509	G2509	U2337	C	C	U2111	G2027	A1906	U1793	A1642	U	A1401	C1265	A
G2717	U2514	U2515	C2338	C	C	G2112	U2034	A1926	G1796	A1643	U	G1402	A1269	A
U2718	C2514	G2515	U2339	C	C	G2117	G2035	C1927	U1811	A1644	U	A1270	G1271	G
U2726	U2516	C2517	A2340	U	U	U2117	U2036	A1928	A1812	G1645	G1513	C1408	U1291	A
C2727	U2517	G2518	U2341	C	C	G2118	G2037	G1931	A1813	G1646	U1514	U1409	U1292	C
G2728	U2518	C2519	U2342	C	C	G2119	G2038	G1932	U1822	A1647	C1515	C1410	G1293	G
U2732	U2519	U2520	C2343	U	U	G2120	U2039	G1933	A1823	G1648	U1523	A1424	U1294	A
G2733	U2521	U2522	U2344	C	C	G2123	U2040	G1934	G1804	A	A1525	G1426	G1295	C
U2738	U2523	U2524	U2345	G	G	U	U2041	U1935	U1811	G	G1528	G1436	U1296	U
A2739	U2525	U2526	U2346	U	U	G	U2042	U1936	A1812	C1652	C1529	A1433	U1297	A
C2740	U2527	U2528	U2347	C	C	G	U2043	A	A1813	U1653	C1522	A1415	G1298	C
C2746	U2529	U2530	U2348	C	C	U	U2044	C	A1820	A1654	U1524	A1424	U1299	A
A2747	U2531	U2532	U2349	C	C	C	U2045	U	A1821	A1655	A1525	G1426	G1299	G
A2753	U2533	U2534	U2350	C	C	U	U2046	G	U1822	G1661	G1528	G1436	U1296	U
A2754	U2535	U2536	U2351	C	C	U	U2047	U	A1823	A1668	C1529	A1530	G1300	A
G2760	U2537	U2538	U2352	C	C	U	U2048	G	A1826	A1671	U1545	C1443	G1304	C
A2761	U2539	U2540	U2353	C	C	U	U2049	A	U1830	A1679	G1545	U1444	G1304	C
C2644	U2541	U2542	U2354	C	C	U	U2050	C	A1831	A1679	C1545	A1445	A1446	A
G2646	U2543	U2544	U2355	C	C	U	U2051	U	G1839	C1684	C1550	A1447	G1312	U
	U2545	U2546	U2356	C	C	A	U2052	U	C1840					C

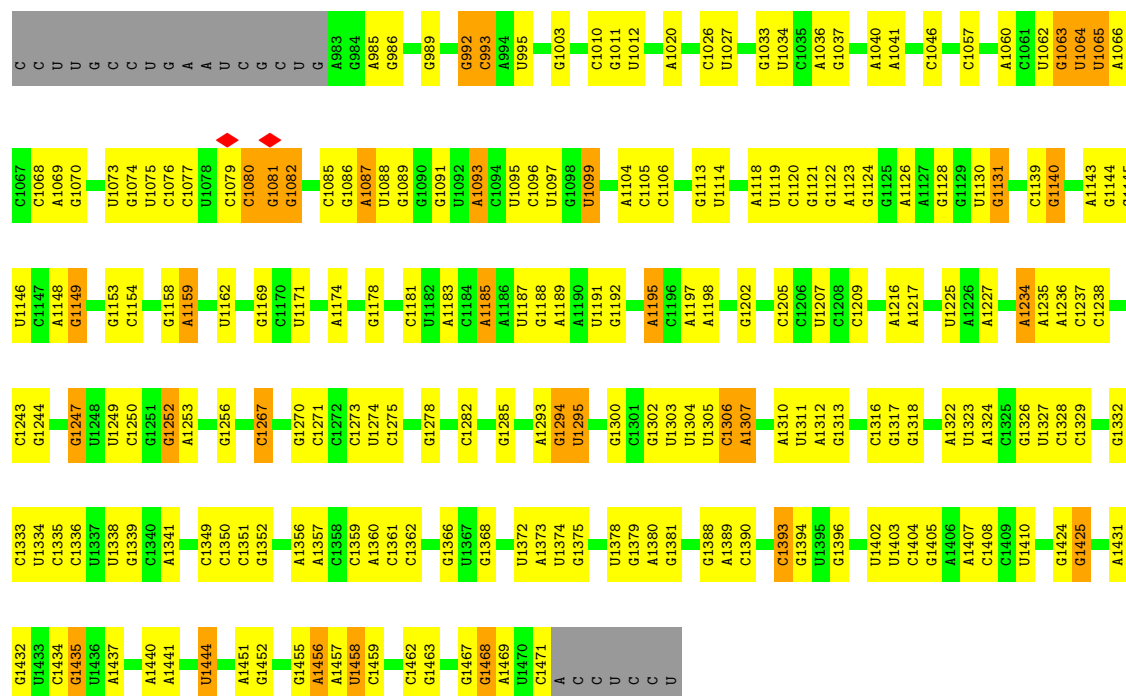


• Molecule 2: 5S rRNA

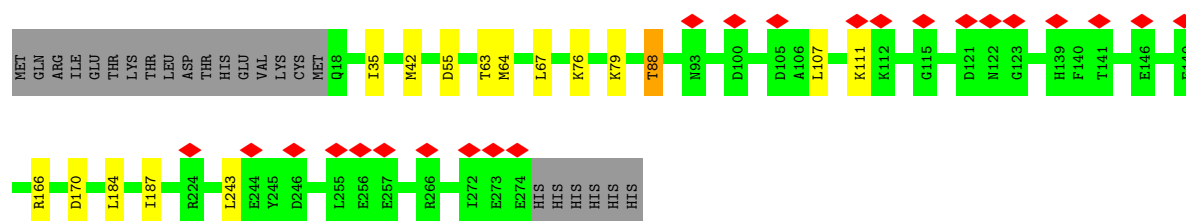
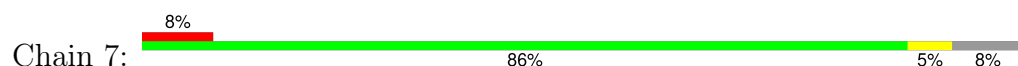


• Molecule 3: 16S rRNA

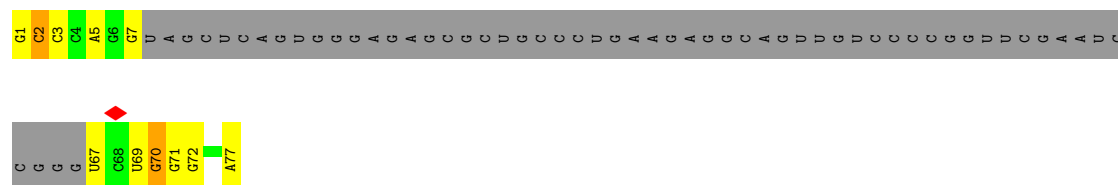




• Molecule 4: CBS domain-containing protein



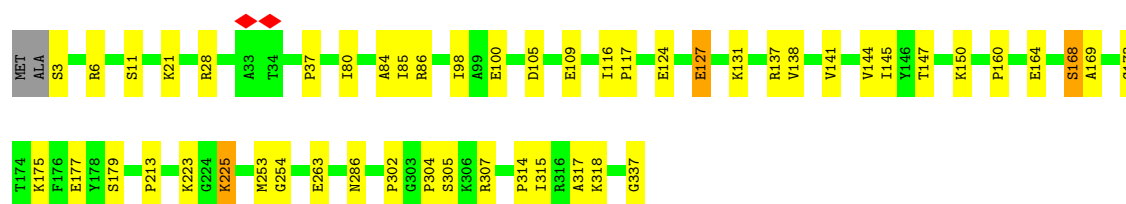
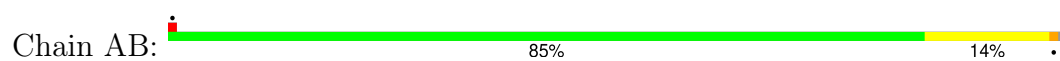
• Molecule 5: E-site tRNA



• Molecule 6: Large ribosomal subunit protein uL2



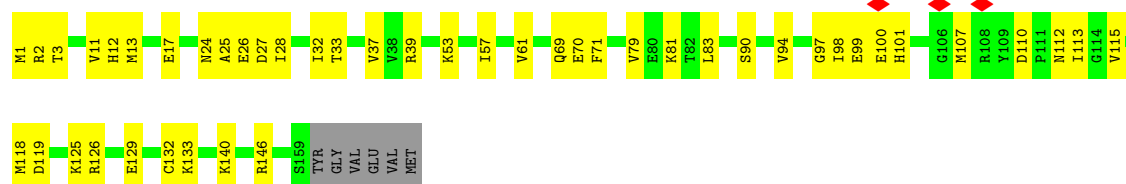
• Molecule 7: Large ribosomal subunit protein uL3



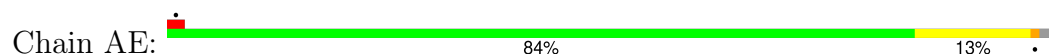
- Molecule 8: Large ribosomal subunit protein uL4



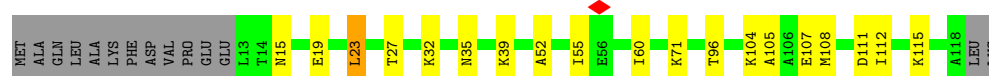
- Molecule 9: Large ribosomal subunit protein uL5



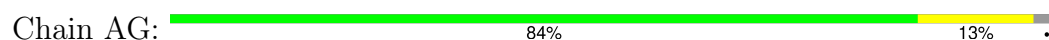
- Molecule 10: Large ribosomal subunit protein uL6



- Molecule 11: Large ribosomal subunit protein eL8



- Molecule 12: Large ribosomal subunit protein uL13



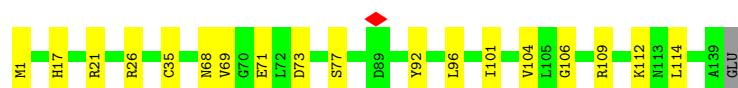
- Molecule 13: Large ribosomal subunit protein uL14

Chain AH:  82% 17%



- Molecule 14: Large ribosomal subunit protein uL15

Chain AI:  86% 13%



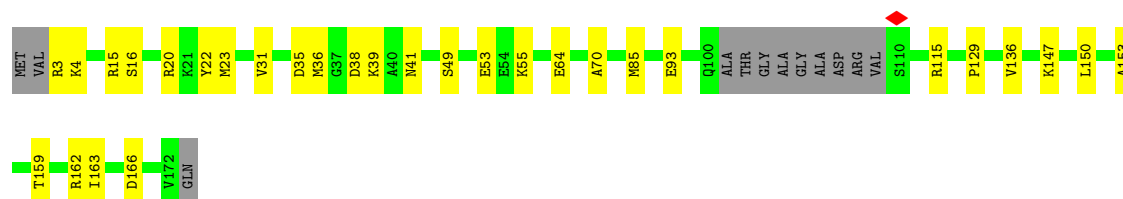
- Molecule 15: Large ribosomal subunit protein eL15

Chain AJ:  91% 8%



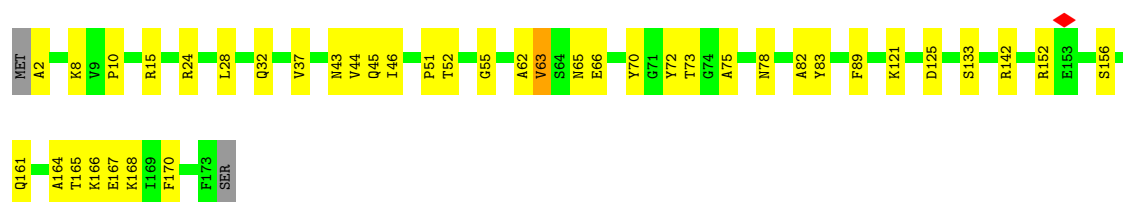
- Molecule 16: Large ribosomal subunit protein uL16

Chain AK:  76% 17% 7%



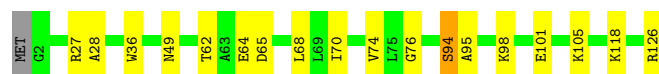
- Molecule 17: Large ribosomal subunit protein uL18

Chain AL:  76% 22% ..



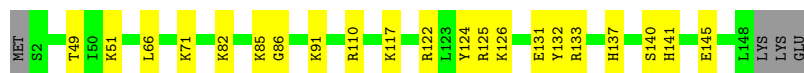
- Molecule 18: Large ribosomal subunit protein eL18

Chain AM:  85% 13% ..



- Molecule 19: Large ribosomal subunit protein eL19

Chain AN:  83% 14%



- Molecule 20: Large ribosomal subunit protein eL20

Chain AO:  75% 16% 8%



- Molecule 21: Large ribosomal subunit protein eL21

Chain AP:  93% 6%



- Molecule 22: Large ribosomal subunit protein uL22

Chain AQ:  89% 10%



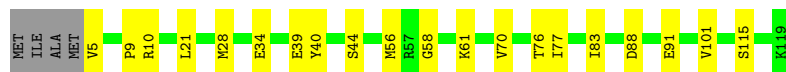
- Molecule 23: Large ribosomal subunit protein uL23

Chain AR:  79% 18%



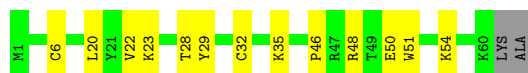
- Molecule 24: Large ribosomal subunit protein uL24

Chain AS:  80% 17%



- Molecule 25: Large ribosomal subunit protein eL24

Chain AT:  76% 21%



- Molecule 26: Large ribosomal subunit protein uL29

Chain AU:  78% 19%



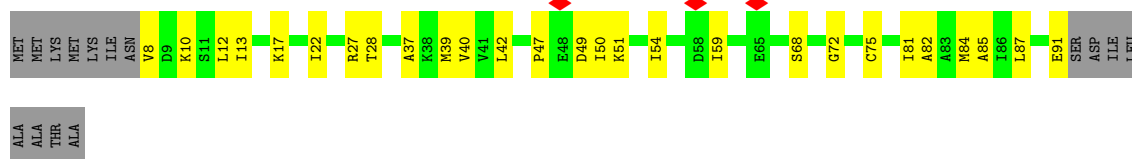
- Molecule 27: Large ribosomal subunit protein uL30

Chain AV:  91% 9%



- Molecule 28: Large ribosomal subunit protein eL30

Chain AW:  58% 27% 15%



- Molecule 29: Large ribosomal subunit protein eL31

Chain AX:  84% 9% 6%



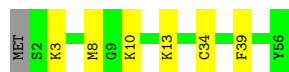
- Molecule 30: Large ribosomal subunit protein eL32

Chain AY:  87% 11%



- Molecule 31: Large ribosomal subunit protein eL37

Chain AZ:  88% 11%



- Molecule 32: Large ribosomal subunit protein eL39

Chain Aa:  86% 12%



- Molecule 33: Large ribosomal subunit protein eL40

Chain Ab:  63% 24% 12%



- Molecule 34: Large ribosomal subunit protein eL42

Chain Ac:  89% 10%



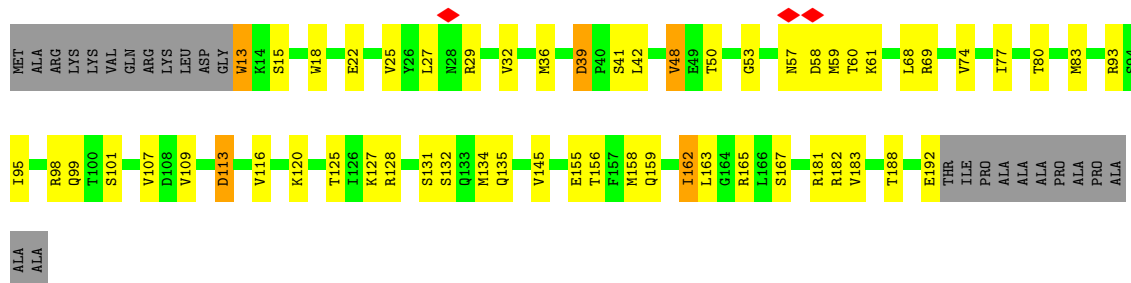
- Molecule 35: Large ribosomal subunit protein eL43

Chain Ad:  79% 16% 5%



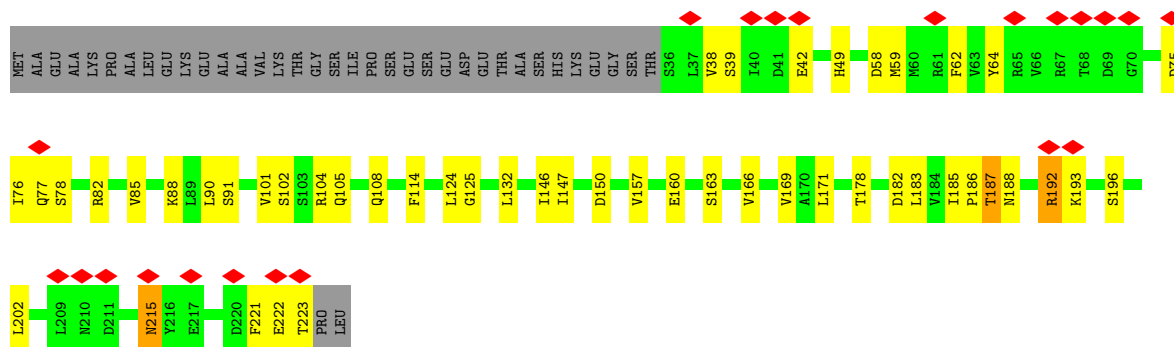
- Molecule 36: Small ribosomal subunit protein eS1

Chain BA:  60% 26% 12%

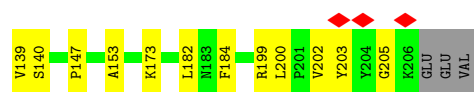


- Molecule 37: Small ribosomal subunit protein uS2

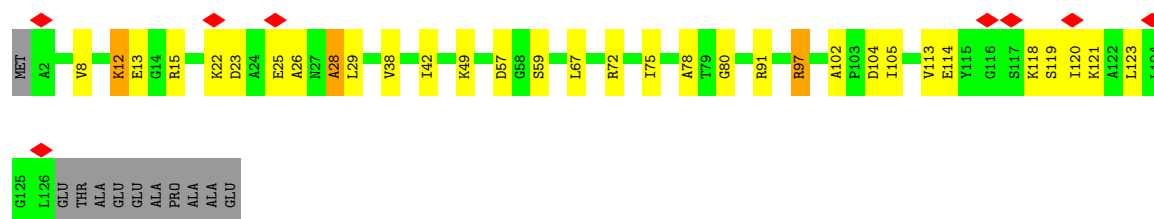
Chain BB:  10% 61% 21% 16%



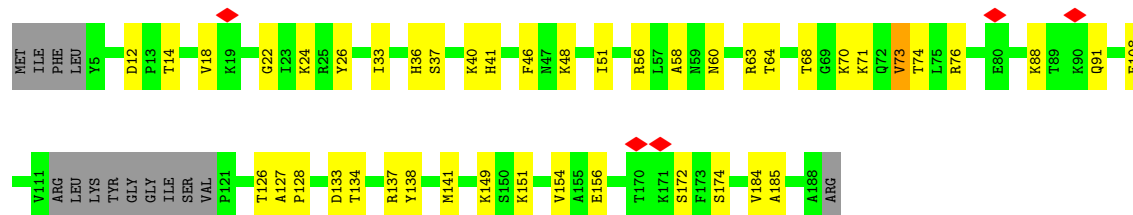
- Molecule 38: Small ribosomal subunit protein uS3



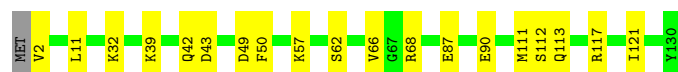
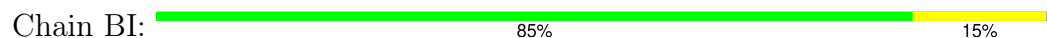
- Molecule 42: Small ribosomal subunit protein eS6



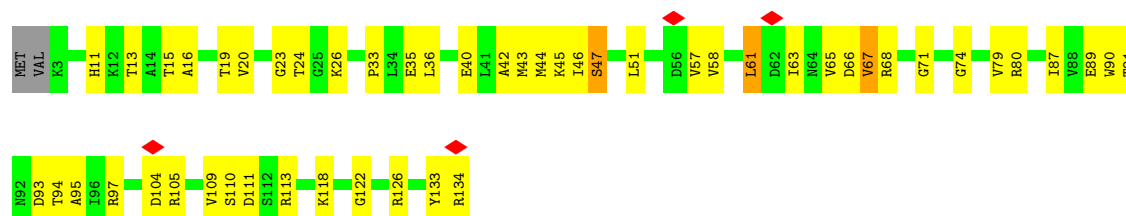
- Molecule 43: Small ribosomal subunit protein uS7



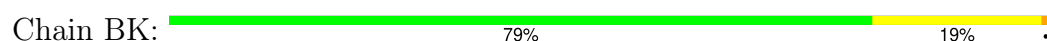
- Molecule 44: Small ribosomal subunit protein uS8

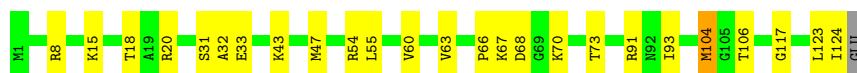


- Molecule 45: Small ribosomal subunit protein uS9

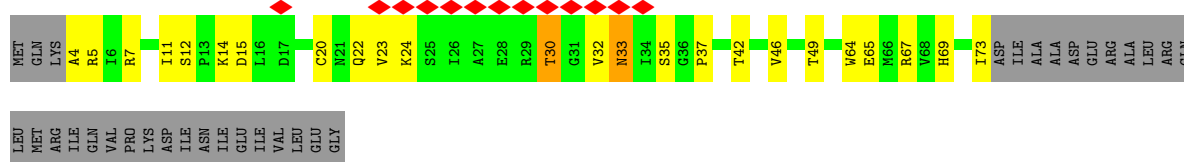


- Molecule 46: Small ribosomal subunit protein eS8

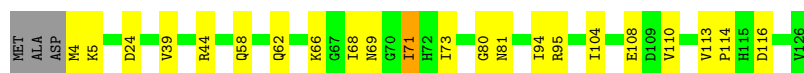
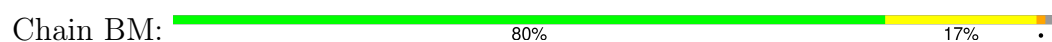




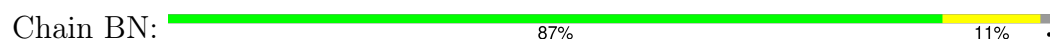
- Molecule 47: Small ribosomal subunit protein uS10



- Molecule 48: Small ribosomal subunit protein uS11



- Molecule 49: Small ribosomal subunit protein uS12



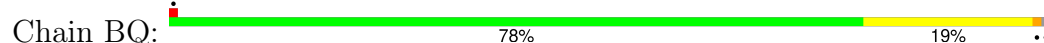
- Molecule 50: Small ribosomal subunit protein uS13



- Molecule 51: Small ribosomal subunit protein uS14

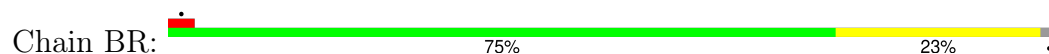


- Molecule 52: Small ribosomal subunit protein uS15





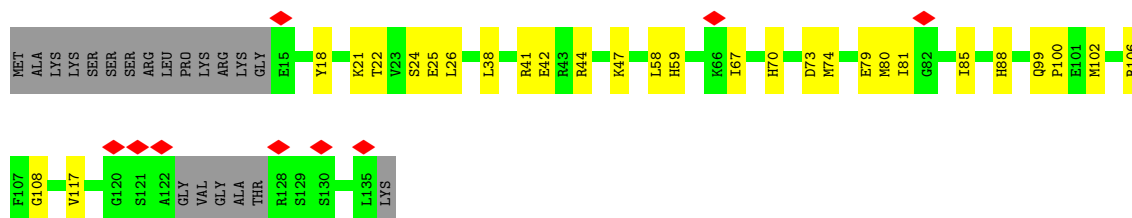
- Molecule 53: Small ribosomal subunit protein uS17A



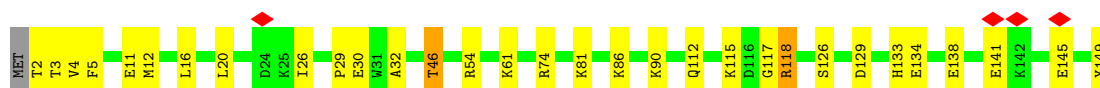
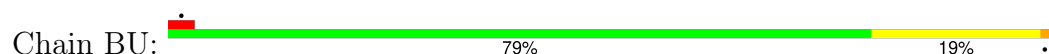
- Molecule 54: Small ribosomal subunit protein eS17



- Molecule 55: Small ribosomal subunit protein uS19



- Molecule 56: Small ribosomal subunit protein eS19

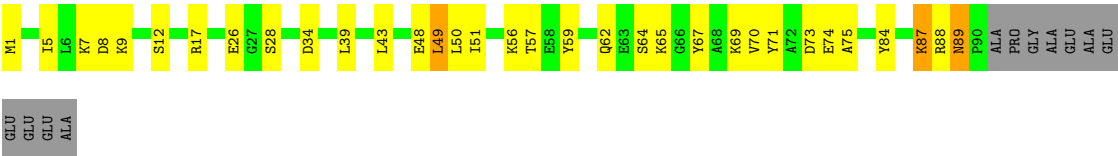


- Molecule 57: Putative zinc finger domain-containing protein

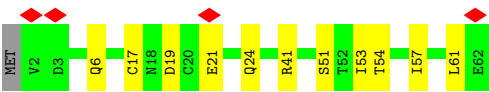
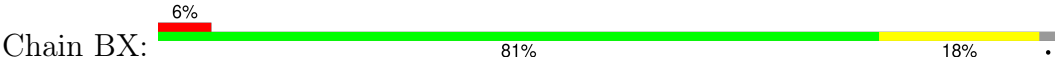


- Molecule 58: Small ribosomal subunit protein eS24

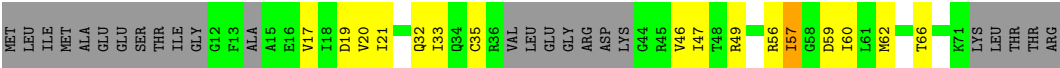




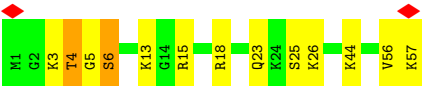
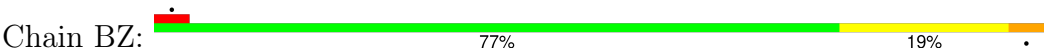
- Molecule 59: Small ribosomal subunit protein eS27



- Molecule 60: Small ribosomal subunit protein eS28



- Molecule 61: DUF5350 family protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68687	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	0.879	Depositor
Minimum map value	-0.222	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	423.1168, 423.1168, 423.1168	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8264, 0.8264, 0.8264	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.18	0/64866	0.34	0/101141
2	2	0.15	0/3011	0.31	0/4689
3	3	0.35	0/34071	0.36	0/53137
4	7	0.72	0/2019	1.25	0/2731
5	8	0.13	0/424	0.25	0/657
6	AA	0.16	0/1821	0.34	0/2462
7	AB	0.23	0/2632	0.40	0/3552
8	AC	0.20	0/1963	0.35	0/2654
9	AD	0.18	0/1261	0.39	0/1697
10	AE	0.24	0/1350	0.36	0/1816
11	AF	0.14	0/784	0.27	0/1055
12	AG	0.23	0/1107	0.36	0/1484
13	AH	0.19	0/1009	0.32	0/1355
14	AI	0.21	0/1061	0.41	0/1413
15	AJ	0.20	0/1616	0.37	0/2166
16	AK	0.14	0/1300	0.30	0/1741
17	AL	0.15	0/1367	0.31	0/1845
18	AM	0.16	0/966	0.33	0/1302
19	AN	0.17	0/1173	0.31	0/1558
20	AO	0.14	0/454	0.26	0/602
21	AP	0.16	0/779	0.31	0/1042
22	AQ	0.15	0/1169	0.34	0/1564
23	AR	0.13	0/647	0.30	0/864
24	AS	0.14	0/889	0.28	0/1189
25	AT	0.14	0/493	0.25	0/652
26	AU	0.15	0/517	0.30	0/695
27	AV	0.22	0/1258	0.37	0/1692
28	AW	0.15	0/610	0.38	0/825
29	AX	0.14	0/697	0.29	0/937
30	AY	0.24	0/997	0.42	0/1333
31	AZ	0.15	0/443	0.38	0/583
32	Aa	0.14	0/439	0.32	0/585

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.24	0/350	0.33	0/461
34	Ac	0.14	0/767	0.31	0/1017
35	Ad	0.14	0/712	0.32	0/950
36	BA	0.25	0/1453	0.41	0/1959
37	BB	0.20	0/1504	0.33	0/2045
38	BC	0.24	0/1102	0.42	0/1477
39	BD	0.31	0/1325	0.39	0/1779
40	BE	0.29	0/1822	0.38	0/2451
41	BF	0.27	0/1552	0.40	0/2105
42	BG	0.47	0/948	0.64	0/1273
43	BH	0.20	0/1380	0.33	0/1858
44	BI	0.36	0/996	0.42	0/1343
45	BJ	0.22	0/1013	0.39	0/1364
46	BK	0.29	0/962	0.31	0/1288
47	BL	0.24	0/549	0.36	0/744
48	BM	0.26	0/915	0.34	0/1230
49	BN	0.27	0/1071	0.31	0/1438
50	BO	0.21	0/1039	0.35	0/1396
51	BP	0.33	0/388	0.46	0/510
52	BQ	0.28	0/1227	0.32	0/1654
53	BR	0.31	0/846	0.43	0/1144
54	BS	0.22	0/481	0.43	0/645
55	BT	0.30	0/959	0.42	0/1279
56	BU	0.22	0/1177	0.37	0/1586
57	BV	0.22	0/402	0.35	0/539
58	BW	0.31	0/744	0.46	0/995
59	BX	0.23	0/479	0.33	0/645
60	BY	0.19	0/389	0.43	0/518
61	BZ	0.26	0/459	0.34	0/603
All	All	0.26	0/160204	0.38	0/237314

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
8	AC	0	1
42	BG	0	1
58	BW	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	AC	82	ARG	Sidechain
42	BG	15	ARG	Sidechain
58	BW	88	ARG	Sidechain

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	1	58043	0	29262	568	0
2	2	2697	0	1371	43	0
3	3	30541	0	15402	360	0
4	7	1995	0	2061	8	0
5	8	381	0	199	9	0
6	AA	1779	0	1804	20	0
7	AB	2583	0	2674	33	0
8	AC	1929	0	1989	24	0
9	AD	1241	0	1272	43	0
10	AE	1329	0	1375	16	0
11	AF	779	0	820	15	0
12	AG	1092	0	1142	17	0
13	AH	998	0	1059	17	0
14	AI	1048	0	1038	12	0
15	AJ	1584	0	1625	13	0
16	AK	1277	0	1318	19	0
17	AL	1341	0	1341	28	0
18	AM	953	0	1009	13	0
19	AN	1159	0	1233	17	0
20	AO	447	0	457	8	0
21	AP	765	0	777	4	0
22	AQ	1149	0	1186	11	0
23	AR	639	0	667	15	0
24	AS	880	0	935	13	0
25	AT	484	0	497	9	0
26	AU	515	0	524	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AV	1236	0	1269	10	0
28	AW	605	0	643	26	0
29	AX	685	0	723	7	0
30	AY	981	0	1033	10	0
31	AZ	436	0	443	4	0
32	Aa	430	0	467	10	0
33	Ab	348	0	369	10	0
34	Ac	750	0	791	6	0
35	Ad	699	0	730	12	0
36	BA	1435	0	1483	49	0
37	BB	1476	0	1482	33	0
38	BC	1085	0	1098	37	0
39	BD	1303	0	1350	51	0
40	BE	1796	0	1878	46	0
41	BF	1527	0	1581	31	0
42	BG	935	0	988	17	0
43	BH	1363	0	1415	34	0
44	BI	980	0	1008	14	0
45	BJ	1001	0	1034	35	0
46	BK	954	0	1022	18	0
47	BL	538	0	564	17	0
48	BM	910	0	936	15	0
49	BN	1057	0	1104	10	0
50	BO	1025	0	1078	26	0
51	BP	382	0	384	10	0
52	BQ	1206	0	1280	32	0
53	BR	831	0	852	23	0
54	BS	476	0	499	30	0
55	BT	941	0	952	21	0
56	BU	1154	0	1185	29	0
57	BV	394	0	388	19	0
58	BW	736	0	769	29	0
59	BX	474	0	481	8	0
60	BY	389	0	397	11	0
61	BZ	452	0	502	10	0
62	1	236	0	0	0	0
62	2	2	0	0	0	0
62	3	64	0	0	0	0
62	7	1	0	0	0	0
62	AA	2	0	0	0	0
62	AB	2	0	0	0	0
62	AH	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	AI	2	0	0	0	0
62	AN	1	0	0	0	0
62	AZ	1	0	0	0	0
62	BF	1	0	0	0	0
62	BM	1	0	0	0	0
63	AT	1	0	0	0	0
63	AZ	1	0	0	0	0
63	Ab	1	0	0	0	0
63	Ac	1	0	0	0	0
63	Ad	1	0	0	0	0
63	BF	1	0	0	0	0
63	BP	1	0	0	0	0
63	BR	1	0	0	0	0
63	BV	2	0	0	0	0
63	BX	1	0	0	0	0
64	1	6124	0	0	120	0
64	2	109	0	0	4	0
64	3	2579	0	0	75	0
64	7	22	0	0	2	0
64	8	5	0	0	0	0
64	AA	80	0	0	0	0
64	AB	101	0	0	5	0
64	AC	100	0	0	4	0
64	AD	11	0	0	3	0
64	AE	20	0	0	0	0
64	AF	11	0	0	0	0
64	AG	55	0	0	4	0
64	AH	27	0	0	1	0
64	AI	54	0	0	1	0
64	AJ	77	0	0	3	0
64	AK	42	0	0	2	0
64	AL	24	0	0	2	0
64	AM	27	0	0	2	0
64	AN	57	0	0	3	0
64	AO	6	0	0	1	0
64	AP	41	0	0	0	0
64	AQ	31	0	0	3	0
64	AR	30	0	0	4	0
64	AS	28	0	0	1	0
64	AT	16	0	0	0	0
64	AU	13	0	0	0	0
64	AV	36	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	AW	9	0	0	0	0
64	AX	27	0	0	2	0
64	AY	34	0	0	2	0
64	AZ	27	0	0	0	0
64	Aa	23	0	0	5	0
64	Ab	7	0	0	2	0
64	Ac	36	0	0	2	0
64	Ad	24	0	0	2	0
64	BA	22	0	0	5	0
64	BB	8	0	0	2	0
64	BC	14	0	0	3	0
64	BD	36	0	0	13	0
64	BE	56	0	0	10	0
64	BF	38	0	0	5	0
64	BG	14	0	0	2	0
64	BH	22	0	0	6	0
64	BI	42	0	0	2	0
64	BJ	20	0	0	2	0
64	BK	29	0	0	1	0
64	BL	12	0	0	2	0
64	BM	27	0	0	2	0
64	BN	42	0	0	3	0
64	BO	19	0	0	2	0
64	BP	12	0	0	1	0
64	BQ	31	0	0	4	0
64	BR	36	0	0	6	0
64	BS	3	0	0	7	0
64	BT	22	0	0	4	0
64	BU	23	0	0	9	0
64	BV	9	0	0	4	0
64	BW	7	0	0	1	0
64	BX	7	0	0	3	0
64	BY	4	0	0	4	0
64	BZ	8	0	0	1	0
All	All	159419	0	105215	1904	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 1904 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)
43:BH:70:LYS:HD2	64:BH:218:HOH:O	1.31	1.31
1:1:360:G:H1'	64:1:4892:HOH:O	1.28	1.29
1:1:347:A:H4'	64:1:3900:HOH:O	1.33	1.24
3:3:916:C:H3'	64:3:2278:HOH:O	1.36	1.23
1:1:359:A:H3'	64:1:4380:HOH:O	1.46	1.15

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	7	255/280 (91%)	250 (98%)	5 (2%)	0	100	100
6	AA	233/238 (98%)	230 (99%)	2 (1%)	1 (0%)	30	23
7	AB	333/337 (99%)	326 (98%)	7 (2%)	0	100	100
8	AC	250/253 (99%)	245 (98%)	5 (2%)	0	100	100
9	AD	157/165 (95%)	153 (98%)	4 (2%)	0	100	100
10	AE	169/176 (96%)	163 (96%)	6 (4%)	0	100	100
11	AF	104/120 (87%)	101 (97%)	3 (3%)	0	100	100
12	AG	137/143 (96%)	136 (99%)	1 (1%)	0	100	100
13	AH	130/132 (98%)	128 (98%)	2 (2%)	0	100	100
14	AI	137/140 (98%)	134 (98%)	3 (2%)	0	100	100
15	AJ	193/196 (98%)	190 (98%)	3 (2%)	0	100	100
16	AK	157/173 (91%)	153 (98%)	4 (2%)	0	100	100
17	AL	170/174 (98%)	169 (99%)	1 (1%)	0	100	100
18	AM	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
19	AN	145/151 (96%)	143 (99%)	2 (1%)	0	100	100
20	AO	54/61 (88%)	53 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	AP	94/97 (97%)	93 (99%)	1 (1%)	0	100	100
22	AQ	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
23	AR	78/82 (95%)	77 (99%)	1 (1%)	0	100	100
24	AS	113/119 (95%)	112 (99%)	1 (1%)	0	100	100
25	AT	58/62 (94%)	58 (100%)	0	0	100	100
26	AU	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
27	AV	151/153 (99%)	150 (99%)	1 (1%)	0	100	100
28	AW	82/99 (83%)	78 (95%)	4 (5%)	0	100	100
29	AX	82/89 (92%)	82 (100%)	0	0	100	100
30	AY	124/129 (96%)	123 (99%)	1 (1%)	0	100	100
31	AZ	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
32	Aa	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
33	Ab	41/49 (84%)	41 (100%)	0	0	100	100
34	Ac	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
35	Ad	87/94 (93%)	83 (95%)	4 (5%)	0	100	100
36	BA	177/203 (87%)	170 (96%)	7 (4%)	0	100	100
37	BB	186/225 (83%)	182 (98%)	4 (2%)	0	100	100
38	BC	138/318 (43%)	134 (97%)	4 (3%)	0	100	100
39	BD	158/218 (72%)	152 (96%)	6 (4%)	0	100	100
40	BE	226/235 (96%)	217 (96%)	9 (4%)	0	100	100
41	BF	199/209 (95%)	182 (92%)	17 (8%)	0	100	100
42	BG	123/136 (90%)	115 (94%)	7 (6%)	1 (1%)	16	8
43	BH	171/189 (90%)	164 (96%)	7 (4%)	0	100	100
44	BI	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
45	BJ	130/134 (97%)	125 (96%)	5 (4%)	0	100	100
46	BK	122/125 (98%)	117 (96%)	5 (4%)	0	100	100
47	BL	68/102 (67%)	64 (94%)	4 (6%)	0	100	100
48	BM	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
49	BN	137/142 (96%)	132 (96%)	5 (4%)	0	100	100
50	BO	129/162 (80%)	126 (98%)	3 (2%)	0	100	100
51	BP	44/50 (88%)	40 (91%)	4 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	BQ	148/152 (97%)	146 (99%)	2 (1%)	0	100	100
53	BR	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
54	BS	56/64 (88%)	55 (98%)	1 (2%)	0	100	100
55	BT	112/136 (82%)	111 (99%)	1 (1%)	0	100	100
56	BU	146/149 (98%)	144 (99%)	2 (1%)	0	100	100
57	BV	50/56 (89%)	49 (98%)	1 (2%)	0	100	100
58	BW	88/101 (87%)	84 (96%)	4 (4%)	0	100	100
59	BX	59/62 (95%)	55 (93%)	4 (7%)	0	100	100
60	BY	46/76 (60%)	42 (91%)	3 (6%)	1 (2%)	5	1
61	BZ	55/57 (96%)	51 (93%)	4 (7%)	0	100	100
All	All	7176/7921 (91%)	6980 (97%)	193 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	BG	28	ALA
60	BY	46	VAL
6	AA	120	VAL

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	7	228/251 (91%)	222 (97%)	6 (3%)	40	37
6	AA	185/188 (98%)	185 (100%)	0	100	100
7	AB	276/277 (100%)	269 (98%)	7 (2%)	42	38
8	AC	197/198 (100%)	197 (100%)	0	100	100
9	AD	135/140 (96%)	129 (96%)	6 (4%)	25	19
10	AE	143/148 (97%)	138 (96%)	5 (4%)	32	26
11	AF	79/91 (87%)	77 (98%)	2 (2%)	42	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	AG	115/119 (97%)	115 (100%)	0	100	100
13	AH	109/109 (100%)	106 (97%)	3 (3%)	38	34
14	AI	107/108 (99%)	104 (97%)	3 (3%)	38	34
15	AJ	165/166 (99%)	162 (98%)	3 (2%)	51	51
16	AK	134/141 (95%)	133 (99%)	1 (1%)	76	79
17	AL	141/143 (99%)	138 (98%)	3 (2%)	47	45
18	AM	103/104 (99%)	102 (99%)	1 (1%)	68	71
19	AN	119/123 (97%)	118 (99%)	1 (1%)	73	77
20	AO	49/54 (91%)	49 (100%)	0	100	100
21	AP	85/86 (99%)	85 (100%)	0	100	100
22	AQ	122/124 (98%)	122 (100%)	0	100	100
23	AR	71/73 (97%)	70 (99%)	1 (1%)	59	60
24	AS	97/100 (97%)	95 (98%)	2 (2%)	47	45
25	AT	53/54 (98%)	53 (100%)	0	100	100
26	AU	55/57 (96%)	54 (98%)	1 (2%)	51	51
27	AV	134/134 (100%)	132 (98%)	2 (2%)	57	58
28	AW	66/78 (85%)	66 (100%)	0	100	100
29	AX	74/78 (95%)	73 (99%)	1 (1%)	59	60
30	AY	103/106 (97%)	100 (97%)	3 (3%)	37	33
31	AZ	48/49 (98%)	47 (98%)	1 (2%)	47	45
32	Aa	47/48 (98%)	46 (98%)	1 (2%)	47	45
33	Ab	37/40 (92%)	37 (100%)	0	100	100
34	Ac	81/82 (99%)	81 (100%)	0	100	100
35	Ad	73/76 (96%)	73 (100%)	0	100	100
36	BA	158/173 (91%)	150 (95%)	8 (5%)	21	14
37	BB	164/193 (85%)	158 (96%)	6 (4%)	30	24
38	BC	111/250 (44%)	102 (92%)	9 (8%)	11	5
39	BD	138/178 (78%)	133 (96%)	5 (4%)	31	25
40	BE	204/209 (98%)	196 (96%)	8 (4%)	28	23
41	BF	163/170 (96%)	159 (98%)	4 (2%)	42	38
42	BG	96/103 (93%)	86 (90%)	10 (10%)	7	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	BH	147/159 (92%)	138 (94%)	9 (6%)	17	9
44	BI	104/105 (99%)	103 (99%)	1 (1%)	68	71
45	BJ	105/107 (98%)	97 (92%)	8 (8%)	12	6
46	BK	104/105 (99%)	103 (99%)	1 (1%)	68	71
47	BL	61/89 (68%)	56 (92%)	5 (8%)	10	5
48	BM	91/93 (98%)	88 (97%)	3 (3%)	33	28
49	BN	109/112 (97%)	107 (98%)	2 (2%)	51	51
50	BO	107/135 (79%)	101 (94%)	6 (6%)	19	12
51	BP	40/44 (91%)	37 (92%)	3 (8%)	12	6
52	BQ	136/138 (99%)	132 (97%)	4 (3%)	37	33
53	BR	94/96 (98%)	94 (100%)	0	100	100
54	BS	52/57 (91%)	49 (94%)	3 (6%)	18	11
55	BT	103/118 (87%)	102 (99%)	1 (1%)	68	71
56	BU	122/123 (99%)	118 (97%)	4 (3%)	33	28
57	BV	44/48 (92%)	42 (96%)	2 (4%)	24	18
58	BW	81/87 (93%)	76 (94%)	5 (6%)	16	9
59	BX	55/56 (98%)	52 (94%)	3 (6%)	19	12
60	BY	42/62 (68%)	39 (93%)	3 (7%)	13	7
61	BZ	47/47 (100%)	42 (89%)	5 (11%)	6	2
All	All	6109/6602 (92%)	5938 (97%)	171 (3%)	38	34

5 of 171 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	BJ	47	SER
52	BQ	104	VAL
45	BJ	89	GLU
49	BN	89	VAL
56	BU	112	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
39	BD	137	HIS

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Mol	Chain	Res	Type
44	BI	98	ASN
39	BD	141	ASN
41	BF	194	GLN
45	BJ	114	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2704/2904 (93%)	321 (11%)	13 (0%)
2	2	126/133 (94%)	13 (10%)	3 (2%)
3	3	1422/1478 (96%)	222 (15%)	16 (1%)
5	8	16/75 (21%)	3 (18%)	0
All	All	4268/4590 (92%)	559 (13%)	32 (0%)

5 of 559 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 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	3	1080	C
3	3	1148	A
1	1	2671	G
1	1	2447	A
3	3	1294	G

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	$\# Z > 2$
3	MA6	3	1456	3	23,26,27	0.30	0	33,38,41	0.74	1 (3%)
1	5MC	1	2516	1	19,22,23	0.98	1 (5%)	26,32,35	0.61	0
1	5MC	1	2514	62,1	19,22,23	0.82	1 (5%)	26,32,35	0.53	0
48	IAS	BM	116	48	6,7,8	1.38	1 (16%)	3,8,10	0.72	0
3	MA6	3	1457	3	23,26,27	0.28	0	33,38,41	0.73	1 (3%)
1	OMU	1	2567	62,1	19,22,23	0.22	0	25,31,34	0.46	0
3	5MU	3	1222	3	19,22,23	0.26	0	27,32,35	0.39	0
1	OMG	1	2568	1	23,26,27	0.32	0	32,38,41	0.42	0
3	6MZ	3	1438	62,3	22,25,26	0.41	0	29,36,39	0.70	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
3	MA6	3	1456	3	-	0/11/29/30	0/3/3/3
1	5MC	1	2516	1	-	2/7/25/26	0/2/2/2
1	5MC	1	2514	62,1	-	0/7/25/26	0/2/2/2
48	IAS	BM	116	48	-	0/7/7/8	-
3	MA6	3	1457	3	-	3/11/29/30	0/3/3/3
1	OMU	1	2567	62,1	-	0/9/27/28	0/2/2/2
3	5MU	3	1222	3	-	0/7/25/26	0/2/2/2
1	OMG	1	2568	1	-	1/9/27/28	0/3/3/3
3	6MZ	3	1438	62,3	-	0/9/27/28	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2516	5MC	C5-C4	-3.94	1.41	1.44
1	1	2514	5MC	C5-C4	-3.32	1.41	1.44
48	BM	116	IAS	CB-CG	2.31	1.56	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	1456	MA6	C2-N1-C6	2.84	118.77	111.83
3	3	1457	MA6	C2-N1-C6	2.80	118.67	111.83

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	C5-C6-N6-C10
3	3	1457	MA6	C3'-C4'-C5'-O5'
1	1	2516	5MC	O4'-C1'-N1-C6
1	1	2568	OMG	C3'-C2'-O2'-CM2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	3	1456	MA6	1	0
1	1	2516	5MC	3	0
1	1	2514	5MC	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 325 ligands modelled in this entry, 325 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 ⓘ

There are no chain breaks in this entry.

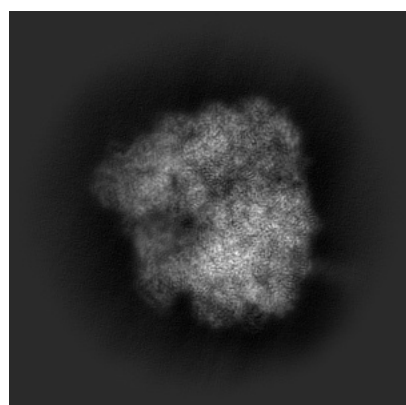
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74447. These allow visual inspection of the internal detail of the map and identification of artifacts.

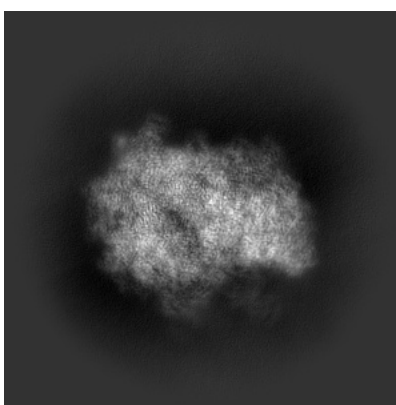
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

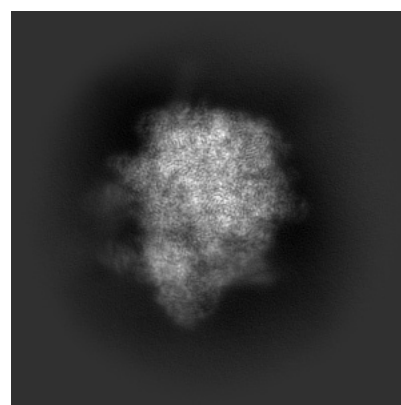
6.1.1 Primary map



X



Y

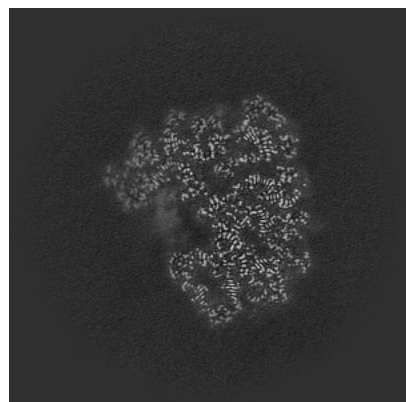


Z

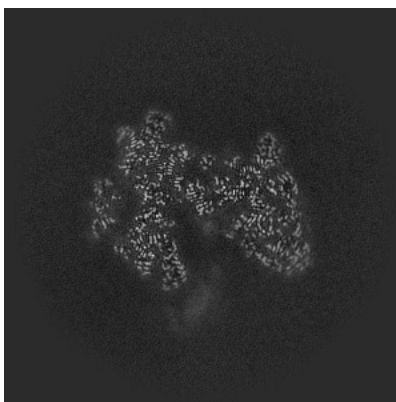
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

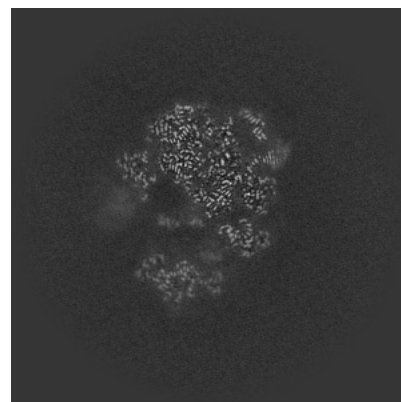
6.2.1 Primary map



X Index: 256



Y Index: 256

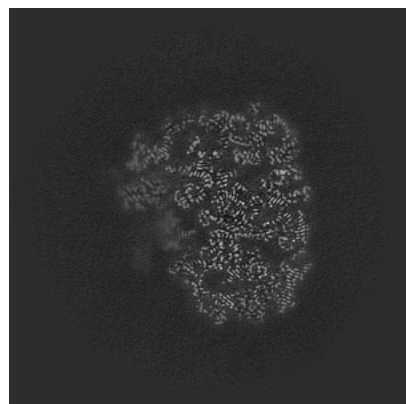


Z Index: 256

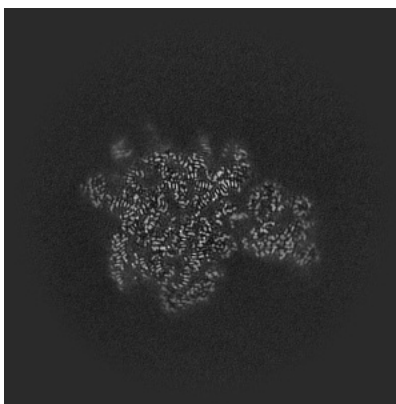
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

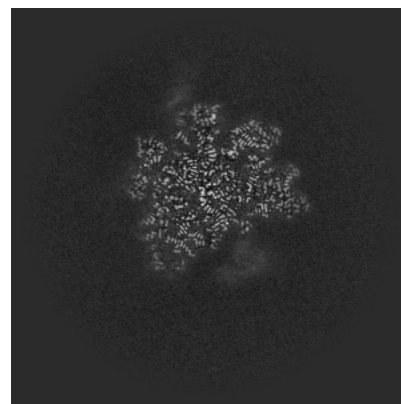
6.3.1 Primary map



X Index: 267



Y Index: 312

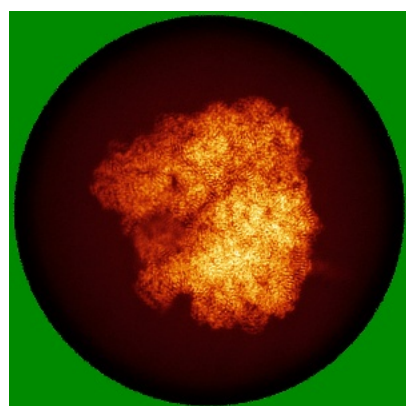


Z Index: 188

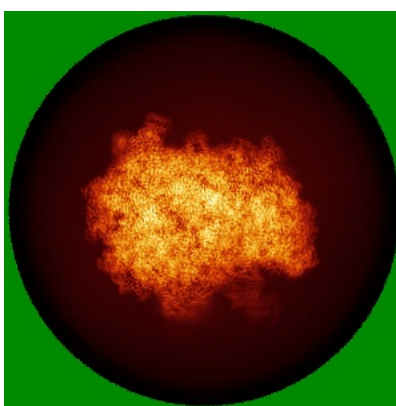
The images above show the largest variance slices of the map in three orthogonal directions.

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

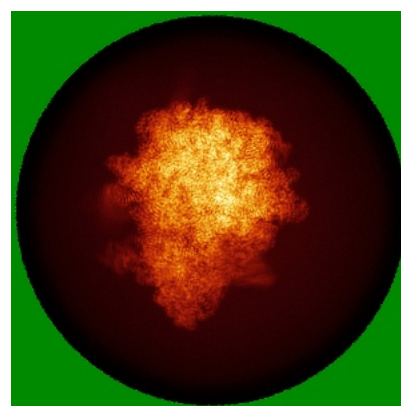
6.4.1 Primary map



X



Y

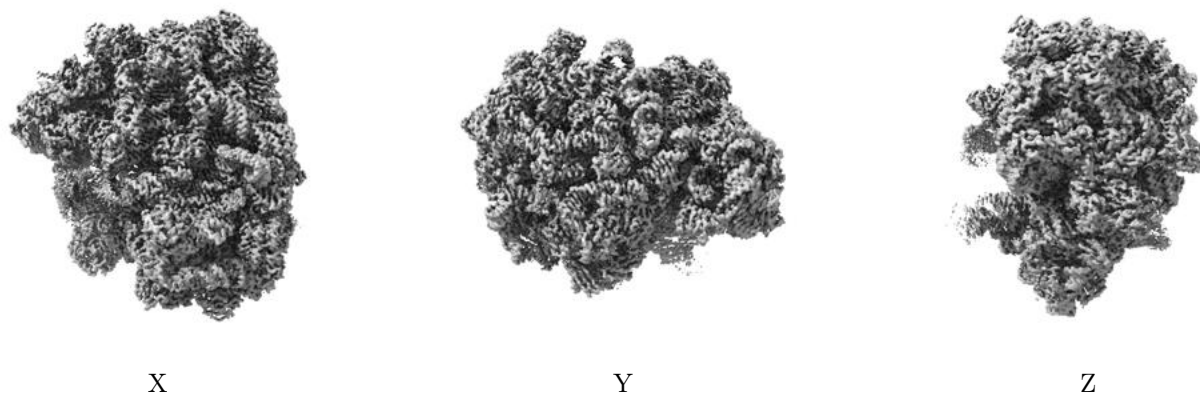


Z

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 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

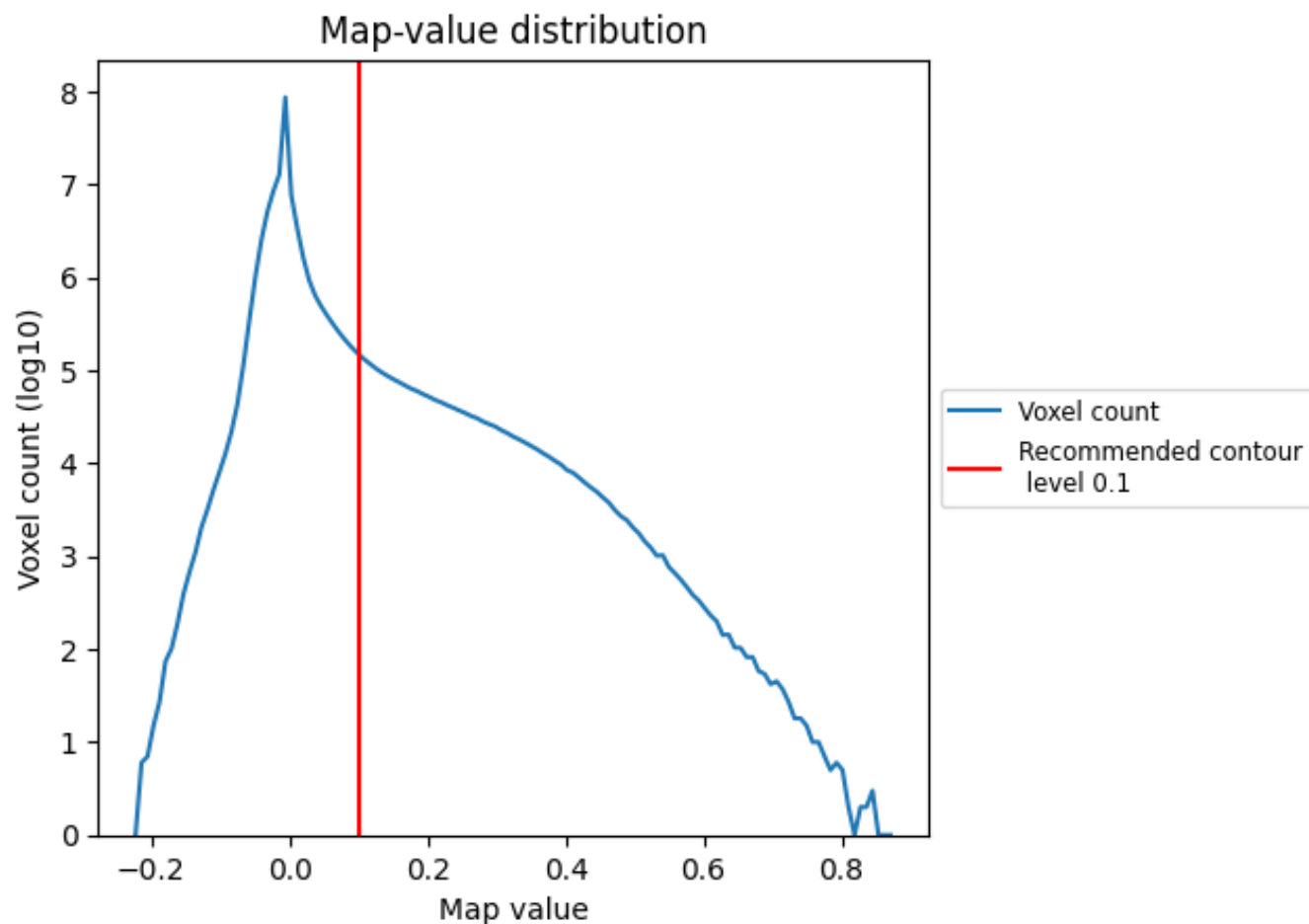
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

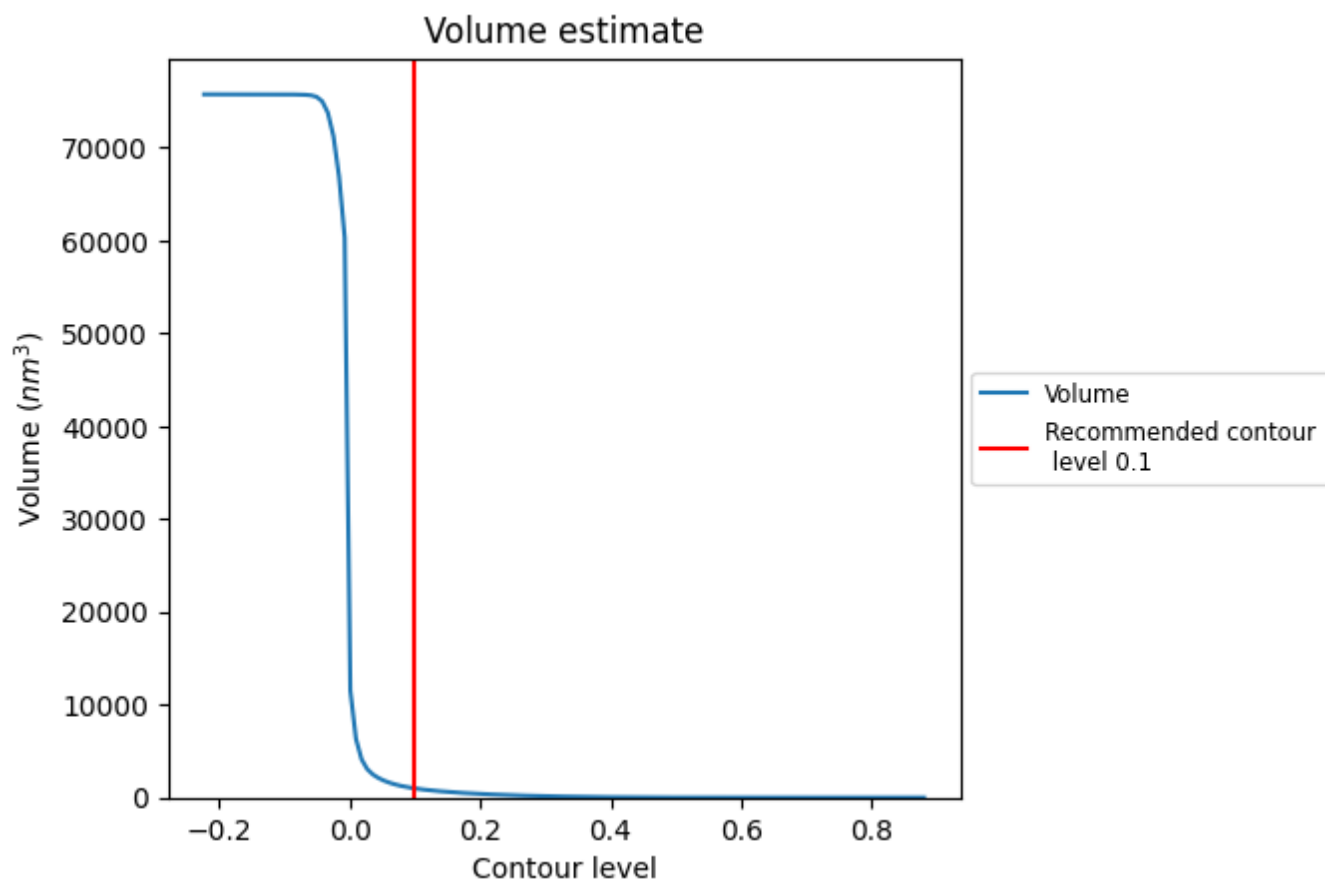
This section contains the results of statistical analysis of the map.

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.

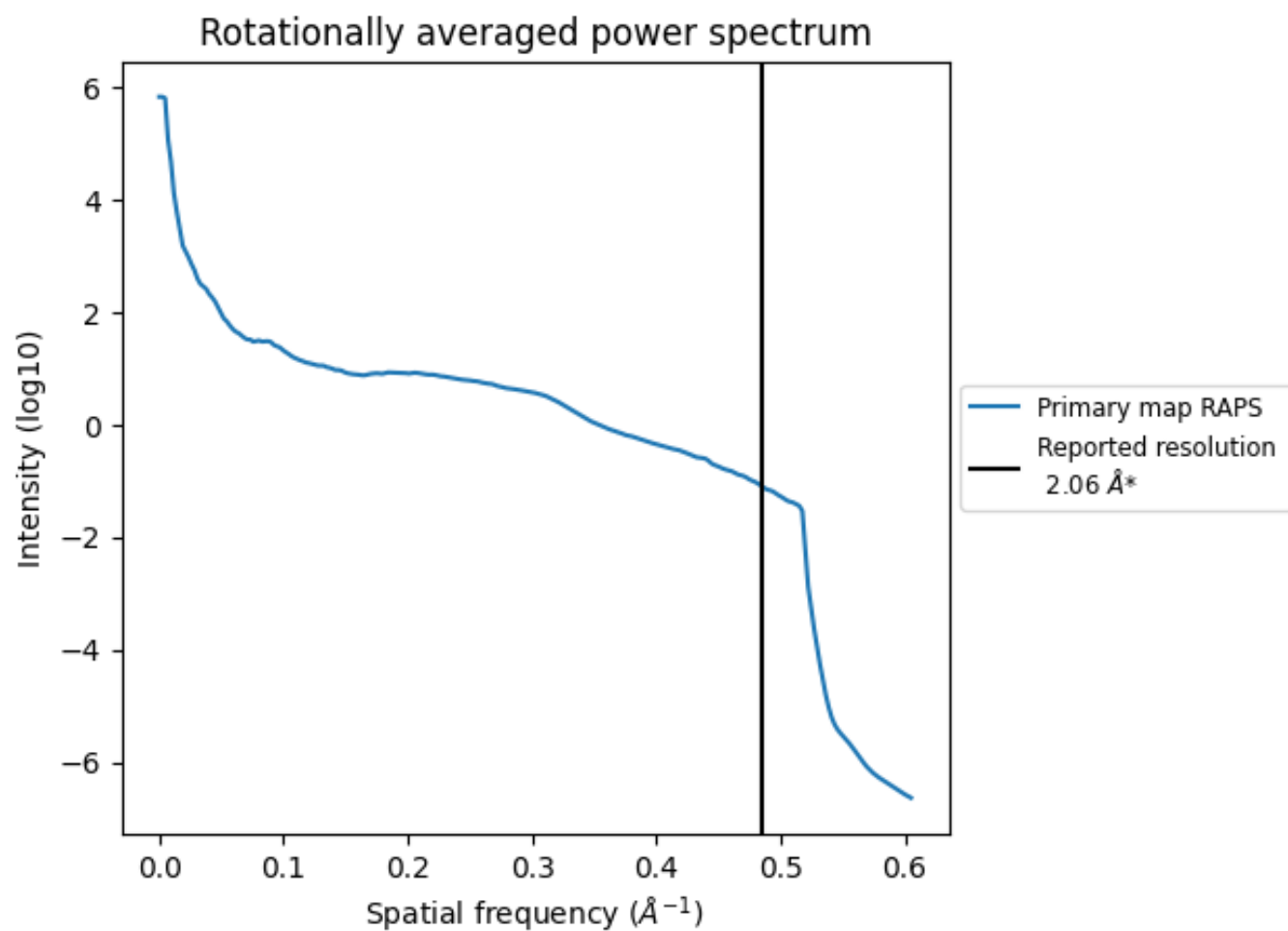
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 989 nm^3 ; this corresponds to an approximate mass of 894 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 0.485 Å⁻¹

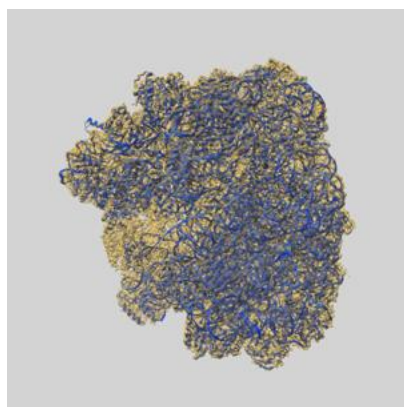
8 Fourier-Shell correlation

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

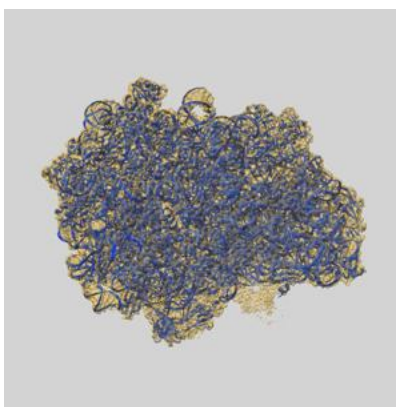
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74447 and PDB model 9ZNG. Per-residue inclusion information can be found in section 3 on page 20.

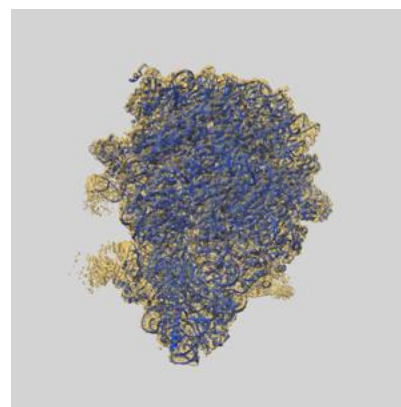
9.1 Map-model overlay [i](#)



X



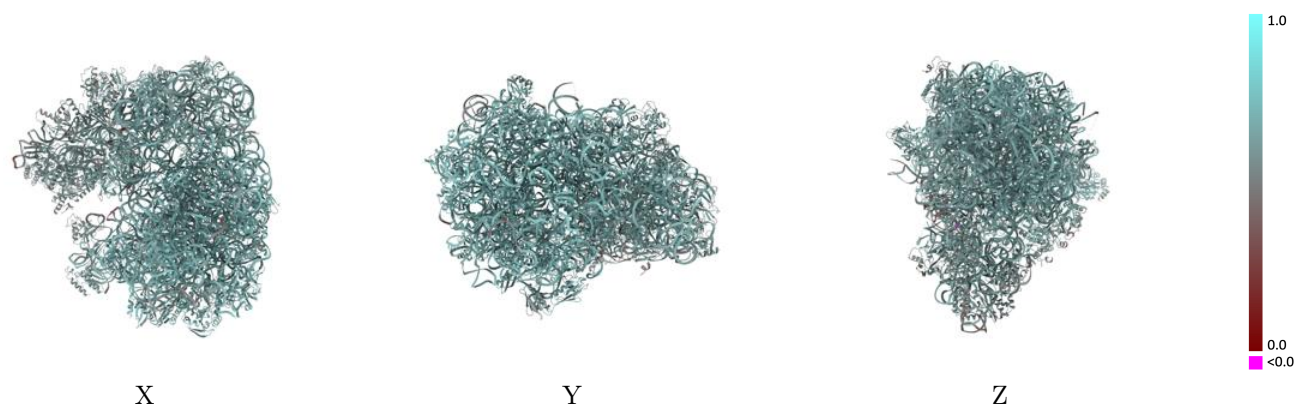
Y



Z

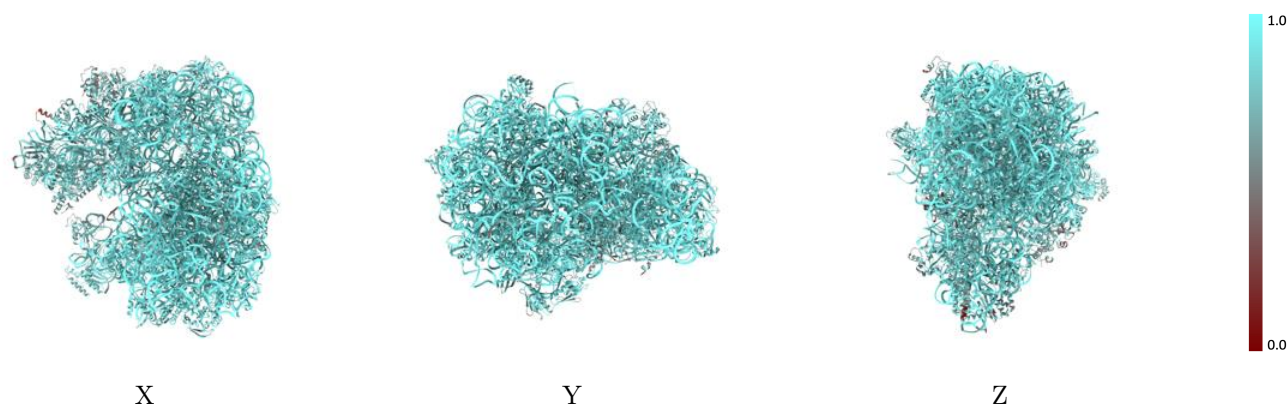
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



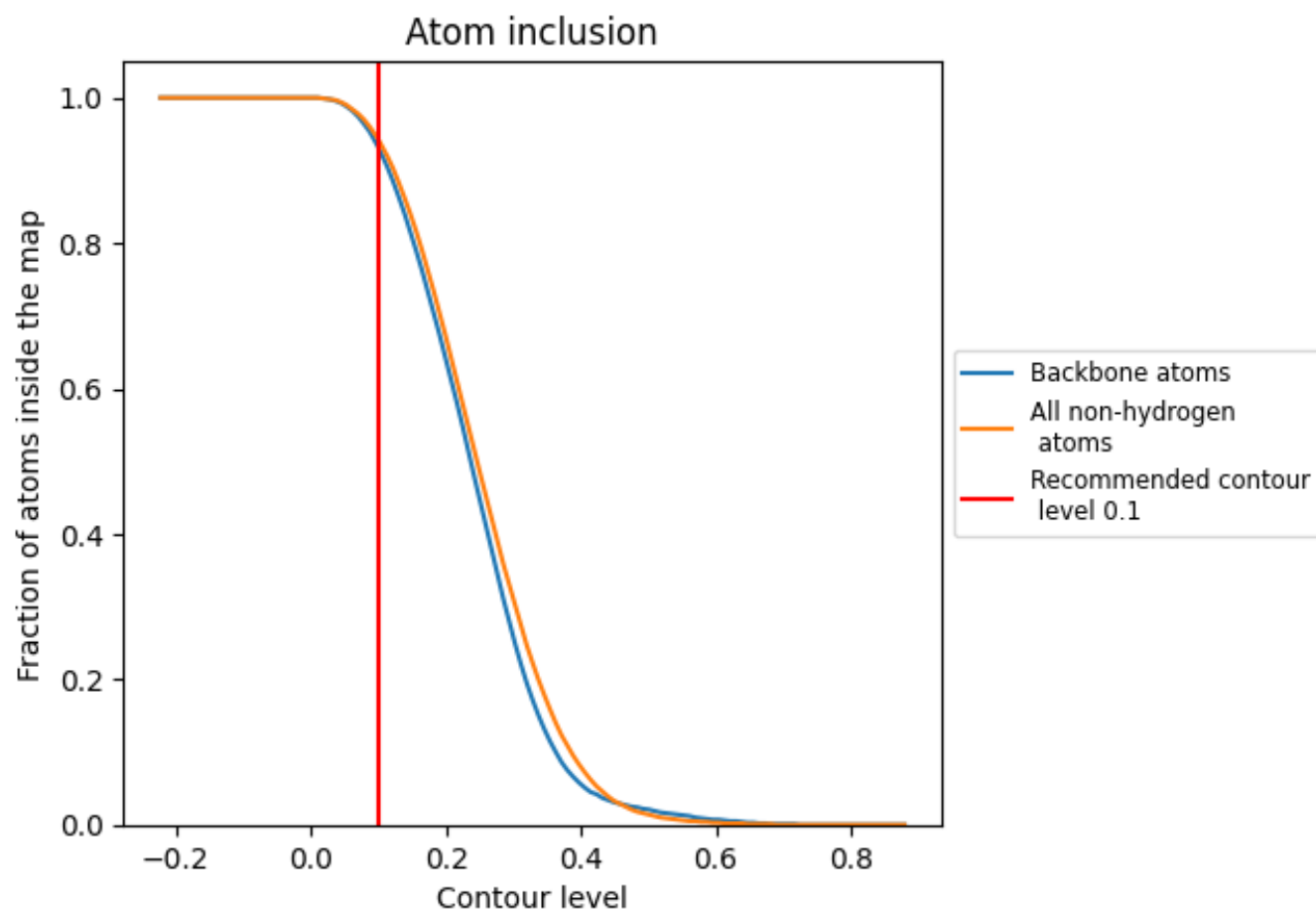
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.9430	 0.6490
1	 0.9870	 0.6760
2	 0.9740	 0.6260
3	 0.9850	 0.6310
7	 0.7080	 0.5340
8	 0.8080	 0.5840
AA	 0.9630	 0.6970
AB	 0.9440	 0.6910
AC	 0.9330	 0.6850
AD	 0.7970	 0.5680
AE	 0.8370	 0.6160
AF	 0.8450	 0.6280
AG	 0.9360	 0.6900
AH	 0.9310	 0.6840
AI	 0.9140	 0.6730
AJ	 0.9800	 0.7060
AK	 0.9350	 0.6780
AL	 0.9150	 0.6420
AM	 0.9270	 0.6740
AN	 0.9300	 0.6720
AO	 0.8560	 0.6530
AP	 0.9670	 0.7000
AQ	 0.9440	 0.6880
AR	 0.9210	 0.6690
AS	 0.9390	 0.6720
AT	 0.9580	 0.6960
AU	 0.8750	 0.6420
AV	 0.9170	 0.6800
AW	 0.8340	 0.5960
AX	 0.9460	 0.6880
AY	 0.9480	 0.6860
AZ	 0.9950	 0.7230
Aa	 0.9850	 0.7010
Ab	 0.8950	 0.6610
Ac	 0.9520	 0.6960



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Chain	Atom inclusion	Q-score
Ad	 0.9500	 0.6870
BA	 0.7990	 0.5850
BB	 0.6710	 0.5570
BC	 0.7590	 0.5540
BD	 0.8970	 0.6000
BE	 0.8960	 0.6090
BF	 0.8790	 0.6130
BG	 0.7860	 0.5570
BH	 0.7910	 0.5580
BI	 0.9530	 0.6440
BJ	 0.8020	 0.5710
BK	 0.9380	 0.6510
BL	 0.7100	 0.5550
BM	 0.9150	 0.6360
BN	 0.9120	 0.6360
BO	 0.7800	 0.5620
BP	 0.8970	 0.6020
BQ	 0.8960	 0.6240
BR	 0.9060	 0.6280
BS	 0.8000	 0.5420
BT	 0.7340	 0.5500
BU	 0.8130	 0.5660
BV	 0.7540	 0.6040
BW	 0.8510	 0.5790
BX	 0.7760	 0.6040
BY	 0.7760	 0.5400
BZ	 0.8970	 0.5970