## Pablo Cárdenas R.

Cambridge, MA, USA (citizen of Colombia, F1 visa status)

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### **Education**

Massachusetts Institute of Technology (MIT) — Cambridge, MA, USA PhD Candidate, Department of Biological Engineering (GPA: 5.0/5.0)

**Ongoing** 

Universidad de los Andes (Uniandes) — Bogotá, Colombia

Mar. 2018

Bachelor of Science Summa Cum Laude in Microbiology, minor in Bioinformatics (GPA: 4.84/5.0)

### Research

### **Department of Biological Engineering, MIT** — Cambridge, MA

Graduate Research Assistant

Sep 2018 ++

- → Designing molecular and computational tools for transcriptional control, functional genetics, and drug discovery in the malarial parasite *Plasmodium falciparum* (Prof. Jacquin C. Niles)
- → Helped model, construct, and test a control system for managing a shared cell resource in genetic circuits (Prof. Domitilla Del Vecchio, Mechanical Engineering)
- → Designed a mathematical model to guide *in vitro* studies of the efficacy and dynamics of a synthetic probiotic system for prevention of gut dysbiosis (Prof. James J. Collins)
- → Created an epidemiological modeling framework for pathogen population genetics and evolution.
- → Created a bioinformatic pipeline to identify cross-reactive T cell epitopes in SARS-CoV-2 (Profs. Mauricio Calvo-Calle & Lawrence Stern, University of Massachusetts Medical School)

# **Department of Systems Biology, Harvard Medical School** — Boston, MA

Undergraduate Researcher

Feb – Jul 2018

- → Constructed and applied microfluidic systems to study bacterial physiology and persister cell formation
- → Helped develop computational workflows for analysis of single-cell imaging (Prof. Johan Paulsson)

#### **Eligo Bioscience** — Paris, France

Research Intern in Synthetic Biology

Aug 2017 – Jan 2018

- → Created DNA constructs and bacterial strains for phage production using CRISPR-Cas9 editing
- → Screened libraries of synthetic phage candidates against bacterial strains

### Mathematical and Theoretical Biology Institute, Arizona State University — Tempe, AZ Undergraduate Researcher

Jun - Jul 2017

→ Created a 3D, spatially explicit computational model of bacterial resistance to antibiotics in a biofilm

#### **Department of Biological Engineering, MIT** — Cambridge, MA

Undergraduate Researcher

May - Aug 2016

→ Assembled CRISPR-Cas9 constructs for gene editing in the malaria parasite (Prof. Jacquin Niles)

### **Department of Biological Sciences, Uniandes** — Bogotá, Colombia

Undergraduate Researcher

May 2015 - Aug 2017

- → Designed and experimentally tested an ODE model of phage-host dynamics (Prof. Martha Vives)
- → Applied Hidden Markov Models to identify phages in human gut metagenomes (Prof. Alejandro Reyes)
- → Helped build DNA parts for a cholera biosensor with the 2014 Uniandes iGEM team (Prof. J.M. Pedraza)

## **Selected Publications**

Selected i ublications		
Peer-reviewed research:	*These authors contributed equally to	the work.
GeneTargeter: automated, in silico design for genome P. Cárdenas, L.Y. Esherick, G. Chambonnier, S. I The CRISPR Journal. doi: 10.1089/crispr.2021.00	Dey, C.V. Turlo, A.S. Nasamu, J.C. Niles	2022
Preventing antibiotic-induced dysbiosis with an engin A. Cubillos-Ruiz, M.A. Alcantar, N.M. Donghia, Nature Biomedical Engineering. Accepted.	• • • • • • • • • • • • • • • • • • •	2022
dCas9 regulator to neutralize competition in CRISPRi HH. Huang*, M. Bellato*, Y. Qian, P. Cárdenas Nature Communications; doi: 10.1038/s41467-0	, L. Pasotti, P. Magni, & D. Del Vecchio	2021
Host resistance, genomics and population dynamics A.V. Holguín, P. Cárdenas, C. Prada-Peñaranda, Viruses. doi: 10.3390/v11020188	in α Salmonella <i>Enteritidis and phage system.</i> L. Rabelo Leite, C. Buitrago, V. Clavijo, , & M.J.	
Preprints:	*These authors contributed equally to	the work.
Resolving drug selection and migration in an inbred S population with identity-by-descent analysis M. Carrasquilla*, A.M. Early*, A.R. Taylor, A. Knu S. Aponte, P. Cárdenas, C.O. Buckee, J.C. Rayne Preprint doi: 10.1101/2022.02.18.480973	s Idson, D.F. Echeverry, T.J.C. Anderson, E. Mancilla	<b>2022</b> a,
Genomic epidemiological models describe pathogen P. Cárdenas, M. Santos-Vega Preprint doi: 10.1101/2021.12.16.473045	evolution across fitness valleys	2021
<b>Selected Teaching &amp; Mentorsh</b>	nip	
Department of Biological Engineering (BE), MIT -	•	
Coding Support Fellow, Biological Engineering Data L		2019 ++
Teaching Assistant, Principles of Molecular Bioengine	ering Sep – D	ec 2019
Peer Counselor, BE Resources for Easing Friction and	Stress (REFS) Jan	2018 ++
Depts. Biological Science, Biomedical Engineerin	<mark>g, &amp; Student Affairs; Uniandes —</mark> Bogotá, Co	olombia
Teaching Assistant, Quantitative Human Physiology I	and II Jan – D	ec 2016
Teaching Assistant, Parasitology Laboratory	Jan – J	un 2015
Teaching and Coordination Assistant; high school tuto	or, Social Practice Program Jul – D	Dec 2015
<b>Selected Awards &amp; Fellowship</b>	S	
S. & P. Eurnekian Biotechnology Fellowship, (Office Awarded by competition. (1 semester tuition, insur	ce of Graduate Education, MIT)	pr 2021
<b>Teaching Assistant Excellence Award</b> , (Departmer Best teaching assistant in MIT BE-Fall 2019, base	d on student and faculty feedback. (1000 USD)	ec 2020
Summa Cum Laude (Faculty of Sciences, Uniande		1ar 2018
Awarded to top 1% Faculty of Sciences historic groups Best Saber Pro Graduate National Exam, Biology Awarded to nation-wide top scores on Colombian	•	service. lov 2017
Ramón de Zubiría Awards (4) (Uniandes) For the highest GPA in a program, won in Microbio	Nov 2015—Cology (1x) and Biomedical Engineering (3x).	Oct 2017