



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 08:02 AM EDT

PDB ID : 6N8M
EMDB ID : EMD-0372
Title : Cryo-EM structure of pre-Lsg1 (PL) pre-60S ribosomal subunit
Authors : Zhou, Y.; Musalgaonkar, S.; Johnson, A.W.; Taylor, D.W.
Deposited on : 2018-11-29
Resolution : 3.50 Å (reported)
Based on initial model : 5T62

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

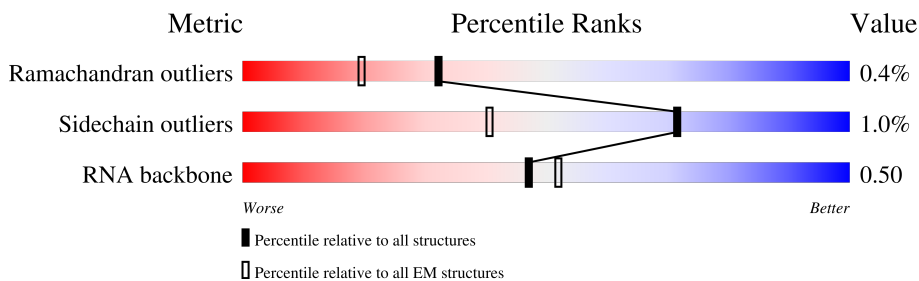
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.50 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3396	
2	B	121	
3	C	158	
4	Y	364	
5	D	254	
6	E	387	
7	F	362	
8	G	297	

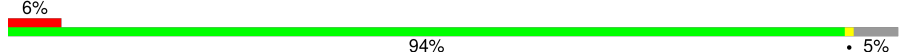
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Mol	Chain	Length	Quality of chain
9	H	176	88% 12%
10	I	244	89% 10%
11	J	256	87% 11%
12	K	191	97%
13	M	174	95%
14	N	199	96%
15	O	138	99%
16	Q	106	96%
17	R	92	95%
18	S	217	7% 96%
19	a	204	99%
20	b	199	98%
21	c	184	5% 99%
22	d	186	98%
23	e	189	79% 20%
24	f	172	97%
25	g	160	97%
26	h	121	80% 20%
27	i	137	96%
28	j	155	39% 61%
29	k	142	85% 15%
30	l	127	97%
31	m	136	99%
32	n	149	95%
33	o	59	8% 97%

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Mol	Chain	Length	Quality of chain
34	p	105	 90% 9%
35	q	113	 94% 5%
36	r	130	 95%
37	s	107	 98%
38	t	121	 87% 10%
39	u	120	 98%
40	v	100	 98%
41	w	88	 91% 5% 5%
42	x	78	 99%
43	y	51	 96%
44	z	128	 40% 60%
45	V	518	 72% 24% 6%
46	L	165	 88% 11% 65%
47	X	245	 95%

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 128867 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 RNA.

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 60S ribosomal protein L2-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	282	2271	1435	395	439	2	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 18 is a protein called Ribosomal Protein uL1.

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

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L25.

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

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L28.

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

- Molecule 33 is a protein called 60S ribosomal protein L29.

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

- Molecule 34 is a protein called 60S ribosomal protein L30.

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

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 45 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	393	Total	C	N	O	S	0	0
			3065	1947	528	570	20		

- Molecule 46 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	L	147	Total	C	N	O	0	0
			825	504	160	161		

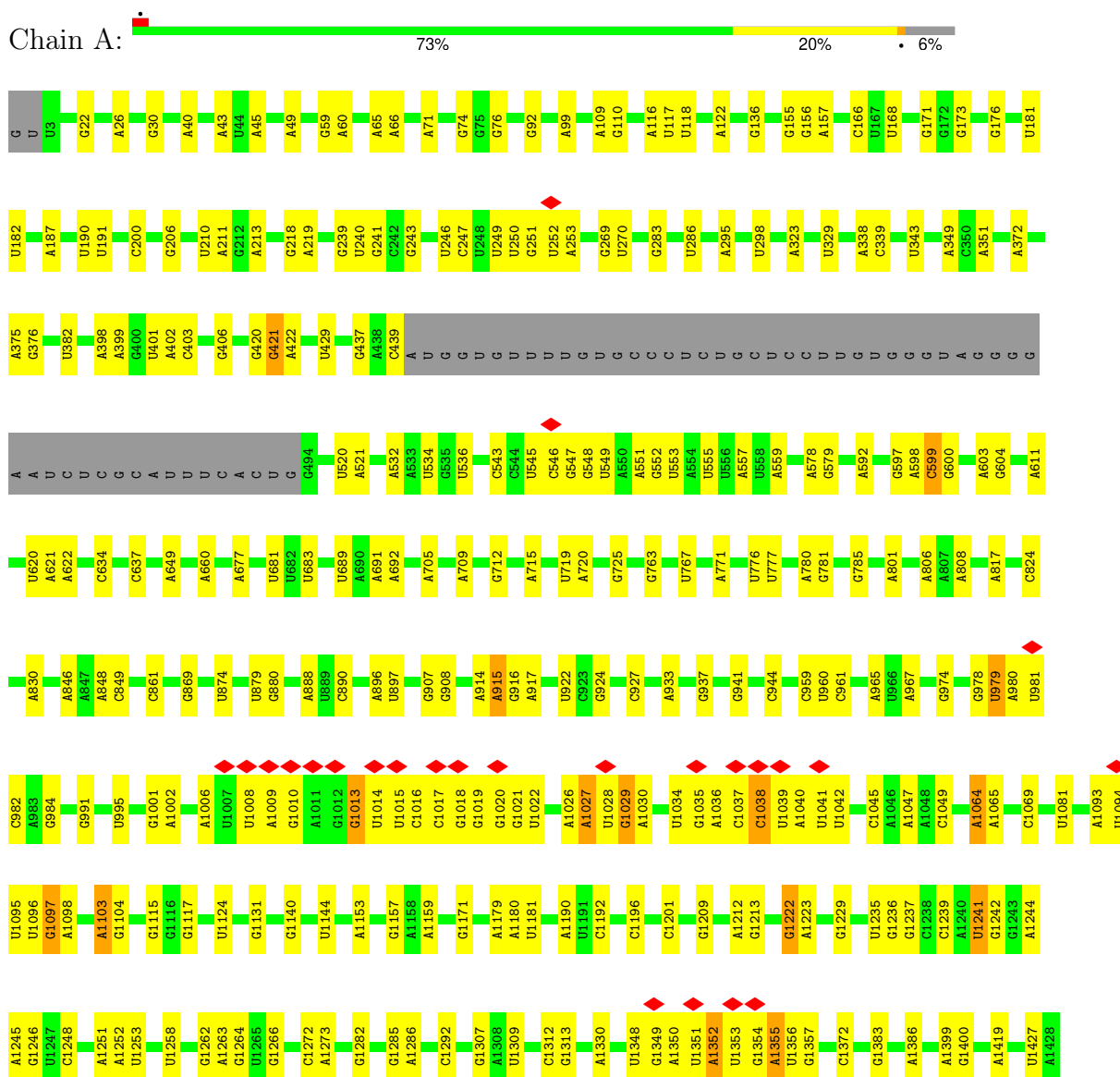
- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

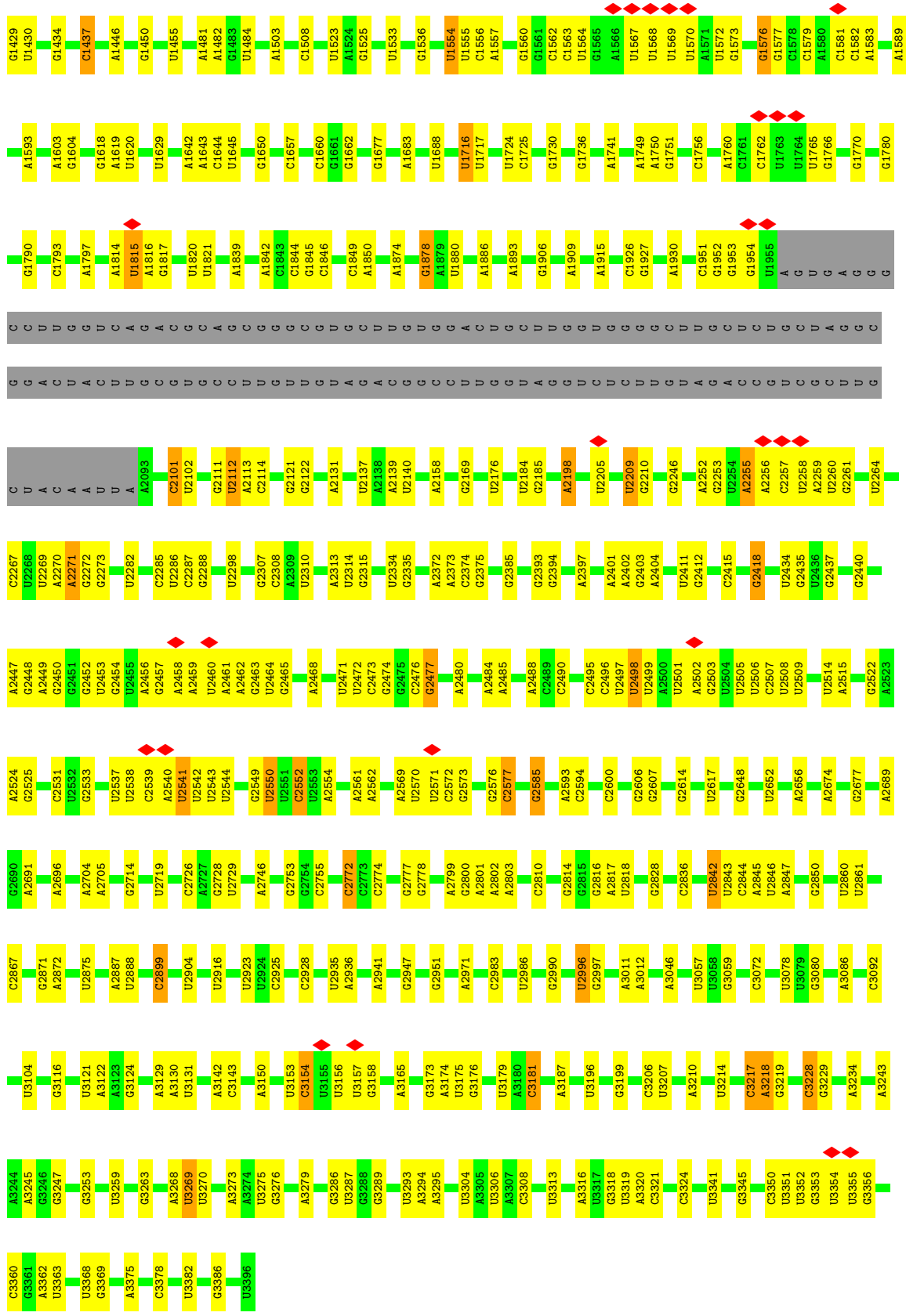
Mol	Chain	Residues	Atoms					AltConf	Trace
47	X	234	Total	C	N	O	S	0	0
			1710	1063	294	346	7		

3 Residue-property plots [i](#)

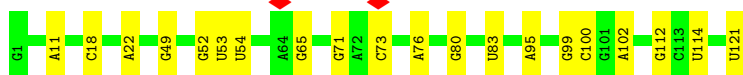
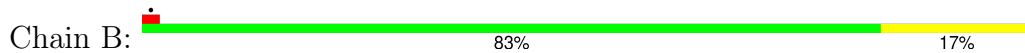
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

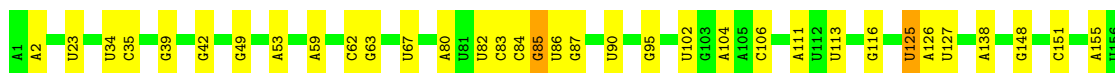
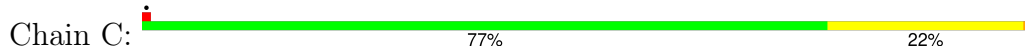




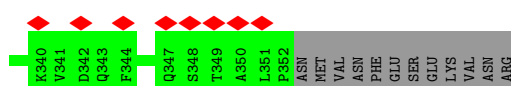
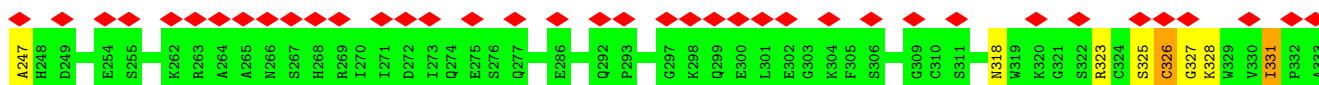
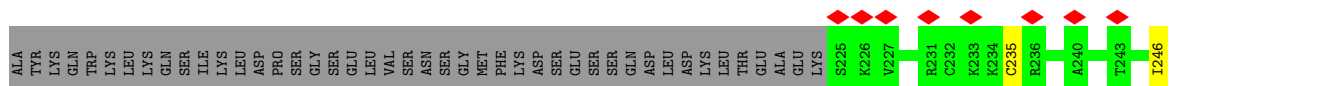
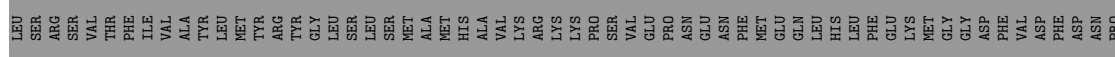
● Molecule 2: 5S rRNA



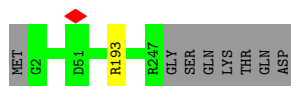
- Molecule 3: 5.8S RNA



- Molecule 4: Tyrosine-protein phosphatase YVH1

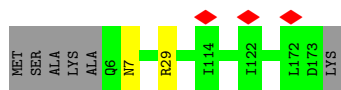


- Molecule 5: 60S ribosomal protein L2-A

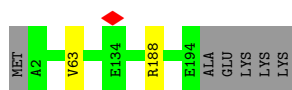


- Molecule 6: 60S ribosomal protein L3

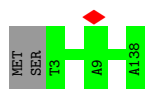




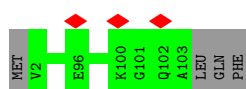
• Molecule 14: 60S ribosomal protein L13-A



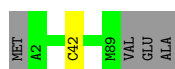
• Molecule 15: 60S ribosomal protein L14-A



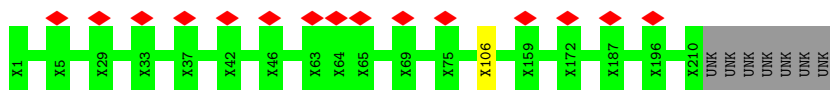
• Molecule 16: 60S ribosomal protein L42-A



• Molecule 17: 60S ribosomal protein L43-A



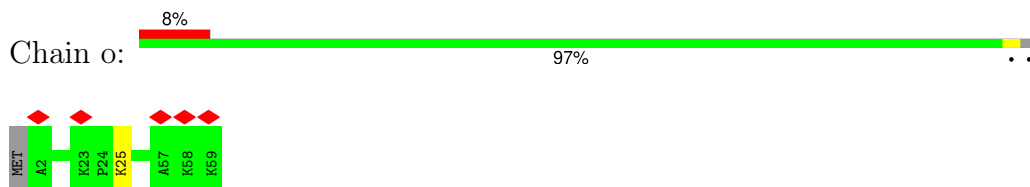
• Molecule 18: Ribosomal Protein uL1



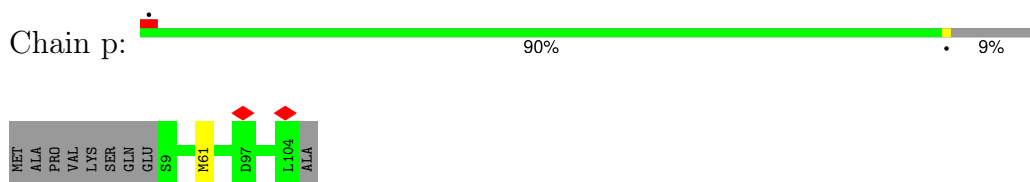
• Molecule 19: 60S ribosomal protein L15-A



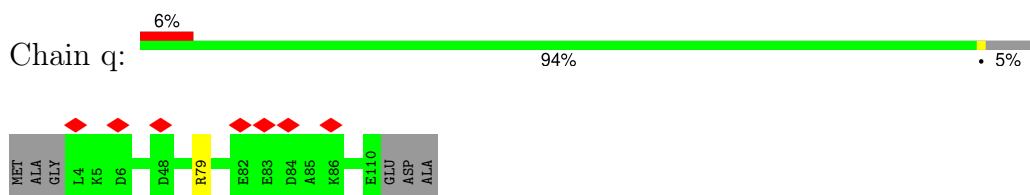
- Molecule 33: 60S ribosomal protein L29



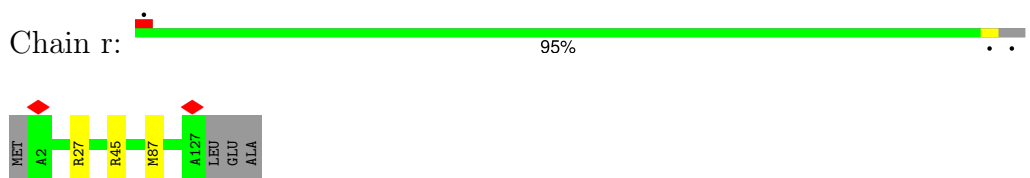
- Molecule 34: 60S ribosomal protein L30



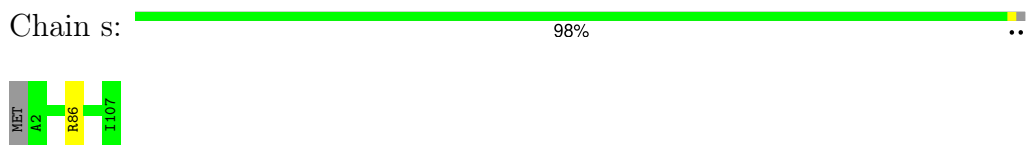
- Molecule 35: 60S ribosomal protein L31-A



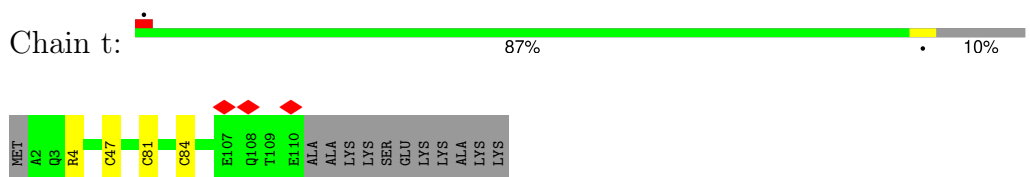
- Molecule 36: 60S ribosomal protein L32



- Molecule 37: 60S ribosomal protein L33-A

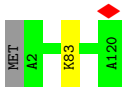


- Molecule 38: 60S ribosomal protein L34-A

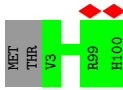


- Molecule 39: 60S ribosomal protein L35-A

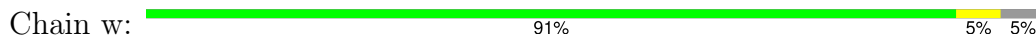




- Molecule 40: 60S ribosomal protein L36-A



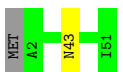
- Molecule 41: 60S ribosomal protein L37-A



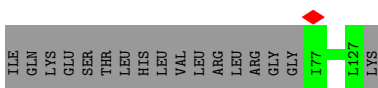
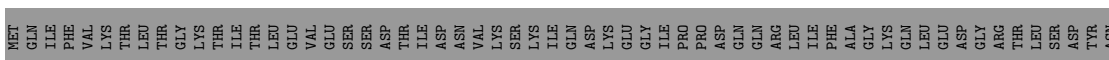
- Molecule 42: 60S ribosomal protein L38



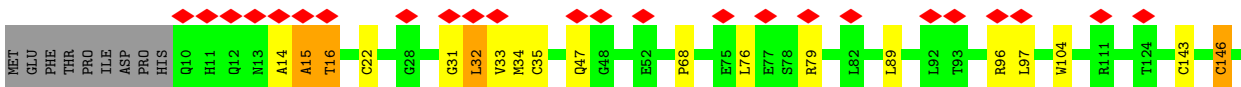
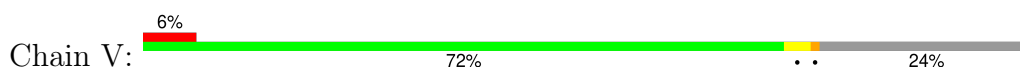
- Molecule 43: 60S ribosomal protein L39



- Molecule 44: Ubiquitin-60S ribosomal protein L40



- Molecule 45: 60S ribosomal export protein NMD3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98980	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	0.153	Depositor
Minimum map value	-0.088	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (\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 (\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	0/76692	0.92	121/119572 (0.1%)
2	B	0.55	0/2883	0.85	0/4491
3	C	0.67	0/3746	0.87	2/5832 (0.0%)
4	Y	0.36	0/1016	0.85	4/1368 (0.3%)
5	D	0.40	0/1908	0.57	0/2564
6	E	0.40	0/3130	0.57	0/4206
7	F	0.37	0/2800	0.58	1/3790 (0.0%)
8	G	0.34	0/2320	0.55	0/3131
9	H	0.35	0/1236	0.56	0/1661
10	I	0.37	0/1807	0.54	0/2432
11	J	0.36	0/1794	0.58	0/2425
12	K	0.38	0/1514	0.56	1/2039 (0.0%)
13	M	0.29	0/1365	0.59	0/1831
14	N	0.36	0/1564	0.57	0/2102
15	O	0.35	0/1068	0.50	0/1438
16	Q	0.35	0/831	0.54	0/1097
17	R	0.40	0/680	0.58	0/905
19	a	0.42	0/1757	0.53	0/2354
20	b	0.38	0/1585	0.51	0/2128
21	c	0.40	0/1443	0.57	0/1944
22	d	0.36	0/1465	0.55	0/1965
23	e	0.36	0/1236	0.55	1/1650 (0.1%)
24	f	0.38	0/1468	0.57	0/1973
25	g	0.37	0/1300	0.52	0/1743
26	h	0.35	0/781	0.52	0/1058
27	i	0.37	0/996	0.54	0/1340
28	j	0.35	0/521	0.50	0/691
29	k	0.39	0/979	0.57	0/1321
30	l	0.35	0/995	0.55	1/1329 (0.1%)
31	m	0.37	0/1118	0.57	0/1497
32	n	0.38	0/1204	0.65	2/1612 (0.1%)
33	o	0.33	0/473	0.56	0/629
34	p	0.35	0/745	0.55	0/1001
35	q	0.39	0/880	0.54	0/1182

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	r	0.37	0/1033	0.54	0/1383
37	s	0.43	0/868	0.54	0/1168
38	t	0.43	0/871	0.66	2/1164 (0.2%)
39	u	0.34	0/978	0.56	0/1301
40	v	0.32	0/759	0.57	0/1009
41	w	0.41	0/680	0.60	1/901 (0.1%)
42	x	0.32	0/614	0.54	0/822
43	y	0.34	0/443	0.58	0/588
44	z	0.31	0/414	0.51	0/551
45	V	0.38	0/3124	0.70	5/4246 (0.1%)
46	L	0.30	0/367	0.68	1/498 (0.2%)
47	X	0.31	0/1729	0.54	0/2355
All	All	0.56	0/137180	0.81	142/202287 (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
6	E	0	1
7	F	0	1
10	I	0	1
11	J	0	2
12	K	0	1
13	M	0	1
18	S	0	1
24	f	0	2
32	n	0	1
33	o	0	1
39	u	0	1
45	V	0	8
47	X	0	1
All	All	0	25

There are no bond length outliers.

The worst 5 of 142 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3217	C	N1-C2-O2	11.25	125.65	118.90
38	t	81	CYS	CA-CB-SG	10.13	132.23	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3217	C	C2-N1-C1'	9.84	129.62	118.80
1	A	922	U	C2-N1-C1'	8.69	128.13	117.70
1	A	3217	C	N3-C2-O2	-8.61	115.88	121.90

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	E	346	THR	Peptide
7	F	4	PRO	Peptide
4	Y	325	SER	Peptide
4	Y	327	GLY	Peptide
4	Y	331	ILE	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%)	96 (76%)	26 (21%)	4 (3%)	3	25
5	D	244/254 (96%)	229 (94%)	15 (6%)	0	100	100
6	E	382/387 (99%)	355 (93%)	26 (7%)	1 (0%)	37	68
7	F	359/362 (99%)	328 (91%)	28 (8%)	3 (1%)	16	51
8	G	280/297 (94%)	263 (94%)	16 (6%)	1 (0%)	30	64
9	H	151/176 (86%)	140 (93%)	11 (7%)	0	100	100
10	I	218/244 (89%)	209 (96%)	8 (4%)	1 (0%)	25	59
11	J	225/256 (88%)	217 (96%)	7 (3%)	1 (0%)	30	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	K	186/191 (97%)	173 (93%)	13 (7%)	0	100	100
13	M	166/174 (95%)	151 (91%)	15 (9%)	0	100	100
14	N	191/199 (96%)	172 (90%)	18 (9%)	1 (0%)	25	59
15	O	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
16	Q	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
17	R	86/92 (94%)	80 (93%)	6 (7%)	0	100	100
19	a	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
20	b	195/199 (98%)	187 (96%)	8 (4%)	0	100	100
21	c	181/184 (98%)	170 (94%)	11 (6%)	0	100	100
22	d	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
23	e	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
24	f	168/172 (98%)	158 (94%)	8 (5%)	2 (1%)	11	43
25	g	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
26	h	95/121 (78%)	90 (95%)	5 (5%)	0	100	100
27	i	130/137 (95%)	129 (99%)	1 (1%)	0	100	100
28	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	7	36
29	k	119/142 (84%)	112 (94%)	7 (6%)	0	100	100
30	l	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
31	m	133/136 (98%)	117 (88%)	16 (12%)	0	100	100
32	n	146/149 (98%)	127 (87%)	16 (11%)	3 (2%)	5	32
33	o	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
34	p	94/105 (90%)	90 (96%)	4 (4%)	0	100	100
35	q	105/113 (93%)	99 (94%)	6 (6%)	0	100	100
36	r	124/130 (95%)	119 (96%)	5 (4%)	0	100	100
37	s	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
38	t	107/121 (88%)	101 (94%)	6 (6%)	0	100	100
39	u	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
40	v	96/100 (96%)	87 (91%)	9 (9%)	0	100	100
41	w	82/88 (93%)	74 (90%)	8 (10%)	0	100	100
42	x	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	z	49/128 (38%)	48 (98%)	1 (2%)	0	100	100
45	V	391/518 (76%)	338 (86%)	46 (12%)	7 (2%)	7	35
46	L	53/165 (32%)	48 (91%)	5 (9%)	0	100	100
47	X	230/245 (94%)	219 (95%)	11 (5%)	0	100	100
All	All	6618/7629 (87%)	6158 (93%)	435 (7%)	25 (0%)	32	64

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	F	339	LEU
4	Y	326	CYS
8	G	259	LYS
11	J	36	ILE
14	N	63	VAL

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%)	108 (98%)	2 (2%)	54	74
5	D	189/196 (96%)	188 (100%)	1 (0%)	86	93
6	E	318/323 (98%)	315 (99%)	3 (1%)	75	86
7	F	288/289 (100%)	285 (99%)	3 (1%)	73	84
8	G	235/245 (96%)	230 (98%)	5 (2%)	48	71
9	H	131/153 (86%)	131 (100%)	0	100	100
10	I	185/205 (90%)	183 (99%)	2 (1%)	70	83
11	J	182/208 (88%)	181 (100%)	1 (0%)	86	93
12	K	168/171 (98%)	167 (99%)	1 (1%)	84	91
13	M	146/150 (97%)	145 (99%)	1 (1%)	81	89
14	N	153/159 (96%)	152 (99%)	1 (1%)	81	89
15	O	107/109 (98%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	87/91 (96%)	87 (100%)	0	100	100
17	R	69/72 (96%)	68 (99%)	1 (1%)	62	79
19	a	175/176 (99%)	173 (99%)	2 (1%)	70	83
20	b	160/162 (99%)	158 (99%)	2 (1%)	65	81
21	c	140/146 (96%)	139 (99%)	1 (1%)	81	89
22	d	150/151 (99%)	148 (99%)	2 (1%)	65	81
23	e	125/154 (81%)	125 (100%)	0	100	100
24	f	155/156 (99%)	154 (99%)	1 (1%)	84	91
25	g	136/137 (99%)	132 (97%)	4 (3%)	37	64
26	h	84/107 (78%)	84 (100%)	0	100	100
27	i	102/105 (97%)	102 (100%)	0	100	100
28	j	54/129 (42%)	54 (100%)	0	100	100
29	k	104/118 (88%)	104 (100%)	0	100	100
30	l	108/110 (98%)	107 (99%)	1 (1%)	75	86
31	m	115/116 (99%)	115 (100%)	0	100	100
32	n	118/119 (99%)	116 (98%)	2 (2%)	56	75
33	o	46/47 (98%)	46 (100%)	0	100	100
34	p	81/88 (92%)	80 (99%)	1 (1%)	67	82
35	q	92/97 (95%)	91 (99%)	1 (1%)	70	83
36	r	108/111 (97%)	105 (97%)	3 (3%)	38	65
37	s	90/91 (99%)	89 (99%)	1 (1%)	70	83
38	t	94/103 (91%)	92 (98%)	2 (2%)	48	71
39	u	104/105 (99%)	104 (100%)	0	100	100
40	v	78/82 (95%)	78 (100%)	0	100	100
41	w	69/71 (97%)	66 (96%)	3 (4%)	25	54
42	x	67/69 (97%)	67 (100%)	0	100	100
43	y	45/46 (98%)	44 (98%)	1 (2%)	47	70
44	z	46/116 (40%)	46 (100%)	0	100	100
45	V	339/467 (73%)	333 (98%)	6 (2%)	54	74
46	L	32/65 (49%)	32 (100%)	0	100	100
47	X	186/211 (88%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5571/6349 (88%)	5517 (99%)	54 (1%)	71 84

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	f	12	ARG
32	n	120	ASN
45	V	79	ARG
25	g	79	MET
25	g	146	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
32	n	74	ASN
43	y	43	ASN
32	n	120	ASN
39	u	59	ASN
45	V	108	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3200/3396 (94%)	675 (21%)	32 (1%)
2	B	120/121 (99%)	20 (16%)	0
3	C	157/158 (99%)	35 (22%)	1 (0%)
All	All	3477/3675 (94%)	730 (20%)	33 (0%)

5 of 730 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	22	G
1	A	26	A
1	A	30	G
1	A	40	A
1	A	43	A

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3121	U
1	A	3218	A
3	C	85	G
1	A	1241	U
1	A	1222	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

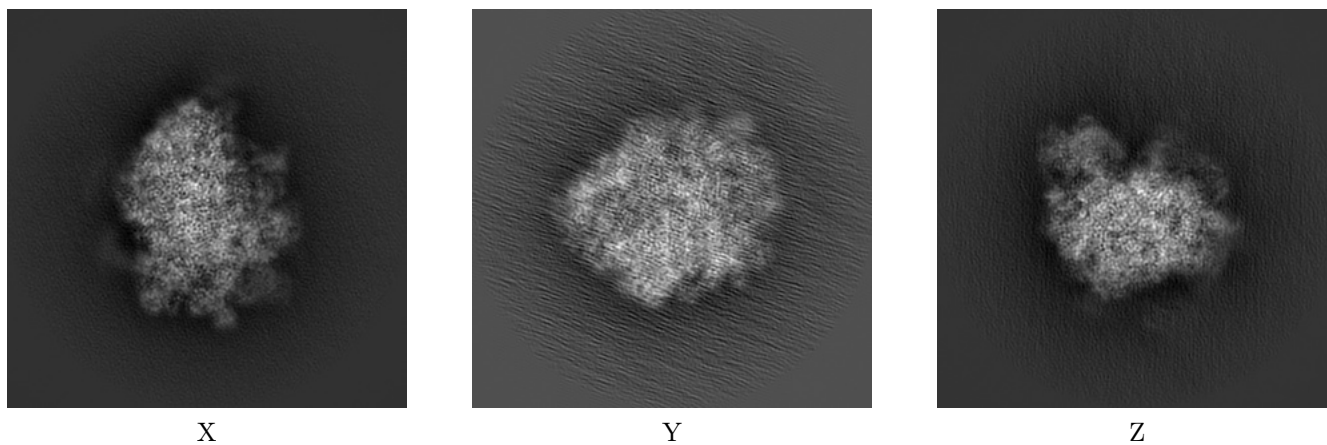
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0372. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

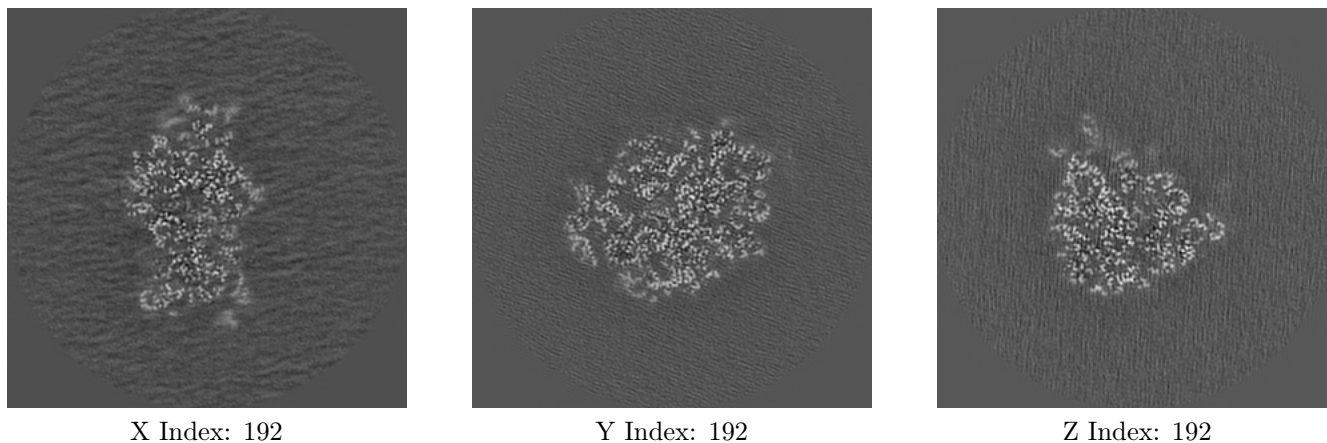
6.1.1 Primary map



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

6.2 Central slices [i](#)

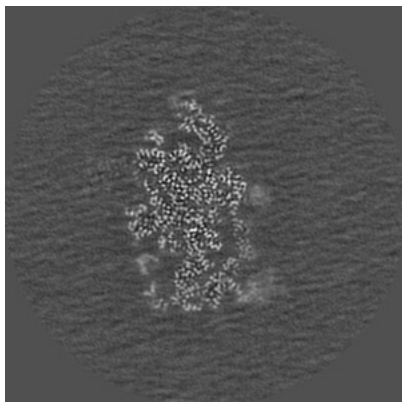
6.2.1 Primary map



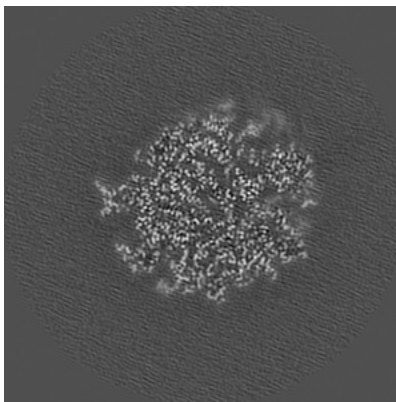
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

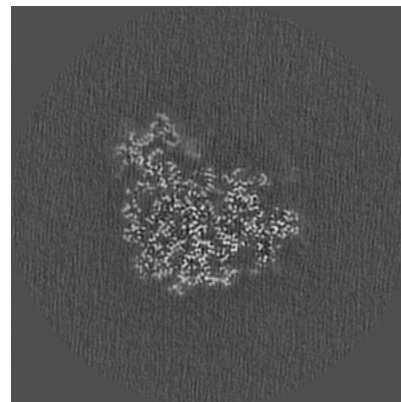
6.3.1 Primary map



X Index: 207



Y Index: 176

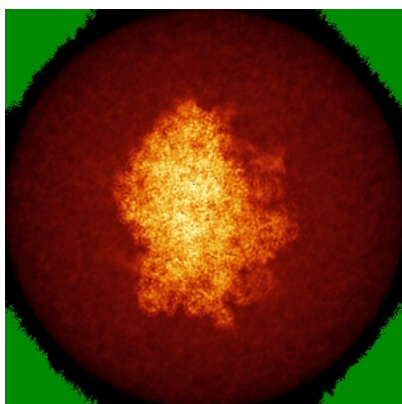


Z Index: 185

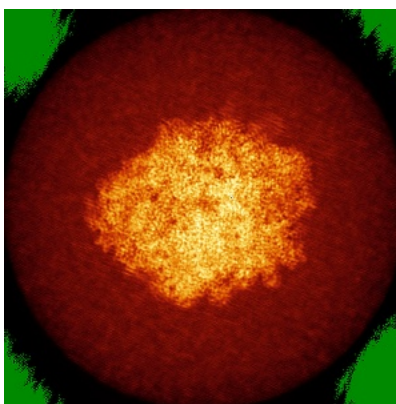
The images above show the largest variance slices of the map in three orthogonal directions.

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

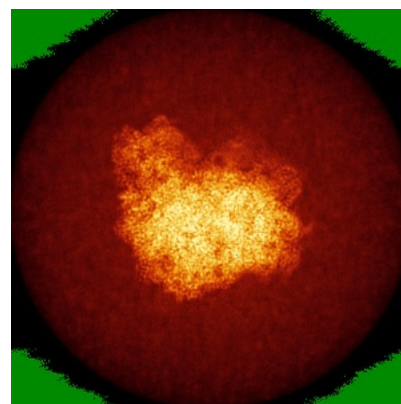
6.4.1 Primary map



X



Y

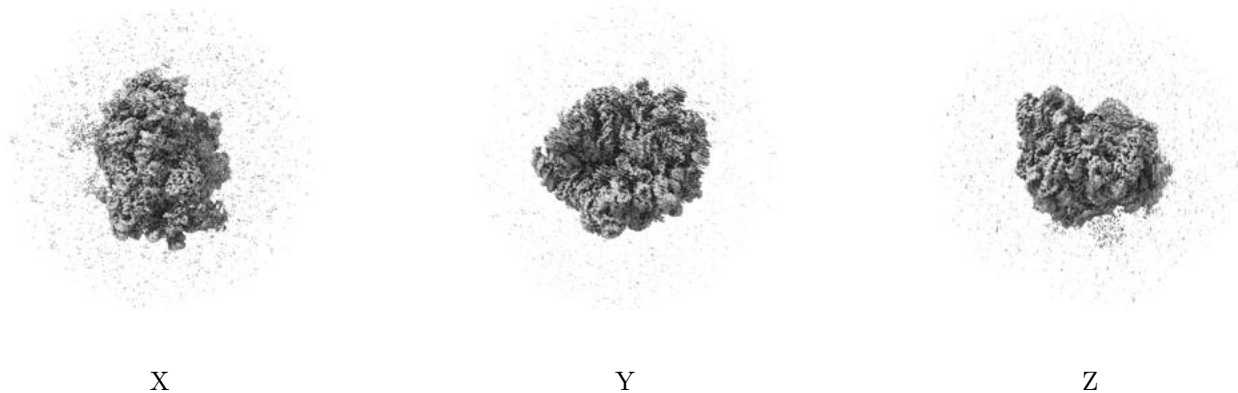


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

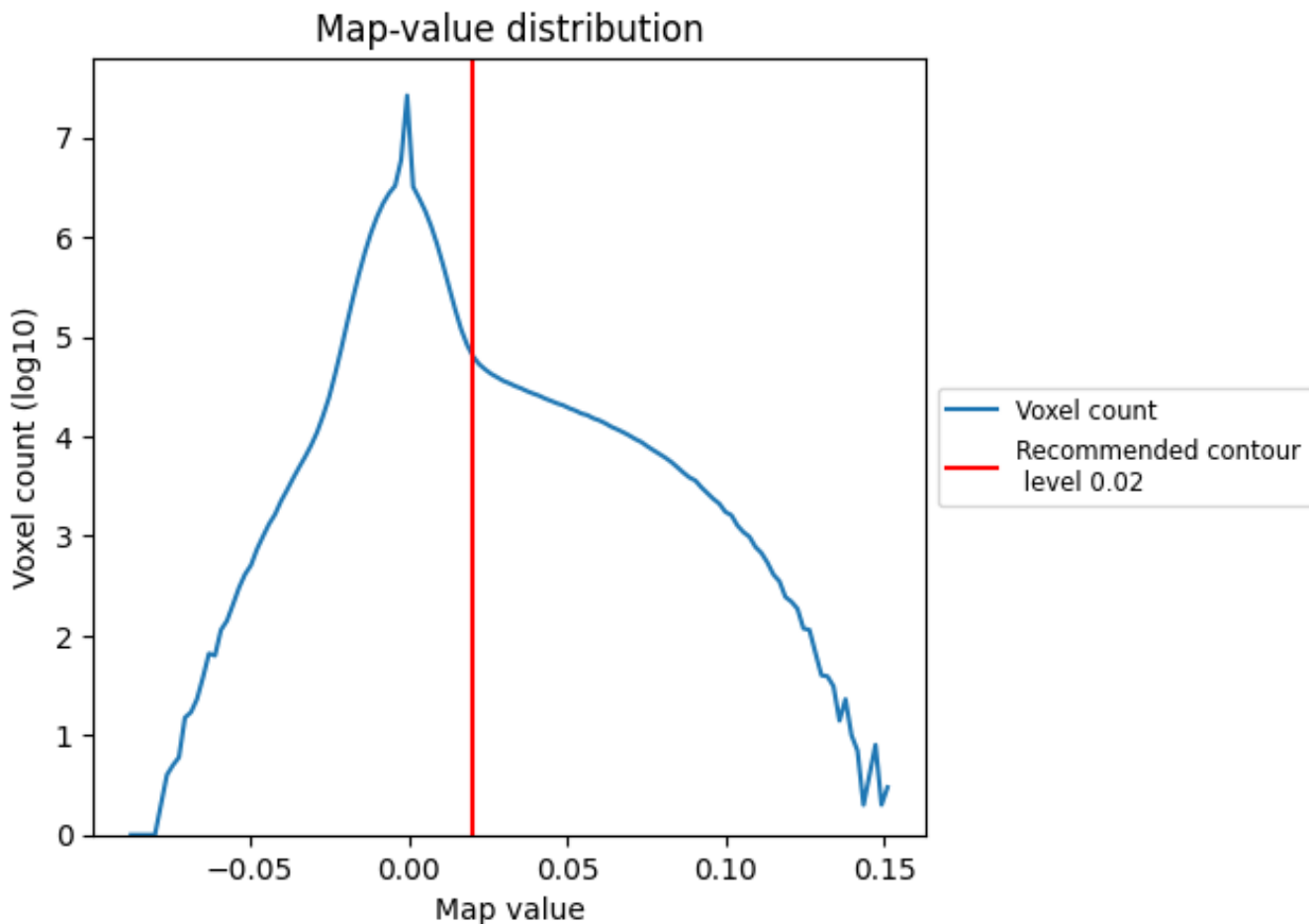
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

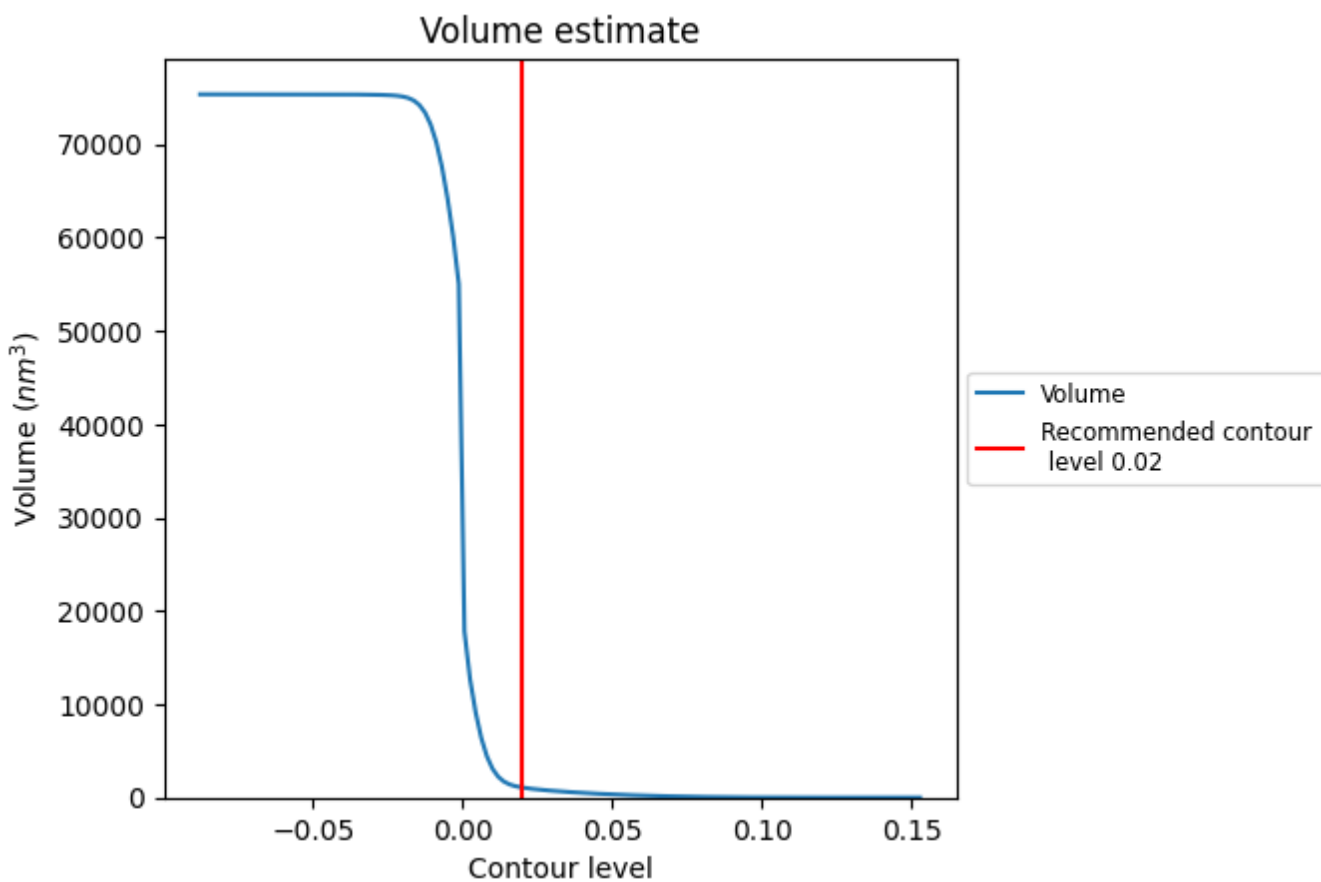
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

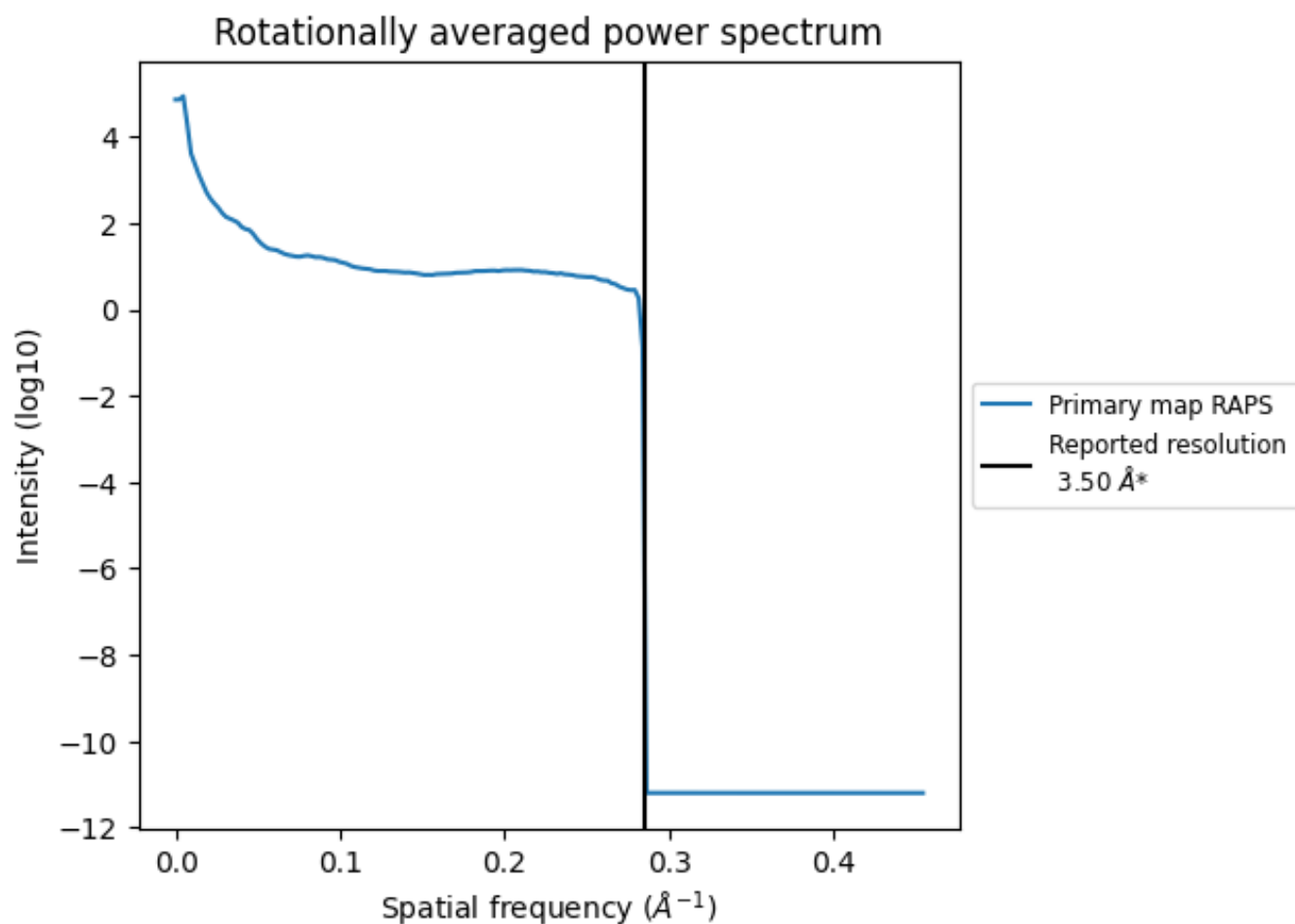
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1078 nm³; this corresponds to an approximate mass of 974 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 [\(i\)](#)

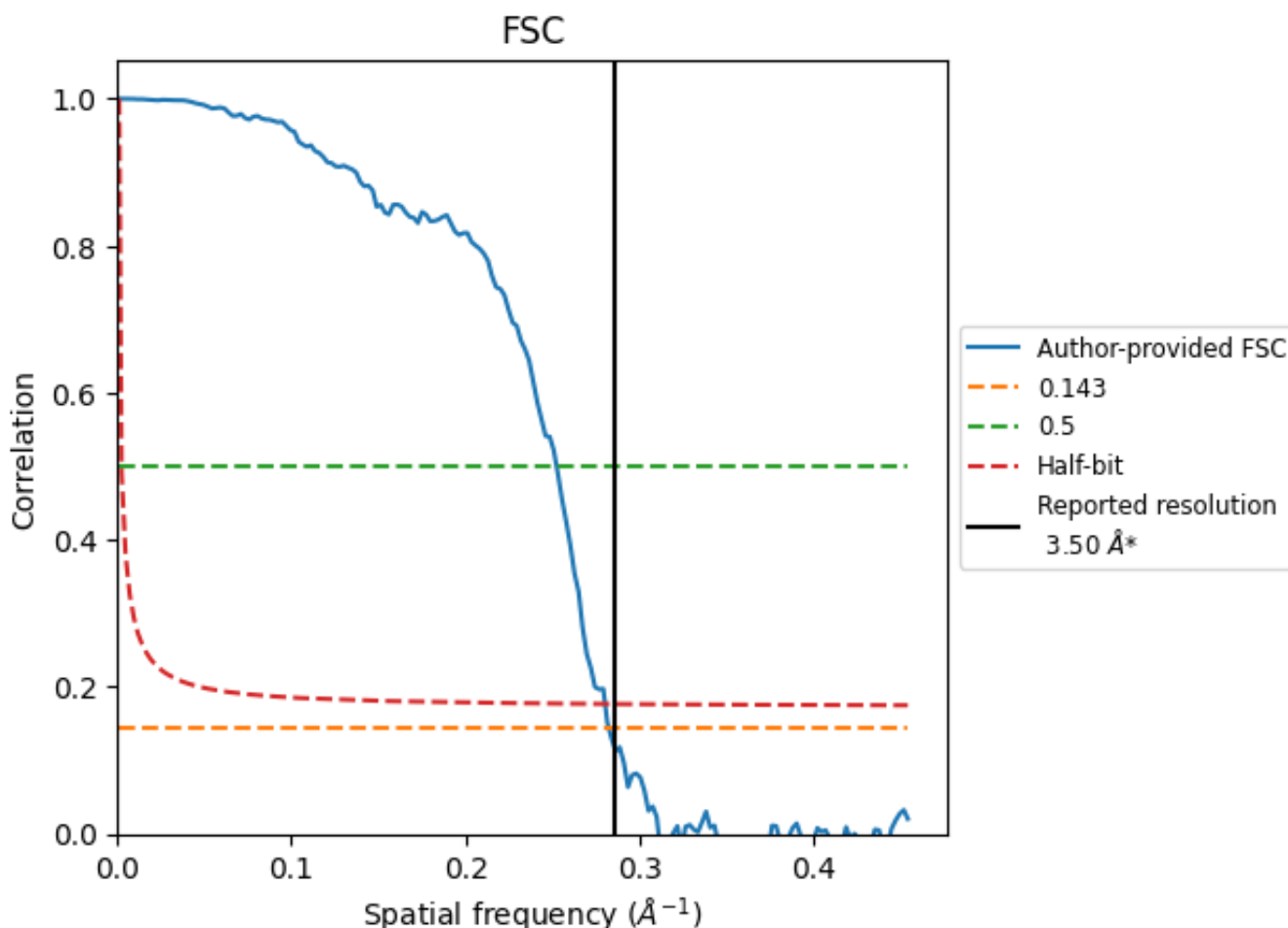


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

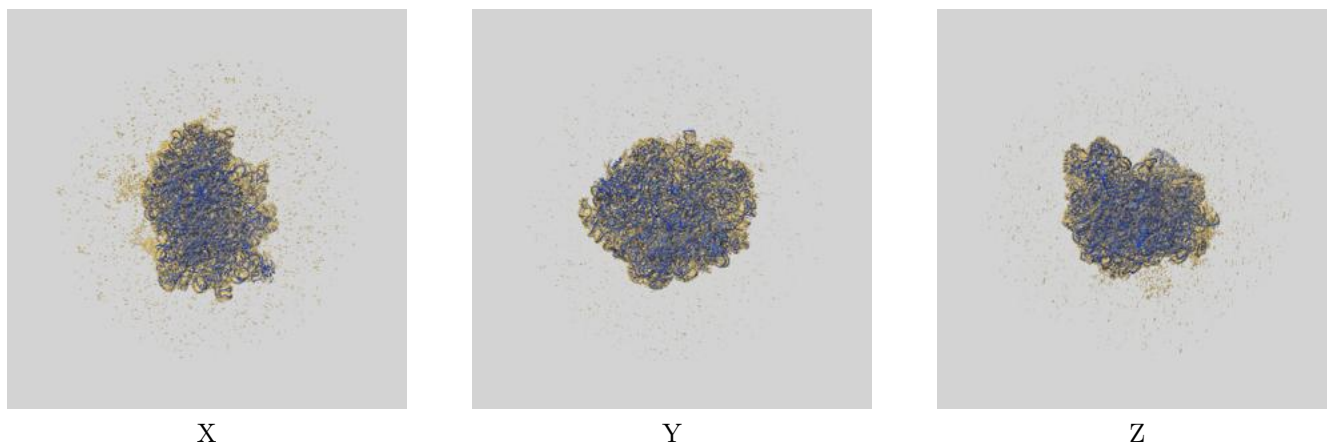
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.54	3.96	3.57
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

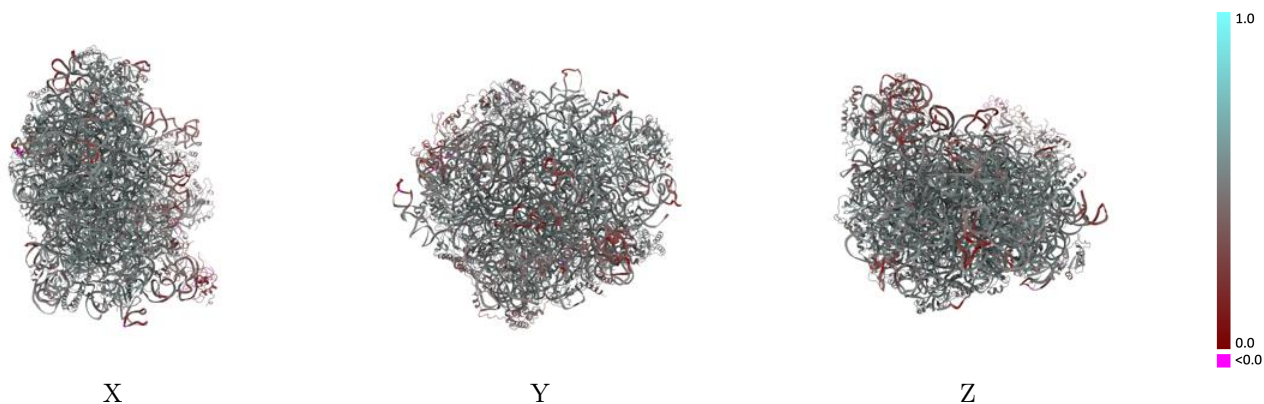
This section contains information regarding the fit between EMDB map EMD-0372 and PDB model 6N8M. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



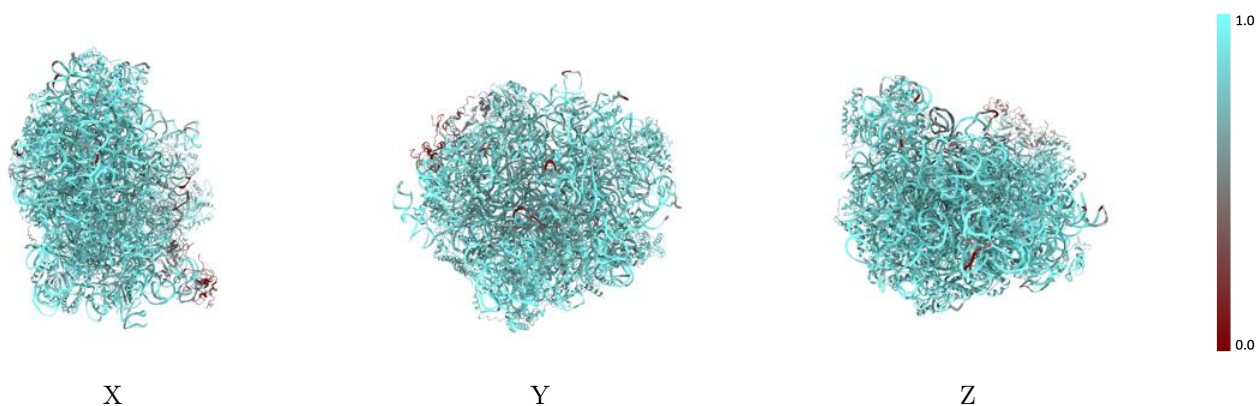
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



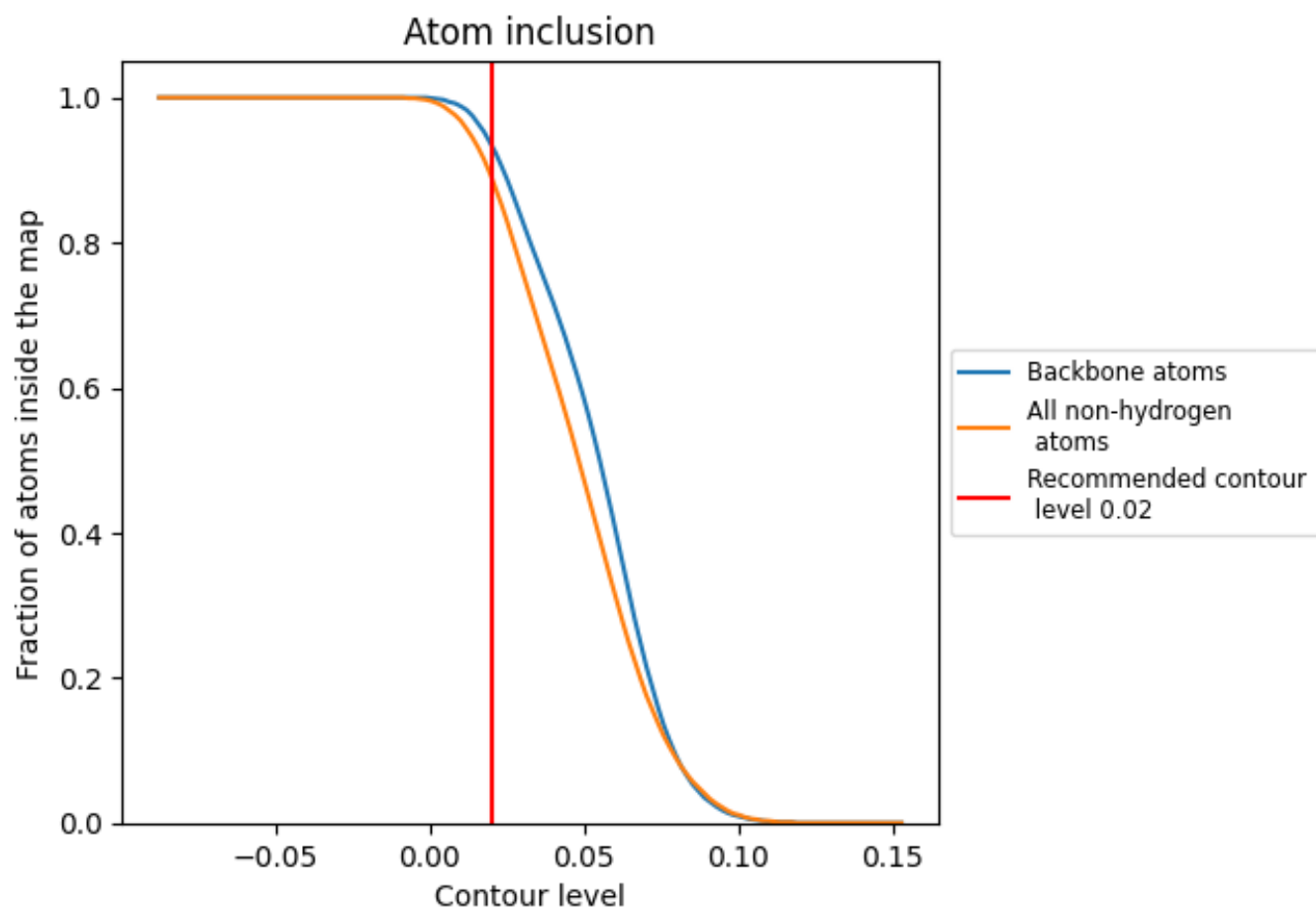
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 89% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.4880
A	 0.9380	 0.4870
B	 0.9640	 0.4810
C	 0.9570	 0.5010
D	 0.8710	 0.5280
E	 0.8770	 0.5190
F	 0.8540	 0.5060
G	 0.8240	 0.4460
H	 0.8370	 0.4930
I	 0.8500	 0.4970
J	 0.8610	 0.4860
K	 0.8610	 0.5020
L	 0.2670	 0.2670
M	 0.7810	 0.4210
N	 0.8540	 0.4950
O	 0.8720	 0.5020
Q	 0.8250	 0.5110
R	 0.8740	 0.5210
S	 0.8270	 0.3980
V	 0.7140	 0.4440
X	 0.7670	 0.4660
Y	 0.4550	 0.3580
a	 0.8750	 0.5260
b	 0.8580	 0.5200
c	 0.8370	 0.5000
d	 0.8440	 0.5070
e	 0.8740	 0.5180
f	 0.8500	 0.5060
g	 0.8200	 0.4970
h	 0.8590	 0.4600
i	 0.8220	 0.5190
j	 0.8740	 0.5150
k	 0.8540	 0.5040
l	 0.8510	 0.5060
m	 0.8550	 0.4940



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Chain	Atom inclusion	Q-score
n	 0.8630	 0.5180
o	 0.7990	 0.4670
p	 0.8320	 0.4860
q	 0.8190	 0.4880
r	 0.8450	 0.5220
s	 0.8660	 0.5330
t	 0.8280	 0.5170
u	 0.8590	 0.5010
v	 0.8310	 0.4790
w	 0.9080	 0.5350
x	 0.7850	 0.4760
y	 0.8430	 0.5210
z	 0.7510	 0.4850