



wwPDB EM Validation Summary Report ⓘ

Mar 2, 2025 – 02:43 PM JST

PDB ID : 8ZDC
EMDB ID : EMD-39957
Title : Cryo-EM structure of the human ubiquitylated pre-40S ribosome with RIOK3
Authors : Huang, Z.; Wang, M.; Li, Y.; Beckmann, R.; Cheng, J.
Deposited on : 2024-05-01
Resolution : 3.80 Å(reported)

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 : **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

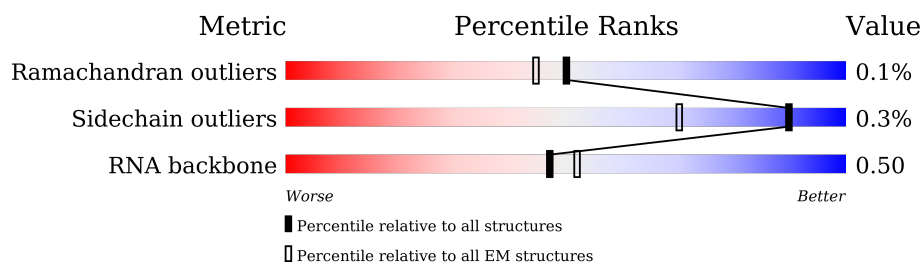
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	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 $\leq 5\%$.

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	

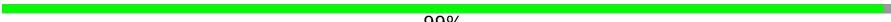



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Mol	Chain	Length	Quality of chain
10	J	194	
11	L	158	
12	N	151	
13	O	151	
14	V	83	
15	W	130	
16	X	143	
17	Y	133	
18	b	84	
19	x	252	
20	y	412	
21	u	804	
22	t	475	
23	d	56	
24	D	243	
25	F	204	
26	K	165	
27	M	132	
28	P	145	
29	Q	146	
30	S	152	
31	T	145	
32	U	119	
33	Z	125	
34	c	69	

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Mol	Chain	Length	Quality of chain
35	g	317	 99%.
36	p	519	 75%25%
37	i	76	 96%.
37	j	76	 96%.

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 84228 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	1659	Total	C	N	O	P	0	0
			35427	15813	6366	11590	1658		

- 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 RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	y	325	Total	C	N	O	S	0	0
			2568	1622	473	463	10		

- Molecule 21 is a protein called Pre-rRNA-processing protein TSR1 homolog.

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

- Molecule 22 is a protein called Protein LTV1 homolog.

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

- Molecule 23 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 26 is a protein called Small ribosomal subunit protein eS10.

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

- Molecule 27 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 30 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 31 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 32 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 33 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 34 is a protein called Small ribosomal subunit protein eS28.

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

- Molecule 35 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 36 is a protein called Serine/threonine-protein kinase RIO3.

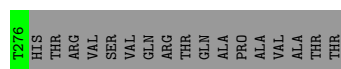
Mol	Chain	Residues	Atoms					AltConf	Trace
36	p	389	Total	C	N	O	S	0	0
			2419	1468	462	483	6		

- Molecule 37 is a protein called Ubiquitin.

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

- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	y	1	Total	Zn	0
			1	1	
38	d	1	Total	Zn	0
			1	1	



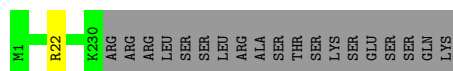
- Molecule 6: Small ribosomal subunit protein eS4, X isoform

Chain E: 98% .



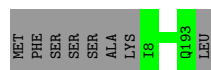
- Molecule 7: Small ribosomal subunit protein eS6

Chain G: 92% 8%



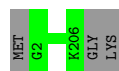
- Molecule 8: Small ribosomal subunit protein eS7

Chain H: 96% .



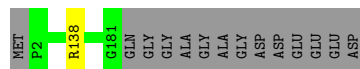
- Molecule 9: Small ribosomal subunit protein eS8

Chain I: 99% .



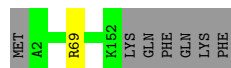
- Molecule 10: Small ribosomal subunit protein uS4

Chain J: 92% . 7%



- Molecule 11: Small ribosomal subunit protein uS17

Chain L: 95% . .



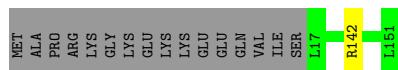
- Molecule 12: Small ribosomal subunit protein uS15

Chain N: 97% ..



- Molecule 13: Small ribosomal subunit protein uS11

Chain O: 89% 11%



- Molecule 14: Small ribosomal subunit protein eS21

Chain V: 99%



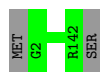
- Molecule 15: Small ribosomal subunit protein uS8

Chain W: 97%



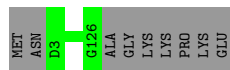
- Molecule 16: Small ribosomal subunit protein uS12

Chain X: 99%



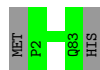
- Molecule 17: Small ribosomal subunit protein eS24

Chain Y: 93% 7%



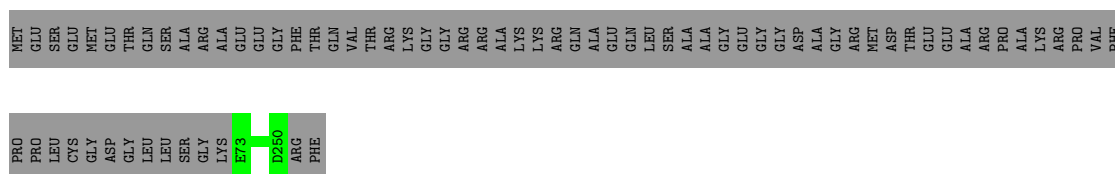
- Molecule 18: Small ribosomal subunit protein eS27

Chain b: 98%

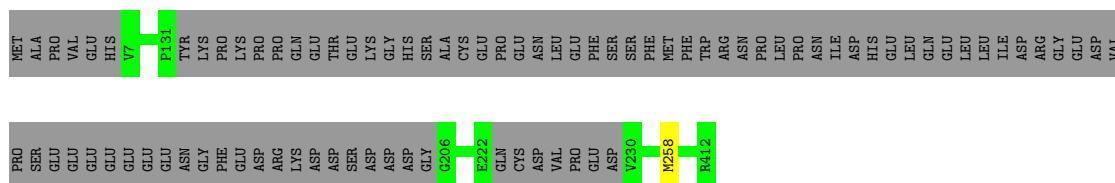
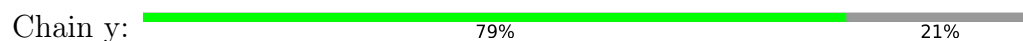


- Molecule 19: RNA-binding protein PNO1

Chain x: 71% 29%



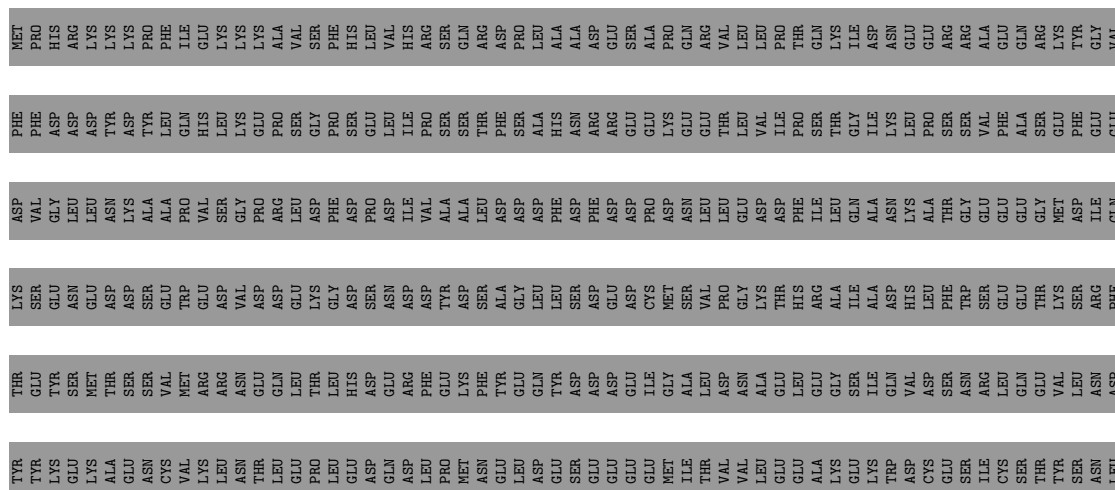
- Molecule 20: RNA-binding protein NOB1

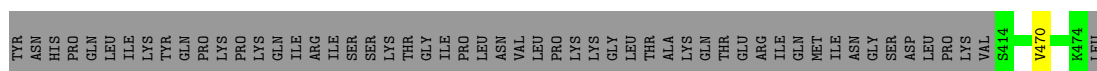


- Molecule 21: Pre-rRNA-processing protein TSR1 homolog



- Molecule 22: Protein LTV1 homolog





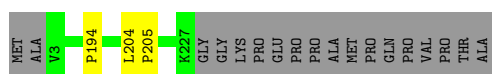
- Molecule 23: Small ribosomal subunit protein uS14

Chain d: 96%



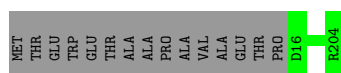
- Molecule 24: Small ribosomal subunit protein uS3

Chain D: 91%



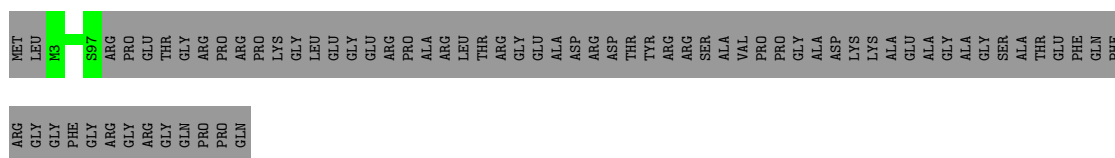
- Molecule 25: Small ribosomal subunit protein uS7

Chain F: 93%



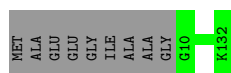
- Molecule 26: Small ribosomal subunit protein eS10

Chain K: 58%



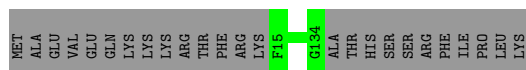
- Molecule 27: Small ribosomal subunit protein eS12

Chain M: 93%



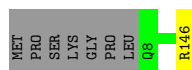
- Molecule 28: Small ribosomal subunit protein uS19

Chain P: 83%



- Molecule 29: Small ribosomal subunit protein uS9

Chain Q:  95% • 5%



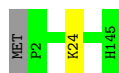
- Molecule 30: Small ribosomal subunit protein uS13

Chain S:  94% 6%




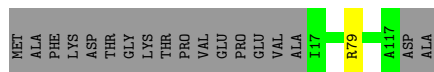
- Molecule 31: Small ribosomal subunit protein eS19

Chain T:  99% ..



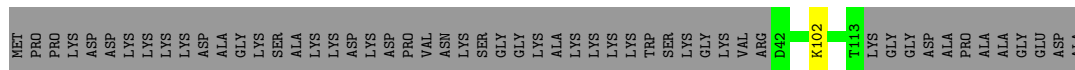
- Molecule 32: Small ribosomal subunit protein uS10

Chain U:  84% • 15%




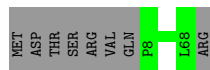
- Molecule 33: Small ribosomal subunit protein eS25

Chain Z:  57% • 42%



- Molecule 34: Small ribosomal subunit protein eS28

Chain c:  88% 12%



- Molecule 35: Small ribosomal subunit protein RACK1

Chain g:  99% •



- Molecule 36: Serine/threonine-protein kinase RIO3

[illegible]

- | | | | | |
|----|-----|-----|-----|-----|
| M1 | L73 | ARG | GLY | GLY |
|----|-----|-----|-----|-----|

- | | | | | |
|----|-----|-----|-----|-----|
| M1 | 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	29221	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	0.42	2/39613 (0.0%)	1.00	148/61728 (0.2%)
2	R	0.32	0/1002	0.69	0/1345
3	A	0.33	0/1742	0.62	0/2367
4	B	0.27	0/1756	0.58	0/2350
5	C	0.35	0/1726	0.64	0/2332
6	E	0.32	0/2118	0.63	2/2849 (0.1%)
7	G	0.28	0/1885	0.59	0/2510
8	H	0.27	0/1524	0.57	0/2042
9	I	0.32	0/1711	0.63	0/2282
10	J	0.31	0/1524	0.62	0/2035
11	L	0.35	0/1250	0.64	0/1673
12	N	0.32	0/1226	0.62	1/1649 (0.1%)
13	O	0.28	0/1022	0.62	0/1372
14	V	0.31	0/631	0.67	0/844
15	W	0.33	0/1051	0.61	0/1406
16	X	0.30	0/1116	0.59	0/1490
17	Y	0.32	0/1031	0.62	0/1370
18	b	0.27	0/653	0.55	0/876
19	x	0.24	0/879	0.41	0/1223
20	y	0.27	0/2618	0.59	1/3536 (0.0%)
21	u	0.26	0/5076	0.56	0/6860
22	t	0.25	0/518	0.53	0/677
23	d	0.30	0/470	0.59	0/623
24	D	0.32	0/1780	0.64	0/2397
25	F	0.26	0/1516	0.59	0/2037
26	K	0.27	0/824	0.60	0/1112
27	M	0.25	0/963	0.53	0/1291
28	P	0.27	0/1003	0.60	0/1341
29	Q	0.29	0/1126	0.63	0/1506
30	S	0.24	0/1202	0.57	0/1610
31	T	0.27	0/1142	0.58	0/1530
32	U	0.29	0/813	0.63	0/1092

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Z	0.27	0/580	0.59	0/780
34	c	0.25	0/481	0.66	0/643
35	g	0.25	0/2497	0.52	0/3399
36	p	0.26	0/2444	0.46	0/3338
37	i	0.24	0/360	0.44	0/500
37	j	0.24	0/360	0.43	0/500
All	All	0.35	2/89233 (0.0%)	0.81	152/128515 (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
15	W	0	1
24	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1363	C	N3-C4	-7.35	1.28	1.33
1	2	926	A	C6-N1	-5.86	1.31	1.35

The worst 5 of 152 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	914	U	C5-C4-O4	20.08	137.95	125.90
1	2	914	U	N3-C4-O4	-19.52	105.74	119.40
1	2	1363	C	C6-N1-C2	-11.84	115.56	120.30
1	2	872	A	N1-C6-N6	-11.03	111.98	118.60
1	2	72	C	N1-C2-O2	10.50	125.20	118.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	D	194	PRO	Peptide
15	W	28	ARG	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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%)	110 (92%)	9 (8%)	1 (1%)	16	49
3	A	214/295 (72%)	204 (95%)	10 (5%)	0	100	100
4	B	211/264 (80%)	199 (94%)	12 (6%)	0	100	100
5	C	216/293 (74%)	206 (95%)	10 (5%)	0	100	100
6	E	260/263 (99%)	248 (95%)	12 (5%)	0	100	100
7	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
8	H	184/194 (95%)	181 (98%)	3 (2%)	0	100	100
9	I	203/208 (98%)	192 (95%)	11 (5%)	0	100	100
10	J	178/194 (92%)	167 (94%)	10 (6%)	1 (1%)	22	55
11	L	149/158 (94%)	139 (93%)	10 (7%)	0	100	100
12	N	147/151 (97%)	142 (97%)	5 (3%)	0	100	100
13	O	133/151 (88%)	126 (95%)	7 (5%)	0	100	100
14	V	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
15	W	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	49
16	X	139/143 (97%)	132 (95%)	7 (5%)	0	100	100
17	Y	122/133 (92%)	118 (97%)	4 (3%)	0	100	100
18	b	80/84 (95%)	75 (94%)	5 (6%)	0	100	100
19	x	176/252 (70%)	172 (98%)	4 (2%)	0	100	100
20	y	319/412 (77%)	305 (96%)	14 (4%)	0	100	100
21	u	607/804 (76%)	575 (95%)	32 (5%)	0	100	100
22	t	59/475 (12%)	56 (95%)	2 (3%)	1 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	d	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
24	D	223/243 (92%)	207 (93%)	15 (7%)	1 (0%)	30	63
25	F	187/204 (92%)	177 (95%)	10 (5%)	0	100	100
26	K	93/165 (56%)	90 (97%)	3 (3%)	0	100	100
27	M	121/132 (92%)	117 (97%)	4 (3%)	0	100	100
28	P	118/145 (81%)	117 (99%)	1 (1%)	0	100	100
29	Q	137/146 (94%)	125 (91%)	12 (9%)	0	100	100
30	S	141/152 (93%)	136 (96%)	5 (4%)	0	100	100
31	T	142/145 (98%)	137 (96%)	5 (4%)	0	100	100
32	U	99/119 (83%)	94 (95%)	5 (5%)	0	100	100
33	Z	70/125 (56%)	68 (97%)	2 (3%)	0	100	100
34	c	59/69 (86%)	55 (93%)	4 (7%)	0	100	100
35	g	312/317 (98%)	297 (95%)	15 (5%)	0	100	100
36	p	385/519 (74%)	367 (95%)	18 (5%)	0	100	100
37	i	71/76 (93%)	71 (100%)	0	0	100	100
37	j	71/76 (93%)	71 (100%)	0	0	100	100
All	All	6234/7760 (80%)	5945 (95%)	284 (5%)	5 (0%)	50	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	R	42	PRO
10	J	138	ARG
24	D	205	PRO
22	t	470	VAL
15	W	29	PRO

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%)	109 (99%)	1 (1%)	75	82
3	A	180/243 (74%)	180 (100%)	0	100	100
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%)	223 (100%)	1 (0%)	89	91
7	G	200/218 (92%)	199 (100%)	1 (0%)	86	90
8	H	167/174 (96%)	167 (100%)	0	100	100
9	I	178/180 (99%)	178 (100%)	0	100	100
10	J	160/168 (95%)	160 (100%)	0	100	100
11	L	135/142 (95%)	134 (99%)	1 (1%)	81	86
12	N	130/131 (99%)	129 (99%)	1 (1%)	79	84
13	O	105/119 (88%)	104 (99%)	1 (1%)	73	80
14	V	66/67 (98%)	66 (100%)	0	100	100
15	W	112/113 (99%)	111 (99%)	1 (1%)	75	82
16	X	113/115 (98%)	113 (100%)	0	100	100
17	Y	108/115 (94%)	108 (100%)	0	100	100
18	b	74/76 (97%)	74 (100%)	0	100	100
20	y	285/367 (78%)	285 (100%)	0	100	100
21	u	539/705 (76%)	537 (100%)	2 (0%)	89	91
22	t	56/434 (13%)	56 (100%)	0	100	100
23	d	48/49 (98%)	47 (98%)	1 (2%)	48	66
24	D	189/202 (94%)	188 (100%)	1 (0%)	86	90
25	F	159/170 (94%)	159 (100%)	0	100	100
26	K	86/136 (63%)	86 (100%)	0	100	100
27	M	104/108 (96%)	104 (100%)	0	100	100
28	P	107/130 (82%)	107 (100%)	0	100	100
29	Q	115/121 (95%)	114 (99%)	1 (1%)	75	82
30	S	124/132 (94%)	124 (100%)	0	100	100
31	T	114/115 (99%)	113 (99%)	1 (1%)	75	82
32	U	93/107 (87%)	92 (99%)	1 (1%)	70	79
33	Z	64/103 (62%)	63 (98%)	1 (2%)	58	73
34	c	54/62 (87%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	g	272/275 (99%)	271 (100%)	1 (0%)	89	91
36	p	136/454 (30%)	136 (100%)	0	100	100
All	All	4985/6334 (79%)	4969 (100%)	16 (0%)	90	92

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	Z	102	LYS
32	U	79	ARG
21	u	499	ARG
31	T	24	LYS
21	u	139	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
36	p	104	ASN
24	D	159	HIS
12	N	101	HIS
10	J	154	GLN
12	N	105	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1646/1873 (87%)	435 (26%)	22 (1%)

5 of 435 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	11	A
1	2	14	C

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1403	C
1	2	1534	C
1	2	1494	U
1	2	1558	C
1	2	472	C

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 2 ligands modelled in this entry, 2 are 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 [i](#)

There are no chain breaks in this entry.