



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2025 – 08:37 AM EDT

PDB ID : 6N8O / pdb\_00006n8o  
EMDB ID : EMD-0374  
Title : Cryo-EM structure of Rpl10-inserted (RI) 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](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:

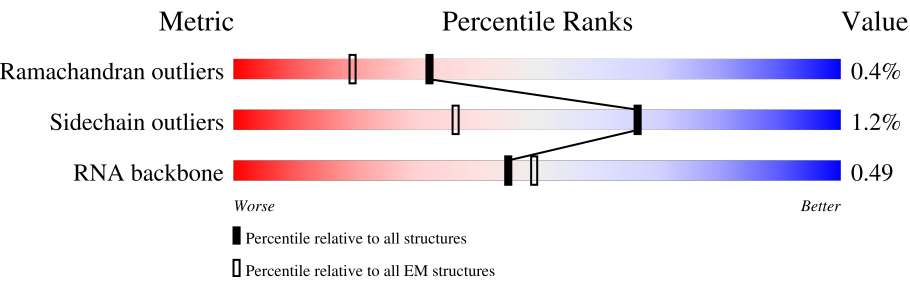
EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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.



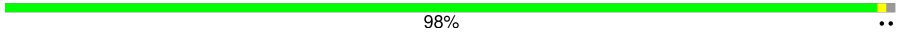
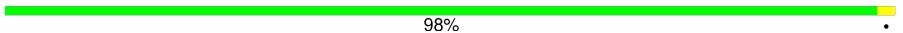













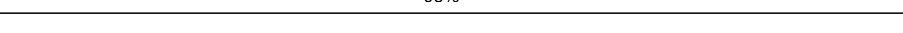
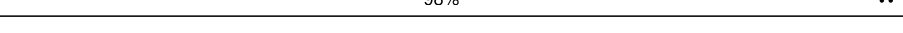
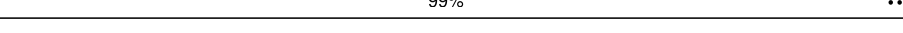
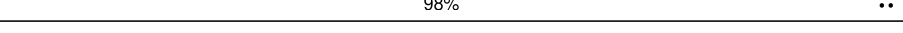

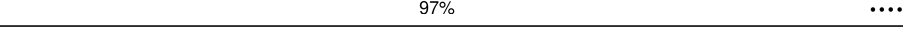
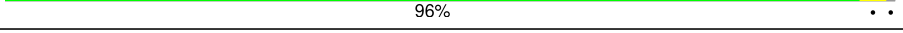

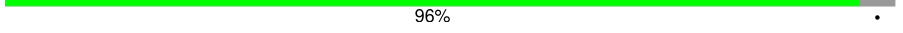

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	3396	<div><div>74%19%6%</div></div>
2	B	121	<div><div>87%13%</div></div>
3	C	158	<div><div>82%18%</div></div>
4	Y	364	<div><div>33%65%</div></div>
5	X	245	<div><div>95%</div></div>
6	L	165	<div><div>88%11%</div></div>
7	W	640	<div><div>55%41%</div></div>
8	V	518	<div><div>73%24%</div></div>
9	D	254	<div><div>96%</div></div>

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Mol	Chain	Length	Quality of chain
10	E	387	 98% ..
11	F	362	 98% .
12	G	297	 95% . .
13	H	176	 88% . 12%
14	I	244	 88% . 10%
15	J	256	 87% . 11%
16	K	191	 97% . .
17	Z	221	 89% . 9%
18	M	174	 95% . .
19	N	199	 96% . .
20	O	138	 99% .
21	Q	106	 96% .
22	R	92	 93% . .
23	S	217	 96% .
24	a	204	 98% .
25	b	199	 98% ..
26	c	184	 99% ..
27	d	186	 98% ..
28	e	189	 79% . 20%
29	f	172	 97% ....
30	g	160	 96% . .
31	h	121	 80% 20%
32	i	137	 96% .
33	j	155	 39% . 61%
34	k	142	 85% 15%

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Mol	Chain	Length	Quality of chain
35	l	127	 97% . .
36	m	136	 99% .
37	n	149	 94% . .
38	o	59	 95% . .
39	p	105	 90% . 9%
40	q	113	 94% . 5%
41	r	130	 95% . .
42	s	107	 98% ..
43	t	121	 86% . 10%
44	u	120	 98% ..
45	v	100	 97% . .
46	w	88	 91% 5% 5%
47	x	78	 99% .
48	y	51	 96% . .
49	z	128	 40% 60%

## 2 Entry composition [i](#)

There are 49 unique types of molecules in this entry. The entry contains 133453 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called *Saccharomyces cerevisiae* S288C 35S pre-ribosomal RNA (RDN37-1), miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3201	Total	C	N	O	P	0	0
			68470	30584	12346	22339	3201		

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

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

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

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

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

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

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

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

- Molecule 6 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	147	Total	C	N	O		0	0
			817	499	159	159			

- Molecule 7 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	377	Total	C	N	O	S	0	0
			2976	1905	516	548	7		

- Molecule 8 is a protein called 60S ribosomal export protein NMD3.

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

- Molecule 9 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L3.

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

- Molecule 11 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	289	Total	C	N	O	S	0	0
			2315	1464	403	446	2		

- Molecule 13 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Z	201	Total	C	N	O	S	0	0
			1648	1050	309	284	5		

- Molecule 18 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 23 is a protein called Ribosomal Protein uL1.

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

- Molecule 24 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L19-A.



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

- Molecule 29 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L25.

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

- Molecule 35 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L28.

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

- Molecule 38 is a protein called 60S ribosomal protein L29.

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

- Molecule 39 is a protein called 60S ribosomal protein L30.

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

- Molecule 40 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L32.

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

- Molecule 42 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L38.

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

- Molecule 48 is a protein called 60S ribosomal protein L39.

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

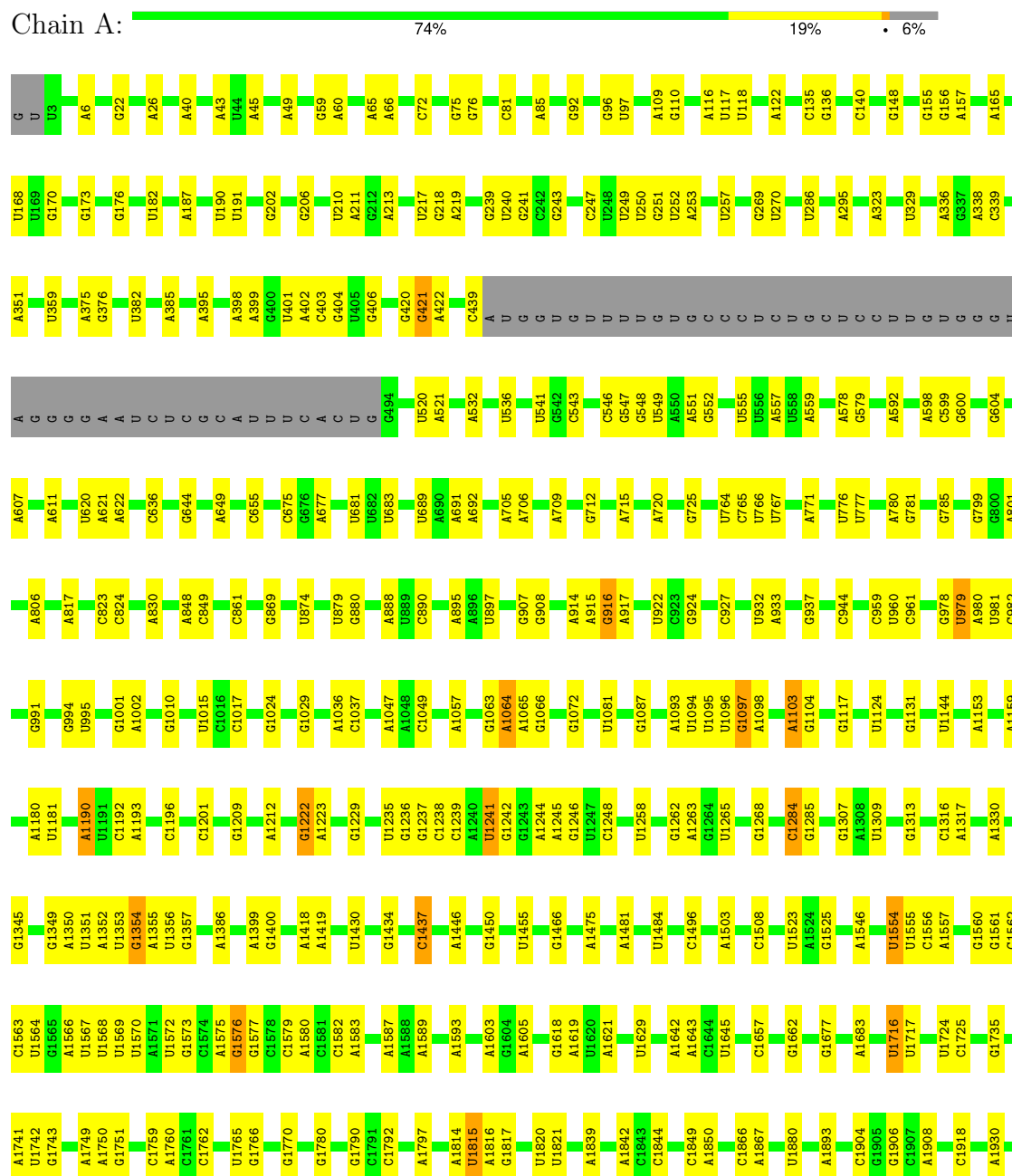
- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

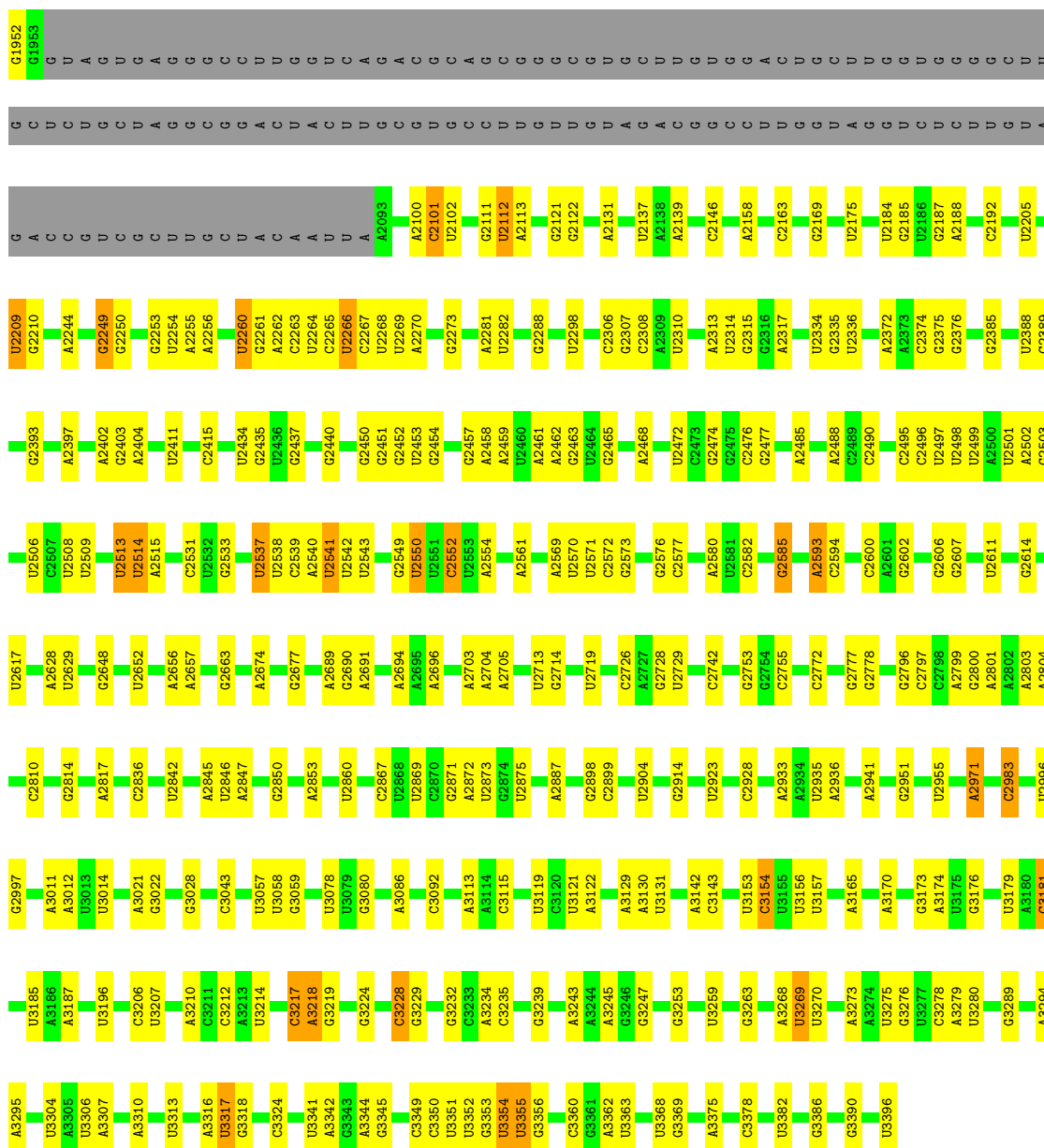
Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	51	Total	C	N	O	S	0	0
			408	253	84	66	5		

### 3 Residue-property plots

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





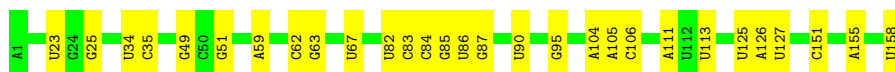
- Molecule 2: 5S rRNA

Chain B:



- Molecule 3: 5.8S rRNA

Chain C:



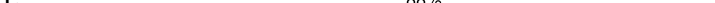
- Molecule 4: Tyrosine-protein phosphatase YVH1

- Molecule 5: Eukaryotic translation initiation factor 6

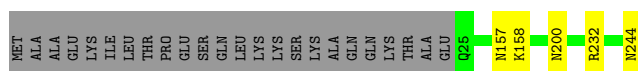
- Molecule 6: Ribosomal protein L12

- Molecule 7: Large subunit GTPase 1



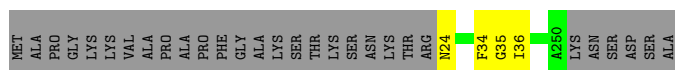
- Chain I:  88% • 10%





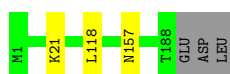
- Molecule 15: 60S ribosomal protein L8-A

Chain J: 87% 11%



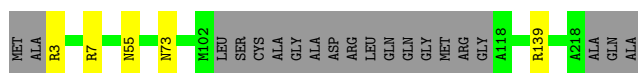
- Molecule 16: 60S ribosomal protein L9-A

Chain K: 97% ..



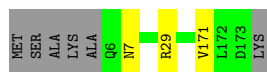
- Molecule 17: 60S ribosomal protein L10

Chain Z: 89% 9%



- Molecule 18: 60S ribosomal protein L11-A

Chain M: 95% ..



- Molecule 19: 60S ribosomal protein L13-A

Chain N: 96% ..



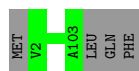
- Molecule 20: 60S ribosomal protein L14-A

Chain O: 99% .



- Molecule 21: 60S ribosomal protein L42-A

Chain Q: 96% .



- Molecule 22: 60S ribosomal protein L43-A

Chain R: 93%



- Molecule 23: Ribosomal Protein uL1

Chain S: 96%



- Molecule 24: 60S ribosomal protein L15-A

Chain a: 98%



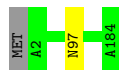
- Molecule 25: 60S ribosomal protein L16-A

Chain b: 98%



- Molecule 26: 60S ribosomal protein L17-A

Chain c: 99%



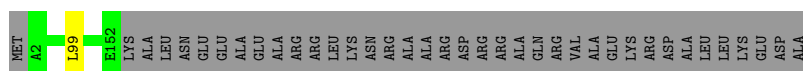
- Molecule 27: 60S ribosomal protein L18-A

Chain d: 98%



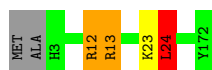
- Molecule 28: 60S ribosomal protein L19-A

Chain e: 79%



- Molecule 29: 60S ribosomal protein L20-A

Chain f: 97%



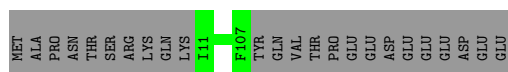
- Molecule 30: 60S ribosomal protein L21-A

Chain g: 96%



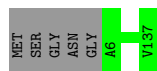
- Molecule 31: 60S ribosomal protein L22-A

Chain h: 80% 20%



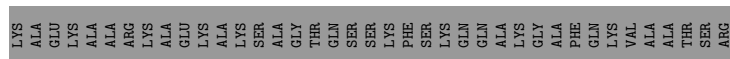
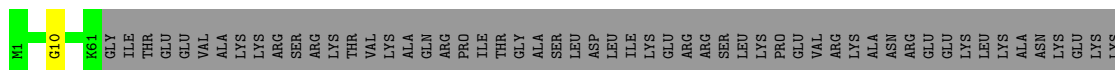
- Molecule 32: 60S ribosomal protein L23-A

Chain i: 96%



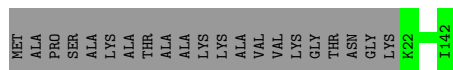
- Molecule 33: 60S ribosomal protein L24-A

Chain j: 39% 61%




- Molecule 34: 60S ribosomal protein L25

Chain k: 85% 15%



- Molecule 35: 60S ribosomal protein L26-A

Chain l:  97% ..



- Molecule 36: 60S ribosomal protein L27-A

Chain m:  99% .



- Molecule 37: 60S ribosomal protein L28

Chain n:  94% ..



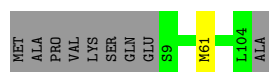
- Molecule 38: 60S ribosomal protein L29

Chain o:  95% ..



- Molecule 39: 60S ribosomal protein L30

Chain p:  90% . 9%



- Molecule 40: 60S ribosomal protein L31-A

Chain q:  94% . 5%



- Molecule 41: 60S ribosomal protein L32

Chain r:  95% ..




- Molecule 42: 60S ribosomal protein L33-A

Chain s:  98% ..



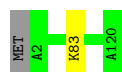
- Molecule 43: 60S ribosomal protein L34-A

Chain t:  86% • 10%



- Molecule 44: 60S ribosomal protein L35-A

Chain u:  98% ..



- Molecule 45: 60S ribosomal protein L36-A

Chain v:  97% ..



- Molecule 46: 60S ribosomal protein L37-A

Chain w:  91% 5% 5%



- Molecule 47: 60S ribosomal protein L38

Chain x:  99% •



- Molecule 48: 60S ribosomal protein L39

Chain y:  96% • •



- Molecule 49: Ubiquitin-60S ribosomal protein L40

Chain z: 

40%

60%

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

ILE  
GLN  
LYS  
GLU  
THR  
LEU  
HIS  
LEU  
VAL  
LEU  
ARG  
LEU  
ARG  
GLY  
GLY  
I77  
L127  
LYS

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	112292	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

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.75	0/76644	0.94	118/119497 (0.1%)
2	B	0.67	0/2883	0.87	0/4491
3	C	0.76	0/3746	0.92	0/5832
4	Y	0.37	0/1016	0.85	2/1368 (0.1%)
5	X	0.34	0/1729	0.55	0/2355
6	L	0.32	0/359	0.73	1/489 (0.2%)
7	W	0.33	0/3039	0.70	1/4124 (0.0%)
8	V	0.36	0/3093	0.64	2/4203 (0.0%)
9	D	0.43	0/1908	0.57	0/2564
10	E	0.44	0/3130	0.58	0/4206
11	F	0.39	0/2800	0.59	1/3790 (0.0%)
12	G	0.37	0/2364	0.57	1/3190 (0.0%)
13	H	0.38	0/1236	0.56	0/1661
14	I	0.39	0/1807	0.55	0/2432
15	J	0.38	0/1794	0.58	0/2425
16	K	0.40	0/1514	0.57	1/2039 (0.0%)
17	Z	0.36	0/1684	0.51	0/2259
18	M	0.31	0/1365	0.60	0/1831
19	N	0.39	0/1564	0.59	0/2102
20	O	0.37	0/1068	0.52	0/1438
21	Q	0.38	0/831	0.56	0/1097
22	R	0.43	0/680	0.59	0/905
24	a	0.46	0/1757	0.56	0/2354
25	b	0.41	0/1585	0.52	0/2128
26	c	0.42	0/1443	0.59	0/1944
27	d	0.38	0/1465	0.55	0/1965
28	e	0.40	0/1236	0.57	1/1650 (0.1%)
29	f	0.42	0/1468	0.58	1/1973 (0.1%)
30	g	0.40	0/1300	0.54	0/1743
31	h	0.38	0/781	0.54	0/1058
32	i	0.41	0/996	0.54	0/1340
33	j	0.37	0/521	0.50	0/691
34	k	0.42	0/979	0.59	0/1321
35	l	0.35	0/995	0.56	1/1329 (0.1%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
36	m	0.39	0/1118	0.58	0/1497
37	n	0.41	0/1204	0.65	3/1612 (0.2%)
38	o	0.34	0/473	0.61	0/629
39	p	0.38	0/745	0.55	0/1001
40	q	0.43	0/880	0.55	0/1182
41	r	0.38	0/1033	0.54	0/1383
42	s	0.46	0/868	0.54	0/1168
43	t	0.45	0/871	0.66	2/1164 (0.2%)
44	u	0.36	0/978	0.55	0/1301
45	v	0.34	0/759	0.57	0/1009
46	w	0.45	0/680	0.61	0/901
47	x	0.34	0/614	0.53	0/822
48	y	0.39	0/443	0.59	0/588
49	z	0.36	0/414	0.50	0/551
All	All	0.63	0/141860	0.82	135/208602 (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	1
7	W	0	10
8	V	0	2
10	E	0	1
11	F	0	2
14	I	0	2
15	J	0	2
16	K	0	1
18	M	0	2
23	S	0	1
29	f	0	2
37	n	0	3
38	o	0	1
44	u	0	1
All	All	0	34

There are no bond length outliers.

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3217	C	N1-C2-O2	11.39	125.73	118.90
1	A	3217	C	C2-N1-C1'	10.59	130.45	118.80
43	t	81	CYS	CA-CB-SG	10.48	132.87	114.00
1	A	3217	C	N3-C2-O2	-9.21	115.45	121.90
1	A	2550	U	C2-N1-C1'	8.35	127.72	117.70

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	W	134	LEU	Peptide
5	X	7	PHE	Peptide
4	Y	325	SER	Peptide
4	Y	326	CYS	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%)	99 (79%)	23 (18%)	4 (3%)	3	25
5	X	230/245 (94%)	222 (96%)	8 (4%)	0	100	100
6	L	53/165 (32%)	48 (91%)	5 (9%)	0	100	100
7	W	373/640 (58%)	313 (84%)	53 (14%)	7 (2%)	6	34
8	V	388/518 (75%)	332 (86%)	52 (13%)	4 (1%)	13	46
9	D	244/254 (96%)	227 (93%)	17 (7%)	0	100	100
10	E	382/387 (99%)	357 (94%)	24 (6%)	1 (0%)	37	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	F	359/362 (99%)	328 (91%)	28 (8%)	3 (1%)	16	51
12	G	287/297 (97%)	266 (93%)	20 (7%)	1 (0%)	37	68
13	H	151/176 (86%)	144 (95%)	7 (5%)	0	100	100
14	I	218/244 (89%)	204 (94%)	13 (6%)	1 (0%)	25	59
15	J	225/256 (88%)	215 (96%)	9 (4%)	1 (0%)	30	64
16	K	186/191 (97%)	173 (93%)	13 (7%)	0	100	100
17	Z	197/221 (89%)	187 (95%)	10 (5%)	0	100	100
18	M	166/174 (95%)	153 (92%)	13 (8%)	0	100	100
19	N	191/199 (96%)	170 (89%)	20 (10%)	1 (0%)	25	59
20	O	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
21	Q	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
22	R	86/92 (94%)	80 (93%)	6 (7%)	0	100	100
24	a	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
25	b	195/199 (98%)	187 (96%)	8 (4%)	0	100	100
26	c	181/184 (98%)	167 (92%)	14 (8%)	0	100	100
27	d	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
28	e	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
29	f	168/172 (98%)	156 (93%)	10 (6%)	2 (1%)	11	43
30	g	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
31	h	95/121 (78%)	89 (94%)	6 (6%)	0	100	100
32	i	130/137 (95%)	127 (98%)	3 (2%)	0	100	100
33	j	59/155 (38%)	56 (95%)	2 (3%)	1 (2%)	7	36
34	k	119/142 (84%)	110 (92%)	9 (8%)	0	100	100
35	l	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
36	m	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
37	n	146/149 (98%)	129 (88%)	14 (10%)	3 (2%)	5	32
38	o	56/59 (95%)	51 (91%)	4 (7%)	1 (2%)	7	35
39	p	94/105 (90%)	90 (96%)	4 (4%)	0	100	100
40	q	105/113 (93%)	96 (91%)	9 (9%)	0	100	100
41	r	124/130 (95%)	120 (97%)	4 (3%)	0	100	100
42	s	104/107 (97%)	99 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	t	107/121 (88%)	101 (94%)	6 (6%)	0	100	100
44	u	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
45	v	96/100 (96%)	86 (90%)	9 (9%)	1 (1%)	13	46
46	w	82/88 (93%)	72 (88%)	10 (12%)	0	100	100
47	x	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
48	y	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
49	z	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
All	All	7192/8490 (85%)	6643 (92%)	518 (7%)	31 (0%)	32	64

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	W	135	ILE
8	V	95	VAL
8	V	97	LEU
11	F	339	LEU
12	G	259	LYS

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Y	110/323 (34%)	107 (97%)	3 (3%)	40	65
5	X	186/211 (88%)	186 (100%)	0	100	100
6	L	30/65 (46%)	30 (100%)	0	100	100
7	W	317/555 (57%)	310 (98%)	7 (2%)	47	70
8	V	332/467 (71%)	328 (99%)	4 (1%)	67	82
9	D	189/196 (96%)	188 (100%)	1 (0%)	86	93
10	E	317/323 (98%)	315 (99%)	2 (1%)	84	91
11	F	288/289 (100%)	285 (99%)	3 (1%)	73	84
12	G	238/245 (97%)	234 (98%)	4 (2%)	56	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	H	131/153 (86%)	130 (99%)	1 (1%)	79	88
14	I	185/205 (90%)	183 (99%)	2 (1%)	70	83
15	J	182/208 (88%)	181 (100%)	1 (0%)	86	93
16	K	168/171 (98%)	167 (99%)	1 (1%)	84	91
17	Z	175/187 (94%)	170 (97%)	5 (3%)	37	64
18	M	146/150 (97%)	145 (99%)	1 (1%)	81	89
19	N	153/159 (96%)	152 (99%)	1 (1%)	81	89
20	O	107/109 (98%)	107 (100%)	0	100	100
21	Q	87/91 (96%)	87 (100%)	0	100	100
22	R	69/72 (96%)	67 (97%)	2 (3%)	37	64
24	a	175/176 (99%)	171 (98%)	4 (2%)	45	69
25	b	160/162 (99%)	158 (99%)	2 (1%)	65	81
26	c	140/146 (96%)	139 (99%)	1 (1%)	81	89
27	d	150/151 (99%)	148 (99%)	2 (1%)	65	81
28	e	125/154 (81%)	125 (100%)	0	100	100
29	f	155/156 (99%)	152 (98%)	3 (2%)	52	73
30	g	136/137 (99%)	131 (96%)	5 (4%)	29	58
31	h	84/107 (78%)	84 (100%)	0	100	100
32	i	102/105 (97%)	102 (100%)	0	100	100
33	j	54/129 (42%)	54 (100%)	0	100	100
34	k	104/118 (88%)	104 (100%)	0	100	100
35	l	108/110 (98%)	107 (99%)	1 (1%)	75	86
36	m	115/116 (99%)	115 (100%)	0	100	100
37	n	118/119 (99%)	116 (98%)	2 (2%)	56	75
38	o	46/47 (98%)	46 (100%)	0	100	100
39	p	81/88 (92%)	80 (99%)	1 (1%)	67	82
40	q	92/97 (95%)	91 (99%)	1 (1%)	70	83
41	r	108/111 (97%)	105 (97%)	3 (3%)	38	65
42	s	90/91 (99%)	89 (99%)	1 (1%)	70	83
43	t	94/103 (91%)	91 (97%)	3 (3%)	34	62
44	u	104/105 (99%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	v	78/82 (95%)	78 (100%)	0	100	100
46	w	69/71 (97%)	65 (94%)	4 (6%)	17	44
47	x	67/69 (97%)	67 (100%)	0	100	100
48	y	45/46 (98%)	44 (98%)	1 (2%)	47	70
49	z	46/116 (40%)	46 (100%)	0	100	100
All	All	6056/7091 (85%)	5984 (99%)	72 (1%)	66	82

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	n	120	ASN
48	y	43	ASN
40	q	79	ARG
43	t	47	CYS
13	H	166	LYS

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

Mol	Chain	Res	Type
18	M	109	HIS
32	i	98	ASN
19	N	25	HIS
25	b	55	HIS
37	n	74	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3198/3396 (94%)	642 (20%)	33 (1%)
2	B	120/121 (99%)	16 (13%)	0
3	C	157/158 (99%)	28 (17%)	1 (0%)
All	All	3475/3675 (94%)	686 (19%)	34 (0%)

5 of 686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	A
1	A	22	G

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

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3218	A
1	A	3228	C
1	A	3353	G
1	A	1576	G
1	A	1554	U

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no 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

This section contains visualisations of the EMDB entry EMD-0374. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

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



## 7 Map analysis ⓘ

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

### 7.1 Map-value distribution ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

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

## 9 Map-model fit

This section was not generated.