wwPDB EM Validation Summary Report ⓘ

Nov 1, 2023 – 11:36 AM EDT

PDB ID	:	8FMW
EMDB ID	:	EMD-29298
Title	:	The structure of a hibernating ribosome in the Lyme disease pathogen
Authors	:	Sharma, M.R.; Manjari, S.R.; Agrawal, E.K.; Keshavan, P.; Koripella, R.K.; Majumdar, S.; Marcinkiewicz, A.L.; Lin, Y.P.; Agrawal, R.K.; Banavali, N.K.
Deposited on	:	2022-12-25
Resolution	:	2.86 Å(reported)

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

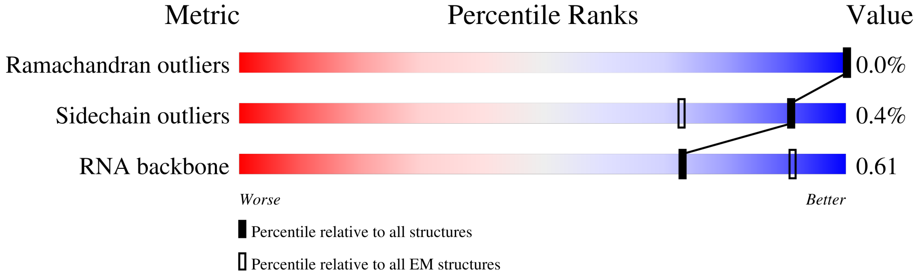
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

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

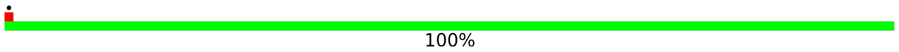
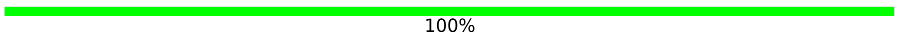
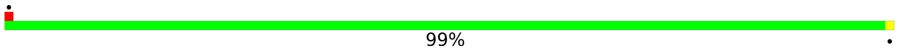
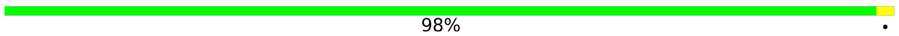
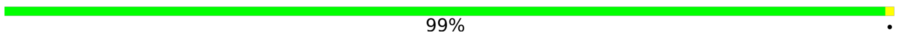
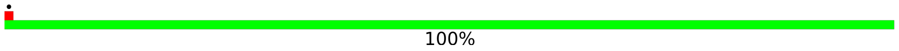
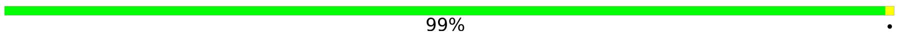
The reported resolution of this entry is 2.86 Å.

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	A	1529	
2	C	206	
3	D	208	
4	E	158	
5	F	97	
6	G	157	
7	H	132	
8	I	131	

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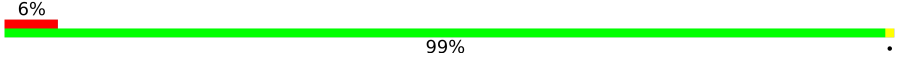
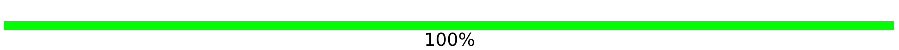
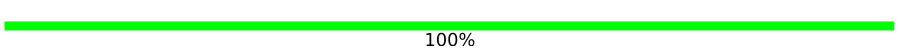
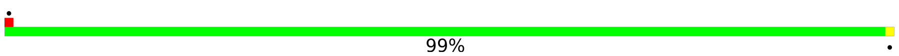
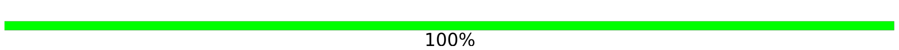
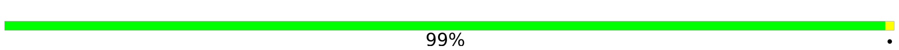
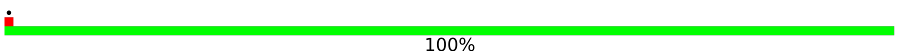
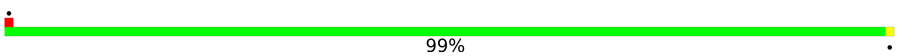
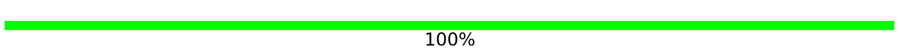
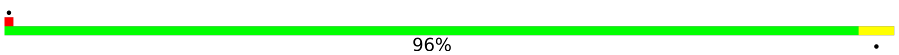
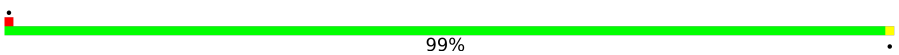
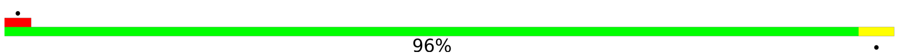
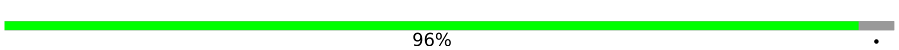
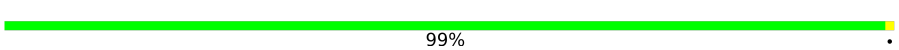
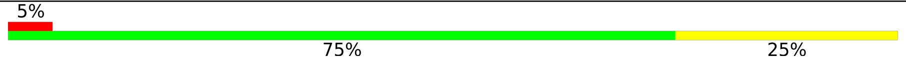
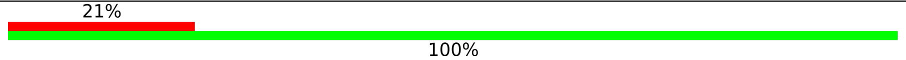
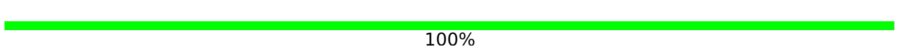
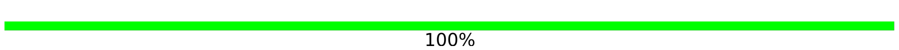
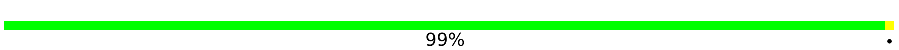
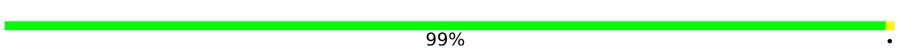
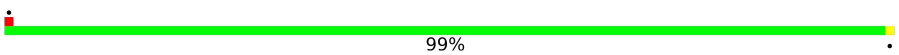
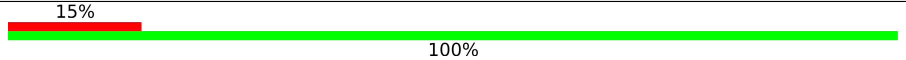
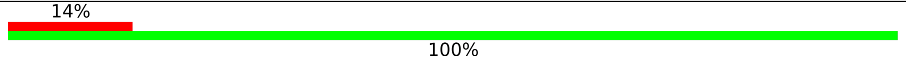
Mol	Chain	Length	Quality of chain
9	J	102	
10	K	117	
11	L	124	
12	M	114	
13	N	60	
14	O	88	
15	P	83	
16	Q	82	
17	R	63	
18	S	84	
19	T	85	
20	U	69	
21	V	28	
22	W	97	
23	X	76	
24	AA	2929	
25	AB	112	
26	AC	221	
27	AD	277	
28	AE	206	
29	AF	209	
30	AG	182	
31	AH	180	
32	AI	148	
33	AJ	162	

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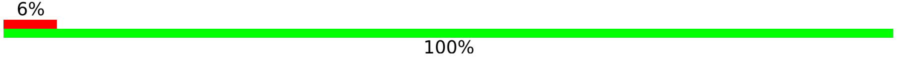
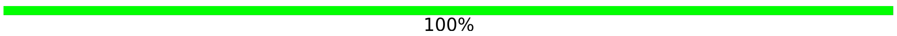
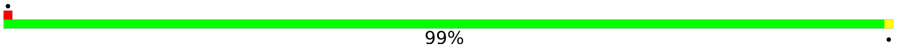
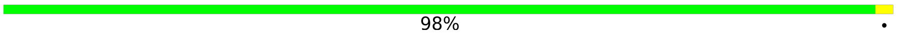
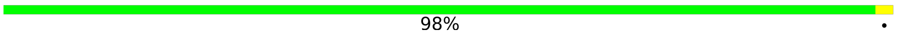
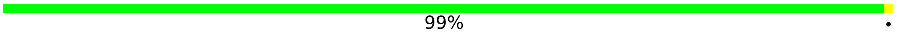
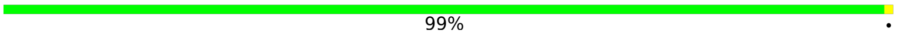
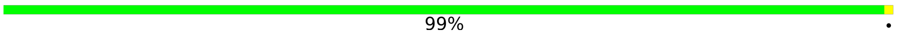
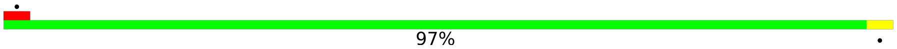
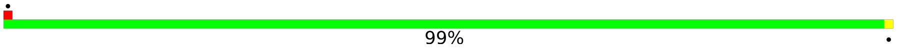
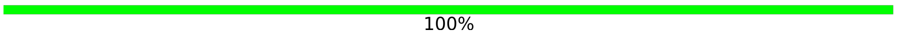
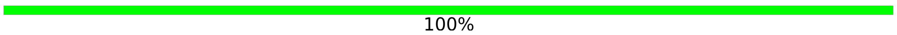
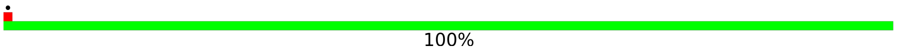
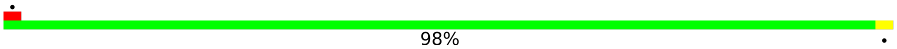
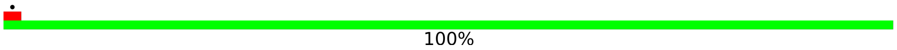
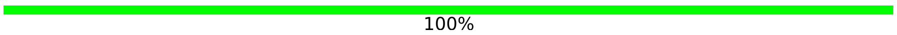
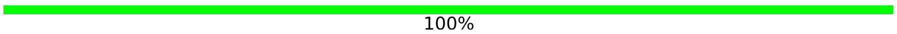
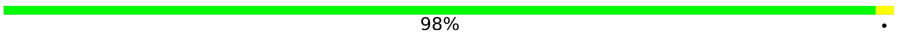
Mol	Chain	Length	Quality of chain
34	AK	139	
35	AL	145	
36	AM	122	
37	AN	145	
38	AO	138	
39	AP	121	
40	AQ	119	
41	AR	117	
42	AS	114	
43	AT	103	
44	AU	115	
45	AV	98	
46	AW	101	
47	AX	181	
48	AY	74	
49	AZ	91	
50	Aa	65	
51	Ab	100	
52	Ac	81	
53	Ad	59	
54	Ae	51	
55	Af	50	
56	Ag	66	
57	Ah	37	
58	Ai	46	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 147910 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1529	32780	14645	5986	10621	1528	0	0

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	206	1646	1066	294	284	2	0	0

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	208	1689	1069	321	296	3	0	0

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	158	1196	763	222	206	5	0	0

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	97	814	529	137	144	4	0	0

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	157	1282	809	235	231	7	0	0

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	132	Total	C	N	O	S	0	0
			1039	662	183	188	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	131	Total	C	N	O	S	0	0
			1043	651	201	188	3		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	102	Total	C	N	O	S	0	0
			817	524	145	145	3		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	117	Total	C	N	O	S	0	0
			876	551	163	159	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	124	Total	C	N	O	S	0	0
			968	601	198	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	114	Total	C	N	O	S	0	0
			901	554	181	161	5		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	60	Total	C	N	O	S	0	0
			491	309	99	76	7		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	88	718	455	135	126	2	0	0

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	83	676	425	127	119	5	0	0

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	82	678	436	122	118	2	0	0

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	63	521	337	95	86	3	0	0

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	84	669	435	114	119	1	0	0

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	85	697	439	143	112	3	0	0

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	U	69	603	382	119	100	2	0	0

- Molecule 21 is a protein called 30S ribosomal protein bS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	27	240	147	61	31	1	0	0

- Molecule 22 is a protein called Ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	97	818	528	145	144	1	0	0

- Molecule 23 is a RNA chain called E-site t-RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
23	X	76	1618	722	284	536	76	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	?	-	U	deletion	GB AE000783.1
X	74	C	U	conflict	GB AE000783.1
X	75	C	U	conflict	GB AE000783.1

- Molecule 24 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
24	AA	2929	62816	28077	11503	20307	2929	0	0

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	AB	112	2398	1071	434	781	112	0	0

- Molecule 26 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	AC	221	884	442	221	221	0	0

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AD	277	Total	C	N	O	S	0	0
			2156	1354	414	383	5		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AE	206	Total	C	N	O	S	0	0
			1564	995	278	286	5		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AF	209	Total	C	N	O	S	0	0
			1658	1056	301	299	2		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AG	182	Total	C	N	O	S	0	0
			1439	930	240	265	4		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	180	Total	C	N	O	S	0	0
			1405	895	249	259	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AI	148	Total	C	N	O	S	0	0
			751	423	161	166	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	AJ	162	Total	C	N	O	0	0
			648	324	162	162		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	AK	139	556	278	139	139	0	0

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	AL	145	1171	756	211	202	2	0	0

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	AM	122	942	593	174	170	5	0	0

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	AN	145	1129	716	210	201	2	0	0

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	AO	138	1092	693	204	188	7	0	0

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AP	121	1004	643	193	164	4	0	0

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AQ	119	968	613	184	170	1	0	0

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AR	117	Total 951	C 613	N 174	O 161	S 3	0	0

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AS	114	Total 943	C 597	N 189	O 155	S 2	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	40	ARG	UNK	conflict	UNP O51206

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AT	103	Total 859	C 552	N 148	O 157	S 2	0	0

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AU	115	Total 918	C 574	N 180	O 158	S 6	0	0

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AV	98	Total 784	C 507	N 134	O 140	S 3	0	0

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AW	101	Total 800	C 501	N 155	O 140	S 4	0	0

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	AX	181	1432	912	245	273	2	0	0

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	AY	74	571	359	112	100	0	0

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	AZ	91	705	452	135	115	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Aa	65	553	352	102	95	4	0	0

- Molecule 51 is a protein called 50S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Ab	100	814	518	158	133	5	0	0

- Molecule 52 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Ac	81	656	419	114	121	2	0	0

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	Ad	59	484	300	99	80	5	0	0

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Ae	51	425	266	80	76	3	0	0

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	Af	50	422	260	95	64	3	0	0

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Ag	66	548	346	111	88	3	0	0

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	Ah	37	305	192	63	46	4	0	0

- Molecule 58 is a protein called 50S ribosomal protein bL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	Ai	46	375	236	72	65	2	0	0

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

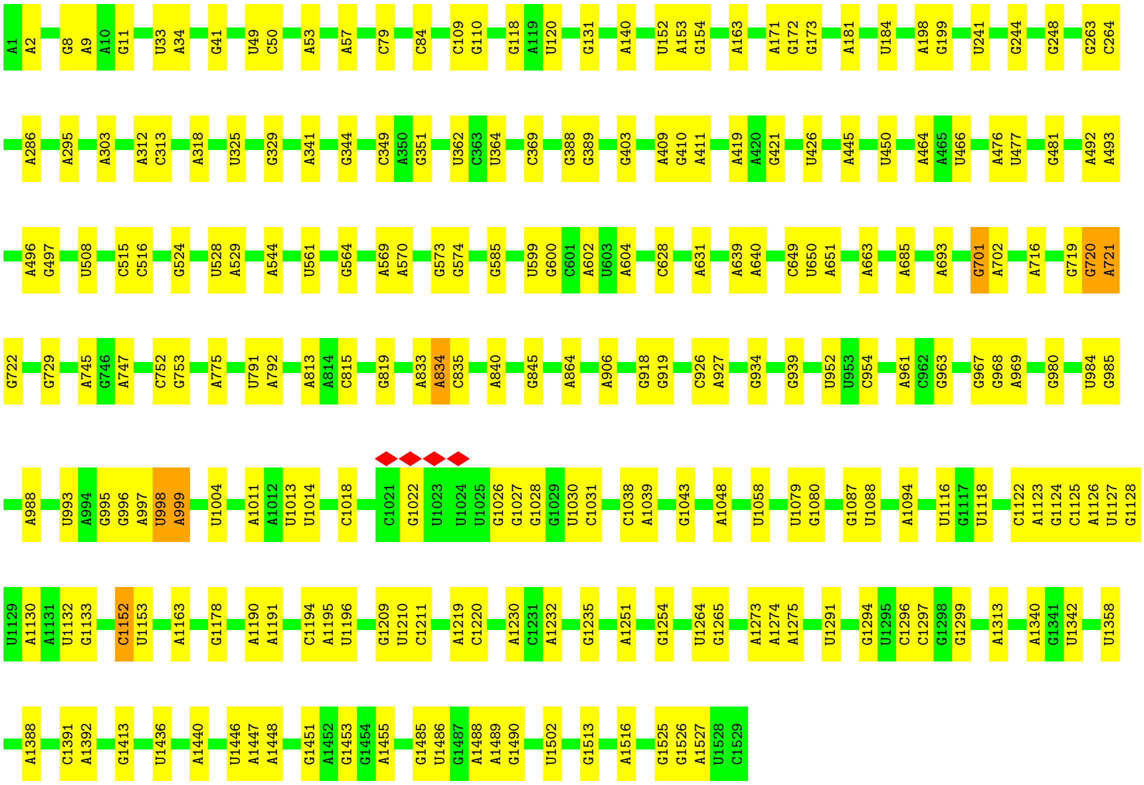
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
59	N	1	1	1	0
			Total	Zn	
59	R	1	1	1	0
			Total	Zn	
59	Ad	1	1	1	0
			Total	Zn	
59	Ah	1	1	1	0

3 Residue-property plots ⓘ

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

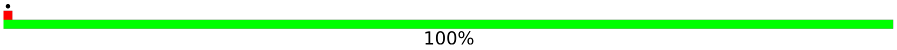
- Molecule 1: 16S ribosomal RNA

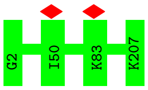
Chain A:



- Molecule 2: 30S ribosomal protein S3

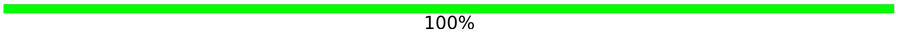
Chain C:

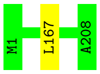




- Molecule 3: 30S ribosomal protein S4

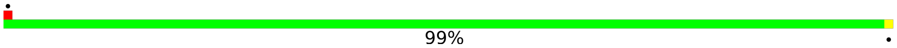
Chain D:

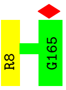




- Molecule 4: 30S ribosomal protein S5

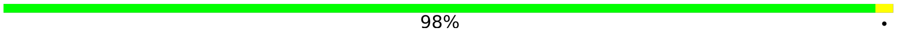
Chain E:

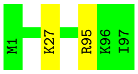




- Molecule 5: 30S ribosomal protein S6

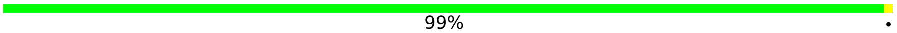
Chain F:

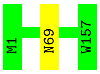




- Molecule 6: 30S ribosomal protein S7

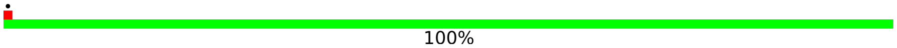
Chain G:

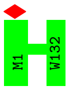




- Molecule 7: 30S ribosomal protein S8

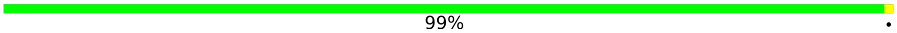
Chain H:

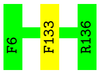




- Molecule 8: 30S ribosomal protein S9

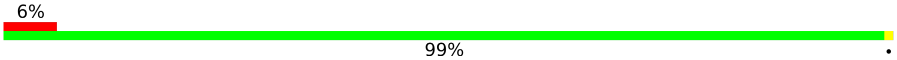
Chain I:

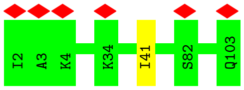




- Molecule 9: 30S ribosomal protein S10

Chain J:





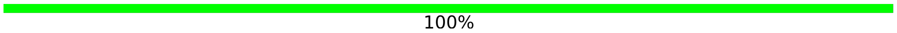
- Molecule 10: 30S ribosomal protein S11

Chain K:

There are no outlier residues recorded for this chain.

- Molecule 11: 30S ribosomal protein S12

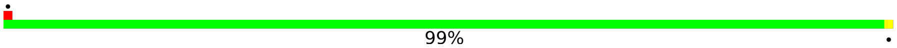
Chain L:

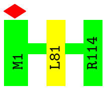


There are no outlier residues recorded for this chain.

- Molecule 12: 30S ribosomal protein S13

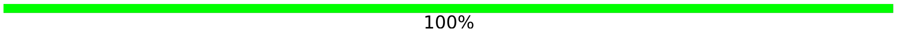
Chain M:





- Molecule 13: 30S ribosomal protein S14 type Z

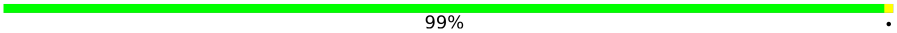
Chain N:

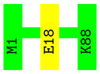


There are no outlier residues recorded for this chain.

- Molecule 14: 30S ribosomal protein S15

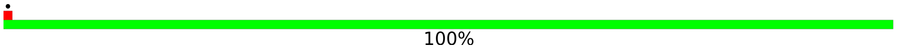
Chain O:

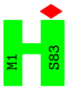




- Molecule 15: 30S ribosomal protein S16

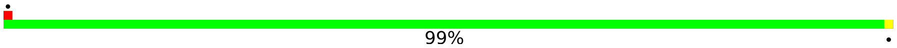
Chain P:

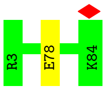




- Molecule 16: 30S ribosomal protein S17

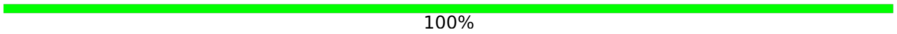
Chain Q:





- Molecule 17: 30S ribosomal protein S18

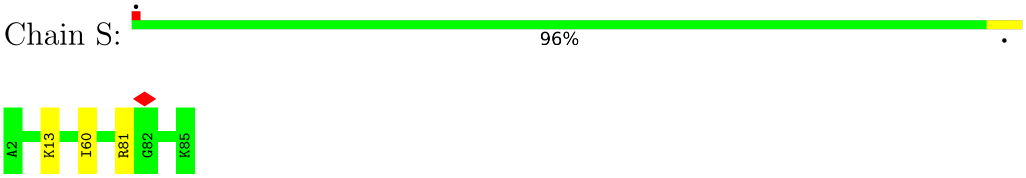
Chain R:



There are no outlier residues recorded for this chain.

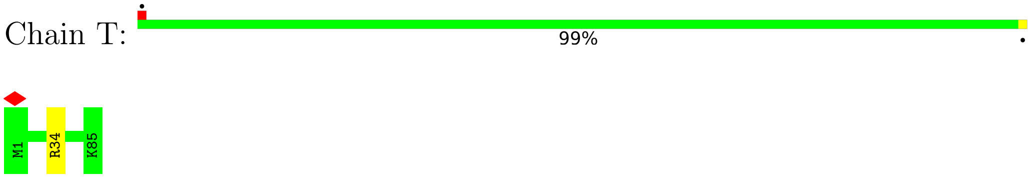
- Molecule 18: 30S ribosomal protein S19

Chain S:



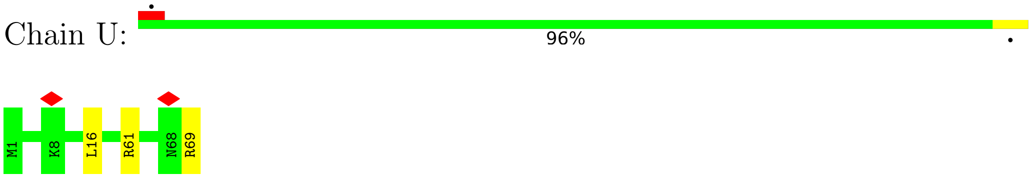
- Molecule 19: 30S ribosomal protein S20

Chain T:



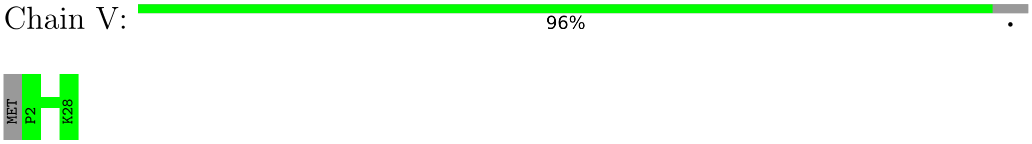
- Molecule 20: 30S ribosomal protein S21

Chain U:



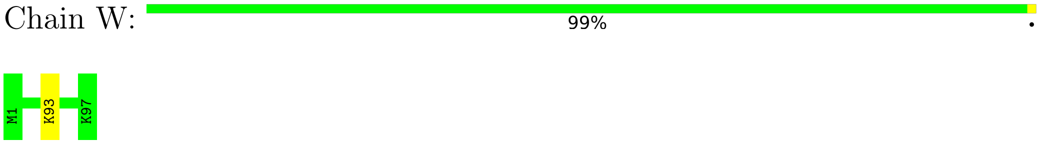
- Molecule 21: 30S ribosomal protein bS22

Chain V:



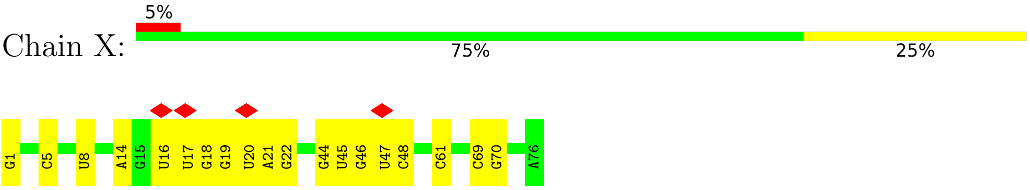
- Molecule 22: Ribosomal subunit interface protein

Chain W:



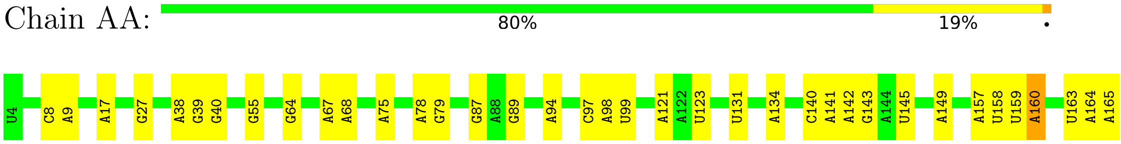
- Molecule 23: E-site t-RNA

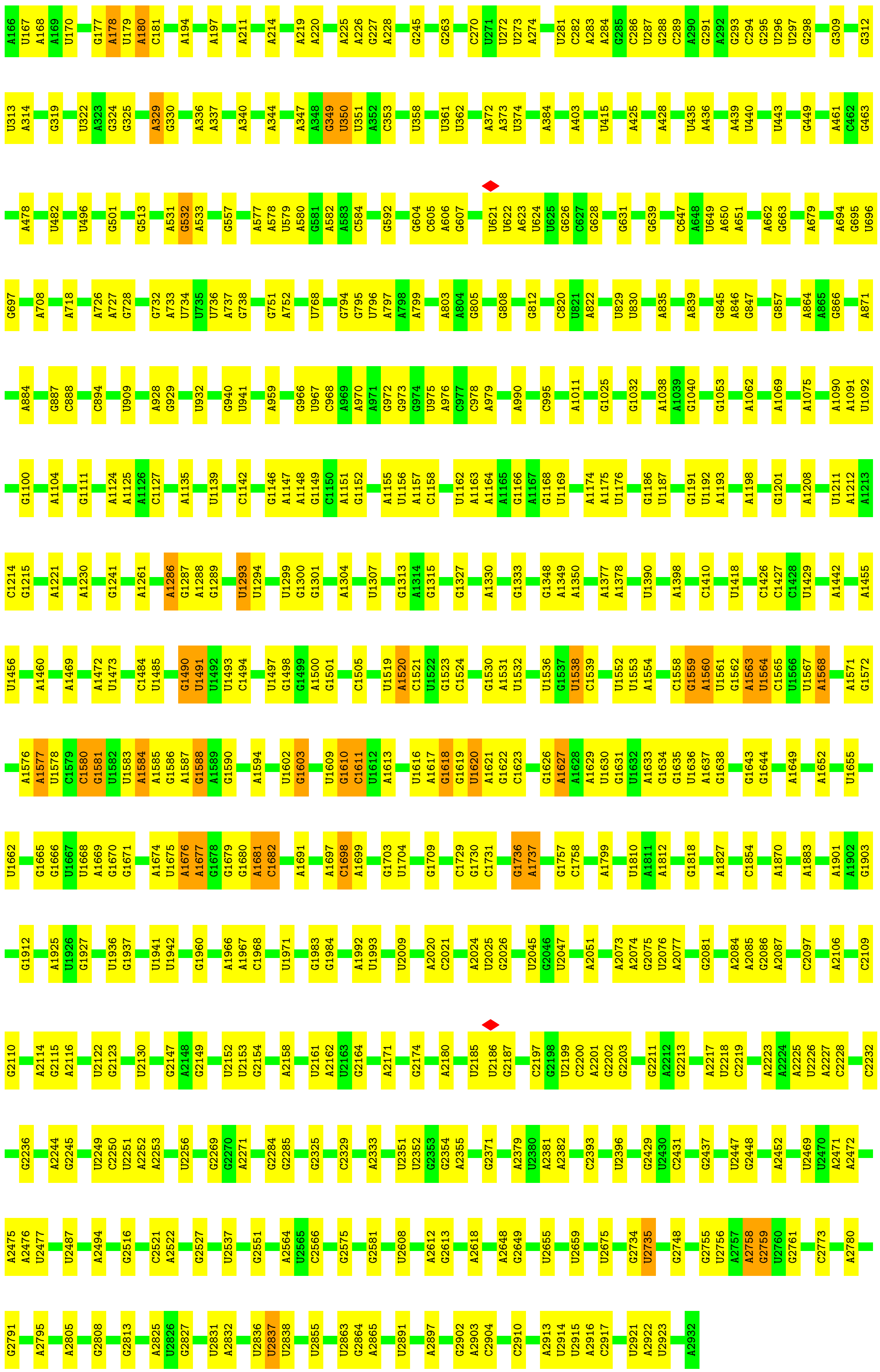
Chain X:



- Molecule 24: 23S ribosomal RNA

Chain AA:

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U167
A168
A169
U170
G177
A178
U179
A180
C181
A194
A197
A211
A214
A219
A220
A225
A226
G227
A228
G245
G263
C270
U271
U272
U273
A274
U281
C282
A283
A284
G285
C286
U287
G288
C289
A290
G291
A292
G293
C294
G295
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A352
C353
U358
U361
U362
A372
A373
U374
A384
A403
U415
A425
A428
U435
A436
A439
U440
U443
G449
A461
C462
G463
A478
U482
U496
G501
G513
A531
G532
A533
G557
A577
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A580
G581
A582
A583
C584
G592
G604
C605
A606
G607
U621
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U625
G626
C627
G628
G631
G639
C647
A648
U649
A650
A651
A662
G663
A679
A694
G695
U696
G697
A708
A718
A726
A727
G728
G732
A733
U734
U735
U736
A737
G738
G751
A752
U768
G794
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A797
A798
A799
A803
A804
G805
G808
G812
C820
U821
A822
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G845
A846
G847
G857
A864
A865
G866
A871
A884
G887
C888
C894
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U1299
G1300
G1301
A1304
U1307
G1313
A1314
G1315
G1327
A1330
G1333
G1348
A1349
A1350
A1377
A1378
U1390
A1398
C1410
U1418
C1426
C1427
C1428
U1429
A1442
A1455
U1456
A1460
A1469
A1472
U1473
C1484
U1485
G1490
U1491
U1492
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C1494
U1497
G1498
G1499
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G1501
C1505
U1519
A1520
C1521
U1522
G1523
C1524
G1530
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U1536
G1537
U1538
C1539
U1552
U1553
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C1558
G1559
A1560
U1561
G1562
A1563
U1564
C1565
U1566
U1567
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U1582
U1583
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A1585
G1586
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G1588
A1589
G1590
A1594
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G1603
U1609
G1610
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U1616
A1617
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A1628
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A1637
G1638
G1643
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A1652
U1655
U1662
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G1818
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A1870
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G1903
G1912
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G1927
U1936
G1937
U1941
U1942
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U1971
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G1984
A1992
U1993
U2009
A2020
C2021
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U2025
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G2046
U2047
A2051
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G2086
A2087
C2097
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U2226
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U2760
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U2891
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G2902
A2903
C2904
C2910
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U2914
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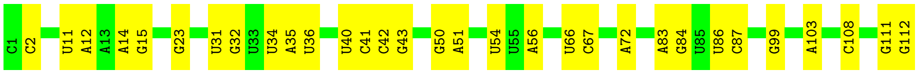
C2917
U2921
A2922
U2923
A2932

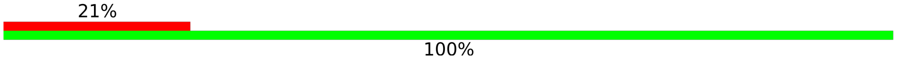
- Molecule 25: 5S ribosomal RNA

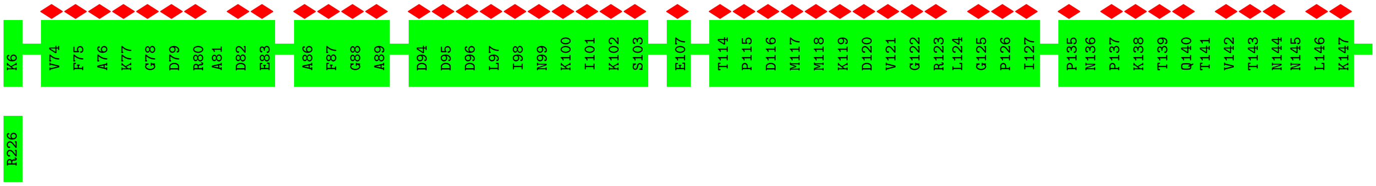
Chain AB:



- Molecule 26: 50S ribosomal protein L1

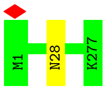
Chain AC:





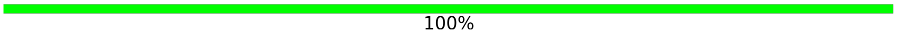
- Molecule 27: 50S ribosomal protein L2

Chain AD:



- Molecule 28: 50S ribosomal protein L3

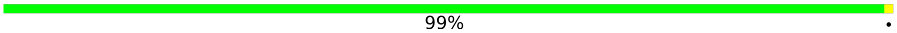
Chain AE:



There are no outlier residues recorded for this chain.

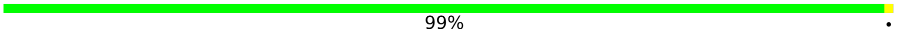
- Molecule 29: 50S ribosomal protein L4

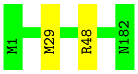
Chain AF:



- Molecule 30: 50S ribosomal protein L5

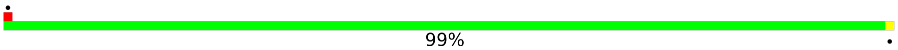
Chain AG:

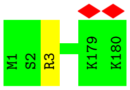




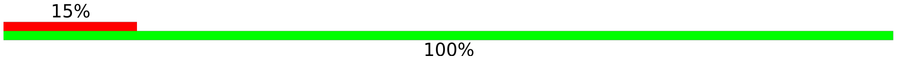
- Molecule 31: 50S ribosomal protein L6

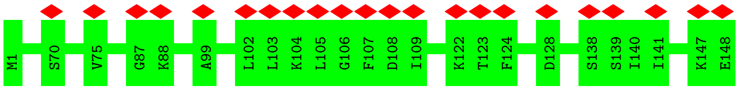
Chain AH:



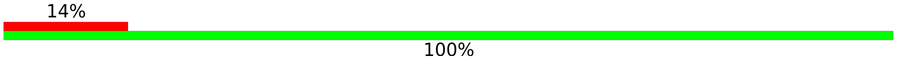


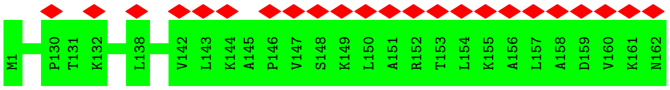
- Molecule 32: 50S ribosomal protein L9

Chain AI:


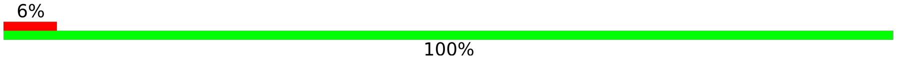


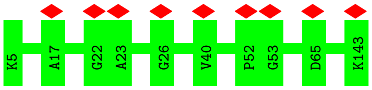
- Molecule 33: 50S ribosomal protein L10

Chain AJ:


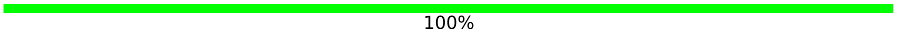


- Molecule 34: 50S ribosomal protein L11

Chain AK:


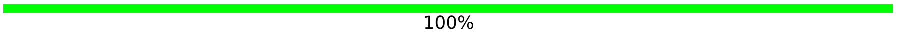


- Molecule 35: 50S ribosomal protein L13

Chain AL:


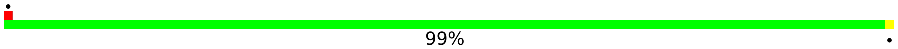
There are no outlier residues recorded for this chain.

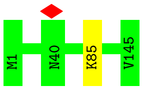
- Molecule 36: 50S ribosomal protein L14

Chain AM:


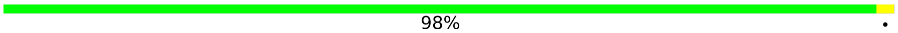
There are no outlier residues recorded for this chain.

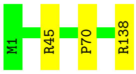
- Molecule 37: 50S ribosomal protein L15

Chain AN:


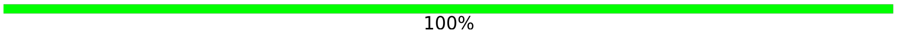


- Molecule 38: 50S ribosomal protein L16

Chain AO:


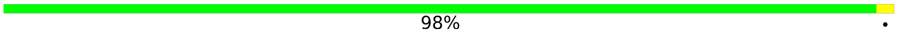


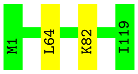
- Molecule 39: 50S ribosomal protein L17

Chain AP:


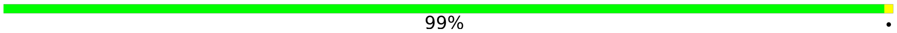
There are no outlier residues recorded for this chain.

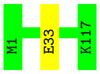
- Molecule 40: 50S ribosomal protein L18

Chain AQ:


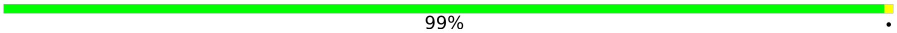


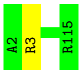
- Molecule 41: 50S ribosomal protein L19

Chain AR:


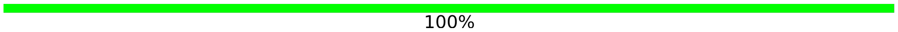


- Molecule 42: 50S ribosomal protein L20

Chain AS:


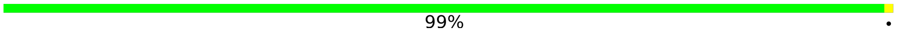


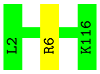
- Molecule 43: 50S ribosomal protein L21

Chain AT:


There are no outlier residues recorded for this chain.

- Molecule 44: 50S ribosomal protein L22

Chain AU:




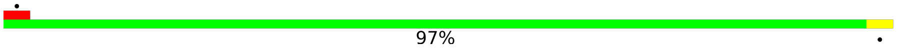
- Molecule 45: 50S ribosomal protein L23

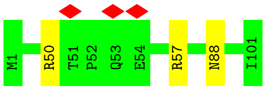
Chain AV:


There are no outlier residues recorded for this chain.

- Molecule 46: 50S ribosomal protein L24

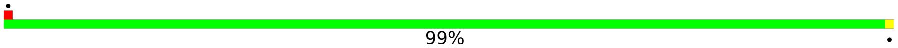
Chain AW:

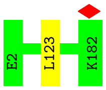




- Molecule 47: 50S ribosomal protein L25

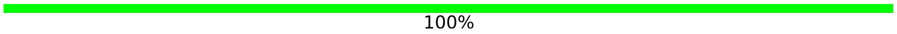
Chain AX:





- Molecule 48: 50S ribosomal protein L27

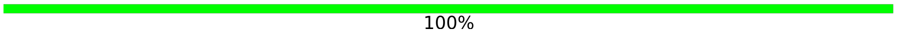
Chain AY:



There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L28

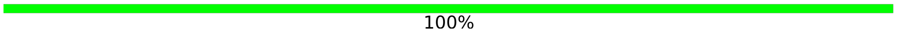
Chain AZ:



There are no outlier residues recorded for this chain.

- Molecule 50: 50S ribosomal protein L29

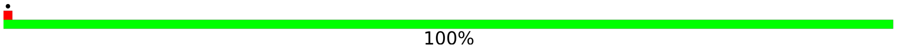
Chain Aa:

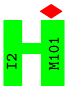


There are no outlier residues recorded for this chain.

- Molecule 51: 50S ribosomal protein uL30

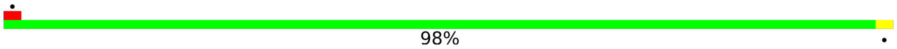
Chain Ab:

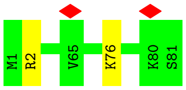




- Molecule 52: 50S ribosomal protein L31 type B

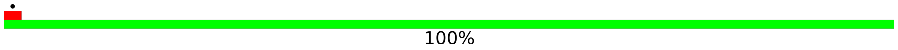
Chain Ac:

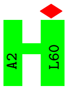




- Molecule 53: 50S ribosomal protein L32

Chain Ad:





- Molecule 54: 50S ribosomal protein L33

Chain Ae:

There are no outlier residues recorded for this chain.

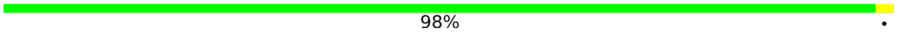
- Molecule 55: 50S ribosomal protein L34

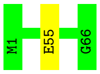
Chain Af:

There are no outlier residues recorded for this chain.

- Molecule 56: 50S ribosomal protein L35

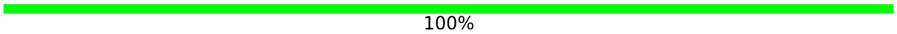
Chain Ag:





- Molecule 57: 50S ribosomal protein L36

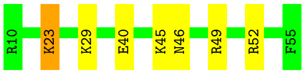
Chain Ah:



There are no outlier residues recorded for this chain.

- Molecule 58: 50S ribosomal protein bL38

Chain Ai:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	288776	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	67.527	Depositor
Minimum defocus (nm)	820	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.084	Depositor
Minimum map value	-0.439	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	493.245, 493.245, 493.245	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.25	0/36721	0.79	28/57268 (0.0%)
2	C	0.39	0/1673	0.53	0/2240
3	D	0.36	0/1716	0.55	1/2298 (0.0%)
4	E	0.42	0/1215	0.56	0/1626
5	F	0.38	0/826	0.62	0/1098
6	G	0.32	0/1302	0.55	0/1734
7	H	0.46	0/1053	0.58	0/1406
8	I	0.32	0/1056	0.50	0/1405
9	J	0.36	0/828	0.59	1/1108 (0.1%)
10	K	0.42	0/891	0.56	0/1201
11	L	0.39	0/983	0.52	0/1318
12	M	0.33	0/907	0.69	2/1208 (0.2%)
13	N	0.37	0/500	0.55	0/662
14	O	0.40	0/724	0.57	1/956 (0.1%)
15	P	0.36	0/685	0.48	0/913
16	Q	0.52	1/686 (0.1%)	0.61	0/910
17	R	0.39	0/532	0.54	0/705
18	S	0.33	0/683	0.79	5/917 (0.5%)
19	T	0.39	0/700	0.68	1/918 (0.1%)
20	U	0.34	0/609	0.74	3/800 (0.4%)
21	V	0.38	0/242	0.45	0/307
22	W	0.37	0/832	0.58	1/1110 (0.1%)
23	X	0.34	1/1807 (0.1%)	0.77	0/2812
24	AA	0.33	0/70389	0.83	156/109770 (0.1%)
25	AB	0.27	0/2684	0.72	0/4183
26	AC	0.24	0/883	0.45	0/1102
27	AD	0.54	0/2196	0.59	1/2935 (0.0%)
28	AE	0.52	0/1588	0.54	0/2122
29	AF	0.50	0/1682	0.54	1/2249 (0.0%)
30	AG	0.35	0/1460	0.53	1/1955 (0.1%)
31	AH	0.38	0/1422	0.50	0/1903
32	AI	0.30	0/756	0.51	0/973

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	AJ	0.23	0/647	0.43	0/807
34	AK	0.25	0/555	0.46	0/692
35	AL	0.54	0/1197	0.54	0/1612
36	AM	0.56	0/951	0.59	0/1276
37	AN	0.49	0/1142	0.59	0/1515
38	AO	0.51	0/1110	0.68	1/1480 (0.1%)
39	AP	0.52	0/1020	0.54	0/1353
40	AQ	0.38	0/979	0.62	2/1299 (0.2%)
41	AR	0.61	1/962 (0.1%)	0.65	0/1280
42	AS	0.59	0/954	0.60	0/1264
43	AT	0.56	0/872	0.53	0/1163
44	AU	0.53	0/931	0.57	0/1245
45	AV	0.47	0/796	0.54	0/1065
46	AW	0.40	0/803	0.55	0/1059
47	AX	0.38	0/1451	0.52	1/1955 (0.1%)
48	AY	0.53	0/577	0.52	0/760
49	AZ	0.45	0/713	0.53	0/943
50	Aa	0.41	0/559	0.58	0/739
51	Ab	0.47	0/818	0.55	0/1079
52	Ac	0.31	0/669	0.52	0/893
53	Ad	0.55	0/492	0.51	0/654
54	Ae	0.44	0/429	0.68	0/568
55	Af	0.53	0/425	0.57	0/551
56	Ag	0.57	0/554	0.61	2/726 (0.3%)
57	Ah	0.49	0/306	0.54	0/400
58	Ai	0.72	1/381 (0.3%)	1.31	7/502 (1.4%)
All	All	0.35	4/160524 (0.0%)	0.76	215/238992 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	X	1	G	OP3-P	-10.73	1.48	1.61
16	Q	78	GLU	CG-CD	-5.97	1.43	1.51
58	Ai	40	GLU	CD-OE2	-5.81	1.19	1.25
41	AR	33	GLU	CB-CG	-5.18	1.42	1.52

The worst 5 of 215 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	999	A	O5'-P-OP1	-31.82	72.51	110.70
24	AA	1559	G	O5'-P-OP1	-31.12	73.36	110.70
24	AA	1967	A	O5'-P-OP1	-31.07	73.41	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	AA	1677	A	O5'-P-OP1	-31.06	73.43	110.70
1	A	1265	G	O5'-P-OP1	-29.81	74.93	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
3	D	206/208 (99%)	196 (95%)	10 (5%)	0	100	100
4	E	156/158 (99%)	147 (94%)	9 (6%)	0	100	100
5	F	95/97 (98%)	88 (93%)	7 (7%)	0	100	100
6	G	155/157 (99%)	138 (89%)	17 (11%)	0	100	100
7	H	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
8	I	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
9	J	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
10	K	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
11	L	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
12	M	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
13	N	58/60 (97%)	57 (98%)	1 (2%)	0	100	100
14	O	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
15	P	81/83 (98%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
17	R	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
18	S	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
19	T	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
20	U	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
21	V	25/28 (89%)	24 (96%)	1 (4%)	0	100	100
22	W	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
26	AC	219/221 (99%)	211 (96%)	8 (4%)	0	100	100
27	AD	275/277 (99%)	259 (94%)	16 (6%)	0	100	100
28	AE	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
29	AF	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
30	AG	180/182 (99%)	168 (93%)	12 (7%)	0	100	100
31	AH	178/180 (99%)	170 (96%)	8 (4%)	0	100	100
32	AI	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
33	AJ	160/162 (99%)	153 (96%)	7 (4%)	0	100	100
34	AK	137/139 (99%)	131 (96%)	6 (4%)	0	100	100
35	AL	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
36	AM	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
37	AN	143/145 (99%)	116 (81%)	27 (19%)	0	100	100
38	AO	136/138 (99%)	118 (87%)	17 (12%)	1 (1%)	22	50
39	AP	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
40	AQ	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
41	AR	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
42	AS	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
43	AT	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
44	AU	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
45	AV	96/98 (98%)	92 (96%)	4 (4%)	0	100	100
46	AW	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
47	AX	179/181 (99%)	168 (94%)	11 (6%)	0	100	100
48	AY	72/74 (97%)	69 (96%)	3 (4%)	0	100	100
49	AZ	89/91 (98%)	86 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	Aa	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
51	Ab	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
52	Ac	79/81 (98%)	67 (85%)	12 (15%)	0	100	100
53	Ad	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
54	Ae	49/51 (96%)	42 (86%)	7 (14%)	0	100	100
55	Af	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
56	Ag	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
57	Ah	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
58	Ai	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
All	All	6239/6348 (98%)	5831 (94%)	407 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	AO	70	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	179/179 (100%)	179 (100%)	0	100	100
3	D	184/184 (100%)	184 (100%)	0	100	100
4	E	125/125 (100%)	124 (99%)	1 (1%)	81	93
5	F	88/88 (100%)	86 (98%)	2 (2%)	50	78
6	G	136/136 (100%)	135 (99%)	1 (1%)	84	94
7	H	115/115 (100%)	115 (100%)	0	100	100
8	I	113/113 (100%)	112 (99%)	1 (1%)	78	92
9	J	93/93 (100%)	93 (100%)	0	100	100
10	K	91/91 (100%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	106/106 (100%)	106 (100%)	0	100	100
12	M	99/99 (100%)	99 (100%)	0	100	100
13	N	53/53 (100%)	53 (100%)	0	100	100
14	O	79/79 (100%)	79 (100%)	0	100	100
15	P	75/75 (100%)	75 (100%)	0	100	100
16	Q	79/79 (100%)	79 (100%)	0	100	100
17	R	56/56 (100%)	56 (100%)	0	100	100
18	S	76/76 (100%)	76 (100%)	0	100	100
19	T	75/75 (100%)	75 (100%)	0	100	100
20	U	65/65 (100%)	64 (98%)	1 (2%)	65	86
21	V	26/27 (96%)	26 (100%)	0	100	100
22	W	91/91 (100%)	91 (100%)	0	100	100
27	AD	229/229 (100%)	229 (100%)	0	100	100
28	AE	168/168 (100%)	168 (100%)	0	100	100
29	AF	181/181 (100%)	180 (99%)	1 (1%)	86	95
30	AG	155/155 (100%)	154 (99%)	1 (1%)	86	95
31	AH	156/156 (100%)	155 (99%)	1 (1%)	86	95
32	AI	34/134 (25%)	34 (100%)	0	100	100
35	AL	127/127 (100%)	127 (100%)	0	100	100
36	AM	103/103 (100%)	103 (100%)	0	100	100
37	AN	124/124 (100%)	123 (99%)	1 (1%)	81	93
38	AO	115/115 (100%)	114 (99%)	1 (1%)	78	92
39	AP	110/110 (100%)	110 (100%)	0	100	100
40	AQ	104/104 (100%)	103 (99%)	1 (1%)	76	91
41	AR	103/103 (100%)	103 (100%)	0	100	100
42	AS	99/99 (100%)	98 (99%)	1 (1%)	76	91
43	AT	96/96 (100%)	96 (100%)	0	100	100
44	AU	100/100 (100%)	99 (99%)	1 (1%)	76	91
45	AV	88/88 (100%)	88 (100%)	0	100	100
46	AW	89/89 (100%)	86 (97%)	3 (3%)	37	67
47	AX	163/163 (100%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	AY	60/60 (100%)	60 (100%)	0	100	100
49	AZ	76/76 (100%)	76 (100%)	0	100	100
50	Aa	61/61 (100%)	61 (100%)	0	100	100
51	Ab	93/93 (100%)	93 (100%)	0	100	100
52	Ac	73/73 (100%)	71 (97%)	2 (3%)	44	74
53	Ad	54/54 (100%)	54 (100%)	0	100	100
54	Ae	48/48 (100%)	48 (100%)	0	100	100
55	Af	44/44 (100%)	44 (100%)	0	100	100
56	Ag	61/61 (100%)	61 (100%)	0	100	100
57	Ah	36/36 (100%)	36 (100%)	0	100	100
58	Ai	40/40 (100%)	37 (92%)	3 (8%)	13	34
All	All	4994/5095 (98%)	4972 (100%)	22 (0%)	91	96

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	AW	50	ARG
52	Ac	2	ARG
46	AW	88	ASN
52	Ac	76	LYS
29	AF	21	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
39	AP	31	HIS
40	AQ	69	ASN
52	Ac	75	ASN
46	AW	88	ASN
36	AM	110	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1528/1529 (99%)	217 (14%)	17 (1%)
23	X	75/76 (98%)	18 (24%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	AA	2928/2929 (99%)	524 (17%)	42 (1%)
25	AB	111/112 (99%)	31 (27%)	4 (3%)
All	All	4642/4646 (99%)	790 (17%)	64 (1%)

5 of 790 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	9	A
1	A	11	G
1	A	33	U
1	A	34	A

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	AA	2831	U
24	AA	2922	A
24	AA	372	A
24	AA	350	U
25	AB	31	U

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

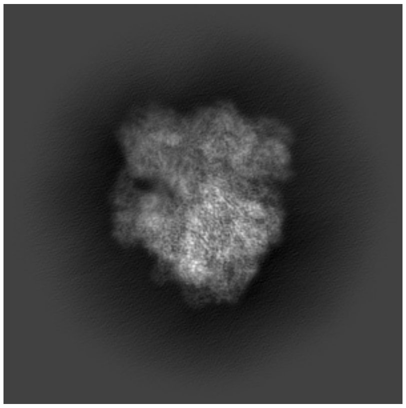
6 Map visualisation ⓘ

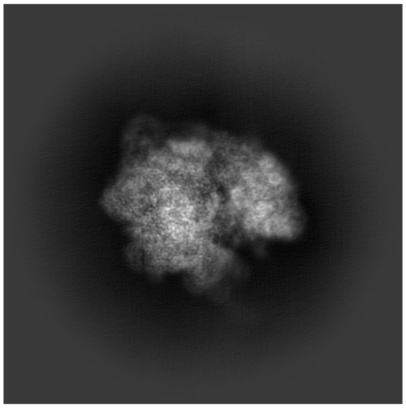
This section contains visualisations of the EMDB entry EMD-29298. These allow visual inspection of the internal detail of the map and identification of artifacts.

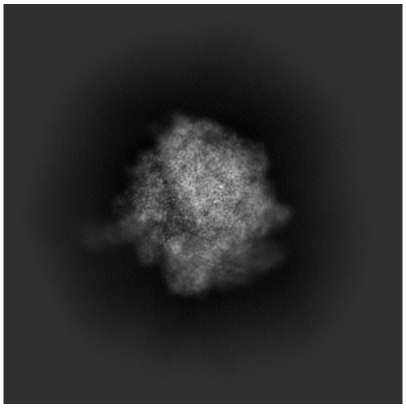
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ

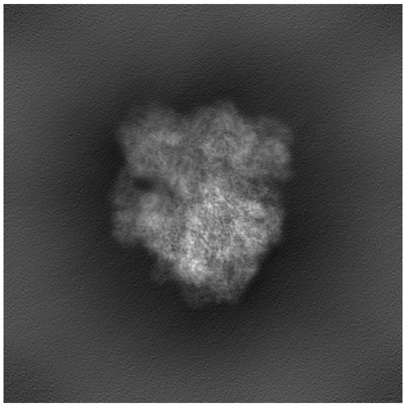
6.1.1 Primary map

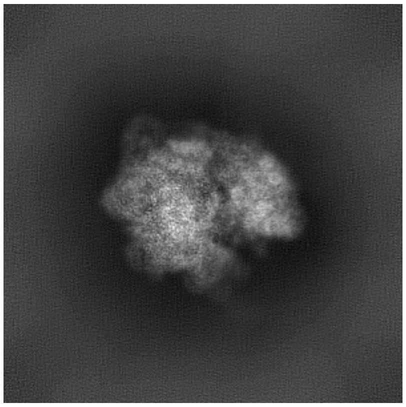

X

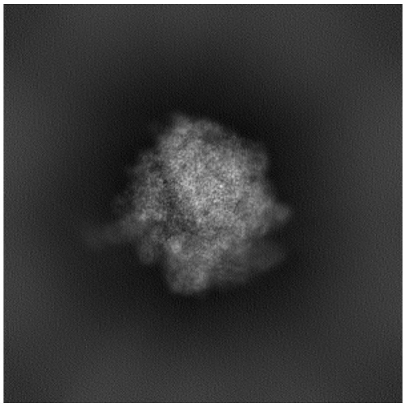

Y


Z

6.1.2 Raw map


X

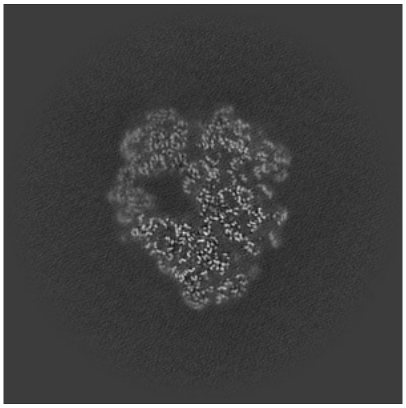

Y


Z

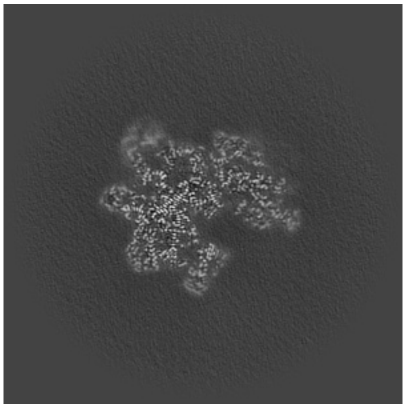
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

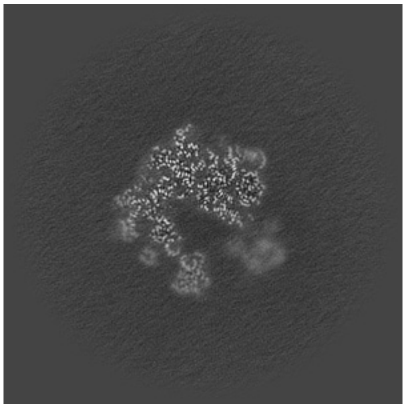
6.2.1 Primary map



X Index: 225

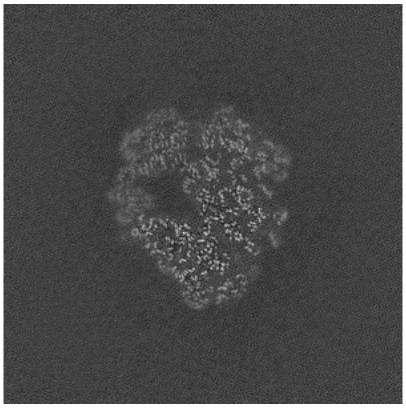


Y Index: 225

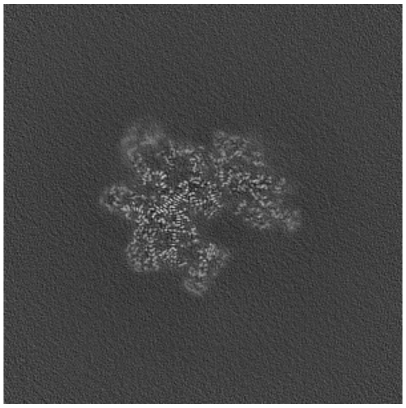


Z Index: 225

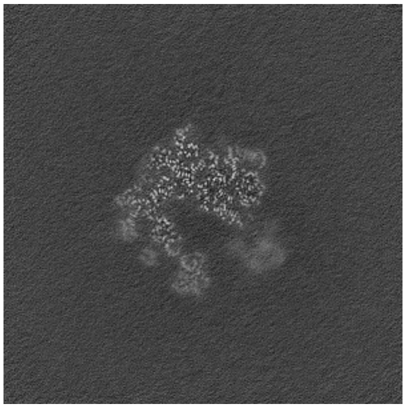
6.2.2 Raw map



X Index: 225



Y Index: 225

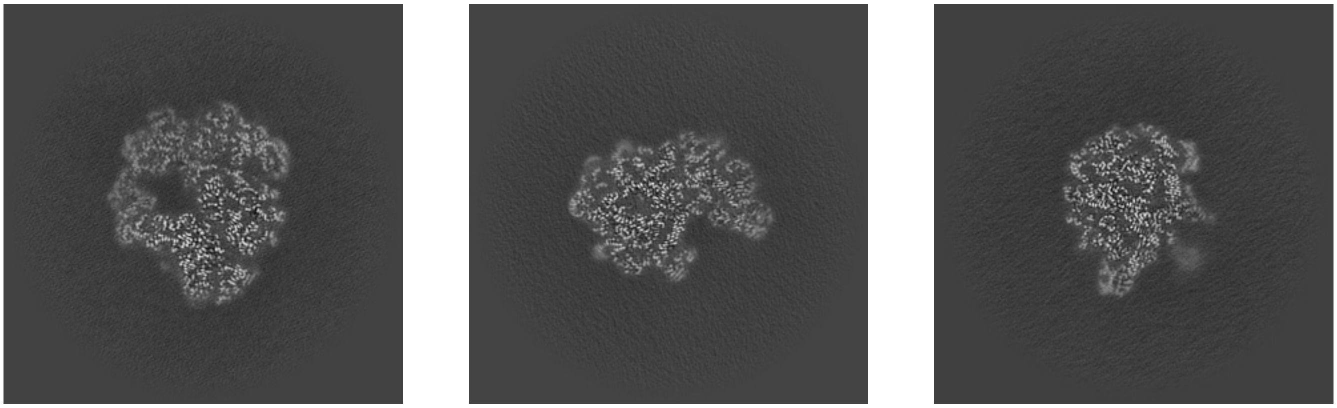


Z Index: 225

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

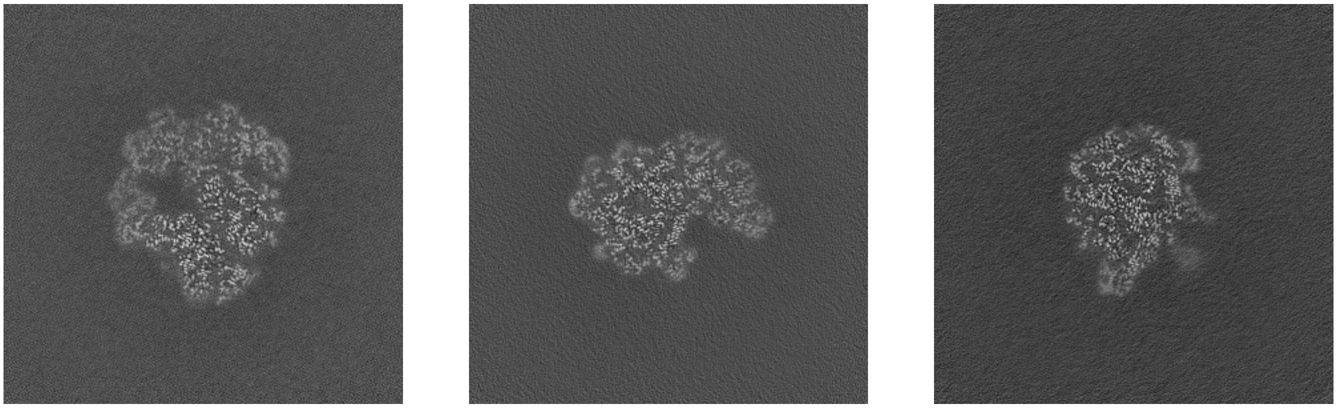
6.3 Largest variance slices

6.3.1 Primary map



X Index: 220 Y Index: 243 Z Index: 191

6.3.2 Raw map

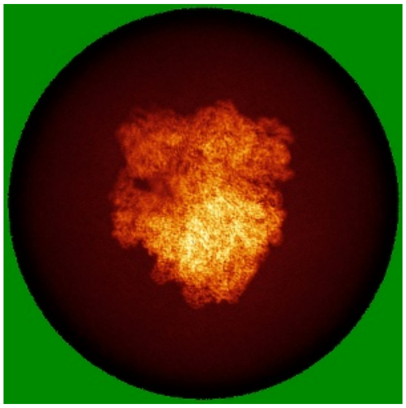


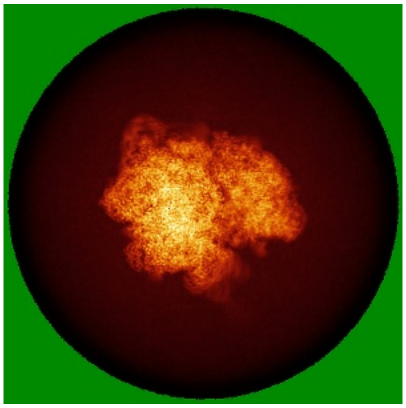
X Index: 220 Y Index: 243 Z Index: 191

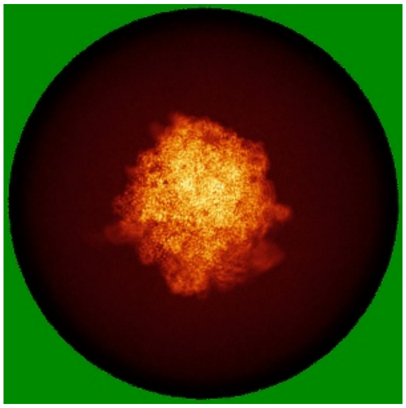
The images above show the largest variance slices of the map in three orthogonal directions.

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

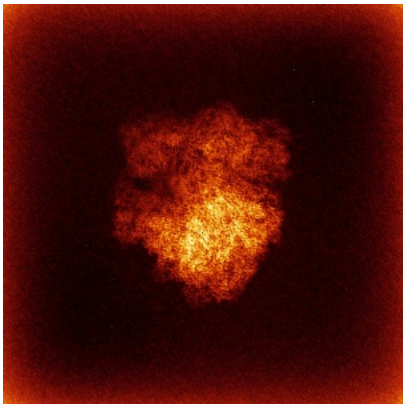
6.4.1 Primary map

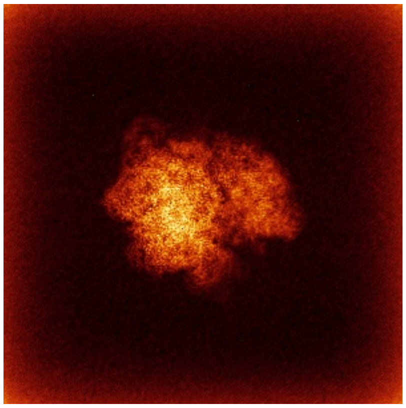

X

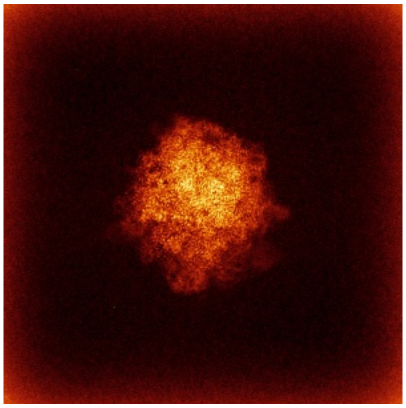

Y


Z

6.4.2 Raw map


X

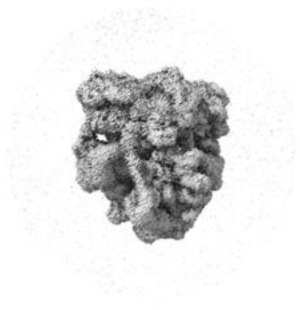

Y


Z

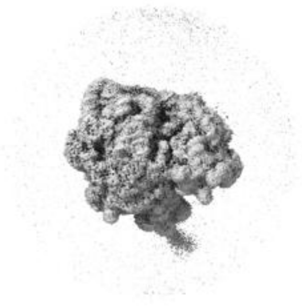
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

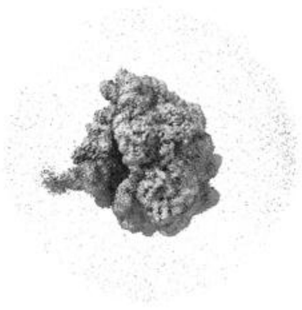
6.5.1 Primary map



X



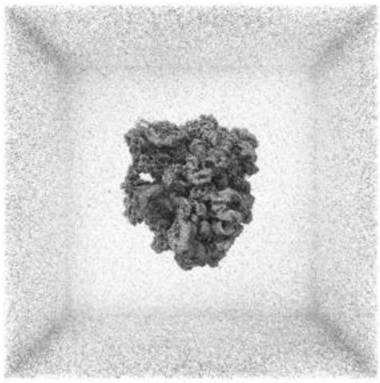
Y



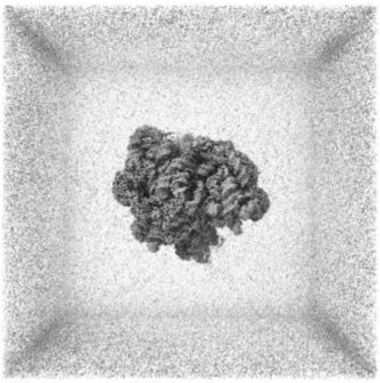
Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

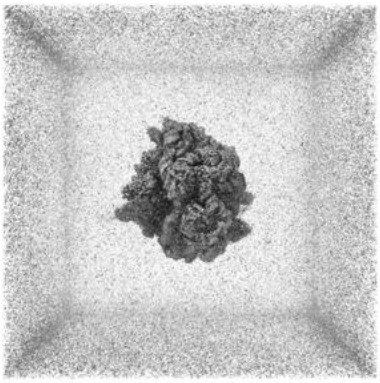
6.5.2 Raw map



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.

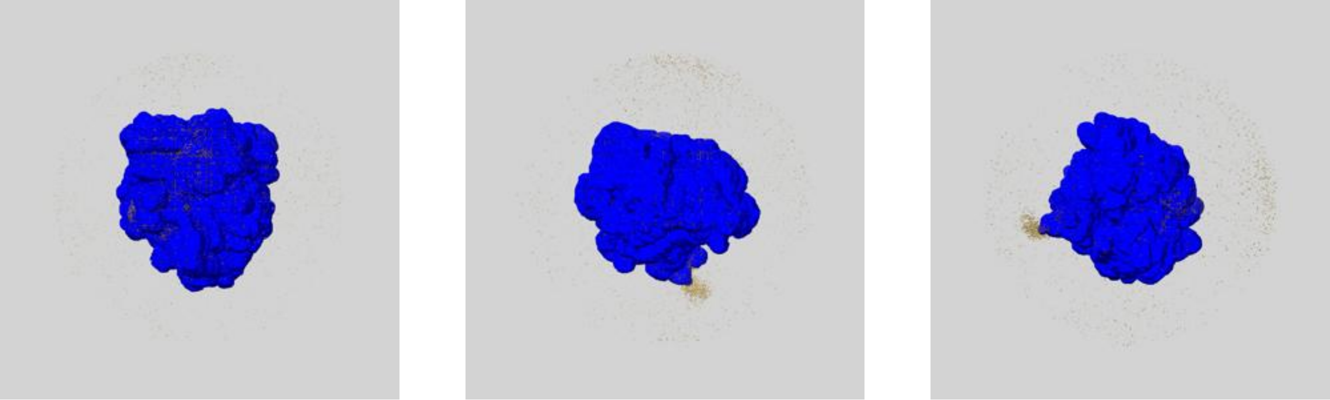
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

6.6.1 emd_29298_msk_1.map (i)

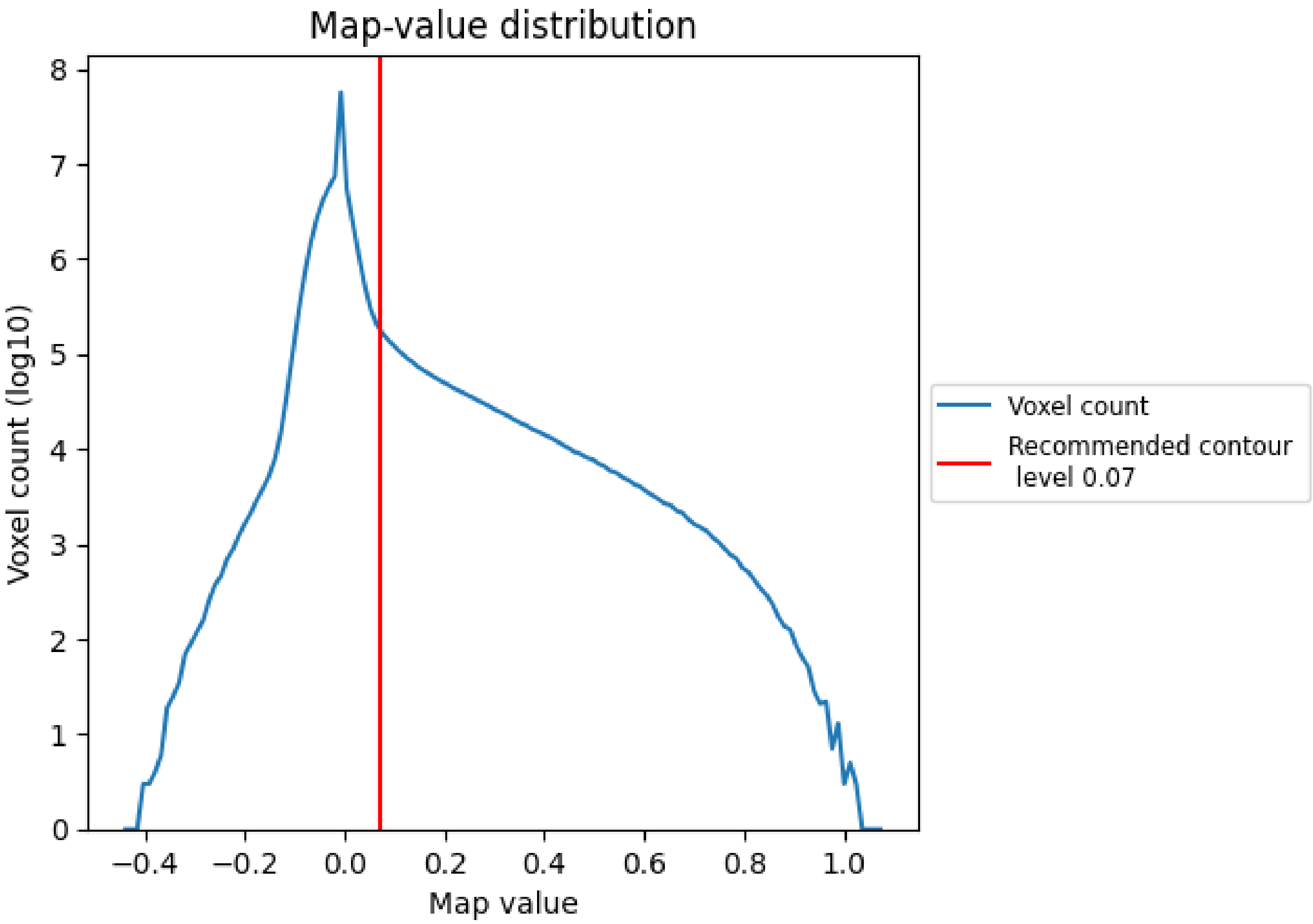


X Y Z

7 Map analysis ⓘ

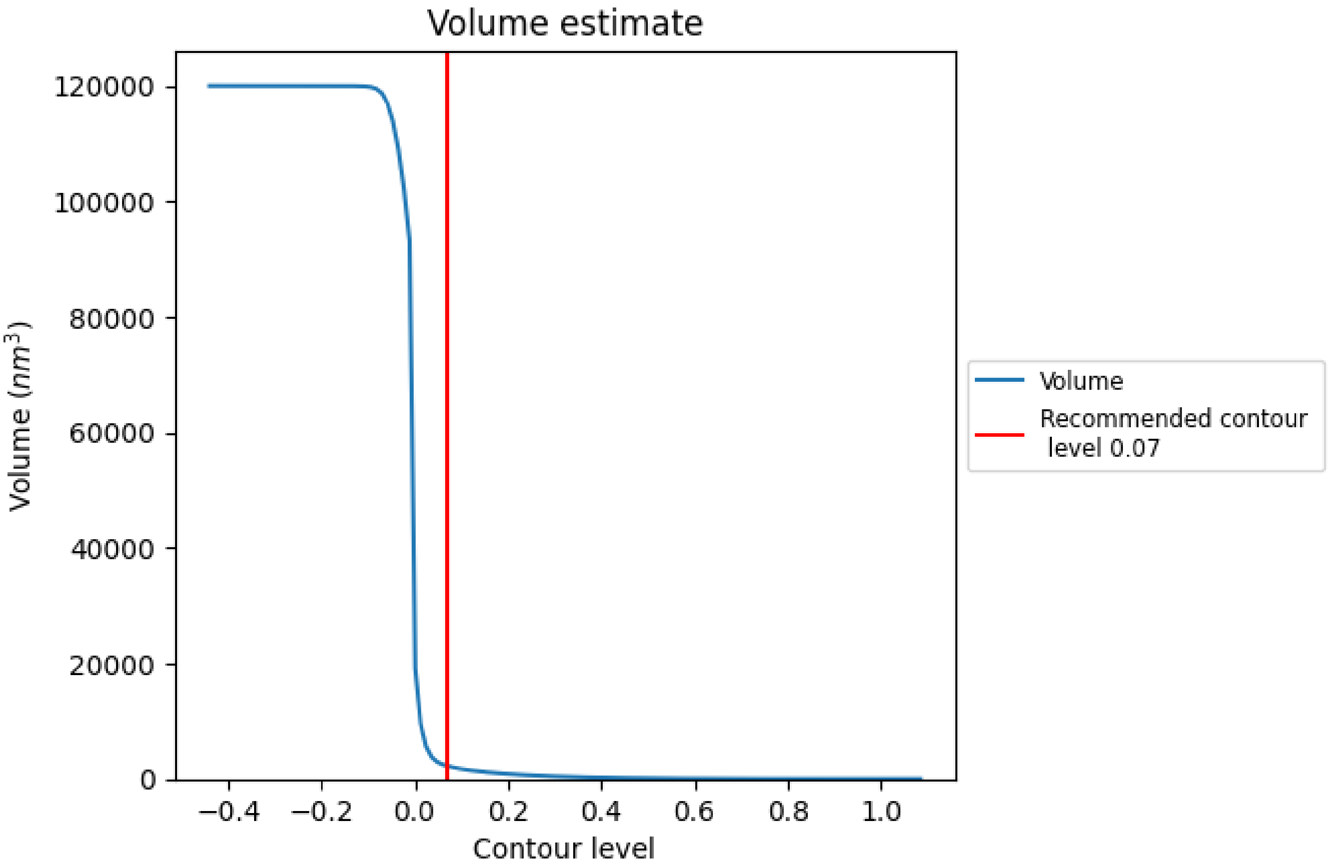
This section contains the results of statistical analysis of the map.

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.

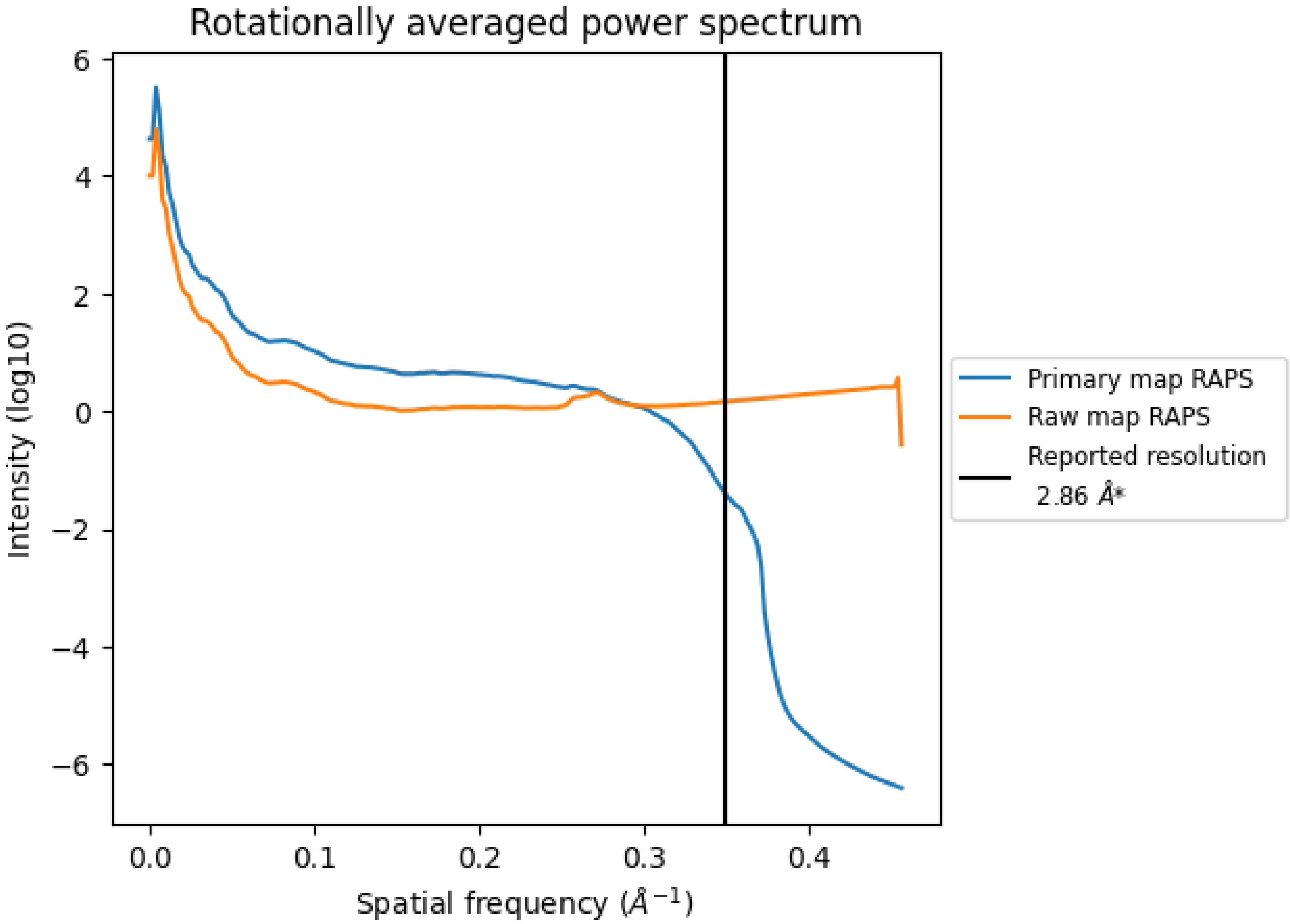
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 2290 nm^3; this corresponds to an approximate mass of 2069 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 ⓘ

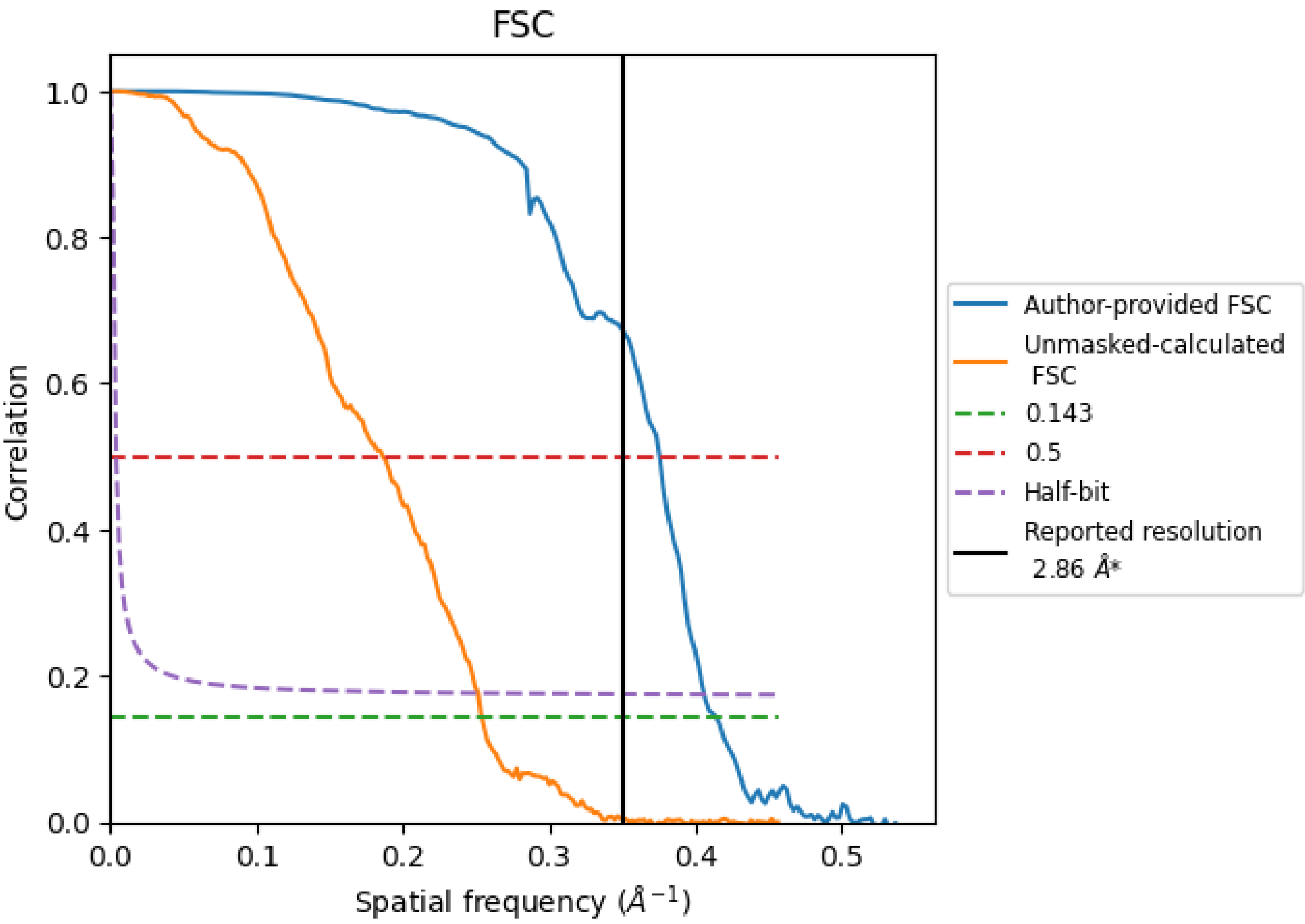


*Reported resolution corresponds to spatial frequency of 0.350 Å^{-1}

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 0.350 $Å^{-1}$

8.2 Resolution estimates ⓘ

Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.41	2.66	2.46
Unmasked-calculated*	3.94	5.36	3.98

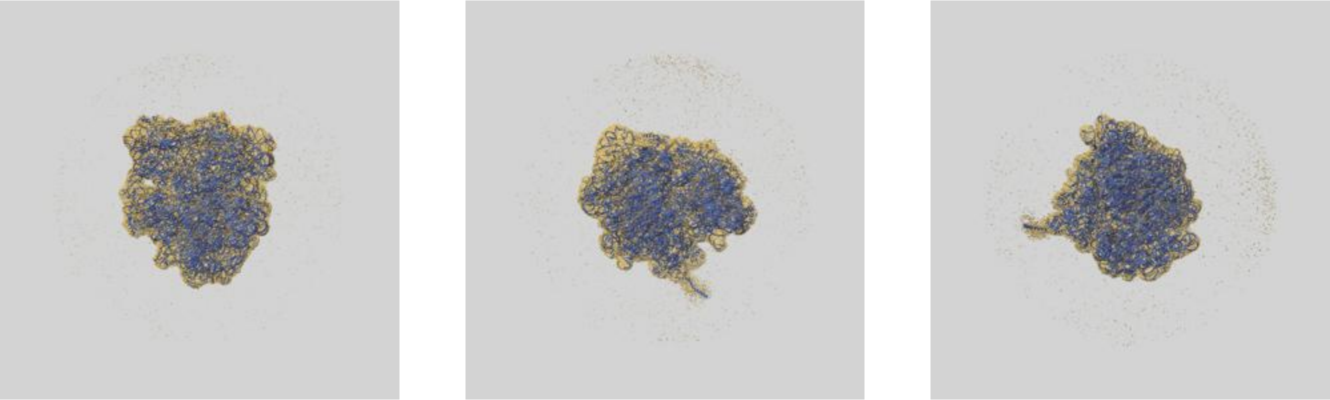
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.41 differs from the reported value 2.86 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.94 differs from the reported value 2.86 by more than 10 %

9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-29298 and PDB model 8FMW. Per-residue inclusion information can be found in section 3 on page 14.

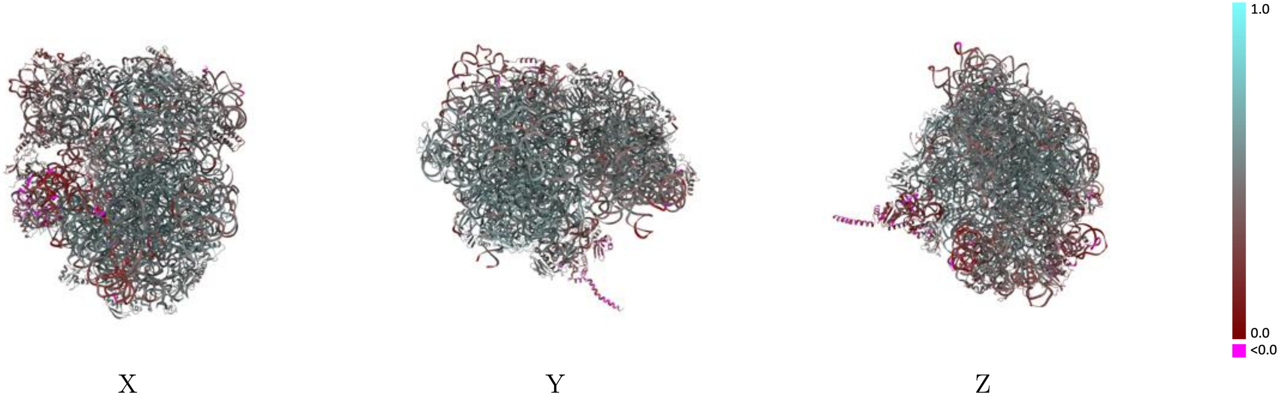
9.1 Map-model overlay (i)



X Y Z

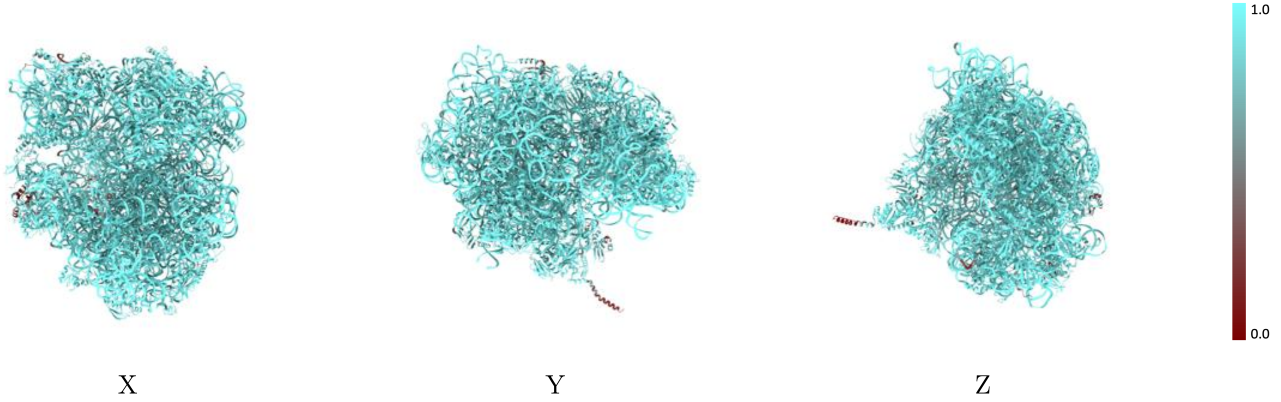
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ



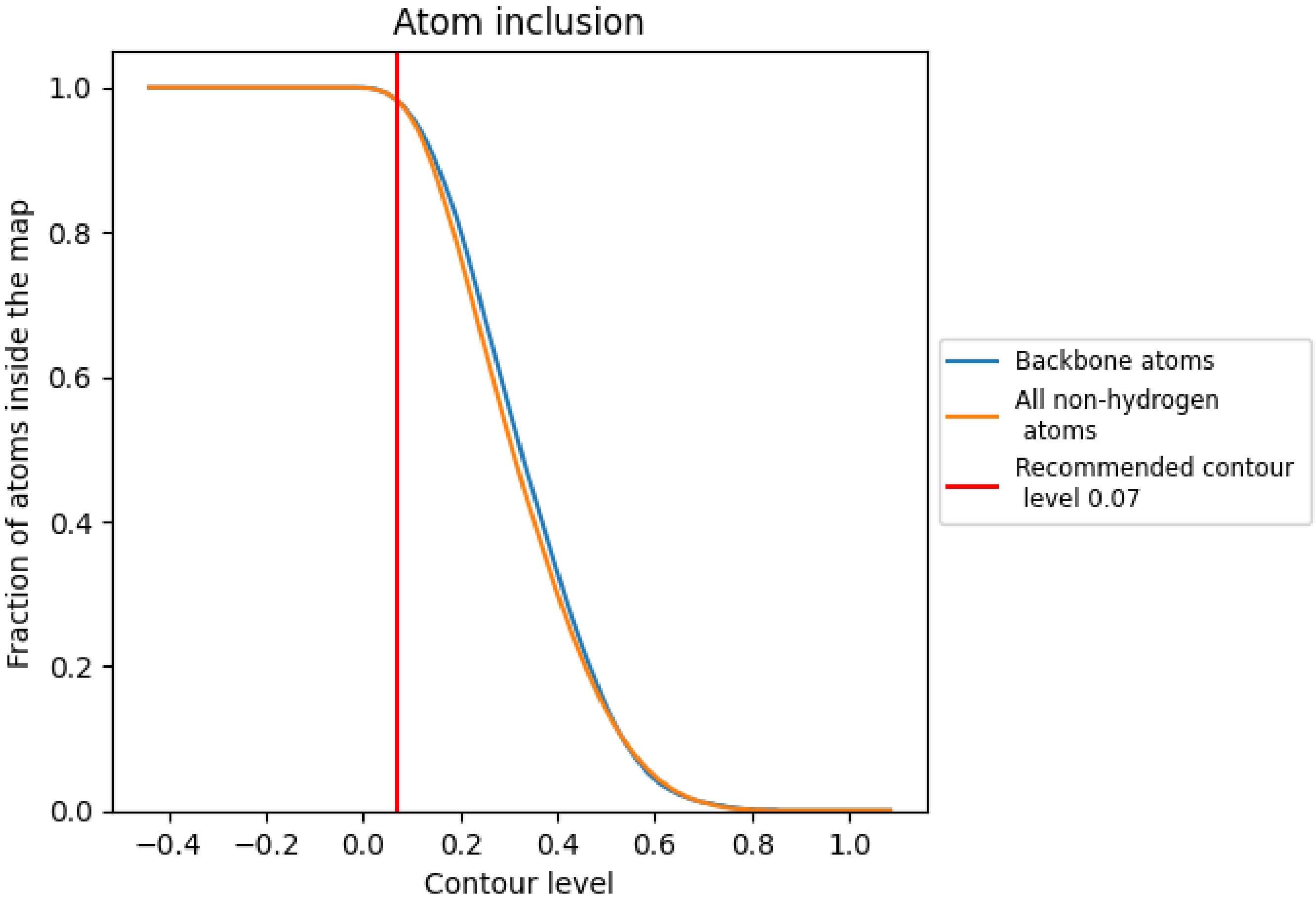
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9820	0.4840
A	0.9910	0.4700
AA	0.9930	0.5000
AB	0.9970	0.4510
AC	0.7340	0.1960
AD	0.9880	0.5780
AE	0.9940	0.5670
AF	0.9970	0.5480
AG	0.9860	0.4340
AH	0.9800	0.4740
AI	0.8320	0.3580
AJ	0.8300	0.2170
AK	0.8880	0.2360
AL	0.9930	0.5700
AM	0.9880	0.5760
AN	0.9730	0.5120
AO	0.9830	0.5420
AP	0.9890	0.5660
AQ	0.9870	0.4740
AR	0.9910	0.5480
AS	0.9820	0.5510
AT	0.9850	0.5370
AU	0.9880	0.5640
AV	0.9790	0.5280
AW	0.9400	0.4880
AX	0.9780	0.4350
AY	0.9980	0.5920
AZ	0.9860	0.5530
Aa	0.9760	0.4790
Ab	0.9910	0.5640
Ac	0.9290	0.3210
Ad	0.9810	0.5560
Ae	0.9810	0.5340
Af	0.9980	0.5930
Ag	0.9910	0.5820

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Chain	Atom inclusion	Q-score
Ah	■ 0.9770	■ 0.5590
Ai	■ 0.9640	■ 0.3980
C	■ 0.9450	■ 0.4380
D	■ 0.9760	■ 0.4510
E	■ 0.9750	■ 0.5080
F	■ 0.9750	■ 0.4180
G	■ 0.9620	■ 0.3930
H	■ 0.9820	■ 0.4960
I	■ 0.9670	■ 0.3780
J	■ 0.8770	■ 0.3970
K	■ 0.9840	■ 0.4780
L	■ 0.9820	■ 0.5340
M	■ 0.9460	■ 0.4190
N	■ 0.9550	■ 0.4430
O	■ 0.9870	■ 0.4820
P	■ 0.9880	■ 0.4870
Q	■ 0.9850	■ 0.5020
R	■ 0.9880	■ 0.4800
S	■ 0.9620	■ 0.3940
T	■ 0.9440	■ 0.4220
U	■ 0.8830	■ 0.3720
V	■ 0.9830	■ 0.5760
W	■ 0.9490	■ 0.5020
X	■ 0.8620	■ 0.2780