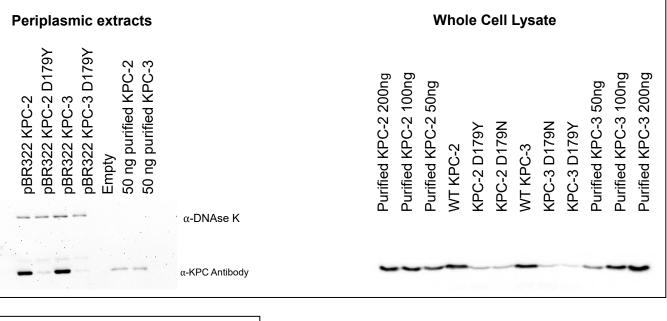
Supplementary File

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Isolate*	CAZ	CZA	FEP	PIP	PIP/TAZO	IMI	IMI/REL	MEM	MEM/VAB	ATM
E. coli DH10B										
<i>Ыа</i> крс-2	64	≤ 0.5/4	8	512	512/4	8	0.5/4	4	0.03/8	256
E. coli DH10B										
Ыа крс-2(D179Y)	512	64/4	4	128	8/4	0.25	0.5/4	0.06	0.03/8	8
E. coli DH10B										
<i>bla</i> кРС-3	512	2/4	16	512	512/4	4	0.5/4	4	0.03/8	512
E. coli DH10B										
bla крс-з(D179Y)	> 512	64/4	4	128	8/4	0.25	0.5/4	0.06	0.03/8	8
<i>E. coli</i> DH10B	≤ 0.5	≤ 0.5/4	≤ 0.5	2	2/4	0.125	0.25/4	0.03	0.03/8	≤ 0.5

- 4 **Table S1. AST results of the study isolates.** Mueller-Hinton (MH) agar-dilution MICs (mg/L) were interpreted according to 2020 CLSI criteria for *Enterobacterales* as follows: for aztreonam (ATM) and ceftazidime (CAZ), MIC \leq 4 is susceptible (S), MIC = 8 is
- 6 intermediate (I), and MIC ≥ 16 is resistant (R); for cefepime (FEP), MIC ≤ 2 is S, MIC = 4-8 is susceptible dose dependent (SDD),
 and MIC ≥ 16 is R; for piperacillin (PIP), MIC ≤ 16 is S, MIC = 32-64 is I, and MIC ≥ 128 is R; for meropenem (MEM) and imipenem
- 8 (IMI), MIC ≤ 1 is S, MIC = 2 is I, and MIC ≥ 4 is R; for ceftazidime/avibactam (CZA), MIC ≤ 8/4 is S, and MIC ≥ 16/4 is R; for piperacillin/tazobactam (PIP/TAZO), MIC ≤ 16/4 is S, MIC = 32/4-64/4 is I, and MIC ≥ 128/4 is R; for meropenem/vaborbactam
- 10 (MEM/VAB), MIC \leq 4/8 is S, MIC = 8/8 is I, and MIC \geq 16/8 is R. Imipenem/relebactam (IMI/REL) MICs were interpreted according to FDA breakpoints: MIC \leq 2/4 is S, MIC = 4/4 is I, and MIC \geq 8/4 is R. Relebactam was tested at fixed concentration of 4 mg/L while
- imipenem concentration was in doubling dilutions as a 1:1 mixture of imipenem:cilastatin. *All KPC variants cloned into pBR322 and transformed into *E. coli* DH10B cells. **AVI/TAZO/MEM/REL are kept at 4µg/ml, VAB at 8µg/ml per CLSI criteria.



	Purified KPC-2 100ng	Purified KPC-2 D179Y 100ng	Purified KPC-3 100ng	Purified KPC-3 D179Y 100ng	
	(47.6)	(37.3)	(60.8)	(24.4)	
a-KPC Antibody	-		-		

- 18 Figure S1. Immunoblots of periplasmic extracts, whole cell lysates, and 100 ngs each of purified KPC-2,
- 19 KPC-2 D179Y, KPC-3, and KPC-3 D179Y. ImageJ analysis of equal amounts of enzyme (100 ngs) show
- 20 varying recognition by the polyclonal anti-KPC-2 antibody (values shown in parentheses).

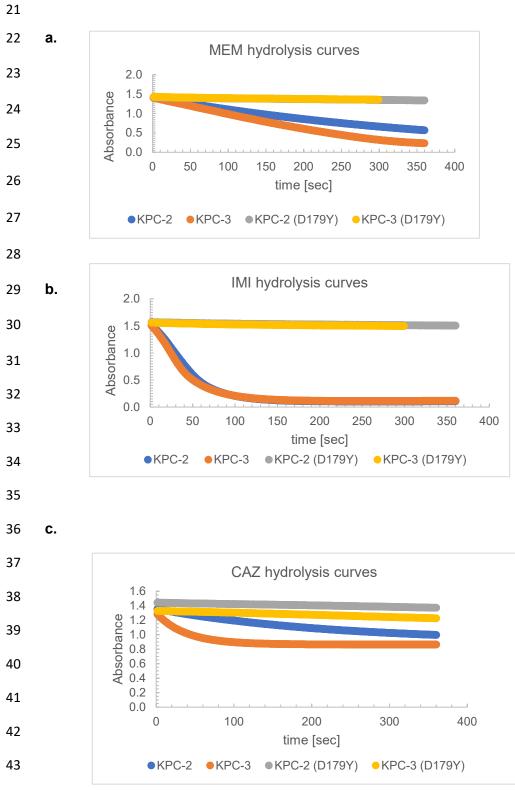
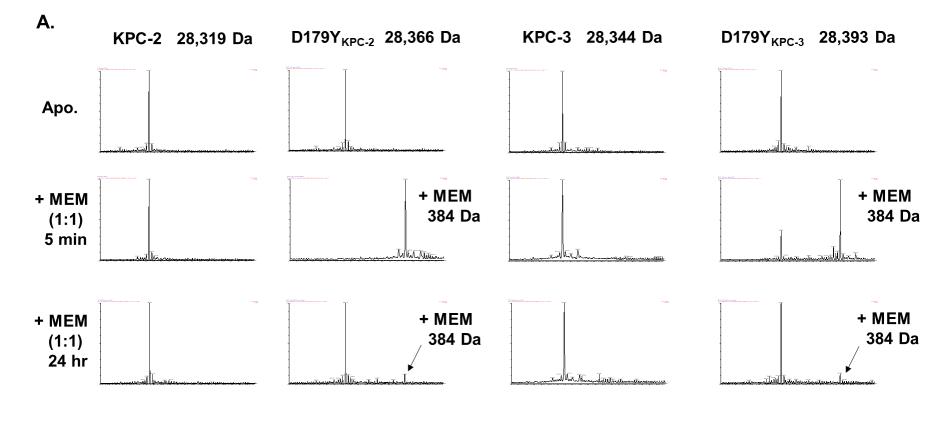
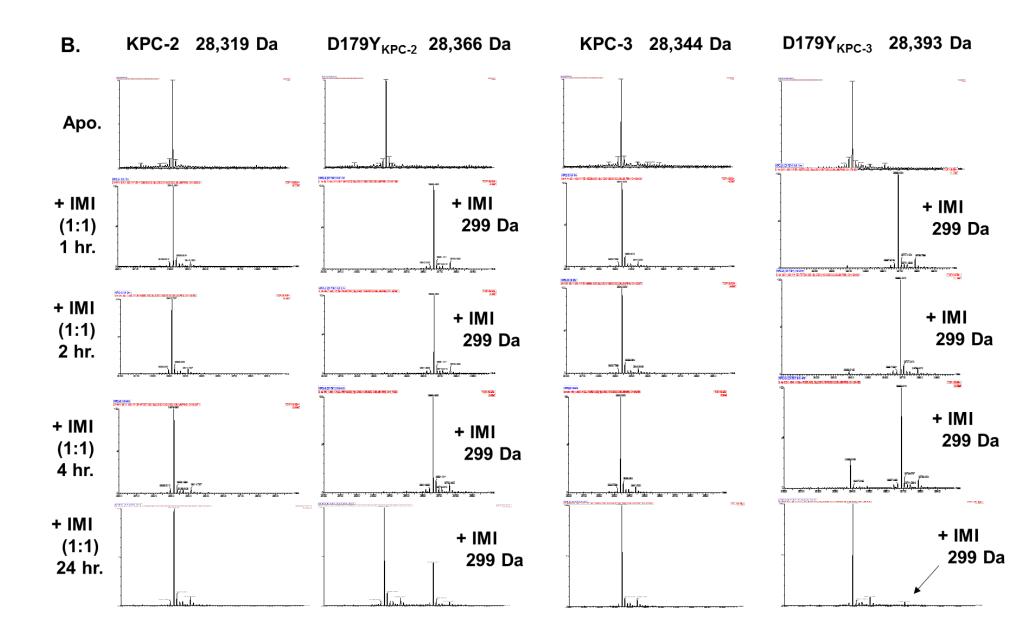
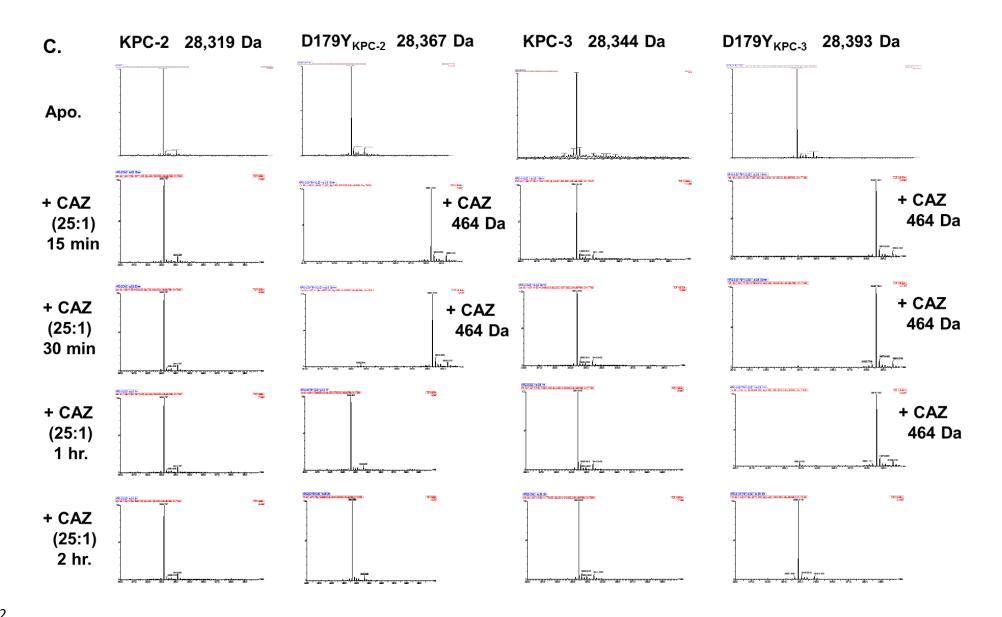


Figure S2. Steady state kinetics. (a.) MEM, (b.) IMI, and (c.) CAZ hydrolysis curves. WT KPC-2 and
KPC-3 can hydrolyze MEM, IMI, and CAZ. D179Y variants showed no catalytic activity against IMI and
MEM, and minimal hydrolysis against CAZ.







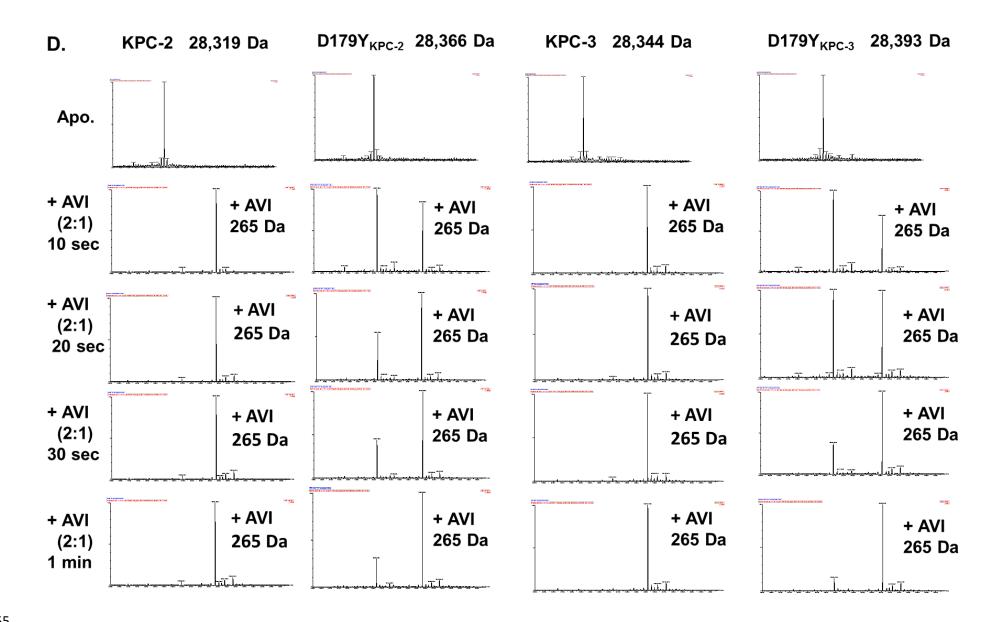


Figure S3. Timed Mass Spectrometry. Both KPC-2 and KPC-3 D179Y variants form prolonged (24h) acyl-complexes with MEM (**A**) and IMI (**B**). The prolonged trapping of MEM and IMI by wild type KPCs is not evident. However, the D179Y variants of KPC-2 and KPC-3 trap MEM and IMI similarly. D179Y variants were able to form acyl-enzyme complex with CAZ (**C**) using a 25x molar excess of CAZ to enzyme, but the acyl-enzyme complex was reduced to < 2 hours ($b/a_{KPC-2 D179Y}, k_{cat} \le 0.014 \text{ s}^{-1}$; $b/a_{KPC-3 D179Y}, k_{cat} \le 0.007 \text{ s}^{-1}$). KPC-2 and KPC-3 formed the acyl-enzyme with AVI immediately, in the first 10 sec of incubation, and at a ratio of 2:1. For the KPC-2 D179Y variant, the complex was formed after 1 min incubation (**D**).

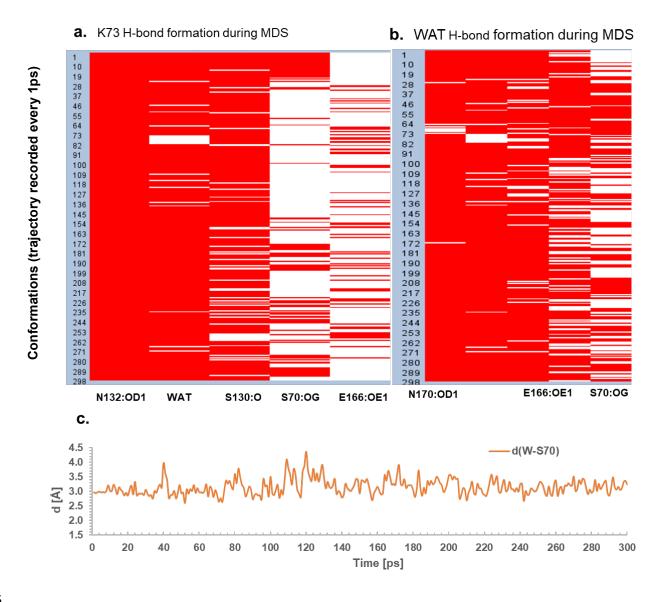


Figure S4. During the 300ps MDS, we follow the possible interactions and H-bond formation of K73 (a),
and deacylation water (b, c). K73 residue is forming and maintaining a H-bonds network with N132:OD1,
S70:O and a water molecule (a). The de-acylation water molecule (b.) Preserve the H-bonds with K73,
and is positioned at H-bond distance during the simulation.

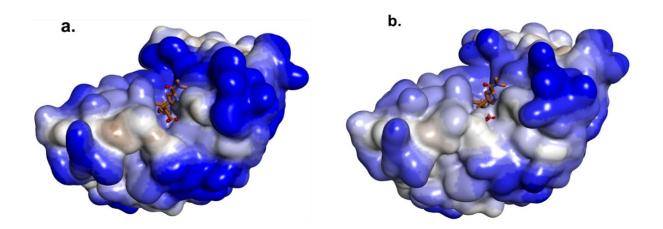


Figure S5. The Connolly electrostatic surface representation of KPC-2 (3) and D179Y variants with CAZ docked into the active site, shows the active site volumes and surface potential variability.

Supplementary Materials and Methods

80 MICs. Mueller-Hinton (MH) agar-dilution MIC measurements were performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines as previously described (1). The MICs are reported as 82 the concentrations at which bacterial growth was no longer observed. Avibactam, relebactam, and vaborbactam were tested at a constant 4 µg/ml in combination with their respective antibiotic partners.

84 All MICs were performed in triplicate.

Immunoblotting. Immunoblotting was used to evaluate the expression levels of wild-type KPC-2, KPC-3. and D179Y variants as previously described (2). Five-milliliter cultures of E. coli DH10B cells containing 86 pBR322 phagemids harboring the *bla*_{KPC} genes in Mueller-Hinton II broth containing 20 µg/mL chloramphenicol were grown at 37 °C to an optical density at 600 nm (OD₆₀₀) of 0.8. Fifty-microliter 88 aliguots of whole cells from these cultures were pelleted and frozen overnight. Pellets were resuspended in 20 µL of loading buffer. Whole cells were then separated via SDS-PAGE and subsequently transferred 90 to a polyvinylidene difluoride (PVDF) membranes (Novex, Life Technologies, Carlsbad, CA) by electroblotting. After blocking for 1 h with 5% nonfat dry milk, the presence of KPC was detected by 92 incubation in 5% nonfat dry milk with anti-KPC-2 polyclonal antibodies (1µg/ml) (3, 4) and anti-DnaK (Enzo Life Science, Farmingdale, New York) (1/10,000 dilution) overnight at 4°C. The membranes were 94 washed four times, 15 min each, in Tris-buffered saline (pH 7.4) containing 0.1% Tween 20 and subsequently incubated in 5% nonfat dry milk with a 1/10,000 dilution of horseradish peroxidase (HRP)-96 protein G conjugate (Bio-Rad, Hercules, California) and 1/10,000 dilution of goat anti-mouse IgG-HRP (Santa Cruz Biotechnology, Santa Cruz, California). After four additional washes, the membranes were 98 processed for exposure using the ECL kit (GE Healthcare, Chicago, Illinois) and FOTO/AnalystVR FX (Fotodyne, Hartland, Wisconsin). Additional immunoblotting was done with 100 ng each of KPC-2, KPC-100

3, KPC-2 (D179Y), and KPC-3 (D179Y). ImageJ analysis software (version 1.52, National Institutes of Health) was used to determine protein band intensities.

104 **References**

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