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EDUCATION	<p><b>Brown University</b>, Providence, RI Sc. M., Ph.D., Physics (2007)</p> <p><b>Sharif University of Technology</b>, Tehran, Iran Sc. B., Physics (2001)</p>
INTERESTS	<ul style="list-style-type: none"><li>• Cancer genomics, Evolutionary dynamics of clonal populations, Molecular epidemiology of infectious diseases, Bioinformatics</li><li>• In my past life: Observational cosmology, Gravitational lensing</li></ul>
APPOINTMENTS	<p><b>Assistant Professor</b> (2015 – present) <b>Rutgers University</b>, Rutgers Cancer Institute</p> <p><b>Associate Research Scientist</b> (2013 – 2015) <b>Columbia University</b>, Departments of Biomedical Informatics &amp; Systems Biology</p> <p><b>Postdoctoral Research Scientist</b> (2008 – 2012) <b>Columbia University</b>, Center for Computational Biology and Bioinformatics</p> <p><b>Postdoctoral Research Associate</b> (2007 – 2008) <b>Brown University</b>, Department of Physics</p> <p><b>Graduate Teaching Assistant and Research Fellow</b> (2001 – 2007) <b>Brown University</b>, Department of Physics</p> <p><b>Undergraduate Research Fellow</b> (1997 – 1999) <b>Institute for Research in Fundamental Sciences (IPM)</b>, School of Physics</p>
PEER-REVIEWED PUBLICATIONS	<ol style="list-style-type: none"><li>1 Gorshein E., Wei C., ..., <b>Khiabanian H.</b><sup>†</sup>, Strair, R.<sup>†</sup>. <i>Lactobacillus rhamnosus GG</i> probiotic enteric regimen does not provide protection against GVHD after allogeneic hematopoietic stem cell transplantation. <i>Clinical Transplantation</i> 2017 <u>Contribution:</u> Designed 16S sequencing analyses, interpreted data, and wrote the manuscript</li><li>2 Uhlemann AC., et al. Evolutionary Dynamics of Pandemic Methicillin-Sensitive <i>S. aureus</i> ST398 and Its International Spread via Routes of Human Migration. <i>mBio</i> 2017 <u>Contribution:</u> Performed molecular evolution analyses</li><li>3 Abate F., Almeida da Silva A., et al. Activating mutations and translocations in the guanine exchange factor VAV1 in peripheral T-cell lymphomas. <i>PNAS</i> 2017 <u>Contribution:</u> Interpreted sequencing data for the study</li><li>4 Oshima K.<sup>†</sup>, <b>Khiabanian H.</b><sup>†</sup>, et al. Mutational landscape, clonal evolution patterns and role of RAS mutations in relapsed acute lymphoblastic leukemia. <i>PNAS</i> 2016 <u>Contribution:</u> Designed computational pipeline, interpreted data, and wrote the manuscript</li><li>5 Spina V.<sup>†</sup>, <b>Khiabanian H.</b><sup>†</sup>, Messina M. et al. The Genetics of Nodal Marginal Zone Lymphoma. <i>Blood</i> 2016 <u>Contribution:</u> Performed sequence data analysis and wrote the manuscript</li><li>6 Rasi S.<sup>†</sup>, <b>Khiabanian H.</b><sup>†</sup>, et al. Clinical impact of small subclones harboring <i>NOTCH1</i>, <i>SF3B1</i>, or <i>BIRC3</i> mutations in chronic lymphocytic leukemia. <i>Haematologica</i> 2016 <u>Contribution:</u> Designed computational pipeline, interpreted data, and wrote the manuscript</li><li>7 Paratala B., Dolfi SC., <b>Khiabanian H.</b>, et al. Emerging role of genomic rearrangements in breast cancer: applying knowledge from other cancers. <i>Biomarkers in Cancer</i> 2016 <u>Contribution:</u> Interpreted data for the review</li><li>8 Paganin M., et al. A Case of T-cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. <i>Pediatric Blood &amp; Cancer</i> 2016 <u>Contribution:</u> Interpreted data for the study</li></ol>

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<sup>†</sup> Equal contribution

✉ Corresponding author

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- 9 Almeida da Silva A.<sup>†</sup>, Abate F.<sup>†</sup>, **Khiabani H.**, et al. The mutational landscape of cutaneous T cell lymphoma and Sézary syndrome. *Nature Genetics* 2015  
Contribution: Interpreted data and wrote the manuscript
  - 10 Emmett K., Lee A., **Khiabani H.**<sup>✉</sup>, Rabadan R.<sup>✉</sup> High-resolution genomic surveillance of 2014 ebolavirus using shared subclonal variants. *PLoS Currents* 2015  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 11 Lee A., Kulcsar K., Elliott O., **Khiabani H.**, et al. Transcriptome Reconstruction and Annotation of the Egyptian Roussette Bat. *BMC Genomics* 2015  
Contribution: Interpreted data and wrote the manuscript
  - 12 Rossi D.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Clinical impact of small *TP53* mutated subclones in chronic lymphocytic leukemia. *Blood* 2014 (Plenary paper)  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 13 Palomero T.<sup>†</sup>, Couronné L.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Recurrent mutations in epigenetic regulators, *RHOA* and *FYN* kinase in peripheral T cell lymphomas. *Nature Genetics* 2014  
Contribution: Performed exome and RNA-seq mutation analysis, and wrote the manuscript
  - 14 Wang J.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, Rossi D.<sup>†</sup>, et al. Tumor Evolutionary Directed Graphs and the History of Chronic Lymphocytic Leukemia. *eLife* 2014  
Contribution: Developed statistical tools, interpreted data, and wrote the manuscript
  - 15 **Khiabani H.**<sup>✉</sup>, et al. Viral diversity and clonal evolution from unphased genomic data. *BMC Genomics* 2014  
Contribution: Designed the study, developed mathematical tools, and wrote the manuscript
  - 16 Lee A.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Transcriptome Reconstruction and Annotation of Cynomolgus and African Green Monkey. *BMC Genomics* 2014  
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
  - 17 Zairis S., **Khiabani H.**, Blumberg A., Rabadan R. Moduli spaces of phylogenetic trees describing tumor evolutionary patterns. *Lecture Notes in Comp. Science Volume 8609* 2014  
Contribution: Interpreted data and wrote the manuscript
  - 18 Pasqualucci L., **Khiabani H.**, et al. Genetics of follicular lymphoma transformation. *Cell Reports* 2014  
Contribution: Developed bioinformatics tools and performed sequencing analysis
  - 19 Melamed R., **Khiabani H.**, Rabadan R. Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. *BMC Bioinformatics* 2014  
Contribution: Developed statistical tools
  - 20 Messina M., Del Giudice I., **Khiabani H.**, et al. Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. *Blood* 2014  
Contribution: Performed sequencing analysis and developed statistical tools
  - 21 Kode A. et al. Leukemogenesis Induced by an Activating  $\beta$ -catenin mutation in Osteoblasts. *Nature* 2014  
Contribution: Performed mouse sequencing analysis and interpreted data
  - 22 Fabbri G.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. *The Journal of Experimental Medicine* 2013  
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
  - 23 Tzoneva G.<sup>†</sup>, Perez Garcia A.<sup>†</sup>, Carpenter Z.<sup>†</sup>, **Khiabani H.**, et al. Activating mutations in the *NT5C2* gene drive chemotherapy resistance in relapsed ALL. *Nature Medicine* 2013  
Contribution: Performed sequencing analysis and interpreted data
  - 24 Blair D.R., et al. A nondegenerate code of deleterious variants in mendelian Loci contributes to complex disease risk. *Cell* 2013  
Contribution: Contributed data to the study
  - 25 Rossi D., et al. Integrated Mutational and Cytogenetic Analysis Identifies New Prognostics Subgroups in Chronic Lymphocytic Leukemia. *Blood* 2013  
Contribution: Interpreted data for the study
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- 26 Dapito D.H., et al. Promotion of hepatocellular carcinoma by the intestinal microbiota and TLR4. *Cancer Cell* 2012  
Contribution: Performed 16S sequencing analysis and interpreted data
  - 27 Holmes A.B., ..., **Khiabani H.**<sup>✉</sup>, Rabadan R.<sup>✉</sup> Discovering Disease Associations by Integrating Electronic Clinical Data and Medical Literature. *PLoS One* 2011  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 28 Rossi D., Brusca A., Spina V., Rasi S., **Khiabani H.**, et al. Mutations of the *SF3B1* splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. *Blood* 2011  
Contribution: Performed sequencing analysis
  - 29 Fabbri G., Rasi S., Rossi D., Trifonov V., **Khiabani H.**, et al. Analysis of the Chronic Lymphocytic Leukemia Coding Genome: Role of *NOTCH1* Mutational Activation. *The Journal of Experimental Medicine* 2011  
Contribution: Developed bioinformatics tools and performed deep-sequencing analysis
  - 30 Van Vlierberghe P.<sup>†</sup>, Palomero T.<sup>†</sup>, **Khiabani H.**, et al. *PHF6* mutations in T-cell acute lymphoblastic leukemia. *Nature Genetics* 2010  
Contribution: Developed bioinformatics tools and performed sequencing analysis
  - 31 **Khiabani H.**<sup>✉</sup>, et al. Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. *PLoS One* 2010  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 32 **Khiabani H.**<sup>✉</sup>, et al. ParMap, an algorithm for the identification of small genomic insertions and deletions in nextgen sequencing data. *BMC Research Notes* 2010  
Contribution: Designed computational tools interpreted data, and wrote the manuscript
  - 33 **Khiabani H.**<sup>✉</sup>, Trifonov V., Rabadan R. Reassortment Patterns in Swine Influenza Viruses. *PLoS One* 2009  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 34 **Khiabani H.**<sup>✉</sup>, et al. Differences in Patient Age Distribution between Influenza A Subtypes. *PLoS One* 2009  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 35 Trifonov V., **Khiabani H.**, Rabadan R. Geographic Dependence, Surveillance and the Origins of the 2009 Influenza A (H1N1) Virus. *The New England Journal of Medicine* 2009  
Contribution: Performed sequencing analysis, interpreted data, and wrote the manuscript
  - 36 Trifonov V., **Khiabani H.**, Greenbaum B., Rabadan R. The origin of the recent swine influenza A (H1N1) virus infecting humans. *Eurosurveillance* 2009  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 37 Kubo J., **Khiabani H.**, Dell'Antonio I., et al. Dark Matter Halos in the Deep Lens Survey. *The Astrophysical Journal* 2009  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 38 **Khiabani H.**, Dell'Antonio I. A Multi-Resolution Weak Lensing Reconstruction Method. *The Astrophysical Journal* 2008  
Contribution: Designed the study, developed mathematical tools, and wrote the manuscript
  - 39 Kubo J., et al. The Mass of Coma Cluster from Weak Lensing in SDSS. *The Astrophysical Journal* 2007  
Contribution: Contributed data and statistical tools to the study

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PRE-PRINTS,  
ETC.

- 1 Rabadan R., Marsilio S., Chiorazzi N., Pasqualucci L., **Khiabani H.**<sup>✉</sup> Highly sensitive detection of small variants in multi-sample ultra-deep tumor sequencing. *bioRxiv* 2017  
Contribution: Designed the study, interpreted data, and wrote the manuscript
  - 2 Zairis S., **Khiabani H.**, Blumberg A., Rabadan R. Genomic data analysis in tree spaces. *arXiv* 2016  
Contribution: Interpreted data and wrote the manuscript
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- 3 Hernandez C., Chan J., **Khiabani H.**, Rabadan R. Understanding the Origins of a Pandemic Virus. arXiv 2011  
Contribution: Interpreted data and wrote the manuscript
  - 4 Greenbaum B., Trifonov V., **Khiabani H.**, Levine A., Rabadan R. The Emergence of 2009 H1N1 Pandemic Influenza. In: G. Del Giudice and R. Rappuoli (eds.). Influenza Vaccines for the Future. 2nd edition 2010  
Contribution: Interpreted data and wrote the book chapter
  - 5 **Khiabani H.** A Maximum-Likelihood Multi-Resolution Weak Lensing Mass Reconstruction Method. Doctoral Dissertation. Brown University 2008  
Contribution: Designed the study, interpreted data, and wrote the thesis
- 

#### PROFESSIONAL ACTIVITIES

- Assistant Professor of Pathology in Medical Informatics, tenure-track, Rutgers Robert Wood Johnson Medical School (2015 – present)
  - Resident Member at Rutgers Cancer Institute, Center for Systems and Computational Biology, the Genome Instability and Cancer Genetics Program (2015 – present)
  - Member of the graduate faculties at Rutgers University in the Department of Physics and Astronomy (2016 – present), the Institute for Quantitative Biomedicine (2016 – present), and the Microbiology and Molecular Genetics graduate program (2017 – present)
  - Scientific Coordinator in Education and Outreach in the Center for Topology of Cancer Evolution and Heterogeneity, Columbia University (2015 – 2017)
  - Member of the faculty in the Department of Biomedical Informatics at Columbia University College of Physicians and Surgeons (2013 – 2015)
  - Academic editor: PeerJ (2017 – present)
  - Proposal review panelist: National Science Foundation (2017)
  - *Ad Hoc* Reviewer: JCO Precision Oncology, Nature Communications, PLoS Pathogens, PLoS Computational Biology, Scientific Reports, PLoS One, Bioinformatics, Journal of Virology, Virology Journal, BMC Evolutionary Biology, BMC Bioinformatics, BMC Genomics, AMIA Joint Summits on Translational Science, etc.
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#### TEACHING EXPERIENCE

- Organizer and Lecturer. Workshop on Quantitative Methods in Cancer Genomics. Center for Systems and Computational Biology, Rutgers Cancer Institute of New Jersey, Rutgers University (September 2016)
  - Faculty Mentor. Research Experience for Undergraduates Program, DIMACS, Rutgers University (2017), Distinction in Research Program, Rutgers Robert Wood Johnson Medical School (2015 – present)
  - Faculty Moderator. Molecular Medicine Seminar Course, Rutgers Cancer Institute of New Jersey (2015 – 2017)
  - Guest Lecturer (*Introduction to Molecular Epidemiology: Dynamics of Clonal Evolution*). Introduction to Biomedical Informatics, Columbia University (Fall 2014)
  - Guest Lecturer (*Clonal Expansions & Introduction to DNA Sequencing Methods*). Quantitative and Computational Aspects of Infectious Diseases, Columbia University (Spring 2011 – 2013)
  - Guest Lecturer (*Introduction to Computational Biology and Genomics*). Advanced Seminar on Modeling for Public Health and Clinical Research, Columbia University (Spring 2013)
  - Instructor (*Introduction to Bioinformatics Tools*). Quantitative Approaches to Biological Problems, International Centre for Theoretical Physics, Trieste, Italy (October 2011)
  - Teaching Assistant. Experiments in Modern Physics, Brown University (Spring 2002)
  - Teaching Assistant. Introduction to Astronomy, Brown University (Fall 2001)
  - Course grader and Tutor. Introductory undergraduate courses in Physics, Astrophysics, and Cosmology, Brown University (2002 – 2007)
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## ADVISING

- Postdoctoral fellow: Mohammad Hadigol (NJCCR Fellow, 2016 – present)
- Doctoral students: Amartya Singh (Physics, 2016 – present), Jui Wan Loh (Molecular Biosciences, 2017 – present)
- Undergraduate students: Anthony Fratella-Calabrese (Biochemistry, 2016 – 2017), Simon Bird (DIMACS, 2017)
- Doctoral thesis committee membership: Saurabh Laddha (IQB), Anshuman Panda (Physics), Manasi Pethe (Chemistry), Albert Lee (Bioinformatics, Columbia U.)

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## PRESENTATIONS

### **Invited Talks and Oral Presentations**

- Genomic data analysis and dimensionality reduction in tree spaces  
Center for Quantitative Biology, Rutgers University, Piscataway, NJ, January 2017
  - Clonal Evolution and Relapse in Leukemia  
Schools of Biological Sciences, Institute for research in fundamental Sciences (IPM), Tehran, Iran, December 2016
  - Statistical Inference and dimensionality reduction in evolutionary tree spaces  
Schloss Dagstuhl Seminar, Leibniz Center for Informatics, Wadern, Germany, June 2016
  - Clonal Dynamics in Cancer Evolution  
The Feinstein Institute for Medical Research, Manhasset, NY, April 2016
  - High-resolution surveillance of viral clonal evolution  
Institute for Quantitative Biomedicine, Rutgers University, Piscataway, NJ, February 2016
  - Intra-host evolution and high-resolution genomic surveillance of filoviruses  
Columbia University Systems Biology Retreat, Tarrytown, NY, June 2015
  - Dynamics of Clonal Evolution in Leukemia  
Rutgers Cancer Institute of New Jersey, New Brunswick, NJ, January 2015
  - Dynamics of Clonal Evolution in Leukemia  
Department of Pathology, Weill Cornell Medical College, New York, NY, December 2014
  - Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns  
The 5<sup>th</sup> Beyond the Genome Conference, Harvard Medical School, Boston, MA, October 2014
  - Viral Diversity and Clonal Evolution from Unphased Genomic Data  
The 12<sup>th</sup> Recomb-CG Meeting, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, October 2014
  - Intra-host Evolution & Subclonal Diversity in Acute Infections using Unphased Genomic Data  
AMIA Joint Summits on Translational Science, San Francisco, CA, April 2014
  - Data Mining Electronic Health Records at New York Presbyterian Hospital  
The Conte Center 1<sup>st</sup> Annual Meeting, The University of Chicago, Chicago, IL, March 2012
  - Tracking the Evolution of Influenza Viruses  
The 2<sup>nd</sup> Systems Biology and New Sequencing Meeting, International Centre for Theoretical Physics, Trieste, Italy, November 2011
  - Emergence of a Pandemic Virus  
University of Bologna, Bologna, Italy, October 2011
  - Data Mining Electronic Health Records  
Columbia University Center for Infection and Immunity, New York, NY, June 2011
  - Fancy Counting in Large Biological Datasets  
Department of Physics, Sharif University of Technology, Tehran, Iran, April 2011
  - Reassortment Patterns in Influenza Viruses  
The Simons Center for Systems Biology, IAS, Princeton, NJ, March 2011
  - Influenza Virus and its Evolution  
Sharif University of Technology, Tehran, Iran, April 2010
  - Statistics of Dark Matter Halos via Maximum-Likelihood Weak Lensing Mass Reconstruction  
The BioMaPS Institute, Rutgers University, Piscataway, NJ, May 2008
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## Selected Peer-reviewed Abstracts

- Oshima K.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Mutational landscape, clonal evolution patterns and role of RAS mutations in relapsed acute lymphoblastic leukemia. 58<sup>th</sup> ASH Annual Meeting, San Diego, Dec. 2016
- Zairis S., **Khiabani H.**<sup>□</sup>, Blumberg A., Rabadan R. Machine learning and statistical inference in evolutionary moduli spaces. Keystone Conference on the Cancer Genome, Banff, Alberta, Feb. 2016
- Spina V.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. The Coding Genome of Nodal Marginal Zone Lymphoma Reveals Recurrent Molecular Alterations of *PTPRD* and Other Jak/Stat Signaling Genes. 56<sup>th</sup> ASH Annual Meeting, San Francisco, CA, Dec. 2014
- Rossi D.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Small Subclones Harboring *NOTCH1*, *SF3B1* or *BIRC3* Mutations Are Clinically Irrelevant in Chronic Lymphocytic Leukemia. 56<sup>th</sup> ASH Annual Meeting, San Francisco, CA, Dec. 2014
- Rossi D.<sup>†</sup>, **Khiabani H.**<sup>†</sup>, et al. Clinical Impact Of Small *TP53* Mutated Subclones In Chronic Lymphocytic Leukemia. 55<sup>th</sup> ASH Annual Meeting, New Orleans, LA, Dec. 2013
- Palomero T.<sup>†</sup>, Couronné L.<sup>†</sup>, **Khiabani, H.**<sup>†</sup>, et al. Recurrent *Rhoa* Mutations In Peripheral T-Cell Lymphoma. 55<sup>th</sup> ASH Annual Meeting, New Orleans, LA, Dec. 2013
- Kubo J., **Khiabani H.**, et al. Dark Matter Structures in the Deep Lens Survey. AAS 213<sup>th</sup> Meeting, Long Beach, CA, Jan. 2009
- **Khiabani H.**, Dell'Antonio I., A Multi-Resolution Weak Lensing Reconstruction Method. AAS 207<sup>th</sup> Meeting, Washington, DC, Jan. 2005

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## COMMENTARY, SELECTED PRESS

- An American Cancer Society Institutional Research Grant is awarded to the Khiabani lab. Rutgers Faculty & Staff Bulletin, October 19, 2016
  - Genetic drivers of vulnerability and resistance in relapsed acute lymphoblastic leukemia. PNAS Commentary, September 22, 2016
  - Shedding Light on the Mutational Landscape of the Most Common Pediatric Cancer. Rutgers Cancer Institute Newsroom, September 21, 2016
  - Nodal marginal zone mutational signature. Blood, September 8, 2016
  - Center for Systems and Computational Biology hosts the Workshop on Quantitative Methods in Cancer Genomics. Rutgers Faculty & Staff Bulletin, August 24, 2016
  - Columbia Investigators Awarded New NCI Physical Sciences in Oncology Center. Columbia Systems Biology News, May 21, 2015
  - Distinguishing Patterns of Tumor Evolution in Chronic Lymphocytic Leukemia. Columbia System Biology News, January 5, 2015
  - CLLonal selection: survival of the fittest? Blood, April 3, 2014
  - *RHOA* mutations in peripheral T cell lymphoma. Nature Genetics, March 27, 2014
  - *RHOA* Mutations Are a Hallmark of Angioimmunoblastic T-cell Lymphoma. Cancer Discovery, January 23, 2014
  - Richter's transformation in CLL — a distinct lymphoma. Nature Reviews Clinical Oncology, November 26, 2013
  - Resistance revealed in acute lymphoblastic leukemia. Nature Medicine, March 6, 2013
  - Of Swine and Men. Science News, February 12, 2010
  - Flu Fighters. Columbia Magazine, Fall 2009
  - Swine flu origins mysterious in 'genetic arms race.' CNN, May 6, 2009
  - New flu virus may be a real mongrel: study. Reuters, May 1, 2009
  - Computational Analysis Helps Researchers Understand Emerging H1N1 Flu Strain. Phys.org, May 3, 2009
  - Swine Flu Name Change? Flu Genes Spell Pig. The Guardian, April 30, 2009
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OTHER  
PUBLICATIONS

**Photography**

- Published, PhotoVogue web site, Vogue Italia, 2013-2014, 2017
  - Featured, *Eyes on Iran*, Print Magazine web site, November 2012
  - Contributor, B|ta'arof Magazine, Inaugural Issue, New York, NY, Fall 2012
  - Invited Artist, Unbound Press, Inaugural Issue, Glasgow, UK, Winter 2007
  - Contributor, Issues Magazine, Brown University-RISD, Providence, RI, Winter 2007
-