



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 05:16 PM UTC

PDB ID : 9UDI / pdb_00009udi
EMDB ID : EMD-64070
Title : Cryo-EM structure of the RdCas12n-sgRNA-DNA ternary complex, Conformation 2
Authors : Fu, W.; Ji, Q.
Deposited on : 2025-04-06
Resolution : 3.01 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

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 : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

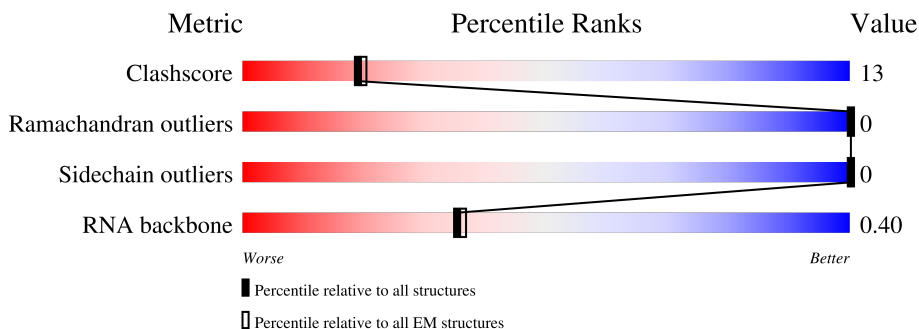
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	A	540	
2	C	40	
3	D	14	
4	R	214	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4986 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 Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	257	Total	C	N	O	S	0	0
			2025	1281	382	360	2		

- Molecule 2 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	22	Total	C	N	O	P	0	0
			445	212	79	132	22		

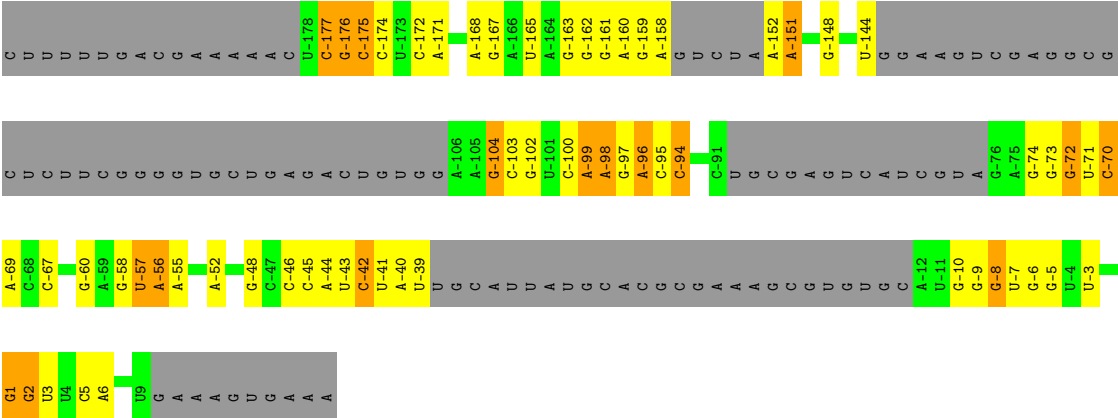
- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*CP*TP*GP*TP*GP*AP*GP*AP*AP*AP*CP*CP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	12	Total	C	N	O	P	0	0
			250	118	50	70	12		

- Molecule 4 is a RNA chain called sgRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	106	Total	C	N	O	P	0	0
			2266	1013	414	734	105		

Chain R: 20% 21% 8% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	879820	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/2074	0.45	1/2812 (0.0%)
2	C	0.22	0/497	0.41	0/763
3	D	0.21	0/281	0.34	0/432
4	R	0.14	0/2532	0.30	0/3937
All	All	0.17	0/5384	0.37	1/7944 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	PRO	CA-N-CD	-7.42	101.61	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A	2025	0	1950	57	0
2	C	445	0	248	11	0
3	D	250	0	135	5	0
4	R	2266	0	1150	42	0
All	All	4986	0	3483	103	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 13.

All (103) 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)
1:A:221:LEU:HD12	1:A:227:ILE:HD12	1.64	0.80
1:A:200:LEU:HB2	1:A:220:ARG:HH12	1.47	0.79
1:A:99:THR:HG23	1:A:100:PRO:HD2	1.66	0.76
1:A:228:ARG:NH1	4:R:-70:C:OP2	2.20	0.74
2:C:27:DG:H1	3:D:-11:DC:H42	1.35	0.72
1:A:199:TYR:HE1	1:A:213:ILE:HG13	1.58	0.67
1:A:18:ARG:NH1	4:R:-171:A:OP1	2.27	0.67
1:A:90:TYR:HB2	1:A:146:LEU:HB3	1.76	0.67
4:R:-41:U:H3	4:R:-10:G:H1	1.43	0.67
4:R:-144:U:O2	4:R:-104:G:O6	2.15	0.65
1:A:51:ASN:OD1	1:A:87:GLN:NE2	2.30	0.64
1:A:140:ARG:NH1	2:C:18:DT:O4	2.31	0.64
1:A:47:ASN:ND2	1:A:87:GLN:OE1	2.24	0.63
1:A:216:TYR:CE2	4:R:-52:A:H5''	2.33	0.63
1:A:188:ALA:HB2	1:A:192:MET:HE2	1.82	0.62
4:R:-175:C:H42	4:R:-161:G:H22	1.49	0.61
4:R:-41:U:H2'	4:R:-40:A:H8	1.66	0.60
1:A:216:TYR:CE1	1:A:237:VAL:HG21	2.36	0.60
1:A:200:LEU:HB2	1:A:220:ARG:NH1	2.15	0.60
2:C:23:DC:H2''	2:C:24:DA:C8	2.37	0.60
4:R:-41:U:H2'	4:R:-40:A:C8	2.36	0.59
1:A:216:TYR:HE1	1:A:237:VAL:HG21	1.66	0.59
4:R:-73:G:H2'	4:R:-72:G:H8	1.68	0.59
1:A:217:ARG:HH21	1:A:228:ARG:HH22	1.52	0.58
4:R:-43:U:H3	4:R:-8:G:H1	1.52	0.57
3:D:-5:DG:H2''	3:D:-4:DA:C8	2.39	0.57
1:A:195:TYR:HB3	1:A:237:VAL:HG11	1.85	0.57
2:C:10:DT:C2	2:C:11:DG:C8	2.93	0.57
1:A:109:GLU:HA	1:A:112:ILE:HG22	1.87	0.57
1:A:183:SER:OG	4:R:3:U:OP1	2.12	0.57
1:A:217:ARG:HH21	1:A:228:ARG:NH2	2.03	0.56
4:R:-158:A:O2'	4:R:-152:A:N1	2.35	0.55
2:C:12:DA:H2''	2:C:13:DA:H8	1.70	0.55
4:R:-45:C:H2'	4:R:-44:A:H8	1.71	0.55
2:C:26:DA:H2''	2:C:27:DG:C8	2.42	0.54
4:R:-168:A:N6	4:R:-167:G:O6	2.39	0.54
4:R:-177:C:O2'	4:R:-176:G:OP1	2.24	0.54
4:R:-159:G:H21	4:R:-151:A:H62	1.56	0.54
1:A:247:ARG:HH11	1:A:265:LYS:HD2	1.73	0.53
4:R:-58:G:N2	4:R:-56:A:O2'	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:PHE:HD1	1:A:231:ASN:HB2	1.74	0.52
4:R:-45:C:H2'	4:R:-44:A:C8	2.45	0.52
1:A:32:ALA:HA	1:A:141:VAL:HG11	1.92	0.51
1:A:159:SER:HA	1:A:164:ARG:HB3	1.93	0.50
4:R:-175:C:N4	4:R:-161:G:H22	2.09	0.50
1:A:99:THR:HA	1:A:102:LYS:HB2	1.94	0.50
4:R:-172:C:H1'	4:R:-98:A:C8	2.47	0.49
4:R:-73:G:H2'	4:R:-72:G:C8	2.47	0.48
4:R:-40:A:H2'	4:R:-39:U:C6	2.48	0.48
2:C:10:DT:H2''	2:C:11:DG:H5'	1.95	0.48
1:A:228:ARG:HD2	4:R:-71:U:OP2	2.14	0.48
1:A:29:LEU:HD22	1:A:251:VAL:HG11	1.96	0.48
4:R:-100:C:H2'	4:R:-99:A:O4'	2.13	0.48
1:A:186:VAL:HB	1:A:249:TYR:CZ	2.49	0.48
4:R:-42:C:H2'	4:R:-41:U:C6	2.49	0.48
4:R:-94:C:O2'	4:R:-57:U:O4	2.25	0.47
1:A:19:LEU:HB3	1:A:21:PRO:HD3	1.96	0.47
1:A:221:LEU:HD22	1:A:249:TYR:CD2	2.49	0.47
2:C:9:DC:H2'	2:C:10:DT:H71	1.96	0.47
1:A:35:ALA:HB1	1:A:142:LEU:HD23	1.96	0.47
1:A:181:ARG:HH21	1:A:252:SER:HB3	1.79	0.47
3:D:-11:DC:H2''	3:D:-10:DT:C5	2.49	0.46
4:R:-177:C:O2	4:R:-159:G:N2	2.48	0.46
1:A:247:ARG:NH1	1:A:265:LYS:HD2	2.30	0.46
2:C:12:DA:H2''	2:C:13:DA:C8	2.49	0.46
1:A:39:THR:HA	1:A:42:MET:HE3	1.97	0.46
4:R:1:G:H2'	4:R:2:G:C8	2.51	0.45
4:R:-103:C:H2'	4:R:-102:G:C8	2.52	0.45
1:A:188:ALA:HA	1:A:190:GLU:H	1.81	0.45
4:R:-158:A:H1'	4:R:-152:A:H61	1.81	0.45
1:A:143:VAL:O	1:A:147:GLN:HG2	2.15	0.45
1:A:40:TYR:CE2	1:A:175:LYS:HG3	2.53	0.44
4:R:-96:A:H2'	4:R:-95:C:C6	2.53	0.44
1:A:107:GLN:HA	1:A:110:HIS:HB2	1.99	0.44
1:A:238:LYS:HD3	1:A:238:LYS:HA	1.74	0.44
4:R:-175:C:H42	4:R:-161:G:H1	1.65	0.43
4:R:-177:C:HO2'	4:R:-176:G:P	2.38	0.43
1:A:192:MET:HE1	1:A:247:ARG:C	2.44	0.43
1:A:135:HIS:CE1	1:A:136:THR:HG23	2.54	0.42
4:R:-163:G:OP2	4:R:-163:G:N2	2.44	0.42
1:A:16:LYS:NZ	4:R:2:G:OP1	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:25:DC:H2''	2:C:26:DA:C8	2.55	0.42
1:A:153:TRP:CE2	1:A:172:PRO:HG2	2.54	0.42
1:A:191:LYS:HE3	3:D:-6:DA:OP2	2.19	0.42
1:A:99:THR:HG23	1:A:100:PRO:CD	2.42	0.42
4:R:-6:G:H2'	4:R:-5:G:C8	2.55	0.42
1:A:218:HIS:NE2	4:R:-71:U:OP1	2.53	0.42
1:A:137:ALA:HB3	1:A:142:LEU:HD11	2.01	0.42
1:A:200:LEU:HD11	3:D:-6:DA:H3'	2.00	0.42
1:A:11:ASN:ND2	1:A:266:PHE:O	2.52	0.42
1:A:233:THR:O	1:A:237:VAL:HG13	2.19	0.42
1:A:246:ILE:HG21	1:A:262:PHE:HD1	1.85	0.42
4:R:-46:C:H2'	4:R:-45:C:C6	2.54	0.42
1:A:23:GLN:NE2	4:R:-74:G:OP1	2.53	0.42
1:A:156:PHE:N	1:A:156:PHE:CD1	2.89	0.41
4:R:-60:G:N3	4:R:-60:G:H2'	2.35	0.41
1:A:234:LYS:HA	1:A:237:VAL:HG22	2.03	0.41
2:C:10:DT:C2'	2:C:11:DG:H5'	2.51	0.41
4:R:5:C:H2'	4:R:6:A:C8	2.56	0.41
1:A:253:ARG:NH1	1:A:255:ALA:O	2.53	0.41
4:R:-98:A:C8	4:R:-69:A:H2	2.39	0.41
1:A:43:LEU:HD23	1:A:149:ALA:HB3	2.02	0.40
1:A:99:THR:CG2	1:A:100:PRO:HD2	2.45	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	A	255/540 (47%)	228 (89%)	27 (11%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	195/449 (43%)	195 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	R	101/214 (47%)	28 (27%)	1 (0%)

All (28) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	R	-176	G
4	R	-175	C
4	R	-174	C
4	R	-165	U
4	R	-162	G
4	R	-160	A
4	R	-151	A
4	R	-148	G
4	R	-104	G
4	R	-99	A
4	R	-98	A
4	R	-97	G
4	R	-96	A
4	R	-94	C
4	R	-72	G
4	R	-70	C

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Mol	Chain	Res	Type
4	R	-67	C
4	R	-57	U
4	R	-56	A
4	R	-55	A
4	R	-48	G
4	R	-42	C
4	R	-9	G
4	R	-8	G
4	R	-7	U
4	R	-3	U
4	R	1	G
4	R	2	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	R	-177	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.