

Albert C. Vill

Institutional email → acv46@cornell.edu
Personal email → albertcvill@gmail.com
Website → metageno.me
Twitter → [@_AlbertVill](https://twitter.com/_AlbertVill)

Education

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

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

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

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

- Vill AC, Rice EJ, De Vlaminc I, Danko CG, Brito IL. Run-on sequencing reveals transcriptional dynamics within the human microbiome. In Review
- 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[†], 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
[†] 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**[‡]; 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
[‡] consortium member, data contributor