



wwPDB X-ray Structure Validation Summary Report

Mar 8, 2026 – 12:23 AM UTC

PDB ID : 2ACI / pdb_00002aci
Title : Structure of D166A arginine deiminase
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Deposited on : 2005-07-18
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

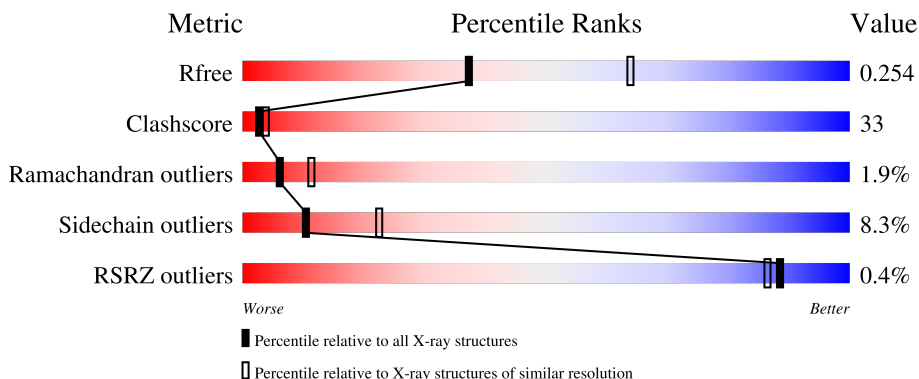
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	418	 39% 45% 11% .
1	B	418	 52% 39% 6% ..
1	C	418	 41% 45% 9% .
1	D	418	 41% 47% 9% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 12953 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Arginine deiminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	402	3139	1988	546	588	17	0	0	0
1	B	409	3193	2020	556	600	17	0	0	0
1	C	403	3147	1992	547	591	17	0	0	0
1	D	406	3174	2009	553	595	17	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	ALA	ASP	engineered mutation	UNP P13981
B	166	ALA	ASP	engineered mutation	UNP P13981
C	166	ALA	ASP	engineered mutation	UNP P13981
D	166	ALA	ASP	engineered mutation	UNP P13981

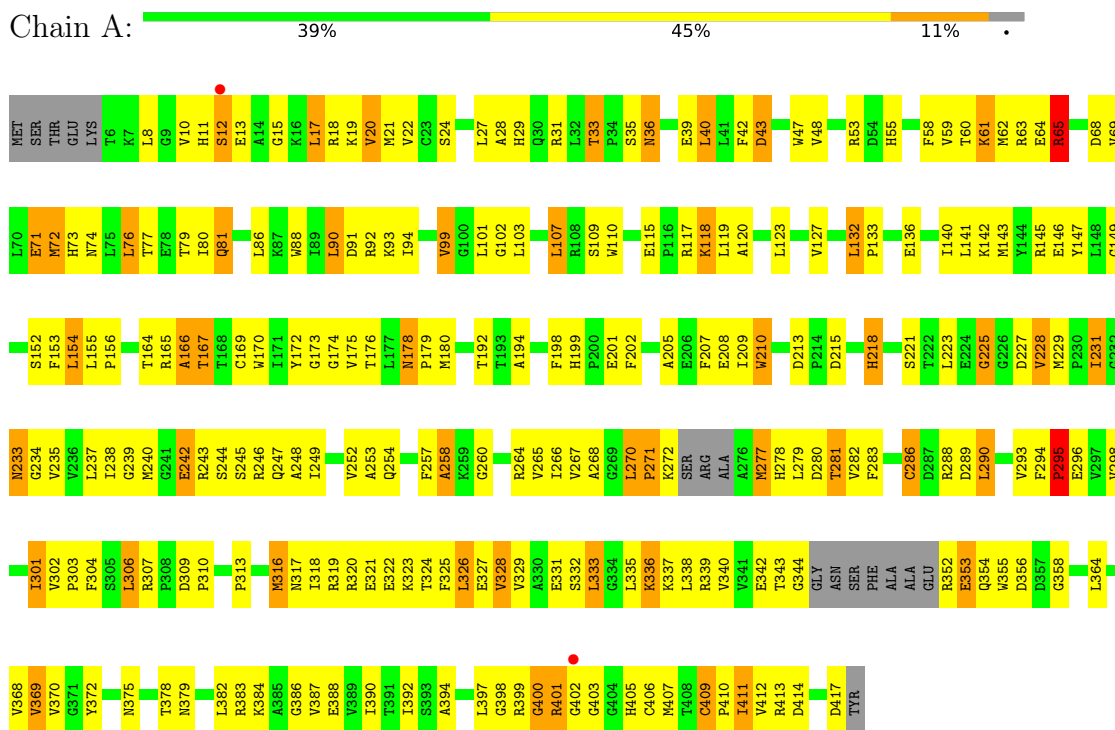
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	60	Total 60	O 60	0	0
2	B	90	Total 90	O 90	0	0
2	C	86	Total 86	O 86	0	0
2	D	64	Total 64	O 64	0	0

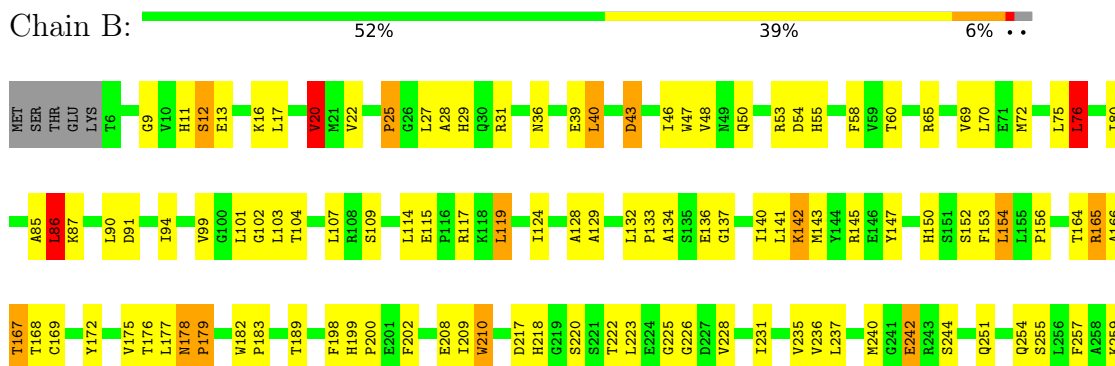
3 Residue-property plots

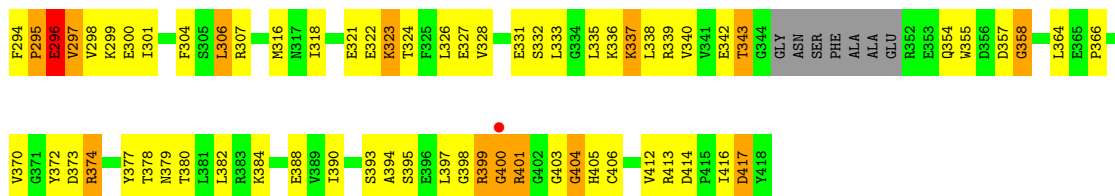
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Arginine deiminase



- Molecule 1: Arginine deiminase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.20Å 123.90Å 150.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.50) 93.5 (20.00-2.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.16 (at 2.88Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.198 , 0.272 0.182 , 0.254	Depositor DCC
R_{free} test set	1806 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtrriage
Anisotropy	0.128	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12953	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.88	3/3205 (0.1%)	1.30	35/4346 (0.8%)
1	B	0.92	0/3261	1.36	44/4422 (1.0%)
1	C	0.90	4/3213 (0.1%)	1.37	36/4356 (0.8%)
1	D	0.89	0/3242	1.35	39/4396 (0.9%)
All	All	0.90	7/12921 (0.1%)	1.34	154/17520 (0.9%)

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
1	C	0	1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	303	PRO	N-CD	10.60	1.62	1.47
1	C	156	PRO	CA-C	-6.16	1.48	1.52
1	C	354	GLN	C-N	6.01	1.41	1.33
1	C	214	PRO	N-CD	-5.66	1.39	1.47
1	A	295	PRO	C-N	-5.46	1.26	1.33

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	329	VAL	N-CA-C	-11.75	102.39	111.90
1	C	48	VAL	N-CA-C	11.19	121.16	110.42
1	A	178	ASN	N-CA-C	10.36	122.31	109.57
1	D	48	VAL	N-CA-C	10.19	120.83	110.23
1	C	354	GLN	OE1-CD-NE2	-10.13	112.47	122.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	TYR	Sidechain

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	3139	0	3128	270	0
1	B	3193	0	3177	166	0
1	C	3147	0	3132	221	0
1	D	3174	0	3161	216	0
2	A	60	0	0	24	0
2	B	90	0	0	22	0
2	C	86	0	0	15	0
2	D	64	0	0	14	0
All	All	12953	0	12598	840	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 33.

The worst 5 of 840 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:D:43:ASP:HB2	1:D:401:ARG:HH12	1.05	1.19
1:C:277:MET:HE2	1:C:281:THR:CG2	1.77	1.14
1:C:33:THR:HG22	1:C:35:SER:H	1.17	1.10
1:A:17:LEU:HD11	1:A:20:VAL:HG13	1.34	1.08
1:D:343:THR:HG21	1:D:358:GLY:N	1.69	1.07

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 X-ray entries followed by that with respect to entries of similar resolution.

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	396/418 (95%)	342 (86%)	45 (11%)	9 (2%)	5	8
1	B	405/418 (97%)	366 (90%)	36 (9%)	3 (1%)	18	34
1	C	397/418 (95%)	346 (87%)	45 (11%)	6 (2%)	8	16
1	D	402/418 (96%)	336 (84%)	53 (13%)	13 (3%)	3	4
All	All	1600/1672 (96%)	1390 (87%)	179 (11%)	31 (2%)	6	11

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	ASP
1	D	152	SER
1	D	276	ALA
1	D	323	LYS
1	A	172	TYR

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 X-ray entries followed by that with respect to entries of similar resolution.

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	342/354 (97%)	311 (91%)	31 (9%)	9	19
1	B	346/354 (98%)	312 (90%)	34 (10%)	7	16
1	C	343/354 (97%)	315 (92%)	28 (8%)	10	23
1	D	345/354 (98%)	324 (94%)	21 (6%)	17	35
All	All	1376/1416 (97%)	1262 (92%)	114 (8%)	10	22

5 of 114 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	363	CYS
1	D	306	LEU
1	C	116	PRO
1	D	295	PRO
1	D	147	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	187	GLN
1	C	317	ASN
1	D	375	ASN
1	D	150	HIS
1	D	218	HIS

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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	402/418 (96%)	-0.41	2 (0%) 87 85	18, 41, 64, 78	0
1	B	409/418 (97%)	-0.56	1 (0%) 91 89	16, 30, 60, 78	0
1	C	403/418 (96%)	-0.50	2 (0%) 87 85	17, 36, 62, 78	0
1	D	406/418 (97%)	-0.43	1 (0%) 91 89	17, 39, 66, 79	0
All	All	1620/1672 (96%)	-0.47	6 (0%) 88 86	16, 37, 64, 79	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	SER	3.1
1	B	276	ALA	2.8
1	D	400	GLY	2.5
1	C	313	PRO	2.5
1	A	402	GLY	2.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.