



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 10:09 am BST

PDB ID : 6RZZ
EMDB ID : EMD-10068
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-06-13
Resolution : 3.20 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:

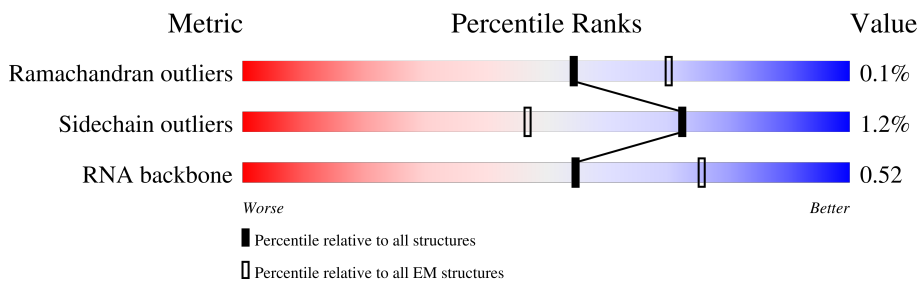
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	

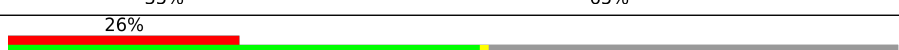
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Mol	Chain	Length	Quality of chain
9	J	198	99%
10	K	199	92% 7%
11	L	137	99%
12	M	138	98% 6%
13	N	149	99%
14	O	204	100%
15	P	297	90% 9%
16	Q	186	99%
17	R	189	79% 21%
18	S	172	98%
19	T	160	98%
20	U	184	84% 16%
21	V	121	82% 18%
22	W	142	83% 15%
23	X	127	98%
24	Y	136	99%
25	Z	120	97%
26	a	59	88% 12%
27	b	244	89% 10%
28	c	105	91% 8%
29	d	113	93% 8%
30	e	130	96%
31	f	107	98%
32	g	121	83% 15%
33	h	100	98% 18%

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Mol	Chain	Length	Quality of chain
34	i	88	 93% 5%
35	j	78	 96%
36	k	51	 98%
37	l	106	 87% 11%
38	m	92	 95%
39	n	245	 90% 9%
40	o	640	 49% 37% 50%
41	p	210	 100% 31%
42	r	593	 86% 43% 13%
43	s	364	 65% 35% 35%
44	u	393	 46% 26% 53%
45	v	155	 61% 19% 39%
46	w	518	 72% 25% 25%
47	x	121	 84% 16%
48	y	158	 81% 17%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 134359 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 Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	320	Total	C	N	O	S	0	0
			2574	1648	444	475	7		

- Molecule 41 is a protein called uL1.

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

- Molecule 42 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	r	516	3999	2530	688	766	15	0	0

- Molecule 43 is a protein called Tyrosine-protein phosphatase YVH1.

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

- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	u	211	1724	1095	307	314	8	0	0

- Molecule 45 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 46 is a protein called 60S ribosomal export protein NMD3.

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

- Molecule 47 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 48 is a RNA chain called 5.8S ribosomal RNA.

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

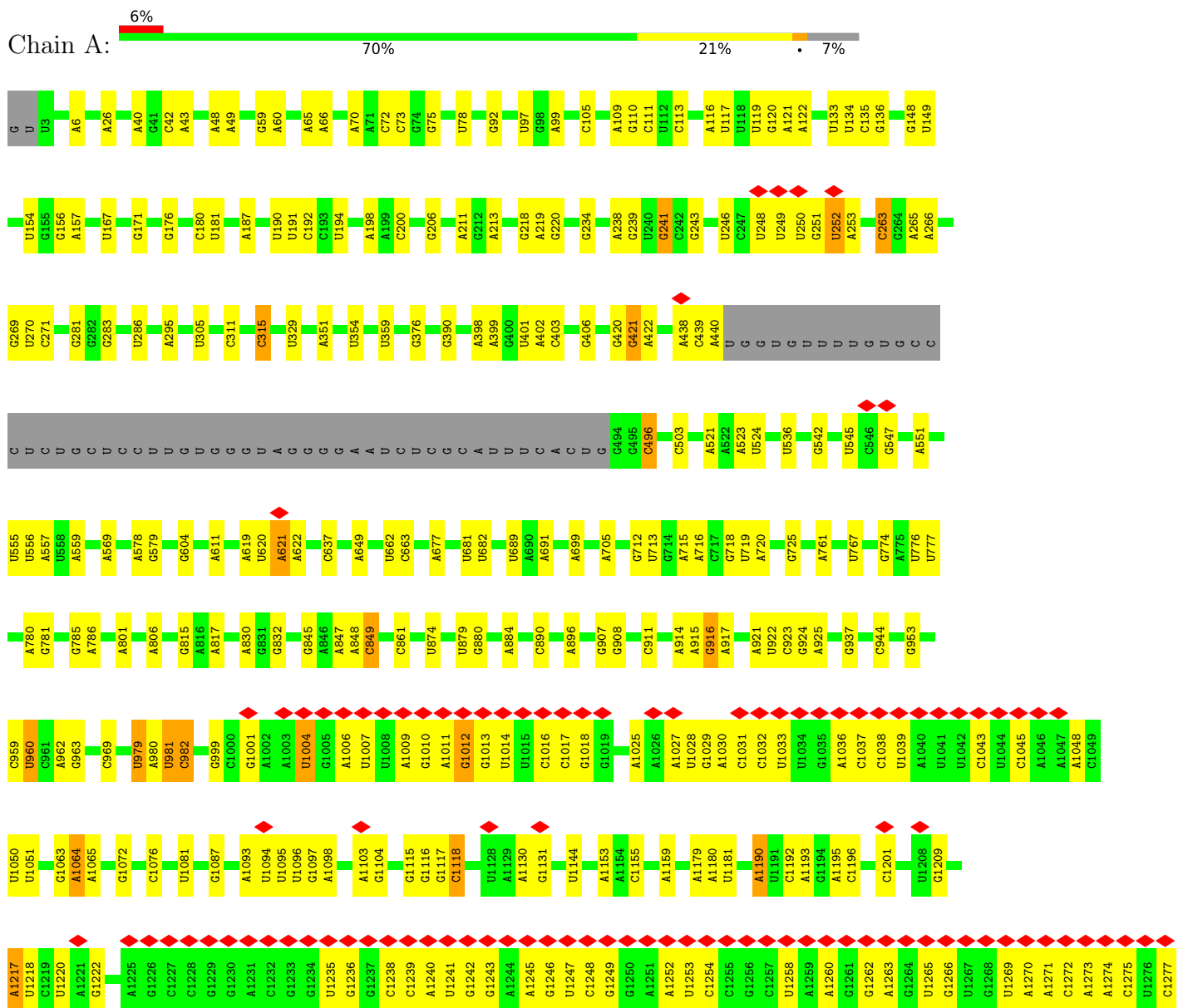
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	g	1	Total 1	Zn 1	0
49	i	1	Total 1	Zn 1	0
49	l	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	s	2	Total 2	Zn 2	0
49	u	2	Total 2	Zn 2	0
49	w	2	Total 2	Zn 2	0

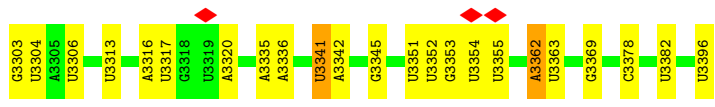
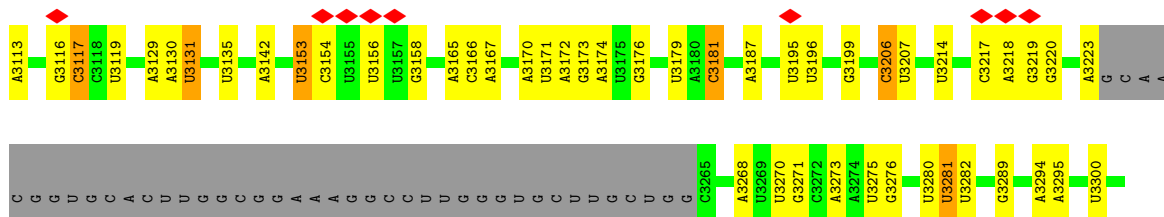
3 Residue-property plots

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.

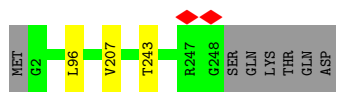
- Molecule 1: 25S ribosomal RNA



C2989	U2843	U2729	G2585	A2488	A2402	U2258	U2200	U1805	G1590	U1448	A1278
A2940	C2844	G2753	A2593	C2489	G2403	A2259	A	A1813	A1593	A1449	C1279
C2942	A2845	G2754	C2594	C2490	A2404	G2260	G	A1814	A1593	G1450	C1280
G2947	U2846	C2755	C2600	C2491	C2405	G2261	C	U1815	C1597	U1455	G1281
C2948	A2847	G2761	G2606	A2492	C2406	A2262	C	A1816	G1604	A1467	G1282
U2954	C2848	C2764	G2607	A2493	C2407	U2266	C	U1819	C1604	C1283	C1283
A2971	C2849	C2766	G2607	A2494	U2411	C2267	C	U1820	C1608	A1475	C1284
G2977	G2850	U2771	G2614	A2495	G2418	U2268	C	U1821	G1618	A1481	G1285
C2983	A2851	C2772	U2617	C2496	A2419	A2270	C	A1885	A1619	A1482	A1286
C2988	A2852	C2773	U2618	U2497	G2437	G2273	C	U1889	U1620	A1287	A1287
U2989	A2853	C2774	G2622	U2498	U2411	U2274	C	A1893	U1629	U1288	G1289
G2990	U2854	G2777	C2622	A2502	G2440	U2274	C	A1893	U1630	A1495	G1289
G2997	G2855	G2778	A2626	U2503	A2441	A2281	C	A1893	C1631	C1499	A1302
A3011	U2856	U2783	A2626	U2504	A2442	U2282	C	A1893	A1642	A1303	A1303
A3012	C2857	G2791	A2626	U2505	A2443	U2282	C	A1893	A1643	A1304	A1304
G3022	U2858	G2796	A2626	U2506	C2444	A2295	C	A1893	C1644	U1305	U1305
A3027	U2859	G2799	A2626	A2511	A2445	U2298	C	A1893	U1645	G1306	G1306
G3028	U2860	C2800	A2626	U2514	A2446	U2298	C	A1893	C1657	G1307	G1307
C3034	U2861	G2800	A2626	U2515	A2447	C2304	C	A1893	C1658	U1309	U1309
U3042	A2862	A2801	A2626	G2550	A2447	G2307	C	A1893	G1677	G1313	G1313
A3046	U2863	U2802	A2626	C	A2448	C2308	C	A1893	U1533	U1325	U1325
U3056	A2864	A2802	A2626	U	A2449	A2309	C	A1893	A1546	A1330	A1330
U3058	U2865	U2802	A2626	U	A2450	U2310	C	A1893	A1546	U1331	U1331
G3059	U2866	G2807	A2626	U	G2451	U2311	C	A1893	U1555	U1332	U1332
U3078	C2867	G2810	A2626	U	G2452	A2313	C	A1893	C1706	A1333	A1333
U3079	U2868	U2814	A2626	U	U2453	G2314	C	A1893	C1710	U1333	U1333
G3080	C2869	G2814	A2626	U	U2454	G2315	C	A1893	U1555	U1333	U1333
C3084	G2870	A2817	A2626	U	U2455	G2315	C	A1893	C1562	U1348	U1348
C3092	G2871	U2818	A2626	U	U2456	G2334	C	A1893	C1563	G1349	G1349
C3097	A2872	U2819	A2626	U	U2461	U2336	C	A1893	U1564	U1350	U1350
G3101	A2873	A2820	A2626	U	A2462	U2336	C	A1893	G1565	U1351	U1351
U3104	C2887	A2820	A2626	U	A2463	A2356	C	A1893	A1566	A1352	A1352
U3105	U2888	A2820	A2626	U	U2464	U2356	C	A1893	A1567	U1353	U1353
G3109	C2889	C2821	A2626	U	G2465	C2359	C	A1893	U1568	G1354	G1354
	U2890	U2822	A2626	U	G2466	C2366	C	A1893	U1569	U1355	U1355
	G2898	G2823	A2626	U	G2467	G2366	C	A1893	A1570	U1356	U1356
	C2899	C2824	A2626	U	G2468	C2366	C	A1893	A1571	A1386	A1386
	U2904	C2825	A2626	U	U2470	A2372	C	A1893	U1572	A1386	A1386
	A2911	U2826	A2626	U	U2471	A2372	C	A1893	G1573	A1392	A1392
	G2914	U2827	A2626	U	U2472	C2374	C	A1893	C1574	A1399	A1399
	G2918	G2828	A2626	U	G2474	G2375	C	A1893	G1576	G1400	G1400
	G2922	U2829	A2626	U	G2475	C2378	C	A1893	C1577	G1400	G1400
	U2923	G2830	A2626	U	G2476	C2378	C	A1893	U1578	C1578	C1578
	C2928	C2831	A2626	U	C2476	U2388	C	A1893	C1579	A1418	A1418
	A2933	C2832	A2626	U	C2479	G2388	C	A1893	A1580	A1419	A1419
	U2934	C2833	A2626	U	A2480	G2388	C	A1893	C1581	U1425	U1425
	U2935	U2715	A2626	U	G2481	G2389	C	A1893	A1583	G1434	G1434
	G2936	U2716	A2626	U	U2482	A2397	C	A1893	A1587	A1587	A1587
	A2937	U2719	A2626	U	U2483	A2397	C	A1893	A1588	A1588	A1588
	C2937	C2726	A2626	U	A2484	U2400	C	A1893	A1589	A1589	A1589
	G2938	A2727	A2626	U	A2485	A2401	C	A1893	A1589	A1589	A1589
		G2728	A2626	U	A2486	A2401	C	A1893	A1589	A1589	A1589
			A2626	U	U2487	A2401	C	A1893	A1589	A1589	A1589



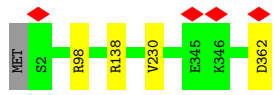
● Molecule 2: 60S ribosomal protein L2-A



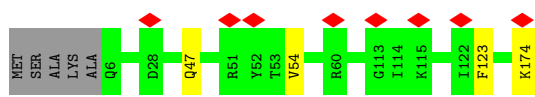
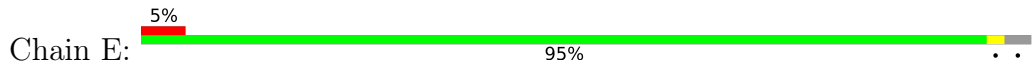
● Molecule 3: 60S ribosomal protein L3



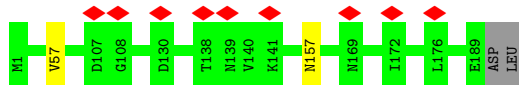
● Molecule 4: 60S ribosomal protein L4-A



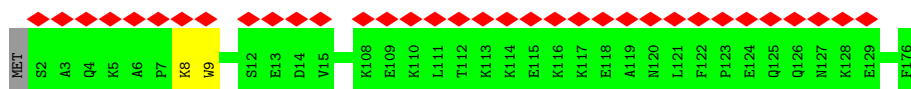
● Molecule 5: 60S ribosomal protein L11-A



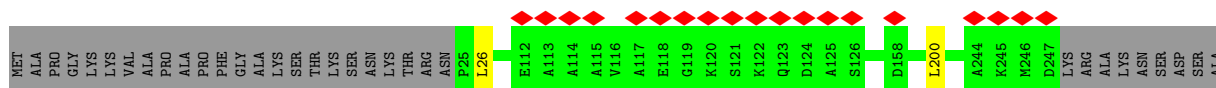
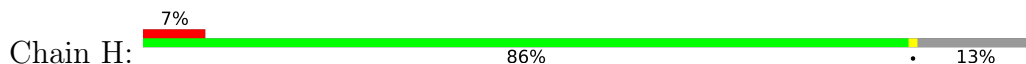
● Molecule 6: 60S ribosomal protein L9-A



● Molecule 7: 60S ribosomal protein L6-A



- Molecule 8: 60S ribosomal protein L8-A



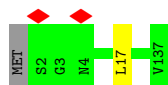
- Molecule 9: 60S ribosomal protein L16-B



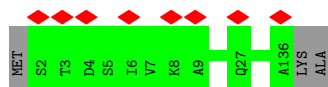
- Molecule 10: 60S ribosomal protein L13-A



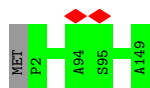
- Molecule 11: 60S ribosomal protein L23-A



- Molecule 12: 60S ribosomal protein L14-A



- Molecule 13: 60S ribosomal protein L28



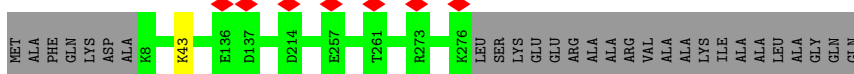
- Molecule 14: 60S ribosomal protein L15-A

Chain O:  100%



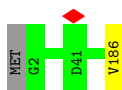
- Molecule 15: 60S ribosomal protein L5

Chain P:  90%




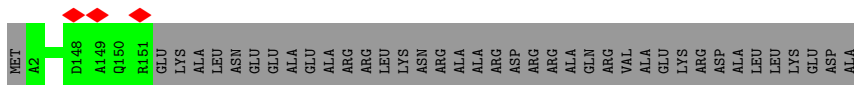
- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  99%



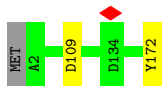
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  79%



- Molecule 18: 60S ribosomal protein L20-A

Chain S:  98%




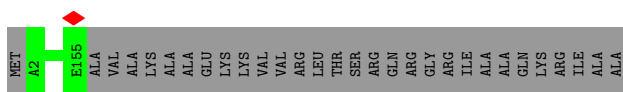
- Molecule 19: 60S ribosomal protein L21-A

Chain T:  98%

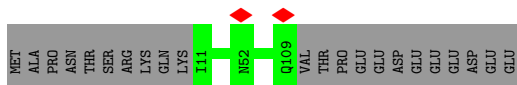
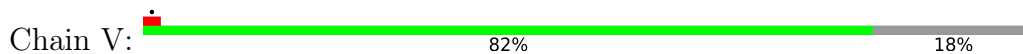


- Molecule 20: 60S ribosomal protein L17-A

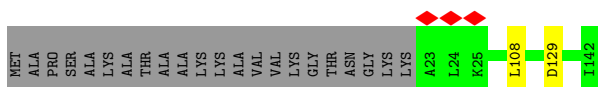
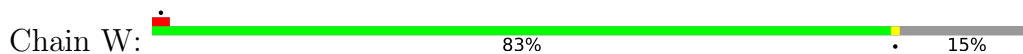
Chain U:  84%



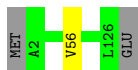
- Molecule 21: 60S ribosomal protein L22-A



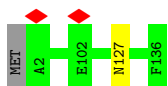
- Molecule 22: 60S ribosomal protein L25



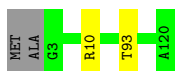
- Molecule 23: 60S ribosomal protein L26-A



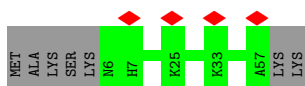
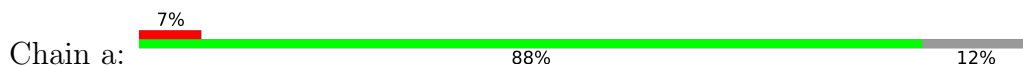
- Molecule 24: 60S ribosomal protein L27-A



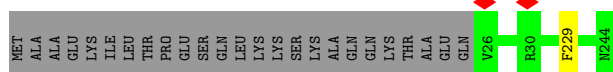
- Molecule 25: 60S ribosomal protein L35-A



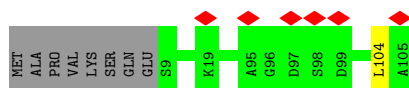
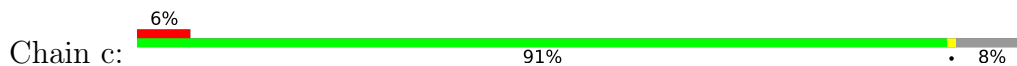
- Molecule 26: 60S ribosomal protein L29



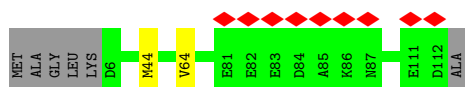
- Molecule 27: 60S ribosomal protein L7-A



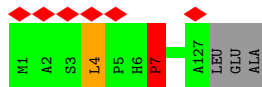
• Molecule 28: 60S ribosomal protein L30



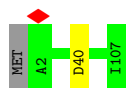
• Molecule 29: 60S ribosomal protein L31-A



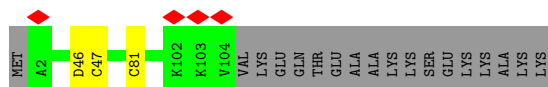
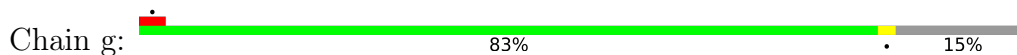
• Molecule 30: 60S ribosomal protein L32



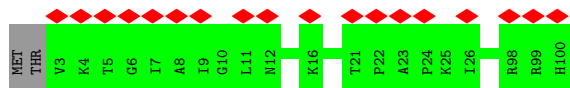
• Molecule 31: 60S ribosomal protein L33-A



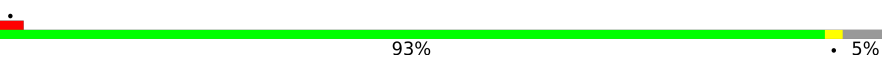
• Molecule 32: 60S ribosomal protein L34-A

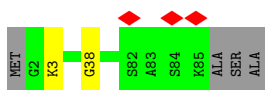


• Molecule 33: 60S ribosomal protein L36-A

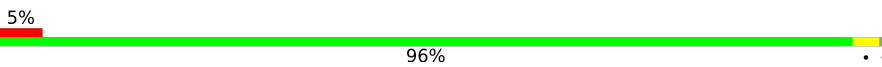


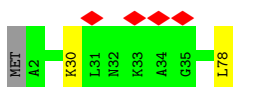
- Molecule 34: 60S ribosomal protein L37-A

Chain i:  93% 5%



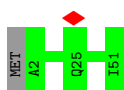
- Molecule 35: 60S ribosomal protein L38

Chain j:  96% 5%




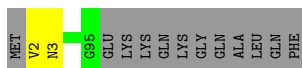
- Molecule 36: 60S ribosomal protein L39

Chain k:  98%



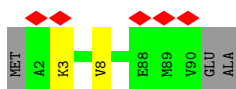
- Molecule 37: 60S ribosomal protein L42-A

Chain l:  87% 11%

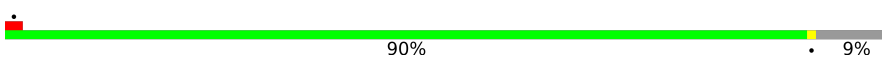


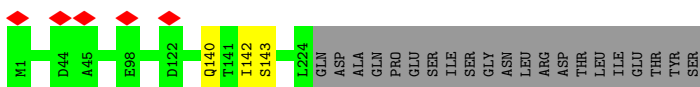
- Molecule 38: 60S ribosomal protein L43-A

Chain m:  95%



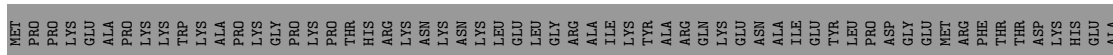
- Molecule 39: Eukaryotic translation initiation factor 6

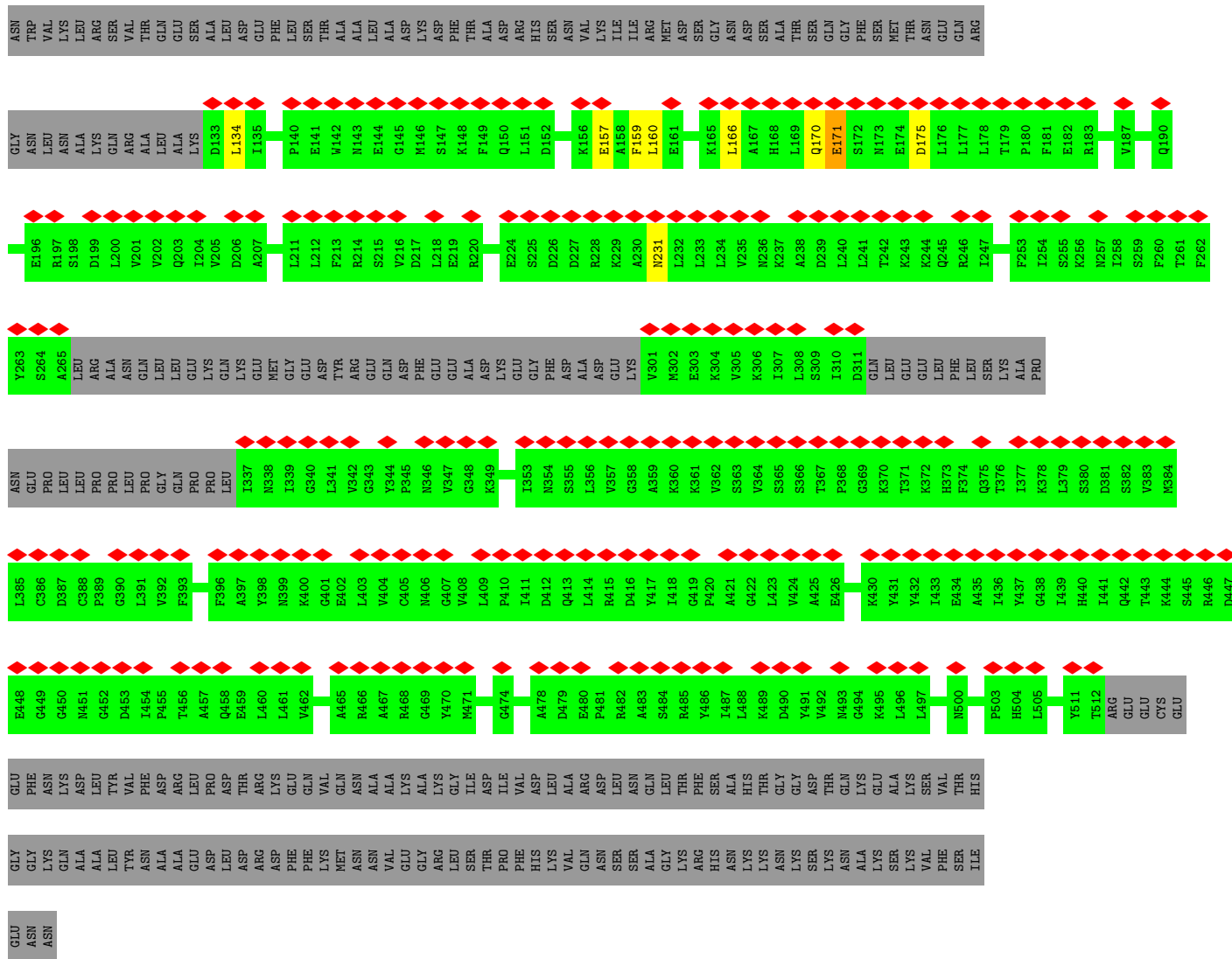
Chain n:  90% 9%



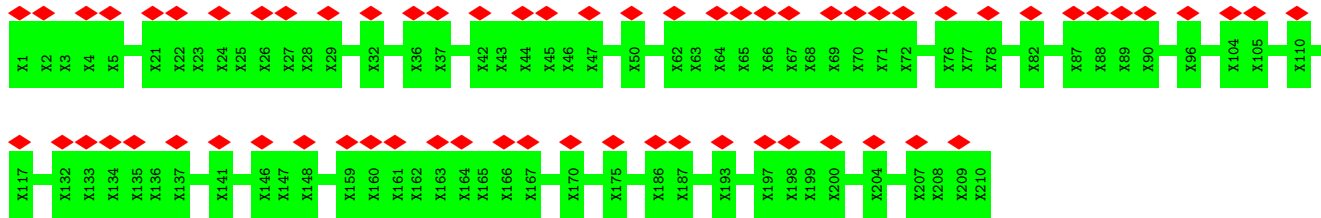
- Molecule 40: Large subunit GTPase 1

Chain o:  49% 37% 50%

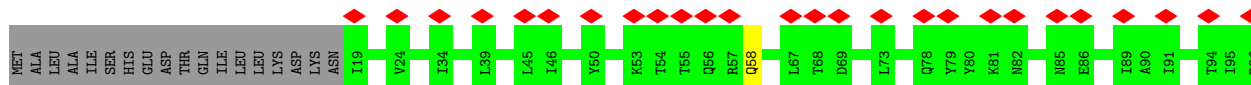
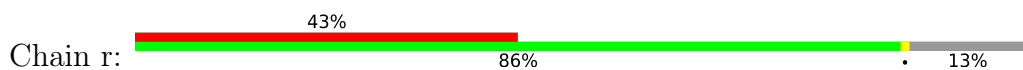


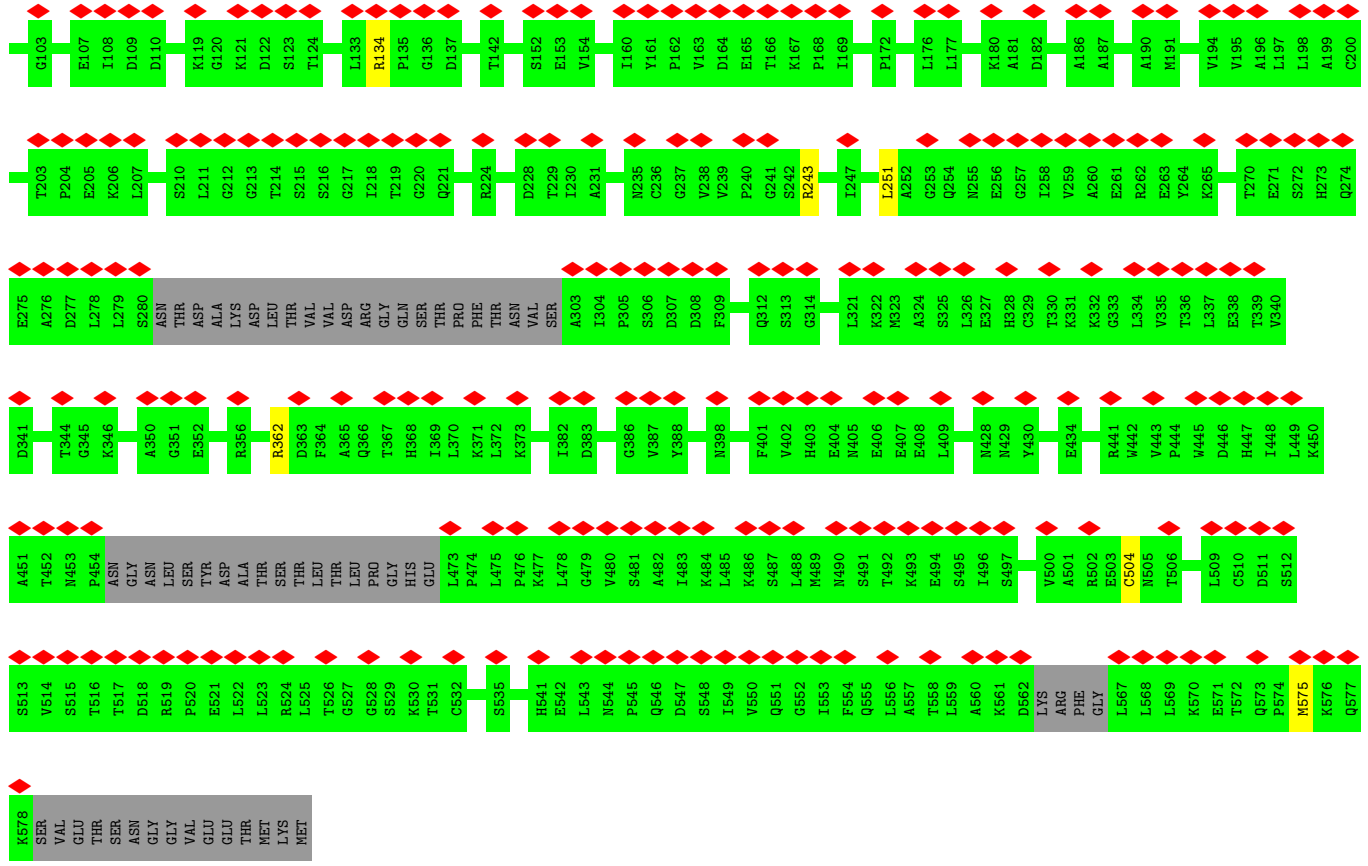


• Molecule 41: uL1

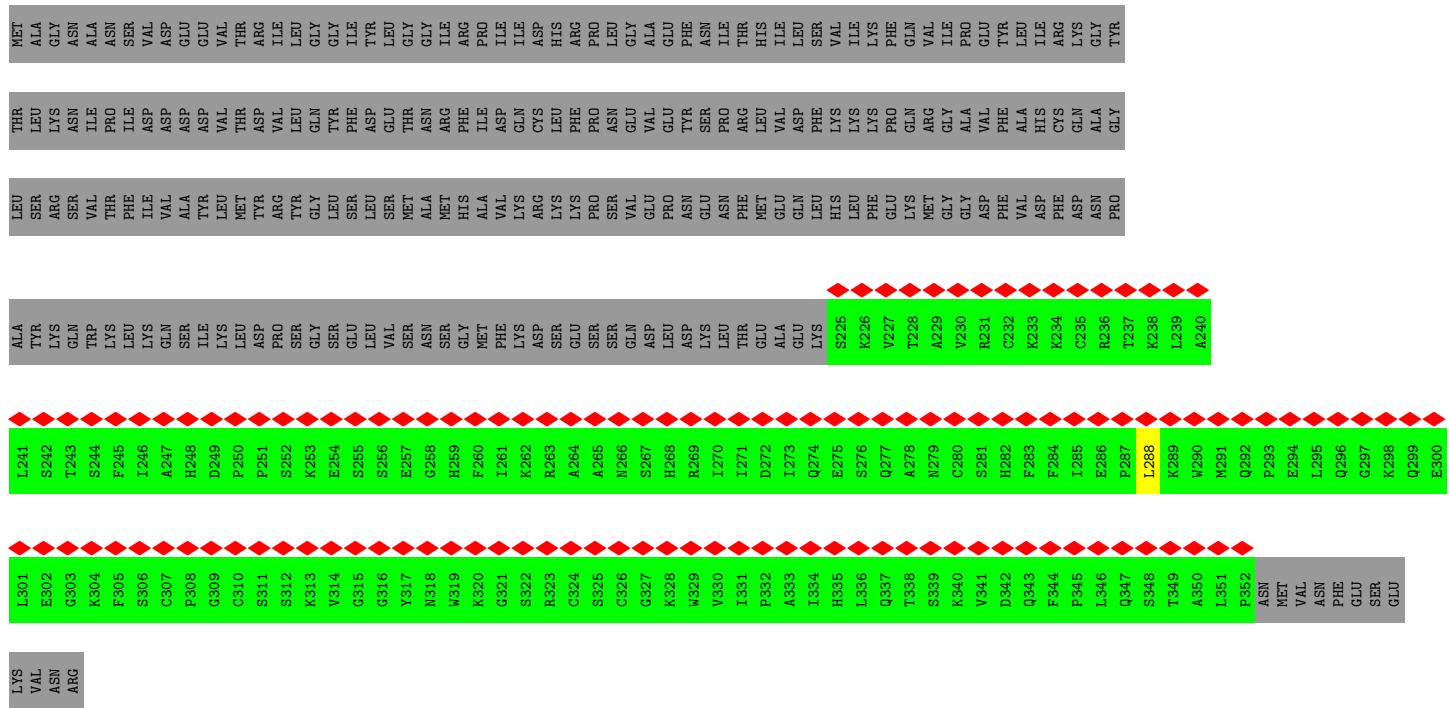


• Molecule 42: Probable metalloprotease ARX1

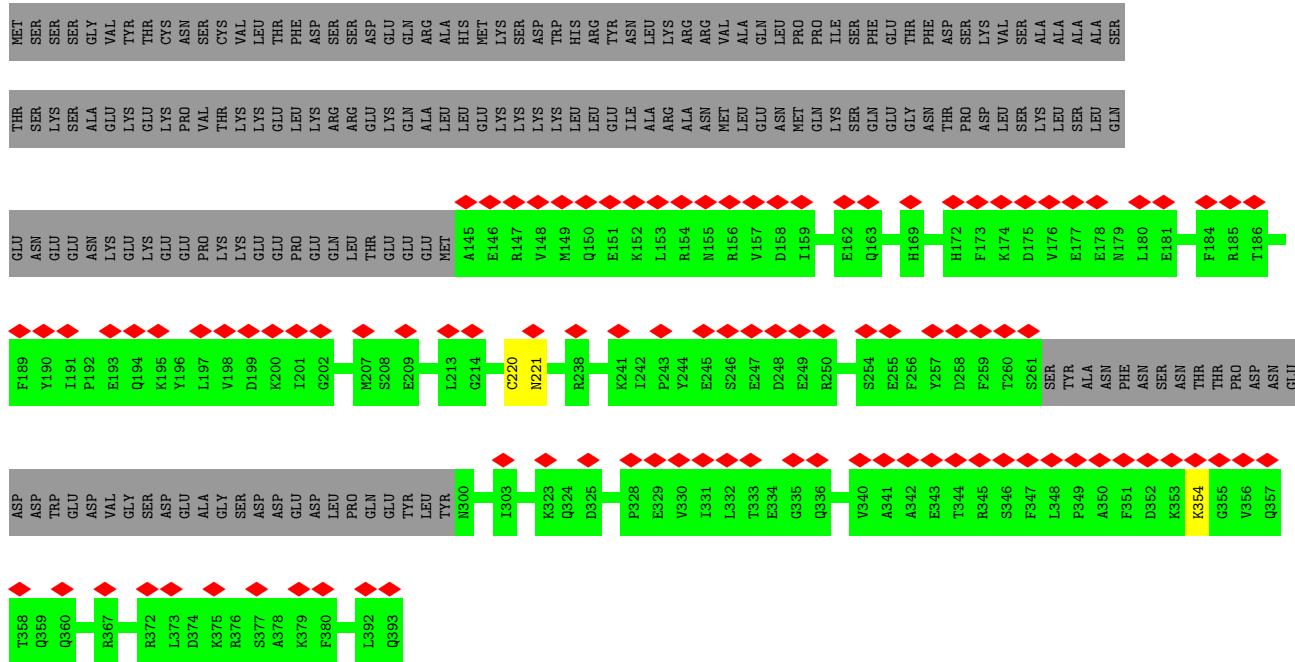




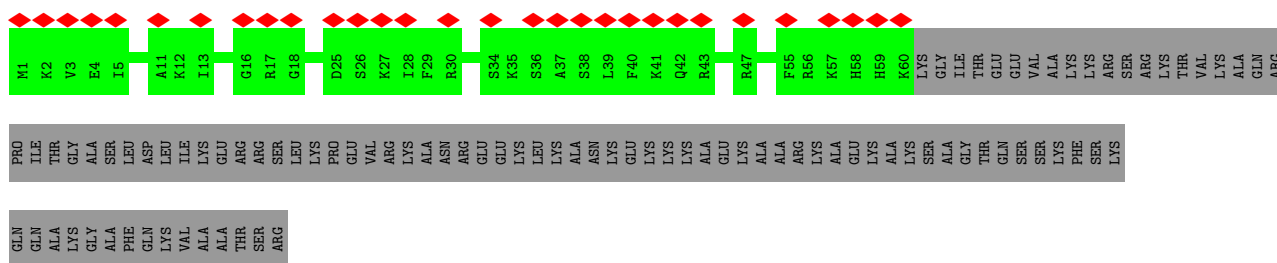
● Molecule 43: Tyrosine-protein phosphatase YVH1



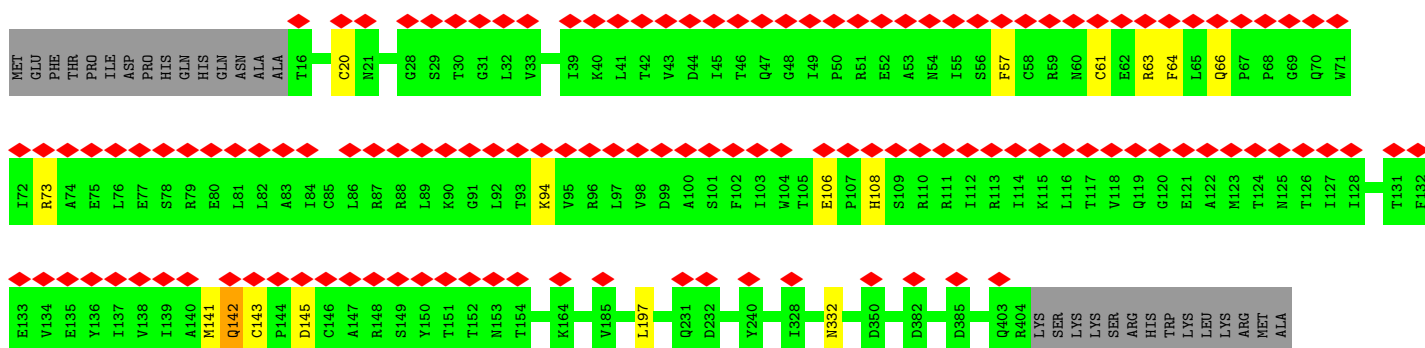
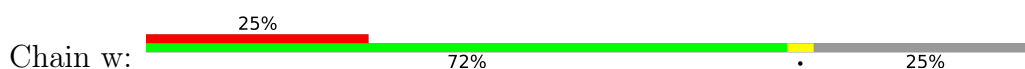
● Molecule 44: Cytoplasmic 60S subunit biogenesis factor REI1



● Molecule 45: 60S ribosomal protein L24-A



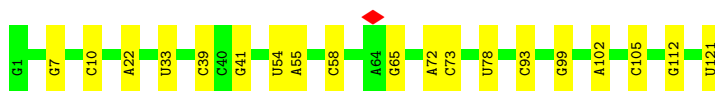
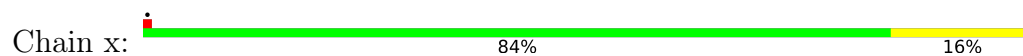
● Molecule 46: 60S ribosomal export protein NMD3



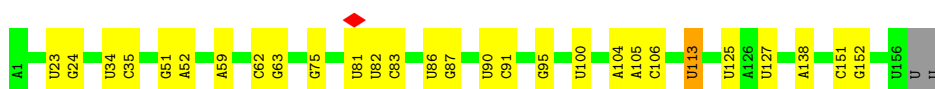
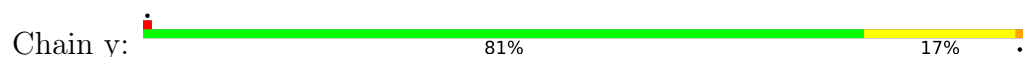
LYS
GLU
HIS
LYS
ASP
ILE
ASP
ALA
SER
LEU
ASP
TYR
ASN
SER
ARG
ALA
GLN
LYS
GLN
GLU
MET
GLU
LEU
ARG
ALA
GLU
LYS
MET
THR
LEU
GLU
TYR
ASP
GLY
LEU
PHE
LEU
GLN
GLU
LEU
PRO
VAL
GLU
ASP
ALA
GLU
LEU
ARG
GLN
SER
VAL
ASN
LEU
TYR
LYS
ASN
ARG
GLU
ALA
VAL
PRO
PRO
GLU
HIS

GLU
MET
ASP
GLU
ASP
GLU
ASP
GLU
ALA
PRO
GLN
ASN
ILE
ASP
GLU
LEU
LEU
ASP
GLU
LEU
ASP
GLU
MET
THR
LEU
GLU
ASP
GLY
VAL
GLU
ASN
THR
PRO
VAL
SER
GLN
GLN

• Molecule 47: 5S ribosomal RNA



• Molecule 48: 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	216403	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	0.638	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.023	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	0.80	2/75327 (0.0%)	1.07	302/117440 (0.3%)
2	B	0.46	0/1912	0.60	1/2569 (0.0%)
3	C	0.47	0/3110	0.62	3/4184 (0.1%)
4	D	0.46	0/2800	0.56	0/3791
5	E	0.31	0/1373	0.54	0/1841
6	F	0.33	0/1523	0.54	0/2051
7	G	0.35	0/1423	0.57	0/1911
8	H	0.38	0/1774	0.55	2/2395 (0.1%)
9	J	0.42	0/1593	0.52	0/2137
10	K	0.40	0/1511	0.52	0/2031
11	L	0.43	0/1017	0.58	1/1368 (0.1%)
12	M	0.36	0/1060	0.55	0/1428
13	N	0.48	0/1203	0.53	0/1611
14	O	0.50	0/1756	0.57	0/2353
15	P	0.37	0/2225	0.53	0/3004
16	Q	0.42	0/1464	0.54	0/1964
17	R	0.40	0/1226	0.48	0/1637
18	S	0.45	0/1472	0.55	1/1979 (0.1%)
19	T	0.44	0/1299	0.53	0/1742
20	U	0.47	0/1245	0.55	0/1676
21	V	0.38	0/802	0.55	0/1087
22	W	0.43	0/973	0.62	2/1313 (0.2%)
23	X	0.43	0/995	0.57	0/1329
24	Y	0.36	0/1117	0.52	0/1496
25	Z	0.38	0/972	0.51	0/1293
26	a	0.34	0/426	0.47	0/570
27	b	0.45	0/1797	0.56	0/2419
28	c	0.34	0/749	0.56	1/1007 (0.1%)
29	d	0.47	0/886	0.59	1/1190 (0.1%)
30	e	0.43	0/1041	0.56	1/1393 (0.1%)
31	f	0.48	0/867	0.68	1/1167 (0.1%)
32	g	0.44	0/822	0.54	0/1099

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.32	0/770	0.52	0/1023
34	i	0.50	0/680	0.59	0/901
35	j	0.37	0/617	0.54	0/825
36	k	0.41	0/442	0.51	0/587
37	l	0.44	0/768	0.55	0/1016
38	m	0.49	0/687	0.57	0/915
39	n	0.34	0/1712	0.58	0/2330
40	o	0.35	0/2628	0.66	3/3557 (0.1%)
42	r	0.28	0/4069	0.58	1/5520 (0.0%)
43	s	0.31	0/1016	0.66	1/1368 (0.1%)
44	u	0.32	0/1759	0.57	0/2363
45	v	0.30	0/512	0.48	0/680
46	w	0.36	0/3135	0.61	1/4255 (0.0%)
47	x	0.67	0/2880	1.01	9/4487 (0.2%)
48	y	0.83	0/3699	1.02	4/5760 (0.1%)
All	All	0.66	2/143134 (0.0%)	0.90	335/210062 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2258	U	C1'-N1	5.95	1.57	1.48
1	A	2971	A	N9-C4	5.11	1.41	1.37

The worst 5 of 335 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1012	G	N1-C6-O6	-10.55	113.57	119.90
1	A	2567	C	N3-C2-O2	-10.35	114.66	121.90
1	A	2567	C	N1-C2-O2	9.86	124.82	118.90
1	A	960	U	C2-N1-C1'	9.65	129.28	117.70
1	A	922	U	C2-N1-C1'	9.58	129.19	117.70

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%)	224 (91%)	21 (9%)	0	100	100
3	C	379/387 (98%)	352 (93%)	26 (7%)	1 (0%)	41	74
4	D	359/362 (99%)	342 (95%)	17 (5%)	0	100	100
5	E	167/174 (96%)	154 (92%)	13 (8%)	0	100	100
6	F	187/191 (98%)	178 (95%)	9 (5%)	0	100	100
7	G	173/176 (98%)	159 (92%)	13 (8%)	1 (1%)	25	64
8	H	221/256 (86%)	210 (95%)	11 (5%)	0	100	100
9	J	195/198 (98%)	193 (99%)	2 (1%)	0	100	100
10	K	184/199 (92%)	174 (95%)	10 (5%)	0	100	100
11	L	134/137 (98%)	125 (93%)	9 (7%)	0	100	100
12	M	133/138 (96%)	128 (96%)	5 (4%)	0	100	100
13	N	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
14	O	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
15	P	267/297 (90%)	253 (95%)	14 (5%)	0	100	100
16	Q	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
17	R	148/189 (78%)	147 (99%)	1 (1%)	0	100	100
18	S	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
19	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	U	152/184 (83%)	144 (95%)	8 (5%)	0	100	100
21	V	97/121 (80%)	91 (94%)	6 (6%)	0	100	100
22	W	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
23	X	123/127 (97%)	118 (96%)	5 (4%)	0	100	100
24	Y	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
25	Z	116/120 (97%)	114 (98%)	2 (2%)	0	100	100
26	a	50/59 (85%)	45 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	b	217/244 (89%)	209 (96%)	8 (4%)	0	100	100
28	c	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
29	d	105/113 (93%)	92 (88%)	13 (12%)	0	100	100
30	e	125/130 (96%)	118 (94%)	5 (4%)	2 (2%)	9	43
31	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
32	g	101/121 (84%)	92 (91%)	8 (8%)	1 (1%)	15	54
33	h	96/100 (96%)	95 (99%)	1 (1%)	0	100	100
34	i	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	13	49
35	j	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
36	k	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
37	l	92/106 (87%)	89 (97%)	3 (3%)	0	100	100
38	m	87/92 (95%)	80 (92%)	6 (7%)	1 (1%)	14	51
39	n	222/245 (91%)	208 (94%)	14 (6%)	0	100	100
40	o	314/640 (49%)	265 (84%)	48 (15%)	1 (0%)	41	74
42	r	508/593 (86%)	475 (94%)	33 (6%)	0	100	100
43	s	126/364 (35%)	105 (83%)	21 (17%)	0	100	100
44	u	207/393 (53%)	193 (93%)	13 (6%)	1 (0%)	29	67
45	v	58/155 (37%)	58 (100%)	0	0	100	100
46	w	387/518 (75%)	348 (90%)	38 (10%)	1 (0%)	41	74
All	All	7486/8961 (84%)	7006 (94%)	470 (6%)	10 (0%)	54	83

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
32	g	81	CYS
30	e	7	PRO
44	u	221	ASN
7	G	9	TRP

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%)	187 (99%)	2 (1%)	73	88
3	C	317/323 (98%)	311 (98%)	6 (2%)	57	81
4	D	288/289 (100%)	284 (99%)	4 (1%)	67	86
5	E	147/150 (98%)	143 (97%)	4 (3%)	44	75
6	F	169/171 (99%)	167 (99%)	2 (1%)	71	88
7	G	152/153 (99%)	151 (99%)	1 (1%)	84	94
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%)	146 (98%)	3 (2%)	55	80
11	L	104/105 (99%)	104 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
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%)	226 (100%)	1 (0%)	91	95
16	Q	150/151 (99%)	149 (99%)	1 (1%)	84	94
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%)	134 (98%)	2 (2%)	65	85
20	U	125/146 (86%)	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%)	114 (99%)	1 (1%)	78	91
25	Z	104/105 (99%)	102 (98%)	2 (2%)	57	81
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	183 (100%)	1 (0%)	88	95
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	93 (99%)	1 (1%)	73	88
30	e	109/111 (98%)	107 (98%)	2 (2%)	59	82
31	f	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	88/103 (85%)	86 (98%)	2 (2%)	50	78
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%)	66 (97%)	2 (3%)	42	74
36	k	45/46 (98%)	45 (100%)	0	100	100
37	l	81/91 (89%)	79 (98%)	2 (2%)	47	77
38	m	70/72 (97%)	69 (99%)	1 (1%)	67	86
39	n	192/211 (91%)	189 (98%)	3 (2%)	62	84
40	o	282/555 (51%)	276 (98%)	6 (2%)	53	79
42	r	453/520 (87%)	447 (99%)	6 (1%)	69	87
43	s	110/323 (34%)	110 (100%)	0	100	100
44	u	181/359 (50%)	179 (99%)	2 (1%)	73	88
45	v	53/129 (41%)	53 (100%)	0	100	100
46	w	348/467 (74%)	333 (96%)	15 (4%)	29	64
All	All	6414/7604 (84%)	6338 (99%)	76 (1%)	72	88

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	r	504	CYS
46	w	141	MET
44	u	220	CYS
46	w	64	PHE
46	w	332	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
20	U	125	GLN
40	o	170	GLN
40	o	399	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	678 (21%)	15 (0%)
47	x	120/121 (99%)	15 (12%)	0
48	y	155/158 (98%)	27 (17%)	0
All	All	3416/3675 (92%)	720 (21%)	15 (0%)

5 of 720 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	A
1	A	26	A
1	A	40	A
1	A	43	A
1	A	48	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1815	U
1	A	3027	A
1	A	2101	C
1	A	3206	C
1	A	2404	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 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

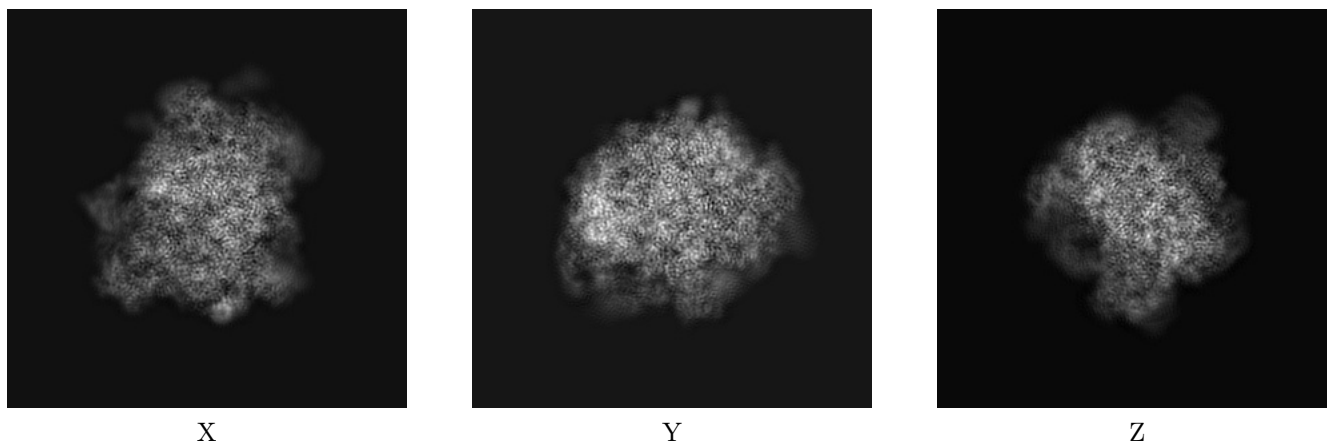
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10068. 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](#)

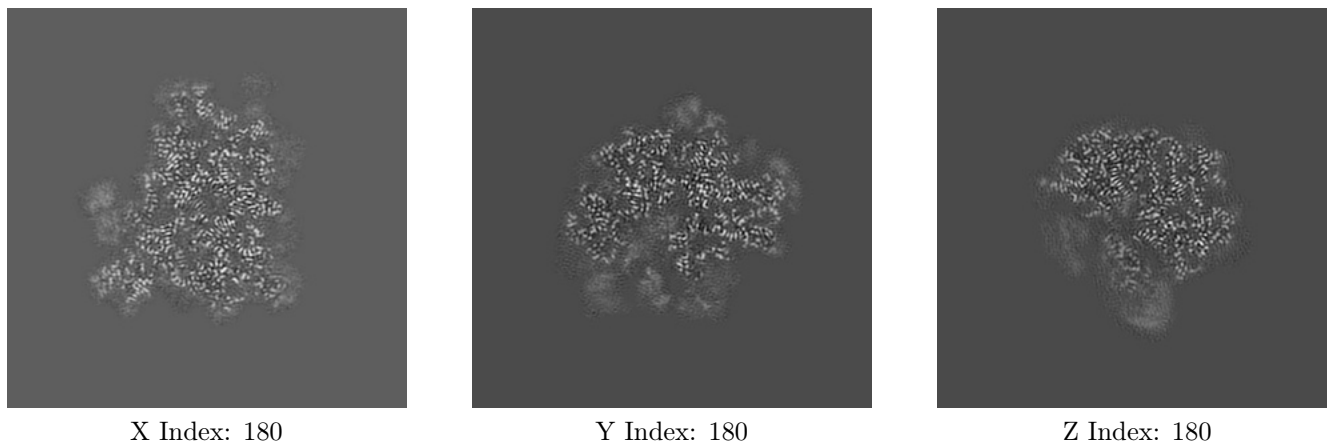
6.1.1 Primary map



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

6.2 Central slices [i](#)

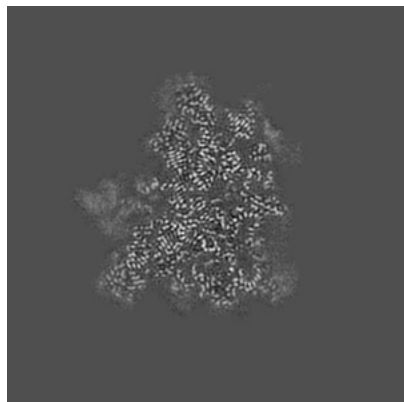
6.2.1 Primary map



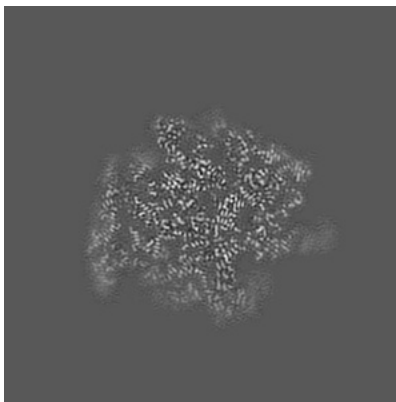
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

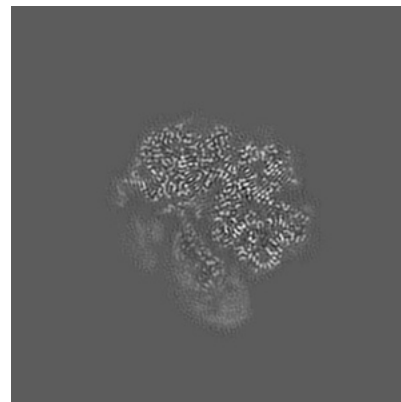
6.3.1 Primary map



X Index: 189



Y Index: 196

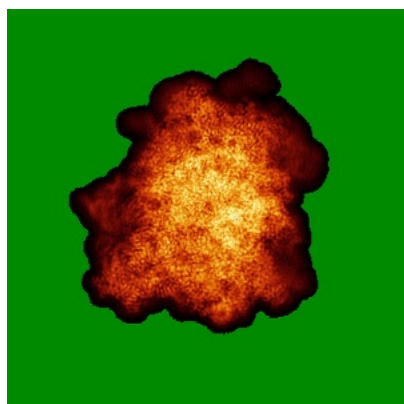


Z Index: 177

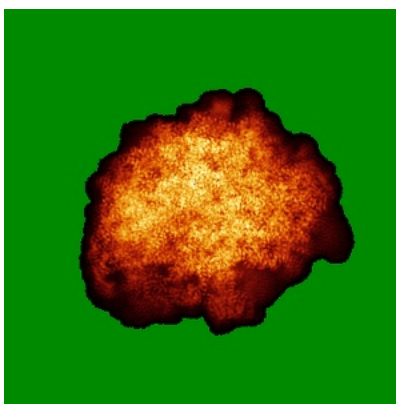
The images above show the largest variance slices of the map in three orthogonal directions.

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

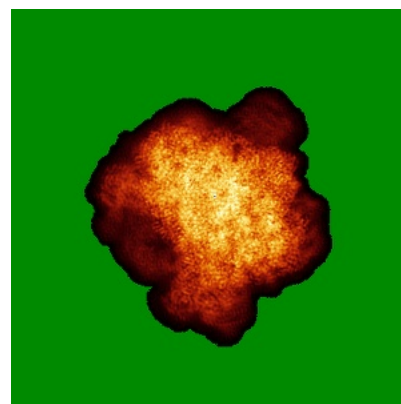
6.4.1 Primary map



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

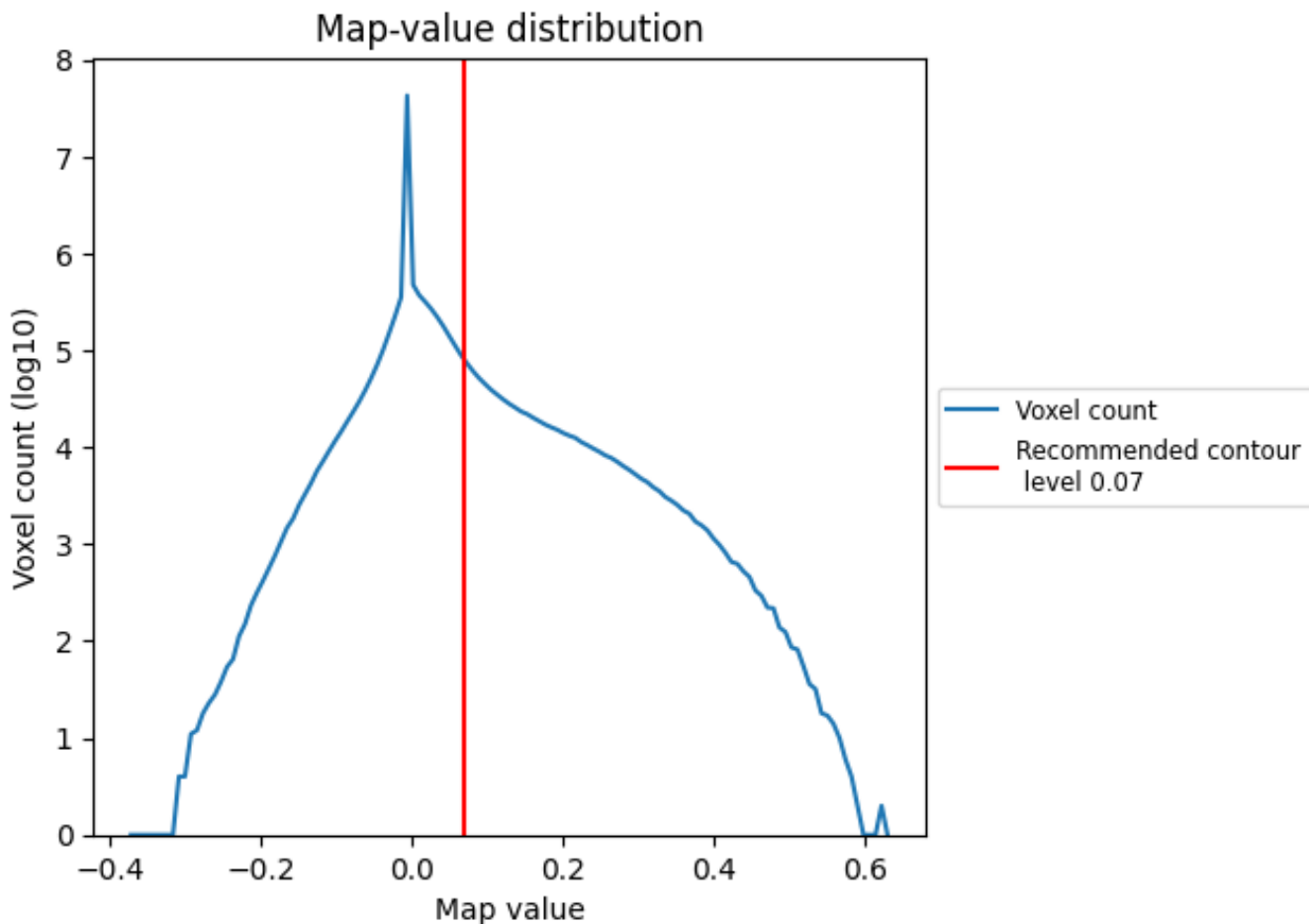
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

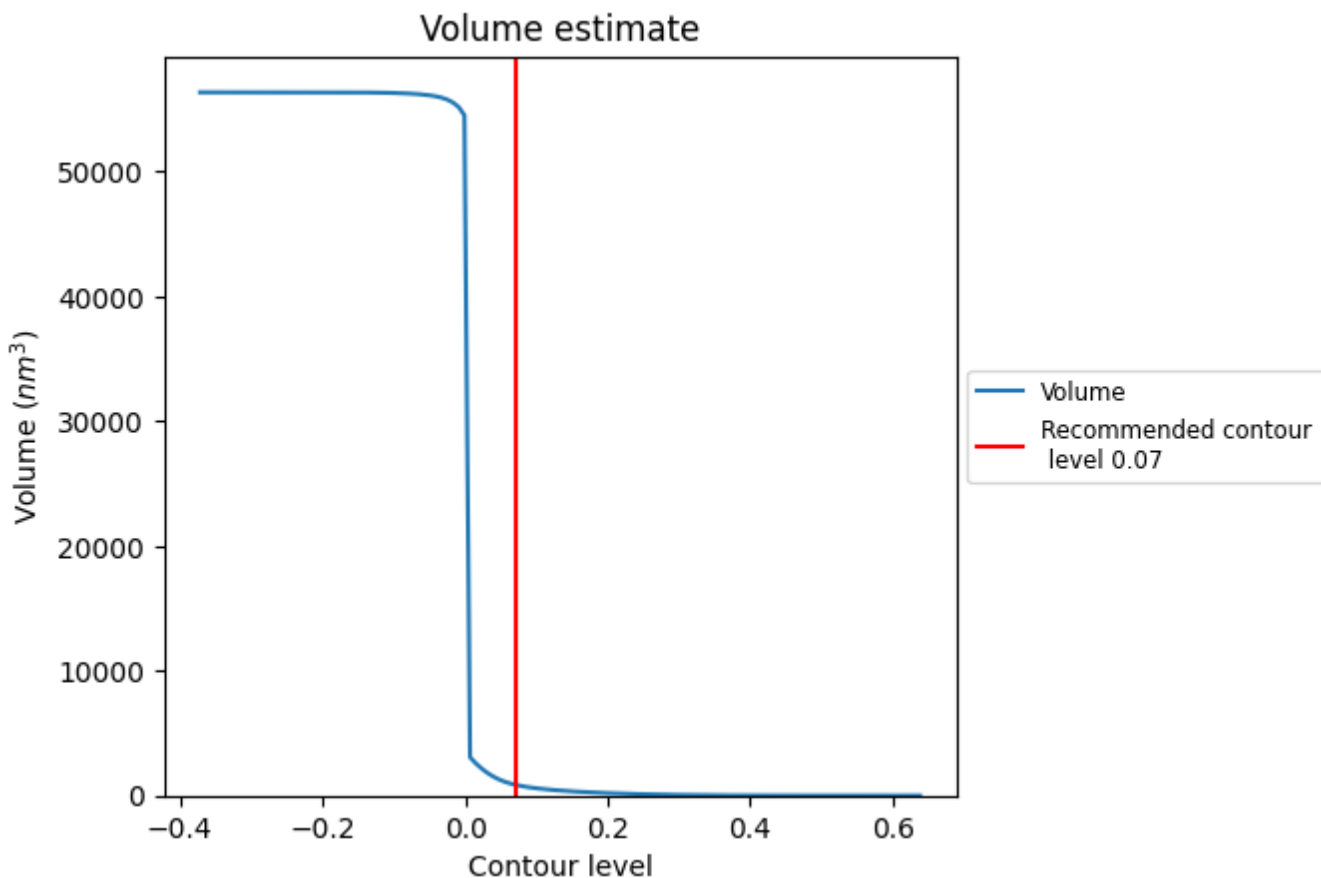
This section contains the results of statistical analysis of the map.

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.

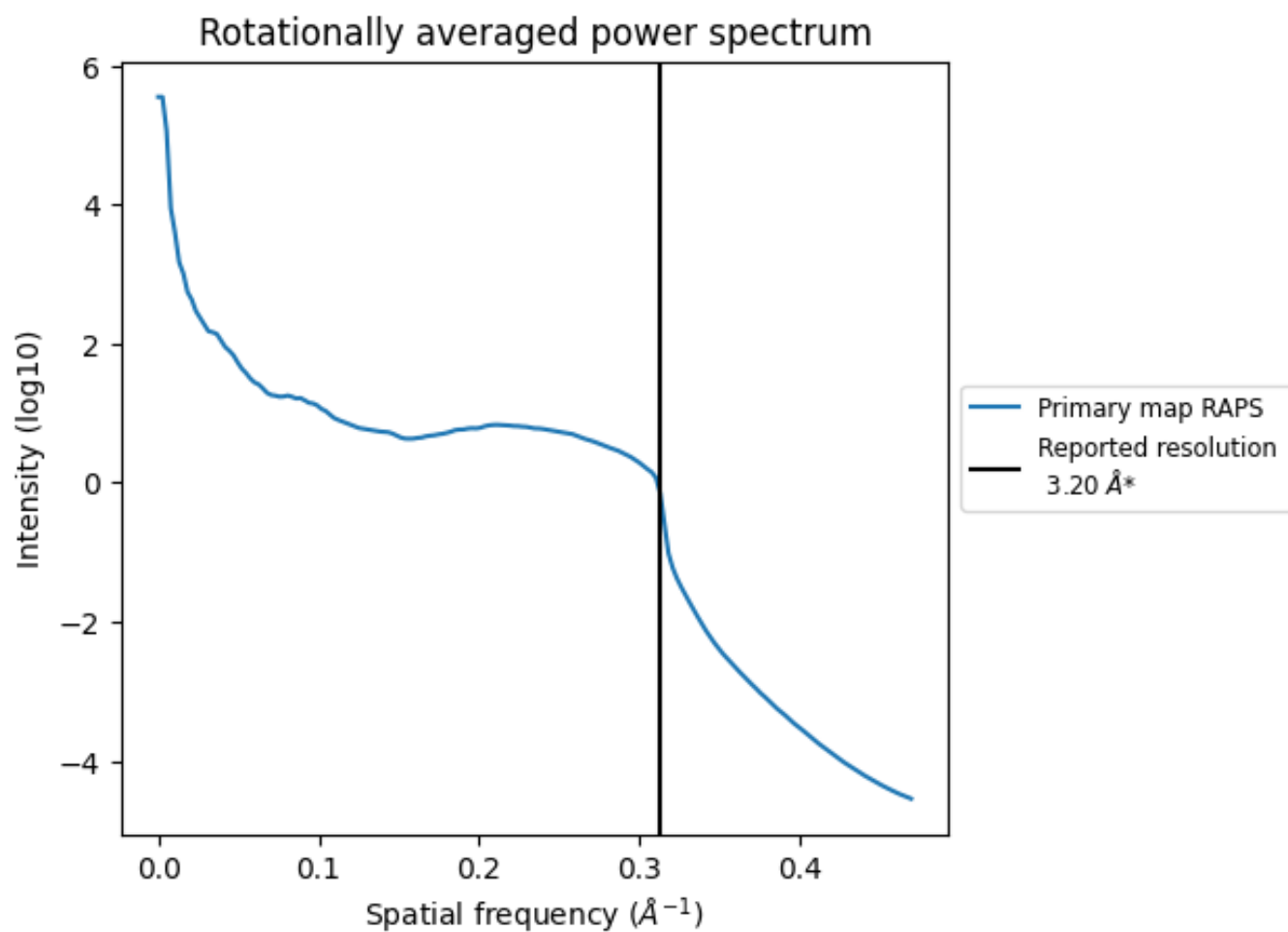
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 0.312\AA^{-1}

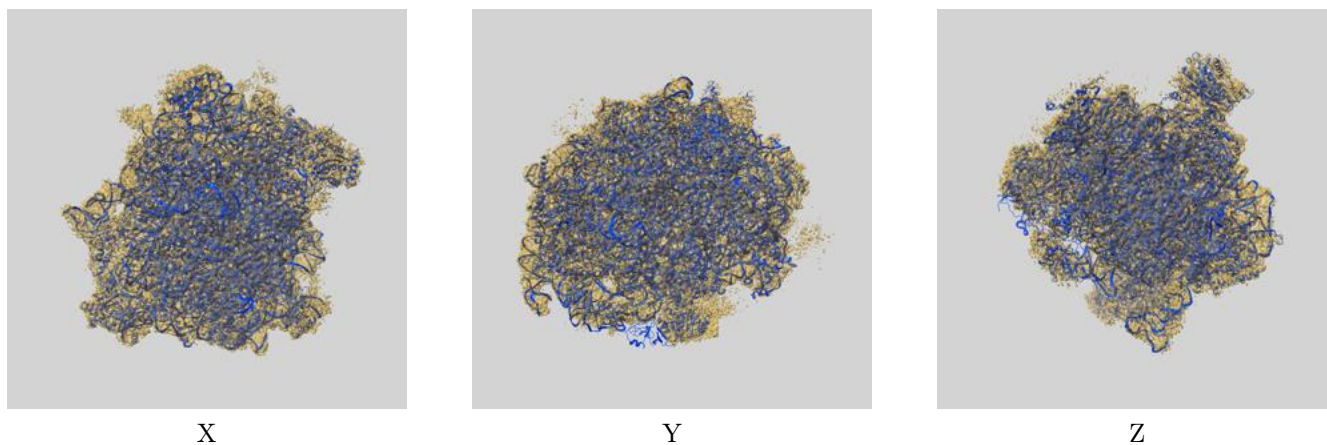
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

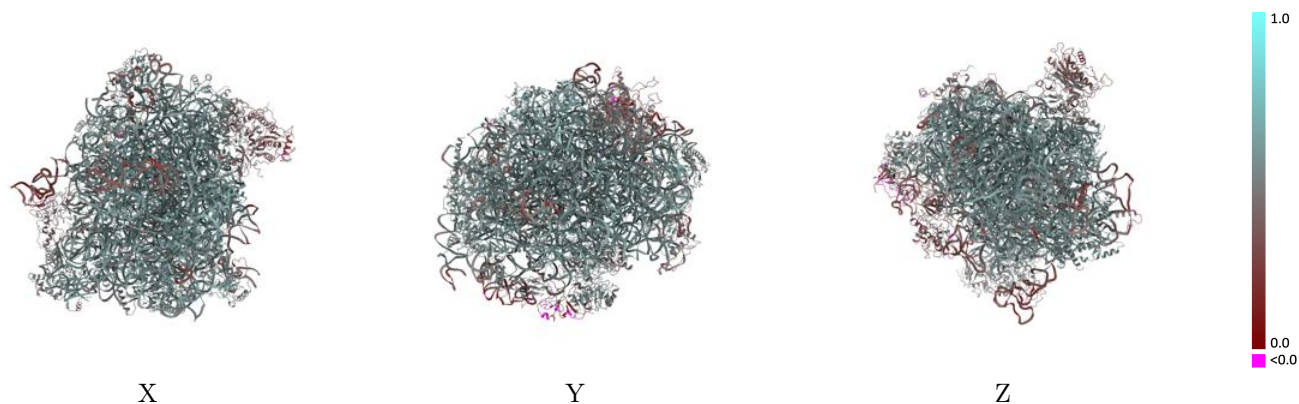
This section contains information regarding the fit between EMDB map EMD-10068 and PDB model 6RZZ. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



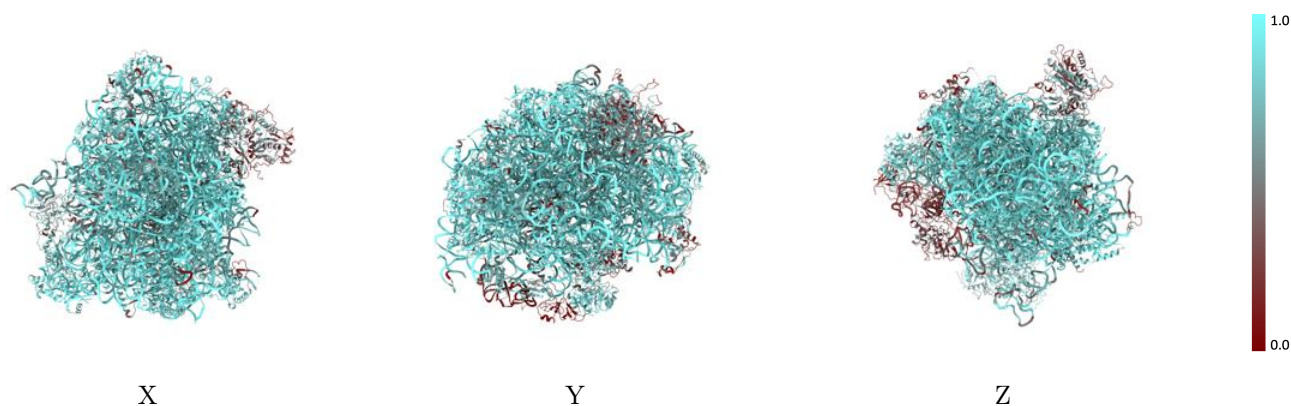
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



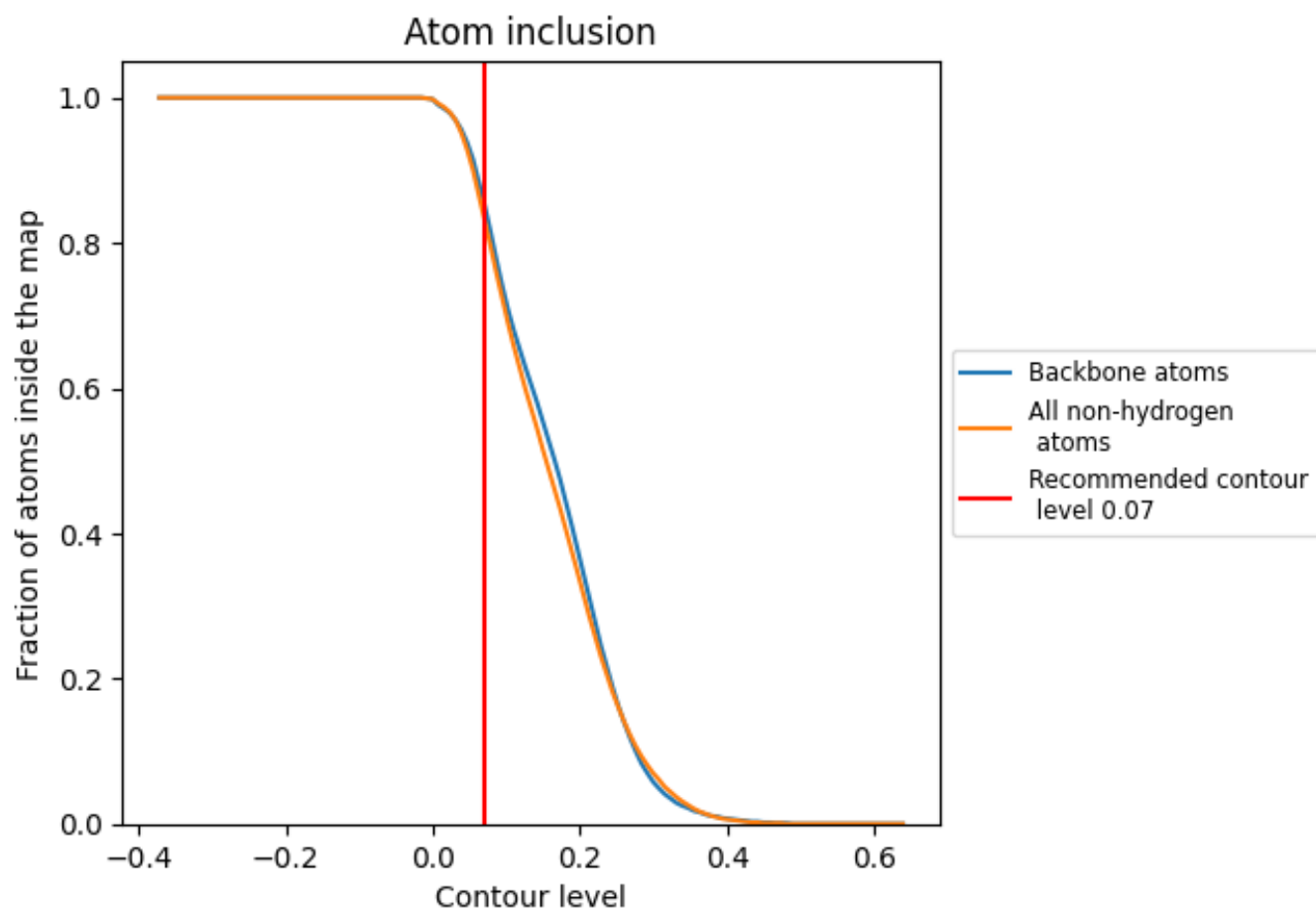
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 85% 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	 0.8320	 0.5300
A	 0.8910	 0.5350
B	 0.8990	 0.5870
C	 0.8930	 0.5770
D	 0.8980	 0.5820
E	 0.7620	 0.4720
F	 0.7440	 0.5210
G	 0.7010	 0.4950
H	 0.8180	 0.5400
J	 0.8840	 0.5770
K	 0.8550	 0.5680
L	 0.8790	 0.5830
M	 0.8390	 0.5480
N	 0.9120	 0.5870
O	 0.9080	 0.5990
P	 0.8560	 0.5380
Q	 0.9250	 0.5930
R	 0.8790	 0.5690
S	 0.8950	 0.5770
T	 0.8480	 0.5610
U	 0.9060	 0.5900
V	 0.8430	 0.5390
W	 0.8470	 0.5700
X	 0.8900	 0.5840
Y	 0.8240	 0.5210
Z	 0.8710	 0.5690
a	 0.8070	 0.5630
b	 0.9050	 0.5810
c	 0.8080	 0.5110
d	 0.8310	 0.5690
e	 0.8700	 0.5790
f	 0.9050	 0.5900
g	 0.8780	 0.5820
h	 0.7030	 0.5210
i	 0.9170	 0.6030



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Chain	Atom inclusion	Q-score
j	 0.8280	 0.5320
k	 0.8620	 0.5950
l	 0.8930	 0.5930
m	 0.8430	 0.5700
n	 0.7920	 0.4990
o	 0.2820	 0.3550
p	 0.6140	 0.3850
r	 0.4140	 0.3880
s	 0.0040	 0.1110
u	 0.4260	 0.4540
v	 0.4440	 0.5140
w	 0.5320	 0.4450
x	 0.9740	 0.5520
y	 0.9610	 0.5760