



Full wwPDB EM Validation Report ⓘ

Feb 24, 2025 – 12:07 pm GMT

PDB ID : 9FCV
EMDB ID : EMD-50322
Title : Cas nuclease-CRISPR (cr)RNA ribonucleoprotein (RNP) complex
Authors : Schmelz, S.; Lukat, P.; Blankenfeldt, W.
Deposited on : 2024-05-16
Resolution : 3.09 Å(reported)
Based on initial model : 6DTD

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 : 4.02b-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

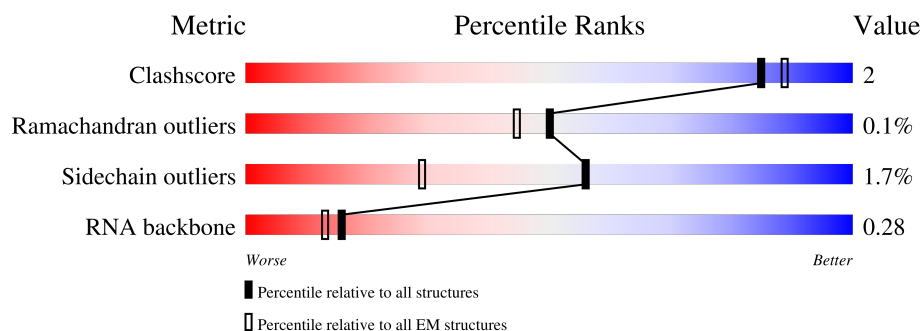
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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	210492	15764
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	A	1127	 88% 6% 6%
2	B	81	 26% 22% 6% 46%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 19225 atoms, of which 9402 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 Phage head-tail adaptor.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1057	Total	C	H	N	O	S	0	0
			17817	5698	8931	1557	1597	34		

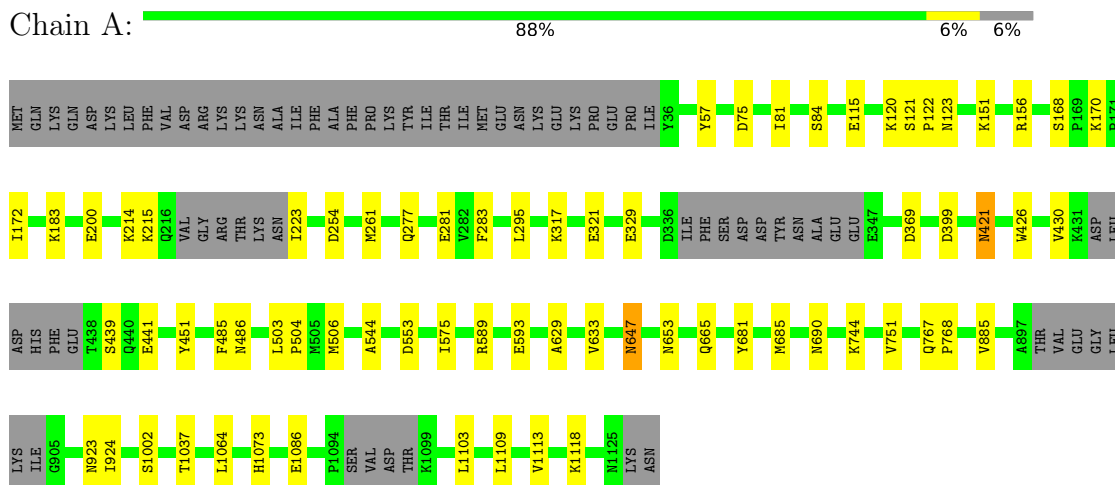
- Molecule 2 is a RNA chain called crRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	44	Total	C	H	N	O	P	0	0
			1408	420	471	167	306	44		

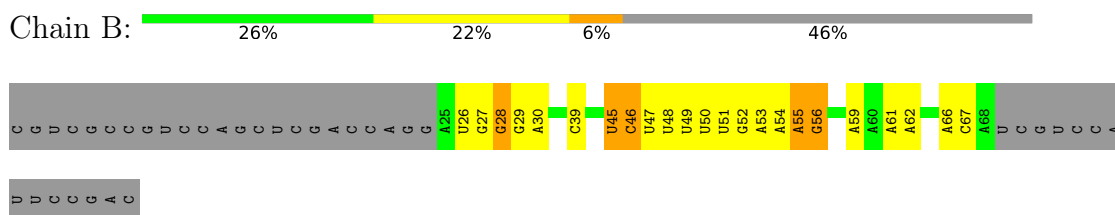
3 Residue-property plots [i](#)

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: Phage head-tail adaptor



- Molecule 2: crRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	356629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.24	0/9083	0.47	0/12212
2	B	0.18	0/1048	0.74	0/1630
All	All	0.24	0/10131	0.51	0/13842

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	8886	8931	8925	36	0
2	B	937	471	472	5	0
All	All	9823	9402	9397	40	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 2.

All (40) 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:1086:GLU:N	1:A:1086:GLU:OE2	2.12	0.82
2:B:59:A:O2'	2:B:61:A:N7	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:ASP:OD2	1:A:451:TYR:OH	2.07	0.69
1:A:151:LYS:NZ	1:A:172:ILE:O	2.16	0.69
1:A:426:TRP:O	1:A:430:VAL:HG23	1.92	0.69
1:A:653:ASN:OD1	2:B:67:C:O2'	2.12	0.66
1:A:544:ALA:HB2	1:A:751:VAL:HG21	1.81	0.62
2:B:28:G:N2	2:B:28:G:OP2	2.31	0.62
1:A:1064:LEU:CD2	1:A:1113:VAL:HG13	2.32	0.60
1:A:647:ASN:O	1:A:647:ASN:ND2	2.32	0.59
1:A:629:ALA:O	1:A:633:VAL:HG23	2.01	0.59
1:A:120:LYS:O	1:A:123:ASN:ND2	2.39	0.56
1:A:1064:LEU:HD21	1:A:1113:VAL:HG13	1.89	0.53
1:A:1109:LEU:O	1:A:1113:VAL:HG23	2.09	0.52
1:A:1037:THR:HG22	1:A:1037:THR:O	2.10	0.51
2:B:55:A:O2'	2:B:56:G:OP1	2.25	0.49
1:A:923:ASN:OD1	1:A:924:ILE:N	2.46	0.49
1:A:589:ARG:NH1	1:A:593:GLU:OE2	2.42	0.49
1:A:503:LEU:CD1	1:A:885:VAL:HG21	2.44	0.48
1:A:170:LYS:O	1:A:172:ILE:N	2.46	0.48
1:A:399:ASP:OD1	1:A:399:ASP:C	2.53	0.47
1:A:215:LYS:O	1:A:223:ILE:N	2.47	0.47
1:A:575:ILE:HD11	1:A:744:LYS:O	2.16	0.46
1:A:277:GLN:O	1:A:281:GLU:HG3	2.16	0.45
1:A:439:SER:OG	1:A:441:GLU:OE1	2.24	0.45
1:A:503:LEU:HB3	1:A:504:PRO:HD3	1.98	0.45
1:A:681:TYR:O	1:A:685:MET:HG3	2.17	0.45
1:A:295:LEU:H	1:A:295:LEU:HD23	1.82	0.44
1:A:115:GLU:OE1	1:A:183:LYS:NZ	2.51	0.44
1:A:1103:LEU:H	1:A:1103:LEU:HD12	1.83	0.44
1:A:767:GLN:HB3	1:A:768:PRO:HD3	1.99	0.43
1:A:421:ASN:N	1:A:421:ASN:OD1	2.51	0.43
1:A:81:ILE:HA	1:A:84:SER:OG	2.19	0.42
1:A:1064:LEU:HD23	1:A:1113:VAL:HG13	1.99	0.42
1:A:503:LEU:HD12	1:A:885:VAL:HG21	2.02	0.41
1:A:317:LYS:O	1:A:321:GLU:HG2	2.21	0.41
1:A:485:PHE:O	1:A:486:ASN:ND2	2.53	0.41
1:A:121:SER:N	1:A:122:PRO:CD	2.83	0.41
1:A:1002:SER:HB3	1:A:1103:LEU:HD11	2.03	0.41
2:B:45:U:H3'	2:B:46:C:C5'	2.51	0.40

There are no symmetry-related clashes.

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
1	A	1045/1127 (93%)	1021 (98%)	23 (2%)	1 (0%)	48 79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	SER

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	974/1039 (94%)	957 (98%)	17 (2%)	56 78

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	TYR
1	A	75	ASP
1	A	156	ARG
1	A	200	GLU
1	A	214	LYS
1	A	254	ASP
1	A	261	MET
1	A	283	PHE
1	A	329	GLU
1	A	421	ASN

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Mol	Chain	Res	Type
1	A	506	MET
1	A	553	ASP
1	A	647	ASN
1	A	665	GLN
1	A	690	ASN
1	A	1073	HIS
1	A	1118	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	43/81 (53%)	19 (44%)	1 (2%)

All (19) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	26	U
2	B	27	G
2	B	28	G
2	B	29	G
2	B	30	A
2	B	39	C
2	B	45	U
2	B	46	C
2	B	47	U
2	B	48	U
2	B	49	U
2	B	50	U
2	B	51	U
2	B	52	G
2	B	53	A
2	B	54	A
2	B	56	G
2	B	62	A
2	B	66	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	55	A

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.