wwPDB X-ray Structure Validation Summary Report (i)

Dec 9, 2023 – 08:27 am GMT

PDB ID	:	1GK1
Title	:	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	:	2001-08-07
Resolution	:	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 (i)) were used in the production of this report:

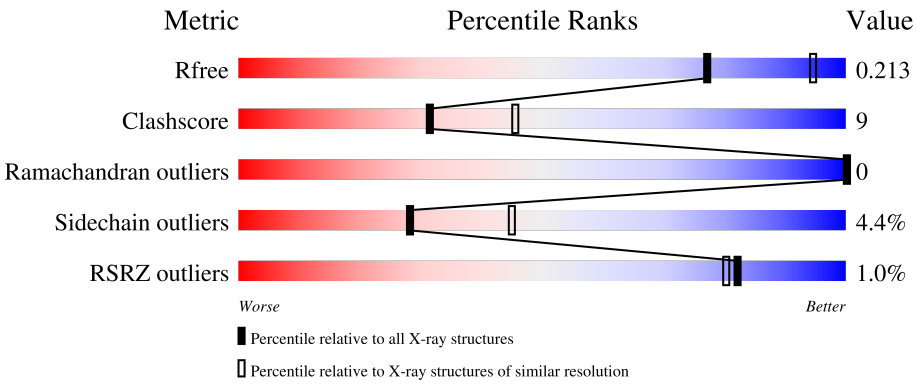
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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-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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
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	A	153	3% 88% 10% •
1	C	153	2% 90% 8% •
2	B	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.

- Molecule 1 is a protein called CEPHALOSPORIN ACYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	153	1203	765	212	225	1	0	0	0
1	C	153	1203	765	212	225	1	0	0	0

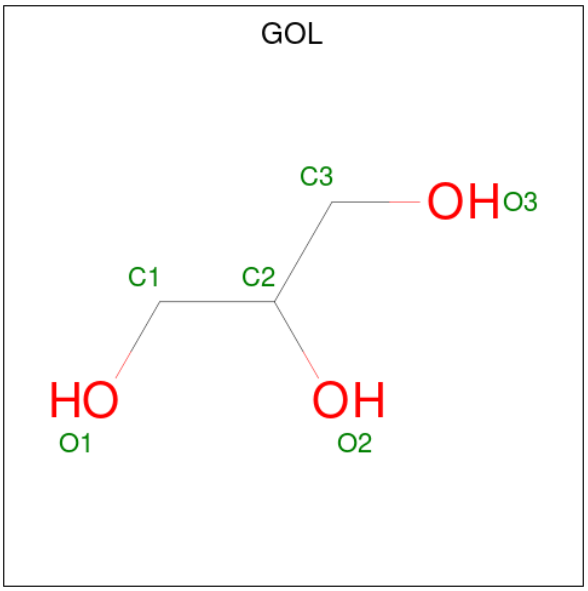
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	126	GLU	ASP	conflict	UNP O86089
C	126	GLU	ASP	conflict	UNP O86089

- Molecule 2 is a protein called CEPHALOSPORIN ACYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	522	4122	2606	727	778	11	0	0	0
2	D	522	4122	2606	727	778	11	0	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	D	1	6	3	3	0	0

- Molecule 4 is water.

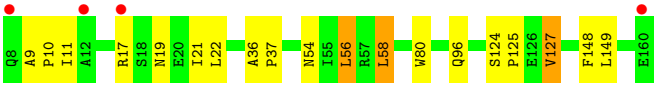
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	70	70	70	0	0
			Total	O		
4	B	257	257	257	0	0
			Total	O		
4	C	81	81	81	0	0
			Total	O		
4	D	251	251	251	0	0

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.

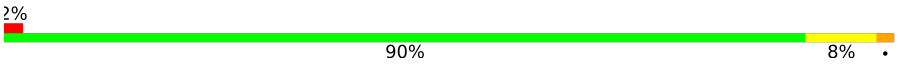
• Molecule 1: CEPHALOSPORIN ACYLASE

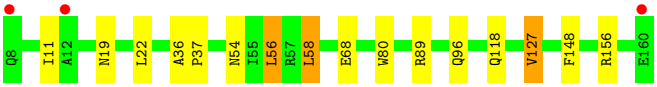
Chain A:



• Molecule 1: CEPHALOSPORIN ACYLASE

Chain C:



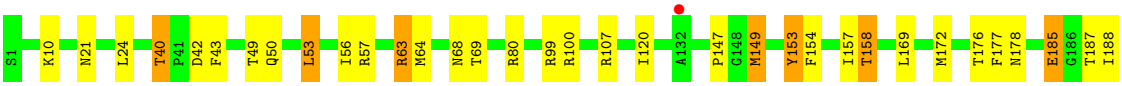


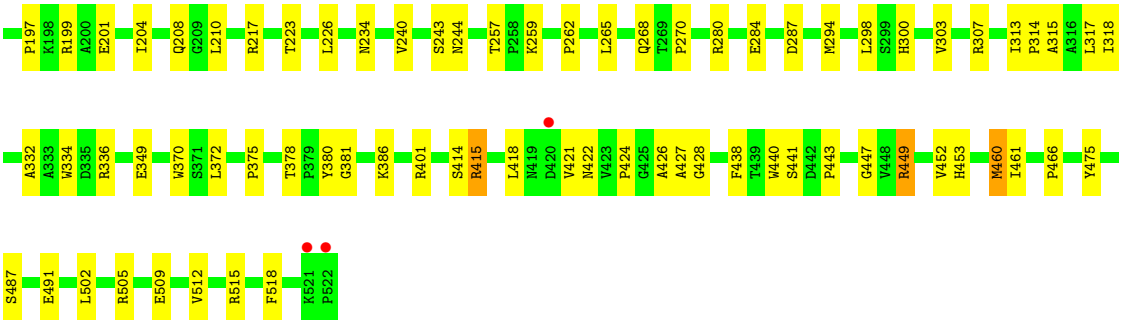
• Molecule 2: CEPHALOSPORIN ACYLASE

Chain B:

• Molecule 2: CEPHALOSPORIN ACYLASE

Chain D:




P197 K198 R199 A200 E201 I204 Q208 G209 L210 R217 T223 L226 N234 V240 S243 N244 T257 P258 K259 P262 L265 Q268 T269 P270 R280 E284 D287 M294 L298 S299 H300 V303 R307 I313 P314 A315 A316 L317 I318
A332 A333 W334 D335 R336 E349 W370 S371 L372 P375 T378 P379 Y380 G381 K386 R401 S414 R415 L418 N419 D420 V421 N422 V423 P424 G425 A426 A427 G428 F438 T439 W440 S441 D442 P443 G447 V448 R449 V452 H453 M460 I461 P466 Y475
S487 E491 L502 R505 E509 V512 R515 F518 K521 P522

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	230.29Å 70.44Å 114.80Å 90.00° 97.48° 90.00°	Depositor
Resolution (Å)	14.63 – 2.40 14.63 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.1 (14.63-2.40) 94.2 (14.63-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.23 (at 2.39Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.180 , 0.219 0.176 , 0.213	Depositor 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[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	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.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

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	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.33	0/1242	0.53	0/1698
1	C	0.32	0/1242	0.53	0/1698
2	B	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	A	1203	0	1120	14	0
1	C	1203	0	1120	13	0
2	B	4122	0	3956	88	0
2	D	4122	0	3956	85	0
3	B	6	0	8	1	0
3	D	6	0	8	1	0
4	A	70	0	0	1	0
4	B	257	0	0	9	0
4	C	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	Percentiles	
1	A	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
1	C	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
2	B	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	A	117/117 (100%)	114 (97%)	3 (3%)	46	66
1	C	117/117 (100%)	113 (97%)	4 (3%)	37	56
2	B	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	C	127	VAL
2	D	158	THR
2	D	21	ASN
2	D	63	ARG
2	D	240	VAL

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

Mol	Chain	Res	Type
1	C	8	GLN
2	D	446	ASN
1	C	117	GLN
2	D	268	GLN
1	C	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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	B	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	B	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	B	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, 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	153/153 (100%)	-0.69	4 (2%)	56	54	10, 16, 43, 72	0
1	C	153/153 (100%)	-0.72	3 (1%)	65	63	10, 17, 43, 76	0
2	B	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	Res	Type	RSRZ
2	D	522	PRO	6.0
2	B	522	PRO	4.6
2	D	521	LYS	3.6
1	A	12	ALA	3.1
1	C	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, 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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	D	1523	6/6	0.71	0.35	41,44,48,53	0
3	GOL	B	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.