



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 02:24 PM UTC

PDB ID : 6NU2 / pdb_00006nu2
EMDB ID : EMD-0514
Title : Structural insights into unique features of the human mitochondrial ribosome recycling
Authors : Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.
Deposited on : 2019-01-30
Resolution : 3.90 Å(reported)
Based on initial model : 3JD5

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

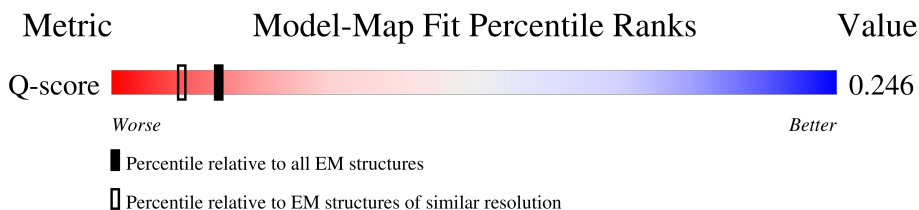
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	8855 (3.40 - 4.40)

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

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 294948 atoms, of which 134991 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	1472	47118	14025	15857	5642	10122	1472	0	0

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	B	56	1794	534	603	214	387	56	0	0

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	D	236	3738	1145	1896	373	315	9	0	0

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	300	4743	1523	2378	410	422	10	0	0

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	F	250	4058	1294	2045	365	348	6	0	0

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
6	H	95	1616	498	832	152	134	0	0

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
7	I	158	Total	C	H	N	O	S	0	0
			2652	828	1369	235	210	10		

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
8	J	140	Total	C	H	N	O	S	0	0
			2202	680	1141	192	187	2		

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
9	K	177	Total	C	H	N	O	S	0	0
			2899	934	1448	259	251	7		

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
10	L	115	Total	C	H	N	O	S	0	0
			1830	559	941	171	154	5		

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
11	M	287	Total	C	H	N	O	S	0	0
			4683	1472	2378	425	402	6		

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
12	N	205	Total	C	H	N	O	S	0	0
			3334	1056	1680	308	280	10		

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
13	O	152	Total	C	H	N	O	S	0	0
			2528	784	1283	239	215	7		

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
14	P	133	Total	C	H	N	O	S	0	0
			2162	677	1082	209	189	5		

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	Q	219	Total	C	H	N	O	S	0	0
			3681	1168	1859	322	323	9		

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
16	R	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
17	S	156	Total	C	H	N	O	S	0	0
			2573	806	1322	222	219	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
18	T	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	U	111	Total	C	H	N	O	S	0	0
			1857	591	935	176	153	2		

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
20	V	189	Total	C	H	N	O	S	0	0
			3109	987	1558	278	278	8		

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	W	115	1816	571	922	169	151	3	0	0

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	X	243	4089	1317	2054	351	362	5	0	0

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	Y	176	3078	970	1561	291	252	4	0	0

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	Z	120	2008	626	1030	183	166	3	0	0

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	0	108	1782	545	902	172	157	6	0	0

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	1	52	908	278	475	83	70	2	0	0

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	2	46	782	233	406	83	59	1	0	0

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	3	95	1714	539	883	162	127	3	0	0

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	4	36	666	203	344	70	46	3	0	0

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	5	376	6123	1987	3059	529	538	10	0	0

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	6	325	5087	1692	2451	465	470	9	0	0

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	7	266	4331	1383	2173	371	388	16	0	0

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	8	99	1680	535	844	144	155	2	0	0

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	9	109	1751	565	878	152	154	2	0	0

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	a	82	1344	434	658	124	123	5	0	0

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	b	148	2358	733	1180	229	213	3	0	0

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	c	275	4437	1415	2220	383	410	9	0	0

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	d	162	2690	870	1343	234	235	8	0	0

- Molecule 39 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	e	217	3529	1124	1767	310	323	5	0	0

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	f	131	2083	663	1044	169	203	4	0	0

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	g	129	2123	690	1056	185	190	2	0	0

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	h	100	1633	524	806	146	155	2	0	0

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	i	97	1684	532	857	165	126	4	0	0

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
44	j	85	1357	423	673	133	126	2	0	0

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	k	84	1311	407	656	122	121	5	0	0

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	H	N			O
46	l	23	448	137	227	52	32	0	0

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
47	m	45	759	232	387	76	62	2	0	0

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
48	o	94	1601	501	804	165	128	3	0	0

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
49	p	127	2141	661	1083	201	192	4	0	0

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
50	q	128	2125	671	1049	208	192	5	0	0

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	r	146	2423	764	1220	232	199	8	0	0

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	s	370	6058	1946	3022	542	534	14	0	0

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
53	t	28	170	84	30	28	28	0	0

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
54	u	2	65	19	23	8	13	2	0	0

- Molecule 55 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
55	z	204	3240	974	1665	285	308	8	0	0

- Molecule 56 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
56	AA	923	29552	8790	9946	3535	6358	923	0	0

- Molecule 57 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
57	AB	217	3533	1131	1765	321	306	10	0	0

- Molecule 58 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
58	AC	132	2170	699	1088	195	184	4	0	0

- Molecule 59 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
59	AD	322	5153	1611	2596	476	457	13	0	0

- Molecule 60 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
60	AE	122	1973	614	1001	177	177	4	0	0

- Molecule 61 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
61	AF	201	3385	1069	1717	305	283	11	0	0

- Molecule 62 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
62	AG	305	5019	1599	2503	448	455	14	0	0

- Molecule 63 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
63	AH	122	2023	643	1024	168	185	3	0	0

- Molecule 64 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	AI	136	2063	637	1052	192	178	4	0	0

- Molecule 65 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	AJ	108	1725	521	887	169	142	6	0	0

- Molecule 66 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
66	AK	101	1746	537	885	179	140	5	0	0

- Molecule 67 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	AL	164	2855	883	1473	257	235	7	0	0

- Molecule 68 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	AM	116	1870	582	950	182	150	6	0	0

- Molecule 69 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	AN	107	1754	549	908	153	141	3	0	0

- Molecule 70 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	AO	185	3016	970	1488	285	267	6	0	0

- Molecule 71 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	AP	96	1578	498	804	133	135	8	0	0

- Molecule 72 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	AQ	86	1481	455	746	147	124	9	0	0

- Molecule 73 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	AR	242	4039	1285	2031	343	372	8	0	0

- Molecule 74 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	AS	126	2079	673	1037	183	185	1	0	0

- Molecule 75 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
75	AT	162	2674	850	1344	231	238	11	0	0

- Molecule 76 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
76	AU	173	2932	900	1471	294	263	4	0	0

- Molecule 77 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
77	AV	328	5392	1737	2690	452	502	11	0	0

- Molecule 78 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
78	AW	97	1551	486	785	137	139	4	0	0

- Molecule 79 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
79	AX	316	5051	1625	2520	440	455	11	0	0

- Molecule 80 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
80	AY	108	1773	593	859	150	169	2	0	0

- Molecule 81 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
81	AZ	87	1487	473	747	133	130	4	0	0

- Molecule 82 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
82	A0	201	3369	1065	1685	322	292	5	0	0

- Molecule 83 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
83	A1	256	4173	1321	2097	350	395	10	0	0

- Molecule 84 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
84	A2	116	1887	574	962	181	162	8	0	0

- Molecule 85 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
85	A3	69	1292	393	682	130	86	1	0	0

- Molecule 86 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
86	A4	414	5103	1805	2265	490	529	14	0	0

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	A	97	Total	Mg	0
			97	97	
87	M	1	Total	Mg	0
			1	1	
87	g	1	Total	Mg	0
			1	1	
87	AA	28	Total	Mg	0
			28	28	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	0	1	Total	Zn	0
			1	1	
88	4	1	Total	Zn	0
			1	1	
88	r	1	Total	Zn	0
			1	1	
88	AB	1	Total	Zn	0
			1	1	
88	AO	1	Total	Zn	0
			1	1	
88	AP	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
88	AT	1	1	1	0

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	67116	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.994	Depositor
Minimum map value	-0.628	Depositor
Average map value	0.023	Depositor
Map value standard deviation	0.112	Depositor
Recommended contour level	0.188	Depositor
Map size (\AA)	414.2, 414.2, 414.2	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.09, 1.09, 1.09	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 134 ligands modelled in this entry, 134 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 [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
1	A	14
86	A4	13
56	AA	8
2	B	4

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2218:C	O3'	2228:A	P	35.95
1	AA	955:A	O3'	965:C	P	34.65
1	A	2760:A	O3'	2792:A	P	26.71
1	A	2881:C	O3'	2889:C	P	26.07
1	A	1760:G	O3'	1766:U	P	25.62

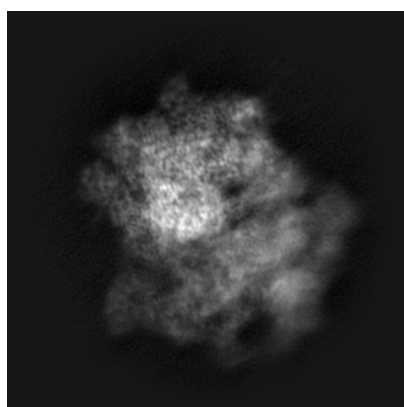
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0514. These allow visual inspection of the internal detail of the map and identification of artifacts.

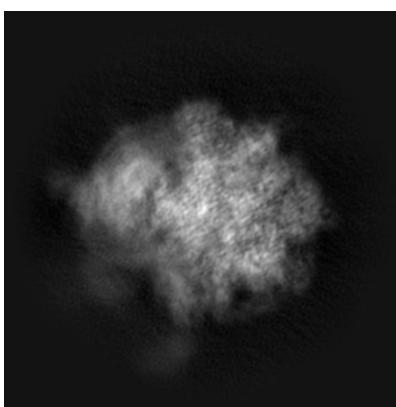
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

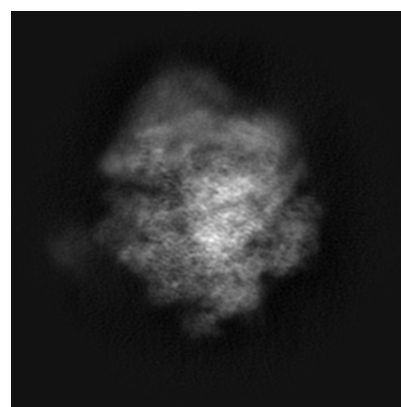
5.1.1 Primary map



X



Y

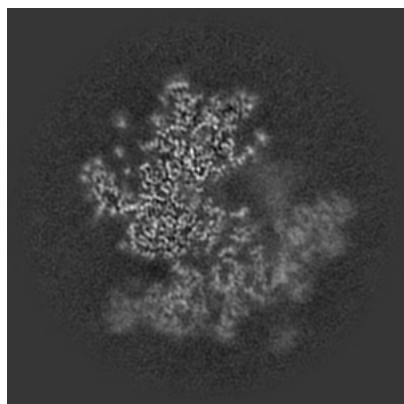


Z

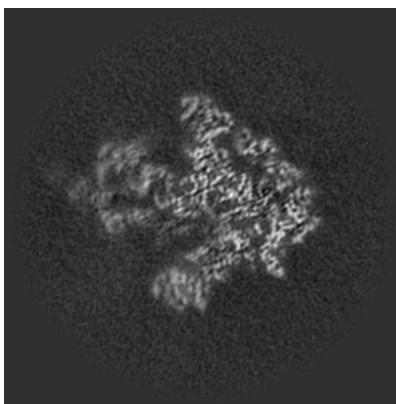
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

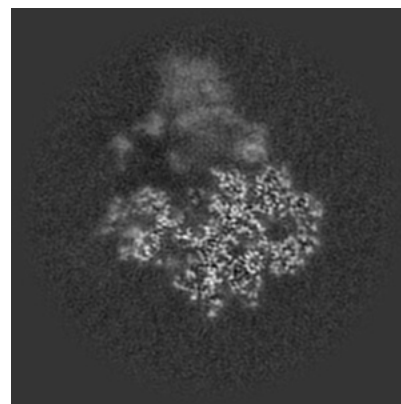
5.2.1 Primary map



X Index: 190



Y Index: 190

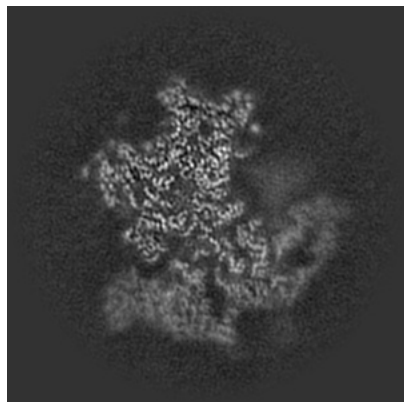


Z Index: 190

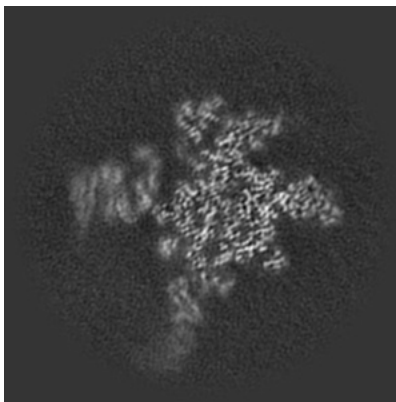
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

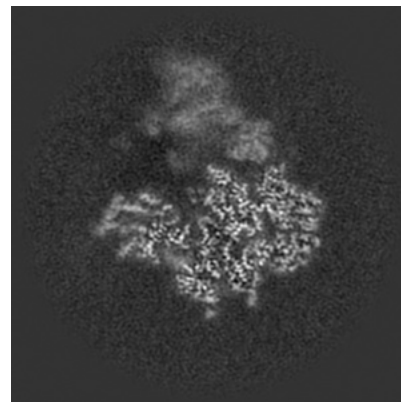
5.3.1 Primary map



X Index: 199



Y Index: 162

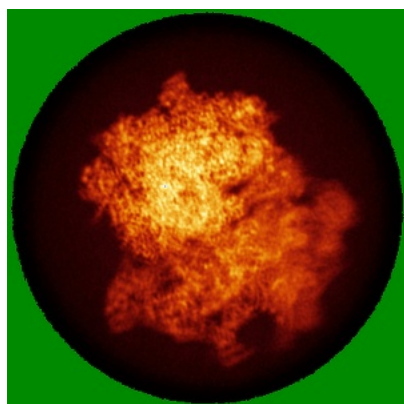


Z Index: 186

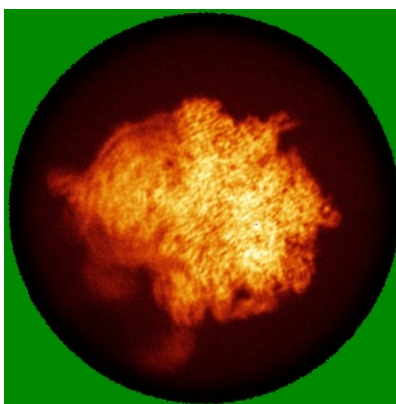
The images above show the largest variance slices of the map in three orthogonal directions.

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

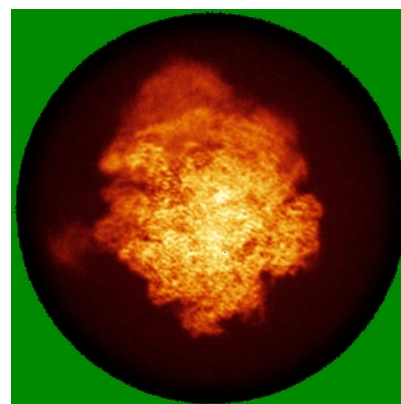
5.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.188. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

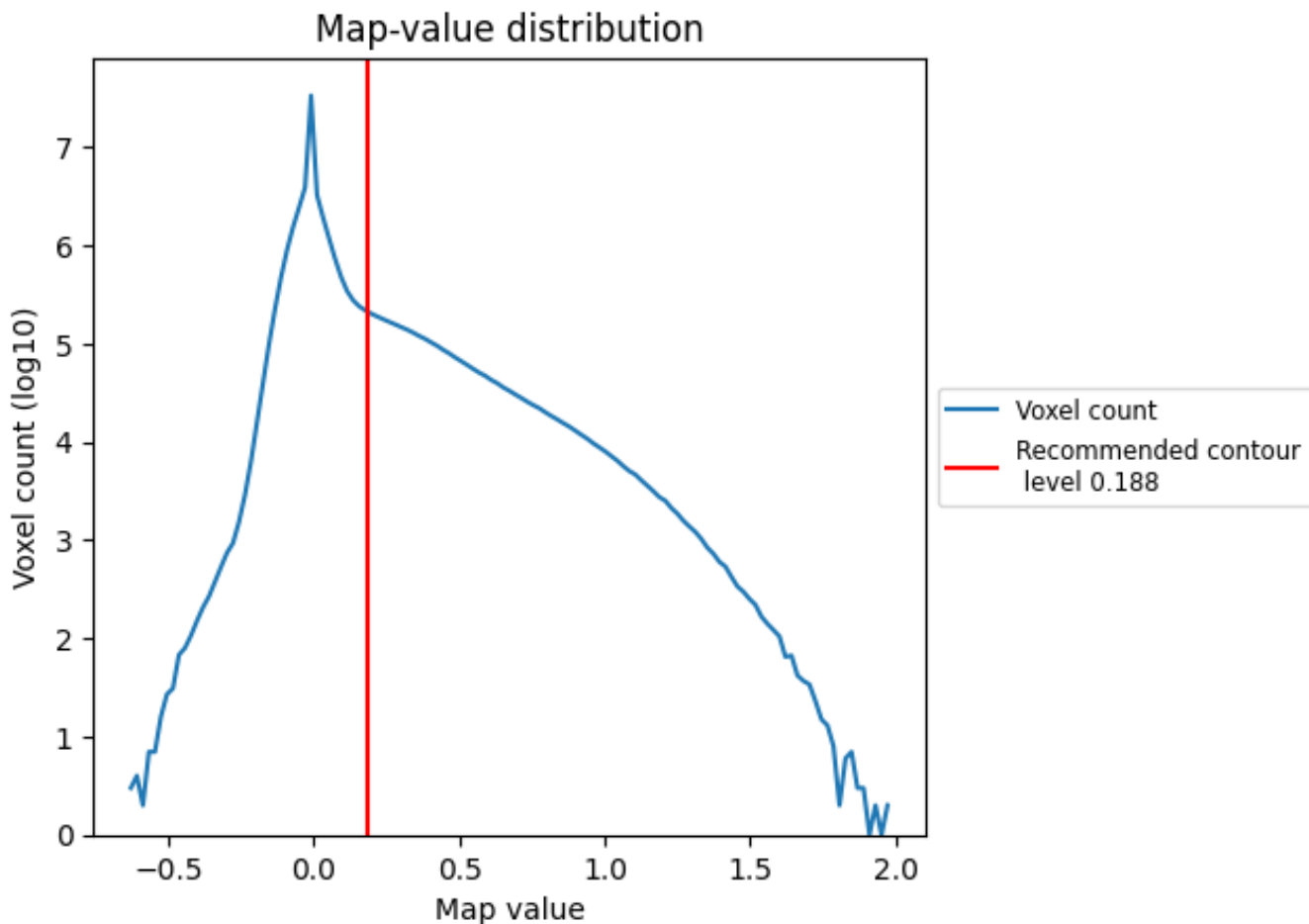
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

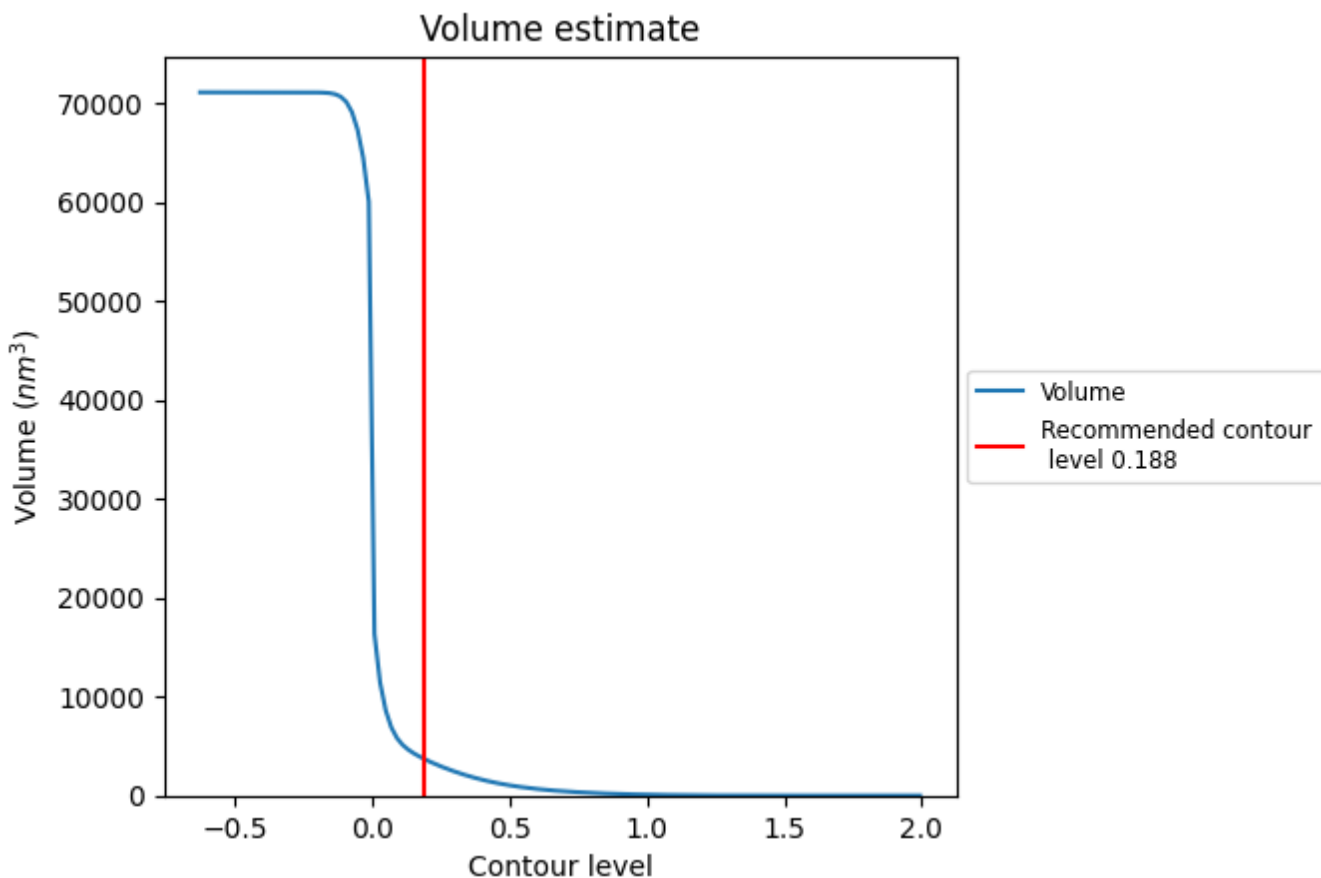
This section contains the results of statistical analysis of the map.

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.

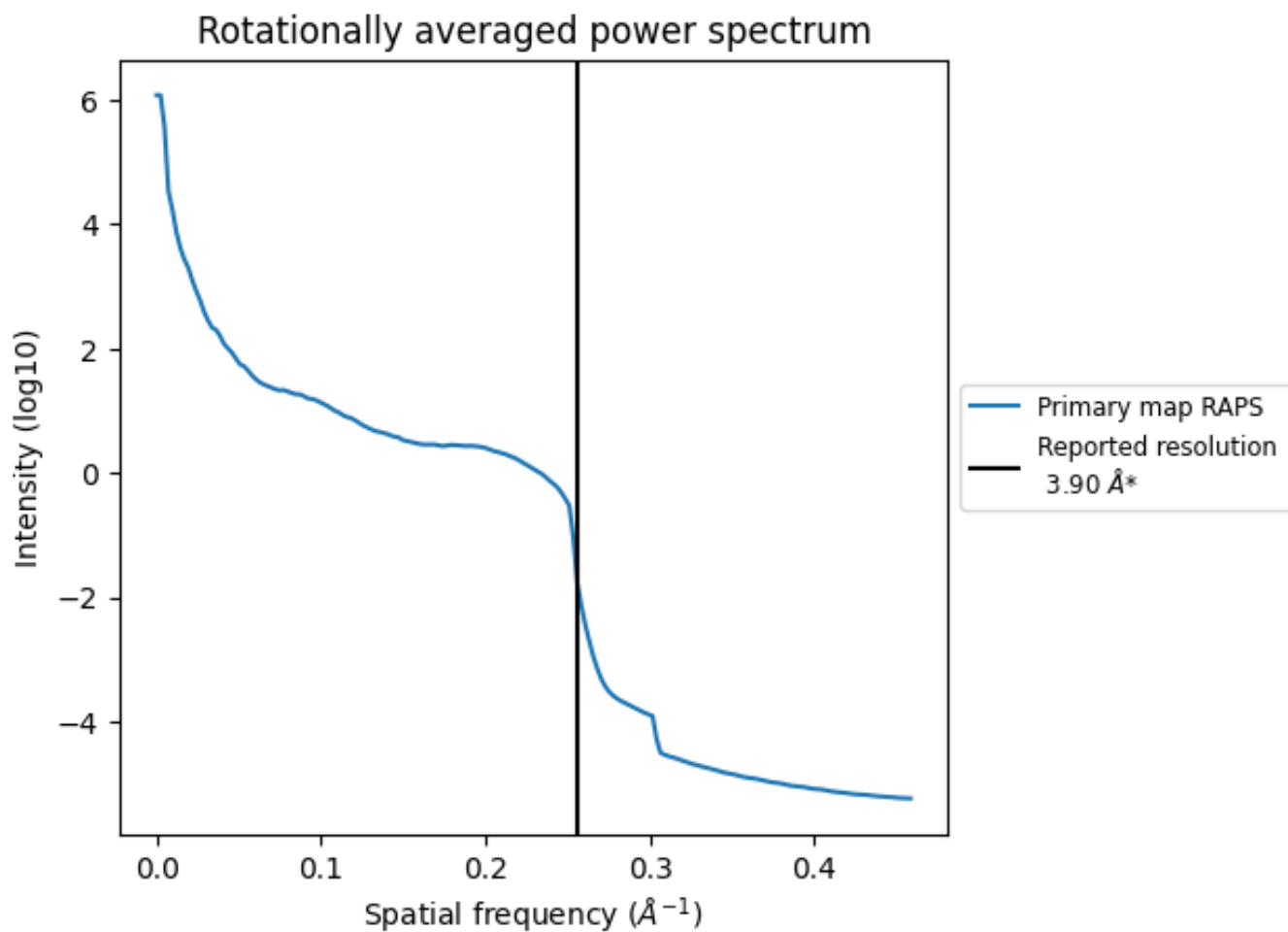
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 3701 nm³; this corresponds to an approximate mass of 3343 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.256\AA^{-1}

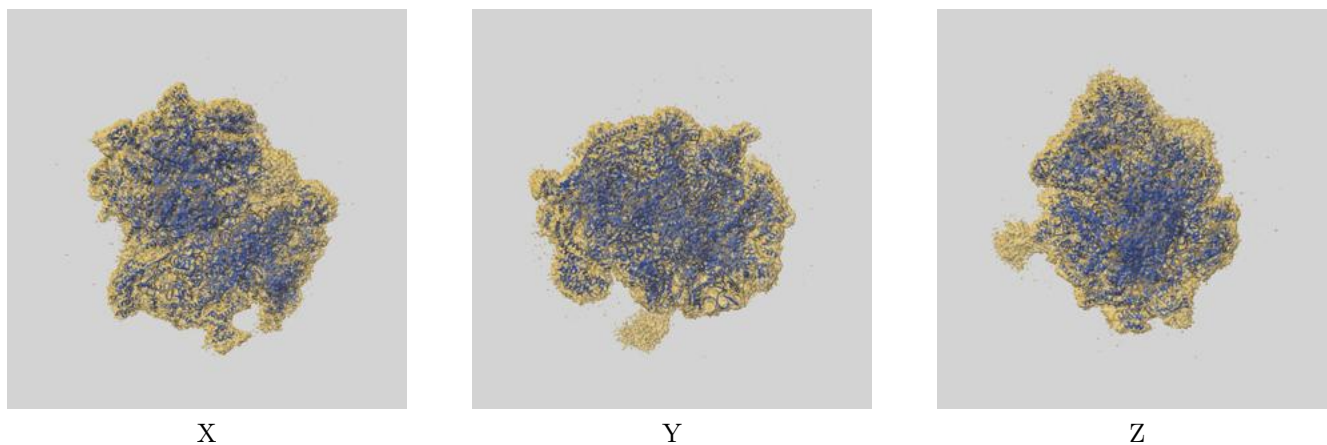
7 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit [i](#)

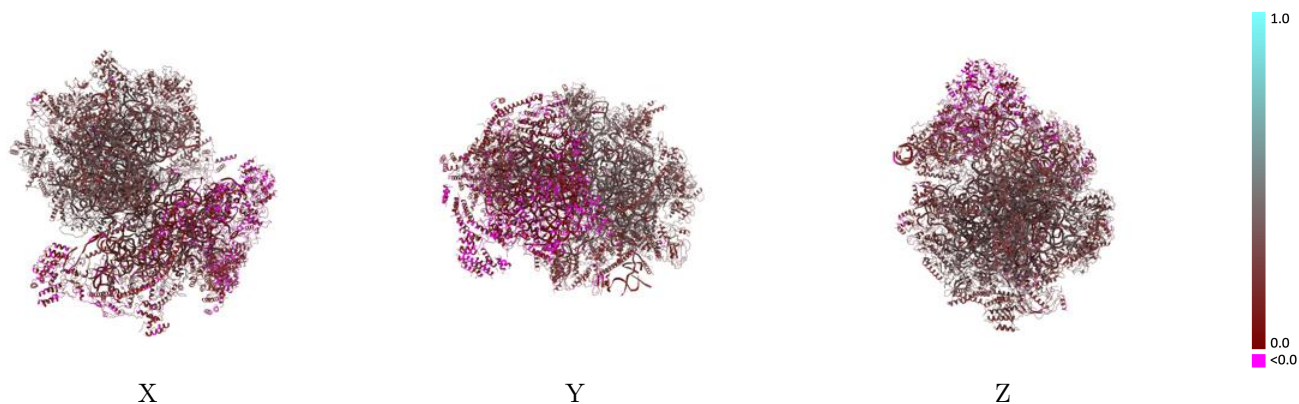
This section contains information regarding the fit between EMDB map EMD-0514 and PDB model 6NU2. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



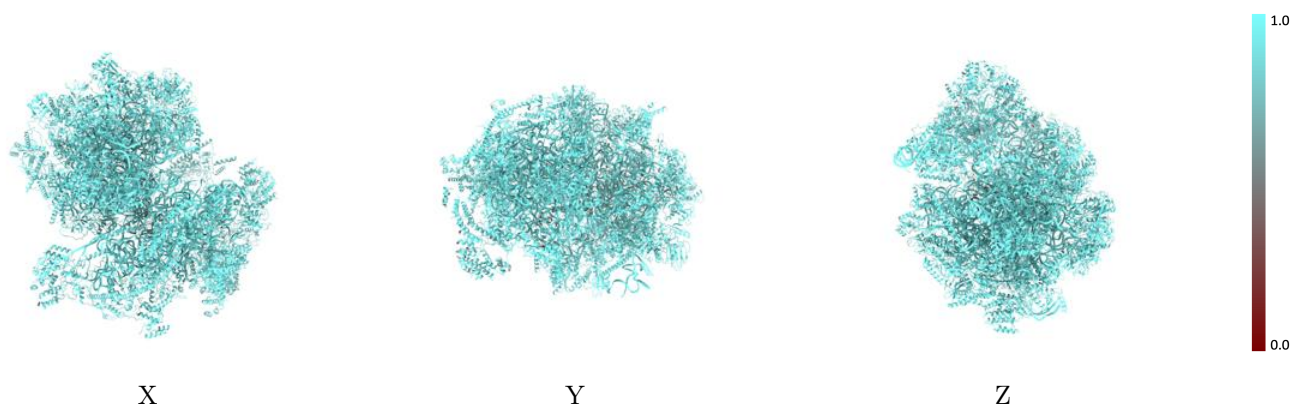
The images above show the 3D surface view of the map at the recommended contour level 0.188 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



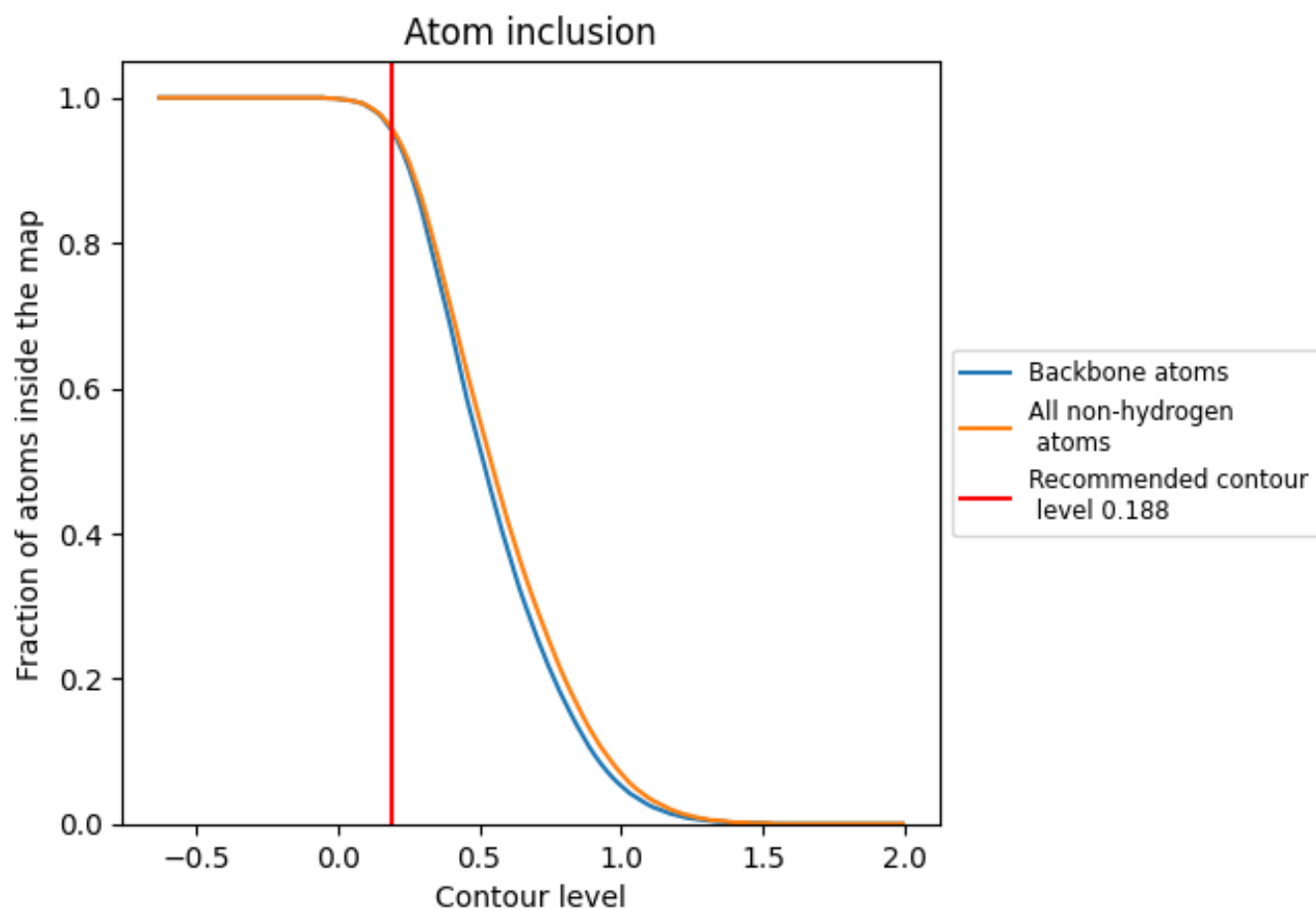
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.188).







































































8.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.188) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.2460
0	 0.9440	 0.3210
1	 0.9550	 0.3150
2	 0.9720	 0.3500
3	 0.9510	 0.3560
4	 0.9840	 0.3390
5	 0.9770	 0.3250
6	 0.9720	 0.2830
7	 0.9650	 0.3020
8	 0.9390	 0.1880
9	 0.9730	 0.3050
A	 0.9850	 0.3120
A0	 0.9630	 0.1740
A1	 0.9320	 0.0800
A2	 0.9430	 0.1570
A3	 0.9310	 0.2570
A4	 0.8980	 0.0690
AA	 0.9910	 0.1890
AB	 0.9710	 0.1830
AC	 0.9600	 0.0820
AD	 0.9410	 0.1860
AE	 0.9760	 0.1230
AF	 0.9480	 0.0880
AG	 0.9560	 0.1010
AH	 0.9410	 0.0720
AI	 0.9840	 0.1470
AJ	 0.9050	 0.2560
AK	 0.9580	 0.0530
AL	 0.9690	 0.1530
AM	 0.9400	 0.1630
AN	 0.9830	 0.2210
AO	 0.9420	 0.1650
AP	 0.9670	 0.1720
AQ	 0.9770	 0.1780
AR	 0.9130	 0.1630























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Chain	Atom inclusion	Q-score
AS	 0.9540	 0.1750
AT	 0.9660	 0.2240
AU	 0.9470	 0.1460
AV	 0.9140	 0.0940
AW	 0.9810	 0.1540
AX	 0.9470	 0.0440
AY	 0.9030	 0.0700
AZ	 0.8640	 0.0780
B	 1.0000	 0.2260
D	 0.9760	 0.3600
E	 0.9600	 0.3490
F	 0.9570	 0.3340
H	 0.9620	 0.3030
I	 0.9530	 0.2300
J	 0.9620	 0.1840
K	 0.9700	 0.3500
L	 0.9160	 0.3400
M	 0.9500	 0.3120
N	 0.9610	 0.3220
O	 0.9600	 0.3360
P	 0.9610	 0.2840
Q	 0.9270	 0.3350
R	 0.9530	 0.3390
S	 0.9690	 0.3620
T	 0.9360	 0.3580
U	 0.9750	 0.3270
V	 0.9560	 0.2980
W	 0.9450	 0.3240
X	 0.9560	 0.3060
Y	 0.9500	 0.2950
Z	 0.9530	 0.3620
a	 0.9790	 0.3520
b	 0.9650	 0.3480
c	 0.9530	 0.3150
d	 0.9570	 0.2550
e	 0.9480	 0.1540
f	 0.9350	 0.2300
g	 0.9710	 0.3270
h	 0.9550	 0.2900
i	 0.9350	 0.3210
j	 0.9530	 0.3350
k	 0.9440	 0.2110

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Chain	Atom inclusion	Q-score
l	 0.9950	 0.2280
m	 0.9830	 0.1930
o	 0.9580	 0.3390
p	 0.9540	 0.2720
q	 0.9450	 0.2700
r	 0.9810	 0.3210
s	 0.9690	 0.3230
t	 1.0000	 0.2650
u	 0.7140	 0.1450
z	 0.6270	 0.2530