

# Nikolai Slavov

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## CONTACT INFORMATION

Mugar # 334, Boston, MA 02115  
*E-mail:* [n.slavov@northeastern.edu](mailto:n.slavov@northeastern.edu)

WWW: [slavovlab.net](http://slavovlab.net)  
ORCID ID: [0000-0003-2035-1820](https://orcid.org/0000-0003-2035-1820)

## EDUCATION

Princeton University, Princeton, USA  
**Ph.D.** in Molecular and Quantitative Cell Biology **06.2010**  
**M.A.** in Molecular Biology **02.2006**  
**Dissertation:** Universality, specificity and regulation of *S. cerevisiae* growth rate response in different carbon sources and nutrient limitations  
**Mentor:** David Botstein  
Massachusetts Institute of Technology (MIT), Cambridge, USA  
**B.S.** in Biology **06.2004**

## ACADEMIC APPOINTMENTS

Northeastern University, Boston, USA  
Department of Bioengineering  
Assistant Professor **2015–present**  
Broad Institute of Harvard and MIT, Cambridge, USA  
Proteomics Platform **2015–2017**  
Harvard University, Cambridge, USA  
Departments of Systems Biology and Statistics **2014–2015**  
Massachusetts Institute of Technology (MIT), Cambridge, USA  
Departments of Biology and Physics  
Postdoc in the van Oudenaarden Laboratory **2011–2013**

## AWARDS & FELLOWSHIPS

✓ NIH Director's New Innovator Award (\$ 2,352,750) **2016**  
✓ Broad Institute of Harvard and MIT SPARC Award **2014**  
✓ Princeton University Dean's Award **2010**  
✓ IRCSET Postgraduate Research Fellowship (72,000 €) **2007**  
✓ Finalist in the Young European Entrepreneur Competition **2006**  
✓ Princeton Graduate Fellowship (\$ 45,000) **2004**  
✓ MIT Undergraduate Fellowship (\$ 125,000) **2001**  
✓ Eureka Fellowship for Academic Excellence (10,000 €) **2000**  
✓ Bronze Medal in the 31<sup>st</sup> International Chemistry Olympiad (*IChO*) **1999**  
✓ National Diploma for Exceptional Achievements in Chemistry **1999**

2019

2019

- ✓ Huffman RG, Chen AT, Specht H & **Slavov N.**<sup>✉</sup> (2019)  
DO-MS: Data-Driven Optimization of Mass Spectrometry Methods  
*Journal of Proteome Research*, DOI: [10.1021/acs.jproteome.9b00039](https://doi.org/10.1021/acs.jproteome.9b00039)
- ✓ Chen AT, Franks A & **Slavov N.**<sup>✉</sup> (2019)  
DART-ID increases single-cell proteome coverage  
*PLoS Computational Biology*, DOI: [10.1371/journal.pcbi.1007082](https://doi.org/10.1371/journal.pcbi.1007082) [OA]
- ✓ Emmott EP, Jovanovic M & **Slavov N.**<sup>✉</sup>  
Approaches for studying ribosome specialization  
*Trends in Biochemical Sciences*, DOI: [10.1016/j.tibs.2019.01.008](https://doi.org/10.1016/j.tibs.2019.01.008)

2018

2018

- ✓ Emmott EP, Jovanovic M & **Slavov N.**<sup>✉</sup>  
Ribosome stoichiometry: from form to function  
*Trends in Biochemical Sciences*, DOI: [10.1016/j.tibs.2018.10.009](https://doi.org/10.1016/j.tibs.2018.10.009)
- ✓ Malioutov D., Chen T., Jaffe J., Airoidi E., Budnik B. & **Slavov N.**<sup>✉</sup>  
Quantifying homologous proteins and proteoforms  
*Molecular & Cellular Proteomics*, DOI: [10.1074/mcp.TIR118.000947](https://doi.org/10.1074/mcp.TIR118.000947)
- ✓ Budnik B., Levy E., Harmange G. & **Slavov N.**<sup>✉</sup>  
SCoPE-MS: mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation  
*Genome Biology*, DOI: [10.1186/s13059-018-1547-5](https://doi.org/10.1186/s13059-018-1547-5) [OA]  
↔ [SCoPE-MS – We can finally do single cell proteomics!!!](#), highlight by *Proteomics News*  
↔ [Researchers Apply Mass Spec to Single-Cell Proteomics](#), highlight by *GenomeWeb*  
↔ [Interview](#), highlight by *Front Line Genomics*  
↔ [Single-cell proteomics](#) highlight by *the NIH Director's office*
- ✓ Levy E. & **Slavov N.**<sup>✉</sup>  
Single cell protein analysis for systems biology  
*Essays in Biochemistry*, DOI: [10.1042/EBC20180014](https://doi.org/10.1042/EBC20180014)
- ✓ Specht H. & **Slavov N.**<sup>✉</sup>  
Transformative opportunities for single cell proteomics  
*Journal of Proteome Research*, 17 (8), 2565 - 2571 , DOI: [10.1021/acs.jproteome.8b00257](https://doi.org/10.1021/acs.jproteome.8b00257)  
↔ [Innovations in Proteomics: The Drive to Single Cells](#), editorial highlight  
↔ [Through the Looking Glass of Single Cell Proteomics](#), highlight by *Technology Networks*

2017

2017

- ✓ Franks A., Airoidi E.M., **Slavov N.**<sup>✉</sup>  
Post-transcriptional regulation across human tissues  
*PLoS Computational Biology*, 13(5): e1005535, DOI: [10.1371/journal.pcbi.1005535](https://doi.org/10.1371/journal.pcbi.1005535) [OA]  
↔ [How Statistics Weakened mRNAs Predictive Power](#) highlight by *The Scientist*

- ✓ Saleh D, Najjar M, Zelic M, Shah S, Nogusa S, Polykratis A, Paczosa MK, Gough PJ, Bertin J, Whalen M, Fitzgerald KA, **Slavov N.**, Pasparakis M, Balachandran S, Kelliher M, Meccas J, Degterev A. Kinase Activities of RIPK1 and RIPK3 Can Direct IFN- Synthesis Induced by Lipopolysaccharide. *The Journal of Immunology*, 198(11):4435-4447, DOI: [10.4049/jimmunol.1601717](https://doi.org/10.4049/jimmunol.1601717)

2016

2016

- ✓ Klionsky, *et al.*, **Slavov N.**, *et al.*. Guidelines for the use and interpretation of assays for monitoring autophagy *Autophagy*, vol. 12, issue 1, 1–222, DOI: [10.1080/15548627.2015.1100356](https://doi.org/10.1080/15548627.2015.1100356)
- ✓ Di Luca A, Hamill RM, Mullen AM, **Slavov N.**, Elia G. Comparative Proteomic Profiling of Divergent Phenotypes for Water Holding Capacity across the Post Mortem Ageing Period in Porcine Muscle Exudate *PLoS One*, 11(3): e0150605, DOI: [10.1371/journal.pone.0150605](https://doi.org/10.1371/journal.pone.0150605) [OA]

2015





2015

- ✓ **Slavov N.**  Making the most of peer review *eLife*, 4:e12708, DOI: [10.7554/eLife.12708](https://doi.org/10.7554/eLife.12708) [OA]
- ✓ **Slavov N.** , Semrau S., Airoidi E.M., Budnik B., van Oudenaarden A. Differential stoichiometry among core ribosomal proteins *Cell Reports*, vol. 13, issue 5, 865–873, DOI: [10.1016/j.celrep.2015.09.056](https://doi.org/10.1016/j.celrep.2015.09.056) [OA]  
 ↪ [All Ribosomes Are Created Equal. Really?](#), highlight by *Trends in Biochemical Sciences*  
 ↪ [New direction for tissue engineering and cancer therapeutics](#), highlight by *Science X*
- ✓ Alvarez JR, Zhiqiang B, Xu D, Yuan B, Lo KA, Yoon MJ, Lim YC, Knoll M, **Slavov N.**, *et al.* De-Novo Reconstruction of Adipose Tissue Transcriptomes Reveals Long Non-coding RNA Regulators of Brown Adipocyte Development *Cell Metabolism*, vol. 21, issue 5, 764–776, DOI: [10.1016/j.cmet.2015.04.003](https://doi.org/10.1016/j.cmet.2015.04.003)

Started Slavov Lab at Northeastern University, August 2015

2014

2014

- ✓ Malioutov D. , **Slavov N.**  Convex Total Least Squares *Journal of Machine Learning Research, W&CP*, vol. 32, issue 1, 109–117 [OA]
- ✓ **Slavov N.** , Budnik B., Schwab D., Airoidi E., van Oudenaarden A.  Constant Growth Rate Can Be Supported by Decreasing Energy Flux and Increasing Aerobic Glycolysis *Cell Reports* vol. 7, issue 3, 705–714 [OA]

2013

2013

✓ **Slavov N.**<sup>✉</sup>, Carey, J., Linse, S.<sup>✉</sup>  
Calmodulin transduces  $Ca^{+2}$  oscillations into differential regulation of its target proteins  
*ACS Chemical Neuroscience*, vol. 4, 601–612 [OA]

✓ **Slavov N.**<sup>✉</sup>, Botstein D.<sup>✉</sup>  
Decoupling Nutrient Signaling from Growth Rate Causes Aerobic Glycolysis and Deregulation of Cell Size and Gene Expression  
*Molecular Biology of the Cell*, vol. 24, issue 2, 157–168 [OA]

**2012**

**2012**

✓ **Slavov N.**<sup>✉</sup>, van Oudenaarden A.<sup>✉</sup>  
How to Regulate a Gene: To Repress or to Activate?  
*Molecular Cell*, vol. 46, issue 5, 551–552 [OA]

✓ **Slavov N.**<sup>✉</sup>, Airoidi E.M., van Oudenaarden A., Botstein D.<sup>✉</sup>  
A Conserved Cell Growth Cycle Can Account for the Environmental Stress Responses of Divergent Eukaryotes  
*Molecular Biology of the Cell*, vol. 23, no. 10, 1986–1997 [OA]

**2011**

**2011**

✓ **Slavov N.**<sup>✉</sup>, Macinskas J., Caudy A., Botstein D.<sup>✉</sup>  
Metabolic Cycling without Cell Division Cycling in Respiring Yeast  
*PNAS*, vol. 108, no. 47, 19090–19095 [OA]

✓ **Slavov N.**<sup>✉</sup>, Botstein D.<sup>✉</sup>  
Coupling among Growth Rate Response, Metabolic Cycle and Cell Division Cycle in Yeast  
*Molecular Biology of the Cell*, vol. 22, no. 12, 1997–2009 [OA]

**2010**

**2010**

✓ **Slavov N.**<sup>✉</sup>  
Inference of Sparse networks with Unobserved Variables. Application to Gene Regulatory Networks  
*Journal of Machine Learning Research, W&CP*, vol. 9, 757–764 [OA]

✓ **Slavov N.**<sup>✉</sup>, Botstein, D.  
Universality, Specificity and Regulation of *S. cerevisiae* Growth Rate Response in Different Carbon Sources and Nutrient Limitations  
*Dissertation*, Princeton University [OA]

✓ Silverman SJ., **Slavov N.**, Petti A., Parsons L., Briehof R., Thiberge S., Zenklusen D., Gandhi SJ., Larson D., Singer R., Botstein D.<sup>✉</sup>  
Metabolic cycling in single yeast cells from unsynchronized steady-state populations limited on glucose or phosphate  
*PNAS*, vol. 107, no. 15, 6946–6951 [OA]

**2009 and before****2009 and before**

- ✓ **Slavov N.**<sup>✉</sup>, Dawson KA. (2009)  
Correlation Signature of the Macroscopic States of the Gene Regulatory Network in Cancer  
*PNAS*, vol. 106, no. 11, 4079-4084 (“In This Issue” article) [\[OA\]](#)
- ✓ Tagkopoulos I.<sup>✉</sup>, **Slavov N.**<sup>✉</sup>, Kung S.<sup>✉</sup> (2005)  
Multi-Class Biclustering and Classification Based on Modeling of Gene Regulatory Networks  
5<sup>th</sup> IEEE Symposium on Bioinformatics and Bioengineering (BIBE'05).


PUBLISHED  
PREPRINTS  
[GOOGLE SCHOLAR](#)

- ▷ Specht H, Emmott E, Koller T, **Slavov N.**<sup>✉</sup> (2019)  
High-throughput single-cell proteomics quantifies the emergence of macrophage heterogeneity  
bioRxiv, DOI: [10.1101/665307](#) [\[OA\]](#)
- ▷ Huffman G, Specht H, Chen AT, **Slavov N.**<sup>✉</sup> (2019)  
DO-MS: Data-Driven Optimization of Mass Spectrometry Methods  
bioRxiv, DOI: [10.1101/512152](#) [\[OA\]](#)
- ▷ Specht H, Harmange G, Perlman DH, Emmott E, Niziolek Z, Budnik B, **Slavov N.**<sup>✉</sup> (2018)  
Automated sample preparation for high-throughput single-cell proteomics  
bioRxiv, DOI: [10.1101/399774](#) [\[OA\]](#)
- ▷ Chen A, Franks A, **Slavov N.**<sup>✉</sup> (2018)  
DART-ID increases single-cell proteome coverage  
bioRxiv, DOI: [10.1101/399121](#) [\[OA\]](#)
- ▷ Levy E. & **Slavov N.**<sup>✉</sup> (2018)  
Single cell protein analysis for systems biology  
*PeerJ Preprint*, DOI: [10.7287/peerj.preprints.26965v1](#) [\[OA\]](#)
- ▷ Emmott EP, Jovanovic M & **Slavov N.**<sup>✉</sup> (2018)  
Ribosome stoichiometry: from form to function  
*PeerJ Preprint*, DOI: [10.7287/peerj.preprints.26991v1](#) [\[OA\]](#)
- ▷ Specht H. & **Slavov N.**<sup>✉</sup> (2018)  
Routinely quantifying single cell proteomes: A new age in quantitative biology and medicine  
*PeerJ Preprint*, DOI: [10.7287/peerj.preprints.26821v1](#) [\[OA\]](#)
- ▷ Malioutov D., Chen T., Jaffe J., Airoidi E., Carr S., Budnik B., **Slavov N.**<sup>✉</sup> (2017)  
Quantifying homologous proteins and proteoforms  
*bioRxiv*, DOI: [10.1101/168765](#) [\[OA\]](#)

- ▷ Berg P., Budnik B., **Slavov N.**<sup>✉</sup>, Semrau S. (2017)  
Dynamic post-transcriptional regulation during embryonic stem cell differentiation  
*bioRxiv*, DOI: [10.1101/123497](https://doi.org/10.1101/123497) [OA]
- ▷ Budnik B., Levy E., **Slavov N.**<sup>✉</sup> (2017)  
Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation  
*bioRxiv*, DOI: [10.1101/102681](https://doi.org/10.1101/102681) [OA]  
↔ [SCoPE-MS – We can finally do single cell proteomics!!!](#), highlight by *Proteomics News*  
↔ [Researchers Apply Mass Spec to Single-Cell Proteomics](#), highlight by *GenomeWeb*  
↔ [Interview](#), highlight by *Front Line Genomics*
- ▷ **Slavov N.**<sup>✉</sup> (2015)  
From differential transcription of ribosomal proteins to differential structure of ribosomes  
*PeerJ Preprint*, DOI: [10.7287/peerj.preprints.1504v1](https://doi.org/10.7287/peerj.preprints.1504v1) [OA]
- ▷ Franks A., Airoidi E.M., **Slavov N.**<sup>✉</sup> (2015)  
Post-transcriptional regulation across human tissues  
*bioRxiv*, DOI: [10.1101/020206](https://doi.org/10.1101/020206) [OA]
- ▷ **Slavov N.**<sup>✉</sup>, Botstein, D., Caudy A. (2014)  
Extensive regulation of metabolism and growth during the cell division cycle  
*bioRxiv*, DOI: [10.1101/005629](https://doi.org/10.1101/005629) [OA]
- ▷ **Slavov N.**<sup>✉</sup>, Semrau S., Airoidi E.M., Budnik B., van Oudenaarden A. (2014)  
Differential stoichiometry among core ribosomal proteins  
*bioRxiv*, DOI: [10.1101/005553](https://doi.org/10.1101/005553) [OA]

OPINIONS &  
POPULAR SCIENCE  
PUBLICATIONS

- ▷ **Slavov N.**<sup>✉</sup> (2018) We Must Demand Evidence of Peer Review  
*The Scientist*, [Link](#)
- ▷ **Slavov N.**<sup>✉</sup> (2017) What was rate limiting was the idea, not the technology  
*Front Line Genomics*, [Link](#)
- ▷ **Slavov N.**<sup>✉</sup> (2015) Making the most of peer review  
*eLife*, [Link](#)
- ▷ **Slavov N.**<sup>✉</sup> (2014) Accomplishments Over Accolades!  
*The Scientist*, [Link](#)
- ▷ **Slavov N.**<sup>✉</sup> (2014) Discoveries lie hidden behind the façade of popular assumptions  
*Cell Reporter*, [Link](#)
- ▷ **Slavov N.**<sup>✉</sup> (2013) The Best Projects Are Least Obvious  
*The Scientist*, [Link](#)

▷ Slavov N.  (2013) A Wonderful Christmas with Mysterious Oscillations  
*PubChase*, [Link](#)

▷ Slavov N.  (2012) The Mission of MIT  
*The MIT Tech*, [Link](#)

ORGANIZED  
CONFERENCES

- [Single Cell Proteomics](#), Northeastern University **June 8–10 2020**
- [Single Cell Proteomics](#), Northeastern University **June 10–12 2019**
- [Chair for the Single Cell Proteomics session](#), HUPO **Oct 1–3 2018**
- [Single Cell Proteomics](#), Northeastern University **June 9–10 2018**

INVITED RESEARCH  
TALKS

- Single-cell proteomics for studying regeneration and aging  
*MDI Biological Symposium for Regeneration and Aging* **Oct.9.2019**
- High-throughput single-cell proteomics quantifies the emergence of macrophage heterogeneity  
*European Single Cell Proteomics Conference* , **Aug.27.2019**
- Mapping the Transcriptome and Proteome of Human Testis in 3D  
*CZI Human Cell Atlas Seed Networks Meeting* , **Jul.30.2019**
- DO-MS: Data-Driven Optimization of Mass Spectrometry Methods  
*MaxQuant Summer School* **Jul.25.2019**
- Welcome to the Single Cell Proteomics Conference  
*Single Cell Proteomics Conference (SCP2019)* **Jun.10-12.2019**
- Mass-spectrometry of single cells quantifies proteome heterogeneity during cell differentiation  
*Winter Q-bio* **Feb.20.2019**
- Transformative opportunities for single cell proteomics  
*The Greater Boston Mass Spectrometry Discussion Group* **Dec.13.2018**
- Understanding and controlling cell differentiation based on comprehensive mass-spec quantification of proteins and signaling in single cells  
*UPENN Single Cell Biology Symposium*, [Video](#) **Nov.13.2018**
- Chair for the Single Cell Proteomics session of HUPO  
*Automated sample preparation for high-throughput single-cell proteomics* **Oct.3.2018**

- Using single-cell proteomics to engineer directed cell differentiation  
*Bioengineering & Translational Medicine Conference* **Sept.27.2018**
- Analyzing single cell proteomics data  
*ETH, Biognosys Discovery Proteomics Seminar* **Jul.7.2018**
- Progress, challenges and standards for single cell proteomics  
*Single-cell proteomics conference, [Video](#)* **June.9.2018**
- Understanding and controlling cell differentiation using single-cell mass-spectrometry  
*HMS Theory Lunch* **May.18.2018**
- Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation  
*CSHL Meeting: Single Cell Analyses* **Nov.10.2017**
- Single cell proteomics quantifies proteome heterogeneity during cell differentiation  
*Annual Single Cell Analysis USA Congress, Boston* **Oct.23.2017**
- Quantifying protein heterogeneity during the differentiation of single stem cells  
*Global CESI-MS Symposium* **Oct.06.2017**
- Single cell proteomics quantifies proteome heterogeneity during cell differentiation  
*Festival of Genomics, Boston* **Oct.04.2017**
- Exploring and characterizing system-level proteome heterogeneity during cell differentiation by single cell mass spectrometry  
*HUPO, Dublin* **Sept.18.2017**
- From differential transcription of ribosomal proteins to differential structure of ribosomes  
*Genetics, Genomics and Beyond, Calico* **Sept.16.2017**
- Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation  
*American Society for Mass Spectrometry Meeting* **June.05.2017**
- Principles of ribosome-mediated translational regulation  
*The Center for Engineering in Medicine, Massachusetts General Hospital* **Mar.17.2017**
- Principles of ribosome-mediated translational regulation  
*Systems Biology Seminar, Boston University* **Oct.13.2016**
- Differential stoichiometry among core ribosomal proteins  
*CSHL Translational Control, Cold Spring Harbor Laboratory* **Sept.08.2016**
- Ribosome-mediated translational regulation: Direct methods for quantifying the ribosome code  
*Center for Systems Biology, Columbia University* **Apr.20.2016**



- Coordinating metabolism and ribosome-mediated translational regulation  
*Department of Biology, New York University* **Apr.19.2016**
- Principles of ribosome-mediated translational regulation  
*Center for Interdisciplinary Research on Complex Systems* **Apr.12.2016**
- Quantifying homologous proteins and proteoforms  
*US HUPO Conference* **Mar.14.2016**
- Coordination among cell growth, cell division and gene expression  
*Broad Institute of MIT and Harvard, YSB* **Dec.9.2015**
- Coordinating cell growth and metabolism with ribosome-mediated translational regulation  
*Northeastern University, Biology Department Colloquium* **Oct.19.2015**
- Quantifying protein isoforms  
*Broad Institute of MIT and Harvard* **Sep.14.2015**
- Variable stoichiometry among core ribosomal proteins  
*2014 ASCB/IFCB Annual Meeting* **Dec.8.2014**
- Direct quantification of highly homologous proteins by mass-spectrometry indicates physiological changes in the protein composition of the ribosome  
*Broad Institute of MIT and Harvard, CBBO* **Jun.25.2014**
- Variable stoichiometry among core ribosomal proteins  
*Broad Institute of MIT and Harvard* **Jun.19.2014**
- Quantification of translational regulation of homologous proteins with unprecedented accuracy  
*Harvard HMS Systems Biology Theory Lunch* **Mar.21.2014**
- Exponentially growing cells can support a constant growth rate by very different metabolic strategies  
*Fourth Annual Physical Sciences in Oncology Meeting, NCI* **Apr.18.2013**
- Experimentally identified trade-offs of aerobic glycolysis  
*Center of Cancer Systems Biology at Tufts* **Dec.18.2012**
- Trade-offs of aerobic glycolysis  
*Harvard HMS Systems Biology Theory Lunch* **Sep.12.2012**
- The dynamics of exponential growth  
*GSA Yeast Meeting, Princeton University* **Aug.5.2012**
- The dynamics of exponential cell growth at constant growth rate  
*MIT Physical Sciences-Oncology Center* **Jun.11.2012**
- The dynamics of exponential growth  
*Broad Institute of Harvard and MIT* **Apr.17.2012**

- Metabolic cycling without cell division cycling  
*Bauer Forum at Harvard FAS Systems Biology* **Apr.15.2011**
- Inference of Sparse Networks with Unobserved Variables. Application to Gene Regulatory Networks  
*International Conference on Artificial Intelligence and Statistics* **May.14.2010**
- Dynamics in the calcium-calmodulin signaling network  
*International Conference on Chaos and Nonlinear Dynamics* **Jan.8.2006**

PROFESSIONAL  
ACTIVITIES

- **Peer-review:** PNAS, Nature Molecular and Structural Biology, Molecular Biology of the Cell, PLoS, Nucleic Acids Research, Bioinformatics, Annals of Applied Statistics, Cell Reports, eLife, Nature Communications || [Publons Profile](#)
- **Editorial roles:** Editor for PeerJ, bioRxiv Affiliate, Member of the editorial board of Journal of Proteome Research

TEACHING &  
RESIDENTIAL  
ADVISING

- Method and Logic in Systems Biology and Bioengineering**, Northeastern University **2019 – 2019**  
Discussion of seminal papers
- Mathematical Methods for Engineers**, Northeastern University **2016 – 2018**  
Introduction to major concepts and methods in linear algebra differential equations
- Method and Logic in Quantitative Biology**, Princeton University **2009 – 2010**  
Introduction to major ideas and concepts in quantitative biology based on primary literature
- Residential Graduate Student at Forbes College**, Princeton University **2009 – 2010**  
Advised students; organized language tables, sport events and trips
- Integrated Quantitative Introduction to Natural Sciences**, Princeton University **2006 – 2010**  
Interdisciplinary curriculum including physics, computer science, biochemistry, genetics, physiology and emphasizing quantitative problem solving and the connections among these disciplines
- Terrascope**, MIT **2002 – 2003**  
Selected for two subsequent years to lead undergraduate student groups working on complex real-world problems
- Biochemistry**, MIT **2003 – 2004**  
Taught precepts and helped undergraduate students prepare for examinations

CURRENT FUNDING

- ✓ NIH Director's New Innovator Award (\$ 2, 352, 750) **2016-2021**
- ✓ Sanofi iAward (\$ 125, 000) **2018**
- ✓ CZI Seed Networks (\$ 400, 000) **2019**
- ✓ Merck Award (\$ 242, 827) **2019**

COMPLETED  
FUNDING

- ✓ NEU Tier I Award (\$ 50, 000) **2016**
- ✓ Broad Institute of Harvard and MIT SPARC Award (\$ 100, 000) **2014**

✓ IRCSET Postgraduate Research Fellowship (72,000 €)

**2007**