



## Full wwPDB EM Validation Report ⓘ

Mar 2, 2025 – 02:41 PM JST

PDB ID : 8ZDD  
EMDB ID : EMD-39958  
Title : Cryo-EM structure of the human ubiquitylated pre-40S ribosome with R1OK3  
(without NOB1)  
Authors : Huang, Z.; Wang, M.; Li, Y.; Beckmann, R.; Cheng, J.  
Deposited on : 2024-05-01  
Resolution : 3.70 Å(reported)

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 : **FAILED**  
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) : 2.41.2

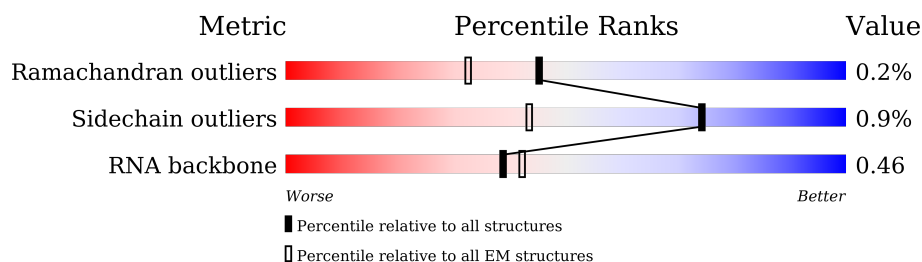
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.70 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.





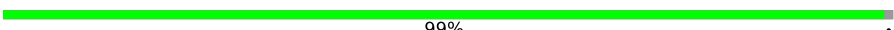

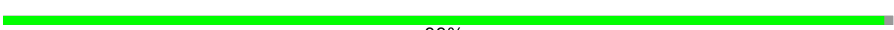





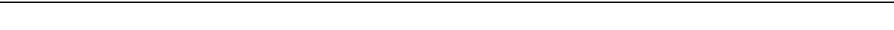

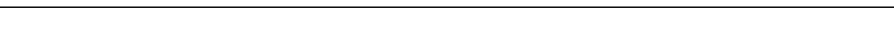
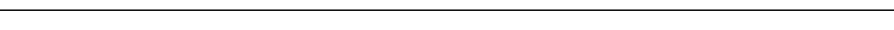



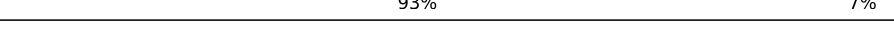

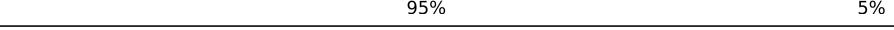
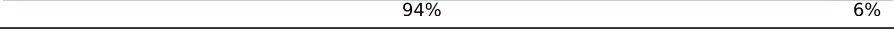
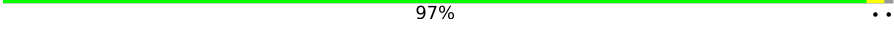



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	1873	
2	R	135	
3	A	295	
4	B	264	
5	C	293	
6	E	263	
7	G	249	
8	H	194	
9	I	208	


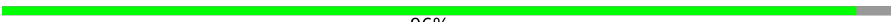

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Mol	Chain	Length	Quality of chain
10	J	194	 92% 7%
11	L	158	 95% ..
12	N	151	 99% .
13	O	151	 89% 11%
14	V	83	 99% .
15	W	130	 96% ..
16	X	143	 97% ..
17	Y	133	 91% 7%
18	b	84	 98% .
19	x	252	 71% 29%
20	u	804	 76% 24%
21	t	475	 13% 87%
22	d	56	 98% .
23	D	243	 88% 7%
24	F	204	 89% 7%
25	K	165	 56% 42%
26	M	132	 93% 7%
27	P	145	 83% 17%
28	Q	146	 95% 5%
29	S	152	 94% 6%
30	T	145	 97% ..
31	U	119	 84% 15%
32	Z	125	 58% 42%
33	c	69	 87% 12%
34	g	317	 99% .

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Mol	Chain	Length	Quality of chain
35	p	519	 75%25%
36	i	76	 96%.
36	j	76	 96%.

## 2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 81515 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1652	Total	C	N	O	P	0	0
			35283	15748	6344	11540	1651		

- Molecule 2 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	122	Total	C	N	O	S	0	0
			990	621	184	182	3		

- Molecule 3 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	216	Total	C	N	O	S	0	0
			1705	1083	299	315	8		

- Molecule 4 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 7 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 9 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 11 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 12 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 13 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	135	Total	C	N	O	S	0	0
			1009	618	198	187	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 16 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 17 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 18 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 19 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	178	Total	C	N	O	0	0
			880	524	178	178		

- Molecule 20 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	615	Total	C	N	O	S	0	0
			4954	3179	885	866	24		

- Molecule 21 is a protein called Protein LTV1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	t	61	Total	C	N	O	0	0
			517	316	107	94		

- Molecule 22 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 23 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 24 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 25 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	K	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 26 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 27 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 28 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 29 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 30 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 31 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 32 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 35 is a protein called Serine/threonine-protein kinase RIO3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	389	Total	C	N	O	S	0	0
			2419	1468	462	483	6		

- Molecule 36 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	i	73	Total	C	N	O	0	0
			361	215	73	73		
36	j	73	Total	C	N	O	0	0
			361	215	73	73		

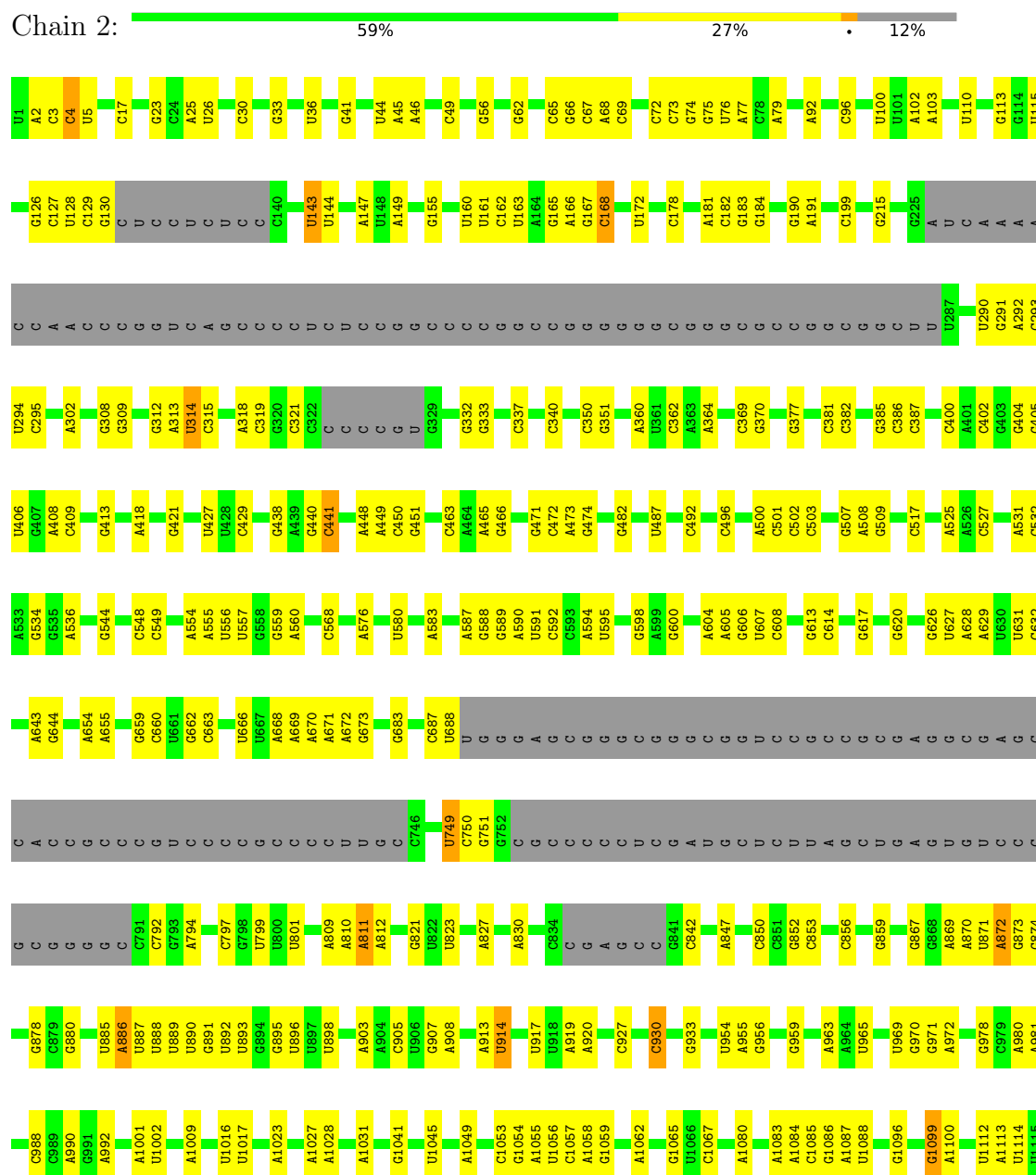
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

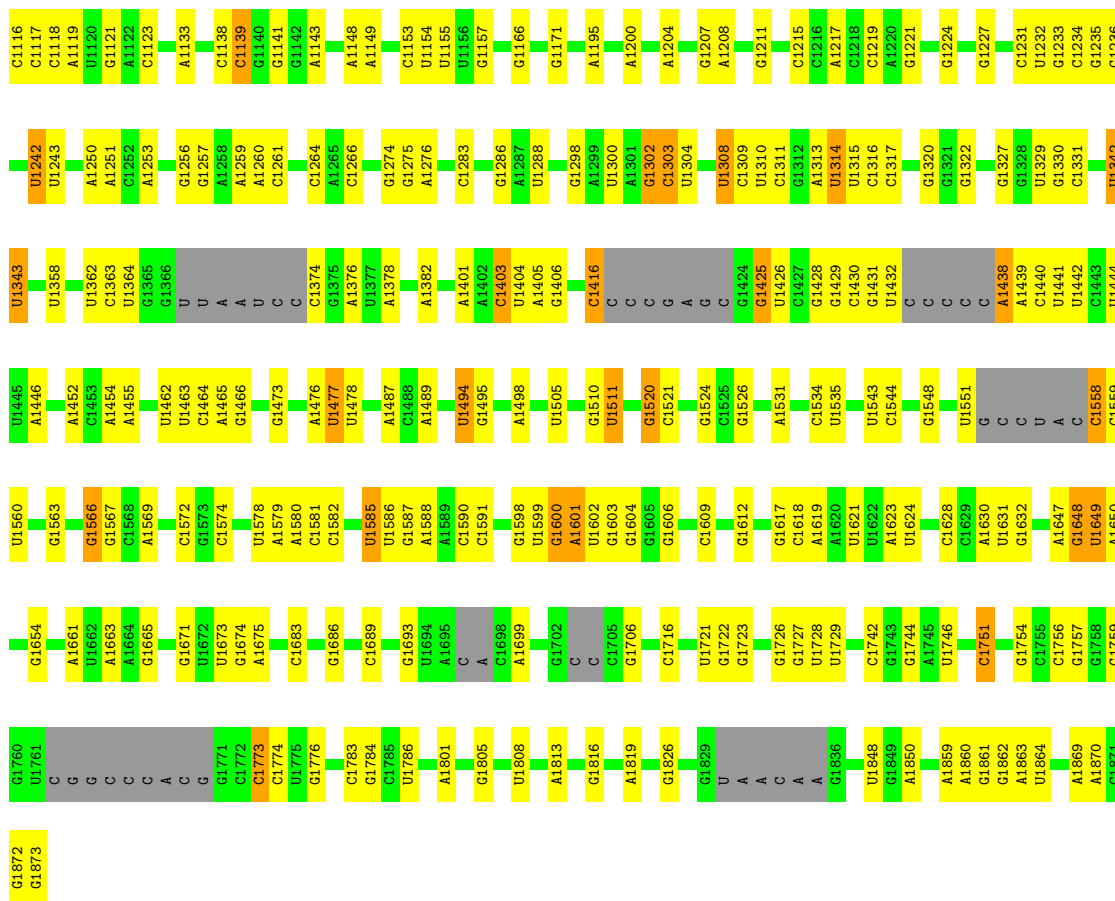
Mol	Chain	Residues	Atoms		AltConf
37	d	1	Total	Zn	0
			1	1	

### 3 Residue-property plots

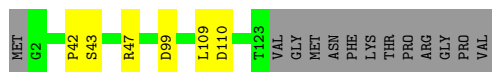
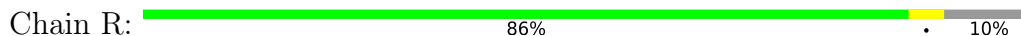
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: 18S rRNA

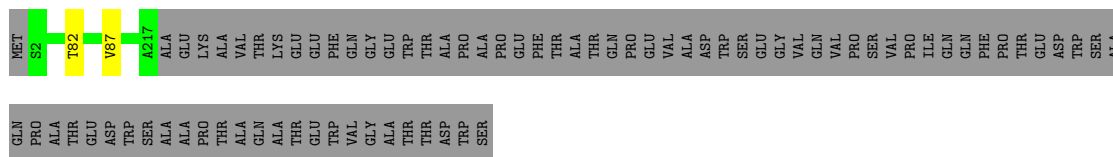




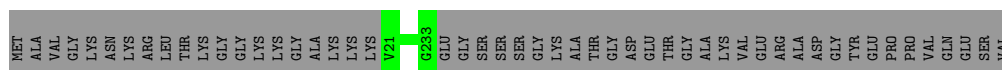
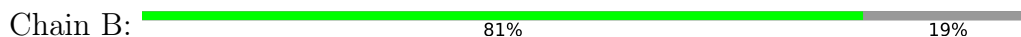
- Molecule 2: Small ribosomal subunit protein eS17



- Molecule 3: Small ribosomal subunit protein uS2

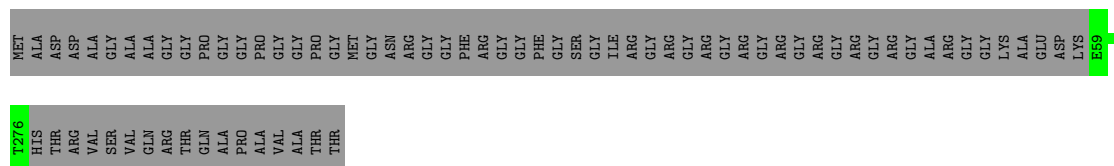


- Molecule 4: Small ribosomal subunit protein eS1



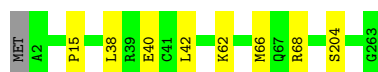
- Molecule 5: Small ribosomal subunit protein uS5

Chain C:  74% 26%



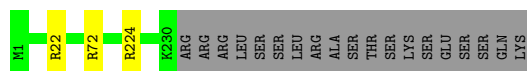
- Molecule 6: Small ribosomal subunit protein eS4, X isoform

Chain E:  97% .



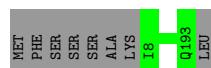
- Molecule 7: Small ribosomal subunit protein eS6

Chain G:  91% 8%



- Molecule 8: Small ribosomal subunit protein eS7

Chain H:  96% .



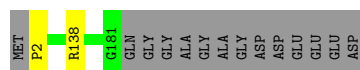
- Molecule 9: Small ribosomal subunit protein eS8

Chain I:  97% ..



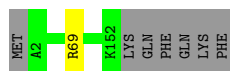
- Molecule 10: Small ribosomal subunit protein uS4

Chain J:  92% 7%



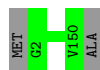
- Molecule 11: Small ribosomal subunit protein uS17

Chain L:  95% ..



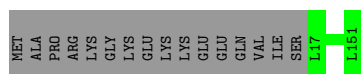
- Molecule 12: Small ribosomal subunit protein uS15

Chain N: 99% .



- Molecule 13: Small ribosomal subunit protein uS11

Chain O: 89% 11%



- Molecule 14: Small ribosomal subunit protein eS21

Chain V: 99% .



- Molecule 15: Small ribosomal subunit protein uS8

Chain W: 96% ..



- Molecule 16: Small ribosomal subunit protein uS12

Chain X: 97% ..



- Molecule 17: Small ribosomal subunit protein eS24

Chain Y: 91% 7%



- Molecule 18: Small ribosomal subunit protein eS27

Chain b: 98% .




- Molecule 22: Small ribosomal subunit protein uS14

Chain d:  98%



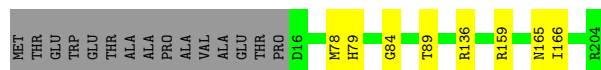
- Molecule 23: Small ribosomal subunit protein uS3

Chain D:  88%



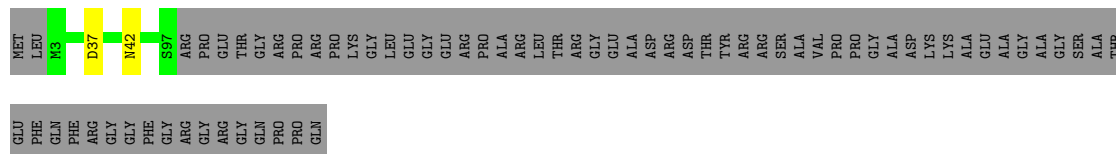
- Molecule 24: Small ribosomal subunit protein uS7

Chain F:  89%



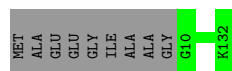
- Molecule 25: Small ribosomal subunit protein eS10

Chain K:  56%




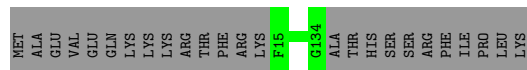
- Molecule 26: Small ribosomal subunit protein eS12

Chain M:  93%



- Molecule 27: Small ribosomal subunit protein uS19

Chain P:  83%



- Molecule 28: Small ribosomal subunit protein uS9

Chain Q:  95%



MET ASP LEU VAL GLY VAL ALA SER PRO GLU PRO GLY THR ALA ALA TRP GLY PRO SER LYS CYS PRO TRP ALA TLE PRO GLN ASN THR TLE SER CYS SER LEU ASP VAL MET SER GLU GLN LEU ALA LYS GLU GLN GLU GLU GLU VAL ALA VAL PHE PRO GLU VAL ALA

VAL ALA PHE LEU LYS PRO PHE TLE THR GLY GLU PRO ASN ASP THR SER S76 S227 THR ALA GLU LYS T233 S469 GLY LEU ASN THR TLE THR ALA ASP ASN GLU ALA ASP PHE LEU ALA GLU TLE GLU ALA LEU GLU LYS MET ASN GLU ASP HIS VAL GLN LYS ASN GLY ARG LYS ALA

ALA SER PHE LEU LYS ASP ASP GLY ASP PRO PRO LEU LEU TYR ASP GLU

● Molecule 36: Ubiquitin



H1 L73 ARG GLY GLY

● Molecule 36: Ubiquitin



H1 L73 ARG GLY GLY

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34363	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	2	0.61	0/39452	1.04	132/61476 (0.2%)
2	R	0.35	0/1002	0.78	3/1345 (0.2%)
3	A	0.39	0/1742	0.62	0/2367
4	B	0.29	0/1756	0.56	0/2350
5	C	0.43	0/1726	0.65	0/2332
6	E	0.48	0/2118	0.68	0/2849
7	G	0.33	0/1885	0.65	0/2510
8	H	0.29	0/1524	0.57	0/2042
9	I	0.43	0/1711	0.67	0/2282
10	J	0.42	0/1524	0.67	0/2035
11	L	0.49	0/1250	0.62	0/1673
12	N	0.34	0/1226	0.57	0/1649
13	O	0.29	0/1022	0.62	0/1372
14	V	0.38	0/631	0.67	0/844
15	W	0.48	0/1051	0.71	1/1406 (0.1%)
16	X	0.44	0/1116	0.69	1/1490 (0.1%)
17	Y	0.41	0/1031	0.65	0/1370
18	b	0.32	0/653	0.61	0/876
19	x	0.25	0/879	0.41	0/1223
20	u	0.30	0/5076	0.59	1/6860 (0.0%)
21	t	0.32	0/518	0.62	0/677
22	d	0.36	0/470	0.62	0/623
23	D	0.42	0/1780	0.70	1/2397 (0.0%)
24	F	0.31	0/1516	0.60	0/2037
25	K	0.32	0/824	0.64	1/1112 (0.1%)
26	M	0.25	0/963	0.52	0/1291
27	P	0.31	0/1003	0.65	0/1341
28	Q	0.36	0/1126	0.67	0/1506
29	S	0.27	0/1202	0.60	0/1610
30	T	0.31	0/1142	0.62	0/1530
31	U	0.36	0/813	0.66	0/1092
32	Z	0.28	0/580	0.60	0/780

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.27	0/481	0.69	1/643 (0.2%)
34	g	0.28	0/2497	0.54	0/3399
35	p	0.31	0/2444	0.51	0/3338
36	i	0.24	0/360	0.44	0/500
36	j	0.24	0/360	0.43	0/500
All	All	0.49	0/86454	0.85	141/124727 (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
9	I	0	1
24	F	0	1
30	T	0	1
All	All	0	3

There are no bond length outliers.

All (141) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	914	U	C5-C4-O4	21.37	138.72	125.90
1	2	914	U	N3-C4-O4	-20.54	105.02	119.40
1	2	872	A	N1-C6-N6	-12.11	111.33	118.60
1	2	1343	U	C2-N1-C1'	11.14	131.07	117.70
1	2	293	C	N1-C2-O2	10.78	125.37	118.90
1	2	293	C	C2-N1-C1'	10.23	130.05	118.80
1	2	1774	C	N3-C2-O2	-9.83	115.02	121.90
1	2	293	C	N3-C2-O2	-9.11	115.52	121.90
1	2	1343	U	N3-C2-O2	-8.94	115.94	122.20
1	2	853	C	C2-N1-C1'	8.82	128.50	118.80
1	2	1374	C	N3-C2-O2	-8.28	116.11	121.90
1	2	1016	U	N1-C2-O2	8.27	128.59	122.80
1	2	1751	C	C2-N1-C1'	8.07	127.68	118.80
1	2	1374	C	N1-C2-O2	8.05	123.73	118.90
1	2	1343	U	N1-C2-O2	7.98	128.39	122.80
1	2	1016	U	N3-C2-O2	-7.85	116.70	122.20
1	2	853	C	N1-C2-O2	7.83	123.60	118.90
1	2	1139	C	N3-C2-O2	-7.75	116.48	121.90
1	2	1016	U	C2-N1-C1'	7.56	126.77	117.70
1	2	1628	C	N3-C2-O2	-7.55	116.61	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1311	C	N1-C2-O2	7.46	123.37	118.90
1	2	1139	C	N1-C2-O2	7.34	123.30	118.90
1	2	1590	C	N1-C2-O2	7.23	123.24	118.90
1	2	872	A	C5-C6-N6	7.20	129.46	123.70
1	2	1343	U	C6-N1-C1'	-7.20	111.12	121.20
1	2	1751	C	N1-C2-O2	7.10	123.16	118.90
1	2	293	C	C6-N1-C1'	-7.06	112.33	120.80
2	R	99	ASP	CB-CG-OD1	6.99	124.59	118.30
1	2	1624	U	C2-N1-C1'	6.94	126.03	117.70
1	2	1628	C	C6-N1-C2	-6.89	117.54	120.30
1	2	293	C	C6-N1-C2	-6.72	117.61	120.30
1	2	1123	C	C2-N1-C1'	6.61	126.07	118.80
1	2	749	U	C2-N1-C1'	6.58	125.59	117.70
1	2	1314	U	C2-N1-C1'	6.53	125.54	117.70
1	2	1551	U	C2-N1-C1'	6.53	125.53	117.70
1	2	853	C	N3-C2-O2	-6.49	117.36	121.90
1	2	1591	C	C6-N1-C2	-6.45	117.72	120.30
1	2	853	C	C6-N1-C1'	-6.45	113.07	120.80
1	2	811	A	C2'-C3'-O3'	6.43	123.99	113.70
1	2	914	U	C4-C5-C6	-6.43	115.84	119.70
1	2	1139	C	C2-N1-C1'	6.42	125.86	118.80
1	2	1624	U	N1-C2-O2	6.41	127.29	122.80
1	2	1403	C	P-O3'-C3'	6.38	127.36	119.70
1	2	1219	C	N1-C2-O2	6.37	122.72	118.90
1	2	1310	U	N1-C2-O2	6.23	127.16	122.80
1	2	914	U	C2-N3-C4	6.20	130.72	127.00
1	2	1477	U	N1-C2-O2	6.15	127.11	122.80
1	2	1477	U	C2-N1-C1'	6.15	125.08	117.70
1	2	856	C	N1-C2-O2	6.12	122.57	118.90
1	2	49	C	N3-C2-O2	-6.11	117.62	121.90
2	R	110	ASP	CB-CG-OD1	6.02	123.72	118.30
1	2	1591	C	N1-C2-O2	5.97	122.48	118.90
1	2	1648	G	P-O3'-C3'	5.96	126.85	119.70
1	2	1591	C	N3-C2-O2	-5.96	117.73	121.90
1	2	1494	U	P-O3'-C3'	5.93	126.82	119.70
33	c	37	ASP	CB-CG-OD1	5.92	123.62	118.30
1	2	369	C	N1-C2-O2	5.91	122.45	118.90
1	2	850	C	N1-C2-O2	5.89	122.43	118.90
1	2	1585	U	P-O3'-C3'	5.88	126.76	119.70
1	2	1308	U	P-O3'-C3'	5.88	126.75	119.70
1	2	1520	G	N1-C6-O6	-5.87	116.38	119.90
1	2	1511	U	C2-N1-C1'	5.87	124.75	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	427	U	N3-C2-O2	-5.86	118.10	122.20
1	2	1751	C	C6-N1-C1'	-5.86	113.77	120.80
1	2	314	U	N3-C2-O2	-5.85	118.11	122.20
25	K	37	ASP	CB-CG-OD1	5.81	123.53	118.30
1	2	1310	U	C2-N1-C1'	5.81	124.67	117.70
1	2	1600	G	C4-N9-C1'	5.81	134.05	126.50
1	2	1558	C	P-O3'-C3'	5.79	126.65	119.70
1	2	1566	G	O5'-P-OP1	5.78	117.64	110.70
1	2	856	C	N3-C2-O2	-5.75	117.87	121.90
1	2	402	C	N1-C2-O2	5.75	122.35	118.90
1	2	1139	C	C6-N1-C2	-5.74	118.00	120.30
1	2	1774	C	N1-C2-O2	5.71	122.33	118.90
1	2	1311	C	N3-C2-O2	-5.69	117.91	121.90
1	2	1773	C	N1-C2-O2	5.67	122.30	118.90
1	2	1551	U	N3-C2-O2	-5.67	118.23	122.20
1	2	1624	U	N3-C2-O2	-5.66	118.24	122.20
1	2	1591	C	C2-N1-C1'	5.65	125.02	118.80
1	2	872	A	N1-C2-N3	-5.63	126.48	129.30
1	2	1551	U	N1-C2-O2	5.63	126.74	122.80
1	2	1303	C	N1-C2-O2	5.62	122.27	118.90
1	2	1601	A	P-O3'-C3'	5.62	126.45	119.70
1	2	168	C	N1-C2-O2	5.61	122.27	118.90
1	2	17	C	C6-N1-C2	-5.61	118.06	120.30
1	2	527	C	N3-C2-O2	-5.61	117.97	121.90
1	2	1123	C	N1-C2-O2	5.56	122.24	118.90
1	2	1343	U	C6-N1-C2	-5.56	117.67	121.00
1	2	1242	U	N1-C2-O2	5.56	126.69	122.80
1	2	1716	C	C2-N1-C1'	5.56	124.91	118.80
1	2	1683	C	N1-C2-O2	5.54	122.22	118.90
2	R	109	LEU	C-N-CA	5.54	135.54	121.70
1	2	850	C	N3-C2-O2	-5.53	118.03	121.90
1	2	1123	C	C6-N1-C2	-5.52	118.09	120.30
1	2	914	U	N1-C2-N3	-5.50	111.60	114.90
1	2	4	C	C6-N1-C2	-5.49	118.10	120.30
1	2	162	C	C6-N1-C2	-5.49	118.10	120.30
1	2	369	C	C2-N1-C1'	5.47	124.81	118.80
1	2	1310	U	N3-C2-O2	-5.46	118.38	122.20
1	2	1600	G	N3-C4-N9	5.45	129.27	126.00
1	2	1600	G	N3-C4-C5	-5.42	125.89	128.60
1	2	1099	G	O4'-C1'-N9	5.40	112.52	108.20
1	2	1342	U	P-O3'-C3'	5.39	126.17	119.70
1	2	659	G	C4-N9-C1'	5.37	133.49	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1343	U	C5-C6-N1	5.36	125.38	122.70
1	2	1438	A	P-O3'-C3'	5.34	126.11	119.70
1	2	1416	C	C2-N1-C1'	5.34	124.67	118.80
1	2	666	U	C2-N1-C1'	5.33	124.10	117.70
1	2	1628	C	N1-C2-N3	5.33	122.93	119.20
1	2	178	C	N1-C2-O2	5.32	122.09	118.90
1	2	1628	C	C6-N1-C1'	5.32	127.18	120.80
1	2	1416	C	N1-C2-O2	5.29	122.08	118.90
1	2	441	C	C2-N1-C1'	5.28	124.61	118.80
1	2	1590	C	N3-C2-O2	-5.27	118.21	121.90
1	2	5	U	C5-C6-N1	5.26	125.33	122.70
1	2	1219	C	N3-C2-O2	-5.24	118.23	121.90
20	u	96	LEU	CA-CB-CG	5.21	127.29	115.30
1	2	930	C	N1-C2-O2	5.20	122.02	118.90
1	2	1774	C	C6-N1-C2	-5.18	118.23	120.30
1	2	1673	U	P-O3'-C3'	5.18	125.91	119.70
1	2	143	U	P-O3'-C3'	5.17	125.91	119.70
1	2	532	C	C2-N1-C1'	5.17	124.49	118.80
1	2	886	A	C4-N9-C1'	5.17	135.60	126.30
1	2	199	C	N1-C2-O2	5.16	122.00	118.90
1	2	749	U	N1-C2-O2	5.16	126.41	122.80
1	2	1649	U	C5-C6-N1	5.15	125.28	122.70
1	2	1759	G	N1-C2-N2	-5.14	111.58	116.20
16	X	60	LYS	C-N-CA	5.12	134.50	121.70
1	2	1302	G	P-O3'-C3'	5.11	125.83	119.70
1	2	1477	U	N3-C2-O2	-5.10	118.63	122.20
1	2	1649	U	P-O3'-C3'	5.09	125.81	119.70
1	2	580	U	N1-C2-O2	5.09	126.36	122.80
1	2	965	U	N1-C2-O2	5.09	126.36	122.80
1	2	1053	C	C2-N1-C1'	5.08	124.39	118.80
23	D	14	ASP	CB-CG-OD1	5.06	122.86	118.30
1	2	1219	C	C2-N1-C1'	5.06	124.36	118.80
1	2	162	C	C5-C6-N1	5.05	123.53	121.00
1	2	662	G	C3'-C2'-C1'	-5.04	97.47	101.50
1	2	1425	G	P-O3'-C3'	5.04	125.75	119.70
15	W	104	LEU	CA-CB-CG	5.02	126.84	115.30
1	2	168	C	N3-C2-O2	-5.00	118.40	121.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	F	165	ASN	Peptide
9	I	140	LYS	Peptide
30	T	36	THR	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	
2	R	120/135 (89%)	108 (90%)	11 (9%)	1 (1%)	16	49
3	A	214/295 (72%)	205 (96%)	9 (4%)	0	100	100
4	B	211/264 (80%)	203 (96%)	8 (4%)	0	100	100
5	C	216/293 (74%)	206 (95%)	10 (5%)	0	100	100
6	E	260/263 (99%)	246 (95%)	13 (5%)	1 (0%)	30	62
7	G	228/249 (92%)	220 (96%)	8 (4%)	0	100	100
8	H	184/194 (95%)	182 (99%)	2 (1%)	0	100	100
9	I	203/208 (98%)	197 (97%)	6 (3%)	0	100	100
10	J	178/194 (92%)	166 (93%)	11 (6%)	1 (1%)	22	54
11	L	149/158 (94%)	144 (97%)	5 (3%)	0	100	100
12	N	147/151 (97%)	142 (97%)	5 (3%)	0	100	100
13	O	133/151 (88%)	127 (96%)	6 (4%)	0	100	100
14	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
15	W	127/130 (98%)	125 (98%)	1 (1%)	1 (1%)	16	49
16	X	139/143 (97%)	134 (96%)	4 (3%)	1 (1%)	19	51
17	Y	122/133 (92%)	116 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	b	80/84 (95%)	77 (96%)	3 (4%)	0	100	100
19	x	176/252 (70%)	171 (97%)	5 (3%)	0	100	100
20	u	607/804 (76%)	577 (95%)	30 (5%)	0	100	100
21	t	59/475 (12%)	55 (93%)	3 (5%)	1 (2%)	7	36
22	d	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
23	D	223/243 (92%)	214 (96%)	8 (4%)	1 (0%)	30	62
24	F	187/204 (92%)	172 (92%)	13 (7%)	2 (1%)	12	43
25	K	93/165 (56%)	87 (94%)	6 (6%)	0	100	100
26	M	121/132 (92%)	117 (97%)	4 (3%)	0	100	100
27	P	118/145 (81%)	118 (100%)	0	0	100	100
28	Q	137/146 (94%)	129 (94%)	8 (6%)	0	100	100
29	S	141/152 (93%)	130 (92%)	11 (8%)	0	100	100
30	T	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
31	U	99/119 (83%)	95 (96%)	4 (4%)	0	100	100
32	Z	70/125 (56%)	68 (97%)	2 (3%)	0	100	100
33	c	59/69 (86%)	55 (93%)	4 (7%)	0	100	100
34	g	312/317 (98%)	290 (93%)	22 (7%)	0	100	100
35	p	385/519 (74%)	368 (96%)	17 (4%)	0	100	100
36	i	71/76 (93%)	71 (100%)	0	0	100	100
36	j	71/76 (93%)	71 (100%)	0	0	100	100
All	All	5915/7348 (80%)	5651 (96%)	255 (4%)	9 (0%)	45	72

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	X	61	GLN
23	D	194	PRO
24	F	166	ILE
10	J	138	ARG
15	W	5	ASN
6	E	68	ARG
2	R	42	PRO
24	F	84	GLY
21	t	470	VAL

### 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	
2	R	110/122 (90%)	108 (98%)	2 (2%)	54	71
3	A	180/243 (74%)	178 (99%)	2 (1%)	70	80
4	B	194/231 (84%)	194 (100%)	0	100	100
5	C	184/225 (82%)	184 (100%)	0	100	100
6	E	224/225 (100%)	217 (97%)	7 (3%)	35	57
7	G	200/218 (92%)	197 (98%)	3 (2%)	60	75
8	H	167/174 (96%)	167 (100%)	0	100	100
9	I	178/180 (99%)	176 (99%)	2 (1%)	70	80
10	J	160/168 (95%)	159 (99%)	1 (1%)	84	90
11	L	135/142 (95%)	134 (99%)	1 (1%)	81	88
12	N	130/131 (99%)	130 (100%)	0	100	100
13	O	105/119 (88%)	105 (100%)	0	100	100
14	V	66/67 (98%)	66 (100%)	0	100	100
15	W	112/113 (99%)	110 (98%)	2 (2%)	54	71
16	X	113/115 (98%)	113 (100%)	0	100	100
17	Y	108/115 (94%)	105 (97%)	3 (3%)	38	60
18	b	74/76 (97%)	74 (100%)	0	100	100
20	u	539/705 (76%)	535 (99%)	4 (1%)	81	88
21	t	56/434 (13%)	56 (100%)	0	100	100
22	d	48/49 (98%)	48 (100%)	0	100	100
23	D	189/202 (94%)	181 (96%)	8 (4%)	25	51
24	F	159/170 (94%)	154 (97%)	5 (3%)	35	57
25	K	86/136 (63%)	85 (99%)	1 (1%)	67	79
26	M	104/108 (96%)	104 (100%)	0	100	100
27	P	107/130 (82%)	107 (100%)	0	100	100
28	Q	115/121 (95%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	S	124/132 (94%)	124 (100%)	0	100	100
30	T	114/115 (99%)	112 (98%)	2 (2%)	54	71
31	U	93/107 (87%)	92 (99%)	1 (1%)	70	80
32	Z	64/103 (62%)	64 (100%)	0	100	100
33	c	54/62 (87%)	54 (100%)	0	100	100
34	g	272/275 (99%)	272 (100%)	0	100	100
35	p	136/454 (30%)	136 (100%)	0	100	100
All	All	4700/5967 (79%)	4656 (99%)	44 (1%)	74	84

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	R	43	SER
2	R	47	ARG
3	A	82	THR
3	A	87	VAL
6	E	15	PRO
6	E	38	LEU
6	E	40	GLU
6	E	42	LEU
6	E	62	LYS
6	E	66	MET
6	E	204	SER
7	G	22	ARG
7	G	72	ARG
7	G	224	ARG
9	I	18	ARG
9	I	19	LYS
10	J	2	PRO
11	L	69	ARG
15	W	32	LYS
15	W	33	VAL
17	Y	103	SER
17	Y	104	ARG
17	Y	107	ARG
20	u	128	ARG
20	u	479	ARG
20	u	497	ARG
20	u	499	ARG
23	D	164	VAL

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Mol	Chain	Res	Type
23	D	192	TRP
23	D	193	ASP
23	D	197	LYS
23	D	198	ILE
23	D	201	LYS
23	D	202	LYS
23	D	204	LEU
24	F	78	MET
24	F	79	HIS
24	F	89	THR
24	F	136	ARG
24	F	159	ARG
25	K	42	ASN
30	T	51	ASN
30	T	122	LYS
31	U	79	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	186	ASN
15	W	92	ASN
18	b	49	HIS
20	u	286	ASN
20	u	298	GLN
27	P	32	GLN
29	S	134	GLN
33	c	29	GLN
33	c	45	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1639/1873 (87%)	481 (29%)	35 (2%)

All (481) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C

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Mol	Chain	Res	Type
1	2	4	C
1	2	23	G
1	2	25	A
1	2	26	U
1	2	30	C
1	2	33	G
1	2	36	U
1	2	41	G
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	62	G
1	2	65	C
1	2	66	G
1	2	67	C
1	2	68	A
1	2	69	C
1	2	72	C
1	2	73	C
1	2	74	G
1	2	75	G
1	2	76	U
1	2	77	A
1	2	79	A
1	2	92	A
1	2	96	C
1	2	100	U
1	2	103	A
1	2	110	U
1	2	113	G
1	2	115	U
1	2	126	G
1	2	127	C
1	2	128	U
1	2	129	C
1	2	130	G
1	2	143	U
1	2	144	U
1	2	147	A
1	2	149	A
1	2	155	G

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Mol	Chain	Res	Type
1	2	160	U
1	2	161	U
1	2	163	U
1	2	165	G
1	2	166	A
1	2	167	G
1	2	168	C
1	2	172	U
1	2	181	A
1	2	182	C
1	2	183	G
1	2	184	G
1	2	190	G
1	2	191	A
1	2	215	G
1	2	290	U
1	2	291	G
1	2	292	A
1	2	294	U
1	2	295	C
1	2	302	A
1	2	308	G
1	2	309	G
1	2	312	G
1	2	313	A
1	2	315	C
1	2	318	A
1	2	319	C
1	2	321	C
1	2	332	G
1	2	333	G
1	2	337	C
1	2	340	C
1	2	350	C
1	2	351	G
1	2	360	A
1	2	362	C
1	2	364	A
1	2	370	G
1	2	377	G
1	2	381	C
1	2	382	C

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Mol	Chain	Res	Type
1	2	385	G
1	2	386	C
1	2	387	C
1	2	400	C
1	2	404	G
1	2	405	G
1	2	406	U
1	2	408	A
1	2	409	C
1	2	413	G
1	2	418	A
1	2	421	G
1	2	429	C
1	2	438	G
1	2	441	C
1	2	448	A
1	2	449	A
1	2	450	C
1	2	451	G
1	2	463	C
1	2	466	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	482	G
1	2	487	U
1	2	492	C
1	2	496	C
1	2	500	A
1	2	501	C
1	2	502	C
1	2	503	C
1	2	507	G
1	2	508	A
1	2	509	G
1	2	517	C
1	2	525	A
1	2	531	A
1	2	534	G
1	2	536	A
1	2	544	G

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Mol	Chain	Res	Type
1	2	548	C
1	2	549	C
1	2	555	A
1	2	556	U
1	2	557	U
1	2	559	G
1	2	560	A
1	2	568	C
1	2	576	A
1	2	583	A
1	2	587	A
1	2	588	G
1	2	589	G
1	2	590	A
1	2	591	U
1	2	592	C
1	2	594	A
1	2	595	U
1	2	598	G
1	2	600	G
1	2	605	A
1	2	606	G
1	2	607	U
1	2	608	C
1	2	613	G
1	2	614	C
1	2	617	G
1	2	620	G
1	2	626	G
1	2	627	U
1	2	628	A
1	2	629	A
1	2	632	C
1	2	643	A
1	2	644	G
1	2	654	A
1	2	655	A
1	2	660	C
1	2	663	C
1	2	668	A
1	2	669	A
1	2	670	A

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Mol	Chain	Res	Type
1	2	671	A
1	2	672	A
1	2	673	G
1	2	683	G
1	2	687	C
1	2	688	U
1	2	749	U
1	2	750	C
1	2	751	G
1	2	792	C
1	2	794	A
1	2	797	C
1	2	799	U
1	2	801	U
1	2	809	A
1	2	810	A
1	2	812	A
1	2	821	G
1	2	823	U
1	2	827	A
1	2	830	A
1	2	842	C
1	2	847	A
1	2	852	G
1	2	859	G
1	2	867	G
1	2	869	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	874	G
1	2	878	G
1	2	880	G
1	2	885	U
1	2	886	A
1	2	887	U
1	2	888	U
1	2	889	U
1	2	890	U
1	2	891	G
1	2	892	U

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Mol	Chain	Res	Type
1	2	893	U
1	2	895	G
1	2	896	U
1	2	898	U
1	2	903	A
1	2	905	C
1	2	907	G
1	2	908	A
1	2	913	A
1	2	914	U
1	2	917	U
1	2	919	A
1	2	920	A
1	2	927	C
1	2	930	C
1	2	933	G
1	2	954	U
1	2	955	A
1	2	956	G
1	2	959	G
1	2	963	A
1	2	969	U
1	2	970	G
1	2	971	G
1	2	972	A
1	2	978	G
1	2	981	A
1	2	988	C
1	2	990	A
1	2	992	A
1	2	1001	A
1	2	1002	U
1	2	1009	A
1	2	1017	U
1	2	1023	A
1	2	1027	A
1	2	1028	A
1	2	1031	A
1	2	1041	G
1	2	1045	U
1	2	1049	A
1	2	1054	G

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Mol	Chain	Res	Type
1	2	1055	A
1	2	1056	U
1	2	1057	C
1	2	1058	A
1	2	1059	G
1	2	1062	A
1	2	1065	G
1	2	1067	C
1	2	1080	A
1	2	1083	A
1	2	1084	A
1	2	1085	C
1	2	1086	G
1	2	1087	A
1	2	1088	U
1	2	1096	G
1	2	1099	G
1	2	1100	A
1	2	1112	U
1	2	1113	A
1	2	1114	U
1	2	1116	C
1	2	1117	C
1	2	1118	C
1	2	1119	A
1	2	1121	G
1	2	1133	A
1	2	1138	C
1	2	1139	C
1	2	1141	G
1	2	1143	A
1	2	1148	A
1	2	1149	A
1	2	1153	C
1	2	1154	U
1	2	1155	U
1	2	1157	G
1	2	1166	G
1	2	1171	G
1	2	1195	A
1	2	1200	A
1	2	1204	A

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Mol	Chain	Res	Type
1	2	1207	G
1	2	1208	A
1	2	1211	G
1	2	1215	C
1	2	1217	A
1	2	1221	G
1	2	1224	G
1	2	1227	G
1	2	1232	U
1	2	1233	G
1	2	1234	C
1	2	1235	G
1	2	1236	G
1	2	1242	U
1	2	1243	U
1	2	1250	A
1	2	1251	A
1	2	1253	A
1	2	1257	G
1	2	1259	A
1	2	1260	A
1	2	1261	C
1	2	1264	C
1	2	1266	C
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1283	C
1	2	1286	G
1	2	1288	U
1	2	1298	G
1	2	1300	U
1	2	1302	G
1	2	1303	C
1	2	1304	U
1	2	1308	U
1	2	1309	C
1	2	1313	A
1	2	1314	U
1	2	1315	U
1	2	1317	C
1	2	1320	G

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Mol	Chain	Res	Type
1	2	1322	G
1	2	1327	G
1	2	1329	U
1	2	1331	C
1	2	1343	U
1	2	1358	U
1	2	1362	U
1	2	1363	C
1	2	1364	U
1	2	1376	A
1	2	1378	A
1	2	1382	A
1	2	1401	A
1	2	1404	U
1	2	1405	A
1	2	1406	G
1	2	1416	C
1	2	1426	U
1	2	1428	G
1	2	1429	G
1	2	1430	C
1	2	1431	G
1	2	1432	U
1	2	1439	A
1	2	1441	U
1	2	1442	U
1	2	1444	U
1	2	1446	A
1	2	1452	A
1	2	1454	A
1	2	1455	A
1	2	1462	U
1	2	1463	U
1	2	1465	A
1	2	1466	G
1	2	1473	G
1	2	1476	A
1	2	1477	U
1	2	1478	U
1	2	1487	A
1	2	1489	A
1	2	1494	U

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Mol	Chain	Res	Type
1	2	1495	G
1	2	1498	A
1	2	1505	U
1	2	1510	G
1	2	1511	U
1	2	1520	G
1	2	1521	C
1	2	1524	G
1	2	1526	G
1	2	1531	A
1	2	1535	U
1	2	1543	U
1	2	1544	C
1	2	1548	G
1	2	1559	C
1	2	1560	U
1	2	1563	G
1	2	1566	G
1	2	1567	G
1	2	1569	A
1	2	1572	C
1	2	1574	C
1	2	1578	U
1	2	1579	A
1	2	1580	A
1	2	1581	C
1	2	1582	C
1	2	1585	U
1	2	1586	U
1	2	1587	G
1	2	1588	A
1	2	1598	G
1	2	1599	U
1	2	1600	G
1	2	1601	A
1	2	1602	U
1	2	1603	G
1	2	1604	G
1	2	1606	G
1	2	1609	C
1	2	1612	G
1	2	1617	G

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Mol	Chain	Res	Type
1	2	1618	C
1	2	1619	A
1	2	1621	U
1	2	1623	A
1	2	1630	A
1	2	1631	U
1	2	1632	G
1	2	1647	A
1	2	1649	U
1	2	1650	A
1	2	1654	G
1	2	1661	A
1	2	1663	A
1	2	1665	G
1	2	1671	G
1	2	1674	G
1	2	1675	A
1	2	1686	G
1	2	1689	C
1	2	1693	G
1	2	1699	A
1	2	1706	G
1	2	1721	U
1	2	1722	G
1	2	1723	G
1	2	1727	G
1	2	1728	U
1	2	1729	U
1	2	1742	C
1	2	1744	G
1	2	1746	U
1	2	1751	C
1	2	1754	G
1	2	1756	C
1	2	1757	G
1	2	1773	C
1	2	1776	G
1	2	1783	C
1	2	1784	G
1	2	1786	U
1	2	1801	A
1	2	1805	G

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Mol	Chain	Res	Type
1	2	1808	U
1	2	1813	A
1	2	1816	G
1	2	1819	A
1	2	1826	G
1	2	1848	U
1	2	1850	A
1	2	1859	A
1	2	1860	A
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1869	A
1	2	1870	A
1	2	1872	G
1	2	1873	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	102	A
1	2	143	U
1	2	291	G
1	2	314	U
1	2	332	G
1	2	440	G
1	2	465	A
1	2	473	A
1	2	554	A
1	2	604	A
1	2	631	U
1	2	811	A
1	2	870	A
1	2	980	A
1	2	1231	C
1	2	1256	G
1	2	1302	G
1	2	1308	U
1	2	1316	C
1	2	1330	G
1	2	1342	U

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Mol	Chain	Res	Type
1	2	1403	C
1	2	1425	G
1	2	1430	C
1	2	1438	A
1	2	1440	C
1	2	1464	C
1	2	1494	U
1	2	1534	C
1	2	1558	C
1	2	1585	U
1	2	1601	A
1	2	1648	G
1	2	1649	U
1	2	1726	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.