

Full wwPDB X-ray Structure Validation Report (i)

Aug 3, 2023 – 02:41 AM EDT

PDB ID : 1GHI

Title : STRUCTURE OF BETA-LACTAMASE GLU166ASP:ASN170GLN MU-

TANT

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Deposited on : 2000-12-18

Resolution : 2.30 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 : 2.34

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

 $Refmac \quad : \quad 5.8.0158$

 $\begin{tabular}{lll} CCP4 & : & 7.0.044 & (Gargrove) \end{tabular}$

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

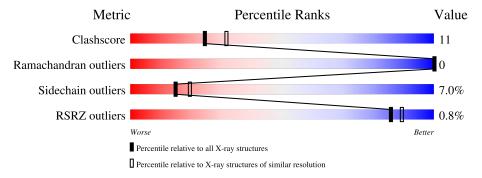
Validation Pipeline (wwPDB-VP) : 2.34

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 2.30 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	Similar resolution
	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	258	75%	21%	•



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2171 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.

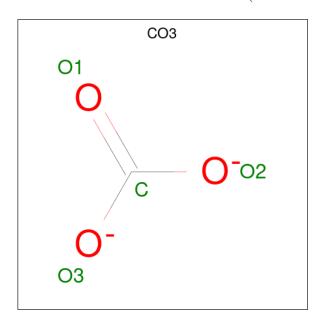
• Molecule 1 is a protein called BETA-LACTAMASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	257	Total 2029	C 1293	N 341	O 392	S 3	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	SEE REMARK 999	UNP P00807
A	166	ASP	GLU	engineered mutation	UNP P00807
A	170	GLN	ASN	engineered mutation	UNP P00807

• Molecule 2 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	A	1	Total 4	C 1	O 3	0	0

• Molecule 3 is water.



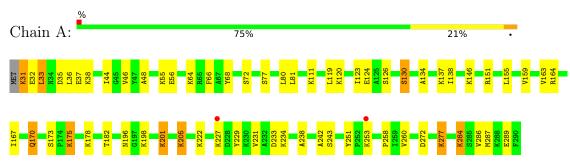
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	138	Total O 138 138	0	0



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.







4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	54.00Å 93.80Å 139.30Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 - 2.30	Depositor
Resolution (A)	34.32 - 2.17	EDS
% Data completeness	82.0 (8.00-2.30)	Depositor
(in resolution range)	80.2 (34.32-2.17)	EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.20 (at 2.18Å)	Xtriage
Refinement program	X-PLOR 3.7	Depositor
D D.	0.153 , 0.263	Depositor
R, R_{free}	0.177 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 109.5	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	0.94	EDS
Total number of atoms	2171	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.95% 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: CO3

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	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.92	0/2059	0.98	$1/2764 \ (0.0\%)$

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	119	LEU	CA-CB-CG	5.43	127.78	115.30

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	2029	0	2115	45	0
2	A	4	0	0	0	0
3	A	138	0	0	3	0
All	All	2171	0	2115	45	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 11.

All (45) 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)
1:A:31:LYS:HG3	1:A:32:GLU:H	1.27	0.98
1:A:32:GLU:HB3	1:A:35:ASP:HB2	1.51	0.93
1:A:31:LYS:HG3	1:A:32:GLU:N	1.99	0.78
1:A:229:TYR:HE2	1:A:287:MET:HE2	1.50	0.75
1:A:120:LYS:O	1:A:124:GLU:HG3	1.92	0.70
1:A:222:LYS:HG2	1:A:231:VAL:HB	1.75	0.69
1:A:159:VAL:HG11	1:A:182:THR:HG23	1.75	0.67
1:A:222:LYS:HE2	1:A:231:VAL:O	1.97	0.65
1:A:163:VAL:HG11	1:A:178:LYS:HD2	1.81	0.62
1:A:201:LYS:O	1:A:205:LYS:HG2	1.98	0.62
1:A:222:LYS:HG3	3:A:307:HOH:O	1.98	0.62
1:A:173:SER:OG	1:A:175:LYS:HG3	1.99	0.61
1:A:251:TYR:CE1	1:A:258:PRO:HB3	2.40	0.56
1:A:33:LEU:HD12	1:A:36:LEU:HD12	1.87	0.56
1:A:229:TYR:CE2	1:A:287:MET:HE2	2.39	0.52
1:A:201:LYS:HE2	1:A:205:LYS:NZ	2.24	0.52
1:A:201:LYS:CE	1:A:201:LYS:HA	2.40	0.51
1:A:48:ALA:O	1:A:56:GLU:HA	2.13	0.49
1:A:229:TYR:CD1	1:A:229:TYR:N	2.80	0.49
1:A:238:ALA:HB3	1:A:243:SER:HB2	1.94	0.49
1:A:242:ALA:HB2	1:A:272:ASP:O	2.13	0.48
1:A:46:VAL:HG11	1:A:286:VAL:HG21	1.96	0.48
1:A:277:LYS:NZ	3:A:371:HOH:O	2.48	0.47
1:A:222:LYS:HG2	1:A:231:VAL:CB	2.42	0.46
1:A:68:TYR:CD2	1:A:72:SER:HB3	2.52	0.45
1:A:80:LEU:HD23	1:A:123:ILE:HD11	1.98	0.45
1:A:151:ARG:NH2	1:A:155:LEU:HD21	2.32	0.45
1:A:229:TYR:N	1:A:229:TYR:HD1	2.14	0.45
1:A:44:ILE:HG22	1:A:46:VAL:HG23	1.99	0.44
1:A:222:LYS:HE3	1:A:233:ASP:OD2	2.17	0.44
1:A:234:LYS:HD2	1:A:234:LYS:HA	1.73	0.43
1:A:126:SER:O	1:A:130:SER:HA	2.18	0.43
1:A:134:ALA:O	1:A:138:ILE:HG13	2.18	0.43
1:A:48:ALA:HA	1:A:260:VAL:O	2.19	0.42
1:A:111:LYS:HA	1:A:111:LYS:HD3	1.83	0.42
1:A:55:LYS:NZ	1:A:289:GLU:O	2.51	0.42
1:A:164:ARG:CZ	1:A:178:LYS:HE2	2.49	0.42
1:A:32:GLU:HG3	3:A:403:HOH:O	2.20	0.42
1:A:284:LYS:HB2	1:A:284:LYS:NZ	2.34	0.42
1:A:167:ILE:O	1:A:170:GLN:HB2	2.20	0.41
1:A:201:LYS:HE2	1:A:205:LYS:HZ2	1.84	0.41
1:A:33:LEU:O	1:A:37:GLU:HG3	2.21	0.41
1.11.00.1110.0	1.11.57.615.1166		0.11

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Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \mathring{A}) \end{array}$	Clash overlap (Å)
1:A:64:LYS:HG2	1:A:66:PHE:CE1	2.56	0.41
1:A:163:VAL:HG12	1:A:164:ARG:HG3	2.03	0.40
1:A:77:SER:O	1:A:81:LEU:HG	2.20	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	Percentiles		
1	A	255/258~(99%)	246 (96%)	9 (4%)	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	227/228 (100%)	211 (93%)	16 (7%)	15 19		

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

Mol	Chain	Res	Type
1	A	31	LYS
1	A	33	LEU
1	A	38	LYS

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Mol	Chain	Res	Type
1	A	130	SER
1	A	137	LYS
1	A	146	LYS
1	A	170	GLN
1	A	175	LYS
1	A	196	ASN
1	A	198	LYS
1	A	201	LYS
1	A	205	LYS
1	A	227	LYS
1	A	253	LYS
1	A	277	LYS
1	A	284	LYS

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

Mol	Chain	Res	Type
1	A	191	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)

1 ligand 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 Res Lin		Link	B	ond leng	gths	Bond angles			
	MIOI	Type	Chain	iii nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
ſ	2	CO3	A	1	-	2,3,3	0.39	0	2,3,3	1.24	0

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.

No monomer is involved in short contacts.

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	<rsrz></rsrz>	$\#\mathrm{RSRZ}{>}2$		$OWAB(Å^2)$	Q<0.9	
1	A	257/258 (99%)	-0.67	2 (0%)	86	89	4, 16, 39, 66	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	LYS	3.2
1	A	227	LYS	2.3

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	CO3	A	1	4/4	0.88	0.28	39,45,47,50	0

6.5 Other polymers (i)

There are no such residues in this entry.

