



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 12:00 pm GMT

PDB ID : 6QIK
EMDB ID : EMD-4560
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-01-20
Resolution : 3.10 Å (reported)
Based on initial model : 4V88

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

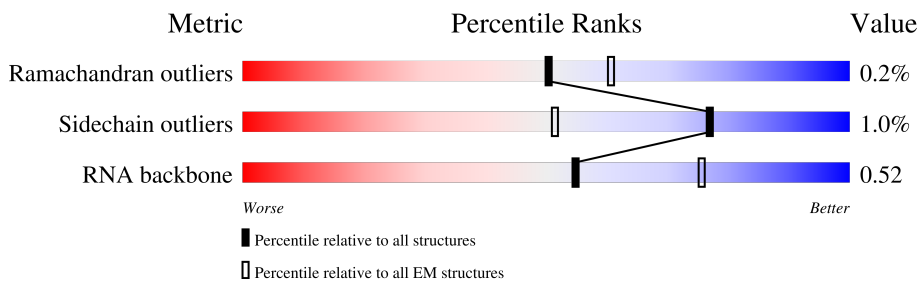
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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	A	3396	
2	B	254	
3	C	387	
4	D	362	
5	E	174	
6	F	191	
7	G	176	
8	H	256	

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Mol	Chain	Length	Quality of chain
9	J	198	99%
10	K	199	92% 7%
11	L	137	98%
12	M	138	96% 7%
13	N	149	99%
14	O	204	100%
15	P	297	91% 9%
16	Q	186	98%
17	R	189	78% 21%
18	S	172	99%
19	T	160	99%
20	U	154	99%
21	V	121	82% 18%
22	W	142	85% 15%
23	X	127	98%
24	Y	136	99%
25	Z	120	97%
26	a	59	88% 12%
27	b	244	89% 10%
28	c	105	92% 8%
29	d	113	93% 5%
30	e	130	97%
31	f	107	98%
32	g	121	82% 15%
33	h	100	98% 21%

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Mol	Chain	Length	Quality of chain
34	i	88	93% . 5%
35	j	78	97% ..
36	k	51	98% .
37	l	106	86% . 11%
38	m	92	96% ..
39	n	245	91% 9%
40	z	432	5% 13% 87%
41	w	518	28% 72% .. 25%
42	v	155	39% 61%
43	o	640	49% 47% . 50%
44	p	210	30% 100%
45	t	128	41% 41% 59%
46	x	121	84% 16%
47	y	158	73% 25% ..

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 128569 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 RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3146	67292	30062	12142	21944	3144	0	0

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	247	1878	1170	381	326	1	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	381	3039	1928	577	526	8	0	0

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	361	2748	1730	522	493	3	0	0

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	169	1352	847	253	248	4	0	0

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	189	1502	953	272	273	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	175	1399	902	251	245	1	0	0

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	223	1742	1117	309	313	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	197	1563	1005	292	265	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	K	186	1486	929	304	253	0	0

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	136	1002	628	189	178	7	0	0

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	135	1045	669	197	177	2	0	0

- Molecule 13 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	148	1172	749	231	189	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	203	Total	C	N	O	S	0	0
			1719	1077	361	280	1		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	269	Total	C	N	O	S	0	0
			2176	1378	375	421	2		

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1440	908	290	240	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	150	Total	C	N	O	S	0	0
			1209	752	257	200			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	171	Total	C	N	O	S	0	0
			1436	925	266	242	3		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1275	805	246	220	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	154	Total	C	N	O	S	0	0
			1222	761	237	224			

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	99	Total	C	N	O	0	0
			786	510	129	147		

- Molecule 22 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	120	Total	C	N	O	S	0	0
			958	617	168	171	2		

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	135	Total	C	N	O	0	0
			1091	710	202	179		

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	118	Total	C	N	O	S	0	0
			963	612	185	165	1		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	52	Total	C	N	O	0	0
			415	259	90	66		

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	219	Total	C	N	O	S	0	0
			1760	1138	320	301	1		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	97	741	479	124	137	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	107	872	553	165	153	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	127	1020	646	205	167	2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	106	849	540	165	143	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	g	103	812	504	167	137	4	0	0

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	h	98	763	477	155	129	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	i	84	665	405	145	110	5	0	0

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	j	77	Total	C	N	O	0	0
			611	391	115	105		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	50	Total	C	N	O	S	0	0
			435	272	97	64	2		

- Molecule 37 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	94	Total	C	N	O	S	0	0
			756	476	153	122	5		

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	224	Total	C	N	O	S	0	0
			1691	1051	293	340	7		

- Molecule 40 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	z	58	Total	C	N	O	S	0	0
			491	301	100	87	3		

- Molecule 41 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	389	Total	C	N	O	S	0	0
			3076	1955	530	571	20		

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	v	60	Total	C	N	O	S	0	0
			500	322	98	79	1		

- Molecule 43 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	322	Total	C	N	O	S	0	0
			2593	1660	449	477	7		

- Molecule 44 is a protein called uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	p	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	156	Total	C	N	O	P	0	0
			3310	1482	582	1091	155		

- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
48	g	1	Total	Zn	0
			1	1	
48	i	1	Total	Zn	0
			1	1	
48	l	1	Total	Zn	0
			1	1	

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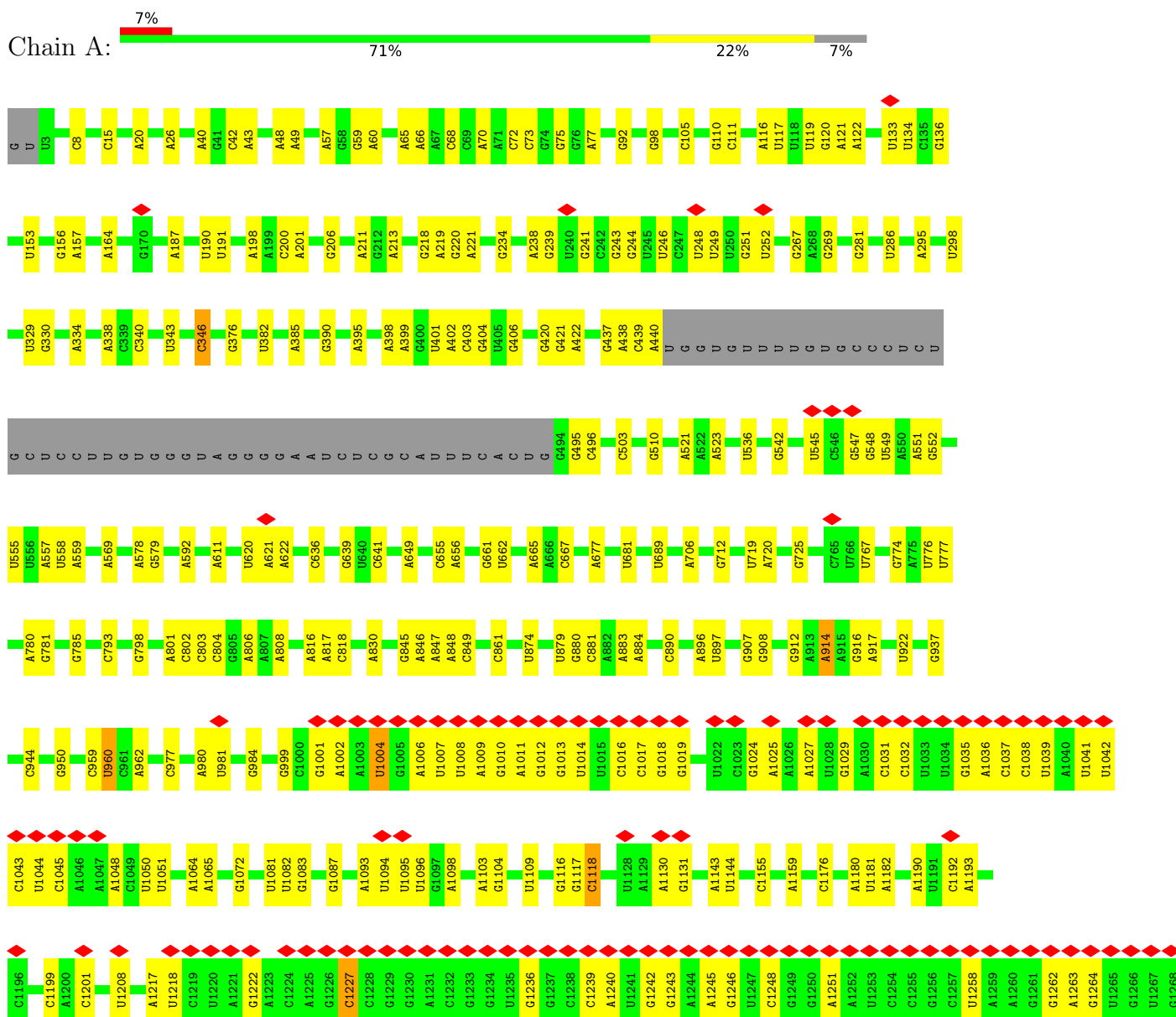
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Mol	Chain	Residues	Atoms		AltConf
48	m	1	Total 1	Zn 1	0
48	w	2	Total 2	Zn 2	0
48	t	1	Total 1	Zn 1	0

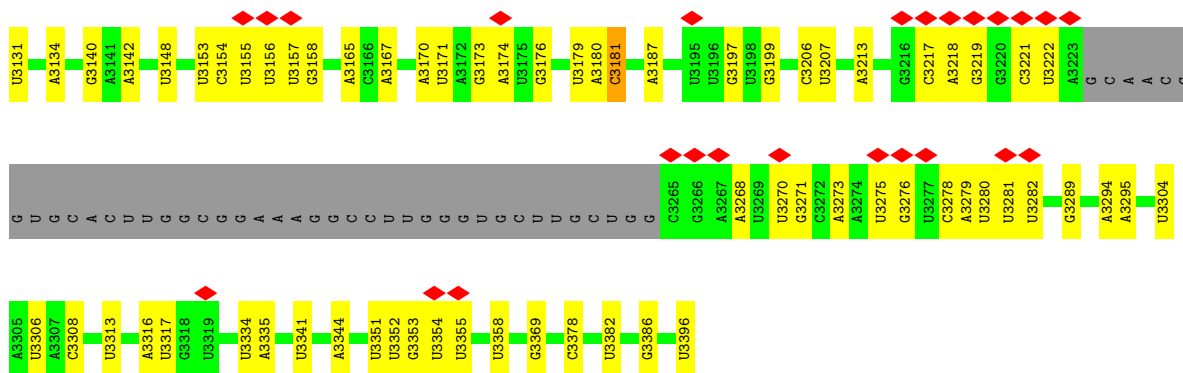
3 Residue-property plots [i](#)

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

• Molecule 1: 25S ribosomal RNA



G2951	G2841	A2703	A2547	A2468	U2336	A2188	G1952	C1762	C1562	G1400	U1269
U2954	U2842	A2704	C2548	G2469	C2337	U2189	G1953	U1563	C1563	C1403	A1270
A2971	U2843	C2708	G2549	C2470	C2338	U2190	G1954	G1564	U1564	G1404	A1271
A2845	C2844	G2714	U2551	U2471	C2339	C2197	U1955	A1566	U1566	U1405	C1272
U2846	A2845	G2714	C2560	G2474	C2350	U2205	A	U1567	U1567	C1411	A1273
A2847	A2561	U2719	A2562	G2475	C2366	G2206	G	U1568	U1568	A1274	A1274
C2983	A2562	G2728	C2566	C2476	A2372	U2209	U	U1569	U1569	C1275	C1275
G2990	C2567	U2482	C2567	A2480	A2373	G2251	G	U1570	U1570	A1418	U1276
G2997	C2568	G2483	C2568	U2482	C2374	A2252	G	U1571	U1571	A1419	U1277
A3011	C2569	A2484	C2569	G2483	G2375	G2253	G	U1572	U1572	A1428	A1278
A3012	A2570	A2485	U2570	A2484	C2383	U2254	C	C1573	U1573	A1432	C1279
A3016	U2571	A2486	C2572	A2485	U2388	A2255	U	A1574	C1574	A1433	C1280
G3022	C2573	A2486	G2573	C2490	U2389	U2256	U	G1574	C1574	G1434	G1281
A3027	G2585	U2492	G2585	A2491	C2393	U2259	C	U1575	A1575	A1435	G1282
G3028	A2593	U2493	A2593	U2493	A2397	U2260	G	C1578	C1578	A1436	G1283
U3038	G2606	A2494	G2606	C2495	A2401	G2261	G	U1579	C1579	A1437	C1284
U3055	G2607	C2496	G2607	U2497	A2402	U2262	A	A1580	C1580	G1443	C1284
U3056	U2612	U2498	U2612	U2498	G2403	A2263	G	C1581	C1581	U1444	G1285
U3057	U2613	U2499	U2613	U2499	A2404	U2264	C	A1581	C1581	U1445	G1285
U3058	G2614	A2500	G2614	A2500	C2405	C2265	C	U1582	C1582	A1446	G1286
U3059	G2614	U2501	G2614	U2501	U2411	U2266	U	U1583	C1583	G1446	G1286
U3067	G2618	C2502	G2618	C2502	G2412	U2269	U	U1584	C1584	G1447	G1287
U3078	G2619	U2504	G2619	U2504	G2418	A2270	U	U1585	C1585	U1455	G1295
U3079	A2626	U2506	A2626	U2506	G2435	G2273	G	U1586	C1586	A1465	A1302
G3080	A2635	A2511	A2635	A2511	U2436	U2274	G	U1587	C1587	A1467	A1303
C3092	G2648	U2514	G2648	U2514	G2437	A2279	U	U1588	C1588	A1475	A1304
A3094	U2652	A2515	U2652	A2515	A2444	A2281	A	U1589	C1589	A1481	G1307
G3101	A2656	A2524	A2656	A2524	A2445	U2282	C	U1590	C1590	G1487	U1309
G3102	A2657	C2530	A2657	C2530	U2446	A2295	U	U1591	C1591	C1496	G1313
G3103	G2672	C	G2672	C	G2448	U2298	G	U1592	C1592	U1512	C1316
G3104	A2673	U	A2673	U	U2453	C2304	C	U1593	C1593	G1525	A1330
G3105	A2674	G	A2674	G	G2454	G2307	U	U1594	C1594	U1526	U1331
G3109	A2677	A	A2677	A	U2455	C2308	C	U1595	C1595	C1527	A1332
G3115	A2678	U	A2678	U	A2456	U2310	U	U1596	C1596	G1542	C1339
G3116	A2679	C	A2679	C	A2458	A2313	U	U1597	C1597	G1547	G1349
G3117	A2680	A	A2680	A	A2459	U2314	G	U1598	C1598	U1551	A1350
G3118	U2681	U	U2681	U	A2461	G2315	U	U1599	C1599	U1555	U1351
A3122	A2682	U	A2682	U	A2462	G2316	C	U1600	C1600	U1556	U1352
A3129	A2689	U	A2689	U	U2464	A2317	U	U1601	C1601	U1556	U1353
A3130	A2690	C	A2690	C	G2465	U2184	U	U1602	C1602	A1750	U1354
U2875	A2691	U	A2691	U	G2466	G2187	U	U1603	C1603	G1751	U1355
U2881	A2694	C	A2694	C	G2466	G2187	A	U1604	C1604	U1386	U1356
U2887	G2872	U	G2872	U	G2466	G2187	U	U1605	C1605	A1399	U1357
U2888	U2875	U	U2875	U	G2466	G2187	U	U1606	C1606		
U2889	C2881	U	C2881	U	G2466	G2187	U	U1607	C1607		
U2898	A2887	U	A2887	U	G2466	G2187	U	U1608	C1608		
C2899	U2888	U	U2888	U	G2466	G2187	U	U1609	C1609		
A2900	C2889	U	C2889	U	G2466	G2187	U	U1610	C1610		
U2916	G2898	U	G2898	U	G2466	G2187	U	U1611	C1611		
U2923	C2899	U	C2899	U	G2466	G2187	U	U1612	C1612		
U2935	A2900	U	A2900	U	G2466	G2187	U	U1613	C1613		
A2936	U2916	U	U2916	U	G2466	G2187	U	U1614	C1614		
G2937	U2923	U	U2923	U	G2466	G2187	U	U1615	C1615		
G2938	U2935	U	U2935	U	G2466	G2187	U	U1616	C1616		
G2939	A2936	U	A2936	U	G2466	G2187	U	U1617	C1617		
A2940	G2937	U	G2937	U	G2466	G2187	U	U1618	C1618		
C2942	G2938	U	G2938	U	G2466	G2187	U	U1619	C1619		
G2947	A2939	U	A2939	U	G2466	G2187	U	U1620	C1620		



• Molecule 2: 60S ribosomal protein L2-A



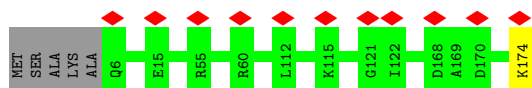
• Molecule 3: 60S ribosomal protein L3



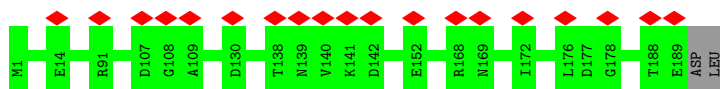
• Molecule 4: 60S ribosomal protein L4-A



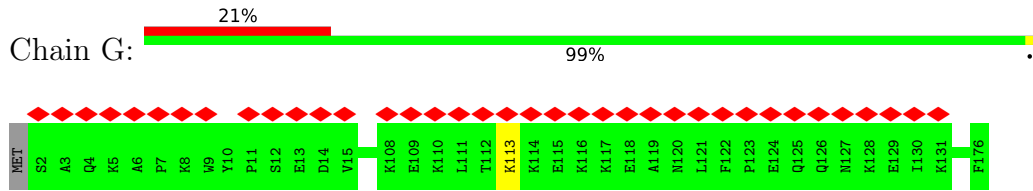
• Molecule 5: 60S ribosomal protein L11-A



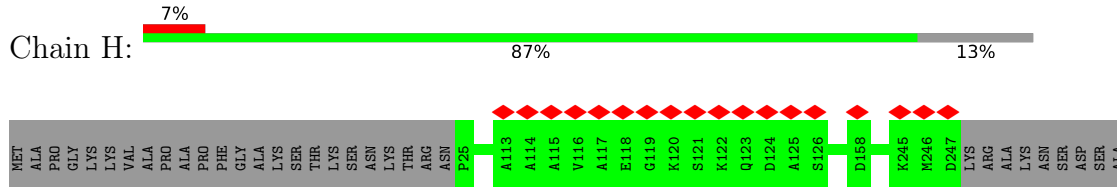
• Molecule 6: 60S ribosomal protein L9-A



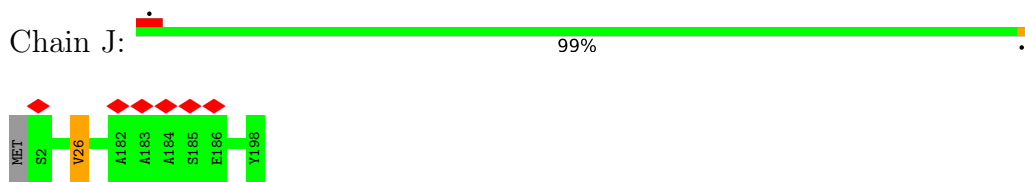
• Molecule 7: 60S ribosomal protein L6-A



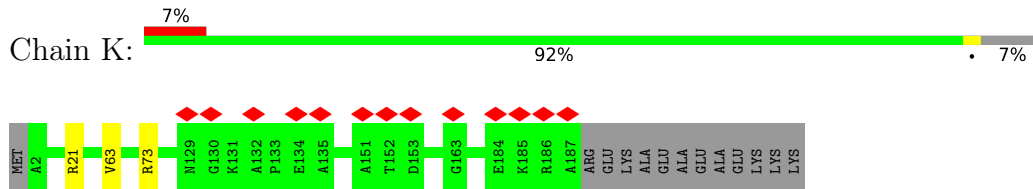
• Molecule 8: 60S ribosomal protein L8-A



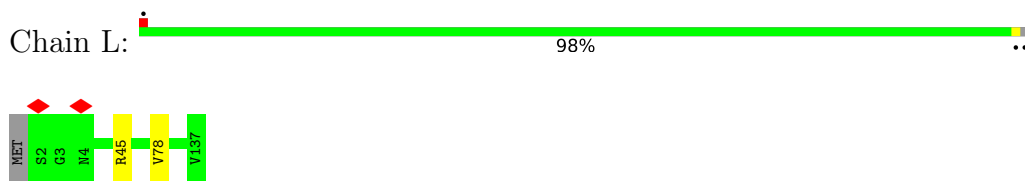
• Molecule 9: 60S ribosomal protein L16-B



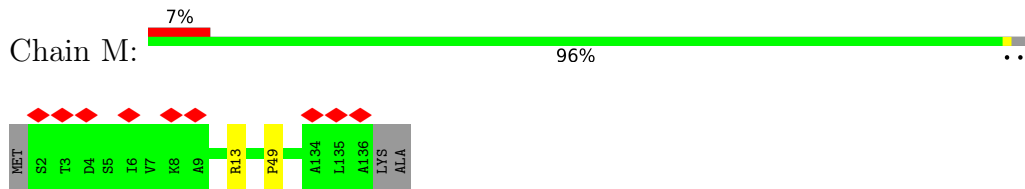
• Molecule 10: 60S ribosomal protein L13-A



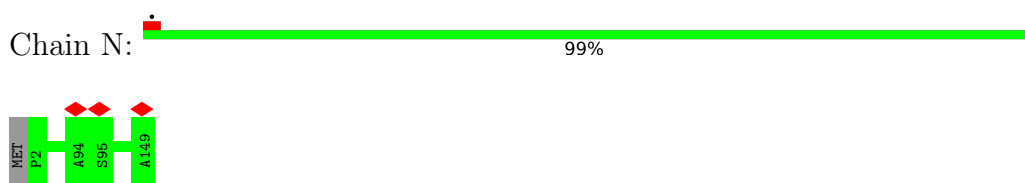
• Molecule 11: 60S ribosomal protein L23-A



• Molecule 12: 60S ribosomal protein L14-A



• Molecule 13: 60S ribosomal protein L28



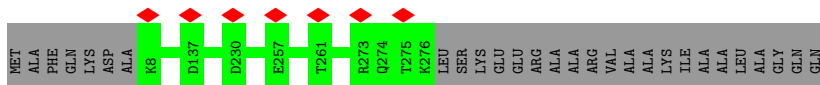
- Molecule 14: 60S ribosomal protein L15-A

Chain O:  100%



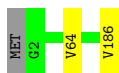
- Molecule 15: 60S ribosomal protein L5

Chain P:  91%




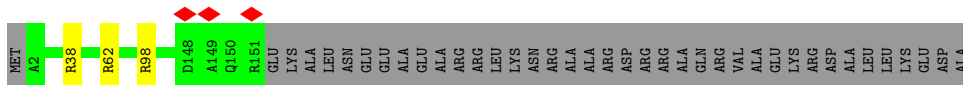
- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  98%



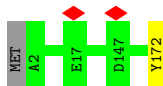
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  78%



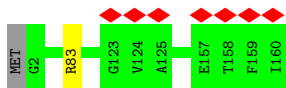
- Molecule 18: 60S ribosomal protein L20-A

Chain S:  99%



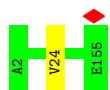
- Molecule 19: 60S ribosomal protein L21-A

Chain T:  99%

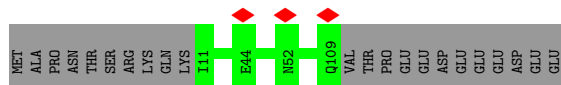
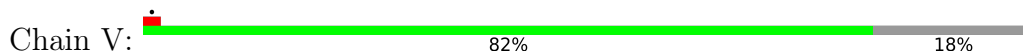


- Molecule 20: 60S ribosomal protein L17-A

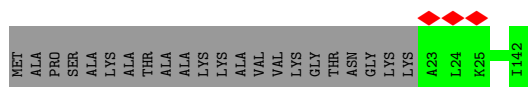
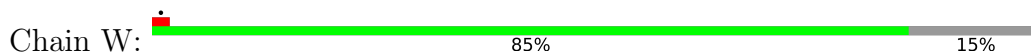
Chain U:  99%



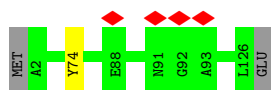
- Molecule 21: 60S ribosomal protein L22-A



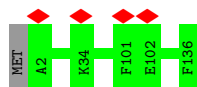
- Molecule 22: 60S ribosomal protein L25



- Molecule 23: 60S ribosomal protein L26-A



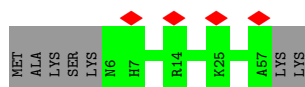
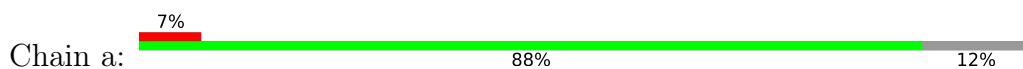
- Molecule 24: 60S ribosomal protein L27-A



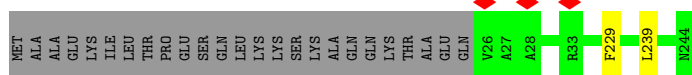
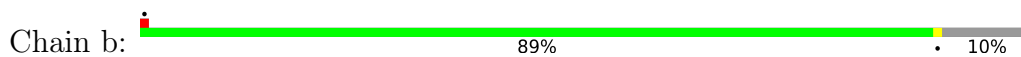
- Molecule 25: 60S ribosomal protein L35-A



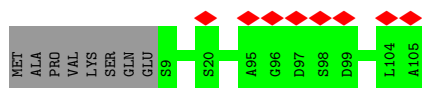
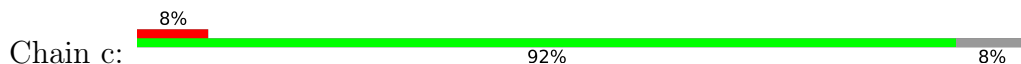
- Molecule 26: 60S ribosomal protein L29



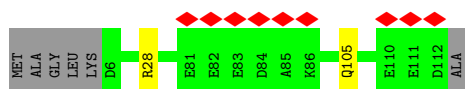
- Molecule 27: 60S ribosomal protein L7-A



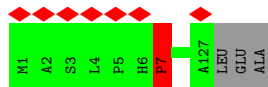
• Molecule 28: 60S ribosomal protein L30



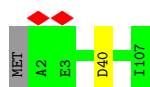
• Molecule 29: 60S ribosomal protein L31-A



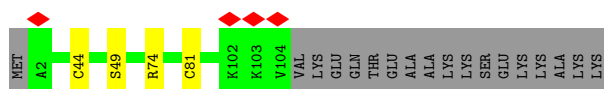
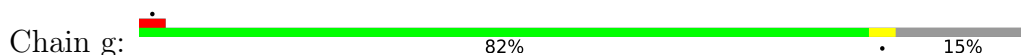
• Molecule 30: 60S ribosomal protein L32



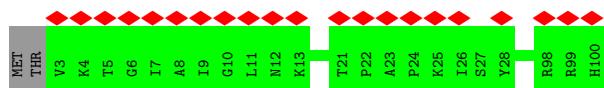
• Molecule 31: 60S ribosomal protein L33-A



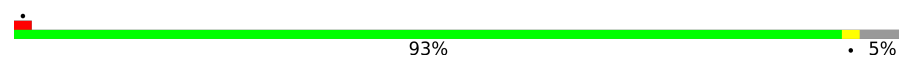
• Molecule 32: 60S ribosomal protein L34-A



• Molecule 33: 60S ribosomal protein L36-A



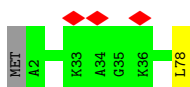
- Molecule 34: 60S ribosomal protein L37-A

Chain i:  93% 5%



- Molecule 35: 60S ribosomal protein L38

Chain j:  97%




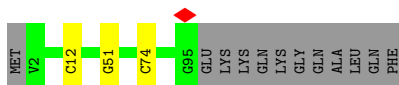
- Molecule 36: 60S ribosomal protein L39

Chain k:  98%



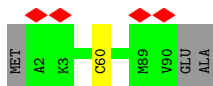
- Molecule 37: 60S ribosomal protein L42-A

Chain l:  86% 11%

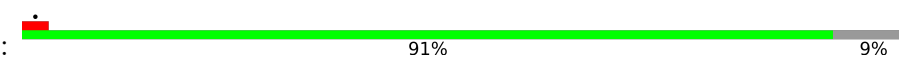


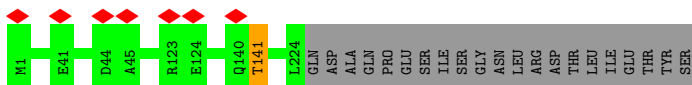
- Molecule 38: 60S ribosomal protein L43-A

Chain m:  96%



- Molecule 39: Eukaryotic translation initiation factor 6

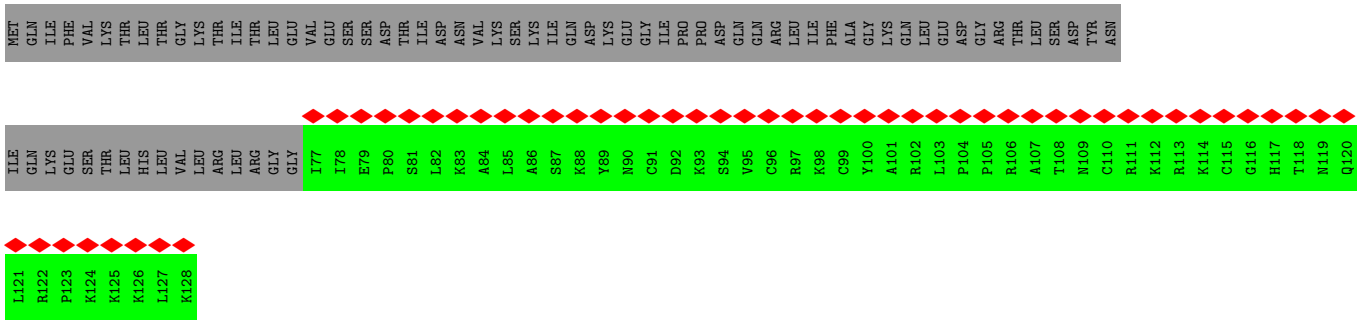
Chain n:  91% 9%



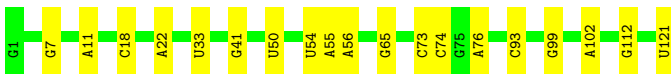
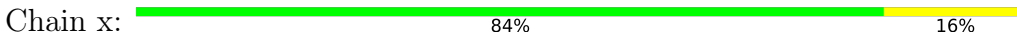
- Molecule 40: Cytoplasmic 60S subunit biogenesis factor REH1

Chain z:  5% 13% 87%

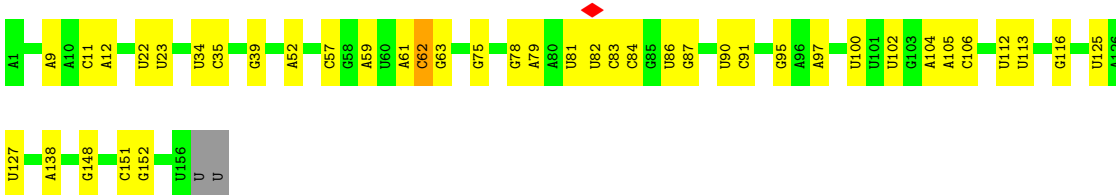




• Molecule 46: 5S ribosomal RNA



• Molecule 47: 5.8S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	260853	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	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	0.560	Depositor
Minimum map value	-0.287	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	A	1.25	40/75327 (0.1%)	1.14	104/117440 (0.1%)
2	B	0.89	2/1912 (0.1%)	0.78	3/2569 (0.1%)
3	C	0.87	0/3110	0.80	3/4184 (0.1%)
4	D	0.86	1/2800 (0.0%)	0.68	1/3791 (0.0%)
5	E	0.45	0/1373	0.63	0/1841
6	F	0.44	0/1523	0.61	0/2051
7	G	0.57	0/1423	0.63	0/1911
8	H	0.68	0/1774	0.62	0/2395
9	J	0.86	1/1593 (0.1%)	0.69	0/2137
10	K	0.79	0/1511	0.77	1/2031 (0.0%)
11	L	0.81	1/1017 (0.1%)	0.74	1/1368 (0.1%)
12	M	0.62	0/1060	0.66	0/1428
13	N	0.89	0/1203	0.70	0/1611
14	O	1.00	0/1756	0.79	0/2353
15	P	0.65	0/2225	0.61	0/3004
16	Q	0.86	1/1464 (0.1%)	0.74	0/1964
17	R	0.83	0/1226	0.75	4/1637 (0.2%)
18	S	0.76	0/1472	0.63	0/1979
19	T	0.78	0/1299	0.66	0/1742
20	U	0.94	1/1245 (0.1%)	0.71	0/1676
21	V	0.60	0/802	0.60	0/1087
22	W	0.80	0/973	0.65	0/1313
23	X	0.77	0/995	0.73	0/1329
24	Y	0.59	0/1117	0.65	0/1496
25	Z	0.72	0/972	0.71	2/1293 (0.2%)
26	a	0.62	0/426	0.61	0/570
27	b	0.87	0/1797	0.67	0/2419
28	c	0.68	0/749	0.63	0/1007
29	d	0.80	0/886	0.75	1/1190 (0.1%)
30	e	0.81	0/1041	0.70	1/1393 (0.1%)
31	f	0.91	0/867	0.79	1/1167 (0.1%)
32	g	0.87	0/822	0.77	1/1099 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.56	0/770	0.67	0/1023
34	i	0.90	0/680	0.81	0/901
35	j	0.58	0/617	0.63	0/825
36	k	0.86	0/442	0.73	0/587
37	l	0.79	0/768	0.77	0/1016
38	m	0.85	0/687	0.76	0/915
39	n	0.48	0/1712	0.60	0/2330
40	z	0.41	0/494	0.67	0/654
41	w	0.59	3/3135 (0.1%)	0.63	1/4255 (0.0%)
42	v	0.57	0/512	0.61	0/680
43	o	0.49	3/2647 (0.1%)	0.67	2/3582 (0.1%)
45	t	0.29	0/423	0.56	0/562
46	x	1.08	0/2880	1.08	0/4487
47	y	1.40	5/3699 (0.1%)	1.19	7/5760 (0.1%)
All	All	1.07	58/137226 (0.0%)	1.00	133/202052 (0.1%)

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	w	25	PRO	N-CA	14.19	1.71	1.47
43	o	394	PRO	N-CA	13.54	1.70	1.47
43	o	179	THR	C-N	8.59	1.50	1.34
1	A	42	C	C4-C5	-6.82	1.37	1.43
1	A	346	C	N1-C6	-6.18	1.33	1.37

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	18	PRO	CA-N-CD	-15.99	89.11	111.50
1	A	962	A	N1-C6-N6	8.65	123.79	118.60
43	o	394	PRO	CA-N-CD	-8.28	99.91	111.50
1	A	962	A	C5-C6-N6	-7.93	117.36	123.70
1	A	406	G	O4'-C1'-N9	7.53	114.22	108.20

There are no chirality outliers.

There are no planarity outliers.

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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	245/254 (96%)	221 (90%)	24 (10%)	0	100	100
3	C	379/387 (98%)	347 (92%)	31 (8%)	1 (0%)	41	73
4	D	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
5	E	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
6	F	187/191 (98%)	175 (94%)	12 (6%)	0	100	100
7	G	173/176 (98%)	156 (90%)	17 (10%)	0	100	100
8	H	221/256 (86%)	204 (92%)	17 (8%)	0	100	100
9	J	195/198 (98%)	187 (96%)	8 (4%)	0	100	100
10	K	184/199 (92%)	173 (94%)	11 (6%)	0	100	100
11	L	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
12	M	133/138 (96%)	123 (92%)	9 (7%)	1 (1%)	19	54
13	N	146/149 (98%)	123 (84%)	23 (16%)	0	100	100
14	O	201/204 (98%)	184 (92%)	17 (8%)	0	100	100
15	P	267/297 (90%)	253 (95%)	14 (5%)	0	100	100
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	148/189 (78%)	146 (99%)	2 (1%)	0	100	100
18	S	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	U	152/154 (99%)	142 (93%)	10 (7%)	0	100	100
21	V	97/121 (80%)	88 (91%)	9 (9%)	0	100	100
22	W	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
23	X	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
24	Y	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
25	Z	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
26	a	50/59 (85%)	43 (86%)	7 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	b	217/244 (89%)	200 (92%)	17 (8%)	0	100	100
28	c	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
29	d	105/113 (93%)	91 (87%)	14 (13%)	0	100	100
30	e	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	19	54
31	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
32	g	101/121 (84%)	88 (87%)	13 (13%)	0	100	100
33	h	96/100 (96%)	88 (92%)	8 (8%)	0	100	100
34	i	82/88 (93%)	70 (85%)	11 (13%)	1 (1%)	13	44
35	j	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
36	k	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
37	l	92/106 (87%)	85 (92%)	6 (6%)	1 (1%)	14	46
38	m	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
39	n	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	29	64
40	z	56/432 (13%)	48 (86%)	8 (14%)	0	100	100
41	w	387/518 (75%)	340 (88%)	41 (11%)	6 (2%)	9	37
42	v	58/155 (37%)	57 (98%)	1 (2%)	0	100	100
43	o	316/640 (49%)	246 (78%)	68 (22%)	2 (1%)	25	59
45	t	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
All	All	6753/8141 (83%)	6178 (92%)	561 (8%)	14 (0%)	50	79

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
41	w	148	ARG
41	w	20	CYS
41	w	68	PRO
30	e	7	PRO

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	189/196 (96%)	189 (100%)	0	100	100
3	C	317/323 (98%)	312 (98%)	5 (2%)	62	84
4	D	288/289 (100%)	287 (100%)	1 (0%)	92	96
5	E	147/150 (98%)	146 (99%)	1 (1%)	84	93
6	F	169/171 (99%)	169 (100%)	0	100	100
7	G	152/153 (99%)	151 (99%)	1 (1%)	84	93
8	H	183/208 (88%)	183 (100%)	0	100	100
9	J	163/164 (99%)	162 (99%)	1 (1%)	86	94
10	K	149/159 (94%)	147 (99%)	2 (1%)	69	87
11	L	104/105 (99%)	104 (100%)	0	100	100
12	M	107/109 (98%)	106 (99%)	1 (1%)	78	91
13	N	118/119 (99%)	118 (100%)	0	100	100
14	O	175/176 (99%)	175 (100%)	0	100	100
15	P	227/245 (93%)	227 (100%)	0	100	100
16	Q	150/151 (99%)	149 (99%)	1 (1%)	84	93
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	154 (99%)	1 (1%)	86	94
19	T	136/137 (99%)	135 (99%)	1 (1%)	84	93
20	U	125/125 (100%)	125 (100%)	0	100	100
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	104 (100%)	0	100	100
23	X	108/110 (98%)	107 (99%)	1 (1%)	78	91
24	Y	115/116 (99%)	115 (100%)	0	100	100
25	Z	104/105 (99%)	104 (100%)	0	100	100
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	182 (99%)	2 (1%)	73	89
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	93 (99%)	1 (1%)	73	89
30	e	109/111 (98%)	108 (99%)	1 (1%)	78	91
31	f	90/91 (99%)	90 (100%)	0	100	100
32	g	88/103 (85%)	85 (97%)	3 (3%)	37	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	80/82 (98%)	80 (100%)	0	100	100
34	i	69/71 (97%)	68 (99%)	1 (1%)	67	86
35	j	68/69 (99%)	67 (98%)	1 (2%)	65	85
36	k	45/46 (98%)	45 (100%)	0	100	100
37	l	81/91 (89%)	79 (98%)	2 (2%)	47	75
38	m	70/72 (97%)	69 (99%)	1 (1%)	67	86
39	n	192/211 (91%)	191 (100%)	1 (0%)	88	94
40	z	53/392 (14%)	53 (100%)	0	100	100
41	w	348/467 (74%)	338 (97%)	10 (3%)	42	72
42	v	53/129 (41%)	53 (100%)	0	100	100
43	o	284/555 (51%)	266 (94%)	18 (6%)	18	48
45	t	47/116 (40%)	47 (100%)	0	100	100
All	All	5772/6889 (84%)	5715 (99%)	57 (1%)	77	90

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	n	141	THR
43	o	400	LYS
41	w	145	ASP
43	o	395	ASN
43	o	179	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
43	o	395	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	664 (21%)	22 (0%)
46	x	120/121 (99%)	19 (15%)	0
47	y	155/158 (98%)	34 (21%)	0
All	All	3416/3675 (92%)	717 (20%)	22 (0%)

5 of 717 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	15	C
1	A	26	A
1	A	40	A
1	A	43	A
1	A	48	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2404	A
1	A	2497	U
1	A	2459	A
1	A	3027	A
1	A	1287	A

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 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

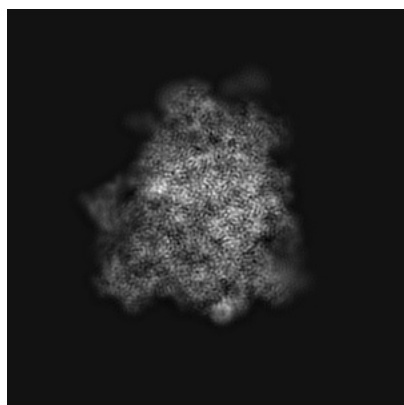
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4560. These allow visual inspection of the internal detail of the map and identification of artifacts.

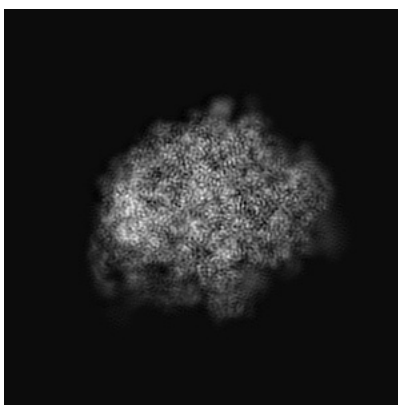
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

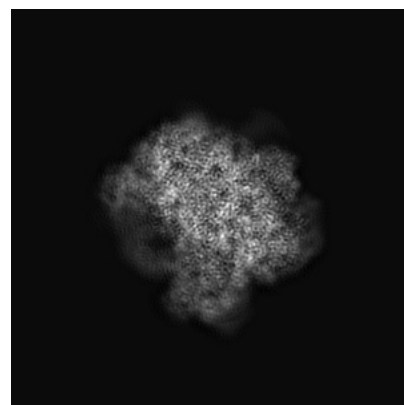
6.1.1 Primary map



X



Y

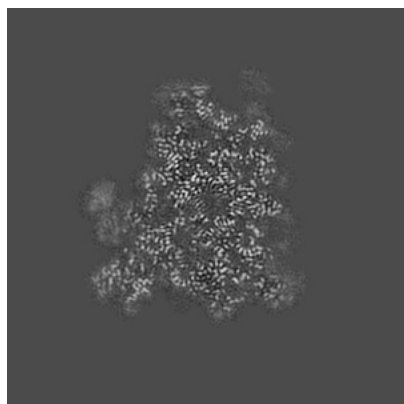


Z

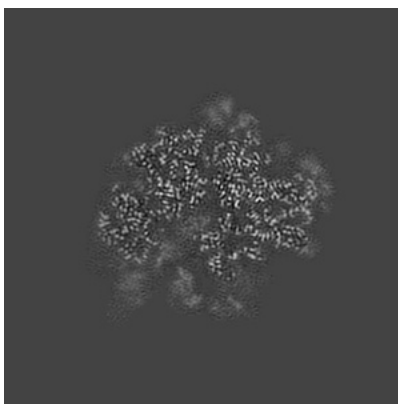
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

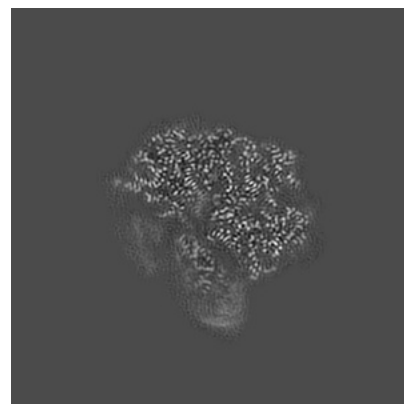
6.2.1 Primary map



X Index: 180



Y Index: 180

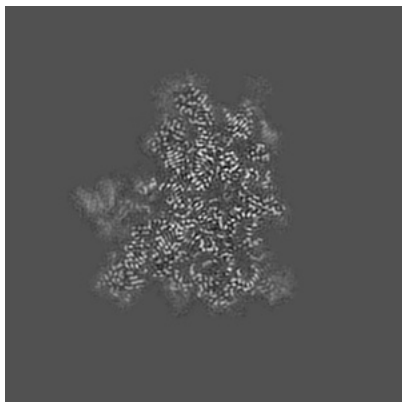


Z Index: 180

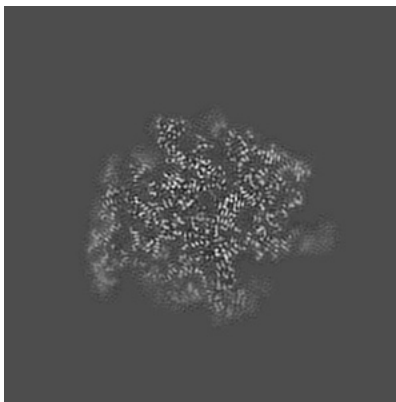
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

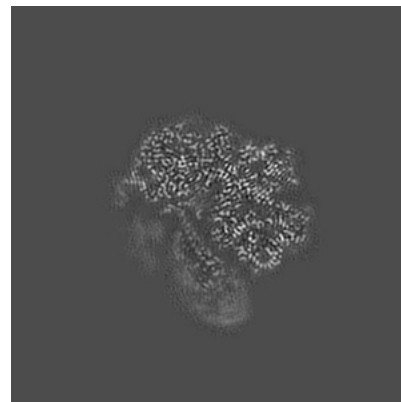
6.3.1 Primary map



X Index: 189



Y Index: 196

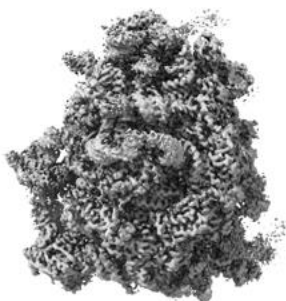


Z Index: 177

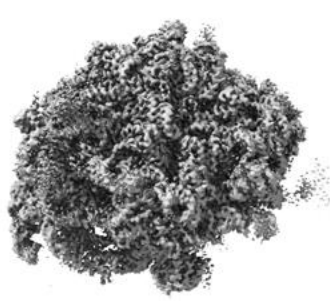
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

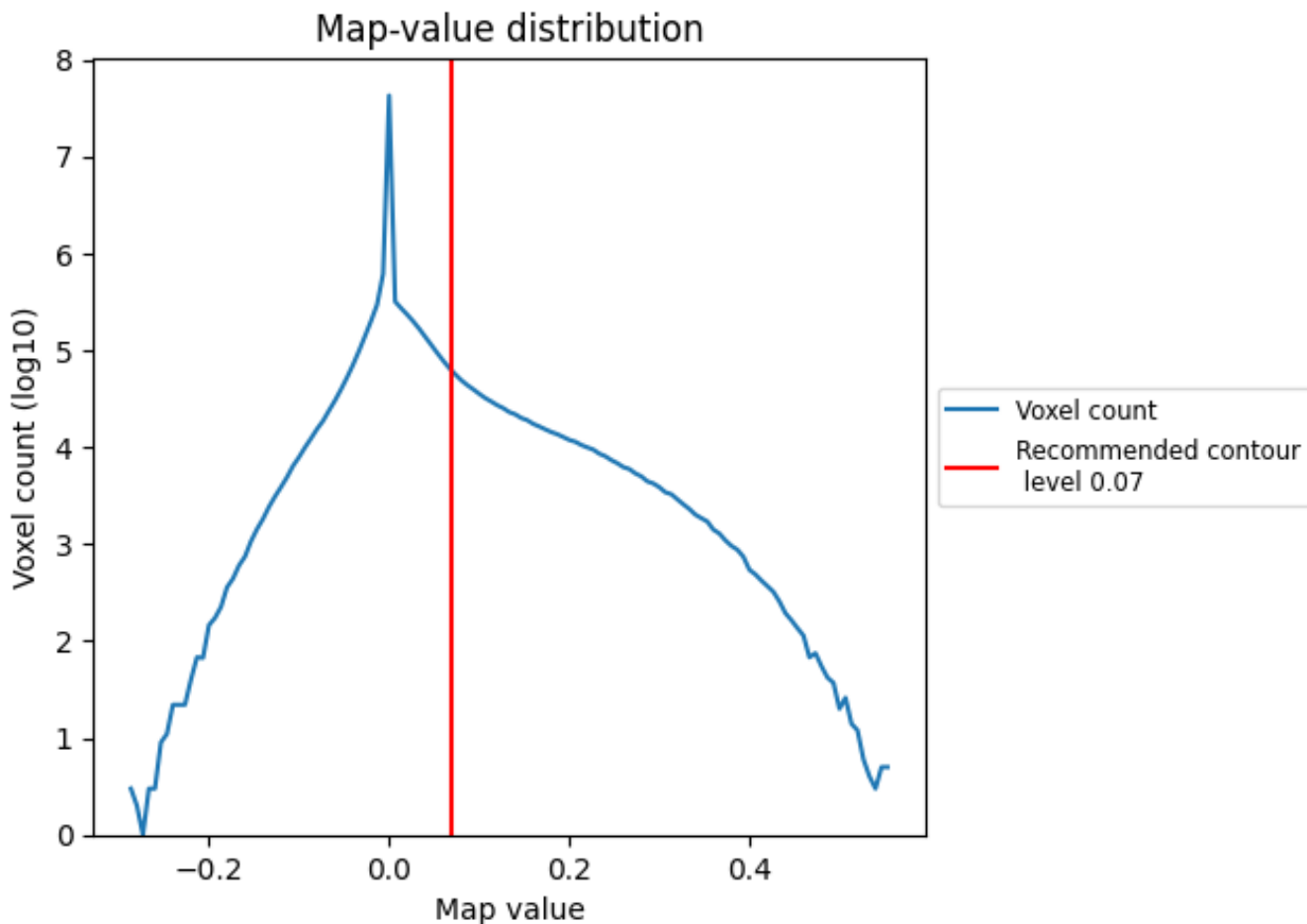
6.5 Mask visualisation

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

7 Map analysis [i](#)

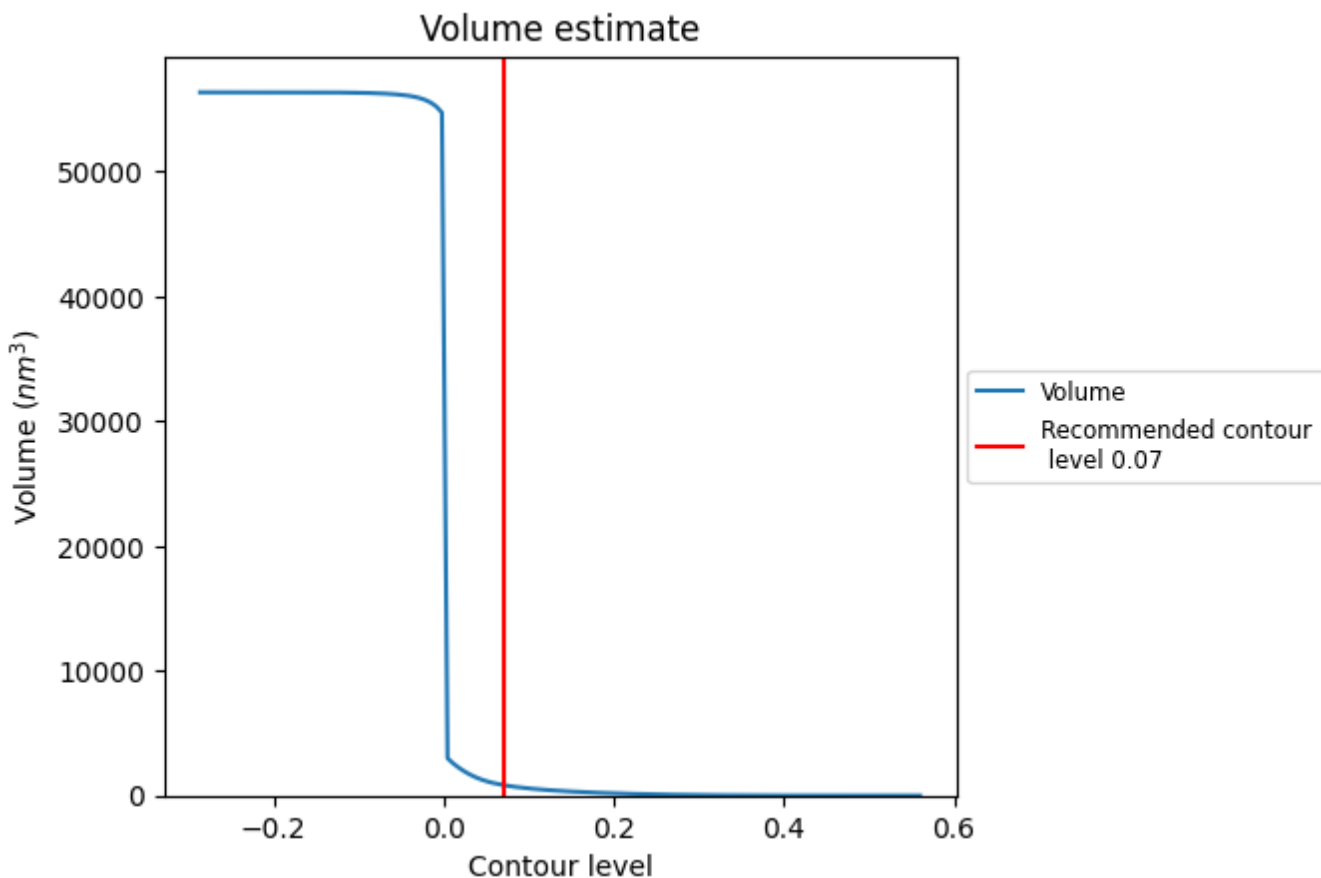
This section contains the results of statistical analysis of the map.

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.

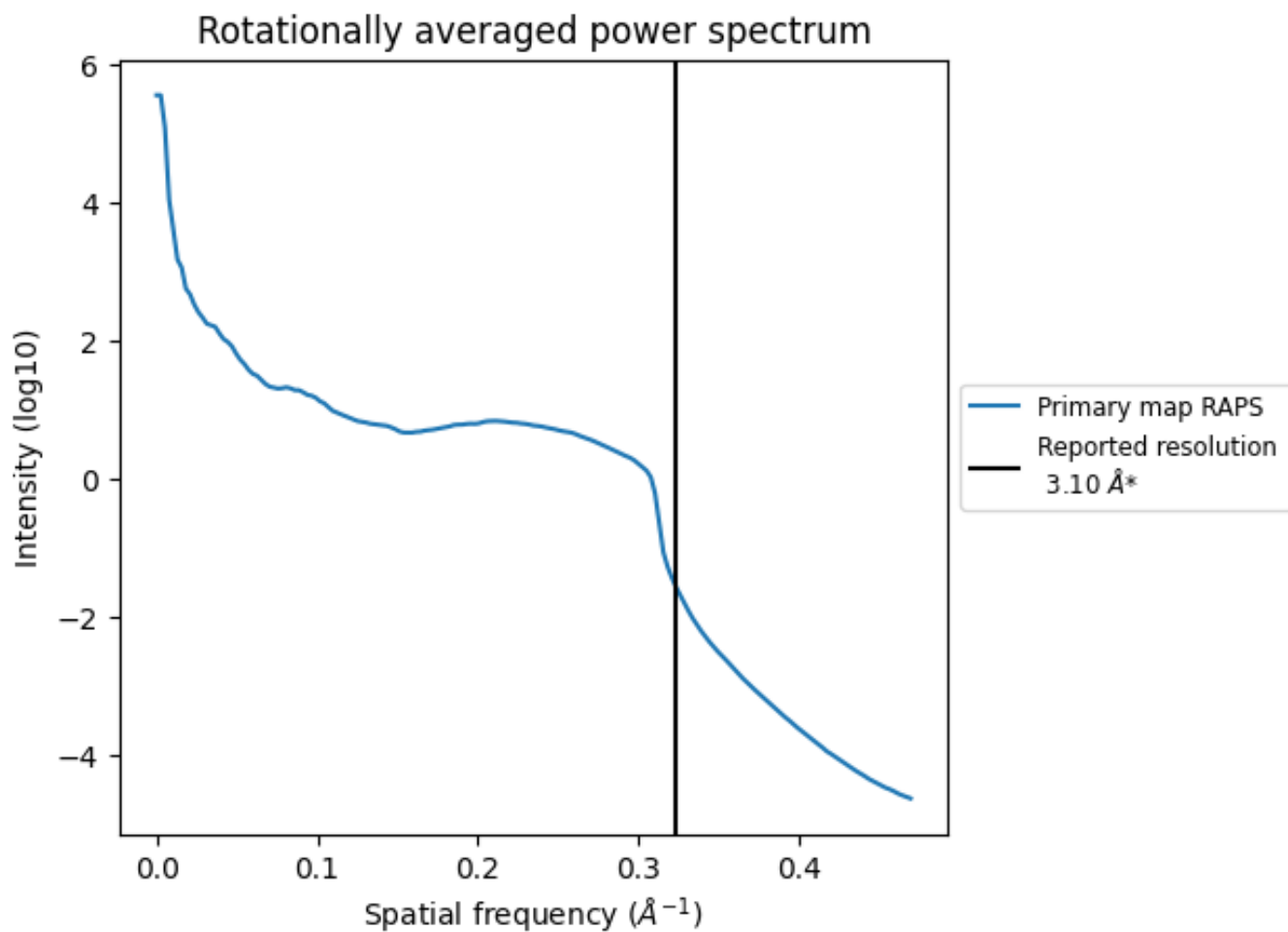
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 838 nm³; this corresponds to an approximate mass of 757 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 0.323\AA^{-1}

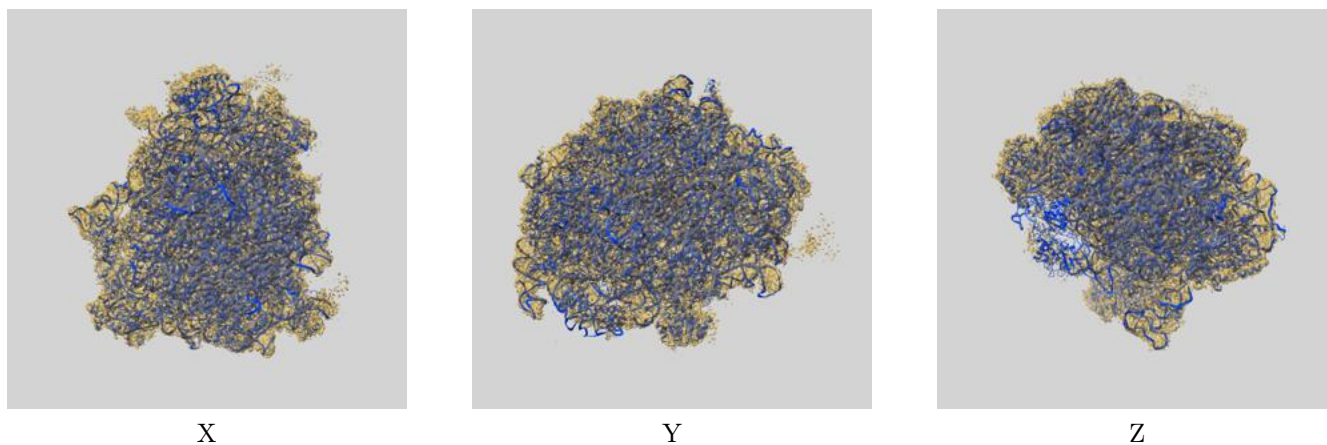
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

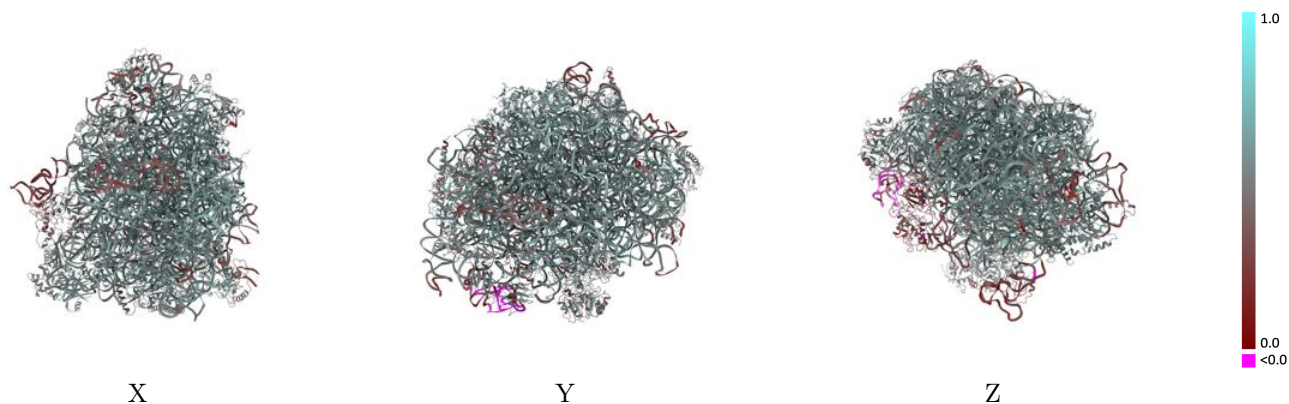
This section contains information regarding the fit between EMDB map EMD-4560 and PDB model 6QIK. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



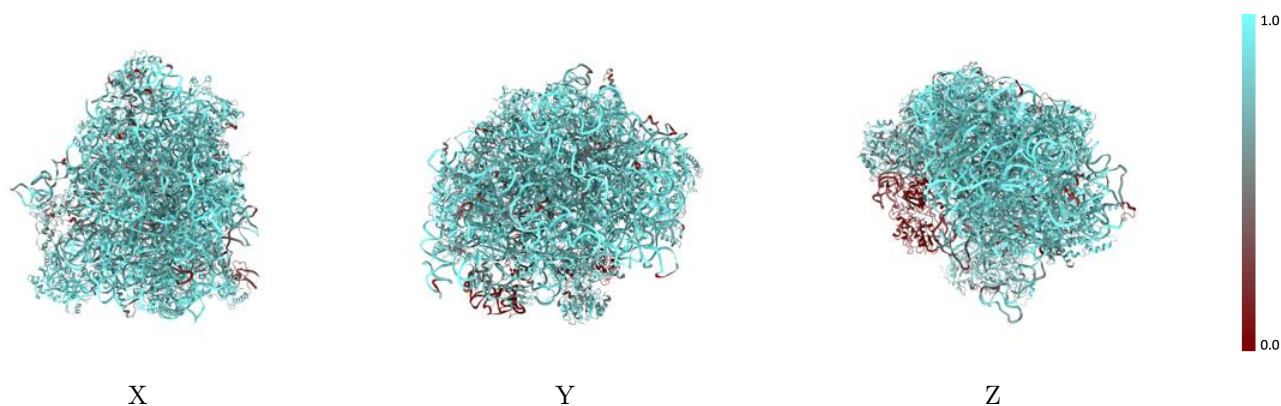
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



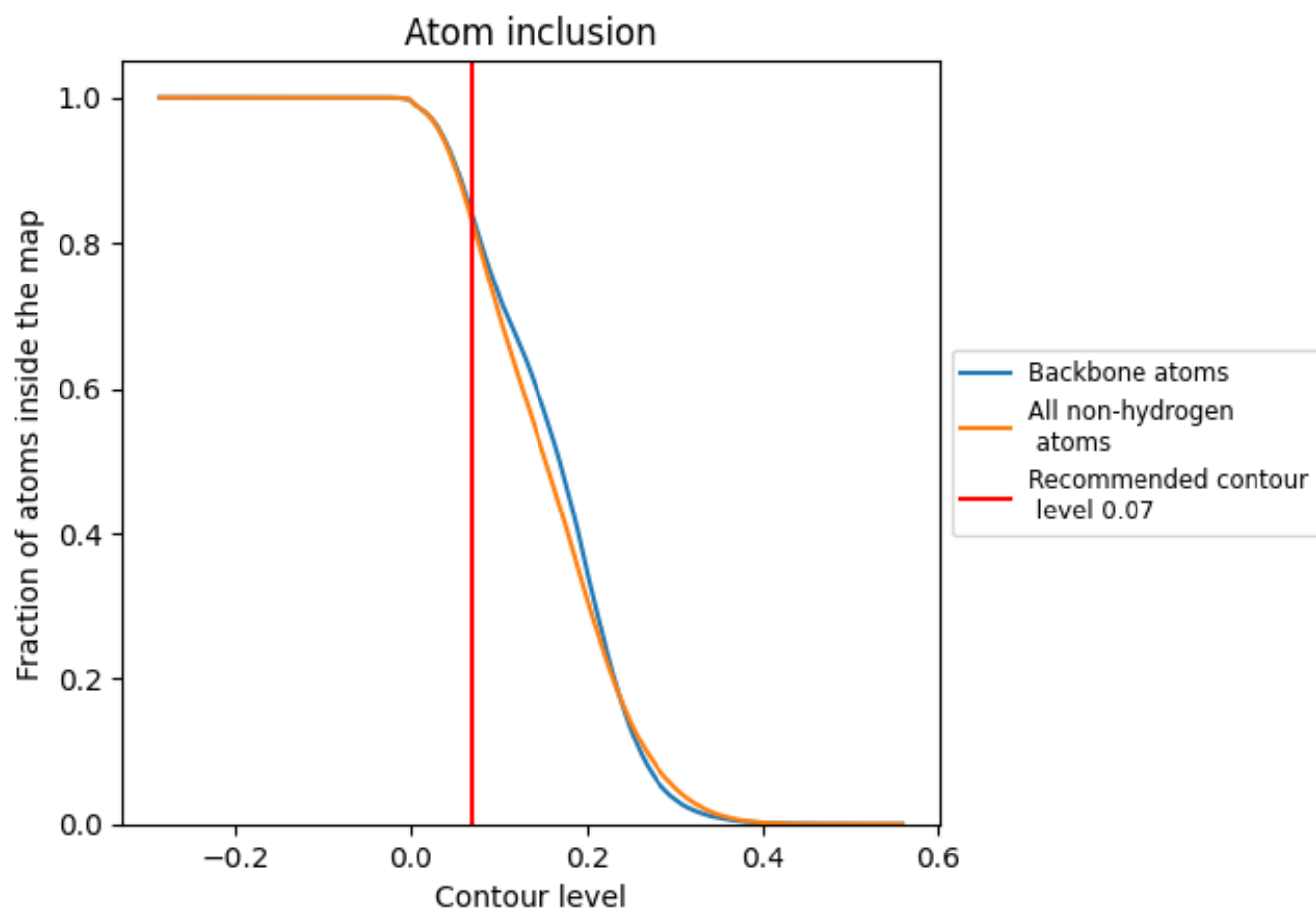
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8278	 0.5190
A	 0.8778	 0.5150
B	 0.8614	 0.5770
C	 0.8639	 0.5630
D	 0.8518	 0.5690
E	 0.7489	 0.4610
F	 0.6791	 0.4980
G	 0.6781	 0.4830
H	 0.7845	 0.5170
J	 0.8336	 0.5540
K	 0.8031	 0.5460
L	 0.8292	 0.5690
M	 0.7967	 0.5290
N	 0.8764	 0.5670
O	 0.8796	 0.5860
P	 0.8356	 0.5290
Q	 0.8716	 0.5780
R	 0.8349	 0.5530
S	 0.8435	 0.5580
T	 0.8039	 0.5440
U	 0.8592	 0.5720
V	 0.8070	 0.5060
W	 0.8333	 0.5540
X	 0.8433	 0.5640
Y	 0.8159	 0.5130
Z	 0.8335	 0.5500
a	 0.7802	 0.5470
b	 0.8527	 0.5570
c	 0.7805	 0.5000
d	 0.7920	 0.5430
e	 0.8119	 0.5700
f	 0.8451	 0.5750
g	 0.8431	 0.5660
h	 0.6472	 0.5110
i	 0.8688	 0.5840



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Chain	Atom inclusion	Q-score
j	 0.7977	 0.5120
k	 0.8502	 0.5830
l	 0.8550	 0.5810
m	 0.8201	 0.5570
n	 0.7449	 0.4860
o	 0.0668	 0.2950
p	 0.6143	 0.3640
t	 0.0025	 0.3180
v	 0.7335	 0.5290
w	 0.4819	 0.4100
x	 0.9686	 0.5410
y	 0.9677	 0.5680
z	 0.4609	 0.5160