

Curriculum Vitae

Name: Raja Jothi
Office address: National Institute of Environmental Health Sciences (NIEHS)
National Institutes of Health (NIH)
111 T.W. Alexander Drive, MD A3-03
Research Triangle Park, NC 27709
Telephone: 984-287-3696
Email: jothi@mail.nih.gov
Web: <http://www.niehs.nih.gov/research/atniehs/labs/escbl/pi/systemsbiology/>

EDUCATION

2001 - 2004 **Ph.D., Computer Science**, University of Texas at Dallas, Richardson, Texas, USA
2000 **M.S., Computer Science**, University of Texas at Dallas, Richardson, Texas, USA
1994 - 1998 **B.E., Computer Science & Engineering**, University of Madras, Chennai, India

ACADEMIC & PROFESSIONAL POSITIONS

2015 - **Senior Investigator** (with tenure) NIH, NIEHS, Epigenetics & Stem Cell Biology Laboratory, Research Triangle Park, NC.
2009 - 2015 **Investigator** (tenure-track) NIH, NIEHS, Epigenetics & Stem Cell Biology Laboratory, Research Triangle Park, NC
2007 - 2009 **Research Fellow** NIH, NHLBI, Laboratory of Molecular Immunology, Bethesda, MD (Mentor: Keji Zhao)
2004 - 2007 **Research Associate** NIH, NCBI/NLM, Computational Biology Branch, Bethesda, MD (Mentor: Teresa Przytycka)
2001 - 2004 **Research Assistant** University of Texas at Dallas, Department of Computer Science, Richardson, TX
2000 - 2001 **Software Engineer** Westwave Communications (acquired by Alcatel), Richardson, TX
1998 - 1999 **Database Engineer** P'Four Software and Marketing Services, Chennai, India

HONORS AND AWARDS

2018 Khairallah Lecture, University of Connecticut
2018 NIH Director's Seminar Series Lecture
2017 NIH Award of Merit
2017 Paper of the Year Award, NIEHS, NIH
2016 Ruth L. Kirschstein Mentoring Award, National Institutes of Health
2014 Paper of the Year Award, NIEHS, National Institutes of Health
2009 Early Career "Rising Star" Award, NIEHS, National Institutes of Health

PROFESSIONAL SERVICES

NIH Institutional Service

- 2017 - 2018 Search Committee for NIH Earl Stadtman Investigator in Chromosome Biology/Epigenetics/Transcription
- 2017 Review Panel, NIDDK/NIDDK Joint Fellowship Program
- 2016 - 2017 Search Committee for NIH Earl Stadtman Investigator in Chromosome Biology/Epigenetics/Transcription
- 2015 - 2016 Search Committee for NIH Earl Stadtman Investigator in Chromosome Biology/Epigenetics/Transcription
- 2013 - 2014 Search Committee for NIH Earl Stadtman Investigator in Stem Cells
- 2014 Review panel, NIH Fellows Award for Research Excellence
- 2012 - 2013 Search Committee for NIH Earl Stadtman Investigator in Stem Cells
- 2013 Review panel, NIH Fellows Award for Research Excellence
- 2012 Review panel, NIH Fellows Award for Research Excellence
- 2011 Review panel, NIH Fellows Award for Research Excellence
- 2010 Review panel, applications for the NIH National Graduate Student Research Festival
- 2010 Review panel, NIH Fellows Award for Research Excellence

NIEHS Institutional Service

- 2018 - 2019 Chair, Search Committee for ESCBL Stem Cell Biology Staff Scientist, NIEHS
- 2018 Selection Committee for the NIEHS Fellow of the Year Award
- 2018 Search Committee for GISBL Structural Cell Biology Staff Scientist, NIEHS
- 2017 - 2018 Elected Councilor, Assembly of Scientists, NIEHS, NIH
- 2017 - Search Committee for Tenure-Track Investigator in Transcription, Epigenetics, or Chromatin Biology, NIEHS
- 2017 - Search Committee for Biostatistics Staff Scientist, NIEHS
- 2017 Organizer, Epigenetics & Stem Cell Biology Laboratory Retreat, NIEHS
- 2016 - Oversight Committee for the Viral Vector Core, NIEHS
- 2016 Organizing Committee, Division of Intramural Research Retreat
- 2016 Organizer, Epigenetics & Stem Cell Biology Laboratory Retreat
- 2015 - 2018 IT Management Committee, NIEHS
- 2015 - 2017 Committee on Promotions IV to review appointment, tier advancement, and renewal requests of Title 42 Staff Scientists, NIEHS, NIH
- 2013 - 2014 Search Committee for Tenure-Track/Tenure-Eligible Investigator in Biostatistics/Computational Biology, NIEHS, NIH
- 2014 Organizer, Laboratory of Molecular Carcinogenesis Retreat
- 2013 - 2015 Member, NIEHS Scientific Director's DIR General Council

- 2012 Stem Cells Committee, NIEHS Cross-Divisional Strategic Plan Implementation
- 2012 Epigenetics Committee, NIEHS Cross-Divisional Strategic Plan Implementation
- 2009 - 2013 Review Committee, Next Generation Sequencing Projects, NIEHS, NIH
- 2009 - 2010 Search Committee for Bioinformatics Staff Scientist, NIEHS, NIH

Conference/Symposium Organizing Committee

- 2017 Organizing Committee - NIEHS/NIH Symposium on Epigenetics & Stem Cells, RTP, NC, June 1-2, 2017
- 2015 Program Committee - International Conference on Bioinformatics and Biomedicine (BIBM), Washington DC, Nov 9-12, 2015.
- 2014 Program Committee - International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, Beijing, China, Aug 18-19, 2014.
- 2013 Program Committee - Workshop on Epigenomics and Cell Function, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, Washington D.C., Sep 22-25, 2013.
- 2013 Program Committee - International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, Niagara Falls, Canada, Aug 25-28, 2013.
- 2013 Co-chair - NIEHS/NIH Symposium on Unlocking the Promise of Stem Cells, RTP, NC, April 11-12, 2013.
- 2012 Organizing Committee - Toxicology 2012, San Antonio, TX, Sep 17-19 2012.
- 2012 Program Committee - International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics Istanbul, Turkey, Aug 2012.
- 2011 Workshop Co-chair - IEEE International Conference on Computational Advances in Bio and medical Sciences, Orlando, FL, Feb 2011
- 2010 Co-chair - Symposium on "Epigenetics, Chromatin, and Gene Regulation", NIH Research Festival, Bethesda, MD, Oct 2010.
- 2010 Program Committee - ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, Aug 2-4, 2010
- 2010 Program Committee - The 8th International Bioinformatics Workshop (IBW), Wuhan, China, June 4-6, 2010
- 2009 Chair - Symposium on "Epigenetics, Chromatin, and Gene Regulation", NIH Research Festival, Bethesda, MD, Oct 2009.
- 2009 Program Committee - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Washington DC, Nov 1-4, 2009
- 2008 Vice-chair - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Philadelphia, CA, Nov 7-9, 2008.
- 2007 Program Committee - 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB), Vienna, Austria, Jul 21-25, 2007.
- 2007 Program Committee - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Silicon Valley, CA, Nov 2-4, 2007.

- 2004 Session Chair, 7th INFORMS Telecommunications Conference, Boca Raton, FL, 2004.
2004 Session Chair, 3rd IEEE International Conference on Networking, 2004.
2003 Session Chair, 15th IASTED International Conference on Parallel and Distributed Computing and Systems, Las Vegas, NV, 2003.

Ad-hoc Reviewer

- Grants** Wellcome Trust
The Biotechnology and Biological Sciences Research Council (BBSRC) – UK
- Journals** *Nature Genetics*
Nature Communications
Nature Methods
Nature Protocols
PNAS
Cell Reports
Genome Research
Genome Biology
Nucleic Acids Research
eLife
Bioinformatics
Trends in Genetics
PLoS Genetics
PLoS Computational Biology
PLoS ONE
Molecular Biology and Evolution
Stem Cells and Development
Proteins
Molecular Biosystems
BMC Bioinformatics
BMC Genomics
BMC Systems Biology
Toxicological Sciences
Oncotarget
IEEE/ACM Transactions on Computational Biology and Bioinformatics
IEEE Transactions on NanoBioscience
Pattern Recognition Letters
Discrete and Computational Geometry
Networks
Journal of Graph Algorithms and Applications

Journal Editorial Board

2011 - Frontiers in Bioinformatics and Computational Biology
2010 – 2017 PLoS ONE

Membership: International Society for Computational Biology (ISCB)

INVITED TALKS

- Jan 2019 **North Carolina State University, NC** – Uncovering unknown unknowns of gene regulation
- Nov 2018 **Wake Forest University, NC** – Uncovering unknown unknowns of gene regulation
- Oct 2018 **Khairallah Lecture, University of Connecticut, CT** – Uncovering unknown unknowns of gene regulation
- Sep 2018 **CSHL Meeting on Meeting on Epigenetics & Chromatin, NY** – Crm1 promotes the formation of broad H3K27me3 repressive domains at developmental genes (presenter: Conway AE)
- May 2018 **CSHL Meeting on Nuclear Organization & Function, NY** – Crm1 promotes the formation of broad H3K27me3 repressive domains at developmental genes (presenter: Conway AE)
- Apr 2018 **NIH Director's Seminar Series Lecture, NIH, MD** – Uncovering unknown unknowns of Gene Regulation
- Oct 2017 **University of North Carolina at Chapel Hill, NC** – Uncovering unknown unknowns of Gene Regulation
- Oct 2017 **Keynote Lecture, NCBI Retreat, NLM, NIH, MD** – Uncovering unknown unknowns of Gene Regulation
- Sep 2017 **CSHL Meeting on Mechanisms of Eukaryotic Transcription, NY** – Transcription at intragenic enhancers attenuate gene expression
- May 2016 **CSHL Meeting on Nuclear Organization & Function, NY** – A non-canonical role for nuclear export receptor CRM1 in developmental gene regulation (presenter: Conway AE)
- May 2016 **NAEHS Council Meeting, NIEHS, NIH, NC** –Why not to look under the lamppost?
- Mar 2016 **Keystone Symposium on Chromatin and Epigenetics, Whistler, Canada** – Transcription at intragenic enhancers attenuates gene expression.
- Mar 2015 **Symposium on Systems Biology of Stem Cells, Oberstdorf, Germany**– Gene networks controlling ES cell identity and homeostasis.
- Oct 2014 **Systems Biology Forum, NIH, Bethesda, MD** – Gene networks controlling embryonic stem cell identity and homeostasis.

- Sep 2014 **NHGRI, NIH**, Bethesda, MD – Gene networks controlling embryonic stem cell identity and homeostasis.
- Apr 2013 **Symposium on Unlocking the Promise of Stem Cells**, RTP, NC – ES cell identity and homeostasis.
- Sep 2012 **Genomics Day Lecture, NIEHS, NIH**, RTP, NC – Meta-analysis identifies determinants of embryonic stem cell identity.
- Aug 2012 **FASEB Meeting** on Biological Methylation: From DNA and Histones to Disease, Snowmass, CO – Tet1-dependent 5hmC is required for maintaining pluripotency.
- Oct 2011 **Laboratory of Toxicology and Pharmacology (LTP), NIEHS, NIH**, RTP, NC – Embryonic stem cells and gene regulation.
- Sep 2011 **Bertinoro Computational Biology Meeting** on Computational Methods in Functional Genomics, Bertinoro, Italy – Embryonic stem cells and gene regulation.
- Sep 2011 **Laboratory of Molecular Carcinogenesis (LMC), NIEHS, NIH**, RTP, NC – esBAF facilitates pluripotency by conditioning the genome for LIF/STAT3 signaling and by regulating Polycomb function.
- Apr 2011 **University of Texas at Dallas**, Richardson, TX – Embryonic stem cells and gene regulation.
- Mar 2011 **New York University**, New York, NY – Embryonic stem cells and gene regulation.
- Feb 2011 **University of Michigan**, Ann Arbor, MI - Embryonic stem cells and gene regulation.
- Oct 2010 **Duke University**, Institute for Genome Sciences & Policy, Durham, NC – Embryonic stem cells and gene regulation
- Oct 2010 **Symposium on Epigenetics, Chromatin, and Gene Regulation**, Bethesda, MD - esBAF conditions the pluripotent genome for LIF/STAT3 signaling by opposing polycomb
- Mar 2010 **Keystone Meeting** on Biomolecular Interaction Networks: Function and Disease, Quebec, Canada – Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture.
- Feb 2010 **North Carolina State University**, Department of Environmental and Molecular Toxicology, Raleigh, NC – Systems biology and epigenetics of gene regulation
- Dec 2009 **RECOMB Conference on Regulatory Genomics**, Cambridge, MA – Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture.
- Nov 2009 **Laboratory of Signal Transduction (LST), NIEHS, NIH**, RTP, NC – Seeing the forest for the trees: stories on Brg1 and CTCF.
- Nov 2009 **NIEHS Early Career Award Lecture, NIH**, RTP, NC – Seeing the forest for the trees: a systems level understanding of differential cell-fate outcome.
- Oct 2009 **Indian Institute of Technology**, Chennai, India – Systems biology and epigenetics of gene regulation.

- Oct 2009 **Center for Cellular and Molecular Biology (CCMB)**, Hyderabad, India – Systems biology and epigenetics of gene regulation.
- Oct 2009 **Center for DNA Finger Printing and Diagnostics (CDFD)**, Hyderabad, India – Systems biology and epigenetics of gene regulation.
- Oct 2009 **Indian Institute of Science**, Bangalore, India – Systems biology and epigenetics of gene regulation.
- Sep 2009 **Biostatistics Branch, NIEHS, NIH**, RTP, NC – Systems biology and epigenetics of gene regulation.
- Nov 2008 **RECOMB Conference on Regulatory Genomics**, Cambridge, MA – Genome-wide identification of in vivo protein-DNA binding sites from CHIP-Seq data.
- Jun 2008 **NIEHS, NIH**, RTP, NC – Chromatin modifications, gene expression, and regulatory networks.
- May 2008 **NCBI/NLM, NIH**, Bethesda, MD – Chromatin modifications, gene expression, and regulatory networks.
- Jan 2008 **Rutgers University**, Camden, NJ - Regulatory proteins within a hierarchical framework have distinct dynamic properties.
- Aug 2007 **Department of Defense Biotechnology HPC Software Applications Institute (BHSI)**, Fort Detrick, Frederick, MD - Inferring protein and domain interactions using sequence co-evolution and combinatorial optimization approaches.
- May 2007 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD - Inferring molecular interactions using sequence co-evolution and co-inheritance: biases, strengths and weaknesses
- Apr 2007 **George Mason University**, Fairfax, VA – Co-evolution (correlated mutations) as an indicator of protein and domain interactions.
- Mar 2007 **Philips Research**, Briarcliff Manor, NY– Co-evolution as an indicator of protein and domain interactions.
- Feb 2007 **University of Connecticut**, Storrs, CT – Co-evolution as an indicator of protein and domain interactions.
- Oct 2006 **9th Annual Computational Genomics Conference**, Baltimore, MD – Co-evolutionary analysis of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions.
- Sep 2005 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD - A new phylogenetic approach to delineate orthologous groups
- Jun 2005 **International Conference on Intelligent Systems for Molecular Biology (ISMB)**, Detroit, MI –Predicting protein-protein interaction by searching evolutionary tree automorphism space.

- May 2005 **DIMACS Workshop on Biomolecular Networks: Topological Properties and Evolution**, Rutgers University, New Brunswick, NJ – An Evolution-Based Clustering Method to Separate Orthologous Genes from Out-Paralogs.
- Dec 2004 **University of Maryland**, College Park, MD – The effects of evolutionary tree topology on predicting protein interaction specificity.
- Dec 2004 **Georgetown University**, Washington D.C – The effects of evolutionary tree topology on predicting protein interaction specificity.
- Apr 2004 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD – Protein folding in the Hydrophobic-Hydrophilic Model.
- Mar 2004 **7th INFORMS Telecommunications Conference**, Boca Raton, FL – Survivable Network design: the capacitated minimum spanning network problem.
- Nov 2003 **International Conference on Parallel and Distributed Computing and Systems**, Marina del Rey, CA – Design of local access networks.
- May 2003 **DIMACS Workshop on Geometric Optimization**, Rutgers University, New Brunswick, NJ – Leave no stones unturned: improved approximation algorithms for degree-bounded minimum spanning trees.
- Apr 2003 **University of Maryland**, College Park, MD – Approximation algorithms for capacitated minimum spanning tree problem and its variants in network design.
- Jan 2003 **14th ACM-SIAM Symposium on Discrete Algorithms**, Baltimore, MD – A 5/4-approximation algorithm for minimum 2-edge-connectivity.

MENTORING

Trainees

Name	Type	Duration	Next Position
Sailu Yellaboina*	Postdoctoral Fellow	2009 – 2011	Associate Professor, CR Rao Institute, Hyderabad, India
Johannes Freudenberg*	Postdoctoral Fellow	2010 – 2011	Scientific Investigator GlaxoSmithKline, RTP, NC, USA
Leelavati Narlikar*	Special Volunteer	2009 – 2013	Group Leader, Wellcome Trust Early Career Fellow, National Chemical Laboratory, Pune, India
Viju Mathew†	High School Student Summer Intern	2010, 2011	Undergraduate Student, Duke University
Swati Ghosh*	Postdoctoral Fellow	2010 – 2012	Postdoctoral Fellow, NIEHS
Pengyi Yang*	Postdoctoral Fellow	2013 – 2015	Lecturer (Assistant Professor), University of Sydney, Australia
Senthilkumar Cinghu*	Postdoctoral Fellow	2011 – 2019	Staff Scientist, NIEHS, NIH

Andrew Oldfield*	Postdoctoral Fellow	2012 – 2016	ARC Foundation Fellow, Institut de Génétique Humaine Montpellier, France
Amanda Conway*	Postdoctoral Fellow	2013 -	
Rajneesh Pathania*	Postdoctoral Fellow	2015 -	
Brian Deskin*	Postdoctoral Fellow	2016 -	
Dhirendra Kumar	Postdoctoral Fellow	2016 -	
Wilfred Wong	Undergraduate Summer Intern	2018	Doctoral Student
Julie Dickerson	Undergraduate Summer Intern	2018, 2019	

*Recipient, NIH Fellows Award for Research Excellence (FARE)

† High school student; contributing author on a manuscript published in *Nucleic Acids Research* (2013), >100 citations

AWARDS/HONORS TO TRAINEES

- Dhirendra Kumar, Ph.D., Postdoctoral Fellow (2016 – present)
 - ✓ Winner, “Big Picture, Small Talk” competition, NIEHS (2018)
- Brian Deskin, Ph.D., Postdoctoral Fellow (2016 – present)
 - ✓ NIH Fellows Award for Research Excellence (2017-2018)
- Rajneesh Pathania, Ph.D., Postdoctoral Fellow (2015 - present)
 - ✓ NIH Fellows Award for Research Excellence (2016-2017)
 - ✓ NIEHS Science Day Best Poster Award (2017)
- Amanda Conway, Ph.D., Postdoctoral Fellow (2013 - present)
 - ✓ Oral Presentation, CSHL Meeting on Chromatin & Epigenetics (2018)
 - ✓ Oral Presentation, CSHL Meeting on Nuclear Function & Organization (2018)
 - ✓ NIGMS PRAT Fellowship (2014 - 2017)
 - ✓ NIH Fellows Award for Research Excellence (2017-2018)
 - ✓ Oral Presentation, CSHL Meeting on Nuclear Function & Organization (2016)
 - ✓ NIH Fellows Award for Research Excellence (2015-2016)
- Pengyi Yang, Ph.D., Postdoctoral Fellow, Ph.D., (2013 - present)
 - ✓ NIH Fellows Award for Research Excellence (2015-2016)
 - ✓ NIH Fellows Award for Research Excellence (2014-2015)
- Andrew Oldfield, Ph.D., Postdoctoral Fellow (2012 - present)
 - ✓ NIH Fellows Award for Research Excellence (2014-2015)
 - ✓ Intramural Research Paper of the Year (2014)
 - ✓ Best Scientific Presentation, LMC Retreat (2014)
 - ✓ Intramural Research Paper of the Month (Oct 2014)
- Senthilkumar Cinghu, Ph.D., Postdoctoral Fellow (2011 - present)
 - ✓ Intramural Research Paper of the Year (2017)
 - ✓ Intramural Research Paper of the Month (Dec 2017)

- ✓ NIH Fellows Award for Research Excellence (2014-2015)
- ✓ NIH Fellows Award for Research Excellence (2013-2014)
- ✓ Intramural Research Paper of the Month (June 2014)
- Swati Ghosh, Ph.D., Postdoctoral Fellow (2010 - 2012)
 - ✓ NIH Fellows Award for Research Excellence (2012-2013)
- Johannes Freudenberg, Ph.D., Postdoctoral Fellow (2010 - 2011)
 - ✓ NIH Fellows Award for Research Excellence (2011-2012)
 - ✓ Invited Oral Presentation, NIH Research Festival, Bethesda, MD (2011)
 - ✓ Intramural Research Paper of the Month (June 2014)
- Leelavati Narlikar, Ph.D., Special Volunteer (2009 - 2013)
 - ✓ NIH Fellows Award for Research Excellence (2011-2012)
 - ✓ Wellcome Trust/DBT Early Career Fellowship (2012 - 2016)
 - ✓ Ramanujan Fellowship (2010 - 2011)
- Sailu Yellaboina, Ph.D., Postdoctoral Fellow (2009 - 2011)
 - ✓ NIH Fellows Award for Research Excellence (2010-2011)
 - ✓ Young Investigator Fellowship, IndiaBioScience.org (2011)
 - ✓ Invited Oral Presentation, NIH Research Festival, Bethesda, MD (2010)

PUBLICATIONS

Peer-Reviewed Articles (in reverse chronological order)

† Co-first author

* Corresponding/Co-corresponding author

Under Revision

- Oldfield AJ, Henriques T, Burkholder AB, Kumar D, Agirre E, Paulet D, Scruggs, BS, Lavender CA, Yang P, Bennett B, Adelman K, **Jothi R***. NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. [*Nature Communications*](#), *under review*

2019

1. Yang P[†], Humphrey SJ[†], Cinghu S[†], Pathania R, Oldfield AJ, Kumar D, Perera KD, Yang JYH, James DE, Mann M, **Jothi R***. Multi-omic profiling reveals dynamics of the phased progression of pluripotency. [*Cell Systems*](#), *accepted*.
2. Jeon K, Kumar D, Conway AE, Park K, **Jothi R**, Jetten AM. GLIS3 Transcriptionally Activates WNT Genes to Promote Differentiation of Human Embryonic Stem Cells into Posterior Neural Progenitors. [*Stem Cells*](#), 37(2):202-215

2017

3. Cinghu S[†], Yang P[†], Kosak J, Conway AE, Kumar D, Oldfield AJ, Adelman K, **Jothi R***. Intragenic enhancers attenuate gene expression. [Molecular Cell](#). 68(1):104-117. (13 citations)
 - Commentary in Nature Reviews in Genetics, doi:10.1038/nrg.2017.90
 - Commentary in Nature Reviews in Molecular Cell Biology, doi:10.1038/nrm.2017.111
 - Paper of the Year, NIEHS Intramural Research (2017)
4. Kang HS, Kumar D, Liao G, Lichti-Kaiser K, Gerrish K, Liao X-H, Refetoff S, **Jothi R**, Jetten AM. GLIS3 is indispensable for TSH/TSHR-dependent thyroid hormone biosynthesis and follicular cell proliferation. [The Journal of Clinical Investigation](#). 127(12):4326-4337 (7 citations)
 - Paper of the Year, NIEHS Intramural Research (2017)

2016

5. Zheng X, Yang P, Lackford B, Bennett B, Wang L, Li H, Miao Y, Fargo D, Jin Y, Williams CJ, **Jothi R**, Hu G (2016). CNOT3-dependent mRNA deadenylation safeguards the pluripotent state. [Stem Cell Reports](#). 7(5):897-910. (9 citations)
6. Yang P, Humphrey SJ, James DE, Yang YH, **Jothi R*** (2016). Positive-unlabeled ensemble learning for kinase substrate prediction from phosphoproteomics data. [Bioinformatics](#). 32(2):252-9. (15 citations)
7. Minard AY, Tan S-X, Yang P, Fazakerley DJ, Domanova W, Parker BL, Humphrey SJ, **Jothi R**, Stockli J, James DE (2016). mTORC1 is a major regulatory node of the FGF21 signaling network. [Cell Reports](#). 17(1):29-36. (19 citations)
8. Yang P, Ellis P, Humphrey SJ, James DE, **Jothi R**, Yang YH (2016). KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. [Proteomics](#). 16(130):1868-71. (5 citations)

2015

9. Yang P, Zheng X, Jayaswal, V, Hu G, Yang YH, **Jothi R*** (2015). Knowledge-based analysis for detecting key signaling events from time-series phosphoproteomics data. [PLoS Computational Biology](#) 11(8):e1004403. (12 citations)
10. Hoffman NJ, Parker BL, Chaudhuri R, Fisher-Wellman KH, Kleinert M, Humphrey SJ, Yang P, Holliday M, Trefely S, Fazakerley DJ, Stöckli J, Burchfield JG, Jensen TE, **Jothi R**, Kiens B, Wojtaszewski JF, Richter EA, James DE (2015). Global Phosphoproteomic Analysis of Human Skeletal Muscle Reveals a Network of Exercise-Regulated Kinases and AMPK Substrates. [Cell Metabolism](#). 22(5):922-35 (>105 citations).
 - Recommended by Faculty of 1000 Biology
11. Pathania R, Ramachandran S, Elangovan S, Padia R, Yang P, Cinghu S, Veeranan-Karmegam R, Arjunan P, Gnana-Prakasam JP, Sadanand F, Pei L, Chang CS, Choi JH, Shi H, Manicassamy S, Prasad PD, Sharma S, Ganapathy V, **Jothi R**, Thangaraju M. (2015) DNMT1 is essential for mammary and cancer stem cell maintenance and tumorigenesis. [Nature Communications](#) 6:6910 (>90 citations).

- Recommended by Faculty of 1000 Biology

2014

- Oldfield AJ[†], Yang P[†] (†Co-first authors), Conway AE, Cinghu S, Freudenberg JM, Yellaboina S, **Jothi R*** (2014). Histone-fold domain protein NF-Y promotes chromatin accessibility for cell type-specific master transcription factors. [Molecular Cell](#) 55(5):708-722 (>60 citations).
 - Paper of the Year, NIEHS Intramural Research (2014)
- Takeda Y, Kang HS, Freudenberg JM, DeGraff LM, **Jothi R**, Jetten AM (2014) Retinoic Acid-Related Orphan Receptor γ (ROR γ): A Novel Participant in the Diurnal Regulation of Hepatic Gluconeogenesis and Insulin Sensitivity. [PLoS Genetics](#) 10(5), e1004331 (>30 citations).
- Wang L, Du Y, Ward JM, Shimbo T, Lackford B, Zheng X, Miao Y, Zhou B, Fargo DC, **Jothi R**, Williams CJ, Wade PA, Hu G (2014) An essential role of INO80 in the core pluripotency transcription circuitry. [Cell Stem Cell](#) 14(5):575-91 (>90 citations).
- Cinghu S[†], Yellaboina S[†] (†Co-first authors), Freudenberg JM, Ghosh S, Zheng X, Oldfield AJ, Lackford B, Zaykin DV, Hu G, **Jothi R*** (2014). Integrative framework for identification of key cell identity genes uncovers determinants of ES cell identity and homeostasis. [PNAS](#) 111(16):E1581-90 (>20 citations).
- Li R, Mav D, Grimm S, **Jothi R**, Shah R, Wade PA (2014). Fine-tuning of epigenetic regulation with respect to promoter CpG content in a cell type-specific manner. [Epigenetics](#) 9(5):747-49 (10 citations).
- Lackford B, Yao C, Charles G, Weng L, Zheng X, Choi E-A, Xie X, Wan J, Xing Y, Freudenberg JM, Yang P, **Jothi R**, Hu G, Shi Y (2014) Fip1 regulates mRNA alternative polyadenylation to promote stem cell self-renewal. [EMBO J](#) 33(8):878-89 (>65 citations).

2013

- Li L[†], Freudenberg JM[†] (†Co-first author), Cui K, Dean A, Zhao K, **Jothi R* (*Co-corresponding author)**, Love PE* (2013). Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. [Blood](#) 121(22):4575-85 (>55 citations).
- Mendez D[†], Nguyen TA[†], Freudenberg JM[†] (†Co-first authors), Mathew VJ, Anderson C, **Jothi R* (*Corresponding author)**, Resnick MA (2013). Diverse stresses dramatically alter genome-wide p53 binding and transactivation landscape in human cancer cells. [Nucleic Acids Research](#) 41(15):7286-7301 (>105 citations).

2012

- Freudenberg JM[†], Ghosh S[†], Lackford B[†], Yellaboina S, Zheng X, Li R, Cuddapah S, Wade PA, Hu G, **Jothi R*** (2012). Acute depletion of Tet1-dependent 5-hydroxymethylcytosine levels impairs LIF/Stat3 signaling and results in loss of embryonic stem cell identity. [Nucleic Acids Research](#), 40:3364-77 (>80 citations).
 - Highlighted as one of journal's featured articles representing "top 5% of papers in terms of originality, significance and scientific excellence".

21. Takeda Y, **Jothi R**, Birault V, Jetten A (2012). ROR γ directly regulates the circadian expression of clock genes and downstream targets in vivo. [Nucleic Acids Research](#) 40(17):8519-35 (>75 citations).
22. Agarwal SK* and **Jothi R*** (2012). Genome-wide characterization of menin-dependent H3K4me3 reveals a specific role for menin in the regulation of genes implicated in MEN-1 associated tumors. [PLoS ONE](#), 7(5):e37952 (>40 citations).
 - Recommended as "Must Read" by Faculty of 1000 Biology
23. Zheng X, Dumitru R, Lackford B, Freudenberg JM, Singh A, Archer T, **Jothi R**, Hu G (2012). Cnot1, Cnot2, and Cnot3 maintain mouse and human ES cell identity and inhibit extraembryonic differentiation. [Stem Cells](#) 30:910-22 (>35 citations).
24. Narlikar L and **Jothi R** (2012). ChIP-Seq Data Analysis: Identification of Protein-DNA Binding Sites with SISR Peak Finder. [Methods in Molecular Biology](#), 802:305-22 (>35 citations).
25. Chalancon G, Ravarani C, Balaji S, Martinez-Ariez A, Aravind L, **Jothi R**, M Madan Babu (2012). Interplay between gene expression noise and regulatory network architecture. [Trends in Genetics](#) 28:221–32 PMID: PMC3340541 (>165 citations)
 - Featured on the cover page

2011

26. Ho L[†], Miller EL, Ronan JL, Ho W, **Jothi R^{†*}** (***Co-corresponding author**), Crabtree GR* (2011). esBAF facilitates pluripotency by conditioning the genome for LIF/STAT3 signaling and by regulating Polycomb function. [Nature Cell Biology](#) 13:903-913 (>190 citations).
 - News and Views commentary in *Nature Cell Biology*, " esBAF safeguards Stat3 binding to maintain pluripotency" (Novershtern & Hanna, *Nature Cell Biology* 13:886-888, 2011).
 - Recommended by Faculty of 1000 Biology
27. Wei G[†], Abraham B[†], Yagi R[†], **Jothi R[†]** (**†Co-first author**), Cui K, Sharma S, Narlikar L, Northrup DL, Tang Q, Paul WE, Zhu J, Zhao K (2011). Genome-wide analyses of GATA3-mediated gene regulation in distinct T cell types. [Immunity](#) 35(2):299-311. (>230 citations)
 - Recommended as "Must Read" by Faculty of 1000 Biology
28. Li L, **Jothi R**, Cui K, Lee JY, Cohen T, Gorivodsky M, Tzchori I, Zhao Y, Hayes SM, Zhao K, Westphal H, Love PE (2011). Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. [Nature Immunology](#), 12(20):129-136 (>95 citations).
 - News and Views commentary in *Nature Immunology*, "Ldb1, a new guardian of hematopoietic stem cell maintenance" (Welinder & Murre, *Nature Immunology* 12:113-114, 2011).
 - Recommended by Faculty of 1000 Biology
29. Yellaboina S, Tasneem A, Zaykin DV, Raghavachari B, **Jothi R*** (2011). DOMINE: a comprehensive collection of known and predicted domain-domain interactions. [Nucleic Acids Research](#), 39(Database issue): D730-735. (>160 citations)
30. Yu S[†], Cui K[†], **Jothi R[†]** (**†Co-first author**), Zhao DM, Jing X, Zhao K, Xue HH (2011). GABP controls a critical transcription regulatory module that is essential for maintenance and differentiation of hematopoietic stem/progenitor cells. [Blood](#) 117(7):2166-78. (>65 citations)

2010

31. Yu S, Zhao DM, **Jothi R**, and Xue HH (2010). Critical requirement of GABP α for normal T Cell Development. [Journal of Biological Chemistry](#), 285(14): 10179-88. (>25 citations)

2009

32. **Jothi R*** (***Corresponding author**), Balaji S, Wuster A, Grochow JA, Gsponer J, Przytycka TM, Aravind L, and Madan Babu M* (2009). Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. [Molecular Systems Biology](#), 5:294 (>135 citations).
- Work highlighted in Nature Reviews Genetics, October 2009
 - 2nd, 2nd, and 5th most downloaded article for the months of Aug, Sept, and Oct 2009, respectively.
33. Barski A[†], **Jothi R**[†] (**†Co-first author**), Cuddapah S[†], Cui K, Roh TY, Schones DE, and Zhao K (2009). Chromatin poises miRNA- and protein-coding genes for activation. [Genome Research](#), 19: 1742-51 (>145 citations).
- Featured on the cover page
34. Ho L[†], **Jothi R**[†] (**†Co-first author**), Ronan JL, Cui K, Zhao K, and Crabtree GR (2009). An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. [PNAS](#), 106(13):5187-91 (>350 citations).
35. Cuddapah S[†], **Jothi R**[†] (**†Co-first author**), Schones DE, Roh TY, Cui K, and Zhao K (2009). Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. [Genome Research](#), 19(1):24-32 (>580 citations)
- Recommended as "Must Read" by Faculty of 1000 Biology
36. Liu M, Chen XW, and **Jothi R** (2009), Knowledge-guided inference of domain-domain interactions from incomplete protein-protein interaction networks, [Bioinformatics](#), 25(19):2492-99 (>30 citations).
37. Kallin E, Cao R, **Jothi R**, Xia K, Cui K, Zhao K, and Zhang Y (2009). Genome wide uH2A localization analysis highlights Bmi1-dependent deposition of the mark at repressed genes. [PLoS Genetics](#), Jun;5(6):e1000506 (>60 citations).
38. **Jothi R*** (***Corresponding author**) and Raghavachari B (2009). Improved approximation algorithms for single-sink buy-at-bulk network design problem. [Journal of Discrete Algorithms](#), 7(2):249-55 (>35 citations).
39. **Jothi R*** (***Corresponding author**) and Raghavachari B (2009). Degree-bounded minimum spanning trees, [Discrete Applied Mathematics](#), 157(5):960-70 PMID: N/A (>25 citations)

2008

40. **Jothi R**, Cuddapah S, Barski A, Cui K, and Zhao K (2008). Genome-wide identification of in vivo protein-DNA binding sites from ChIP-Seq data. [Nucleic Acids Research](#), 36(16):5221-31 (>600 citations).
- Featured on the cover page

41. Przytycka TM, **Jothi R**, Aravind L, and Lipman DJ (2008). Differences in evolutionary pressure acting within highly conserved ortholog groups. [BMC Evolutionary Biology](#), 8:208. PMID: PMC2488352 (5 citations).
42. Ragavachari R, Tasneem A, Przytycka TM, and **Jothi R** (2008), DOMINE: a database of protein domain interactions, [Nucleic Acids Research](#), 36:D656-D661 (>140 citations).
43. **Jothi R** and Przytycka TM (2008). Computational approaches to predict protein-protein and domain-domain interactions, [Bioinformatics Algorithms: Techniques and Applications](#), (Eds: Alexander Zelikovsky and Ion Mandoiu), Wiley, John & Sons. (10 citations)

2007

44. **Jothi R* (*Co-corresponding author)**, Przytycka TM*, and Aravind L (2007). Discovering functional linkages and uncharacterized cellular pathways using phylogenetic profile comparisons: a comprehensive assessment, [BMC Bioinformatics](#), 8:173. PMID: PMC1904249 (>85 citations)
 - Biomed Central “Highly Accessed” distinction
45. Kann MG, **Jothi R**, Cherukuri PF, and Przytycka TM (2007). Predicting protein domain interactions from coevolution of conserved regions, [Proteins](#), 67(4):811-20. (>55 citations)
46. **Jothi R* (*Corresponding author)** and Raghavachari B (2007). Approximating the k-traveling repairment problem with repair times, [Journal of Discrete Algorithms](#), 5(2): 293-303. (>45 citations)

2006

47. Guimaraes K, **Jothi R**, Zotenko E, and Przytycka TM (2006). Predicting Domain-Domain Interactions Using a Parsimony Approach, [Genome Biology](#), 7: R104 (>110 citations).
 - Biomed Central “Highly Accessed” distinction
48. **Jothi R* (*Co-corresponding author)**, Cherukuri PF, Tasneem A, and Przytycka TM* (2006). Co-evolutionary analysis of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions, [Journal of Molecular Biology](#), 362(4):861-75 (>145 citations).
 - Recommended by Faculty of 1000 Biology
49. Zotenko E, Guimaraes K, **Jothi R**, and Przytycka TM (2006). Decomposition of overlapping protein complexes: a graph theoretical method for analyzing static and dynamic protein associations, [Algorithms for Molecular Biology](#), 1: 7 (>50 citations).
 - Biomed Central “Highly Accessed” distinction
50. **Jothi R* (*Co-corresponding author)**, Zotenko E, Tasneem A, and Przytycka TM* (2006). COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations, [Bioinformatics](#), 22(7), 779-88 (>70 citations).
51. Gong C, Sarac K, Daescu O, Raghavachari B, and **Jothi R (2006)**. Load balanced agent activation for value added network services, [Computer Communications](#), 29(11), 1905-16 (8 citations).

2005

52. **Jothi R**, Kann MG, and Przytycka TM (2005). Predicting protein-protein interaction by searching evolutionary tree automorphism space, [Bioinformatics](#), 21 Suppl 1, i240-i250 (>70 citations).
53. **Jothi R* (*Corresponding author)** and Raghavachari B (2005). Approximation algorithms for the capacitated minimum spanning tree problem and its variants in network design, [ACM Transactions on Algorithms](#), 1(2), 265-82. (>65 citations)
54. Wang J, Vokkarane V, **Jothi R**, Qi X, Raghavachari B, and Jue J (2005). Dual-homing protection in IP-over-WDM networks, [Journal of Lightwave Technology](#), Vol. 23 (10), 3111-24. (>30 citations)

2004

55. **Jothi R* (*Co-corresponding author)** and Raghavachari B* (2004). Survivable network design: the capacitated minimum spanning network problem, [Information Processing Letters](#), 91(4), 183-90. (9 citations)
56. Daescu O*, **Jothi R* (*Co-corresponding author)**, Raghavachari B*, and Sarac K* (2004). Optimal placement of NAK-suppressing agents for reliable multicast: a partial deployment case, [Proc. 19th ACM Symposium on Applied Computing](#), 334-38. (8 citations)

2003

57. **Jothi R* (*Co-corresponding author)**, Varadarajan S*, and Raghavachari B*, A 5/4-approximation algorithm for minimum 2-edge-connectivity, [Proc. 14th Annual ACM/SIAM Symposium on Discrete Algorithms](#), 725-34, 2003. (>65 citations)
58. **Jothi R* (*Co-corresponding author)** and Raghavachari B*, Design of local access networks, [Proc. 15th IASTED International Conference on Parallel and Distributed Computing and Systems](#), 883-888, 2003. (4 citations)

Extended Abstracts

59. **Jothi R*** and Vokkarane V (2004). Threshold-based differentiated intermediate-node initiated (TDINI) signaling for optical burst-switched networks, [Proc. 7th INFORMS Telecommunications Conference](#), 190-91.
60. **Jothi R** (2004). A note on Altinkemer-Gavish's algorithm for the design of tree networks, [Proc. 7th INFORMS Telecommunications Conference](#), 78-80.
61. **Jothi R*** and Raghavachari B* (2004). Revisiting Esau-Williams' algorithm: on the design of local access networks, [Proc. 7th INFORMS Telecommunications Conference](#), 104-107.
62. **Jothi R*** and Raghavachari B* (2004). Dynamic capacitated minimum spanning trees, [Proc. 3rd IEEE International Conference on Networking](#), ISBN 0-86341-326-9, 2004.
63. **Jothi R*** and Raghavachari B*, Placement of proxy servers to support server-based reliable multicast, [Proc. 3rd IEEE International Conference on Networking](#), ISBN 0-86341-326-9, 2004.