



wwPDB EM Validation Summary Report ⓘ

Jun 2, 2025 – 03:09 pm BST

PDB ID : 9I05 / pdb_00009i05
EMDB ID : EMD-52551
Title : Cryo-EM structure of the large subunit of the mitochondrial ribosome from
Toxoplasma gondii
Authors : Tobiasson, V.; Shikha, S.; Muhleip, A.
Deposited on : 2025-01-14
Resolution : 2.20 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.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : **FAILED**
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

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 2.20 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 109 unique types of molecules in this entry. The entry contains 323886 atoms, of which 152518 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 protein called Putative LSU ribosomal protein L2P.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	Aa	349	Total	C	H	N	O	S	0	0
			5504	1698	2803	543	453	7		

- Molecule 2 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	Ab	298	Total	C	H	N	O	S	0	0
			4759	1515	2384	432	413	15		

- Molecule 3 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	Ac	423	Total	C	H	N	O	S	0	0
			7057	2251	3546	654	593	13		

- Molecule 4 is a protein called HECT-domain (Ubiquitin-transferase) domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	Ad	213	Total	C	H	N	O	S	0	0
			3371	1078	1688	307	291	7		

- Molecule 5 is a protein called Ribosomal protein L9, N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	Ae	84	Total	C	H	N	O	S	0	0
			1382	431	709	129	113			

- Molecule 6 is a protein called Putative ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	Af	180	Total	C	H	N	O	S	0	0
			2879	885	1475	263	244	12		

- Molecule 7 is a protein called Putative 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	Ag	221	Total	C	H	N	O	S	0	0
			3529	1115	1785	330	290	9		

- Molecule 8 is a protein called Putative LSU ribosomal protein L14P.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	Ah	112	Total	C	H	N	O	S	0	0
			1867	566	969	179	147	6		

- Molecule 9 is a protein called Ribosomal protein L15, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Ai	296	Total	C	H	N	O	S	0	0
			5016	1556	2554	488	413	5		

- Molecule 10 is a protein called Putative 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	Aj	178	Total	C	H	N	O	S	0	0
			2916	913	1483	281	236	3		

- Molecule 11 is a protein called Putative 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	Ak	240	Total	C	H	N	O	S	0	0
			4007	1277	1996	382	345	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ak	246	ASP	ARG	conflict	UNP A0A7J6KEY9

- Molecule 12 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	Al	367	Total	C	H	N	O	S	0	0
			6225	1952	3157	593	511	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Al	670	TRP	TYR	conflict	UNP A0A7J6JZ22
Al	673	TRP	TYR	conflict	UNP A0A7J6JZ22

- Molecule 13 is a protein called Putative ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Am	121	Total	C	H	N	O	S	0	0
			2075	657	1048	200	165	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Am	38	SER	TYR	conflict	UNP B9PY19

- Molecule 14 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	An	369	Total	C	H	N	O	S	0	0
			6125	1909	3077	601	526	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
An	401	GLN	ALA	conflict	UNP A0A7J6K7U7
An	405	ARG	SER	conflict	UNP A0A7J6K7U7

- Molecule 15 is a protein called Ribosomal L22p/L17e protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Ao	346	Total	C	H	N	O	S	0	0
			5903	1861	2990	561	482	9		

- Molecule 16 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Ap	215	Total	C	H	N	O	S	0	0
			3582	1150	1806	321	299	6		

- Molecule 17 is a protein called Large ribosomal subunit protein uL24c.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Aq	182	Total	C	H	N	O	S	0	0
			3039	937	1552	281	262	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Aq	398	LYS	ARG	conflict	UNP A0A7J6JXG2
Aq	399	ASP	ALA	conflict	UNP A0A7J6JXG2
Aq	400	THR	GLY	conflict	UNP A0A7J6JXG2

- Molecule 18 is a protein called Ribosomal l25 family protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	Ar	234	Total	C	H	N	O	S	0	0
			3734	1213	1848	331	332	10		

- Molecule 19 is a protein called bL27m.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	As	174	Total	C	H	N	O	S	0	0
			2936	923	1482	281	245	5		

- Molecule 20 is a protein called Putative ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	At	281	Total	C	H	N	O	S	0	0
			4656	1475	2313	461	398	9		

- Molecule 21 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Au	216	Total	C	H	N	O	S	0	0
			3745	1168	1900	352	316	9		

- Molecule 22 is a protein called bL32m.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	Av	78	Total	C	H	N	O	S	0	0
			1337	443	665	122	105	2		

- Molecule 23 is a protein called Putative 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Aw	112	Total	C	H	N	O	S	0	0
			1959	616	1003	182	155	3		

- Molecule 24 is a protein called bL35m.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Ax	113	Total	C	H	N	O	S	0	0
			2023	626	1037	205	153	2		

- Molecule 25 is a protein called bL36m.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Ay	90	Total	C	H	N	O	S	0	0
			1502	473	759	154	111	5		

- Molecule 26 is a protein called mL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Az	183	Total	C	H	N	O	S	0	0
			3009	975	1485	272	270	7		

- Molecule 27 is a protein called Putative 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AA	80	Total	C	H	N	O	S	0	0
			1285	408	664	110	99	4		

- Molecule 28 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	AB	188	Total	C	H	N	O	S	0	0
			3132	988	1574	305	262	3		

- Molecule 29 is a protein called Ribosomal protein L46.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AC	233	Total	C	H	N	O	S	0	0
			3801	1234	1893	329	340	5		

- Molecule 30 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	AD	80	Total	C	H	N	O	S	0	0
			1310	407	675	119	107	2		

- Molecule 31 is a protein called mL53.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	AE	111	Total	C	H	N	O	S	0	0
			1826	587	907	162	164	6		

- Molecule 32 is a protein called Large ribosomal subunit protein mL54.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AF	70	Total	C	H	N	O	S	0	0
			1186	384	601	98	101	2		

- Molecule 33 is a protein called BIR protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	AG	219	Total	C	H	N	O	S	0	0
			3786	1211	1881	364	324	6		

- Molecule 34 is a protein called mL102.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	AH	34	Total	C	H	N	O	S	0	0
			580	165	304	67	41	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AH	35	ASN	ARG	conflict	UNP A0A0F7V869

- Molecule 35 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	AI	329	Total	C	H	N	O	S	0	0
			5401	1698	2707	506	480	10		

- Molecule 36 is a protein called mL130.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	Xa	69	Total	C	H	N	O	S	0	0
			1272	420	630	131	90	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Xa	113	TRP	LYS	conflict	UNP A0A7J6JZ23
Xa	114	LYS	GLY	conflict	UNP A0A7J6JZ23
Xa	115	GLY	ASN	conflict	UNP A0A7J6JZ23
Xa	116	ASN	ARG	conflict	UNP A0A7J6JZ23

- Molecule 37 is a protein called RRM domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	Xb	343	Total	C	H	N	O	S	0	0
			5801	1863	2900	537	487	14		

- Molecule 38 is a protein called mL132.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Xc	197	Total	C	H	N	O	S	0	0
			3206	1014	1613	304	267	8		

- Molecule 39 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	Xd	492	Total	C	H	N	O	S	0	0
			7539	2356	3796	680	688	19		

- Molecule 40 is a protein called Large ribosomal subunit protein uL24c.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	Xe	228	Total	C	H	N	O	S	0	0
			3694	1153	1883	333	314	11		

- Molecule 41 is a protein called FAS1 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	Xf	264	Total	C	H	N	O	S	0	0
			4138	1311	2073	384	361	9		

- Molecule 42 is a protein called DUF6832 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	Xg	486	Total	C	H	N	O	S	0	0
			7931	2555	3972	695	694	15		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Xg	1	VAL	-	expression tag	UNP A0A7J6KC93
Xg	2	GLY	-	expression tag	UNP A0A7J6KC93
Xg	3	VAL	-	expression tag	UNP A0A7J6KC93
Xg	4	LEU	-	expression tag	UNP A0A7J6KC93
Xg	5	ALA	-	expression tag	UNP A0A7J6KC93
Xg	6	SER	-	expression tag	UNP A0A7J6KC93
Xg	7	LEU	-	expression tag	UNP A0A7J6KC93
Xg	8	THR	-	expression tag	UNP A0A7J6KC93
Xg	9	SER	-	expression tag	UNP A0A7J6KC93
Xg	10	GLY	-	expression tag	UNP A0A7J6KC93
Xg	11	GLN	-	expression tag	UNP A0A7J6KC93

- Molecule 43 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	Xh	421	Total	C	H	N	O	S	0	0
			6863	2171	3449	624	601	18		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Xh	600	ARG	-	insertion	UNP A0A7J6KAP7
Xh	601	ARG	-	insertion	UNP A0A7J6KAP7
Xh	602	LYS	-	insertion	UNP A0A7J6KAP7
Xh	603	ARG	-	insertion	UNP A0A7J6KAP7
Xh	604	GLU	-	insertion	UNP A0A7J6KAP7
Xh	605	ASN	-	insertion	UNP A0A7J6KAP7
Xh	606	PHE	-	insertion	UNP A0A7J6KAP7

- Molecule 44 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	Xi	444	Total	C	H	N	O	S	0	0
			7329	2318	3684	691	617	19		

- Molecule 45 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	Xj	585	Total	C	H	N	O	S	0	0
			9609	3029	4866	885	811	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Xj	781	HIS	LEU	conflict	UNP A0A7J6K4L1

- Molecule 46 is a protein called RNA recognition motif-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	Xk	119	Total	C	H	N	O	S	0	0
			1932	618	942	187	183	2		

- Molecule 47 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	Xl	421	Total	C	H	N	O	S	0	0
			6792	2148	3421	597	610	16		
47	Xv	394	Total	C	H	N	O	S	0	0
			6386	2016	3222	559	575	14		

- Molecule 48 is a protein called Macro domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	Xm	361	Total	C	H	N	O	S	0	0
			5586	1735	2820	523	498	10		

- Molecule 49 is a protein called AP2 domain transcription factor AP2VIIb-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	Xn	183	Total	C	H	N	O	S	0	0
			2979	964	1486	266	257	6		

- Molecule 50 is a protein called mL144.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	Xo	580	Total	C	H	N	O	S	0	0
			8835	2787	4447	796	787	18		

- Molecule 51 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	Xp	200	Total	C	H	N	O	S	0	0
			3175	1028	1556	295	286	10		

- Molecule 52 is a protein called mL146.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	Xq	644	Total	C	H	N	O	S	0	0
			10123	3185	5104	930	883	21		

- Molecule 53 is a protein called RAP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	Xr	451	Total	C	H	N	O	S	0	0
			7423	2349	3757	671	629	17		

- Molecule 54 is a protein called mL149.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Xs	220	Total	C	H	N	O	S	0	0
			3476	1099	1746	306	315	10		

- Molecule 55 is a protein called mL148.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	Xt	123	Total	C	H	N	O	S	0	0
			2017	615	1031	201	166	4		

- Molecule 56 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Xw	281	Total	C	H	N	O	S	0	0
			4424	1398	2217	419	380	10		

- Molecule 57 is a protein called mL152.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Xx	104	Total	C	H	N	O	S	0	0
			1747	565	886	149	141	6		

- Molecule 58 is a protein called mL153.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Xy	68	Total	C	H	N	O	0	0
			1194	375	607	118	94		

- Molecule 59 is a protein called AP2 domain transcription factor AP2IV-1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
59	Xz	151	Total	C	H	N	O	S	0	0
			2557	806	1277	254	216	4		

- Molecule 60 is a protein called mL155.

Mol	Chain	Residues	Atoms					AltConf	Trace	
60	XA	86	Total	C	H	N	O	S	0	0
			1472	467	758	134	112	1		

- Molecule 61 is a protein called mL156.

Mol	Chain	Residues	Atoms					AltConf	Trace	
61	XB	90	Total	C	H	N	O	S	0	0
			1521	489	757	130	140	5		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XB	85	VAL	LYS	conflict	UNP A0A7J6K9K6
XB	86	ALA	GLU	conflict	UNP A0A7J6K9K6
XB	88	VAL	ILE	conflict	UNP A0A7J6K9K6
XB	89	LYS	VAL	conflict	UNP A0A7J6K9K6
XB	90	GLU	ALA	conflict	UNP A0A7J6K9K6

- Molecule 62 is a protein called mL157.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	XC	296	Total	C	H	N	O	S	0	0
			4680	1458	2358	423	435	6		

- Molecule 63 is a protein called mL158.

Mol	Chain	Residues	Atoms					AltConf	Trace	
63	XD	94	Total	C	H	N	O	S	0	0
			1554	484	790	144	131	5		

- Molecule 64 is a protein called mL159.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	XE	59	Total	C	H	N	O	S	0	0
			997	316	501	96	83	1		

- Molecule 65 is a protein called mL160.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	XF	95	Total	C	H	N	O	S	0	0
			1620	509	830	142	135	4		

- Molecule 66 is a protein called mL161.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	XG	29	Total	C	H	N	O	S	0	0
			546	162	286	61	35	2		

- Molecule 67 is a protein called Ribosomal protein RPL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	XH	181	Total	C	H	N	O	S	0	0
			3088	987	1542	301	254	4		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XH	-145	HIS	GLN	conflict	UNP A0A7J6JUA9
XH	-113	GLY	ARG	conflict	UNP A0A7J6JUA9
XH	-71	VAL	LEU	conflict	UNP A0A7J6JUA9
XH	-19	THR	PRO	conflict	UNP A0A7J6JUA9
XH	-1	ARG	SER	conflict	UNP A0A7J6JUA9
XH	81	VAL	ILE	conflict	UNP A0A7J6JUA9

- Molecule 68 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	XI	35	Total	C	H	N	O	S	0	0
			630	192	322	72	43	1		

- Molecule 69 is a protein called Chain Ua.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	XJ	46	Total	C	H	N	O	S	0	0
			807	240	415	92	59	1		

- Molecule 70 is a protein called Ribosomal l25 family protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	Ua	26	Total	C	H	N	O	S	0	0
			385	118	188	34	44	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ua	2	ALA	ARG	conflict	UNP A0A7J6JXW0

- Molecule 71 is a protein called Chain Uc.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ub	21	Total	C	H	N	O	0	0
			353	112	176	40	25		

- Molecule 72 is a protein called Chain Ud.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Uc	19	Total	C	H	N	O	0	0
			241	76	121	23	21		

- Molecule 73 is a protein called Chain Ue.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ud	28	Total	C	H	N	O	0	0
			426	139	204	37	46		

- Molecule 74 is a protein called Chain Uf.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Ue	13	Total	C	H	N	O	S	0	0
			204	63	103	20	17	1		

- Molecule 75 is a protein called LSU-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Uf	6	Total	C	H	N	O	0	0
			56	18	26	6	6		

- Molecule 76 is a RNA chain called LSU-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	RA	35	Total	C	H	N	O	P	0	0
			1112	331	373	124	249	35		

- Molecule 77 is a RNA chain called LSU-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	RB	27	Total	C	H	N	O	P	0	0
			876	261	293	112	183	27		

- Molecule 78 is a RNA chain called LSU-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	RC	33	Total	C	H	N	O	P	0	0
			1071	322	358	143	215	33		

- Molecule 79 is a RNA chain called LSU-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	RD	91	Total	C	H	N	O	P	0	0
			2928	875	978	361	623	91		

- Molecule 80 is a RNA chain called LSU-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	RE	44	Total	C	H	N	O	P	0	0
			1413	419	477	170	303	44		

- Molecule 81 is a RNA chain called LSU-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	RF	29	Total	C	H	N	O	P	0	0
			948	282	315	124	198	29		

- Molecule 82 is a RNA chain called LSU-8.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	RG	84	Total	C	H	N	O	P	0	0
			2683	802	899	318	580	84		

- Molecule 83 is a RNA chain called LSU-9.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	RI	36	Total	C	H	N	O	P	0	0
			1168	347	390	147	248	36		

- Molecule 84 is a RNA chain called LSU-10.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	RJ	59	Total	C	H	N	O	P	0	0
			1887	562	635	224	407	59		

- Molecule 85 is a RNA chain called LSU-11.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	RK	10	Total	C	H	N	O	P	0	0
			329	97	111	44	67	10		

- Molecule 86 is a RNA chain called LSU-12.

Mol	Chain	Residues	Atoms						AltConf	Trace
86	RL	178	Total	C	H	N	O	P	0	0
			5702	1701	1905	678	1240	178		

- Molecule 87 is a RNA chain called LSU-13.

Mol	Chain	Residues	Atoms						AltConf	Trace
87	RM	71	Total	C	H	N	O	P	0	0
			2285	682	766	283	483	71		

- Molecule 88 is a RNA chain called LSU-14.

Mol	Chain	Residues	Atoms						AltConf	Trace
88	RN	26	Total	C	H	N	O	P	0	0
			831	247	280	97	181	26		

- Molecule 89 is a RNA chain called LSU-15.

Mol	Chain	Residues	Atoms						AltConf	Trace
89	RO	26	Total	C	H	N	O	P	0	0
			844	252	283	110	173	26		

- Molecule 90 is a RNA chain called LSU-16.

Mol	Chain	Residues	Atoms						AltConf	Trace
90	RP	11	Total	C	H	N	O	P	0	0
			369	110	122	55	71	11		

- Molecule 91 is a RNA chain called LSU-17.

Mol	Chain	Residues	Atoms						AltConf	Trace
91	RQ	68	Total	C	H	N	O	P	0	0
			2192	656	732	275	461	68		

- Molecule 92 is a RNA chain called LSU-18.

Mol	Chain	Residues	Atoms						AltConf	Trace
92	RS	94	Total	C	H	N	O	P	0	0
			2996	893	1005	346	658	94		

- Molecule 93 is a RNA chain called LSU-19.

Mol	Chain	Residues	Atoms						AltConf	Trace
93	RT	28	Total	C	H	N	O	P	0	0
			915	275	305	126	181	28		

- Molecule 94 is a RNA chain called LSU-20.

Mol	Chain	Residues	Atoms						AltConf	Trace
94	RU	15	Total	C	H	N	O	P	0	0
			489	146	163	64	101	15		

- Molecule 95 is a RNA chain called LSU-21.

Mol	Chain	Residues	Atoms						AltConf	Trace
95	RV	35	Total	C	H	N	O	P	0	0
			1133	339	380	147	232	35		

- Molecule 96 is a RNA chain called LSU-22.

Mol	Chain	Residues	Atoms						AltConf	Trace
96	RW	91	Total	C	H	N	O	P	0	0
			2901	864	975	336	635	91		

- Molecule 97 is a RNA chain called LSU-23.

Mol	Chain	Residues	Atoms						AltConf	Trace
97	RX	277	Total	C	H	N	O	P	0	0
			8851	2633	2968	1031	1942	277		

- Molecule 98 is a RNA chain called LSU-24.

Mol	Chain	Residues	Atoms						AltConf	Trace
98	RY	47	Total	C	H	N	O	P	0	0
			1529	457	510	201	314	47		

- Molecule 99 is a RNA chain called LSU-25.

Mol	Chain	Residues	Atoms						AltConf	Trace
99	RZ	45	Total	C	H	N	O	P	0	0
			1470	440	493	202	290	45		

- Molecule 100 is a RNA chain called LSU-26.

Mol	Chain	Residues	Atoms						AltConf	Trace
100	Ra	50	Total	C	H	N	O	P	0	0
			1609	480	538	197	344	50		

- Molecule 101 is a RNA chain called LSU-27.

Mol	Chain	Residues	Atoms						AltConf	Trace
101	Rb	28	Total	C	H	N	O	P	0	0
			891	265	298	99	201	28		

- Molecule 102 is a RNA chain called LSU-28.

Mol	Chain	Residues	Atoms						AltConf	Trace
102	Rc	201	Total	C	H	N	O	P	0	0
			6437	1917	2156	763	1400	201		

- Molecule 103 is a RNA chain called LSU-29.

Mol	Chain	Residues	Atoms						AltConf	Trace
103	Rd	80	Total	C	H	N	O	P	0	0
			2570	765	859	308	558	80		

- Molecule 104 is a RNA chain called LSU-30.

Mol	Chain	Residues	Atoms						AltConf	Trace
104	Rf	29	Total	C	H	N	O	P	0	0
			948	285	316	131	187	29		

- Molecule 105 is a RNA chain called LSU-31.

Mol	Chain	Residues	Atoms						AltConf	Trace
105	Rg	14	Total	C	H	N	O	P	0	0
			455	136	152	59	94	14		

- Molecule 106 is a RNA chain called LSU-32.

Mol	Chain	Residues	Atoms						AltConf	Trace
106	Rh	49	Total	C	H	N	O	P	0	0
			1586	473	533	204	327	49		

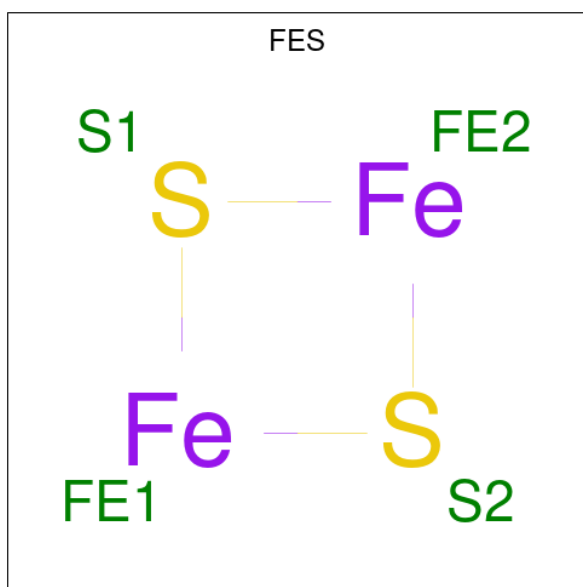
- Molecule 107 is a RNA chain called LSU-32.

Mol	Chain	Residues	Atoms						AltConf	Trace
107	Ri	44	Total	C	H	N	O	P	0	0
			1407	420	468	163	312	44		

- Molecule 108 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
108	Ay	1	Total	Zn	0
			1	1	

- Molecule 109 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			AltConf
109	Xw	1	Total	Fe	S	0
			4	2	2	
109	XD	1	Total	Fe	S	0
			4	2	2	

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, Not provided	
Number of particles used	375745	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	1.903	Depositor
Minimum map value	-1.113	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	581.0, 581.0, 581.0	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
109	FES	Xw	401	56	0,4,4	-	-	-		
109	FES	XD	301	63	0,4,4	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
109	FES	Xw	401	56	-	-	0/1/1/1
109	FES	XD	301	63	-	-	0/1/1/1

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 [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
102	Rc	4
82	RG	2
97	RX	2
103	Rd	1
50	Xo	1
83	RI	1
99	RZ	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Rd	20:U	O3'	28:U	P	25.99
1	RG	4:A	O3'	12:A	P	24.64
1	Rc	74:A	O3'	79:C	P	24.09
1	Xo	732:THR	C	978:ILE	N	16.87
1	Rc	81:C	O3'	87:C	P	15.74

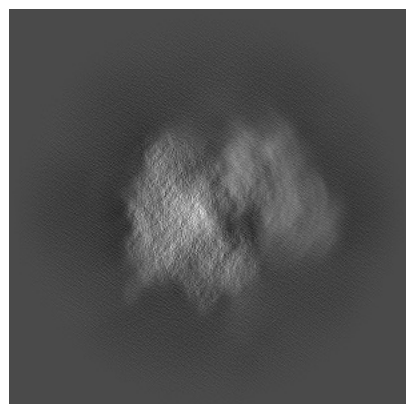
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52551. These allow visual inspection of the internal detail of the map and identification of artifacts.

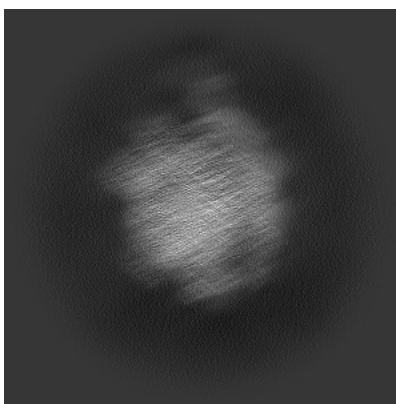
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

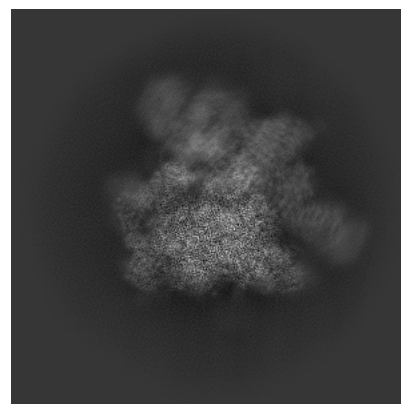
5.1.1 Primary map



X

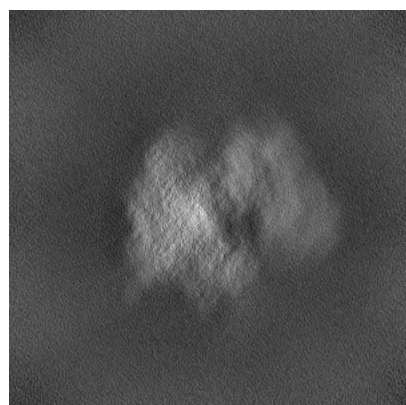


Y

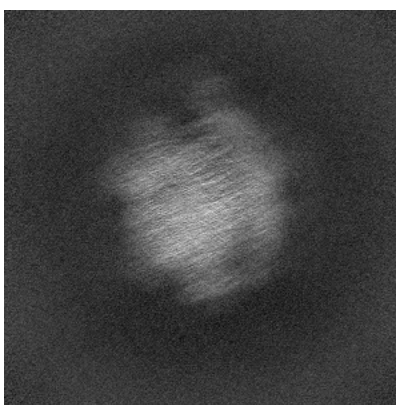


Z

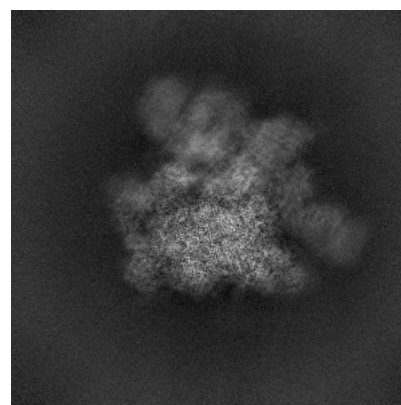
5.1.2 Raw map



X



Y

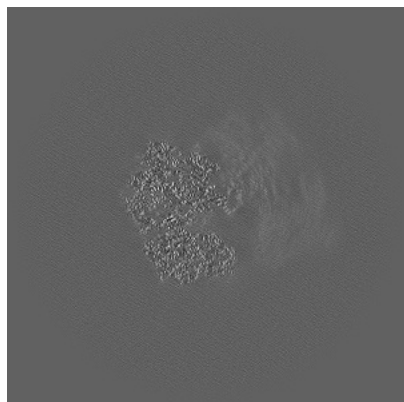


Z

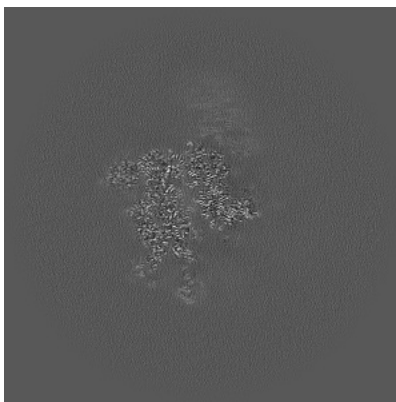
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

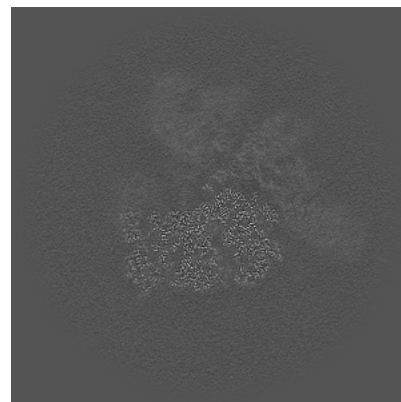
5.2.1 Primary map



X Index: 350

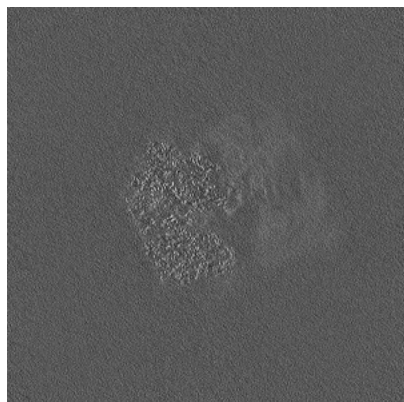


Y Index: 350

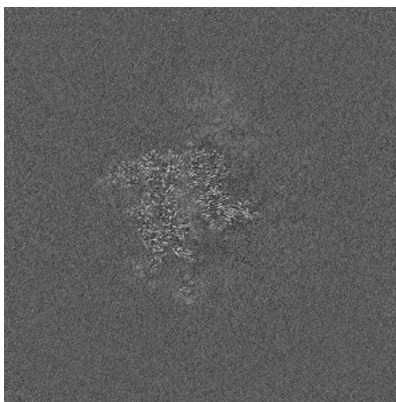


Z Index: 350

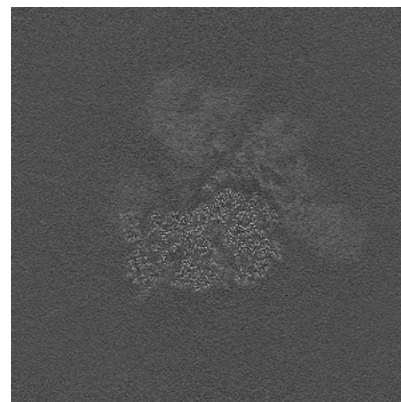
5.2.2 Raw map



X Index: 350



Y Index: 350

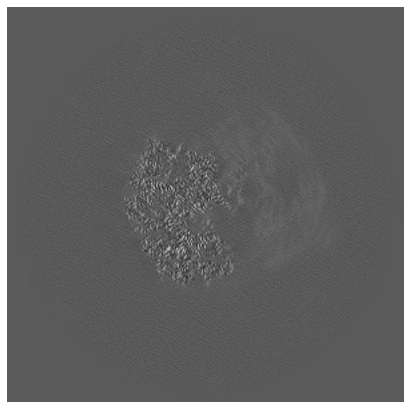


Z Index: 350

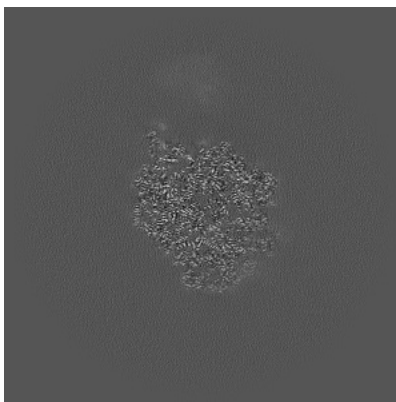
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

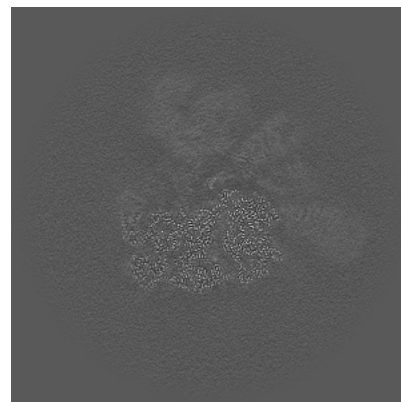
5.3.1 Primary map



X Index: 344

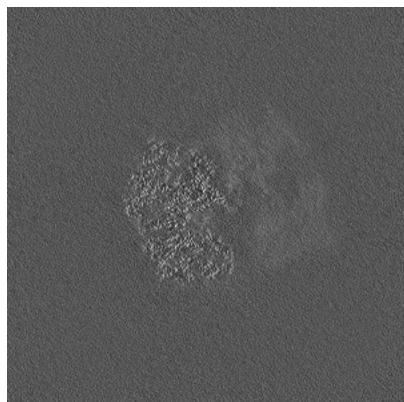


Y Index: 286

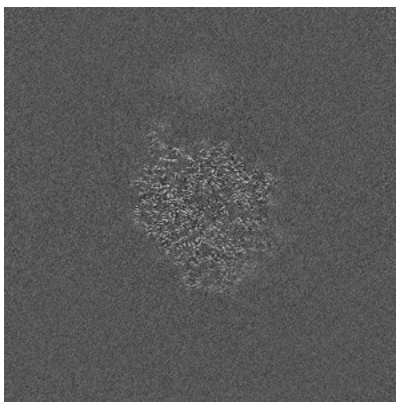


Z Index: 342

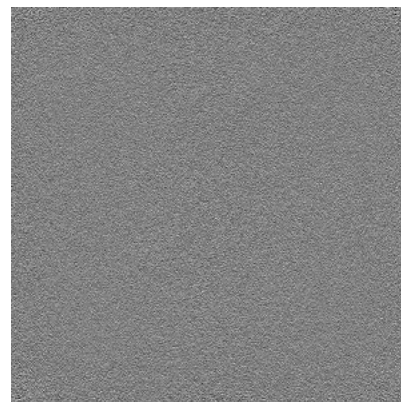
5.3.2 Raw map



X Index: 346



Y Index: 286

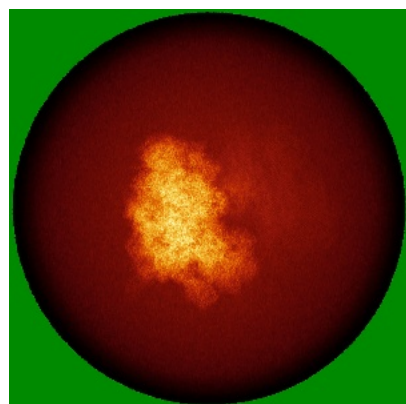


Z Index: 0

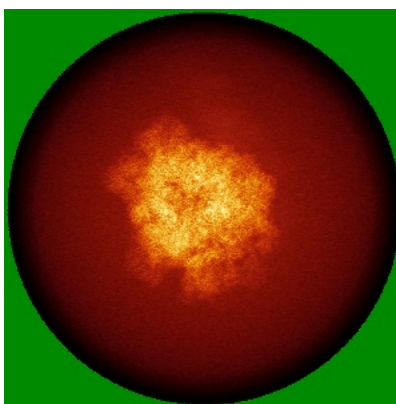
The images above show the largest variance slices of the map in three orthogonal directions.

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

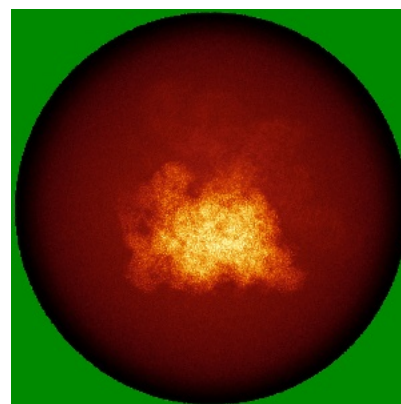
5.4.1 Primary map



X

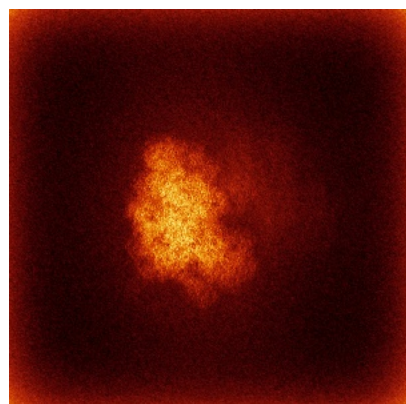


Y

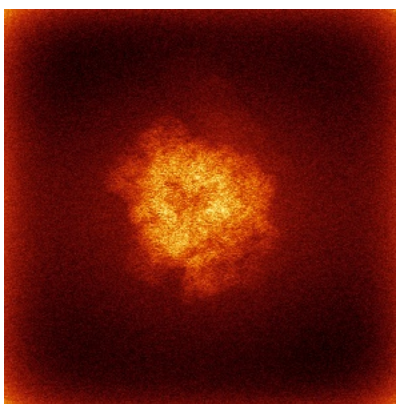


Z

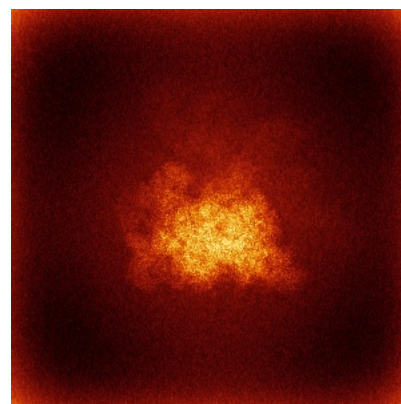
5.4.2 Raw map



X



Y



Z

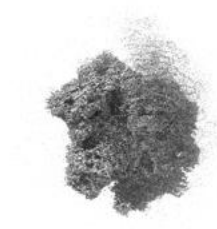
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



X



Y



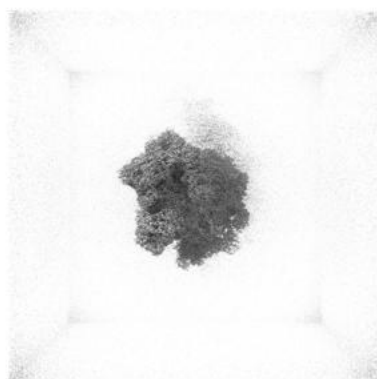
Z

The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

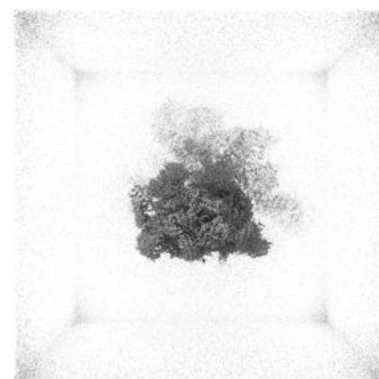
5.5.2 Raw map



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.

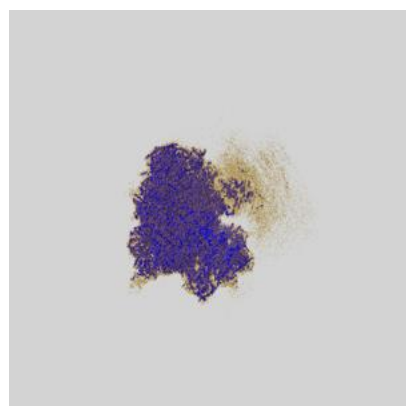
5.6 Mask visualisation [i](#)

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

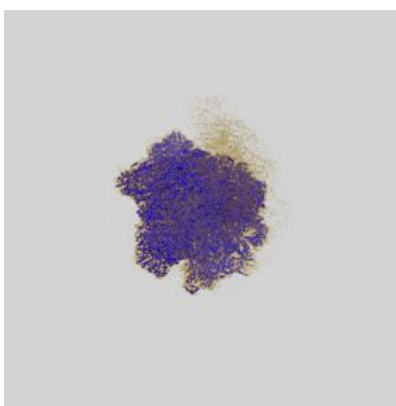
A mask typically either:

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

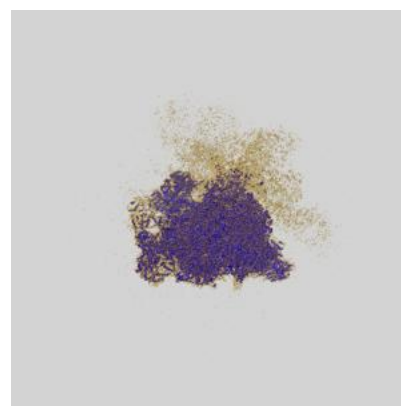
5.6.1 emd_52551_msk_1.map [i](#)



X



Y

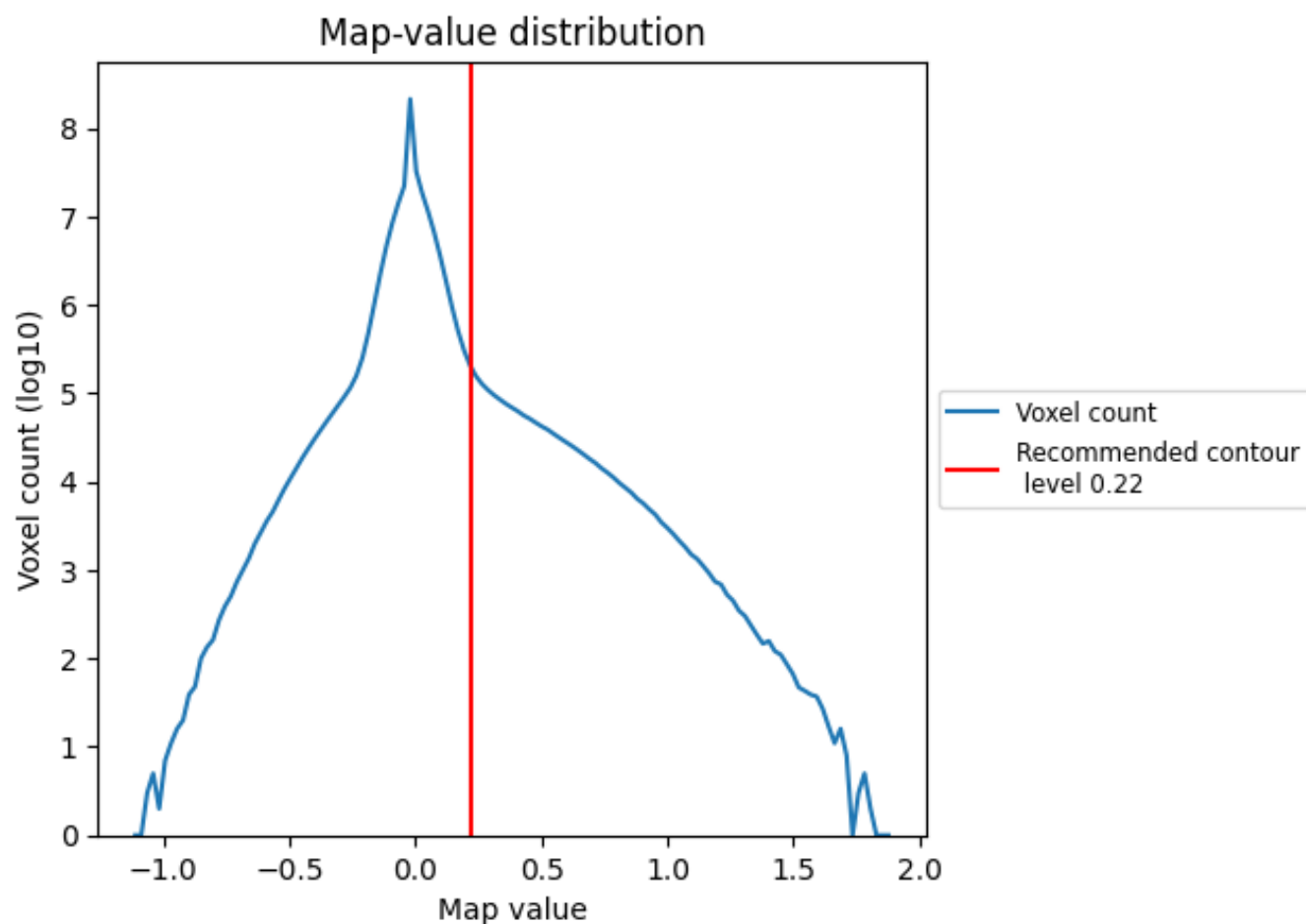


Z

6 Map analysis [i](#)

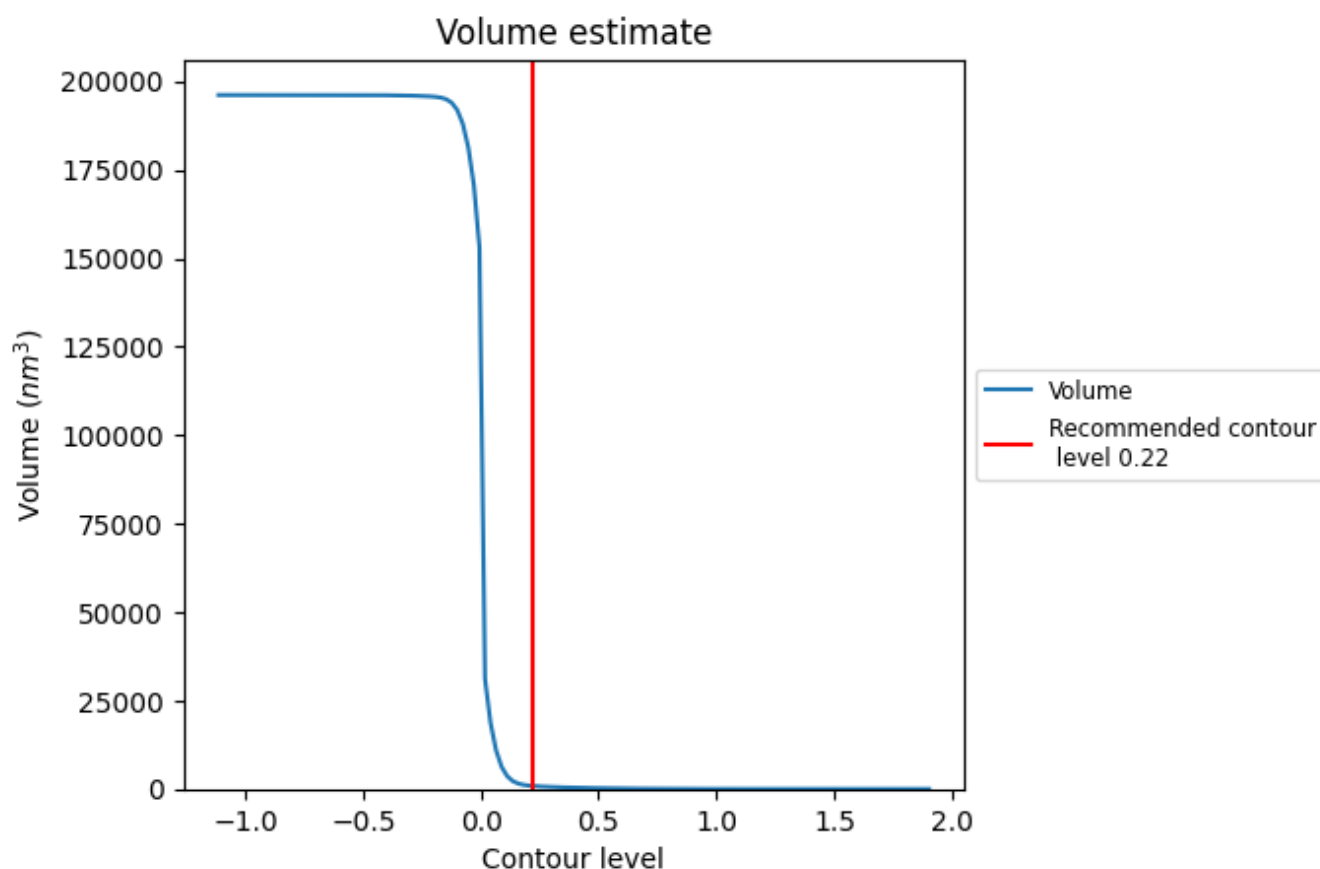
This section contains the results of statistical analysis of the map.

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.

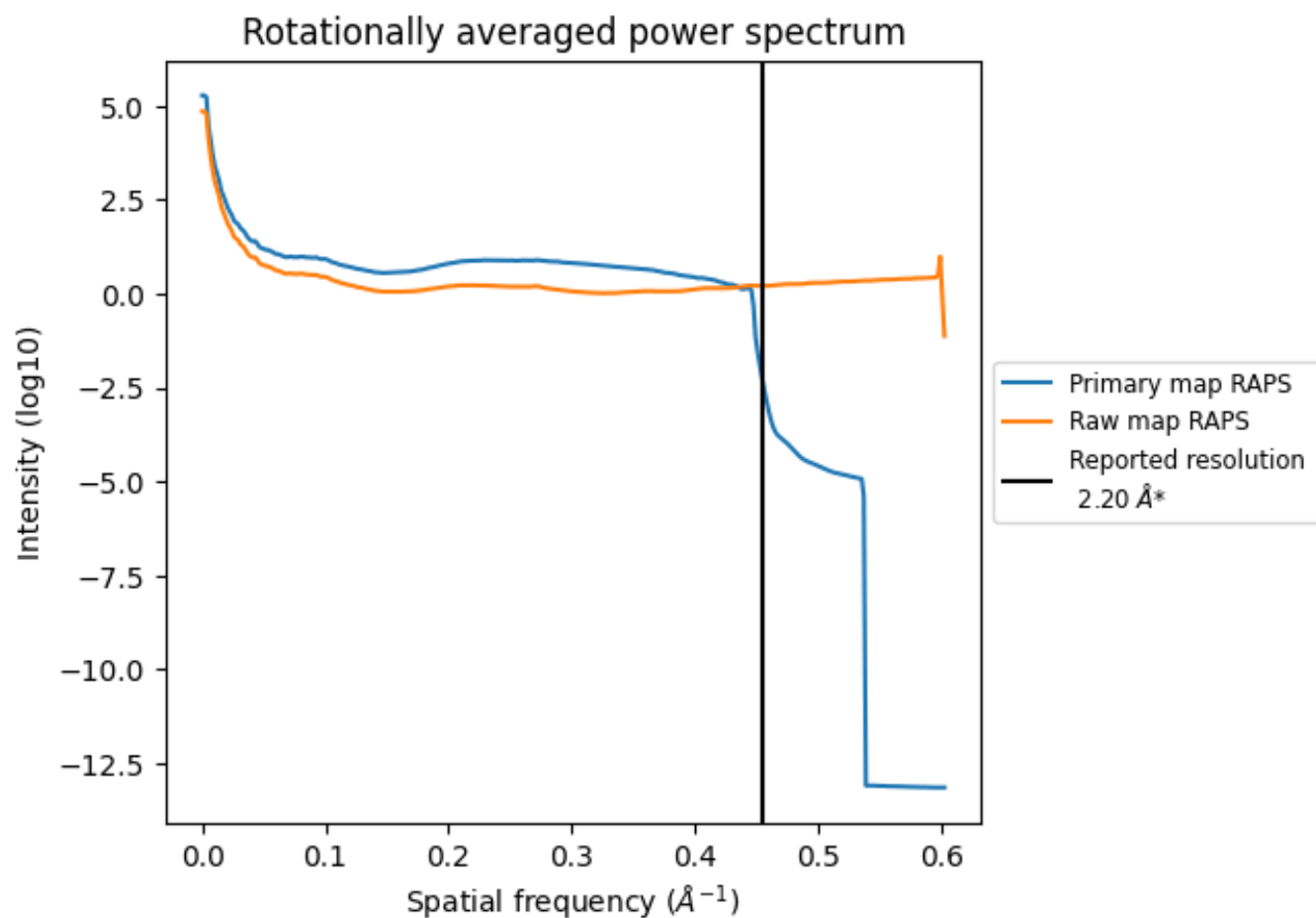
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 859 nm^3 ; this corresponds to an approximate mass of 776 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 ⓘ

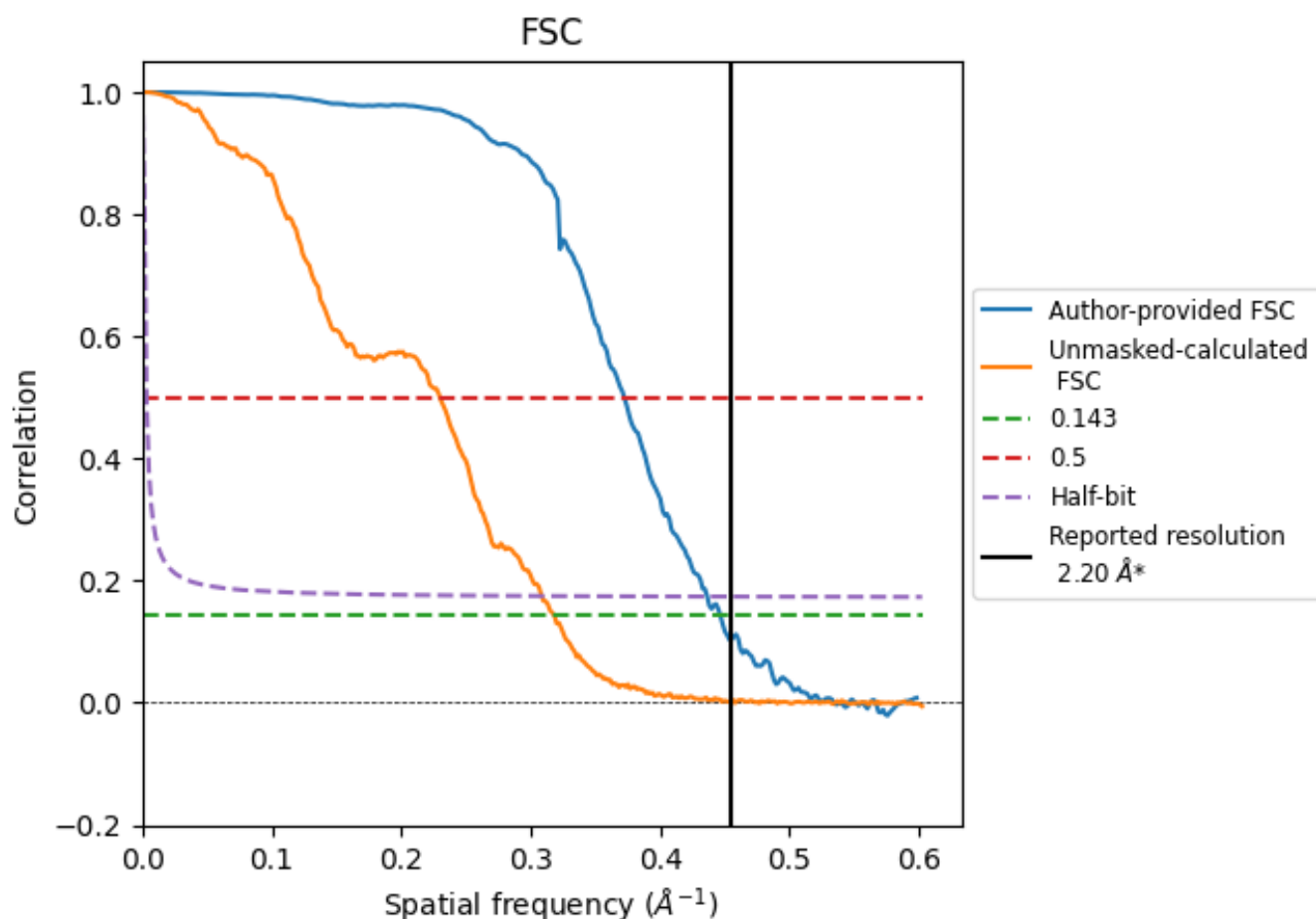


*Reported resolution corresponds to spatial frequency of 0.455 \AA^{-1}

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 0.455 Å⁻¹

7.2 Resolution estimates [i](#)

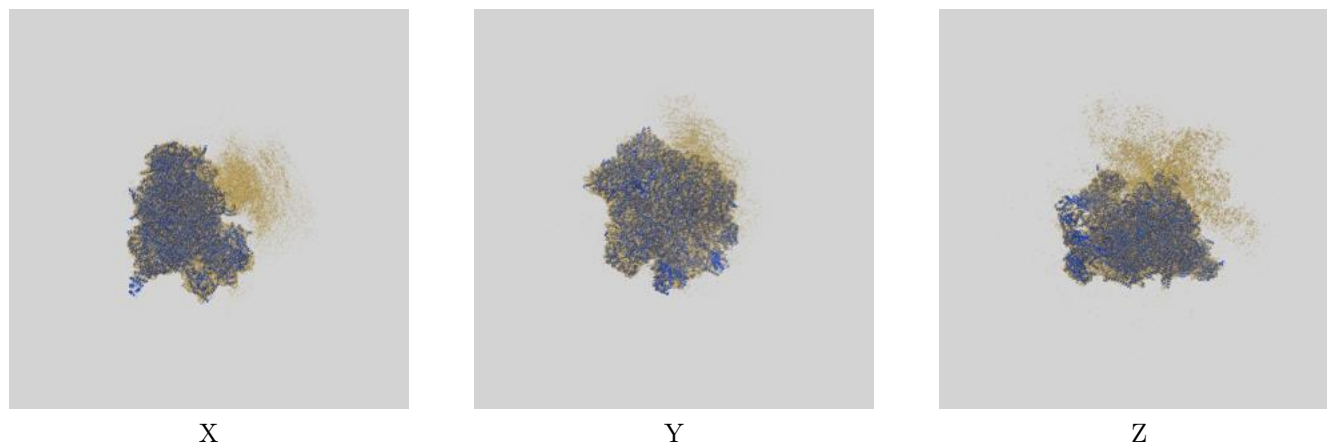
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.24	2.69	2.29
Unmasked-calculated*	3.14	4.35	3.24

*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 3.14 differs from the reported value 2.2 by more than 10 %

8 Map-model fit [i](#)

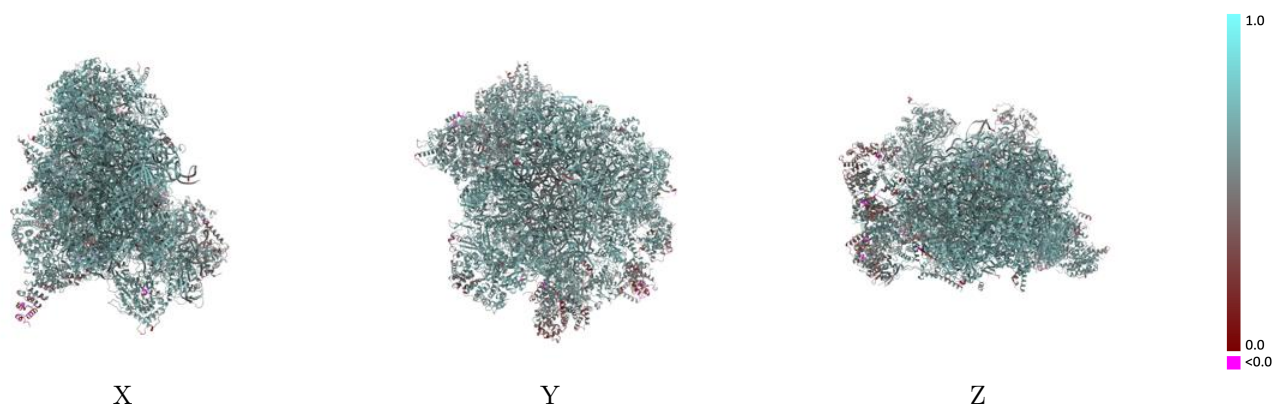
This section contains information regarding the fit between EMDB map EMD-52551 and PDB model 9I05. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



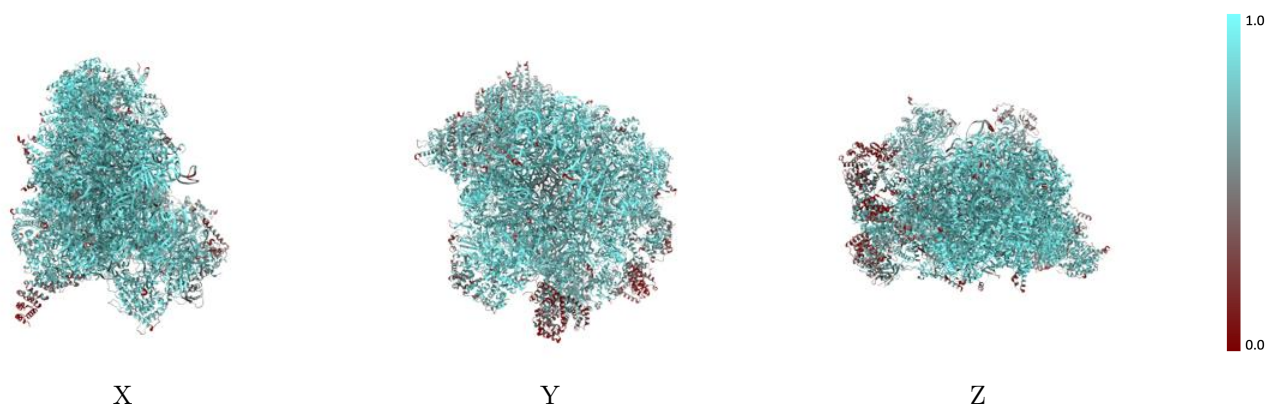
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



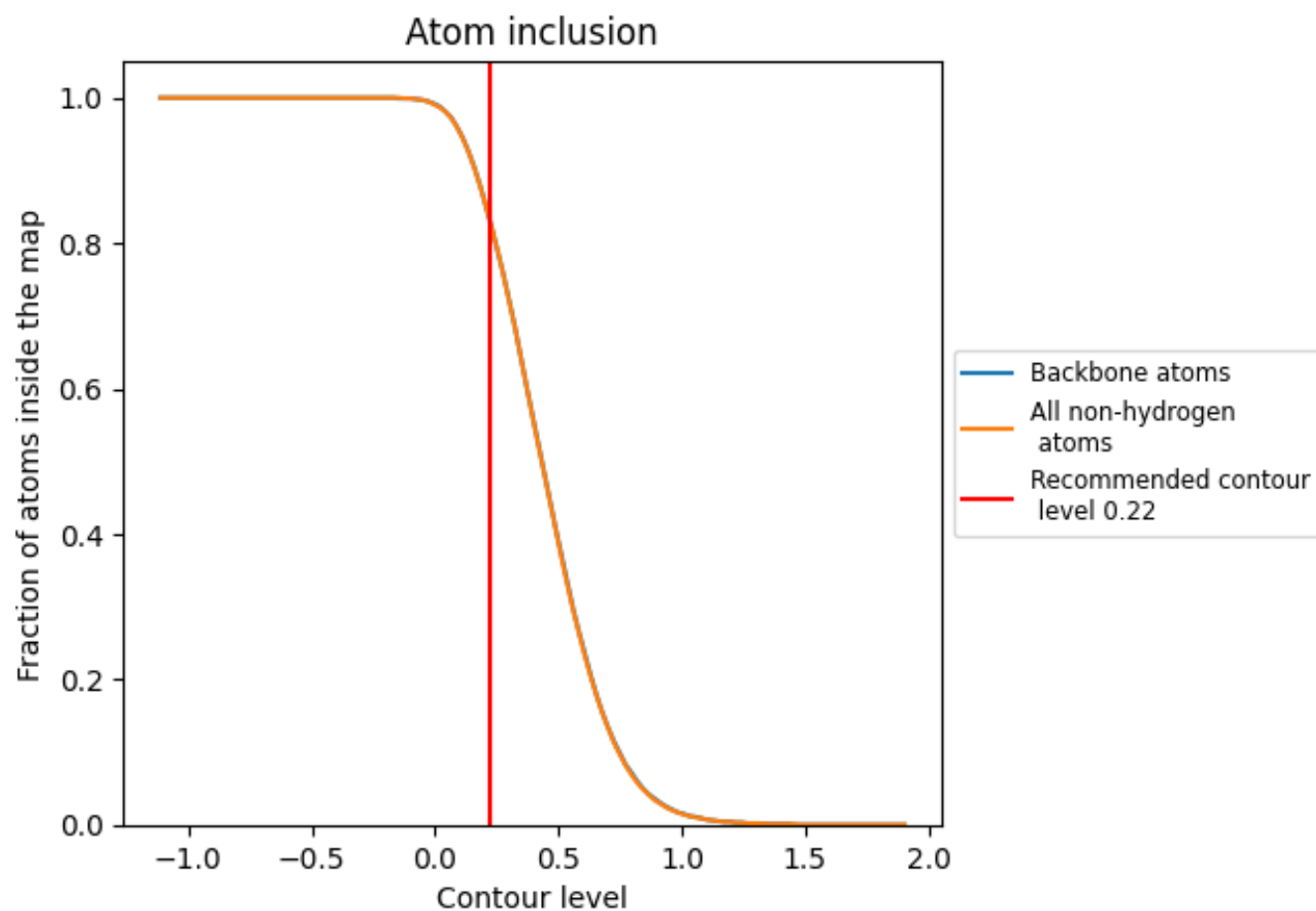
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).







































































8.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8340	 0.6110
AA	 0.8630	 0.6160
AB	 0.8560	 0.6180
AC	 0.7360	 0.5620
AD	 0.9320	 0.6570
AE	 0.7760	 0.6130
AF	 0.7710	 0.5990
AG	 0.8780	 0.6430
AH	 0.9150	 0.6250
AI	 0.8140	 0.6100
Aa	 0.8940	 0.6440
Ab	 0.9400	 0.6600
Ac	 0.8550	 0.6250
Ad	 0.8280	 0.6050
Ae	 0.8280	 0.6020
Af	 0.4620	 0.4590
Ag	 0.8900	 0.6300
Ah	 0.8900	 0.6430
Ai	 0.8790	 0.6420
Aj	 0.8600	 0.6330
Ak	 0.9110	 0.6410
Al	 0.8790	 0.6400
Am	 0.9360	 0.6560
An	 0.8890	 0.6290
Ao	 0.9180	 0.6480
Ap	 0.9360	 0.6520
Aq	 0.8250	 0.6150
Ar	 0.9010	 0.6470
As	 0.9410	 0.6610
At	 0.9300	 0.6600
Au	 0.9260	 0.6530
Av	 0.9280	 0.6610
Aw	 0.8810	 0.6270
Ax	 0.9690	 0.6730
Ay	 0.9550	 0.6510



































































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Chain	Atom inclusion	Q-score
Az	 0.7330	 0.5740
RA	 0.7640	 0.5180
RB	 0.8780	 0.6030
RC	 0.9000	 0.6110
RD	 0.9230	 0.6280
RE	 0.8830	 0.6010
RF	 0.8520	 0.6010
RG	 0.8460	 0.6020
RI	 0.8420	 0.5900
RJ	 0.9400	 0.6370
RK	 0.9770	 0.6730
RL	 0.9340	 0.6280
RM	 0.9190	 0.6250
RN	 0.7600	 0.5160
RO	 0.8000	 0.5260
RP	 0.8990	 0.6110
RQ	 0.9200	 0.6330
RS	 0.9320	 0.6370
RT	 0.9180	 0.6370
RU	 0.9080	 0.6180
RV	 0.8750	 0.6020
RW	 0.9460	 0.6440
RX	 0.8980	 0.6180
RY	 0.8540	 0.5880
RZ	 0.9140	 0.6080
Ra	 0.9110	 0.6200
Rb	 0.8600	 0.6070
Rc	 0.8960	 0.6120
Rd	 0.9210	 0.6180
Rf	 0.9220	 0.6350
Rg	 0.8350	 0.5620
Rh	 0.9120	 0.6140
Ri	 0.8810	 0.5960
Ua	 0.5700	 0.5100
Ub	 0.7680	 0.5800
Uc	 0.6120	 0.5430
Ud	 0.7560	 0.5400
Ue	 0.8450	 0.6150
Uf	 0.6670	 0.4380
XA	 0.9100	 0.6520
XB	 0.8650	 0.6290
XC	 0.5740	 0.4890

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Chain	Atom inclusion	Q-score
XD	 0.8160	 0.6010
XE	 0.9320	 0.6530
XF	 0.5770	 0.5320
XG	 0.9460	 0.6650
XH	 0.8650	 0.6310
XI	 0.9510	 0.6700
XJ	 0.9080	 0.6370
Xa	 0.9490	 0.6610
Xb	 0.8870	 0.6350
Xc	 0.8890	 0.6380
Xd	 0.7350	 0.5800
Xe	 0.9080	 0.6460
Xf	 0.8600	 0.6320
Xg	 0.7950	 0.5990
Xh	 0.8110	 0.6060
Xi	 0.9160	 0.6470
Xj	 0.8250	 0.6150
Xk	 0.9070	 0.6420
Xl	 0.3520	 0.4320
Xm	 0.8270	 0.6140
Xn	 0.8870	 0.6410
Xo	 0.7120	 0.5680
Xp	 0.9360	 0.6580
Xq	 0.7700	 0.5890
Xr	 0.7450	 0.5840
Xs	 0.8630	 0.6280
Xt	 0.8610	 0.6190
Xv	 0.4240	 0.4550
Xw	 0.8360	 0.6120
Xx	 0.8540	 0.6360
Xy	 0.9630	 0.6760
Xz	 0.9090	 0.6400