



wwPDB EM Validation Summary Report ⓘ

Feb 27, 2025 – 10:07 PM JST

PDB ID : 8Z40
EMDB ID : EMD-39759
Title : The structure of type III CRISPR-associated deaminase apo form
Authors : Chen, M.R.; Li, Z.X.; Xiao, Y.B.
Deposited on : 2024-04-16
Resolution : 3.26 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

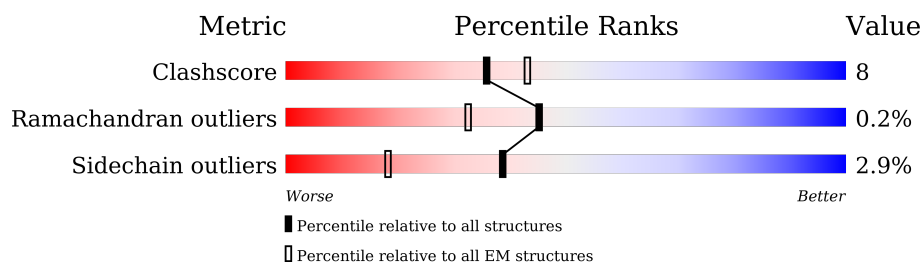
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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

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	635	
1	B	635	
1	C	635	
1	D	635	
1	E	635	
1	F	635	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21893 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 Adenosine deaminase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	614	Total	C	N	O	S	0	0
			4802	3031	892	857	22		
1	B	613	Total	C	N	O	S	0	0
			4807	3037	892	856	22		
1	C	395	Total	C	N	O	S	0	0
			3065	1922	575	554	14		
1	D	396	Total	C	N	O	S	0	0
			3075	1930	576	555	14		
1	E	396	Total	C	N	O	S	0	0
			3072	1929	576	553	14		
1	F	396	Total	C	N	O	S	0	0
			3072	1929	576	553	14		

There are 36 discrepancies between the modelled and reference sequences:

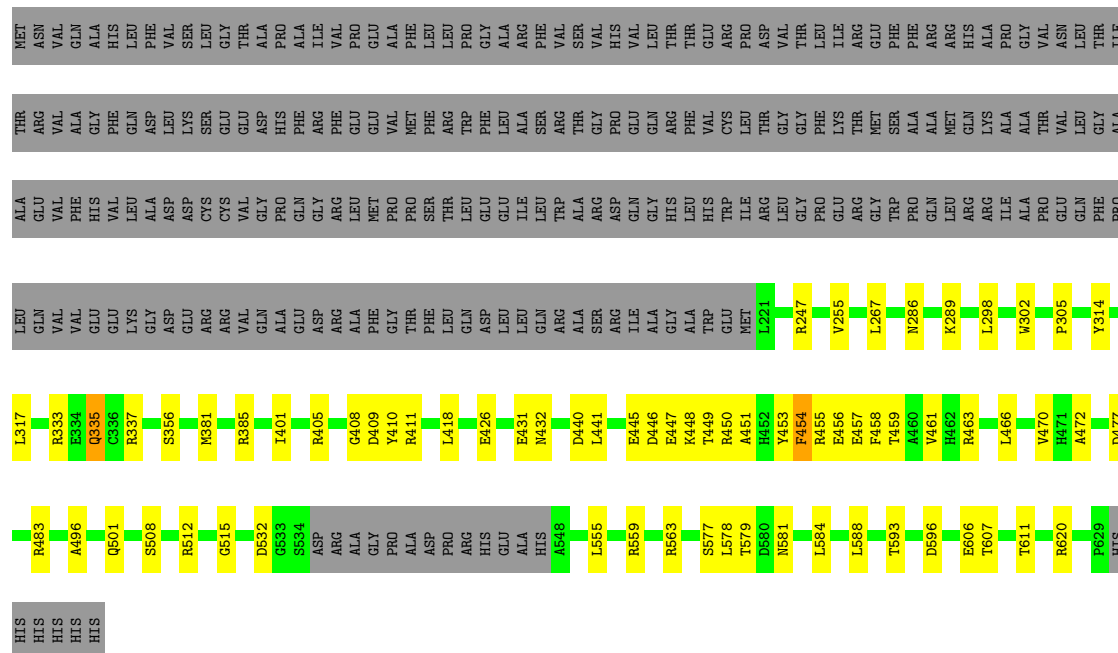
Chain	Residue	Modelled	Actual	Comment	Reference
A	630	HIS	-	expression tag	UNP A0A6M1RED6
A	631	HIS	-	expression tag	UNP A0A6M1RED6
A	632	HIS	-	expression tag	UNP A0A6M1RED6
A	633	HIS	-	expression tag	UNP A0A6M1RED6
A	634	HIS	-	expression tag	UNP A0A6M1RED6
A	635	HIS	-	expression tag	UNP A0A6M1RED6
B	630	HIS	-	expression tag	UNP A0A6M1RED6
B	631	HIS	-	expression tag	UNP A0A6M1RED6
B	632	HIS	-	expression tag	UNP A0A6M1RED6
B	633	HIS	-	expression tag	UNP A0A6M1RED6
B	634	HIS	-	expression tag	UNP A0A6M1RED6
B	635	HIS	-	expression tag	UNP A0A6M1RED6
C	630	HIS	-	expression tag	UNP A0A6M1RED6
C	631	HIS	-	expression tag	UNP A0A6M1RED6
C	632	HIS	-	expression tag	UNP A0A6M1RED6
C	633	HIS	-	expression tag	UNP A0A6M1RED6
C	634	HIS	-	expression tag	UNP A0A6M1RED6
C	635	HIS	-	expression tag	UNP A0A6M1RED6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	630	HIS	-	expression tag	UNP A0A6M1RED6
D	631	HIS	-	expression tag	UNP A0A6M1RED6
D	632	HIS	-	expression tag	UNP A0A6M1RED6
D	633	HIS	-	expression tag	UNP A0A6M1RED6
D	634	HIS	-	expression tag	UNP A0A6M1RED6
D	635	HIS	-	expression tag	UNP A0A6M1RED6
E	630	HIS	-	expression tag	UNP A0A6M1RED6
E	631	HIS	-	expression tag	UNP A0A6M1RED6
E	632	HIS	-	expression tag	UNP A0A6M1RED6
E	633	HIS	-	expression tag	UNP A0A6M1RED6
E	634	HIS	-	expression tag	UNP A0A6M1RED6
E	635	HIS	-	expression tag	UNP A0A6M1RED6
F	630	HIS	-	expression tag	UNP A0A6M1RED6
F	631	HIS	-	expression tag	UNP A0A6M1RED6
F	632	HIS	-	expression tag	UNP A0A6M1RED6
F	633	HIS	-	expression tag	UNP A0A6M1RED6
F	634	HIS	-	expression tag	UNP A0A6M1RED6
F	635	HIS	-	expression tag	UNP A0A6M1RED6

- Molecule 1: Adenosine deaminase domain-containing protein.



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	247410	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (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	0.25	0/4916	0.56	1/6683 (0.0%)
1	B	0.25	0/4923	0.54	0/6693
1	C	0.25	0/3134	0.55	0/4266
1	D	0.25	0/3144	0.53	0/4278
1	E	0.24	0/3142	0.52	0/4278
1	F	0.25	0/3142	0.53	0/4278
All	All	0.25	0/22401	0.54	1/30476 (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	105	LYS	CA-CB-CG	6.01	126.62	113.40

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	4802	0	4771	94	0
1	B	4807	0	4776	86	0
1	C	3065	0	3043	37	0
1	D	3075	0	3056	42	0
1	E	3072	0	3057	38	0
1	F	3072	0	3057	42	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	21893	0	21760	332	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 8.

The worst 5 of 332 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:C:445:GLU:HB3	1:C:450:ARG:HA	1.61	0.82
1:A:182:GLN:HB3	1:A:194:GLN:HE21	1.48	0.76
1:A:63:VAL:HG21	1:A:66:PHE:HB2	1.66	0.75
1:A:167:GLY:O	1:A:172:ARG:NH2	2.20	0.75
1:B:187:LYS:HB3	1:B:190:GLU:HB3	1.69	0.74

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	610/635 (96%)	569 (93%)	38 (6%)	3 (0%)	25	56
1	B	609/635 (96%)	569 (93%)	38 (6%)	2 (0%)	37	66
1	C	391/635 (62%)	368 (94%)	22 (6%)	1 (0%)	37	66
1	D	390/635 (61%)	377 (97%)	13 (3%)	0	100	100
1	E	392/635 (62%)	378 (96%)	14 (4%)	0	100	100
1	F	392/635 (62%)	373 (95%)	19 (5%)	0	100	100
All	All	2784/3810 (73%)	2634 (95%)	144 (5%)	6 (0%)	45	71

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	ALA
1	C	442	ALA
1	B	445	GLU
1	A	52	HIS
1	A	445	GLU

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	A	493/511 (96%)	480 (97%)	13 (3%)	41	64
1	B	494/511 (97%)	480 (97%)	14 (3%)	38	62
1	C	313/511 (61%)	304 (97%)	9 (3%)	37	61
1	D	315/511 (62%)	308 (98%)	7 (2%)	47	68
1	E	314/511 (61%)	302 (96%)	12 (4%)	28	54
1	F	314/511 (61%)	303 (96%)	11 (4%)	31	56
All	All	2243/3066 (73%)	2177 (97%)	66 (3%)	39	61

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	381	MET
1	F	410	TYR
1	F	620	ARG
1	B	457	GLU
1	B	450	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	GLN
1	D	462	HIS
1	E	321	ASN
1	E	335	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	397	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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.