

Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 04:09 am BST

PDB ID : 3UYI

Title : Crystal Structure of Perakine Reductase, Founder Member of a Novel AKR

Subfamily with Unique Conformational Changes during NADPH Binding

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Deposited on : 2011-12-06

Resolution : 2.31 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp

with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.11

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

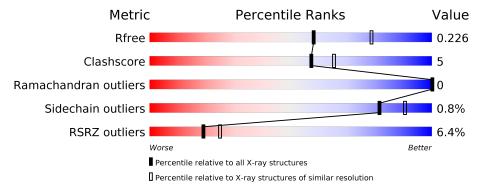
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.31 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 on 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 <=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		
			6%		
1	A	337	82%	11%	7%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4832 atoms, of which 2356 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 Perakine reductase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	313	Total	С	Н	N	О	S	0	0	0
	11	319	4783	1553	2356	412	453	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	EXPRESSION TAG	UNP Q3L181

• Molecule 2 is water.

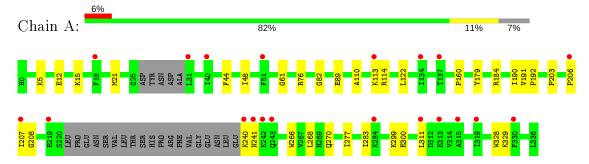
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	$\mathbf{AltConf}$
2	A	49	Total O 49 49	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Perakine reductase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	58.80Å 93.05Å 143.01Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 - 2.31	Depositor
resolution (A)	19.80 - 2.31	EDS
% Data completeness	96.8 (19.80-2.31)	Depositor
(in resolution range)	96.8 (19.80-2.31)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.28 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
P. P.	0.189 , 0.237	Depositor
R, R_{free}	0.183 , 0.226	DCC
R_{free} test set	932 reflections (5.50%)	wwPDB-VP
Wilson B-factor (Å ²)	49.9	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 42.5	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4832	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MLZ

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).

Mal	Chain	Bond	lengths	Bond angles		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.70	0/2462	0.73	0/3328	

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 (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	$\mathbf{H}(\mathbf{model})$	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2427	2356	2482	24	0
2	A	49	0	0	5	0
All	All	2476	2356	2482	24	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 5.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
1:A:21:MET:HE1	2:A:447:HOH:O	1.75	0.85
1:A:114:ARG:O	2:A:417:HOH:O	2.13	0.66

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A + a ma 1	A 4 0 mg 2	Interatomic	Clash
Atom-1	Atom-2	${\bf distance} \ ({\rm \AA})$	$\text{overlap } (\text{\AA})$
1:A:110:ALA:HA	1:A:113:LYS:HE2	1.77	0.64
1:A:206:PRO:HA	2:A:447:HOH:O	2.00	0.61
1:A:15:LYS:HE3	1:A:268:LEU:HD22	1.91	0.53
1:A:207:ILE:N	2:A:447:HOH:O	2.22	0.52
1:A:44:PHE:HA	1:A:48:ILE:O	2.09	0.52
1:A:299:LYS:HE2	1:A:300:GLU:OE2	2.09	0.52
1:A:191:VAL:HB	1:A:192:PRO:HD3	1.91	0.51
1:A:179:TYR:HB3	1:A:203:PRO:HB3	1.93	0.51
1:A:277:ILE:HG13	1:A:277:ILE:O	2.12	0.48
1:A:5:LYS:HD3	1:A:12:GLU:HG3	1.97	0.47
1:A:328:TRP:O	1:A:329:LYS:C	2.54	0.46
1:A:184:ARG:CZ	1:A:311:LEU:HD21	2.46	0.45
1:A:240:LYS:CD	1:A:241:ASN:H	2.31	0.44
1:A:266:TRP:O	1:A:270:GLN:HG2	2.19	0.43
1:A:160:PRO:HD3	1:A:190:ILE:HD11	2.03	0.41
1:A:283:ILE:N	1:A:283:ILE:HD12	2.35	0.41
1:A:82:GLY:HA2	1:A:122:LEU:O	2.20	0.41
1:A:15:LYS:HE3	1:A:268:LEU:CD2	2.50	0.41
1:A:207:ILE:HD12	1:A:208:GLY:H	1.84	0.41
1:A:61:GLY:HA2	2:A:401:HOH:O	2.21	0.41
1:A:191:VAL:N	1:A:192:PRO:CD	2.83	0.41
1:A:240:LYS:HG3	1:A:241:ASN:N	2.36	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 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	Perce	ntiles
1	A	306/337 (91%)	297 (97%)	9 (3%)	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 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.

Mo	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	264/286 (92%)	262 (99%)	2 (1%)	81 90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	ARG
1	A	89	GLU

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

Mol	Chain	${f Res}$	Type
1	A	287	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol Type Chain	n Res	Link	Bond lengths			Bond angles				
	туре	Chain	res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLZ	A	142	1	8,9,10	0.67	0	4,9,11	2.18	1 (25%)



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLZ	A	142	1	-	1/7/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	ms Z Observ		$\operatorname{Ideal}({}^{o})$
1	A	142	MLZ	CM-NZ-CE	-4.18	99.89	111.95

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	142	MLZ	CG-CD-CE-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates 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.



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, 95^{th} 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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	312/337 (92%)	0.18	20 (6%) 19	25	34, 52, 89, 129	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	330	PHE	4.2
1	A	31	LEU	3.7
1	A	240	LYS	3.6
1	A	241	ASN	3.6
1	A	207	ILE	3.2
1	A	242	LYS	3.0
1	A	243	GLN	3.0
1	A	134	ILE	2.8
1	A	18	PHE	2.8
1	A	137	THR	2.8
1	A	51	PHE	2.7
1	A	319	ILE	2.5
1	A	313	GLU	2.5
1	A	40	ILE	2.3
1	A	206	PRO	2.2
1	A	219	GLU	2.1
1	A	284	LYS	2.1
1	A	315	ALA	2.1
1	A	113	LYS	2.0
1	A	311	LEU	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column



labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

\mathbf{M}	d Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	MLZ	A	142	10/11	0.88	0.13	42,51,66,66	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.

