wwPDB EM Validation Summary Report (i)

Nov 7, 2022 – 08:13 AM EST

PDB ID	:	6N8N
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 (i) 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 (i)) were used in the production of this report:

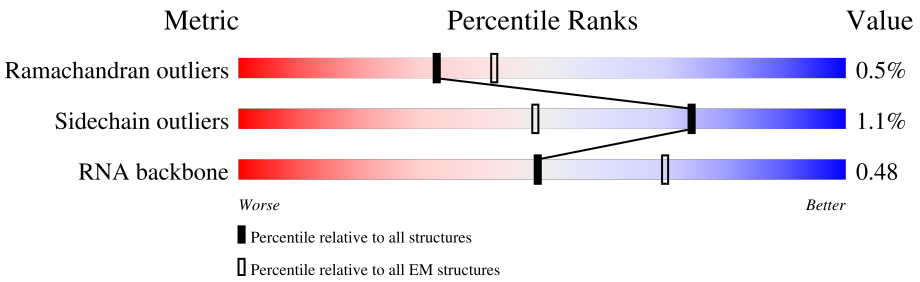
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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)
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 <=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	72% 20% 6%
2	B	121	88% 12%
3	C	158	80% 19%
4	Y	364	19% 32% 65%
5	X	245	95%
6	W	640	9% 54% 41%
7	V	518	15% 73% 24%
8	D	254	96%

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Mol	Chain	Length	Quality of chain
9	E	387	98%
10	F	362	98%
11	G	297	93% 5%
12	H	176	88% 12%
13	I	244	87% 10%
14	J	256	87% 11%
15	K	191	97%
16	M	174	95%
17	N	199	95%
18	O	138	99%
19	Q	106	7% 96%
20	R	92	95%
21	S	217	21% 97%
22	a	204	99%
23	b	199	98%
24	c	184	7% 99%
25	d	186	99%
26	e	189	79% 20%
27	f	172	97%
28	g	160	96%
29	h	121	79% 20%
30	i	137	96%
31	j	155	39% 61%
32	k	142	85% 15%
33	l	127	97%

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Mol	Chain	Length	Quality of chain
34	m	136	99%
35	n	149	94%
36	o	59	5% 95%
37	p	105	90% 9%
38	q	113	93% 5%
39	r	130	95%
40	s	107	98%
41	t	121	86% 10%
42	u	120	98%
43	v	100	98%
44	w	88	92% 5%
45	x	78	99%
46	y	51	96%
47	z	128	7% 40% 60%
48	L	165	74% 88% 11%

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
			Total	C	N	O	P		
1	A	3203	68513	30603	12353	22354	3203	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Ribosomal Protein uL1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 48 is a protein called Ribosomal protein L12.

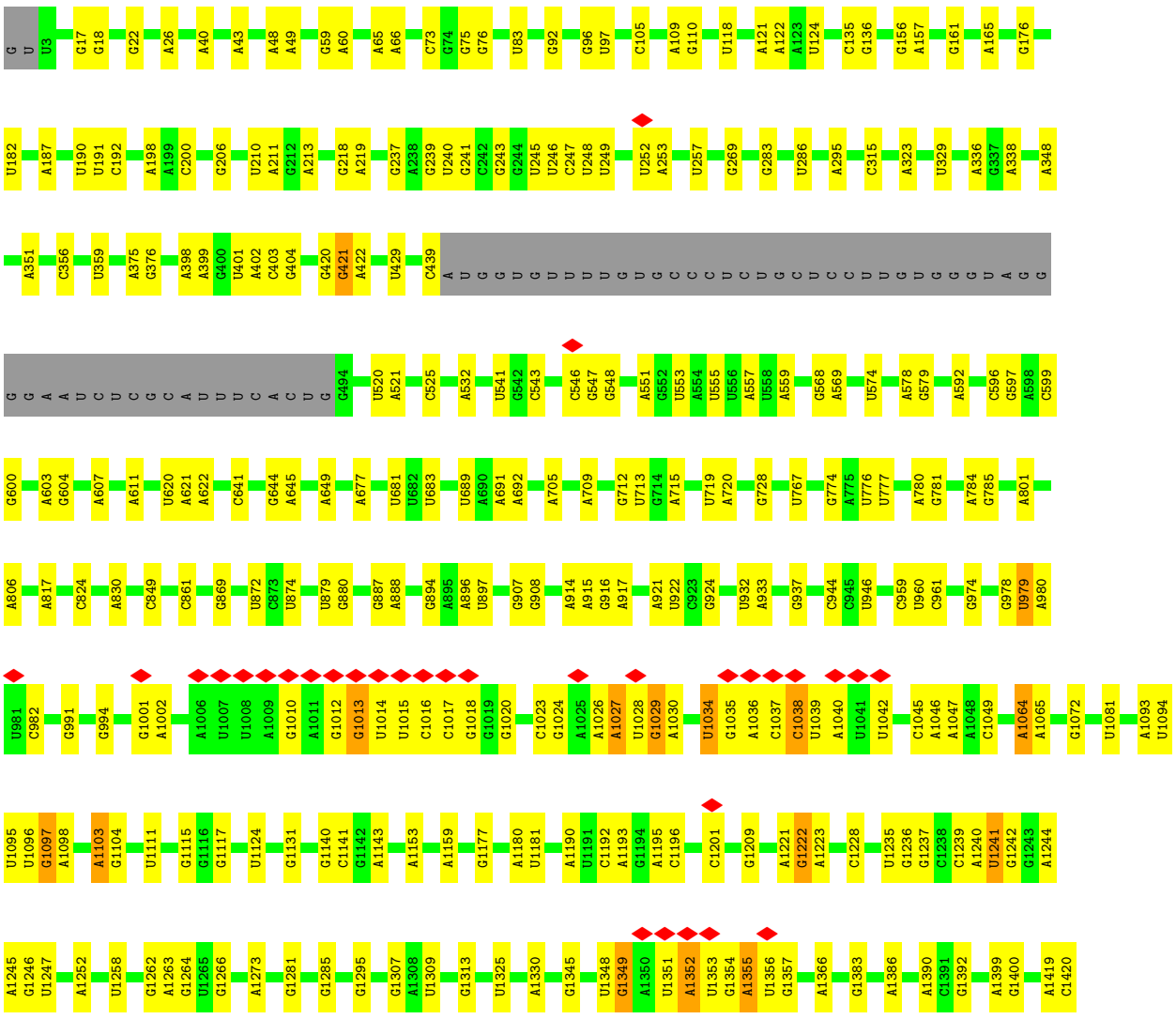
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	L	147	821	502	160	159	0	0

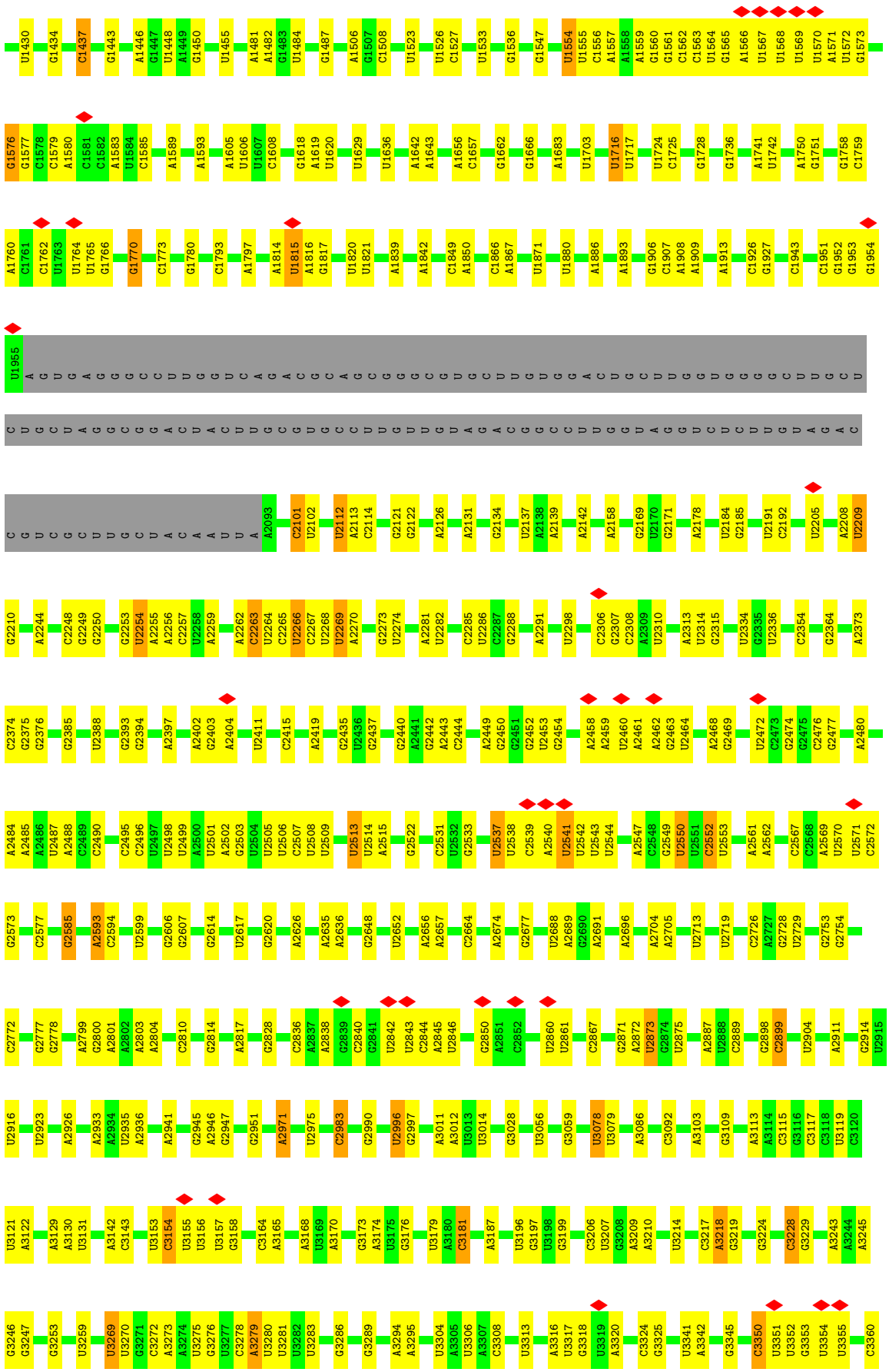
3 Residue-property plots (i)

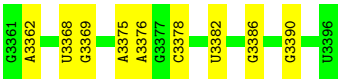
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

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

Chain A: 72% 20% • 6%

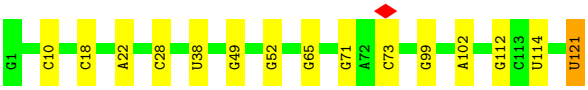



U1430 G1434 C1437 G1443 A1446 G1447 U1448 A1449 G1450 U1455 A1481 A1482 G1483 U1484 G1487 A1506 G1507 C1508 U1523 U1526 C1527 U1533 G1536 G1547 U1554 U1555 C1556 A1557 A1558 A1559 G1560 G1561 C1562 C1563 U1564 G1565 A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1573
G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 U1584 C1585 A1589 A1593 A1605 U1606 U1607 C1608 G1618 A1619 U1620 U1629 U1636 A1642 A1643 A1656 C1657 G1662 G1666 A1683 U1703 U1716 U1717 U1724 C1725 G1728 G1736 A1741 U1742 A1750 G1751 G1758 C1759
A1760 C1761 C1762 U1763 U1764 U1765 G1766 G1770 C1773 G1780 C1793 A1797 A1814 U1815 A1816 G1817 U1820 U1821 A1839 A1842 C1849 A1850 C1866 A1867 U1871 U1880 A1886 A1893 G1906 C1907 A1908 A1909 A1913 C1926 G1927 C1943 C1951 G1952 G1953 G1954
U1955 A G U G A G G C C U A C U G G U C A G A C G U G C A G C U G G U C G U U G C G G A C U U G U A G G U C U U G U G A C
C U G C U A G G C G C U A C U U G C A A G U U C G C G U G C C U U G U U G G G A G A C U G G C G G C C U U G G U C U C U G U G G A G G U C U G G U A G A C
C G U C G C U U G C U A C A U U A A2093 C2101 U2102 U2112 A2113 C2114 G2121 G2122 A2126 A2131 G2134 U2137 A2138 A2139 A2142 A2158 G2169 U2170 G2171 A2178 U2184 G2185 U2191 C2192 U2205 A2208 U2209
G2210 A2244 C2248 G2249 G2250 G2253 U2254 A2255 A2256 C2257 U2258 A2259 A2262 C2263 U2264 C2265 U2266 C2267 U2268 U2269 A2270 G2273 U2274 A2281 U2282 C2285 U2286 C2287 G2288 A2291 U2298 C2306 G2307 C2308 A2309 U2310 A2313 U2314 G2315 U2334 G2335 U2336 C2354 G2364 A2373
C2374 G2375 G2376 G2385 U2388 G2393 G2394 A2397 A2402 G2403 A2404 U2411 C2415 A2419 G2435 U2436 G2437 G2440 A2441 G2442 A2443 C2444 A2449 G2450 G2451 G2452 U2453 G2454 A2458 A2459 U2460 A2461 A2462 G2463 U2464 A2468 G2469 U2472 C2473 G2474 G2475 C2476 G2477 A2480
A2484 A2485 A2486 U2487 A2488 C2489 C2490 C2495 C2496 U2497 U2498 U2499 A2500 U2501 A2502 G2503 U2504 U2505 U2506 C2507 U2508 U2509 U2513 U2514 A2515 G2522 C2531 U2532 C2533 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 A2547 C2548 G2549 U2550 U2551 C2552 U2553 A2561 A2562 C2567 C2568 A2569 U2570 U2571 C2572
G2573 C2577 G2585 A2593 C2594 U2599 G2606 G2607 G2614 U2617 G2620 A2626 A2635 A2636 G2648 U2652 A2656 A2657 C2664 A2674 G2677 U2688 A2689 G2690 A2691 A2696 A2704 A2705 U2713 U2719 C2726 A2727 G2728 U2729 G2753 G2754
C2772 G2777 G2778 A2799 G2800 A2801 A2802 A2803 A2804 C2810 G2814 A2817 G2828 C2836 A2837 A2838 G2839 C2840 G2841 U2842 U2843 C2844 A2845 U2846 G2850 A2851 C2852 U2860 U2861 C2867 G2871 A2872 U2873 G2874 U2875 A2887 U2888 C2889 G2898 C2899 U2904 A2911 G2914 U2915
U2916 U2923 A2926 A2933 A2934 U2935 A2936 A2941 G2945 A2946 G2947 G2951 A2971 U2975 C2983 G2990 U2996 G2997 A3011 A3012 U3013 U3014 G3028 U3056 G3059 U3078 U3079 A3086 C3092 A3103 G3109 A3113 A3114 C3115 G3116 C3117 C3118 U3119 C3120
U3121 A3122 A3129 A3130 U3131 A3142 C3143 U3153 C3154 U3155 U3156 U3157 G3158 C3164 A3165 A3168 U3169 A3170 G3173 A3174 U3175 G3176 U3179 A3180 C3181 A3187 U3196 G3197 U3198 G3199 C3206 U3207 G3208 A3209 A3210 U3214 C3217 A3218 G3219 G3224 C3228 G3229 A3243 A3244 A3245
G3246 G3247 G3253 U3259 U3269 U3270 G3271 C3272 A3273 A3274 U3275 G3276 U3277 C3278 A3279 U3280 U3281 U3282 U3283 G3286 G3289 A3294 A3295 U3304 A3305 U3306 A3307 C3308 U3313 A3316 U3317 G3318 U3319 A3320 C3324 G3325 U3341 A3342 G3345 C3350 U3351 U3352 G3353 U3354 U3355 C3360



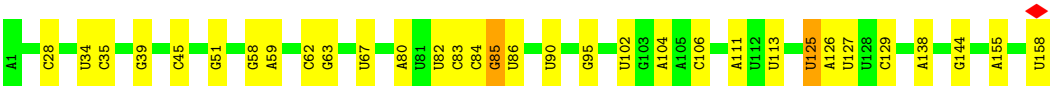
• Molecule 2: 5S rRNA

Chain B:



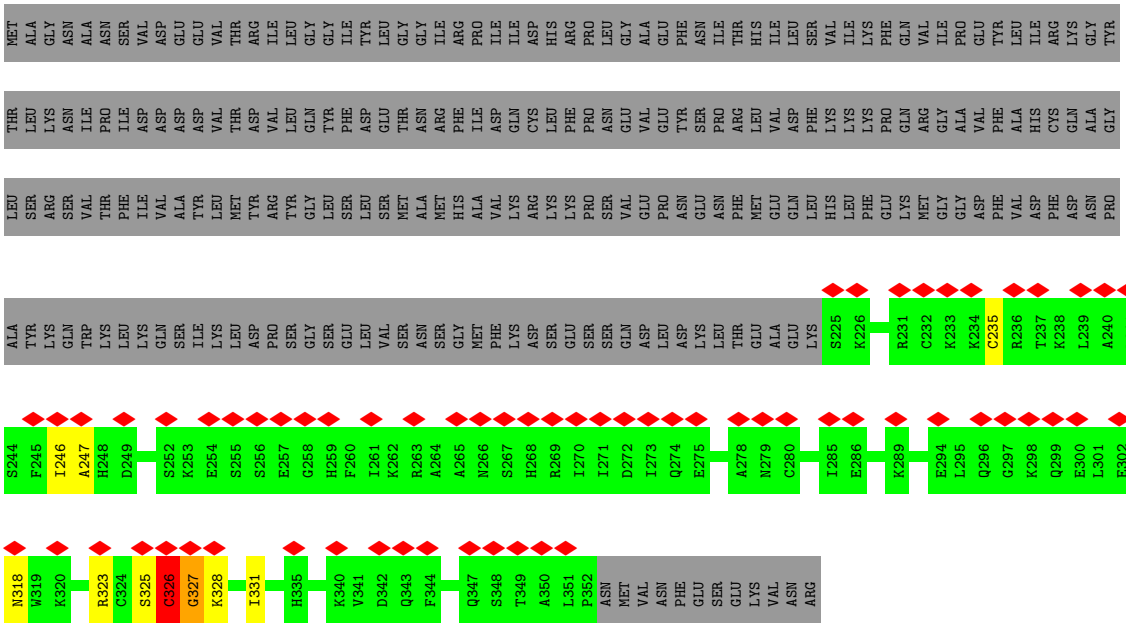
• Molecule 3: 5.8S rRNA

Chain C:



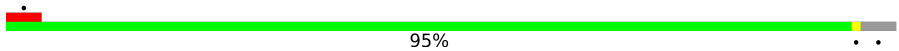
• Molecule 4: Tyrosine-protein phosphatase YVH1

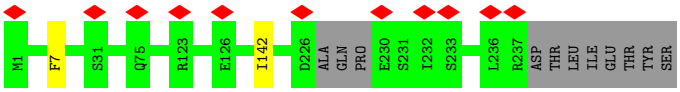
Chain Y:



• Molecule 5: Eukaryotic translation initiation factor 6

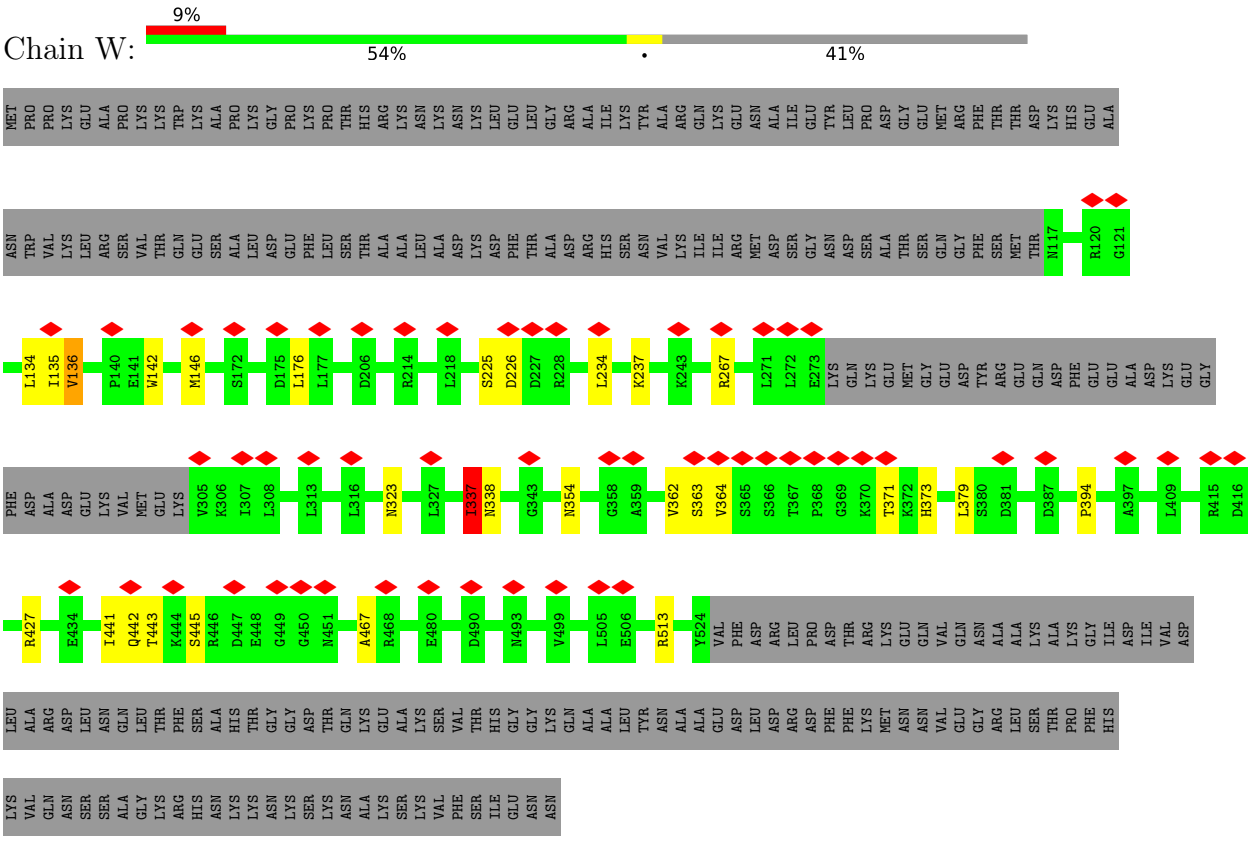
Chain X:





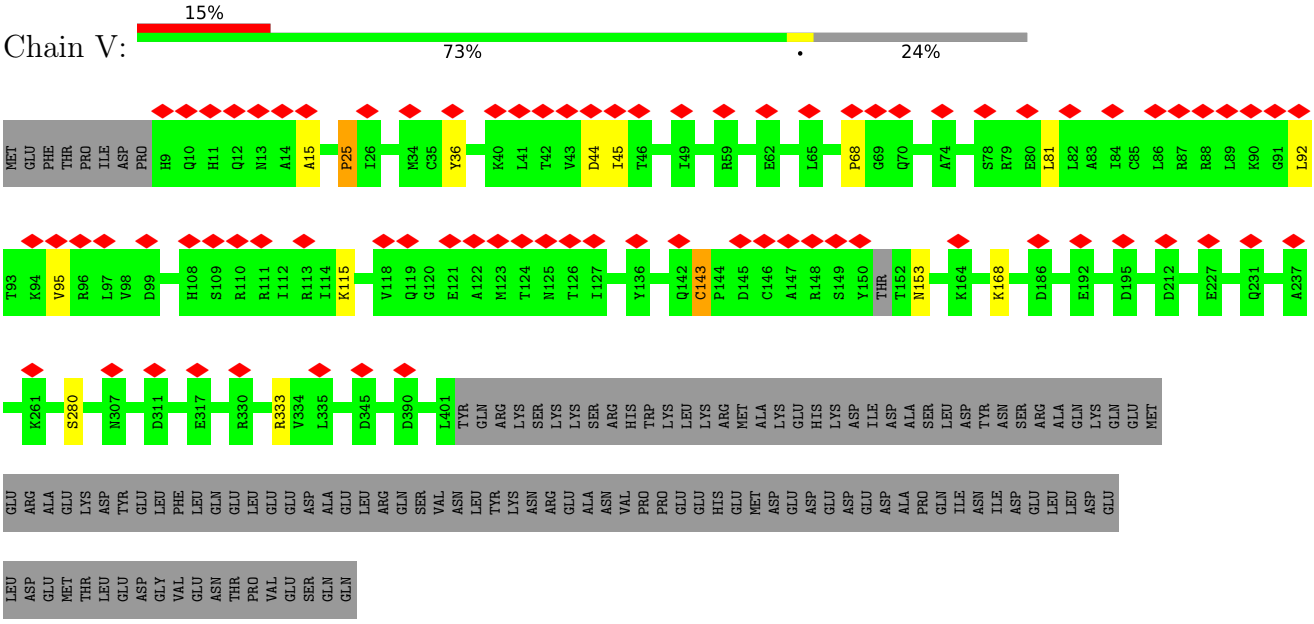
• Molecule 6: Large subunit GTPase 1

Chain W:



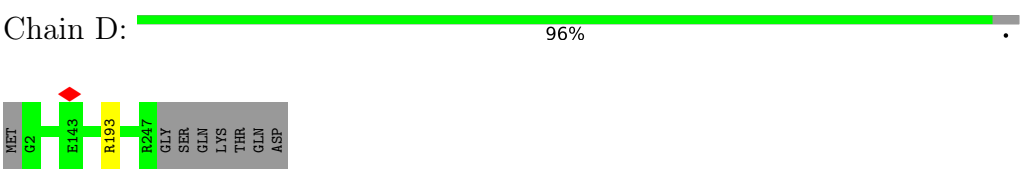
- Molecule 7: 60S ribosomal export protein NMD3

Chain V:



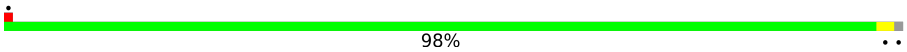
- Molecule 8: 60S ribosomal protein L2-A

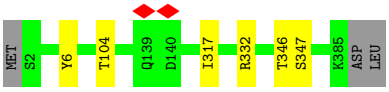
Chain D:



- Molecule 9: 60S ribosomal protein L3

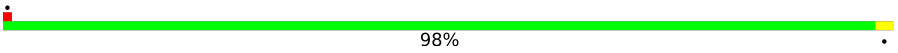
Chain E:

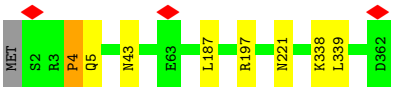




- Molecule 10: 60S ribosomal protein L4-A

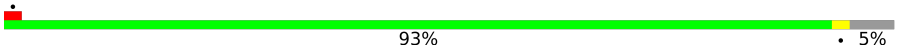
Chain F:

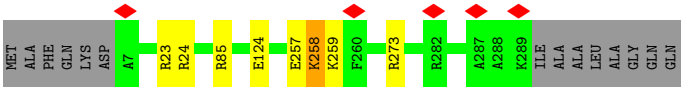




- Molecule 11: 60S ribosomal protein L5

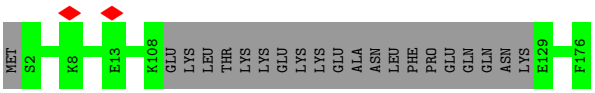
Chain G:





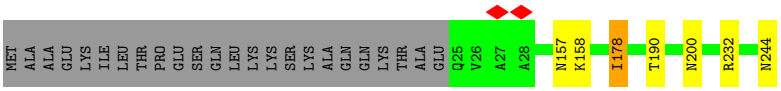
- Molecule 12: 60S ribosomal protein L6-A

Chain H:



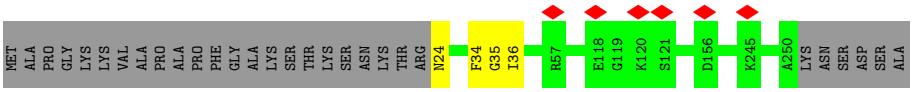
- Molecule 13: 60S ribosomal protein L7-A

Chain I:



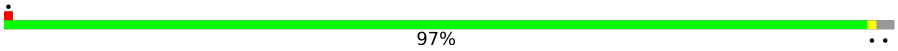
- Molecule 14: 60S ribosomal protein L8-A

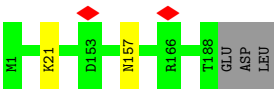
Chain J:



- Molecule 15: 60S ribosomal protein L9-A

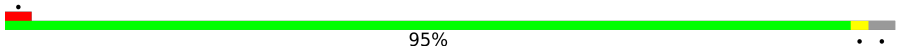
Chain K:

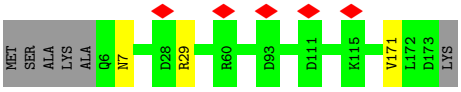




• Molecule 16: 60S ribosomal protein L11-A

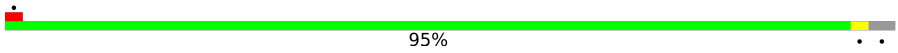
Chain M:

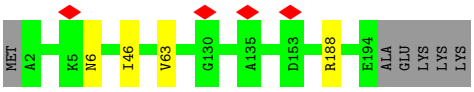




• Molecule 17: 60S ribosomal protein L13-A

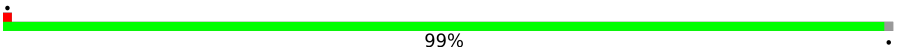
Chain N:

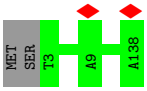




• Molecule 18: 60S ribosomal protein L14-A

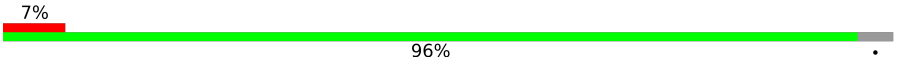
Chain O:

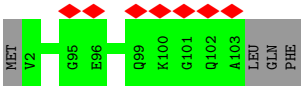




• Molecule 19: 60S ribosomal protein L42-A

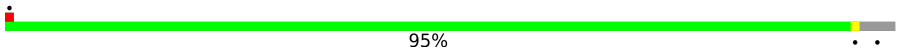
Chain Q:

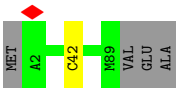




• Molecule 20: 60S ribosomal protein L43-A

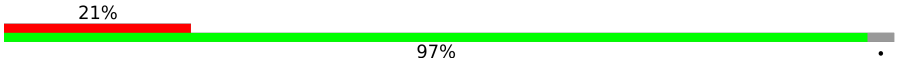
Chain R:

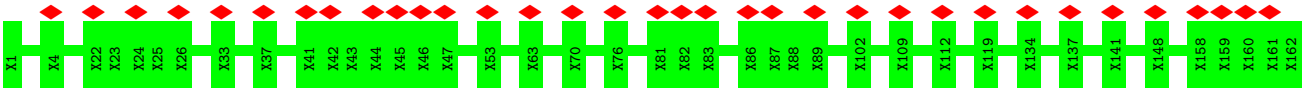


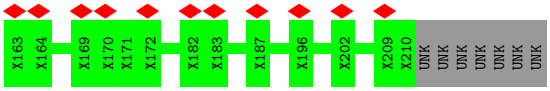


• Molecule 21: Ribosomal Protein uL1

Chain S:

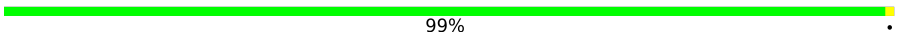






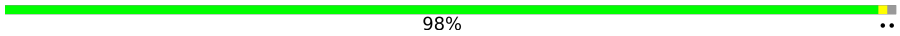
• Molecule 22: 60S ribosomal protein L15-A

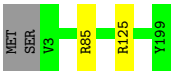
Chain a:



• Molecule 23: 60S ribosomal protein L16-A

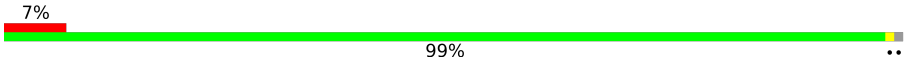
Chain b:

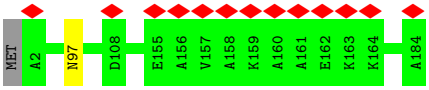




• Molecule 24: 60S ribosomal protein L17-A

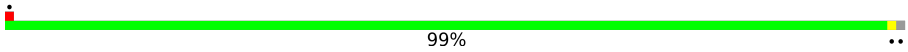
Chain c:

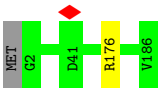




• Molecule 25: 60S ribosomal protein L18-A

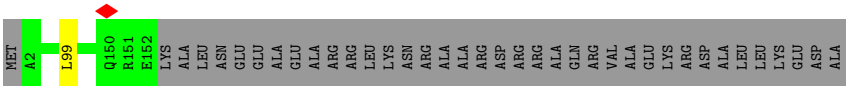
Chain d:





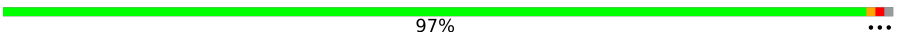
• Molecule 26: 60S ribosomal protein L19-A

Chain e:



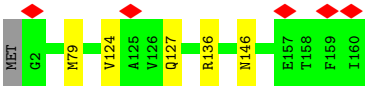
• Molecule 27: 60S ribosomal protein L20-A

Chain f:



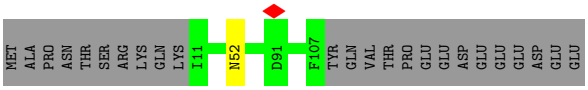
• Molecule 28: 60S ribosomal protein L21-A

Chain g: 96%



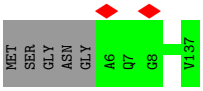
• Molecule 29: 60S ribosomal protein L22-A

Chain h: 79% 20%



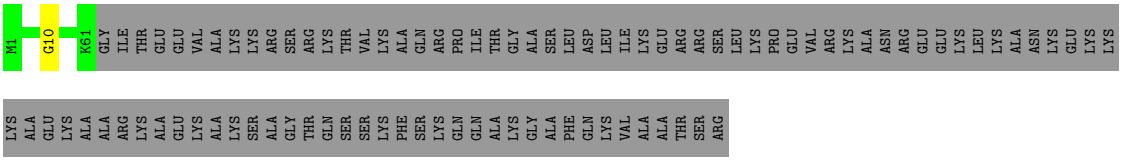
• Molecule 30: 60S ribosomal protein L23-A

Chain i: 96%



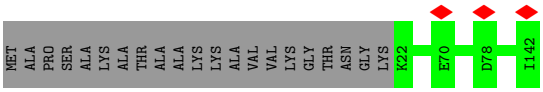
• Molecule 31: 60S ribosomal protein L24-A

Chain j: 39% 61%



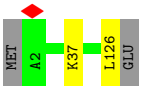
• Molecule 32: 60S ribosomal protein L25

Chain k: 85% 15%



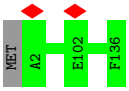
• Molecule 33: 60S ribosomal protein L26-A

Chain l: 97%

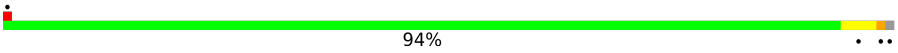


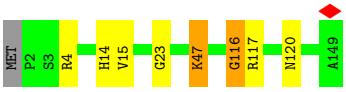
• Molecule 34: 60S ribosomal protein L27-A

Chain m: 99%

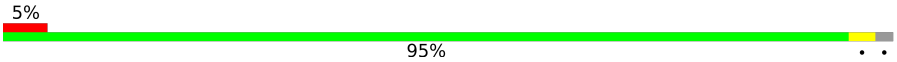


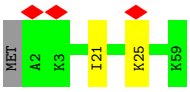
• Molecule 35: 60S ribosomal protein L28

Chain n: 



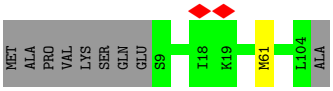
• Molecule 36: 60S ribosomal protein L29

Chain o: 

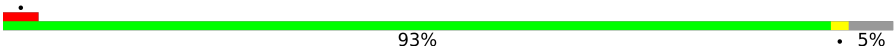


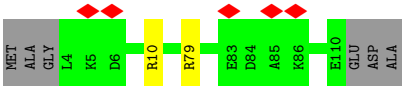
• Molecule 37: 60S ribosomal protein L30

Chain p:

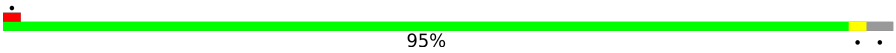


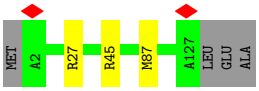
• Molecule 38: 60S ribosomal protein L31-A

Chain q: 

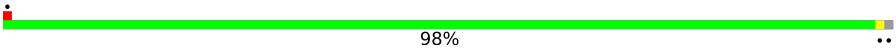


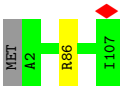
• Molecule 39: 60S ribosomal protein L32

Chain r: 



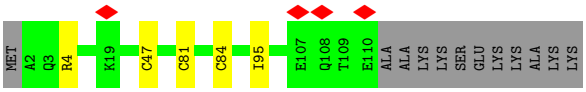
• Molecule 40: 60S ribosomal protein L33-A

Chain s: 

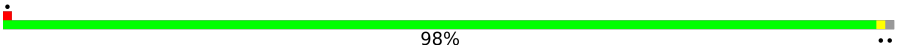


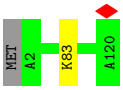
• Molecule 41: 60S ribosomal protein L34-A

Chain t:

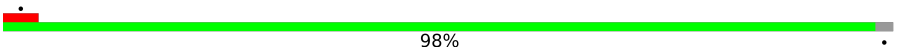


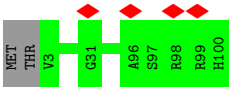
- Molecule 42: 60S ribosomal protein L35-A

Chain u: 



- Molecule 43: 60S ribosomal protein L36-A

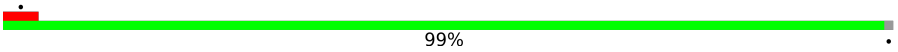
Chain v: 

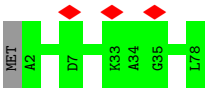


- Molecule 44: 60S ribosomal protein L37-A

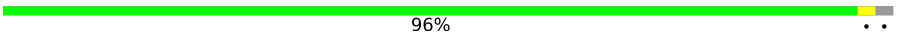
Chain w:

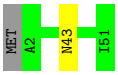
- Molecule 45: 60S ribosomal protein L38

Chain x: 



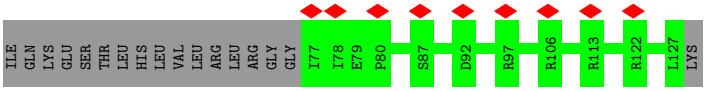
- Molecule 46: 60S ribosomal protein L39

Chain y: 



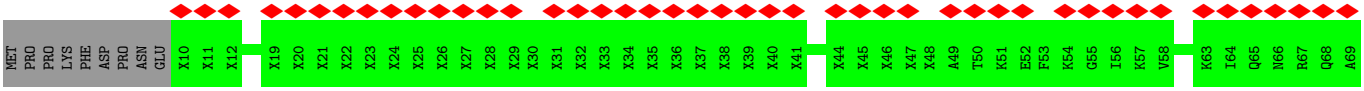
- Molecule 47: Ubiquitin-60S ribosomal protein L40

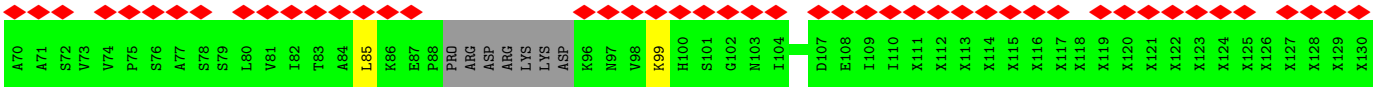
Chain z:

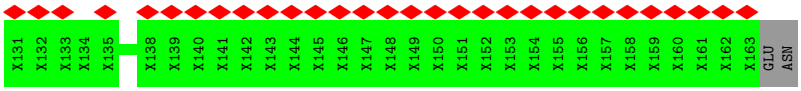


• Molecule 48: Ribosomal protein L12

Chain L:







4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0.66	1/76692 (0.0%)	0.94	131/119572 (0.1%)
2	B	0.57	0/2883	0.93	5/4491 (0.1%)
3	C	0.68	0/3746	0.92	5/5832 (0.1%)
4	Y	0.38	0/1016	0.91	4/1368 (0.3%)
5	X	0.31	0/1729	0.55	0/2355
6	W	0.34	0/3035	0.71	2/4119 (0.0%)
7	V	0.35	0/3093	0.66	2/4203 (0.0%)
8	D	0.39	0/1908	0.58	0/2564
9	E	0.41	0/3130	0.58	0/4206
10	F	0.37	0/2800	0.59	1/3790 (0.0%)
11	G	0.36	0/2329	0.58	2/3142 (0.1%)
12	H	0.34	0/1236	0.56	0/1661
13	I	0.37	0/1807	0.56	1/2432 (0.0%)
14	J	0.37	0/1794	0.58	0/2425
15	K	0.36	0/1514	0.57	0/2039
16	M	0.30	0/1365	0.61	0/1831
17	N	0.38	0/1564	0.59	0/2102
18	O	0.33	0/1068	0.50	0/1438
19	Q	0.37	0/831	0.57	0/1097
20	R	0.40	0/680	0.60	0/905
22	a	0.41	0/1757	0.54	0/2354
23	b	0.38	0/1585	0.51	0/2128
24	c	0.39	0/1443	0.58	0/1944
25	d	0.36	0/1465	0.57	0/1965
26	e	0.36	0/1236	0.56	1/1650 (0.1%)
27	f	0.38	0/1468	0.60	2/1973 (0.1%)
28	g	0.36	0/1300	0.55	0/1743
29	h	0.35	0/781	0.51	0/1058
30	i	0.39	0/996	0.55	0/1340
31	j	0.35	0/521	0.50	0/691
32	k	0.40	0/979	0.57	0/1321
33	l	0.34	0/995	0.56	1/1329 (0.1%)
34	m	0.39	0/1118	0.56	0/1497
35	n	0.38	0/1204	0.66	2/1612 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
36	o	0.33	0/473	0.60	0/629
37	p	0.35	0/745	0.54	0/1001
38	q	0.39	0/880	0.57	0/1182
39	r	0.36	0/1033	0.56	0/1383
40	s	0.44	0/868	0.56	0/1168
41	t	0.43	1/871 (0.1%)	0.66	2/1164 (0.2%)
42	u	0.34	0/978	0.56	0/1301
43	v	0.33	0/759	0.56	0/1009
44	w	0.41	0/680	0.60	0/901
45	x	0.33	0/614	0.58	0/822
46	y	0.36	0/443	0.60	0/588
47	z	0.27	0/414	0.51	0/551
48	L	0.31	0/363	0.75	1/493 (0.2%)
All	All	0.56	2/140189 (0.0%)	0.83	162/206369 (0.1%)

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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2259	A	C1'-N9	-5.70	1.38	1.46
41	t	81	CYS	CB-SG	5.03	1.90	1.82

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
41	t	81	CYS	CA-CB-SG	10.98	133.76	114.00
4	Y	331	ILE	CG1-CB-CG2	-10.01	89.38	111.40
1	A	2263	C	N1-C2-O2	8.71	124.13	118.90
2	B	121	U	N3-C2-O2	-8.67	116.13	122.20
1	A	2137	U	N1-C2-O2	8.64	128.85	122.80

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)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	Y	126/364 (35%)	99 (79%)	22 (18%)	5 (4%)	3 28
5	X	230/245 (94%)	221 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	W	373/640 (58%)	313 (84%)	54 (14%)	6 (2%)	9	44
7	V	388/518 (75%)	323 (83%)	59 (15%)	6 (2%)	10	46
8	D	244/254 (96%)	225 (92%)	19 (8%)	0	100	100
9	E	382/387 (99%)	354 (93%)	26 (7%)	2 (0%)	29	66
10	F	359/362 (99%)	330 (92%)	26 (7%)	3 (1%)	19	57
11	G	281/297 (95%)	268 (95%)	12 (4%)	1 (0%)	34	70
12	H	151/176 (86%)	142 (94%)	9 (6%)	0	100	100
13	I	218/244 (89%)	207 (95%)	9 (4%)	2 (1%)	17	54
14	J	225/256 (88%)	217 (96%)	7 (3%)	1 (0%)	34	70
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%)	15	52
18	O	134/138 (97%)	129 (96%)	5 (4%)	0	100	100
19	Q	100/106 (94%)	94 (94%)	6 (6%)	0	100	100
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%)	13	50
28	g	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
29	h	95/121 (78%)	91 (96%)	3 (3%)	1 (1%)	14	51
30	i	130/137 (95%)	129 (99%)	1 (1%)	0	100	100
31	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	9	43
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%)	7	40
36	o	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
37	p	94/105 (90%)	93 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	32	66

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 (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	
4	Y	110/323 (34%)	107 (97%)	3 (3%)	44	69
5	X	186/211 (88%)	186 (100%)	0	100	100
6	W	316/555 (57%)	309 (98%)	7 (2%)	52	72
7	V	332/467 (71%)	327 (98%)	5 (2%)	65	81
8	D	189/196 (96%)	188 (100%)	1 (0%)	88	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	E	317/323 (98%)	314 (99%)	3 (1%)	78	88
10	F	288/289 (100%)	285 (99%)	3 (1%)	76	86
11	G	236/245 (96%)	232 (98%)	4 (2%)	60	78
12	H	131/153 (86%)	131 (100%)	0	100	100
13	I	185/205 (90%)	183 (99%)	2 (1%)	73	85
14	J	182/208 (88%)	181 (100%)	1 (0%)	88	94
15	K	168/171 (98%)	167 (99%)	1 (1%)	86	92
16	M	146/150 (97%)	145 (99%)	1 (1%)	84	91
17	N	153/159 (96%)	152 (99%)	1 (1%)	84	91
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%)	67	81
22	a	175/176 (99%)	173 (99%)	2 (1%)	73	85
23	b	160/162 (99%)	158 (99%)	2 (1%)	69	82
24	c	140/146 (96%)	139 (99%)	1 (1%)	84	91
25	d	150/151 (99%)	149 (99%)	1 (1%)	84	91
26	e	125/154 (81%)	125 (100%)	0	100	100
27	f	155/156 (99%)	153 (99%)	2 (1%)	69	82
28	g	136/137 (99%)	131 (96%)	5 (4%)	34	62
29	h	84/107 (78%)	84 (100%)	0	100	100
30	i	102/105 (97%)	102 (100%)	0	100	100
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%)	107 (99%)	1 (1%)	78	88
34	m	115/116 (99%)	115 (100%)	0	100	100
35	n	118/119 (99%)	116 (98%)	2 (2%)	60	78
36	o	46/47 (98%)	46 (100%)	0	100	100
37	p	81/88 (92%)	80 (99%)	1 (1%)	71	84
38	q	92/97 (95%)	90 (98%)	2 (2%)	52	72
39	r	108/111 (97%)	105 (97%)	3 (3%)	43	68
40	s	90/91 (99%)	89 (99%)	1 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	t	94/103 (91%)	91 (97%)	3 (3%)	39	65
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%)	66 (96%)	3 (4%)	29	58
45	x	67/69 (97%)	67 (100%)	0	100	100
46	y	45/46 (98%)	44 (98%)	1 (2%)	52	72
47	z	46/116 (40%)	46 (100%)	0	100	100
48	L	31/65 (48%)	30 (97%)	1 (3%)	39	65
All	All	5879/6904 (85%)	5815 (99%)	64 (1%)	74	85

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	t	47	CYS
44	w	22	CYS
11	G	85	ARG
11	G	24	ARG
44	w	25	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
17	N	25	HIS
24	c	97	ASN
17	N	137	GLN
22	a	37	HIS
28	g	146	ASN

5.3.3 RNA (i)

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 (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)

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.

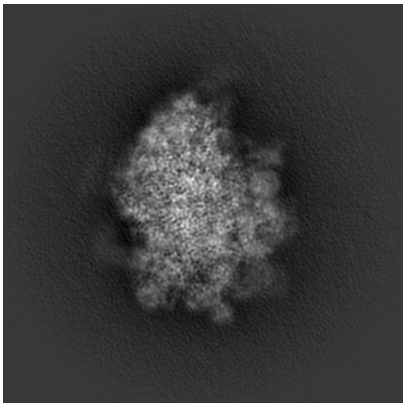
6 Map visualisation (i)

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.

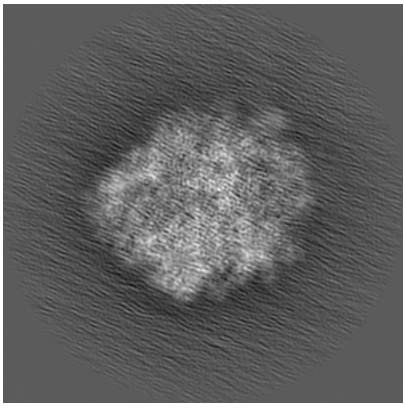
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

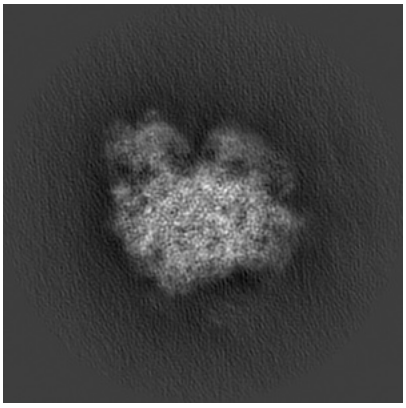
6.1.1 Primary map



X



Y

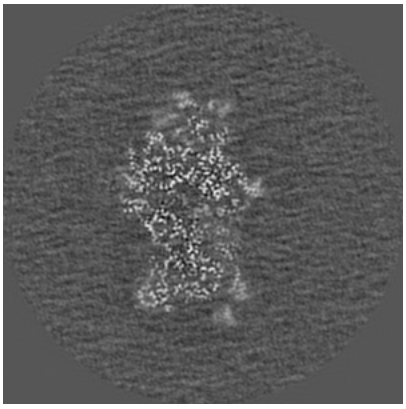


Z

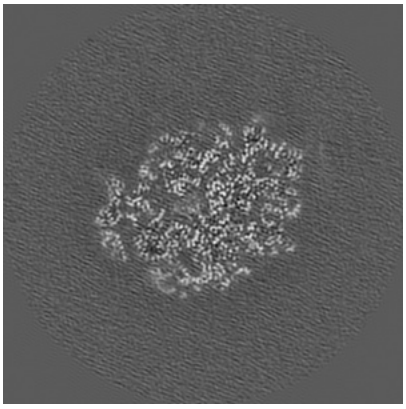
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

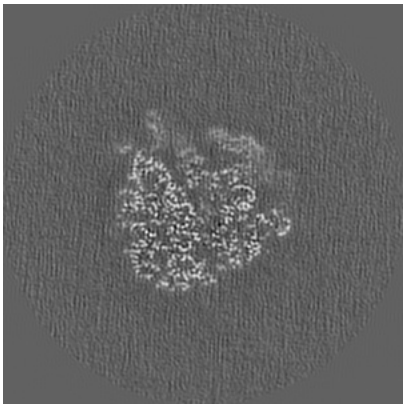
6.2.1 Primary map



X Index: 192



Y Index: 192

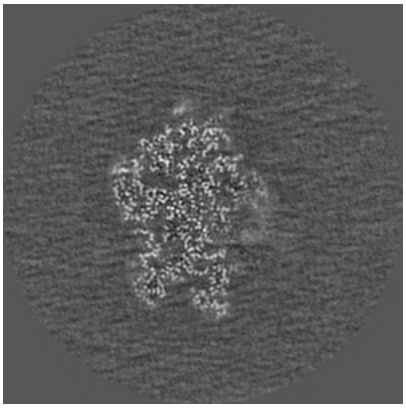


Z Index: 192

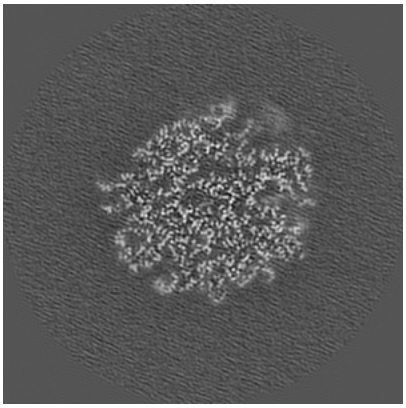
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

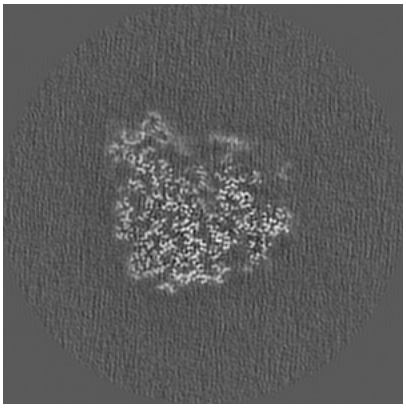
6.3.1 Primary map



X Index: 173



Y Index: 173

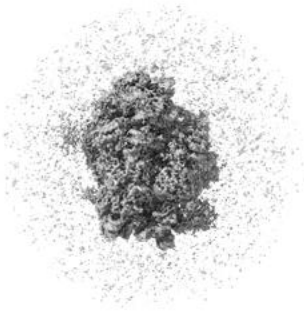


Z Index: 185

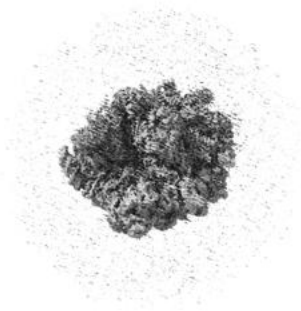
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

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

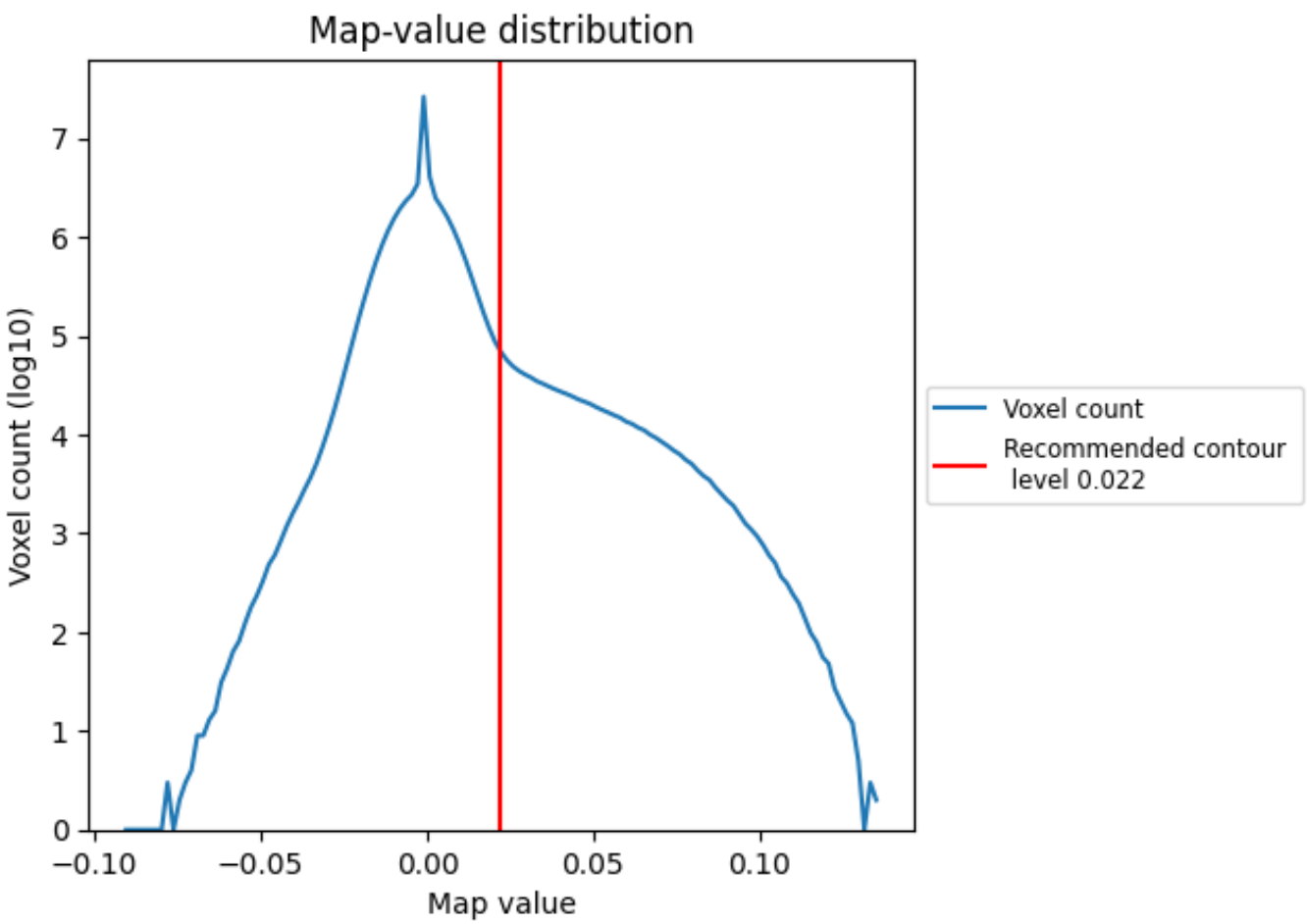
6.5 Mask visualisation (i)

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

7 Map analysis (i)

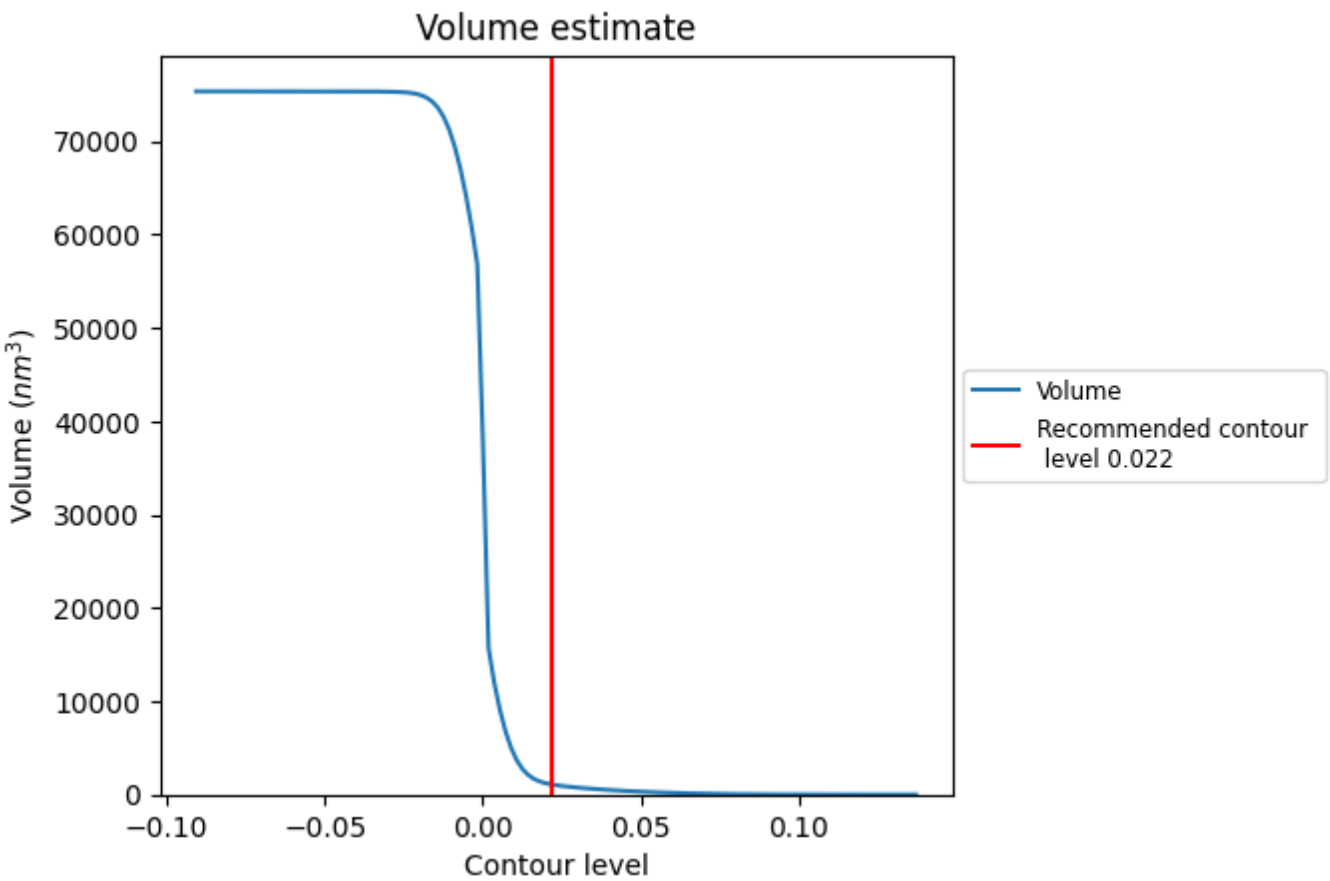
This section contains the results of statistical analysis of the map.

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.

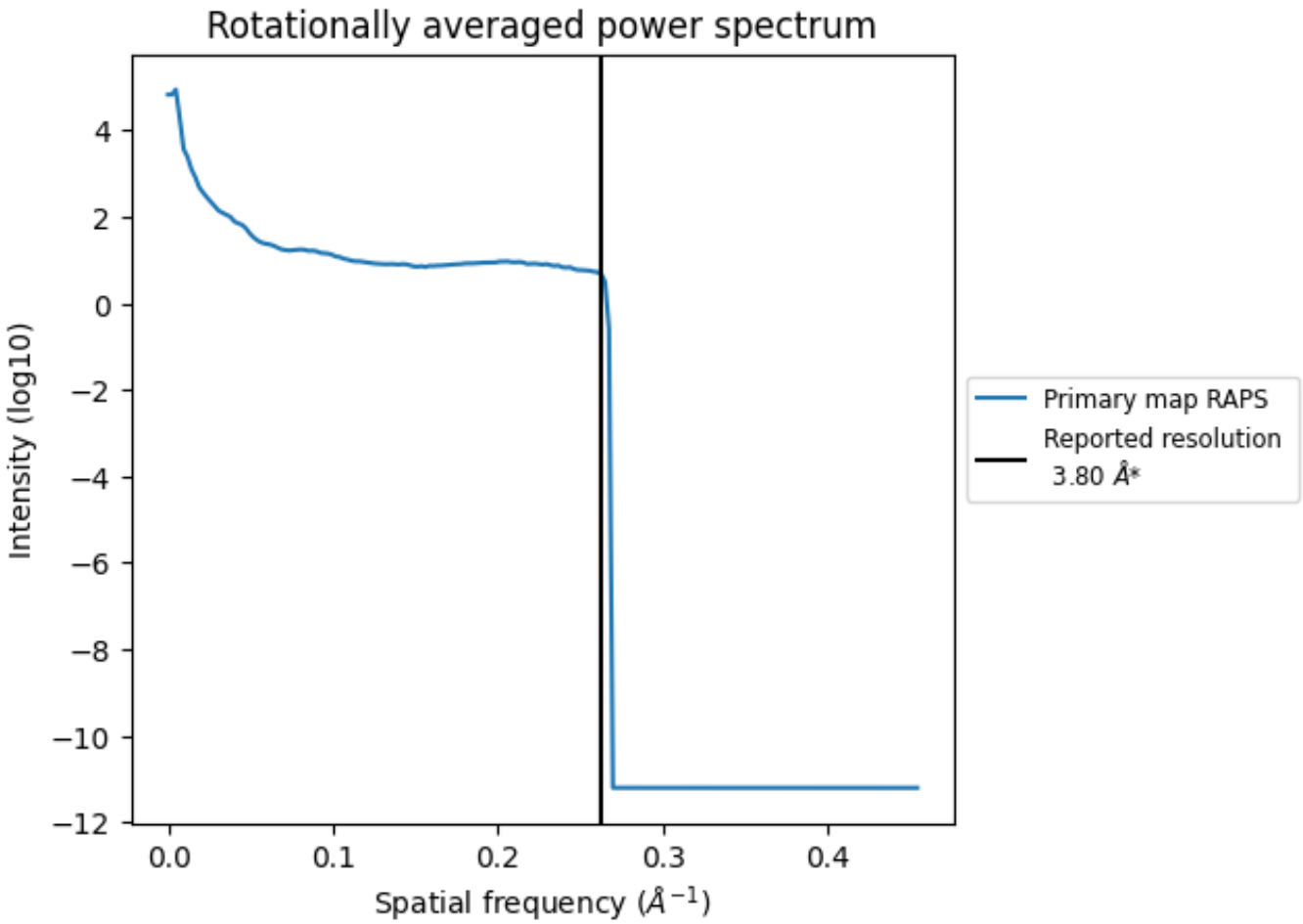
7.2 Volume estimate (i)



The volume at the recommended contour level is 1068 nm^3; 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 (i)

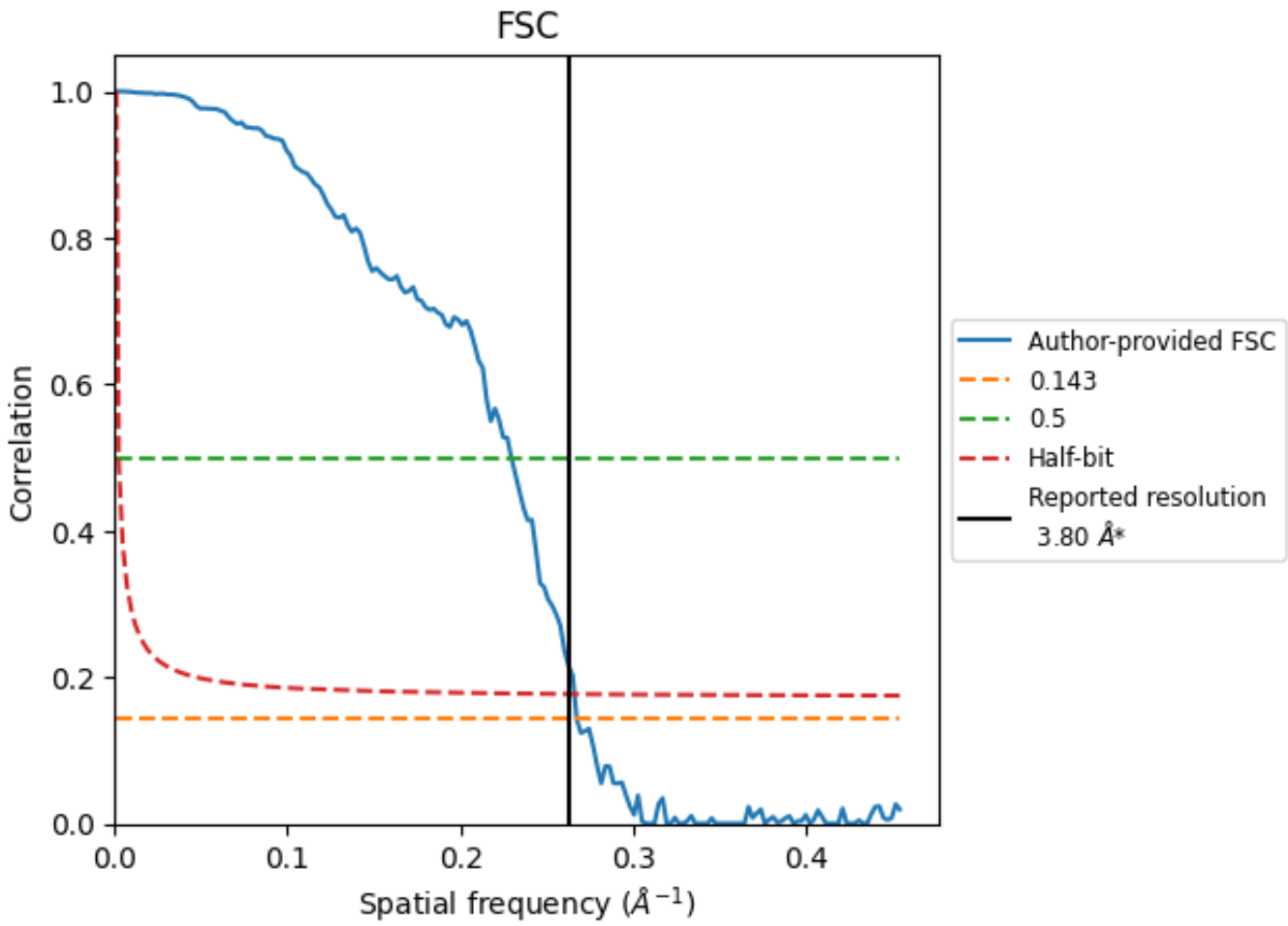


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8.2 Resolution estimates (i)

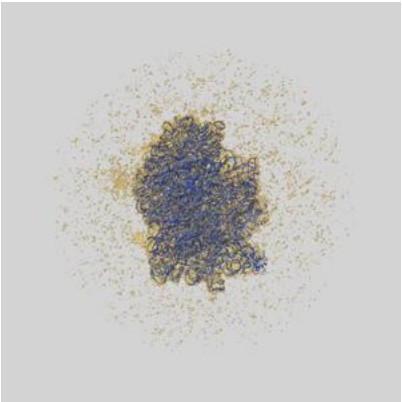
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.74	4.35	3.76
Unmasked-calculated*	-	-	-

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

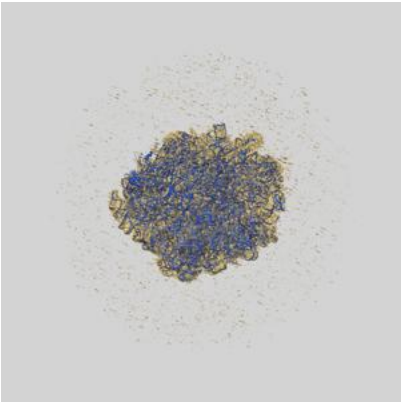
9 Map-model fit (i)

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.

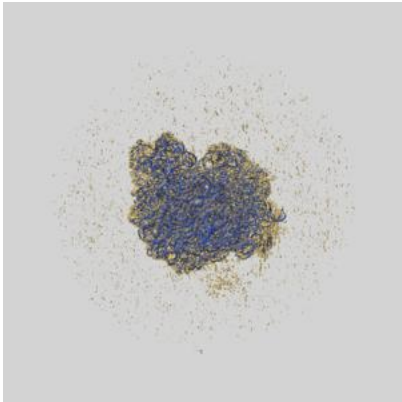
9.1 Map-model overlay (i)



X



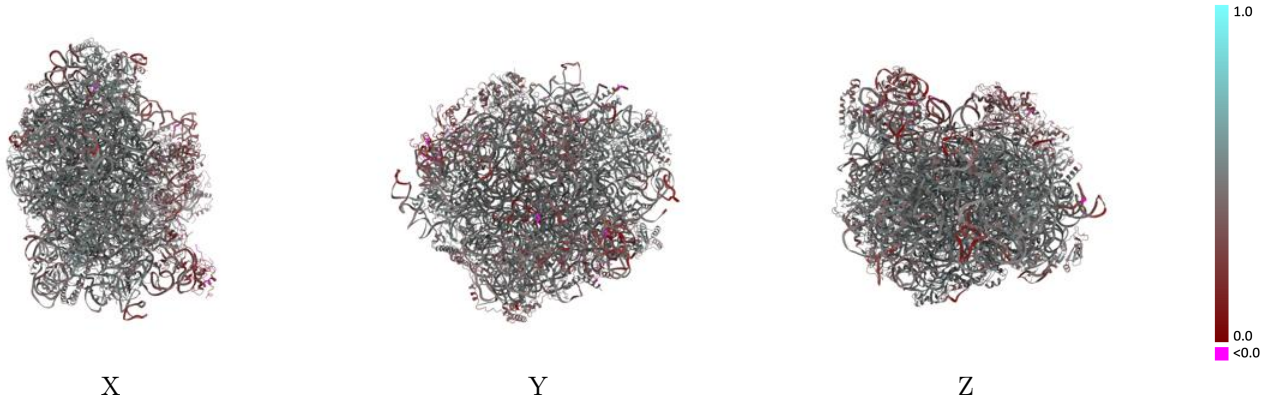
Y



Z

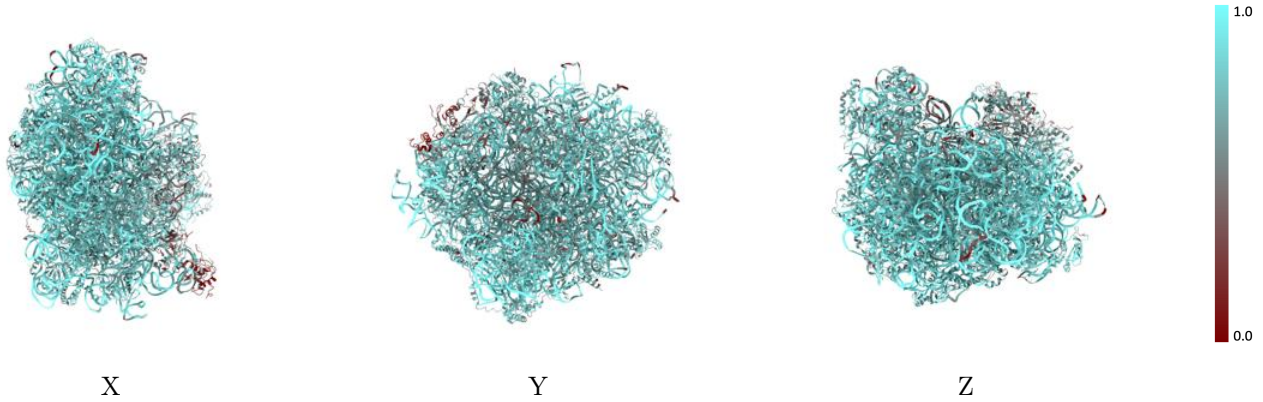
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



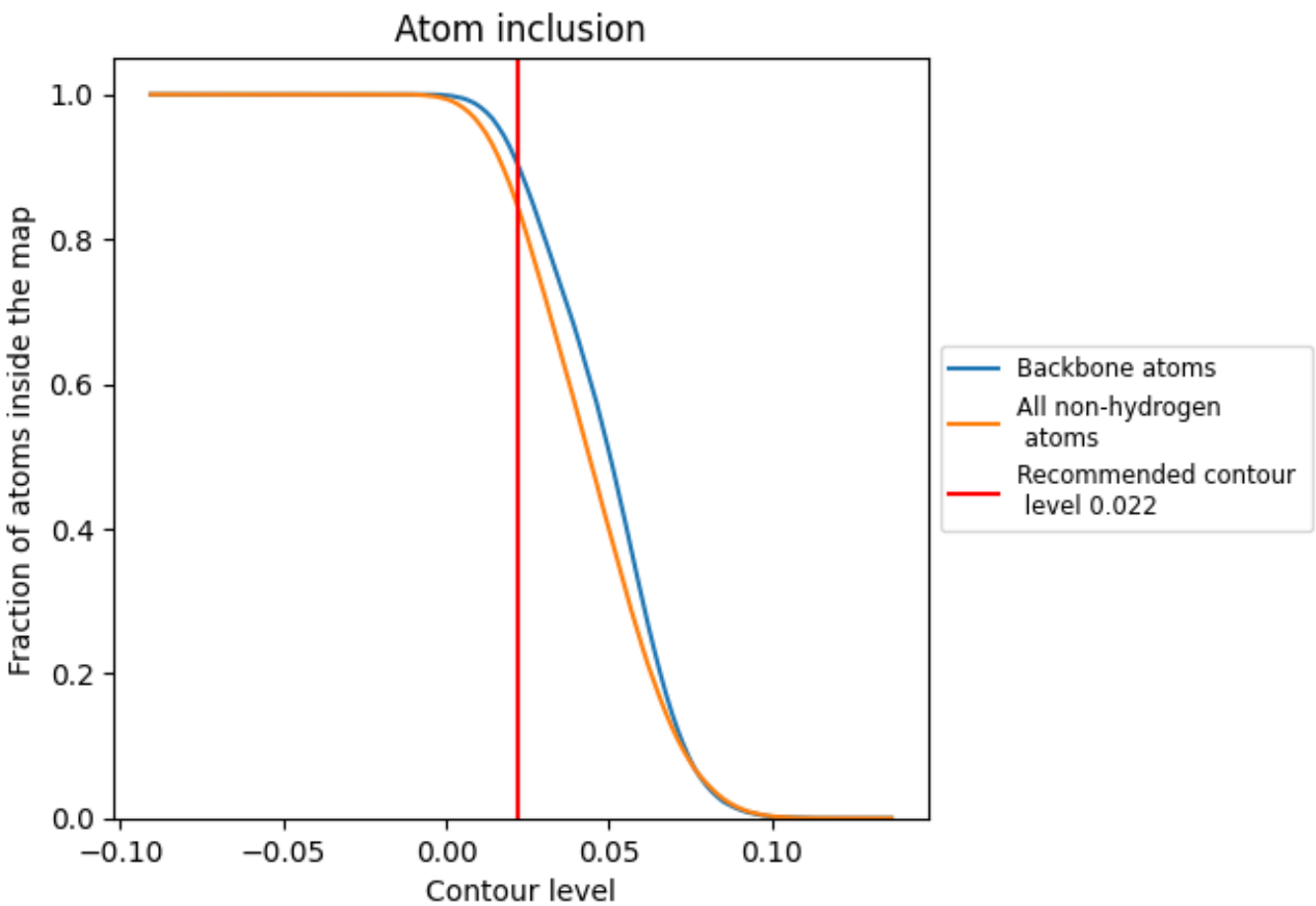
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	0.9519	0.4610
C	0.9404	0.4730
D	0.8241	0.5080
E	0.8272	0.4900
F	0.7952	0.4810
G	0.7754	0.4170
H	0.7869	0.4620
I	0.8079	0.4740
J	0.8029	0.4600
K	0.7870	0.4730
L	0.2100	0.2090
M	0.7243	0.3840
N	0.7876	0.4620
O	0.8051	0.4690
Q	0.7450	0.4820
R	0.8133	0.4930
S	0.7010	0.3340
V	0.6163	0.4010
W	0.6463	0.3470
X	0.7028	0.4330
Y	0.3889	0.3310
a	0.8247	0.5050
b	0.8184	0.4940
c	0.7805	0.4820
d	0.7957	0.4860
e	0.8312	0.4900
f	0.8099	0.4800
g	0.7685	0.4780
h	0.7928	0.4390
i	0.7576	0.4890
j	0.7850	0.4810
k	0.7941	0.4690
l	0.7973	0.4860

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Chain	Atom inclusion	Q-score
m	0.8217	0.4730
n	0.8161	0.4950
o	0.7257	0.4380
p	0.7766	0.4580
q	0.7679	0.4640
r	0.7890	0.4950
s	0.8319	0.5030
t	0.7849	0.4920
u	0.8081	0.4660
v	0.7641	0.4510
w	0.8701	0.5130
x	0.7479	0.4440
y	0.7928	0.5030
z	0.5558	0.4530