



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 12:53 PM EDT

PDB ID : 5MMJ
EMDB ID: : EMD-3532
Title : Structure of the small subunit of the chloroplast ribosome
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.
Deposited on : unknown
Resolution : 3.65 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

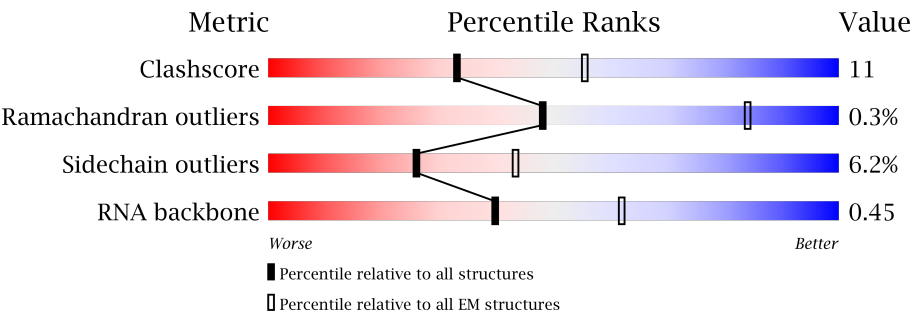
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

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 3.65 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.



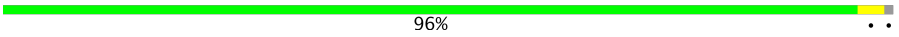




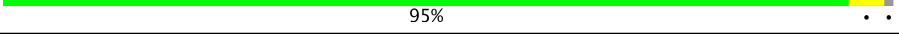


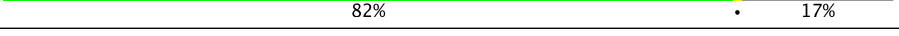

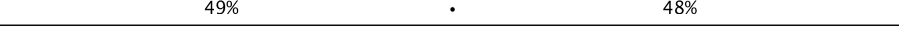
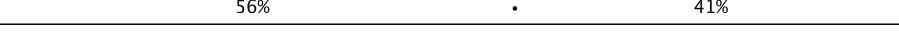

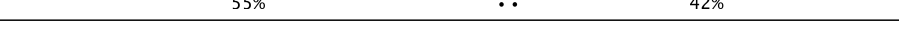


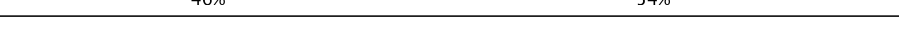

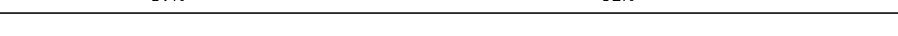
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	0	130	<div><div>8%</div><div>92%</div></div>
2	8	174	<div><div>99%</div><div>.</div></div>
3	a	1491	<div><div>71%</div><div>27%</div><div>.</div></div>
4	b	236	<div><div>92%</div><div>7%</div><div>.</div></div>
5	c	218	<div><div>92%</div><div>7%</div><div>.</div></div>
6	d	201	<div><div>93%</div><div>6%</div><div>.</div></div>
7	e	308	<div><div>58%</div><div>.</div><div>39%</div></div>
8	f	211	<div><div>51%</div><div>.</div><div>46%</div></div>

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Mol	Chain	Length	Quality of chain
9	g	155	 96% . .
10	h	134	 92% 7% .
11	i	208	 62% 8% 31%
12	j	195	 47% . 49%
13	k	138	 79% 6% 15%
14	l	123	 95% . .
15	m	172	 59% 5% 36%
16	n	100	 88% 11% .
17	o	90	 82% . 17%
18	p	88	 85% 6% 9%
19	q	165	 49% . 48%
20	r	101	 56% . 41%
21	s	92	 82% . 15%
22	t	183	 55% . . 42%
23	u	180	 33% . 64%
24	v	260	 31% 69%
25	w	179	 46% 54%
26	x	101	 39% . 60%
27	y	302	 37% . 62%

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 55315 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 protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	11	Total	C	N	O	0	0
			98	63	18	17		

- Molecule 2 is a protein called plastid ribosomal protein bS1c.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	8	174	Total	C	N	O	0	0
			870	522	174	174		

- Molecule 3 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	1484	Total	C	N	O	P	0	0
			31868	14208	5881	10295	1484		

- Molecule 4 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	233	Total	C	N	O	S	0	0
			1844	1163	339	329	13		

- Molecule 5 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	216	Total	C	N	O	S	0	0
			1736	1108	313	309	6		

- Molecule 6 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 7 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e	187	Total	C	N	O	S	0	0
			1331	826	259	240	6		

- Molecule 8 is a protein called plastid ribosomal protein bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f	113	Total	C	N	O	S	0	0
			911	583	152	172	4		

- Molecule 9 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g	154	Total	C	N	O	S	0	0
			1210	753	244	210	3		

- Molecule 10 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	h	133	Total	C	N	O	S	0	0
			1079	679	210	185	5		

- Molecule 11 is a protein called plastid ribosomal protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	i	144	Total	C	N	O	S	0	0
			1119	712	211	195	1		

- Molecule 12 is a protein called plastid ribosomal protein uS10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	j	99	Total	C	N	O	S	0	0
			805	517	144	139	5		

- Molecule 13 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	k	117	Total	C	N	O	S	0	0
			882	546	181	150	5		

- Molecule 14 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	l	122	Total	C	N	O	S	0	0
			959	599	197	161	2		

- Molecule 15 is a protein called plastid ribosomal protein uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	m	110	Total	C	N	O	S	0	0
			904	556	182	161	5		

- Molecule 16 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	n	99	Total	C	N	O	S	0	0
			820	507	174	136	3		

- Molecule 17 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	o	75	Total	C	N	O	S	0	0
			635	404	123	107	1		

- Molecule 18 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 19 is a protein called plastid ribosomal protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	q	86	Total	C	N	O	S	0	0
			693	434	136	119	4		

- Molecule 20 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	60	Total	C	N	O	S	0	0
			490	308	96	85	1		

- Molecule 21 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	s	78	Total	C	N	O	S	0	0
			631	406	119	104	2		

- Molecule 22 is a protein called plastid ribosomal protein bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	t	107	Total	C	N	O	S	0	0
			853	528	173	151	1		

- Molecule 23 is a protein called plastid ribosomal protein bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	u	65	Total	C	N	O	S	0	0
			568	339	127	100	2		

- Molecule 24 is a protein called 30S ribosomal protein 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	80	Total	C	N	O		0	0
			613	388	104	121			

- Molecule 25 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	w	82	Total	C	N	O	S	0	0
			686	454	113	116	3		

- Molecule 26 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	x	40	Total	C	N	O		0	0
			309	192	69	48			

- Molecule 27 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	y	116	Total	C	N	O	S	0	0
			919	567	181	169	2		

- Molecule 28 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
28	x	1	Total 1	Mg 1	0
28	a	182	Total 182	Mg 182	0
28	l	1	Total 1	Mg 1	0
28	k	1	Total 1	Mg 1	0

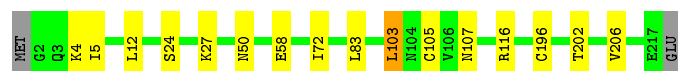
- Molecule 4: 30S ribosomal protein S2, chloroplastic

Chain b: 92% 7%



- Molecule 5: 30S ribosomal protein S3, chloroplastic

Chain c: 92% 7%



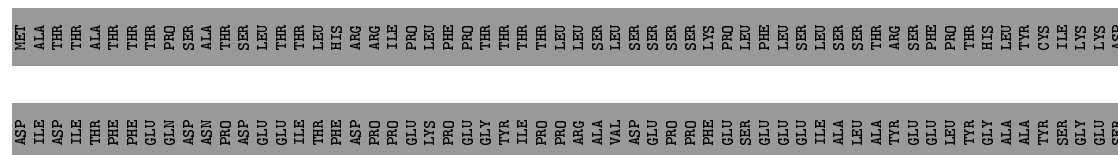
- Molecule 6: 30S ribosomal protein S4, chloroplastic

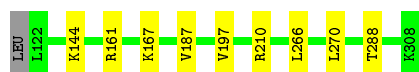
Chain d:  93% 6%



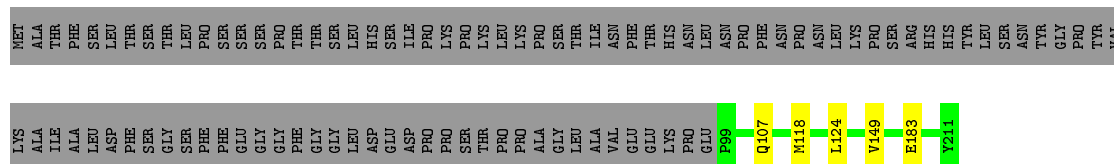
- Molecule 7: 30S ribosomal protein S5, chloroplastic

Chain e: 58% 1% 39%





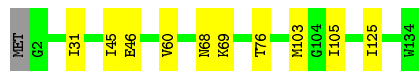
- Molecule 8: plastid ribosomal protein bS6c



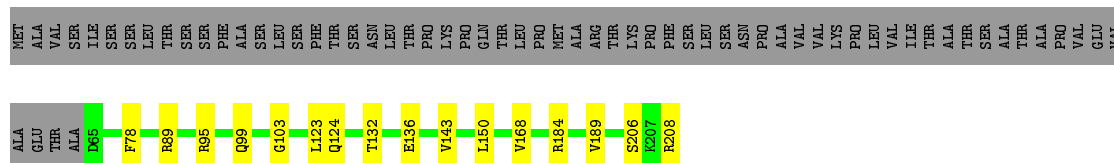
- Molecule 9: 30S ribosomal protein S7, chloroplastic



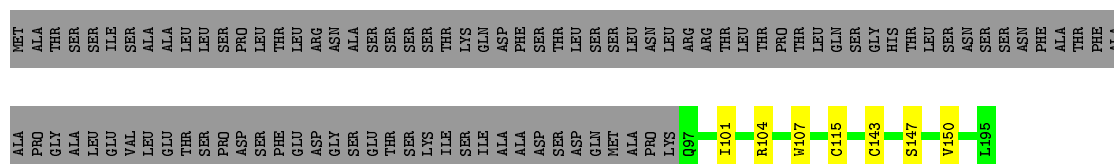
- Molecule 10: 30S ribosomal protein S8, chloroplastic



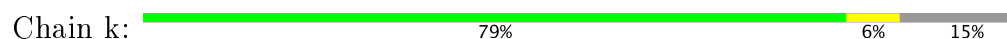
- Molecule 11: plastid ribosomal protein uS9c

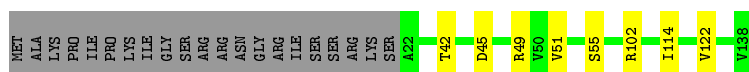


- Molecule 12: plastid ribosomal protein uS10c



- Molecule 13: 30S ribosomal protein S11, chloroplastic





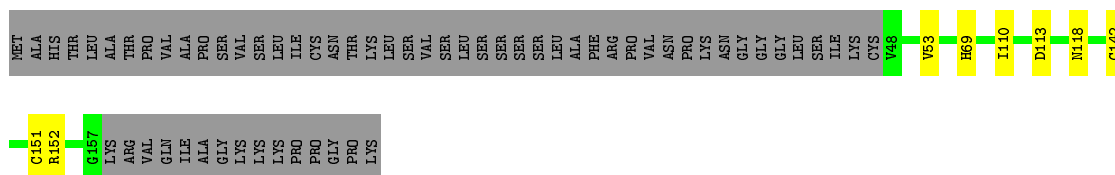
- Molecule 14: 30S ribosomal protein S12, chloroplastic

Chain l: 95%



- Molecule 15: plastid ribosomal protein uS13c

Chain m: 59% 5% 36%



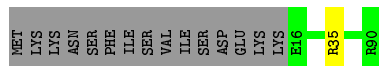
- Molecule 16: 30S ribosomal protein S14, chloroplastic

Chain n: 88% 11%



- Molecule 17: 30S ribosomal protein S15, chloroplastic

Chain o: 82% 17%



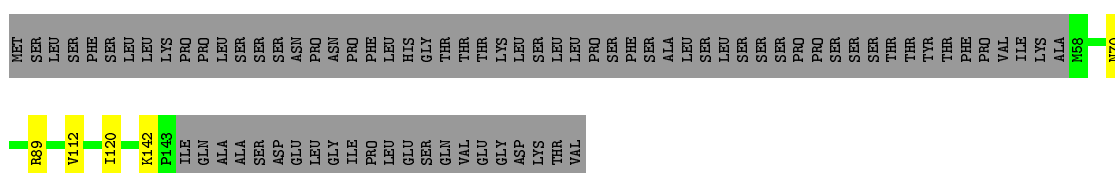
- Molecule 18: 30S ribosomal protein S16, chloroplastic

Chain p: 85% 6% 9%



- Molecule 19: plastid ribosomal protein uS17c

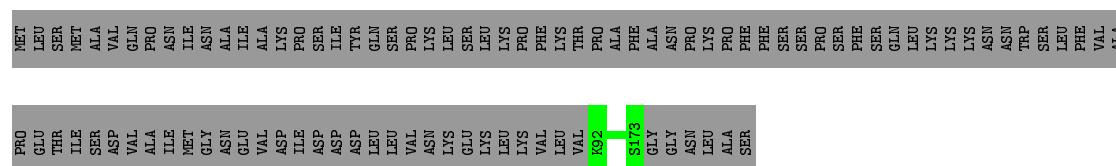
Chain q: 49% 48%



- E181 A260

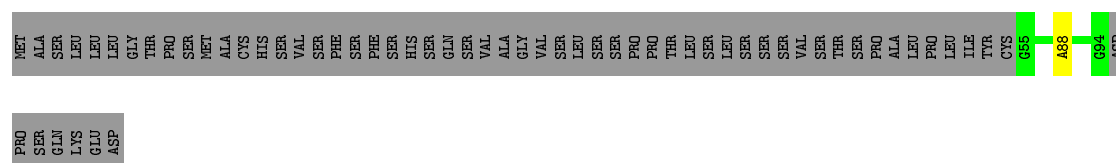
- Molecule 25: 30S ribosomal protein 3, chloroplastic

Chain w:  46% 54%



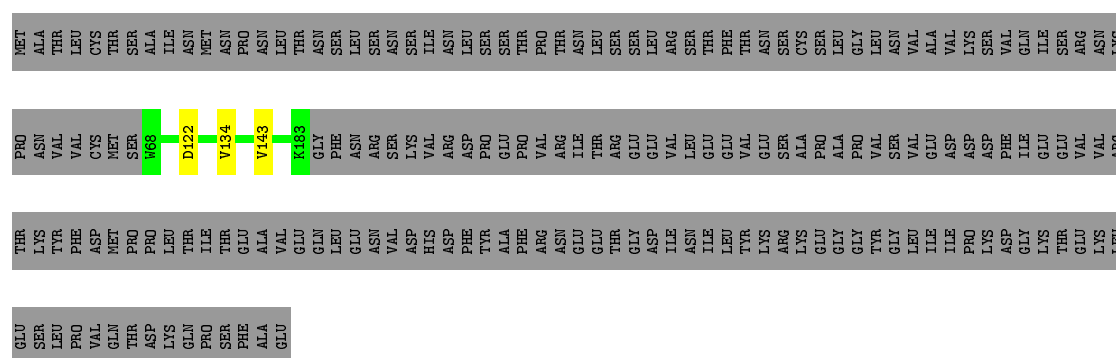
- Molecule 26: 30S ribosomal protein S31, chloroplastic

Chain x:  39% . 60%



- Molecule 27: Ribosome-binding factor PSRP1, chloroplastic

Chain v:  37% 62%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	127031	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 ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k 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: MG

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	0	0.34	0/99	0.47	0/128
10	h	0.48	0/1094	0.68	0/1467
11	i	0.52	0/1138	0.76	2/1526 (0.1%)
12	j	0.55	0/822	0.66	0/1111
13	k	0.43	0/896	0.64	0/1206
14	l	0.52	0/975	0.68	0/1312
15	m	0.46	0/912	0.67	0/1219
16	n	0.50	0/836	0.66	0/1116
17	o	0.40	0/642	0.53	0/852
18	p	0.46	0/674	0.70	0/902
19	q	0.44	0/707	0.62	0/949
20	r	0.45	0/494	0.67	0/660
21	s	0.51	0/646	0.77	0/870
22	t	0.49	0/862	0.68	0/1151
23	u	0.39	0/572	0.53	0/754
24	v	0.58	0/621	0.49	0/833
25	w	0.58	0/707	0.55	0/962
26	x	0.67	1/317 (0.3%)	0.80	0/418
27	y	0.45	0/930	0.65	0/1243
3	a	0.74	15/35687 (0.0%)	1.16	92/55680 (0.2%)
4	b	0.44	0/1878	0.60	0/2538
5	c	0.52	0/1763	0.70	1/2370 (0.0%)
6	d	0.46	0/1661	0.66	1/2230 (0.0%)
7	e	0.57	0/1345	0.70	0/1817
8	f	0.43	0/929	0.61	0/1255
9	g	0.39	0/1226	0.59	0/1641
All	All	0.66	16/58433 (0.0%)	1.01	96/86210 (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
22	t	0	2
4	b	0	1
5	c	0	1
7	e	0	1
All	All	0	5

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	a	1152	A	C6-N6	-8.63	1.27	1.33
3	a	1006	G	N3-C4	-7.76	1.30	1.35
3	a	400	U	C4-C5	7.69	1.50	1.43
3	a	1152	A	N7-C5	-7.68	1.34	1.39
3	a	714	A	N9-C4	-7.31	1.33	1.37

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	a	1152	A	C5-C6-N1	21.25	128.32	117.70
3	a	1152	A	C6-N1-C2	-20.10	106.54	118.60
3	a	1006	G	C5-C6-N1	-16.13	103.43	111.50
3	a	1152	A	N1-C2-N3	15.45	137.03	129.30
3	a	1006	G	N7-C8-N9	-15.28	105.46	113.10

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	b	74	VAL	Peptide
5	c	103	LEU	Peptide
7	e	144	LYS	Peptide
22	t	173	TRP	Peptide
22	t	75	LYS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	98	0	99	0	0
2	8	870	0	184	1	0
3	a	31868	0	16048	0	0
4	b	1844	0	1887	0	0
5	c	1736	0	1819	0	0
6	d	1633	0	1730	0	0
7	e	1331	0	1312	0	0
8	f	911	0	923	0	0
9	g	1210	0	1284	0	0
10	h	1079	0	1137	0	0
11	i	1119	0	1181	0	0
12	j	805	0	849	0	0
13	k	882	0	928	0	0
14	l	959	0	1035	0	0
15	m	904	0	943	0	0
16	n	820	0	858	0	0
17	o	635	0	686	0	0
18	p	664	0	703	0	0
19	q	693	0	729	0	0
20	r	490	0	532	0	0
21	s	631	0	661	0	0
22	t	853	0	915	0	0
23	u	568	0	576	0	0
24	v	613	0	621	0	0
25	w	686	0	706	0	0
26	x	309	0	323	0	0
27	y	919	0	958	0	0
28	a	182	0	0	0	0
28	k	1	0	0	0	0
28	l	1	0	0	0	0
28	x	1	0	0	0	0
All	All	55315	0	39627	1	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (1) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:8:1131:UNK:CB	2:8:1219:UNK:HA	2.51	0.40

There are no symmetry-related clashes.

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	
1	0	9/130 (7%)	8 (89%)	1 (11%)	0	100	100
4	b	231/236 (98%)	220 (95%)	11 (5%)	0	100	100
5	c	214/218 (98%)	200 (94%)	14 (6%)	0	100	100
6	d	197/201 (98%)	181 (92%)	16 (8%)	0	100	100
7	e	185/308 (60%)	181 (98%)	4 (2%)	0	100	100
8	f	111/211 (53%)	106 (96%)	4 (4%)	1 (1%)	20	63
9	g	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
10	h	131/134 (98%)	125 (95%)	4 (3%)	2 (2%)	12	54
11	i	142/208 (68%)	136 (96%)	6 (4%)	0	100	100
12	j	97/195 (50%)	92 (95%)	4 (4%)	1 (1%)	18	61
13	k	115/138 (83%)	107 (93%)	8 (7%)	0	100	100
14	l	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
15	m	108/172 (63%)	97 (90%)	10 (9%)	1 (1%)	20	63
16	n	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
17	o	73/90 (81%)	73 (100%)	0	0	100	100
18	p	78/88 (89%)	72 (92%)	6 (8%)	0	100	100
19	q	84/165 (51%)	78 (93%)	6 (7%)	0	100	100
20	r	58/101 (57%)	55 (95%)	3 (5%)	0	100	100
21	s	76/92 (83%)	74 (97%)	2 (3%)	0	100	100
22	t	105/183 (57%)	100 (95%)	4 (4%)	1 (1%)	18	61
23	u	63/180 (35%)	61 (97%)	2 (3%)	0	100	100
24	v	78/260 (30%)	76 (97%)	2 (3%)	0	100	100
25	w	80/179 (45%)	78 (98%)	2 (2%)	0	100	100
26	x	38/101 (38%)	37 (97%)	1 (3%)	0	100	100
27	y	114/302 (38%)	105 (92%)	8 (7%)	1 (1%)	20	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2756/4270 (64%)	2614 (95%)	135 (5%)	7 (0%)	48 80

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	h	68	ASN
12	j	150	VAL
15	m	53	VAL
22	t	174	TYR
10	h	69	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
1	0	10/117 (8%)	10 (100%)	0	100 100
4	b	198/201 (98%)	182 (92%)	16 (8%)	14 50
5	c	186/188 (99%)	171 (92%)	15 (8%)	14 50
6	d	178/180 (99%)	167 (94%)	11 (6%)	21 61
7	e	121/255 (48%)	113 (93%)	8 (7%)	19 58
8	f	100/186 (54%)	96 (96%)	4 (4%)	36 72
9	g	125/126 (99%)	120 (96%)	5 (4%)	36 72
10	h	116/117 (99%)	108 (93%)	8 (7%)	18 56
11	i	114/169 (68%)	100 (88%)	14 (12%)	5 31
12	j	91/173 (53%)	85 (93%)	6 (7%)	19 58
13	k	91/109 (84%)	83 (91%)	8 (9%)	12 47
14	l	105/106 (99%)	100 (95%)	5 (5%)	30 67
15	m	99/151 (66%)	92 (93%)	7 (7%)	17 55
16	n	89/90 (99%)	78 (88%)	11 (12%)	5 31
17	o	70/85 (82%)	69 (99%)	1 (1%)	71 89
18	p	71/79 (90%)	66 (93%)	5 (7%)	18 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	q	77/149 (52%)	72 (94%)	5 (6%)	20	59
20	r	56/96 (58%)	53 (95%)	3 (5%)	26	64
21	s	68/81 (84%)	65 (96%)	3 (4%)	33	70
22	t	89/156 (57%)	84 (94%)	5 (6%)	25	63
23	u	59/160 (37%)	54 (92%)	5 (8%)	12	48
24	v	67/225 (30%)	67 (100%)	0	100	100
25	w	76/162 (47%)	76 (100%)	0	100	100
26	x	30/85 (35%)	30 (100%)	0	100	100
27	y	104/275 (38%)	102 (98%)	2 (2%)	62	85
All	All	2390/3721 (64%)	2243 (94%)	147 (6%)	26	61

5 of 147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	h	125	ILE
12	j	104	ARG
22	t	121	SER
11	i	89	ARG
11	i	143	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
13	k	127	HIS
15	m	87	ASN
25	w	162	GLN
15	m	52	ASN
16	n	48	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	a	1483/1491 (99%)	389 (26%)	0

5 of 389 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	a	2	C
3	a	3	U
3	a	5	A
3	a	6	U
3	a	7	G

There are no RNA pucker outliers to report.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 185 ligands modelled in this entry, 185 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	1068:UNK	C	1101:UNK	N	66.30
1	8	1143:UNK	C	1201:UNK	N	11.98