# Hani Goodarzi

Assistant Professor

University of California, San Francisco

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#### Academic

Appointments • 2016-present: Assistant Professor.

Department of Biochemistry & Biophysics,

Department of Urology,

and Helen Diller Family Comprehensive Cancer Center.

• 2012-2016: Postdoctoral Fellow in Cancer Genomics. Laboratory of Systems Cancer Biology at Rockefeller University. Dr. Sohail F. Tavazoie.

• 2010-2012: Postdoctoral Associate in Genomics.

Princeton/Columbia University. Continued post-doctoral work in thesis lab. Dr. Saeed Tavazoie.

#### **EDUCATION**

# Princeton University, Princeton, NJ USA

Ph.D., Molecular Biology, November 2010

- Thesis Title: Experimental and Computational Approaches for Genetic Dissection of Complex Phenotypes
- Advisor: Dr. Saeed Tavazoie

# University of Tehran, Tehran, Iran

B.S., Biotechnology, June 2006

# AWARDS AND Honors

- 2015: Blavatnik Regional Award Winner for Life Sciences
- 2015: NIH Pathway to Independence Award (K99/R00)
- 2015: Tri-Institutional Breakout Prize for Junior Investigators
- 2014: Ruth L. Kirschstein National Research Service Award
- 2014: RUCCTS/CDDS/SCBN Pilot Project Award
- 2012: Anderson Cancer Center Postdoctoral Fellowship
- 2006: William G. Bowen Merit Fellowship
- 2006: Top undergraduate researcher, University of Tehran, Iran
- 2004: Ministry of Sciences, Research and Technology Fellowship, Iran
- 2002: University of Tehran Fellowship, Iran
- 2002: Presidential Award for Exceptional Talents, Iran
- 2002: Silver medal, The 13<sup>th</sup> International Biology Olympiad, Latvia

### **Publications**

Goodarzi H<sup>†\*</sup>, Nguyen HCB\*, Zhang S, Dill BD, Molina H, Tavazoie SF<sup>†</sup> (2015). Abundance of specific tRNA species drives cancer progression. Cell, 165: 1416-1427. †Corresponding authors

Alarcon C, **Goodarzi H**, Lee H, Tavazoie S, Tavazoie SF (2015). HN-RNPA2B1 is a mediator of m6A-dependent nuclear RNA processing events. *Cell*, 162: 1299-1308.

**Goodarzi H**, Liu X, Nguyen HCB, Zhang S, Fish L, Tavazoie SF (2015). Endogenous tRNA-derived fragments suppress breast cancer progression via YBX1 displacement. *Cell*, 161: 790-802.

Goodarzi H, Zhang S, Buss CG, Fish L, Tavazoie S, Tavazoie SF (2014). Metastasis-suppressor transcript destabilization through TARBP2 binding of mRNA hairpins. *Nature* 513, 255-260.

Alarcon C, Lee H\*, **Goodarzi H**\*, Tavazoie SF (2014). m<sup>6</sup>A site marks primary miRNAs for processing. *Nature*, 519, 482-485. \*Equal contribution

Goodarzi H, Tavazoie S, Tavazoie SF (2014). TARBP2 binding structured RNA elements drives metastasis. *Cell Cycle* 13:18, 2799-2800. Invited editorial feature.

Oikonomou P\*, **Goodarzi H**\*, Tavazoie S (2014). Systematic Identification of Regulatory Elements in Conserved 3' UTRs of Human Transcripts. *Cell Reports* 7(1): 281-292. \*Equal contribution

Freddolino PL\*, **Goodarzi H**\*, Tavazoie S (2013). Revealing the genetic basis of natural bacterial phenotypic divergence. *J. Bacteriol.* 196(4):825-39. \*Equal contribution

Chiu IM, Morimoto ETA, **Goodarzi H**, et al., Tavazoie S, Myers RM, Maniatis T (2013). A Neurodegeneration-Specific Gene-Expression Signature of Acutely Isolated Microglia from an Amyotrophic Lateral Sclerosis Mouse Model. *Cell Reports* 4(2): 385-401.

Freddolino PL\*, **Goodarzi H**\*, Tavazoie S (2012). Fitness landscape transformation through a single amino acid change in the Rho terminator. **PLoS Genet** 8(5), e1002744. \*Equal contribution

Goodarzi H, Najafabadi HS, Oikonomou P, Greco TM, Fish L, Salavati R, Cristea IM, Tavazoie S (2012). Systematic discovery of structural elements governing stability of mammalian messenger RNAs. *Nature* 485, 264-268.

Goodarzi H, Bennet BD, Amini S, Reaves ML, Hottes AK, Rabinowitz JD, Tavazoie S (2010). Regulatory and metabolic rewiring during laboratory evolution of ethanol tolerance in *E. coli. Mol Syst Biol* 6:378.

Goodarzi H, Elemento O, Tavazoie S (2009). Revealing Global Regulatory Perturbations across Human Cancers. *Mol Cell* 36: 900-911.

Najafabadi HS\*, **Goodarzi H**\*, Salavati R (2009). Universal function-specicity of codon usage. **Nucl Acids Res** 37(21):7014-7023. \*Equal contribution

Goodarzi H, Hottes AK, Tavazoie S (2009). Global discovery of adaptive mutations. *Nature Methods* 6(8):581-3.

Amini S, Goodarzi H, Tavazoie S (2009). Genetic Dissection of an Exogenously Induced Biofilm in Laboratory and Clinical Isolates of *E. coli.* **PLoS Pathog** 5:e1000432.

Goodarzi H<sup>†</sup>, Torabi N, Najafabadi HS, Archetti M (2008). Amino acid and codon usage profiles: adaptive changes in the frequency of amino acids and codons. *Gene* 407(1-2):30-41. <sup>†</sup>Corresponding author

**Goodarzi H**<sup>†</sup>, Katanforoush A, Torabi N, Najafabadi HS (2007). Solvent accessibility, residue charge and residue volume, the three ingredients of a robust amino acid substitution matrix. **J Theor Biol** 245(4):715-25.  $^{\dagger}$ Corresponding author

Torabi N, Goodarzi  $\mathbf{H}^{\dagger}$ , Shateri Najafabadi H. (2007). The case for an error minimizing set of coding amino acids. J Theor Biol 244(4):737-44.  $^{\dagger}$ Corresponding author

Marashi SA, Goodarzi H, Sadeghi M, Eslahchi C, Pezeshk H (2006). Importance of RNA secondary structure information for yeast donor and acceptor splice site predictions by neural networks. *Comput Biol Chem* 30(1):50-7.

Najafabadi HS, **Goodarzi H**, Torabi N, Banihosseini SS.(2006). Applying a neural network to predict the thermodynamic parameters for an expanded nearest-neighbor model. *J Theor Biol* 238(3):657-65.

Goodarzi H<sup>†</sup>, Shateri Najafabadi H, Torabi N (2005). On the coevolution of genes and genetic code. *Gene* 362:133-40. <sup>†</sup>Corresponding author

Goodarzi H<sup>†</sup>, Shateri Najafabadi H, Nejad HA, Torabi N (2005). The impact of including tRNA content on the optimality of the genetic code. **Bull Math Biol** 67(6):1355-68. <sup>†</sup>Corresponding author

Goodarzi  $\mathbf{H}^{\dagger}$ , Shateri Najafabadi H, Torabi N (2005). Designing a neural network for the constraint optimization of the fitness functions devised based on the load minimization of the genetic code. **Biosystems** 81(2):91-100.  $^{\dagger}$ Corresponding author

Najafabadi HS, Goodarzi H, Torabi N (2005). Optimality of codon usage in Escherichia coli due to load minimization. *J Theor Biol* 237(2):203-9.

Goodarzi H<sup>†</sup>, Najafabadi HS, Hassani K, Nejad HA, Torabi N (2005). On the optimality of the genetic code, with the consideration of coevolution theory by comparison of prominent cost measure matrices. *J Theor Biol* 235(3):318-25. <sup>†</sup>Corresponding author

Goodarzi H<sup>†</sup>, Nejad HA, Torabi N (2005). On the optimality of the genetic code, with the consideration of termination codons. *Biosystems* 77(1-3):163-73. <sup>†</sup>Corresponding author

# SEMINARS AND CONFERENCES

Goodarzi H, Najafabadi HS, Tavazoie S (2012). Systematic discovery of structural regulatory elements. Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor Laboratory, USA. Poster

**Goodarzi H**, Bennet BD, Hottes HK, Rabinowitz JD, Tavazoie S (2010). Regulatory and metabolic rewiring in laboratory evolution of ethanol tolerance. 6<sup>th</sup> Annual NIH Directors Pioneer Award Symposium. Bethesda, MD, USA. Poster

Goodarzi H, Elemento O, Tavazoie S (2008). Module-Level Analysis of Genome-wide Datasets. 16<sup>th</sup> Annual International Meeting on Microbial Genomics. Lake Arrowhead, CA USA. Poster

# TEACHING EXPERIENCE

- Teaching "Genes, Health and Society (MOL205)" in Princeton (Spring Semester 2009).
- Teaching "Introduction to Genomics and Computational Molecular Biology (COS551)" in Princeton (Fall Semester 2008).
- Teaching "Introduction to Cellular & Molecular Biology (MOL214)" in Princeton (Spring semester 2008).
- Teaching general biology in Biology Olympiad preparatory classes held by Ministry of Education for talented high school students in different regions of Iran.
- Teaching molecular biology to the members of National Biology Olympiad teams in Young Scholars Club, Tehran, Iran.

# Public Projects

# iGET (integrated Genomic Exploratory Tools)

An online portal for using a suite of information-theoretic software for analyzing whole-genome quantitative datasets. With close to 1,000 users, iGET enables researchers to analyze their data with a variety of tools developed by me and my colleagues (e.g. TEISER, FIRE and iPAGE).

## • Genophoria

A scientific blog with both technical and popular posts on recently published studies and/or other life science-related issues.