



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 09:07 pm BST

PDB ID : 6Z6J
EMDB ID : EMD-11096
Title : Cryo-EM structure of yeast Lso2 bound to 80S ribosomes under native condition
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.
Deposited on : 2020-05-28
Resolution : 3.40 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:

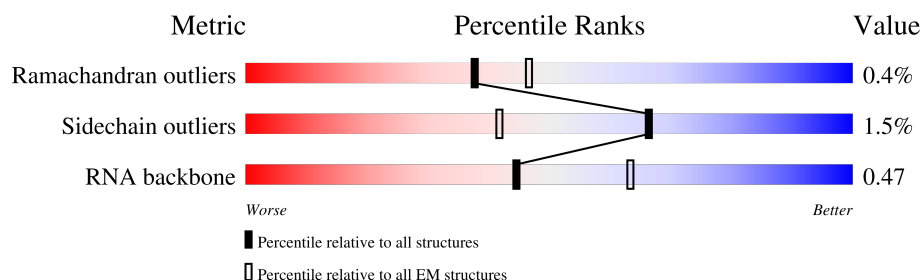
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 3.40 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C2	1800	<div> <div>14%</div> <div>58%</div> <div>31%</div> <div>6%</div> <div>6%</div> </div>
2	C5	92	<div> <div>52%</div> <div>86%</div> <div>14%</div> </div>
3	C1	3396	<div> <div>5%</div> <div>60%</div> <div>28%</div> <div>•</div> <div>8%</div> </div>
4	C4	121	<div> <div>74%</div> <div>26%</div> </div>
5	C3	158	<div> <div>66%</div> <div>30%</div> <div>•</div> <div>•</div> </div>
6	SA	252	<div> <div>9%</div> <div>79%</div> <div>•</div> <div>18%</div> </div>
7	SB	255	<div> <div>11%</div> <div>83%</div> <div>•</div> <div>15%</div> </div>
8	SC	254	<div> <div>83%</div> <div>•</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
9	SD	240	<div> <div>51%</div> <div>90%</div> <div>7%</div> </div>
10	SE	261	<div> <div>7%</div> <div>96%</div> <div></div> </div>
11	SF	225	<div> <div>50%</div> <div>88%</div> <div>8%</div> </div>
12	SG	236	<div> <div>21%</div> <div>90%</div> <div>8%</div> </div>
13	SH	190	<div> <div>26%</div> <div>91%</div> <div>5%</div> </div>
14	SI	200	<div> <div>6%</div> <div>94%</div> <div>6%</div> </div>
15	SJ	197	<div> <div>12%</div> <div>89%</div> <div>6%</div> </div>
16	SK	105	<div> <div>63%</div> <div>86%</div> <div>12%</div> </div>
17	SL	156	<div> <div>11%</div> <div>92%</div> <div>6%</div> </div>
18	SM	143	<div> <div>82%</div> <div>81%</div> <div>5%</div> </div>
19	SN	151	<div> <div>5%</div> <div>96%</div> <div></div> </div>
20	SO	137	<div> <div>6%</div> <div>91%</div> <div>7%</div> </div>
21	SP	142	<div> <div>69%</div> <div>80%</div> <div>16%</div> </div>
22	SQ	143	<div> <div>56%</div> <div>94%</div> <div></div> </div>
23	SR	136	<div> <div>29%</div> <div>83%</div> <div>15%</div> </div>
24	SS	146	<div> <div>66%</div> <div>96%</div> <div></div> </div>
25	ST	144	<div> <div>58%</div> <div>99%</div> <div></div> </div>
26	SU	121	<div> <div>55%</div> <div>79%</div> <div>17%</div> </div>
27	SV	87	<div> <div>8%</div> <div>97%</div> <div></div> </div>
28	SW	130	<div> <div></div> <div>97%</div> <div></div> </div>
29	SX	145	<div> <div>5%</div> <div>97%</div> <div></div> </div>
30	SY	135	<div> <div>15%</div> <div>96%</div> <div></div> </div>
31	SZ	108	<div> <div>42%</div> <div>63%</div> <div>36%</div> </div>
32	Sa	119	<div> <div>9%</div> <div>78%</div> <div>18%</div> </div>
33	Sb	82	<div> <div>18%</div> <div>94%</div> <div></div> </div>

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Mol	Chain	Length	Quality of chain
34	Sc	67	
35	Sd	56	
36	Se	63	
37	Sf	152	
38	Sg	319	
39	LA	254	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 196350 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1700	Total	C	N	O	P	0	0
			36234	16201	6426	11907	1700		

- Molecule 2 is a protein called Protein LSO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C5	79	Total	C	N	O	S	0	0
			633	379	128	125	1		

- Molecule 3 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C1	3127	Total	C	N	O	P	0	0
			66891	29878	12066	21820	3127		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C3	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SA	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 7 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SB	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 8 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 9 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 11 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SG	218	Total	C	N	O	S	0	0
			1751	1100	337	311	3		

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	SH	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 14 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SK	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SL	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 18 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SM	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 19 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 20 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SO	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 21 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SP	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 23 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SR	115	Total	C	N	O	S	0	0
			896	557	172	165	2		

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 26 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SU	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 28 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 31 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SZ	69	Total	C	N	O		0	0
			558	357	103	98			

- Molecule 32 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 35 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Se	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 37 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Sf	33	Total	C	N	O	S	0	0
			248	153	46	45	4		

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Sg	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LI	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	LL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LO	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	LP	175	Total	C	N	O	0	0
			1378	856	273	249		

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	LR	174	Total	C	N	O	0	0
			1359	840	283	236		

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LU	98	Total	C	N	O		0	0
			778	505	127	146			

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LV	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 60 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LW	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LY	124	Total	C	N	O		0	0
			976	614	190	172			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	Lb	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ld	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 68 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Le	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Li	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lj	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

- Molecule 74 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	Lk	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 77 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Lo	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	C2	1	Total	Zn	0
			1	1	
80	Sa	1	Total	Zn	0
			1	1	
80	Sb	1	Total	Zn	0
			1	1	
80	Sf	1	Total	Zn	0
			1	1	
80	Lg	1	Total	Zn	0
			1	1	
80	Lj	1	Total	Zn	0
			1	1	
80	Lm	1	Total	Zn	0
			1	1	
80	Lo	1	Total	Zn	0
			1	1	
80	Lp	1	Total	Zn	0
			1	1	

SEQUENCE-PLOTS INFOmissingINFO

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34951	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.865	Depositor
Minimum map value	-0.566	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

4 Model quality ⓘ

4.1 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	C2	1.06	19/40528 (0.0%)	1.42	623/63141 (1.0%)
2	C5	0.37	0/636	0.51	0/837
3	C1	1.34	50/74873 (0.1%)	1.37	901/116727 (0.8%)
4	C4	1.14	0/2883	1.28	18/4491 (0.4%)
5	C3	1.31	3/3724 (0.1%)	1.28	34/5798 (0.6%)
6	SA	0.51	0/1623	0.71	0/2222
7	SB	0.52	0/1748	0.70	2/2352 (0.1%)
8	SC	0.55	0/1665	0.70	0/2263
9	SD	0.41	0/1759	0.68	1/2368 (0.0%)
10	SE	0.55	0/2109	0.70	1/2839 (0.0%)
11	SF	0.40	0/1629	0.66	0/2202
12	SG	0.45	0/1775	0.68	2/2374 (0.1%)
13	SH	0.50	0/1511	0.76	2/2036 (0.1%)
14	SI	0.62	0/1514	0.66	0/2021
15	SJ	0.49	0/1519	0.65	0/2035
16	SK	0.40	0/757	0.64	0/1022
17	SL	0.64	0/1194	0.63	0/1610
18	SM	0.36	0/898	0.84	1/1220 (0.1%)
19	SN	0.54	0/1215	0.69	1/1638 (0.1%)
20	SO	0.56	0/960	0.70	0/1290
21	SP	0.44	0/959	0.74	1/1288 (0.1%)
22	SQ	0.42	0/1125	0.71	1/1510 (0.1%)
23	SR	0.41	0/904	0.62	0/1210
24	SS	0.39	0/1211	0.64	0/1628
25	ST	0.40	0/1130	0.62	1/1517 (0.1%)
26	SU	0.42	0/815	0.69	0/1102
27	SV	0.55	0/693	0.67	1/935 (0.1%)
28	SW	0.63	0/1038	0.67	0/1395
29	SX	0.58	0/1139	0.67	0/1518
30	SY	0.48	0/1087	0.67	0/1449
31	SZ	0.38	0/566	0.71	0/761
32	Sa	0.56	0/782	0.68	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sb	0.49	0/620	0.73	2/838 (0.2%)
34	Sc	0.40	0/499	0.73	0/670
35	Sd	0.42	0/452	0.65	0/600
36	Se	0.46	0/483	0.62	0/643
37	Sf	0.40	0/253	0.70	0/340
38	Sg	0.37	0/2456	0.69	1/3343 (0.0%)
39	LA	0.72	0/1946	0.74	1/2614 (0.0%)
40	LB	0.69	0/3146	0.67	0/4228
41	LC	0.66	0/2800	0.71	1/3790 (0.0%)
42	LD	0.54	0/2408	0.62	1/3248 (0.0%)
43	LE	0.57	0/1269	0.65	0/1705
44	LF	0.66	0/1828	0.70	3/2461 (0.1%)
45	LG	0.62	0/1795	0.71	0/2429
46	LH	0.54	0/1531	0.64	0/2062
47	LI	0.57	0/1732	0.63	0/2323
48	LJ	0.52	0/1374	0.77	0/1842
49	LL	0.63	0/1573	0.78	3/2113 (0.1%)
50	LM	0.57	0/1074	0.63	0/1446
51	LN	0.75	0/1757	0.72	2/2354 (0.1%)
52	LO	0.63	0/1585	0.67	1/2128 (0.0%)
53	LP	0.69	0/1400	0.67	0/1882
54	LQ	0.60	1/1465 (0.1%)	0.69	0/1965
55	LR	0.66	1/1376 (0.1%)	0.64	0/1842
56	LS	0.66	0/1481	0.65	0/1990
57	LT	0.66	0/1300	0.65	0/1743
58	LU	0.56	0/794	0.60	0/1076
59	LV	0.62	0/1008	0.70	0/1356
60	LW	0.64	0/533	0.64	0/707
61	LX	0.62	0/974	0.69	0/1314
62	LY	0.54	0/987	0.62	0/1318
63	LZ	0.64	0/1118	0.63	0/1497
64	La	0.66	0/1204	0.70	1/1612 (0.1%)
65	Lb	0.47	0/473	0.70	0/629
66	Lc	0.60	0/775	0.67	0/1040
67	Ld	0.66	0/897	0.66	0/1205
68	Le	0.63	0/1041	0.68	0/1394
69	Lf	0.77	0/868	0.67	0/1168
70	Lg	0.65	0/890	0.67	0/1189
71	Lh	0.56	0/974	0.61	0/1297
72	Li	0.51	0/777	0.62	0/1033
73	Lj	0.79	0/665	0.69	0/882
74	Lk	0.53	0/614	0.70	0/822
75	Ll	0.65	0/443	0.68	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lm	0.62	0/423	0.62	0/562
77	Ln	0.49	0/234	0.55	0/300
78	Lo	0.57	0/860	0.60	0/1136
79	Lp	0.70	0/701	0.70	0/934
All	All	1.02	74/210825 (0.0%)	1.16	1606/309504 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	SA	0	4
7	SB	0	1
8	SC	0	1
10	SE	0	3
12	SG	0	1
13	SH	0	5
15	SJ	0	1
16	SK	0	2
18	SM	0	3
19	SN	0	2
20	SO	0	2
21	SP	0	2
22	SQ	0	2
24	SS	0	1
26	SU	0	3
28	SW	0	1
30	SY	0	2
31	SZ	0	1
32	Sa	0	2
33	Sb	0	2
36	Se	0	3
39	LA	0	4
40	LB	0	2
41	LC	0	4
45	LG	0	1
48	LJ	0	1
49	LL	0	4
51	LN	0	1
54	LQ	0	1
56	LS	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
58	LU	0	1
63	LZ	0	2
64	La	0	1
65	Lb	0	2
67	Ld	0	1
71	Lh	0	2
72	Li	0	1
79	Lp	0	1
All	All	0	74

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C2	853	G	N1-C2	-7.62	1.31	1.37
1	C2	818	C	N3-C4	-7.37	1.28	1.33
3	C1	2149	A	N9-C4	-6.94	1.33	1.37
1	C2	163	G	N9-C4	-6.62	1.32	1.38
3	C1	340	C	N1-C6	-6.59	1.33	1.37

The worst 5 of 1606 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	853	G	C2-N3-C4	27.75	125.78	111.90
1	C2	853	G	N1-C6-O6	-24.59	105.14	119.90
1	C2	853	G	N3-C4-C5	-19.87	118.66	128.60
1	C2	853	G	N9-C4-C5	19.21	113.08	105.40
1	C2	818	C	N1-C2-O2	17.25	129.25	118.90

There are no chirality outliers.

5 of 74 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	SA	184	LEU	Peptide
6	SA	186	GLY	Peptide
6	SA	43	ASP	Peptide
6	SA	94	GLY	Peptide
7	SB	105	PHE	Peptide

4.2 Too-close contacts

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

4.3 Torsion angles ⓘ

4.3.1 Protein backbone ⓘ

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	C5	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
6	SA	204/252 (81%)	175 (86%)	29 (14%)	0	100	100
7	SB	214/255 (84%)	190 (89%)	24 (11%)	0	100	100
8	SC	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	29	61
9	SD	221/240 (92%)	196 (89%)	25 (11%)	0	100	100
10	SE	258/261 (99%)	233 (90%)	24 (9%)	1 (0%)	34	67
11	SF	204/225 (91%)	177 (87%)	26 (13%)	1 (0%)	29	61
12	SG	216/236 (92%)	201 (93%)	15 (7%)	0	100	100
13	SH	183/190 (96%)	156 (85%)	24 (13%)	3 (2%)	9	34
14	SI	184/200 (92%)	173 (94%)	11 (6%)	0	100	100
15	SJ	183/197 (93%)	166 (91%)	15 (8%)	2 (1%)	14	44
16	SK	90/105 (86%)	70 (78%)	20 (22%)	0	100	100
17	SL	144/156 (92%)	123 (85%)	21 (15%)	0	100	100
18	SM	122/143 (85%)	83 (68%)	36 (30%)	3 (2%)	5	26
19	SN	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
20	SO	126/137 (92%)	109 (86%)	17 (14%)	0	100	100
21	SP	117/142 (82%)	95 (81%)	20 (17%)	2 (2%)	9	34
22	SQ	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	22	55
23	SR	111/136 (82%)	96 (86%)	15 (14%)	0	100	100
24	SS	143/146 (98%)	123 (86%)	20 (14%)	0	100	100
25	ST	141/144 (98%)	127 (90%)	14 (10%)	0	100	100
26	SU	99/121 (82%)	91 (92%)	7 (7%)	1 (1%)	15	46
27	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	13	41
28	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
29	SX	142/145 (98%)	128 (90%)	12 (8%)	2 (1%)	11	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	SY	132/135 (98%)	113 (86%)	17 (13%)	2 (2%)	10	36
31	SZ	67/108 (62%)	61 (91%)	6 (9%)	0	100	100
32	Sa	95/119 (80%)	80 (84%)	14 (15%)	1 (1%)	14	44
33	Sb	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	12	39
34	Sc	61/67 (91%)	53 (87%)	8 (13%)	0	100	100
35	Sd	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
36	Se	58/63 (92%)	46 (79%)	12 (21%)	0	100	100
37	Sf	31/152 (20%)	23 (74%)	8 (26%)	0	100	100
38	Sg	311/319 (98%)	275 (88%)	36 (12%)	0	100	100
39	LA	250/254 (98%)	213 (85%)	37 (15%)	0	100	100
40	LB	384/387 (99%)	352 (92%)	32 (8%)	0	100	100
41	LC	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	41	72
42	LD	292/297 (98%)	273 (94%)	19 (6%)	0	100	100
43	LE	153/176 (87%)	132 (86%)	21 (14%)	0	100	100
44	LF	221/244 (91%)	207 (94%)	14 (6%)	0	100	100
45	LG	229/256 (90%)	199 (87%)	30 (13%)	0	100	100
46	LH	188/191 (98%)	178 (95%)	10 (5%)	0	100	100
47	LI	205/221 (93%)	189 (92%)	15 (7%)	1 (0%)	29	61
48	LJ	167/174 (96%)	139 (83%)	25 (15%)	3 (2%)	8	32
49	LL	192/199 (96%)	164 (85%)	19 (10%)	9 (5%)	2	15
50	LM	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
51	LN	201/204 (98%)	180 (90%)	20 (10%)	1 (0%)	29	61
52	LO	195/199 (98%)	188 (96%)	6 (3%)	1 (0%)	29	61
53	LP	171/184 (93%)	159 (93%)	12 (7%)	0	100	100
54	LQ	183/186 (98%)	172 (94%)	11 (6%)	0	100	100
55	LR	172/189 (91%)	161 (94%)	11 (6%)	0	100	100
56	LS	170/172 (99%)	157 (92%)	13 (8%)	0	100	100
57	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
58	LU	96/121 (79%)	91 (95%)	5 (5%)	0	100	100
59	LV	132/137 (96%)	122 (92%)	10 (8%)	0	100	100
60	LW	61/155 (39%)	58 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	LX	118/142 (83%)	109 (92%)	9 (8%)	0	100	100
62	LY	122/127 (96%)	114 (93%)	8 (7%)	0	100	100
63	LZ	133/136 (98%)	114 (86%)	18 (14%)	1 (1%)	19	51
64	La	146/149 (98%)	130 (89%)	14 (10%)	2 (1%)	11	37
65	Lb	56/59 (95%)	46 (82%)	9 (16%)	1 (2%)	8	32
66	Lc	98/105 (93%)	89 (91%)	9 (9%)	0	100	100
67	Ld	107/113 (95%)	99 (92%)	8 (8%)	0	100	100
68	Le	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	19	51
69	Lf	104/107 (97%)	91 (88%)	13 (12%)	0	100	100
70	Lg	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
71	Lh	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
72	Li	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
73	Lj	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
74	Lk	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	12	39
75	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
76	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
77	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
78	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
79	Lp	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
All	All	10892/11972 (91%)	9760 (90%)	1088 (10%)	44 (0%)	38	67

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	SQ	116	LEU
41	LC	339	LEU
48	LJ	95	ASN
49	LL	48	PRO
49	LL	62	THR

4.3.2 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	C5	60/70 (86%)	60 (100%)	0	100	100
6	SA	165/210 (79%)	163 (99%)	2 (1%)	71	85
7	SB	192/224 (86%)	190 (99%)	2 (1%)	76	88
8	SC	176/205 (86%)	170 (97%)	6 (3%)	37	65
9	SD	182/195 (93%)	176 (97%)	6 (3%)	38	66
10	SE	221/222 (100%)	217 (98%)	4 (2%)	59	79
11	SF	173/191 (91%)	167 (96%)	6 (4%)	36	65
12	SG	186/201 (92%)	183 (98%)	3 (2%)	62	81
13	SH	165/170 (97%)	161 (98%)	4 (2%)	49	74
14	SI	150/161 (93%)	149 (99%)	1 (1%)	84	92
15	SJ	158/166 (95%)	151 (96%)	7 (4%)	28	58
16	SK	73/98 (74%)	73 (100%)	0	100	100
17	SL	129/137 (94%)	126 (98%)	3 (2%)	50	74
18	SM	88/119 (74%)	86 (98%)	2 (2%)	50	74
19	SN	127/128 (99%)	125 (98%)	2 (2%)	62	81
20	SO	97/105 (92%)	95 (98%)	2 (2%)	53	76
21	SP	98/118 (83%)	95 (97%)	3 (3%)	40	68
22	SQ	117/119 (98%)	115 (98%)	2 (2%)	60	80
23	SR	92/124 (74%)	90 (98%)	2 (2%)	52	75
24	SS	128/129 (99%)	124 (97%)	4 (3%)	40	68
25	ST	115/116 (99%)	114 (99%)	1 (1%)	78	90
26	SU	94/114 (82%)	92 (98%)	2 (2%)	53	76
27	SV	74/74 (100%)	73 (99%)	1 (1%)	67	83
28	SW	110/111 (99%)	108 (98%)	2 (2%)	59	79
29	SX	119/120 (99%)	116 (98%)	3 (2%)	47	72
30	SY	112/113 (99%)	111 (99%)	1 (1%)	78	90
31	SZ	61/89 (68%)	61 (100%)	0	100	100
32	Sa	83/100 (83%)	82 (99%)	1 (1%)	71	85
33	Sb	70/71 (99%)	70 (100%)	0	100	100
34	Sc	56/60 (93%)	55 (98%)	1 (2%)	59	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	Sd	47/49 (96%)	47 (100%)	0	100	100
36	Se	51/54 (94%)	51 (100%)	0	100	100
37	Sf	27/135 (20%)	27 (100%)	0	100	100
38	Sg	255/262 (97%)	253 (99%)	2 (1%)	81	91
39	LA	192/196 (98%)	187 (97%)	5 (3%)	46	72
40	LB	318/323 (98%)	311 (98%)	7 (2%)	52	75
41	LC	288/289 (100%)	285 (99%)	3 (1%)	76	88
42	LD	243/245 (99%)	242 (100%)	1 (0%)	91	95
43	LE	135/153 (88%)	133 (98%)	2 (2%)	65	82
44	LF	187/205 (91%)	186 (100%)	1 (0%)	88	94
45	LG	177/208 (85%)	175 (99%)	2 (1%)	73	86
46	LH	170/171 (99%)	168 (99%)	2 (1%)	71	85
47	LI	177/187 (95%)	176 (99%)	1 (1%)	86	94
48	LJ	147/150 (98%)	143 (97%)	4 (3%)	44	70
49	LL	154/159 (97%)	151 (98%)	3 (2%)	57	78
50	LM	108/109 (99%)	106 (98%)	2 (2%)	57	78
51	LN	175/176 (99%)	174 (99%)	1 (1%)	86	94
52	LO	160/162 (99%)	159 (99%)	1 (1%)	86	94
53	LP	139/146 (95%)	136 (98%)	3 (2%)	52	75
54	LQ	150/151 (99%)	150 (100%)	0	100	100
55	LR	132/154 (86%)	128 (97%)	4 (3%)	41	68
56	LS	156/156 (100%)	155 (99%)	1 (1%)	86	94
57	LT	136/137 (99%)	133 (98%)	3 (2%)	52	75
58	LU	85/107 (79%)	85 (100%)	0	100	100
59	LV	103/105 (98%)	102 (99%)	1 (1%)	76	88
60	LW	55/129 (43%)	54 (98%)	1 (2%)	59	79
61	LX	104/118 (88%)	102 (98%)	2 (2%)	57	78
62	LY	107/110 (97%)	105 (98%)	2 (2%)	57	78
63	LZ	115/116 (99%)	115 (100%)	0	100	100
64	La	118/119 (99%)	118 (100%)	0	100	100
65	Lb	46/47 (98%)	45 (98%)	1 (2%)	52	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Lc	84/88 (96%)	84 (100%)	0	100	100
67	Ld	94/97 (97%)	92 (98%)	2 (2%)	53	76
68	Le	109/111 (98%)	108 (99%)	1 (1%)	78	90
69	Lf	90/91 (99%)	89 (99%)	1 (1%)	73	86
70	Lg	95/103 (92%)	95 (100%)	0	100	100
71	Lh	103/105 (98%)	103 (100%)	0	100	100
72	Li	80/82 (98%)	79 (99%)	1 (1%)	69	84
73	Lj	67/71 (94%)	67 (100%)	0	100	100
74	Lk	67/69 (97%)	67 (100%)	0	100	100
75	Ll	45/46 (98%)	44 (98%)	1 (2%)	52	75
76	Lm	47/116 (40%)	47 (100%)	0	100	100
77	Ln	23/23 (100%)	23 (100%)	0	100	100
78	Lo	90/91 (99%)	90 (100%)	0	100	100
79	Lp	71/72 (99%)	70 (99%)	1 (1%)	67	83
All	All	9193/10053 (91%)	9058 (98%)	135 (2%)	66	82

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	LR	158	GLU
57	LT	82	ASN
68	Le	91	THR
20	SO	26	THR
19	SN	87	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
41	LC	320	ASN
47	LI	163	GLN
71	Lh	34	GLN
42	LD	274	GLN
45	LG	240	ASN

4.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1693/1800 (94%)	472 (27%)	31 (1%)
3	C1	3120/3396 (91%)	699 (22%)	39 (1%)
4	C4	120/121 (99%)	21 (17%)	0
5	C3	156/158 (98%)	37 (23%)	2 (1%)
All	All	5089/5475 (92%)	1229 (24%)	72 (1%)

5 of 1229 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	25	C
1	C2	26	A
1	C2	27	U

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	C1	2522	G
5	C3	106	C
3	C1	2714	G
3	C1	3269	U
1	C2	1255	G

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

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

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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.

4.7 Other polymers

There are no such residues in this entry.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

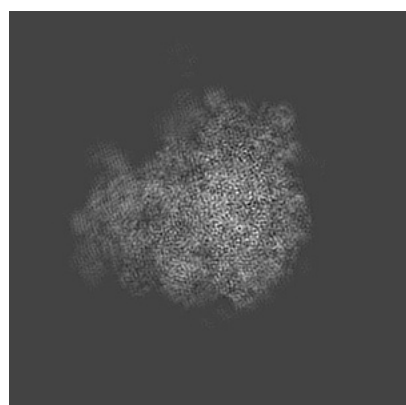
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11096. These allow visual inspection of the internal detail of the map and identification of artifacts.

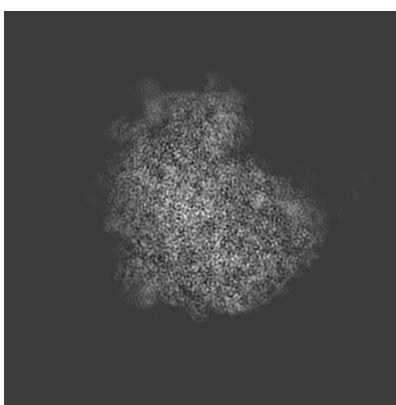
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

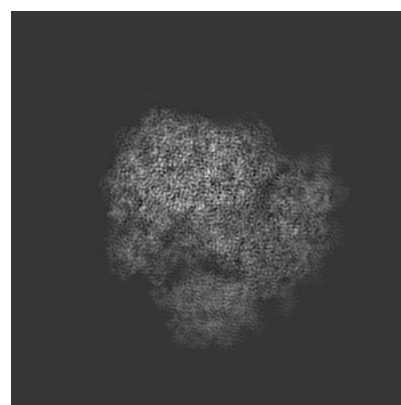
5.1.1 Primary map



X



Y

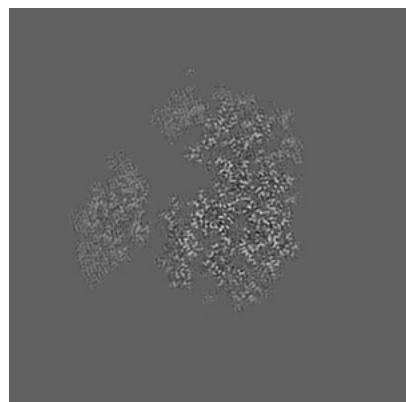


Z

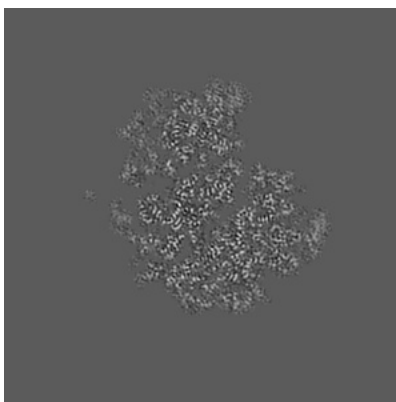
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

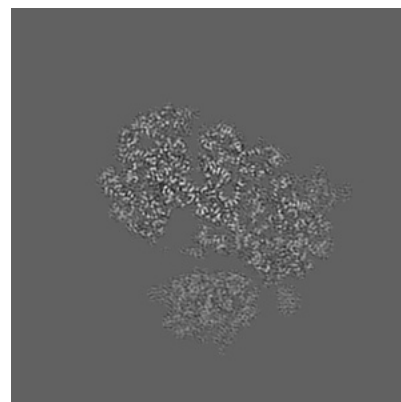
5.2.1 Primary map



X Index: 200



Y Index: 200

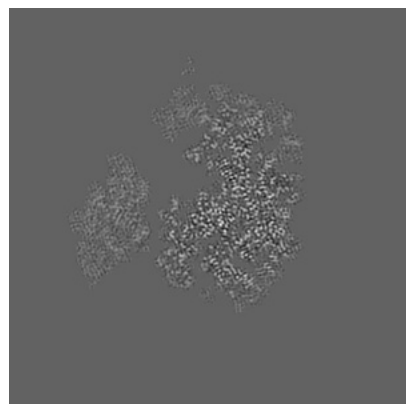


Z Index: 200

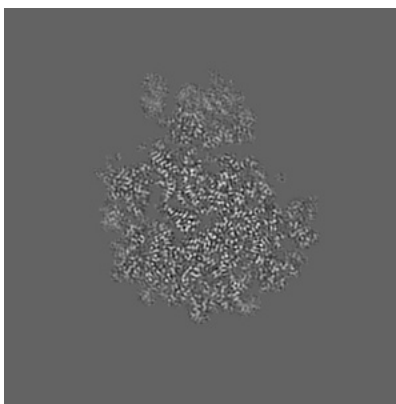
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

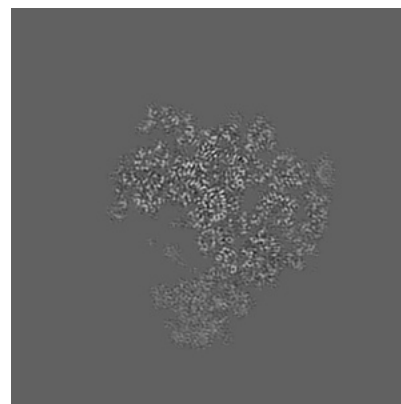
5.3.1 Primary map



X Index: 198



Y Index: 227

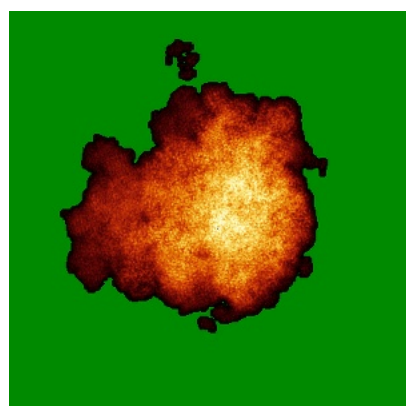


Z Index: 181

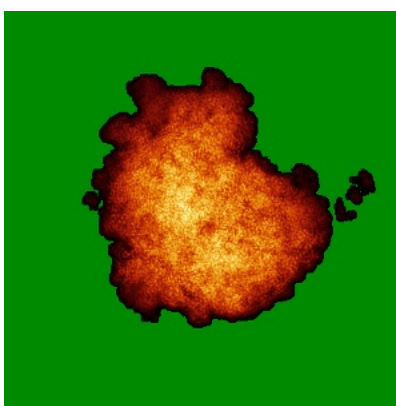
The images above show the largest variance slices of the map in three orthogonal directions.

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

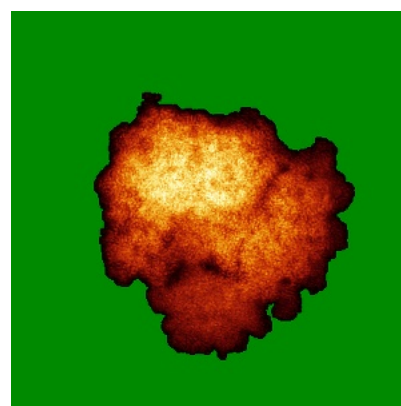
5.4.1 Primary map



X



Y

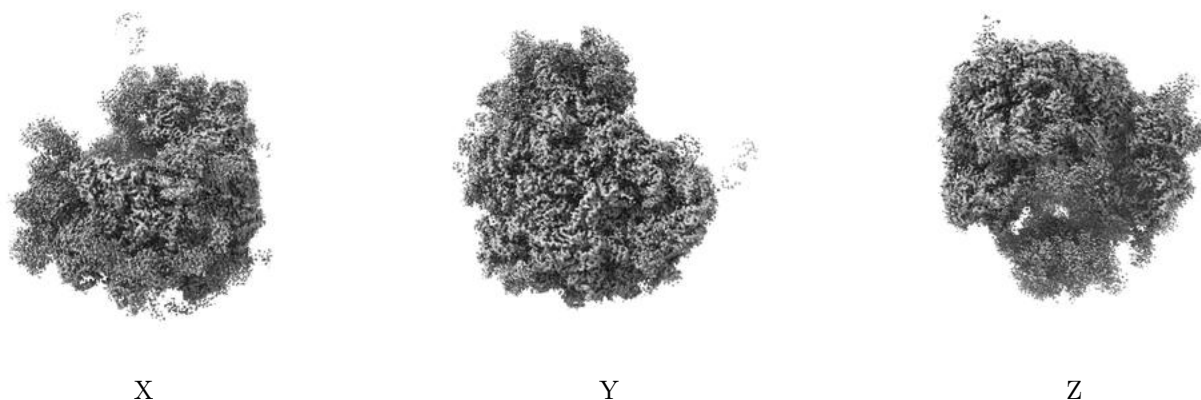


Z

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

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

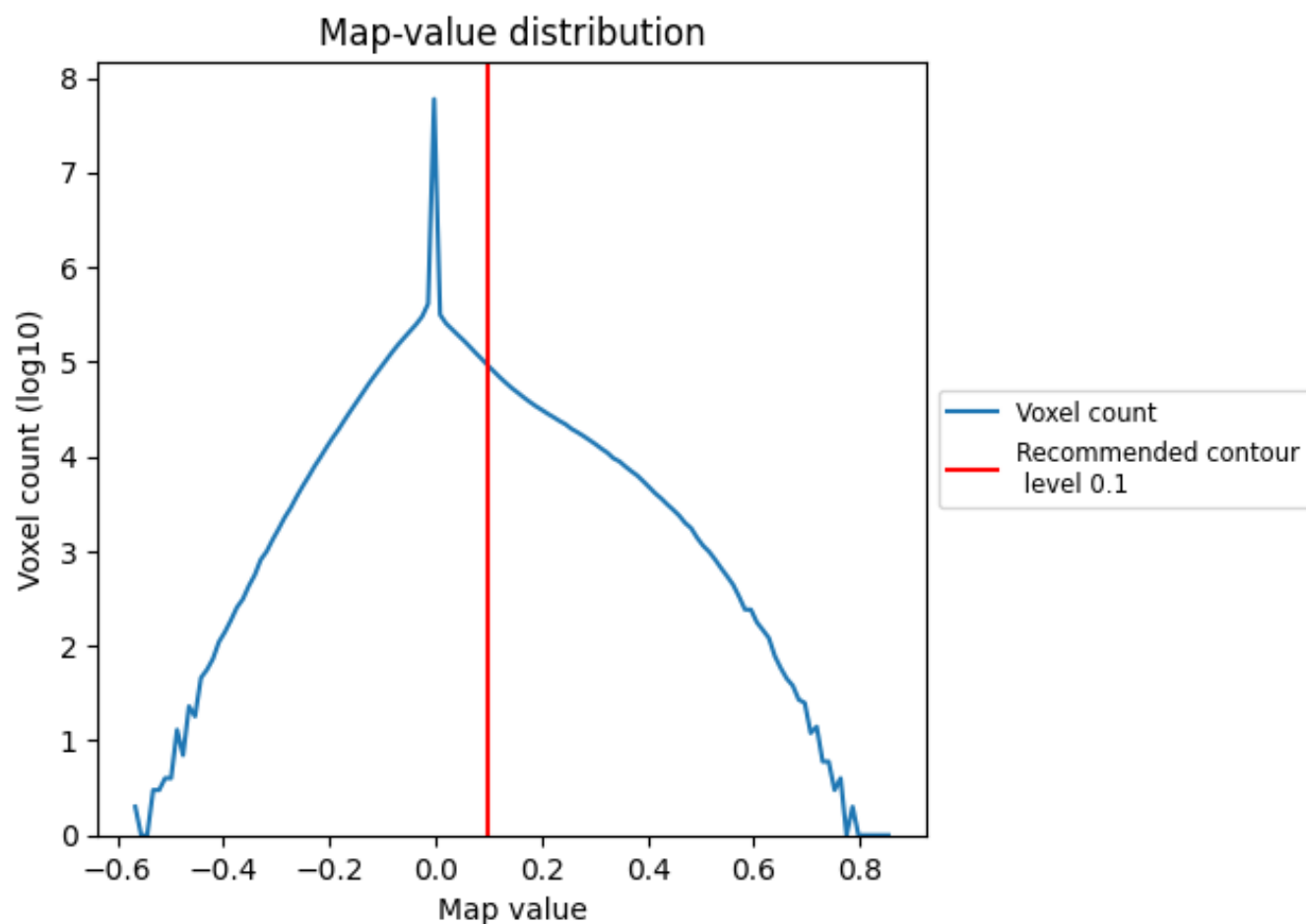
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

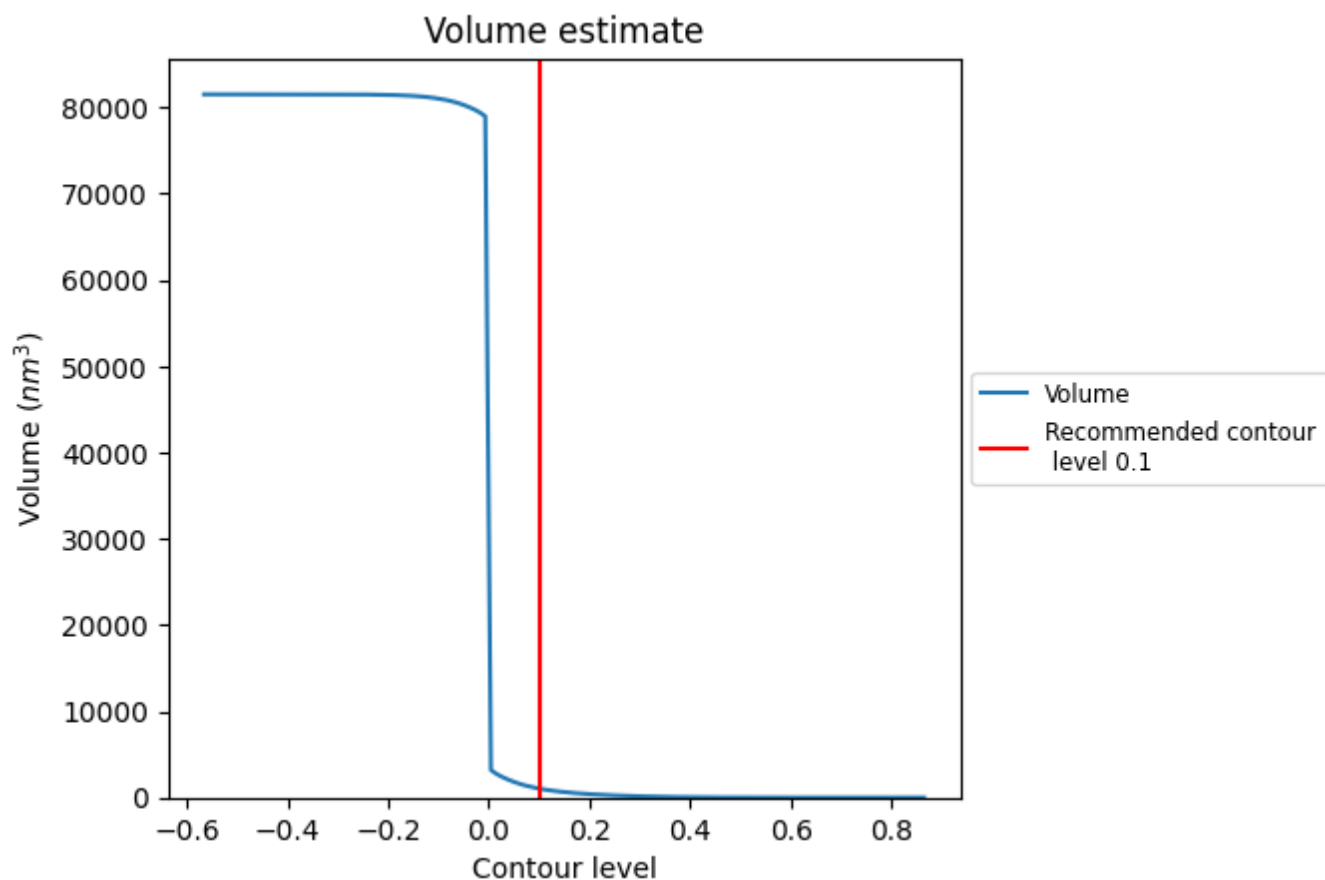
This section contains the results of statistical analysis of the map.

6.1 Map-value distribution [i](#)



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

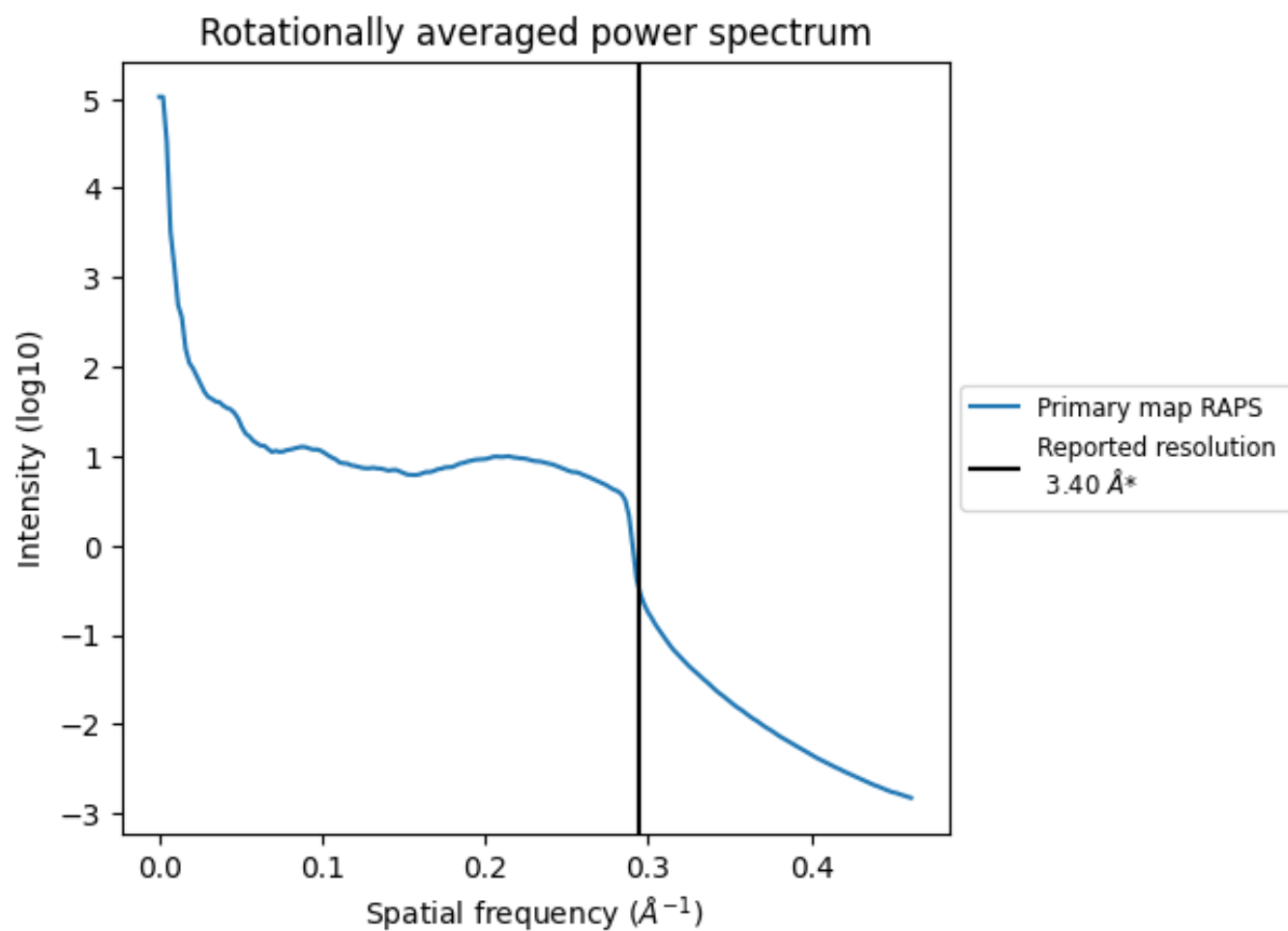
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1042 nm³; this corresponds to an approximate mass of 941 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.

6.3 Rotationally averaged power spectrum ⓘ

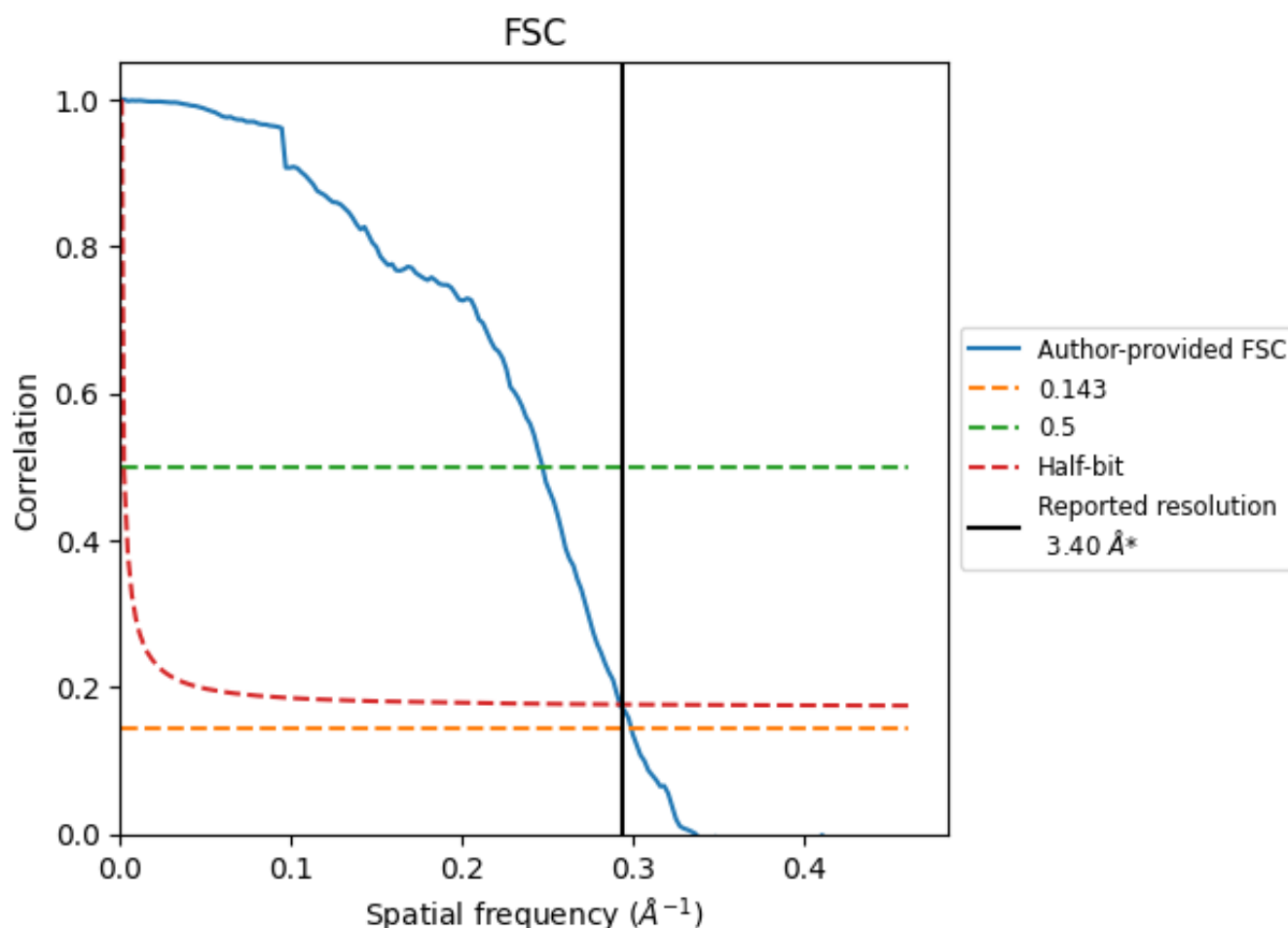


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

7 Fourier-Shell correlation [i](#)

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

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

7.2 Resolution estimates [i](#)

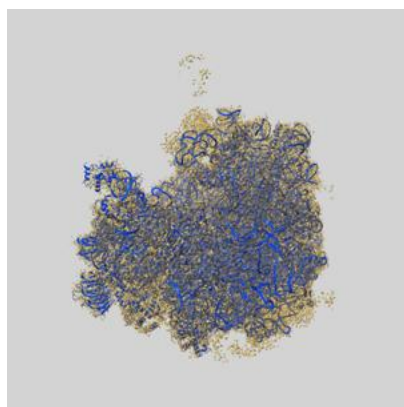
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.34	4.05	3.42
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

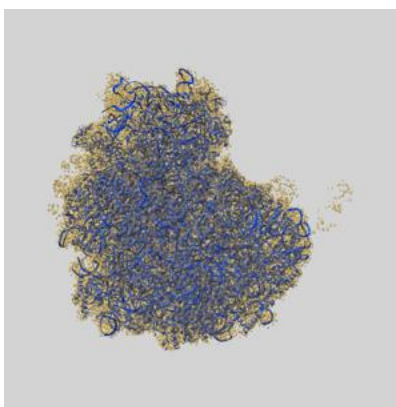
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11096 and PDB model 6Z6J. Per-residue inclusion information can be found in section ?? on page ??.

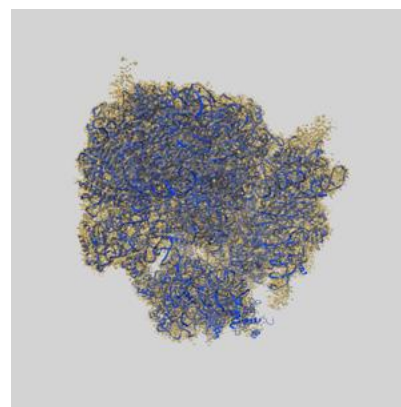
8.1 Map-model overlay [i](#)



X



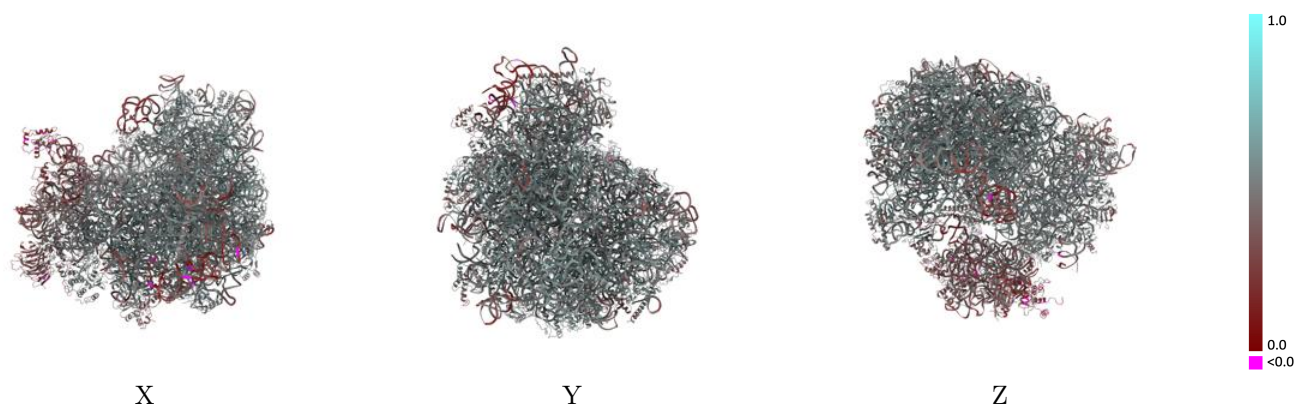
Y



Z

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

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

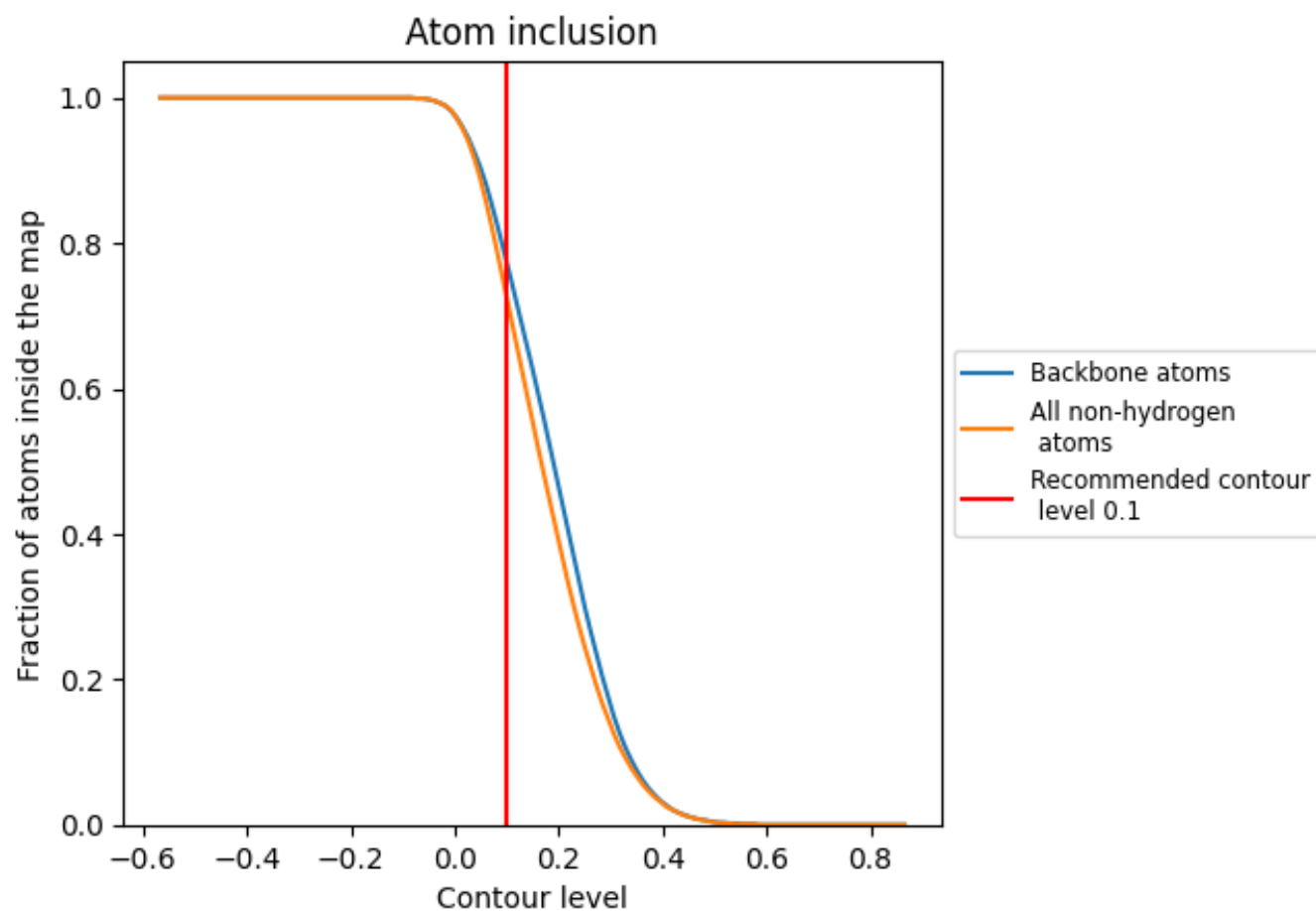


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.







































































8.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ





















































































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

Chain	Atom inclusion	Q-score
All	 0.7250	 0.4820
C1	 0.8260	 0.4970
C2	 0.7010	 0.4390
C3	 0.8490	 0.5050
C4	 0.8490	 0.4930
C5	 0.3880	 0.4340
LA	 0.7900	 0.5480
LB	 0.7780	 0.5390
LC	 0.7640	 0.5270
LD	 0.6610	 0.4830
LE	 0.6730	 0.4960
LF	 0.7440	 0.5260
LG	 0.7020	 0.4990
LH	 0.7090	 0.5130
LI	 0.7150	 0.5200
LJ	 0.6130	 0.4620
LL	 0.7250	 0.5060
LM	 0.7050	 0.5090
LN	 0.8080	 0.5530
LO	 0.7810	 0.5350
LP	 0.7820	 0.5400
LQ	 0.7660	 0.5310
LR	 0.7720	 0.5400
LS	 0.7610	 0.5390
LT	 0.7590	 0.5310
LU	 0.6920	 0.4920
LV	 0.7590	 0.5480
LW	 0.7540	 0.5370
LX	 0.7350	 0.5240
LY	 0.7470	 0.5260
LZ	 0.7330	 0.5200
La	 0.7940	 0.5450
Lb	 0.6990	 0.4940
Lc	 0.7230	 0.5170
Ld	 0.7350	 0.5260









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Chain	Atom inclusion	Q-score
Le	 0.7810	 0.5440
Lf	 0.8160	 0.5600
Lg	 0.7530	 0.5370
Lh	 0.7110	 0.5220
Li	 0.7060	 0.5040
Lj	 0.8500	 0.5630
Lk	 0.6200	 0.4840
Ll	 0.7930	 0.5470
Lm	 0.7380	 0.5310
Ln	 0.6410	 0.5120
Lo	 0.7530	 0.5380
Lp	 0.7210	 0.5370
SA	 0.6610	 0.4790
SB	 0.6320	 0.4930
SC	 0.7100	 0.5160
SD	 0.3830	 0.3800
SE	 0.6970	 0.5080
SF	 0.3740	 0.3930
SG	 0.5800	 0.4690
SH	 0.5580	 0.4420
SI	 0.7210	 0.5260
SJ	 0.6620	 0.4960
SK	 0.2850	 0.3240
SL	 0.7270	 0.5260
SM	 0.1060	 0.2230
SN	 0.7300	 0.5180
SO	 0.6830	 0.5080
SP	 0.2530	 0.2970
SQ	 0.3730	 0.3740
SR	 0.5100	 0.4320
SS	 0.3110	 0.3330
ST	 0.3860	 0.3700
SU	 0.3150	 0.3560
SV	 0.6930	 0.4930
SW	 0.7550	 0.5400
SX	 0.7200	 0.5290
SY	 0.6220	 0.4690
SZ	 0.3140	 0.3300
Sa	 0.7070	 0.5170
Sb	 0.6390	 0.4950
Sc	 0.4170	 0.4190
Sd	 0.4940	 0.4340

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Chain	Atom inclusion	Q-score
Se	 0.5470	 0.4430
Sf	 0.1390	 0.2310
Sg	 0.2000	 0.3160