



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:14 PM UTC

PDB ID : 1KEH / pdb_00001keh
Title : Precursor structure of cephalosporin acylase
Authors : Kim, Y.; Kim, S.
Deposited on : 2001-11-16
Resolution : 2.50 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
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

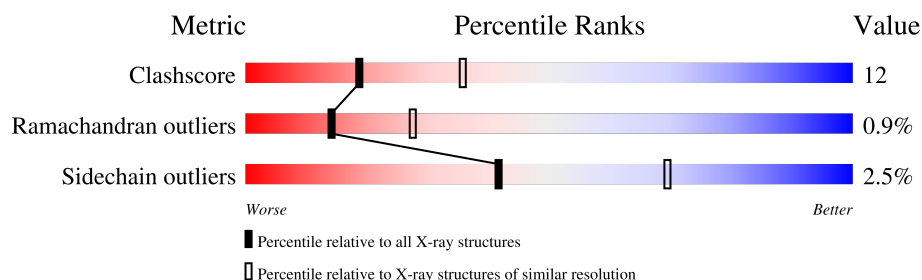
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	689	 74% 23% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5773 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 precursor of cephalosporin acylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	683	Total	C	N	O	S	0	0	0
			5374	3395	952	1013	14			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	170	ALA	SER	engineered mutation	UNP Q9L5D6
A	426	CYS	THR	SEE REMARK 999	UNP Q9L5D6
A	428	ALA	ARG	engineered mutation	UNP Q9L5D6
A	429	ASN	ASP	SEE REMARK 999	UNP Q9L5D6
A	506	ASP	GLU	SEE REMARK 999	UNP Q9L5D6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	399	Total	O	0	0
			399	399		



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	73.70Å 73.70Å 381.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.203 , 0.237	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5773	wwPDB-VP
Average B, all atoms (Å ²)	42.0	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	0.43	0/5532	0.95	22/7558 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	GLY	CA-C-N	9.71	131.97	119.84
1	A	70	GLY	C-N-CA	9.71	131.97	119.84
1	A	606	VAL	N-CA-C	9.17	121.83	108.53
1	A	168	GLN	N-CA-C	-7.01	101.85	110.61
1	A	347	ASN	N-CA-C	-6.80	98.53	109.96
1	A	166	ALA	N-CA-C	-6.69	104.83	114.12
1	A	621	VAL	N-CA-C	-6.55	105.36	111.45
1	A	343	VAL	CA-C-N	6.21	127.61	119.84
1	A	343	VAL	C-N-CA	6.21	127.61	119.84
1	A	169	GLY	N-CA-C	6.09	121.54	112.41
1	A	292	SER	N-CA-C	-5.94	101.13	109.69
1	A	146	ASN	N-CA-C	5.88	118.92	111.69
1	A	477	THR	N-CA-C	5.58	119.87	112.72
1	A	586	ILE	N-CA-C	5.55	115.58	107.37
1	A	667	PHE	N-CA-C	5.43	118.15	110.50
1	A	393	HIS	N-CA-C	5.42	117.57	110.08
1	A	198	ASP	N-CA-C	5.40	117.61	111.02
1	A	543	LYS	CA-C-N	5.14	124.80	119.56
1	A	543	LYS	C-N-CA	5.14	124.80	119.56
1	A	398	LEU	CA-C-N	5.07	125.86	119.98
1	A	398	LEU	C-N-CA	5.07	125.86	119.98
1	A	49	SER	N-CA-C	5.03	118.56	112.23

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	5374	0	5094	124	0
2	A	399	0	0	14	0
All	All	5773	0	5094	124	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 12.

All (124) 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:321:GLN:HE22	1:A:342:GLN:H	1.04	1.04
1:A:463:MET:HG2	1:A:629:MET:HG3	1.37	1.03
1:A:321:GLN:NE2	1:A:342:GLN:H	1.62	0.94
1:A:459:LEU:HG	1:A:463:MET:HE2	1.58	0.84
1:A:164:ASP:HA	1:A:167:ASP:OD2	1.82	0.81
1:A:317:GLY:H	1:A:342:GLN:HE21	1.31	0.78
1:A:138:VAL:HA	2:A:1015:HOH:O	1.84	0.78
1:A:321:GLN:HE22	1:A:342:GLN:N	1.83	0.76
1:A:473:MET:HE1	1:A:535:PHE:HZ	1.50	0.76
1:A:88:ARG:HH11	1:A:142:HIS:HE2	1.34	0.76
1:A:553:ASP:OD1	1:A:555:LYS:HG3	1.87	0.74
1:A:552:ARG:HB3	1:A:552:ARG:HH11	1.52	0.73
1:A:552:ARG:HB3	1:A:552:ARG:NH1	2.03	0.72
1:A:321:GLN:HG2	1:A:325:MET:HE2	1.71	0.71
1:A:141:ALA:HB3	2:A:1015:HOH:O	1.90	0.71
1:A:366:PRO:HD2	1:A:368:ARG:NH2	2.07	0.69
1:A:473:MET:HE1	1:A:535:PHE:CZ	2.29	0.66
1:A:608:THR:O	1:A:621:VAL:HG12	1.98	0.64
1:A:240:ASN:HB3	1:A:347:ASN:ND2	2.13	0.64
1:A:416:PRO:O	1:A:419:PRO:HD3	1.99	0.63
1:A:214:ILE:HG22	1:A:225:ILE:HD12	1.79	0.63
1:A:56:ARG:HD2	2:A:1063:HOH:O	1.99	0.62
1:A:322:TYR:HA	1:A:325:MET:HE3	1.80	0.61
1:A:203:TYR:O	1:A:217:ALA:HA	2.02	0.60
1:A:524:PHE:CE1	1:A:534:ALA:HB1	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:GLN:NE2	1:A:342:GLN:N	2.43	0.58
1:A:418:THR:HG22	1:A:418:THR:O	2.02	0.58
1:A:164:ASP:CA	1:A:167:ASP:OD2	2.51	0.58
1:A:554:PRO:O	1:A:558:VAL:HG23	2.03	0.58
1:A:463:MET:CG	1:A:629:MET:HG3	2.23	0.57
1:A:241:GLY:O	1:A:242:MET:C	2.48	0.57
1:A:321:GLN:O	1:A:325:MET:HG3	2.04	0.57
1:A:321:GLN:CG	1:A:325:MET:HE2	2.35	0.57
1:A:21:LEU:HD22	1:A:684:ARG:HG2	1.88	0.55
1:A:167:ASP:HB2	2:A:1074:HOH:O	2.06	0.55
1:A:88:ARG:NH1	1:A:142:HIS:HE2	2.00	0.55
1:A:552:ARG:HH11	1:A:552:ARG:CB	2.19	0.54
1:A:368:ARG:HD2	1:A:376:TRP:CE2	2.43	0.54
1:A:366:PRO:HB3	1:A:389:TRP:CD2	2.43	0.53
1:A:595:ALA:O	1:A:596:ALA:HB3	2.07	0.53
1:A:345:THR:O	1:A:346:PHE:HB2	2.09	0.52
1:A:321:GLN:HE21	1:A:342:GLN:HB2	1.73	0.52
1:A:632:PHE:HA	1:A:636:VAL:HG12	1.92	0.52
1:A:240:ASN:HB3	1:A:347:ASN:CG	2.34	0.51
1:A:86:PRO:HG2	2:A:985:HOH:O	2.11	0.51
1:A:177:PRO:HB3	1:A:183:GLY:O	2.11	0.51
1:A:612:PRO:HB2	1:A:616:GLY:HA2	1.93	0.51
1:A:317:GLY:H	1:A:342:GLN:NE2	2.03	0.50
1:A:35:ALA:HB3	1:A:36:PRO:HD3	1.92	0.50
1:A:236:THR:HG22	1:A:349:VAL:HB	1.93	0.50
1:A:174:ALA:HB3	1:A:409:VAL:HG22	1.92	0.50
1:A:18:ASN:HB3	1:A:687:PHE:CZ	2.47	0.49
1:A:451:MET:HA	1:A:451:MET:HE2	1.93	0.49
1:A:99:ASP:HB2	2:A:872:HOH:O	2.13	0.49
1:A:373:ILE:HD13	1:A:436:PRO:HG3	1.94	0.49
1:A:10:ILE:HD13	1:A:635:PRO:HB3	1.95	0.49
1:A:317:GLY:N	1:A:342:GLN:HE21	2.06	0.48
1:A:240:ASN:H	1:A:240:ASN:HD22	1.60	0.48
1:A:410:GLN:CD	1:A:410:GLN:C	2.82	0.48
1:A:622:HIS:HB2	2:A:1074:HOH:O	2.14	0.47
1:A:242:MET:HE2	2:A:916:HOH:O	2.13	0.47
1:A:7:GLN:HG3	1:A:8:ALA:N	2.30	0.47
1:A:446:GLN:HG2	1:A:472:VAL:HG21	1.95	0.47
1:A:673:ARG:O	1:A:677:VAL:HG23	2.14	0.47
1:A:539:TRP:HD1	1:A:547:THR:O	1.97	0.47
1:A:541:LEU:O	1:A:544:PRO:HD3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:VAL:HG13	1:A:142:HIS:CD2	2.50	0.47
1:A:145:MET:HG3	1:A:318:MET:HE2	1.97	0.46
1:A:173:TRP:CZ2	1:A:604:PHE:CZ	3.04	0.46
1:A:426:CYS:HB2	1:A:427:PRO:HD2	1.96	0.46
1:A:606:VAL:O	1:A:624:GLU:HG2	2.15	0.46
1:A:321:GLN:NE2	1:A:342:GLN:HB2	2.31	0.45
1:A:678:GLU:O	1:A:681:VAL:HG12	2.16	0.45
1:A:621:VAL:HG13	1:A:622:HIS:ND1	2.32	0.45
1:A:449:ARG:O	1:A:453:GLU:HB2	2.17	0.45
1:A:16:ARG:HB2	1:A:16:ARG:NH1	2.32	0.45
1:A:162:PRO:O	1:A:163:PRO:C	2.60	0.45
1:A:460:GLU:HA	1:A:463:MET:HE3	1.99	0.45
1:A:191:PRO:HD2	1:A:626:TRP:O	2.18	0.44
1:A:232:ARG:HA	1:A:353:ARG:HD2	2.00	0.44
1:A:242:MET:HE3	1:A:242:MET:HA	1.99	0.44
1:A:48:ARG:O	1:A:649:GLN:HG3	2.17	0.43
1:A:229:PHE:HA	1:A:233:MET:O	2.18	0.43
1:A:270:GLN:NE2	1:A:288:GLU:HG3	2.33	0.43
1:A:362:ASN:CG	1:A:363:GLY:N	2.76	0.43
1:A:534:ALA:HB2	2:A:948:HOH:O	2.19	0.43
1:A:9:PRO:HG3	1:A:353:ARG:HD3	2.00	0.43
1:A:240:ASN:HD22	1:A:241:GLY:N	2.15	0.43
1:A:117:GLN:NE2	2:A:903:HOH:O	2.51	0.43
1:A:148:LEU:HD23	1:A:148:LEU:HA	1.90	0.43
1:A:478:LEU:O	1:A:482:ILE:HG12	2.18	0.43
1:A:512:ARG:NH1	1:A:576:ASP:O	2.50	0.43
1:A:549:TYR:CG	1:A:550:GLY:N	2.87	0.43
1:A:248:TYR:HA	1:A:380:VAL:O	2.19	0.42
1:A:431:PRO:HG2	1:A:434:LEU:HG	2.00	0.42
1:A:174:ALA:HB3	1:A:409:VAL:CG2	2.49	0.42
1:A:79:TRP:CD2	1:A:153:PRO:HB3	2.55	0.42
1:A:18:ASN:HB3	1:A:687:PHE:CE1	2.54	0.42
1:A:75:GLN:HB3	2:A:974:HOH:O	2.20	0.42
1:A:649:GLN:O	1:A:650:PRO:C	2.63	0.42
1:A:23:ASP:OD1	1:A:23:ASP:C	2.62	0.42
1:A:160:GLY:O	1:A:161:ASP:CB	2.67	0.42
1:A:382:GLY:HA2	2:A:899:HOH:O	2.19	0.42
1:A:482:ILE:N	1:A:483:PRO:HD2	2.35	0.42
1:A:490:ASP:HB3	1:A:493:VAL:HG23	2.01	0.42
1:A:373:ILE:HG23	1:A:374:ALA:N	2.35	0.42
1:A:240:ASN:ND2	1:A:242:MET:H	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:THR:O	1:A:346:PHE:CB	2.68	0.41
1:A:474:ALA:HB1	1:A:478:LEU:CD1	2.49	0.41
1:A:259:TYR:OH	1:A:385:SER:HA	2.20	0.41
1:A:621:VAL:HG13	1:A:622:HIS:N	2.35	0.41
1:A:18:ASN:HB2	1:A:687:PHE:O	2.21	0.41
1:A:444:ALA:O	1:A:447:SER:HB3	2.20	0.41
1:A:614:GLU:HG3	1:A:615:ASN:CG	2.46	0.41
1:A:294:HIS:HE1	2:A:899:HOH:O	2.03	0.41
1:A:350:TYR:CD2	1:A:351:ALA:N	2.88	0.41
1:A:418:THR:N	1:A:419:PRO:CD	2.84	0.41
1:A:528:ASN:O	1:A:529:PHE:HB2	2.21	0.41
1:A:443:ARG:HB2	1:A:599:GLY:O	2.20	0.41
1:A:473:MET:HE3	1:A:473:MET:HA	2.03	0.40
1:A:325:MET:HE1	1:A:343:VAL:HG21	2.03	0.40
1:A:538:PRO:HD3	2:A:1080:HOH:O	2.20	0.40
1:A:614:GLU:HG3	1:A:615:ASN:OD1	2.22	0.40
1:A:393:HIS:HA	1:A:394:PRO:HD3	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	681/689 (99%)	645 (95%)	30 (4%)	6 (1%)	14 27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	ASP
1	A	163	PRO
1	A	165	LEU
1	A	164	ASP

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Mol	Chain	Res	Type
1	A	346	PHE
1	A	416	PRO

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	551/557 (99%)	537 (98%)	14 (2%)	42 69

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	PRO
1	A	99	ASP
1	A	161	ASP
1	A	163	PRO
1	A	218	THR
1	A	240	ASN
1	A	284	ASP
1	A	410	GLN
1	A	469	HIS
1	A	473	MET
1	A	629	MET
1	A	637	ARG
1	A	644	TYR
1	A	672	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	91	GLN
1	A	146	ASN
1	A	168	GLN
1	A	206	HIS

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Mol	Chain	Res	Type
1	A	240	ASN
1	A	253	GLN
1	A	262	GLN
1	A	294	HIS
1	A	321	GLN
1	A	342	GLN
1	A	377	GLN
1	A	379	ASN
1	A	410	GLN
1	A	429	ASN
1	A	527	GLN
1	A	654	HIS

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](#)

There are no ligands in this entry.

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.