

The Basis of Commensal Bacillota Resistance to a Novel PolC-type DNA Polymerase III Inhibitor, Ibezapolstat, and the “Narrower” Spectrum of Activity Towards *C. difficile*

Jacob McPherson, Pharm.D.

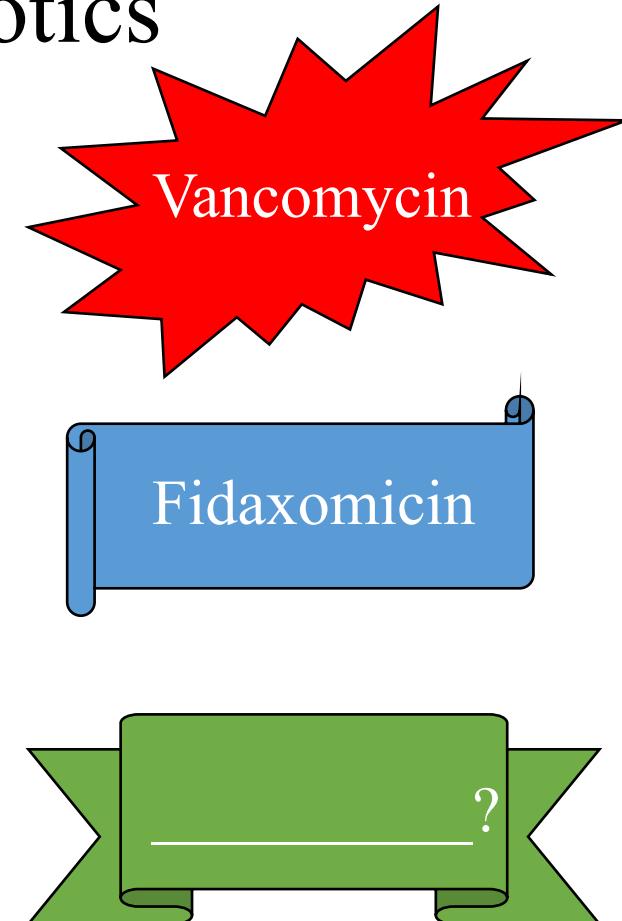
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University of Houston College of Pharmacy

Mentors: Dr. Kevin Garey, Pharm.D., M.S.,
Dr. Julian Hurdle, Ph.D.

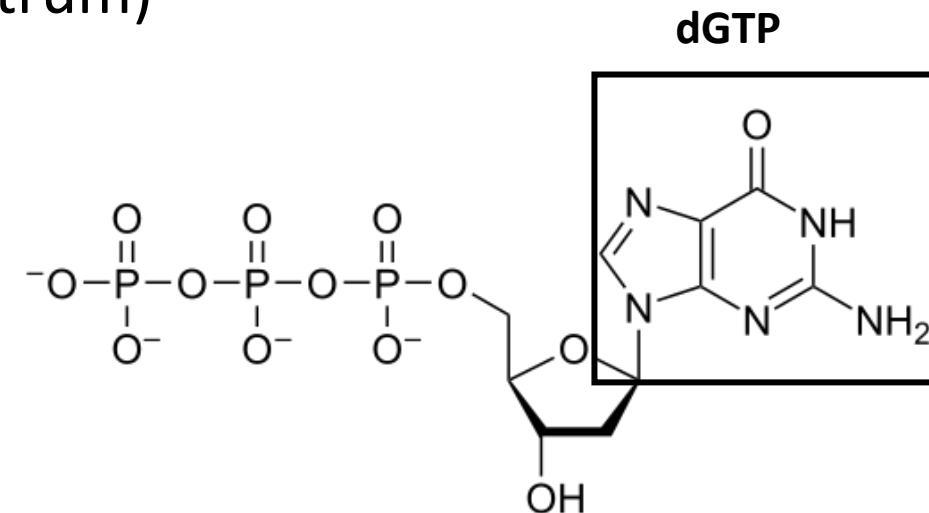
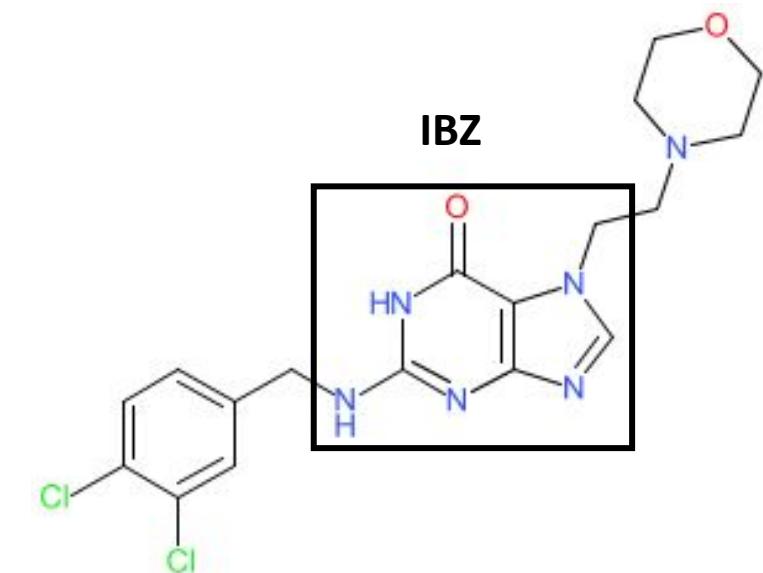
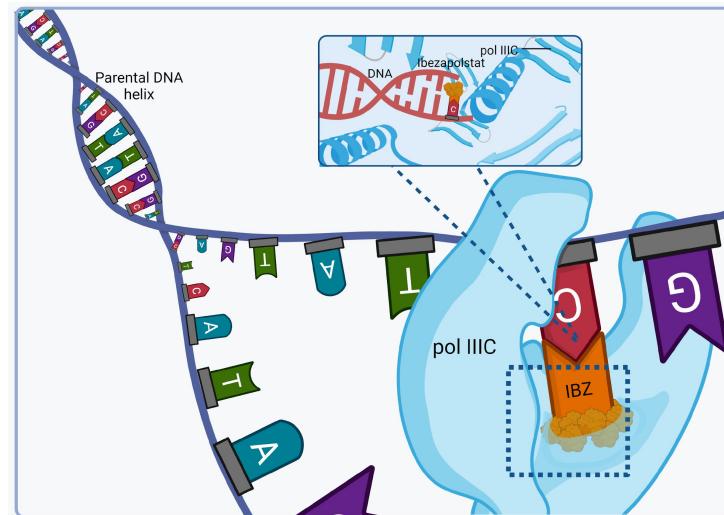
Training Program in Antimicrobial Resistance

Clostridioides difficile infection (CDI): an **Urgent** Threat with **Limited** Narrow-spectrum Antibiotics

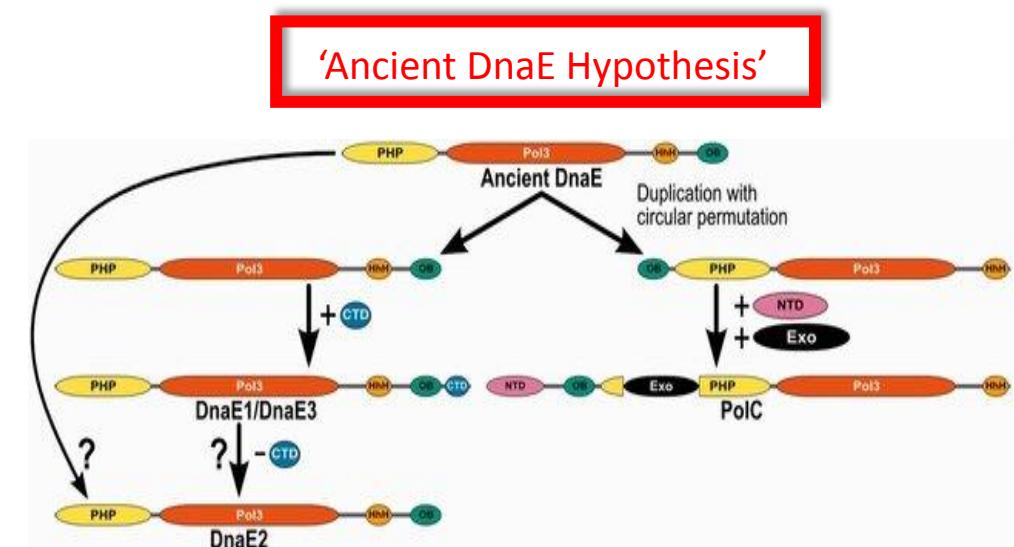
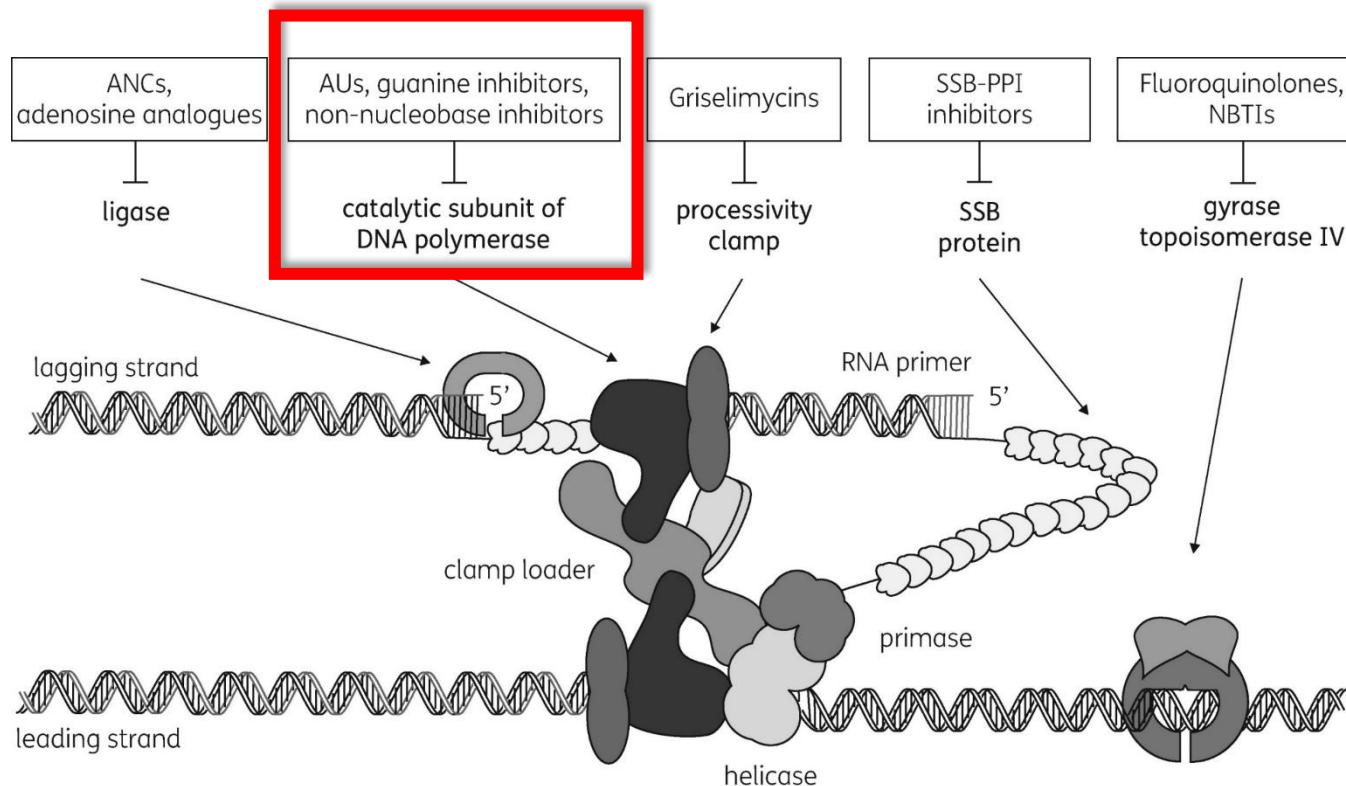


Ibezapolstat (IBZ; ACX362E)

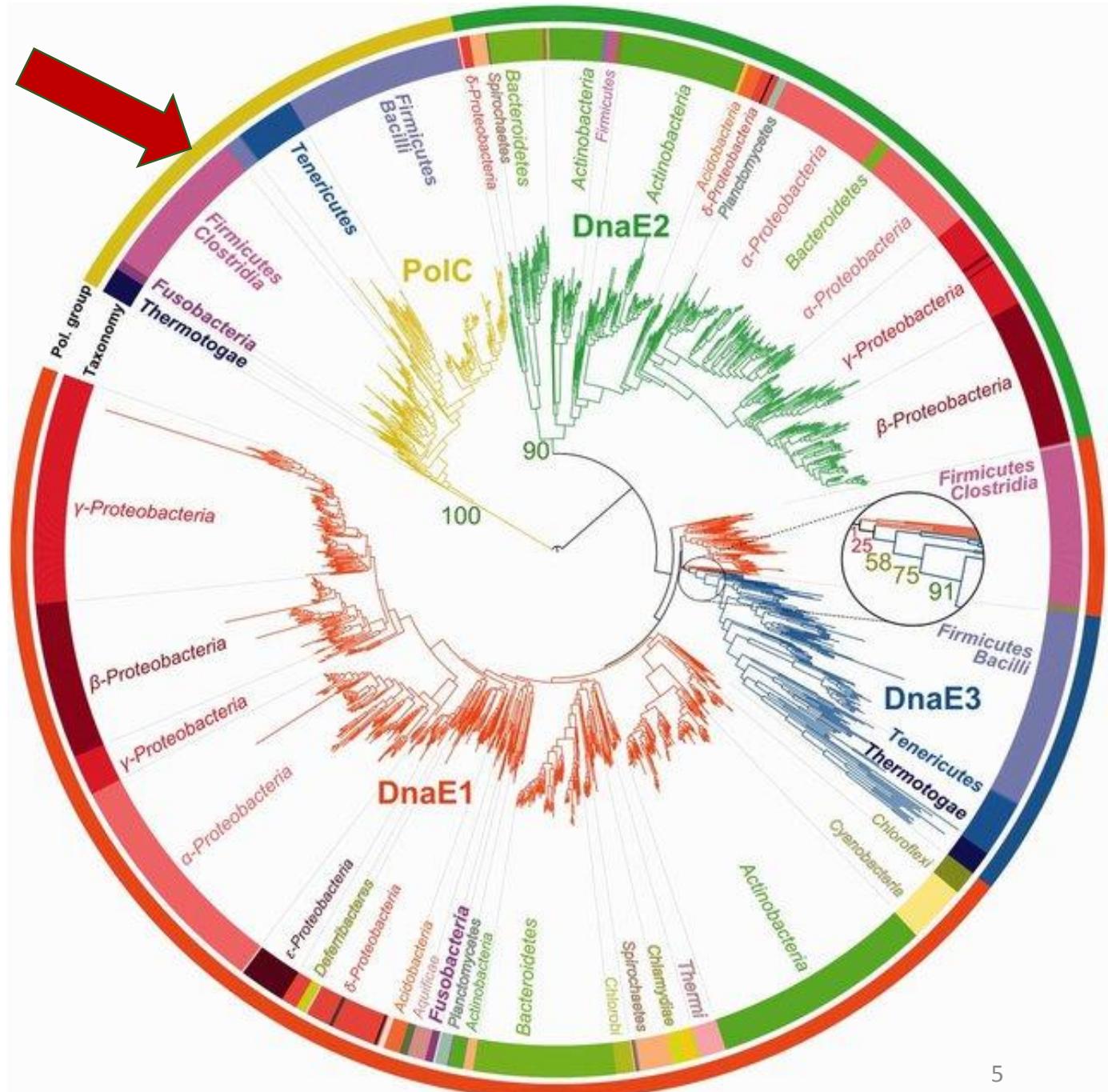
- Deoxyguanosine triphosphate (**dGTP**) analog
- Small-molecule *competitive* inhibitor of the PolC-type DNA Polymerase III (**PolC**)
- PolC is *essential* for replication of low G+C genome Gram-positive bacteria (**Bacillota**)
- **GPSS™ (Gram Positive Selective Spectrum)**
narrow-spectrum of activity



The PolC-type DNA Polymerase III (PolC) is the catalytic subunit of the Bacillota Replisome



polC is found in
Bacillota,
not Proteobacteria,
Bacteroidetes or
Actinobacteria

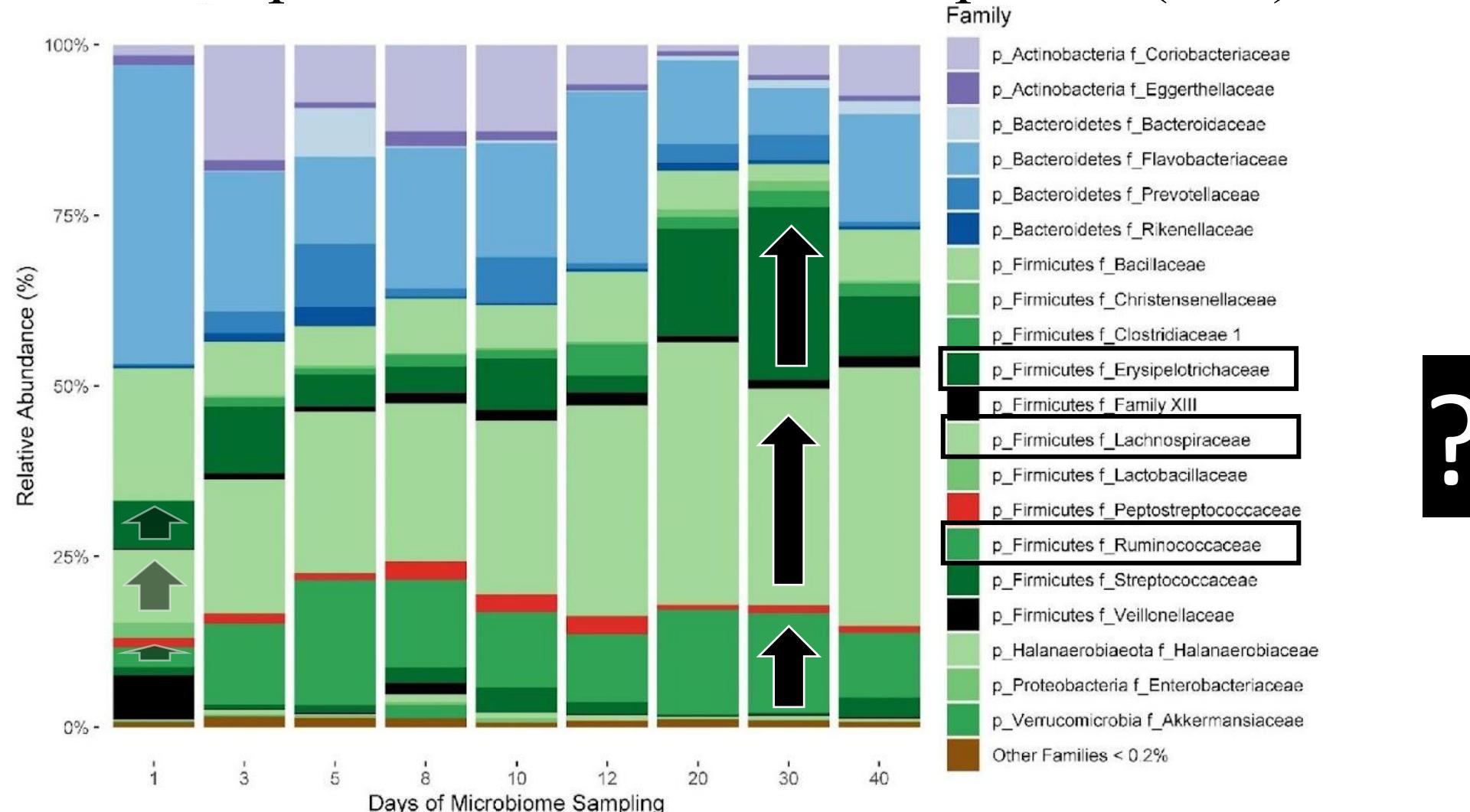


IBZ Clinical update

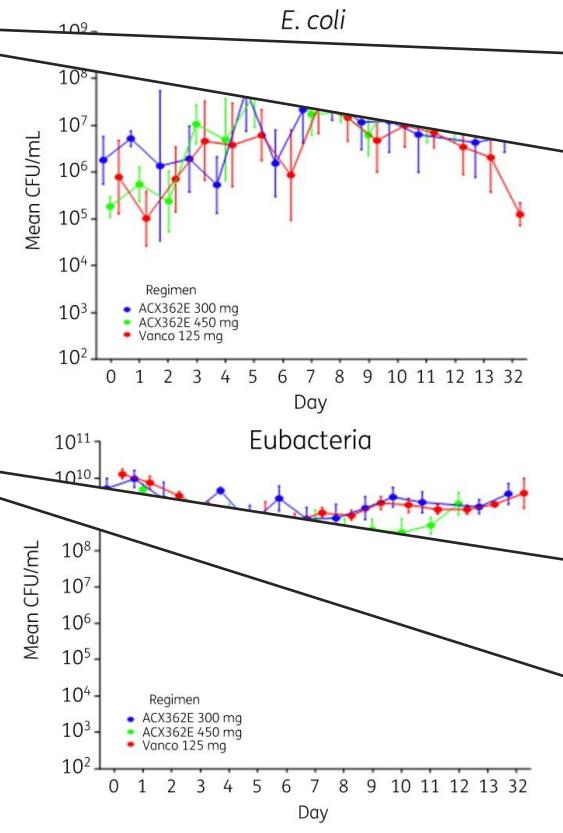
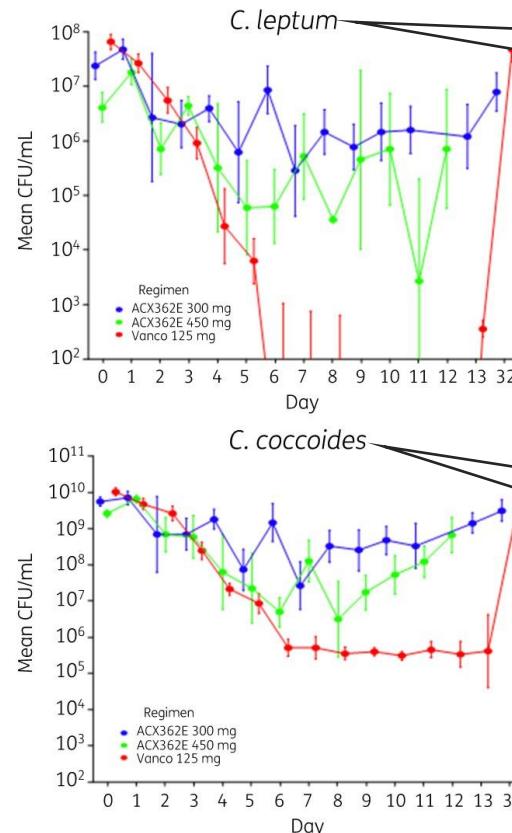
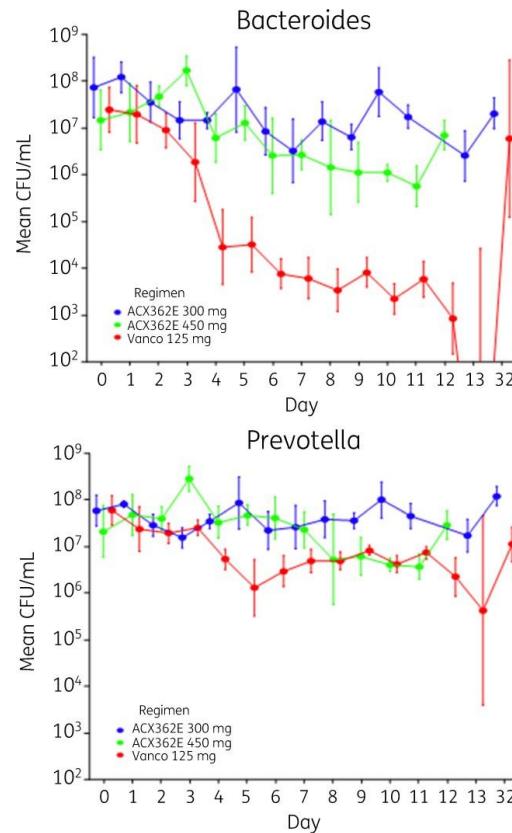
- **Phase 1**, Healthy Volunteer: *Completed*
 - IBZ 450 mg twice daily chosen for phase 2 studies
 - Garey et al. J Antimicrob Chemother 2020
 - *Microbiome evaluations predicted an anti-recurrence effects due *narrower* than expected spectrum of activity
 - *McPherson et al. Antimicrob Agents Chemother 2022
- **Phase 2a** (n=10): *Completed*
 - *10 of 10 patients experienced clinical cure with no recurrence.
 - *Narrower* than expected spectrum of activity also observed
 - *Garey et al. Clin Infect Dis 2022
- **Phase 2b:** *Completed*
 - IBZ 450 mg twice daily vs. vancomycin 125 mg PO four times daily
 - ClinicalTrials.gov Identifier: NCT04247542
 - See poster being presented at lunch today

*In phase I/II studies, an IBZ selective spectrum of activity to certain Bacillota

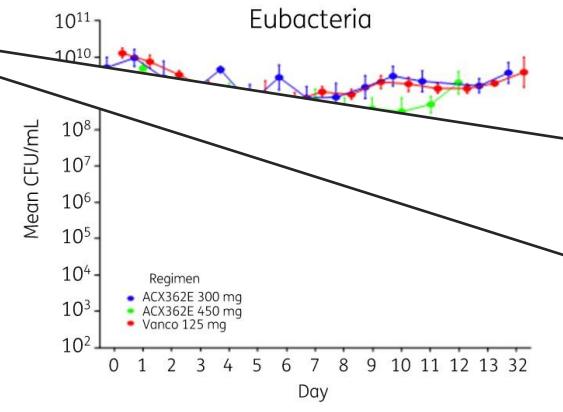
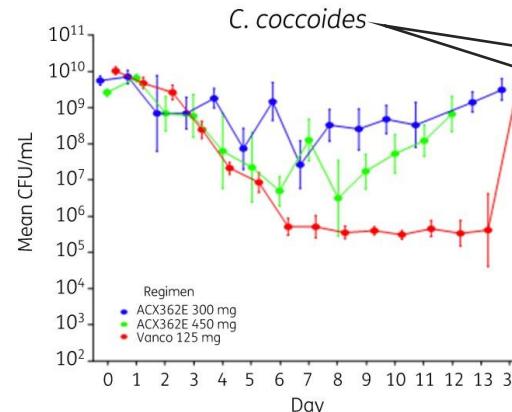
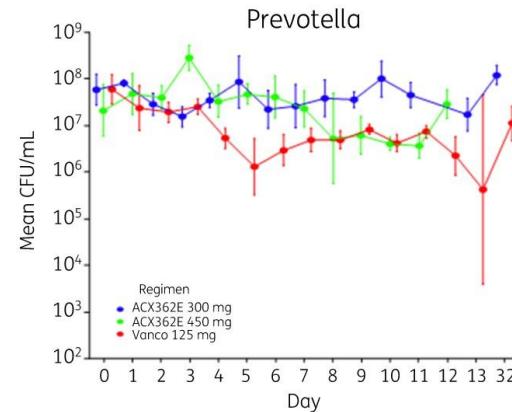
Lachnospiraceae, Ruminococcaceae and Erysipelotrichaceae increased in CDI patients treated with Ibezapolstat (IBZ)



IBZ-mediated Increases in Specific Sub-taxa of Commensal Bacillota Confirmed by qPCR



Many of Clostridium cluster IV (*C. leptum* group) taxonomically reassigned **Oscillospiraceae** (formerly Ruminococcaceae)



Many of Clostridium cluster XIVa (*C. coccoides* group) taxonomically reassigned **Lachnospiraceae**

Specific Aims

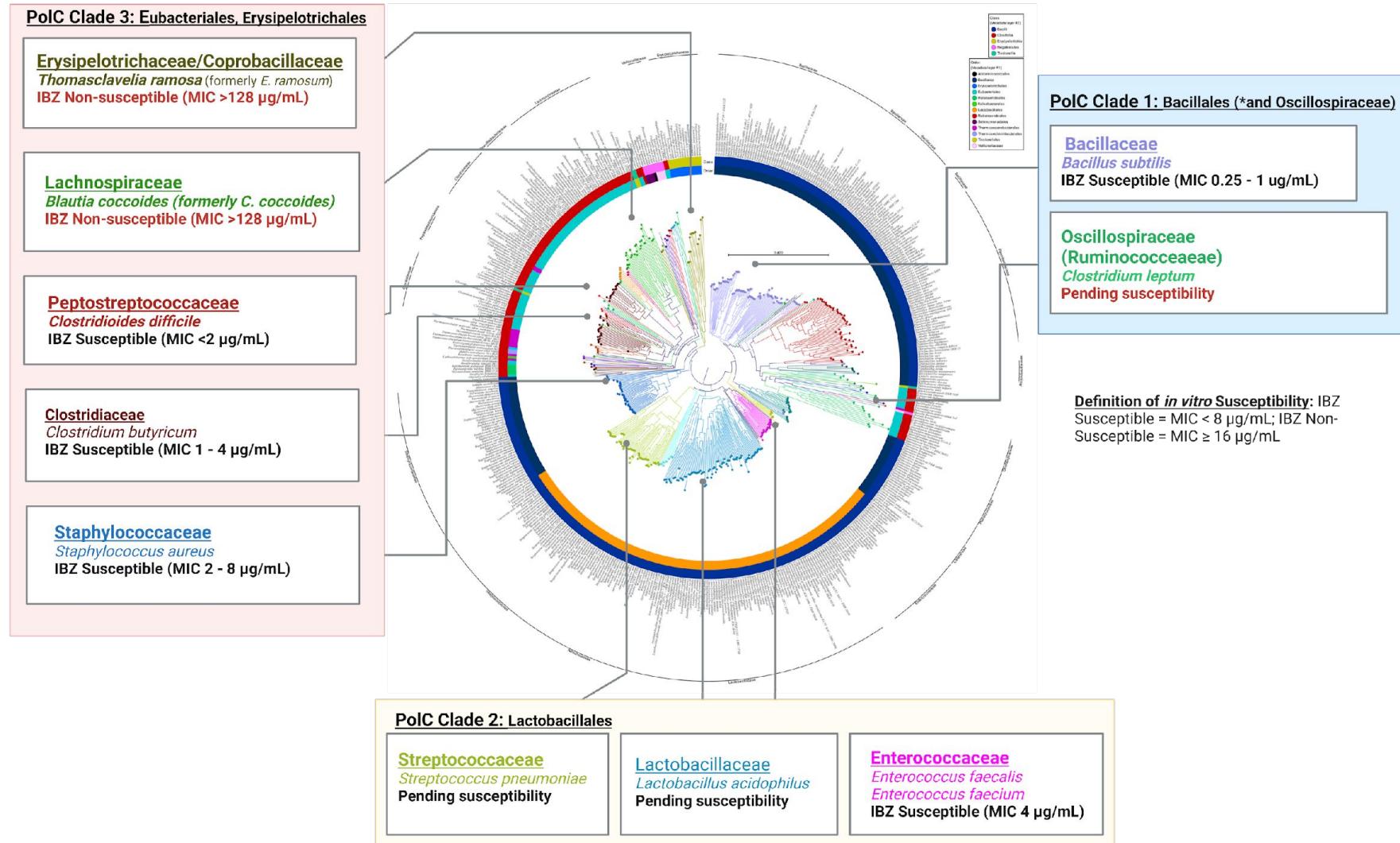
The global aim of my project is to determine the narrower than expected spectrum of IBZ

- Determine the structure, binding pocket and drug-binding residues of the *C. difficile* PolC-IBZ complex
 - Cryogenic-electron microscopy (cryo-EM): Work in progress
 - In silico prediction: Presenting today
 - PolC Phylogenetics
 - In silico binding prediction

In silico Methods

- **PolC sequence relatedness:** mmSeqs2 MSA, Neighbor-joining, and Jukes-Cantor
- **3D protein structure prediction:** AlphaFold2 (ColabFold)
- **Cavity-detection blind drug docking:** CB-Dock2: CurPocket, AutoDock-Vina
- **Homology modeling:** CLC Genomics (Qiagen), Maestro (Schrodinger), UCSF ChimeraX

Sequence Relatedness of the PolC does not predict IBZ susceptibility



IBZ selectivity is likely related to unique binding residues present in select Bacillota taxa

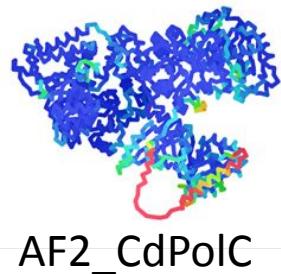


Fig. 3a) Overview of *in silico* chemistry

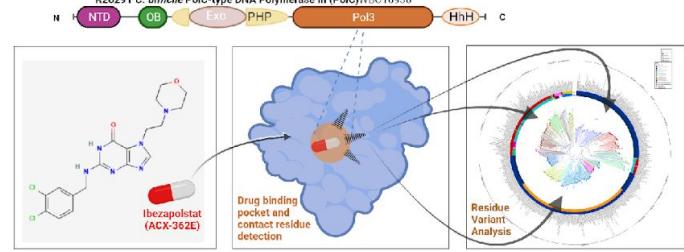


Fig. 3b) Protein Structure Prediction using AlphaFold2 Homology Modeling

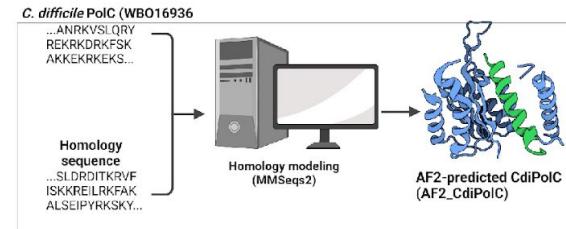


Fig. 3c) Drug-binding residue detection using CB-Dock2, AutoDock-Vina, and PLIP

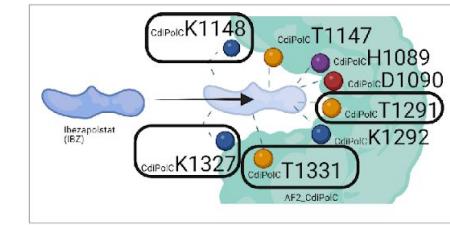
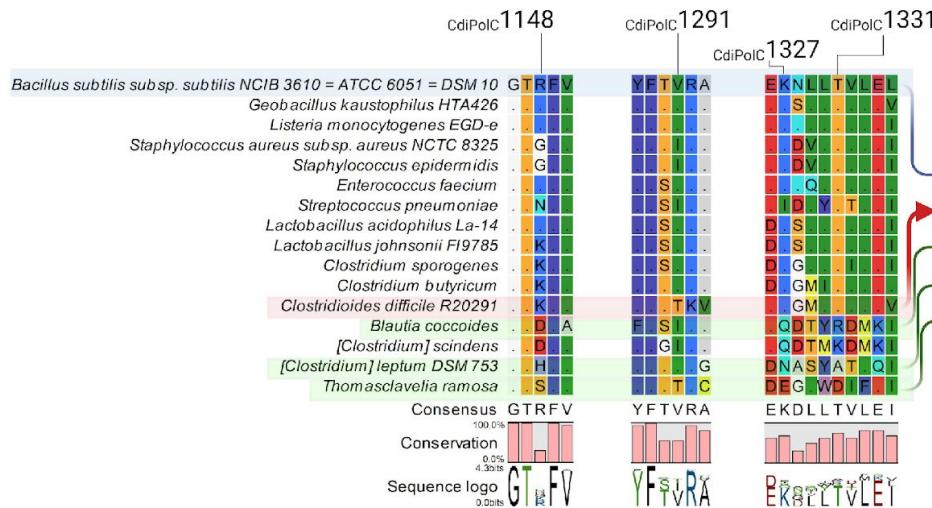


Fig. 3d) Variant analysis of proposed several drug-binding residues across representative species from taxonomic families comprising the Bacillota phylum



Summary
predicted PolC-IBZ interaction variants
across five
representative
species

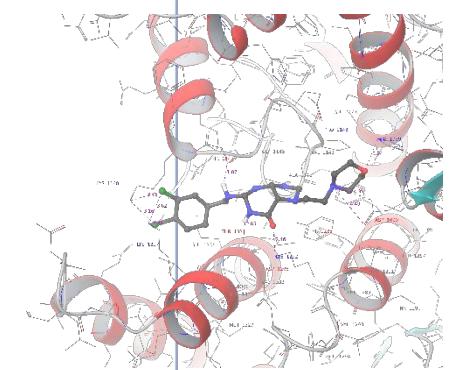
| | Bacillaceae, BsuPolC | Peptostreptococcaceae, CdPolC | Lachnospiraceae, BcoPolC | Oscillospiraceae, ClepPolC | Coprobacillaceae, TraPolC | IBZ MIC (μ g/mL) |
|--|----------------------|-------------------------------|--------------------------|----------------------------|---------------------------|-----------------------|
| | R V K T | K T K T | D I Q R | H V N A | S T E D | 1 - 2 |
| | | | | | | > 128 |
| | | | | | | > 128 |
| | | | | | | pending |

PolC may have (3) 'de-sensitizer residues':

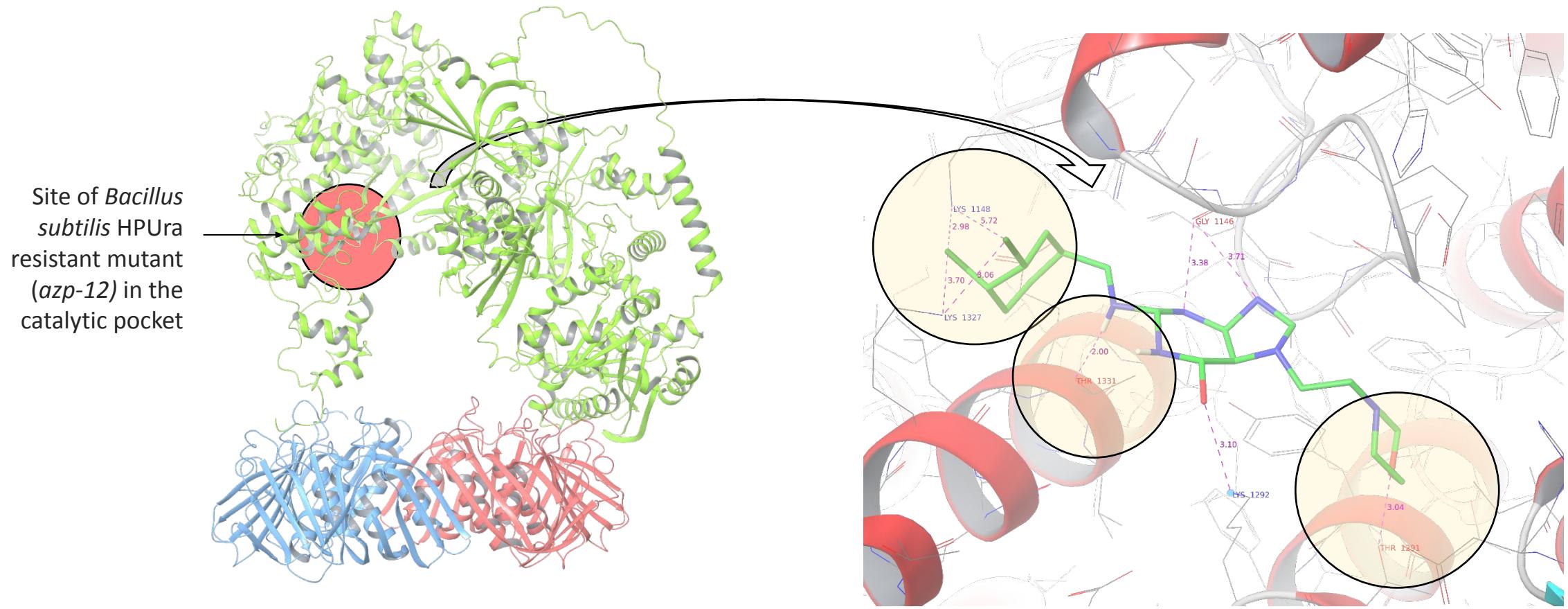
Two lysine "hooks" [CdPolC^{K1148,K1327}] present in *C. difficile* that may bind the IBZ 3,4-dichlorophenyl abolished in LOC. CdPolc Thr1291 interaction with 7-morpholinol is almost C. difficile unique. CdPolc Lys1327 "hook 2" interaction with 3,4-dichlorophenyl abolished in LOC. CdPolc Thr1331 interaction with 2-methylamino abolished in LOC.

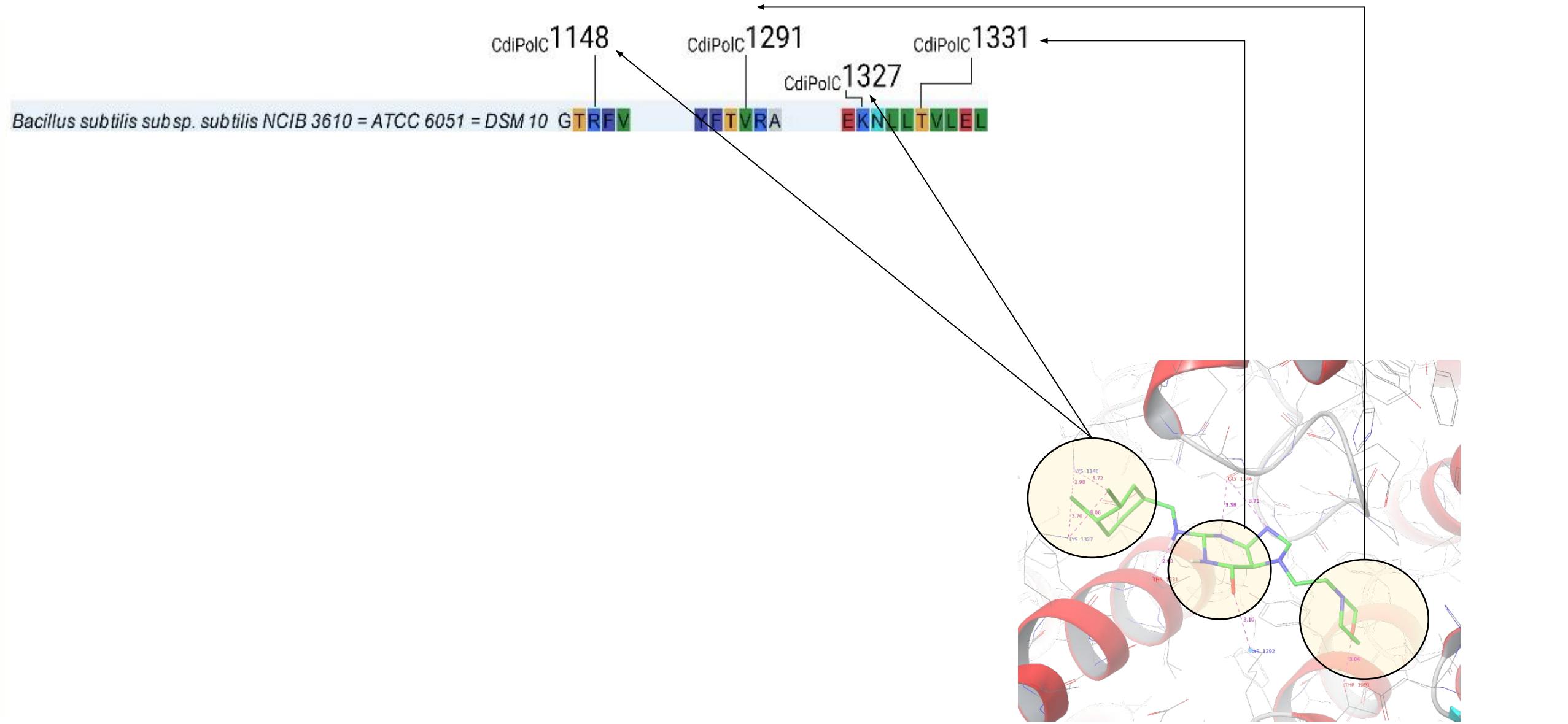
PolC may have (1) 'enhancer residue':

CdPolc^{T1291} that may bind the IBZ 7-morpholinethyl is instead an aliphatic valine or isoleucine across most representative Bacillota species, except for *C. difficile* and *T. ramosa*.



In silico (predicted) IBZ drug-binding residues are conserved across *most* Firmicutes except **Lachnospiraceae, Ruminococcaceae, Erysipelotrichaceae**





Lachnospiraceae: *Blautia coccoides*; [Clostridium] scindens
Ruminococcaceae: [Clostridium] leptum
Erysipelotrichaceae: *Thomasclavelia ramosa*

CB-Dock2 [CurPocket + AutoDock-Vina] of IBZ to AF2-CdiPolC

My hypotheses after *in silico* studies

1. The ***C. difficile* PolC** catalytic pocket contains a '**sensitizer residue**' ($\text{CdiPolC}^{\text{Thr}1291}$) that increases the relative potency of IBZ towards *C. difficile*
2. Lachnospiraceae, Oscillospiraceae, and Erysipelotrichaceae PolC catalytic pockets contain '**de-sensitizer residues**' ($\text{CdiPolC}^{\text{Lys}1148}$, $\text{CdiPolC}^{\text{Lys}1327}$, $\text{CdiPolC}^{\text{Thr}1331}$) that confer IBZ **non-susceptibility**

Conclusions

- Using in silico modeling, we were able to predict the narrower than expected spectrum of activity of IBZ
 - Sensitizer and de-sensitizer residues were identified
- MIC work to date has helped confirm these predictions
- Cryo-EM work to validate this work ongoing

Acknowledgements

The Garey Lab



Faculty

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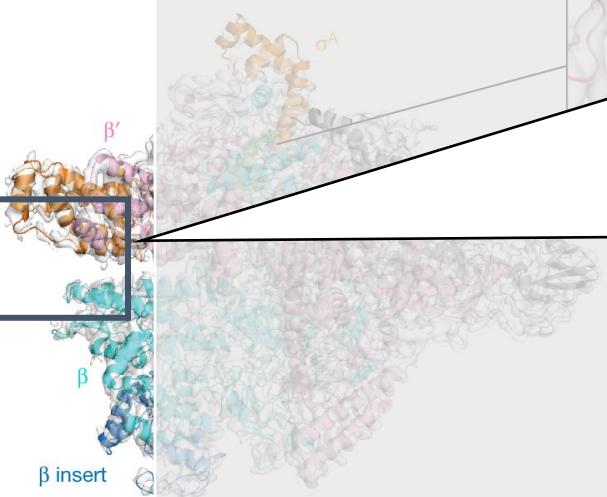
Gulf Coast Consortia



Comparative Structural Biology to determine the Gram-positive selective spectrum activity of PolC inhibitors

CryoEM of the FDX-bound Cdiff RNAP II

c



Peptostreptococceae

?

?

Bacillaceae

?

?

Lactobacillaceae

?

?

Lachnospiraceae

?

?

Ruminococcaceae

?

?

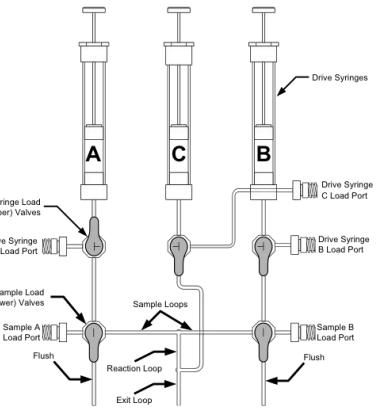
Erysipelotrichaceae

?

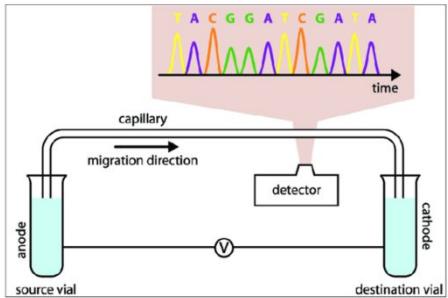
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K84

Enzyme Kinetics of Inhibition



Rapid Quench Flow (RQF)
millisecond-resolution

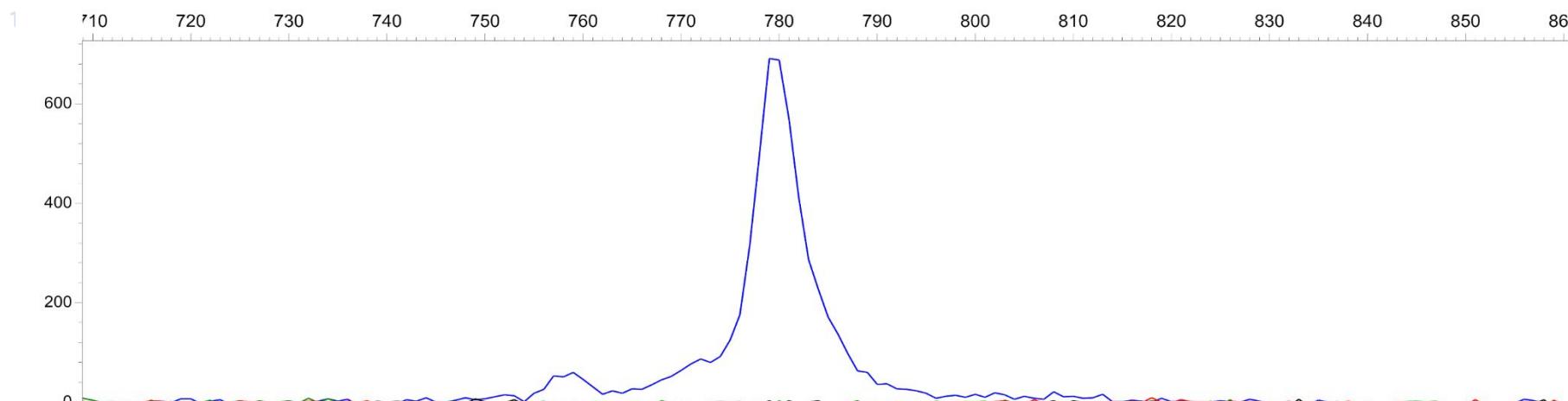


Fluorescence Capillary Electrophoresis: single-nucleotide incorporation resolution

Project Name : 20240114_project
Sample Name : B11
Sample Type : Sample

Stay tuned

Sample File Name : B11_20240115_034701.fsa
Sizing Quality : 0
Plot Type : raw

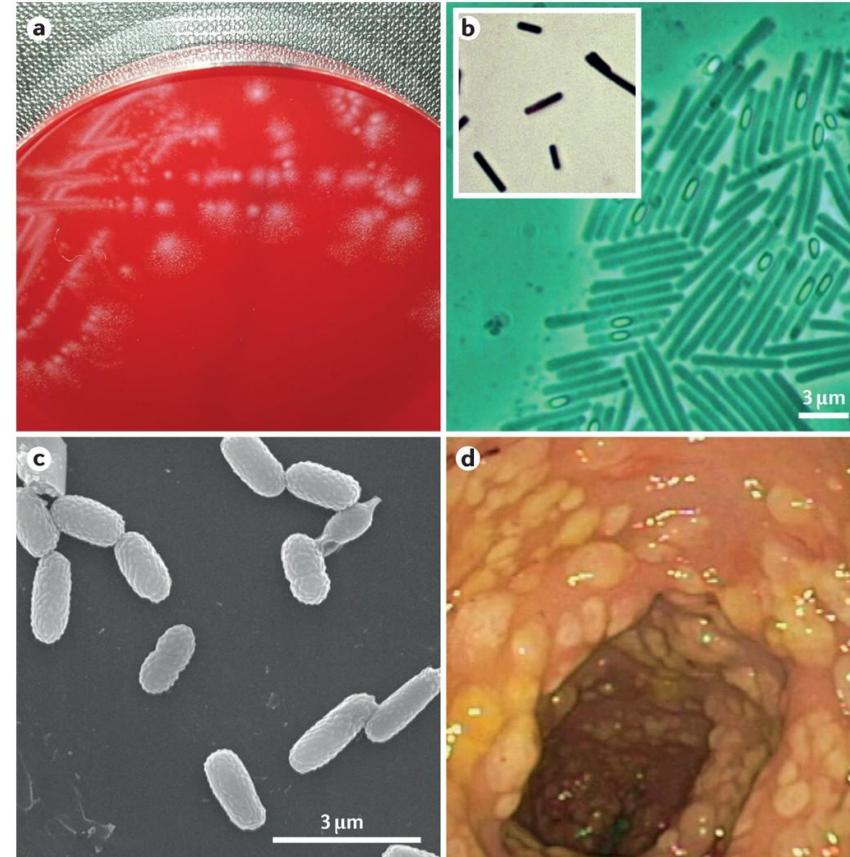
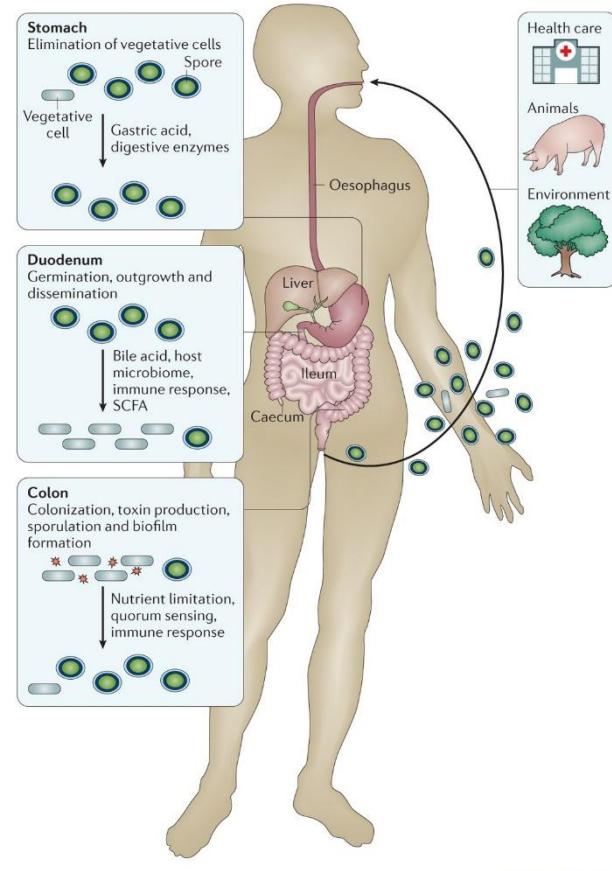


Structural Biology of PolC Pharmacology

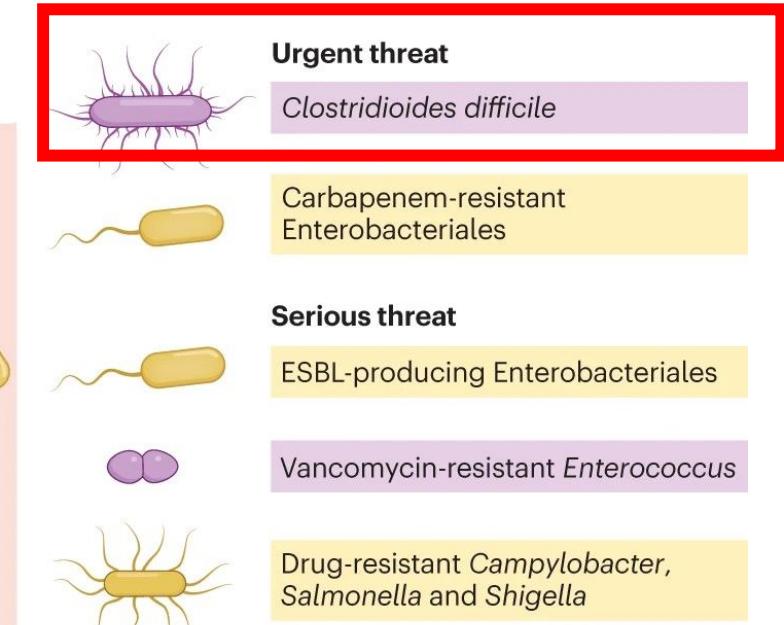
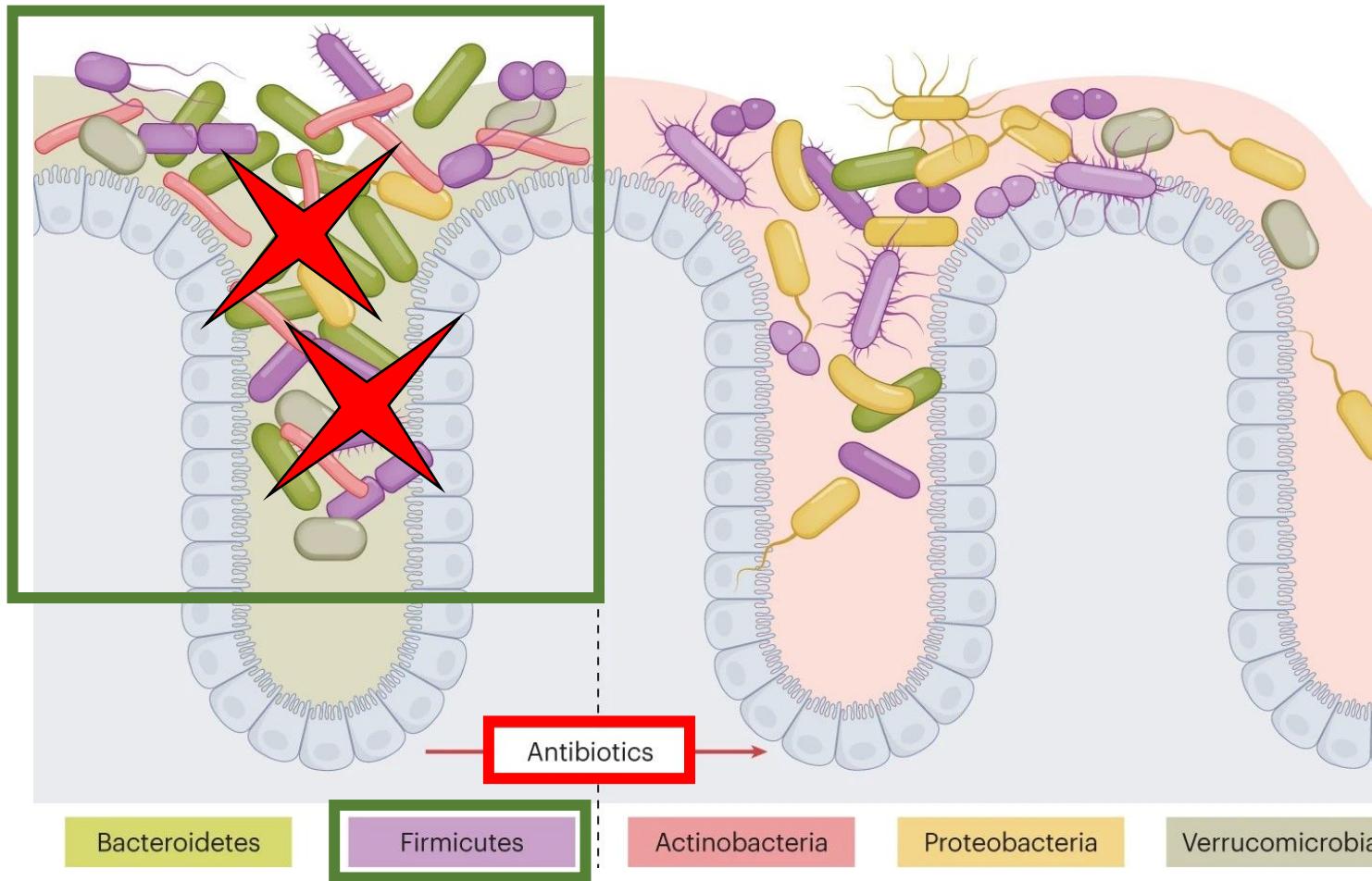
- In collaboration with the University of Texas McGovern School of Medicine cryo-EM core facility

Stay tuned

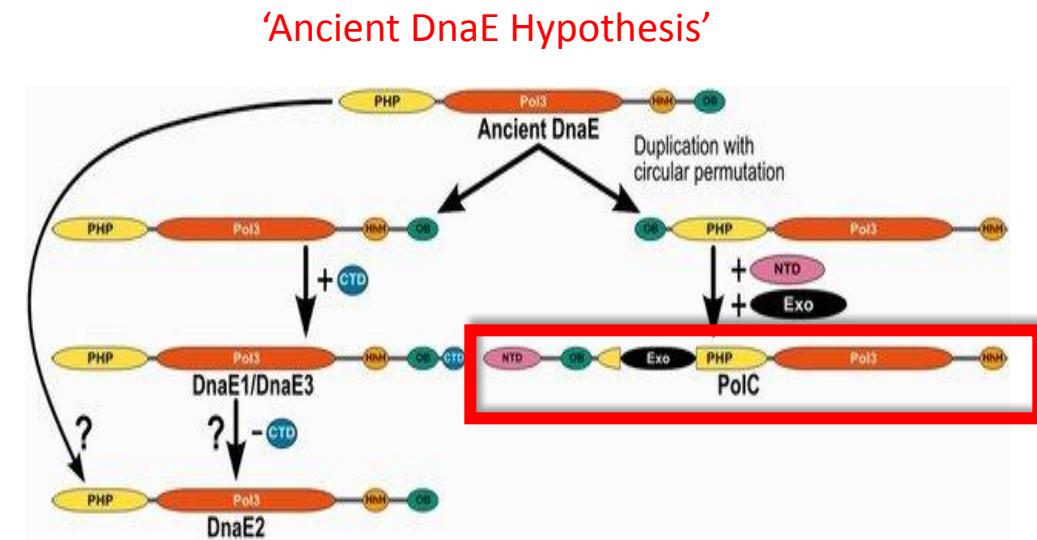
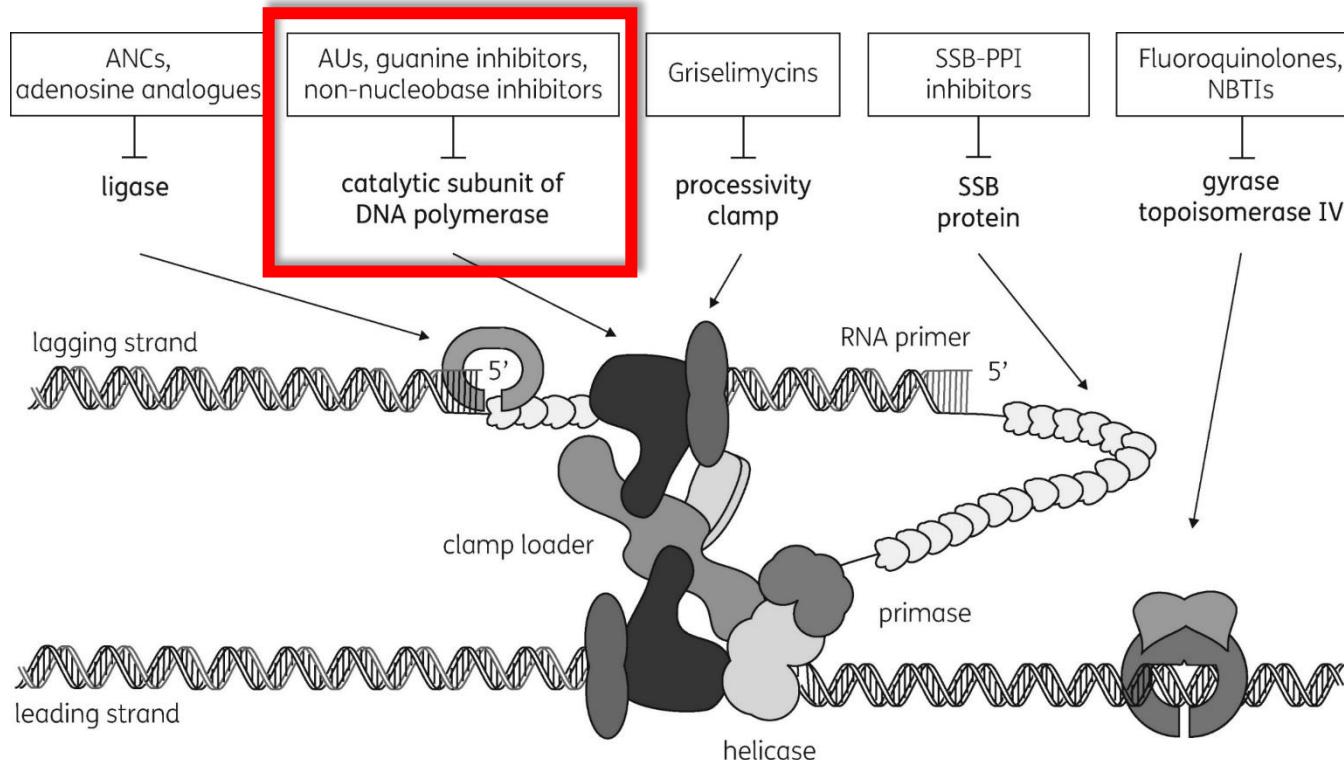
Clostridiooides difficile is a Gram-positive Bacillota pathobiont that leads to antibiotic-associated diarrhea, pseudomembranous colitis, colectomy and death



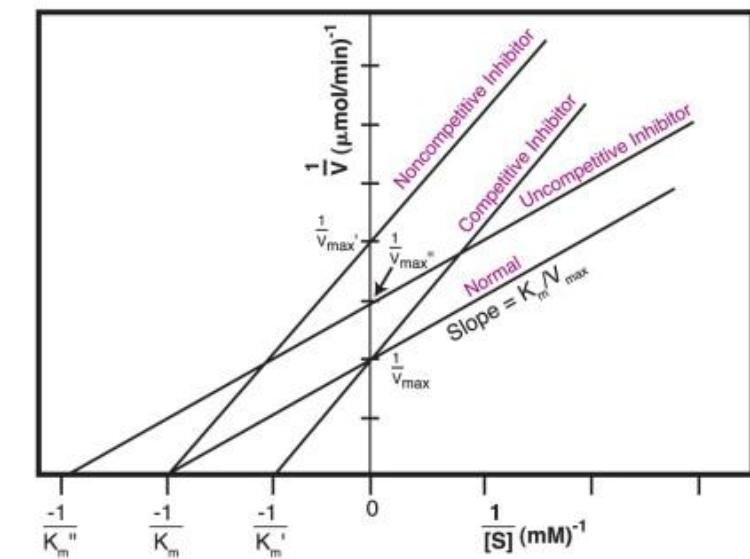
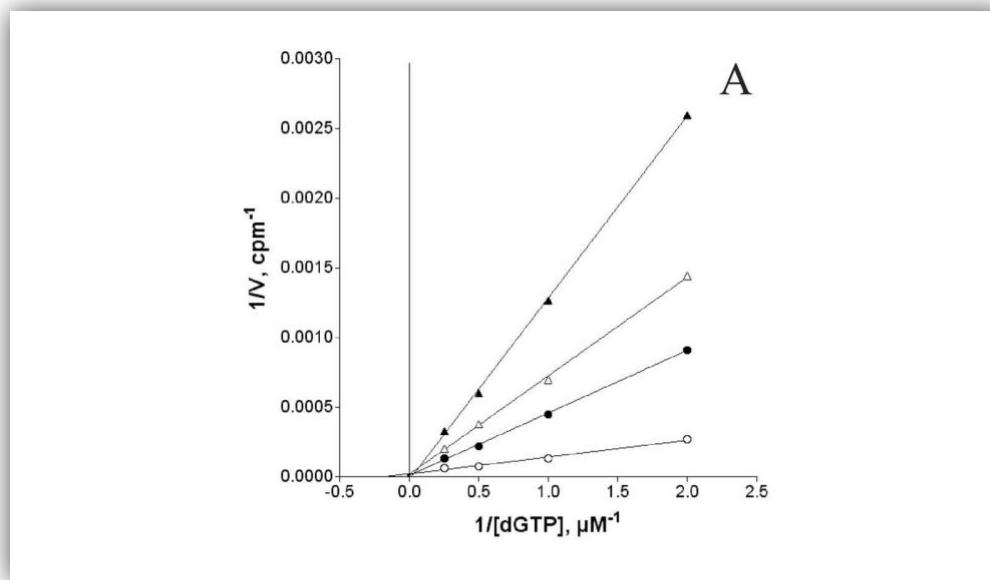
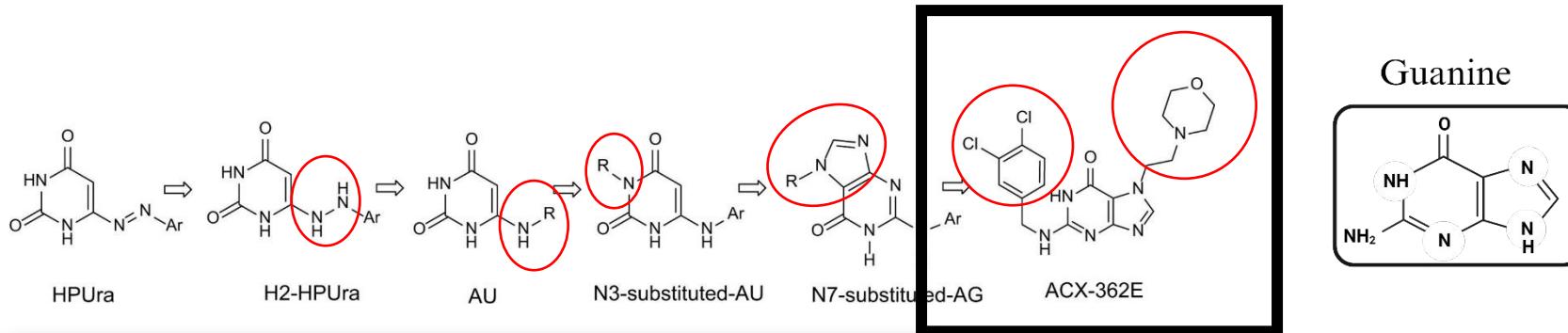
Oral Antibiotics Damage the Human Gut Microbiome



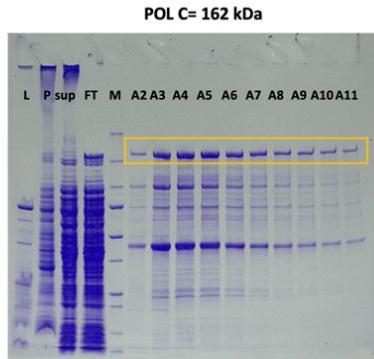
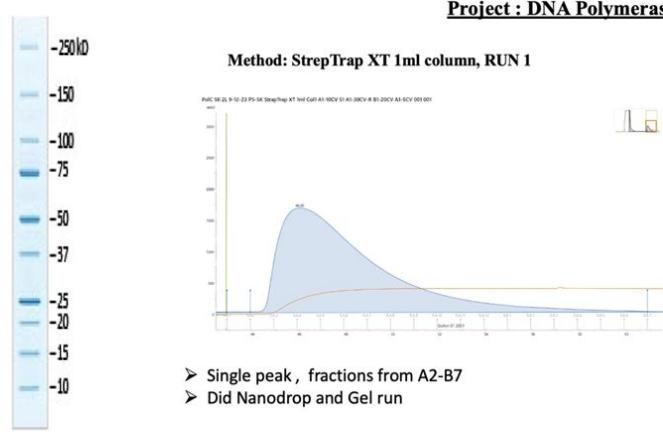
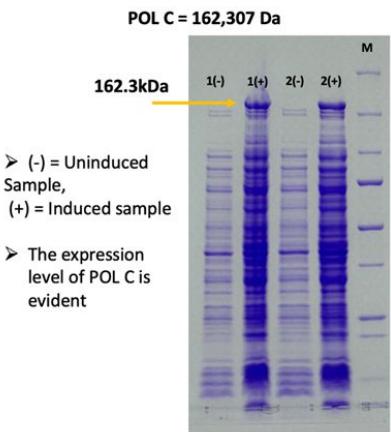
The PolC-type DNA Polymerase III (PolC) is the catalytic subunit of the Firmicute Replisome



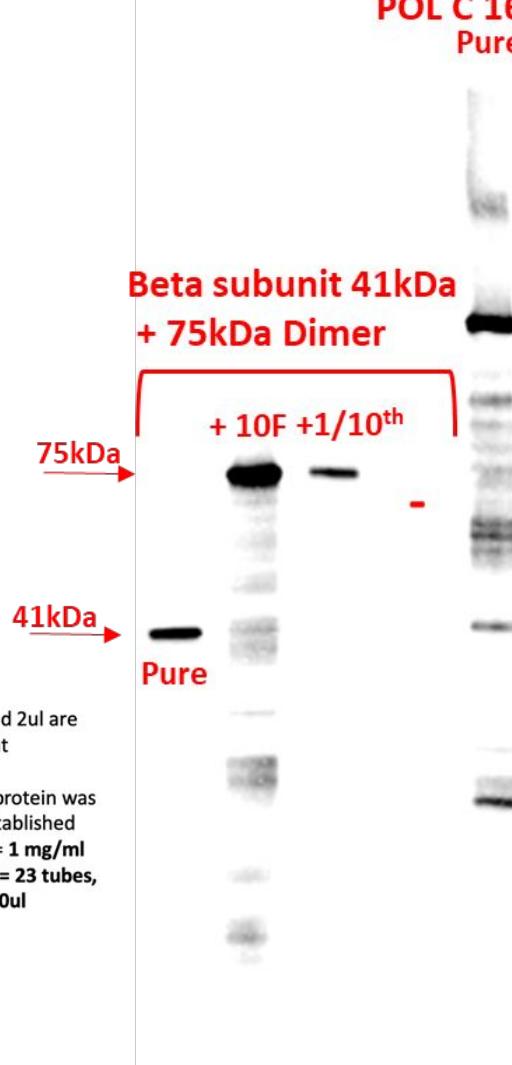
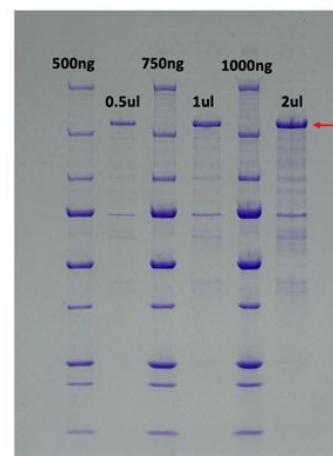
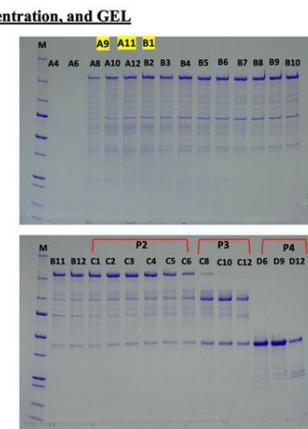
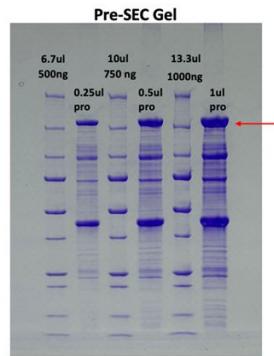
Ibezapolstat (IBZ) is a dGTP-mimetic inhibitor of the *C. difficile* PolC



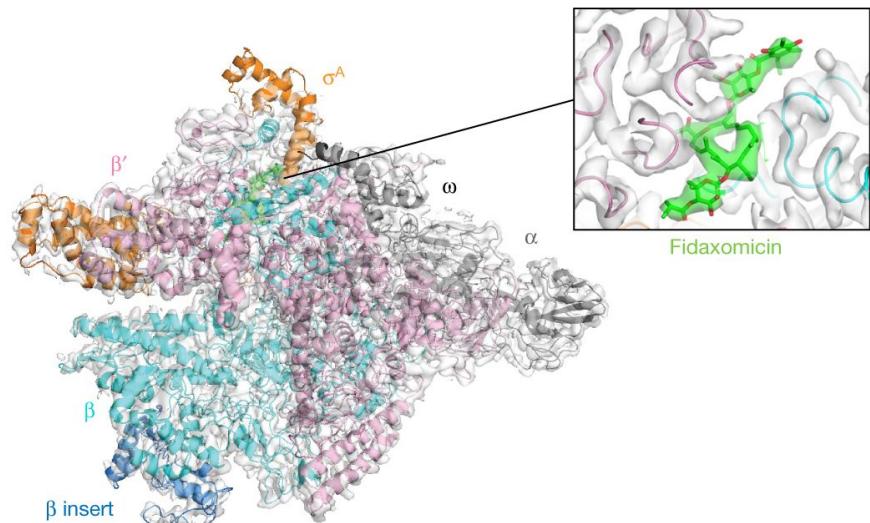
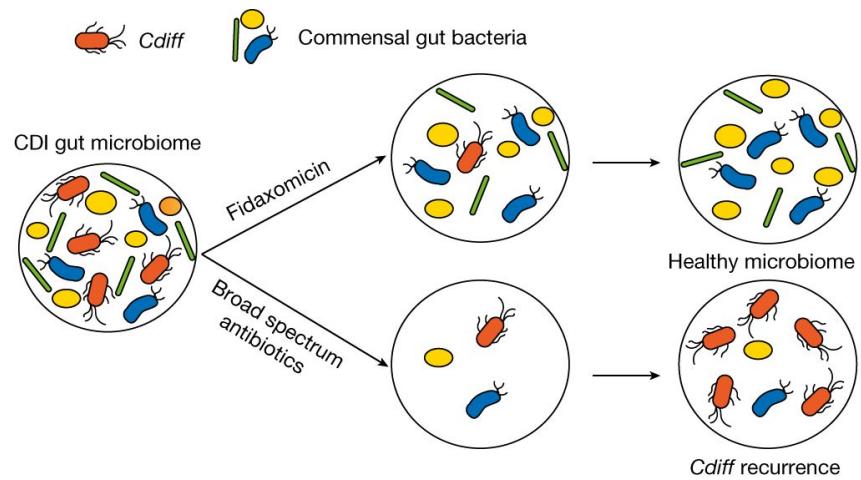
C. difficile PolC and DnaN beta sliding-clamp expression and purification



POL C 162 kDa
Pure

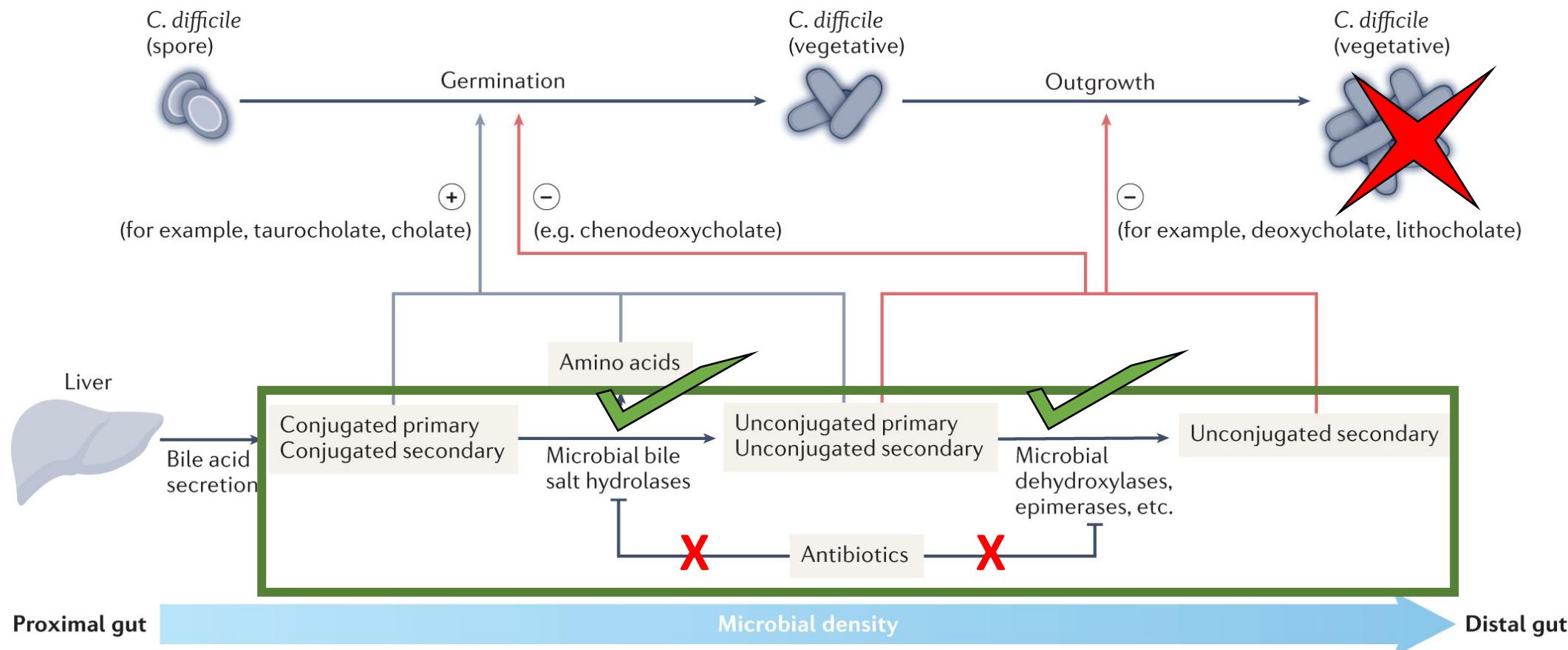


Inspiration from Fidaxomicin

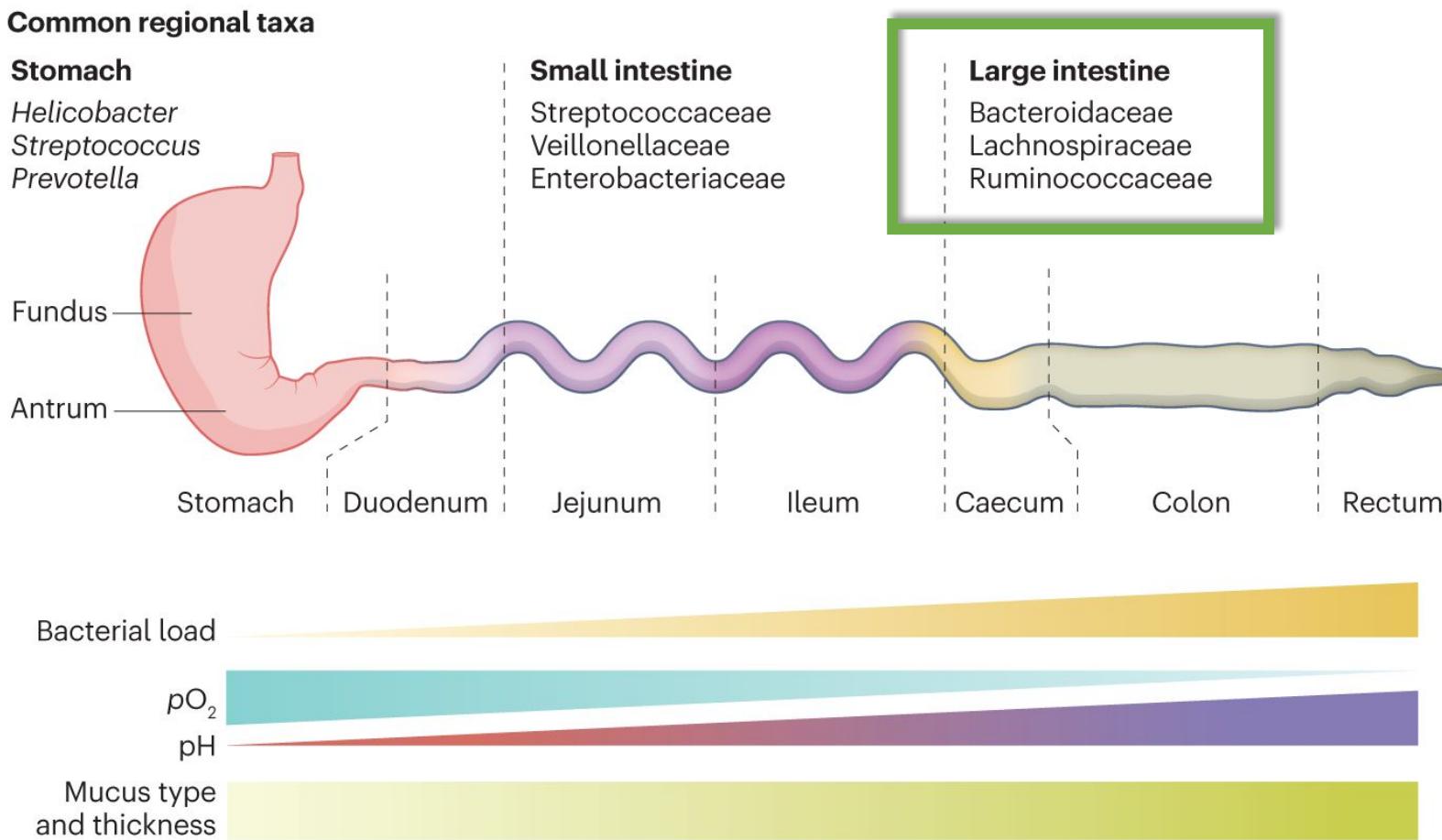


CryoEM of the FDX-bound Cdiff RNAP II

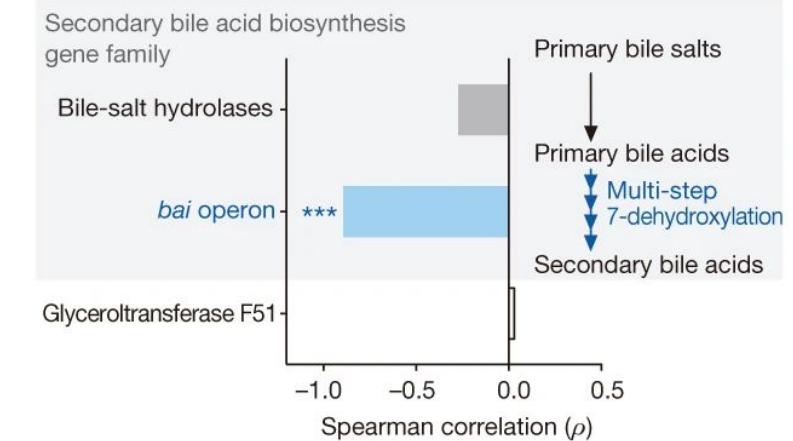
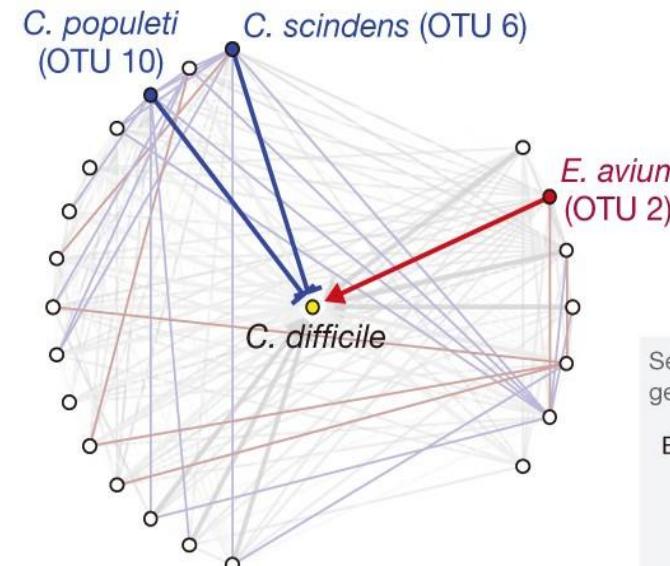
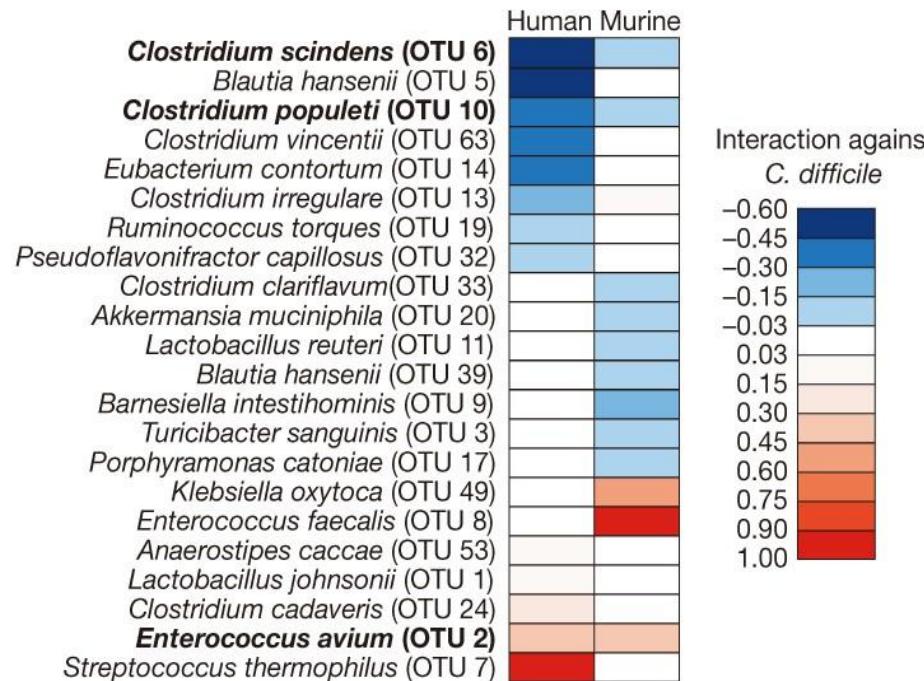
Microbial Bile Salt Metabolism Suppresses *C. difficile* Germination and Outgrowth



Lachnospiraceae and Ruminococcaceae are the dominant Bacillota of the Large Intestine



Lachnospiraceae (*C. scindens*) protects against CDI via bile acid metabolism



Targeting the Bacterial Replisome

