

Within-host evolution of *Staphylococcus aureus* stringent response imparts a fitness advantage under nutrient stress

Edwin Chen MD PhD

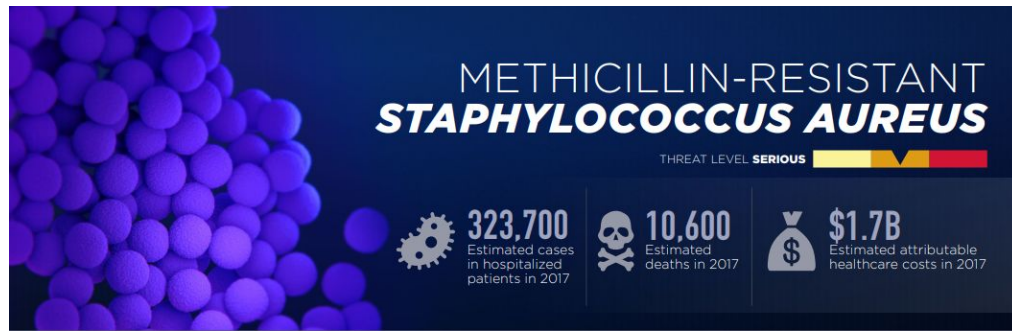
Adult Infectious Diseases Fellow

T32 Postdoctoral Trainee

Laboratory of Dr. Matthew Culyba

University of Pittsburgh

Invasive MRSA infections are a healthcare threat



Persistent MRSA bacteremia is common despite appropriate antibiotic selection (Paul 2010, Hawkins 2007, Leibovici 1998)

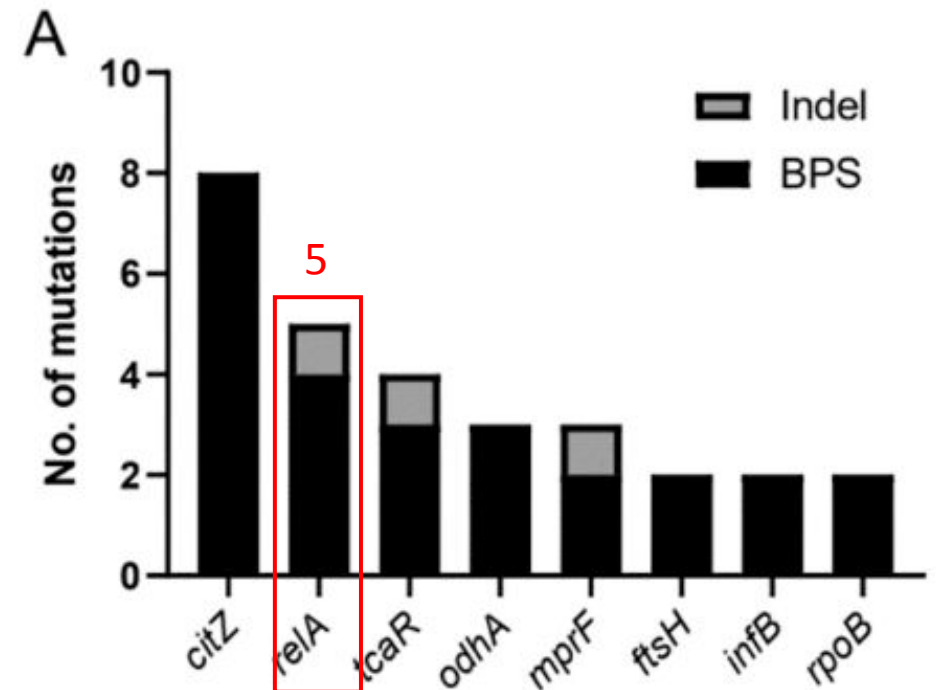
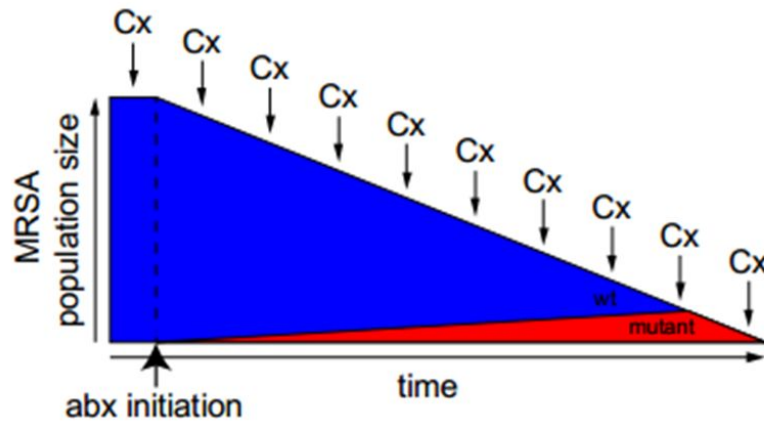
Persistent MRSA bacteremia is associated with a higher mortality:

- **45%** for persisters (>7 days) vs **9%** for non-persisters (≤ 3 days) (Yoon 2010)
- **54%** for persisters (>7 days) vs **31%** for non-persisters (<3 days) (Hawkins 2007)

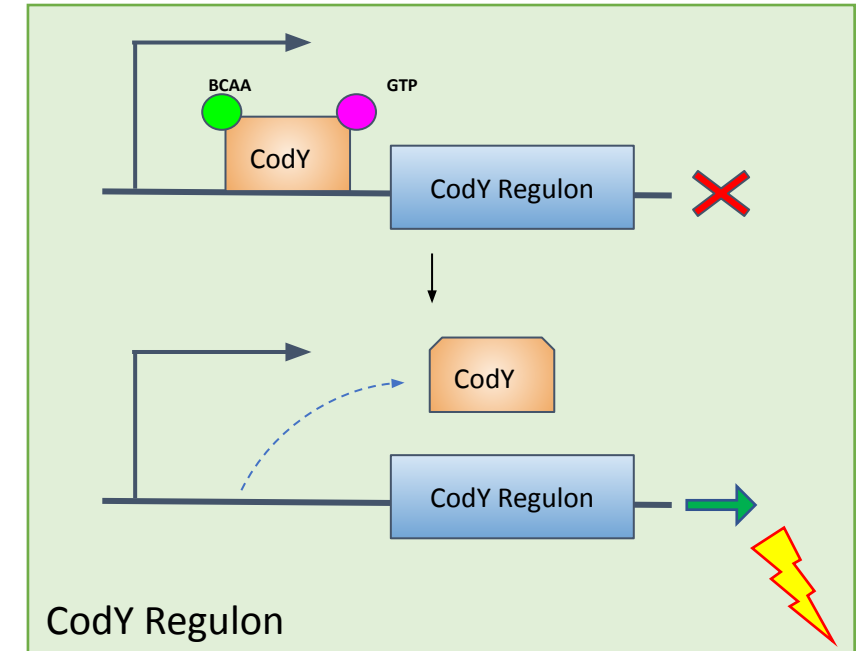
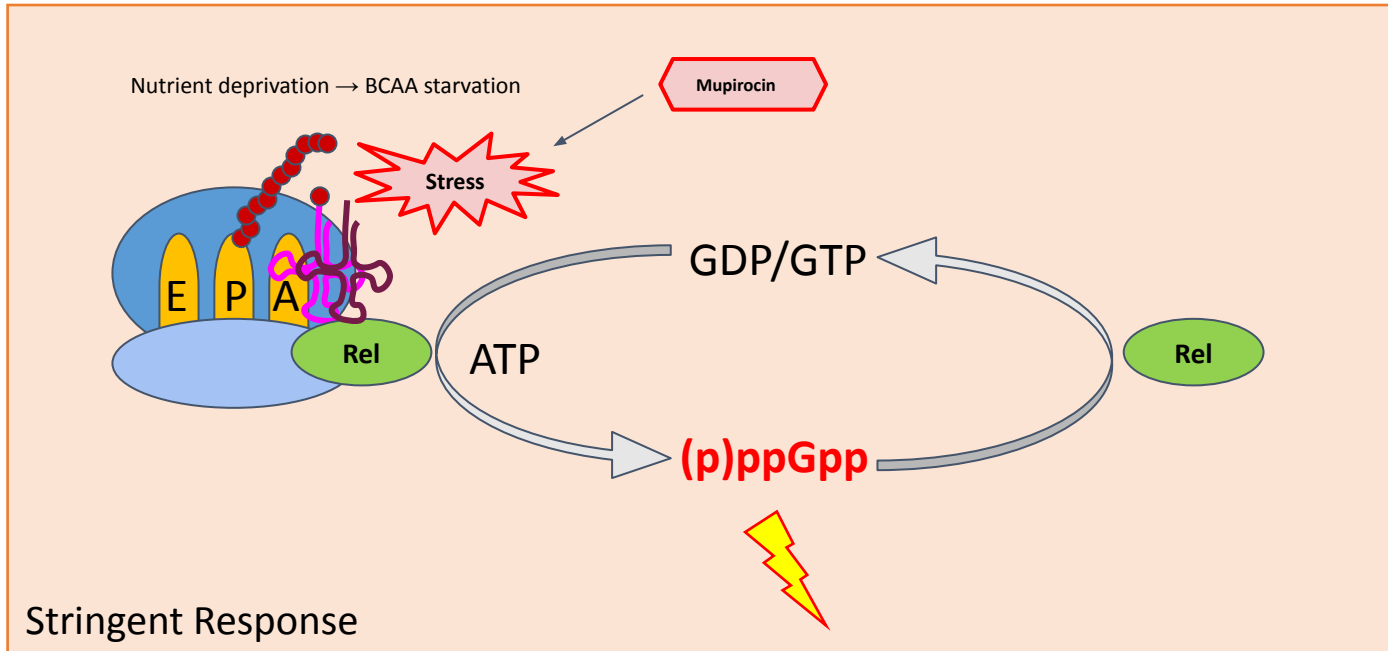
∴ There is great interest in understanding the mechanism(s) underlying persistent clinical infections.

A forward genetic screen to characterize within-host evolution of *S. aureus*

Whole-genome sequenced 206 serially positive MRSA blood cultures from 20 patients with persistent clinical infections to identify evidence of within-host evolution.



The stringent response is a conserved bacterial stress response

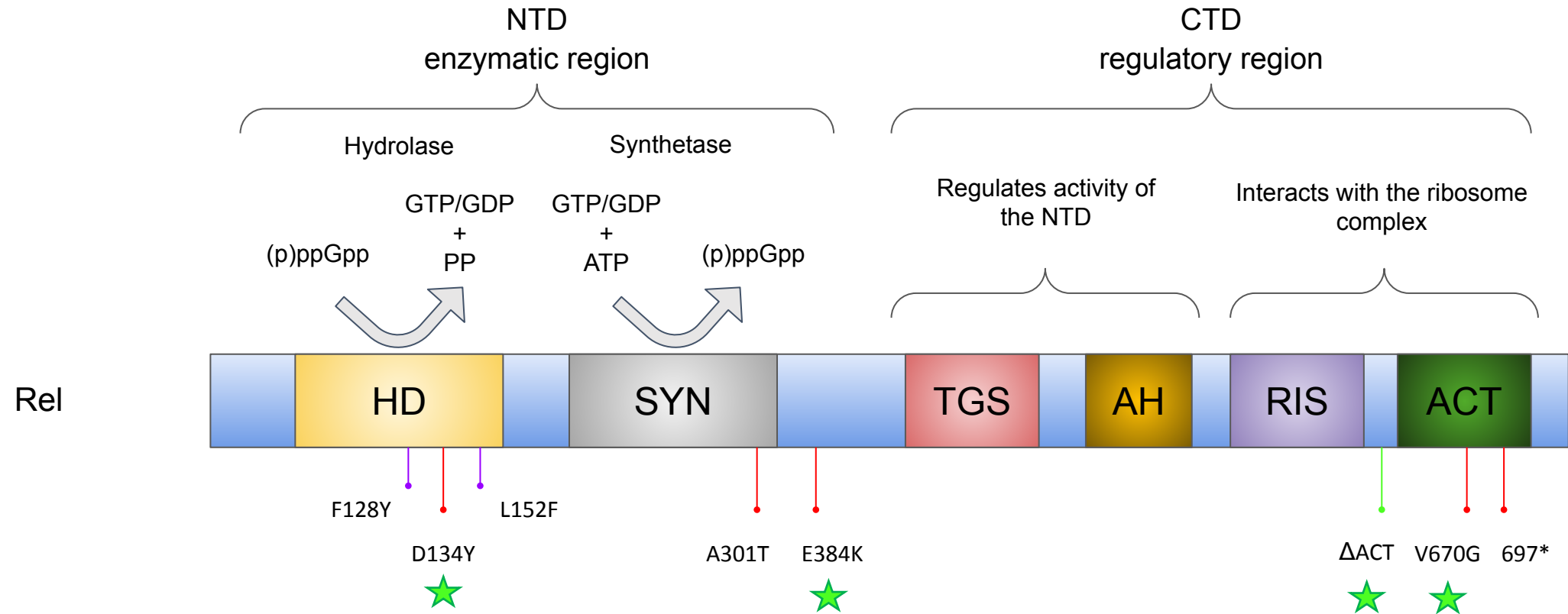


Antibiotic tolerance
Virulence
Phagosomal escape
Transcriptional regulation



Metabolism and growth
Protein translation
DNA replication
Transcriptional regulation

Rel, the central regulator of the stringent response



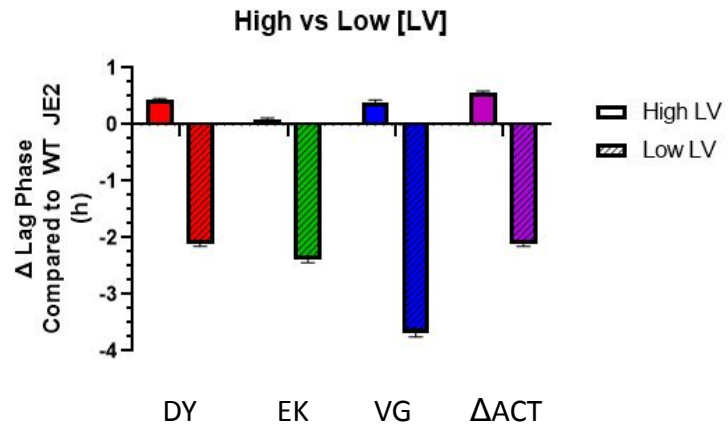
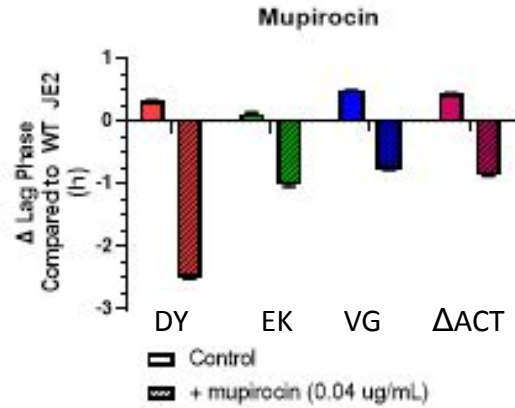
Previously identified clinical *Rel* mutations in persistent Gram(+) infections, found to impart **multidrug tolerance**

Our newly identified clinical *Rel* mutations

Allelic exchange mutants in a MRSA JE2 background

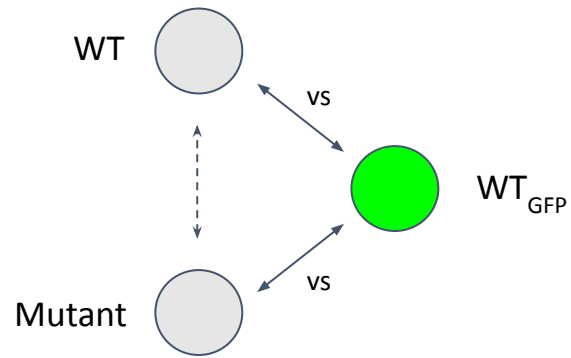
What role do our mutations play in persistent clinical infections?

Clinical *Rel* mutations alter growth

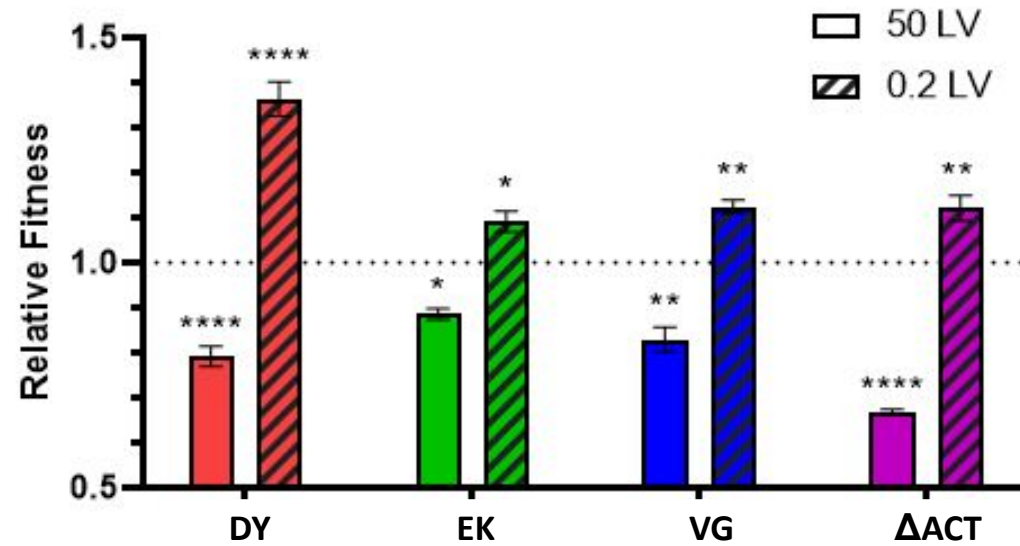


Clinical *Rel* mutations result in an abnormal stringent response phenotype and alter bacterial growth kinetics.

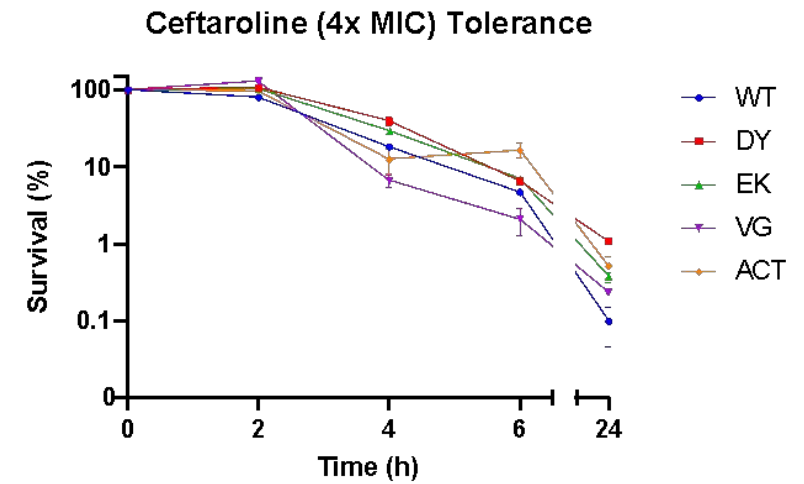
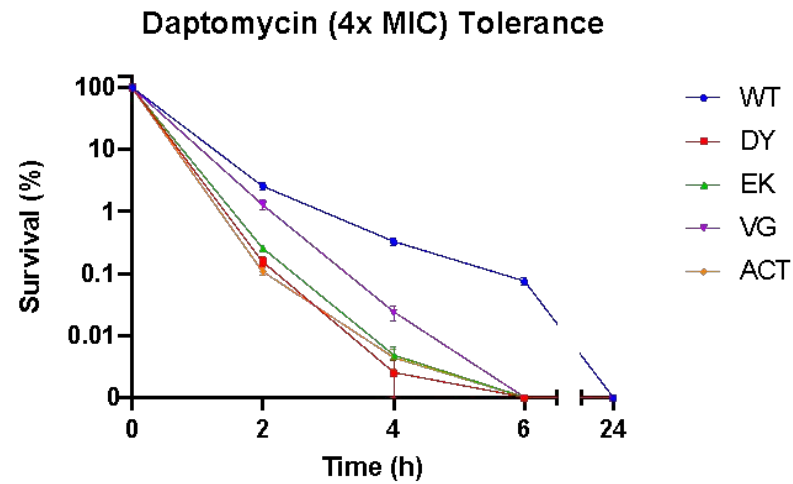
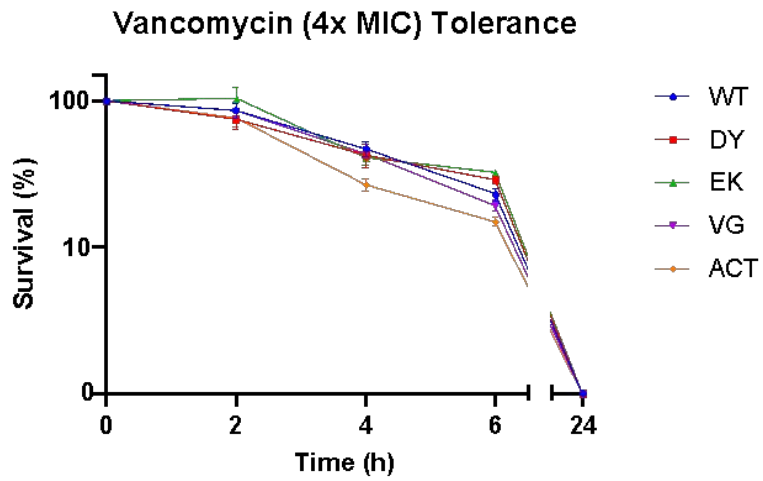
Clinical *Rel* mutations have increased fitness under stringent conditions



$$W = \ln\left(\frac{N_f^{\text{dark}}}{N_i^{\text{dark}}}\right) / \ln\left(\frac{N_f^{\text{bright}}}{N_i^{\text{bright}}}\right)$$



Clinical *Rel* mutations do not impart multidrug tolerance

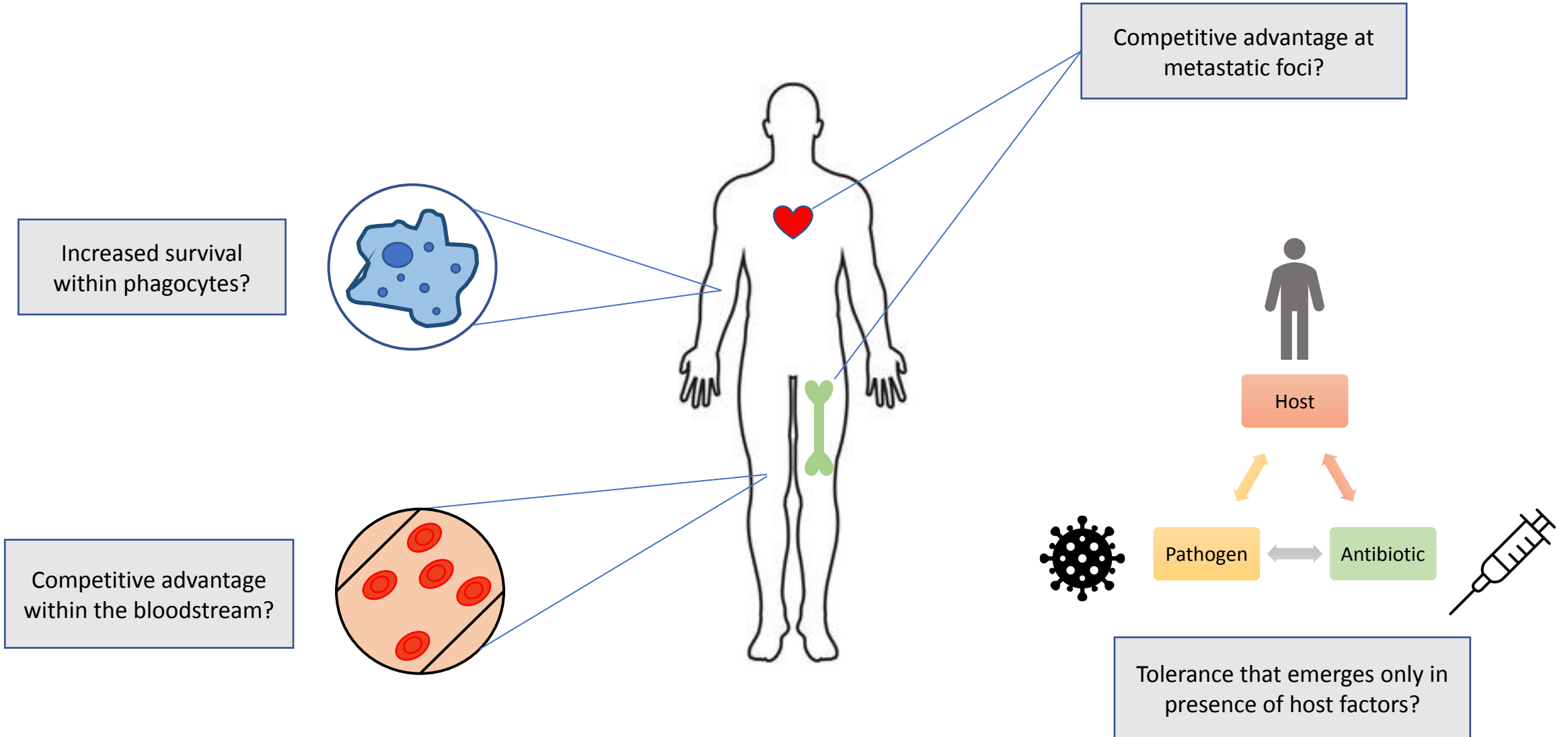


Conclusions

1. Within-host evolution of the stringent response occurs during persistent MRSA bacteremia.
2. We have identified several novel mutations localized throughout the different domains of Rel.
3. Our *Rel* mutations impart a competitive fitness advantage under nutrient limiting conditions.
4. Our *Rel* mutations results in a diverse tolerance phenotype, *not* multidrug tolerance.

∴ Our clinical *Rel* mutations highlight the diverse roles the stringent response plays in host-pathogen interactions.

Future Questions



Acknowledgements

Culyba Lab

Matthew Culyba
Marla Shaffer
Robert Bilodeau

Doi Lab

Christi McElheny
Erin Fowler
Dominic Woods

Shields Lab

Ryan Shields

Sluis-Cremer Lab

John Barnard

Harrison Lab

Urish Lab

Nguyen Lab

Van Tyne Lab

Dimitrov Lab

Cooper Lab

Division of Infectious Diseases

Department of Medicine

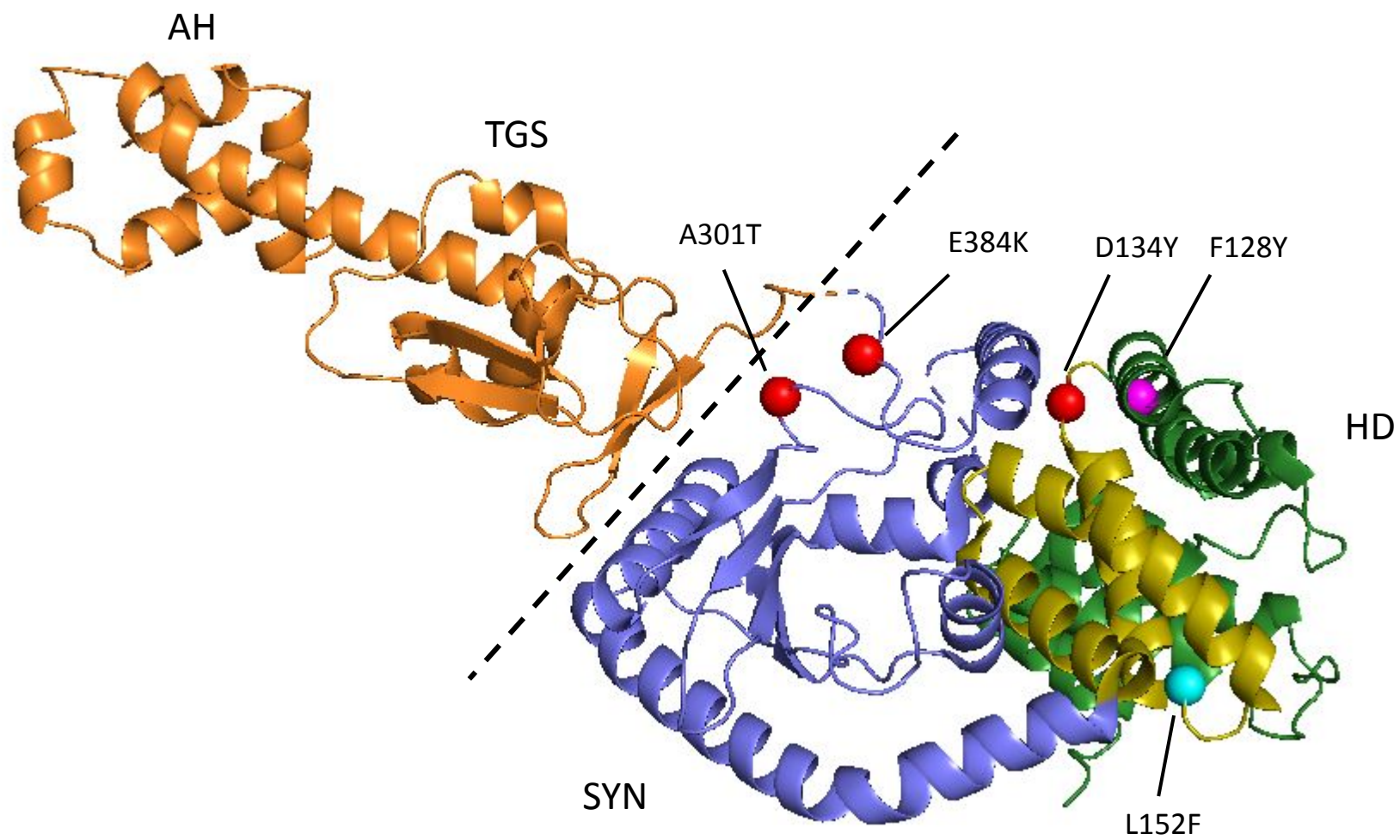
University of Pittsburgh

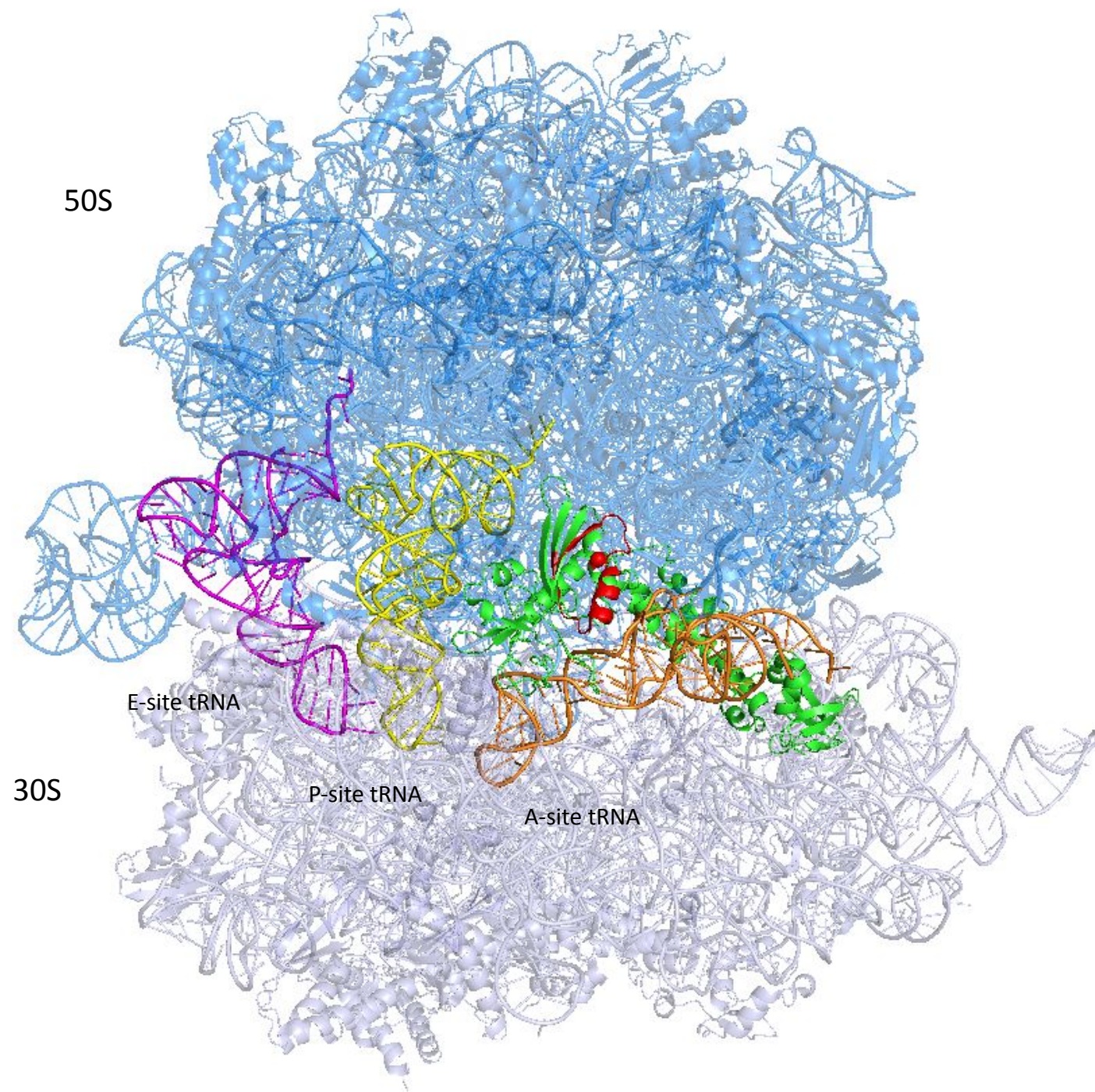


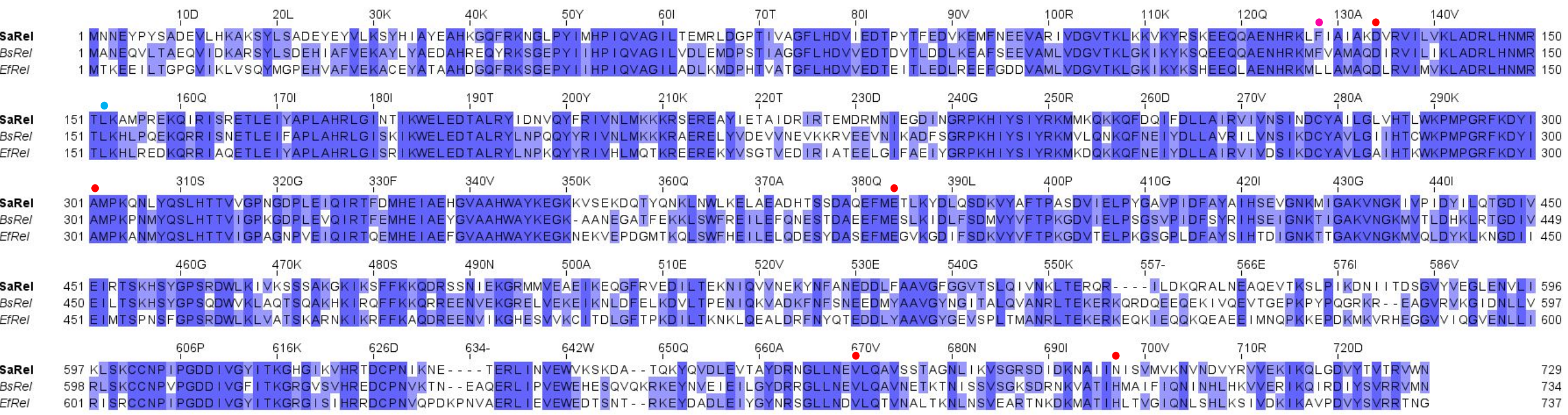
T32 Mentors

Lee Harrison
Nicolas Sluis-Cremer

T32AI138954

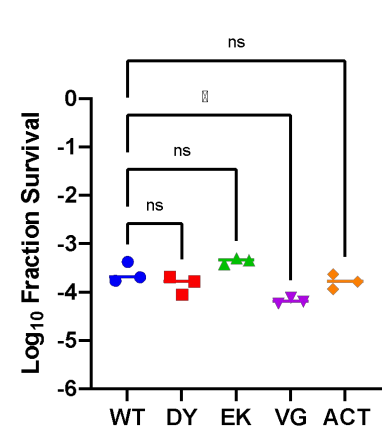




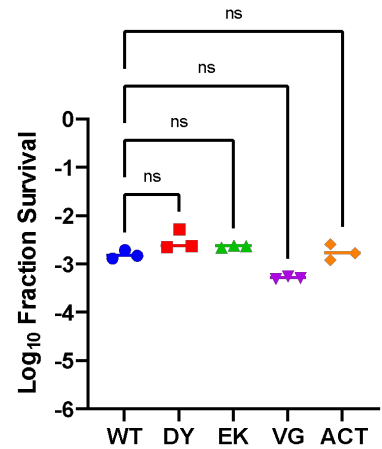


72 h

Vancomycin (4x MIC) Tolerance



Daptomycin (4x MIC) Tolerance



Ceftaroline (4x MIC) Tolerance

