



## Full wwPDB EM Validation Report ⓘ

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

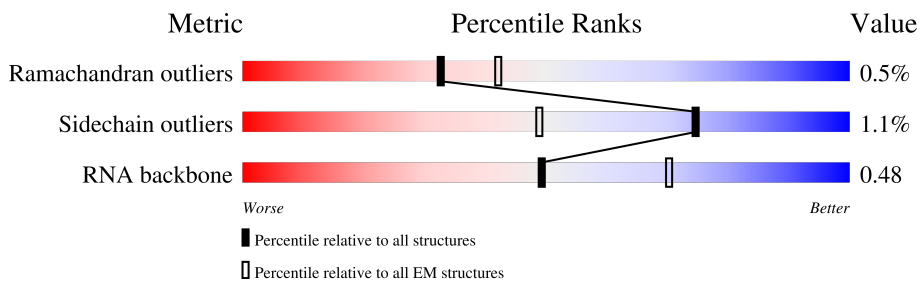
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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

# 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 3.80 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3396	
2	B	121	
3	C	158	
4	Y	364	
5	X	245	
6	W	640	
7	V	518	
8	D	254	

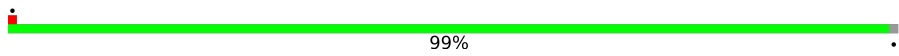
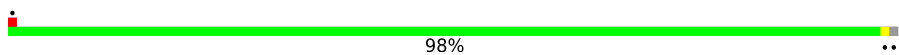
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Mol	Chain	Length	Quality of chain
9	E	387	98%
10	F	362	98%
11	G	297	93% 5%
12	H	176	88% 12%
13	I	244	87% 10%
14	J	256	87% 11%
15	K	191	97%
16	M	174	95%
17	N	199	95%
18	O	138	99%
19	Q	106	7% 96%
20	R	92	95%
21	S	217	21% 97%
22	a	204	99%
23	b	199	98%
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	 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	 40% 60% 7%
48	L	165	 88% 11% 74%

## 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
14	J	227	Total	C	N	O	S	0	0
			1762	1128	315	316	3		

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Ribosomal Protein uL1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

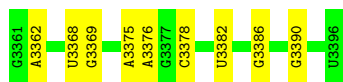
Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	51	Total	C	N	O	S	0	0
			408	253	84	66	5		

- Molecule 48 is a protein called Ribosomal protein L12.

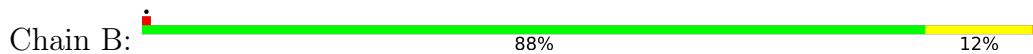
Mol	Chain	Residues	Atoms				AltConf	Trace
48	L	147	Total	C	N	O	0	0
			821	502	160	159		



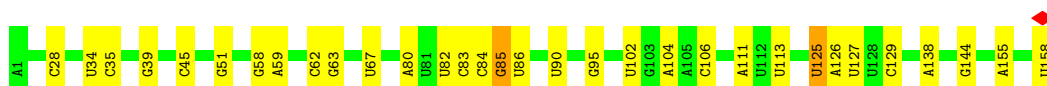
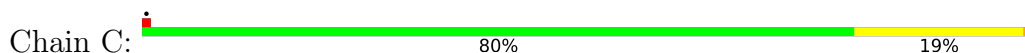
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U3121	A3122	A3129	A3130	U3131	A3142	C3143	U3153	C3154	U3155	U3156	U3157	G3158	C3164	A3165	A3168	U3169	A3170	G3173	A3174	U3175	G3176	A3179	A3180	C3181	U3187	U3196	G3197	U3198	G3199	C3206	G3207	A3209	A3210	U3214	C3217	A3218	G3219	G3224	C3228	G3229	U3243	A3244	A3245					
U2916	U2923	A2926	A2933	U2934	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	U3119	A3244	A3245											
C2772	G2777	G2778	A2799	G2800	A2801	A2803	A2804	C2810	G2814	A2817	G2828	C2836	A2837	A2838	C2839	C2840	U2842	U2843	C2844	A2845	U2846	G2850	A2851	C2852	U2860	U2861	C2867	G2871	A2872	U2873	G2874	U2875	A2887	U2888	C2889	G2896	C2899	U2904	A2911	G2914	U2915							
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													
A2484	A2485	U2486	U2487	A2488	C2489	C2495	C2496	U2497	U2498	U2499	A2500	U2501	A2502	G2503	U2505	U2506	U2508	U2509	U2513	U2514	A2515	G2522	C2531	U2532	G2533	U2537	U2538	C2539	A2540	U2541	U2542	U2543	U2544	A2547	C2546	G2549	U2550	C2551	C2552	U2553	A2561	A2562	C2567	C2568	A2569	U2570	U2571	C2572
G2374	G2375	G2376	G2385	U2388	G2393	G2394	A2397	A2402	G2403	A2404	U2411	C2415	A2419	G2435	U2436	G2437	G2440	A2441	G2442	A2443	C2444	A2449	U2450	G2451	G2452	U2453	G2454	A2458	A2459	U2460	A2461	A2462	G2463	U2464	A2468	G2469	U2472	G2473	G2474	G2475	G2477	A2480						
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	G2288	A2291	U2298	C2306	G2307	C2308	U2310	A2313	U2314	G2315	U2334	G2335	U2336	C2354	G2364	A2373						
C2121	C2122	A2126	A2131	G2134	U2137	A2138	A2139	A2142	A2158	G2169	U2170	C2171	A2178	U2184	G2185	U2191	C2192	U2205	A2208	U2209																												
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G1576	G1577	C1578	C1579	A1580	C1581	A1582	U1583	U1584	C1585	A1589	A1593	A1605	U1606	U1607	U1608	U1609	G1618	A1619	U1620	U1629	U1636	A1642	A1643	U1656	C1657	G1662	G1666	A1683	U1703	U1716	U1717	U1724	C1725	G1728	G1736	A1741	U1742	U1750	A1751	U1752	C1759							
U1430	G1434	C1437	G1443	A1446	U1448	U1449	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	U1564	G1565	A1566	U1567	U1568	U1569	U1570	A1571	U1572	G1573							



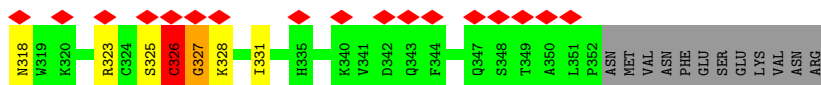
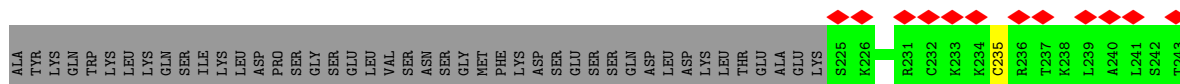
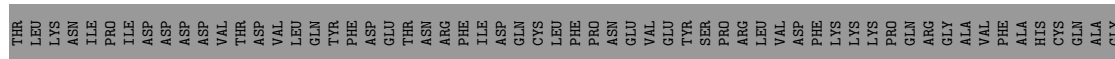
• Molecule 2: 5S rRNA



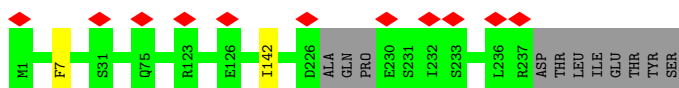
• Molecule 3: 5.8S rRNA



• Molecule 4: Tyrosine-protein phosphatase YVH1



• Molecule 5: Eukaryotic translation initiation factor 6

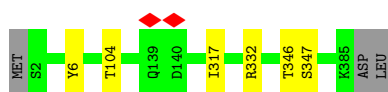


• Molecule 6: Large subunit GTPase 1



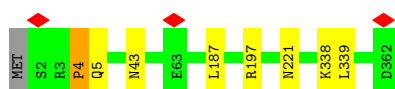
- Molecule 9: 60S ribosomal protein L3

Chain E:  98%

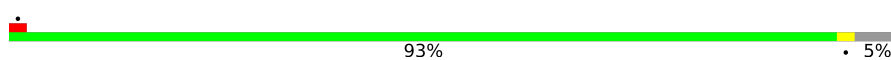


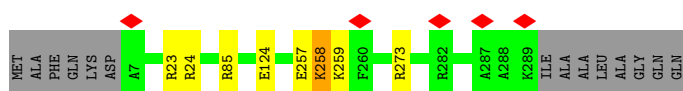
- Molecule 10: 60S ribosomal protein L4-A

Chain F:  98%




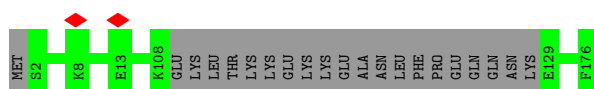
- Molecule 11: 60S ribosomal protein L5

Chain G:  93%




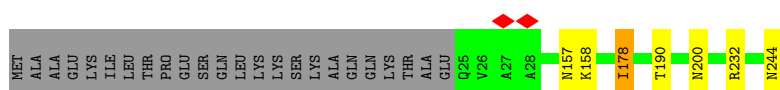
- Molecule 12: 60S ribosomal protein L6-A

Chain H:  88%




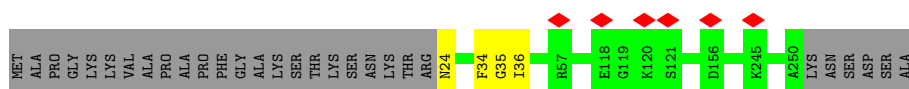
- Molecule 13: 60S ribosomal protein L7-A

Chain I:  87%



- Molecule 14: 60S ribosomal protein L8-A

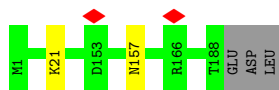
Chain J:  87%



- Molecule 15: 60S ribosomal protein L9-A

Chain K:  97%

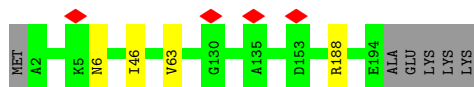




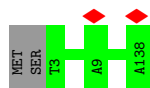
- Molecule 16: 60S ribosomal protein L11-A



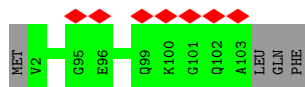
- Molecule 17: 60S ribosomal protein L13-A



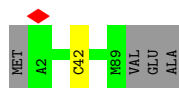
- Molecule 18: 60S ribosomal protein L14-A



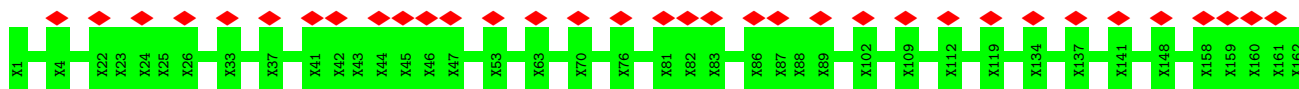
- Molecule 19: 60S ribosomal protein L42-A

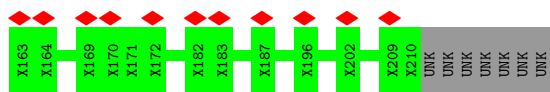


- Molecule 20: 60S ribosomal protein L43-A



- Molecule 21: Ribosomal Protein uL1





- Molecule 22: 60S ribosomal protein L15-A

Chain a: 99%



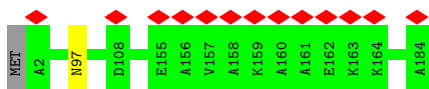
- Molecule 23: 60S ribosomal protein L16-A

Chain b: 98%



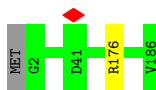
- Molecule 24: 60S ribosomal protein L17-A

Chain c: 99%



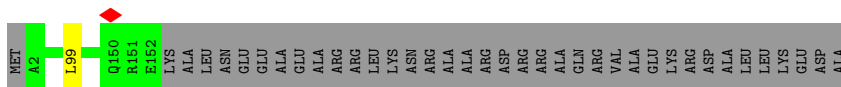
- Molecule 25: 60S ribosomal protein L18-A

Chain d: 99%



- Molecule 26: 60S ribosomal protein L19-A

Chain e: 79% 20%

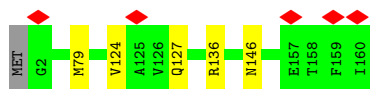


- Molecule 27: 60S ribosomal protein L20-A

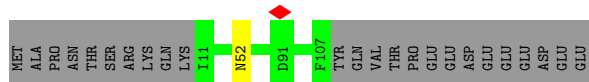
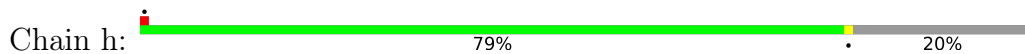
Chain f: 97%



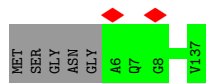
- Molecule 28: 60S ribosomal protein L21-A



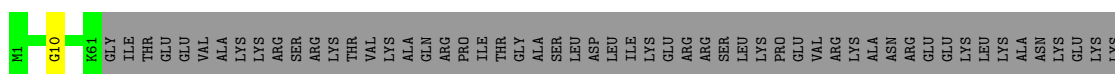
• Molecule 29: 60S ribosomal protein L22-A



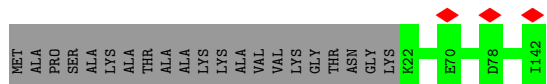
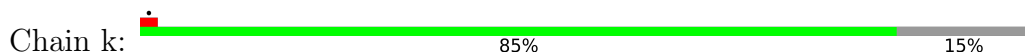
• Molecule 30: 60S ribosomal protein L23-A



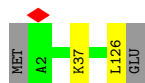
• Molecule 31: 60S ribosomal protein L24-A



• Molecule 32: 60S ribosomal protein L25

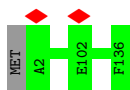


• Molecule 33: 60S ribosomal protein L26-A

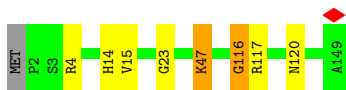


• Molecule 34: 60S ribosomal protein L27-A

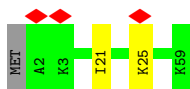
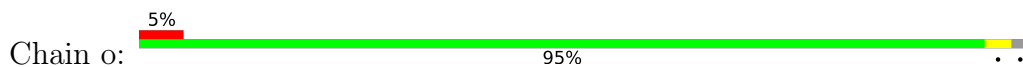




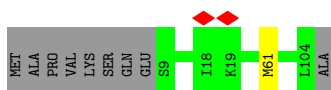
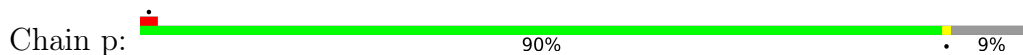
- Molecule 35: 60S ribosomal protein L28



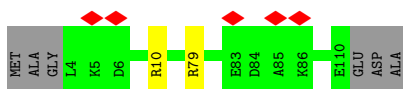
- Molecule 36: 60S ribosomal protein L29



- Molecule 37: 60S ribosomal protein L30



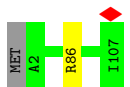
- Molecule 38: 60S ribosomal protein L31-A



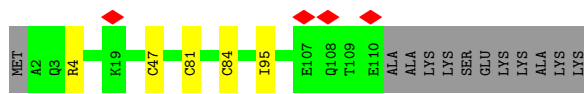
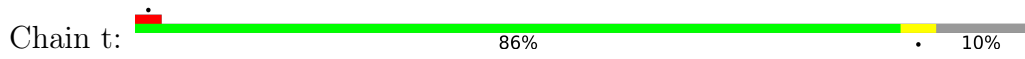
- Molecule 39: 60S ribosomal protein L32



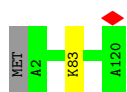
- Molecule 40: 60S ribosomal protein L33-A



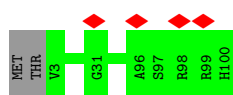
- Molecule 41: 60S ribosomal protein L34-A



• Molecule 42: 60S ribosomal protein L35-A



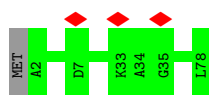
• Molecule 43: 60S ribosomal protein L36-A



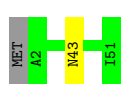
• Molecule 44: 60S ribosomal protein L37-A



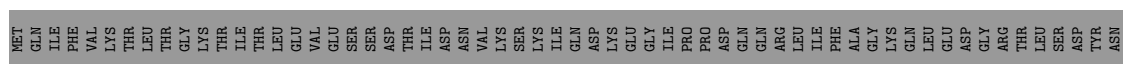
• Molecule 45: 60S ribosomal protein L38

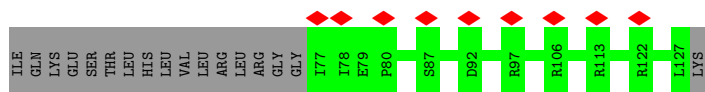


• Molecule 46: 60S ribosomal protein L39

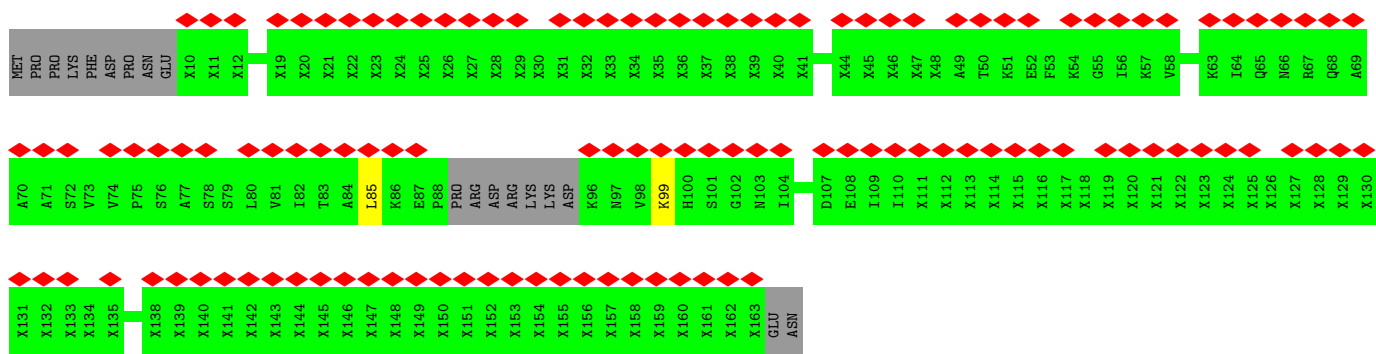
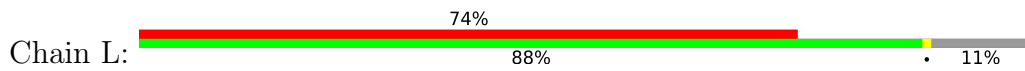


• Molecule 47: Ubiquitin-60S ribosomal protein L40





• Molecule 48: Ribosomal protein L12



## 4 Experimental information

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

## 5 Model quality 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

All (162) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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
1	A	2137	U	C2-N1-C1'	8.62	128.04	117.70
2	B	121	U	N1-C2-O2	8.41	128.69	122.80
1	A	3214	U	C2-N1-C1'	8.30	127.67	117.70
1	A	1437	C	C6-N1-C2	-7.86	117.16	120.30
1	A	1013	G	N3-C4-C5	-7.73	124.73	128.60
1	A	2137	U	N3-C2-O2	-7.72	116.79	122.20
1	A	1013	G	C4-N9-C1'	7.68	136.49	126.50
1	A	1576	G	P-O3'-C3'	7.59	128.81	119.70
1	A	2971	A	C2-N3-C4	7.59	114.39	110.60
1	A	1573	G	C4-N9-C1'	7.50	136.25	126.50
1	A	2541	U	P-O3'-C3'	7.43	128.61	119.70
1	A	1029	G	P-O3'-C3'	7.35	128.52	119.70
33	l	126	LEU	CA-CB-CG	7.29	132.06	115.30
1	A	2263	C	C2-N1-C1'	7.20	126.72	118.80
1	A	1038	C	P-O3'-C3'	7.09	128.21	119.70
1	A	1815	U	P-O3'-C3'	7.08	128.20	119.70
1	A	2617	U	N3-C2-O2	-7.05	117.26	122.20
2	B	121	U	C5-C6-N1	7.02	126.21	122.70
1	A	979	U	P-O3'-C3'	6.95	128.04	119.70
1	A	1573	G	N3-C4-C5	-6.95	125.12	128.60
1	A	2254	U	N1-C2-O2	6.94	127.66	122.80
1	A	922	U	C2-N1-C1'	6.89	125.97	117.70
1	A	3214	U	N3-C2-O2	-6.88	117.39	122.20
1	A	1437	C	N1-C2-O2	6.86	123.02	118.90
1	A	1027	A	P-O3'-C3'	6.81	127.87	119.70
1	A	1573	G	N3-C4-N9	6.75	130.05	126.00
1	A	1013	G	N3-C4-N9	6.75	130.05	126.00
1	A	2254	U	N3-C2-O2	-6.69	117.52	122.20
1	A	3214	U	N1-C2-O2	6.66	127.46	122.80
1	A	2550	U	N3-C2-O2	-6.62	117.57	122.20
1	A	1064	A	P-O3'-C3'	6.58	127.60	119.70
6	W	234	LEU	CA-CB-CG	6.57	130.40	115.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	824	C	C6-N1-C2	-6.54	117.68	120.30
1	A	2101	C	P-O3'-C3'	6.52	127.52	119.70
7	V	143	CYS	CA-CB-SG	6.51	125.72	114.00
1	A	2836	C	C2-N1-C1'	6.48	125.93	118.80
1	A	1716	U	P-O3'-C3'	6.38	127.36	119.70
1	A	2617	U	N1-C2-O2	6.37	127.26	122.80
48	L	85	LEU	CA-CB-CG	6.36	129.92	115.30
1	A	1034	U	N3-C2-O2	-6.34	117.76	122.20
1	A	1190	A	C2-N3-C4	6.33	113.77	110.60
1	A	1241	U	P-O3'-C3'	6.33	127.29	119.70
1	A	1437	C	N3-C2-O2	-6.32	117.47	121.90
1	A	1573	G	C8-N9-C1'	-6.28	118.84	127.00
2	B	121	U	C6-N1-C2	-6.28	117.23	121.00
7	V	81	LEU	CA-CB-CG	6.28	129.73	115.30
1	A	1352	A	P-O3'-C3'	6.27	127.23	119.70
1	A	1013	G	C8-N9-C1'	-6.27	118.85	127.00
1	A	1608	C	C6-N1-C2	-6.27	117.79	120.30
4	Y	331	ILE	N-CA-C	-6.23	94.17	111.00
1	A	3181	C	C2-N1-C1'	6.23	125.65	118.80
1	A	1420	C	C6-N1-C2	-6.18	117.83	120.30
1	A	1222	G	P-O3'-C3'	6.13	127.05	119.70
1	A	1437	C	C5-C6-N1	6.10	124.05	121.00
1	A	2263	C	N3-C2-O2	-6.09	117.64	121.90
1	A	3306	U	N3-C2-O2	-6.07	117.95	122.20
1	A	2617	U	C2-N1-C1'	6.05	124.97	117.70
2	B	121	U	C2-N1-C1'	6.05	124.96	117.70
1	A	2585	G	N3-C4-N9	6.04	129.63	126.00
1	A	1103	A	P-O3'-C3'	6.02	126.93	119.70
1	A	2137	U	C6-N1-C1'	-6.00	112.80	121.20
1	A	1097	G	P-O3'-C3'	5.99	126.88	119.70
1	A	1034	U	N1-C2-O2	5.98	126.99	122.80
10	F	187	LEU	CA-CB-CG	5.96	129.00	115.30
1	A	2899	C	C2-N1-C1'	5.91	125.30	118.80
1	A	2873	U	C2-N1-C1'	5.90	124.78	117.70
1	A	1115	G	C4-N9-C1'	5.89	134.16	126.50
1	A	915	A	C2-N3-C4	5.83	113.52	110.60
1	A	2873	U	N1-C2-O2	5.81	126.87	122.80
1	A	2112	U	P-O3'-C3'	5.80	126.66	119.70
35	n	116	GLY	N-CA-C	5.80	127.60	113.10
1	A	3269	U	P-O3'-C3'	5.79	126.65	119.70
1	A	1437	C	C2-N1-C1'	5.79	125.17	118.80
1	A	2537	U	P-O3'-C3'	5.79	126.64	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2585	G	C4-N9-C1'	5.78	134.01	126.50
1	A	2209	U	P-O3'-C3'	5.77	126.62	119.70
1	A	1355	A	P-O3'-C3'	5.76	126.61	119.70
4	Y	326	CYS	CB-CA-C	-5.75	98.91	110.40
1	A	915	A	C4-N9-C1'	5.74	136.63	126.30
1	A	1585	C	C6-N1-C2	-5.74	118.00	120.30
1	A	2513	U	P-O3'-C3'	5.73	126.57	119.70
1	A	2836	C	N1-C2-O2	5.72	122.33	118.90
1	A	2593	A	P-O3'-C3'	5.71	126.56	119.70
1	A	2553	U	N3-C2-O2	-5.71	118.20	122.20
27	f	13	ARG	N-CA-CB	-5.70	100.33	110.60
1	A	3181	C	N1-C2-O2	5.65	122.29	118.90
1	A	3306	U	C2-N1-C1'	5.63	124.46	117.70
3	C	125	U	C2-N1-C1'	5.63	124.46	117.70
1	A	3228	C	P-O3'-C3'	5.62	126.44	119.70
1	A	1608	C	C2-N1-C1'	5.61	124.97	118.80
1	A	2971	A	N3-C4-N9	5.60	131.88	127.40
1	A	922	U	N1-C2-O2	5.59	126.72	122.80
1	A	1554	U	P-O3'-C3'	5.58	126.40	119.70
1	A	2873	U	N3-C2-O2	-5.58	118.29	122.20
1	A	1554	U	N1-C2-O2	5.57	126.70	122.80
1	A	3078	U	P-O3'-C3'	5.57	126.38	119.70
6	W	337	ILE	C-N-CA	5.56	135.60	121.70
13	I	178	ILE	CG1-CB-CG2	-5.55	99.20	111.40
1	A	2269	U	N1-C2-O2	5.54	126.68	122.80
1	A	2550	U	N1-C2-O2	5.54	126.68	122.80
1	A	2846	U	C2-N1-C1'	5.53	124.34	117.70
27	f	24	LEU	CB-CG-CD2	5.52	120.39	111.00
1	A	3154	C	N1-C2-O2	5.52	122.21	118.90
1	A	2726	C	C2-N1-C1'	5.51	124.87	118.80
41	t	84	CYS	CA-CB-SG	-5.51	104.08	114.00
1	A	1608	C	N1-C2-O2	5.50	122.20	118.90
1	A	1349	G	N3-C4-C5	-5.49	125.86	128.60
3	C	125	U	N1-C2-O2	5.49	126.64	122.80
1	A	1228	C	C6-N1-C2	-5.47	118.11	120.30
1	A	2585	G	N3-C4-C5	-5.47	125.86	128.60
11	G	258	LYS	C-N-CA	5.47	135.37	121.70
1	A	1349	G	N3-C4-N9	5.46	129.28	126.00
1	A	3354	U	C2-N1-C1'	5.46	124.25	117.70
1	A	1349	G	C4-N9-C1'	5.44	133.58	126.50
3	C	28	C	C6-N1-C2	-5.43	118.13	120.30
1	A	824	C	N1-C2-O2	5.42	122.15	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	922	U	N3-C2-O2	-5.42	118.41	122.20
1	A	3218	A	P-O3'-C3'	5.41	126.20	119.70
1	A	2171	G	C4-N9-C1'	5.39	133.51	126.50
1	A	824	C	N3-C2-O2	-5.38	118.13	121.90
1	A	1013	G	C2-N3-C4	5.38	114.59	111.90
1	A	2772	C	N1-C2-O2	5.36	122.12	118.90
1	A	3279	A	C2-N3-C4	5.35	113.28	110.60
1	A	2266	U	OP1-P-O3'	5.34	116.95	105.20
1	A	2550	U	C2-N1-C1'	5.33	124.09	117.70
1	A	2263	C	C6-N1-C1'	-5.32	114.42	120.80
1	A	3214	U	C6-N1-C1'	-5.31	113.76	121.20
1	A	283	G	C4-N9-C1'	5.30	133.39	126.50
1	A	3306	U	N1-C2-O2	5.28	126.49	122.80
1	A	1115	G	C8-N9-C1'	-5.27	120.15	127.00
1	A	1034	U	C2-N1-C1'	5.24	123.99	117.70
1	A	1115	G	N3-C4-N9	5.21	129.13	126.00
1	A	2134	G	C4-N9-C1'	5.21	133.28	126.50
1	A	356	C	C6-N1-C2	-5.21	118.22	120.30
4	Y	328	LYS	C-N-CA	5.21	134.72	121.70
3	C	85	G	P-O3'-C3'	5.20	125.94	119.70
1	A	2552	C	C2-N1-C1'	5.18	124.49	118.80
3	C	125	U	N3-C2-O2	-5.15	118.60	122.20
1	A	2266	U	P-O3'-C3'	5.14	125.87	119.70
1	A	2996	U	N1-C2-O2	5.13	126.39	122.80
1	A	3181	C	N3-C2-O2	-5.12	118.32	121.90
35	n	47	LYS	C-N-CA	5.10	134.45	121.70
1	A	824	C	C2-N1-C1'	5.08	124.38	118.80
1	A	2983	C	N3-C2-O2	-5.07	118.35	121.90
1	A	2553	U	N1-C2-O2	5.06	126.34	122.80
1	A	2567	C	N1-C2-O2	5.05	121.93	118.90
1	A	1222	G	OP2-P-O3'	5.05	116.31	105.20
1	A	1770	G	C4-N9-C1'	5.05	133.06	126.50
26	e	99	LEU	CA-CB-CG	5.05	126.91	115.30
1	A	596	C	C6-N1-C2	-5.04	118.28	120.30
11	G	257	GLU	C-N-CA	5.04	134.30	121.70
1	A	2971	A	N3-C4-C5	-5.04	123.27	126.80
1	A	3350	C	N1-C2-O2	5.04	121.92	118.90
1	A	3214	U	O4'-C1'-N1	5.04	112.23	108.20
1	A	2836	C	N3-C2-O2	-5.03	118.38	121.90
1	A	421	G	C4-N9-C1'	5.03	133.03	126.50
1	A	2137	U	O4'-C1'-N1	5.03	112.22	108.20

There are no chirality outliers.

All (47) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	E	346	THR	Peptide
10	F	338	LYS	Peptide
10	F	4	PRO	Peptide
11	G	124	GLU	Peptide
11	G	258	LYS	Peptide
13	I	157	ASN	Peptide
13	I	190	THR	Peptide
13	I	232	ARG	Peptide
14	J	34	PHE	Peptide
14	J	35	GLY	Peptide
15	K	21	LYS	Peptide
16	M	171	VAL	Peptide
16	M	7	ASN	Peptide
17	N	46	ILE	Peptide
7	V	15	ALA	Peptide
7	V	25	PRO	Peptide
7	V	280	SER	Peptide
7	V	44	ASP	Peptide
6	W	134	LEU	Peptide
6	W	136	VAL	Peptide
6	W	142	TRP	Peptide
6	W	176	LEU	Peptide
6	W	225	SER	Peptide
6	W	337	ILE	Peptide
6	W	362	VAL	Peptide
6	W	363	SER	Peptide
6	W	364	VAL	Peptide
6	W	371	THR	Peptide
6	W	373	HIS	Peptide
6	W	379	LEU	Peptide
6	W	394	PRO	Peptide
6	W	427	ARG	Peptide
6	W	441	ILE	Peptide
6	W	445	SER	Peptide
6	W	467	ALA	Peptide
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
27	f	12	ARG	Peptide
35	n	116	GLY	Peptide

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Mol	Chain	Res	Type	Group
35	n	14	HIS	Peptide
35	n	23	GLY	Peptide
36	o	21	ILE	Peptide
36	o	25	LYS	Peptide
42	u	83	LYS	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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



All (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
6	W	135	ILE
6	W	442	GLN
7	V	45	ILE
14	J	36	ILE
17	N	6	ASN
17	N	63	VAL
27	f	13	ARG
4	Y	247	ALA
6	W	338	ASN
6	W	443	THR
10	F	5	GLN
13	I	158	LYS
27	f	24	LEU
4	Y	323	ARG
6	W	226	ASP
6	W	337	ILE
7	V	36	TYR
10	F	4	PRO
35	n	15	VAL
35	n	47	LYS
35	n	117	ARG
7	V	68	PRO
7	V	143	CYS
9	E	347	SER
29	h	52	ASN
4	Y	246	ILE
9	E	317	ILE
31	j	10	GLY
4	Y	327	GLY
7	V	25	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Y	235	CYS
4	Y	307	CYS
4	Y	318	ASN
6	W	136	VAL
6	W	146	MET
6	W	237	LYS
6	W	267	ARG
6	W	323	ASN
6	W	354	ASN
6	W	513	ARG
7	V	92	LEU
7	V	115	LYS
7	V	153	ASN
7	V	168	LYS
7	V	333	ARG
8	D	193	ARG
9	E	6	TYR
9	E	104	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	E	332	ARG
10	F	43	ASN
10	F	197	ARG
10	F	221	ASN
11	G	23	ARG
11	G	24	ARG
11	G	85	ARG
11	G	273	ARG
13	I	200	ASN
13	I	244	ASN
14	J	24	ASN
15	K	157	ASN
16	M	29	ARG
17	N	188	ARG
20	R	42	CYS
22	a	50	ARG
22	a	71	ARG
23	b	85	ARG
23	b	125	ARG
24	c	97	ASN
25	d	176	ARG
27	f	12	ARG
27	f	13	ARG
28	g	79	MET
28	g	124	VAL
28	g	127	GLN
28	g	136	ARG
28	g	146	ASN
33	l	37	LYS
35	n	4	ARG
35	n	120	ASN
37	p	61	MET
38	q	10	ARG
38	q	79	ARG
39	r	27	ARG
39	r	45	ARG
39	r	87	MET
40	s	86	ARG
41	t	4	ARG
41	t	47	CYS
41	t	95	ILE
44	w	22	CYS

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Mol	Chain	Res	Type
44	w	25	ARG
44	w	45	ARG
46	y	43	ASN
48	L	99	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
4	Y	318	ASN
5	X	50	HIS
5	X	106	ASN
5	X	145	ASN
5	X	170	GLN
6	W	170	GLN
6	W	323	ASN
6	W	413	GLN
7	V	21	ASN
7	V	119	GLN
7	V	153	ASN
7	V	231	GLN
8	D	132	ASN
8	D	140	ASN
8	D	209	HIS
8	D	218	HIS
10	F	43	ASN
10	F	59	GLN
11	G	264	GLN
13	I	200	ASN
13	I	225	GLN
13	I	244	ASN
14	J	24	ASN
14	J	38	GLN
14	J	240	ASN
16	M	109	HIS
16	M	150	ASN
17	N	19	GLN
17	N	25	HIS
17	N	137	GLN
19	Q	22	GLN
19	Q	82	GLN
22	a	37	HIS
23	b	29	ASN

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Mol	Chain	Res	Type
23	b	55	HIS
24	c	97	ASN
27	f	142	GLN
28	g	146	ASN
29	h	25	ASN
35	n	120	ASN
39	r	52	GLN
40	s	88	ASN
42	u	104	GLN
42	u	108	GLN
46	y	11	GLN
46	y	43	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%)

All (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
1	A	43	A
1	A	48	A
1	A	49	A
1	A	59	G
1	A	60	A
1	A	65	A
1	A	66	A
1	A	73	C
1	A	75	G
1	A	76	G
1	A	83	U
1	A	92	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	96	G
1	A	97	U
1	A	105	C
1	A	109	A
1	A	110	G
1	A	118	U
1	A	121	A
1	A	122	A
1	A	124	U
1	A	135	C
1	A	136	G
1	A	156	G
1	A	157	A
1	A	161	G
1	A	165	A
1	A	176	G
1	A	182	U
1	A	187	A
1	A	190	U
1	A	191	U
1	A	192	C
1	A	198	A
1	A	200	C
1	A	206	G
1	A	210	U
1	A	211	A
1	A	213	A
1	A	218	G
1	A	219	A
1	A	237	G
1	A	240	U
1	A	241	G
1	A	243	G
1	A	245	U
1	A	246	U
1	A	247	C
1	A	248	U
1	A	249	U
1	A	252	U
1	A	253	A
1	A	257	U
1	A	269	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	286	U
1	A	295	A
1	A	315	C
1	A	323	A
1	A	329	U
1	A	336	A
1	A	338	A
1	A	348	A
1	A	351	A
1	A	359	U
1	A	375	A
1	A	376	G
1	A	398	A
1	A	399	A
1	A	401	U
1	A	402	A
1	A	403	C
1	A	404	G
1	A	420	G
1	A	421	G
1	A	422	A
1	A	429	U
1	A	439	C
1	A	520	U
1	A	521	A
1	A	525	C
1	A	532	A
1	A	541	U
1	A	543	C
1	A	546	C
1	A	547	G
1	A	548	G
1	A	551	A
1	A	553	U
1	A	555	U
1	A	557	A
1	A	559	A
1	A	568	G
1	A	569	A
1	A	574	U
1	A	578	A
1	A	579	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	592	A
1	A	597	G
1	A	600	G
1	A	603	A
1	A	604	G
1	A	607	A
1	A	611	A
1	A	620	U
1	A	621	A
1	A	622	A
1	A	641	C
1	A	644	G
1	A	645	A
1	A	649	A
1	A	677	A
1	A	681	U
1	A	683	U
1	A	689	U
1	A	691	A
1	A	692	A
1	A	705	A
1	A	709	A
1	A	712	G
1	A	713	U
1	A	715	A
1	A	719	U
1	A	720	A
1	A	728	G
1	A	767	U
1	A	774	G
1	A	776	U
1	A	777	U
1	A	780	A
1	A	781	G
1	A	784	A
1	A	785	G
1	A	801	A
1	A	806	A
1	A	817	A
1	A	830	A
1	A	849	C
1	A	861	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	869	G
1	A	872	U
1	A	874	U
1	A	879	U
1	A	880	G
1	A	887	G
1	A	888	A
1	A	894	G
1	A	896	A
1	A	897	U
1	A	907	G
1	A	908	G
1	A	914	A
1	A	916	G
1	A	917	A
1	A	921	A
1	A	924	G
1	A	932	U
1	A	933	A
1	A	937	G
1	A	944	C
1	A	946	U
1	A	959	C
1	A	960	U
1	A	961	C
1	A	974	G
1	A	978	G
1	A	979	U
1	A	980	A
1	A	982	C
1	A	991	G
1	A	994	G
1	A	1001	G
1	A	1002	A
1	A	1010	G
1	A	1012	G
1	A	1013	G
1	A	1014	U
1	A	1015	U
1	A	1016	C
1	A	1017	C
1	A	1018	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1020	G
1	A	1023	C
1	A	1024	G
1	A	1026	A
1	A	1027	A
1	A	1028	U
1	A	1029	G
1	A	1030	A
1	A	1034	U
1	A	1035	G
1	A	1036	A
1	A	1037	C
1	A	1038	C
1	A	1039	U
1	A	1040	A
1	A	1042	U
1	A	1045	C
1	A	1046	A
1	A	1047	A
1	A	1049	C
1	A	1064	A
1	A	1065	A
1	A	1072	G
1	A	1081	U
1	A	1093	A
1	A	1094	U
1	A	1095	U
1	A	1096	U
1	A	1097	G
1	A	1098	A
1	A	1103	A
1	A	1104	G
1	A	1111	U
1	A	1117	G
1	A	1124	U
1	A	1131	G
1	A	1140	G
1	A	1141	C
1	A	1143	A
1	A	1153	A
1	A	1159	A
1	A	1177	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1180	A
1	A	1181	U
1	A	1192	C
1	A	1193	A
1	A	1195	A
1	A	1196	C
1	A	1201	C
1	A	1209	G
1	A	1221	A
1	A	1222	G
1	A	1223	A
1	A	1235	U
1	A	1236	G
1	A	1237	G
1	A	1239	C
1	A	1240	A
1	A	1241	U
1	A	1242	G
1	A	1244	A
1	A	1245	A
1	A	1246	G
1	A	1247	U
1	A	1252	A
1	A	1258	U
1	A	1262	G
1	A	1263	A
1	A	1264	G
1	A	1266	G
1	A	1273	A
1	A	1281	G
1	A	1285	G
1	A	1295	G
1	A	1307	G
1	A	1309	U
1	A	1313	G
1	A	1325	U
1	A	1330	A
1	A	1345	G
1	A	1348	U
1	A	1349	G
1	A	1351	U
1	A	1352	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1353	U
1	A	1354	G
1	A	1356	U
1	A	1357	G
1	A	1366	A
1	A	1383	G
1	A	1386	A
1	A	1390	A
1	A	1392	G
1	A	1399	A
1	A	1400	G
1	A	1419	A
1	A	1430	U
1	A	1434	G
1	A	1437	C
1	A	1443	G
1	A	1446	A
1	A	1448	U
1	A	1450	G
1	A	1455	U
1	A	1481	A
1	A	1482	A
1	A	1484	U
1	A	1487	G
1	A	1506	A
1	A	1508	C
1	A	1523	U
1	A	1526	U
1	A	1527	C
1	A	1533	U
1	A	1536	G
1	A	1547	G
1	A	1555	U
1	A	1556	C
1	A	1557	A
1	A	1559	A
1	A	1560	G
1	A	1561	G
1	A	1562	C
1	A	1563	C
1	A	1564	U
1	A	1565	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1566	A
1	A	1567	U
1	A	1568	U
1	A	1569	U
1	A	1570	U
1	A	1571	A
1	A	1572	U
1	A	1576	G
1	A	1577	G
1	A	1579	C
1	A	1580	A
1	A	1583	A
1	A	1589	A
1	A	1593	A
1	A	1605	A
1	A	1606	U
1	A	1618	G
1	A	1619	A
1	A	1620	U
1	A	1629	U
1	A	1636	U
1	A	1642	A
1	A	1643	A
1	A	1656	A
1	A	1657	C
1	A	1662	G
1	A	1666	G
1	A	1683	A
1	A	1703	U
1	A	1716	U
1	A	1717	U
1	A	1724	U
1	A	1725	C
1	A	1728	G
1	A	1736	G
1	A	1741	A
1	A	1742	U
1	A	1750	A
1	A	1751	G
1	A	1758	G
1	A	1759	C
1	A	1760	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1762	C
1	A	1764	U
1	A	1765	U
1	A	1766	G
1	A	1770	G
1	A	1773	C
1	A	1780	G
1	A	1793	C
1	A	1797	A
1	A	1814	A
1	A	1816	A
1	A	1817	G
1	A	1820	U
1	A	1821	U
1	A	1839	A
1	A	1842	A
1	A	1849	C
1	A	1850	A
1	A	1866	C
1	A	1867	A
1	A	1871	U
1	A	1880	U
1	A	1886	A
1	A	1893	A
1	A	1906	G
1	A	1907	C
1	A	1908	A
1	A	1909	A
1	A	1913	A
1	A	1926	C
1	A	1927	G
1	A	1943	C
1	A	1951	C
1	A	1952	G
1	A	1953	G
1	A	1954	G
1	A	2101	C
1	A	2102	U
1	A	2113	A
1	A	2114	C
1	A	2121	G
1	A	2122	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2126	A
1	A	2131	A
1	A	2139	A
1	A	2142	A
1	A	2158	A
1	A	2169	G
1	A	2178	A
1	A	2184	U
1	A	2185	G
1	A	2191	U
1	A	2192	C
1	A	2205	U
1	A	2208	A
1	A	2209	U
1	A	2210	G
1	A	2244	A
1	A	2248	C
1	A	2249	G
1	A	2250	G
1	A	2253	G
1	A	2254	U
1	A	2255	A
1	A	2256	A
1	A	2257	C
1	A	2262	A
1	A	2263	C
1	A	2265	C
1	A	2267	C
1	A	2268	U
1	A	2269	U
1	A	2270	A
1	A	2273	G
1	A	2274	U
1	A	2281	A
1	A	2282	U
1	A	2285	C
1	A	2286	U
1	A	2288	G
1	A	2291	A
1	A	2298	U
1	A	2306	C
1	A	2307	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2308	C
1	A	2310	U
1	A	2313	A
1	A	2314	U
1	A	2315	G
1	A	2334	U
1	A	2336	U
1	A	2354	C
1	A	2364	G
1	A	2373	A
1	A	2374	C
1	A	2375	G
1	A	2376	G
1	A	2385	G
1	A	2388	U
1	A	2393	G
1	A	2394	G
1	A	2397	A
1	A	2402	A
1	A	2403	G
1	A	2404	A
1	A	2411	U
1	A	2415	C
1	A	2419	A
1	A	2435	G
1	A	2437	G
1	A	2440	G
1	A	2442	G
1	A	2443	A
1	A	2444	C
1	A	2449	A
1	A	2450	G
1	A	2452	G
1	A	2453	U
1	A	2454	G
1	A	2458	A
1	A	2459	A
1	A	2460	U
1	A	2461	A
1	A	2462	A
1	A	2463	G
1	A	2464	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2468	A
1	A	2469	G
1	A	2472	U
1	A	2474	G
1	A	2476	C
1	A	2477	G
1	A	2480	A
1	A	2484	A
1	A	2485	A
1	A	2487	U
1	A	2488	A
1	A	2490	C
1	A	2495	C
1	A	2496	C
1	A	2498	U
1	A	2499	U
1	A	2501	U
1	A	2502	A
1	A	2503	G
1	A	2505	U
1	A	2506	U
1	A	2507	C
1	A	2508	U
1	A	2509	U
1	A	2514	U
1	A	2515	A
1	A	2522	G
1	A	2531	C
1	A	2533	G
1	A	2537	U
1	A	2538	U
1	A	2539	C
1	A	2540	A
1	A	2541	U
1	A	2542	U
1	A	2543	U
1	A	2544	U
1	A	2547	A
1	A	2549	G
1	A	2550	U
1	A	2552	C
1	A	2561	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2562	A
1	A	2569	A
1	A	2570	U
1	A	2571	U
1	A	2572	C
1	A	2573	G
1	A	2577	C
1	A	2585	G
1	A	2593	A
1	A	2594	C
1	A	2599	U
1	A	2606	G
1	A	2607	G
1	A	2614	G
1	A	2620	G
1	A	2626	A
1	A	2635	A
1	A	2636	A
1	A	2648	G
1	A	2652	U
1	A	2656	A
1	A	2657	A
1	A	2664	C
1	A	2674	A
1	A	2677	G
1	A	2688	U
1	A	2689	A
1	A	2691	A
1	A	2696	A
1	A	2704	A
1	A	2705	A
1	A	2713	U
1	A	2719	U
1	A	2728	G
1	A	2729	U
1	A	2753	G
1	A	2754	G
1	A	2777	G
1	A	2778	G
1	A	2799	A
1	A	2800	G
1	A	2801	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2803	A
1	A	2804	A
1	A	2810	C
1	A	2814	G
1	A	2817	A
1	A	2828	G
1	A	2838	A
1	A	2840	C
1	A	2842	U
1	A	2843	U
1	A	2844	C
1	A	2845	A
1	A	2850	G
1	A	2860	U
1	A	2861	U
1	A	2867	C
1	A	2871	G
1	A	2872	A
1	A	2873	U
1	A	2875	U
1	A	2887	A
1	A	2889	C
1	A	2898	G
1	A	2899	C
1	A	2904	U
1	A	2911	A
1	A	2914	G
1	A	2916	U
1	A	2923	U
1	A	2926	A
1	A	2933	A
1	A	2935	U
1	A	2936	A
1	A	2941	A
1	A	2945	G
1	A	2946	A
1	A	2947	G
1	A	2951	G
1	A	2971	A
1	A	2975	U
1	A	2983	C
1	A	2990	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	2996	U
1	A	2997	G
1	A	3011	A
1	A	3012	A
1	A	3014	U
1	A	3028	G
1	A	3056	U
1	A	3059	G
1	A	3078	U
1	A	3079	U
1	A	3086	A
1	A	3092	C
1	A	3103	A
1	A	3109	G
1	A	3113	A
1	A	3115	C
1	A	3117	C
1	A	3119	U
1	A	3122	A
1	A	3129	A
1	A	3130	A
1	A	3131	U
1	A	3142	A
1	A	3143	C
1	A	3153	U
1	A	3154	C
1	A	3155	U
1	A	3156	U
1	A	3157	U
1	A	3158	G
1	A	3164	C
1	A	3165	A
1	A	3168	A
1	A	3170	A
1	A	3173	G
1	A	3174	A
1	A	3176	G
1	A	3179	U
1	A	3181	C
1	A	3187	A
1	A	3196	U
1	A	3197	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	3199	G
1	A	3206	C
1	A	3207	U
1	A	3209	A
1	A	3210	A
1	A	3217	C
1	A	3218	A
1	A	3219	G
1	A	3224	G
1	A	3229	G
1	A	3243	A
1	A	3245	A
1	A	3246	G
1	A	3247	G
1	A	3253	G
1	A	3259	U
1	A	3269	U
1	A	3270	U
1	A	3272	C
1	A	3273	A
1	A	3275	U
1	A	3276	G
1	A	3278	C
1	A	3279	A
1	A	3280	U
1	A	3281	U
1	A	3283	U
1	A	3286	G
1	A	3289	G
1	A	3294	A
1	A	3295	A
1	A	3304	U
1	A	3308	C
1	A	3313	U
1	A	3316	A
1	A	3317	U
1	A	3318	G
1	A	3320	A
1	A	3324	C
1	A	3325	G
1	A	3341	U
1	A	3342	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	3345	G
1	A	3350	C
1	A	3351	U
1	A	3352	U
1	A	3353	G
1	A	3355	U
1	A	3360	C
1	A	3362	A
1	A	3368	U
1	A	3369	G
1	A	3375	A
1	A	3376	A
1	A	3378	C
1	A	3382	U
1	A	3386	G
1	A	3390	G
2	B	10	C
2	B	18	C
2	B	22	A
2	B	28	C
2	B	38	U
2	B	49	G
2	B	52	G
2	B	65	G
2	B	71	G
2	B	73	C
2	B	99	G
2	B	102	A
2	B	112	G
2	B	114	U
2	B	121	U
3	C	34	U
3	C	35	C
3	C	39	G
3	C	45	C
3	C	51	G
3	C	58	G
3	C	59	A
3	C	62	C
3	C	63	G
3	C	67	U
3	C	80	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	82	U
3	C	83	C
3	C	84	C
3	C	85	G
3	C	86	U
3	C	90	U
3	C	95	G
3	C	102	U
3	C	104	A
3	C	106	C
3	C	111	A
3	C	113	U
3	C	125	U
3	C	126	A
3	C	127	U
3	C	129	C
3	C	138	A
3	C	144	G
3	C	155	A
3	C	158	U

All (39) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	239	G
1	A	547	G
1	A	599	C
1	A	916	G
1	A	979	U
1	A	1027	A
1	A	1029	G
1	A	1038	C
1	A	1064	A
1	A	1097	G
1	A	1103	A
1	A	1222	G
1	A	1241	U
1	A	1352	A
1	A	1355	A
1	A	1554	U
1	A	1576	G
1	A	1716	U

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Mol	Chain	Res	Type
1	A	1815	U
1	A	2101	C
1	A	2112	U
1	A	2209	U
1	A	2249	G
1	A	2264	U
1	A	2266	U
1	A	2453	U
1	A	2495	C
1	A	2501	U
1	A	2513	U
1	A	2537	U
1	A	2541	U
1	A	2593	A
1	A	3078	U
1	A	3121	U
1	A	3218	A
1	A	3228	C
1	A	3269	U
3	C	82	U
3	C	85	G

#### 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

There are no chain breaks in this entry.

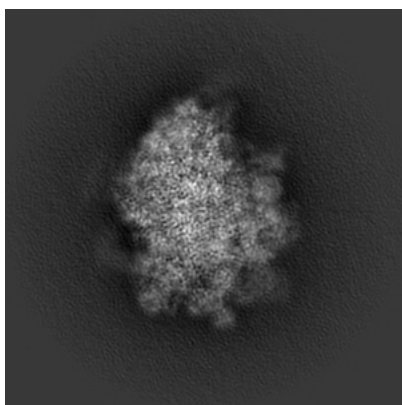
## 6 Map visualisation [i](#)

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.

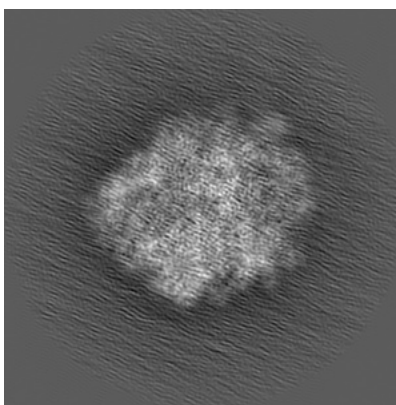
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

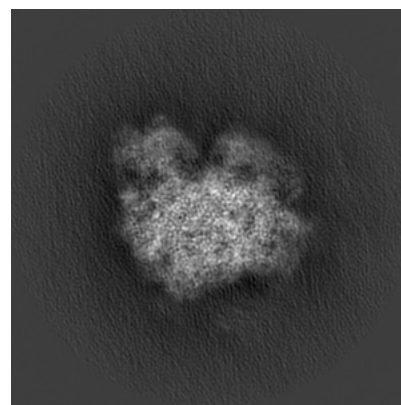
#### 6.1.1 Primary map



X



Y

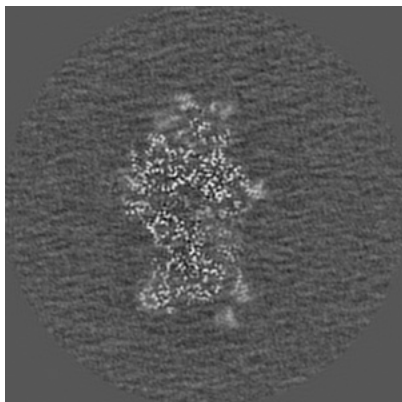


Z

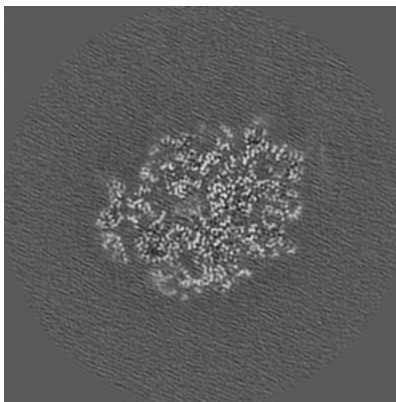
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

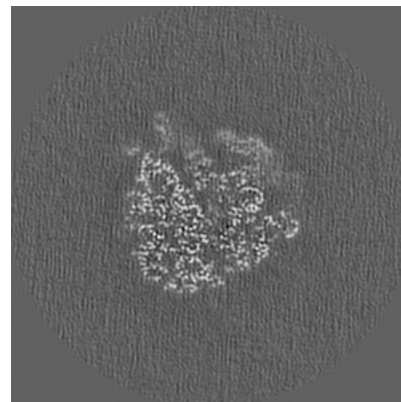
#### 6.2.1 Primary map



X Index: 192



Y Index: 192

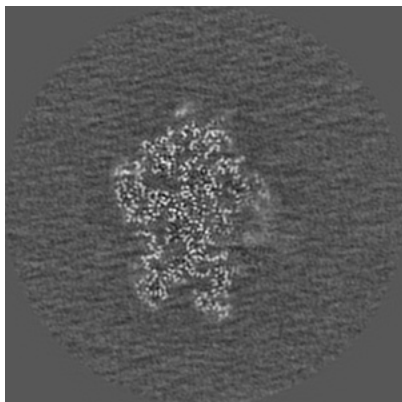


Z Index: 192

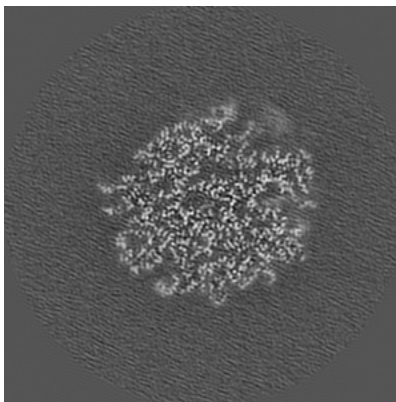
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

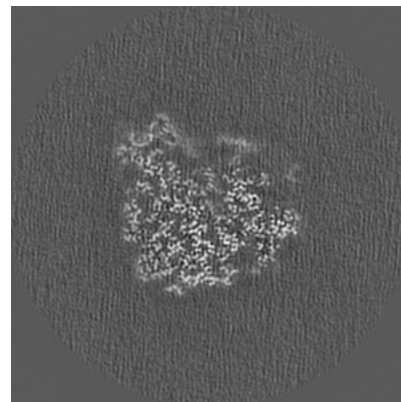
### 6.3.1 Primary map



X Index: 173



Y Index: 173

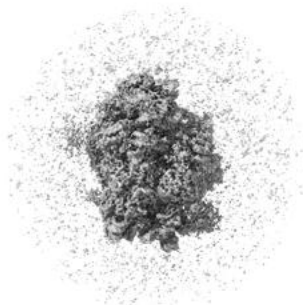


Z Index: 185

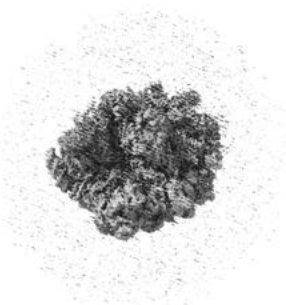
The images above show the largest variance slices of the map in three orthogonal directions.

## 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.

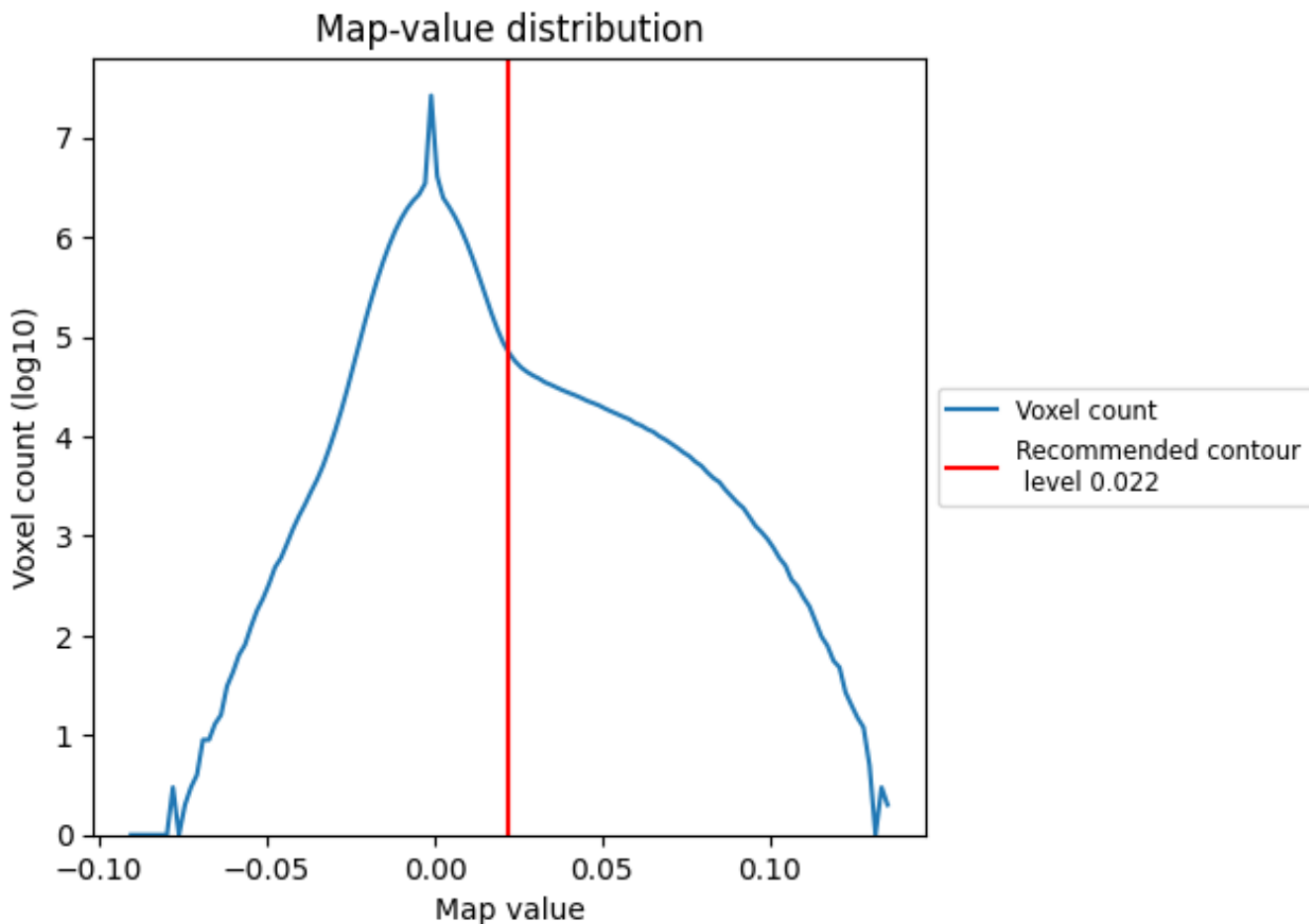
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

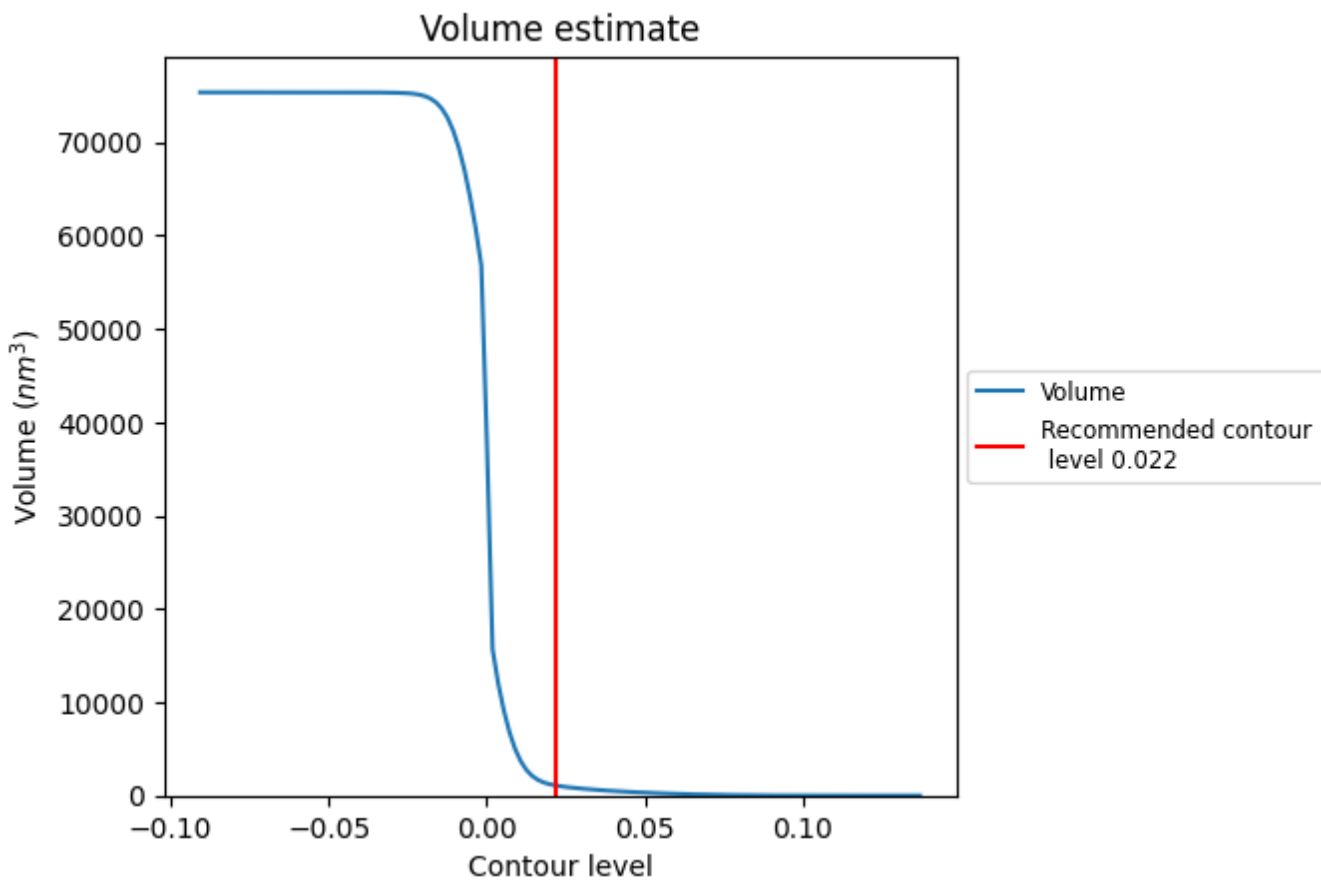
This section contains the results of statistical analysis of the map.

### 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.

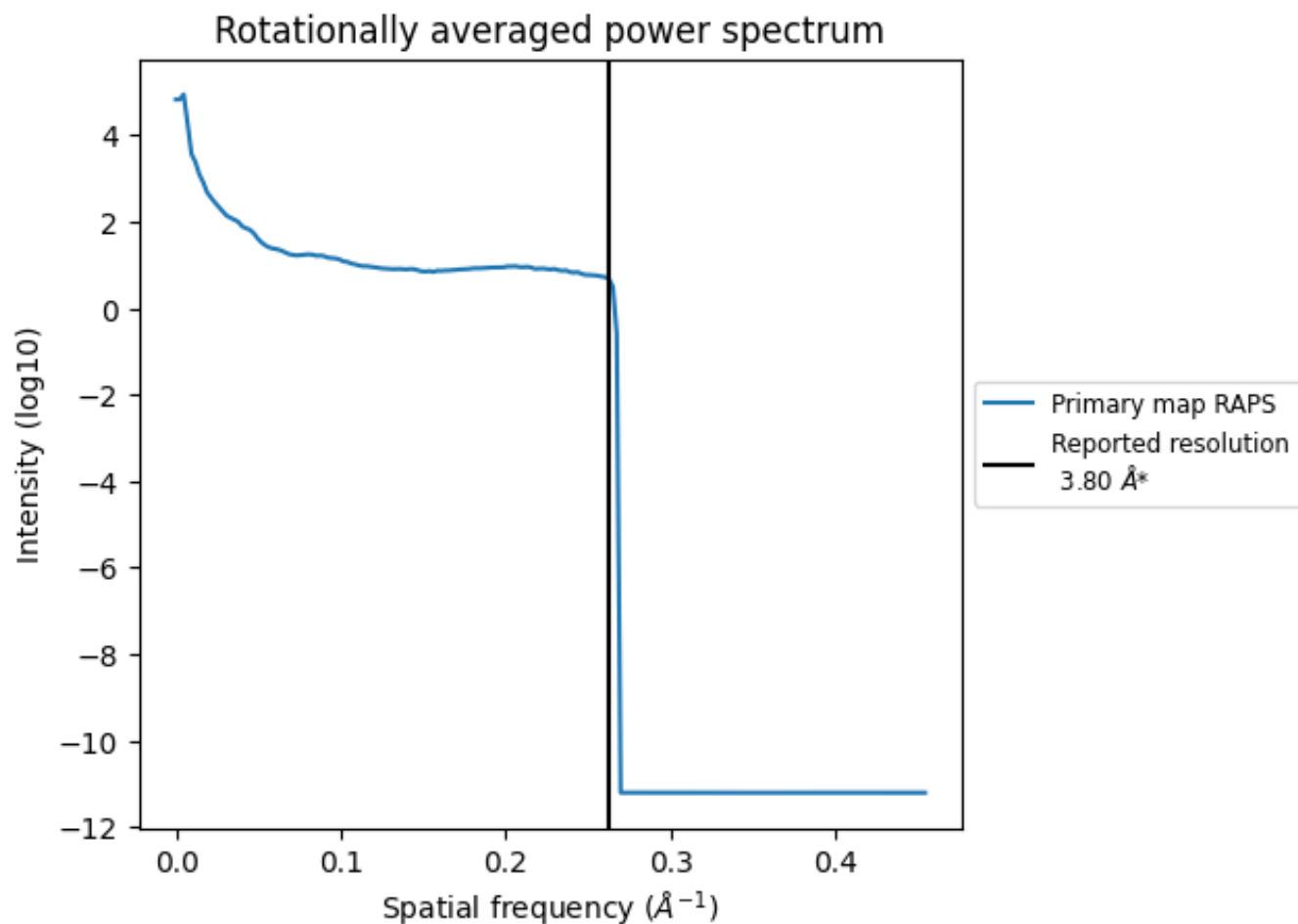
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1068 nm<sup>3</sup>; 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 [\(i\)](#)



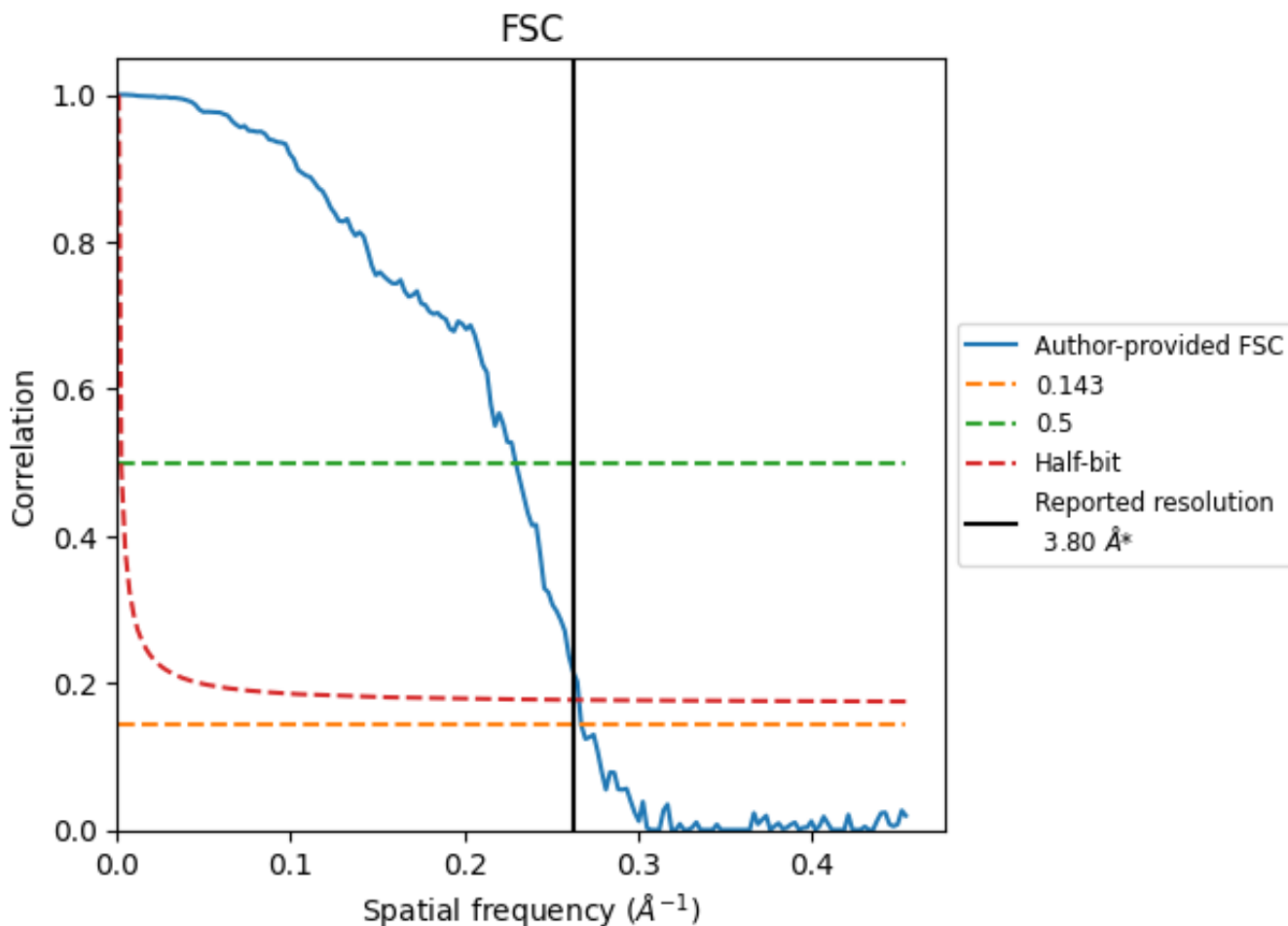
\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>



## 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<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

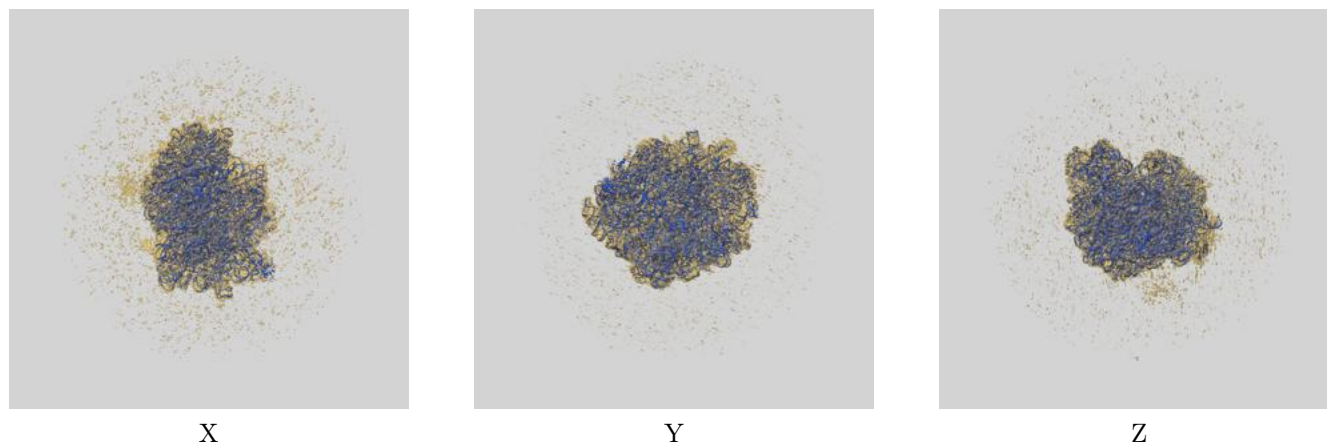
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.74	4.35	3.76
Unmasked-calculated*	-	-	-

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

## 9 Map-model fit [i](#)

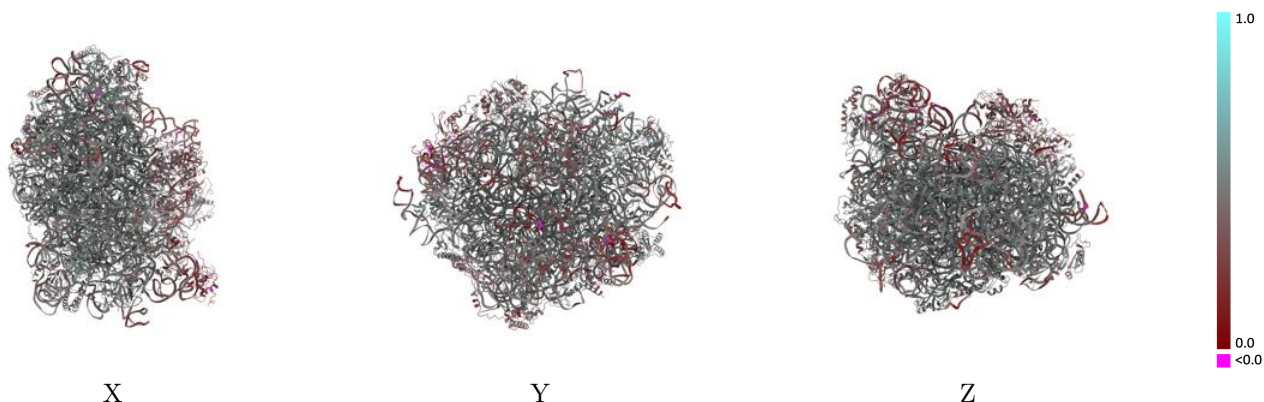
This section contains information regarding the fit between EMDB map EMD-0373 and PDB model 6N8N. Per-residue inclusion information can be found in section 3 on page 12.

### 9.1 Map-model overlay [i](#)



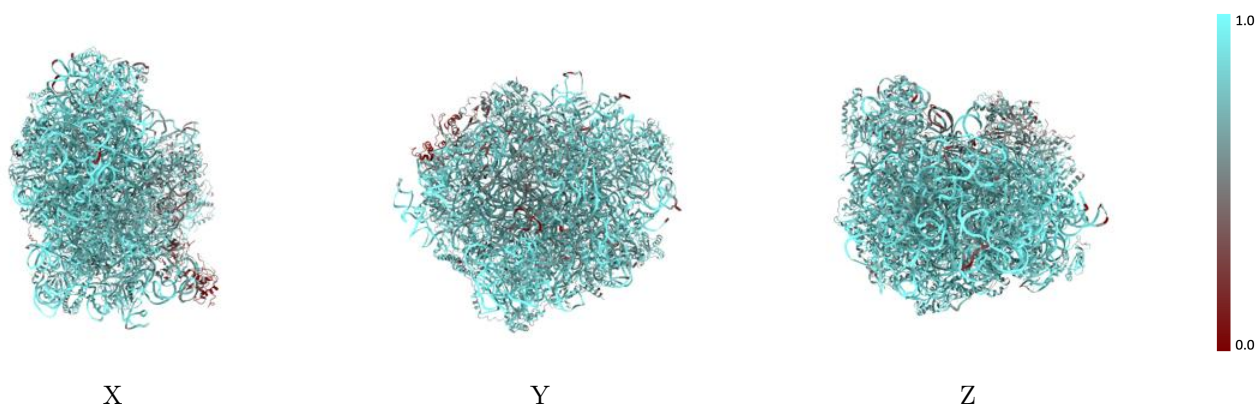
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



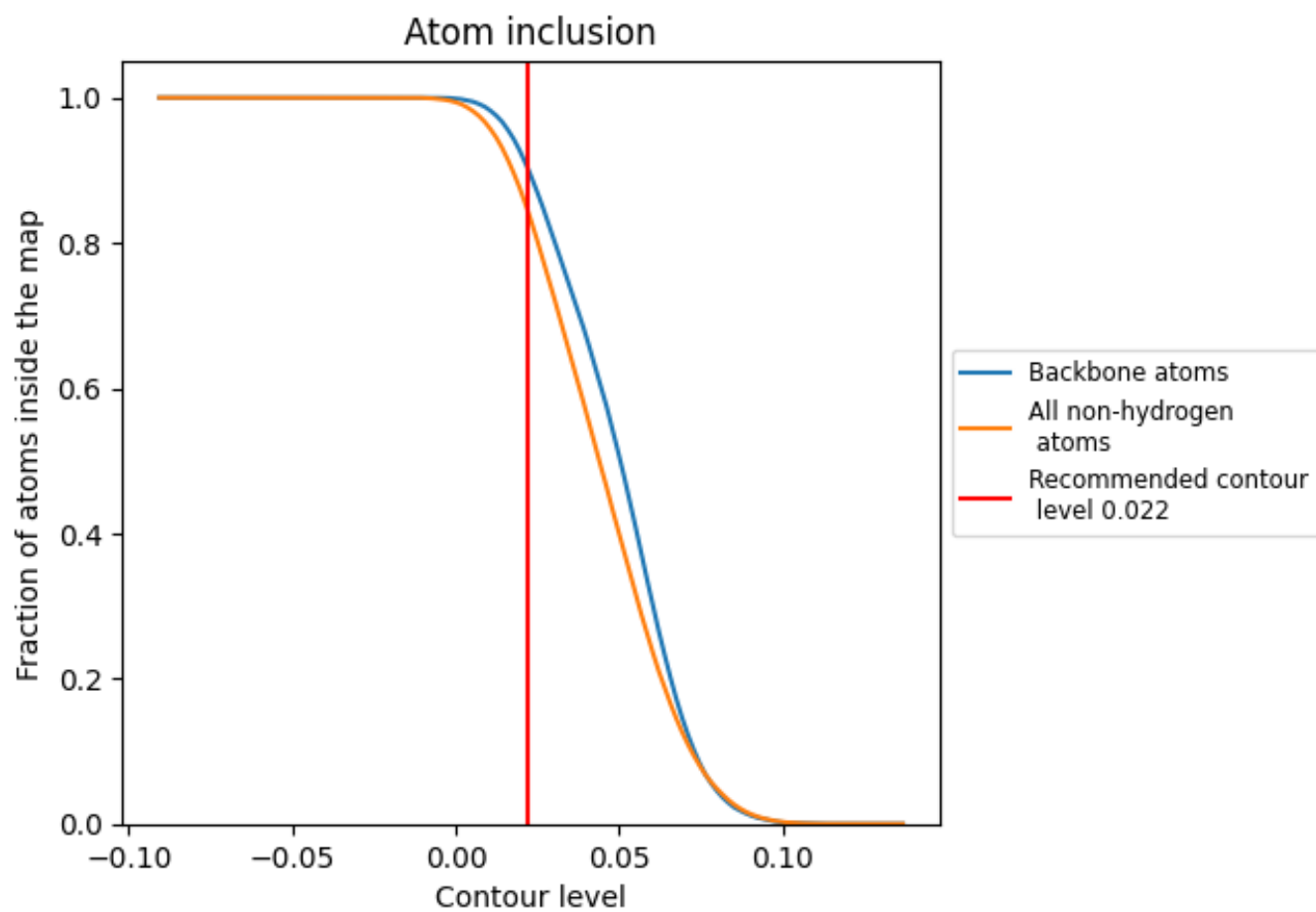
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.022).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





























The table lists the average atom inclusion at the recommended contour level (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4570
A	 0.9100	 0.4590
B	 0.9519	 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