



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:18 PM UTC

PDB ID : 6N8N / pdb_00006n8n
EMDB ID : EMD-0373
Title : Cryo-EM structure of Lsg1-engaged (LE) pre-60S ribosomal subunit
Authors : Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.
Deposited on : 2018-11-29
Resolution : 3.80 Å(reported)
Based on initial model : 5T62

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

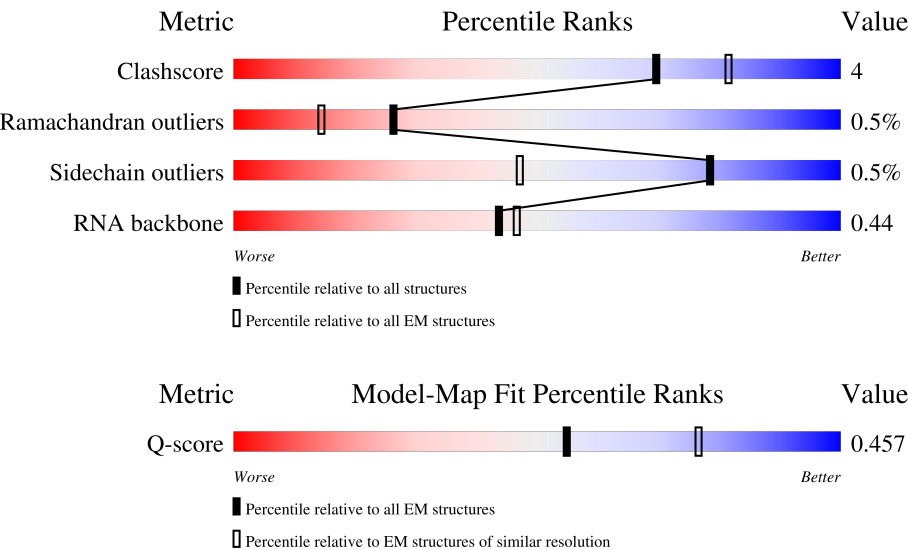
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 Å.

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



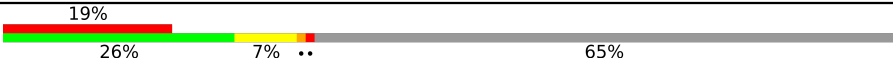
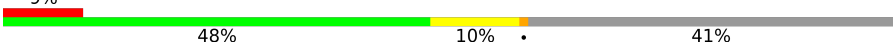
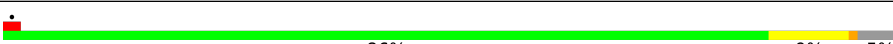
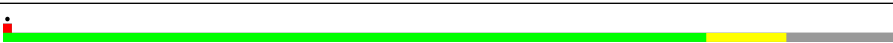
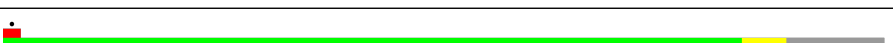
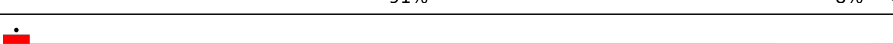
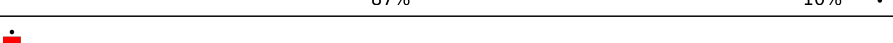
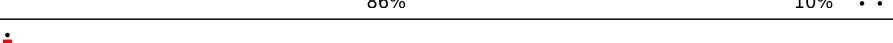
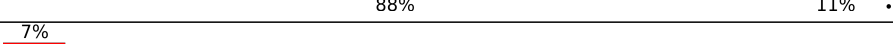
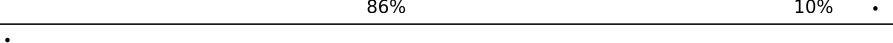
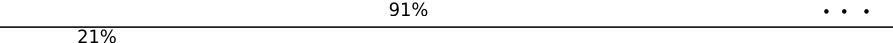
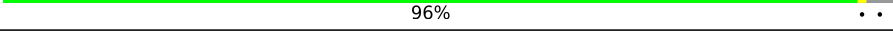
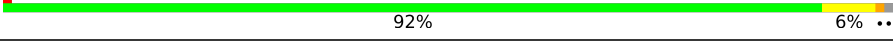
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	121	
3	C	158	

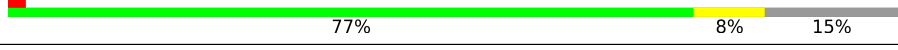
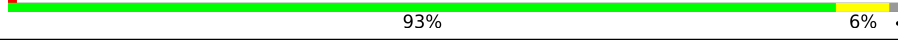
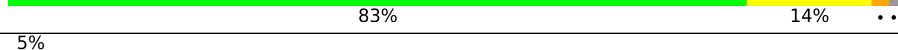
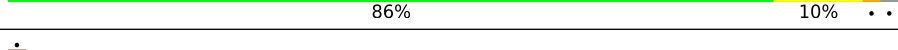
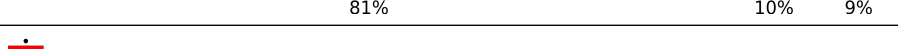
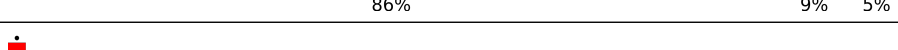
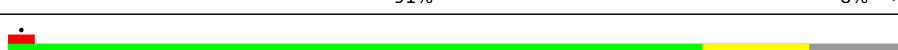
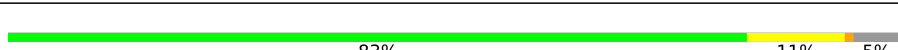
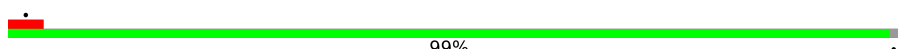
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Mol	Chain	Length	Quality of chain
4	Y	364	
5	X	245	
6	W	640	
7	V	518	
8	D	254	
9	E	387	
10	F	362	
11	G	297	
12	H	176	
13	I	244	
14	J	256	
15	K	191	
16	M	174	
17	N	199	
18	O	138	
19	Q	106	
20	R	92	
21	S	217	
22	a	204	
23	b	199	
24	c	184	
25	d	186	
26	e	189	
27	f	172	
28	g	160	

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Mol	Chain	Length	Quality of chain
29	h	121	
30	i	137	
31	j	155	
32	k	142	
33	l	127	
34	m	136	
35	n	149	
36	o	59	
37	p	105	
38	q	113	
39	r	130	
40	s	107	
41	t	121	
42	u	120	
43	v	100	
44	w	88	
45	x	78	
46	y	51	
47	z	128	
48	L	165	

2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 131813 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 *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3203	Total	C	N	O	P	0	0
			68513	30603	12353	22354	3203		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called Tyrosine-protein phosphatase YVH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	128	Total	C	N	O	S	0	0
			991	625	179	179	8		

- Molecule 5 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	234	Total	C	N	O	S	0	0
			1710	1063	294	346	7		

- Molecule 6 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	W	377	Total	C	N	O	S	0	0
			2972	1903	516	546	7		

- Molecule 7 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V	392	Total	C	N	O	S	0	0
			3034	1930	523	561	20		

- Molecule 8 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	384	Total	C	N	O	S	0	0
			3059	1940	582	529	8		

- Molecule 10 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	283	Total	C	N	O	S	0	0
			2280	1441	397	440	2		

- Molecule 12 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	155	Total	C	N	O	S	0	0
			1217	785	220	211	1		

- Molecule 13 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	220	Total	C	N	O	S	0	0
			1770	1143	322	304	1		

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	227	Total	C	N	O	S	0	0
			1762	1128	315	316	3		

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 16 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	168	Total	C	N	O	S	0	0
			1344	841	251	248	4		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	193	Total	C	N	O		0	0
			1539	959	314	266			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 19 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 20 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	88	Total	C	N	O	S	0	0
			673	416	135	116	6		

- Molecule 21 is a protein called Ribosomal Protein uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	S	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 22 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 23 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 24 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	c	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 25 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 26 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	e	151	Total	C	N	O	0	0
			1219	757	258	204		

- Molecule 27 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 28 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 29 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	97	Total	C	N	O		0	0
			766	496	126	144			

- Molecule 30 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	132	Total	C	N	O	S	0	0
			981	617	184	173	7		

- Molecule 31 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	61	Total	C	N	O	S	0	0
			509	328	100	80	1		

- Molecule 32 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 33 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	p	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 38 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	q	107	Total	C	N	O	S	0	0
			866	550	165	150	1		

- Molecule 39 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	126	Total	C	N	O	S	0	0
			1012	641	204	166	1		

- Molecule 40 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	s	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 41 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	109	Total	C	N	O	S	0	0
			861	533	175	149	4		

- Molecule 42 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 43 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	98	Total	C	N	O	S	0	0
			753	471	150	130	2		

- Molecule 44 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	77	Total	C	N	O		0	0
			608	388	114	106			

- Molecule 46 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 47 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	51	Total	C	N	O	S	0	0
			408	253	84	66	5		

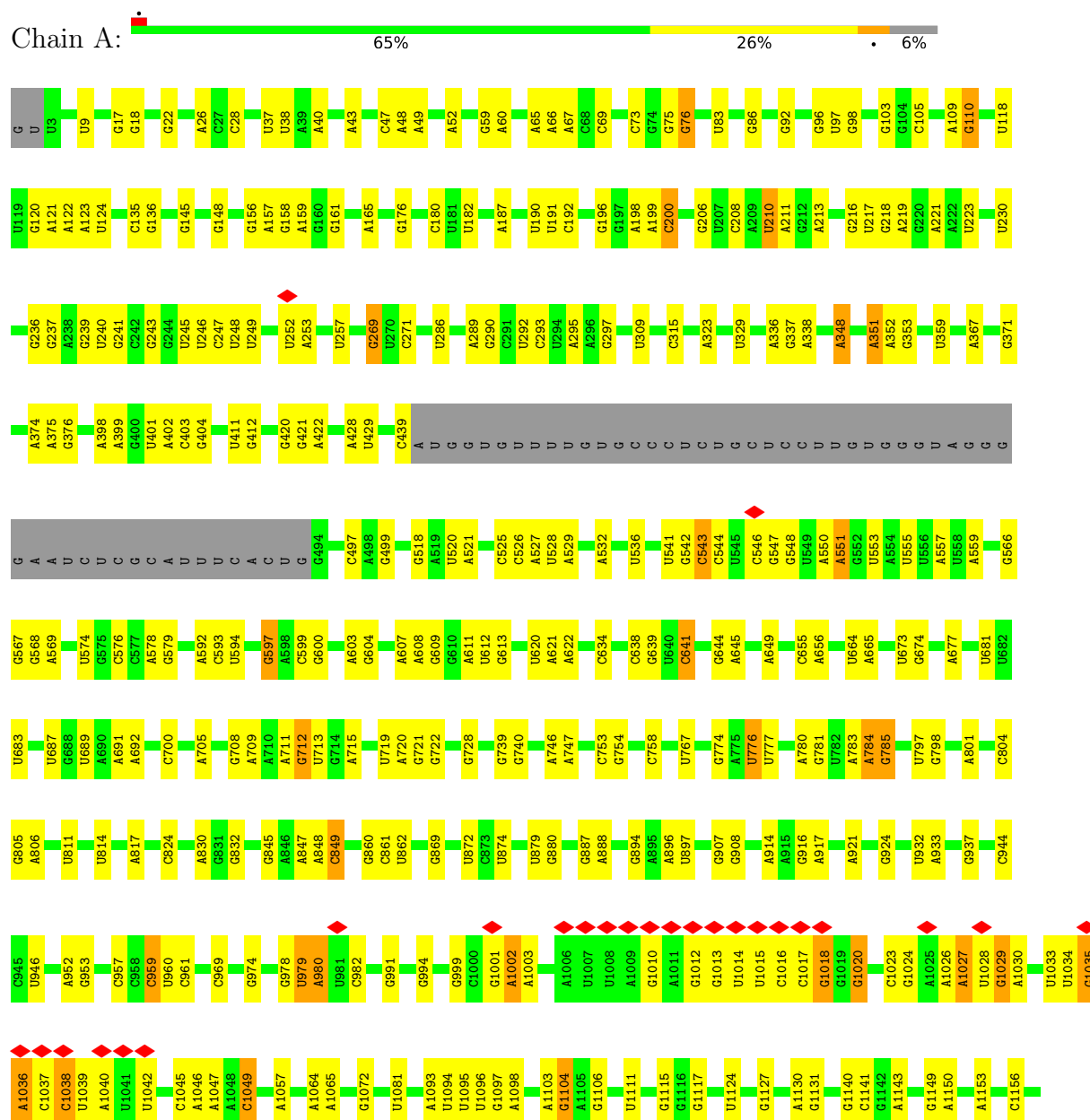
- Molecule 48 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L	147	Total	C	N	O		0	0
			821	502	160	159			

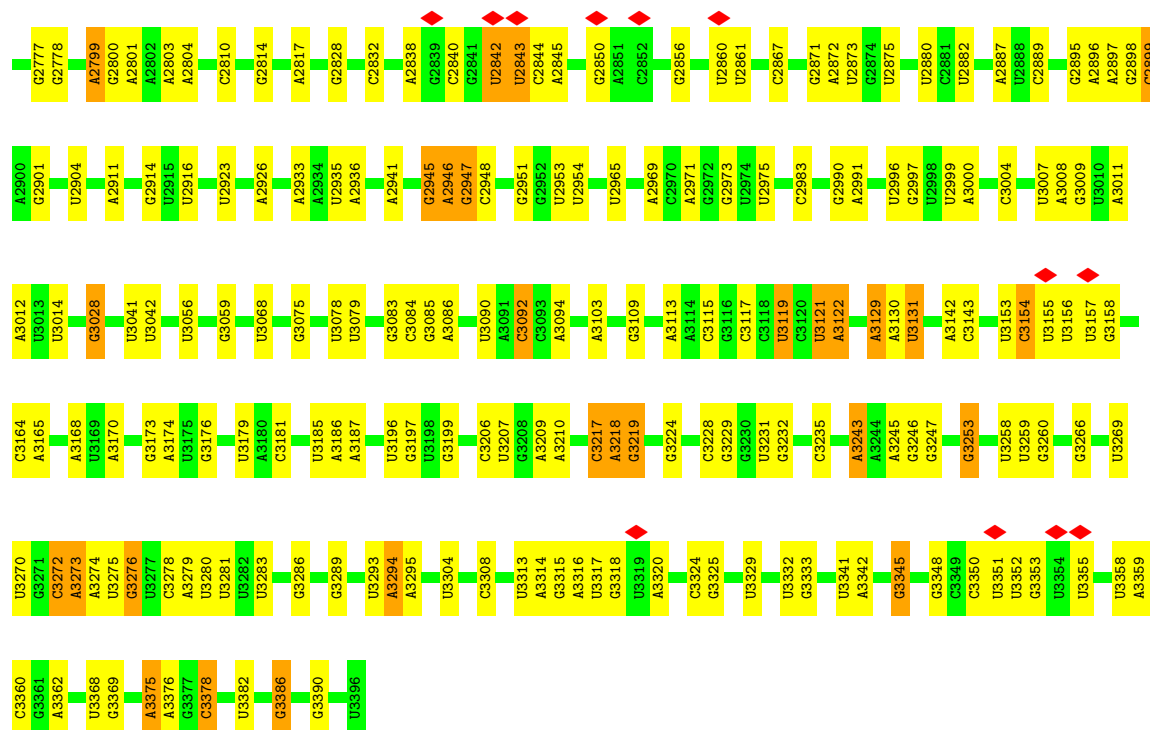
3 Residue-property plots

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

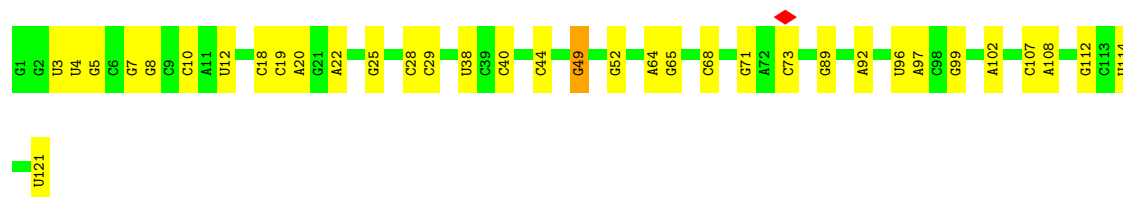
- Molecule 1: *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA



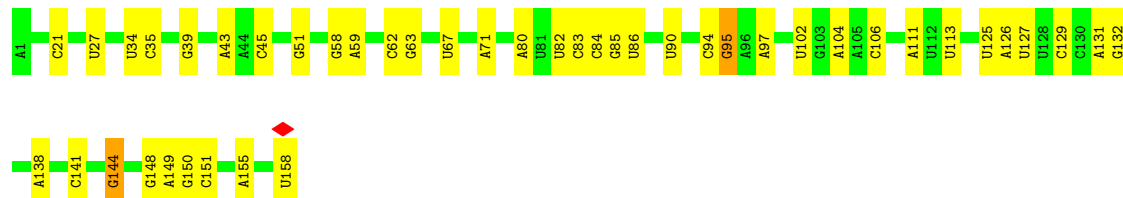
G2619	G2620	A2626	U2631	A2635	A2636	G2648	U2652	A2656	A2657	G2660	G2661	G2664	A2674	G2677	A2680	U2688	A2689	G2690	A2691	A2696	A2704	A2705	G2709	U2712	U2713	U2719	A2727	G2728	U2729	U2743	U2744	U2745	A2748	G2753	G2754	U2768	A2769													
C2507	U2508	U2509	U2513	U2514	A2515	U2516	G2522	C2531	U2532	G2533	G2534	A2535	A2536	U2537	U2538	U2539	A2540	U2541	U2542	U2543	U2544	A2547	G2548	U2549	U2550	U2551	C2552	A2561	A2562	C2568	A2569	U2570	U2571	C2572	G2573	C2577	G2584	G2585	G2586	A2593	U2594	U2599	G2606	G2607	G2608	U2614				
G2435	U2436	G2437	G2440	A2441	G2442	A2443	G2444	A2449	G2450	G2451	G2452	U2453	G2454	G2457	A2458	A2459	U2460	A2461	A2462	G2463	U2464	A2468	G2469	U2472	G2473	G2474	G2475	G2476	G2477	A2480	G2483	A2484	A2485	A2486	U2487	A2488	G2489	C2490	G2495	U2496	U2497	U2498	U2499	A2500	U2501	A2502	G2503	U2504	U2505	U2506
C2287	G2288	U2289	U2290	A2291	U2298	G2306	G2307	C2308	A2309	U2310	G2311	A2312	A2313	U2314	G2315	U2334	G2335	U2336	A2341	C2354	G2364	G2365	G2369	A2373	G2374	G2375	G2376	G2377	G2385	U2388	G2393	G2394	A2397	A2402	G2403	A2404	G2405	C2406	U2411	C2415	A2419	U2424								
C2192	C2196	C2197	A2198	U2205	A2208	U2209	G2210	G2218	A2219	G2220	G2221	A2224	G2236	U2241	A2242	A2243	A2244	G2247	G2248	G2249	G2250	G2253	U2254	A2255	A2256	C2257	U2258	A2259	A2262	U2263	U2264	C2265	U2266	C2267	U2268	U2269	A2270	A2271	G2272	G2273	U2274	A2275	A2281	U2282	G2283	C2284	C2285	U2286		
U	A	C	A	A	U	U	A	A2093	C2094	G2095	C2101	U2102	U2103	A2104	A2107	U2112	A2113	C2114	G2121	G2122	A2126	A2131	U2137	A2138	A2139	A2142	A2149	G2150	G2157	A2158	A2168	C2169	U2170	U2176	G2177	A2178	C2179	G2180	U2184	G2185	U2186	G2187	A2188	U2189	U2190	U2191				
G	A	C	U	A	C	U	U	G	C	C	U	C	C	C	U	U	G	U	A	C	C	C	U	U	U	U	A	G	U	C	U	U	A	A	C	C	C	U	U	C	C	U	U	G	C					
C	U	U	G	G	C	U	C	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C					
G1817	U1820	U1821	U1834	G1838	A1839	A1842	C1849	A1850	G1863	G1866	A1867	U1871	A1874	U1880	A1886	A1893	G1906	C1907	A1908	A1909	A1913	C1926	G1927	C1941	U1942	C1943	G1949	U1950	C1951	G1952	G1953	G1954	U1955	A	G	U	U	G	U	C	C	C	C	C						
G1666	C1671	G1675	A1676	A1683	U1703	A1704	U1705	U1716	U1717	U1724	G1725	G1728	G1736	A1741	U1742	A1750	G1751	C1756	U1757	C1758	A1759	A1760	C1761	C1762	U1763	U1764	U1765	G1766	G1769	G1770	C1773	G1780	G1786	C1793	G1794	U1795	G1796	A1797	A1814	U1815	A1816									
C1556	A1557	A1558	G1560	G1561	C1562	C1563	U1564	A1566	U1567	U1568	U1569	U1570	A1571	U1572	G1576	G1577	C1578	C1579	A1589	G1592	A1593	C1597	U1601	A1605	U1606	U1607	G1618	A1619	U1620	G1624	U1629	G1635	U1636	A1637	A1638	A1642	A1643	A1656	C1657	G1662										
A1419	U1430	G1431	G1434	C1437	G1443	A1446	G1447	U1448	A1449	U1455	A1468	A1474	A1477	A1481	A1482	G1483	U1484	G1485	G1486	G1487	G1488	A1489	C1496	A1506	G1507	C1508	G1513	G1520	G1521	U1522	U1523	A1524	G1525	U1526	C1527	U1533	G1536	G1547	U1554	U1555										
G1285	A1286	G1295	A1301	A1302	G1307	A1308	U1309	G1313	U1325	A1330	C1342	A1343	G1344	G1345	U1348	G1349	A1350	U1351	A1352	U1353	G1354	A1355	U1356	G1357	G1362	A1363	A1366	G1383	U1384	G1385	A1386	A1390	C1391	G1392	A1399	G1400	G1404	A1407	C1411	G1412	A1418									
A1159	G1177	U1180	U1181	A1190	U1191	C1192	A1193	G1194	A1195	G1196	C1199	A1200	C1201	A1203	G1209	U1210	C1219	U1220	A1221	G1222	A1223	C1228	U1235	U1236	G1237	G1238	C1239	A1240	U1241	G1242	G1243	A1244	A1245	G1246	U1247	A1252	U1258	G1262	A1263	G1264	U1265	G1266	A1273	G1281	G1282					



• Molecule 2: 5S rRNA

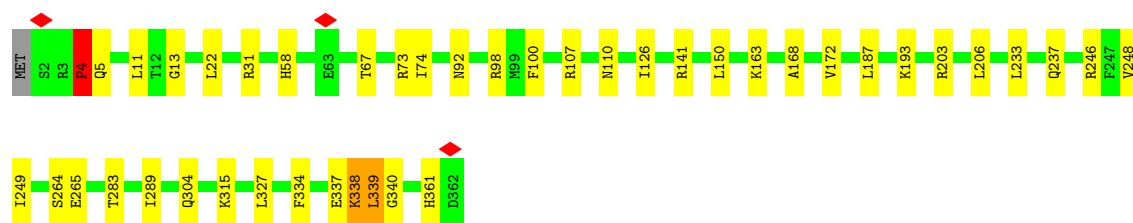


• Molecule 3: 5.8S rRNA



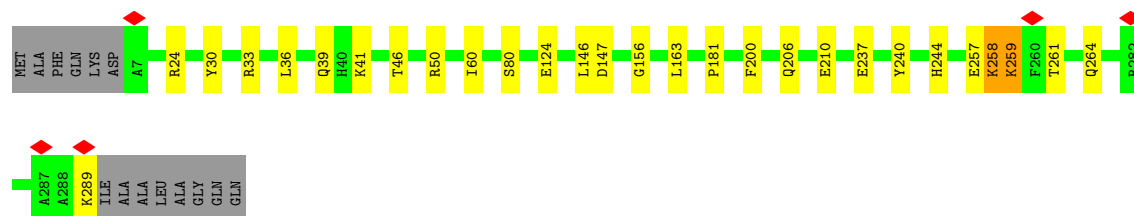
• Molecule 4: Tyrosine-protein phosphatase YVH1





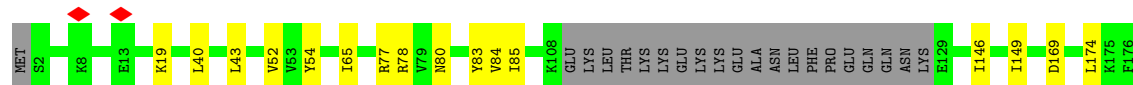
- Molecule 11: 60S ribosomal protein L5

Chain G: 86% 9% 5%



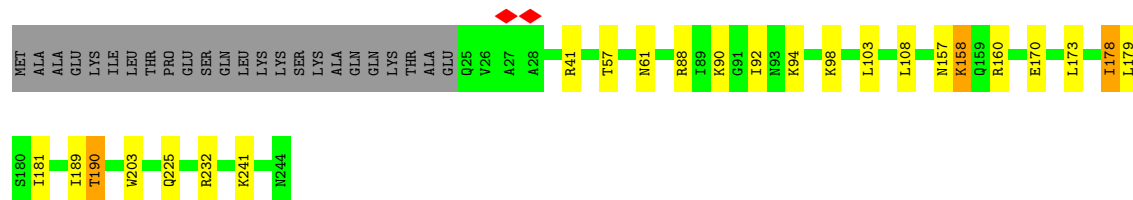
- Molecule 12: 60S ribosomal protein L6-A

Chain H: 79% 9% 12%



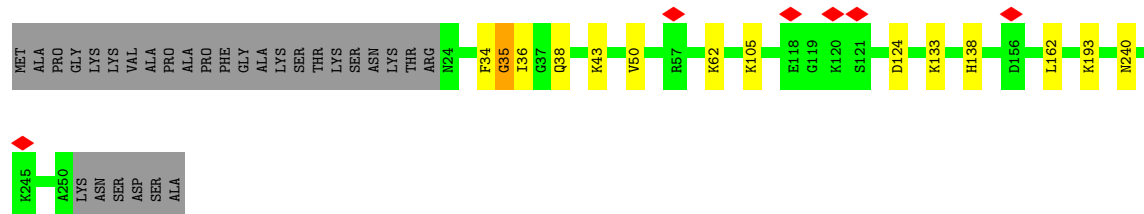
- Molecule 13: 60S ribosomal protein L7-A

Chain I: 80% 9% 10%



- Molecule 14: 60S ribosomal protein L8-A

Chain J: 83% 5% 11%



- Molecule 15: 60S ribosomal protein L9-A

Chain K:  91% 8%



- Molecule 16: 60S ribosomal protein L11-A

Chain M:  87% 10%



- Molecule 17: 60S ribosomal protein L13-A

Chain N:  86% 10%



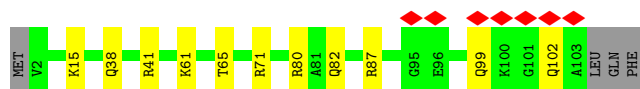
- Molecule 18: 60S ribosomal protein L14-A

Chain O:  88% 11%



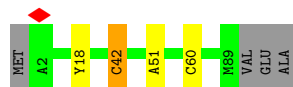
- Molecule 19: 60S ribosomal protein L42-A

Chain Q:  7% 86% 10%

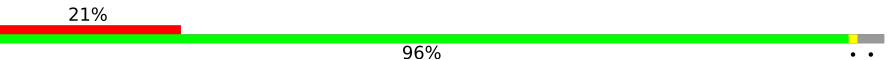


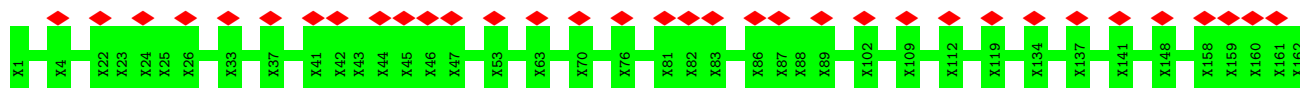
- Molecule 20: 60S ribosomal protein L43-A

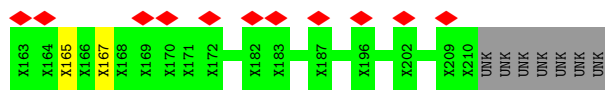
Chain R:  91% 10%



- Molecule 21: Ribosomal Protein uL1

Chain S:  21% 96%





- Molecule 22: 60S ribosomal protein L15-A

Chain a: 83% 17%



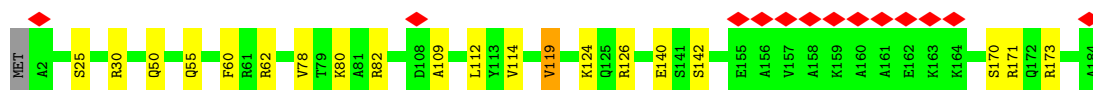
- Molecule 23: 60S ribosomal protein L16-A

Chain b: 89% 10%



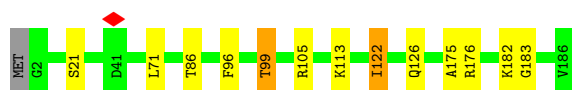
- Molecule 24: 60S ribosomal protein L17-A

Chain c: 7% 89% 10%



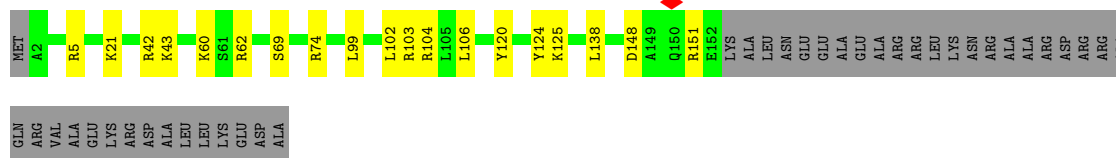
- Molecule 25: 60S ribosomal protein L18-A

Chain d: 92% 6%



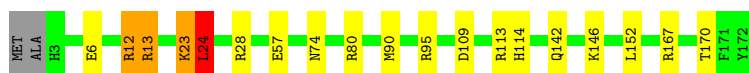
- Molecule 26: 60S ribosomal protein L19-A

Chain e: 70% 10% 20%

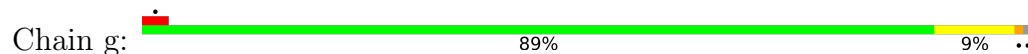


- Molecule 27: 60S ribosomal protein L20-A

Chain f: 88% 9% 9%



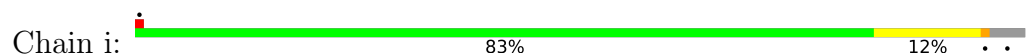
- Molecule 28: 60S ribosomal protein L21-A



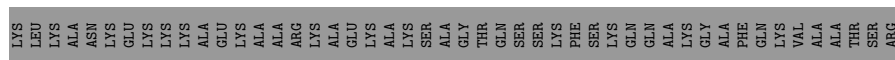
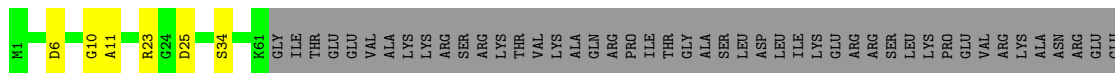
- Molecule 29: 60S ribosomal protein L22-A



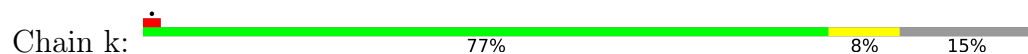
- Molecule 30: 60S ribosomal protein L23-A



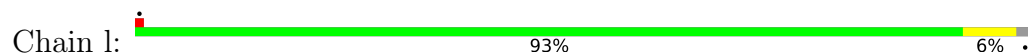
- Molecule 31: 60S ribosomal protein L24-A



- Molecule 32: 60S ribosomal protein L25

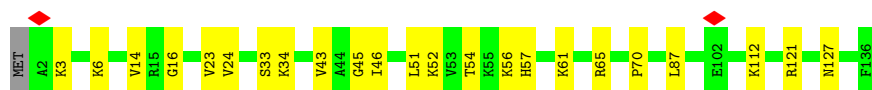


- Molecule 33: 60S ribosomal protein L26-A



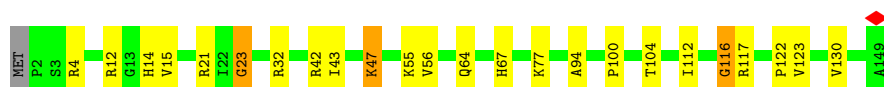
- Molecule 34: 60S ribosomal protein L27-A

Chain m:  82% 17%



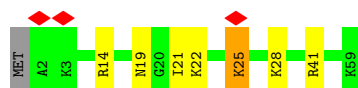
- Molecule 35: 60S ribosomal protein L28

Chain n:  83% 14%



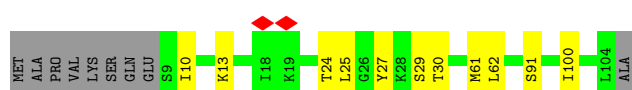
- Molecule 36: 60S ribosomal protein L29

Chain o:  5% 86% 10%



- Molecule 37: 60S ribosomal protein L30

Chain p:  81% 10% 9%



- Molecule 38: 60S ribosomal protein L31-A

Chain q:  86% 9% 5%



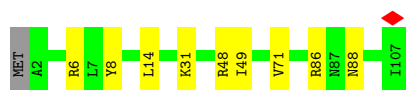
- Molecule 39: 60S ribosomal protein L32

Chain r:  91% 6%

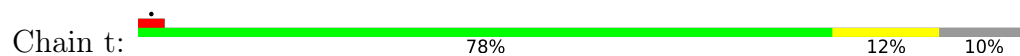


- Molecule 40: 60S ribosomal protein L33-A

Chain s:  91% 8%



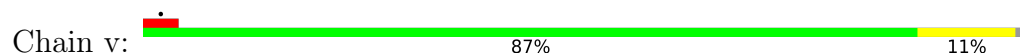
- Molecule 41: 60S ribosomal protein L34-A



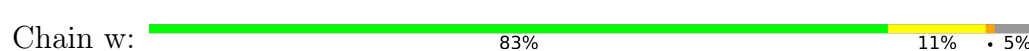
- Molecule 42: 60S ribosomal protein L35-A



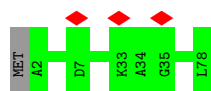
- Molecule 43: 60S ribosomal protein L36-A



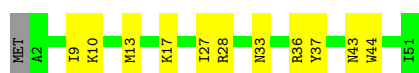
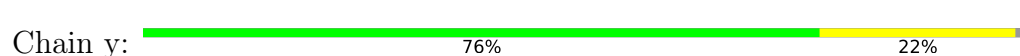
- Molecule 44: 60S ribosomal protein L37-A



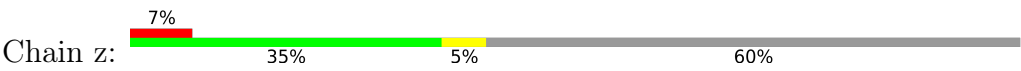
- Molecule 45: 60S ribosomal protein L38



- Molecule 46: 60S ribosomal protein L39



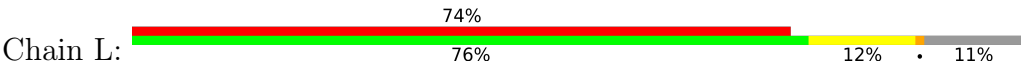
- Molecule 47: Ubiquitin-60S ribosomal protein L40



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

ILE
GLN
LYS
GLU
SER
THR
LEU
HIS
VAL
LEU
LEU
ARG
LEU
ARG
GLY
GLY
I77
I78
E79
P90
K83
S87
D92
R97
Y100
P104
P105
R106
R113
R122
P123
K124
L127
LYS

• Molecule 48: Ribosomal protein L12



MET
PRO
PRO
LYS
PHE
ASP
PRO
ASN
GLU
X10
X11
X12
X17
X18
X19
X20
X21
X22
X23
X24
X25
X26
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X47
X48
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K51
E52
F53
K54
G55
I56
K57
V58
T59
V60
Q61
L62
K63
I64
Q65
N66
R67
Q68
A69
A70
A71
S72
V73
V74
V75
S76
A77
S78
S79
L80
V81
I82
T83
A84
L85
K86
E87
P88
PRO
ARG
ASP
ARG
ARG
LYS
LYS
ASP
K96
N97
V98
K99
H100
S101
G102
N103
I104
I105
L106
D107
E108
I109
I110
X111
E112
X113
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X156
X157
X158
X159
X160
X161
X162
X163
GLU
ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54188	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.137	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.022	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.31	1/76692 (0.0%)	0.36	7/119572 (0.0%)
2	B	0.27	0/2883	0.31	0/4491
3	C	0.32	0/3746	0.34	0/5832
4	Y	0.38	0/1016	1.09	12/1368 (0.9%)
5	X	0.27	0/1729	0.61	2/2355 (0.1%)
6	W	0.33	0/3035	0.86	10/4119 (0.2%)
7	V	0.32	0/3093	0.79	8/4203 (0.2%)
8	D	0.35	0/1908	0.62	2/2564 (0.1%)
9	E	0.35	0/3130	0.64	4/4206 (0.1%)
10	F	0.33	0/2800	0.67	4/3790 (0.1%)
11	G	0.28	0/2329	0.64	4/3142 (0.1%)
12	H	0.28	0/1236	0.58	0/1661
13	I	0.33	0/1807	0.64	1/2432 (0.0%)
14	J	0.30	0/1794	0.61	0/2425
15	K	0.29	0/1514	0.64	0/2039
16	M	0.27	0/1365	0.66	2/1831 (0.1%)
17	N	0.33	0/1564	0.72	3/2102 (0.1%)
18	O	0.29	0/1068	0.56	0/1438
19	Q	0.30	0/831	0.59	0/1097
20	R	0.33	0/680	0.68	0/905
22	a	0.36	0/1757	0.60	0/2354
23	b	0.32	0/1585	0.54	0/2128
24	c	0.34	0/1443	0.64	0/1944
25	d	0.32	0/1465	0.63	1/1965 (0.1%)
26	e	0.31	0/1236	0.56	0/1650
27	f	0.33	0/1468	0.62	3/1973 (0.2%)
28	g	0.30	0/1300	0.63	0/1743
29	h	0.27	0/781	0.60	0/1058
30	i	0.34	0/996	0.55	0/1340
31	j	0.27	0/521	0.55	0/691
32	k	0.32	0/979	0.57	0/1321
33	l	0.29	0/995	0.57	0/1329
34	m	0.33	0/1118	0.62	0/1497
35	n	0.34	0/1204	0.79	5/1612 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	o	0.32	0/473	0.83	1/629 (0.2%)
37	p	0.26	0/745	0.48	0/1001
38	q	0.35	0/880	0.66	0/1182
39	r	0.30	0/1033	0.59	2/1383 (0.1%)
40	s	0.37	0/868	0.60	0/1168
41	t	0.37	0/871	0.61	1/1164 (0.1%)
42	u	0.30	0/978	0.60	0/1301
43	v	0.28	0/759	0.64	0/1009
44	w	0.36	0/680	0.70	0/901
45	x	0.28	0/614	0.56	0/822
46	y	0.33	0/443	0.65	0/588
47	z	0.23	0/414	0.54	0/551
48	L	0.33	0/363	0.94	4/493 (0.8%)
All	All	0.31	1/140189 (0.0%)	0.49	76/206369 (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
4	Y	0	3
5	X	0	2
6	W	0	17
7	V	0	4
9	E	0	1
10	F	0	2
11	G	0	2
13	I	0	3
14	J	0	2
15	K	0	1
16	M	0	2
17	N	0	1
27	f	0	1
35	n	0	3
36	o	0	2
42	u	0	1
All	All	0	47

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2259	A	C1'-N9	-6.05	1.38	1.48

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	t	81	CYS	CA-CB-SG	8.42	133.76	114.40
6	W	337	ILE	CA-C-N	7.36	135.60	121.54
6	W	337	ILE	C-N-CA	7.36	135.60	121.54
11	G	258	LYS	CA-C-N	7.24	135.37	121.54
11	G	258	LYS	C-N-CA	7.24	135.37	121.54

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	X	142	ILE	Peptide
5	X	7	PHE	Peptide
4	Y	325	SER	Peptide
4	Y	326	CYS	Peptide
4	Y	327	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	68513	0	34427	315	0
2	B	2579	0	1304	15	0
3	C	3353	0	1695	14	0
4	Y	991	0	980	19	0
5	X	1710	0	1667	9	0
6	W	2972	0	2973	29	0
7	V	3034	0	3004	70	0
8	D	1874	0	1943	18	0
9	E	3059	0	3127	35	0
10	F	2748	0	2859	30	0
11	G	2280	0	2230	16	0
12	H	1217	0	1308	10	0
13	I	1770	0	1851	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	J	1762	0	1839	10	0
15	K	1493	0	1566	10	0
16	M	1344	0	1370	8	0
17	N	1539	0	1597	12	0
18	O	1053	0	1149	9	0
19	Q	819	0	890	7	0
20	R	673	0	715	3	0
21	S	1050	0	235	1	0
22	a	1720	0	1779	27	0
23	b	1555	0	1659	12	0
24	c	1420	0	1437	12	0
25	d	1441	0	1543	8	0
26	e	1219	0	1301	13	0
27	f	1432	0	1470	14	0
28	g	1276	0	1323	10	0
29	h	766	0	782	6	0
30	i	981	0	1031	13	0
31	j	509	0	537	3	0
32	k	964	0	1025	7	0
33	l	984	0	1075	6	0
34	m	1092	0	1155	15	0
35	n	1173	0	1215	13	0
36	o	462	0	491	5	0
37	p	737	0	792	7	0
38	q	866	0	908	7	0
39	r	1012	0	1079	4	0
40	s	850	0	880	6	0
41	t	861	0	919	10	0
42	u	969	0	1078	4	0
43	v	753	0	826	8	0
44	w	665	0	668	10	0
45	x	608	0	671	0	0
46	y	436	0	475	7	0
47	z	408	0	446	5	0
48	L	821	0	434	19	0
All	All	131813	0	95728	730	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 730 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L:97:ASN:O	48:L:99:LYS:HD2	1.47	1.14
7:V:49:ILE:HG22	7:V:90:LYS:HG3	1.28	1.08
7:V:96:ARG:HD3	7:V:119:GLN:HE22	1.14	1.06
1:A:2247:G:C6	1:A:2248:C:C5	2.44	1.05
7:V:90:LYS:HE2	7:V:90:LYS:HA	1.41	1.00

There are no symmetry-related clashes.

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	Y	126/364 (35%)	99 (79%)	22 (18%)	5 (4%)	2	20
5	X	230/245 (94%)	221 (96%)	9 (4%)	0	100	100
6	W	373/640 (58%)	313 (84%)	54 (14%)	6 (2%)	7	35
7	V	388/518 (75%)	323 (83%)	59 (15%)	6 (2%)	8	36
8	D	244/254 (96%)	225 (92%)	19 (8%)	0	100	100
9	E	382/387 (99%)	354 (93%)	26 (7%)	2 (0%)	24	57
10	F	359/362 (99%)	330 (92%)	26 (7%)	3 (1%)	16	48
11	G	281/297 (95%)	268 (95%)	12 (4%)	1 (0%)	30	62
12	H	151/176 (86%)	142 (94%)	9 (6%)	0	100	100
13	I	218/244 (89%)	207 (95%)	9 (4%)	2 (1%)	14	45
14	J	225/256 (88%)	217 (96%)	7 (3%)	1 (0%)	30	62
15	K	186/191 (97%)	176 (95%)	10 (5%)	0	100	100
16	M	166/174 (95%)	152 (92%)	14 (8%)	0	100	100
17	N	191/199 (96%)	172 (90%)	17 (9%)	2 (1%)	12	43
18	O	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
19	Q	100/106 (94%)	94 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	R	86/92 (94%)	80 (93%)	6 (7%)	0	100	100
22	a	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
23	b	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
24	c	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
25	d	183/186 (98%)	175 (96%)	8 (4%)	0	100	100
26	e	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
27	f	168/172 (98%)	155 (92%)	11 (6%)	2 (1%)	10	40
28	g	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
29	h	95/121 (78%)	91 (96%)	3 (3%)	1 (1%)	11	41
30	i	130/137 (95%)	129 (99%)	1 (1%)	0	100	100
31	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	7	34
32	k	119/142 (84%)	111 (93%)	8 (7%)	0	100	100
33	l	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
34	m	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
35	n	146/149 (98%)	132 (90%)	11 (8%)	3 (2%)	5	31
36	o	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
37	p	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
38	q	105/113 (93%)	98 (93%)	7 (7%)	0	100	100
39	r	124/130 (95%)	118 (95%)	6 (5%)	0	100	100
40	s	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
41	t	107/121 (88%)	103 (96%)	4 (4%)	0	100	100
42	u	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
43	v	96/100 (96%)	90 (94%)	6 (6%)	0	100	100
44	w	82/88 (93%)	75 (92%)	7 (8%)	0	100	100
45	x	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
46	y	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
47	z	49/128 (38%)	46 (94%)	3 (6%)	0	100	100
48	L	53/165 (32%)	48 (91%)	5 (9%)	0	100	100
All	All	6989/8269 (84%)	6483 (93%)	471 (7%)	35 (0%)	26	57

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	V	95	VAL
10	F	339	LEU
11	G	259	LYS
13	I	178	ILE
4	Y	326	CYS

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	Y	110/323 (34%)	109 (99%)	1 (1%)	70	74
5	X	186/211 (88%)	186 (100%)	0	100	100
6	W	316/555 (57%)	313 (99%)	3 (1%)	70	74
7	V	332/467 (71%)	330 (99%)	2 (1%)	78	79
8	D	189/196 (96%)	187 (99%)	2 (1%)	65	73
9	E	317/323 (98%)	316 (100%)	1 (0%)	86	84
10	F	288/289 (100%)	287 (100%)	1 (0%)	86	84
11	G	236/245 (96%)	235 (100%)	1 (0%)	84	83
12	H	131/153 (86%)	131 (100%)	0	100	100
13	I	185/205 (90%)	184 (100%)	1 (0%)	81	81
14	J	182/208 (88%)	182 (100%)	0	100	100
15	K	168/171 (98%)	168 (100%)	0	100	100
16	M	146/150 (97%)	146 (100%)	0	100	100
17	N	153/159 (96%)	151 (99%)	2 (1%)	61	71
18	O	107/109 (98%)	107 (100%)	0	100	100
19	Q	87/91 (96%)	87 (100%)	0	100	100
20	R	69/72 (96%)	68 (99%)	1 (1%)	59	70
22	a	175/176 (99%)	175 (100%)	0	100	100
23	b	160/162 (99%)	159 (99%)	1 (1%)	78	79
24	c	140/146 (96%)	138 (99%)	2 (1%)	59	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	d	150/151 (99%)	149 (99%)	1 (1%)	76	77
26	e	125/154 (81%)	124 (99%)	1 (1%)	73	76
27	f	155/156 (99%)	154 (99%)	1 (1%)	78	79
28	g	136/137 (99%)	134 (98%)	2 (2%)	57	69
29	h	84/107 (78%)	84 (100%)	0	100	100
30	i	102/105 (97%)	101 (99%)	1 (1%)	68	74
31	j	54/129 (42%)	54 (100%)	0	100	100
32	k	104/118 (88%)	104 (100%)	0	100	100
33	l	108/110 (98%)	108 (100%)	0	100	100
34	m	115/116 (99%)	115 (100%)	0	100	100
35	n	118/119 (99%)	117 (99%)	1 (1%)	73	76
36	o	46/47 (98%)	46 (100%)	0	100	100
37	p	81/88 (92%)	81 (100%)	0	100	100
38	q	92/97 (95%)	92 (100%)	0	100	100
39	r	108/111 (97%)	108 (100%)	0	100	100
40	s	90/91 (99%)	90 (100%)	0	100	100
41	t	94/103 (91%)	92 (98%)	2 (2%)	47	64
42	u	104/105 (99%)	104 (100%)	0	100	100
43	v	78/82 (95%)	78 (100%)	0	100	100
44	w	69/71 (97%)	68 (99%)	1 (1%)	59	70
45	x	67/69 (97%)	67 (100%)	0	100	100
46	y	45/46 (98%)	45 (100%)	0	100	100
47	z	46/116 (40%)	46 (100%)	0	100	100
48	L	31/65 (48%)	30 (97%)	1 (3%)	34	56
All	All	5879/6904 (85%)	5850 (100%)	29 (0%)	78	81

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	R	42	CYS
44	w	22	CYS
24	c	119	VAL
35	n	4	ARG
24	c	114	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
24	c	55	GLN
37	p	36	GLN
25	d	15	HIS
29	h	25	ASN
39	r	26	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3200/3396 (94%)	705 (22%)	37 (1%)
2	B	120/121 (99%)	15 (12%)	0
3	C	157/158 (99%)	31 (19%)	2 (1%)
All	All	3477/3675 (94%)	751 (21%)	39 (1%)

5 of 751 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	G
1	A	18	G
1	A	22	G
1	A	26	A
1	A	40	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2513	U
1	A	3228	C
1	A	2537	U
1	A	3078	U
3	C	82	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

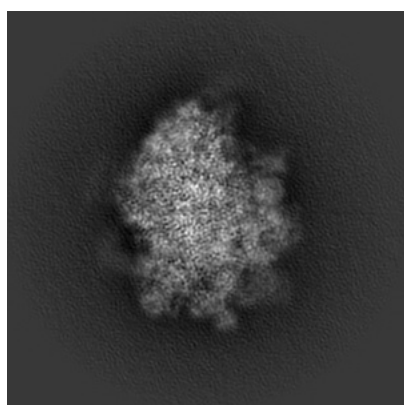
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0373. These allow visual inspection of the internal detail of the map and identification of artifacts.

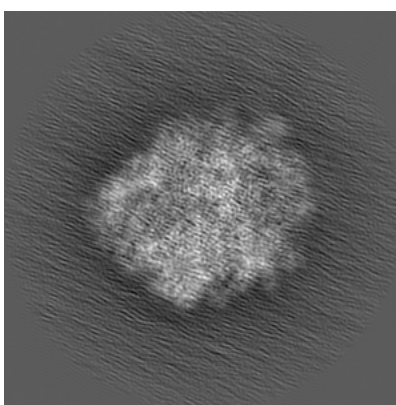
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

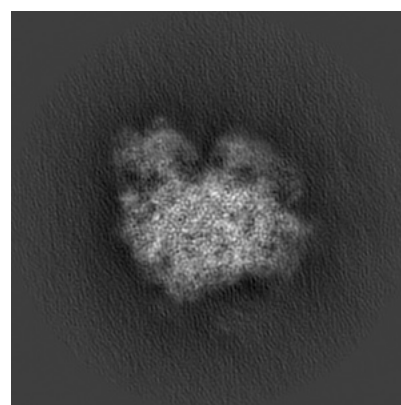
6.1.1 Primary map



X



Y

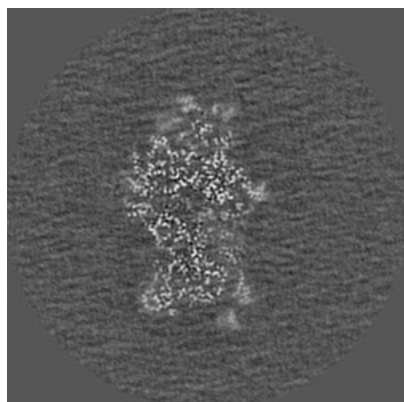


Z

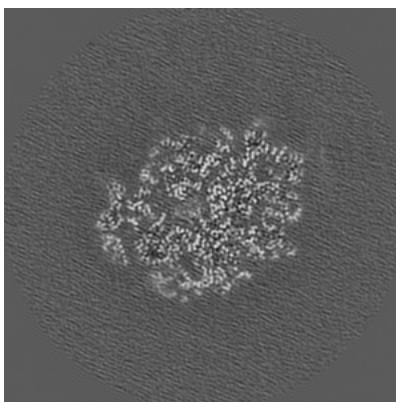
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

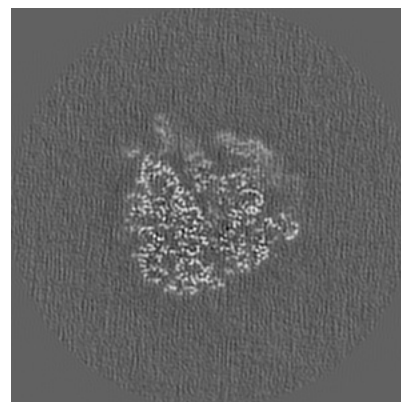
6.2.1 Primary map



X Index: 192



Y Index: 192

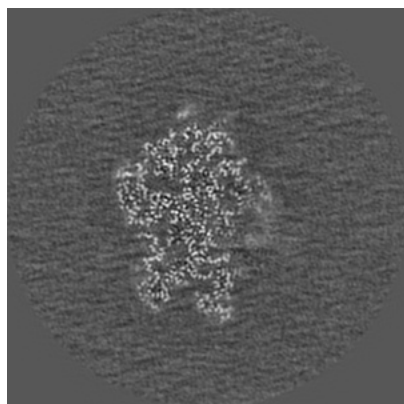


Z Index: 192

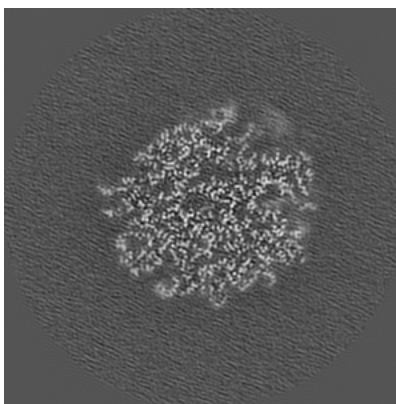
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

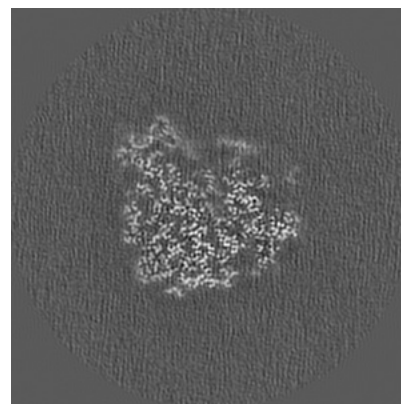
6.3.1 Primary map



X Index: 173



Y Index: 173

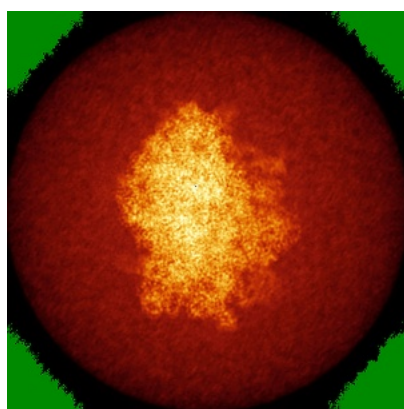


Z Index: 185

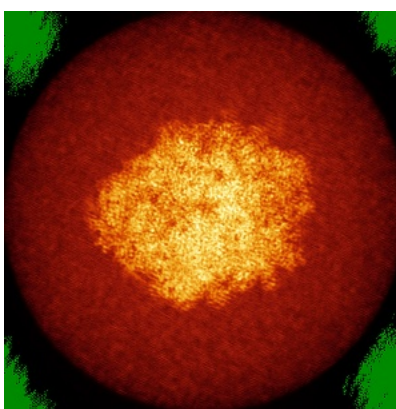
The images above show the largest variance slices of the map in three orthogonal directions.

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

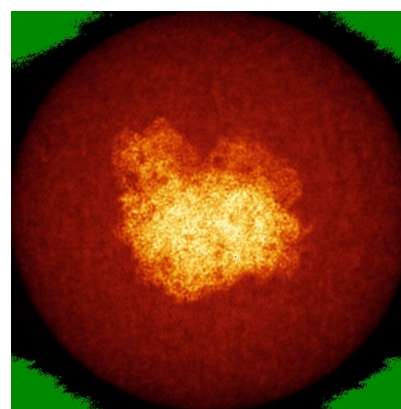
6.4.1 Primary map



X



Y

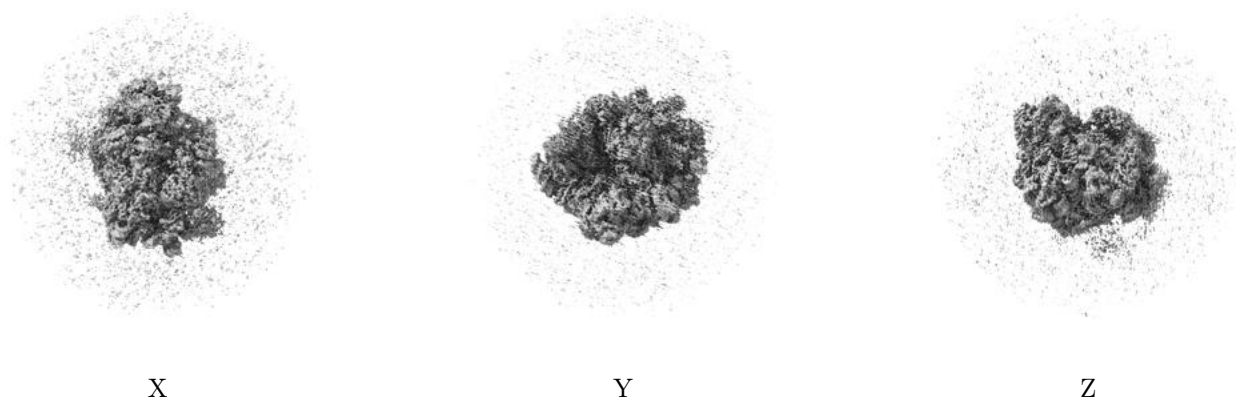


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

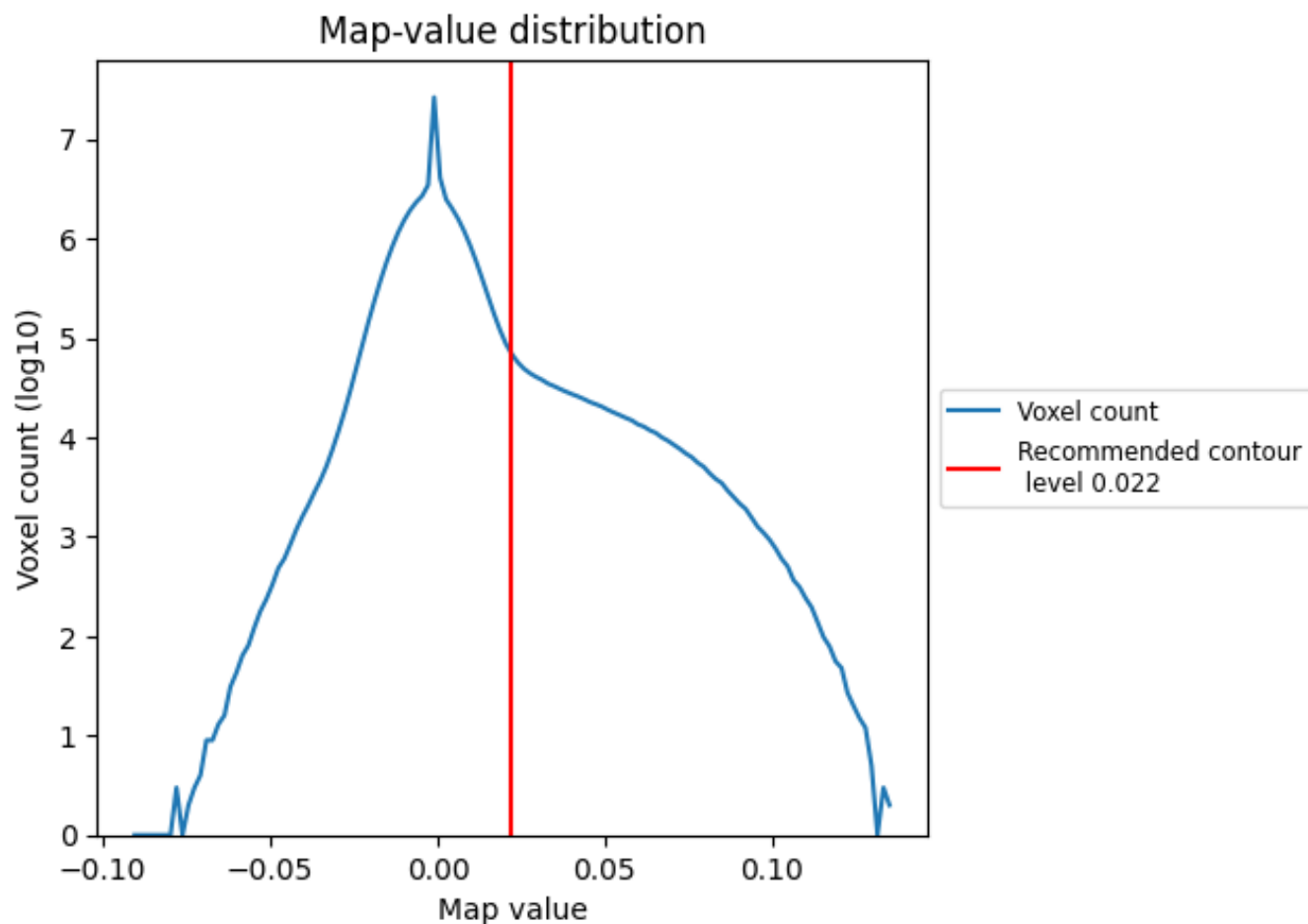
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

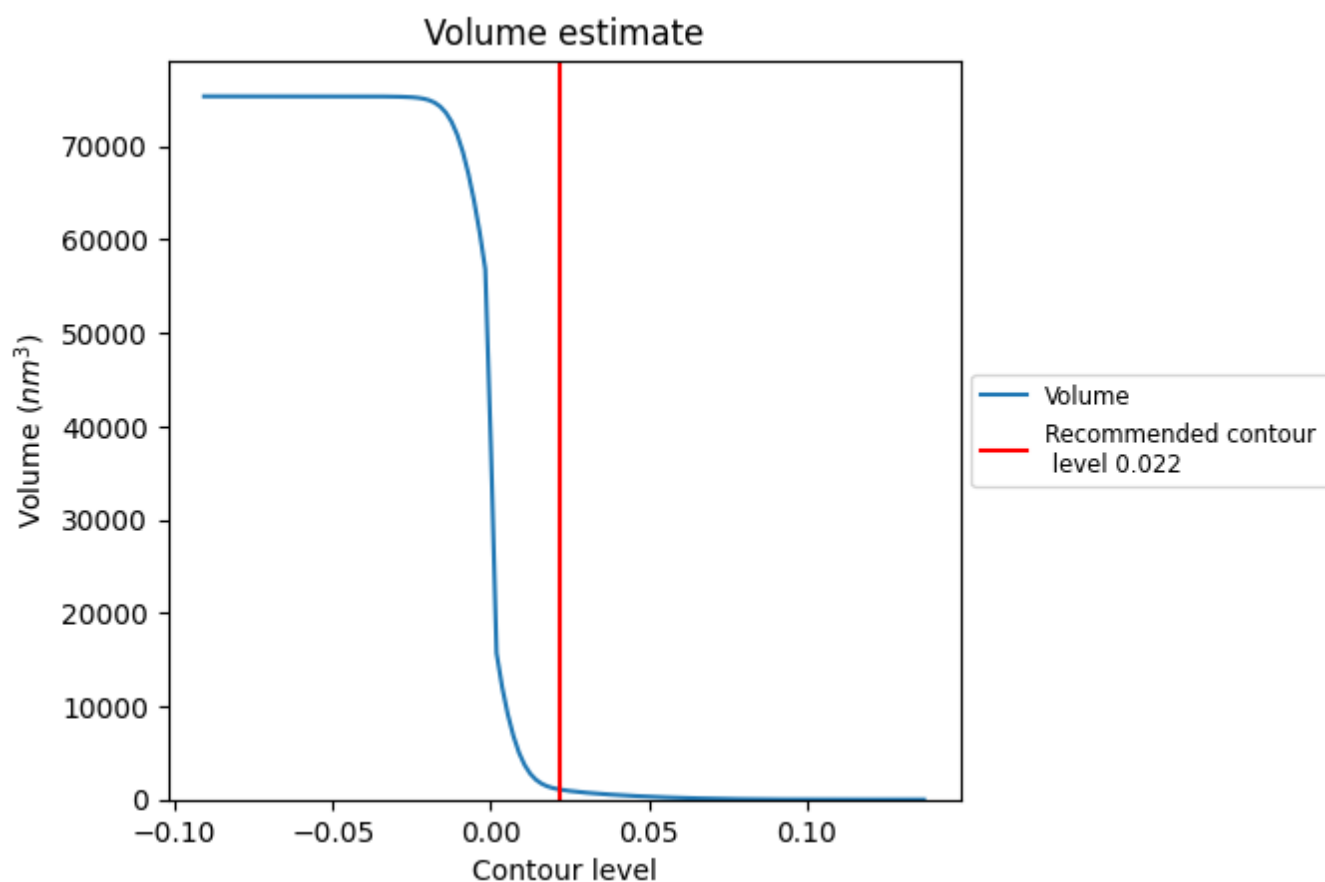
This section contains the results of statistical analysis of the map.

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.

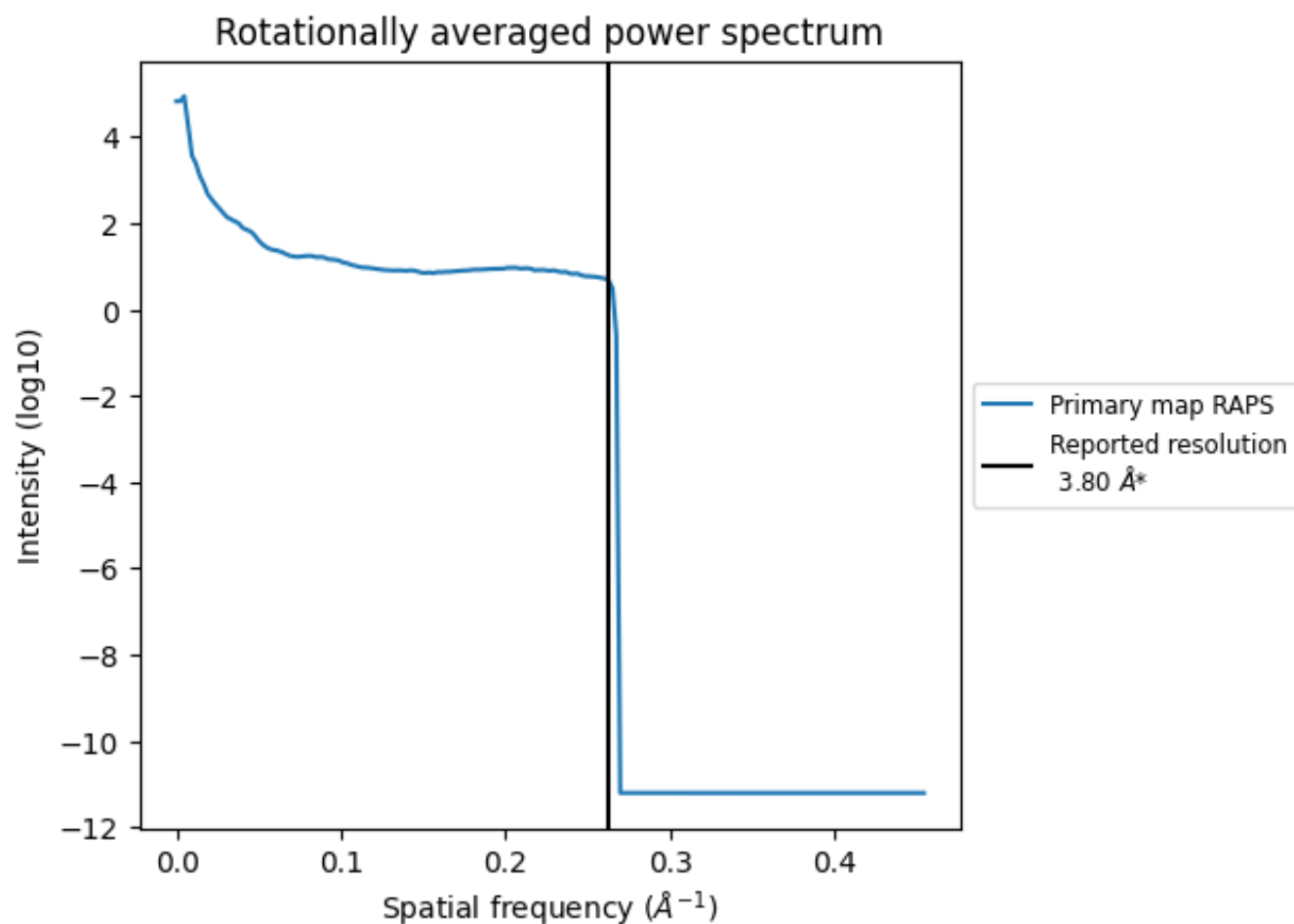
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1068 nm³; this corresponds to an approximate mass of 965 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 ⓘ

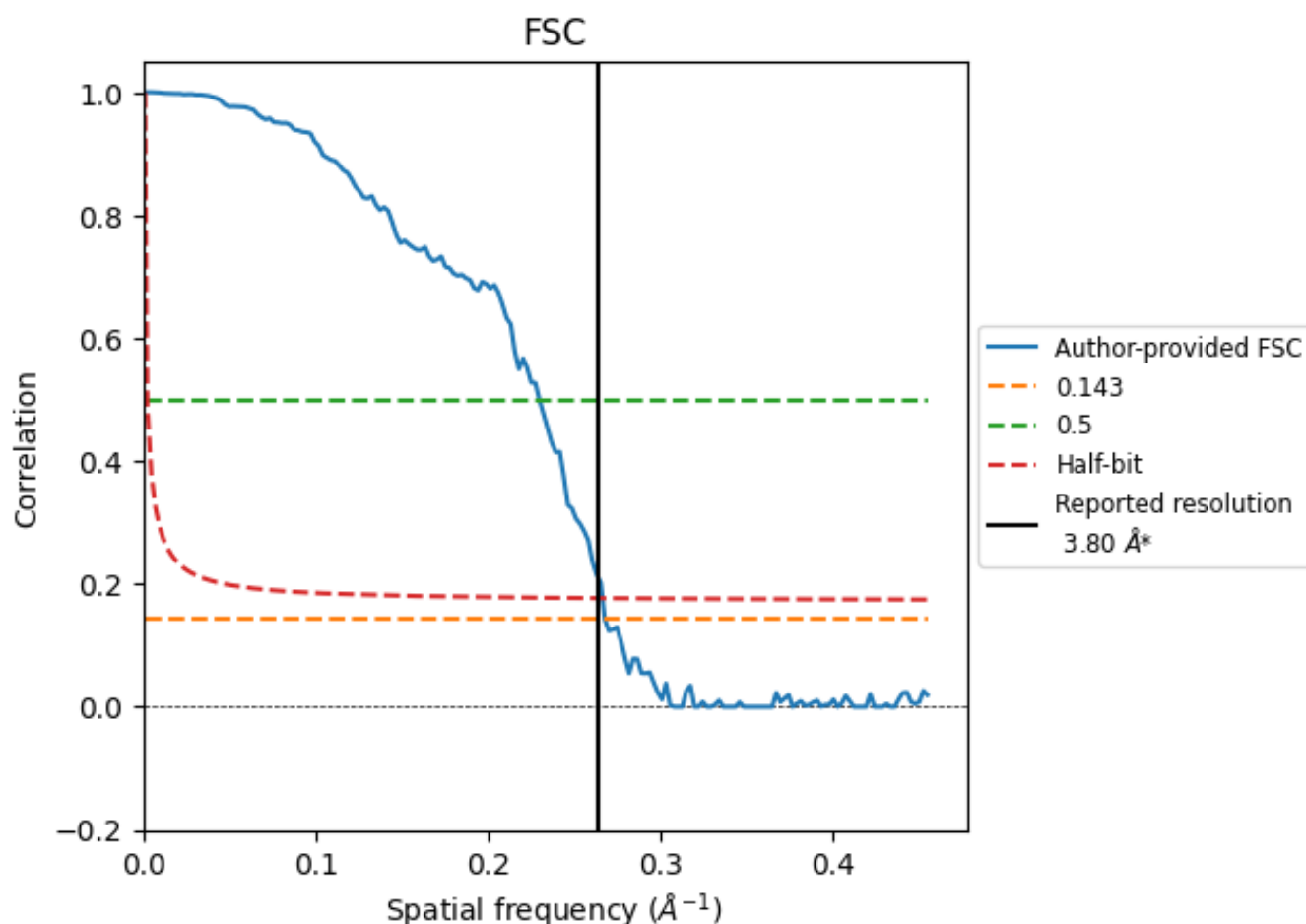


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

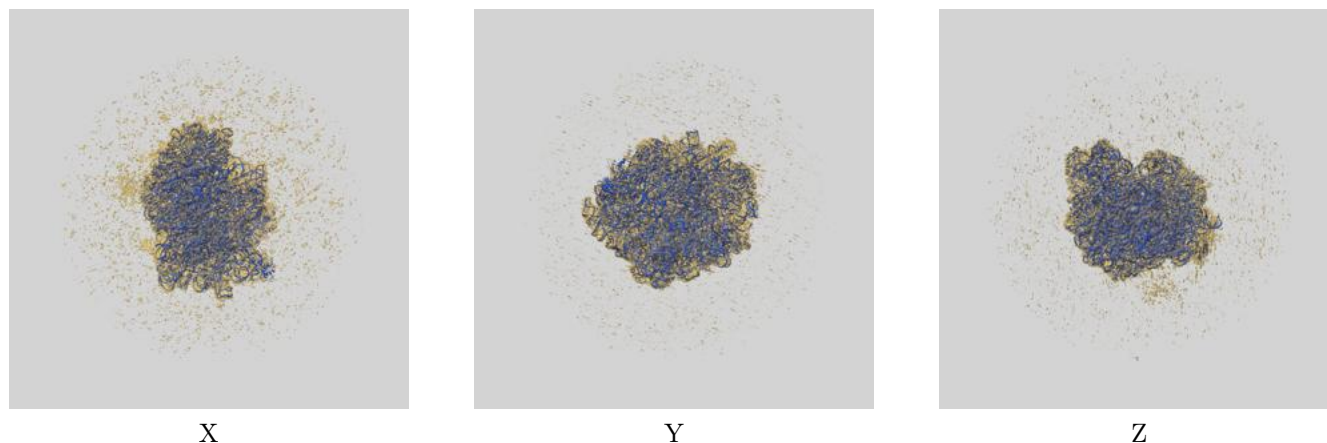
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.74	4.35	3.76
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

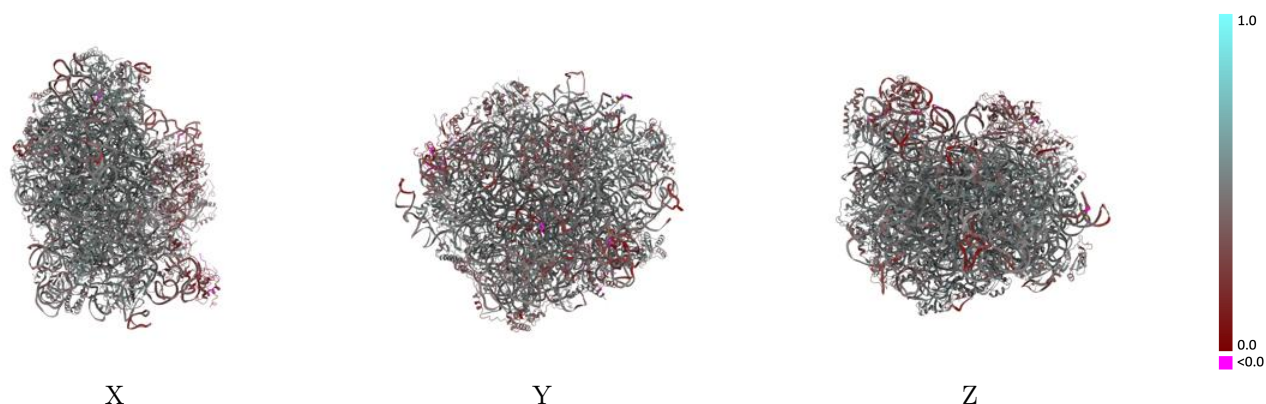
This section contains information regarding the fit between EMDB map EMD-0373 and PDB model 6N8N. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



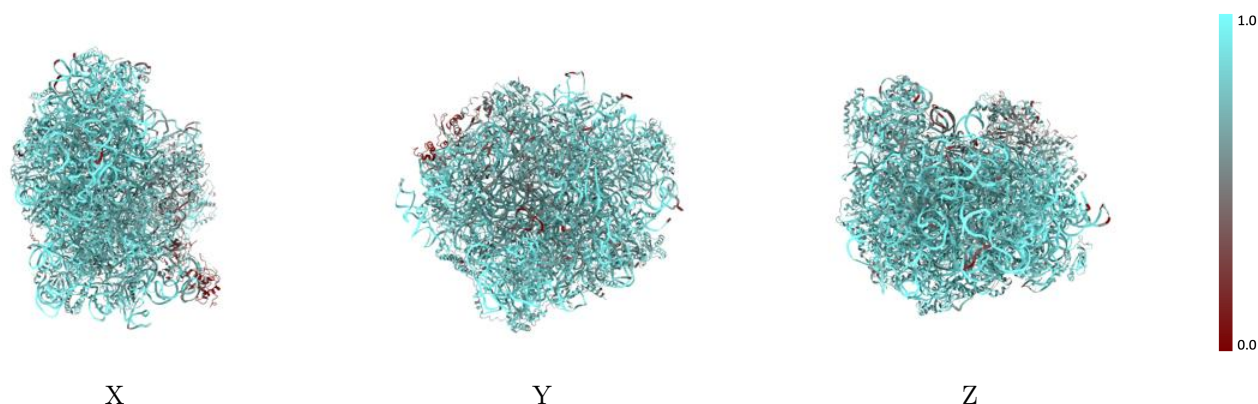
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



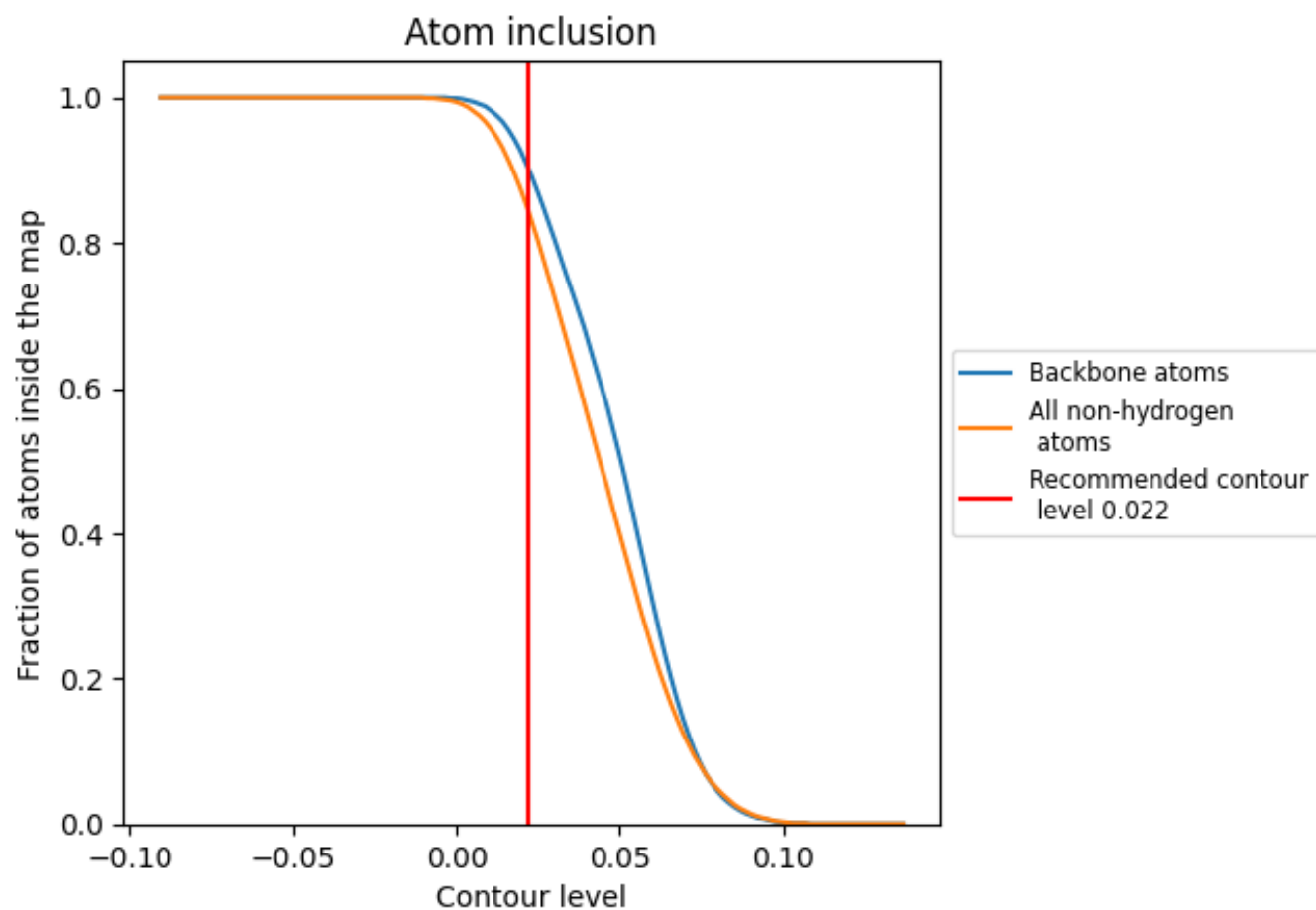
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4570
A	 0.9100	 0.4590
B	 0.9520	 0.4610
C	 0.9400	 0.4730
D	 0.8240	 0.5080
E	 0.8270	 0.4900
F	 0.7950	 0.4810
G	 0.7750	 0.4170
H	 0.7870	 0.4620
I	 0.8080	 0.4740
J	 0.8030	 0.4600
K	 0.7870	 0.4730
L	 0.2100	 0.2090
M	 0.7240	 0.3840
N	 0.7880	 0.4620
O	 0.8050	 0.4690
Q	 0.7450	 0.4820
R	 0.8130	 0.4930
S	 0.7010	 0.3340
V	 0.6160	 0.4010
W	 0.6460	 0.3470
X	 0.7030	 0.4330
Y	 0.3890	 0.3310
a	 0.8250	 0.5050
b	 0.8180	 0.4940
c	 0.7800	 0.4820
d	 0.7960	 0.4860
e	 0.8310	 0.4900
f	 0.8100	 0.4800
g	 0.7680	 0.4780
h	 0.7930	 0.4390
i	 0.7580	 0.4890
j	 0.7850	 0.4810
k	 0.7940	 0.4690
l	 0.7970	 0.4860



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Chain	Atom inclusion	Q-score
m	 0.8220	 0.4730
n	 0.8160	 0.4950
o	 0.7260	 0.4380
p	 0.7770	 0.4580
q	 0.7680	 0.4640
r	 0.7890	 0.4950
s	 0.8320	 0.5030
t	 0.7850	 0.4910
u	 0.8080	 0.4660
v	 0.7640	 0.4510
w	 0.8700	 0.5130
x	 0.7480	 0.4440
y	 0.7930	 0.5030
z	 0.5560	 0.4530