

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: 919-316-4557
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)	National Institutes of Health (NIH) , NIEHS, Epigenetics & Stem Cell Biology Laboratory, Research Triangle Park, NC.
2009 - 2015	Investigator (tenure-track)	National Institutes of Health (NIH) , NIEHS, Epigenetics & Stem Cell Biology Laboratory, Research Triangle Park, NC
2007 - 2009	Research Fellow	National Institutes of Health (NIH) , NHLBI, Laboratory of Molecular Immunology, Bethesda, MD, USA (Mentor: Keji Zhao)
2004 - 2007	Research Associate	National Institutes of Health (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

2017 NIH Award of Merit
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 Earl Stadtman Investigator Search Committee (Chromosome Biology/Epigenetics/Transcription), NIH
- 2016 - 2017 Earl Stadtman Investigator Search Committee (Chromosome Biology/Epigenetics/Transcription), NIH
- 2015 - 2016 Earl Stadtman Investigator Search Committee (Chromosome Biology/Epigenetics/Transcription), NIH
- 2013 - 2014 Earl Stadtman Investigator Search Committee (Stem Cells), NIH
- 2014 Review panel, NIH Fellows Award for Research Excellence
- 2012 - 2013 Earl Stadtman Investigator Search Committee (Stem Cells), NIH
- 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
- 2009 - 2013 Next Generation Sequencing Projects Review Committee, NIEHS, NIH
- 2010 Review panel, applications for the NIH National Graduate Student Research Festival
- 2010 Review panel, NIH Fellows Award for Research Excellence

NIEHS Institutional Service

- 2017 - Councilor, Assembly of Scientists, NIEHS, NIH
- 2017 Organizer, Epigenetics & Stem Cell Biology Laboratory Retreat
- 2016 - Viral Vector Core Oversight Committee, NIEHS
- 2016 Organizing Committee, Division of Intramural Research Retreat
- 2016 Organizer, Epigenetics & Stem Cell Biology Laboratory Retreat
- 2015 - NIEHS IT Management Committee
- 2015 - Committee on Promotions IV to review appointment, tier advancement, and renewal requests of Title 42 Staff Scientists, NIEHS, NIH
- 2013 - 2014 Search Committee, Tenure-Track/Tenure-Eligible Investigator in Biostatistics/Computational Biology, NIEHS, NIH
- 2014 Organizer, Laboratory of Molecular Carcinogenesis Retreat
- 2013 - 2015 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 Next Generation Sequencing Projects Review Committee, NIEHS, NIH
- 2009 - 2010 Search Committee, 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	<i>Nature Genetics</i> <i>Nature Methods</i> <i>Nature Protocols</i> <i>PNAS</i> <i>eLife</i> <i>Genome Research</i> <i>Genome Biology</i> <i>Trends in Genetics</i> <i>PLoS Genetics</i> <i>PLoS Computational Biology</i> <i>PLoS ONE</i> <i>Nucleic Acids Research</i> <i>Molecular Biology and Evolution</i> <i>Stem Cells and Development</i> <i>Proteins</i> <i>Bioinformatics</i> <i>Molecular Biosystems</i> <i>BMC Bioinformatics</i> <i>BMC Genomics</i> <i>BMC Systems Biology</i> <i>Toxicological Sciences</i> <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> <i>IEEE Transactions on NanoBioscience</i> <i>Pattern Recognition Letters</i> <i>Discrete and Computational Geometry</i> <i>Networks</i> <i>Journal of Graph Algorithms and Applications</i>

Membership: International Society for Computational Biology (ISCB)

INVITED TALKS

- Apr 2018 **NIH Director's Seminar Series Lecture**, NIH, MD – Uncovering unknown unknowns of Gene Regulation
- Oct 2017 **University of North Carolina**, NC – Uncovering unknown unknowns of Gene Regulation
- Oct 2017 **NCBI Retreat Keynote**, 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 **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 (BHSAI)**, 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.

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	Sr. Lecturer (Assistant Professor) and DECRA Fellow, University of Sydney, Australia
Senthilkumar Cinghu	Postdoctoral Fellow	2011 -	
Andrew Oldfield	Postdoctoral Fellow	2012 -	ARC Foundation Fellow, Institut de Génétique Humaine Montpellier, France
Amanda Conway	Postdoctoral Fellow	2013 -	
Rajneesh Pathania	Postdoctoral Fellow	2015 -	
Dhirendra Kumar	Postdoctoral Fellow	2016 -	
Brian Deskin	Postdoctoral Fellow	2016 -	

AWARDS/HONORS TO TRAINEES

- 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)
- Amanda Conway, Ph.D., Postdoctoral Fellow (2013 - present)
 - ✓ NIGMS PRAT Fellowship (2014 - 2017)
 - ✓ NIH Fellows Award for Research Excellence (2017-2018)
 - ✓ 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)
 - ✓ Best Scientific Presentation, LMC Retreat (2014)
 - ✓ Intramural Paper of the Year (2014)
 - ✓ Intramural Research Paper of the Month (Oct 2014)
- Senthilkumar Cinghu, Ph.D., Postdoctoral Fellow (2011 - present)
 - ✓ 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

2017

1. Cinghu S[†], Yang P[†], Kosak J, Conway AE, Kumar D, Oldfield AJ, Adelman K, **Jothi R***. Intragenic enhancers attenuate gene expression. [Molecular Cell](#), to appear.
2. 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](#), to appear.

2016

3. 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.
4. 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.
5. 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.
6. 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.

2015

7. 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.
8. 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 (>25 citations).
 - Recommended by Faculty of 1000 Biology
9. 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 (>25 citations).

- Recommended by Faculty of 1000 Biology

2014

10. 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 (>25 citations).
 - Paper of the Year, NIEHS Intramural Research (2014)
11. 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 (>15 citations).
12. 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 (>45 citations).
13. 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 (9 citations).
14. 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 (5 citations).
15. 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 (>30 citations).

2013

16. 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 (>30 citations).
17. Menedez 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 (>65 citations).

2012

18. 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 (>60 citations).
 - Highlighted as one of journal's featured articles representing "top 5% of papers in terms of originality, significance and scientific excellence".

19. 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 (>45 citations).
20. 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 (18 citations).
 - Recommended as "Must Read" by Faculty of 1000 Biology
21. 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 (25 citations).
22. Narlikar L and **Jothi R** (2012). ChIP-Seq Data Analysis: Identification of Protein-DNA Binding Sites with SISR's Peak Finder. [Methods in Molecular Biology](#), 802:305-22 (>25 citations).
23. 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 (>90 citations)
 - Featured on the cover page

2011

24. 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 (>125 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
25. 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. (>150 citations)
 - Recommended as "Must Read" by Faculty of 1000 Biology
26. 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 (>65 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
27. 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. (>115 citations)
28. 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. (>50 citations)

2010

29. 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. (>20 citations)

2009

30. **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 (>110 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.
31. 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 (>120 citations).
- Featured on the cover page
32. 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 (>265 citations).
33. 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 (>440 citations)
- Recommended as "Must Read" by Faculty of 1000 Biology
34. 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 (>25 citations).
35. 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 (>55 citations).
36. **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 (>30 citations).
37. **Jothi R*** (***Corresponding author**) and Raghavachari B (2009). Degree-bounded minimum spanning trees, [*Discrete Applied Mathematics*](#), 157(5):960-70 PMID: N/A (>20 citations)

2008

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