

Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 07:14 AM EDT

PDB ID	:	4PR8
Title	:	URATE OXIDASE AZIDE URIC ACID TERNARY complex
Authors	:	Colloc'h, N.; Prange, T.
Deposited on		
Resolution	:	1.16 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

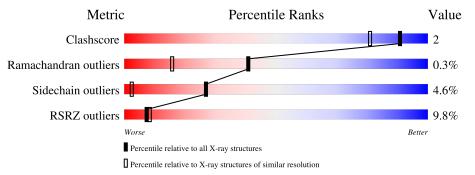
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.16 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	1832 (1.20-1.12)
Ramachandran outliers	138981	1768 (1.20-1.12)
Sidechain outliers	138945	1768 (1.20-1.12)
RSRZ outliers	127900	1724 (1.20-1.12)

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 <=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		
			10%		
1	А	302	86%	11%	••



4PR8

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4986 atoms, of which 2294 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.

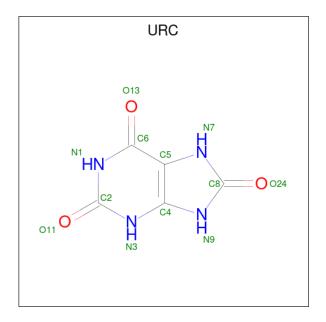
• Molecule 1 is a protein called Uricase.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	А	296	$\begin{array}{c} \text{Total} \\ 4665 \end{array}$	C 1498	Н 2294	N 411	0 454	S 8	0	3	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP Q00511
А	296	SER	-	expression tag	UNP Q00511
А	297	LEU	-	expression tag	UNP Q00511
А	298	LYS	-	expression tag	UNP Q00511
А	299	SER	-	expression tag	UNP Q00511
А	300	LYS	-	expression tag	UNP Q00511
А	301	LEU	-	expression tag	UNP Q00511

• Molecule 2 is URIC ACID (three-letter code: URC) (formula: $C_5H_4N_4O_3$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	А	1	Total 12	C N 5 4	ł	O 3	0	0

• Molecule 3 is AZIDE ION (three-letter code: AZI) (formula: N_3).

	AZI	
N1 N	N2 N⁺── N⁻ N3	

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total N 3 3	0	0
3	А	1	Total N 3 3	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	А	1	Total 1	Na 1	0	0

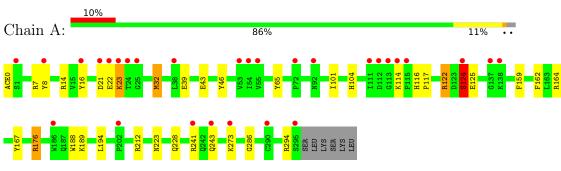
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	302	Total O 302 302	0	0



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 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: Uricase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	78.58Å 95.16Å 104.82Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	11.00 - 1.16	Depositor
Resolution (A)	22.75 - 1.16	EDS
% Data completeness	80.9 (11.00-1.16)	Depositor
(in resolution range)	80.9(22.75-1.16)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.99 (at 1.16 \text{\AA})$	Xtriage
Refinement program	SHELXL-97	Depositor
D D.	0.184 , (Not available)	Depositor
R, R_{free}	0.193 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	15.7	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.47,73.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4986	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.52% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: URC, NA, ACE, AZI

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	Bo	nd lengths	Bond angles	
Mol Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.59	1/2437~(0.0%)	1.42	33/3307~(1.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	0	ACE	C-N	-7.22	1.17	1.34

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	176	ARG	NE-CZ-NH1	14.30	127.45	120.30
1	А	122	ARG	NE-CZ-NH1	11.22	125.91	120.30
1	А	0	ACE	O-C-N	10.98	140.27	122.70
1	А	164	ARG	NE-CZ-NH2	-9.47	115.56	120.30
1	А	32	MET	CG-SD-CE	9.08	114.73	100.20
1	А	188	TRP	CD1-NE1-CE2	8.97	117.08	109.00
1	А	176	ARG	NE-CZ-NH2	-8.59	116.00	120.30
1	А	104	HIS	CG-ND1-CE1	8.31	119.83	108.20
1	А	65	TYR	CB-CG-CD1	-8.13	116.12	121.00
1	А	122	ARG	NE-CZ-NH2	-7.99	116.31	120.30
1	А	7	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	А	65	TYR	CB-CG-CD2	7.37	125.42	121.00
1	А	14	ARG	NE-CZ-NH1	-7.22	116.69	120.30
1	А	167	TYR	CB-CG-CD1	7.03	125.22	121.00
1	А	8	TYR	CB-CG-CD1	-6.90	116.86	121.00
1	А	212	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	А	46	TYR	CG-CD1-CE1	6.78	126.73	121.30
1	А	124	SER	O-C-N	6.77	133.53	122.70
1	А	228	GLN	O-C-N	-6.28	112.65	122.70
1	А	39	GLU	OE1-CD-OE2	6.13	130.66	123.30

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Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	32	MET	CA-CB-CG	6.12	123.71	113.30
1	А	188	TRP	CG-CD1-NE1	-6.06	104.04	110.10
1	А	212	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	А	7	ARG	NE-CZ-NH2	-5.63	117.49	120.30
1	А	188	TRP	NE1-CE2-CD2	-5.62	101.69	107.30
1	А	159	PHE	CB-CG-CD2	5.58	124.70	120.80
1	А	164	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	А	104	HIS	ND1-CG-CD2	-5.52	98.27	106.00
1	А	167	TYR	CB-CG-CD2	-5.51	117.69	121.00
1	А	46	TYR	CZ-CE2-CD2	5.29	124.56	119.80
1	А	46	TYR	CB-CG-CD1	5.12	124.07	121.00
1	А	16	TYR	CA-CB-CG	5.09	123.07	113.40
1	А	162	PHE	CB-CG-CD2	-5.01	117.29	120.80

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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	А	2371	2294	2337	8	0
2	А	12	0	4	1	0
3	А	6	0	0	1	0
4	А	1	0	0	0	0
5	А	302	0	0	2	0
All	All	2692	2294	2341	8	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 (8) 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:176:ARG:HH12	2:A:401:URC:HN3	1.32	0.77
1:A:286:GLY:HA3	3:A:402:AZI:N3	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:ASP:OD2	1:A:23:LYS:HD2	2.04	0.58
1:A:124:SER:HB2	5:A:1089:HOH:O	2.09	0.53
1:A:32:MET:HG2	1:A:101:ILE:CG2	2.43	0.48
1:A:294:ARG:HG3	5:A:1268:HOH:O	2.17	0.45
1:A:116:HIS:CG	1:A:117:PRO:HD2	2.51	0.45
1:A:43:GLU:H	1:A:43:GLU:CD	2.20	0.44

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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	А	297/302~(98%)	292~(98%)	4 (1%)	1 (0%)	41 16

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	124	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed Rotameric		Outliers	Percentiles	
1	А	264/267~(99%)	251~(95%)	13~(5%)	25 2	



Mol	Chain	Res	Type
1	А	22	GLU
1	А	23	LYS
1	А	114[A]	LYS
1	А	114[B]	LYS
1	А	122	ARG
1	А	124	SER
1	А	125	GLU
1	А	189	LYS
1	А	194	LEU
1	А	223	ASN
1	А	241	ARG
1	А	243	GLN
1	А	273	LYS

All (13) residues with a non-rotameric sidechain are listed below:

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	92	ASN
1	А	223	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	Turne	Type Chain Res		Link	Bond lengths			Bond angles		
10101	Type	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	URC	А	401	-	8,13,13	1.41	2 (25%)	$5,\!19,\!19$	7.95	5 (100%)
3	AZI	А	403	-	0,2,2	-	-	0,1,1	-	-
3	AZI	А	402	-	0,2,2	-	-	0,1,1	-	-

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
2	URC	А	401	-	-	-	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
2	А	401	URC	C5-C6	2.36	1.45	1.41
2	А	401	URC	C6-N1	2.15	1.36	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	401	URC	C2-N1-C6	15.05	127.85	115.14
2	А	401	URC	C5-C6-N1	-7.89	112.64	123.43
2	А	401	URC	C4-C5-N7	4.29	113.83	109.47
2	А	401	URC	C4-C5-C6	-2.07	118.82	120.80
2	А	401	URC	C4-N9-C8	2.06	102.37	101.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	401	URC	1	0
3	А	402	AZI	1	0



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	А	0:ACE	С	1:SER	N	1.17



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	<RSRZ $>$	#RSR	RZ>	$\cdot 2$	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	295/302~(97%)	0.95	29~(9%)	7	8	13, 18, 36, 65	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	23	LYS	10.8
1	А	22	GLU	8.6
1	А	113	GLY	5.5
1	А	92	ASN	5.1
1	А	273	LYS	4.6
1	А	137	GLY	4.4
1	А	295	SER	4.3
1	А	115	PRO	4.2
1	А	24	THR	4.2
1	А	114[A]	LYS	3.8
1	А	112	ASP	3.6
1	А	138	LYS	3.5
1	А	243	GLN	3.3
1	А	8	TYR	3.0
1	А	1	SER	2.9
1	А	55	VAL	2.8
1	А	111	ILE	2.8
1	А	21	ASP	2.7
1	А	38	LEU	2.6
1	А	241	ARG	2.5
1	А	202	PRO	2.5
1	А	53	VAL	2.4
1	А	124	SER	2.3
1	А	290[A]	CYS	2.2
1	А	25	GLY	2.2
1	А	186	TRP	2.2
1	А	16	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	А	72	PRO	2.1
1	А	54	ILE	2.0

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 monosaccharides in this entry.

6.4 Ligands (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, 95^{th} 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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q < 0.9
2	URC	А	401	12/12	0.88	0.15	$15,\!19,\!22,\!22$	0
3	AZI	А	403	3/3	0.89	0.14	18,18,22,25	0
3	AZI	А	402	3/3	0.96	0.16	9,9,22,23	0
4	NA	А	404	1/1	0.98	0.07	19,19,19,19	0

6.5 Other polymers (i)

There are no such residues in this entry.

