Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:07 pm BST

PDB ID	:	1OME
Title	:	CRYSTAL STRUCTURE OF THE OMEGA LOOP DELETION MUTANT (RESIDUES 163-178 DELETED) OF BETA-LACTAMASE FROM STAPHYLOCOCCUS AUREUS PC1
Authors	:	Banerjee, S.; Pieper, U.; Herzberg, O.
Deposited on	:	1998-02-09
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 ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

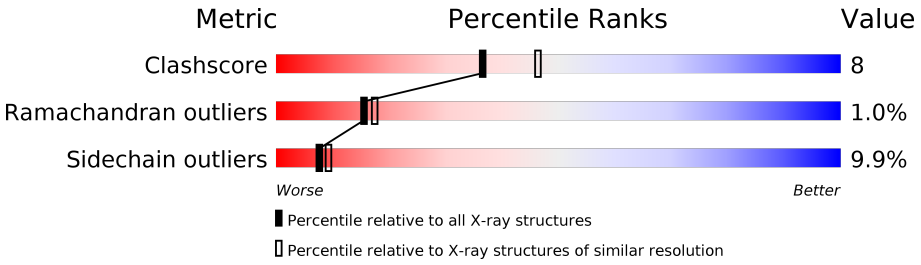
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (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 on 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	69% 21% • 7%
1	B	258	68% 20% • • 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3926 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	241	Total	C	N	O	S	0	0	0
			1877	1192	316	366	3			
1	B	240	Total	C	N	O	S	0	0	0
			1867	1186	313	365	3			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	105	Total	O	0	0
			105	105		
3	B	76	Total	O	0	0
			76	76		

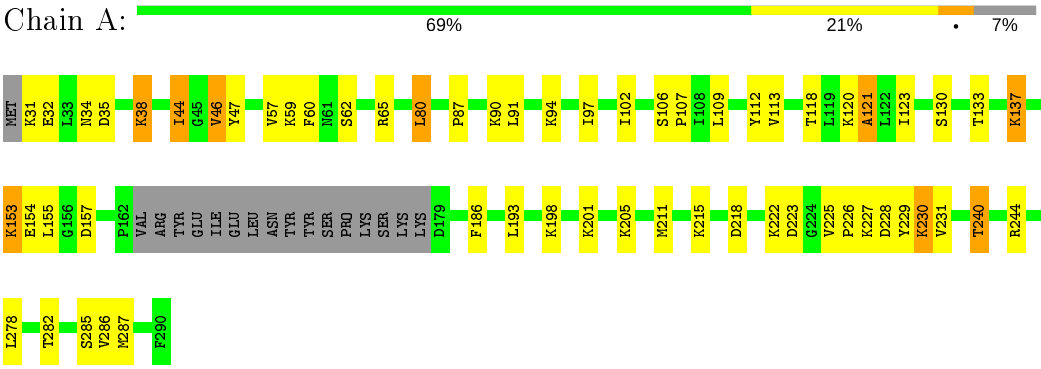
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

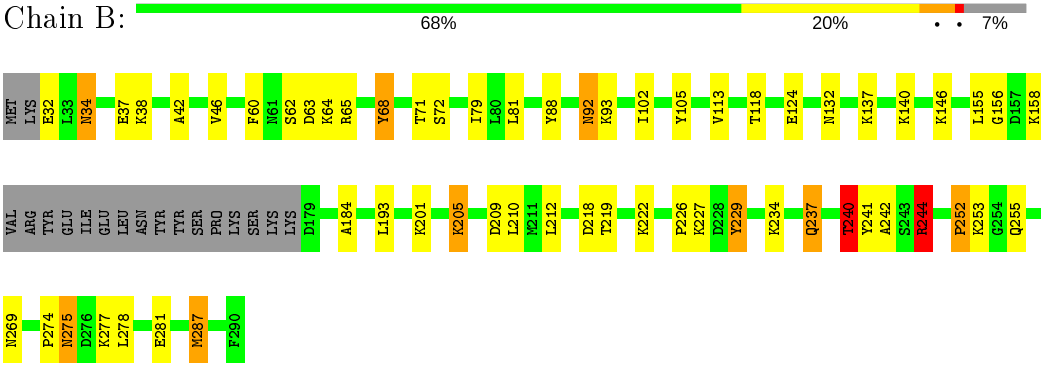
- Molecule 1: BETA-LACTAMASE

Chain A:



- Molecule 1: BETA-LACTAMASE

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.00Å 55.00Å 79.20Å 90.00° 90.25° 90.00°	Depositor
Resolution (Å)	7.00 – 2.30	Depositor
% Data completeness (in resolution range)	79.0 (7.00-2.30)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.190 , 0.298	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3926	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.91	0/1902	1.55	17/2556 (0.7%)
1	B	0.85	0/1892	1.52	15/2545 (0.6%)
All	All	0.88	0/3794	1.53	32/5101 (0.6%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	65	ARG	NE-CZ-NH2	-10.89	114.85	120.30
1	B	65	ARG	NE-CZ-NH2	-9.62	115.49	120.30
1	B	240	THR	N-CA-CB	-8.57	94.02	110.30
1	B	244	ARG	NE-CZ-NH1	8.27	124.44	120.30
1	A	121	ALA	N-CA-CB	7.99	121.29	110.10
1	A	240	THR	N-CA-CB	-7.65	95.76	110.30
1	A	65	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	B	244	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	B	46	VAL	CG1-CB-CG2	-7.18	99.41	110.90
1	A	154	GLU	CA-CB-CG	7.07	128.96	113.40
1	B	275	ASN	CA-C-N	-6.91	101.99	117.20
1	A	121	ALA	CB-CA-C	-6.83	99.85	110.10
1	A	38	LYS	CA-CB-CG	6.64	128.02	113.40
1	A	47	TYR	CB-CG-CD1	-6.57	117.06	121.00
1	A	35	ASP	CB-CG-OD2	-6.50	112.45	118.30
1	B	65	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	B	68	TYR	CB-CG-CD2	-6.35	117.19	121.00
1	B	229	TYR	CB-CG-CD2	-6.10	117.34	121.00
1	A	211	MET	CG-SD-CE	5.97	109.75	100.20
1	B	275	ASN	O-C-N	5.90	132.14	122.70
1	A	80	LEU	CD1-CG-CD2	-5.86	92.92	110.50
1	B	287	MET	CG-SD-CE	5.68	109.29	100.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	35	ASP	CB-CG-OD1	5.43	123.19	118.30
1	A	154	GLU	N-CA-CB	-5.34	100.98	110.60
1	B	160	THR	CA-C-N	-5.32	105.49	117.20
1	A	80	LEU	CA-CB-CG	5.24	127.35	115.30
1	A	157	ASP	CB-CG-OD1	5.22	122.99	118.30
1	A	112	TYR	CB-CG-CD2	-5.17	117.90	121.00
1	A	251	TYR	CB-CG-CD2	-5.12	117.93	121.00
1	B	88	TYR	CB-CG-CD1	-5.10	117.94	121.00
1	B	209	ASP	CB-CG-OD1	5.05	122.84	118.30
1	B	81	LEU	CB-CG-CD1	-5.01	102.48	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	A	1877	0	1940	31	0
1	B	1867	0	1921	33	0
2	B	1	0	0	0	0
3	A	105	0	0	3	0
3	B	76	0	0	1	0
All	All	3926	0	3861	60	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 8.

All (60) 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:80:LEU:HD22	1:A:123:ILE:HD11	1.65	0.78
1:A:155:LEU:HD11	1:A:193:LEU:HG	1.73	0.71
1:B:252:PRO:HB2	1:B:255:GLN:HB3	1.73	0.71
1:B:68:TYR:CE1	1:B:72:SER:HB3	2.26	0.70
1:B:68:TYR:HE1	1:B:72:SER:HB3	1.62	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:GLY:HA2	1:B:158:LYS:NZ	2.14	0.62
1:B:275:ASN:HB3	1:B:278:LEU:HB3	1.82	0.61
1:A:201:LYS:HG3	1:A:205:LYS:HZ3	1.66	0.60
1:B:34:ASN:HA	1:B:37:GLU:HG2	1.84	0.60
1:A:44:ILE:HD11	1:A:278:LEU:HD11	1.83	0.59
1:A:201:LYS:O	1:A:205:LYS:HD3	2.02	0.59
1:B:201:LYS:O	1:B:205:LYS:HG2	2.04	0.58
1:A:106:SER:H	1:B:240:THR:CG2	2.16	0.58
1:A:106:SER:HB2	1:B:240:THR:HG21	1.86	0.57
1:A:222:LYS:HG2	1:A:231:VAL:HB	1.87	0.56
1:A:46:VAL:HG13	1:A:60:PHE:HB3	1.89	0.55
1:B:267:LYS:NZ	1:B:275:ASN:HB2	2.21	0.54
1:A:222:LYS:HG3	3:A:302:HOH:O	2.07	0.54
1:A:102:ILE:HD13	1:A:133:THR:HG21	1.90	0.54
1:B:105:TYR:HB2	1:B:132:ASN:HD22	1.74	0.53
1:B:71:THR:HG22	1:B:234:LYS:O	2.08	0.53
1:B:218:ASP:HA	1:B:222:LYS:HB2	1.92	0.51
1:B:267:LYS:HZ1	1:B:275:ASN:HB2	1.76	0.51
1:B:156:GLY:HA2	1:B:158:LYS:HZ3	1.76	0.50
1:B:268:ASP:HB3	1:B:269:ASN:OD1	2.10	0.50
1:A:228:ASP:HB3	1:A:253:LYS:HD2	1.94	0.50
1:A:87:PRO:HD2	1:A:90:LYS:HG3	1.94	0.50
1:A:94:LYS:HG2	1:A:118:THR:HG22	1.93	0.49
1:A:44:ILE:HD11	1:A:278:LEU:HD21	1.95	0.49
1:A:31:LYS:N	1:A:285:SER:HG	2.10	0.49
1:A:282:THR:O	1:A:286:VAL:HG23	2.13	0.48
1:A:57:VAL:HG11	1:A:286:VAL:HG13	1.95	0.48
1:B:275:ASN:HD22	1:B:277:LYS:HG3	1.79	0.47
1:B:42:ALA:HB2	1:B:267:LYS:HD2	1.96	0.47
1:A:153:LYS:N	1:A:153:LYS:HD3	2.29	0.47
1:B:92:ASN:H	1:B:92:ASN:ND2	2.13	0.46
1:A:230:LYS:HB3	1:A:251:TYR:HB2	1.97	0.46
1:B:105:TYR:HB2	1:B:132:ASN:ND2	2.32	0.45
1:A:97:ILE:HD13	3:A:296:HOH:O	2.17	0.44
1:B:244:ARG:HG3	1:B:265:THR:O	2.18	0.44
1:B:267:LYS:O	1:B:268:ASP:HB2	2.18	0.43
1:A:225:VAL:HG12	1:A:287:MET:HG3	2.01	0.43
1:A:218:ASP:O	1:A:223:ASP:HB2	2.17	0.43
1:A:44:ILE:CD1	1:A:278:LEU:HD11	2.49	0.42
1:B:79:ILE:HG12	1:B:193:LEU:HD11	2.01	0.42
1:A:222:LYS:HE3	1:A:231:VAL:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:226:PRO:HG2	1:B:229:TYR:CD1	2.55	0.42
1:B:242:ALA:HB1	1:B:274:PRO:HB3	2.01	0.42
1:A:107:PRO:HA	1:B:241:TYR:CE1	2.55	0.42
1:A:226:PRO:HB2	1:A:229:TYR:CD1	2.55	0.41
1:B:124:GLU:HG2	1:B:210:LEU:HD21	2.03	0.41
1:B:219:THR:HB	3:B:301:HOH:O	2.20	0.41
1:B:155:LEU:HD11	1:B:193:LEU:HB2	2.03	0.41
1:A:91:LEU:HB3	1:A:120:LYS:HB2	2.02	0.41
1:A:137:LYS:HD2	3:A:296:HOH:O	2.21	0.40
1:B:102:ILE:CD1	1:B:113:VAL:HG22	2.50	0.40
1:B:62:SER:HB3	1:B:184:ALA:HB2	2.03	0.40
1:A:106:SER:N	1:A:107:PRO:HD3	2.36	0.40
1:A:107:PRO:HA	1:B:241:TYR:HE1	1.85	0.40
1:B:93:LYS:O	1:B:118:THR:HA	2.22	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	239/258 (93%)	232 (97%)	6 (2%)	1 (0%)	34 42
1	B	238/258 (92%)	221 (93%)	13 (6%)	4 (2%)	9 8
All	All	477/516 (92%)	453 (95%)	19 (4%)	5 (1%)	15 17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	60	PHE
1	A	121	ALA
1	B	227	LYS
1	B	268	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	237	GLN

5.3.2 Protein sidechains

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	208/228 (91%)	187 (90%)	21 (10%)	7 9
1	B	206/228 (90%)	186 (90%)	20 (10%)	8 9
All	All	414/456 (91%)	373 (90%)	41 (10%)	8 9

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	GLU
1	A	34	ASN
1	A	38	LYS
1	A	44	ILE
1	A	46	VAL
1	A	59	LYS
1	A	62	SER
1	A	109	LEU
1	A	113	VAL
1	A	130	SER
1	A	137	LYS
1	A	145	ILE
1	A	147	LYS
1	A	153	LYS
1	A	186	PHE
1	A	198	LYS
1	A	215	LYS
1	A	227	LYS
1	A	230	LYS
1	A	240	THR
1	A	244	ARG
1	B	32	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	34	ASN
1	B	38	LYS
1	B	63	ASP
1	B	64	LYS
1	B	92	ASN
1	B	137	LYS
1	B	140	LYS
1	B	146	LYS
1	B	205	LYS
1	B	212	LEU
1	B	237	GLN
1	B	240	THR
1	B	244	ARG
1	B	252	PRO
1	B	253	LYS
1	B	267	LYS
1	B	268	ASP
1	B	281	GLU
1	B	287	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	196	ASN
1	B	43	HIS
1	B	92	ASN
1	B	132	ASN
1	B	196	ASN
1	B	275	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

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.