



# wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:08 PM UTC

PDB ID : 7OF0 / pdb\_00007of0  
EMDB ID : EMD-12865  
Title : Structure of a human mitochondrial ribosome large subunit assembly intermediate in complex with MTERF4-NSUN4 (dataset1).  
Authors : Hillen, H.S.; Lavdovskaia, E.; Nadler, F.; Hanitsch, E.; Linden, A.; Bohnsack, K.E.; Urlaub, H.; Richter-Dennerlein, R.  
Deposited on : 2021-05-04  
Resolution : 2.20 Å (reported)  
Based on initial model : 5OOL

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

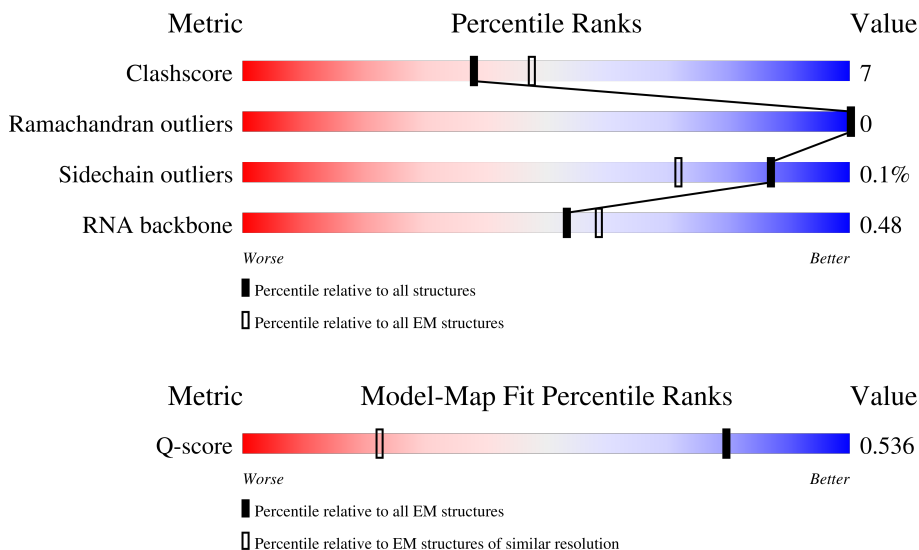
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 ( 1.71 - 2.70 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	188	49% (green), 9% (yellow), 43% (grey)
2	1	65	69% (green), 11% (yellow), 20% (grey)
3	2	92	37% (green), 12% (yellow), 51% (grey)














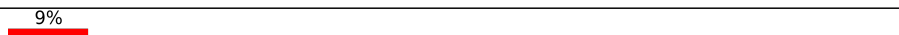
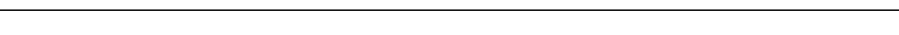
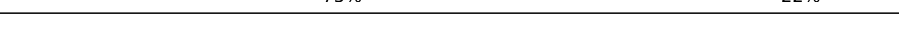

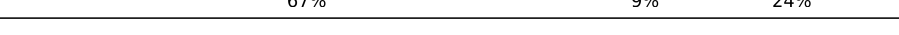





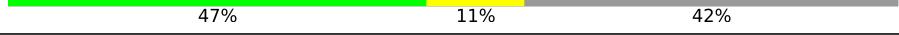

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Mol	Chain	Length	Quality of chain
4	3	188	
5	4	103	
6	5	423	
7	6	380	
8	7	338	
9	8	206	
10	9	137	
11	A	1559	
12	B	69	
13	C	384	
14	D	305	
15	E	348	
16	F	311	
17	G	381	
18	H	267	
19	I	261	
20	J	192	
21	K	178	
22	L	145	
23	M	296	
24	N	251	
25	O	175	
26	P	180	
27	Q	292	
28	R	149	




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Mol	Chain	Length	Quality of chain
29	S	205	
30	T	206	
31	U	153	
32	V	216	
33	W	148	
34	X	256	
35	Y	250	
36	Z	161	
37	a	142	
38	b	215	
39	c	332	
40	d	306	
41	e	279	
42	f	212	
43	g	166	
44	h	158	
45	i	128	
46	j	123	
47	k	112	
48	m	128	
49	o	102	
50	p	206	
51	q	222	
52	r	196	
53	s	439	

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Mol	Chain	Length	Quality of chain
54	u	234	
55	v	70	
56	w	156	

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 99476 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	108	880	545	172	157	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	52	433	278	83	70	2	0	0

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	45	367	227	81	58	1	0	0

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	95	831	539	162	127	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	333	212	71	47	3	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	392	3199	2067	558	563	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	324	2723	1743	488	484	8	0	0

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	287	2334	1495	397	425	17	0	0

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	77	651	413	113	123	2	0	0

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	117	947	614	163	168	2	0	0

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	1376	29219	13111	5277	9455	1376	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3107	U	UNK	conflict	GB 1025814679

- Molecule 12 is a RNA chain called mitochondrial tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	B	56	1191	534	214	387	56	0	0

- Molecule 13 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	C	327	2595	1651	454	474	16	1	0

- Molecule 14 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	D	240	1872	1165	378	320	9	0	0

- Molecule 15 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	E	308	2427	1559	423	434	11	0	0

- Molecule 16 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	F	250	2013	1294	365	348	6	0	0

- Molecule 17 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	238	1943	1243	336	352	12	0	0

- Molecule 18 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	H	95	784	498	152	134	0	0

- Molecule 19 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	I	151	1228	795	222	201	10	0	0

- Molecule 20 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 21 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 22 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 23 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 24 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	183	Total	C	N	O	S	0	0
			1494	960	274	251	9		

- Molecule 25 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 26 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 27 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 28 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	116	Total	C	N	O	S	0	0
			971	616	200	151	4		

- Molecule 29 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 30 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 31 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 32 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	47	Total	C	N	O	S	0	0
			395	255	62	75	3		

- Molecule 33 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	100	Total	C	N	O	S	0	0
			801	518	150	130	3		

- Molecule 34 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 35 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 36 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	115	Total	C	N	O	S	0	0
			937	598	175	161	3		

- Molecule 37 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	71	Total	C	N	O	S	0	0
			597	378	112	103	4		

- Molecule 38 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 40 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	199	Total	C	N	O	S	0	0
			1653	1075	276	293	9		

- Molecule 41 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	197	Total	C	N	O	S	0	0
			1599	1027	277	290	5		

- Molecule 42 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	108	Total	C	N	O	S	0	0
			857	549	140	165	3		

- Molecule 43 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 44 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

- Molecule 45 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 46 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 47 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	m	29	245	157	48	38	2	0	0

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	o	80	676	426	134	113	3	0	0

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	p	127	1058	661	201	192	4	0	0

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	q	128	1076	671	208	192	5	0	0

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	r	146	1203	764	232	199	8	0	0

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	s	370	3036	1946	542	534	14	0	0

- Molecule 54 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	u	111	927	595	155	167	10	0	0

- Molecule 55 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	v	69	588	372	116	100	0	0

- Molecule 56 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	w	79	638	410	95	128	5	0	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	0	1	1	1	0
57	4	1	1	1	0
57	r	1	1	1	0

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

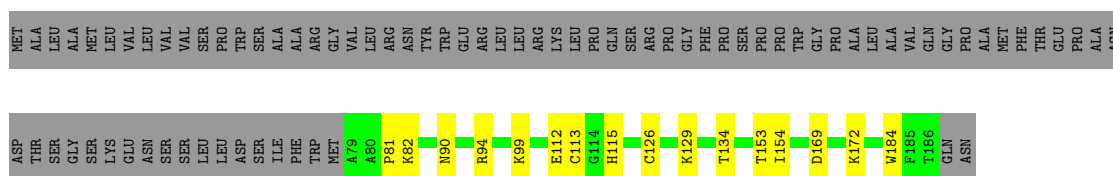
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
58	A	59	59	59	0
58	E	1	1	1	0
58	g	1	1	1	0

### 3 Residue-property plots [i](#)

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

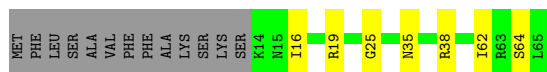
- Molecule 1: 39S ribosomal protein L32, mitochondrial

Chain 0: 




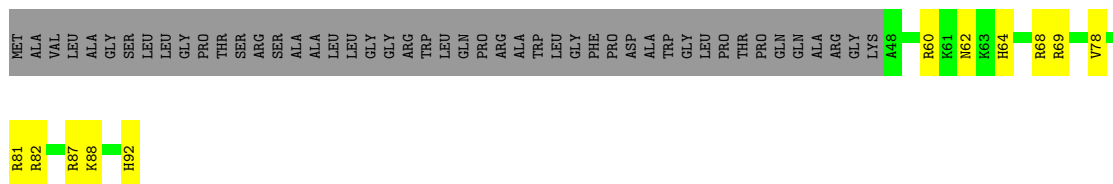
- Molecule 2: 39S ribosomal protein L33, mitochondrial

Chain 1: 



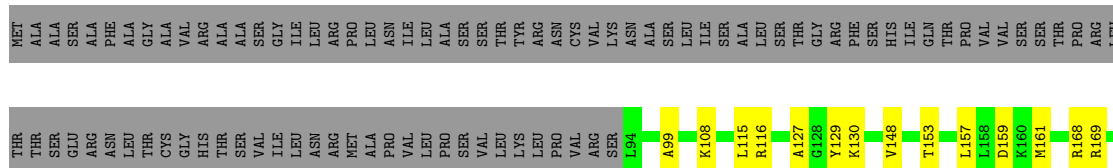
- Molecule 3: 39S ribosomal protein L34, mitochondrial

Chain 2: 



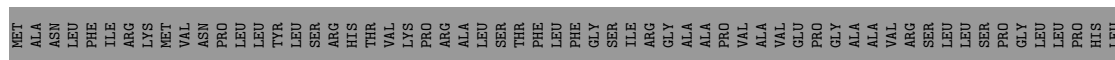
- Molecule 4: 39S ribosomal protein L35, mitochondrial

Chain 3: 

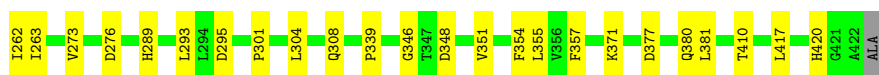
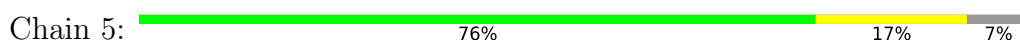




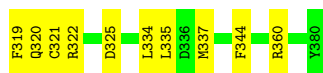
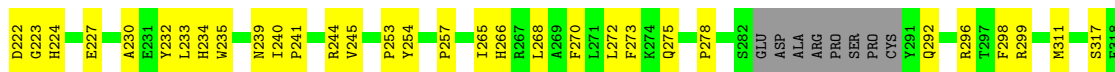
• Molecule 5: 39S ribosomal protein L36, mitochondrial



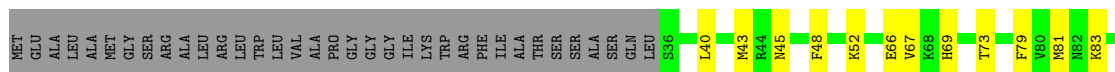
• Molecule 6: 39S ribosomal protein L37, mitochondrial

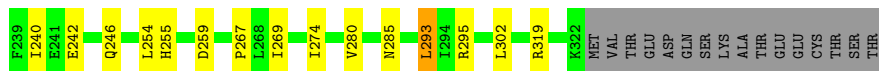


• Molecule 7: 39S ribosomal protein L38, mitochondrial

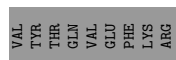
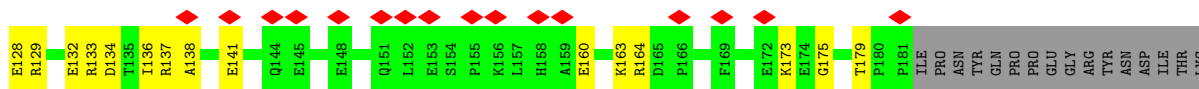
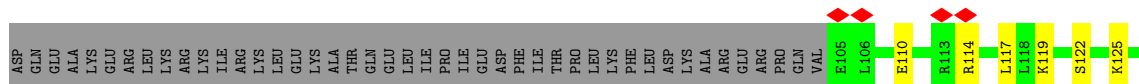


• Molecule 8: 39S ribosomal protein L39, mitochondrial

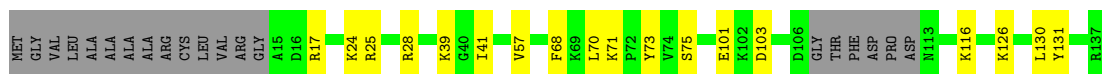




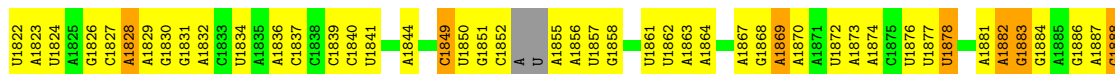
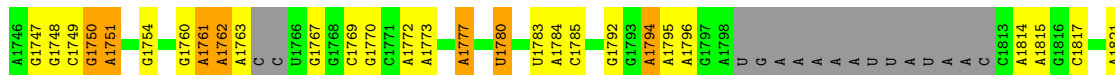
• Molecule 9: 39S ribosomal protein L40, mitochondrial



• Molecule 10: 39S ribosomal protein L41, mitochondrial



• Molecule 11: 16S ribosomal RNA

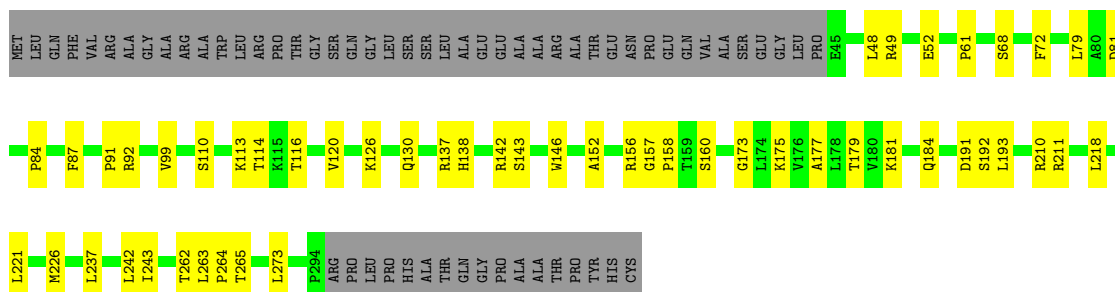


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A3144	A2982	A2914	C2837	U2680	A2457	A2458	A2297	C2210	G2129	C2057
A3145	C2983	C2915	U2838	A2682	A2458	C2379	G2300	A2214	A2134	A2060
C3148	A2984	G2917	C2838	C2684	A2461	C2380	G2300	C2215	A2135	A2060
C3149	C2985	G2917	U2839	U2685	A2462	A2381	A2308	A2216	U2141	A2064
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A3151	U2987	A2919	C2847	C2687	A2463	A2384	G2310	C	G2146	A2065
A3085	C2988	A2920	C2848	C2688	G2470	U2385	G2311	C	G2147	C2068
A3089	A2989	A2921	G2849	A2689	G2471	U2386	U2310	A	A2151	C2068
G3090	U2990	A2922	U2850	A2690	A2472	U2387	G2311	C	A2152	U2072
G3091	U2993	A2925	U2851	A2691	A2473	U2388	A2312	C	A2153	A2074
U3092	U2994	A2926	C2852	A2692	A2474	U2389	A2313	C	A2154	A2074
C3093	C2995	A2927	U2853	A2693	A2475	U2390	A2314	A	U2157	U2075
G3094	U2996	U2925	U2854	A2694	G2478	A2391	A2318	C	A2157	C2076
G3095	C2999	U2929	U2855	G2700	U2484	U2392	A2319	C	A2158	C2077
G3163	A3000	G2930	G2855	G2701	U2485	U2393	A2320	C	U2159	C2078
C3164	G3001	A2931	U2859	G2702	U2485	C2393	A2321	A	A2163	C2079
C3165	G3001	G2832	G2860	G2705	C2493	C2394	A2321	A	U2164	U2080
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U3167	C3099	G2934	A2865	A2707	A2500	U2398	U2524	A	C2166	U2083
C3168	U3100	C2927	U2866	A2707	A2501	U2399	U2524	A	A2167	A2084
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C3175	C3106	A2935	U2874	A2708	A2507	U2411	U2524	A	U2177	U2095
A3176	U3107	G2832	G2875	A2709	A2508	U2412	U2524	A	U2178	U2096
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U3181	C3023	U2947	A2883	C2727	A2512	U2410	U2524	A	G2183	G2107
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U3115	A3025	U2950	U2886	G2732	A2515	U2411	U2524	A	C2186	A2109
C3116	U3026	U2951	A2887	A2732	A2516	C2413	U2524	A	C2187	A2110
C3117	U3027	A2952	U2888	G2733	A2517	C2414	U2524	A	A2188	A2111
C3118	U3028	U2953	A2889	U2734	A2518	C2417	U2524	A	U2193	G2112
C3119	G3040	U2954	C2890	U2735	A2519	U2421	U2524	A	U2194	G2113
C3120	U3041	C2954	U2891	U2736	A2520	G2421	U2524	A	A2195	U2115
C3121	G3042	U2955	U2892	U2737	A2521	U2422	U2524	A	C2196	C2116
C3122	A3044	A2956	U2893	U2738	A2522	U2422	U2524	A	G2197	U2117
G3123	A3045	G2957	U2894	U2739	A2523	A2426	U2524	A	A2198	U2118
U3124	U3045	G2958	U2895	U2740	A2524	A2426	U2524	A	G2188	U2119
U3124	U3045	G2959	U2896	U2741	A2525	A2426	U2524	A	C2186	A2109
G3127	A3051	U2959	U2897	U2742	A2526	A2426	U2524	A	C2187	A2110
A3130	U3052	A2963	A2898	U2743	A2527	A2426	U2524	A	U2187	A2111
G3131	U3053	G2814	U2899	U2744	A2528	A2426	U2524	A	U2193	G2112
G3132	C3054	G2815	U2900	U2745	U2529	A2426	U2524	A	U2194	G2113
A3133	G3055	G2816	C2899	U2746	U2530	A2426	U2524	A	A2195	U2115
G3134	U3056	G2817	C2900	U2747	U2531	A2426	U2524	A	A2196	C2116
C3207	C3057	G2818	U2901	U2748	U2532	A2426	U2524	A	G2197	U2117
C3208	U3058	G2819	U2902	A2749	U2533	A2426	U2524	A	A2198	U2118
A3209	U3059	G2820	U2903	U2750	U2534	A2426	U2524	A	G2188	U2119
C	C3060	C2822	U2904	U2751	A2535	A2426	U2524	A	A2199	U2119
C	U3061	C2823	U2905	U2752	A2536	A2426	U2524	A	A2200	A2200
C3212	U3062	C2824	U2906	U2753	A2537	A2426	U2524	A	G2201	C2202
A3213	U3063	C2825	U2907	U2754	A2538	A2426	U2524	A	U2285	G2202
	U3064	C2826	U2908	U2755	A2539	A2426	U2524	A	U2286	G2202
	U3065	C2827	U2909	U2756	A2540	A2426	U2524	A	U2287	G2202
	U3066	C2828	U2910	U2757	A2541	A2426	U2524	A		
		C2829	U2911	U2758	A2542	A2426	U2524	A		
		A2830		U2759	A2543	A2426	U2524	A		
		C2831		U2760	A2544	A2426	U2524	A		
		C2832		U2761	A2545	A2426	U2524	A		
		C2833		U2762	A2546	A2426	U2524	A		
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		C2835		U2764	A2548	A2426	U2524	A		
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		C2837		U2766	A2550	A2426	U2524	A		
		C2838		U2767	A2551	A2426	U2524	A		
		C2839		U2768	A2552	A2426	U2524	A		
		C2840		U2769	A2553	A2426	U2524	A		
		C2841		U2770	A2554	A2426	U2524	A		
		C2842		U2771	A2555	A2426	U2524	A		
		C2843		U2772	A2556	A2426	U2524	A		
		C2844		U2773	A2557	A2426	U2524	A		
		C2845		U2774	A2558	A2426	U2524	A		
		C2846		U2775	A2559	A2426	U2524	A		
		C2847		U2776	A2560	A2426	U2524	A		
		C2848		U2777	A2561	A2426	U2524	A		
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		C2850		U2779	A2563	A2426	U2524	A		
		C2851		U2780	A2564	A2426	U2524	A		
		C2852		U2781	A2565	A2426	U2524	A		
		C2853		U2782	A2566	A2426	U2524	A		
		C2854		U2783	A2567	A2426	U2524	A		
		C2855		U2784	A2568	A2426	U2524	A		
		C2856		U2785	A2569	A2426	U2524	A		
		C2857		U2786	A2570	A2426	U2524	A		
		C2858		U2787	A2571	A2426	U2524	A		
		C2859		U2788	A2572	A2426	U2524	A		
		C2860		U2789	A2573	A2426	U2524	A		
		C2861		U2790	A2574	A2426	U2524	A		
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		C2871		U2800	A2584	A2426	U2524	A		
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		C2873		U2802	A2586	A2426	U2524	A		
		C2874		U2803	A2587	A2426	U2524	A		
		C2875		U2804	A2588	A2426	U2524	A		
		C2876		U2805	A2589	A2426	U2524	A		
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		C2879		U2808	A2592	A2426	U2524	A		
		C2880		U2809	A2593	A2426	U2524	A		
		C2881		U2810	A2594	A2426	U2524	A		
		C2882		U2811	A2595	A2426	U2524	A		
		C2883		U2812	A2596	A2426	U2524	A		
		C2884		U2813	A2597	A2426	U2524	A		
		C2885		U2814	A2598	A2426	U2524	A		
		C2886		U2815	A2599	A2426	U2524	A		
		C2887		U2816	A2600	A2426	U2524	A		
		C2888		U2817	A2601	A2426	U2524	A		
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		C2892		U2821	A2605	A2426	U2524	A		
		C2893		U2822	A2606	A2426	U2524	A		
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		C2897		U2826	A2610	A2426	U2524	A		
		C2898		U2827	A2611	A2426	U2524	A		
		C2899		U2828	A2612	A2426	U2524	A		
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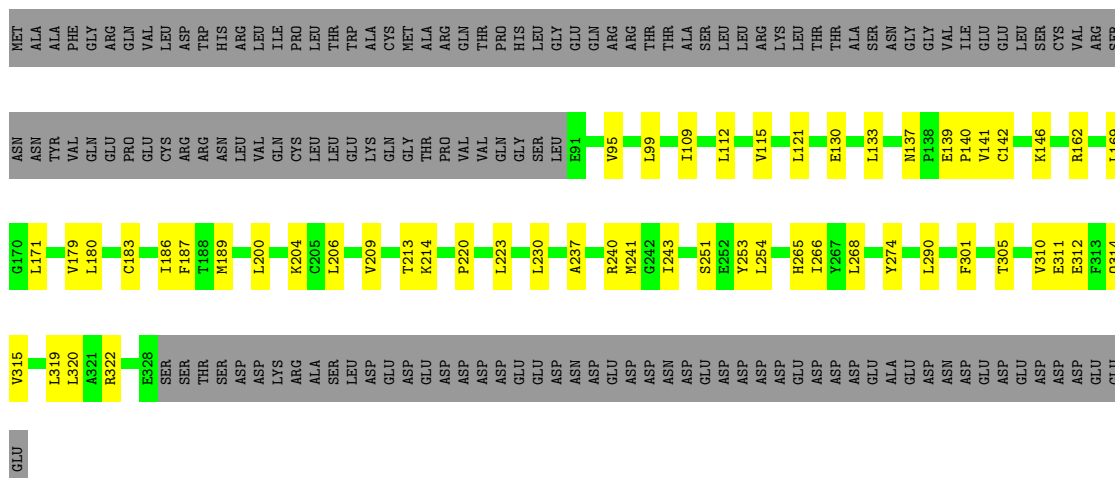




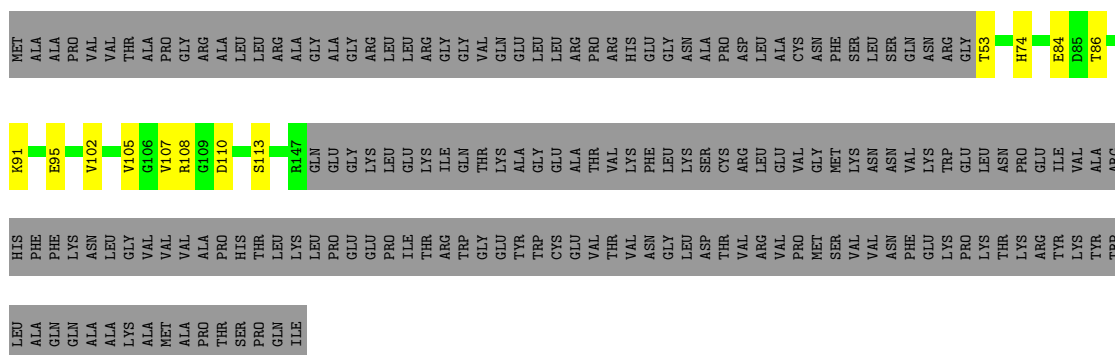
• Molecule 16: 39S ribosomal protein L4, mitochondrial



• Molecule 17: Transcription termination factor 4, mitochondrial

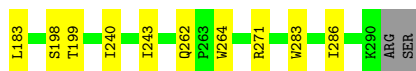


• Molecule 18: 39S ribosomal protein L9, mitochondrial







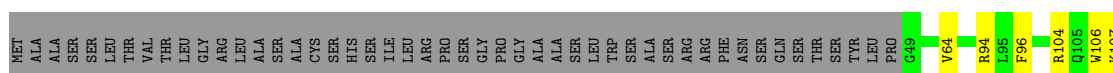


- Molecule 28: 39S ribosomal protein L20, mitochondrial

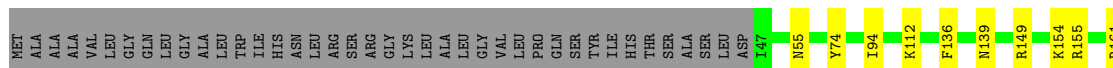


HIS

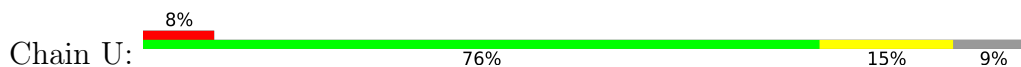
- Molecule 29: 39S ribosomal protein L21, mitochondrial



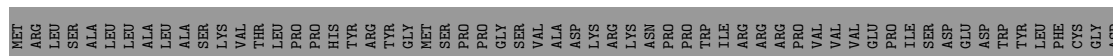
- Molecule 30: 39S ribosomal protein L22, mitochondrial



- Molecule 31: 39S ribosomal protein L23, mitochondrial



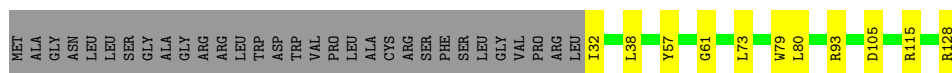
- Molecule 32: 39S ribosomal protein L24, mitochondrial







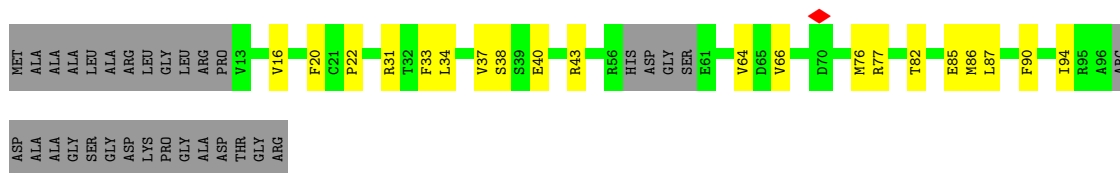




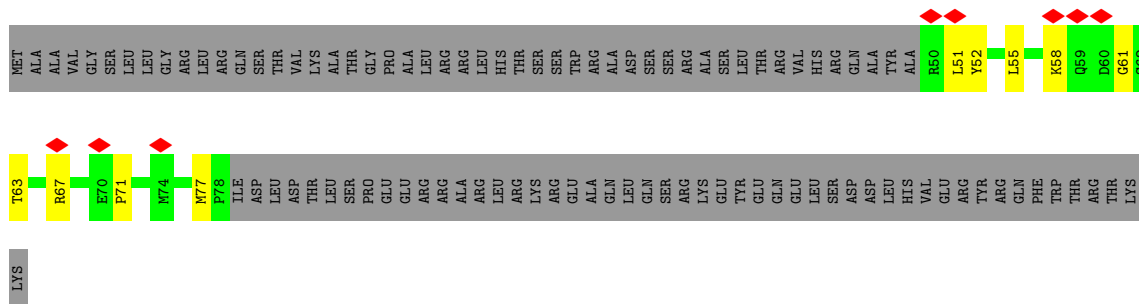
• Molecule 46: 39S ribosomal protein L52, mitochondrial



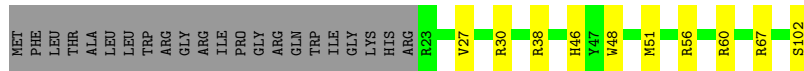
• Molecule 47: 39S ribosomal protein L53, mitochondrial



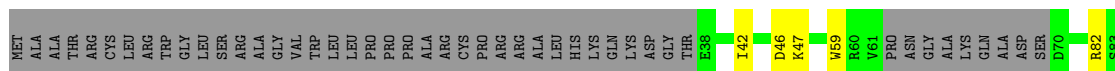
• Molecule 48: 39S ribosomal protein L55, mitochondrial



• Molecule 49: Ribosomal protein 63, mitochondrial



• Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1060638	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	36	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.128	Depositor
Minimum map value	-0.035	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	367.49997, 367.49997, 367.49997	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0	0.24	0/895	0.28	0/1201
2	1	0.09	0/438	0.28	0/583
3	2	0.33	0/373	0.34	0/496
4	3	0.31	0/852	0.32	0/1136
5	4	0.22	0/341	0.34	0/451
6	5	0.22	0/3294	0.33	0/4488
7	6	0.18	0/2809	0.32	0/3818
8	7	0.18	0/2391	0.31	0/3234
9	8	0.11	0/665	0.26	0/894
10	9	0.23	0/972	0.29	0/1306
11	A	0.31	0/32679	0.33	4/50833 (0.0%)
12	B	0.10	0/1328	0.22	0/2056
13	C	0.12	0/2655	0.30	0/3601
14	D	0.26	0/1910	0.36	0/2569
15	E	0.28	0/2497	0.35	0/3386
16	F	0.29	0/2071	0.33	0/2817
17	G	0.14	0/1974	0.27	0/2652
18	H	0.20	0/798	0.27	0/1073
19	I	0.13	0/1252	0.31	0/1686
20	J	0.10	0/1077	0.27	0/1452
21	K	0.30	0/1495	0.34	0/2029
22	L	0.25	0/904	0.32	0/1218
23	M	0.28	0/2359	0.31	0/3185
24	N	0.15	0/1533	0.32	0/2061
25	O	0.28	0/1269	0.33	0/1708
26	P	0.19	0/1173	0.30	0/1588
27	Q	0.25	0/1846	0.34	0/2487
28	R	0.32	0/987	0.32	0/1320
29	S	0.30	0/1276	0.36	0/1729
30	T	0.29	0/1402	0.32	0/1886
31	U	0.27	0/1183	0.33	0/1600
32	V	0.19	0/404	0.23	0/545

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	W	0.26	0/823	0.29	0/1113
34	X	0.24	0/2090	0.29	0/2825
35	Y	0.26	0/1552	0.26	0/2079
36	Z	0.25	0/960	0.33	0/1295
37	a	0.26	0/616	0.29	0/833
38	b	0.28	0/1202	0.37	0/1626
39	c	0.24	0/2264	0.28	0/3059
40	d	0.12	0/1702	0.30	0/2307
41	e	0.10	0/1633	0.29	0/2204
42	f	0.12	0/873	0.28	0/1180
43	g	0.27	0/1102	0.35	0/1503
44	h	0.17	0/884	0.28	0/1203
45	i	0.32	0/849	0.33	0/1135
46	j	0.22	0/698	0.27	0/940
47	k	0.12	0/635	0.33	0/855
48	m	0.14	0/250	0.38	0/336
49	o	0.24	0/693	0.28	0/931
50	p	0.17	0/1071	0.26	0/1433
51	q	0.17	0/1107	0.25	0/1498
52	r	0.22	0/1238	0.29	0/1676
53	s	0.28	0/3114	0.33	0/4225
54	u	0.18	0/949	0.34	0/1281
55	v	0.13	0/597	0.31	0/796
56	w	0.12	0/647	0.38	0/871
All	All	0.26	0/104651	0.32	4/148292 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	2543	C	C2'-C3'-O3'	6.86	123.99	113.70
11	A	2543	C	C3'-C2'-O2'	5.69	119.24	110.70
11	A	2635	G	C2'-C3'-O3'	5.08	121.32	113.70
11	A	2635	G	C3'-C2'-O2'	5.07	118.30	110.70

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	880	0	902	13	0
2	1	433	0	475	5	0
3	2	367	0	393	11	0
4	3	831	0	883	12	0
5	4	333	0	352	6	0
6	5	3199	0	3196	47	0
7	6	2723	0	2615	59	0
8	7	2334	0	2343	49	0
9	8	651	0	649	20	0
10	9	947	0	949	18	0
11	A	29219	0	14850	465	0
12	B	1191	0	607	20	0
13	C	2595	0	2576	36	0
14	D	1872	0	1932	36	0
15	E	2427	0	2436	35	0
16	F	2013	0	2044	39	0
17	G	1943	0	2030	40	0
18	H	784	0	832	9	0
19	I	1228	0	1310	34	0
20	J	1061	0	1141	14	0
21	K	1451	0	1448	24	0
22	L	889	0	941	25	0
23	M	2305	0	2378	26	0
24	N	1494	0	1512	26	0
25	O	1245	0	1283	24	0
26	P	1148	0	1148	23	0
27	Q	1805	0	1841	26	0
28	R	971	0	1045	16	0
29	S	1251	0	1322	31	0
30	T	1368	0	1410	13	0
31	U	1154	0	1154	19	0
32	V	395	0	392	9	0
33	W	801	0	826	14	0
34	X	2035	0	2054	22	0
35	Y	1517	0	1561	17	0
36	Z	937	0	983	8	0
37	a	597	0	584	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	1178	0	1180	23	0
39	c	2217	0	2220	27	0
40	d	1653	0	1632	31	0
41	e	1599	0	1604	32	0
42	f	857	0	852	18	0
43	g	1067	0	1056	6	0
44	h	862	0	845	10	0
45	i	827	0	857	10	0
46	j	684	0	673	5	0
47	k	627	0	636	13	0
48	m	245	0	263	5	0
49	o	676	0	676	11	0
50	p	1058	0	1083	18	0
51	q	1076	0	1049	16	0
52	r	1203	0	1219	24	0
53	s	3036	0	3022	46	0
54	u	927	0	921	30	0
55	v	588	0	604	16	0
56	w	638	0	637	19	0
57	0	1	0	0	0	0
57	4	1	0	0	0	0
57	r	1	0	0	0	0
58	A	59	0	0	0	0
58	E	1	0	0	0	0
58	g	1	0	0	0	0
All	All	99476	0	85426	1356	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1356 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:2394:A:H2	11:A:2397:C:H42	1.25	0.85
1:0:113:CYS:SG	1:0:115:HIS:ND1	2.50	0.84
11:A:2528:G:OP1	14:D:135:ARG:NH2	2.12	0.83
11:A:1747:G:N2	11:A:1750:G:O2'	2.13	0.82
11:A:3121:C:O2	11:A:3135:A:N6	2.15	0.80

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	106/188 (56%)	104 (98%)	2 (2%)	0	100	100
2	1	50/65 (77%)	48 (96%)	2 (4%)	0	100	100
3	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
5	4	35/103 (34%)	34 (97%)	1 (3%)	0	100	100
6	5	390/423 (92%)	382 (98%)	8 (2%)	0	100	100
7	6	316/380 (83%)	305 (96%)	11 (4%)	0	100	100
8	7	285/338 (84%)	271 (95%)	14 (5%)	0	100	100
9	8	75/206 (36%)	73 (97%)	2 (3%)	0	100	100
10	9	113/137 (82%)	111 (98%)	2 (2%)	0	100	100
13	C	324/384 (84%)	312 (96%)	12 (4%)	0	100	100
14	D	238/305 (78%)	230 (97%)	8 (3%)	0	100	100
15	E	306/348 (88%)	300 (98%)	6 (2%)	0	100	100
16	F	248/311 (80%)	245 (99%)	3 (1%)	0	100	100
17	G	236/381 (62%)	227 (96%)	9 (4%)	0	100	100
18	H	93/267 (35%)	88 (95%)	5 (5%)	0	100	100
19	I	147/261 (56%)	140 (95%)	7 (5%)	0	100	100
20	J	138/192 (72%)	132 (96%)	6 (4%)	0	100	100
21	K	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
22	L	113/145 (78%)	112 (99%)	1 (1%)	0	100	100
23	M	285/296 (96%)	282 (99%)	3 (1%)	0	100	100
24	N	177/251 (70%)	174 (98%)	3 (2%)	0	100	100
25	O	150/175 (86%)	146 (97%)	4 (3%)	0	100	100
26	P	139/180 (77%)	132 (95%)	7 (5%)	0	100	100
27	Q	215/292 (74%)	211 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R	114/149 (76%)	113 (99%)	1 (1%)	0	100	100
29	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
30	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
31	U	135/153 (88%)	134 (99%)	1 (1%)	0	100	100
32	V	45/216 (21%)	44 (98%)	1 (2%)	0	100	100
33	W	98/148 (66%)	98 (100%)	0	0	100	100
34	X	241/256 (94%)	238 (99%)	3 (1%)	0	100	100
35	Y	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
36	Z	113/161 (70%)	111 (98%)	2 (2%)	0	100	100
37	a	67/142 (47%)	67 (100%)	0	0	100	100
38	b	146/215 (68%)	141 (97%)	5 (3%)	0	100	100
39	c	271/332 (82%)	268 (99%)	3 (1%)	0	100	100
40	d	189/306 (62%)	186 (98%)	3 (2%)	0	100	100
41	e	191/279 (68%)	175 (92%)	16 (8%)	0	100	100
42	f	102/212 (48%)	92 (90%)	10 (10%)	0	100	100
43	g	127/166 (76%)	121 (95%)	6 (5%)	0	100	100
44	h	101/158 (64%)	98 (97%)	3 (3%)	0	100	100
45	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
46	j	83/123 (68%)	82 (99%)	1 (1%)	0	100	100
47	k	76/112 (68%)	71 (93%)	5 (7%)	0	100	100
48	m	27/128 (21%)	19 (70%)	8 (30%)	0	100	100
49	o	78/102 (76%)	78 (100%)	0	0	100	100
50	p	119/206 (58%)	116 (98%)	3 (2%)	0	100	100
51	q	126/222 (57%)	126 (100%)	0	0	100	100
52	r	140/196 (71%)	136 (97%)	4 (3%)	0	100	100
53	s	366/439 (83%)	363 (99%)	3 (1%)	0	100	100
54	u	109/234 (47%)	103 (94%)	6 (6%)	0	100	100
55	v	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
56	w	77/156 (49%)	70 (91%)	7 (9%)	0	100	100
All	All	8285/11756 (70%)	8058 (97%)	227 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	97/164 (59%)	97 (100%)	0	100	100
2	1	49/60 (82%)	49 (100%)	0	100	100
3	2	39/72 (54%)	39 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	353 (100%)	0	100	100
7	6	286/332 (86%)	286 (100%)	0	100	100
8	7	263/303 (87%)	261 (99%)	2 (1%)	73	85
9	8	70/190 (37%)	70 (100%)	0	100	100
10	9	99/112 (88%)	99 (100%)	0	100	100
13	C	284/328 (87%)	284 (100%)	0	100	100
14	D	194/245 (79%)	194 (100%)	0	100	100
15	E	262/290 (90%)	261 (100%)	1 (0%)	84	92
16	F	217/262 (83%)	217 (100%)	0	100	100
17	G	221/350 (63%)	221 (100%)	0	100	100
18	H	86/228 (38%)	86 (100%)	0	100	100
19	I	139/232 (60%)	139 (100%)	0	100	100
20	J	113/150 (75%)	113 (100%)	0	100	100
21	K	155/156 (99%)	155 (100%)	0	100	100
22	L	98/124 (79%)	97 (99%)	1 (1%)	68	81
23	M	245/249 (98%)	245 (100%)	0	100	100
24	N	156/211 (74%)	156 (100%)	0	100	100
25	O	133/150 (89%)	133 (100%)	0	100	100
26	P	123/155 (79%)	123 (100%)	0	100	100
27	Q	199/256 (78%)	199 (100%)	0	100	100
28	R	101/126 (80%)	101 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	S	141/180 (78%)	141 (100%)	0	100	100
30	T	146/176 (83%)	146 (100%)	0	100	100
31	U	124/135 (92%)	124 (100%)	0	100	100
32	V	43/191 (22%)	43 (100%)	0	100	100
33	W	83/119 (70%)	83 (100%)	0	100	100
34	X	219/229 (96%)	219 (100%)	0	100	100
35	Y	159/223 (71%)	159 (100%)	0	100	100
36	Z	106/147 (72%)	106 (100%)	0	100	100
37	a	67/133 (50%)	67 (100%)	0	100	100
38	b	130/186 (70%)	130 (100%)	0	100	100
39	c	241/288 (84%)	241 (100%)	0	100	100
40	d	184/274 (67%)	183 (100%)	1 (0%)	81	90
41	e	171/236 (72%)	171 (100%)	0	100	100
42	f	95/188 (50%)	95 (100%)	0	100	100
43	g	119/148 (80%)	119 (100%)	0	100	100
44	h	100/148 (68%)	100 (100%)	0	100	100
45	i	86/110 (78%)	86 (100%)	0	100	100
46	j	68/97 (70%)	68 (100%)	0	100	100
47	k	71/90 (79%)	71 (100%)	0	100	100
48	m	27/113 (24%)	27 (100%)	0	100	100
49	o	69/87 (79%)	69 (100%)	0	100	100
50	p	117/181 (65%)	117 (100%)	0	100	100
51	q	110/178 (62%)	110 (100%)	0	100	100
52	r	133/169 (79%)	133 (100%)	0	100	100
53	s	326/381 (86%)	325 (100%)	1 (0%)	86	93
54	u	105/200 (52%)	105 (100%)	0	100	100
55	v	59/60 (98%)	59 (100%)	0	100	100
56	w	73/136 (54%)	73 (100%)	0	100	100
All	All	7478/10171 (74%)	7472 (100%)	6 (0%)	87	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	L	75	LEU
40	d	51	LYS
53	s	66	TRP
8	7	293	LEU
8	7	143	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
35	Y	147	GLN
40	d	47	GLN
53	s	107	GLN
35	Y	225	ASN
38	b	66	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1357/1559 (87%)	323 (23%)	17 (1%)
12	B	52/69 (75%)	17 (32%)	1 (1%)
All	All	1409/1628 (86%)	340 (24%)	18 (1%)

5 of 340 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1677	C
11	A	1678	C
11	A	1679	U
11	A	1680	A
11	A	1681	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	3072	U
12	B	1607	U
11	A	3196	G
11	A	2530	A
11	A	3041	U

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 64 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

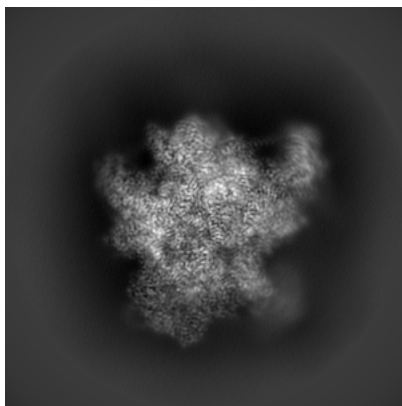
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12865. These allow visual inspection of the internal detail of the map and identification of artifacts.

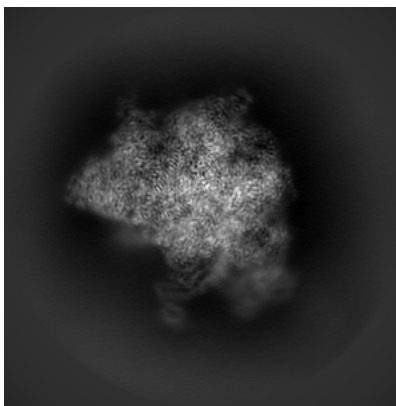
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

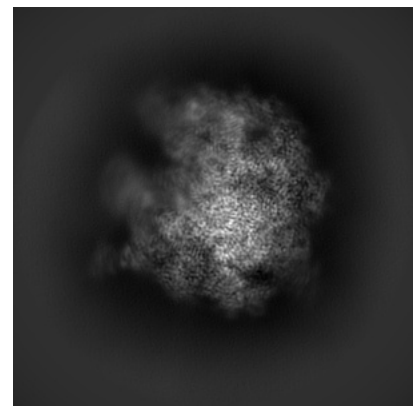
#### 6.1.1 Primary map



X

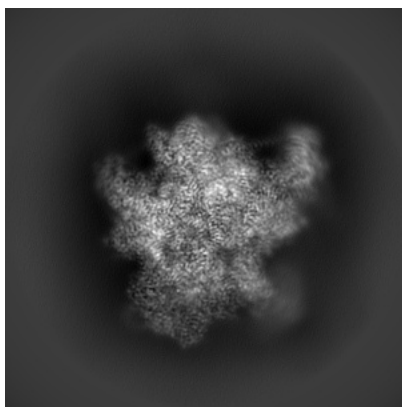


Y

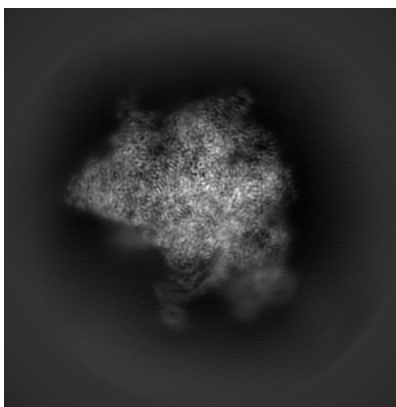


Z

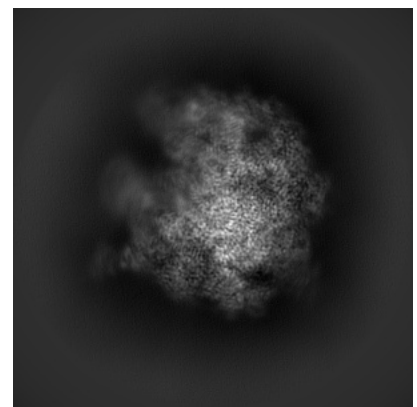
#### 6.1.2 Raw map



X



Y

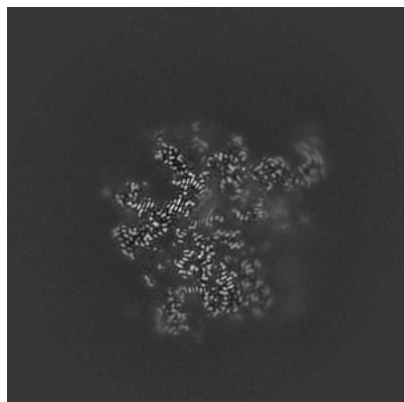


Z

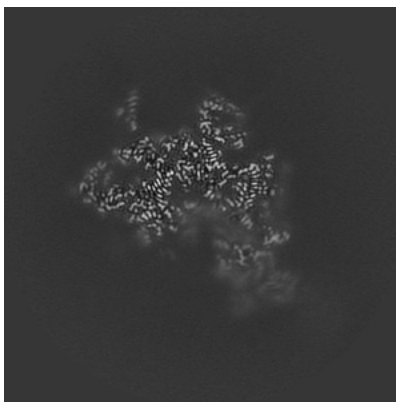
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

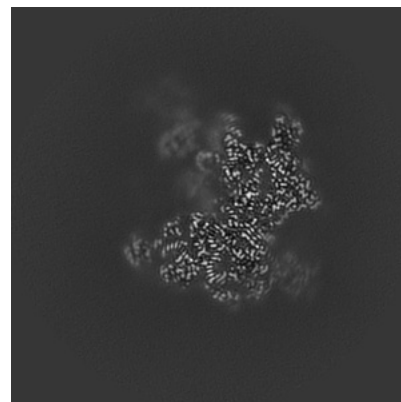
### 6.2.1 Primary map



X Index: 175

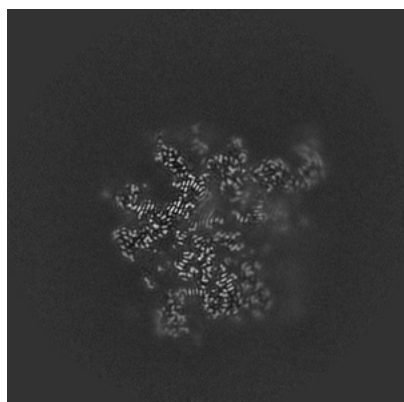


Y Index: 175

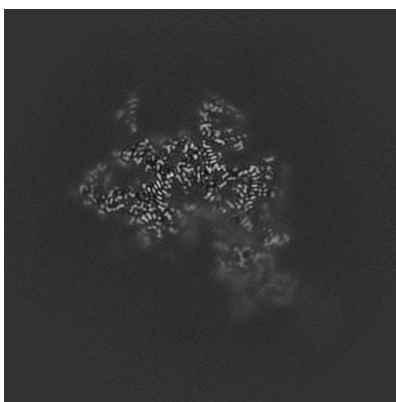


Z Index: 175

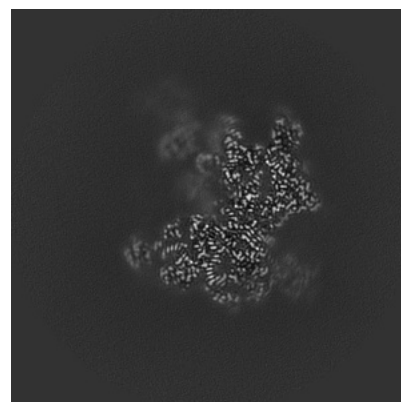
### 6.2.2 Raw map



X Index: 175



Y Index: 175

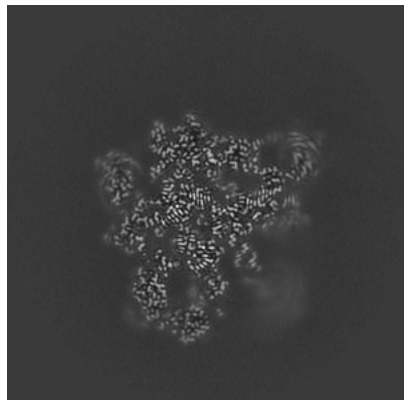


Z Index: 175

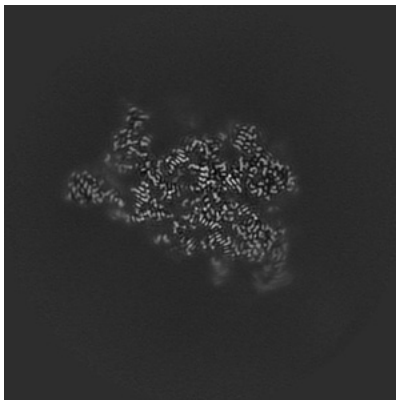
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

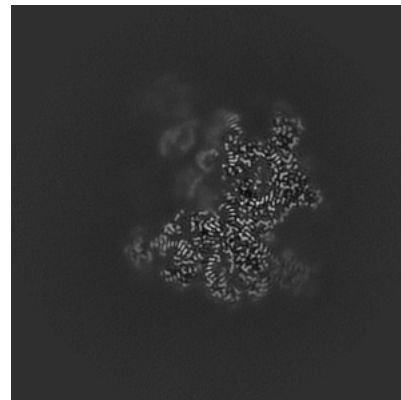
### 6.3.1 Primary map



X Index: 192

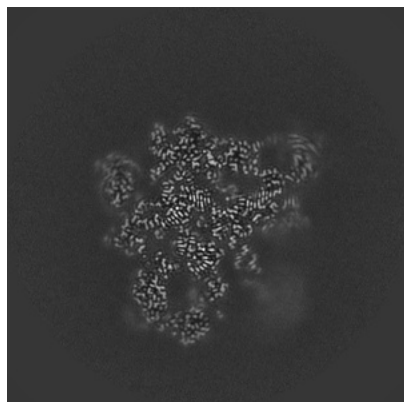


Y Index: 159

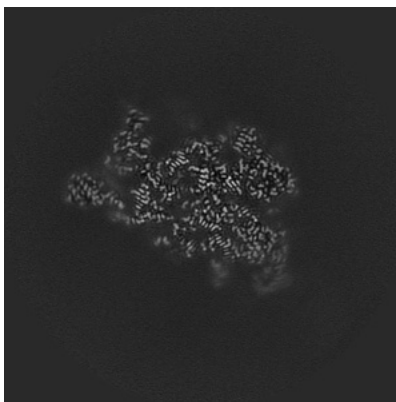


Z Index: 177

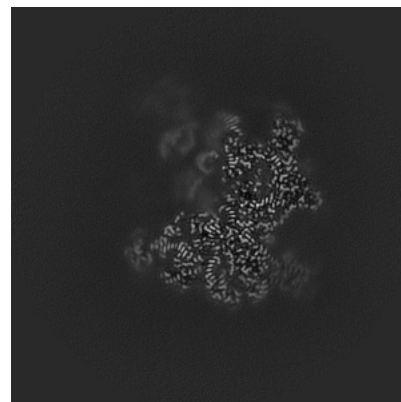
### 6.3.2 Raw map



X Index: 192



Y Index: 159



Z Index: 177

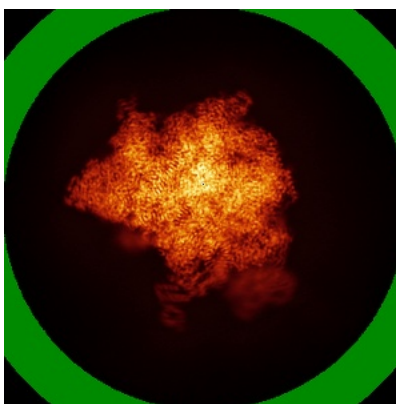
The images above show the largest variance slices of the map in three orthogonal directions.

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

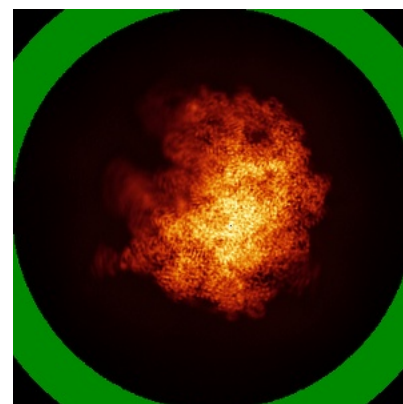
### 6.4.1 Primary map



X

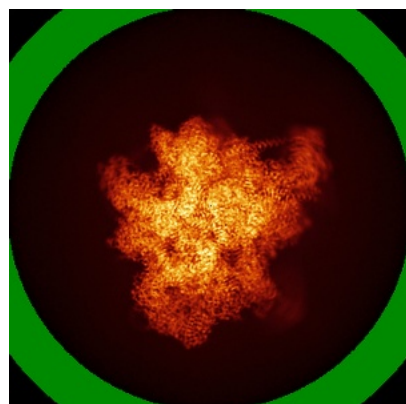


Y

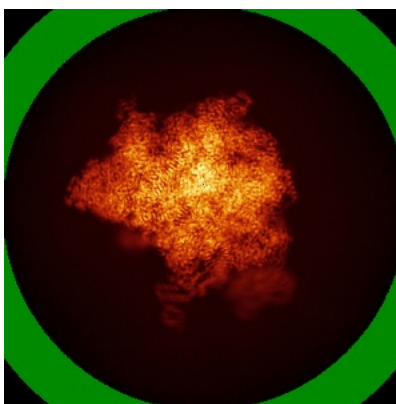


Z

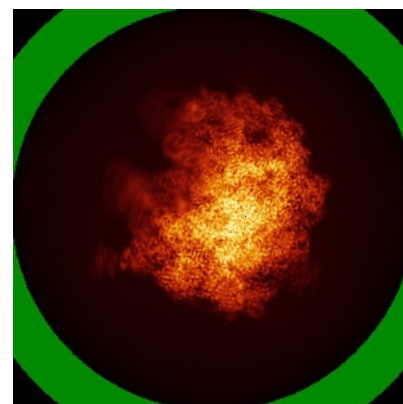
### 6.4.2 Raw map



X



Y

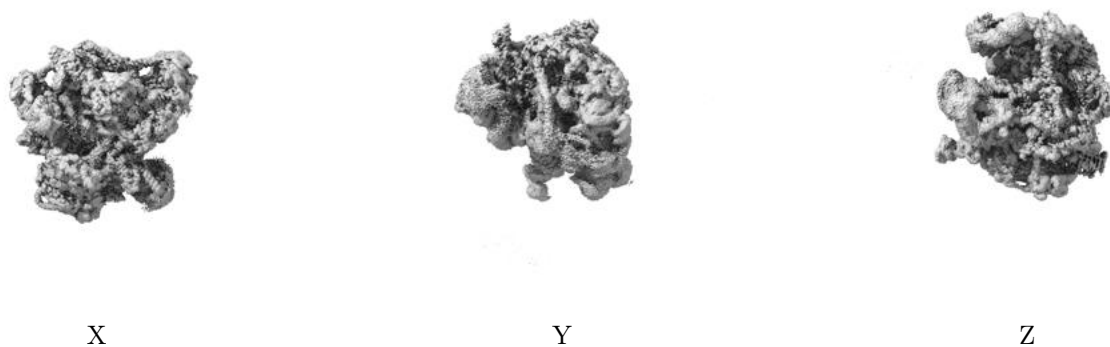


Z

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

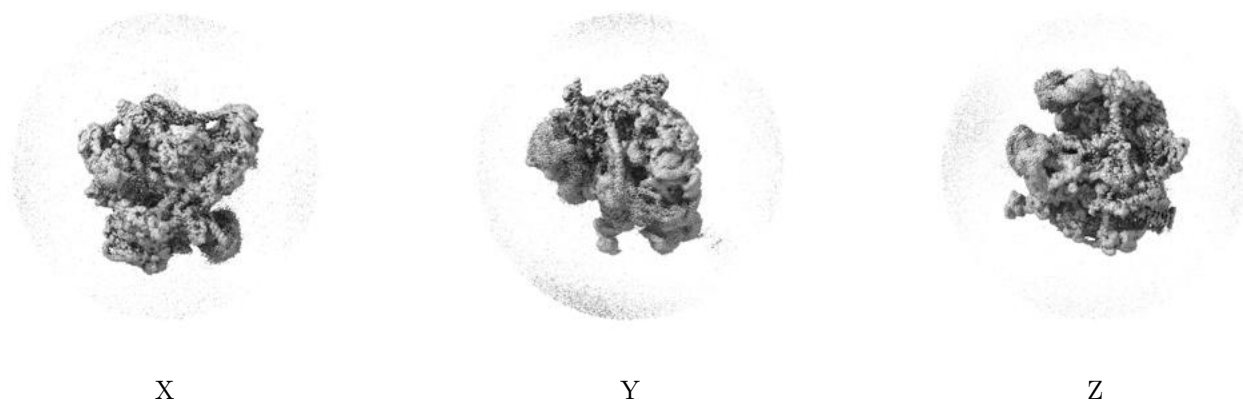
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

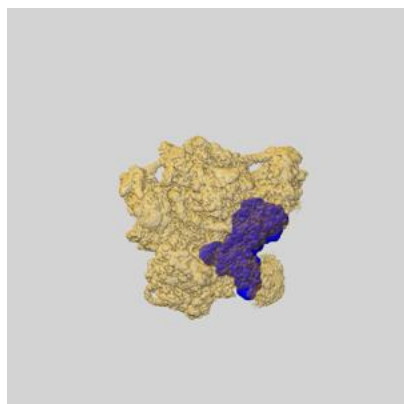
## 6.6 Mask visualisation [i](#)

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

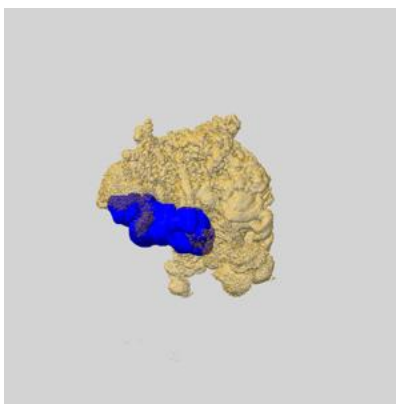
A mask typically either:

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

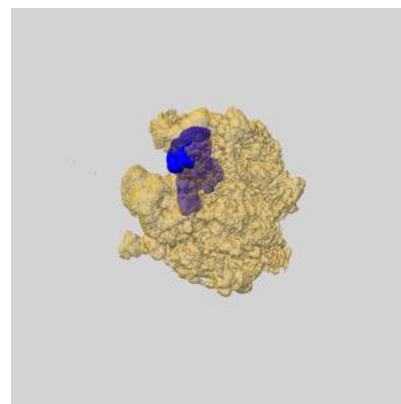
### 6.6.1 emd\_12865\_msk\_1.map [i](#)



X

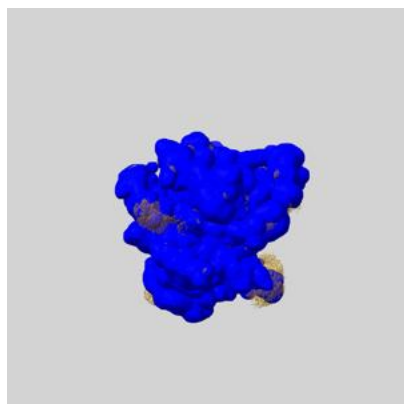


Y

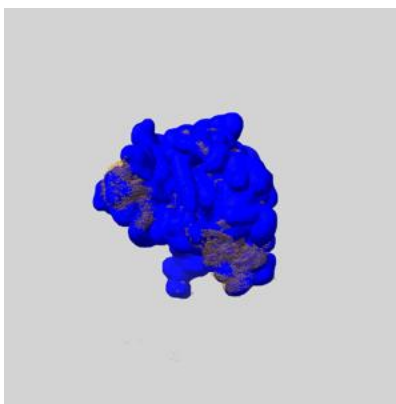


Z

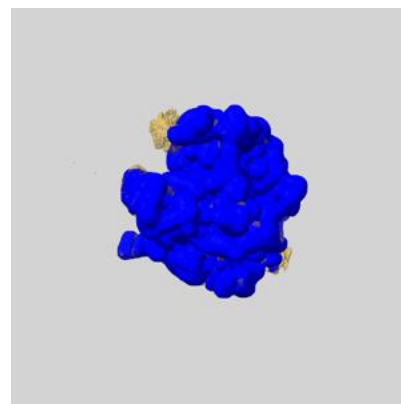
### 6.6.2 emd\_12865\_msk\_2.map [i](#)



X



Y

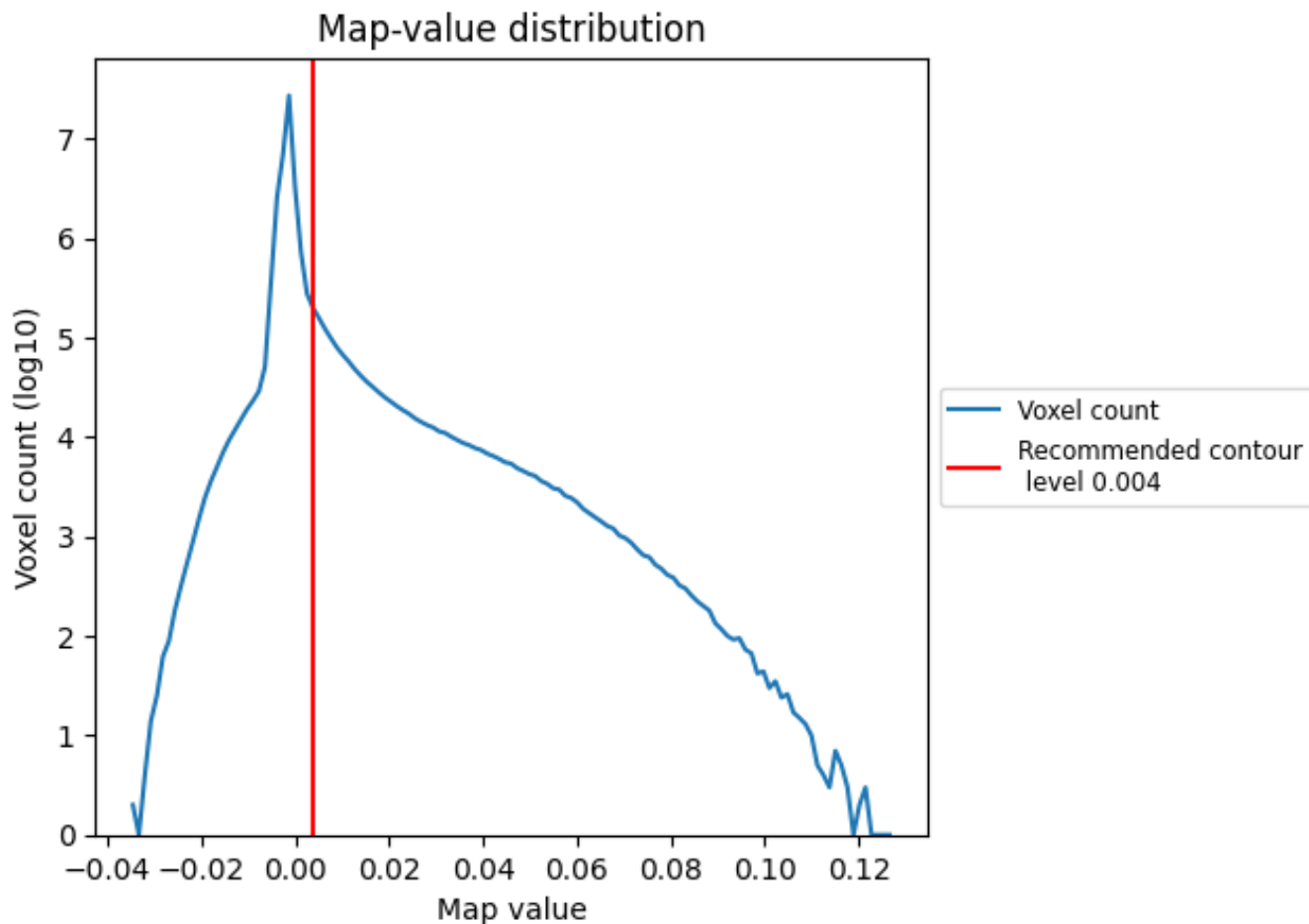


Z

## 7 Map analysis [i](#)

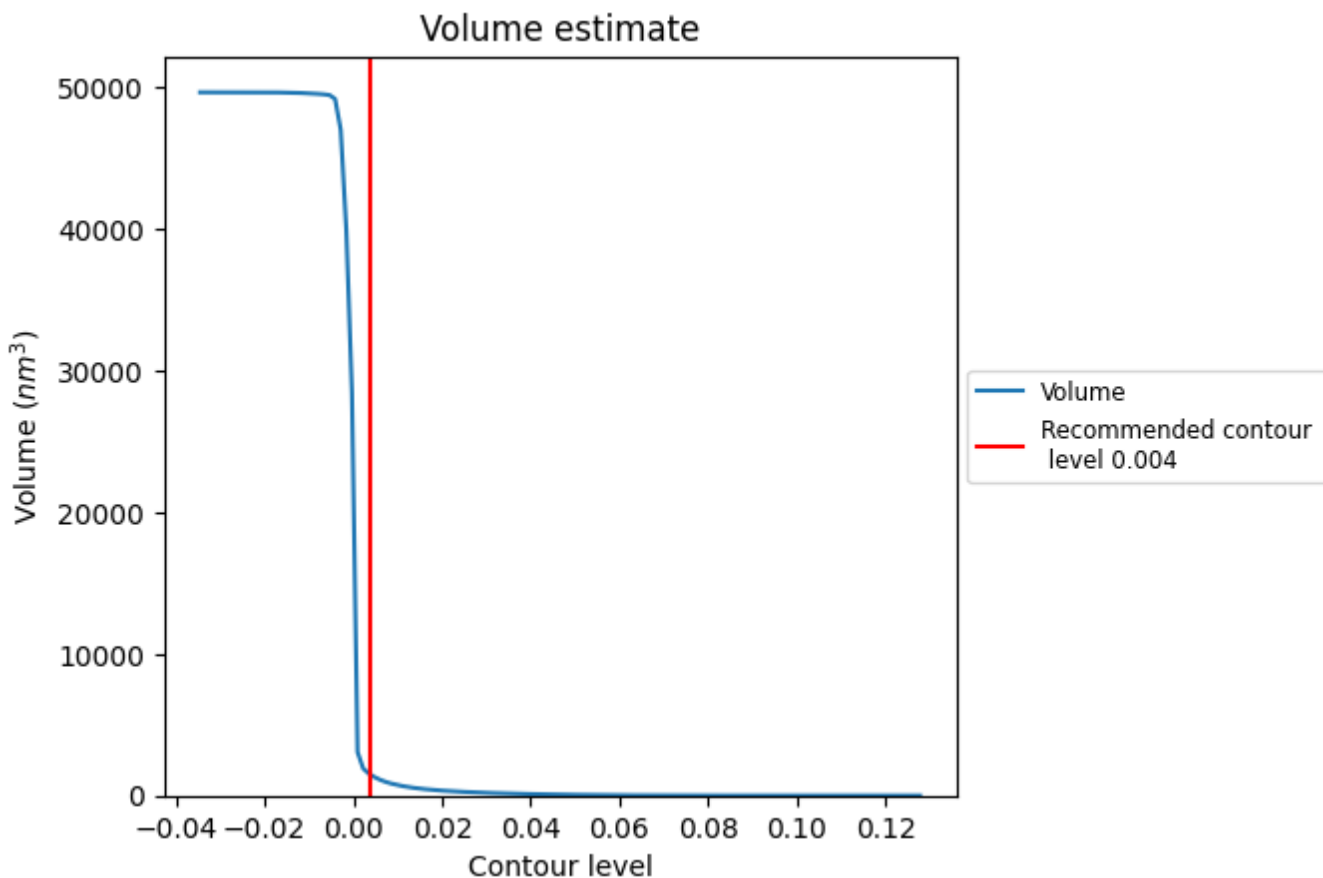
This section contains the results of statistical analysis of the map.

### 7.1 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.

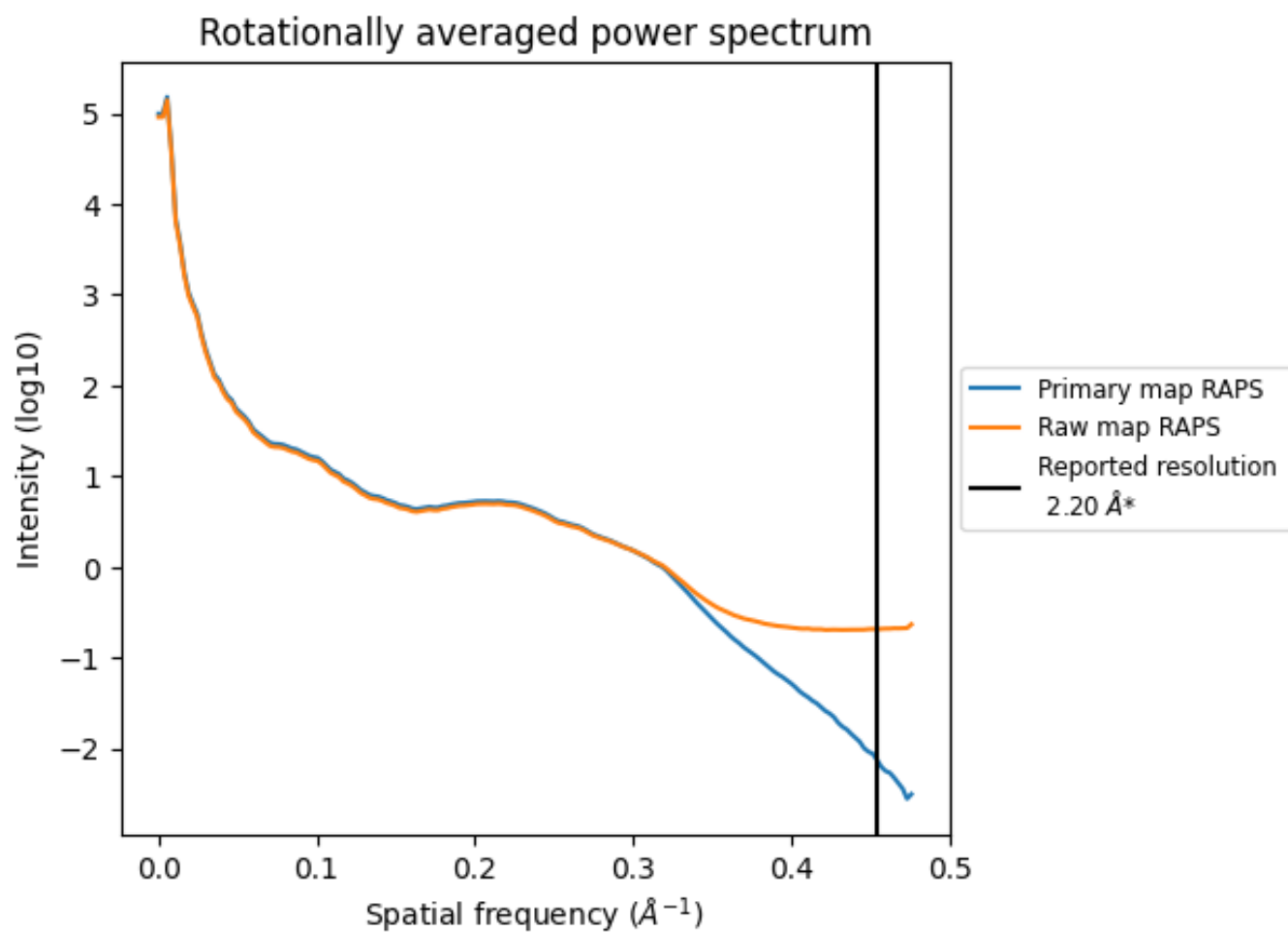
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1458 nm<sup>3</sup>; this corresponds to an approximate mass of 1317 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

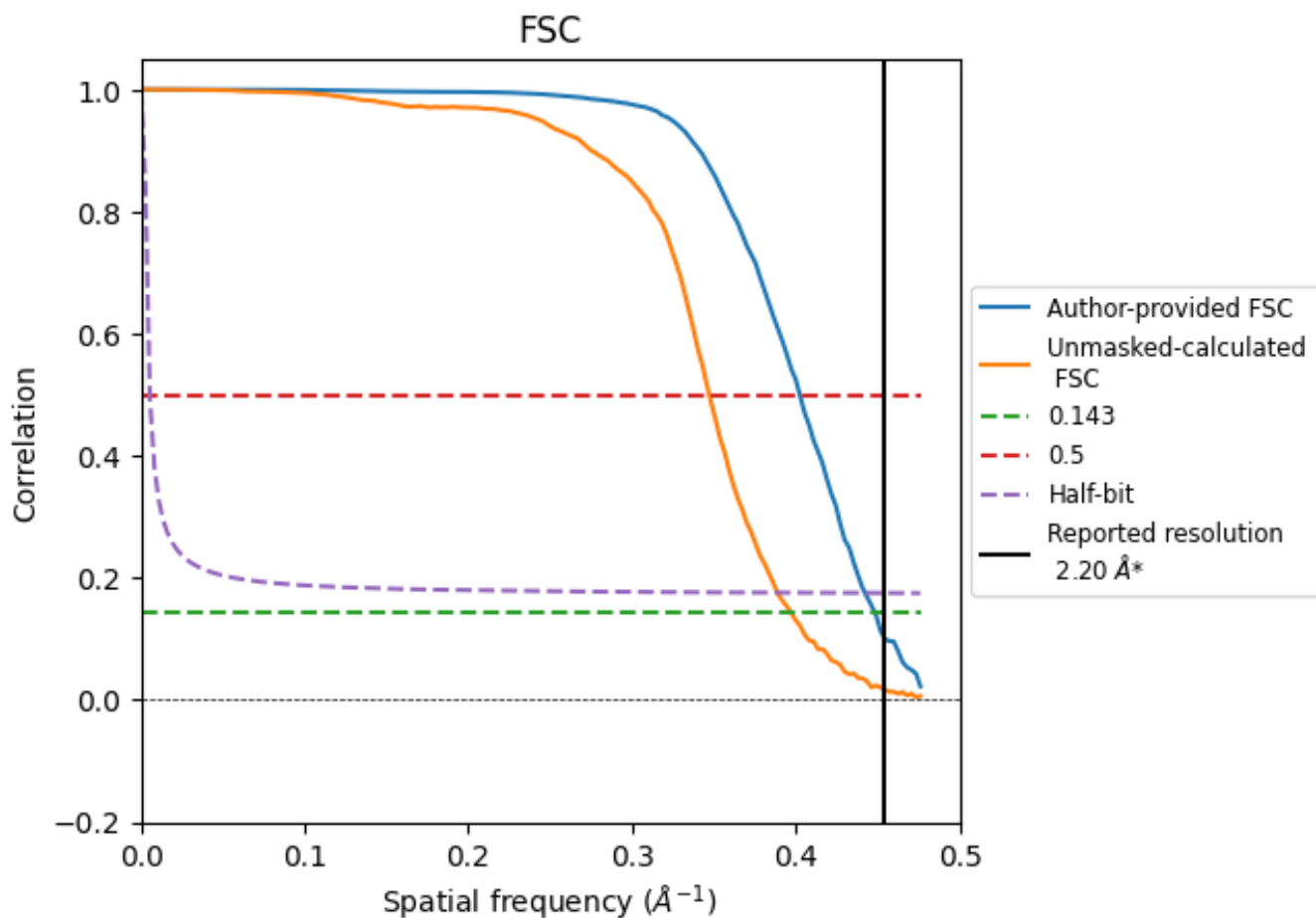


\*Reported resolution corresponds to spatial frequency of 0.455 Å<sup>-1</sup>

## 8 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.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.455 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

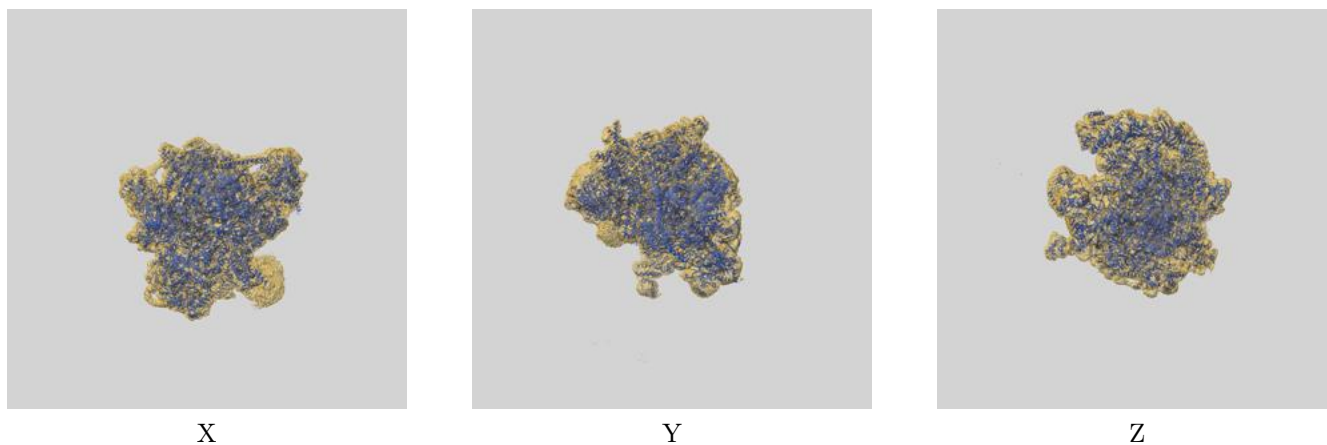
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.23	2.48	2.26
Unmasked-calculated*	2.52	2.88	2.57

\*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 2.52 differs from the reported value 2.2 by more than 10 %

## 9 Map-model fit [i](#)

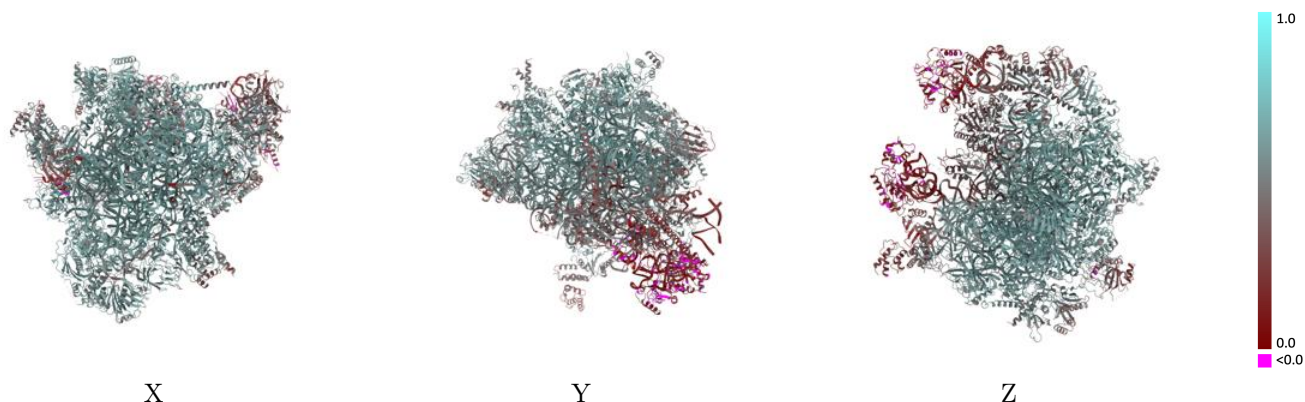
This section contains information regarding the fit between EMDB map EMD-12865 and PDB model 7OF0. Per-residue inclusion information can be found in section 3 on page 15.

### 9.1 Map-model overlay [i](#)



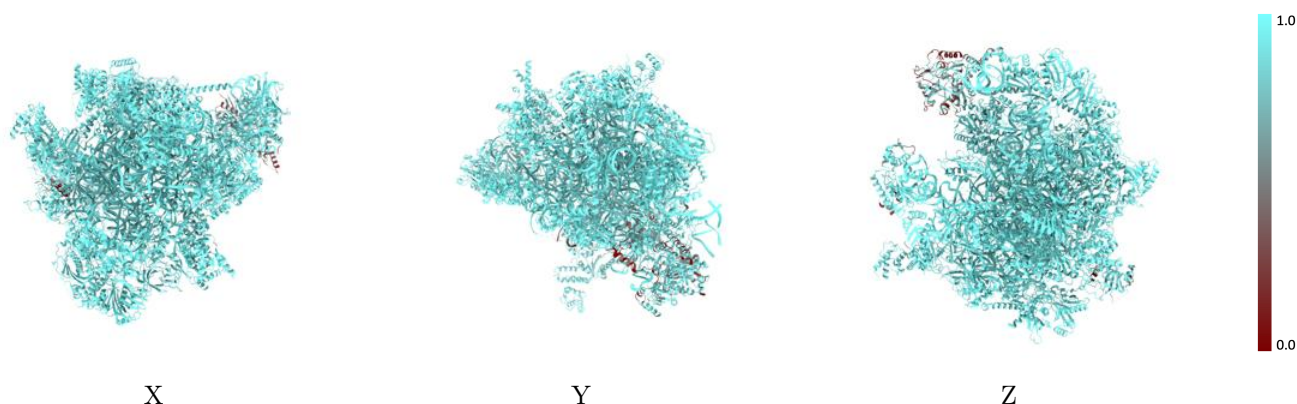
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



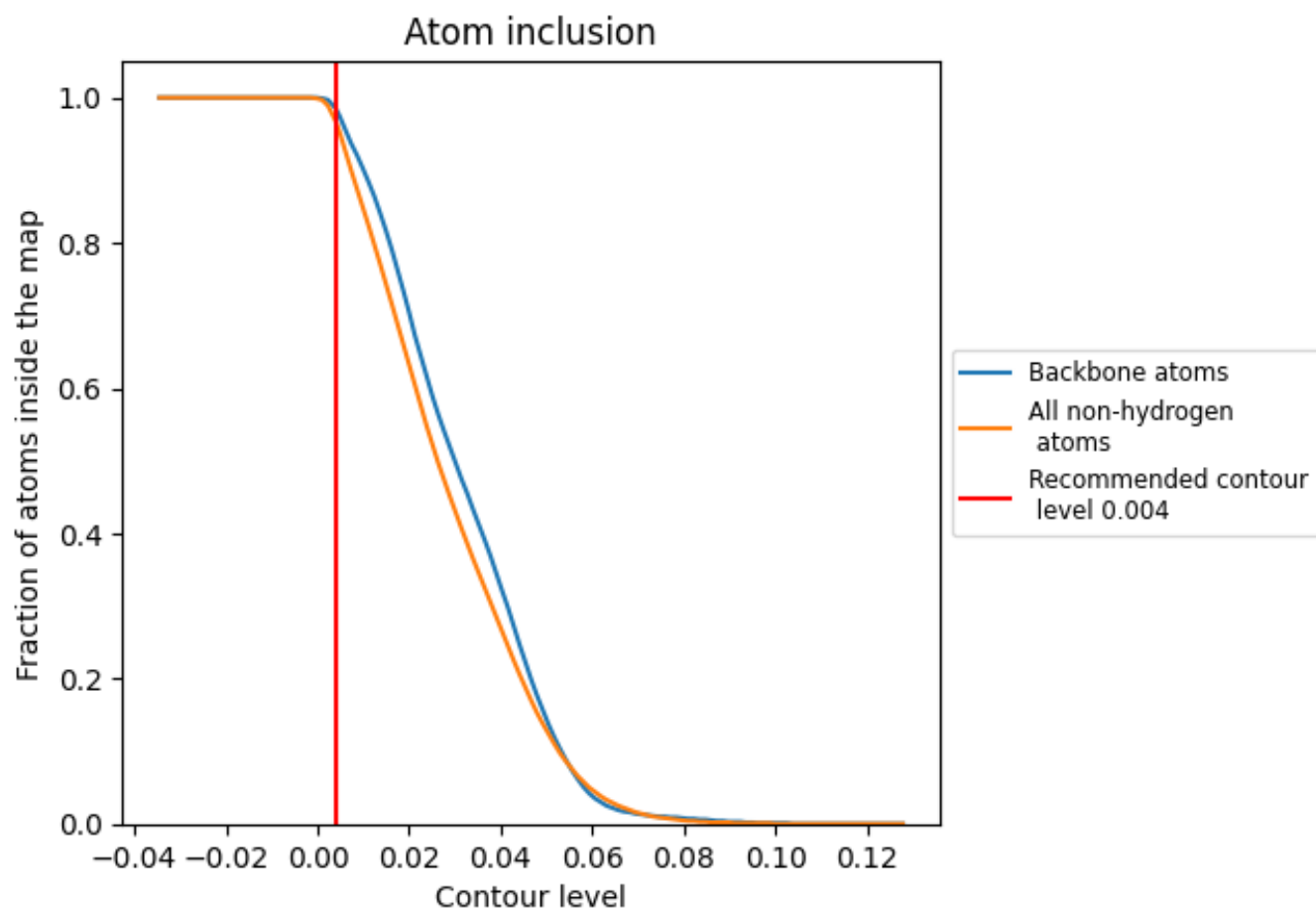
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

## 9.3 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 (0.004).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary













































The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.5360
0	 0.9720	 0.5920
1	 0.9670	 0.3880
2	 1.0000	 0.6690
3	 0.9930	 0.6490
4	 1.0000	 0.5770
5	 0.9850	 0.5650
6	 0.9780	 0.4590
7	 0.9800	 0.5180
8	 0.5940	 0.1780
9	 0.9810	 0.5830
A	 0.9950	 0.5770
B	 0.9760	 0.2960
C	 0.9710	 0.3940
D	 0.9800	 0.6020
E	 0.9900	 0.6120
F	 0.9950	 0.6350
G	 0.9540	 0.4480
H	 0.9720	 0.5520
I	 0.9400	 0.2380
J	 0.8390	 0.0850
K	 0.9940	 0.6290
L	 0.9890	 0.5960
M	 0.9900	 0.6230
N	 0.9700	 0.4400
O	 0.9910	 0.6230
P	 0.9880	 0.5190
Q	 0.9840	 0.5940
R	 0.9900	 0.6430
S	 0.9870	 0.6140
T	 0.9850	 0.6350
U	 0.8900	 0.5600
V	 0.9790	 0.5590
W	 0.9910	 0.6110
X	 0.9800	 0.5940



*Continued on next page...*

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Chain	Atom inclusion	Q-score
Y	 0.9820	 0.6120
Z	 0.9890	 0.6050
a	 0.9880	 0.6180
b	 0.9900	 0.6230
c	 0.9800	 0.5840
d	 0.8620	 0.3900
e	 0.5420	 0.1240
f	 0.6860	 0.3110
g	 0.9920	 0.6180
h	 0.9800	 0.5220
i	 0.9980	 0.6570
j	 0.9890	 0.5920
k	 0.9590	 0.2990
m	 0.5790	 0.1720
o	 0.9880	 0.6200
p	 0.9630	 0.5160
q	 0.9540	 0.4880
r	 0.9910	 0.5620
s	 0.9870	 0.6100
u	 0.9740	 0.4640
v	 0.9540	 0.3520
w	 0.9100	 0.2280