

# Albert C. Vill

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## Education

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- Doctor of Philosophy — Cornell University** May 2022  
*Field of Genetics, Genomics & Development*  
*Thesis: “Metagenomic Methods to Investigate Mobile Element Context and Nascent Transcription in the Human Gut Microbiome”*
- Bachelor of Science, Magna Cum Laude — Gettysburg College** May 2016  
*Biochemistry and Molecular Biology major, 3.70 GPA*  
*Lincoln Scholar – highest merit-based scholarship awarded*

## Research Experience

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- Graduate Research Assistant — Lab of Dr. Ilana Brito, Cornell University** Spring 2017 – present  
*Designing and implementing methods to quantify changes in the composition and function of the human gut microbiome during perturbation and disease*
- HMI Summer Research Fellow — Gettysburg College** Summers 2014 & 2015  
*Characterizing bacteriophages by host-range screens and comparative genomics*

## Publications

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- Vill AC**, Rice EJ, De Vlaminck I, Danko CG, Brito IL. Run-on sequencing reveals nascent transcriptomics of the human microbiome. Preprint
- Kent AG, **Vill AC**<sup>†</sup>, Shi Q, Satlin MJ, Brito IL. Widespread transfer of mobile antibiotic resistance genes within individual gut microbiomes revealed through bacterial Hi-C. *Nature Communications*. 2020 Sep 1;11(1):4379.  
<sup>†</sup> *co-first author*
- Delesalle VA, **Vill AC**, Tomko BE, Boas K, Burton EA, Guffey AA, Loney R, Simões MS, Tanke NT, Krukoni GP. Comparative genomics of fourteen novel Siphoviridae phages of *Bacillus subtilis*, including three phages closely related to SPP1. In preparation
- Delesalle VA, Tanke NT, **Vill AC**, Krukoni GP. Testing hypotheses for the presence of tRNA genes in mycobacteriophage genomes. *Bacteriophage*. 2016 Aug 5;6(3):e1219441. 2016
- Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF; **Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science** ‡; Phage Hunters Integrating Research and Education; Mycobacterial Genetics Course. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *eLife*. 2015 Apr 28;4:e06416. 2015  
<sup>‡</sup> *consortium member, data contributor*

## Honors and Awards

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Travel Award Recipient, Cornell Center for Vertebrate Genomics	2022
Seed Grant Recipient, Genomics Innovation Hub	2020
Distinguished Scholar, Cornell Center for Vertebrate Genomics	2019
Honorable Mention, NSF Graduate Research Fellowship	2018
Herzog Teaching Fellow, Gettysburg College	2015
HHMI Summer Research Fellow, Gettysburg College	2014 & 2015

## Presentations

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<b>Poster</b> — The Human Microbiome: Ecology and Evolution Symposium <i>Run-on sequencing enables nascent metatranscriptomics of the human microbiome</i>	(canceled) 2022
<b>Poster</b> — Lake Arrowhead Microbial Genomics Meeting <i>Bacterial nascent transcriptomics with precision run-on sequencing</i>	(canceled) 2021
<b>Poster</b> — Biomedical Engineering Society Annual Meeting <i>Monitoring the Transfer of Antibiotic Resistance Genes in Patients with Neutropenia using Bacterial Hi-C</i>	2019

## Service and Outreach

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Coordinator, Cornell Center for Vertebrate Genomics Journal Club	Fall 2021 – Spring 2022
Graduate Mentor, Microbial Friends & Foes Research Experience for non-Cornell Undergraduates	Summer 2019
Workshop Facilitator, 4-H Career Explorations “Engineering the Microbiome” Focus Program	June 2018
Graduate Fellow, Cornell Graduate Student School Outreach Program	Spring 2018

## Skills

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R programming language <ul style="list-style-type: none"><li>▪ tidyverse evangelist</li><li>▪ ggplot2 devotee</li></ul>	Bash programming language / shell scripting <ul style="list-style-type: none"><li>▪ awk, sed, grep</li><li>▪ Sun Grid Engine queuing system</li></ul>
NGS software proficiency <ul style="list-style-type: none"><li>▪ samtools</li><li>▪ bedtools</li><li>▪ bwa, bowtie2, minimap2</li></ul>	Sequencing library preparation <ul style="list-style-type: none"><li>▪ Hi-C, PRO-seq, RNA-seq</li><li>▪ Nextera XT kit</li><li>▪ NEBNext Ultra II DNA / RNA kits</li></ul>