

# Albert C. Vill

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## Education

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**Bachelor of Science, *Magna Cum Laude* — Gettysburg College** Graduated May 2016  
*Biochemistry and Molecular Biology major, 3.70 GPA*  
*Lincoln Scholar – highest merit-based scholarship awarded*

## Research Experience

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**PhD Candidate — 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*

**HHMI Summer Research Fellow — Gettysburg College** Summers, 2014 & 2015  
*Characterizing bacteriophages by host-range screens and comparative genomics*

## 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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**Poster** — The Human Microbiome: Ecology and Evolution Symposium (canceled) 2022  
*Run-on sequencing enables nascent metatranscriptomics of the human microbiome*

**Poster** — Lake Arrowhead Microbial Genomics Meeting (canceled) 2021  
*Bacterial nascent transcriptomics with precision run-on sequencing*

**Poster** — Biomedical Engineering Society Annual Meeting 2019  
*Monitoring the Transfer of Antibiotic Resistance Genes in Patients with Neutropenia using Bacterial Hi-C*

## Publications

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- Vill AC, Rice EJ, De Vlaminck I, Danko CG, Brito IL. Run-on sequencing reveals transcriptional dynamics within the human microbiome. Submitted Jan. 2022
- 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
- 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. 2020  
<sup>†</sup> *co-first author*
- 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**<sup>‡</sup>; 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*