



wwPDB EM Validation Summary Report ⓘ

Feb 23, 2022 – 09:58 pm GMT

PDB ID : 7QH6
EMDB ID : EMD-13965
Title : Cryo-EM structure of the human mtLSU assembly intermediate upon MRM2 depletion - class 1
Authors : Rebelo-Guiomar, P.; Pellegrino, S.; Dent, K.C.; Warren, A.J.; Minczuk, M.
Deposited on : 2021-12-10
Resolution : 3.08 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

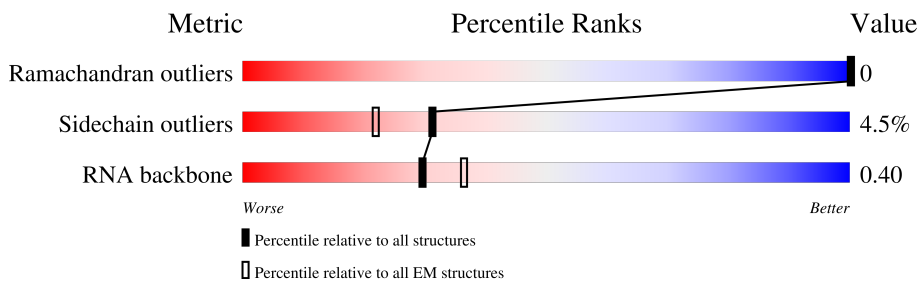
EMDB validation analysis : 0.0.0.dev97
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

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 3.08 Å.

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





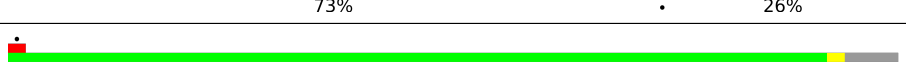
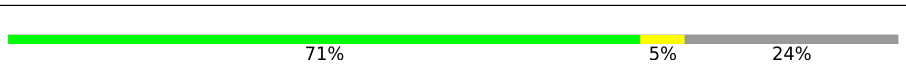


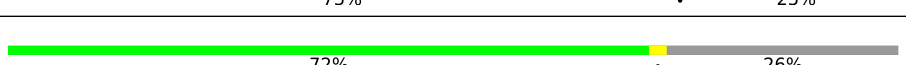
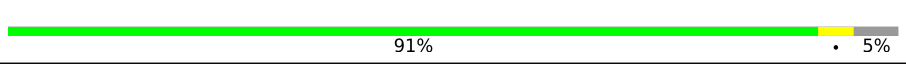
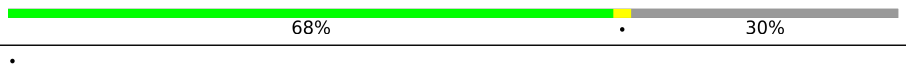


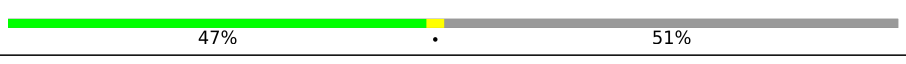

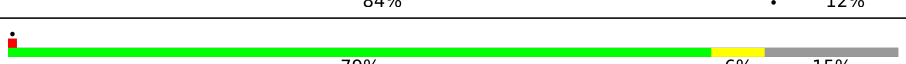

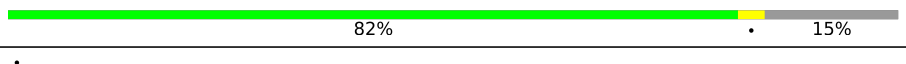

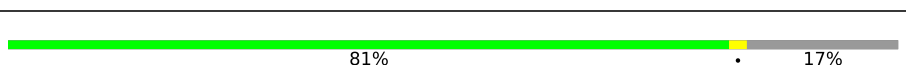





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	D	305	
2	E	348	
3	F	311	
4	H	267	
5	K	178	
6	L	145	
7	M	296	
8	N	251	








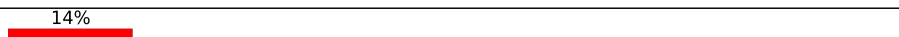
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Mol	Chain	Length	Quality of chain
9	O	175	 81% 6% 13%
10	P	180	 73% 6% 22%
11	Q	292	 73% 26%
12	R	149	 92% 6%
13	S	205	 71% 5% 24%
14	T	206	 6% 75% 6% 19%
15	U	153	 5% 88% 9%
16	V	216	 20% 75% 25%
17	W	148	 72% 26%
18	X	256	 91% 5%
19	Y	250	 68% 30%
20	Z	161	 69% 27%
21	0	188	 54% 43%
22	1	65	 80% 20%
23	2	92	 47% 51%
24	3	188	 48% 49%
25	5	423	 84% 12%
26	6	380	 79% 6% 15%
27	7	338	 83% 15%
28	9	137	 82% 15%
29	a	142	 55% 42%
30	b	215	 66% 31%
31	c	332	 81% 17%
32	d	306	60% 40%
33	g	166	74% 22%

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Mol	Chain	Length	Quality of chain
34	h	158	
35	i	128	
36	j	123	
37	o	102	
38	p	206	
39	q	222	
40	r	196	
41	s	439	
42	u	234	
43	v	70	
44	w	156	
45	A	1559	
46	B	69	

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 83425 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 L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	174	1349	834	268	240	7	0	0

- Molecule 2 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	284	2249	1451	382	405	11	0	0

- Molecule 3 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 4 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 5 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 6 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	N	205	1654	1056	308	280	10	0	0

- Molecule 9 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L18, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	R	140	1153	732	231	186	4	0	0

- Molecule 13 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 14 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 15 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	V	163	1333	848	231	247	7	0	0

- Molecule 17 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	W	109	859	552	162	142	3	0	0

- Molecule 18 is a protein called 39S ribosomal protein L28, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Z	117	955	610	179	163	3	0	0

- Molecule 21 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	0	108	880	545	172	157	6	0	0

- Molecule 22 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	1	52	433	278	83	70	2	0	0

- Molecule 23 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	2	45	367	227	81	58	1	0	0

- Molecule 24 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	3	95	831	539	162	127	3	0	0

- Molecule 25 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	5	373	3037	1964	526	536	11	0	0

- Molecule 26 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	6	324	2640	1694	470	468	8	0	0

- Molecule 27 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	7	287	2334	1495	397	425	17	0	0

- Molecule 28 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 29 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 30 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 31 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	185	Total	C	N	O	S	0	0
			1529	989	260	271	9		

- Molecule 33 is a protein called 39S ribosomal protein L49, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 35 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 37 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	91	Total	C	N	O	S	0	0
			771	487	156	125	3		

- Molecule 38 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 39 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 40 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	130	Total	C	N	O	S	0	0
			1075	683	210	174	8		

- Molecule 41 is a protein called 39S ribosomal protein S30, mitochondrial.

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

- Molecule 42 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

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

- Molecule 43 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 44 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 45 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	A	1133	24063	10801	4361	7768	1133	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 46 is a RNA chain called mitochondrial tRNAVal.

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

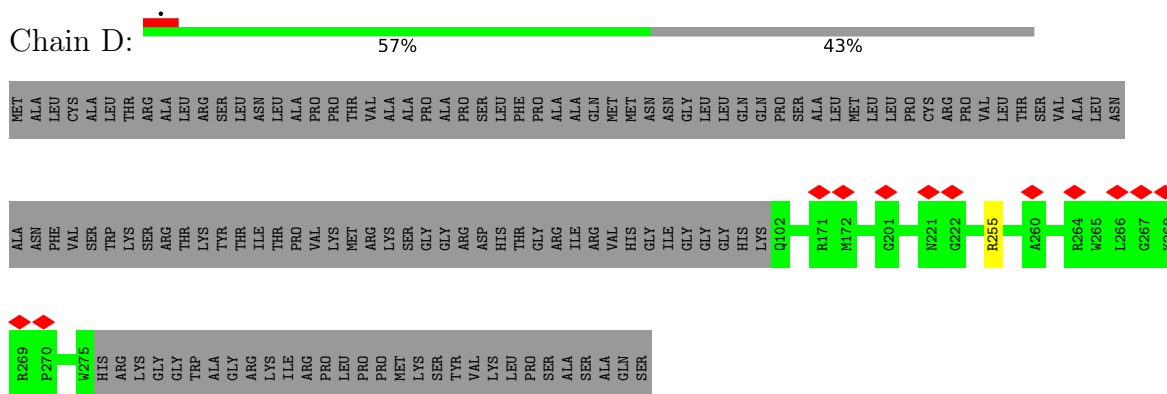
- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	0	1	Total	Zn	0
			1	1	

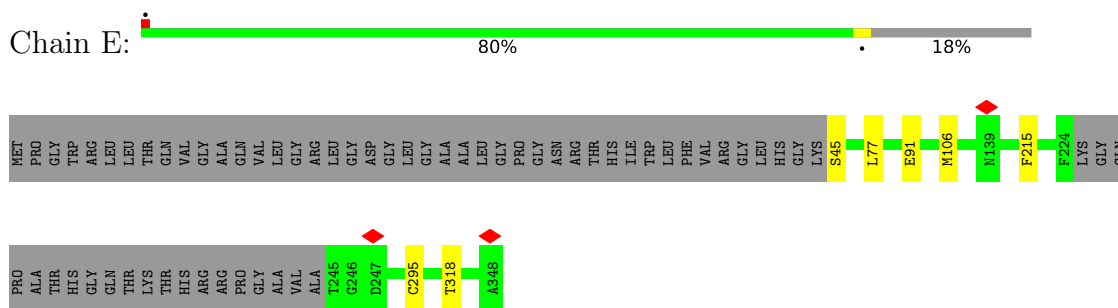
3 Residue-property plots

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.

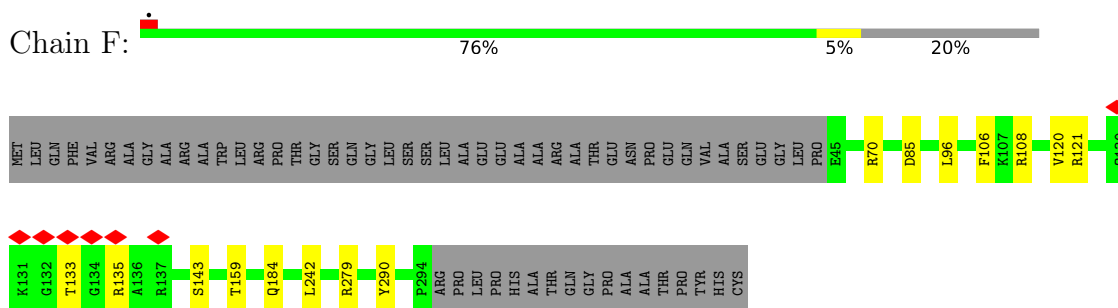
- Molecule 1: 39S ribosomal protein L2, mitochondrial



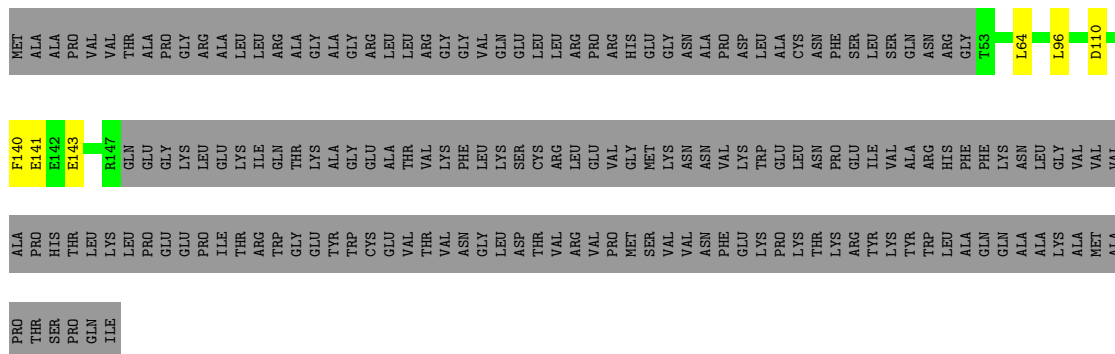
- Molecule 2: 39S ribosomal protein L3, mitochondrial



- Molecule 3: 39S ribosomal protein L4, mitochondrial



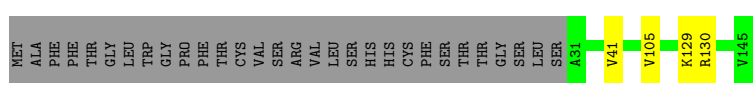
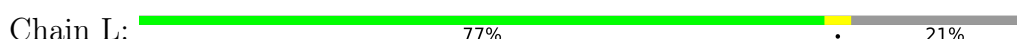
- Molecule 4: 39S ribosomal protein L9, mitochondrial



- Molecule 5: 39S ribosomal protein L13, mitochondrial



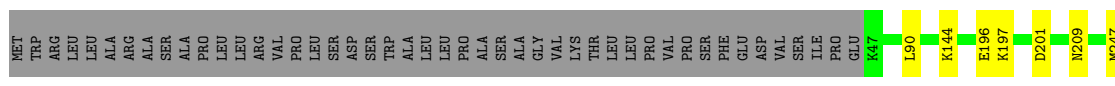
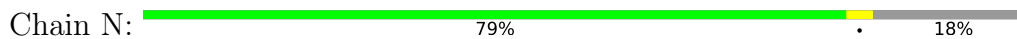
- Molecule 6: 39S ribosomal protein L14, mitochondrial



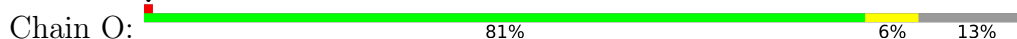
- Molecule 7: 39S ribosomal protein L15, mitochondrial



- Molecule 8: 39S ribosomal protein L16, mitochondrial

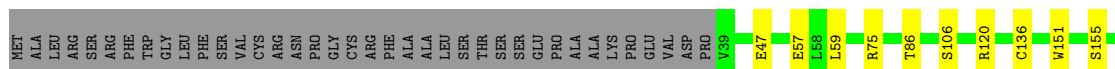


- Molecule 9: 39S ribosomal protein L17, mitochondrial

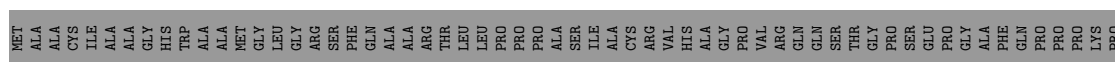




- Molecule 10: 39S ribosomal protein L18, mitochondrial



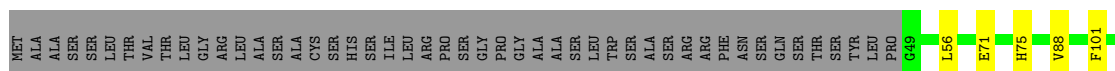
- Molecule 11: 39S ribosomal protein L19, mitochondrial



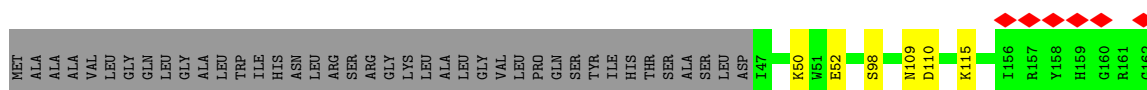
- Molecule 12: 39S ribosomal protein L20, mitochondrial



- Molecule 13: 39S ribosomal protein L21, mitochondrial

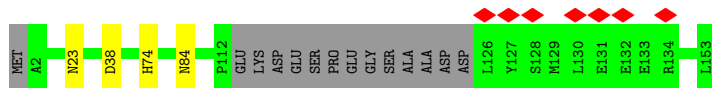
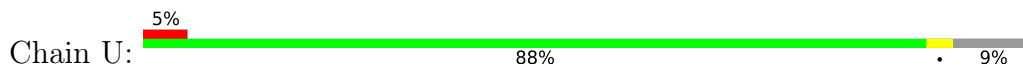


- Molecule 14: 39S ribosomal protein L22, mitochondrial

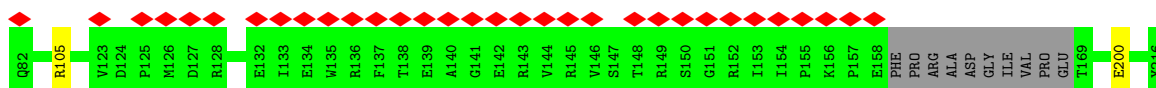
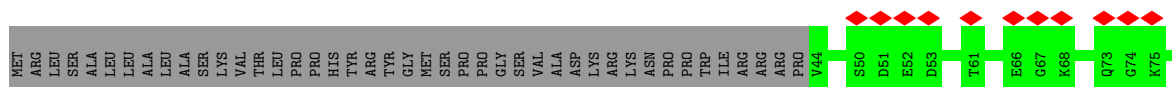
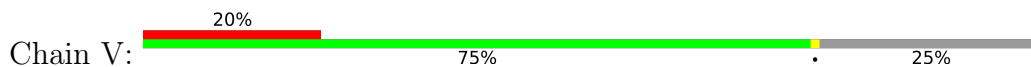




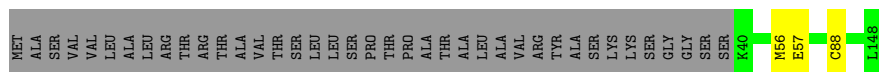
- Molecule 15: 39S ribosomal protein L23, mitochondrial



- Molecule 16: 39S ribosomal protein L24, mitochondrial



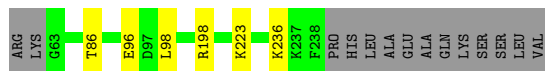
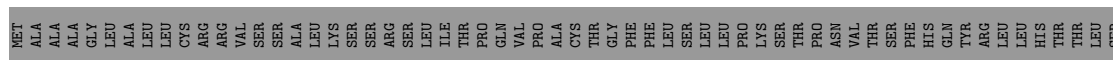
- Molecule 17: 39S ribosomal protein L27, mitochondrial



- Molecule 18: 39S ribosomal protein L28, mitochondrial

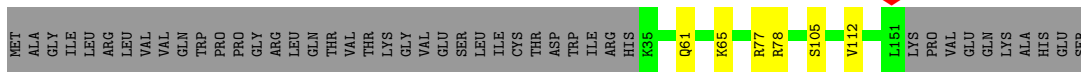


- Molecule 19: 39S ribosomal protein L47, mitochondrial

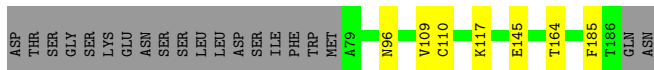


- Molecule 20: 39S ribosomal protein L30, mitochondrial

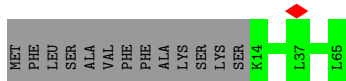
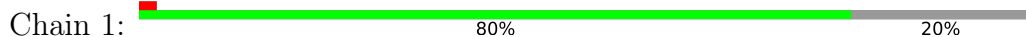




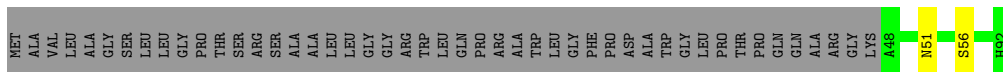
• Molecule 21: 39S ribosomal protein L32, mitochondrial



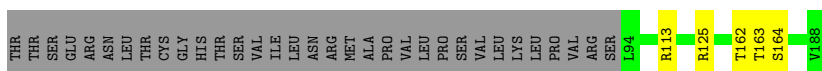
• Molecule 22: 39S ribosomal protein L33, mitochondrial



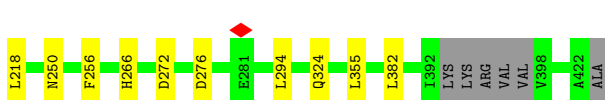
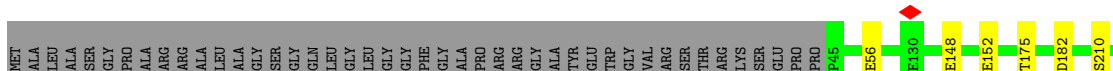
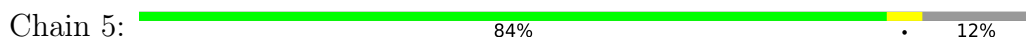
• Molecule 23: 39S ribosomal protein L34, mitochondrial



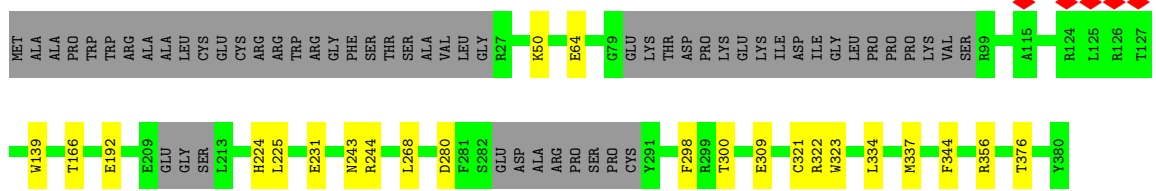
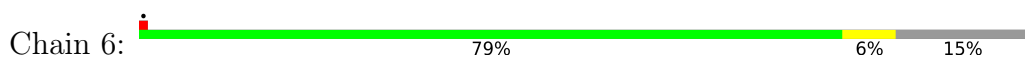
• Molecule 24: 39S ribosomal protein L35, mitochondrial



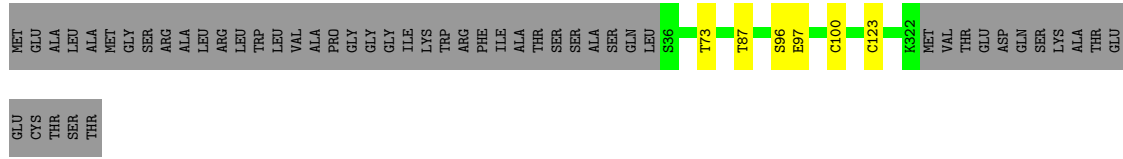
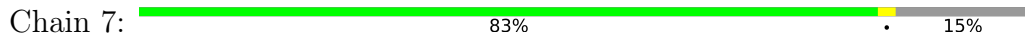
• Molecule 25: 39S ribosomal protein L37, mitochondrial



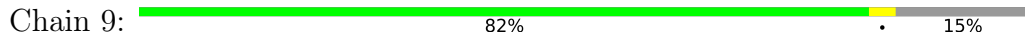
• Molecule 26: 39S ribosomal protein L38, mitochondrial



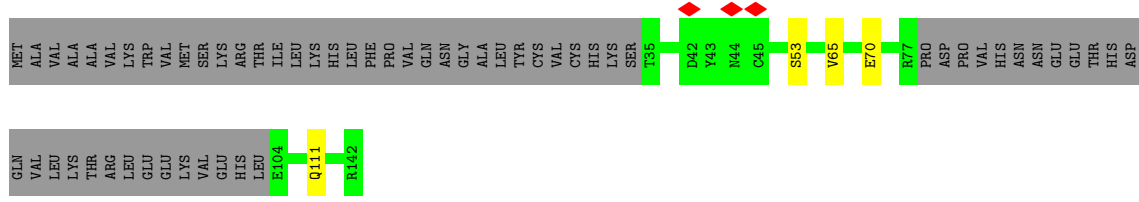
• Molecule 27: 39S ribosomal protein L39, mitochondrial



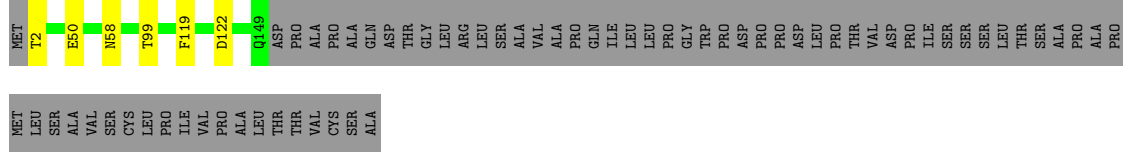
• Molecule 28: 39S ribosomal protein L41, mitochondrial



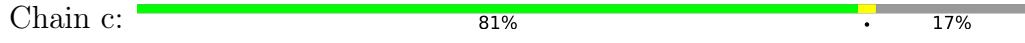
• Molecule 29: 39S ribosomal protein L42, mitochondrial

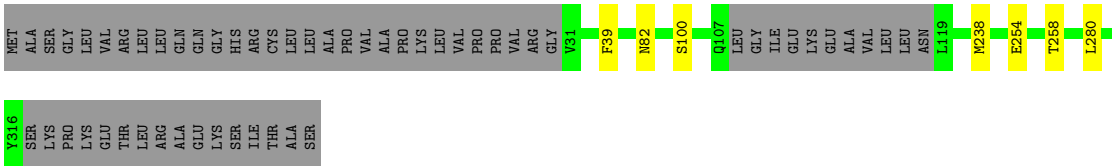


• Molecule 30: 39S ribosomal protein L43, mitochondrial

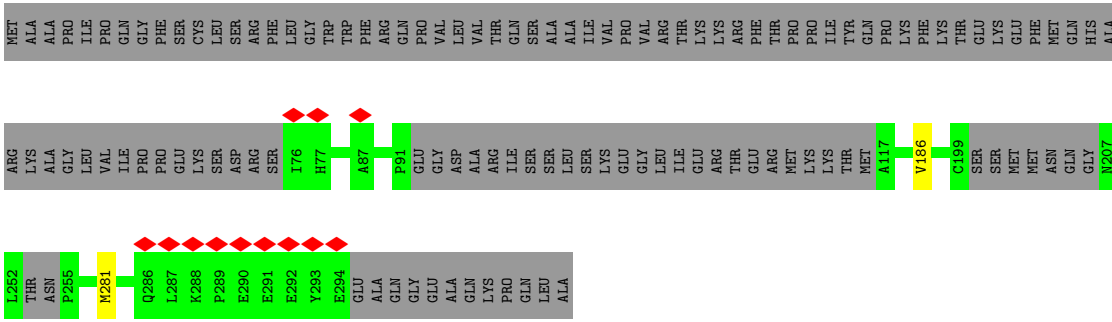


• Molecule 31: 39S ribosomal protein L44, mitochondrial

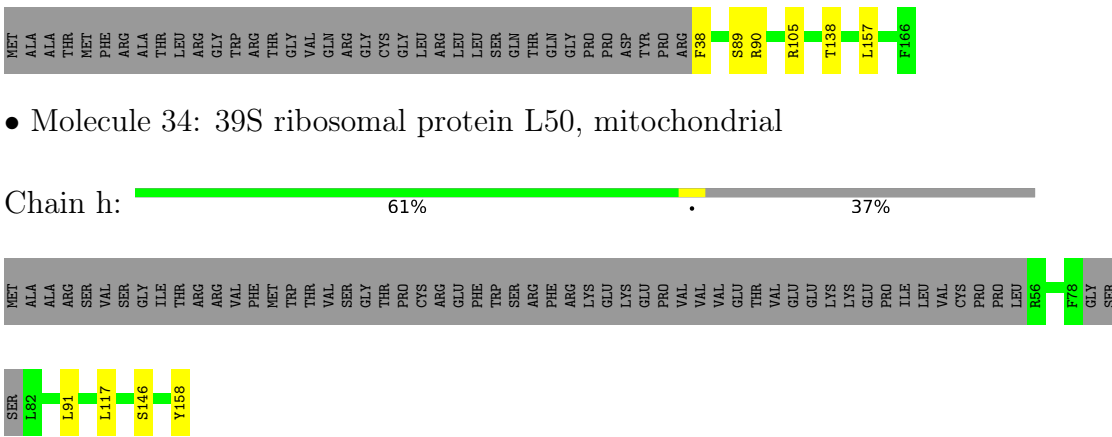




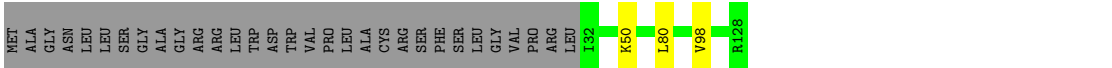
● Molecule 32: 39S ribosomal protein L45, mitochondrial



● Molecule 33: 39S ribosomal protein L49, mitochondrial



● Molecule 34: 39S ribosomal protein L50, mitochondrial



● Molecule 35: 39S ribosomal protein L51, mitochondrial

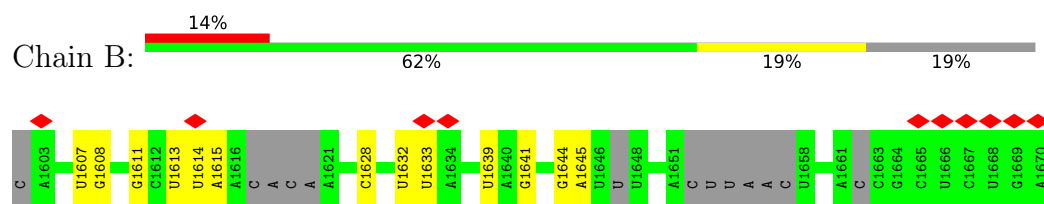


● Molecule 36: 39S ribosomal protein L52, mitochondrial



U3188	C3189	A3190	A3101	A3102	U3108	U3109	C	A3113	U3114	C3117	U3118	C3119	C3120	C3121	U3122	G3123	U3124	A3125	C3126	G3127	A3128	A3129	A3130	G3131	C3134	A3135	A3140	A3141	C3149	U3150	A3151	U3154	C3157	A3158	G3162	G3163	C3164	C3168	C3169	C3170	C3171	C3172	A3177	G3184	A3185																
U	C	A	A	A	C	C	A	A	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C												
U3189	A3191	U3193	G3196	U	A	U	U	U	A3201	A3207	C	A	C	C3212	A3217	A3218	G3219	A3220	U3228	U																																									
U	A	A	C	U	A	U	U	U	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C											
A2446	A2451	A2452	G2453	A2457	A2458	A2473	U	U	C	A2481	C2484	A2487	C	C	C	C	C	C	C	C	C	C	C	C	C	U2499	A2500	C2501	C2502	A2503	A2504	A2507	C2508	C2511	G2519	C2520	A2521	U2522	C2523	A2524	C2525	C2526	A2527	G2528	U2529	A2530	U2531	C2540	C2544	U	G										
C	C	C	C	U	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C								
U	G	U	U	U	C	C	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U					
G2686	C2689	A2694	G2695	A2696	C2699	A2706	A2709	C2710	C2718	G2719	G2721	A2722	A2723	G2724	A2725	C2726	U2731	G2732	A2733	G2735	U2738	U2739	A2740	U2743	U2750	A2755	C2756	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U			
U	U	C	C	U	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A						
C2889	U2890	C2891	U2895	U2898	A2905	C2906	U2907	U2908	G2909	A2910	C2911	C2912	A2913	G2916	G2917	A2918	U2919	A2922	U2924	U2925	A2926	C2927	C2928	C2929	U2930	A2931	G2932	G2933	G2934	A2935	U2936	A2937	A2938	C2939	A2940	G2943	A2946	U2947	A2951	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
A	U	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C			
U	U	A	A	C	C	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
U3100	U3102	U3108	U3109	C	A3113	U3114	C3117	U3118	C3119	C3120	C3121	U3122	G3123	U3124	A3125	C3126	G3127	A3128	A3129	A3130	G3131	C3134	A3135	A3140	A3141	C3149	U3150	A3151	U3154	C3157	A3158	G3162	G3163	C3164	C3168	C3169	C3170	C3171	C3172	A3177	G3184	A3185																			
U	C	A	A	A	A	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C					
U2072	A2073	A2074	C2079	U2080	U2083	A2084	A2085	U2089	U2096	G2105	G2113	U2126	G2129	A2132	A2135	C2136	U2139	G2140	U2141	G2147	A2148	G2149	A2154	A2155	U2157	U2158	U	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A					
U	A	A	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C							
A2239	C2240	A2241	A2245	A2246	A2250	C2257	A2260	A2261	C2262	C2263	A2278	C2282	C2283	C2284	A2297	C2298	U2299	G2300	A2306	U2307	A2308	A2309	G2317	A2321	C2322	A2324	C2329	U2330	C2331	C2332	U2342	C2343	C2344	G2345	G2349	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U			
U	A	A	A	G	C	A	C	C	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A				
U	A	A	A	G	C	A	C	C	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A			
A2363	A2364	A2369	A2370	A2371	U2372	A2373	A2374	C2375	A2376	C2377	C2378	C2379	A2384	U2385	U2387	A2388	C2389	A2390	A2391	U2392	A2394	A2395	C2396	A2399	C2400	A2401	U2404	U2407	U2408	A2409	C2414	C2415	U2416	C2417	A2418	C2426	A2430	C2431	A2432	C2433	A2434	U2442	C2443	A2444	U2445																
G	A	A	A	A	C	A	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C						
U	A	A	A	G	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C						

● Molecule 46: mitochondrial tRNAVal



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	119341	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 ($e^-/\text{\AA}^2$)	52.5	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-2600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.020	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	D	0.26	0/1371	0.54	0/1848
2	E	0.33	0/2313	0.50	0/3137
3	F	0.42	0/2071	0.55	0/2817
4	H	0.35	0/798	0.60	0/1073
5	K	0.39	0/1495	0.51	0/2029
6	L	0.27	0/904	0.56	0/1218
7	M	0.39	0/2359	0.58	0/3185
8	N	0.31	0/1697	0.52	0/2281
9	O	0.36	0/1269	0.56	0/1708
10	P	0.30	0/1173	0.55	0/1588
11	Q	0.31	0/1846	0.56	0/2487
12	R	0.42	0/1174	0.56	0/1572
13	S	0.38	0/1276	0.61	1/1729 (0.1%)
14	T	0.41	0/1402	0.56	0/1886
15	U	0.36	0/1183	0.55	0/1600
16	V	0.28	0/1362	0.48	0/1842
17	W	0.40	0/881	0.56	0/1188
18	X	0.35	0/2090	0.51	0/2825
19	Y	0.36	0/1552	0.51	0/2079
20	Z	0.34	0/979	0.53	0/1321
21	0	0.34	0/895	0.59	0/1201
22	1	0.27	0/438	0.55	0/583
23	2	0.43	0/373	0.61	0/496
24	3	0.47	0/852	0.57	0/1136
25	5	0.29	0/3126	0.51	0/4259
26	6	0.34	0/2726	0.53	0/3715
27	7	0.31	0/2391	0.49	0/3234
28	9	0.35	0/972	0.53	0/1306
29	a	0.38	0/709	0.56	0/963
30	b	0.39	0/1202	0.60	0/1626
31	c	0.34	0/2264	0.51	0/3059
32	d	0.27	0/1573	0.50	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.40	0/1102	0.55	0/1503
34	h	0.31	0/847	0.51	0/1150
35	i	0.47	0/849	0.59	0/1135
36	j	0.37	0/698	0.59	0/940
37	o	0.38	0/792	0.58	0/1064
38	p	0.29	0/1071	0.55	0/1433
39	q	0.33	0/1107	0.52	0/1498
40	r	0.33	0/1110	0.55	0/1504
41	s	0.34	0/3114	0.53	0/4225
42	u	0.26	0/949	0.47	0/1281
43	v	0.26	0/597	0.50	0/796
44	w	0.25	0/647	0.44	0/871
45	A	0.62	0/26912	0.93	27/41848 (0.1%)
46	B	0.22	0/1328	0.83	0/2056
All	All	0.45	0/87839	0.70	28/124429 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	S	0	1

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	A	2484	C	C2-N1-C1'	8.06	127.66	118.80
45	A	2484	C	N1-C2-O2	6.99	123.09	118.90
45	A	1833	C	C6-N1-C2	-6.12	117.85	120.30
45	A	2493	C	N1-C2-O2	6.07	122.54	118.90
45	A	3134	C	C6-N1-C2	-6.02	117.89	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	S	101	PHE	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	D	172/305 (56%)	158 (92%)	14 (8%)	0	100	100
2	E	280/348 (80%)	262 (94%)	18 (6%)	0	100	100
3	F	248/311 (80%)	230 (93%)	18 (7%)	0	100	100
4	H	93/267 (35%)	86 (92%)	7 (8%)	0	100	100
5	K	175/178 (98%)	161 (92%)	14 (8%)	0	100	100
6	L	113/145 (78%)	105 (93%)	8 (7%)	0	100	100
7	M	285/296 (96%)	265 (93%)	20 (7%)	0	100	100
8	N	203/251 (81%)	189 (93%)	14 (7%)	0	100	100
9	O	150/175 (86%)	142 (95%)	8 (5%)	0	100	100
10	P	139/180 (77%)	132 (95%)	7 (5%)	0	100	100
11	Q	215/292 (74%)	198 (92%)	17 (8%)	0	100	100
12	R	138/149 (93%)	128 (93%)	10 (7%)	0	100	100
13	S	154/205 (75%)	144 (94%)	10 (6%)	0	100	100
14	T	164/206 (80%)	152 (93%)	12 (7%)	0	100	100
15	U	135/153 (88%)	128 (95%)	7 (5%)	0	100	100
16	V	159/216 (74%)	150 (94%)	9 (6%)	0	100	100
17	W	107/148 (72%)	100 (94%)	7 (6%)	0	100	100
18	X	241/256 (94%)	229 (95%)	12 (5%)	0	100	100
19	Y	174/250 (70%)	165 (95%)	9 (5%)	0	100	100
20	Z	115/161 (71%)	107 (93%)	8 (7%)	0	100	100
21	0	106/188 (56%)	102 (96%)	4 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	1	50/65 (77%)	45 (90%)	5 (10%)	0	100	100
23	2	43/92 (47%)	36 (84%)	7 (16%)	0	100	100
24	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
25	5	369/423 (87%)	342 (93%)	27 (7%)	0	100	100
26	6	316/380 (83%)	290 (92%)	26 (8%)	0	100	100
27	7	285/338 (84%)	262 (92%)	23 (8%)	0	100	100
28	9	113/137 (82%)	107 (95%)	6 (5%)	0	100	100
29	a	78/142 (55%)	72 (92%)	6 (8%)	0	100	100
30	b	146/215 (68%)	132 (90%)	14 (10%)	0	100	100
31	c	271/332 (82%)	258 (95%)	13 (5%)	0	100	100
32	d	177/306 (58%)	166 (94%)	11 (6%)	0	100	100
33	g	127/166 (76%)	120 (94%)	7 (6%)	0	100	100
34	h	96/158 (61%)	90 (94%)	6 (6%)	0	100	100
35	i	95/128 (74%)	85 (90%)	10 (10%)	0	100	100
36	j	83/123 (68%)	79 (95%)	4 (5%)	0	100	100
37	o	89/102 (87%)	81 (91%)	8 (9%)	0	100	100
38	p	119/206 (58%)	112 (94%)	7 (6%)	0	100	100
39	q	126/222 (57%)	119 (94%)	7 (6%)	0	100	100
40	r	126/196 (64%)	118 (94%)	8 (6%)	0	100	100
41	s	366/439 (83%)	340 (93%)	26 (7%)	0	100	100
42	u	109/234 (47%)	98 (90%)	11 (10%)	0	100	100
43	v	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
44	w	77/156 (49%)	67 (87%)	10 (13%)	0	100	100
All	All	6987/9498 (74%)	6503 (93%)	484 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	140/245 (57%)	139 (99%)	1 (1%)	84	92
2	E	245/290 (84%)	238 (97%)	7 (3%)	42	70
3	F	217/262 (83%)	202 (93%)	15 (7%)	15	44
4	H	86/228 (38%)	80 (93%)	6 (7%)	15	43
5	K	155/156 (99%)	151 (97%)	4 (3%)	46	72
6	L	98/124 (79%)	94 (96%)	4 (4%)	30	62
7	M	245/249 (98%)	232 (95%)	13 (5%)	22	53
8	N	172/211 (82%)	165 (96%)	7 (4%)	30	62
9	O	133/150 (89%)	122 (92%)	11 (8%)	11	37
10	P	123/155 (79%)	113 (92%)	10 (8%)	11	37
11	Q	199/256 (78%)	195 (98%)	4 (2%)	55	78
12	R	118/126 (94%)	115 (98%)	3 (2%)	47	74
13	S	141/180 (78%)	131 (93%)	10 (7%)	14	43
14	T	146/176 (83%)	134 (92%)	12 (8%)	11	37
15	U	124/135 (92%)	120 (97%)	4 (3%)	39	68
16	V	146/191 (76%)	144 (99%)	2 (1%)	67	84
17	W	89/119 (75%)	86 (97%)	3 (3%)	37	67
18	X	219/229 (96%)	209 (95%)	10 (5%)	27	58
19	Y	159/223 (71%)	153 (96%)	6 (4%)	33	64
20	Z	108/147 (74%)	102 (94%)	6 (6%)	21	51
21	0	97/164 (59%)	90 (93%)	7 (7%)	14	42
22	1	49/60 (82%)	49 (100%)	0	100	100
23	2	39/72 (54%)	37 (95%)	2 (5%)	24	54
24	3	88/166 (53%)	83 (94%)	5 (6%)	20	50
25	5	335/368 (91%)	319 (95%)	16 (5%)	25	57
26	6	265/332 (80%)	242 (91%)	23 (9%)	10	35
27	7	263/303 (87%)	257 (98%)	6 (2%)	50	75
28	9	99/112 (88%)	95 (96%)	4 (4%)	31	63
29	a	78/133 (59%)	74 (95%)	4 (5%)	24	54
30	b	130/186 (70%)	124 (95%)	6 (5%)	27	58
31	c	241/288 (84%)	234 (97%)	7 (3%)	42	70
32	d	170/274 (62%)	168 (99%)	2 (1%)	71	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	g	119/148 (80%)	113 (95%)	6 (5%)	24	55
34	h	95/148 (64%)	91 (96%)	4 (4%)	30	61
35	i	86/110 (78%)	83 (96%)	3 (4%)	36	67
36	j	68/97 (70%)	65 (96%)	3 (4%)	28	59
37	o	78/87 (90%)	74 (95%)	4 (5%)	24	54
38	p	117/181 (65%)	108 (92%)	9 (8%)	13	40
39	q	110/178 (62%)	106 (96%)	4 (4%)	35	66
40	r	119/169 (70%)	113 (95%)	6 (5%)	24	55
41	s	326/381 (86%)	308 (94%)	18 (6%)	21	52
42	u	105/200 (52%)	102 (97%)	3 (3%)	42	70
43	v	59/60 (98%)	57 (97%)	2 (3%)	37	67
44	w	73/136 (54%)	71 (97%)	2 (3%)	44	72
All	All	6272/8205 (76%)	5988 (96%)	284 (4%)	31	59

5 of 284 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	i	80	LEU
37	o	54	MET
41	s	75	SER
14	T	98	SER
13	S	197	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
38	p	184	ASN
29	a	44	ASN
14	T	125	GLN
11	Q	158	GLN
19	Y	110	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	A	1113/1559 (71%)	358 (32%)	15 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	B	51/69 (73%)	13 (25%)	0
All	All	1164/1628 (71%)	371 (31%)	15 (1%)

5 of 371 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	A	1679	U
45	A	1680	A
45	A	1681	G
45	A	1685	C
45	A	1689	C

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	A	2653	C
45	A	3130	A
45	A	2905	A
45	A	3168	C
45	A	3117	C

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

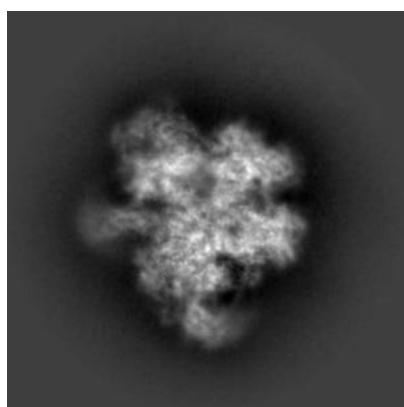
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13965. These allow visual inspection of the internal detail of the map and identification of artifacts.

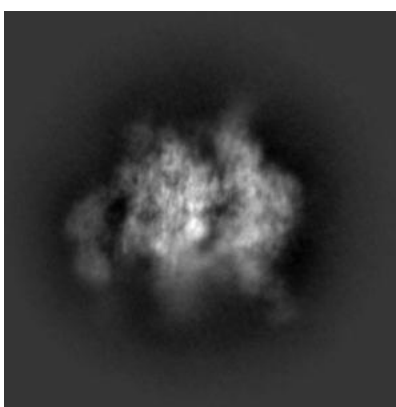
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

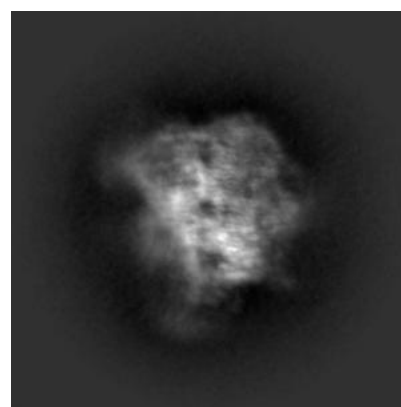
6.1.1 Primary map



X



Y

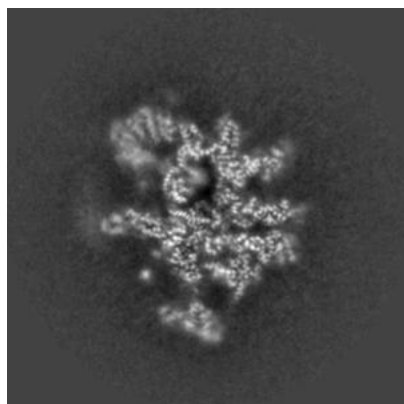


Z

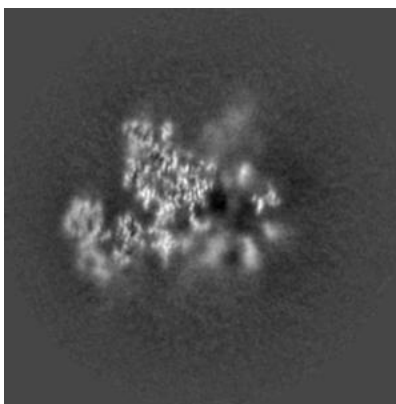
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

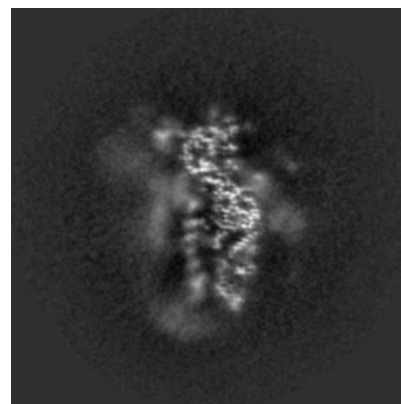
6.2.1 Primary map



X Index: 180



Y Index: 180

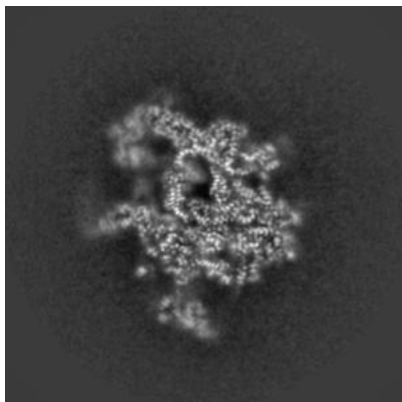


Z Index: 180

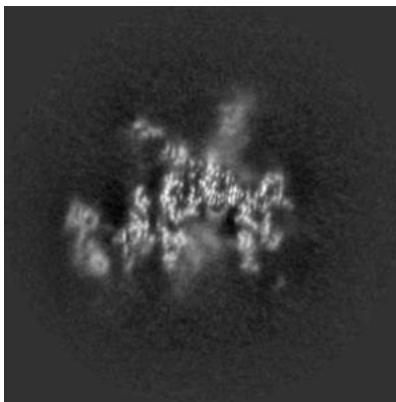
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

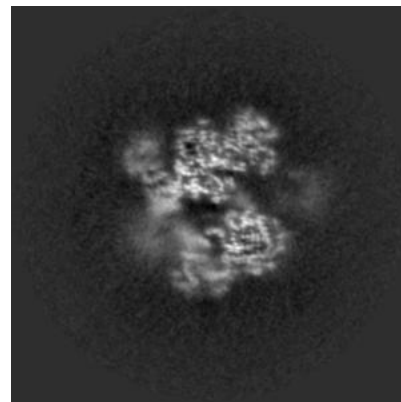
6.3.1 Primary map



X Index: 186



Y Index: 191



Z Index: 221

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

6.4 Orthogonal surface views [i](#)

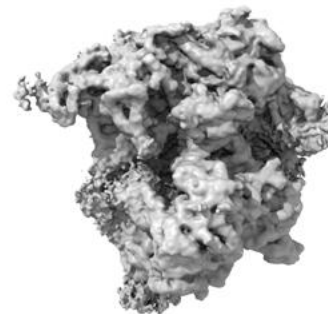
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

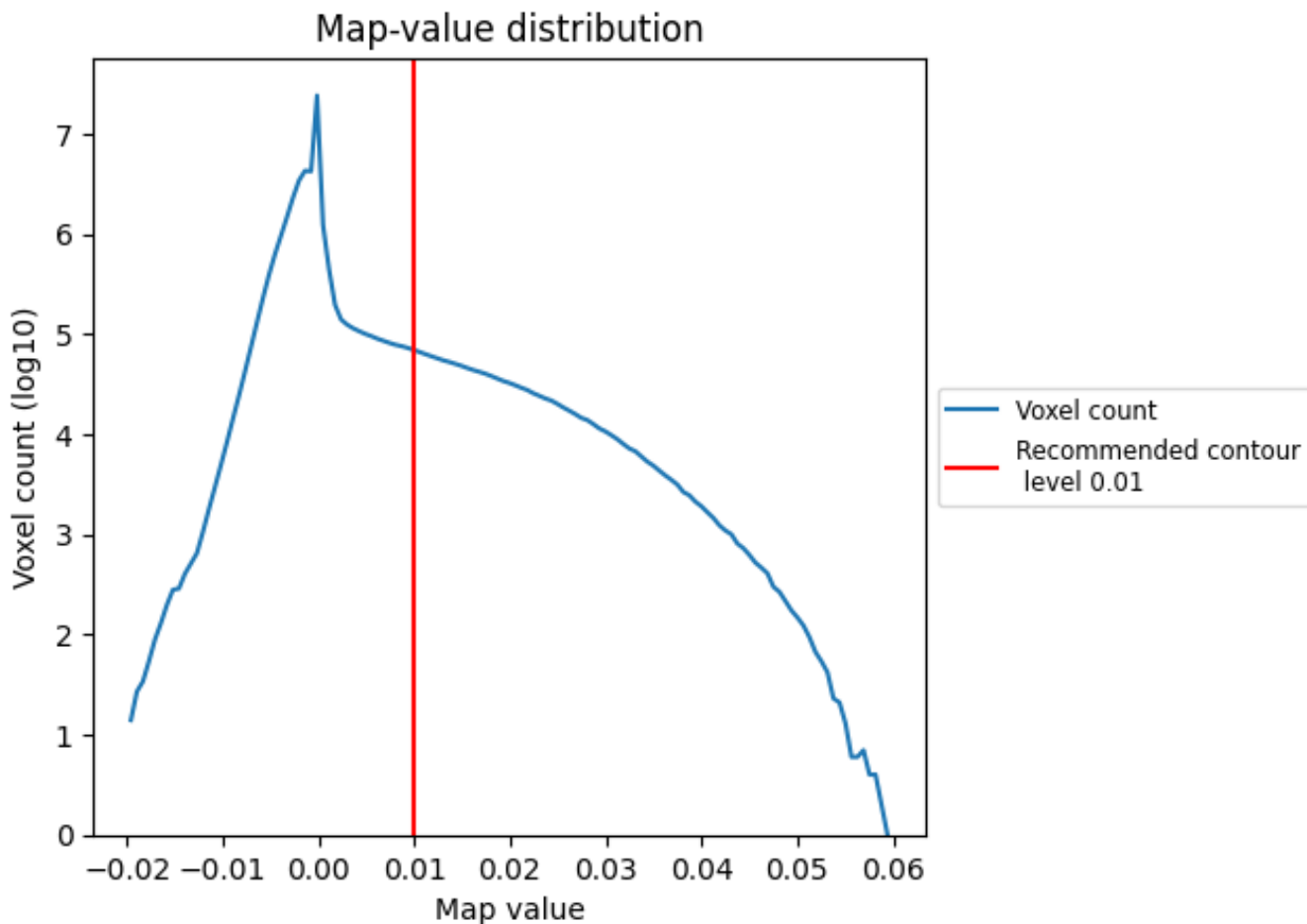
6.5 Mask visualisation

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

7 Map analysis [i](#)

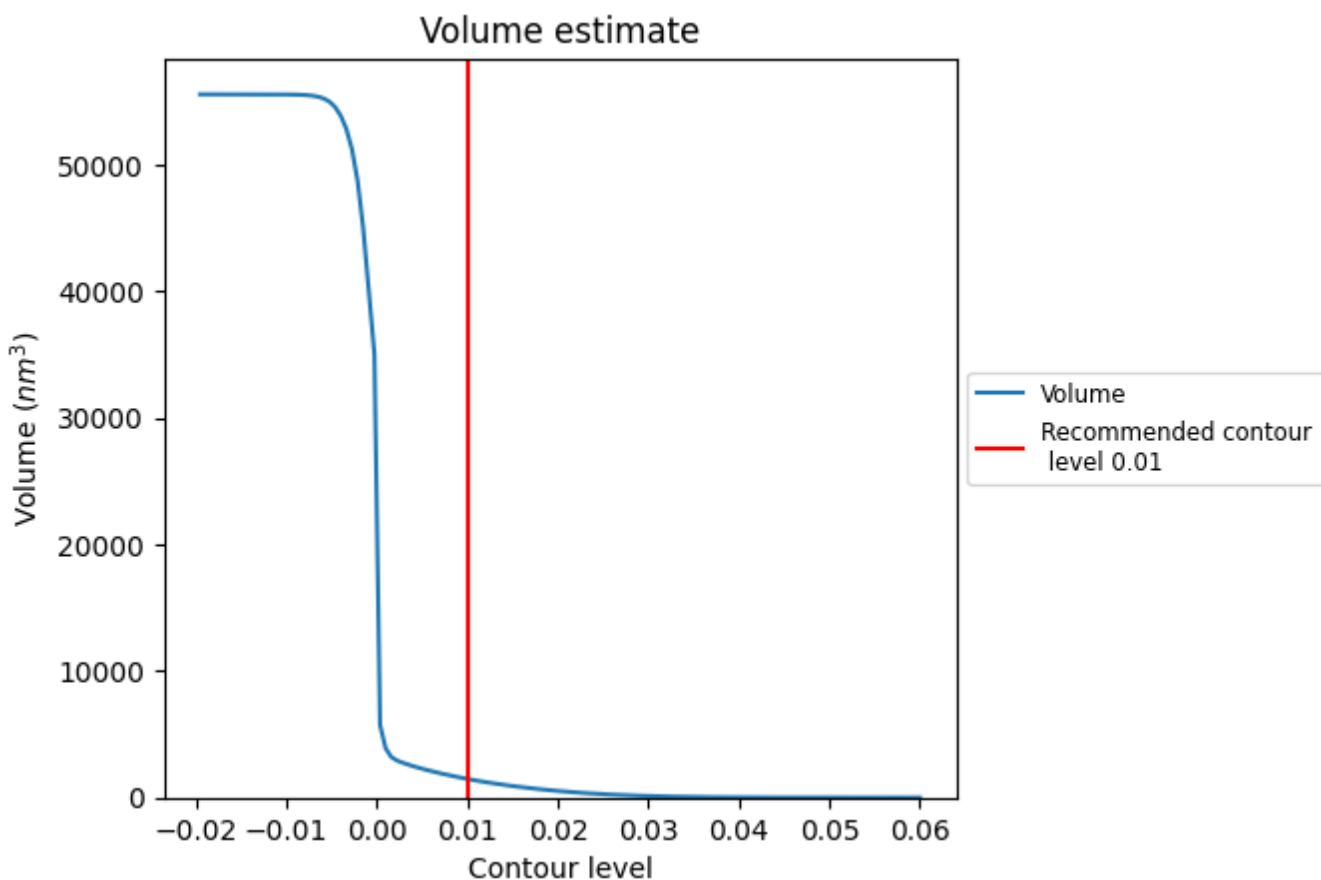
This section contains the results of statistical analysis of the map.

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.

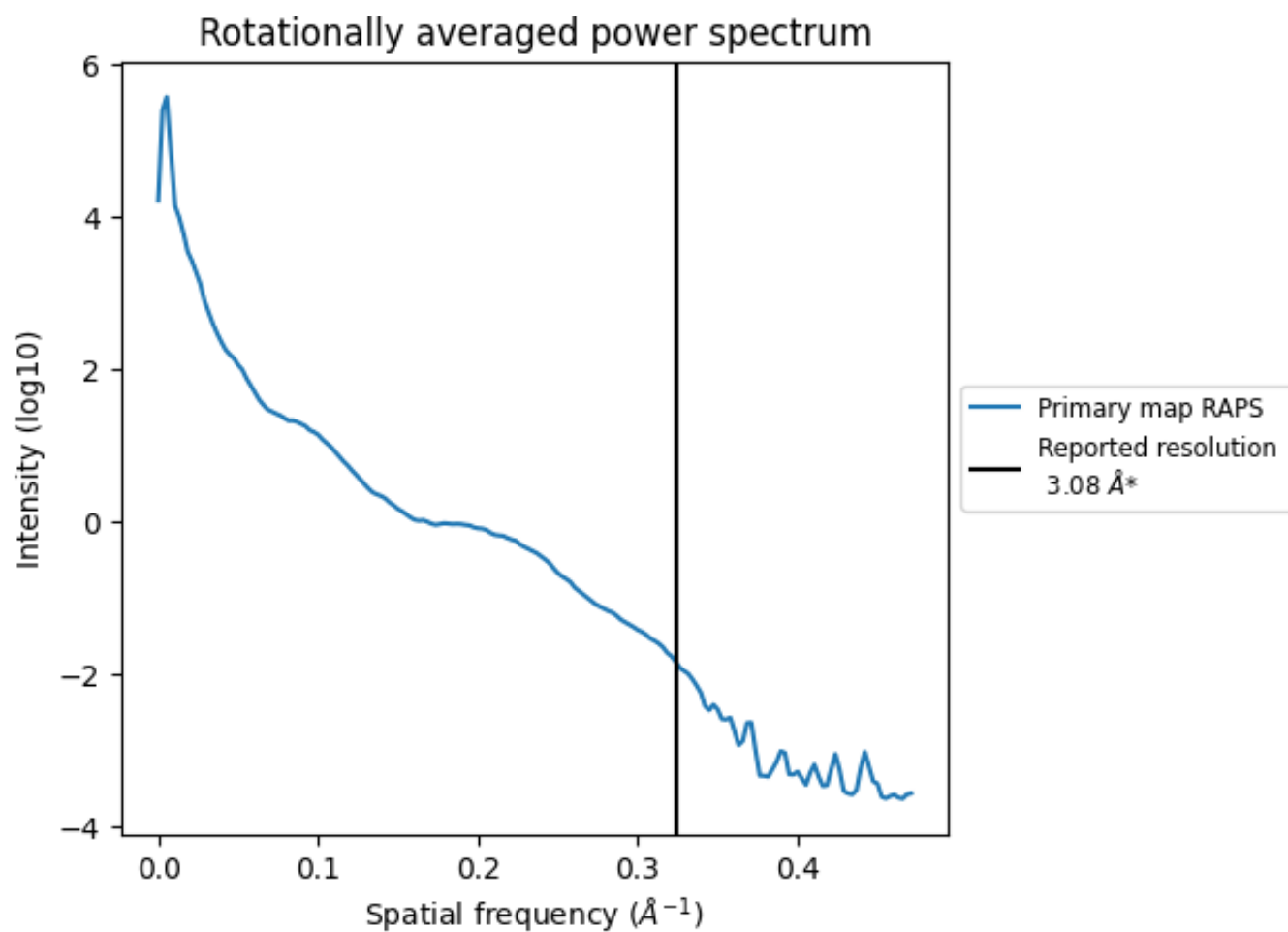
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1470 nm^3 ; this corresponds to an approximate mass of 1328 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

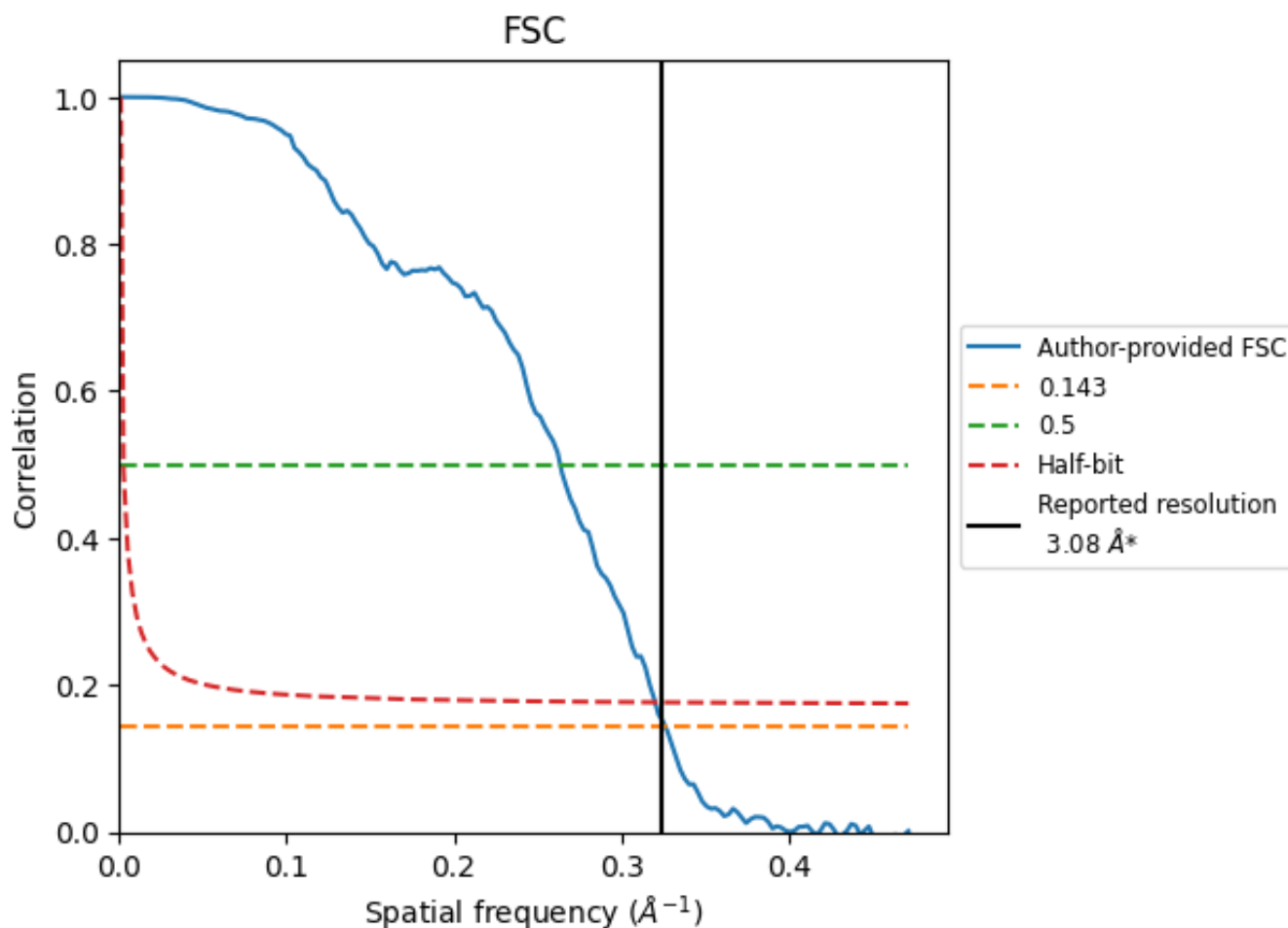


*Reported resolution corresponds to spatial frequency of 0.325 Å⁻¹

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 0.325 Å⁻¹

8.2 Resolution estimates [i](#)

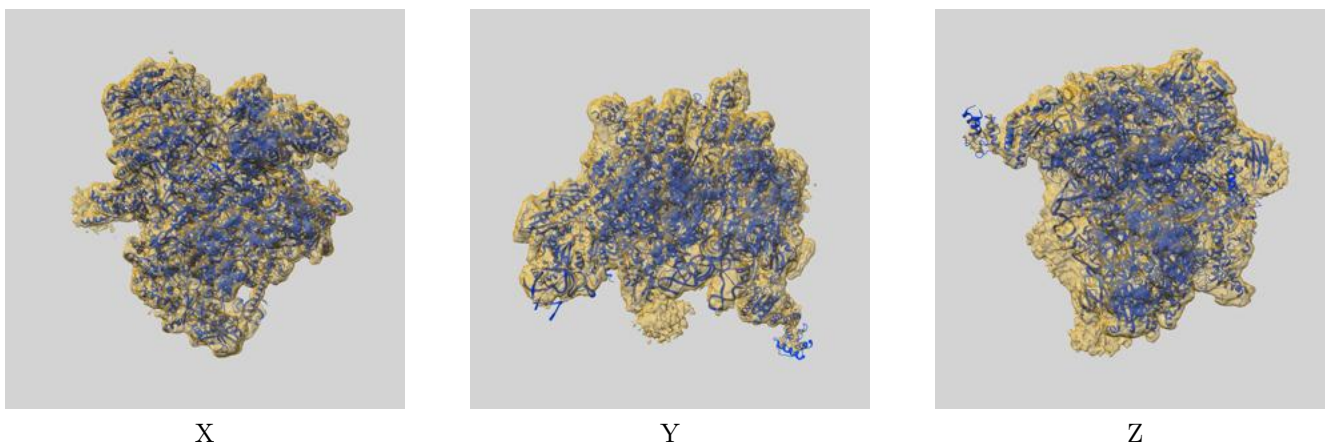
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.06	3.79	3.12
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

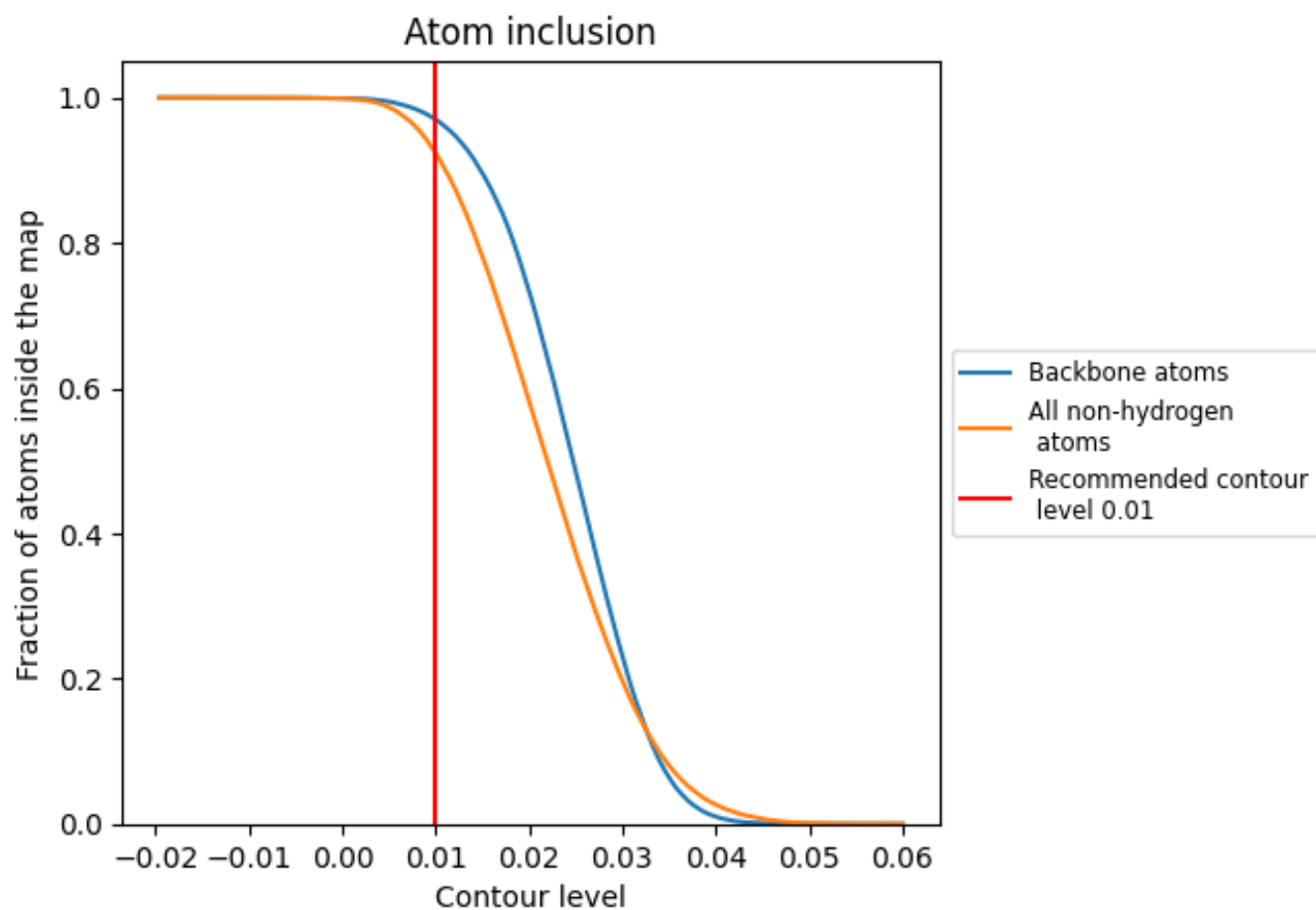
This section contains information regarding the fit between EMDB map EMD-13965 and PDB model 7QH6. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.01 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 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.