

# Albert C. Vill, Ph.D.

**Institutional email** → [albert.vill@yale.edu](mailto:albert.vill@yale.edu)  
**Personal email** → [albertcvill@gmail.com](mailto:albertcvill@gmail.com)  
**Website** → [albertvill.com](http://albertvill.com)

## Education

---

- 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

---

- Postdoctoral Associate — Lab of Dr. Paul Turner, Yale University** March 2023 – present  
Studying the evolutionary dynamics of phages of human pathogens as part of the ongoing efforts at the Center for Phage Biology and Therapy at Yale
- Graduate Research Assistant — Lab of Dr. Ilana Brito, Cornell University** May 2017 – May 2022  
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

---

- 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

## Service and Outreach

---

- 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

---

### R programming language

- tidyverse evangelist
- ggplot2 devotee

### Linux-based NGS software

- samtools
- bedtools
- bwa, bowtie2, minimap2

### Bash programming language / shell scripting

- awk, sed, grep
- Sun Grid Engine queuing system

### Microbiology

- anaerobic and BSL-2 culture
- phage isolation and propagation

### Nucleic acid sequencing

- metagenomic sequencing, assembly, binning, and annotation
- RNA-seq and differential expression analysis

## Publications

---

**Vill AC**, Rice EJ, De Vlaminck I, Danko CG, Brito IL. Run-on sequencing reveals nascent transcriptomics of the human microbiome. Preprint

Chivu AG, Abuhashem A, Barshad G, Rice EJ, Leger MM, **Vill AC**, Wong W, Brady R, Smith JJ, Wikramanayake AH, Arenas-Mena C, Brito IL, Ruiz-Trillo I, Hadjantonakis AK, Lis JT, Lewis JJ, Danko CG. Evolution of promoter-proximal pausing enabled a new layer of transcription control. Preprint

Grodner B, Shi H, Farchione O, **Vill AC**, Ntekas I, Diebold PJ, Zipfel WR, Brito IL, De Vlaminck I. Spatial Mapping of Mobile Genetic Elements and their Cognate Hosts in Complex Microbiomes. Preprint

**Vill AC**, Delesalle VA, Tomko BE, Lichty KB, Simões MS, Guffey AA, Burton EA, Tanke NT, Krukonis GP. Comparative genomics of six lytic *Bacillus subtilis* phages from the Southwest United States. *PHAGE*. 3(3):171-178. 2022

Delesalle VA, Tomko BE, **Vill AC**, Boas K, Krukonis GP. Forty Years without Family: Three Novel Bacteriophages with High Similarity to SPP1 Reveal Decades of Evolutionary Stasis since the Isolation of Their Famous Relative. *Viruses*. 14(10):2106. 2022

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*. 11(1):4379. 2020

<sup>†</sup> co-first author

Delesalle VA, Tanke NT, **Vill AC**, Krukonis GP. Testing hypotheses for the presence of tRNA genes in mycobacteriophage genomes. *Bacteriophage*. 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*. 4:e06416. 2015

<sup>‡</sup> consortium member, data contributor