



wwPDB EM Validation Summary Report ⓘ

Mar 18, 2026 – 12:37 AM UTC

PDB ID : 9R9O / pdb_00009r9o
EMDB ID : EMD-53860
Title : Yeast 80S with nascent chain in complex with Ssb1-ADP in the S1 state
Authors : Grundmann, L.; Zhang, Y.; Grishkovskaya, I.; Rospert, S.; Haselbach, D.
Deposited on : 2025-05-20
Resolution : 2.90 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>.

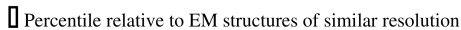
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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ELECTRON MICROSCOPY

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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	13054 (2.40 - 3.40)

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 339152 atoms, of which 144364 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 mRNA_Flag-Pgk-1-70.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	5	7	Total	C	H	N	O	P	0	0
			229	68	76	29	49	7		

- Molecule 2 is a RNA chain called tRNA Methionin elongator.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	6	76	Total	C	H	N	O	P	0	0
			2440	724	820	292	528	76		

- Molecule 3 is a protein called Ribosome-associated molecular chaperone SSB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A	214	Total	C	H	N	O	S	0	0
			2293	788	999	247	258	1		

- Molecule 4 is a protein called Phosphoglycerate kinase.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	17	Total	C	H	N	O	S	0	0
			283	89	143	29	19	3		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P00560
B	2	ASP	-	expression tag	UNP P00560
B	3	TYR	-	expression tag	UNP P00560
B	4	LYS	-	expression tag	UNP P00560
B	5	ASP	-	expression tag	UNP P00560
B	6	ASP	-	expression tag	UNP P00560
B	7	ASP	-	expression tag	UNP P00560
B	8	ASP	-	expression tag	UNP P00560
B	9	LYS	-	expression tag	UNP P00560

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Chain	Residue	Modelled	Actual	Comment	Reference
B	10	GLU	-	expression tag	UNP P00560
B	76	MET	-	expression tag	UNP P00560
B	77	MET	-	expression tag	UNP P00560
B	78	MET	-	expression tag	UNP P00560

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C1	3063	Total	C	H	N	O	P	0	0
			98458	29270	32926	11827	21372	3063		

- Molecule 6 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	C2	1642	Total	C	H	N	O	P	0	0
			52622	15656	17607	6227	11490	1642		

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	C3	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C4	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 9 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	LA	251	Total	C	H	N	O	S	0	0
			3857	1182	1958	385	331	1		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	LB	386	Total	C	H	N	O	S	0	0
			6238	1954	3159	584	533	8		

- Molecule 11 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	LC	361	Total	C	H	N	O	S	0	0
			5613	1730	2864	522	494	3		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	LD	294	Total	C	H	N	O	S	0	0
			4646	1484	2295	410	455	2		

- Molecule 13 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	LE	156	Total	C	H	N	O		0	0
			2547	802	1306	222	217			

- Molecule 14 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	LF	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 15 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	LG	229	Total	C	H	N	O	S	0	0
			3638	1138	1859	319	319	3		

- Molecule 16 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	LH	191	Total	C	H	N	O	S	0	0
			3080	957	1572	274	273	4		

- Molecule 17 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	LI	208	Total	C	H	N	O	S	0	0
			3429	1076	1734	321	293	5		

- Molecule 18 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	LJ	169	Total	C	H	N	O	S	0	0
			2732	846	1382	253	247	4		

- Molecule 19 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	LL	193	Total	C	H	N	O		0	0
			3152	962	1609	315	266			

- Molecule 20 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	LM	136	Total	C	H	N	O	S	0	0
			2203	675	1150	199	177	2		

- Molecule 21 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	LN	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 22 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	LO	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 23 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	LP	183	Total	C	H	N	O		0	0
			2850	879	1434	284	253			

- Molecule 24 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	LQ	185	Total	C	H	N	O	S	0	0
			2986	908	1545	290	241	2		

- Molecule 25 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	188	Total	C	H	N	O	0	0
			3122	932	1607	323	260		

- Molecule 26 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	LS	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 27 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	LT	159	Total	C	H	N	O	S	0	0
			2600	805	1324	246	221	4		

- Molecule 28 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	100	Total	C	H	N	O	0	0
			1609	516	813	131	149		

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
29	LV	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 30 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace	
30	LW	63	Total	C	H	N	O	S	0	0
			1050	332	533	102	82	1		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace	
31	LX	121	Total	C	H	N	O	S	0	0
			1992	620	1027	169	174	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	125	Total	C	H	N	O	0	0
			2060	620	1076	191	173		

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	H	N	O	0	0
			2248	710	1156	202	180		

- Molecule 34 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	La	148	Total	C	H	N	O	S	0	0
			2388	749	1215	231	190	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	58	Total	C	H	N	O	0	0
			954	289	492	100	73		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	Lc	96	Total	C	H	N	O	S	0	0
			1530	476	793	123	137	1		

- Molecule 37 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Ld	108	Total	C	H	N	O	S	0	0
			1782	553	911	166	151	1		

- Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
38	Le	127	Total	C	H	N	O	S	0	0
			2099	644	1082	205	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	Lf	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 40 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	Lg	112	Total	C	H	N	O	S	0	0
			1826	545	946	179	152	4		

- Molecule 41 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	Lh	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 42 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	Li	99	Total	C	H	N	O	S	0	0
			1611	478	845	154	132	2		

- Molecule 43 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	Lj	85	Total	C	H	N	O	S	0	0
			1348	408	678	146	111	5		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	Lk	77	Total	C	H	N	O		0	0
			1295	391	683	115	106			

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	Ll	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 46 is a protein called Large ribosomal subunit protein eL41B.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	Ln	25	Total	C	H	N	O	S	0	0
			502	139	273	62	27	1		

- Molecule 47 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	Lo	103	Total	C	H	N	O	S	0	0
			1717	517	893	167	135	5		

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	Lp	91	Total	C	H	N	O	S	0	0
			1433	429	739	138	121	6		

- Molecule 49 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	SA	206	Total	C	H	N	O	S	0	0
			3214	1030	1611	284	287	2		

- Molecule 50 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	SB	226	Total	C	H	N	O	S	0	0
			3690	1139	1892	330	325	4		

- Molecule 51 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	SC	216	Total	C	H	N	O	S	0	0
			3342	1042	1716	287	295	2		

- Molecule 52 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	SD	222	Total	C	H	N	O	S	0	0
			3542	1098	1813	312	313	6		

- Molecule 53 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	SE	258	Total	C	H	N	O	S	0	0
			4197	1308	2141	387	358	3		

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	SF	205	Total	C	H	N	O	S	0	0
			3256	996	1662	298	297	3		

- Molecule 55 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	SG	228	Total	C	H	N	O	S	0	0
			3709	1138	1894	351	323	3		

- Molecule 56 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	SH	184	Total	C	H	N	O		0	0
			3028	946	1555	263	264			

- Molecule 57 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	SI	187	Total	C	H	N	O	S	0	0
			2979	916	1503	295	263	2		

- Molecule 58 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	SJ	184	Total	C	H	N	O	S	0	0
			3035	935	1556	285	258	1		

- Molecule 59 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	SK	80	Total	C	H	N	O	S	0	0
			1362	446	677	109	128	2		

- Molecule 60 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	SL	142	Total	C	H	N	O	S	0	0
			2360	735	1214	217	191	3		

- Molecule 61 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	SN	150	Total	C	H	N	O	S	0	0
			2448	759	1256	224	207	2		

- Molecule 62 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	SO	127	Total	C	H	N	O	S	0	0
			1877	569	951	185	169	3		

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	SP	114	Total	C	H	N	O	S	0	0
			1816	571	921	168	150	6		

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	SQ	141	Total	C	H	N	O	S	0	0
			2272	708	1167	203	194			

- Molecule 65 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	SR	121	Total	C	H	N	O	S	0	0
			1940	596	992	179	171	2		

- Molecule 66 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	SS	145	Total	C	H	N	O	S	0	0
			2415	743	1223	237	210	2		

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	ST	143	Total	C	H	N	O	S	0	0
			2236	694	1124	208	208	2		

- Molecule 68 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	SU	100	Total	C	H	N	O	S	0	0
			1661	506	864	144	146	1		

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	SV	87	Total	C	H	N	O	S	0	0
			1335	415	662	125	131	2		

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	SW	129	Total	C	H	N	O	S	0	0
			2082	650	1061	188	180	3		

- Molecule 71 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	SX	144	Total	C	H	N	O	S	0	0
			2318	708	1197	220	191	2		

- Molecule 72 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	SY	133	Total	C	H	N	O		0	0
			2196	673	1129	207	187			

- Molecule 73 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	SZ	67	Total	C	H	N	O		0	0
			1123	346	584	98	95			

- Molecule 74 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Sa	97	Total	C	H	N	O	S	0	0
			1587	475	818	160	129	5		

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	Sb	81	Total	C	H	N	O	S	0	0
			1244	382	634	110	113	5		

- Molecule 76 is a protein called Small ribosomal subunit protein eS28B.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	Sc	63	Total	C	H	N	O	S	0	0
			1016	303	525	96	91	1		

- Molecule 77 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	Sd	45	Total	C	H	N	O	S	0	0
			749	227	378	80	60	4		

- Molecule 78 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	Se	60	Total	C	H	N	O	S	0	0
			994	298	522	97	76	1		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	Sg	312	Total	C	H	N	O	S	0	0
			4717	1514	2334	409	452	8		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32921	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.314	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.0392	Depositor
Map size (Å)	476.00003, 476.00003, 476.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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 oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

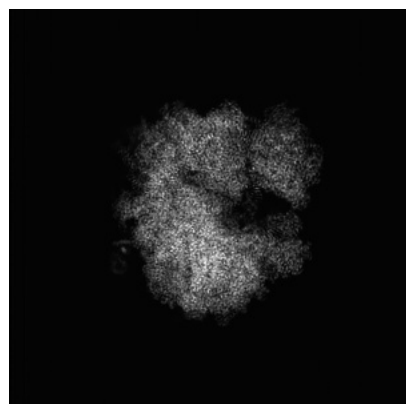
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53860. These allow visual inspection of the internal detail of the map and identification of artifacts.

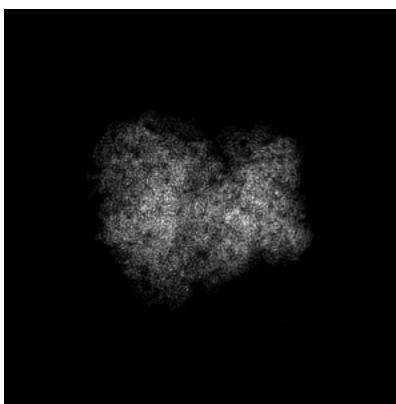
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

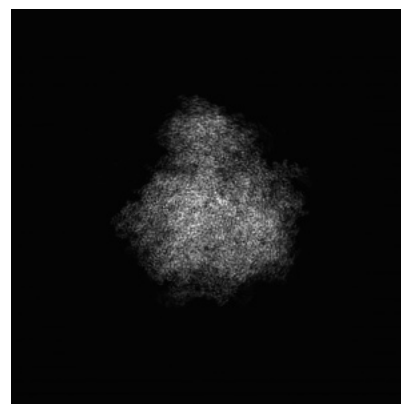
5.1.1 Primary map



X

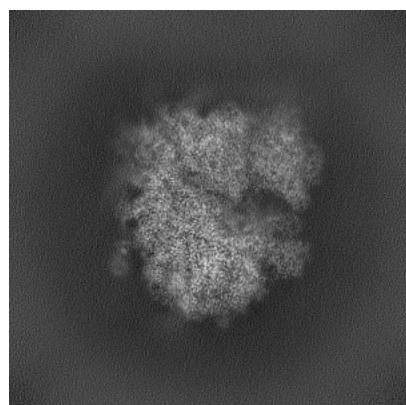


Y

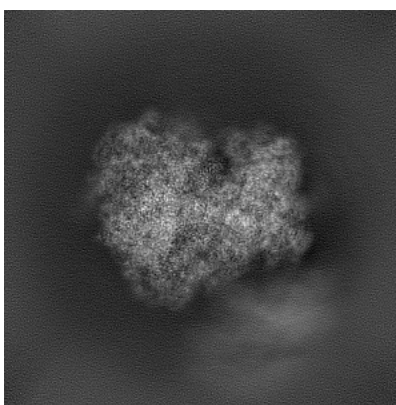


Z

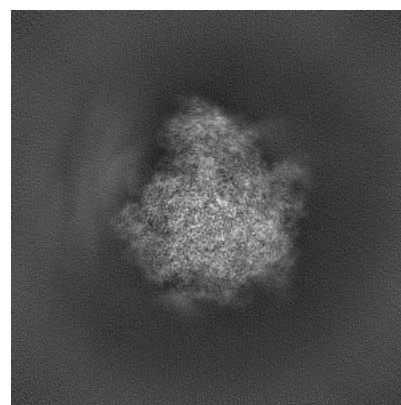
5.1.2 Raw map



X



Y

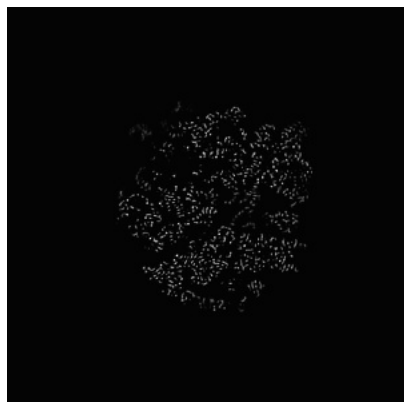


Z

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

5.2 Central slices [i](#)

5.2.1 Primary map



X Index: 200

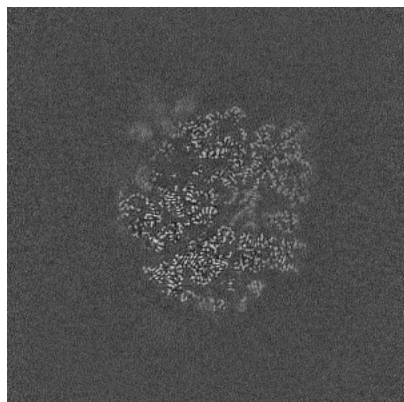


Y Index: 200

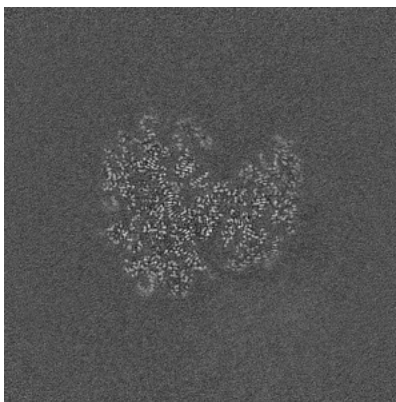


Z Index: 200

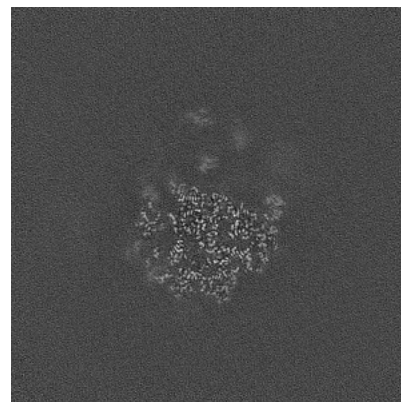
5.2.2 Raw map



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: 185

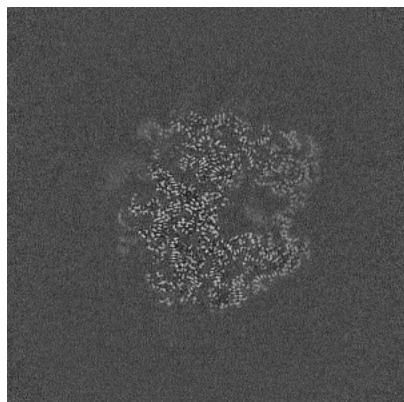


Y Index: 183

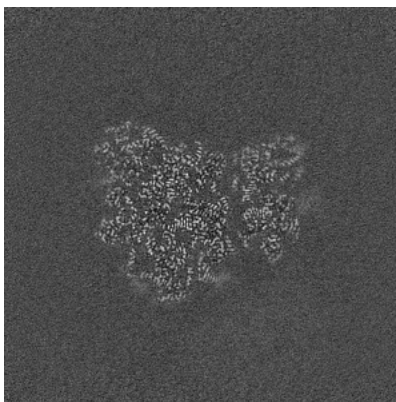


Z Index: 150

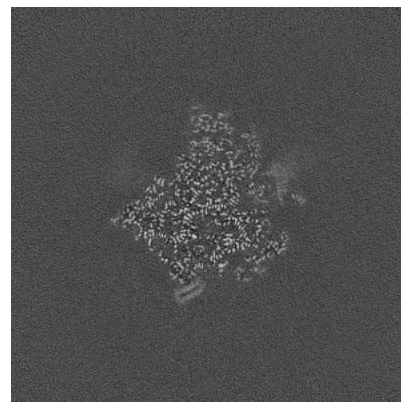
5.3.2 Raw map



X Index: 188



Y Index: 183

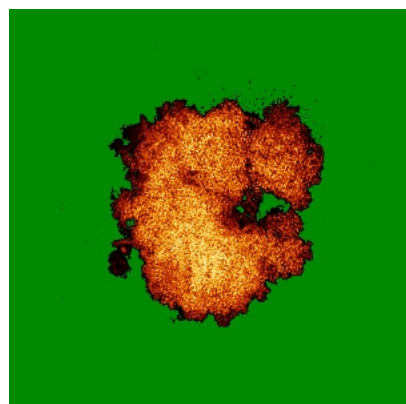


Z Index: 166

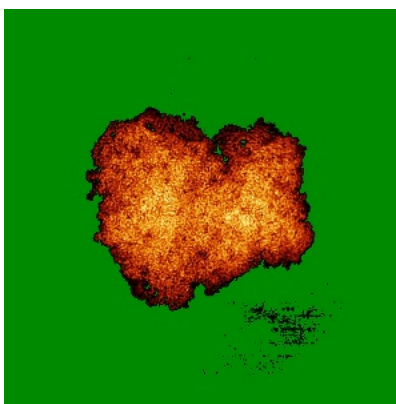
The images above show the largest variance slices of the map in three orthogonal directions.

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

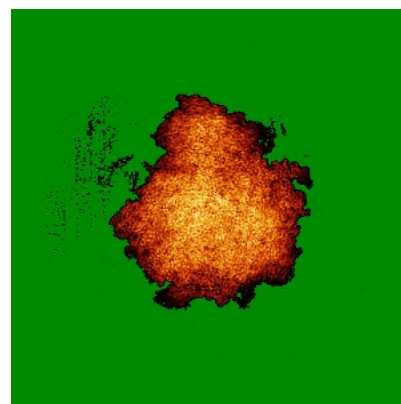
5.4.1 Primary map



X

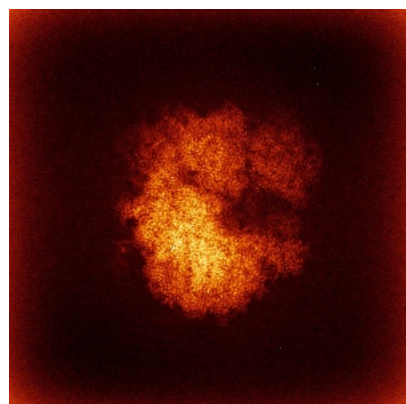


Y

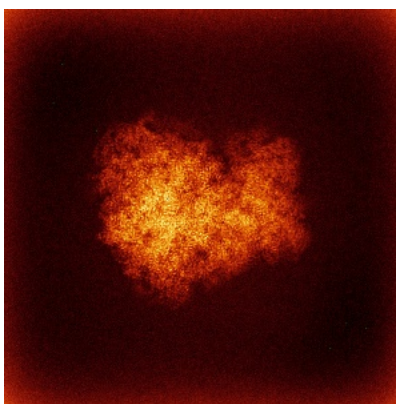


Z

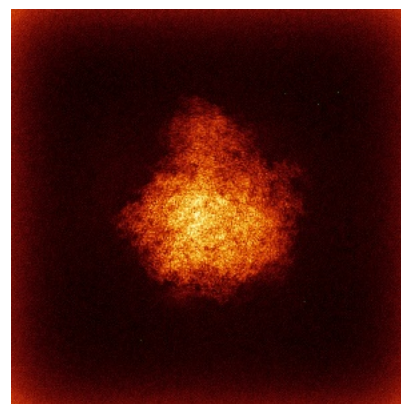
5.4.2 Raw map



X



Y



Z

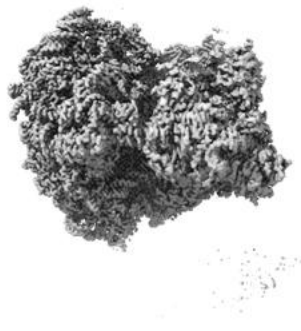
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

5.5 Orthogonal surface views [i](#)

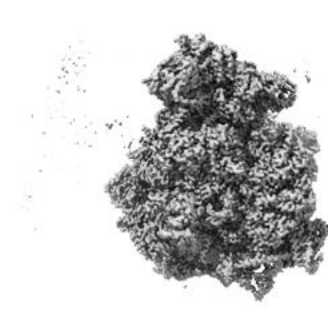
5.5.1 Primary map



X



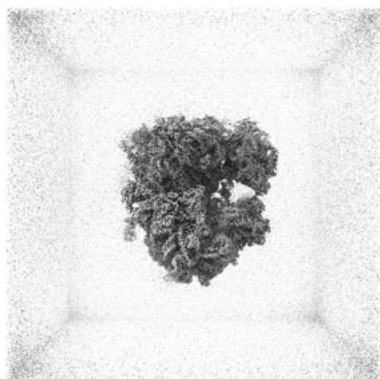
Y



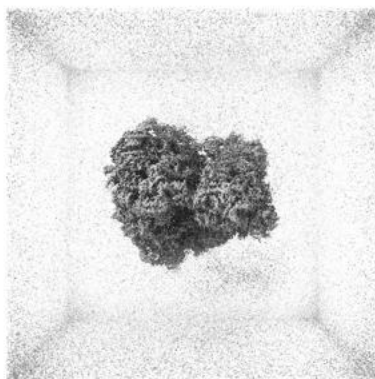
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0392. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

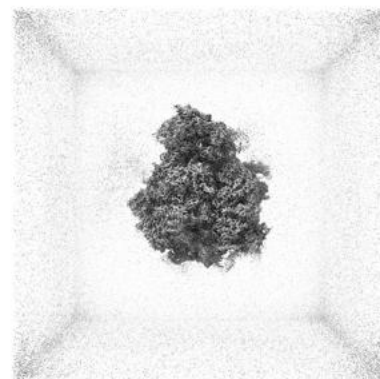
5.5.2 Raw map



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.

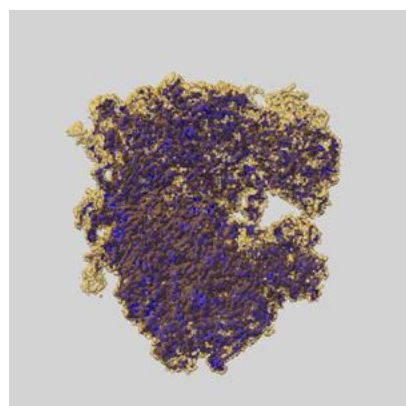
5.6 Mask visualisation [i](#)

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

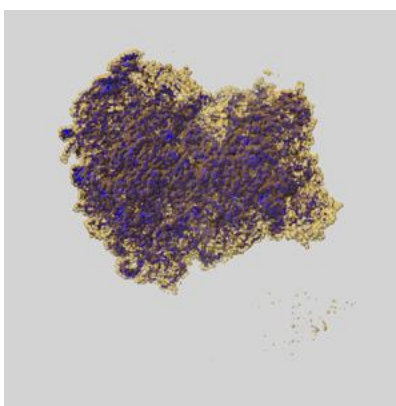
A mask typically either:

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

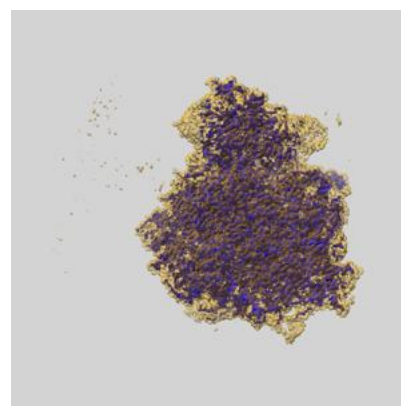
5.6.1 emd_53860_msk_1.map [i](#)



X



Y

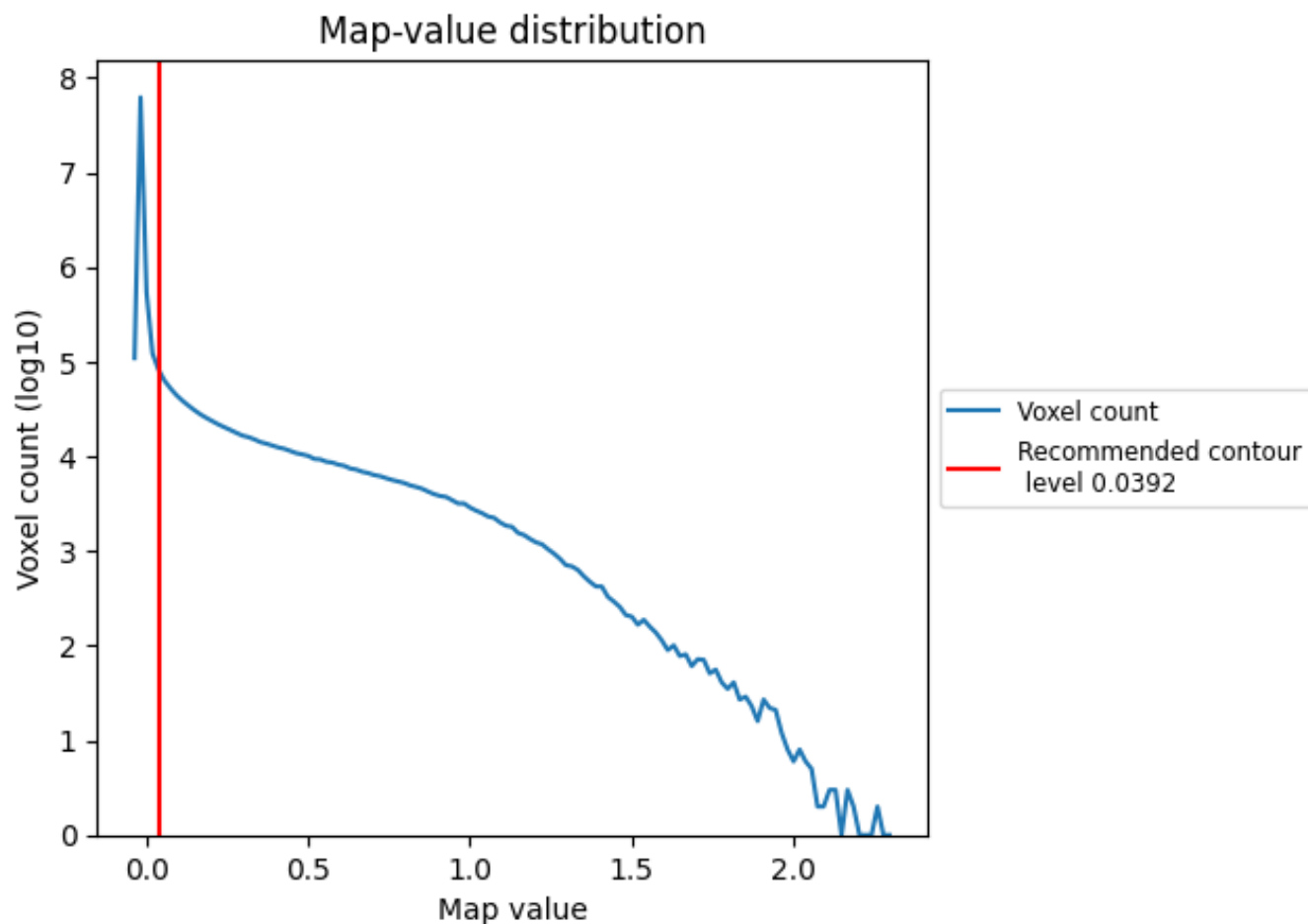


Z

6 Map analysis [i](#)

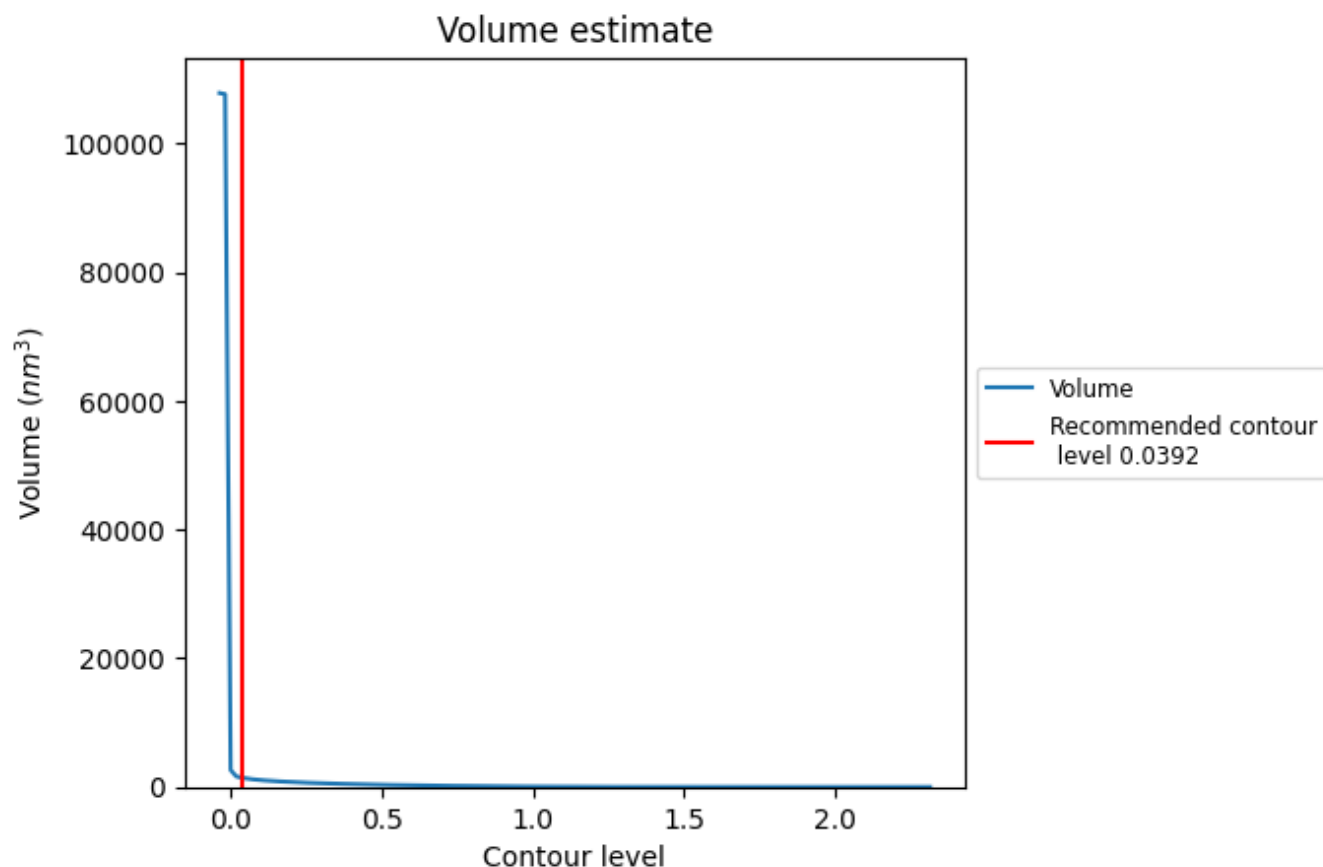
This section contains the results of statistical analysis of the map.

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.

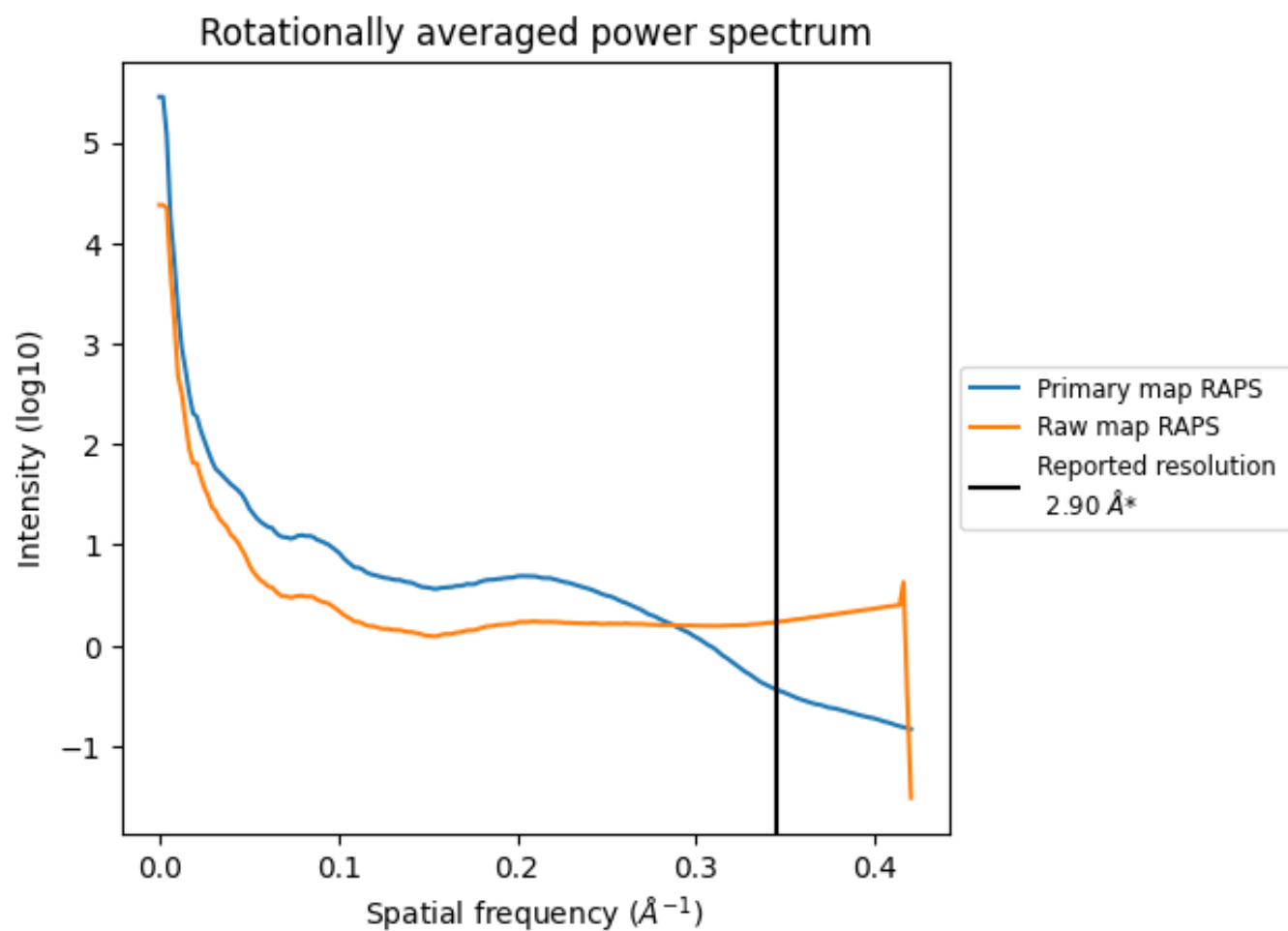
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1425 nm^3 ; this corresponds to an approximate mass of 1288 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 ⓘ

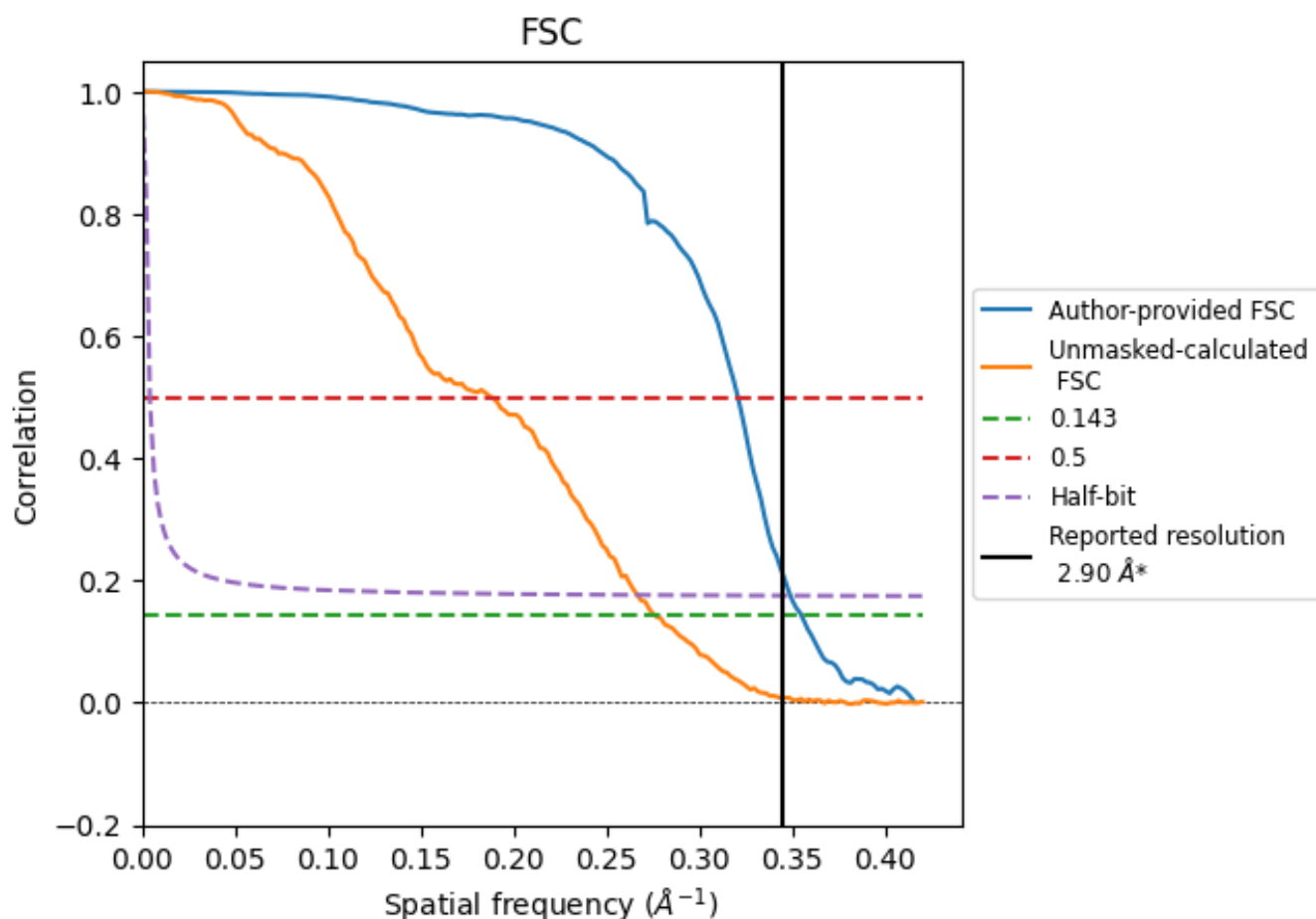


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 Å⁻¹

7.2 Resolution estimates [i](#)

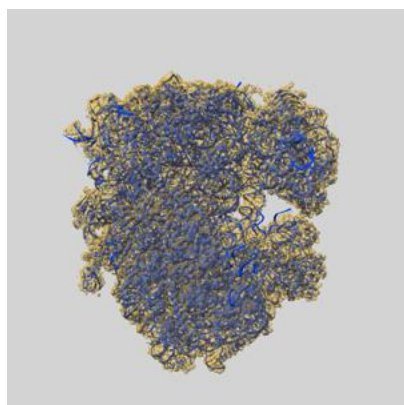
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.82	3.12	2.86
Unmasked-calculated*	3.62	5.31	3.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.62 differs from the reported value 2.9 by more than 10 %

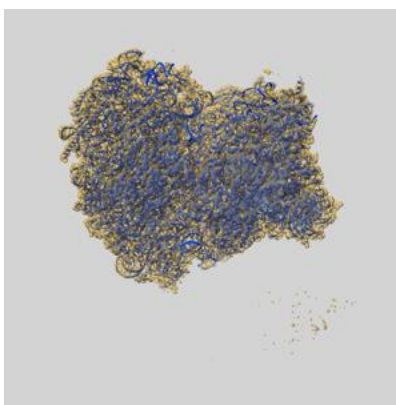
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53860 and PDB model 9R9O. Per-residue inclusion information can be found in section ?? on page ??.

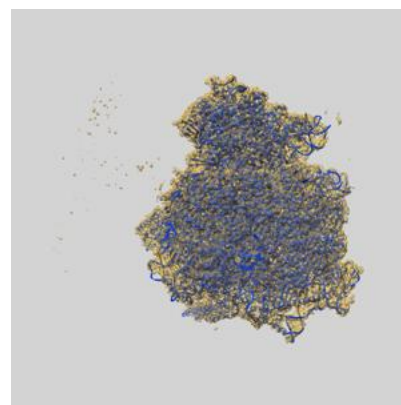
8.1 Map-model overlay [i](#)



X



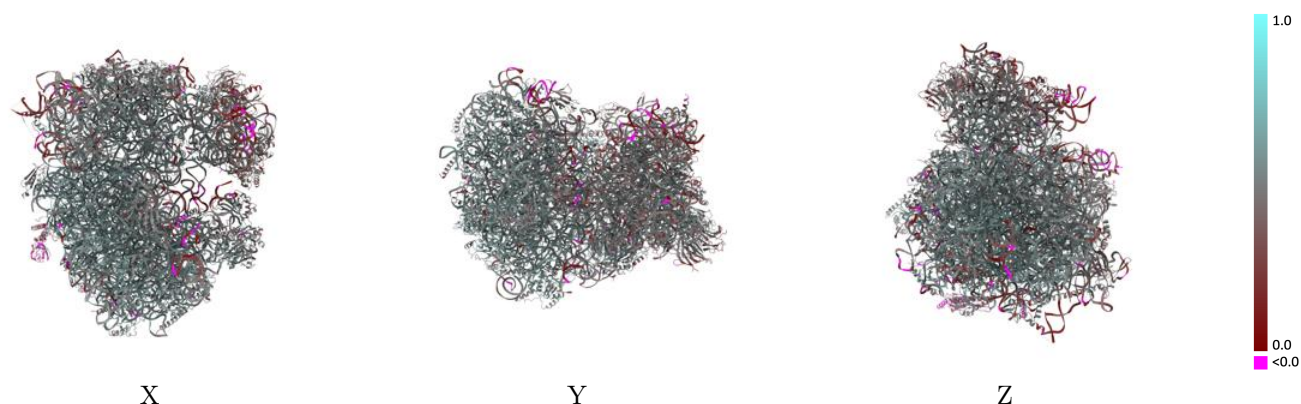
Y



Z

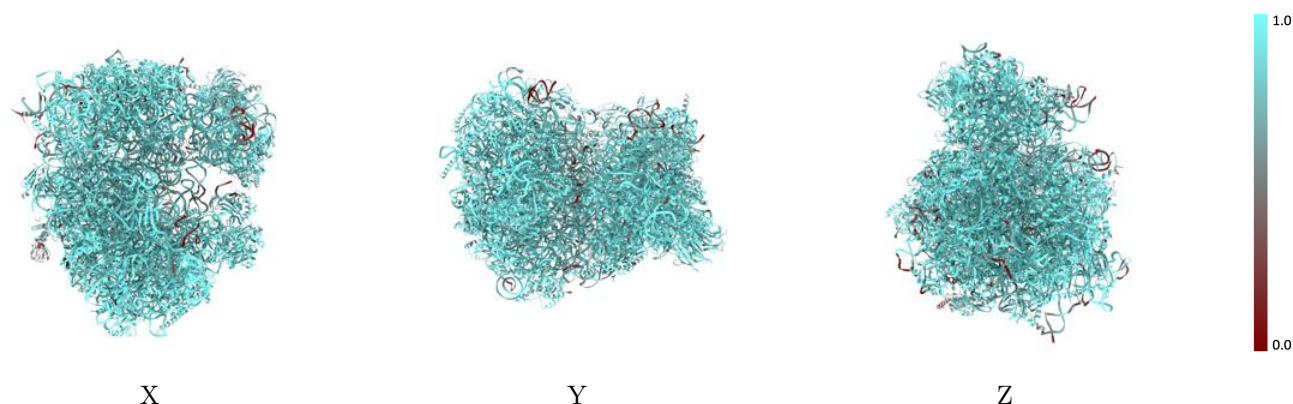
The images above show the 3D surface view of the map at the recommended contour level 0.0392 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



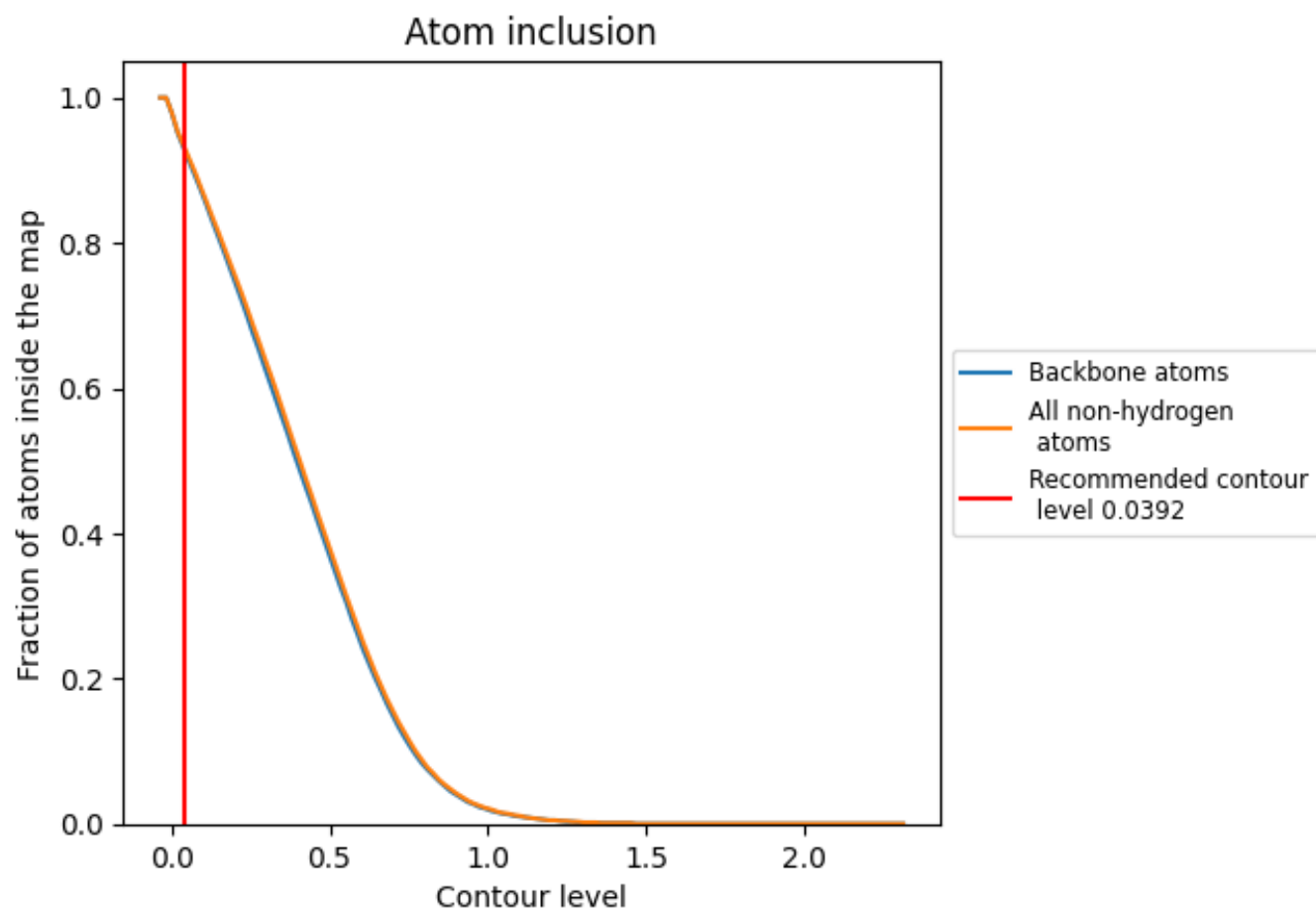
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.0392).

8.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.0392) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.5010
5	 0.9410	 0.5090
6	 0.7910	 0.3300
A	 0.5320	 0.1640
B	 0.4670	 0.2320
C1	 0.9530	 0.5240
C2	 0.9230	 0.4650
C3	 0.9700	 0.5560
C4	 0.9810	 0.5240
LA	 0.9730	 0.5710
LB	 0.9710	 0.5570
LC	 0.9670	 0.5660
LD	 0.9000	 0.4740
LE	 0.9400	 0.5250
LF	 0.9660	 0.5480
LG	 0.9400	 0.5350
LH	 0.9000	 0.4540
LI	 0.9270	 0.4850
LJ	 0.9020	 0.4530
LL	 0.9460	 0.5490
LM	 0.9590	 0.5280
LN	 0.9830	 0.5890
LO	 0.9750	 0.5540
LP	 0.9290	 0.5370
LQ	 0.9690	 0.5610
LR	 0.9070	 0.5120
LS	 0.9510	 0.5180
LT	 0.9520	 0.5340
LU	 0.8980	 0.4820
LV	 0.9520	 0.5360
LW	 0.9620	 0.5430
LX	 0.9490	 0.5560
LY	 0.9560	 0.5720
LZ	 0.9180	 0.5260
La	 0.9690	 0.5640



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Chain	Atom inclusion	Q-score
Lb	 0.8610	 0.4770
Lc	 0.9750	 0.5470
Ld	 0.9400	 0.5470
Le	 0.9620	 0.5680
Lf	 0.9700	 0.5600
Lg	 0.9330	 0.5450
Lh	 0.9600	 0.5640
Li	 0.9420	 0.5180
Lj	 0.9720	 0.5740
Lk	 0.9050	 0.5030
Ll	 0.9710	 0.5700
Ln	 0.9330	 0.5190
Lo	 0.9140	 0.5170
Lp	 0.9280	 0.5230
SA	 0.9700	 0.5200
SB	 0.8890	 0.4870
SC	 0.9560	 0.5160
SD	 0.8770	 0.4120
SE	 0.9460	 0.5000
SF	 0.9090	 0.4540
SG	 0.8650	 0.4120
SH	 0.8550	 0.4230
SI	 0.9160	 0.5070
SJ	 0.9200	 0.4680
SK	 0.7870	 0.3100
SL	 0.9360	 0.5200
SN	 0.9350	 0.5180
SO	 0.9620	 0.5270
SP	 0.8530	 0.3650
SQ	 0.9380	 0.4700
SR	 0.9160	 0.4750
SS	 0.8580	 0.3950
ST	 0.8950	 0.4190
SU	 0.8710	 0.4000
SV	 0.9660	 0.5150
SW	 0.9770	 0.5420
SX	 0.9300	 0.5060
SY	 0.9010	 0.4470
SZ	 0.8780	 0.4170
Sa	 0.9580	 0.5290
Sb	 0.9350	 0.5070
Sc	 0.8820	 0.4480

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Chain	Atom inclusion	Q-score
Sd	 0.9410	 0.4770
Se	 0.7810	 0.3930
Sg	 0.8840	 0.4010