



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:11 AM UTC

PDB ID : 1ALQ / pdb_00001alq
Title : CIRCULARLY PERMUTED BETA-LACTAMASE FROM STAPHYLOCOCCUS AUREUS PC1
Authors : Pieper, U.; Herzberg, O.
Deposited on : 1997-06-02
Resolution : 1.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
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

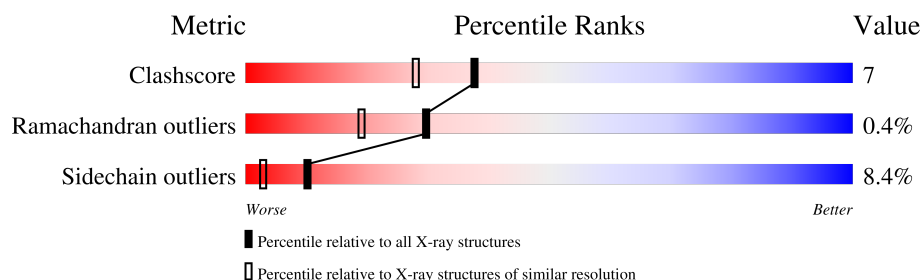
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	266	 62% 27% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2254 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 CP254 BETA-LACTAMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	2033	1296	341	393	3	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	212	Total	O	0	0
			212	212		

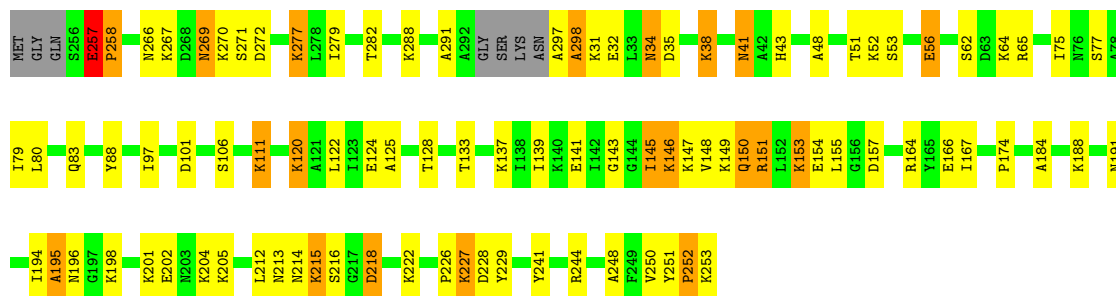
3 Residue-property plots

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: CP254 BETA-LACTAMASE

Chain A: 



4 Data and refinement statistics

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	53.90Å 94.20Å 138.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.80	Depositor
% Data completeness (in resolution range)	88.8 (30.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97, X-PLOR	Depositor
R, R_{free}	0.196 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2254	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: CO3, SO4

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	0.90	0/2062	2.23	90/2769 (3.3%)

There are no bond length outliers.

All (90) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	227	LYS	CA-C-N	14.08	149.06	121.18
1	A	227	LYS	C-N-CA	14.08	149.06	121.18
1	A	226	PRO	CA-C-N	14.06	148.39	121.54
1	A	226	PRO	C-N-CA	14.06	148.39	121.54
1	A	34	ASN	OD1-CG-ND2	12.79	135.40	122.60
1	A	34	ASN	CA-CB-CG	-12.10	100.50	112.60
1	A	145	ILE	CA-C-N	11.80	139.96	121.19
1	A	145	ILE	C-N-CA	11.80	139.96	121.19
1	A	297	ALA	CA-C-N	10.60	137.34	122.72
1	A	297	ALA	C-N-CA	10.60	137.34	122.72
1	A	214	ASN	CA-CB-CG	9.22	121.82	112.60
1	A	213	ASN	CA-CB-CG	-9.03	103.57	112.60
1	A	269	ASN	CA-CB-CG	-8.76	103.84	112.60
1	A	196	ASN	CA-CB-CG	-8.68	103.92	112.60
1	A	101	ASP	CA-C-O	8.66	130.05	119.31
1	A	298	ALA	CA-C-O	8.45	129.64	120.43
1	A	88	TYR	CA-C-O	8.16	129.44	120.63
1	A	298	ALA	N-CA-C	8.14	122.50	109.24
1	A	65	ARG	CD-NE-CZ	8.02	135.63	124.40
1	A	194	ILE	N-CA-CB	-7.51	105.48	111.64
1	A	195	ALA	CA-C-O	7.16	128.01	120.42
1	A	53	SER	CA-C-O	6.97	126.81	119.14
1	A	143	GLY	CA-C-O	6.97	126.31	118.86
1	A	227	LYS	N-CA-CB	-6.78	99.03	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	32	GLU	CA-C-N	6.73	129.29	120.28
1	A	32	GLU	C-N-CA	6.73	129.29	120.28
1	A	41	ASN	CA-CB-CG	-6.71	105.89	112.60
1	A	184	ALA	O-C-N	-6.66	114.89	122.09
1	A	266	ASN	OD1-CG-ND2	6.60	129.20	122.60
1	A	202	GLU	CB-CG-CD	6.60	123.82	112.60
1	A	191	ASN	OD1-CG-ND2	6.56	129.16	122.60
1	A	218	ASP	CA-C-O	6.53	127.39	119.49
1	A	34	ASN	CB-CA-C	-6.53	100.36	110.81
1	A	298	ALA	O-C-N	-6.53	115.89	123.27
1	A	194	ILE	N-CA-C	6.52	116.77	111.62
1	A	188	LYS	CA-C-O	6.46	127.40	119.97
1	A	111	LYS	CB-CG-CD	6.36	125.93	111.30
1	A	77	SER	CA-C-O	6.15	127.27	120.82
1	A	65	ARG	NE-CZ-NH2	6.14	124.73	119.20
1	A	64	LYS	CA-CB-CG	6.14	126.38	114.10
1	A	279	ILE	CA-C-O	6.11	126.85	120.25
1	A	111	LYS	CG-CD-CE	6.10	125.33	111.30
1	A	148	VAL	O-C-N	6.04	127.83	121.91
1	A	218	ASP	O-C-N	-5.99	114.61	122.39
1	A	120	LYS	CA-C-N	5.94	129.34	120.31
1	A	120	LYS	C-N-CA	5.94	129.34	120.31
1	A	80	LEU	CA-C-O	-5.89	114.17	120.42
1	A	166	GLU	CA-C-O	-5.89	114.56	121.16
1	A	157	ASP	CA-CB-CG	5.79	118.39	112.60
1	A	62	SER	CA-C-N	-5.75	113.53	122.67
1	A	62	SER	C-N-CA	-5.75	113.53	122.67
1	A	106	SER	O-C-N	5.71	126.42	121.34
1	A	151	ARG	NE-CZ-NH2	-5.69	114.08	119.20
1	A	128	THR	CA-C-N	5.64	131.22	122.26
1	A	128	THR	C-N-CA	5.64	131.22	122.26
1	A	75	ILE	O-C-N	5.57	127.69	121.90
1	A	79	ILE	CA-C-O	5.56	126.73	120.95
1	A	196	ASN	OD1-CG-ND2	5.56	128.16	122.60
1	A	141	GLU	CB-CG-CD	-5.54	103.17	112.60
1	A	258	PRO	CA-C-N	-5.47	116.03	122.93
1	A	258	PRO	C-N-CA	-5.47	116.03	122.93
1	A	184	ALA	CA-C-O	5.46	126.32	120.70
1	A	56	GLU	CA-C-O	-5.44	114.82	120.70
1	A	164	ARG	NE-CZ-NH2	5.44	124.09	119.20
1	A	65	ARG	O-C-N	5.39	129.41	123.16
1	A	266	ASN	CA-CB-CG	5.33	117.93	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	SER	CA-CB-OG	-5.31	100.47	111.10
1	A	53	SER	CA-C-N	-5.30	113.77	122.20
1	A	53	SER	C-N-CA	-5.30	113.77	122.20
1	A	271	SER	O-C-N	5.28	128.94	122.34
1	A	244	ARG	NE-CZ-NH1	5.28	126.78	121.50
1	A	257	GLU	N-CA-C	-5.26	102.56	110.24
1	A	184	ALA	CA-C-N	5.25	127.63	120.54
1	A	184	ALA	C-N-CA	5.25	127.63	120.54
1	A	43	HIS	CA-CB-CG	-5.16	108.64	113.80
1	A	146	LYS	CA-C-O	5.15	127.05	121.02
1	A	270	LYS	O-C-N	5.13	127.56	122.12
1	A	34	ASN	CB-CG-OD1	-5.13	110.54	120.80
1	A	125	ALA	CA-C-O	5.13	126.20	120.82
1	A	257	GLU	O-C-N	-5.11	115.15	121.64
1	A	282	THR	CA-C-O	5.09	125.94	120.55
1	A	153	LYS	O-C-N	-5.09	116.83	122.07
1	A	122	LEU	N-CA-CB	5.07	117.36	110.01
1	A	248	ALA	N-CA-CB	-5.07	103.71	111.56
1	A	97	ILE	CA-C-N	-5.06	113.81	123.32
1	A	97	ILE	C-N-CA	-5.06	113.81	123.32
1	A	139	ILE	O-C-N	5.06	126.78	121.87
1	A	141	GLU	OE1-CD-OE2	5.06	135.03	122.90
1	A	150	GLN	O-C-N	-5.04	116.08	122.27
1	A	133	THR	N-CA-CB	5.02	117.50	110.12

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	2033	0	2113	29	0
2	A	5	0	0	0	0
3	A	4	0	0	0	0
4	A	212	0	0	11	0
All	All	2254	0	2113	29	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 7.

All (29) 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:215:LYS:HD3	1:A:218:ASP:OD2	1.93	0.68
1:A:291:ALA:HB2	4:A:464:HOH:O	1.93	0.68
1:A:215:LYS:HD2	4:A:415:HOH:O	2.00	0.59
1:A:38:LYS:HE2	4:A:443:HOH:O	2.04	0.57
1:A:150:GLN:O	1:A:154:GLU:HG3	2.07	0.55
1:A:267:LYS:HE3	1:A:41:ASN:O	2.08	0.54
1:A:151:ARG:O	1:A:155:LEU:HG	2.08	0.54
1:A:258:PRO:HB3	1:A:251:TYR:CE2	2.43	0.53
1:A:120:LYS:O	1:A:124:GLU:HG3	2.09	0.53
1:A:222:LYS:HG3	4:A:310:HOH:O	2.08	0.53
1:A:174:PRO:HD3	1:A:241:TYR:CE2	2.43	0.53
1:A:147:LYS:HE2	4:A:445:HOH:O	2.09	0.52
1:A:205:LYS:HE2	4:A:493:HOH:O	2.10	0.52
1:A:229:TYR:CG	1:A:252:PRO:HA	2.45	0.52
1:A:269:ASN:HB2	1:A:272:ASP:CG	2.37	0.49
1:A:288:LYS:HD2	1:A:298:ALA:HB2	1.98	0.45
1:A:195:ALA:O	1:A:204:LYS:NZ	2.49	0.45
1:A:253:LYS:HD3	4:A:499:HOH:O	2.17	0.45
1:A:34:ASN:ND2	1:A:34:ASN:H	2.14	0.44
1:A:147:LYS:NZ	4:A:371:HOH:O	2.50	0.44
1:A:229:TYR:CD2	1:A:252:PRO:HA	2.53	0.43
1:A:198:LYS:HB2	4:A:440:HOH:O	2.19	0.43
1:A:257:GLU:HB3	1:A:51:THR:OG1	2.19	0.43
1:A:250:VAL:O	1:A:252:PRO:HD3	2.18	0.43
1:A:229:TYR:CD1	1:A:252:PRO:HA	2.54	0.42
1:A:277:LYS:HD2	4:A:419:HOH:O	2.20	0.42
1:A:52:LYS:HD3	4:A:429:HOH:O	2.20	0.41
1:A:269:ASN:HB2	1:A:272:ASP:OD1	2.20	0.41
1:A:48:ALA:O	1:A:56:GLU:HA	2.21	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	255/266 (96%)	249 (98%)	5 (2%)	1 (0%)	30	19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	LYS

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	225/231 (97%)	206 (92%)	19 (8%)	10	3

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

Mol	Chain	Res	Type
1	A	257	GLU
1	A	277	LYS
1	A	31	LYS
1	A	35	ASP
1	A	38	LYS
1	A	83	GLN
1	A	111	LYS
1	A	137	LYS
1	A	145	ILE
1	A	146	LYS

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Mol	Chain	Res	Type
1	A	149	LYS
1	A	153	LYS
1	A	167	ILE
1	A	201	LYS
1	A	212	LEU
1	A	215	LYS
1	A	216	SER
1	A	228	ASP
1	A	252	PRO

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	170	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 [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	$\# Z > 2$
2	SO4	A	301	-	4,4,4	0.60	0	6,6,6	0.20	0
3	CO3	A	302	-	3,3,3	0.69	0	2,3,3	0.68	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

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.