



Full wwPDB EM Validation Report ⓘ

Jul 3, 2024 – 05:22 am BST

PDB ID : 7OHQ
EMDB ID : EMD-12905
Title : Nog1-TAP associated immature ribosomal particle population C from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 3.10 Å(reported)
Based on initial model : 3JCT

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

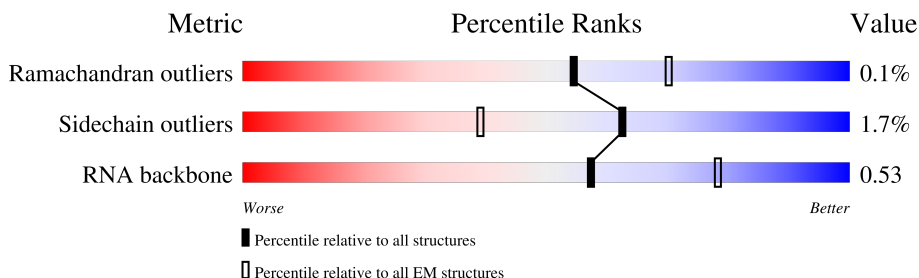
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


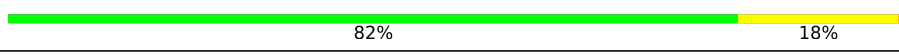

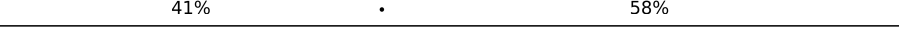

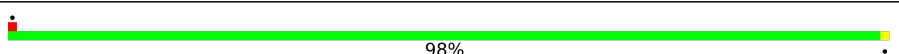
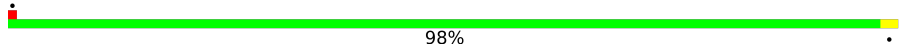

The reported resolution of this entry is 3.10 Å.

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.





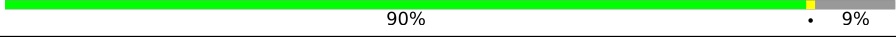

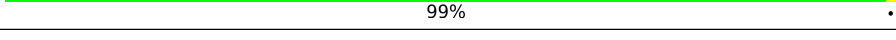
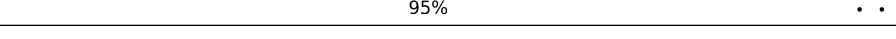
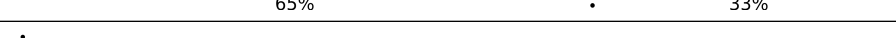
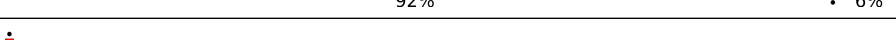
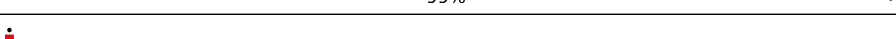
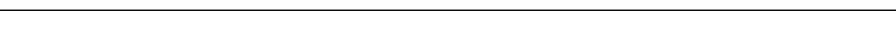






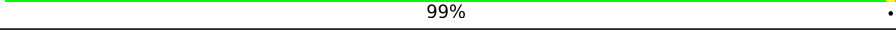
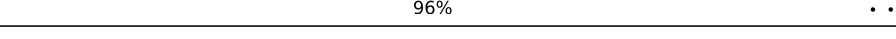
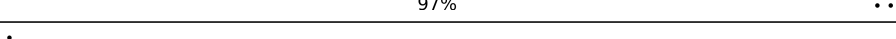
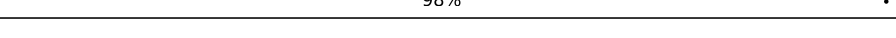
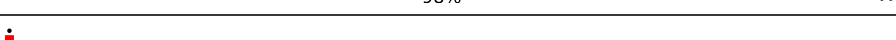
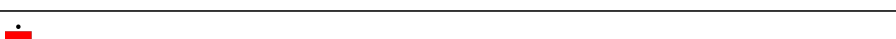



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	3396	
2	2	158	
3	3	121	
4	5	120	
5	6	232	
6	A	254	
7	B	387	
8	C	362	

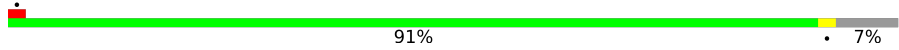
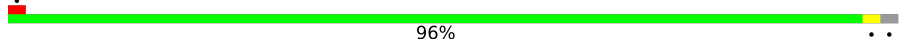
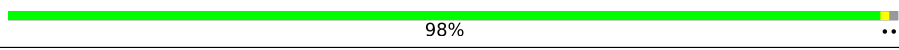
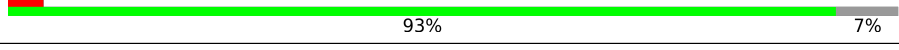
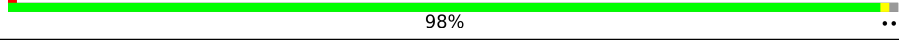
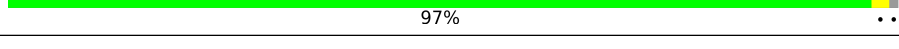
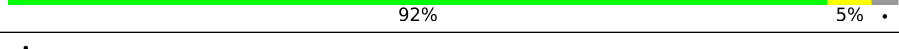
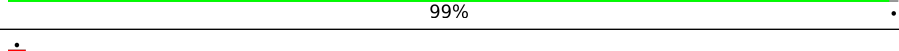
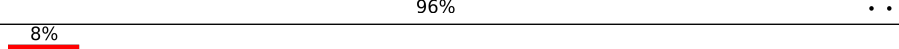
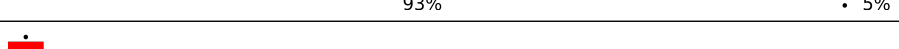
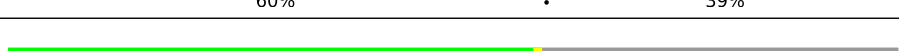









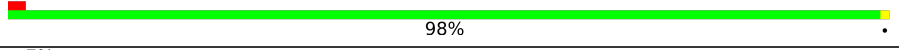


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Mol	Chain	Length	Quality of chain
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	J	174	
15	K	376	
16	L	199	
17	M	138	
18	N	204	
19	O	199	
20	P	184	
21	Q	186	
22	R	189	
23	S	172	
24	T	160	
25	U	121	
26	V	137	
27	W	236	
28	X	142	
29	Y	127	
30	Z	136	
31	a	149	
32	b	647	
33	c	105	

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Mol	Chain	Length	Quality of chain
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	m	486	
44	n	605	
45	o	220	
46	p	92	
47	q	455	
48	r	261	
49	s	520	
50	t	322	
51	u	199	
52	v	344	
53	w	203	
54	x	515	
55	y	245	
56	z	106	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 264865 atoms, of which 115934 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	3053	Total	C	H	N	O	P	0	0
			98146	29178	32819	11796	21300	3053		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 4 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	51	Total	C	H	N	O	S	0	0
			927	280	475	86	85	1		

- Molecule 5 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	6	65	Total	C	H	N	O	P	0	0
			2061	614	691	228	463	65		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	A	212	Total	C	H	N	O	S	0	0
			3314	1021	1684	325	283	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	386	Total	C	H	N	O	S	0	0
			6247	1956	3166	584	533	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	261	Total	C	H	N	O	S	0	0
			4178	1335	2066	372	403	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	156	Total	C	H	N	O	S	0	0
			2567	800	1328	222	216	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	233	Total	C	H	N	O	S	0	0
			3726	1159	1909	326	329	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 14 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	J	169	Total	C	H	N	O	S	0	0
			2737	847	1384	253	249	4		

- Molecule 15 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	K	252	Total	C	H	N	O	S	0	0
			4153	1312	2121	336	381	3		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	L	187	Total	C	H	N	O	S	0	0
			3057	934	1558	307	258			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	P	177	Total	C	H	N	O	S	0	0
			2845	871	1443	280	251			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Q	134	Total	C	H	N	O	S	0	0
			2151	659	1116	196	179	1		

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	R	156	Total	C	H	N	O		0	0
			2601	781	1343	265	212			

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	T	116	Total	C	H	N	O	S	0	0
			1902	584	978	176	161	3		

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	U	101	Total	C	H	N	O		0	0
			1617	519	816	131	151			

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 27 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 28 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	X	141	Total	C	H	N	O	S	0	0
			2288	705	1188	196	197	2		

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Y	126	Total	C	H	N	O		0	0
			2075	625	1082	192	176			

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	93	Total	C	H	N	O	S	0	0
			1512	479	777	130	125	1		

- Molecule 32 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	537	Total	C	H	N	O	S	0	0
			8784	2760	4427	763	811	23		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	97	Total	C	H	N	O	S	0	0
			1541	479	798	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	105	Total	C	H	N	O	S	0	0
			1761	544	905	163	148	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	127	Total	C	H	N	O	S	0	0
			2112	647	1092	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	g	112	Total	C	H	N	O	S	0	0
			1831	546	950	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	i	99	Total	C	H	N	O	S	0	0
			1621	481	850	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L38.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	m	461	Total	C	H	N	O	S	0	0
			7508	2350	3788	675	686	9		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	n	371	Total	C	H	N	O	S	0	0
			6139	1963	3109	523	534	10		

- Molecule 45 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	o	133	Total	C	H	N	O	S	0	0
			2267	716	1160	198	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	p	91	Total	C	H	N	O	S	0	0
			1434	429	740	138	121	6		

- Molecule 47 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	q	147	Total	C	H	N	O	S	0	0
			2501	778	1268	222	232	1		

- Molecule 48 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	s	53	Total	C	H	N	O	S	0	0
			935	274	499	90	70	2		

- Molecule 50 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	t	287	Total	C	H	N	O	S	0	0
			4762	1459	2456	427	417	3		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	u	150	Total	C	H	N	O	S	0	0
			2582	793	1317	253	210	9		

- Molecule 52 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	287	Total	C	H	N	O	S	0	0
			4718	1482	2400	408	412	16		

- Molecule 53 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 54 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	x	413	Total	C	H	N	O	S	0	0
			6438	2030	3207	583	598	20		

- Molecule 55 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	y	244	Total	C	H	N	O	S	0	0
			3685	1146	1836	319	377	7		

- Molecule 56 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	46	Total	C	H	N	O	0	0
			772	228	402	75	67		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	b	1	Total	Mg	0
			1	1	
57	m	1	Total	Mg	0
			1	1	

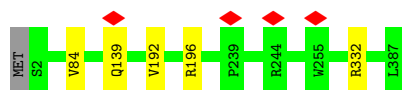
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	j	1	Total	Zn	0
			1	1	
58	p	1	Total	Zn	0
			1	1	
58	u	1	Total	Zn	0
			1	1	

A3180	C3181	A3187	U3195	U3196	U3198	U3207	A3213	C3217	A3218	G3219	G3224	C3228	U3078	A3245	G3246	G3247	C3092	C3093	U3100	G3101	A3129	U3269	U3270	A3273	G3276	U3281	G3289	A3294	U3304	A3307	A3316	U3319	U3334	A3335	U3341	A3342																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
C2867	U2868	U2869	A2872	U2873	U2874	U2875	U2876	G2877	U2878	C2879	A2887	U2888	C2889	G2898	G2901	U2921	G2922	U2923	U2924	C2925	A2926	C2927	C2928	U2935	A2936	A2940	A2945	A2946	G2947	G2952	U2953	U2954	U2955	A2956	G2957	C2970	A2971	U2978	U2979	U2980	U2981	C2982	C2983	C2984																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A2762	U2763	C2764	C2765	U2766	U2767	G2770	U2771	C2772	G2777	U2778	A2779	G2793	U2794	U2795	U2796	C2797	C2798	A2799	G2800	A2801	A2802	A2803	C2810	G2815	U2816	U2817	U2818	A2819	A2820	C2821	U2822	C2823	G2824	C2825	U2826	A2838	U2842	U2843	C2844	A2845	U2846	C2857	U2858	U2859	U2860	U2861	U2862	A2863	U2864	U2865	U2866																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
A2657	G2658	G2659	G2663	A2667	G2672	U2673	A2674	G2677	U2681	A2686	U2687	U2688	A2689	A2690	A2692	C2693	A2694	A2695	A2696	A2702	A2703	A2704	U2713	G2714	A2715	U2719	G2720	U2725	C2726	A2727	U2729	G2730	U2731	G2732	A2740	G2749	U2752	G2753	G2754	U2758	U2759	C2760	G2761																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
U2543	U2544	C2545	A2546	C2547	C2548	U2549	U2550	U2551	C2552	G2555	C2560	A2561	A2562	A2569	U2570	C2572	G2573	G2586	A2593	C2594	A2595	G2606	G2607	C2615	C	U	G	U2619	C2620	G2621	G2624	C2625	A2626	U2629	A2635	A2636	A2637	U2641	C2644	G2651	U2652	C2653	C2654	U2655	A2656																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G	U	G	G	G	A	C	U	U	C	G	C	G	C	A	G	U	A	A	A	A	C	C	A	U	C	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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	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</

- Molecule 7: 60S ribosomal protein L3

Chain B:  98%




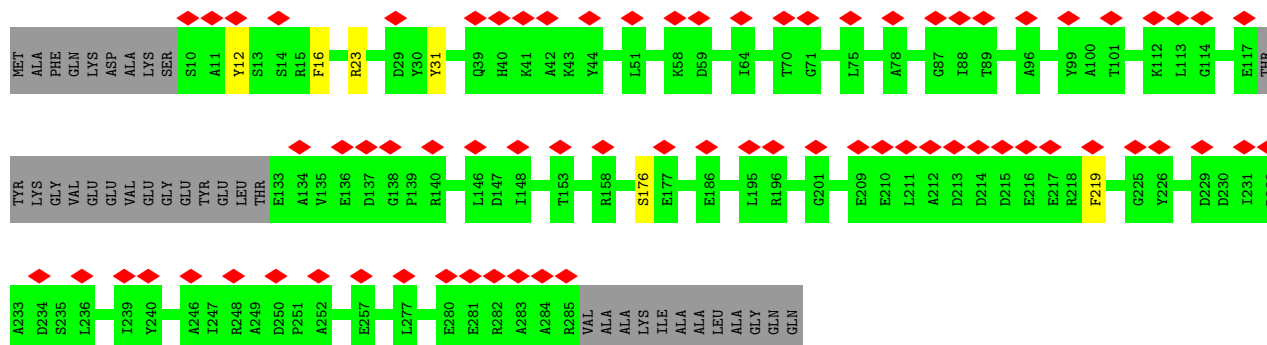
- Molecule 8: 60S ribosomal protein L4-A

Chain C:  98%



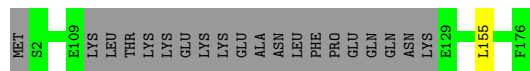
- Molecule 9: 60S ribosomal protein L5

Chain D:  25% 86% 12%




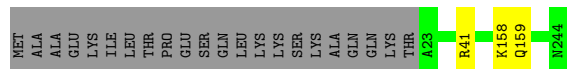
- Molecule 10: 60S ribosomal protein L6-A

Chain E:  88% 11%



- Molecule 11: 60S ribosomal protein L7-A

Chain F:  90% 9%

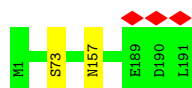


- Molecule 12: 60S ribosomal protein L8-A

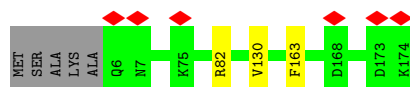
Chain G:  90% 9%



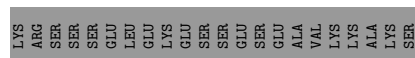
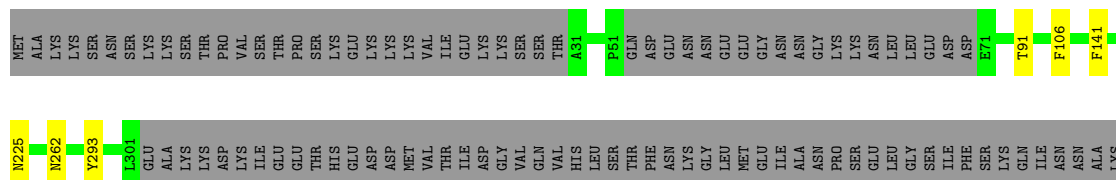
- Molecule 13: 60S ribosomal protein L9-A



- Molecule 14: 60S ribosomal protein L11-A



- Molecule 15: Proteasome-interacting protein CIC1



- Molecule 16: 60S ribosomal protein L13-A

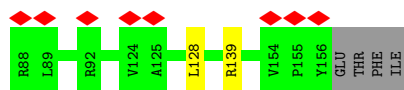


- Molecule 17: 60S ribosomal protein L14-A



- Molecule 18: 60S ribosomal protein L15-A





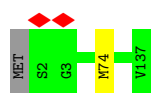
- Molecule 25: 60S ribosomal protein L22-A

Chain U: 81% 17%



- Molecule 26: 60S ribosomal protein L23-A

Chain V: 99% ..



- Molecule 27: Ribosome assembly factor MRT4

Chain W: 96% ..



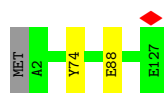
- Molecule 28: 60S ribosomal protein L25

Chain X: 97% ..



- Molecule 29: 60S ribosomal protein L26-A

Chain Y: 98% ..



- Molecule 30: 60S ribosomal protein L27-A

Chain Z: 98% ..




- Molecule 31: 60S ribosomal protein L28

Chain a:  62% 38%

MET PRO SER ARG ARG PHE THR LYS THR ARG LYS HIS HIS ARG GLY HIS VAL SER ALA GLY LYS GLY ARG ARG ILE GLY LYS HIS ARG LYS HIS PRO PRO GLY ARG ARG MET MET ALA GLY GLN HIS HIS HIS HIS ARG ARG ILE ASN MET MET ASP LYS TYR HIS PRO GLY TYR PHE GLY LYS VAL 957 Y60

A149

- Molecule 32: Nucleolar GTP-binding protein 1


Chain b:  81% 17%

M1 Q2 W5 K6 D7 N70 D73 E230 E256 N280 S350 Q351 S352 R353 I354 N355 N356 V357 L358 R369 V427 V432 N470 SER ASP ASP GLU GLU E476 E482 D487 N498 R499 K511 L524 T525 E532 E535 L538 M542

SER ALA LEU LEU ASP GLN LYS LYS ASN ARG ALA ALA ARG LYS ASN ARG TYR VAL GLN ARG GLY SER ASP ASP VAL VAL PHE GLY ASP ASP ASP ALA LEU THR ALA SER THR THR ASN GLY VAL SER ASP LYS LEU LEU ARG GLN THR ASP THR ARG LEU LEU GLY VAL ALA ASP GLY SER MET ARG SER LYS ALA


ASP ARG MET LYS MET GLU ARG ARG GLU GLU ASN ARG HIS LYS GLN GLU SER ASP ARG HIS ASN VAL VAL SER SER LYS HIS LEU PHE SER GLY LYS ARG GLY VAL GLY LYS LEU THR ASP PHE ARG

- Molecule 33: 60S ribosomal protein L30

Chain c:  91% 8%

MET ALA PRO VAL LYS SER GLN S9 N11 A105

- Molecule 34: 60S ribosomal protein L31-A

Chain d:  91% 7%

MET ALA GLY LEU LYS D6 K26 D47 E81 E82 E83 E110 GLU ASP ALA

- Molecule 35: 60S ribosomal protein L32

Chain e:  96% 4%


MET A2 H21 D39 L128 GLU ALA

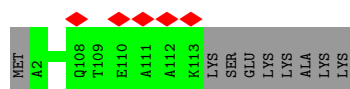
- Molecule 36: 60S ribosomal protein L33-A

Chain f:  98% 2%

MET A2 S28 L107

- Molecule 37: 60S ribosomal protein L34-A

Chain g:  93% 7%



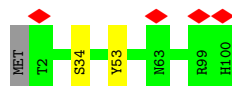
- Molecule 38: 60S ribosomal protein L35-A

Chain h:  98% ..




- Molecule 39: 60S ribosomal protein L36-A

Chain i:  97% ..



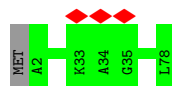
- Molecule 40: 60S ribosomal protein L37-A

Chain j:  92% 5% .



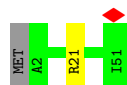
- Molecule 41: 60S ribosomal protein L38

Chain k:  99% .



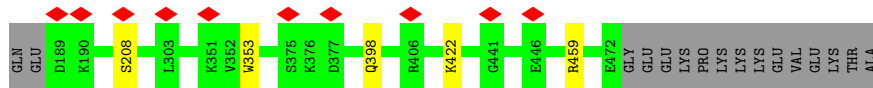
- Molecule 42: 60S ribosomal protein L39

Chain l:  96% ..

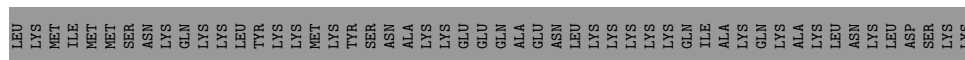
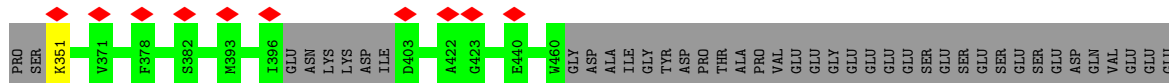
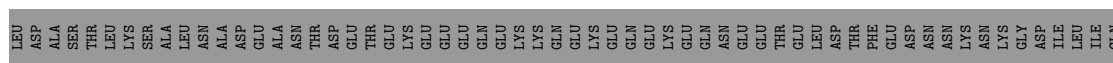
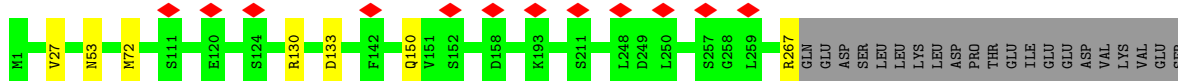


- Molecule 43: Nucleolar GTP-binding protein 2

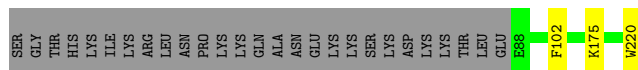
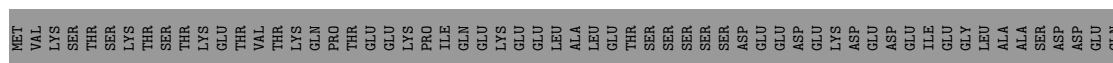
Chain m:  8% 93% . 5%



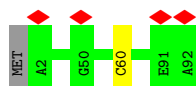
- Molecule 44: Pescadillo homolog



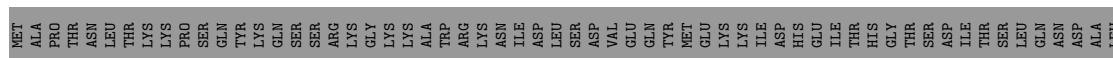
- Molecule 45: Ribosome biogenesis protein 15



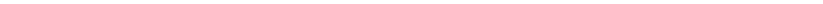
- Molecule 46: 60S ribosomal protein L43-A

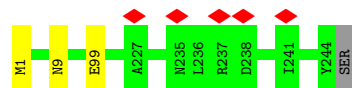


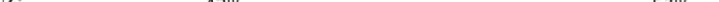
- Molecule 47: Ribosome biogenesis protein NOP53

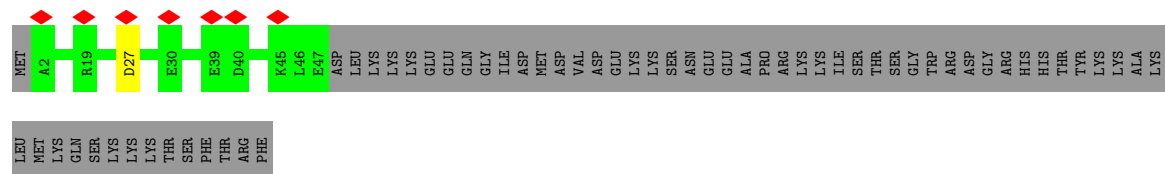




Chain x: 



Chain z:  7% 42% 57%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34162	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 ($e^-/\text{\AA}^2$)	84.67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.165	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	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: MG, 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	1	0.16	0/73123	0.74	30/113993 (0.0%)
2	2	0.16	0/3746	0.76	2/5832 (0.0%)
3	3	0.15	0/2883	0.75	1/4491 (0.0%)
4	5	0.25	0/455	0.35	0/596
5	6	0.17	0/1527	0.77	3/2371 (0.1%)
6	A	0.24	0/1662	0.44	0/2236
7	B	0.24	0/3152	0.43	0/4239
8	C	0.24	0/2801	0.42	0/3792
9	D	0.24	0/2158	0.40	0/2910
10	E	0.25	0/1260	0.42	0/1694
11	F	0.25	0/1821	0.41	0/2451
12	G	0.25	0/1849	0.42	0/2495
13	H	0.24	0/1539	0.43	0/2073
14	J	0.24	0/1374	0.43	0/1842
15	K	0.24	0/2066	0.42	0/2789
16	L	0.24	0/1524	0.43	0/2046
17	M	0.23	0/1074	0.41	0/1446
18	N	0.26	0/1757	0.43	0/2354
19	O	0.25	0/1585	0.39	0/2128
20	P	0.24	0/1424	0.42	0/1911
21	Q	0.25	0/1050	0.41	0/1419
22	R	0.23	0/1275	0.39	0/1702
23	S	0.24	0/1473	0.42	0/1980
24	T	0.25	0/937	0.44	0/1256
25	U	0.25	0/817	0.42	0/1108
26	V	0.25	0/1018	0.42	0/1369
27	W	0.24	0/1918	0.42	0/2586
28	X	0.24	0/1116	0.41	0/1503
29	Y	0.24	0/1004	0.40	0/1341
30	Z	0.26	0/1118	0.43	0/1497
31	a	0.25	0/751	0.40	0/1013
32	b	0.24	0/4435	0.40	0/5971

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	c	0.24	0/751	0.40	0/1008
34	d	0.23	0/870	0.41	0/1168
35	e	0.23	0/1041	0.41	0/1394
36	f	0.25	0/868	0.45	0/1168
37	g	0.23	0/891	0.40	0/1191
38	h	0.24	0/978	0.38	0/1301
39	i	0.23	0/778	0.38	0/1034
40	j	0.25	0/685	0.41	0/908
41	k	0.26	0/618	0.44	0/826
42	l	0.23	0/443	0.41	0/588
43	m	0.24	0/3794	0.43	0/5108
44	n	0.24	0/3101	0.40	0/4187
45	o	0.24	0/1129	0.40	0/1502
46	p	0.24	0/701	0.45	0/934
47	q	0.23	0/1254	0.42	0/1675
48	r	0.24	0/1892	0.44	0/2528
49	s	0.25	0/440	0.40	0/573
50	t	0.24	0/2333	0.43	0/3128
51	u	0.25	0/1287	0.40	0/1711
52	v	0.25	0/2361	0.42	0/3153
53	w	0.24	0/1471	0.40	0/1980
54	x	0.23	0/3313	0.42	0/4490
55	y	0.23	0/1872	0.44	0/2548
56	z	0.24	0/371	0.34	0/489
All	All	0.20	0/158934	0.62	36/231026 (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
11	F	0	1
30	Z	0	1
32	b	0	1
43	m	0	1
50	t	0	2
All	All	0	6

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2376	G	OP1-P-OP2	-6.80	109.39	119.60
1	1	1082	U	OP1-P-OP2	-6.79	109.41	119.60
2	2	1	A	OP1-P-OP2	-6.79	109.41	119.60
1	1	2501	U	OP1-P-OP2	-6.78	109.43	119.60
5	6	1	C	OP1-P-OP2	-6.77	109.45	119.60
3	3	1	G	OP1-P-OP2	-6.76	109.46	119.60
1	1	494	G	OP1-P-OP2	-6.75	109.48	119.60
1	1	1047	A	OP1-P-OP2	-6.74	109.48	119.60
1	1	2313	A	OP1-P-OP2	-6.74	109.48	119.60
1	1	2619	G	OP1-P-OP2	-6.74	109.49	119.60
1	1	2093	A	OP1-P-OP2	-6.73	109.50	119.60
5	6	227	C	OP1-P-OP2	-6.73	109.50	119.60
1	1	2943	G	OP1-P-OP2	-6.72	109.52	119.60
1	1	1	G	OP1-P-OP2	-6.71	109.54	119.60
1	1	1283	C	N3-C2-O2	-6.70	117.21	121.90
1	1	2861	U	C2-N1-C1'	6.41	125.40	117.70
1	1	2572	C	C2-N1-C1'	6.40	125.84	118.80
1	1	2257	C	C2-N1-C1'	6.35	125.78	118.80
1	1	1254	C	N3-C2-O2	-6.07	117.65	121.90
1	1	1239	C	N3-C2-O2	-6.06	117.66	121.90
1	1	2112	U	C2-N1-C1'	6.03	124.94	117.70
1	1	2760	C	C2-N1-C1'	5.78	125.16	118.80
1	1	2552	C	C2-N1-C1'	5.68	125.05	118.80
1	1	2928	C	N3-C2-O2	-5.68	117.93	121.90
2	2	83	C	C2-N1-C1'	5.62	124.99	118.80
1	1	2257	C	N1-C2-O2	5.50	122.20	118.90
1	1	2444	C	C2-N1-C1'	5.49	124.84	118.80
1	1	922	U	C2-N1-C1'	5.42	124.21	117.70
1	1	1711	C	N1-C2-O2	5.42	122.15	118.90
1	1	2572	C	N1-C2-O2	5.39	122.13	118.90
1	1	3058	U	C2-N1-C1'	5.38	124.16	117.70
1	1	1805	C	N3-C2-O2	-5.34	118.16	121.90
5	6	1	C	O4'-C1'-N1	5.21	112.37	108.20
1	1	2928	C	N1-C2-O2	5.15	121.99	118.90
1	1	1805	C	C6-N1-C2	-5.10	118.26	120.30
1	1	1254	C	N1-C2-O2	5.04	121.93	118.90

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	F	158	LYS	Peptide
30	Z	104	PRO	Peptide

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Mol	Chain	Res	Type	Group
32	b	369	ARG	Peptide
43	m	77	TRP	Peptide
50	t	220	ASN	Peptide
50	t	221	GLU	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	
4	5	49/120 (41%)	49 (100%)	0	0	100	100
6	A	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
7	B	384/387 (99%)	358 (93%)	26 (7%)	0	100	100
8	C	359/362 (99%)	336 (94%)	23 (6%)	0	100	100
9	D	257/297 (86%)	246 (96%)	11 (4%)	0	100	100
10	E	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
11	F	220/244 (90%)	210 (96%)	9 (4%)	1 (0%)	29	64
12	G	231/256 (90%)	212 (92%)	19 (8%)	0	100	100
13	H	189/191 (99%)	177 (94%)	12 (6%)	0	100	100
14	J	167/174 (96%)	152 (91%)	15 (9%)	0	100	100
15	K	248/376 (66%)	231 (93%)	17 (7%)	0	100	100
16	L	185/199 (93%)	174 (94%)	10 (5%)	1 (0%)	29	64
17	M	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
18	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	29	64
19	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	173/184 (94%)	168 (97%)	5 (3%)	0	100	100
21	Q	132/186 (71%)	131 (99%)	1 (1%)	0	100	100
22	R	154/189 (82%)	147 (96%)	7 (4%)	0	100	100
23	S	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
24	T	110/160 (69%)	98 (89%)	12 (11%)	0	100	100
25	U	99/121 (82%)	95 (96%)	4 (4%)	0	100	100
26	V	134/137 (98%)	129 (96%)	5 (4%)	0	100	100
27	W	232/236 (98%)	219 (94%)	12 (5%)	1 (0%)	34	69
28	X	139/142 (98%)	133 (96%)	6 (4%)	0	100	100
29	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
30	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
31	a	91/149 (61%)	86 (94%)	5 (6%)	0	100	100
32	b	533/647 (82%)	490 (92%)	43 (8%)	0	100	100
33	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
34	d	103/113 (91%)	97 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
36	f	104/107 (97%)	95 (91%)	9 (9%)	0	100	100
37	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
38	h	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
39	i	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
40	j	83/88 (94%)	78 (94%)	5 (6%)	0	100	100
41	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
42	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
43	m	457/486 (94%)	420 (92%)	36 (8%)	1 (0%)	47	79
44	n	365/605 (60%)	340 (93%)	25 (7%)	0	100	100
45	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
46	p	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
47	q	143/455 (31%)	130 (91%)	13 (9%)	0	100	100
48	r	224/261 (86%)	199 (89%)	25 (11%)	0	100	100
49	s	49/520 (9%)	46 (94%)	3 (6%)	0	100	100
50	t	283/322 (88%)	261 (92%)	20 (7%)	2 (1%)	22	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	u	148/199 (74%)	143 (97%)	5 (3%)	0	100	100
52	v	283/344 (82%)	270 (95%)	13 (5%)	0	100	100
53	w	178/203 (88%)	174 (98%)	4 (2%)	0	100	100
54	x	409/515 (79%)	391 (96%)	18 (4%)	0	100	100
55	y	242/245 (99%)	229 (95%)	13 (5%)	0	100	100
56	z	44/106 (42%)	44 (100%)	0	0	100	100
All	All	9407/11749 (80%)	8864 (94%)	536 (6%)	7 (0%)	54	83

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	159	GLN
50	t	220	ASN
50	t	221	GLU
18	N	146	ALA
43	m	208	SER
16	L	63	VAL
27	W	127	PRO

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	
4	5	48/106 (45%)	46 (96%)	2 (4%)	30	62
6	A	166/196 (85%)	166 (100%)	0	100	100
7	B	322/323 (100%)	317 (98%)	5 (2%)	62	84
8	C	288/289 (100%)	282 (98%)	6 (2%)	53	79
9	D	219/245 (89%)	213 (97%)	6 (3%)	44	74
10	E	134/153 (88%)	133 (99%)	1 (1%)	84	93
11	F	186/205 (91%)	185 (100%)	1 (0%)	88	94
12	G	191/208 (92%)	189 (99%)	2 (1%)	76	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	H	171/171 (100%)	169 (99%)	2 (1%)	71	88
14	J	147/150 (98%)	144 (98%)	3 (2%)	55	80
15	K	233/346 (67%)	227 (97%)	6 (3%)	46	74
16	L	149/159 (94%)	147 (99%)	2 (1%)	69	87
17	M	108/109 (99%)	108 (100%)	0	100	100
18	N	175/176 (99%)	172 (98%)	3 (2%)	60	83
19	O	160/162 (99%)	159 (99%)	1 (1%)	86	94
20	P	142/146 (97%)	138 (97%)	4 (3%)	43	73
21	Q	110/151 (73%)	110 (100%)	0	100	100
22	R	129/154 (84%)	126 (98%)	3 (2%)	50	77
23	S	155/156 (99%)	151 (97%)	4 (3%)	46	74
24	T	100/137 (73%)	98 (98%)	2 (2%)	55	80
25	U	88/107 (82%)	85 (97%)	3 (3%)	37	69
26	V	104/105 (99%)	103 (99%)	1 (1%)	76	90
27	W	211/213 (99%)	205 (97%)	6 (3%)	43	73
28	X	117/118 (99%)	114 (97%)	3 (3%)	46	74
29	Y	109/110 (99%)	107 (98%)	2 (2%)	59	82
30	Z	115/116 (99%)	114 (99%)	1 (1%)	78	91
31	a	76/119 (64%)	75 (99%)	1 (1%)	69	87
32	b	482/573 (84%)	473 (98%)	9 (2%)	57	81
33	c	81/88 (92%)	80 (99%)	1 (1%)	71	88
34	d	92/97 (95%)	90 (98%)	2 (2%)	52	78
35	e	109/111 (98%)	107 (98%)	2 (2%)	59	82
36	f	90/91 (99%)	89 (99%)	1 (1%)	73	89
37	g	95/103 (92%)	95 (100%)	0	100	100
38	h	104/105 (99%)	103 (99%)	1 (1%)	76	90
39	i	81/82 (99%)	79 (98%)	2 (2%)	47	75
40	j	69/71 (97%)	65 (94%)	4 (6%)	20	51
41	k	68/69 (99%)	68 (100%)	0	100	100
42	l	45/46 (98%)	44 (98%)	1 (2%)	52	78
43	m	408/428 (95%)	401 (98%)	7 (2%)	60	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	n	334/548 (61%)	326 (98%)	8 (2%)	49	76
45	o	118/199 (59%)	115 (98%)	3 (2%)	47	75
46	p	71/72 (99%)	70 (99%)	1 (1%)	67	86
47	q	137/420 (33%)	136 (99%)	1 (1%)	84	93
48	r	203/229 (89%)	196 (97%)	7 (3%)	37	69
49	s	47/445 (11%)	45 (96%)	2 (4%)	29	62
50	t	256/287 (89%)	251 (98%)	5 (2%)	55	80
51	u	133/180 (74%)	131 (98%)	2 (2%)	65	85
52	v	258/309 (84%)	257 (100%)	1 (0%)	91	96
53	w	161/179 (90%)	156 (97%)	5 (3%)	40	70
54	x	361/451 (80%)	358 (99%)	3 (1%)	81	92
55	y	210/211 (100%)	207 (99%)	3 (1%)	67	86
56	z	40/95 (42%)	39 (98%)	1 (2%)	47	75
All	All	8206/10119 (81%)	8064 (98%)	142 (2%)	62	83

All (142) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	5	72	ARG
4	5	78	MET
7	B	84	VAL
7	B	139	GLN
7	B	192	VAL
7	B	196	ARG
7	B	332	ARG
8	C	120	TYR
8	C	182	LEU
8	C	246	ARG
8	C	255	PHE
8	C	306	THR
8	C	332	LYS
9	D	12	TYR
9	D	16	PHE
9	D	23	ARG
9	D	31	TYR
9	D	176	SER
9	D	219	PHE

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Mol	Chain	Res	Type
10	E	155	LEU
11	F	41	ARG
12	G	84	ARG
12	G	150	LEU
13	H	73	SER
13	H	157	ASN
14	J	82	ARG
14	J	130	VAL
14	J	163	PHE
15	K	91	THR
15	K	106	PHE
15	K	141	PHE
15	K	225	ASN
15	K	262	ASN
15	K	293	TYR
16	L	55	ARG
16	L	153	ASP
18	N	73	ARG
18	N	83	LYS
18	N	96	ARG
19	O	46	GLU
20	P	3	ARG
20	P	69	ARG
20	P	92	GLN
20	P	180	LYS
22	R	58	HIS
22	R	74	ARG
22	R	138	LEU
23	S	96	ASP
23	S	136	LYS
23	S	171	PHE
23	S	172	TYR
24	T	128	LEU
24	T	139	ARG
25	U	21	SER
25	U	52	ASN
25	U	104	ARG
26	V	74	MET
27	W	3	ARG
27	W	60	TRP
27	W	67	MET
27	W	96	CYS

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Mol	Chain	Res	Type
27	W	139	GLU
27	W	154	ASP
28	X	45	LYS
28	X	73	MET
28	X	137	ASN
29	Y	74	TYR
29	Y	88	GLU
30	Z	67	LYS
31	a	60	TYR
32	b	5	TRP
32	b	70	ASN
32	b	280	ASN
32	b	427	TRP
32	b	432	MET
32	b	482	GLU
32	b	499	ARG
32	b	535	MET
32	b	542	MET
33	c	11	ASN
34	d	26	LYS
34	d	47	ASP
35	e	21	HIS
35	e	39	ASP
36	f	28	SER
38	h	115	LYS
39	i	34	SER
39	i	53	TYR
40	j	25	ARG
40	j	37	CYS
40	j	58	THR
40	j	75	LYS
42	l	21	ARG
43	m	62	GLN
43	m	147	ARG
43	m	151	ARG
43	m	353	TRP
43	m	398	GLN
43	m	422	LYS
43	m	459	ARG
44	n	27	VAL
44	n	53	ASN
44	n	72	MET

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Mol	Chain	Res	Type
44	n	130	ARG
44	n	133	ASP
44	n	150	GLN
44	n	267	ARG
44	n	351	LYS
45	o	102	PHE
45	o	175	LYS
45	o	220	TRP
46	p	60	CYS
47	q	228	ASN
48	r	17	ARG
48	r	54	ARG
48	r	133	MET
48	r	162	THR
48	r	164	ARG
48	r	183	ASN
48	r	210	THR
49	s	33	MET
49	s	47	ASP
50	t	44	GLN
50	t	74	ARG
50	t	216	TYR
50	t	223	GLU
50	t	261	PHE
51	u	81	TYR
51	u	100	ARG
52	v	217	ARG
53	w	29	PHE
53	w	70	MET
53	w	131	LYS
53	w	158	TRP
53	w	162	VAL
54	x	194	TRP
54	x	293	TYR
54	x	406	ASN
55	y	1	MET
55	y	9	ASN
55	y	99	GLU
56	z	27	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
6	A	38	HIS
6	A	140	ASN
6	A	209	HIS
7	B	173	GLN
7	B	198	HIS
7	B	345	ASN
8	C	48	GLN
8	C	307	GLN
11	F	172	ASN
12	G	59	GLN
12	G	85	ASN
13	H	163	GLN
14	J	109	HIS
15	K	262	ASN
16	L	137	GLN
18	N	87	GLN
18	N	95	GLN
20	P	121	GLN
21	Q	58	ASN
22	R	92	GLN
25	U	101	ASN
28	X	19	ASN
29	Y	4	GLN
32	b	70	ASN
32	b	72	ASN
32	b	78	HIS
32	b	152	GLN
32	b	177	ASN
32	b	356	ASN
34	d	57	GLN
38	h	59	ASN
41	k	40	GLN
44	n	53	ASN
45	o	130	ASN
48	r	224	ASN
48	r	256	ASN
49	s	7	GLN
51	u	5	GLN
51	u	130	ASN
52	v	82	ASN
53	w	151	ASN
53	w	157	GLN
53	w	191	ASN

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Mol	Chain	Res	Type
53	w	198	ASN
54	x	208	ASN
54	x	321	HIS
55	y	11	ASN
55	y	79	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3044/3396 (89%)	615 (20%)	78 (2%)
2	2	157/158 (99%)	27 (17%)	2 (1%)
3	3	120/121 (99%)	16 (13%)	2 (1%)
5	6	64/232 (27%)	21 (32%)	5 (7%)
All	All	3385/3907 (86%)	679 (20%)	87 (2%)

All (679) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	13	A
1	1	14	U
1	1	26	A
1	1	40	A
1	1	41	G
1	1	43	A
1	1	45	A
1	1	49	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	76	G
1	1	92	G
1	1	96	G
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G

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Mol	Chain	Res	Type
1	1	148	G
1	1	156	G
1	1	157	A
1	1	161	G
1	1	166	C
1	1	173	G
1	1	187	A
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	213	A
1	1	218	G
1	1	219	A
1	1	221	A
1	1	240	U
1	1	241	G
1	1	243	G
1	1	245	U
1	1	248	U
1	1	249	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	266	A
1	1	269	G
1	1	283	G
1	1	284	A
1	1	285	A
1	1	286	U
1	1	295	A
1	1	305	U
1	1	315	C
1	1	323	A
1	1	325	A
1	1	329	U
1	1	352	A
1	1	361	A
1	1	370	U
1	1	374	A
1	1	375	A
1	1	376	G

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Mol	Chain	Res	Type
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	421	G
1	1	422	A
1	1	429	U
1	1	438	A
1	1	440	A
1	1	521	A
1	1	529	A
1	1	535	G
1	1	536	U
1	1	546	C
1	1	547	G
1	1	552	G
1	1	557	A
1	1	559	A
1	1	578	A
1	1	579	G
1	1	589	A
1	1	592	A
1	1	604	G
1	1	609	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	636	C
1	1	638	C
1	1	641	C
1	1	643	U
1	1	644	G
1	1	645	A
1	1	646	A
1	1	647	A
1	1	649	A
1	1	650	C
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A

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Mol	Chain	Res	Type
1	1	715	A
1	1	716	A
1	1	720	A
1	1	721	G
1	1	722	G
1	1	725	G
1	1	735	A
1	1	761	A
1	1	764	U
1	1	765	C
1	1	766	U
1	1	767	U
1	1	768	C
1	1	769	G
1	1	777	U
1	1	779	G
1	1	780	A
1	1	785	G
1	1	787	G
1	1	808	A
1	1	817	A
1	1	836	A
1	1	850	U
1	1	857	G
1	1	861	C
1	1	875	G
1	1	879	U
1	1	880	G
1	1	895	A
1	1	896	A
1	1	897	U
1	1	907	G
1	1	908	G
1	1	914	A
1	1	916	G
1	1	917	A
1	1	944	C
1	1	957	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	964	G

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Mol	Chain	Res	Type
1	1	965	A
1	1	974	G
1	1	976	U
1	1	977	C
1	1	979	U
1	1	980	A
1	1	981	U
1	1	984	G
1	1	991	G
1	1	992	A
1	1	997	A
1	1	999	G
1	1	1000	C
1	1	1003	A
1	1	1048	A
1	1	1050	U
1	1	1051	U
1	1	1057	A
1	1	1058	U
1	1	1063	G
1	1	1064	A
1	1	1065	A
1	1	1066	G
1	1	1072	G
1	1	1074	U
1	1	1087	G
1	1	1093	A
1	1	1094	U
1	1	1095	U
1	1	1097	G
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1111	U
1	1	1116	G
1	1	1117	G
1	1	1118	C
1	1	1123	U
1	1	1127	G
1	1	1129	A
1	1	1132	C
1	1	1153	A

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Mol	Chain	Res	Type
1	1	1155	C
1	1	1180	A
1	1	1181	U
1	1	1189	C
1	1	1190	A
1	1	1191	U
1	1	1192	C
1	1	1193	A
1	1	1196	C
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1201	C
1	1	1203	A
1	1	1206	G
1	1	1207	G
1	1	1222	G
1	1	1234	G
1	1	1241	U
1	1	1242	G
1	1	1243	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1251	A
1	1	1252	A
1	1	1253	U
1	1	1259	A
1	1	1263	A
1	1	1270	A
1	1	1272	C
1	1	1278	A
1	1	1286	A
1	1	1287	A
1	1	1303	A
1	1	1304	A
1	1	1307	G
1	1	1308	A
1	1	1325	U
1	1	1330	A
1	1	1348	U
1	1	1349	G

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Mol	Chain	Res	Type
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1356	U
1	1	1357	G
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1406	A
1	1	1408	G
1	1	1417	G
1	1	1419	A
1	1	1434	G
1	1	1436	U
1	1	1437	C
1	1	1455	U
1	1	1481	A
1	1	1483	G
1	1	1487	G
1	1	1496	C
1	1	1508	C
1	1	1555	U
1	1	1560	G
1	1	1561	G
1	1	1562	C
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1572	U
1	1	1573	G
1	1	1575	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1583	A
1	1	1588	A
1	1	1589	A
1	1	1593	A
1	1	1607	U

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Mol	Chain	Res	Type
1	1	1613	A
1	1	1620	U
1	1	1629	U
1	1	1638	A
1	1	1639	C
1	1	1643	A
1	1	1647	A
1	1	1683	A
1	1	1687	U
1	1	1688	U
1	1	1694	U
1	1	1713	G
1	1	1716	U
1	1	1717	U
1	1	1724	U
1	1	1725	C
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1760	A
1	1	1763	U
1	1	1765	U
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1796	G
1	1	1797	A
1	1	1808	G
1	1	1812	G
1	1	1813	A
1	1	1816	A
1	1	1817	G
1	1	1820	U
1	1	1821	U
1	1	1839	A
1	1	1841	A
1	1	1849	C
1	1	1851	G
1	1	1863	G
1	1	1866	C
1	1	1878	G
1	1	1906	G

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Mol	Chain	Res	Type
1	1	1909	A
1	1	1952	G
1	1	2094	C
1	1	2100	A
1	1	2102	U
1	1	2114	C
1	1	2121	G
1	1	2122	G
1	1	2131	A
1	1	2158	A
1	1	2163	C
1	1	2167	A
1	1	2169	G
1	1	2188	A
1	1	2191	U
1	1	2192	C
1	1	2193	U
1	1	2194	G
1	1	2195	C
1	1	2205	U
1	1	2207	A
1	1	2208	A
1	1	2210	G
1	1	2223	A
1	1	2239	G
1	1	2243	A
1	1	2244	A
1	1	2246	G
1	1	2247	G
1	1	2248	C
1	1	2249	G
1	1	2250	G
1	1	2264	U
1	1	2265	C
1	1	2266	U
1	1	2267	C
1	1	2270	A
1	1	2271	A
1	1	2274	U
1	1	2277	C
1	1	2278	C
1	1	2279	A

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Mol	Chain	Res	Type
1	1	2316	G
1	1	2318	U
1	1	2335	G
1	1	2336	U
1	1	2371	G
1	1	2378	C
1	1	2388	U
1	1	2393	G
1	1	2397	A
1	1	2398	A
1	1	2401	A
1	1	2402	A
1	1	2404	A
1	1	2410	U
1	1	2411	U
1	1	2412	G
1	1	2413	A
1	1	2414	G
1	1	2418	G
1	1	2419	A
1	1	2433	U
1	1	2444	C
1	1	2502	A
1	1	2503	G
1	1	2507	C
1	1	2514	U
1	1	2522	G
1	1	2523	A
1	1	2533	G
1	1	2536	A
1	1	2538	U
1	1	2540	A
1	1	2541	U
1	1	2542	U
1	1	2543	U
1	1	2544	U
1	1	2546	C
1	1	2547	A
1	1	2548	C
1	1	2549	G
1	1	2550	U
1	1	2552	C

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Mol	Chain	Res	Type
1	1	2555	G
1	1	2560	C
1	1	2561	A
1	1	2562	A
1	1	2570	U
1	1	2573	G
1	1	2586	G
1	1	2593	A
1	1	2594	C
1	1	2595	A
1	1	2606	G
1	1	2607	G
1	1	2621	G
1	1	2625	C
1	1	2626	A
1	1	2629	U
1	1	2635	A
1	1	2636	A
1	1	2641	U
1	1	2644	C
1	1	2651	G
1	1	2652	U
1	1	2653	C
1	1	2654	C
1	1	2655	U
1	1	2656	A
1	1	2657	A
1	1	2659	G
1	1	2663	G
1	1	2667	A
1	1	2672	G
1	1	2674	A
1	1	2677	G
1	1	2681	U
1	1	2686	A
1	1	2688	U
1	1	2690	G
1	1	2691	A
1	1	2692	A
1	1	2693	C
1	1	2694	A
1	1	2696	A

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Mol	Chain	Res	Type
1	1	2702	A
1	1	2704	A
1	1	2713	U
1	1	2714	G
1	1	2715	A
1	1	2719	U
1	1	2720	G
1	1	2725	U
1	1	2726	C
1	1	2727	A
1	1	2728	G
1	1	2729	U
1	1	2730	G
1	1	2731	U
1	1	2732	G
1	1	2740	A
1	1	2749	G
1	1	2752	U
1	1	2754	G
1	1	2758	A
1	1	2759	U
1	1	2762	A
1	1	2763	U
1	1	2764	C
1	1	2766	U
1	1	2767	U
1	1	2770	G
1	1	2771	U
1	1	2772	C
1	1	2777	G
1	1	2778	G
1	1	2779	A
1	1	2793	G
1	1	2794	G
1	1	2795	U
1	1	2796	G
1	1	2798	C
1	1	2799	A
1	1	2800	G
1	1	2801	A
1	1	2802	A
1	1	2803	A

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Mol	Chain	Res	Type
1	1	2810	C
1	1	2815	G
1	1	2817	A
1	1	2818	U
1	1	2819	A
1	1	2820	A
1	1	2821	C
1	1	2822	U
1	1	2824	G
1	1	2826	U
1	1	2838	A
1	1	2842	U
1	1	2844	C
1	1	2845	A
1	1	2846	U
1	1	2858	U
1	1	2859	U
1	1	2861	U
1	1	2863	G
1	1	2865	U
1	1	2866	U
1	1	2867	C
1	1	2868	U
1	1	2869	U
1	1	2872	A
1	1	2873	U
1	1	2875	U
1	1	2876	C
1	1	2877	G
1	1	2878	G
1	1	2879	C
1	1	2887	A
1	1	2889	C
1	1	2898	G
1	1	2901	G
1	1	2921	U
1	1	2923	U
1	1	2925	C
1	1	2926	A
1	1	2935	U
1	1	2936	A
1	1	2945	G

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Mol	Chain	Res	Type
1	1	2947	G
1	1	2952	G
1	1	2953	U
1	1	2954	U
1	1	2955	U
1	1	2956	A
1	1	2957	G
1	1	2970	C
1	1	2971	A
1	1	2978	U
1	1	2980	U
1	1	2981	U
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2995	A
1	1	2996	U
1	1	2997	G
1	1	3003	G
1	1	3012	A
1	1	3017	A
1	1	3022	G
1	1	3026	G
1	1	3029	A
1	1	3030	G
1	1	3031	G
1	1	3032	A
1	1	3059	G
1	1	3078	U
1	1	3079	U
1	1	3086	A
1	1	3092	C
1	1	3093	C
1	1	3100	U
1	1	3101	G
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3163	A
1	1	3164	C

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Mol	Chain	Res	Type
1	1	3165	A
1	1	3170	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3198	U
1	1	3207	U
1	1	3213	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3224	G
1	1	3229	G
1	1	3245	A
1	1	3247	G
1	1	3253	G
1	1	3259	U
1	1	3260	G
1	1	3266	G
1	1	3270	U
1	1	3273	A
1	1	3276	G
1	1	3281	U
1	1	3289	G
1	1	3294	A
1	1	3304	U
1	1	3307	A
1	1	3316	A
1	1	3319	U
1	1	3334	U
1	1	3335	A
1	1	3341	U
1	1	3342	A
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3354	U

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Mol	Chain	Res	Type
1	1	3355	U
1	1	3369	G
1	1	3378	C
1	1	3389	U
2	2	16	G
2	2	34	U
2	2	35	C
2	2	39	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	71	A
2	2	72	A
2	2	80	A
2	2	81	U
2	2	82	U
2	2	83	C
2	2	84	C
2	2	86	U
2	2	90	U
2	2	95	G
2	2	100	U
2	2	104	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	126	A
2	2	151	C
3	3	7	G
3	3	22	A
3	3	27	A
3	3	49	G
3	3	53	U
3	3	54	U
3	3	65	G
3	3	72	A
3	3	74	C
3	3	76	A
3	3	87	G

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Mol	Chain	Res	Type
3	3	95	A
3	3	102	A
3	3	112	G
3	3	113	C
3	3	121	U
5	6	2	C
5	6	5	C
5	6	6	U
5	6	7	C
5	6	8	A
5	6	14	U
5	6	16	U
5	6	17	G
5	6	24	A
5	6	34	A
5	6	37	C
5	6	40	U
5	6	41	G
5	6	52	G
5	6	53	A
5	6	54	A
5	6	56	U
5	6	57	U
5	6	59	C
5	6	231	A
5	6	232	A

All (87) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1	G
1	1	13	A
1	1	40	A
1	1	116	A
1	1	160	G
1	1	284	A
1	1	545	U
1	1	645	A
1	1	649	A
1	1	720	A
1	1	765	C
1	1	849	C

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Mol	Chain	Res	Type
1	1	916	G
1	1	960	U
1	1	999	G
1	1	1057	A
1	1	1064	A
1	1	1097	G
1	1	1102	A
1	1	1103	A
1	1	1128	U
1	1	1205	A
1	1	1241	U
1	1	1302	A
1	1	1307	G
1	1	1329	U
1	1	1355	A
1	1	1405	U
1	1	1482	A
1	1	1567	U
1	1	1568	U
1	1	1570	U
1	1	1579	C
1	1	1581	C
1	1	1716	U
1	1	1816	A
1	1	2101	C
1	1	2166	A
1	1	2209	U
1	1	2243	A
1	1	2245	C
1	1	2263	C
1	1	2269	U
1	1	2317	A
1	1	2392	C
1	1	2501	U
1	1	2513	U
1	1	2537	U
1	1	2541	U
1	1	2569	A
1	1	2593	A
1	1	2624	G
1	1	2625	C
1	1	2651	G

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Mol	Chain	Res	Type
1	1	2652	U
1	1	2658	G
1	1	2690	G
1	1	2728	G
1	1	2753	G
1	1	2761	G
1	1	2770	G
1	1	2795	U
1	1	2802	A
1	1	2817	A
1	1	2857	C
1	1	2868	U
1	1	2875	U
1	1	2946	A
1	1	2954	U
1	1	3030	G
1	1	3078	U
1	1	3195	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3350	C
1	1	3351	U
1	1	3353	G
2	2	123	G
2	2	125	U
3	3	52	G
3	3	86	U
5	6	1	C
5	6	5	C
5	6	16	U
5	6	23	U
5	6	56	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 5 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

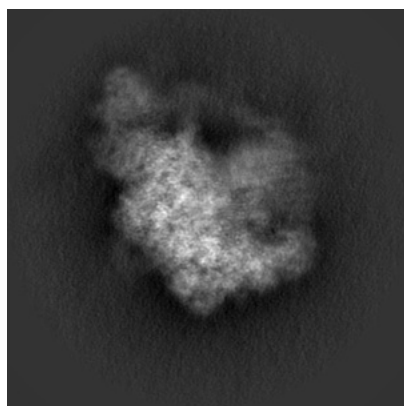
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12905. These allow visual inspection of the internal detail of the map and identification of artifacts.

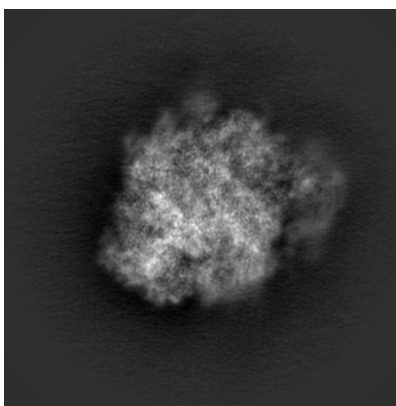
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

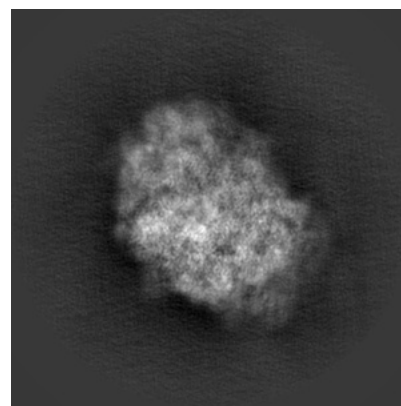
6.1.1 Primary map



X

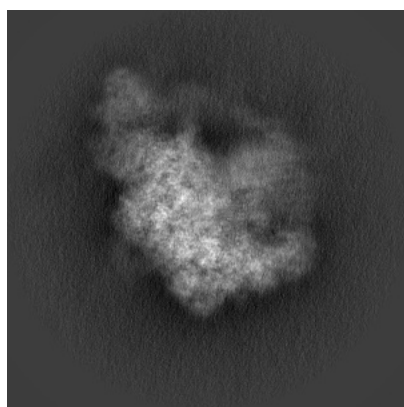


Y

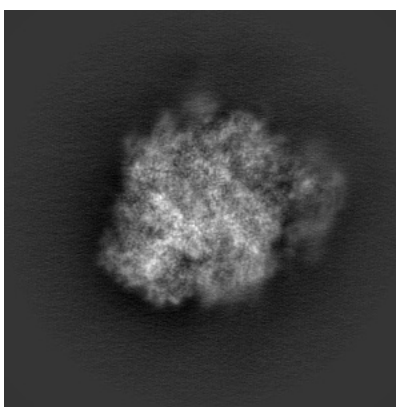


Z

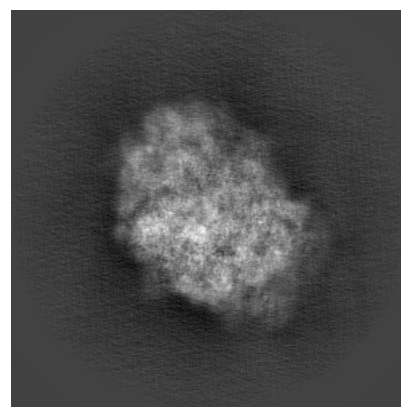
6.1.2 Raw map



X



Y

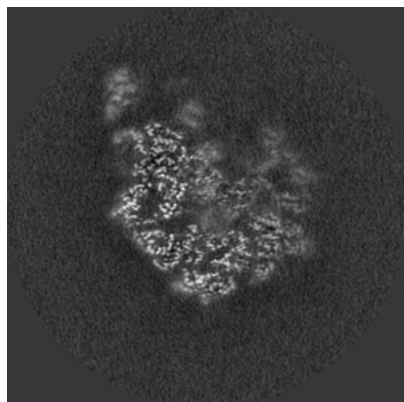


Z

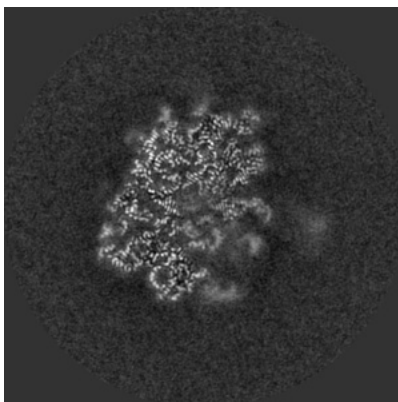
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

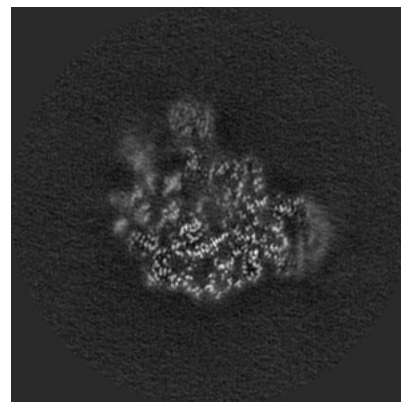
6.2.1 Primary map



X Index: 200

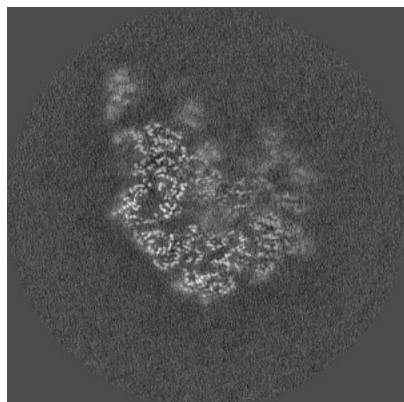


Y Index: 200

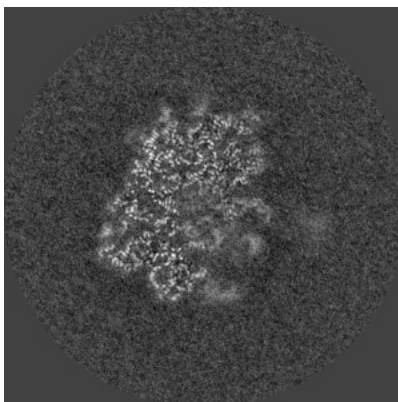


Z Index: 200

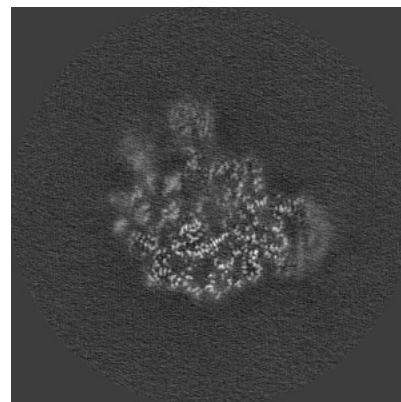
6.2.2 Raw map



X Index: 200



Y Index: 200

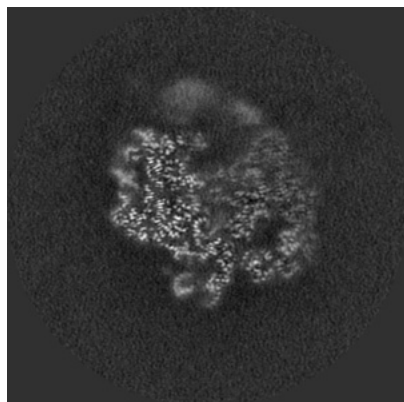


Z Index: 200

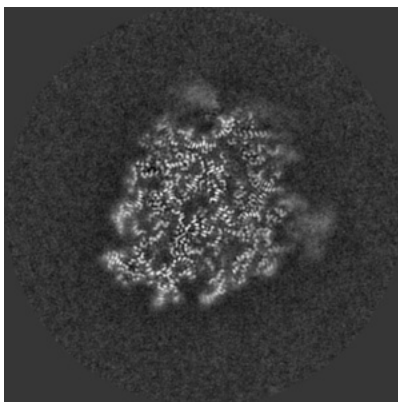
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

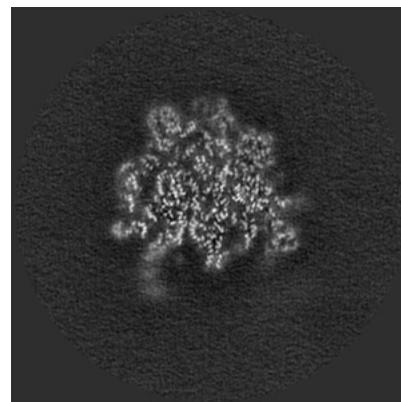
6.3.1 Primary map



X Index: 183

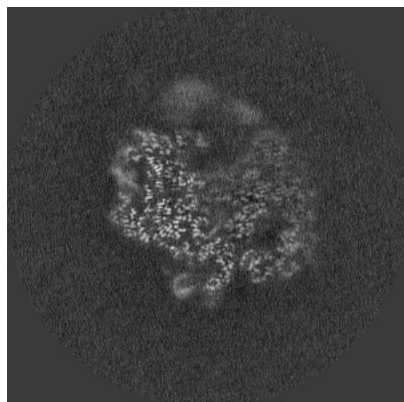


Y Index: 178

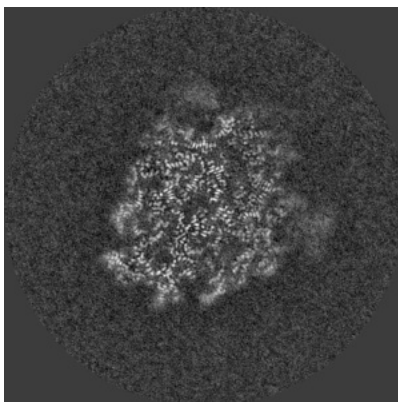


Z Index: 153

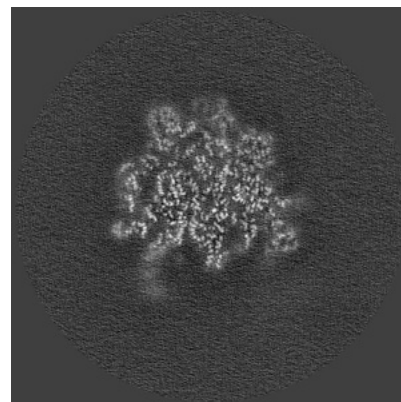
6.3.2 Raw map



X Index: 184



Y Index: 178

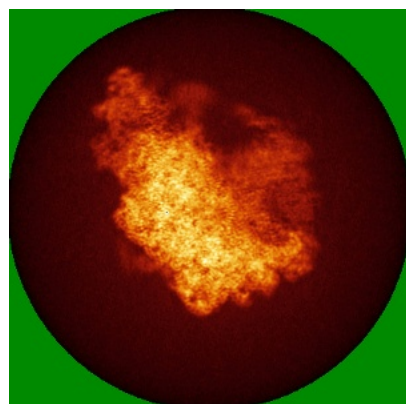


Z Index: 153

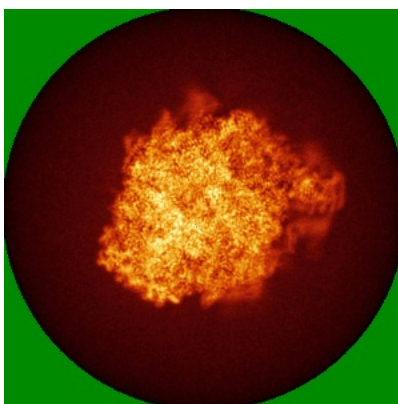
The images above show the largest variance slices of the map in three orthogonal directions.

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

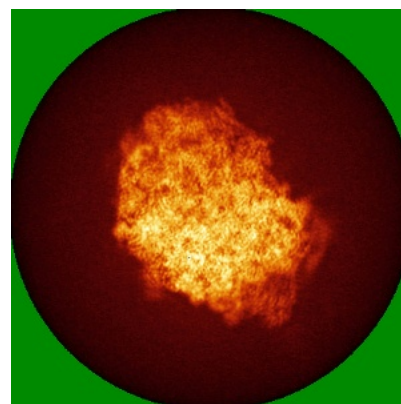
6.4.1 Primary map



X

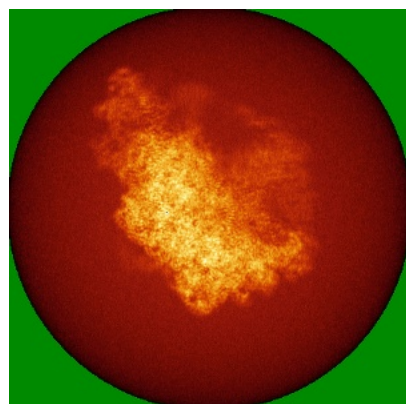


Y

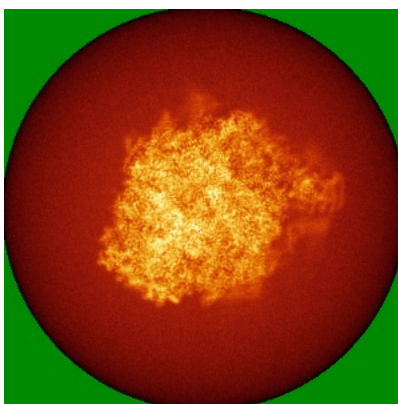


Z

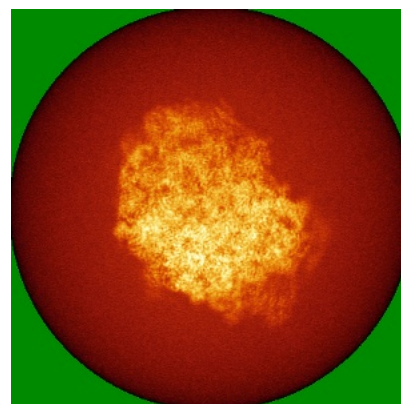
6.4.2 Raw map



X



Y



Z

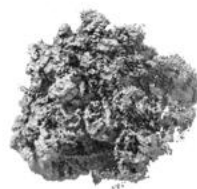
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



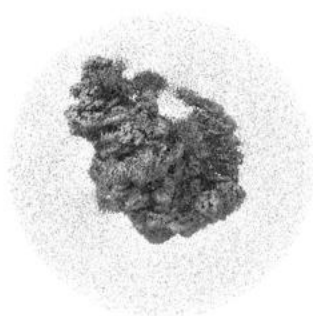
Y



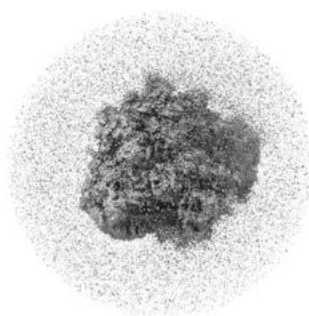
Z

The images above show the 3D surface view of the map at the recommended contour level 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

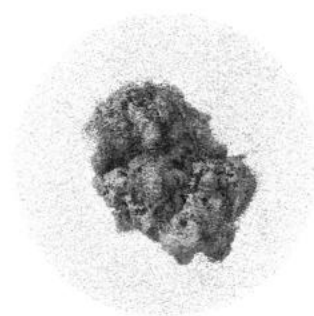
6.5.2 Raw map



X



Y



Z

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

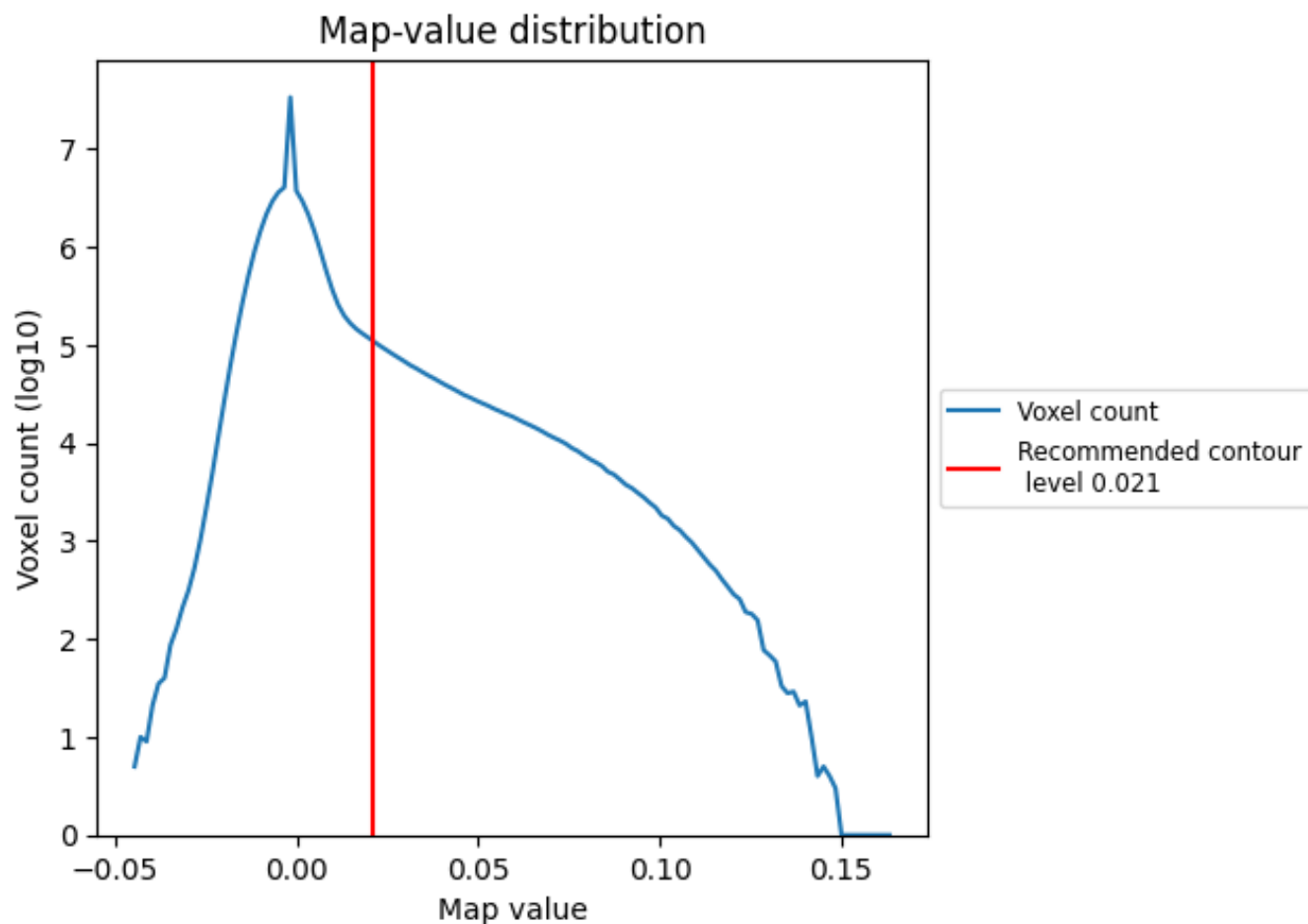
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

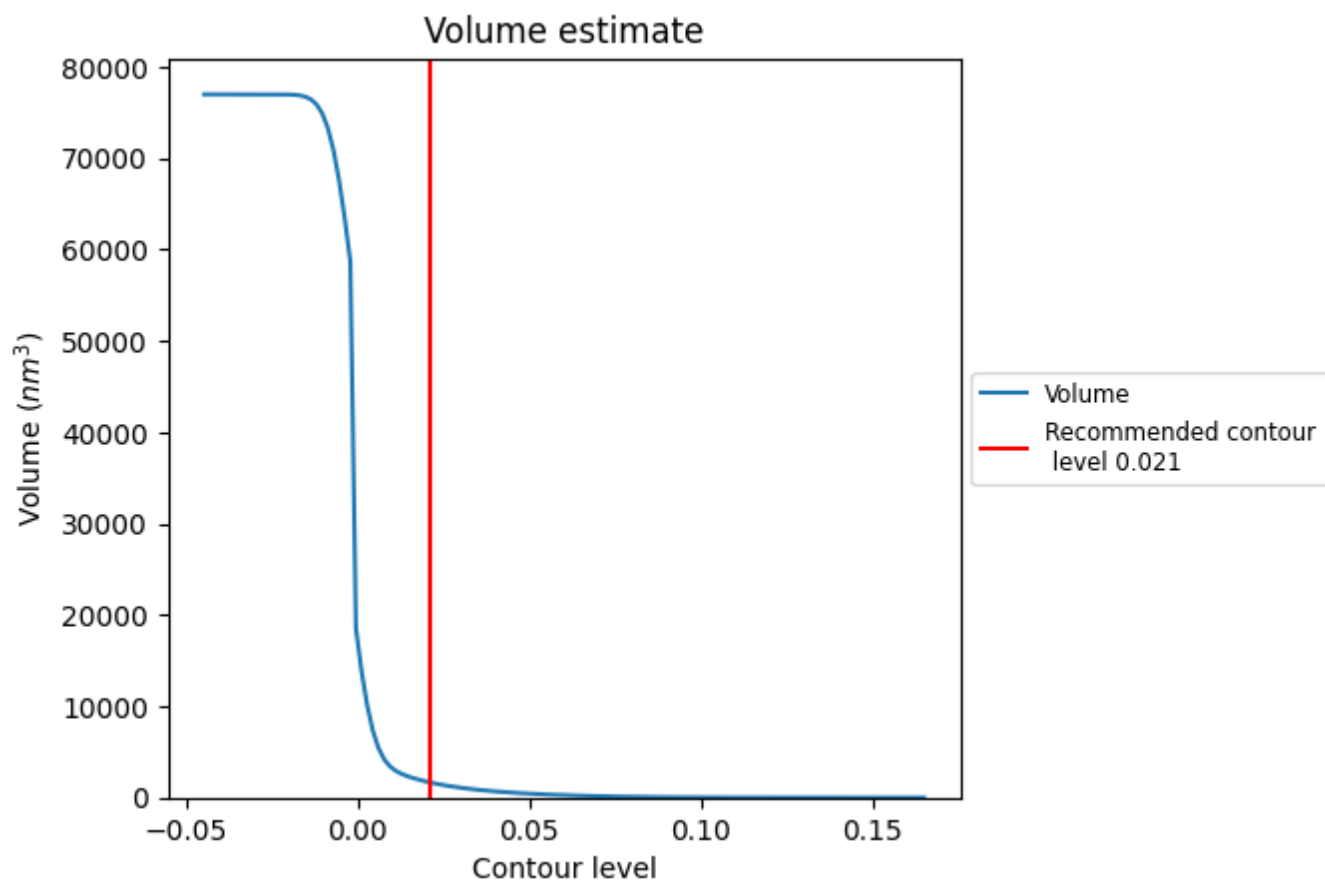
This section contains the results of statistical analysis of the map.

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.

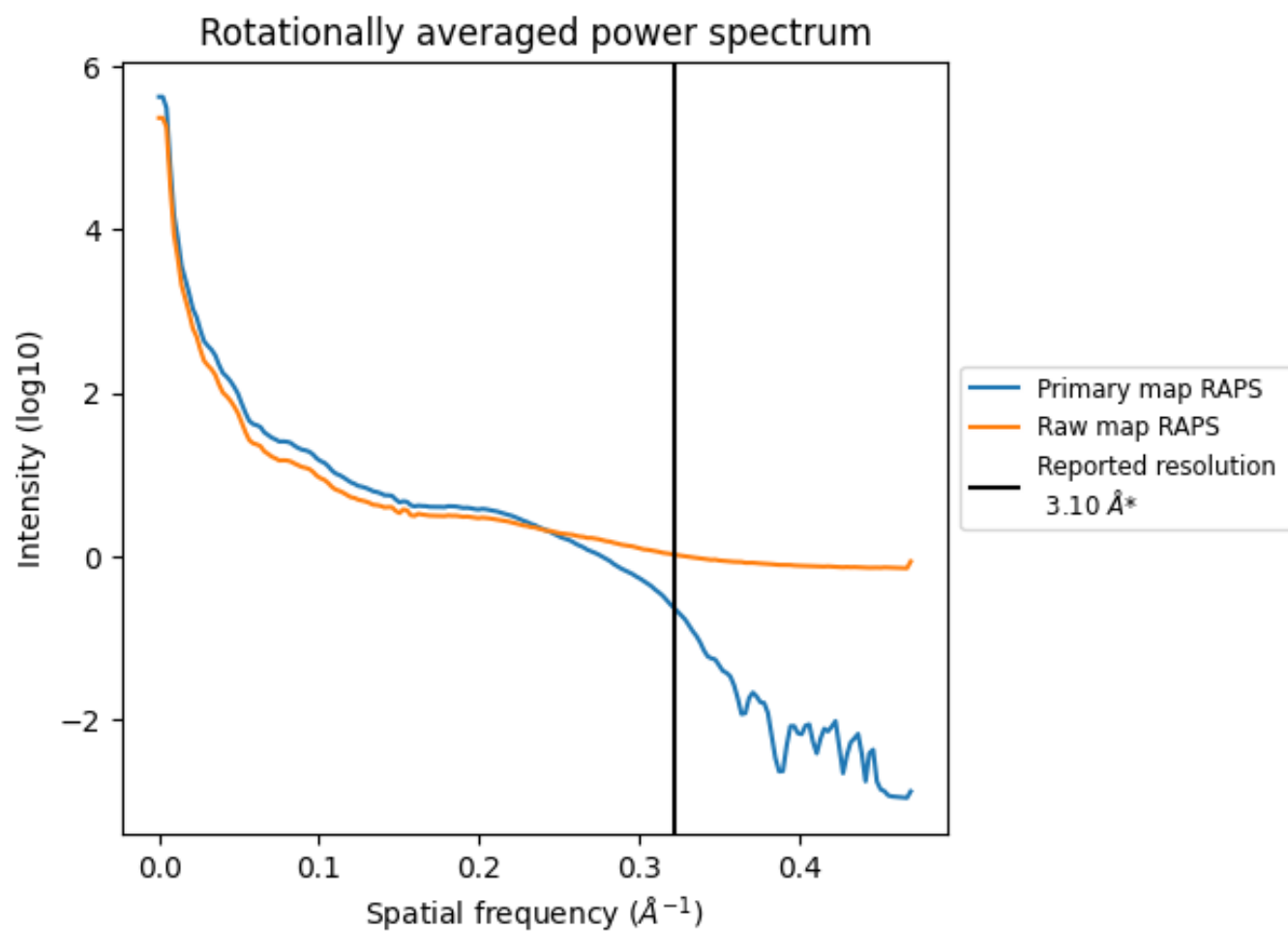
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1666 nm³; this corresponds to an approximate mass of 1505 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 ⓘ

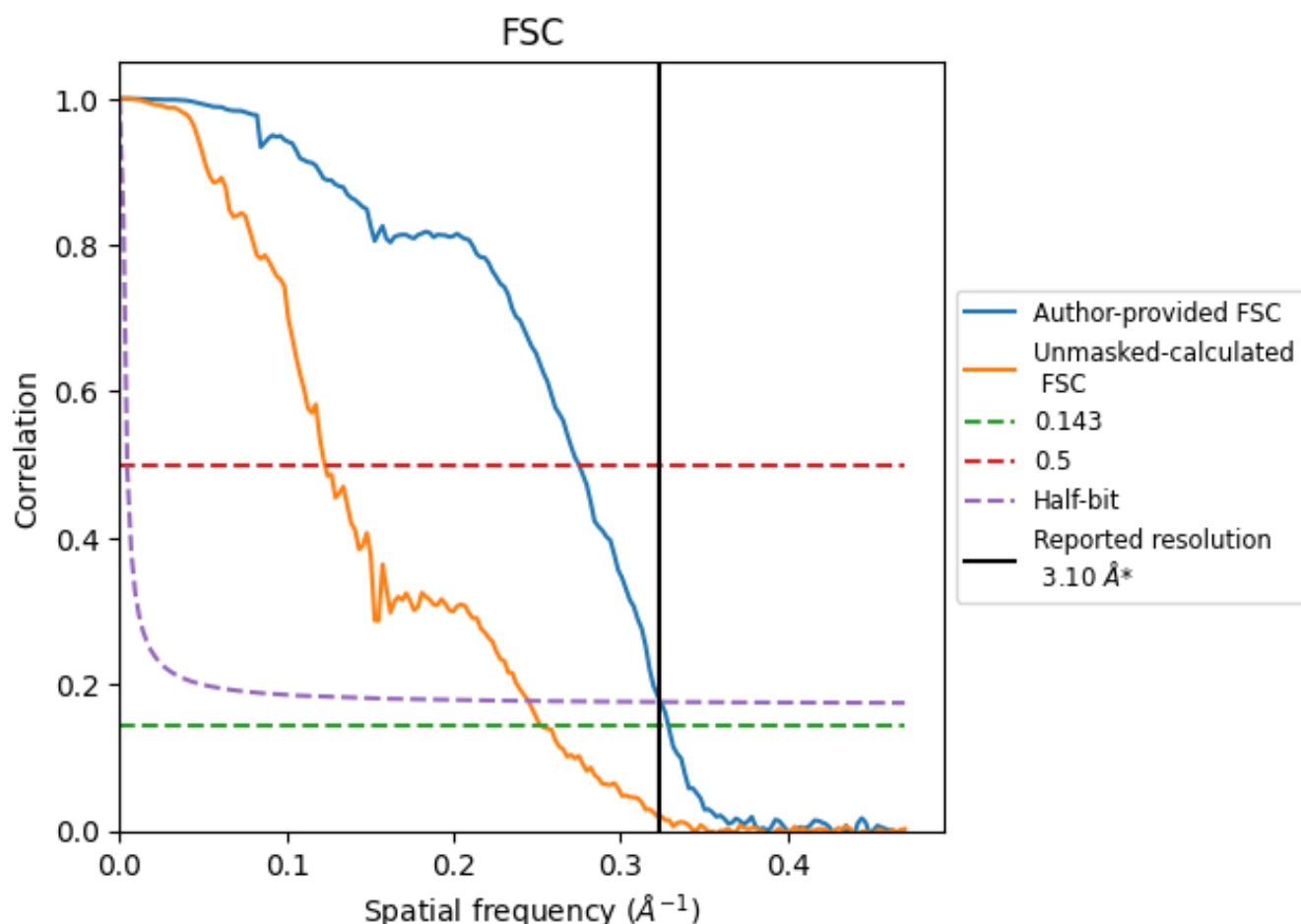


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

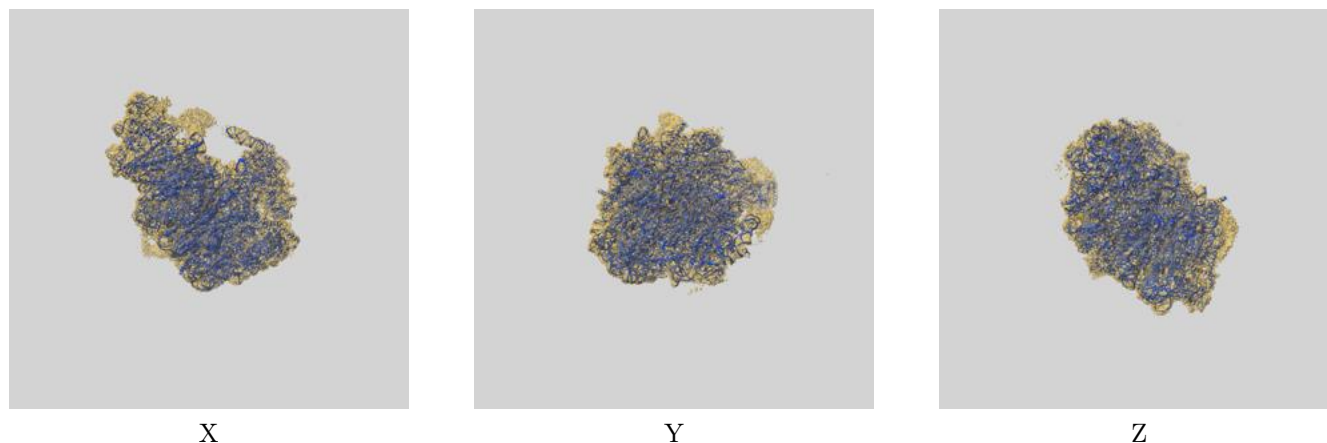
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.64	3.09
Unmasked-calculated*	3.96	8.13	4.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

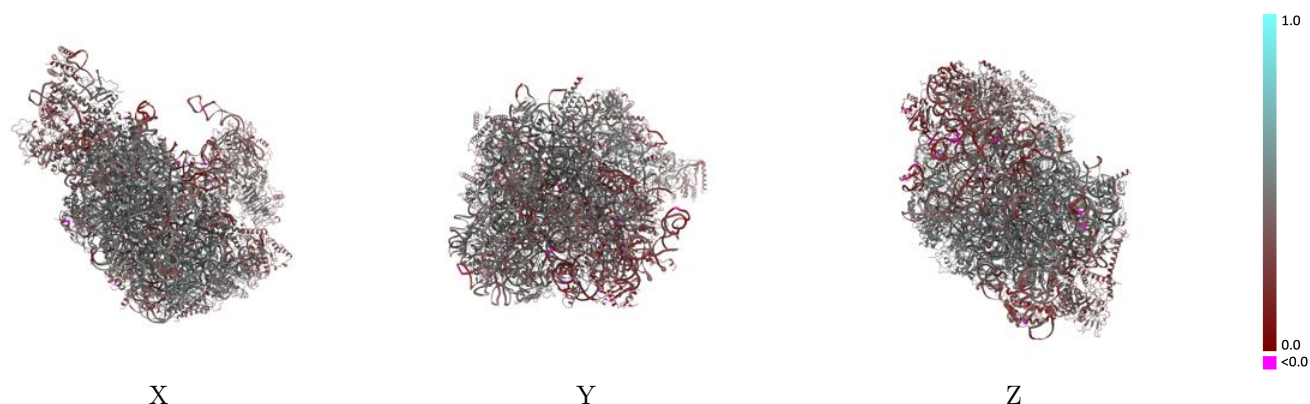
This section contains information regarding the fit between EMDB map EMD-12905 and PDB model 7OHQ. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



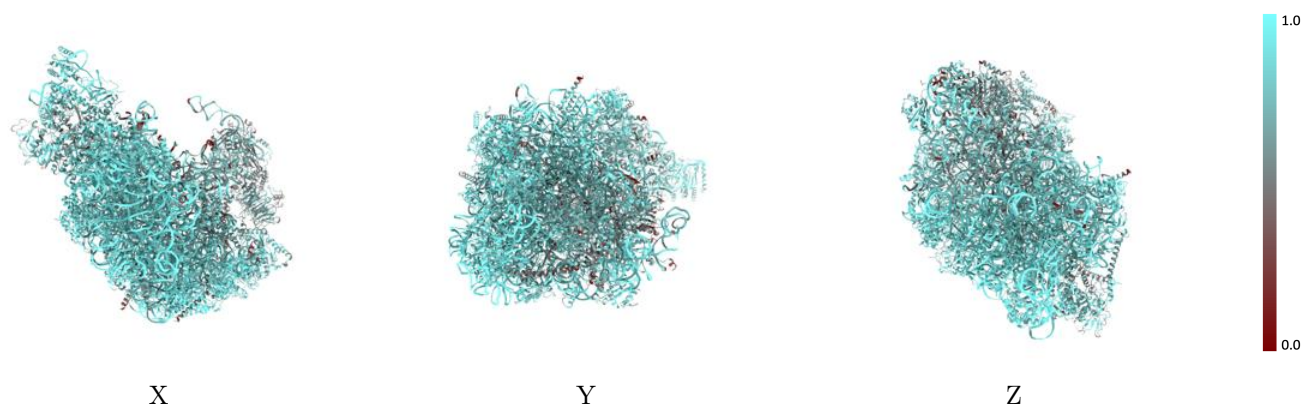
The images above show the 3D surface view of the map at the recommended contour level 0.021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



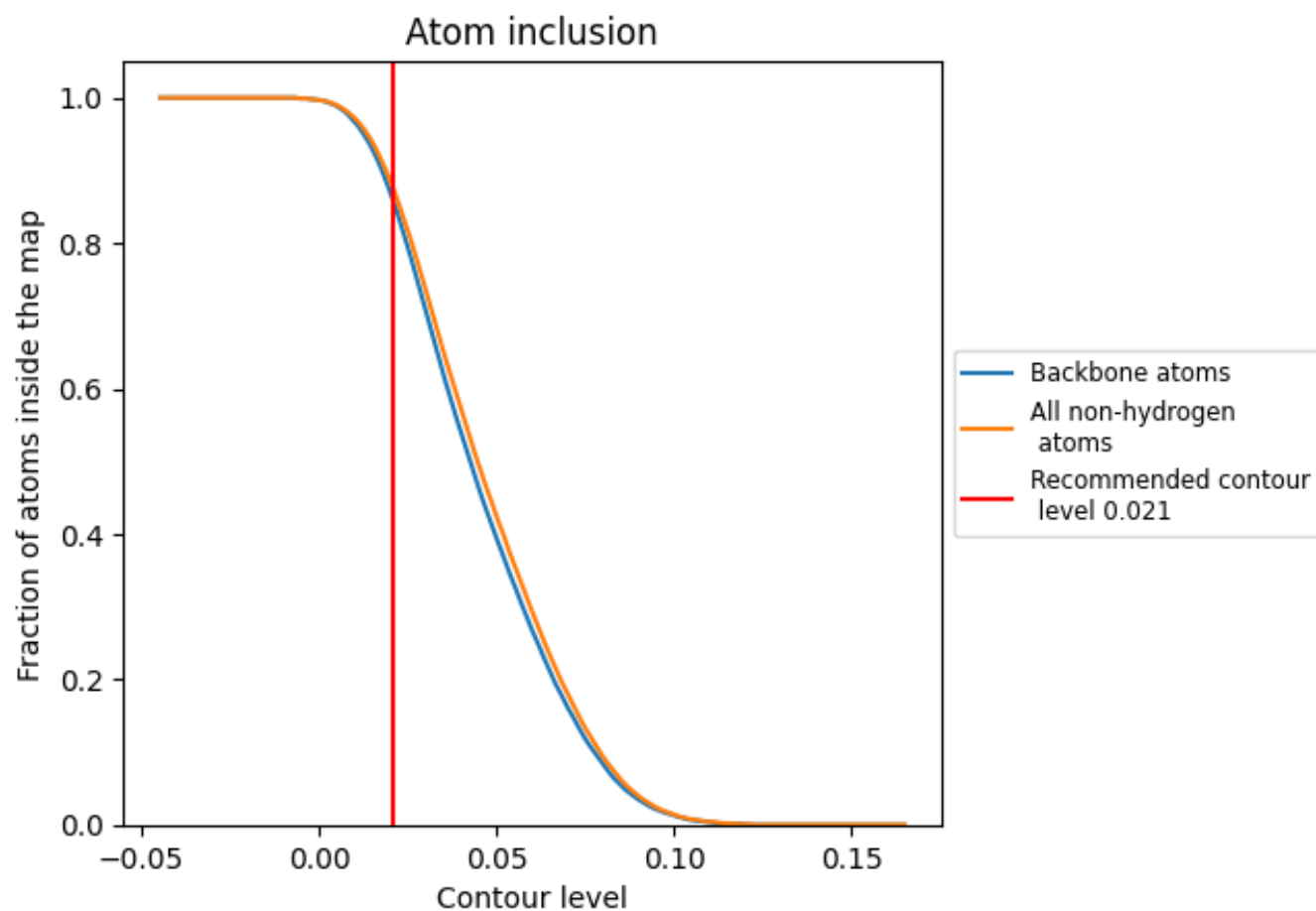
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.4170
1	 0.9350	 0.4130
2	 0.9650	 0.4520
3	 0.8170	 0.2760
5	 0.4060	 0.3030
6	 0.9490	 0.3430
A	 0.8330	 0.4950
B	 0.9060	 0.4830
C	 0.9010	 0.4850
D	 0.5710	 0.3230
E	 0.9200	 0.4710
F	 0.8970	 0.4610
G	 0.8210	 0.4330
H	 0.8650	 0.4550
J	 0.8020	 0.2580
K	 0.8690	 0.3340
L	 0.8770	 0.4590
M	 0.9020	 0.4760
N	 0.8720	 0.4900
O	 0.9130	 0.4980
P	 0.8920	 0.4910
Q	 0.8920	 0.4770
R	 0.8630	 0.4700
S	 0.8710	 0.4460
T	 0.6870	 0.3660
U	 0.8840	 0.4050
V	 0.8920	 0.4860
W	 0.8530	 0.3920
X	 0.8780	 0.4840
Y	 0.9220	 0.4890
Z	 0.8890	 0.4450
a	 0.8780	 0.4650
b	 0.7950	 0.3960
c	 0.9060	 0.4650
d	 0.8660	 0.4800



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Chain	Atom inclusion	Q-score
e	 0.8850	 0.5040
f	 0.9240	 0.5200
g	 0.8560	 0.4790
h	 0.9070	 0.4650
i	 0.8230	 0.4390
j	 0.9260	 0.5020
k	 0.7750	 0.4200
l	 0.8770	 0.4790
m	 0.7340	 0.4130
n	 0.7430	 0.3810
o	 0.8580	 0.3770
p	 0.8580	 0.4650
q	 0.6570	 0.3280
r	 0.7600	 0.4280
s	 0.6480	 0.4110
t	 0.7300	 0.3400
u	 0.8420	 0.4370
v	 0.5730	 0.3560
w	 0.5790	 0.3370
x	 0.6480	 0.3860
y	 0.8930	 0.4510
z	 0.5940	 0.4060