wwPDB EM Validation Summary Report

Oct 27, 2026 – 03:22 AM JST

PDB ID	:	9XHK / pdb_00009xhk
EMDB ID	:	EMD-66877
Title	:	Cryo-EM structure of the native ARC-bound 70S ribosome from stationary-phase Methanolobus
Authors	:	Zhu, L.; Yi, C.; Li, W.
Deposited on	:	2025-11-01
Resolution	:	2.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

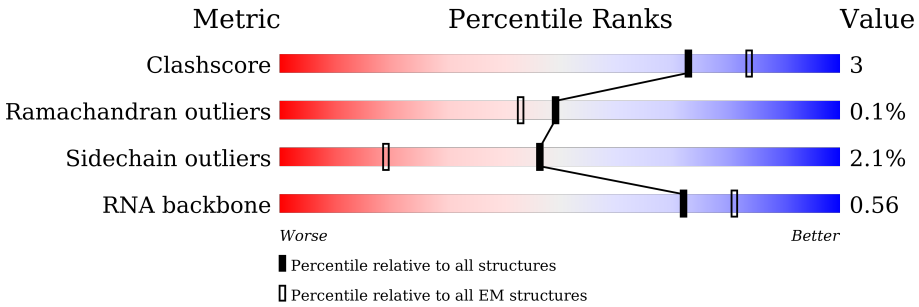
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

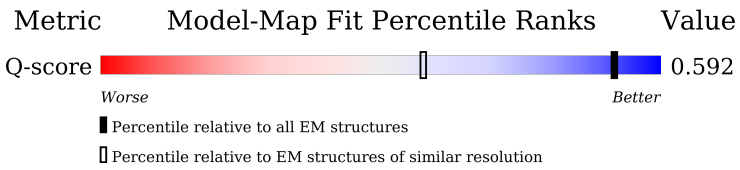
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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.





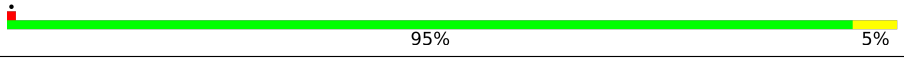
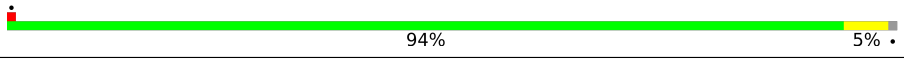
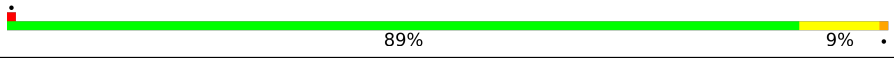
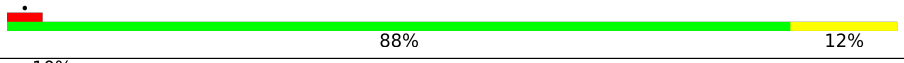
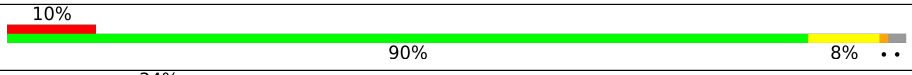
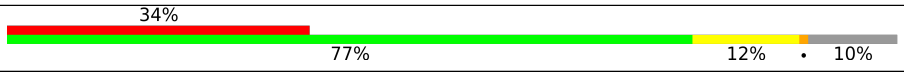
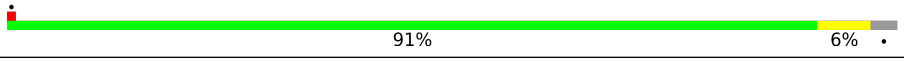
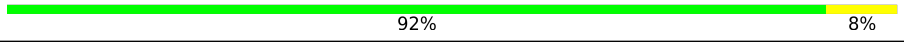
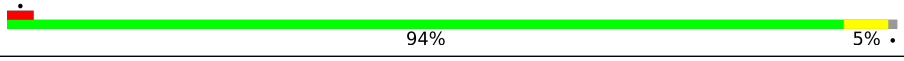
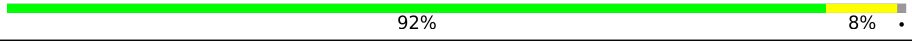
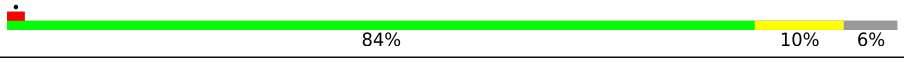
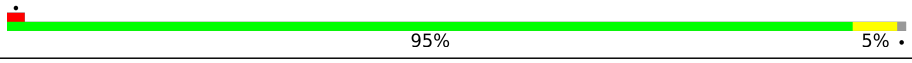
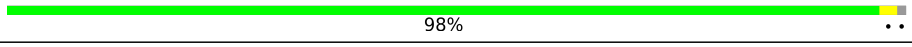
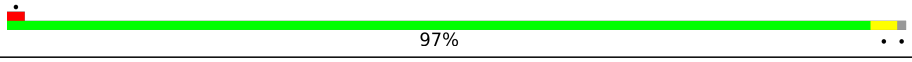
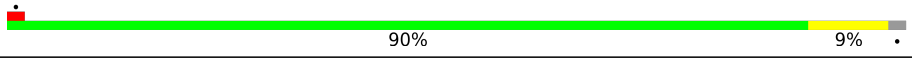
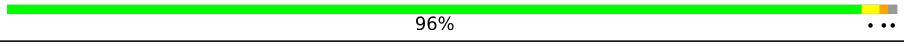
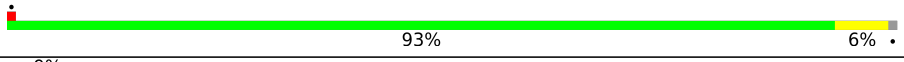
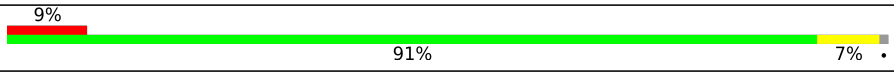
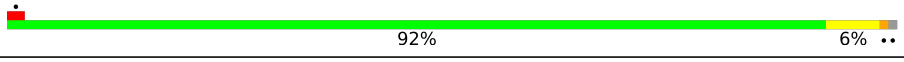
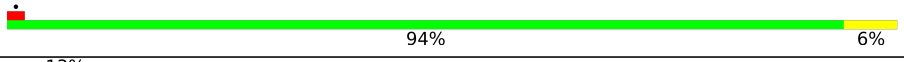
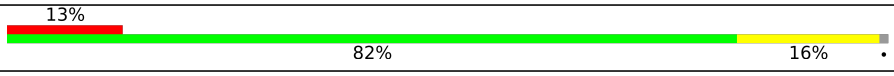
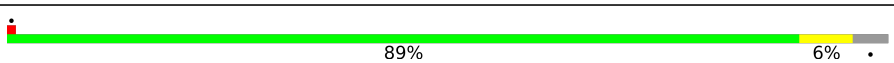
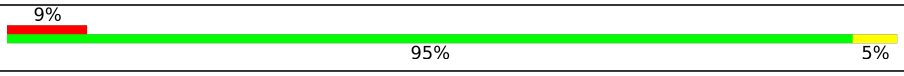
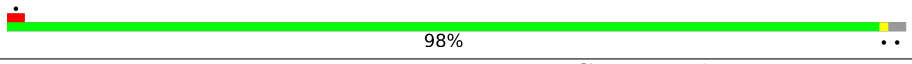
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4254 (1.80 - 2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	2910	7% 76% 20%
2	2	126	73% 25%
3	4	1474	72% 22% 6%

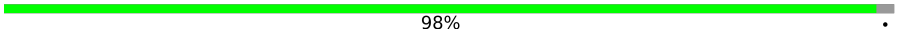
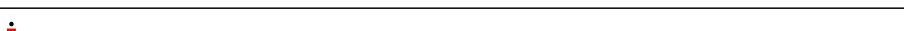
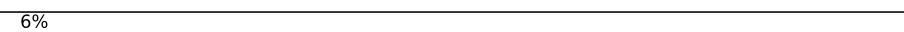
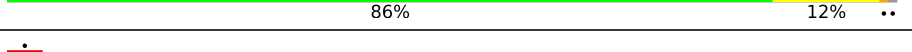
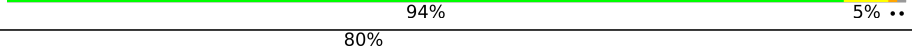
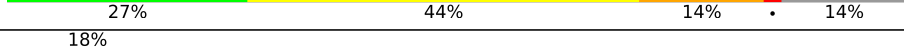
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Mol	Chain	Length	Quality of chain
4	AA	237	
5	AB	337	
6	AC	253	
7	AD	165	
8	AE	177	
9	AF	130	
10	AG	142	
11	AI	132	
12	AL	147	
13	AM	196	
14	AN	172	
15	AO	173	
16	AP	126	
17	AQ	152	
18	AR	58	
19	AS	97	
20	AT	151	
21	AU	82	
22	AV	117	
23	AW	62	
24	AX	67	
25	AY	160	
26	AZ	95	
27	Aa	90	
28	Ab	129	

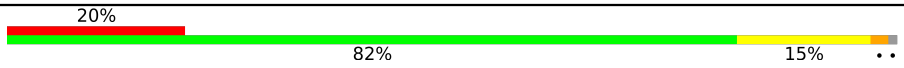
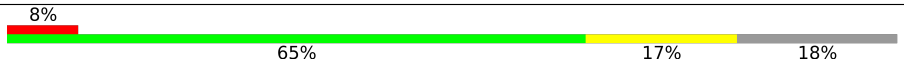
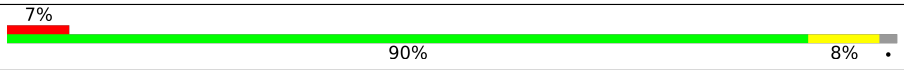
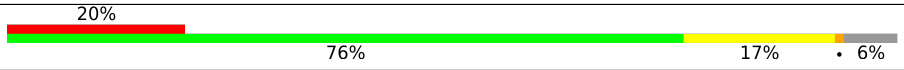
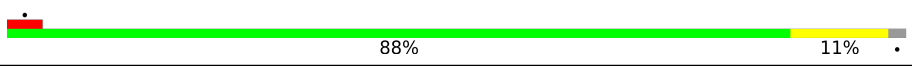
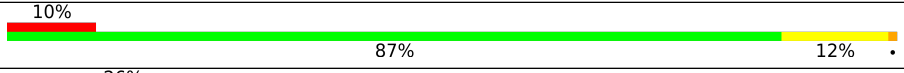
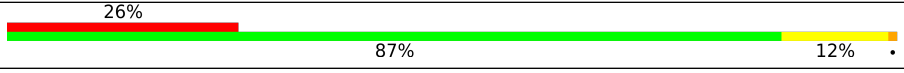
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Mol	Chain	Length	Quality of chain
29	Ad	56	
30	Af	51	
31	Ag	49	
32	Ah	92	
33	Ai	97	
34	BA	196	
35	BB	218	
36	BC	311	
37	BD	186	
38	BE	236	
39	BF	211	
40	BG	139	
41	BH	186	
42	BI	157	
43	BJ	124	
44	BK	134	
45	BL	103	
46	BM	127	
47	BN	142	
48	BO	148	
49	BP	50	
50	BQ	152	
51	BR	109	
52	BS	64	
53	BT	137	

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Mol	Chain	Length	Quality of chain
54	BU	149	
55	BV	114	
56	BY	59	
57	BZ	71	
58	Ba	57	
59	Bc	55	
60	CS	281	
61	LF	258	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
62	ZN	BY	101	-	-	X	-

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 157419 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
			Total	C	N	O	P		
1	1	2910	62358	27842	11402	20204	2910	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	126	2683	1199	479	879	126	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	1474	31571	14081	5738	10278	1474	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AA	236	1783	1114	345	317	7	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AB	335	2570	1620	460	482	8	0	0

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AC	252	1914	1183	365	359	7	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	165	Total	C	N	O	S	0	0
			1305	829	230	241	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	174	Total	C	N	O	S	0	0
			1358	868	228	255	7		

- Molecule 9 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	117	Total	C	N	O	S	0	0
			858	538	143	174	3		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	138	Total	C	N	O	S	0	0
			1088	691	196	195	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AI	132	Total	C	N	O	S	0	0
			1005	623	194	181	7		

- Molecule 12 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	146	Total	C	N	O	S	0	0
			1092	666	207	216	3		

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	195	Total	C	N	O	S	0	0
			1600	985	332	277	6		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	161	Total	C	N	O	S	0	0
			1265	789	251	218	7		

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	172	Total	C	N	O	S	0	0
			1344	844	237	261	2		

- Molecule 16 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	125	Total	C	N	O	S	0	0
			957	604	171	179	3		

- Molecule 17 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	151	Total	C	N	O	S	0	0
			1208	743	248	212	5		

- Molecule 18 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	57	Total	C	N	O	0	0
			454	290	78	86		

- Molecule 19 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	96	Total	C	N	O	S	0	0
			761	472	146	138	5		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	150	Total	C	N	O	S	0	0
			1157	717	222	209	9		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	81	Total	C	N	O	S	0	0
			629	404	103	114	8		

- Molecule 22 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	116	Total	C	N	O	S	0	0
			900	558	171	168	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	62	Total	C	N	O	S	0	0
			504	319	88	92	5		

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	66	Total	C	N	O	S	0	0
			528	318	103	102	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	153	Total	C	N	O	S	0	0
			1199	746	228	219	6		

- Molecule 26 is a protein called Ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	95	Total	C	N	O	S	0	0
			683	429	116	133	5		

- Molecule 27 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	86	Total	C	N	O	S	0	0
			716	460	126	128	2		

- Molecule 28 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	127	Total	C	N	O	S	0	0
			1001	631	196	172	2		

- Molecule 29 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ad	55	Total	C	N	O	S	0	0
			435	264	91	73	7		

- Molecule 30 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Af	50	Total	C	N	O	0	0
			422	261	97	64		

- Molecule 31 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ag	46	Total	C	N	O	S	0	0
			362	218	77	61	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ah	92	Total	C	N	O	S	0	0
			758	472	157	123	6		

- Molecule 33 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ai	94	Total	C	N	O	S	0	0
			737	454	149	128	6		

- Molecule 34 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	188	Total	C	N	O	S	0	0
			1519	960	274	282	3		

- Molecule 35 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BB	195	Total	C	N	O	S	0	0
			1517	968	252	290	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	192	Total	C	N	O	S	0	0
			1471	928	261	270	12		

- Molecule 37 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	177	Total	C	N	O	S	0	0
			1422	893	265	262	2		

- Molecule 38 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	236	Total	C	N	O	S	0	0
			1831	1151	333	342	5		

- Molecule 39 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BF	200	Total	C	N	O	S	0	0
			1512	941	277	287	7		

- Molecule 40 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BG	123	Total	C	N	O	S	0	0
			917	578	160	175	4		

- Molecule 41 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BH	186	Total	C	N	O	S	0	0
			1468	910	281	270	7		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BI	129	Total	C	N	O	S	0	0
			994	638	166	187	3		

- Molecule 43 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BJ	124	Total	C	N	O	S	0	0
			966	586	196	182	2		

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BK	133	Total	C	N	O	S	0	0
			1016	637	185	192	2		

- Molecule 45 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BL	103	Total	C	N	O	S	0	0
			800	499	151	145	5		

- Molecule 46 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BM	123	Total	C	N	O	S	0	0
			899	554	174	167	4		

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BN	141	Total	C	N	O	S	0	0
			1094	675	220	193	6		

- Molecule 48 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BO	142	Total	C	N	O	S	0	0
			1119	688	212	214	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BP	38	Total	C	N	O	S	0	0
			318	199	62	52	5		

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BQ	151	Total	C	N	O	S	0	0
			1224	775	220	223	6		

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BR	108	Total	C	N	O	S	0	0
			851	533	152	161	5		

- Molecule 52 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BS	55	Total	C	N	O	S	0	0
			450	282	87	80	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BT	125	Total	C	N	O	S	0	0
			998	628	184	183	3		

- Molecule 54 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BU	148	Total	C	N	O	S	0	0
			1145	726	200	216	3		

- Molecule 55 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	93	Total	C	N	O	S	0	0
			749	473	131	140	5		

- Molecule 56 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BY	58	Total	C	N	O	S	0	0
			445	275	81	85	4		

- Molecule 57 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	67	Total	C	N	O	S	0	0
			507	309	94	100	4		

- Molecule 58 is a protein called DUF5350 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ba	56	Total	C	N	O	S	0	0
			437	270	93	73	1		

- Molecule 59 is a protein called Putative Zn-ribbon RNA-binding protein with a function in translation.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Bc	51	Total	C	N	O	S	0	0
			378	227	70	72	9		

- Molecule 60 is a protein called CBS-domain-containing membrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CS	281	Total	C	N	O	S	0	0
			2189	1369	385	419	16		

- Molecule 61 is a protein called CBS-domain-containing membrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LF	258	Total	C	N	O	S	0	0
			1968	1230	352	372	14		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
62	AW	1	Total	Zn	0
			1	1	
62	Ad	1	Total	Zn	0
			1	1	

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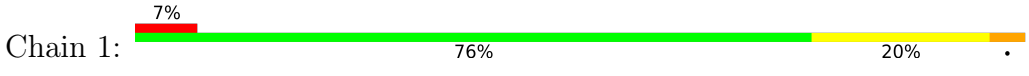
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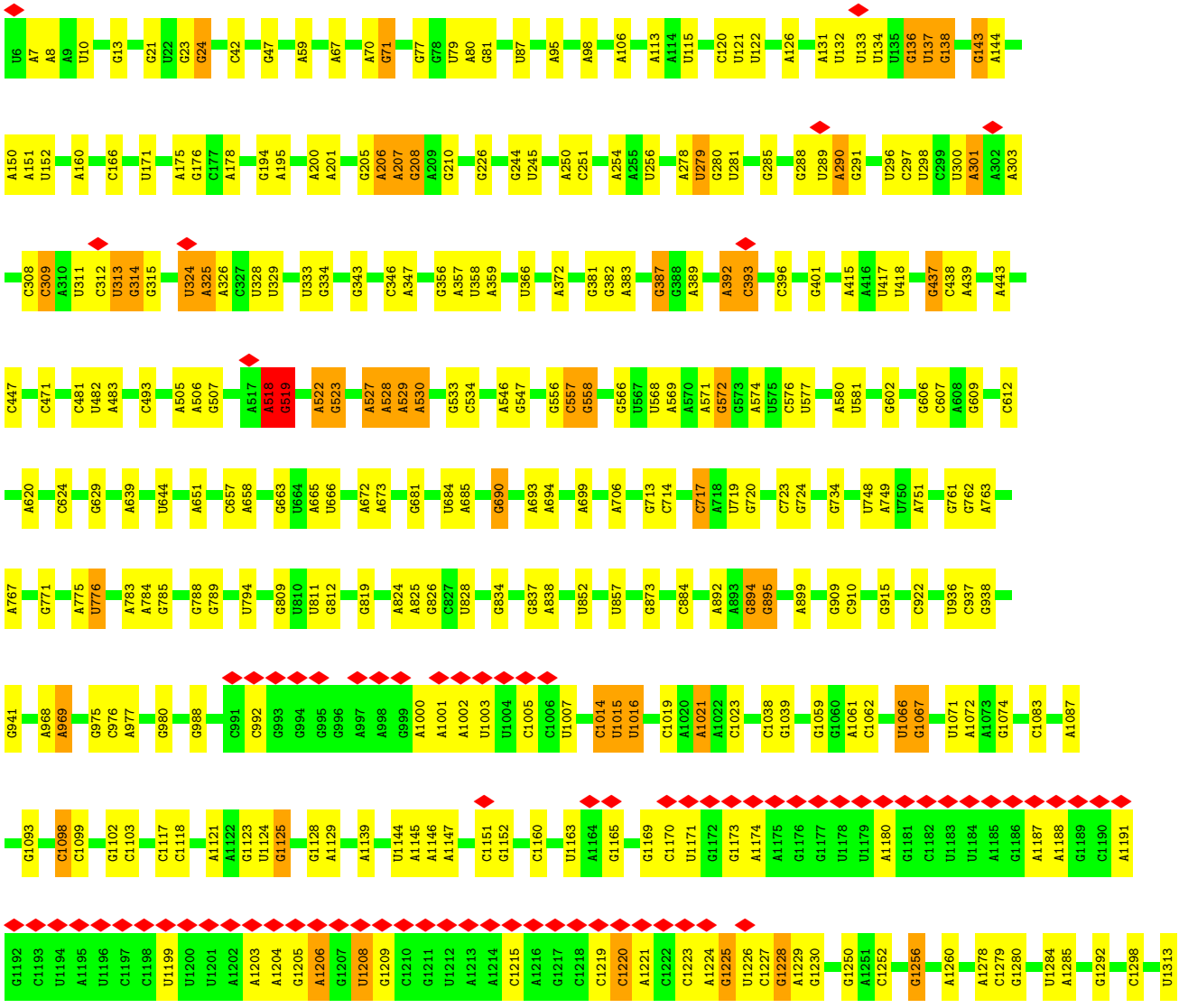
3 Residue-property plots (i)

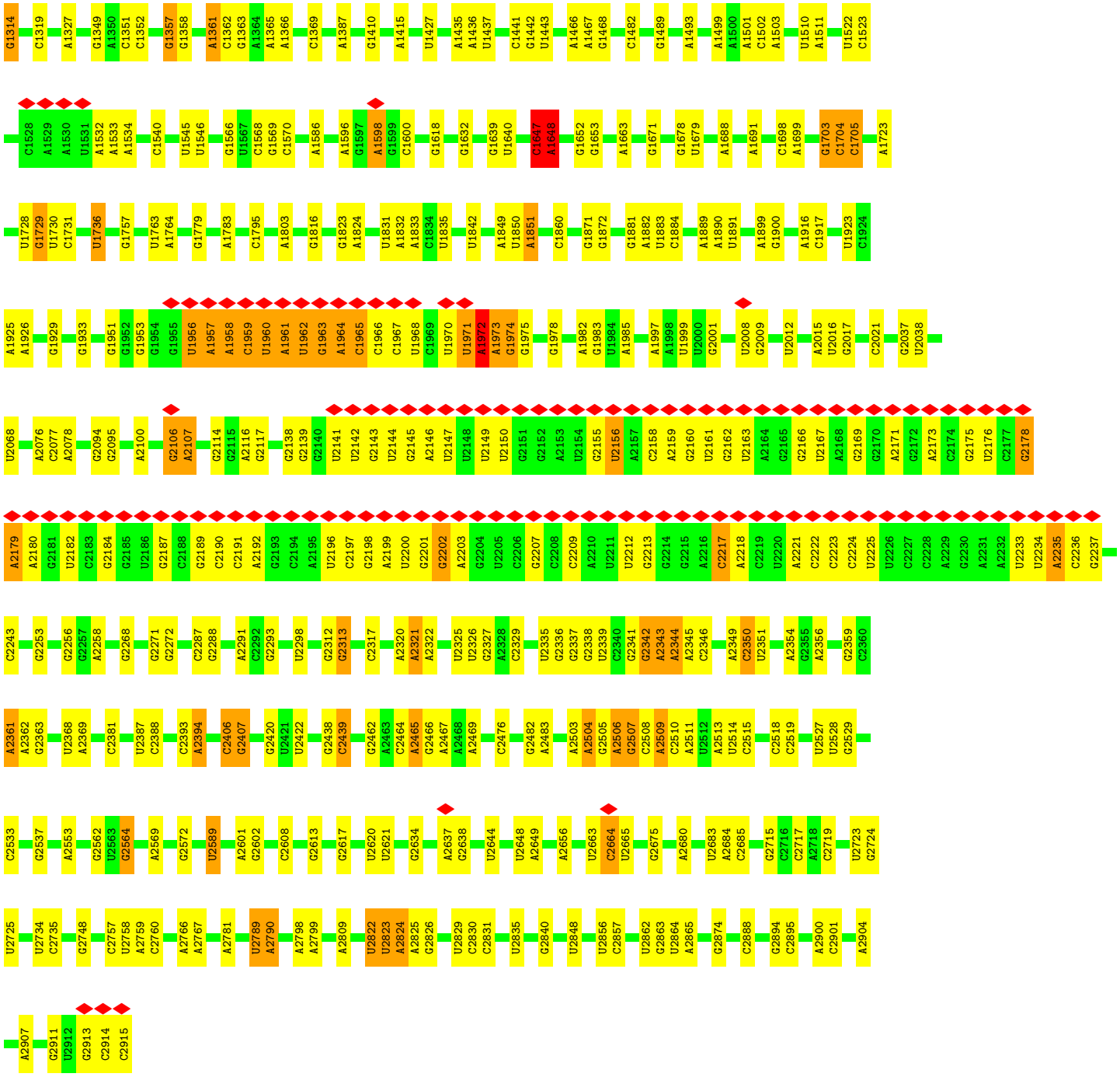
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 23S rRNA

Chain 1:



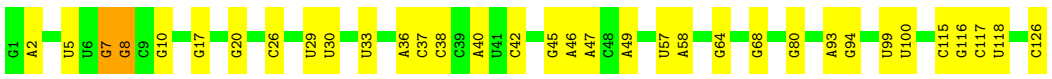




• Molecule 2: 5S rRNA

Chain 2:

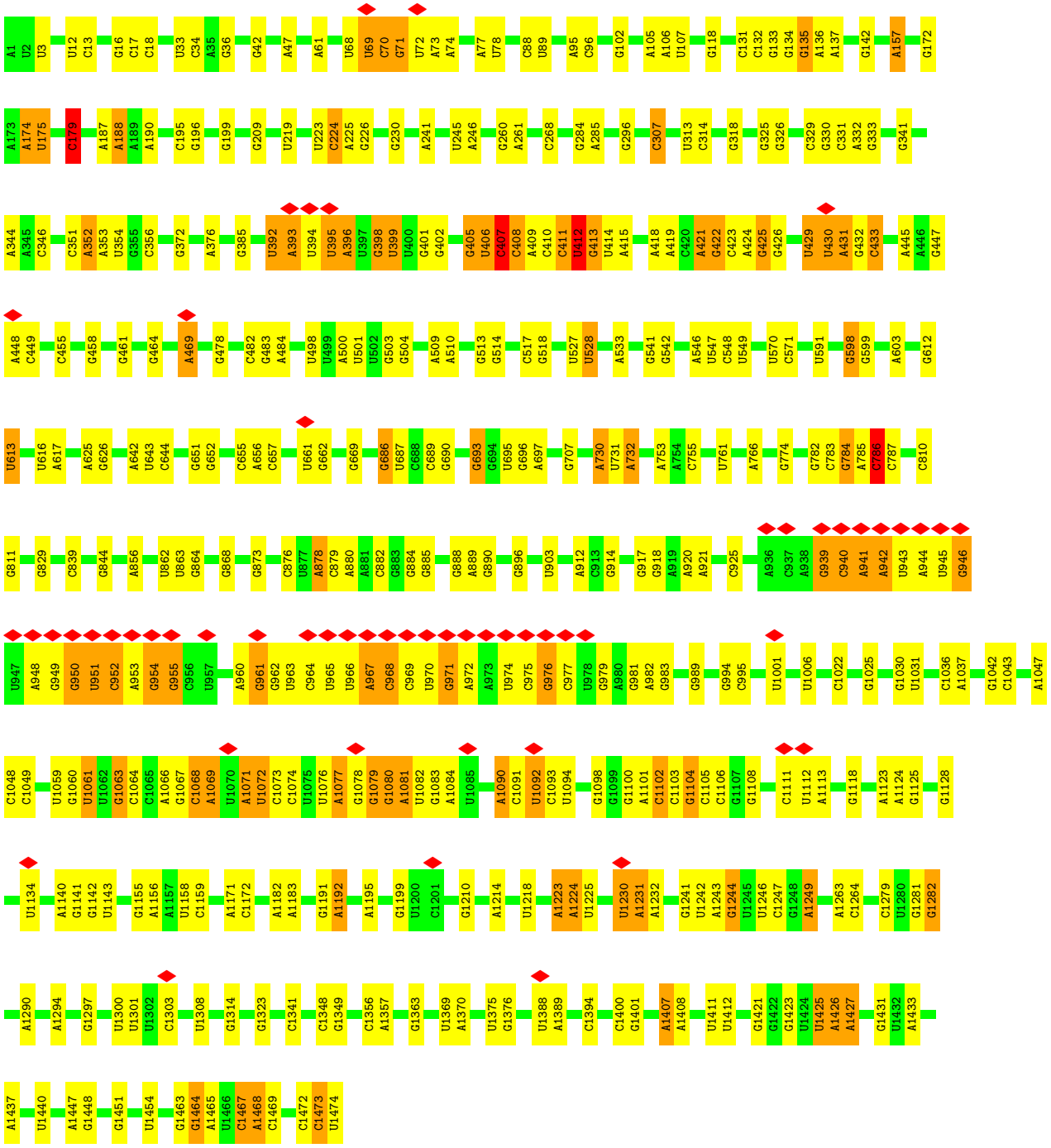




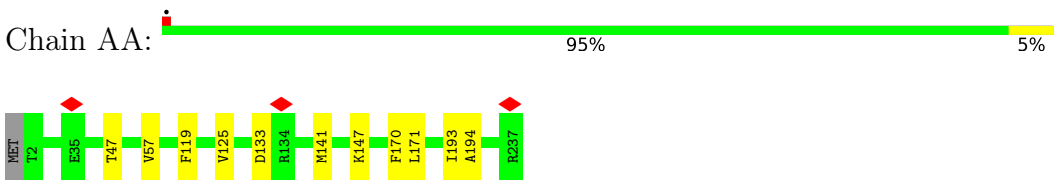
• Molecule 3: 16S rRNA

Chain 4:



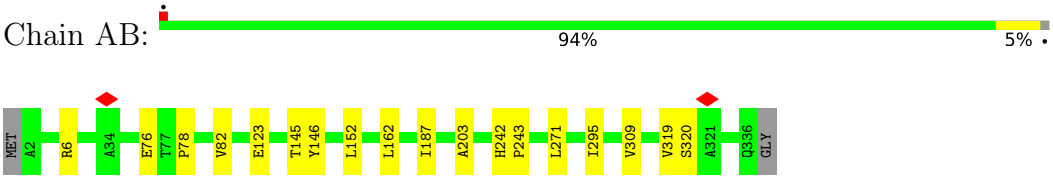


• Molecule 4: Large ribosomal subunit protein uL2



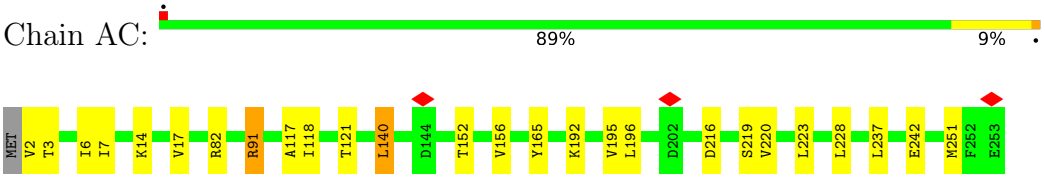
• Molecule 5: Large ribosomal subunit protein uL3

Chain AB:



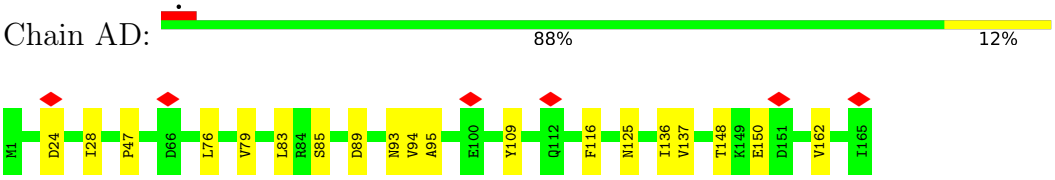
• Molecule 6: 50S ribosomal protein L4

Chain AC:



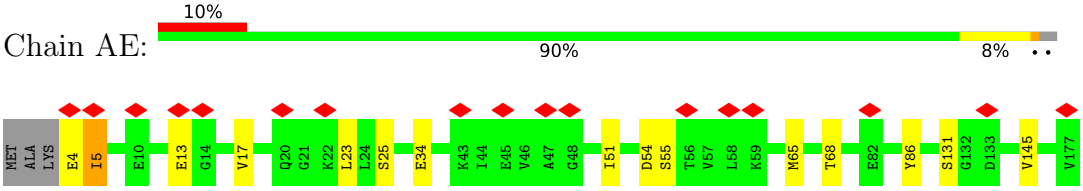
• Molecule 7: Large ribosomal subunit protein uL5

Chain AD:



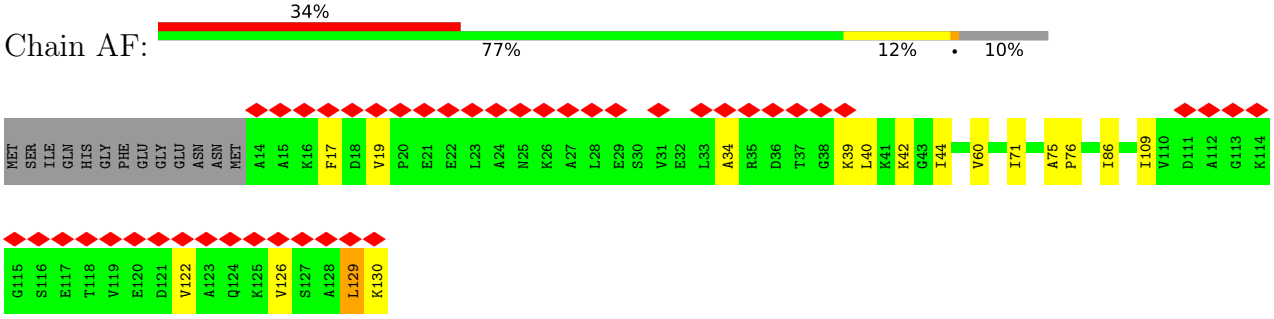
• Molecule 8: Large ribosomal subunit protein uL6

Chain AE:



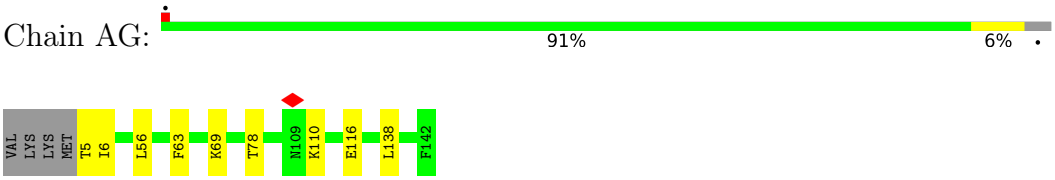
• Molecule 9: 50S ribosomal protein L7Ae

Chain AF:



• Molecule 10: 50S ribosomal protein L13

Chain AG:



• Molecule 11: Large ribosomal subunit protein uL14

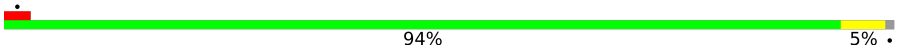
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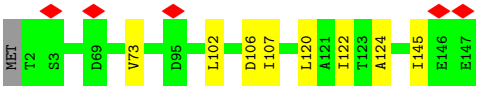




• Molecule 12: Large ribosomal subunit protein uL15

Chain AL:

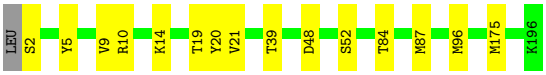




• Molecule 13: 50S ribosomal protein L15e

Chain AM:





• Molecule 14: Large ribosomal subunit protein uL16

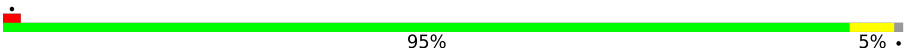
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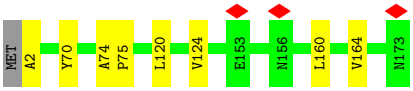




• Molecule 15: Large ribosomal subunit protein uL18

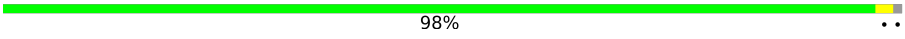
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• Molecule 16: Large ribosomal subunit protein eL18

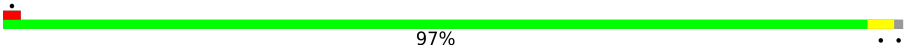
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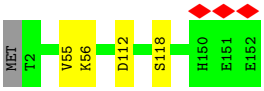




• Molecule 17: Large ribosomal subunit protein eL19

Chain AQ:

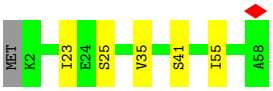




• Molecule 18: Large ribosomal subunit protein eL20

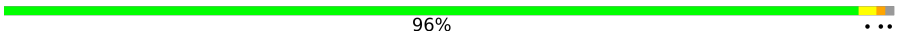
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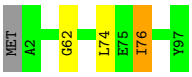




• Molecule 19: Large ribosomal subunit protein eL21

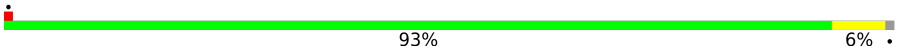
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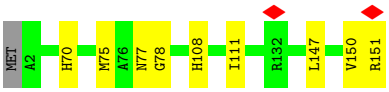




• Molecule 20: 50S ribosomal protein L22

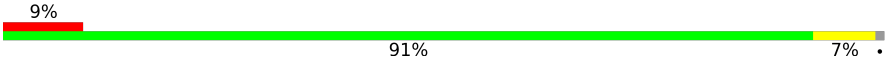
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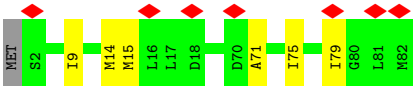




• Molecule 21: 50S ribosomal protein L23

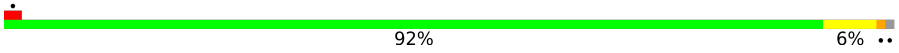
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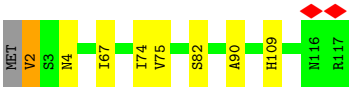




• Molecule 22: Large ribosomal subunit protein uL24

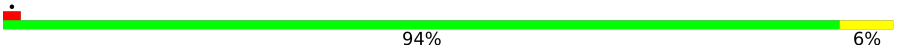
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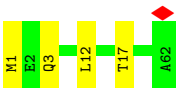




• Molecule 23: Large ribosomal subunit protein eL24

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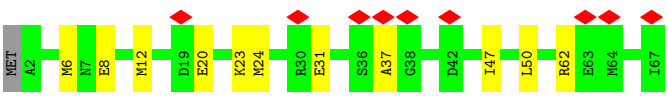




• Molecule 24: Large ribosomal subunit protein uL29

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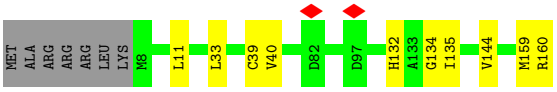




• Molecule 25: 50S ribosomal protein L30

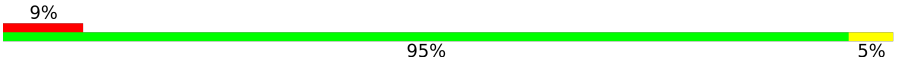
Chain AY:

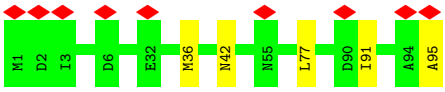




• Molecule 26: Ribosomal protein L30E

Chain AZ:

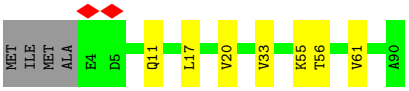




• Molecule 27: 50S ribosomal protein L31e

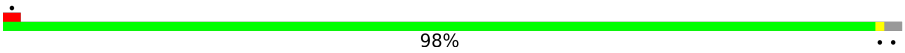
Chain Aa:

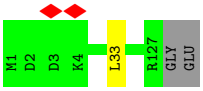




• Molecule 28: 50S ribosomal protein L32e

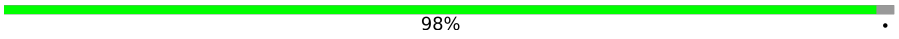
Chain Ab:





• Molecule 29: Large ribosomal subunit protein eL37

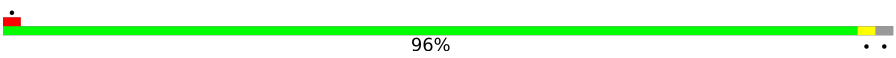
Chain Ad:

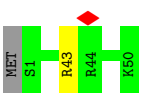




• Molecule 30: Large ribosomal subunit protein eL39

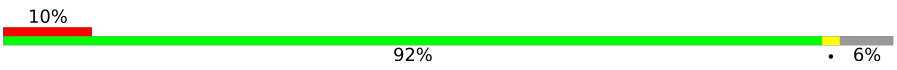
Chain Af:

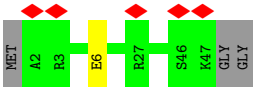




• Molecule 31: Large ribosomal subunit protein eL40

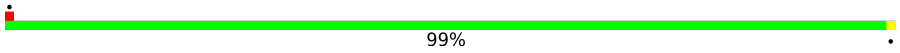
Chain Ag:

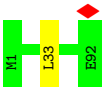




• Molecule 32: Large ribosomal subunit protein eL42

Chain Ah:

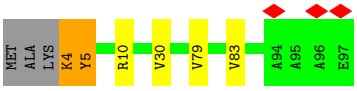




• Molecule 33: Large ribosomal subunit protein eL43

Chain Ai:

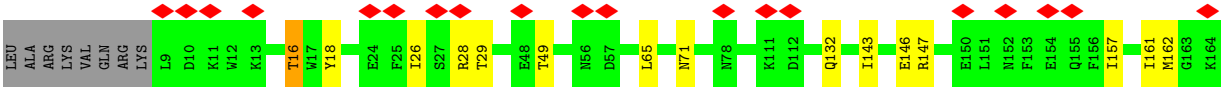


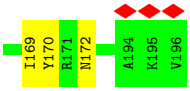


• Molecule 34: 30S ribosomal protein S3Ae

Chain BA:



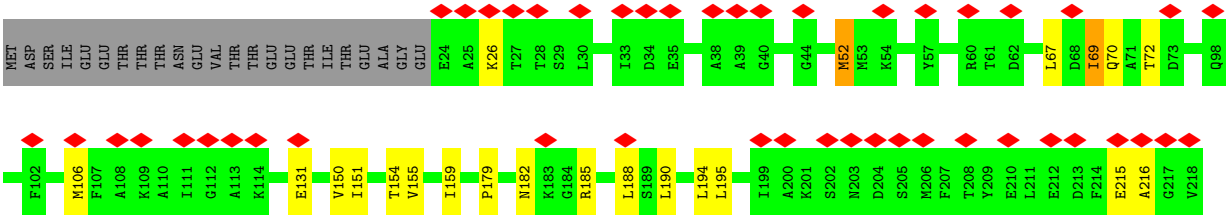




• Molecule 35: Small ribosomal subunit protein uS2

Chain BB:

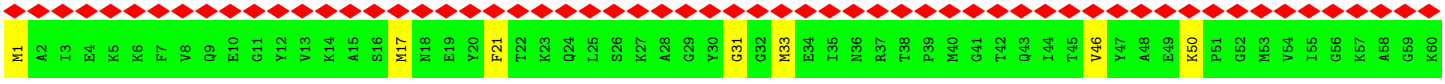


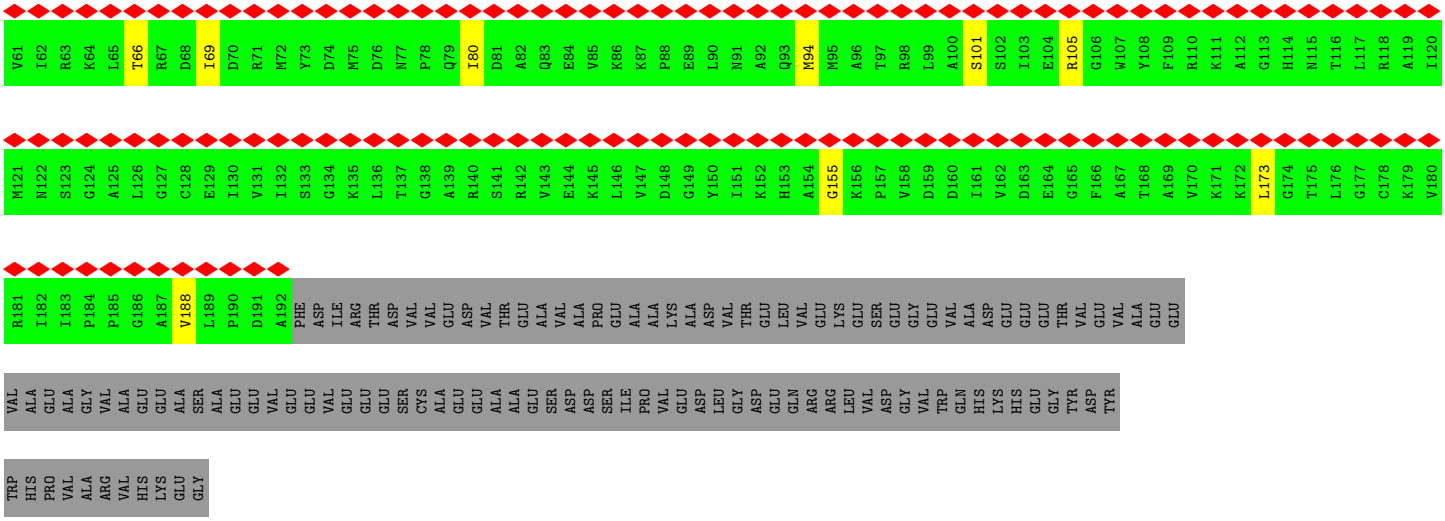


• Molecule 36: 30S ribosomal protein S3

Chain BC:



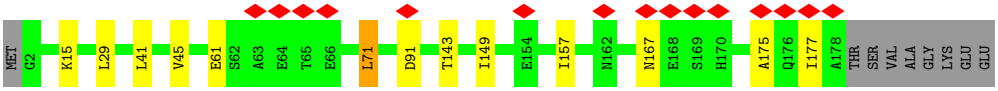




• Molecule 37: Small ribosomal subunit protein uS4

Chain BD:

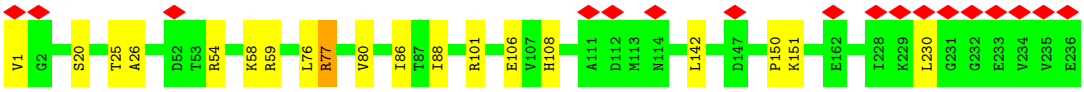




• Molecule 38: 30S ribosomal protein S4e

Chain BE:

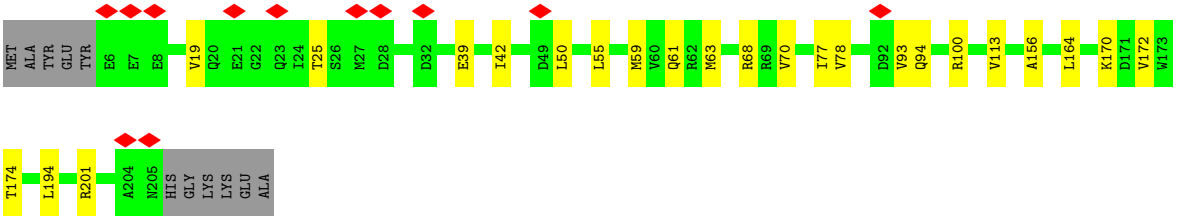




• Molecule 39: Small ribosomal subunit protein uS5

Chain BF:

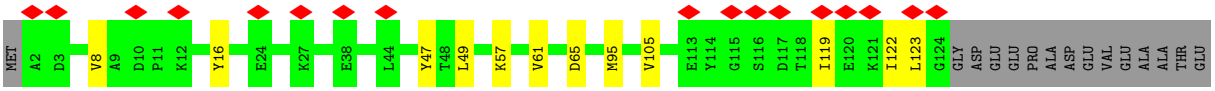




• Molecule 40: 30S ribosomal protein S6e

Chain BG:



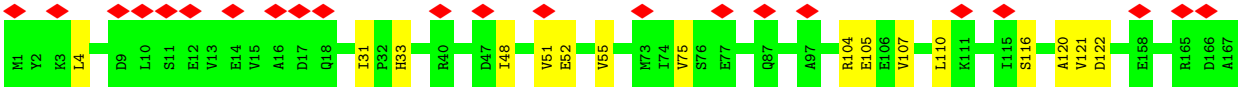




• Molecule 41: Small ribosomal subunit protein uS7

Chain BH:

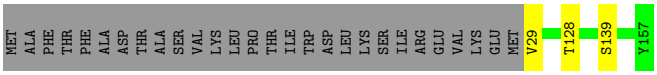




• Molecule 42: 30S ribosomal protein S8

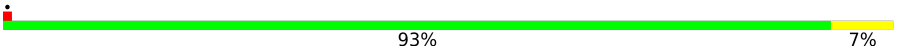
Chain BI:

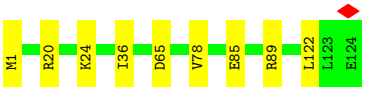




• Molecule 43: Small ribosomal subunit protein eS8

Chain BJ:

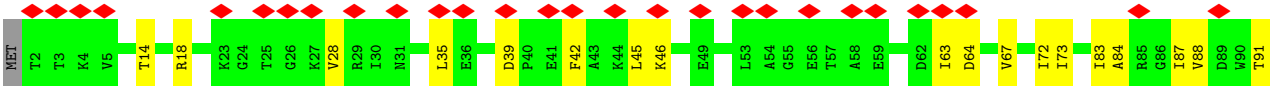




• Molecule 44: Small ribosomal subunit protein uS9

Chain BK:

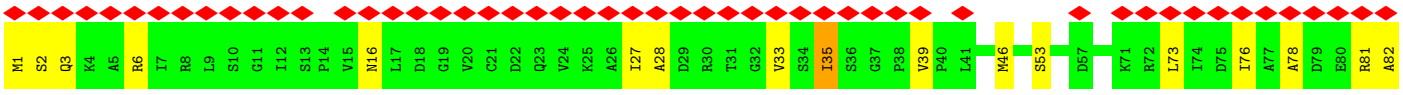




• Molecule 45: Small ribosomal subunit protein uS10

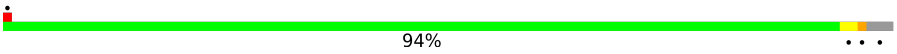
Chain BL:

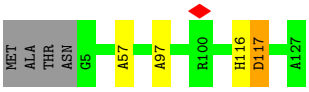




• Molecule 46: Small ribosomal subunit protein uS11

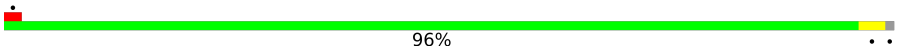
Chain BM:





• Molecule 47: Small ribosomal subunit protein uS12

Chain BN:

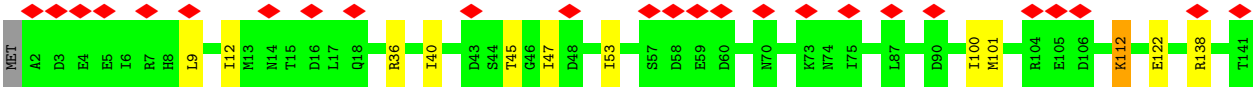


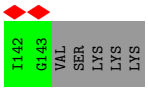


• Molecule 48: Small ribosomal subunit protein uS13

Chain BO:



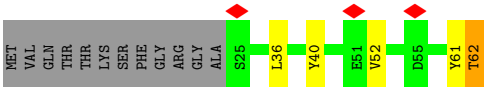




• Molecule 49: Small ribosomal subunit protein uS14

Chain BP:





• Molecule 50: Small ribosomal subunit protein uS15

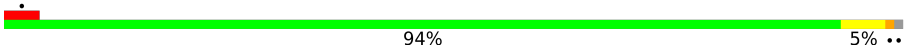
Chain BQ:

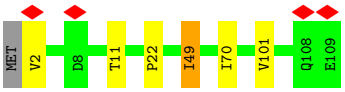




• Molecule 51: Small ribosomal subunit protein uS17

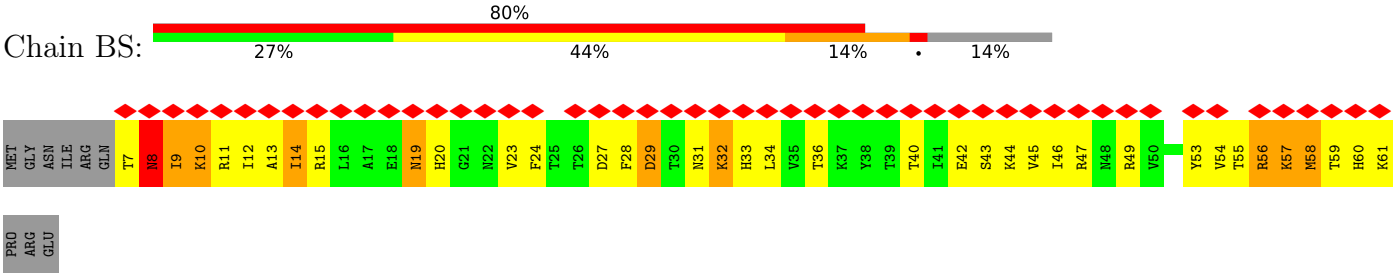
Chain BR:





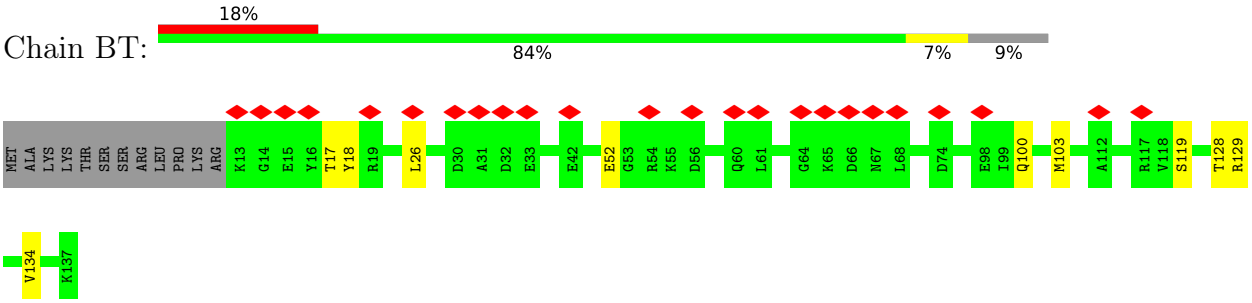
• Molecule 52: Small ribosomal subunit protein eS17

Chain BS:



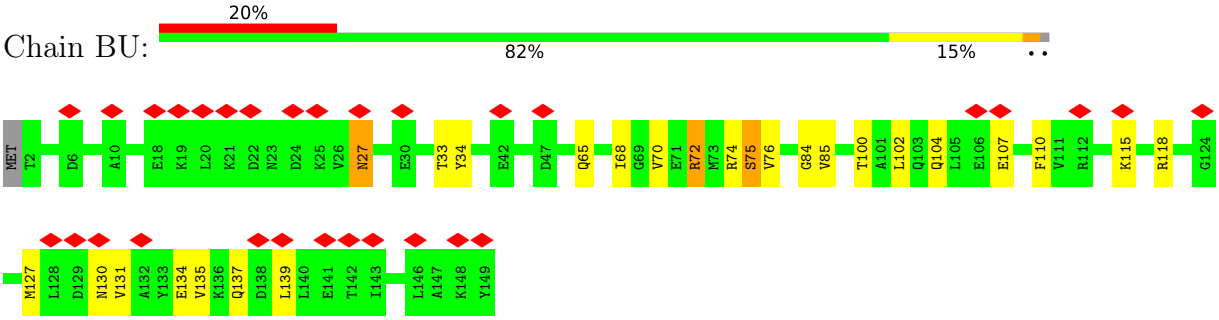
• Molecule 53: Small ribosomal subunit protein uS19

Chain BT:



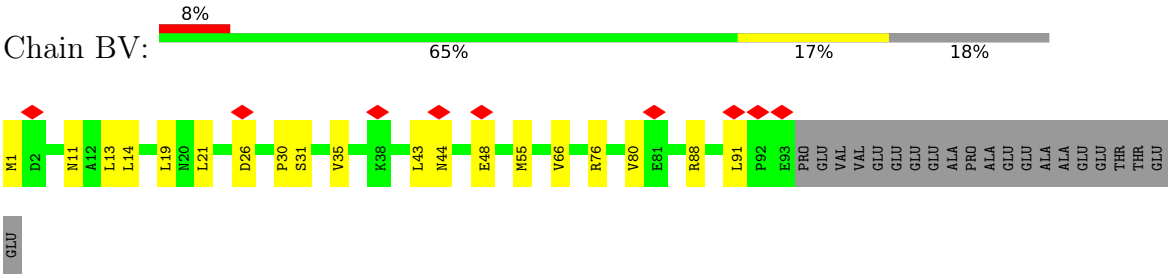
• Molecule 54: 30S ribosomal protein S19e

Chain BU:



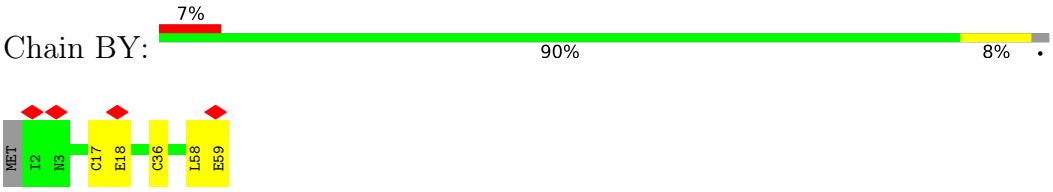
• Molecule 55: Small ribosomal subunit protein eS24

Chain BV:



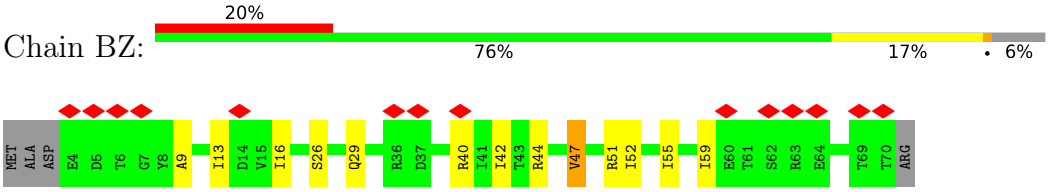
• Molecule 56: Small ribosomal subunit protein eS27

Chain BY:



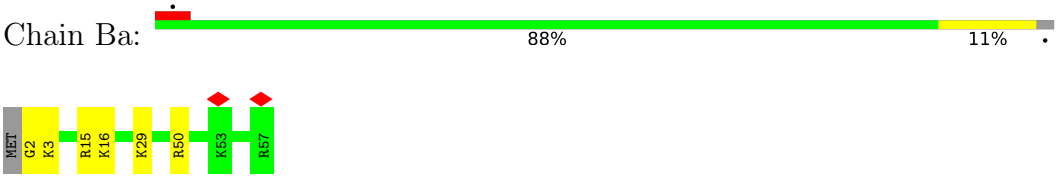
• Molecule 57: Small ribosomal subunit protein eS28

Chain BZ:



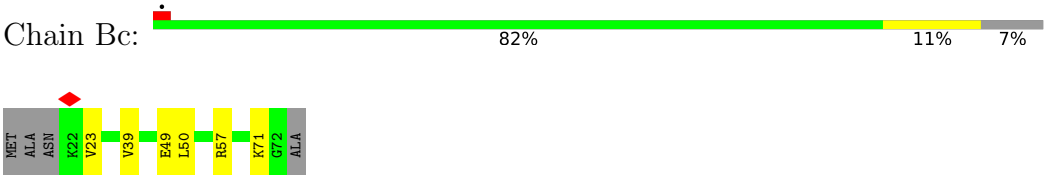
• Molecule 58: DUF5350 domain-containing protein

Chain Ba:



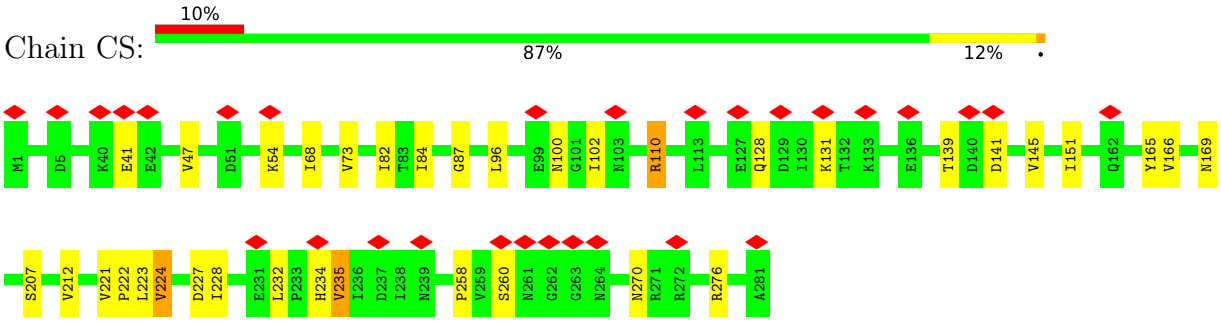
• Molecule 59: Putative Zn-ribbon RNA-binding protein with a function in translation

Chain Bc:



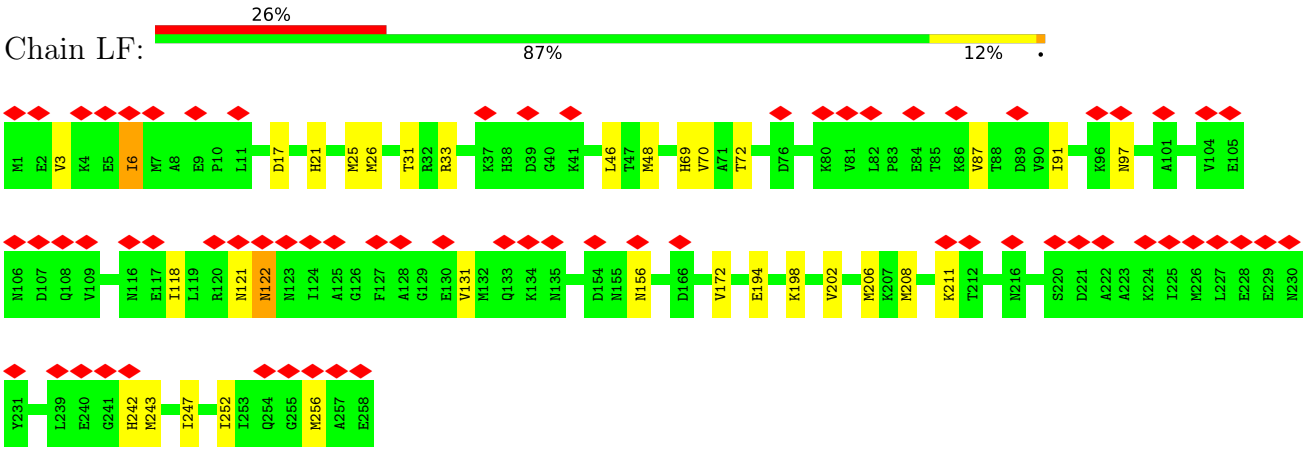
• Molecule 60: CBS-domain-containing membrane protein

Chain CS:



• Molecule 61: CBS-domain-containing membrane protein

Chain LF:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	204924	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.545	Depositor
Minimum map value	-0.582	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	446.4, 446.4, 446.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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

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	0/69829	0.67	10/108904 (0.0%)
2	2	0.25	0/2999	0.67	0/4671
3	4	0.28	0/35333	0.69	6/55109 (0.0%)
4	AA	0.13	0/1821	0.35	0/2454
5	AB	0.14	0/2620	0.32	0/3541
6	AC	0.14	0/1943	0.34	0/2620
7	AD	0.15	0/1328	0.37	0/1784
8	AE	0.12	0/1378	0.32	0/1849
9	AF	0.16	0/864	0.44	0/1165
10	AG	0.15	0/1102	0.33	0/1472
11	AI	0.15	0/1016	0.36	0/1363
12	AL	0.13	0/1102	0.32	0/1470
13	AM	0.15	0/1628	0.35	0/2173
14	AN	0.18	0/1285	0.40	0/1720
15	AO	0.14	0/1369	0.34	0/1846
16	AP	0.12	0/966	0.28	0/1299
17	AQ	0.13	0/1222	0.31	0/1622
18	AR	0.13	0/460	0.28	0/614
19	AS	0.13	0/775	0.30	0/1033
20	AT	0.15	0/1176	0.34	0/1575
21	AU	0.13	0/637	0.33	0/852
22	AV	0.21	0/911	0.32	0/1224
23	AW	0.14	0/514	0.30	0/683
24	AX	0.15	0/530	0.44	0/704
25	AY	0.13	0/1216	0.33	0/1634
26	AZ	0.18	0/689	0.39	0/934
27	Aa	0.13	0/730	0.33	0/980
28	Ab	0.15	0/1015	0.30	0/1354
29	Ad	0.15	0/442	0.36	0/582
30	Af	0.15	0/432	0.30	0/578
31	Ag	0.15	0/363	0.38	0/476
32	Ah	0.15	0/774	0.30	0/1027

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Ai	0.21	0/749	0.41	0/997
34	BA	0.14	0/1541	0.34	0/2078
35	BB	0.15	0/1544	0.39	0/2097
36	BC	0.11	0/1493	0.30	0/2003
37	BD	0.13	0/1447	0.36	0/1951
38	BE	0.15	0/1856	0.35	0/2504
39	BF	0.14	0/1530	0.32	0/2067
40	BG	0.15	0/930	0.38	0/1251
41	BH	0.14	0/1486	0.36	0/1996
42	BI	0.15	0/1010	0.36	0/1361
43	BJ	0.12	0/974	0.32	0/1304
44	BK	0.15	0/1027	0.37	0/1376
45	BL	0.18	0/812	0.44	0/1097
46	BM	0.15	0/913	0.34	0/1229
47	BN	0.13	0/1110	0.31	0/1485
48	BO	0.17	0/1131	0.42	0/1520
49	BP	0.13	0/324	0.39	0/427
50	BQ	0.17	0/1248	0.36	0/1680
51	BR	0.14	0/865	0.31	0/1170
52	BS	0.66	0/456	0.68	0/613
53	BT	0.13	0/1017	0.37	0/1361
54	BU	0.22	0/1168	0.45	0/1582
55	BV	0.16	0/756	0.36	0/1015
56	BY	0.16	0/449	0.36	0/602
57	BZ	0.19	0/509	0.44	0/683
58	Ba	0.14	0/445	0.33	0/588
59	Bc	0.14	0/384	0.35	0/516
60	CS	0.19	0/2222	0.41	1/3013 (0.0%)
61	LF	0.17	0/1987	0.36	0/2674
All	All	0.23	0/169852	0.59	17/251552 (0.0%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	CS	228	ILE	N-CA-C	-6.93	106.55	113.20
1	1	519	G	O5'-C5'-C4'	6.25	114.40	109.40
3	4	407	C	O4'-C1'-N1	6.20	113.16	108.20
3	4	179	C	C2-N1-C1'	6.19	125.61	118.80
1	1	518	A	O4'-C1'-N9	6.01	113.01	108.20

There are no chirality outliers.

There are no planarity outliers.

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	62358	0	31379	281	0
2	2	2683	0	1358	11	0
3	4	31571	0	15901	173	0
4	AA	1783	0	1844	6	0
5	AB	2570	0	2632	12	0
6	AC	1914	0	1949	15	0
7	AD	1305	0	1344	15	0
8	AE	1358	0	1414	12	0
9	AF	858	0	889	13	0
10	AG	1088	0	1161	4	0
11	AI	1005	0	1067	5	0
12	AL	1092	0	1097	4	0
13	AM	1600	0	1648	11	0
14	AN	1265	0	1312	9	0
15	AO	1344	0	1337	5	0
16	AP	957	0	1022	2	0
17	AQ	1208	0	1269	2	0
18	AR	454	0	468	2	0
19	AS	761	0	778	1	0
20	AT	1157	0	1188	6	0
21	AU	629	0	666	6	0
22	AV	900	0	941	6	0
23	AW	504	0	503	2	0
24	AX	528	0	546	10	0
25	AY	1199	0	1227	5	0
26	AZ	683	0	721	3	0
27	Aa	716	0	751	3	0
28	Ab	1001	0	1081	1	0
29	Ad	435	0	449	0	0
30	Af	422	0	451	0	0
31	Ag	362	0	389	1	0
32	Ah	758	0	794	1	0
33	Ai	737	0	761	5	0
34	BA	1519	0	1580	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	BB	1517	0	1532	12	0
36	BC	1471	0	1528	13	0
37	BD	1422	0	1458	7	0
38	BE	1831	0	1911	19	0
39	BF	1512	0	1558	12	0
40	BG	917	0	955	5	0
41	BH	1468	0	1519	13	0
42	BI	994	0	1016	3	0
43	BJ	966	0	1013	3	0
44	BK	1016	0	1070	17	0
45	BL	800	0	844	17	0
46	BM	899	0	924	5	0
47	BN	1094	0	1133	2	0
48	BO	1119	0	1143	13	0
49	BP	318	0	312	3	0
50	BQ	1224	0	1275	14	0
51	BR	851	0	871	3	0
52	BS	450	0	469	29	0
53	BT	998	0	1001	7	0
54	BU	1145	0	1162	18	0
55	BV	749	0	784	16	0
56	BY	445	0	460	5	0
57	BZ	507	0	520	7	0
58	Ba	437	0	471	3	0
59	Bc	378	0	362	4	0
60	CS	2189	0	2237	29	0
61	LF	1968	0	2074	18	0
62	AW	1	0	0	0	0
62	Ad	1	0	0	0	0
62	Ag	1	0	0	0	0
62	Ah	1	0	0	0	0
62	Ai	1	0	0	0	0
62	BF	1	0	0	0	0
62	BP	1	0	0	0	0
62	BR	1	0	0	0	0
62	BY	1	0	0	2	0
62	Bc	1	0	0	0	0
All	All	157419	0	111519	870	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 3.

The worst 5 of 870 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)
38:BE:59:ARG:HH22	55:BV:80:VAL:HG22	1.29	0.97
56:BY:36:CYS:HG	62:BY:101:ZN:ZN	0.55	0.87
1:1:366:U:H5"	22:AV:2:VAL:HG11	1.62	0.80
1:1:2343:A:N6	60:CS:110:ARG:HD3	1.98	0.78
1:1:1957:A:H2'	1:1:1958:A:H4'	1.65	0.77

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	AA	234/237 (99%)	228 (97%)	6 (3%)	0	100	100
5	AB	333/337 (99%)	327 (98%)	6 (2%)	0	100	100
6	AC	250/253 (99%)	244 (98%)	6 (2%)	0	100	100
7	AD	163/165 (99%)	159 (98%)	4 (2%)	0	100	100
8	AE	172/177 (97%)	168 (98%)	3 (2%)	1 (1%)	21	27
9	AF	115/130 (88%)	111 (96%)	4 (4%)	0	100	100
10	AG	136/142 (96%)	134 (98%)	2 (2%)	0	100	100
11	AI	130/132 (98%)	130 (100%)	0	0	100	100
12	AL	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
13	AM	193/196 (98%)	190 (98%)	3 (2%)	0	100	100
14	AN	157/172 (91%)	148 (94%)	9 (6%)	0	100	100
15	AO	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
16	AP	123/126 (98%)	123 (100%)	0	0	100	100
17	AQ	149/152 (98%)	149 (100%)	0	0	100	100
18	AR	55/58 (95%)	55 (100%)	0	0	100	100
19	AS	94/97 (97%)	93 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AT	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
21	AU	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
22	AV	114/117 (97%)	114 (100%)	0	0	100	100
23	AW	60/62 (97%)	60 (100%)	0	0	100	100
24	AX	64/67 (96%)	63 (98%)	1 (2%)	0	100	100
25	AY	151/160 (94%)	150 (99%)	1 (1%)	0	100	100
26	AZ	93/95 (98%)	92 (99%)	1 (1%)	0	100	100
27	Aa	84/90 (93%)	84 (100%)	0	0	100	100
28	Ab	125/129 (97%)	125 (100%)	0	0	100	100
29	Ad	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
30	Af	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
31	Ag	44/49 (90%)	43 (98%)	1 (2%)	0	100	100
32	Ah	90/92 (98%)	90 (100%)	0	0	100	100
33	Ai	92/97 (95%)	88 (96%)	4 (4%)	0	100	100
34	BA	186/196 (95%)	181 (97%)	5 (3%)	0	100	100
35	BB	193/218 (88%)	188 (97%)	5 (3%)	0	100	100
36	BC	190/311 (61%)	189 (100%)	1 (0%)	0	100	100
37	BD	175/186 (94%)	173 (99%)	2 (1%)	0	100	100
38	BE	234/236 (99%)	222 (95%)	12 (5%)	0	100	100
39	BF	198/211 (94%)	195 (98%)	3 (2%)	0	100	100
40	BG	121/139 (87%)	114 (94%)	7 (6%)	0	100	100
41	BH	184/186 (99%)	179 (97%)	5 (3%)	0	100	100
42	BI	127/157 (81%)	121 (95%)	6 (5%)	0	100	100
43	BJ	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
44	BK	131/134 (98%)	128 (98%)	3 (2%)	0	100	100
45	BL	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
46	BM	121/127 (95%)	118 (98%)	2 (2%)	1 (1%)	16	20
47	BN	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
48	BO	140/148 (95%)	135 (96%)	5 (4%)	0	100	100
49	BP	36/50 (72%)	34 (94%)	2 (6%)	0	100	100
50	BQ	149/152 (98%)	147 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	BR	106/109 (97%)	105 (99%)	1 (1%)	0	100 100
52	BS	53/64 (83%)	38 (72%)	14 (26%)	1 (2%)	6 5
53	BT	123/137 (90%)	114 (93%)	9 (7%)	0	100 100
54	BU	146/149 (98%)	139 (95%)	7 (5%)	0	100 100
55	BV	91/114 (80%)	90 (99%)	1 (1%)	0	100 100
56	BY	56/59 (95%)	52 (93%)	4 (7%)	0	100 100
57	BZ	65/71 (92%)	60 (92%)	5 (8%)	0	100 100
58	Ba	54/57 (95%)	51 (94%)	2 (4%)	1 (2%)	6 5
59	Bc	49/55 (89%)	46 (94%)	3 (6%)	0	100 100
60	CS	279/281 (99%)	266 (95%)	10 (4%)	3 (1%)	11 13
61	LF	256/258 (99%)	248 (97%)	8 (3%)	0	100 100
All	All	7688/8166 (94%)	7477 (97%)	204 (3%)	7 (0%)	49 60

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	BM	117	ASP
52	BS	8	ASN
58	Ba	50	ARG
60	CS	224	VAL
60	CS	54	LYS

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	AA	184/185 (100%)	181 (98%)	3 (2%)	55 73
5	AB	277/278 (100%)	276 (100%)	1 (0%)	84 92
6	AC	199/200 (100%)	194 (98%)	5 (2%)	42 60
7	AD	145/145 (100%)	143 (99%)	2 (1%)	59 76
8	AE	149/151 (99%)	147 (99%)	2 (1%)	61 77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AF	89/100 (89%)	87 (98%)	2 (2%)	45	65
10	AG	115/119 (97%)	112 (97%)	3 (3%)	40	59
11	AI	108/108 (100%)	106 (98%)	2 (2%)	50	69
12	AL	113/114 (99%)	112 (99%)	1 (1%)	70	84
13	AM	166/167 (99%)	165 (99%)	1 (1%)	78	89
14	AN	130/136 (96%)	126 (97%)	4 (3%)	35	52
15	AO	143/144 (99%)	143 (100%)	0	100	100
16	AP	103/104 (99%)	103 (100%)	0	100	100
17	AQ	122/123 (99%)	120 (98%)	2 (2%)	55	73
18	AR	49/50 (98%)	47 (96%)	2 (4%)	27	41
19	AS	82/83 (99%)	80 (98%)	2 (2%)	43	62
20	AT	122/123 (99%)	122 (100%)	0	100	100
21	AU	70/71 (99%)	70 (100%)	0	100	100
22	AV	99/100 (99%)	97 (98%)	2 (2%)	48	67
23	AW	55/55 (100%)	54 (98%)	1 (2%)	51	70
24	AX	57/58 (98%)	57 (100%)	0	100	100
25	AY	129/135 (96%)	129 (100%)	0	100	100
26	AZ	73/73 (100%)	72 (99%)	1 (1%)	59	76
27	Aa	78/81 (96%)	77 (99%)	1 (1%)	61	77
28	Ab	105/106 (99%)	105 (100%)	0	100	100
29	Ad	49/50 (98%)	49 (100%)	0	100	100
30	Af	46/47 (98%)	45 (98%)	1 (2%)	45	65
31	Ag	39/40 (98%)	39 (100%)	0	100	100
32	Ah	82/82 (100%)	82 (100%)	0	100	100
33	Ai	75/77 (97%)	73 (97%)	2 (3%)	39	58
34	BA	168/175 (96%)	165 (98%)	3 (2%)	51	70
35	BB	165/186 (89%)	159 (96%)	6 (4%)	31	47
36	BC	154/251 (61%)	154 (100%)	0	100	100
37	BD	150/157 (96%)	147 (98%)	3 (2%)	48	67
38	BE	205/205 (100%)	202 (98%)	3 (2%)	57	75
39	BF	163/171 (95%)	159 (98%)	4 (2%)	42	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	BG	100/112 (89%)	96 (96%)	4 (4%)	28 42
41	BH	157/157 (100%)	156 (99%)	1 (1%)	78 89
42	BI	104/129 (81%)	104 (100%)	0	100 100
43	BJ	105/105 (100%)	101 (96%)	4 (4%)	29 44
44	BK	105/106 (99%)	103 (98%)	2 (2%)	50 69
45	BL	90/90 (100%)	86 (96%)	4 (4%)	25 38
46	BM	91/94 (97%)	91 (100%)	0	100 100
47	BN	113/114 (99%)	111 (98%)	2 (2%)	51 70
48	BO	122/128 (95%)	120 (98%)	2 (2%)	55 73
49	BP	33/42 (79%)	31 (94%)	2 (6%)	17 24
50	BQ	137/138 (99%)	135 (98%)	2 (2%)	57 75
51	BR	99/100 (99%)	97 (98%)	2 (2%)	48 67
52	BS	50/58 (86%)	32 (64%)	18 (36%)	0 0
53	BT	104/115 (90%)	103 (99%)	1 (1%)	68 82
54	BU	119/120 (99%)	111 (93%)	8 (7%)	15 21
55	BV	82/99 (83%)	79 (96%)	3 (4%)	30 45
56	BY	52/53 (98%)	51 (98%)	1 (2%)	50 69
57	BZ	55/58 (95%)	51 (93%)	4 (7%)	13 18
58	Ba	46/47 (98%)	45 (98%)	1 (2%)	45 65
59	Bc	45/47 (96%)	45 (100%)	0	100 100
60	CS	246/246 (100%)	237 (96%)	9 (4%)	30 45
61	LF	220/220 (100%)	211 (96%)	9 (4%)	27 41
All	All	6533/6828 (96%)	6395 (98%)	138 (2%)	46 66

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	BZ	26	SER
58	Ba	29	LYS
61	LF	6	ILE
35	BB	215	GLU
35	BB	195	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
30	Af	3	ASN
60	CS	103	ASN
37	BD	101	GLN
60	CS	30	HIS
60	CS	195	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2909/2910 (99%)	429 (14%)	14 (0%)
2	2	125/126 (99%)	17 (13%)	1 (0%)
3	4	1473/1474 (99%)	278 (18%)	13 (0%)
All	All	4507/4510 (99%)	724 (16%)	28 (0%)

5 of 724 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	8	A
1	1	10	U
1	1	13	G
1	1	21	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	7	G
3	4	1467	C
3	4	174	A
3	4	1077	A
3	4	70	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

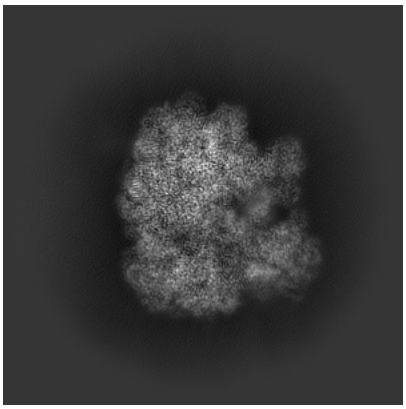
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66877. These allow visual inspection of the internal detail of the map and identification of artifacts.

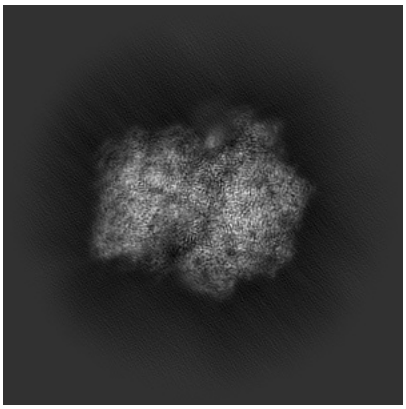
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

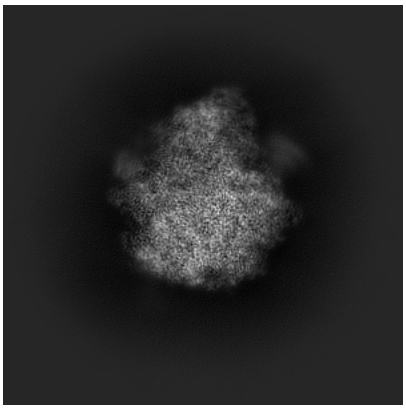
6.1.1 Primary map



X

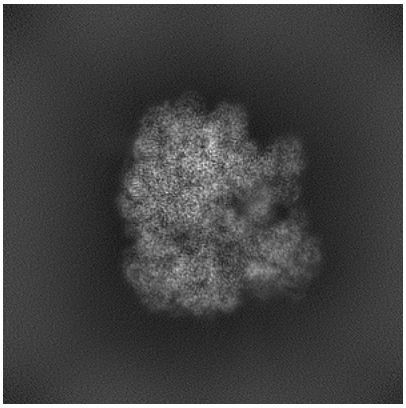


Y

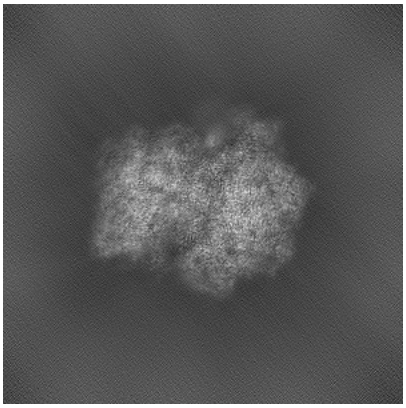


Z

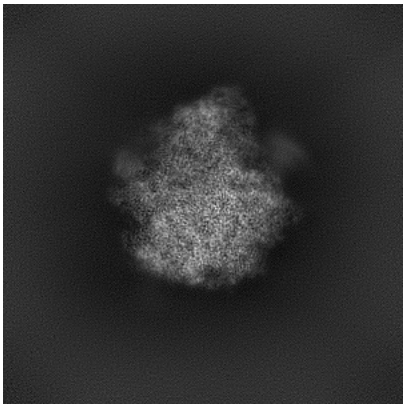
6.1.2 Raw map



X



Y

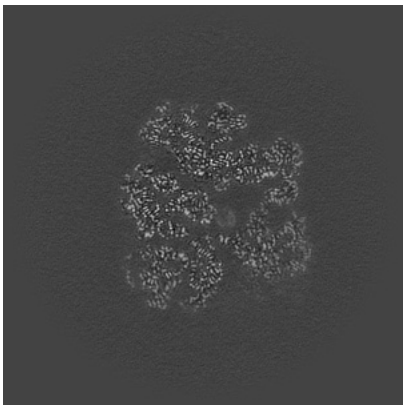


Z

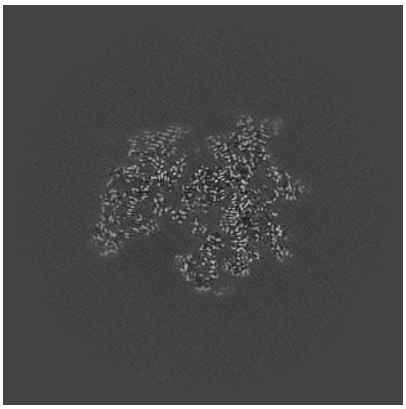
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

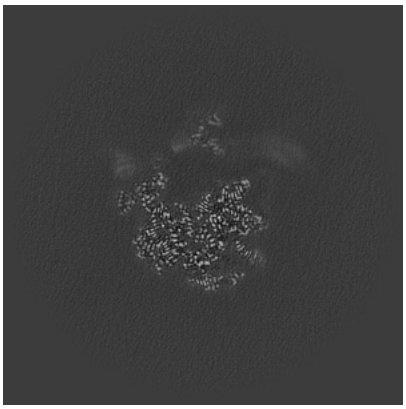
6.2.1 Primary map



X Index: 240



Y Index: 240

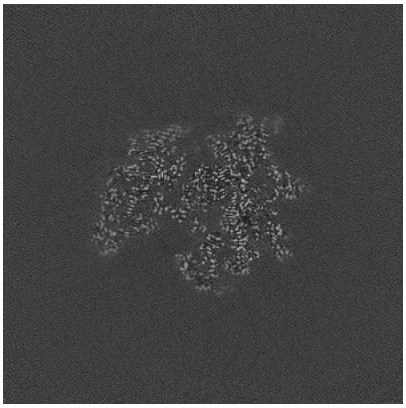


Z Index: 240

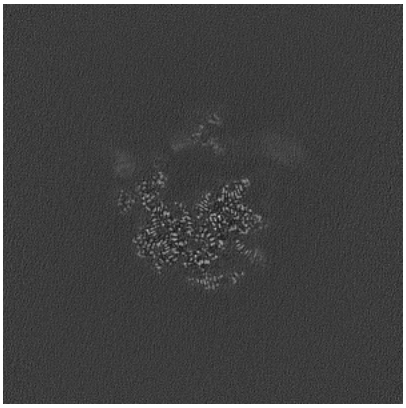
6.2.2 Raw map



X Index: 240



Y Index: 240

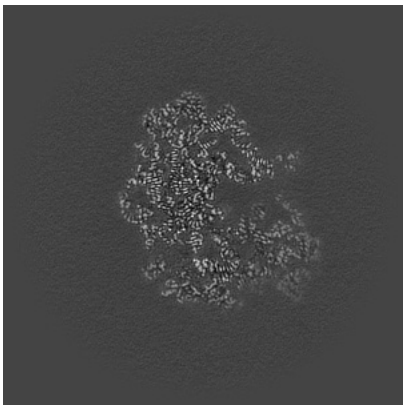


Z Index: 240

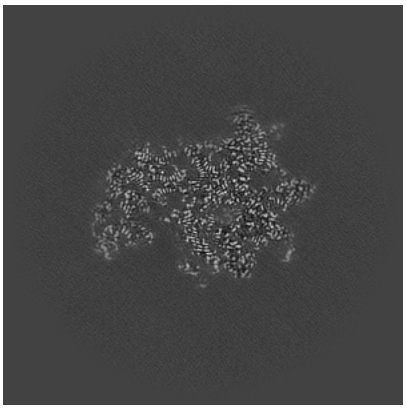
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

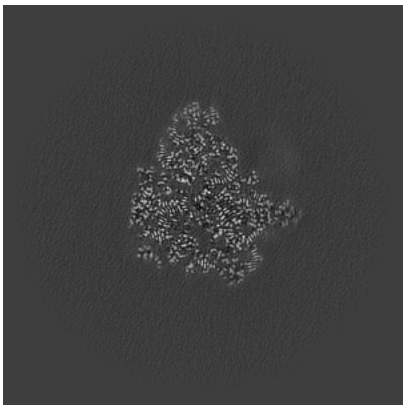
6.3.1 Primary map



X Index: 258

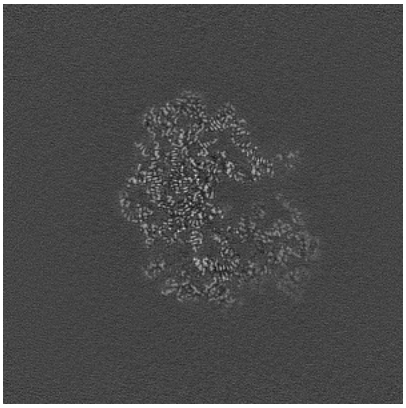


Y Index: 229

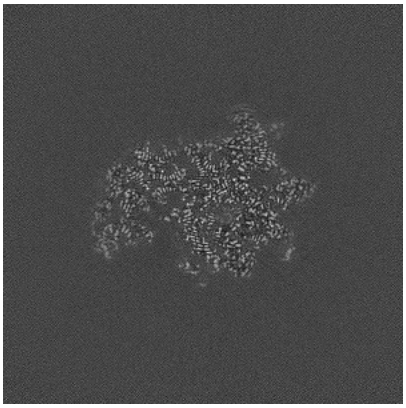


Z Index: 284

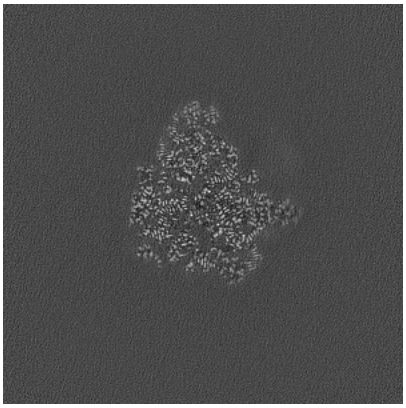
6.3.2 Raw map



X Index: 258



Y Index: 229

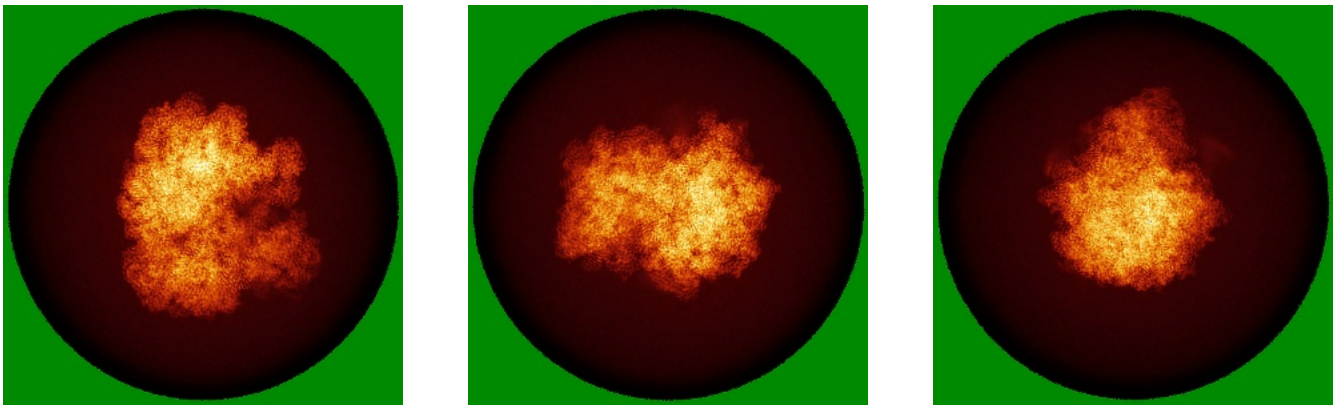


Z Index: 284

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

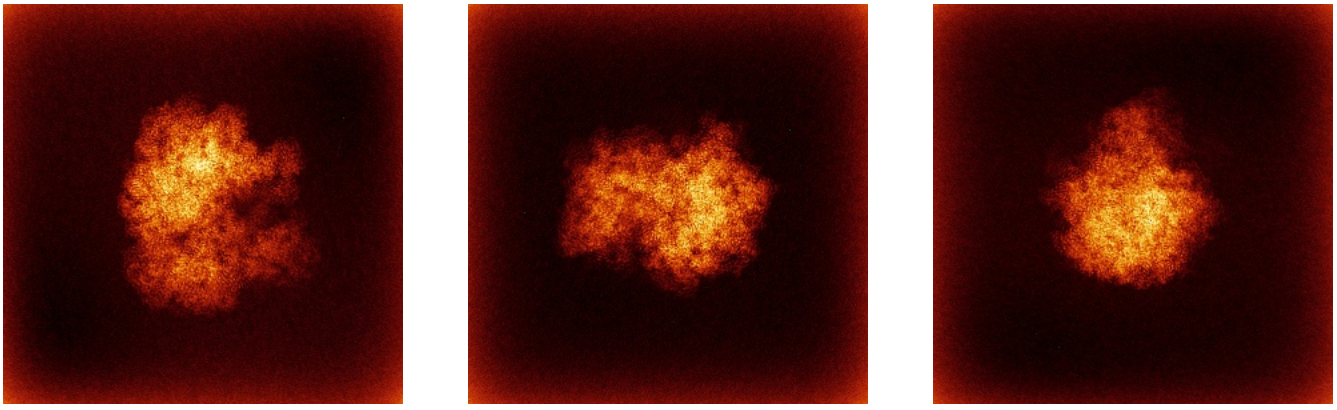
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



X Y Z

6.4.2 Raw map

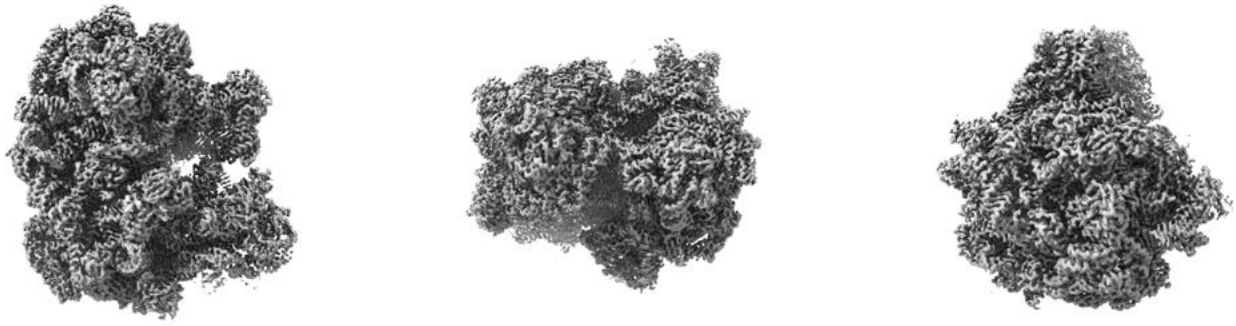


X Y Z

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

6.5 Orthogonal surface views (i)

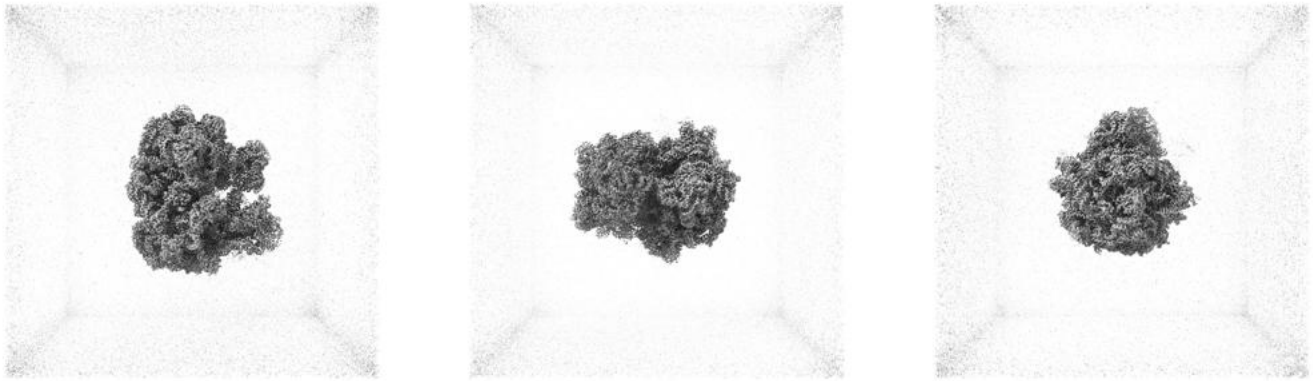
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

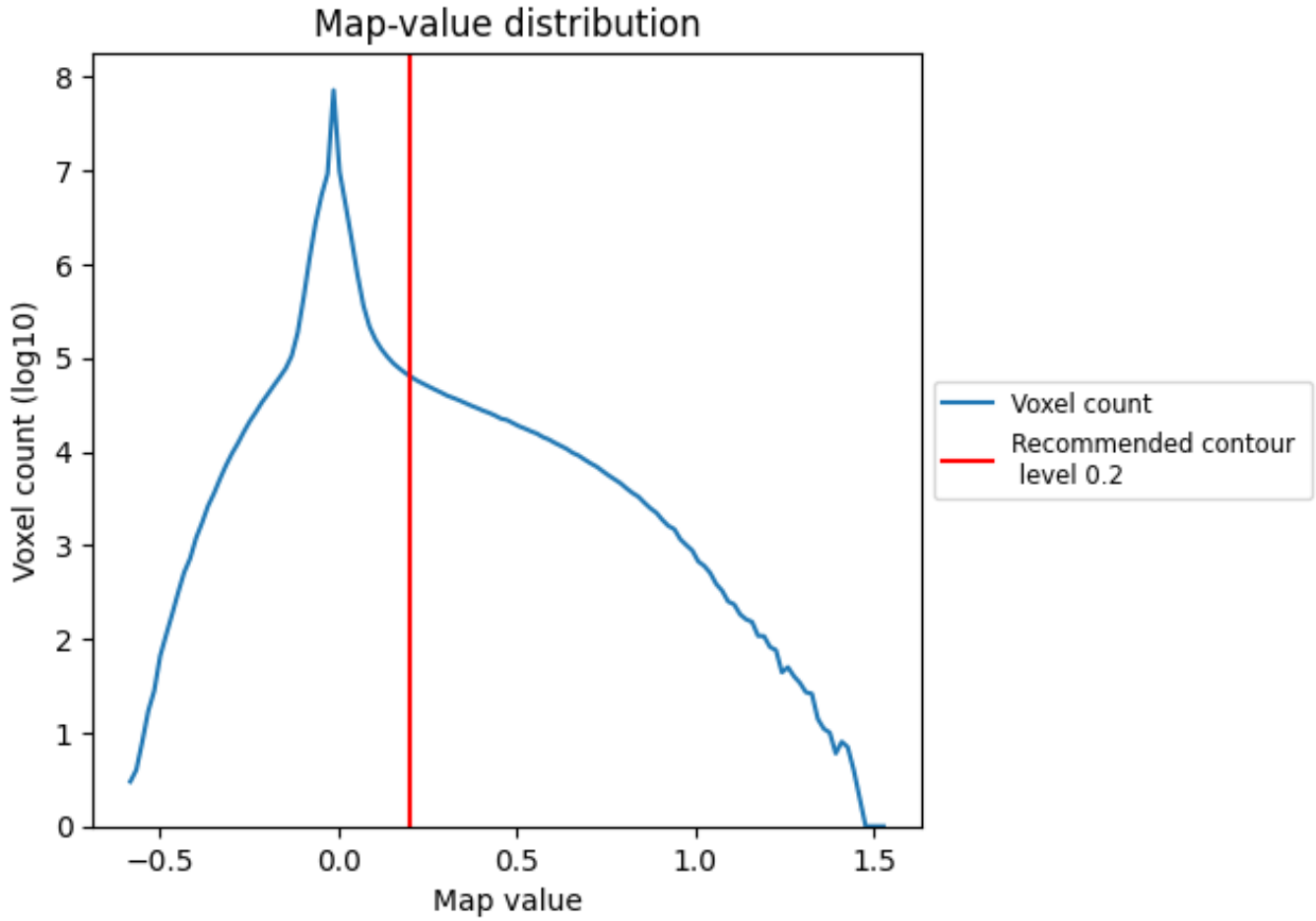
6.6 Mask visualisation (i)

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

7 Map analysis

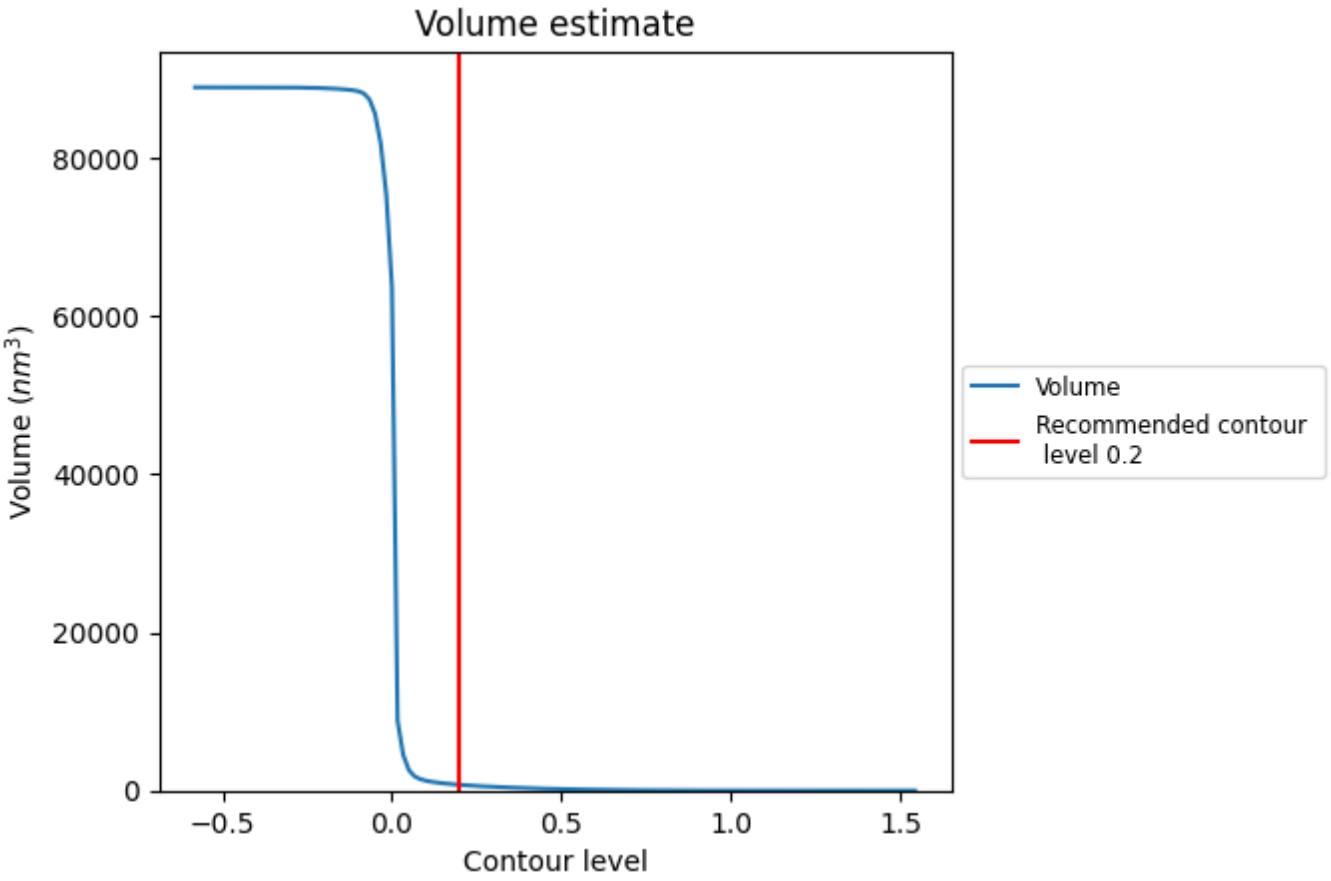
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

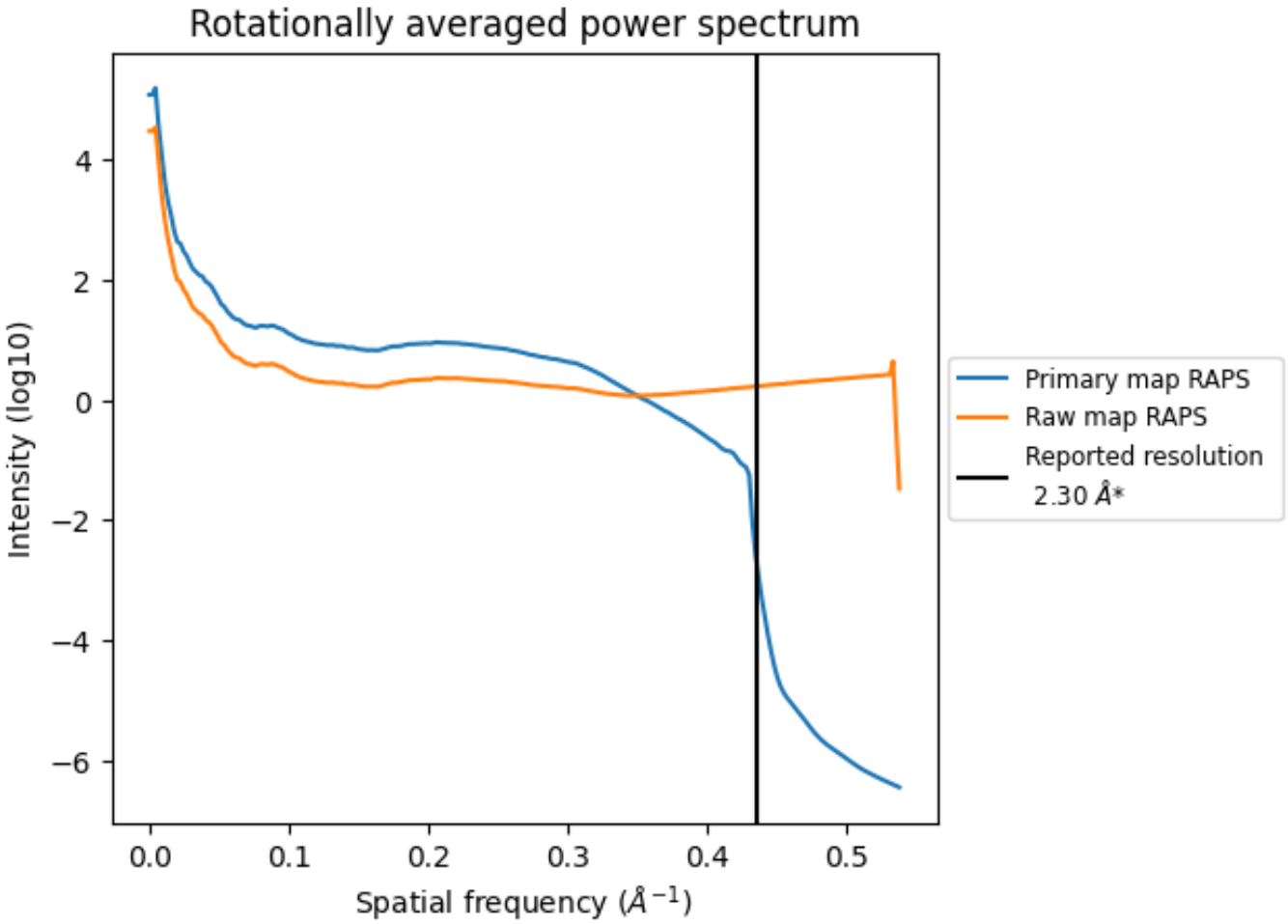
7.2 Volume estimate (i)



The volume at the recommended contour level is 726 nm^3; this corresponds to an approximate mass of 655 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

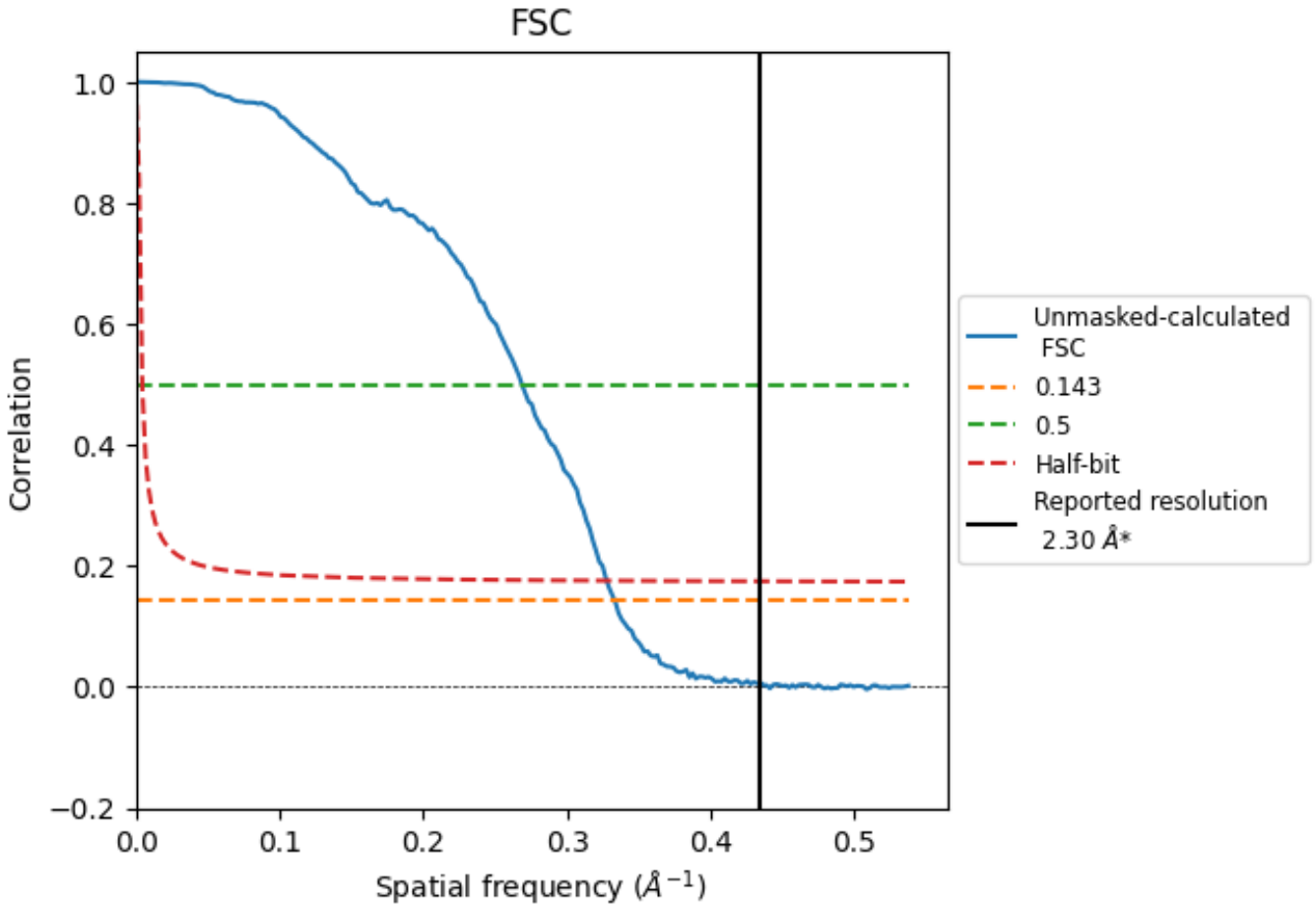


*Reported resolution corresponds to spatial frequency of 0.435 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.435 Å^{-1}

8.2 Resolution estimates (i)

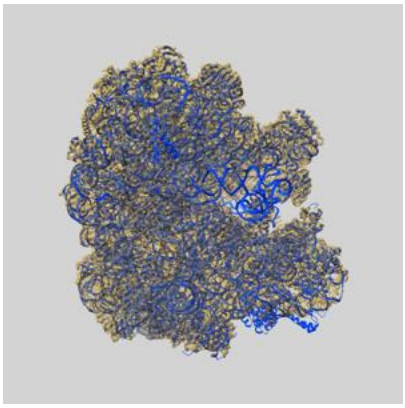
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.72	3.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.00 differs from the reported value 2.3 by more than 10 %

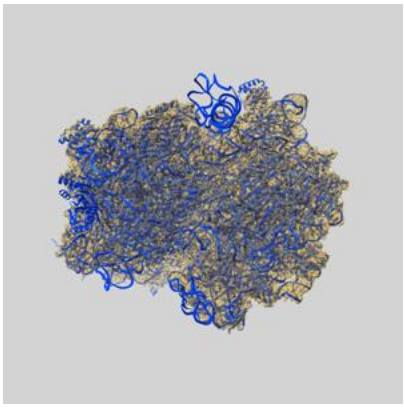
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66877 and PDB model 9XHK. Per-residue inclusion information can be found in section 3 on page 16.

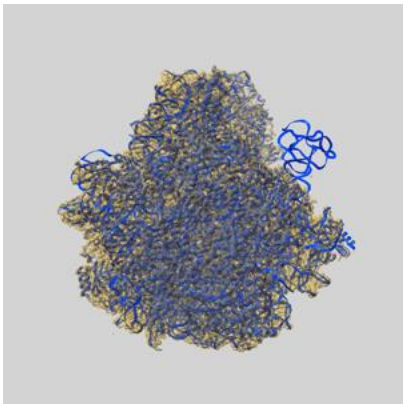
9.1 Map-model overlay



X



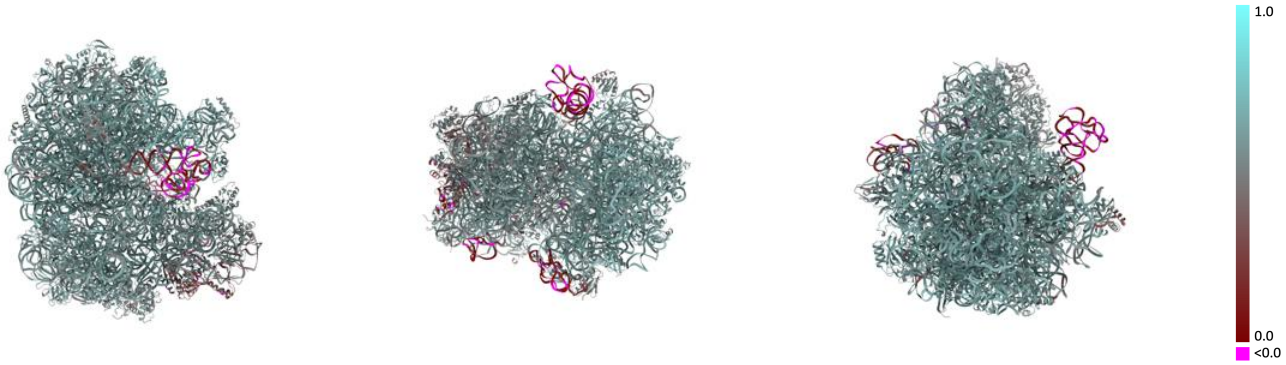
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

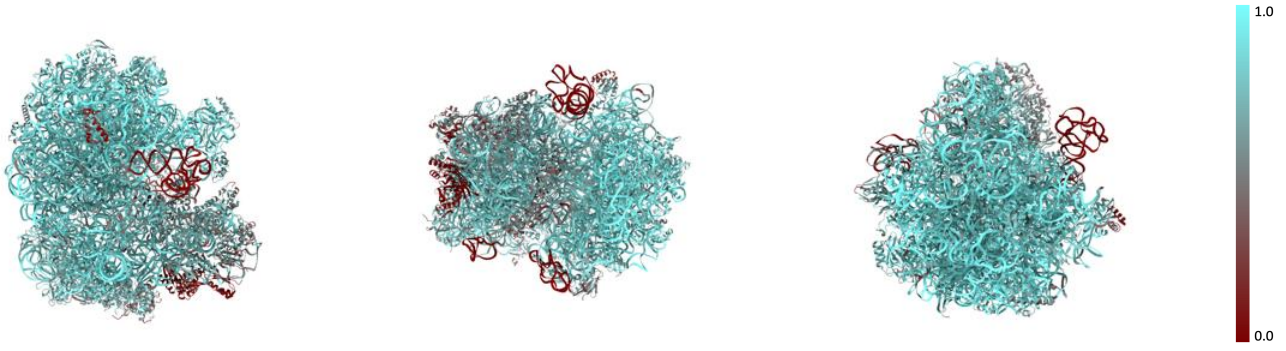
9.2 Q-score mapped to coordinate model



X Y Z

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

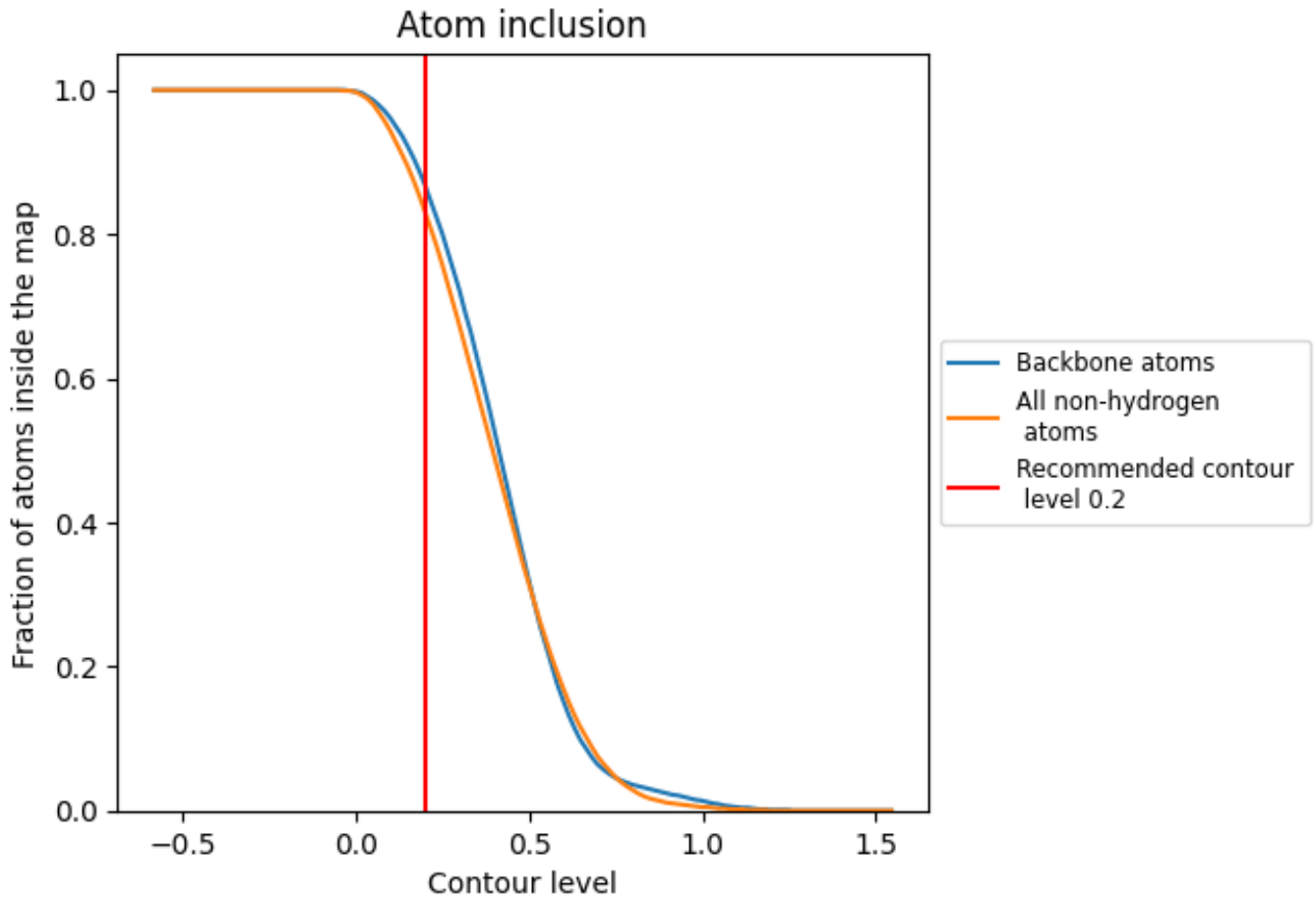
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 83% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8300	0.5920
1	0.8940	0.5950
2	0.9390	0.6140
4	0.8810	0.5870
AA	0.9030	0.6480
AB	0.9010	0.6550
AC	0.8480	0.6260
AD	0.7560	0.6010
AE	0.6730	0.5620
AF	0.4860	0.5220
AG	0.8840	0.6440
AI	0.9010	0.6580
AL	0.8040	0.6240
AM	0.9070	0.6450
AN	0.8740	0.6450
AO	0.8360	0.6140
AP	0.8760	0.6320
AQ	0.8710	0.6300
AR	0.8040	0.6200
AS	0.9310	0.6570
AT	0.9030	0.6470
AU	0.7720	0.6040
AV	0.8420	0.6160
AW	0.8860	0.6520
AX	0.6550	0.5590
AY	0.8810	0.6340
AZ	0.7440	0.5900
Aa	0.8580	0.6370
Ab	0.8880	0.6400
Ad	0.9740	0.6680
Af	0.9010	0.6510
Ag	0.7620	0.6220
Ah	0.9110	0.6490
Ai	0.8480	0.6330
BA	0.6440	0.5610



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Chain	Atom inclusion	Q-score
BB	0.5560	0.5270
BC	0.0030	0.3130
BD	0.7210	0.5830
BE	0.6960	0.5770
BF	0.7680	0.6000
BG	0.6410	0.5640
BH	0.5890	0.5590
BI	0.8190	0.6040
BJ	0.8010	0.6160
BK	0.5350	0.5220
BL	0.2650	0.4190
BM	0.8130	0.6160
BN	0.7960	0.6210
BO	0.5800	0.5550
BP	0.6830	0.5820
BQ	0.7920	0.5940
BR	0.7940	0.6080
BS	0.1390	0.4030
BT	0.5960	0.5600
BU	0.5840	0.5250
BV	0.6390	0.5520
BY	0.7060	0.5560
BZ	0.5360	0.5250
Ba	0.7660	0.6000
Bc	0.7020	0.5720
CS	0.6540	0.5980
LF	0.5620	0.5620