

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

Dec 9, 2023 - 08:27 am GMT

PDB ID Title		1GK1 Structure-based prediction of modifications in glutarylamidase to allow single- step enzymatic production of 7-aminocephalosporanic acid from cephalosporin C
Authors	:	Fritz-Wolf, K.; Koller, K.P.; Lange, G.; Liesum, A.; Sauber, K.; Schreuder, H.; Aretz, W.; Kabsch, W.
Deposited on Resolution		2001-08-07 2.40 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 (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:

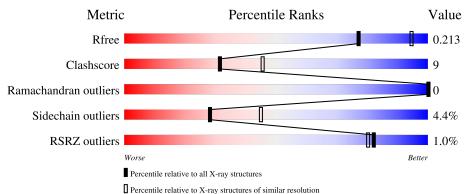
MolProbity	:	4.02b-467
•		1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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 2.40 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	153	88%	10%	•
1	С	153	2% <b>90%</b>	8%	•
2	В	522	80%	17%	•
2	D	522	% 80%	19%	•



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11321 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1 1	153	Total	С	Ν	0	S	0	0	0
	A		1203	765	212	225	1	0		
1	C	153	Total	С	Ν	0	S	0	0	0
	U	155	1203	765	212	225	1	0	0	0

• Molecule 1 is a protein called CEPHALOSPORIN ACYLASE.

There are 2 discrepancies between the modelled and reference sequences:

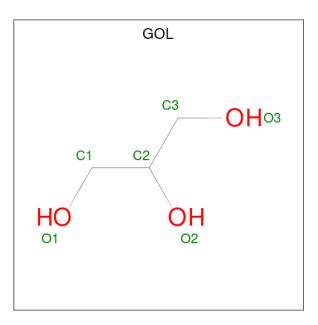
Chain	Residue	Modelled	Actual	Comment	Reference
А	126	GLU	ASP	conflict	UNP 086089
С	126	GLU	ASP	conflict	UNP 086089

• Molecule 2 is a protein called CEPHALOSPORIN ACYLASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	В	522	Total 4122	C 2606		0 778	S 11	0	0	0
2	D	522	Total 4122	-		0 778	S 11	0	0	0

• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

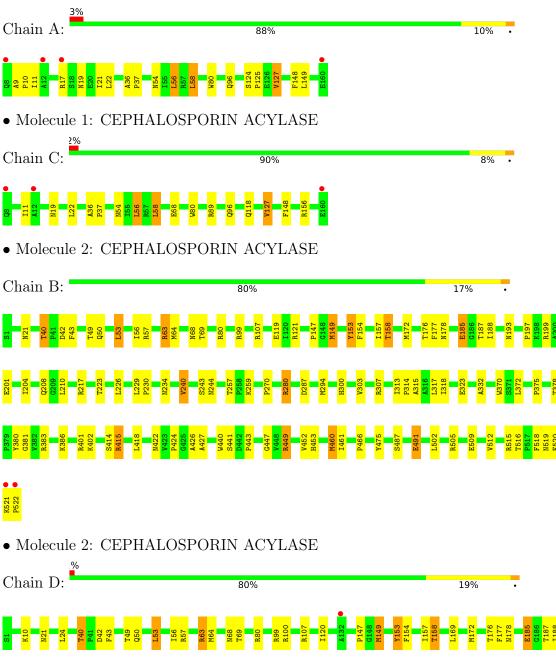
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	70	Total O 70 70	0	0
4	В	257	Total         O           257         257	0	0
4	С	81	Total         O           81         81	0	0
4	D	251	Total O 251 251	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: CEPHALOSPORIN ACYLASE



# 5437 5437 6491 63323 6196 63333 6196 E491 x3334 x3334 x199 E609 x3345 x3345 x109 E105 x3345 x304 x109 E509 x3345 x304 x109 F518 x371 x373 x000 F518 x371 x373 x000 F518 x371 x376 x200 F518 x376 x217 x200 F518 x376 x214 x214 F521 x376 x214 x244 F522 x361 x244 x244 F523 x416 x244 F524 x416 x244 F428 x446 x266 F438 x446 x266 F448 x446 x264 F448 x446</td



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	230.29Å 70.44Å 114.80Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $97.48^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	14.63 - 2.40	Depositor
Resolution (A)	14.63 - 2.40	EDS
% Data completeness	94.1 (14.63-2.40)	Depositor
(in resolution range)	94.2 (14.63-2.40)	EDS
R <sub>merge</sub>	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.23 (at $2.39$ Å)	Xtriage
Refinement program	CNS 1.0	Depositor
D D.	0.180 , $0.219$	Depositor
$R, R_{free}$	0.176 , $0.213$	DCC
$R_{free}$ test set	3362 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	17.5	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , $42.0$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.47, \langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11321	wwPDB-VP
Average B, all atoms $(Å^2)$	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 70.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1857e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<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)

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

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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.33	0/1242	0.53	0/1698	
1	С	0.32	0/1242	0.53	0/1698	
2	В	0.34	0/4237	0.61	0/5783	
2	D	0.34	0/4237	0.61	0/5783	
All	All	0.34	0/10958	0.59	0/14962	

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	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1203	0	1120	14	0
1	С	1203	0	1120	13	0
2	В	4122	0	3956	88	0
2	D	4122	0	3956	85	0
3	В	6	0	8	1	0
3	D	6	0	8	1	0
4	А	70	0	0	1	0
4	В	257	0	0	9	0
4	С	81	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	251	0	0	10	0
All	All	11321	0	10168	188	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 9.

The worst 5 of 188 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)
2:B:172:MET:HE3	2:B:226:LEU:HB2	1.49	0.94
2:D:172:MET:HE3	2:D:226:LEU:HB2	1.52	0.91
2:B:280:ARG:HH11	2:B:280:ARG:HB3	1.37	0.87
2:B:294:MET:HG2	2:B:460:MET:HG3	1.63	0.81
2:D:294:MET:HG2	2:D:460:MET:HG3	1.63	0.80

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	151/153~(99%)	149 (99%)	2(1%)	0	100	100
1	С	151/153~(99%)	147 (97%)	4(3%)	0	100	100
2	В	520/522~(100%)	507~(98%)	13 (2%)	0	100	100
2	D	520/522~(100%)	506~(97%)	14 (3%)	0	100	100
All	All	1342/1350~(99%)	1309 (98%)	33 (2%)	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.

Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	А	117/117~(100%)	114 (97%)	3~(3%)	46	66	
1	С	117/117~(100%)	113~(97%)	4 (3%)	37	56	
2	В	431/431 (100%)	409~(95%)	22~(5%)	24	39	
2	D	431/431~(100%)	412 (96%)	19 (4%)	28	45	
All	All	1096/1096~(100%)	1048 (96%)	48 (4%)	28	45	

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	127	VAL
2	D	158	THR
2	D	21	ASN
2	D	63	ARG
2	D	240	VAL

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such side chains are listed below:

Mol	Chain	Res	Type
1	С	8	GLN
2	D	446	ASN
1	С	117	GLN
2	D	268	GLN
1	С	96	GLN

#### 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)

2 ligands are 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	e Chain	Res	Link	Bond lengths			Bond angles		
IVIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
3	GOL	В	1523	-	$5,\!5,\!5$	0.49	0	$5,\!5,\!5$	0.52	0
3	GOL	D	1523	-	5,5,5	0.49	0	$5,\!5,\!5$	0.53	0

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
3	GOL	В	1523	-	-	0/4/4/4	-
3	GOL	D	1523	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

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
3	В	1523	GOL	1	0
3	D	1523	GOL	1	0



## 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	$OWAB(Å^2)$	Q<0.9
1	А	153/153~(100%)	-0.69	4 (2%) 56 54	10, 16, 43, 72	0
1	С	153/153~(100%)	-0.72	3 (1%) 65 63	10, 17, 43, 76	0
2	В	522/522~(100%)	-0.87	2 (0%) 92 91	6, 16, 30, 67	0
2	D	522/522~(100%)	-0.85	4 (0%) 86 84	7, 17, 31, 81	0
All	All	1350/1350~(100%)	-0.82	13 (0%) 82 80	6, 16, 33, 81	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
2	D	522	PRO	6.0
2	В	522	PRO	4.6
2	D	521	LYS	3.6
1	А	12	ALA	3.1
1	С	8	GLN	3.0

#### 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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
3	GOL	D	1523	6/6	0.71	0.35	41,44,48,53	0
3	GOL	В	1523	6/6	0.80	0.27	44,45,48,52	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

