Full wwPDB X-ray Structure Validation Report (i)

Mar 8, 2026 – 12:13 PM UTC

PDB ID	:	1KGE / pdb_00001kge
Title	:	STRUCTURE OF BETA-LACTAMASE ASN 170 MET MUTANT
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Deposited on	:	1996-10-17
Resolution	:	2.00 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 (i)) were used in the production of this report:

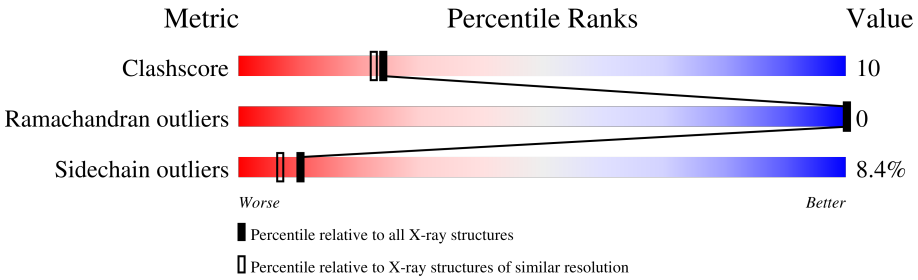
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	258	75% 19%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2191 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	C	N	O	S	0	0	0
			2029	1294	340	391	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	170	MET	ASN	engineered mutation	UNP P00807

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	162	Total	O	0	0
			162	162		

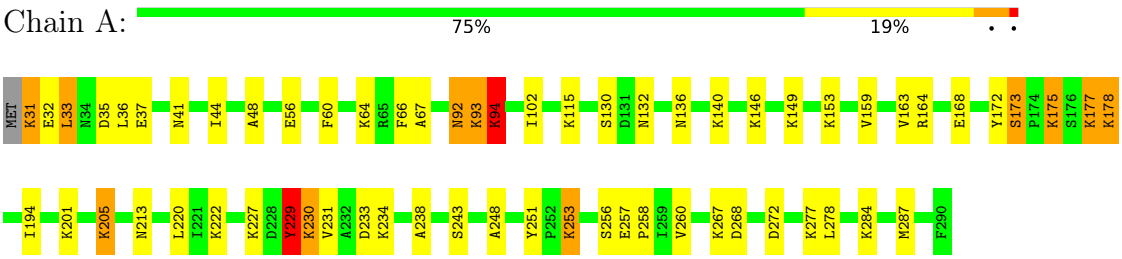
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: BETA-LACTAMASE

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	54.30Å 94.00Å 139.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.156 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2191	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.06	1/2059 (0.0%)	1.22	12/2763 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	LYS	CA-C	-5.03	1.46	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	213	ASN	N-CA-C	6.57	121.31	113.16
1	A	173	SER	CA-C-N	6.42	127.86	119.84
1	A	173	SER	C-N-CA	6.42	127.86	119.84
1	A	102	ILE	N-CA-C	6.01	116.81	109.30
1	A	220	LEU	N-CA-C	5.77	114.29	108.75
1	A	268	ASP	N-CA-C	5.74	120.01	112.89
1	A	159	VAL	N-CA-C	5.73	117.11	111.67
1	A	132	ASN	N-CA-C	5.50	118.20	111.82
1	A	229	TYR	N-CA-C	5.43	118.78	110.20
1	A	194	ILE	N-CA-C	5.35	116.16	111.56
1	A	257	GLU	N-CA-C	-5.30	103.39	110.07
1	A	248	ALA	N-CA-C	5.28	116.31	108.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2118	42	0
2	A	162	0	0	2	0
All	All	2191	0	2118	42	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 10.

All (42) 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:177:LYS:HD3	1:A:177:LYS:H	1.41	0.85
1:A:173:SER:OG	1:A:175:LYS:HG3	1.90	0.70
1:A:201:LYS:O	1:A:205:LYS:HG2	1.92	0.70
1:A:253:LYS:NZ	1:A:253:LYS:HB3	2.08	0.68
1:A:146:LYS:HD2	1:A:146:LYS:H	1.59	0.67
1:A:238:ALA:HB3	1:A:243:SER:HB2	1.77	0.67
1:A:205:LYS:HE2	2:A:431:HOH:O	2.00	0.61
1:A:229:TYR:N	1:A:229:TYR:HD1	1.98	0.61
1:A:177:LYS:H	1:A:177:LYS:CD	2.13	0.60
1:A:44:ILE:HD11	1:A:278:LEU:HD11	1.85	0.59
1:A:229:TYR:HE2	1:A:287:MET:HE2	1.69	0.57
1:A:222:LYS:HG2	1:A:231:VAL:HB	1.86	0.57
1:A:163:VAL:HG11	1:A:178:LYS:HG2	1.86	0.56
1:A:229:TYR:N	1:A:229:TYR:CD1	2.69	0.56
1:A:92:ASN:HD22	1:A:92:ASN:H	1.53	0.55
1:A:229:TYR:CE2	1:A:287:MET:HE2	2.42	0.53
1:A:136:ASN:O	1:A:140:LYS:HG2	2.09	0.52
1:A:33:LEU:HD12	1:A:36:LEU:HD12	1.91	0.52
1:A:92:ASN:HD22	1:A:92:ASN:N	2.08	0.51
1:A:149:LYS:HE2	1:A:153:LYS:NZ	2.26	0.50
1:A:115:LYS:HE3	2:A:372:HOH:O	2.12	0.49
1:A:48:ALA:HA	1:A:260:VAL:O	2.13	0.48
1:A:146:LYS:H	1:A:146:LYS:CD	2.19	0.47
1:A:251:TYR:CE1	1:A:258:PRO:HB3	2.49	0.47
1:A:177:LYS:HD3	1:A:177:LYS:N	2.20	0.47
1:A:164:ARG:CZ	1:A:178:LYS:NZ	2.78	0.47
1:A:284:LYS:HE3	1:A:284:LYS:HB2	1.78	0.46
1:A:230:LYS:HB2	1:A:251:TYR:HB2	1.96	0.46
1:A:229:TYR:HE2	1:A:287:MET:CE	2.28	0.46
1:A:267:LYS:HD3	1:A:272:ASP:HB3	1.97	0.46
1:A:48:ALA:O	1:A:56:GLU:HA	2.16	0.45
1:A:31:LYS:HB3	1:A:32:GLU:H	1.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:LYS:HG2	1:A:66:PHE:CE1	2.53	0.44
1:A:164:ARG:CZ	1:A:178:LYS:HZ3	2.31	0.44
1:A:33:LEU:HB3	1:A:60:PHE:CE2	2.53	0.43
1:A:175:LYS:C	1:A:175:LYS:HD2	2.42	0.43
1:A:222:LYS:HE3	1:A:231:VAL:O	2.18	0.43
1:A:234:LYS:HA	1:A:234:LYS:HD2	1.81	0.42
1:A:253:LYS:HB3	1:A:253:LYS:HZ2	1.81	0.41
1:A:93:LYS:HD3	1:A:94:LYS:N	2.35	0.41
1:A:67:ALA:HB2	1:A:172:TYR:CD1	2.56	0.41
1:A:37:GLU:O	1:A:41:ASN:N	2.53	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%)	248 (97%)	7 (3%)	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%)	208 (92%)	19 (8%)	10 7

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS
1	A	33	LEU
1	A	35	ASP
1	A	92	ASN
1	A	93	LYS
1	A	94	LYS
1	A	130	SER
1	A	168	GLU
1	A	175	LYS
1	A	177	LYS
1	A	178	LYS
1	A	205	LYS
1	A	227	LYS
1	A	229	TYR
1	A	230	LYS
1	A	233	ASP
1	A	253	LYS
1	A	256	SER
1	A	277	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	92	ASN
1	A	196	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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.