

# Douglas L. Huseby

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## **Education**

### Ph.D. Biochemistry and Molecular Biology

August 2004 – September 2012

University of California, Davis

Thesis Advisor: John Roth

### B.S., Biochemistry

August 1998 - May 2002

University of Oklahoma

## **Research Experience**

### Researcher

University of Uppsala

November 2012 - Present

I am researching the evolution of antibiotic resistance in bacterial populations. I am doing this by evolving bacteria in the presence of antibiotics, and then using whole genome sequencing and genetic techniques to reconstruct the evolutionary steps that gave rise to resistance in these populations. I am doing this to understand the selections that bacterial populations are subjected to that lead to the formation of clinical resistance.

Additionally I am involved in the IMI ND4BB ENABLE program as a program co-leader. In this capacity I, together with the hit owner pharmaceutical company, coordinate experiments between academic research groups across Europe to develop a novel antibiotic. The ultimate goal of this program is to develop novel antibiotics to the step of Phase I clinical trials. In addition to this coordinating role, I am also involved experimentally in the microbiology platform determining frequency of resistance and mechanism of action and resistance using genetic techniques and whole-genome sequencing technology.

### Ph.D Candidate

University of California, Davis

March 2005 – October 2012

I examined the role of bacterial microcompartments in the metabolism of ethanolamine by *Salmonella typhimurium*. I discovered that microcompartments encapsulate enzymes requiring cofactors, and that the cofactors are cycled in the microcompartment leading to more efficient metabolism of difficult substrates than otherwise possible.

### Laboratory Technician

Oregon Health & Science University

May 2000 - August 2000; May 2001 - August 2001; May 2002 – August 2004

My investigations included the expression, purification and assembly onto lipid monolayers of retroviral structural proteins, and analysis of assembly using structural electron microscopy and image processing techniques.

### Research Assistant

Oregon Health & Science University

May 1999-August 1999

I was awarded the Elizabeth Glaser Pediatric AIDS Foundation summer internship to study the structure of HIV capsid proteins assembled on synthetic lipid monolayers.

## Awards and Honors

ESCMID Tuition Grant (2016 Advanced Course on Antibiotics)  
Swedish Federation of Microbiologists Travel Grant (2014 EMBO Workshop on Recoding)  
National Merit Scholar  
University of Oklahoma National Scholars Program  
Automatic Data Processing Corporate National Merit Scholarship  
Elizabeth Glaser Pediatric AIDS Summer Intern

## Courses

2017 Swedish Apotekarsocieteten 3-day Drug Development Course  
2016 Advanced Course on Antibiotics (now ICARe)  
2014 Perl Programming with Application to Bioinformatics  
2013 Introduction to Recombineering in Bacterial Genetics

## Publications

1. Juhas, M., Widlake, E., Teo, J., Huseby, D. L., Tyrrell, J. M., Polikanov, Y. S., ... Hobbie, S. N. (2019). In vitro activity of apramycin against multidrug-, carbapenem- and aminoglycoside-resistant Enterobacteriaceae and *Acinetobacter baumannii*. *Journal of Antimicrobial Chemotherapy*, 74(4), 944–952.
2. Vestö, K., Huseby, D. L., Snygg, I., Wang, H., Hughes, D., & Rhen, M. (2018). Muramyl Endopeptidase Spr Contributes to Intrinsic Vancomycin Resistance in *Salmonella enterica* Serovar Typhimurium. *Frontiers in Microbiology*, Vol. 9, p. 2941.
3. Garoff, L., Huseby, D. L., Praski Alzrigat, L., & Hughes, D. (2018). Effect of aminoacyl-tRNA synthetase mutations on susceptibility to ciprofloxacin in *Escherichia coli*. *Journal of Antimicrobial Chemotherapy*, 73(12), 3285–3292.
4. Pantel, L., Florin, T., Dobosz-Bartoszek, M., Racine, E., Sarciaux, M., Serri, M., ... Gualtieri, M. (2018). Odilorhabdins, Antibacterial Agents that Cause Miscoding by Binding at a New Ribosomal Site. *Molecular Cell*, 70(1), 83–94.e7.
5. Jeannot, F., Taillier, T., Despeyroux, P., Renard, S., Rey, A., Mourez, M., ... Bacqué, E. (2018). Imidazopyrazinones (IPYs): Non-Quinolone Bacterial Topoisomerase Inhibitors Showing Partial Cross-Resistance with Quinolones. *Journal of Medicinal Chemistry*, 61(8), 3565–3581.
6. Huseby DL, Hughes D (2018) Methods to Determine Mutational Trajectories After Experimental Evolution of Antibiotic Resistance BT - Antibiotic Resistance Protocols. ed Gillespie SH (Springer New York, New York, NY), pp 95–103.
7. Petursdottir DH, et al. (2017) Early-Life Human Microbiota Associated With Childhood Allergy Promotes the T Helper 17 Axis in Mice. *Front Immunol* 8:1699.
8. Praski Alzrigat L, Huseby DL, Brandis G, Hughes D (2017) Fitness cost constrains the spectrum of marR mutations in ciprofloxacin-resistant *Escherichia coli*. *J Antimicrob Chemother* 72(11):3016–3024.
9. Brandis G, Cao S, Huseby DL, Hughes D (2017) Having your cake and eating it - *Staphylococcus aureus* small colony variants can evolve faster growth rate without losing their antibiotic resistance. *Microb Cell* 4(8):275–277.

10. Cao S, Huseby DL, Brandis G, Hughes D (2017) Alternative Evolutionary Pathways for Drug-Resistant Small Colony Variant Mutants in *Staphylococcus aureus*. *MBio* 8(3):e00358-17.
11. Huseby DL, Pietsch F, Brandis G, et al. (2017) Mutation Supply and Relative Fitness Shape the Genotypes of Ciprofloxacin-Resistant *Escherichia coli*. *Mol Biol Evol* 34(5):1029–1039.
12. De Rosa M, et al. (2017) Design, synthesis and in vitro biological evaluation of oligopeptides targeting *E. coli* type I signal peptidase (LepB). *Bioorg Med Chem* 25(3):897–911.
13. Pietsch F, et al. (2017) Ciprofloxacin selects for RNA polymerase mutations with pleiotropic antibiotic resistance effects. *J Antimicrob Chemother* 72(1):75–84.
14. Huseby DL, Roth JR. (2013) Evidence that a metabolic microcompartment contains and recycles private cofactor pools. *J Bacteriol.* 195(12): 2864-79.
15. Thiennimitr P, Winter SE, Winter MG, Xavier MN, Tolstikov V, Huseby DL, Sterzenbach T, Tsolis RM, Roth JR, Bäumlér AJ. (2011) Intestinal inflammation allows *Salmonella* to use ethanolamine to compete with the microbiota. *Proc Natl Acad Sci U S A.* 108(42): 17480-5.
16. Still A, Huseby D, Barklis E. (2011) Analysis of the N-terminal region of the murine leukemia virus nucleocapsid protein. *Virus Res.* 155(1): 181-8.
17. Winter SE, Thiennimitr P, Winter MG, Butler BP, Huseby DL, Crawford RW, Russell JM, Bevins CL, Adams LG, Tsolis RM, Roth JR, Bäumlér AJ. (2010) Gut inflammation provides a respiratory electron acceptor for *Salmonella*. *Nature.* 467(7314): 426-9.
18. Alfadhli A, Huseby D, Kapit E, Colman D, Barklis E. (2006) Human immunodeficiency virus type 1 matrix protein assembles on membranes as a hexamer. *J Virol.* 81(3): 1472-8.
19. Huseby D, Barklis RL, Alfadhli A, Barklis E. (2005) Assembly of human immunodeficiency virus precursor gag proteins. *J Biol Chem.* 280(18): 17664-70.
20. Scholz I, Arvidson B, Huseby D, Barklis E. (2005) Virus particle core defects caused by mutations in the human immunodeficiency virus capsid N-terminal domain. *J Virol.* 79(3): 1470-9.
21. Mayo K, Huseby D, McDermott J, Arvidson B, Finlay L, Barklis E. (2003) Retrovirus capsid protein assembly arrangements. *J Mol Biol.* 325(1): 225-37.
22. Mayo K, Vana ML, McDermott J, Huseby D, Leis J, Barklis E. Analysis of Rous sarcoma virus capsid protein variants assembled on lipid monolayers. *J Mol Biol.* 316(3): 667-78.