Hani Goodarzi

Assistant Professor
University of California, San Francisco

Contact Information

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Academic Appointments

- **2016-present:** Assistant Professor.
  Department of Biochemistry & Biophysics,
  Bakar Computational Health Scinces Institute,
  Helen Diller Family Comprehensive Cancer Center.
- **2012-2016:** Postdoctoral Fellow in Cancer Genomics.
  Rockefeller University

Education

Princeton University, Princeton, NJ USA
Molecular Biology, November 2010
University of Tehran, Tehran, Iran
B.S., Biotechnology, June 2006

Awards and Honors

- **2019:** Mary Kay Foundation Award
- **2017:** AAAS Martin and Rose Wachtel Cancer Research Award
- **2017:** AACR NextGen Award for Transformative Cancer Research
- **2017:** Sidney Kimmel Cancer Foundation Scholar Award
- **2015:** Blavatnik Regional Award Winner for Life Sciences
- **2015:** Tri-Institutional Breakout Prize for Junior Investigators
- **2015:** NIH Pathway to Independence Award (K99/R00)
- **2014:** Ruth L. Kirschstein National Research Service Award

Professional activity

- **Study sections:** *Ad hoc* member on Biodata Management and Analysis (BDMA) and Molecular Genetic B (MGB) study sections (NIH)
- **Journals:** *Ad hoc* referee for the following journals: Science, Nature, Nature Communications, Nature Reviews Molecular Cell Biology, Molecular Biosystems, Frontiers in Physiology, European Urology, Computational and Structural Biotechnology Journal, Breast Cancer: Basic and Clinical Research, Molecular Biology and Evolution, and BMC Cancer.
- **Teaching:** Dynamical Systems Modeling (BP205B) and Cancer Biology (BMS230).

Intellectual Property

Goodarzi H, Tavazoie SF (2016). Transfer RNA (tRNA) quantification. US patent Application No. 20170298433, Filed April 14, 2016.

Goodarzi H (2017). Non-coding RNA for Detection of Cancer. Provisional US patent Application No. 62/584,899, Filed November 12, 2017.

Selected Publications

Fish L, Fish L, Navickas A, Culbertson B, et al, Ruggero D, and **Goodarzi H** (2018). Nuclear TARBP2 Drives Oncogenic Dysregulation of RNA Splicing and Decay. ***Molecular Cell***, 75(5), 967-81.

Fish L, Zhang S, Yu J, Culbertson B, Zhou A, Goga A, **Goodarzi H** (2018). Cancer cells exploit an orphan RNA to drive metastatic progression. ***Nature Medicine***, 24: 1743-51.

Goodarzi H†*, Nguyen HCB*, Zhang S, Dill BD, Molina H, Tavazoie SF† (2016). Abundance of specific tRNA species drives cancer progression. ***Cell***, 165: 1416-1427. †Corresponding authors

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.

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 (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.

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

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. *Contributed equally.