

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 23, 2021 - 03:47 PM EDT

PDB ID	:	1A5K
Title	:	K217E VARIANT OF KLEBSIELLA AEROGENES UREASE
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Deposited on		
Resolution	:	2.20  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:

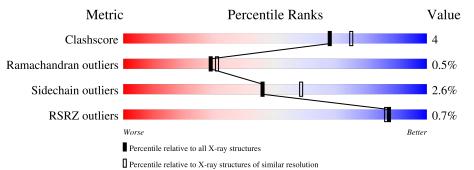
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

# 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 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	
1	А	100	99%	
2	В	101	.% <b>8</b> 9%	11%
3	С	566	% 87%	11% •



## 1A5K

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5964 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 UREASE (GAMMA SUBUNIT).

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	100	Total 776	C 491	N 134	0 146	${ m S}{ m 5}$	0	0	0

• Molecule 2 is a protein called UREASE (BETA SUBUNIT).

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	101	Total 785	C 496	N 150	0 136	${ m S} { m 3}$	0	0	0

• Molecule 3 is a protein called UREASE (ALPHA SUBUNIT).

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	С	566	Total 4226	C 2650	N 740	0 813	S 23	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	217	GLU	LYS	engineered mutation	UNP P18314

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	16	Total O 16 16	0	0
4	В	10	Total O 10 10	0	0
4	С	151	Total O 151 151	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: UREASE (GAMMA SUBUNIT)





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants	170.80Å 170.80Å 170.80Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	10.00 - 2.20	Depositor
Resolution (A)	31.18 - 2.20	EDS
% Data completeness	94.0 (10.00-2.20)	Depositor
(in resolution range)	88.9 (31.18-2.20)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	0.09	Depositor
$< I/\sigma(I) > 1$	$2.56 (at 2.20 \text{\AA})$	Xtriage
Refinement program	X-PLOR 3.1	Depositor
P. P.	0.178 , (Not available)	Depositor
$R, R_{free}$	0.167 , (Not available)	DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	15.4	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.32 , $43.3$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.032 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5964	wwPDB-VP
Average B, all atoms $(Å^2)$	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.32	0/787	0.56	0/1061	
2	В	0.32	0/805	0.61	0/1087	
3	С	0.32	0/4311	0.67	1/5875~(0.0%)	
All	All	0.32	0/5903	0.65	1/8023~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	С	299	ASN	N-CA-C	5.56	126.01	111.00

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	776	0	807	0	0
2	В	785	0	775	8	0
3	С	4226	0	4171	38	0
4	А	16	0	0	0	0
4	В	10	0	0	1	0
4	С	151	0	0	3	0
All	All	5964	0	5753	44	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 4.

All (44) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
		distance (Å)	overlap (Å)	
3:C:545:VAL:O	3:C:548:GLU:HG2	1.93	0.67	
3:C:297:SER:OG	3:C:349:HIS:HE1	1.80	0.65	
3:C:460:ASP:HB3	3:C:463:ALA:HB2	1.79	0.64	
3:C:201:GLN:HE21	3:C:203:ASP:H	1.49	0.58	
3:C:300:PRO:HD3	3:C:365:GLY:HA2	1.84	0.58	
2:B:83:ALA:HB1	2:B:88:ARG:HH21	1.68	0.58	
3:C:299:ASN:HB2	3:C:373:ARG:HD2	1.86	0.57	
3:C:170:CYS:O	3:C:172:PRO:HD3	2.06	0.56	
3:C:218:ILE:HD11	3:C:232:ALA:CB	2.38	0.54	
3:C:515:LYS:HB2	4:C:671:HOH:O	2.07	0.53	
2:B:72:GLU:H	2:B:75:GLN:NE2	2.07	0.51	
3:C:419:HIS:HD2	4:C:641:HOH:O	1.93	0.51	
3:C:218:ILE:HD13	3:C:243:VAL:HG13	1.92	0.51	
2:B:3:PRO:HA	3:C:24:ALA:O	2.12	0.50	
3:C:296:SER:HB3	3:C:356:LEU:HB2	1.94	0.49	
3:C:99:ALA:HA	3:C:110:ILE:O	2.13	0.49	
3:C:238:GLU:HG3	3:C:239:MET:HG3	1.95	0.49	
2:B:100:PRO:O	2:B:101:LEU:HB2	2.13	0.48	
3:C:300:PRO:HG3	3:C:364:MET:O	2.14	0.48	
2:B:50:LYS:HB2	4:B:109:HOH:O	2.12	0.48	
3:C:199:VAL:HG23	3:C:205:LEU:HD21	1.95	0.48	
3:C:219:HIS:HA	3:C:246:HIS:HB3	1.97	0.47	
3:C:395:ASN:C	3:C:395:ASN:HD22	2.19	0.46	
3:C:65:CYS:HA	3:C:111:PRO:HG2	1.96	0.46	
3:C:213:VAL:O	3:C:493:SER:HB3	2.15	0.46	
3:C:236:ALA:O	3:C:518:ARG:HD2	2.15	0.46	
3:C:43:VAL:HG22	4:C:657:HOH:O	2.15	0.45	
3:C:133:THR:HA	3:C:155:VAL:HB	1.98	0.45	
3:C:316:LEU:HD21	3:C:336:ARG:NE	2.31	0.45	
3:C:298:THR:CG2	3:C:360:ASP:HB2	2.48	0.44	
3:C:363:ALA:O	3:C:364:MET:HB2	2.17	0.44	
2:B:100:PRO:O	2:B:101:LEU:CB	2.64	0.44	
2:B:89:ALA:HA	2:B:100:PRO:HA	2.00	0.43	
3:C:281:ALA:HA	3:C:282:PRO:HA	1.78	0.43	
2:B:4:GLY:HA2	3:C:22:ARG:O	2.18	0.43	
3:C:36:LEU:HD22	3:C:84:ALA:HB2	2.01	0.42	
3:C:237:ASP:HA	3:C:518:ARG:HD3	2.00	0.42	
3:C:380:ARG:NE	3:C:555:ALA:HB2	2.34	0.42	

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:324:PRO:HA	3:C:330:VAL:CG1	2.50	0.42
3:C:489:LEU:HD23	3:C:510:ALA:HB3	2.02	0.41
3:C:135:ILE:HG13	3:C:154:MET:HB3	2.03	0.41
3:C:322:LEU:HD13	3:C:332:PHE:CE1	2.56	0.41
3:C:296:SER:CB	3:C:356:LEU:HB2	2.51	0.40
3:C:275:GLY:HA3	3:C:338:ARG:HH22	1.87	0.40

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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	Perce	ntiles
1	А	98/100~(98%)	97~(99%)	1 (1%)	0	100	100
2	В	99/101~(98%)	94 (95%)	5(5%)	0	100	100
3	С	564/566~(100%)	532 (94%)	28~(5%)	4 (1%)	22	22
All	All	761/767~(99%)	723~(95%)	34 (4%)	4 (0%)	29	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	С	481	GLY
3	С	360	ASP
3	С	272	HIS
3	С	364	MET

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	85/85~(100%)	84~(99%)	1 (1%)	71 83
2	В	78/78~(100%)	77~(99%)	1 (1%)	69 81
3	С	443/443 (100%)	429~(97%)	14 (3%)	39 50
All	All	606/606~(100%)	590~(97%)	16 (3%)	46 58

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

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	100	ILE
2	В	97	VAL
3	С	22	ARG
3	С	179	ARG
3	С	199	VAL
3	С	282	PRO
3	С	316	LEU
3	С	332	PHE
3	С	336	ARG
3	С	349	HIS
3	С	392	THR
3	С	394	ASP
3	С	395	ASN
3	С	449	LYS
3	С	507	LEU
3	С	508	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	12	GLN
2	В	16	ASN
2	В	29	HIS
3	С	142	GLN
3	С	166	HIS
3	С	201	GLN
3	С	349	HIS
3	С	362	GLN
3	С	395	ASN
3	С	419	HIS

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Mol	Chain	Res	Type
3	С	469	GLN
3	С	486	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 monosaccharides 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	100/100~(100%)	-0.98	0 100 100	4,10,26,37	0
2	В	101/101 (100%)	-0.58	1 (0%) 82 81	8, 18, 33, 47	0
3	С	566/566~(100%)	-0.86	4 (0%) 87 86	3, 10, 27, 73	0
All	All	767/767~(100%)	-0.84	5 (0%) 87 86	3, 11, 30, 73	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	С	334	GLU	4.8
3	С	333	ALA	4.7
3	С	332	PHE	3.9
3	С	313	LEU	3.0
2	В	101	LEU	2.2

## 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)

There are no ligands in this entry.



## 6.5 Other polymers (i)

There are no such residues in this entry.

