# Mitchell Guttman

Professor, California Institute of Technology
Robertson Investigator, New York Stem Cell Foundation
Investigator, Heritage Medical Research Institute

## OFFICE

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## EDUCATION

**Massachusetts Institute of Technology**, Cambridge, MA.
Department of Biology.
Broad Institute of MIT and Harvard.
Doctor of Philosophy (Ph.D.) in Biology. 2012

**University of Pennsylvania**, Philadelphia, PA.
School of Engineering and Applied Sciences.
Masters of Science in Computational Biology and Bioinformatics. 2006.

**University of Pennsylvania**, Philadelphia, PA.
School of Arts and Sciences.
Bachelors of Arts in Molecular Biology and Computational Biology. 2006.
Magna cum laude
With Distinction in Biology

## POSITIONS

| | |
|---|---|
| ***2019-present*** | **Professor of Biology,** California Institute of Technology |
| ***2013-2018*** | **Assistant Professor of Biology**, California Institute of Technology |
| ***2015-present*** | **Robertson Investigator,** New York Stem Cell Foundation |
| ***2015-present*** | **Investigator,** Heritage Medical Research Institute |
| ***2012- 2013*** | **Fellow**, Broad Institute of MIT and Harvard |
| ***2006-2012*** | **Graduate Student**, Department of Biology, MIT |
| ***2005-2006*** | **Researcher**, Center for Bioinformatics, University of Pennsylvania |
| ***2003-2006*** | **Researcher**, Department of Pathology, University of Pennsylvania |

## RESEARCH TRAINING

***2006-2012*** **Broad Institute of MIT and Harvard,** MIT
-Advisor: Eric S. Lander

- Identified large intergenic ncRNAs (lincRNAs) using a chromatin signature.
- Developed a statistical method to reconstruct a mammalian transcriptome.
- Characterized the role of lincRNAs in regulating embryonic stem cell state.

***2005-2006*** **Center for Bioinformatics**, University of Pennsylvania
-Advisors: Warren J. Ewens and Gregory R. Grant

- Developed a statistical method to identify conserved genomic aberrations in cancer.

*2003-2006* **Department of Pathology**, University of Pennsylvania
-Advisor: Carolyn Mies
- Defined genomic aberrations that drive breast cancer progression.

*2000-2002* **Derald H. Ruttenberg Cancer Center,** Mount Sinai School of Medicine
-Advisor: Rachel B. Hazan
- Identified the molecular basis of cadherin switch that drives metastasis in cancer.

## HONORS AND AWARDS

*2020* **NIH Director's Transformative Research Award**
*2019* **Edward Mallincrodt Scholar**
*2017* **Cell Scientists to Watch,** Journal of Cell Biology
*2016* **Rising Stars,** Third Rock Ventures
*2015* **Agilent Early Career Professor Award,** Agilent Technologies
*2015* **Investigator**, Heritage Medical Research Institute
*2015* **Pew-Steward Scholar for Cancer Research**, The Pew Charitable Trusts
*2015* **Robertson Stem Cell Investigator**, New York Stem Cell Foundation
*2015* **Alfred P. Sloan Research Fellow** for Computational and Evolutionary Biology
*2015* **CSQ Magazine "NextGen 10" in Innovation and Technology**
*2014* **Wilson S. Stone Memorial Award,** MD Anderson Cancer Center
*2014* **Distinguished Scientist Award,** Sontag Foundation
*2014* **Kimmel Scholar,** Sidney Kimmel Foundation for Cancer Research
*2014* **Searle Foundation Scholar**
*2014* **Forbes magazine '30 under 30' in Science and Medicine**
*2013* **Edward Mallincrodt, Jr. Foundation Scholar**
*2013* **Forbes magazine '30 under 30' in Science and Medicine**
*2012* **NIH Director's Early Independence Award**
*2007* **Vertex Pharmaceuticals Scholar**
*2006* **Phi Beta Kappa,** University of Pennsylvania
*2006* **Neysa Cristol Adams Prize in Biology (Best Thesis),** University of Pennsylvania
*2006* **MGED Society Best Presentation**
*2005* **NIH Fellowship for Bioinformatics Research**

## PUBLICATIONS

1) Takei Y, Ollikainen N, Zheng S, Pierson N, White J, Shah S, Thoimassie J, Eng L, **Guttman M**, Yuan GC, Cai, L. Global architecture of the nucleus in single cells by DNA seqFISH+ and multiplexed immunofluorescence. ***Nature*** *(in press)*

2) Banerjee AK, Blanco MR, Bruce EA, Honson DD, Chen L, Chow A, Bhat P, Ollikainen N, Quinodoz SA, Loney C, Thai J, Miller ZD, Lin AE, Schmidt MM, Stewart DG, Goldfarb D, De Lorenzo G, Rihn SJ, Voorhees R, Botten JW, Majumdar D, and **Guttman M** (2020). SARS-CoV-2 suppresses mRNA splicing, translation, and protein trafficking in a multipronged mechanism to evade host defenses. ***Cell*** Nov 25;183(5):1325-1339.e21

3) Quinodoz SA, Bhat P, Ollikainen N, Jachowicz JW, Banerjee AK, Chovanec P, Blanco MR, Chow A, Markaki Y, Plath K, and **Guttman M** (2020). RNA promotes the formation of spatial compartments in the nucleus. ***bioRxiv*** doi: https://doi.org/10.1101/2020.08.25.267435

4) Arrastia MV, Jachowicz JW, Ollikainen N, Curtis MS, Lai C, Quinodoz SA, Selck DA, **Guttman M**[†], Ismagilov RF (2020). A single-cell method to map higher-order 3D genome organization in thousands of individual cells reveals structural heterogeneity in mouse ES cells. ***bioRxiv*** doi: https://doi.org/10.1101/2020.08.11.242081. [†]*Corresponding author*

5) Vangala P, Murphy R, Quinodoz SA, Gellatly K, McDonel PE, **Guttman M**, Garber M (2020). High-resolution mapping of multiway enhancer promoter interactions regulating pathogen detection. ***Molecular Cell*** doi: 10.1016/j.molcel.2020.09.005.

6) Pandya-Jones A, Markaki Y, Serizay J, Chitiashvilli T, Mancia W, Damianov A, Chronis C, Papp B, Chen CK, McKee R, Wang XJ, Chau A, Leonhardt H, Zheng S, **Guttman M**, Black DL, Plath K (2020). An Xist-dependent protein assembly mediates Xist localization and gene silencing. ***Nature*** doi:10.1038/s41586-020-2703-0

7) Cerase A, Armaos A, Neumayer C, Avner P, **Guttman M**[†], Tartaglia GG (2019). Phase separation drives X-chromosome inactivation: a hypothesis. ***Nature Structural and Molecular Biology*** May;26(5):331-334. [†]*Corresponding author*

8) McDonel P and **Guttman M** (2019) . Approaches for Understanding the Mechanisms of Long Noncoding RNA Regulation of Gene Expression. In ***RNA Worlds: New Tools for Deep Exploration*** edited by Thomas R. Cech, Joan A. Steitz, and John F. Atkins

9) van Bemmel JG, Galupa R, Gard C, Servant N, Picard C, Davies J, Szempruch AJ, Zhan Y, Żylicz JJ, Nora EP, Lameiras S, de Wit E, Gentien D, Baulande S, Giorgetti L, **Guttman M**, Hughes JR, Higgs DR, Gribnau J, Heard E (2019). The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. ***Nature Genetics*** June 51(6):1024-1034

10) Quinodoz SA, Ollikainen N, Tabak B, Palla A, Schmidt JM, Detmar E, Lai M, Shishkin A, Bhat P, Trinh V, Aznauryan E, Russell P, Cheng C, Jovanovic M, Chow A, McDonel P, Garber M, and **Guttman M** (2018). Higher-order inter-chromosomal hubs shape 3-dimensional genome organization in the nucleus. ***Cell*** July 26;174(3):744-757.e24. doi: 10.1016/j.cell.2018.05.024

11) Munschauer M, Nguyen CT, Sirokman K, Hartigan CR, Hogstrom L, Engreitz JM, Ulirsch JC, Fulco CP, Subramanian V, Chen J, Schenone M, **Guttman M**, Carr SA, Lander ES (2018). The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. ***Nature*** Sep;561(7721):132-136.

12) Dekker J, Belmont AS, **Guttman M**, Leshyk VO, Lis JT, Lomvardas S, Mirny LA, O'Shea CC, Park PJ, Ren B, Politz JCR, Shendure J, Zhong S (2017). The 4D nucleome project. ***Nature.*** Sep 13;549(7671):219-226. doi: 10.1038/nature23884

13) McHugh CA and **Guttman M** (2017). RAP-MS: A Method to Identify Proteins that Interact Directly with a Specific RNA Molecule in Cells. Methods Molecular Biology doi: 10.1007/978-1-4939-7213-531.

14) Blanco MR and **Guttman M** (2017). Re-evaluating the foundations of lncRNA-Polycomb function. ***EMBO Journal*** Apr 13;36(8):964-966. doi: 10.15252/embj.201796796

15) Szempruch A and **Guttman M** (2017). Linking Protein and RNA Function within the same gene. ***Cell*** Feb 23;168(5):753-755. doi: 10.1016/j.cell.2017.02.014

16) Cirillo D, Blanco MR, Armaos A, Buness A, Avner P, **Guttman M**, Cerase A, Tartaglia GG (2016). Quantitative predictions of protein interactions with long non-coding RNAs. ***Nature Methods*** Dec 29;14(1):5-6. doi: 10.1038/nmeth.4100

17) Engreitz JM, Ollikainen N, **Guttman M** (2016). Long non-coding RNAs (lncRNAs) as spatial amplifiers that control nuclear architecture and gene expression. ***Nature Reviews Molecular Cell Biology*** Dec;17(12):756-770

18) Engreitz JM, Haines JE, Perez EM, Munson G, Chen J, Kane M, McDonel PE, **Guttman M**, Lander ES (2016). Local regulation of gene expression by lncRNA promoters, transcription, and splicing. ***Nature*** Nov 17;539(7629):452-455

19) Chen CK, Blanco M, Jackson C, Aznauryan E, Ollikainen N, Surka C., Chow A, Cerase A, McDonel PE, **Guttman M** (2016). Xist recruits the X chromosome to the nuclear lamina to enable chromosome-wide silencing. ***Science*** Oct 28;354(6311):468-472

20) Patil DP, Chen CK, Pickering BF, Chow A, Jackson C, **Guttman M**, Jaffrey SR (2016). m6A RNA methylation promotes XIST-mediated transcriptional repression. ***Nature*** Sep 7;537(7620):369-373

21) Van Nostrand EL, Pratt GA, Shishkin AA, Gelboin-Burkhart C, Fang M, Sundararaman B, Blue SM, Nguyen TB, Surka C, Elkins K, Stanton R, Rigo F, **Guttman M**, Yeo GW (2016). Enhanced CLIP (eCLIP) enables robust and scalable transcriptome-wide discovery and characterization of RNA binding protein binding sites. ***Nature Methods*** doi:10.1038/nmeth.3810

22) Chen J, Shishkin AA, Zhu X, Kadri S, Maza I, **Guttman M**, Hanna JH, Regev A, Garber M (2016). Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. ***Genome Biology*** doi: 10.1186/s13059-016-0880-9

23) Paten B, Diekhans M, Druker BJ, Friend S, Guinney J, Gassner N, **Guttman M**, Kent WJ, Mantey P, Margolin AA, Massie M, Novak AM, Nothaft F, Pachter L, Patterson D, Smuga-Otto M, Stuart JM, Van't Veer L, Wold B, Haussler D (2015). The NIH BD2K center for big data in translational genomics**.** ***J Am Med Inform Assoc***. doi: 10.1093/jamia/ocv047

24) McHugh CA, Chen CK, Chow A, Surka CF, Tran C, McDonel P, Pandya-Jones A, Blanco MR, Burghard C, Moradian A, Sweredoski MJ, Shishkin AA, Su J, Lander ES, Hess S, Plath K, and **Guttman M** (2015). The Xist lncRNA directly interacts with SHARP to silence transcription through HDAC3. ***Nature*** doi:10.1038/nature14443

25) Shishkin AA, Giannoukos G, Kucukural A, Ciulla D, Busby M, Surka CF, Chen J, Bhattacharyya RP, Rudy RF, Patel MM, Novod N, Hung DT, Gnirke A, Garber M, **Guttman M**[*†], Jonathan Livny[*] (2015). Simultaneous generation of large numbers of strand-specific RNA-Seq cDNA libraries in a single reaction. ***Nature Methods*** doi: 10.1038/nmeth.3313 * *Co-senior authors* †*Corresponding author*

26) Engreitz JM, Lander ES, and **Guttman M** (2015). RNA Antisense Purification (RAP) for mapping RNA interactions with chromatin. ***Methods in Molecular Biology*** 1262:183-97

27) Rinn JL and **Guttman M** (2014). RNA and the dynamics of nuclear organization. ***Science*** 345(6202):1240-1

28) Quinodoz S and **Guttman M** (2014). Long non-coding RNAs: An emerging link between gene regulation and nuclear organization. ***Trends in Cell Biology*** 24(11): 651–663

29) Engreitz JM, Sirokman K, McDonel P, Shishkin A, Surka CF, Russell P, Grossman SR, Chow AY, **Guttman M**[*†], Lander ES[*] (2014). RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites. ***Cell*** Sep 25;159(1):188-99 * *Co-senior authors*, †*Corresponding author*

30) Schwartz S, Bernstein DA, Mumbach MR, Jovanovic M, Herbst RH, León-Ricardo BX, Engreitz JM, **Guttman M**, Satija R, Lander ES, Fink G, Regev A (2014). Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. ***Cell*** Sep 25;159(1):148-62

31) McHugh CA, Russell P, and **Guttman M**[†] (2014). Methods for comprehensive experimental identification of RNA–protein interactions. ***Genome Biology*** 15(1):203 †*Corresponding author*

32) Hacisuleyman E, Goff LA, Trapnell C, Williams A, Henao-Mejia J, Sun L, McClanahan P, Hendrickson DG, Sauvageau M, Kelley DR, Morse M, Engreitz JM, Lander ES, **Guttman M**, Lodish HF, Flavell R, Raj A, and Rinn JL (2014). Topological Organization of Multi-chromosomal Regions by Firre. ***Nature Structural & Molecular Biology*** 21(2):198-206

33) Engreitz JM, Pandya-Jones A, McDonel P, Shishkin A, Sirokman K, Surka C, Kadri S, Lander ES, Plath K, and **Guttman M** (2013). The Xist lncRNA exploits three-dimensional chromosome architecture to spread across the X-chromosome. ***Science*** 341:767

34) **Guttman M**[†], Russell P, Ingolia NT, Weissman JS, and Lander ES (2013). Ribosome profiling provides evidence that large non-coding RNAs do not encode proteins. ***Cell*** 154(1):240-51 †*Corresponding author*

35) Gifford CA, Ziller MJ, Gu H, Trapnell C, Donaghey J, Tsankov A, Shalek AK, Kelley DR, Shishkin AA, Issner R, Zhang X, Coyne M, Fostel JL, Holmes L, Meldrim J, **Guttman M**, Epstein C, Park H, Kohlbacher O, Rinn J, Gnirke A, Lander ES, Bernstein BE, Meissner A. (2013) Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. ***Cell*** 153(5):1149-63

36) Kirby A, Gnirke A, Jaffe DB, Barešová V, Pochet N, Blumenstiel B, Ye C, Aird D, Stevens C, Robinson JT, Cabili MN, Gat-Viks I, Kelliher E, Daza R, DeFelice M, Hůlková H, Sovová J, Vylet'al P, Antignac C, **Guttman M**, Handsaker RE, Perrin D, Steelman S, Sigurdsson S, Scheinman SJ, Sougnez C, Cibulskis K, Parkin M, Green T, Rossin E, Zody MC, Xavier RJ, Pollak MR, Alper SL, Lindblad-Toh K, Gabriel S, Hart PS, Regev A, Nusbaum C, Kmoch S, Bleyer AJ, Lander ES, Daly MJ (2013). Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. ***Nature Genetics*** 45(3):299-303

37) **Guttman M**[†] and Rinn JL. (2012). Modular regulatory principles of large non-coding RNAs. ***Nature*** 482(7385):339-46 [†]*Corresponding author*

38) Garber M, Yosef N, Goren A, Raychowdhury R, Thielke A, **Guttman M**, Robinson J, Minie B, Chevrier N, Itzhaki Z, Blecher-Gonen R, Bornstein C, Amann-Zalcenstein D, Weiner A, Friedrich D, Meldrim J, Ram O, Cheng C, Gnirke A, Fisher S, Friedman N, Wong B, Bernstein BE, Nusbaum C, Hacohen N, Regev A, Amit I. (2012). A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. ***Molecular Cell*** 47(5):810-22

39) **Guttman M**[†]**,** Donaghey J, Carey BW, Garber M, Grenier J, Munson G, Young G, Lucas AB, Ach R, Bruhn L, Yang X, Amit I, Meissner A, Regev A, Rinn JL, Root DE, Lander ES. (2011). lincRNAs act in the circuitry controlling pluripotency and differentiation. ***Nature*** 477(7364):295-300 [†]*Corresponding author*

40) Lindblad-Toh K, Garber M, Or Zuk, Lin MF, Parker BJ, Washietl S, Kheradpour P, Ernst J, Jordan G, Mauceli E, Ward LD, Lowe CB, Holloway AK, Clamp M, Gnerre S, Alfoldi J, Beal K, Chang J, Clawson H, Cuff J, Di Palma F, Fitzgerald S, Flicek P, **Guttman M**, Hubisz MJ, Jaffe DB, Jungreis I, Kent WJ, Kostka D, Lara M, Martins AL, MassinghamT, Moltke I, Raney NJ, Rasmussen MD, Robinson J, Stark A, Vilella AJ, Wen J, Xie X, Zody MC, Worley KC, Kovar CL, Muzny DM, Gibbs RA, Warren WC, Mardis ER, Weinstock GM, Wilson RK, Birney E, Margulies EH, Herrero J, Green ED, Haussler D, Siepel A, Goldman N, Pollard KS, Pedersen JS, Lander ES, Kellis M. (2011). Evolutionary constraint in the human genome based on 29 eutherian mammals. ***Nature.*** doi: 10.1038/nature10530

41) Garber M, Grabherr MG**, Guttman M,** Trapnell C. (2011). Computational methods for transcriptome annotation and quantification using RNA-Seq. ***Nature Methods.*** 8(6):469-77

42) **Guttman M**[†], Garber M, Levin JZ, Donaghey J, Robinson J, Adiconis X, Fan L, Koziol MJ, Gnirke A, Nusbaum C, Rinn JL, Lander ES, Regev A. (2010) Ab initio reconstruction of transcriptomes of pluripotent and lineage committed cells reveals gene structures of thousands of lincRNAs. ***Nature Biotechnology*** 28(5):503-10 [†]*Corresponding author*

43) Huarte M, **Guttman M**, Feldser D, Garber M, Koziol M, Broz D, Khalil AM, Zuk O, Amit I, Rabani M, Attardi L, Regev A, Lander ES, Jacks T, Rinn JL. (2010). A large intergenic noncoding RNA induced by p53 mediates global gene repression in the p53 transcriptional response. ***Cell*** 142(3):409-19

44) Robinson JT, Thorvaldsdóttir H, Winckler W, **Guttman M**, Lander ES, Getz G, Mesirov JP. (2010). Integrative Genomics Viewer. ***Nature Biotechnology*** 29(1):24-6

45) Loewer S, Cabili MN, **Guttman M**, Loh YH, Thomas K, Park IH, Garber M, Curran M, Onder T, Agarwal S, Manos PD, Datta S, Lander ES, Schlaeger TM, Daley GQ, Rinn JL. (2010). Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. ***Nature Genetics*** 42(12):1113-7

46) **Guttman M**, Amit I, Garber M, French C, Lin M, Feldser D, Huarte M, Cabili M, Carey BW, Cassady J, Jaenisch R, Mikkelsen T, Jacks T, Hacohen N, Bernstein BEB, Kellis M, Regev A, Rinn JL, Lander ES. (2009) Chromatin structure reveals over a thousand highly conserved, large non-coding RNAs in mammals. ***Nature***. 458(7235):223-7

47) Khalil AM*, **Guttman M*,** Huarte M, Garber M, Raj A, Rivea Morales D, Thomas K, Presser A, Bernstein BE, van Oudenaarden A, Regev A, Lander ES, Rinn JL. (2009) Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. ***Proceedings of the National Academies of Science*** 106(28):11667-72 **equal contribution*

48) Amit I, Garber M, Chevrier N, Leite AP, Donner Y, Eisenhaure T, **Guttman M**, Grenier JK, Li W, Zuk O, Schubert LA, Birditt B, Shay T, Goren A, Zhang X, Smith Z, Deering R, McDonald RC, Cabili M, Bernstein BE, Rinn JL, Meissner A, Root DE, Hacohen N, Regev A. (2009) Unbiased reconstruction of a mammalian transcriptional network mediating pathogen responses. ***Science*** 326(5950):257-63

49) Ozsolak F, Goren A, Gymrek M, **Guttman M**, Regev A, Bernstein BE, Milos PM. (2010) Digital transcriptome profiling from attomole-level RNA samples. ***Genome Research*** 20(4):519-25

50) Garber M, **Guttman M**, Clamp M, Zody MC, Friedman N, Xie X. (2009). Identifying Novel Constrained Elements by Exploiting Biased Substitution Patterns. Conference on Intelligent Systems for Molecular Biology (ISMB) ***Bioinformatics*** 25(12):i54-62

51) **Guttman M**, Mies C, Dudycz-Sulicz K, Diskin SJ, Baldwin DA, Grant GR. (2007) Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. ***PLoS Genetics*** 3(8):e143

52) Nagi C, **Guttman M**, Jaffer S, Qiao R, Keren R, Triana A, Li M, Godbold J, Bleiweiss IJ, Hazan RB. (2005) N-cadherin expression in breast cancer: Correlation with an aggressive histologic variant-invasive micropapillary carcinoma. ***Breast Cancer Research and Treatment*** 94(3):225-35

53) Suyama K, Shapiro I, **Guttman M**, Hazan RB. (2002) A signaling pathway leading to metastasis is controlled by N-cadherin and the FGF receptor. ***Cancer Cell*** 2(4):301-14

## INVITED TALKS AND LECTURES

2020 **Noncoding RNAs: Mechanism, Function and Therapies**, Keystone Symposia
2020 **Systems Biology: Global Regulation of Gene Expression,** CSHL

2020 **Post-Transcriptional Gene Regulation,** Gordon Research Conference
2020 **The Nuclear Bodies Conference: Hubs of Genomic Activity,** FASEB
2020 **RNA at the bench and bedside**, Nature Conferences
2020 **New Approaches to Early Embryogenesis and Epigenetics** Symposium, Weizmann Institute of Science
2019 9th Annual California ALS Research Summit
2019 **Epigenetics/3D Genome**, Keystone Symposium
2019 **5th Annual Non-coding RNA Symposium**, Harvard Medical School
2019 EMBL Sapienza Seminar Series
2018 **Post-transcriptional gene regulation**, Gordon Research Conference
2018 **Chromatin Structure and Function**, Gordon Research Conference
2018 **Chromatin Architecture and Chromosome Organization/Gene Control in Development and Disease**, Keystone
2018 **CTSI Distinguished Speaker Seminar**, UCLA
2018 **Nuclear Organization & Function**, CSHL
2018 **Danny Thomas Lecture Series**, St. Jude
2018 Rett Translational Group Meeting
2018 **4DN-ASCB Satellite Symposium**: Bridging the 4D Genome with Cell Biology
2017 **Biophysical Society** 61st Annual Meeting
2017 **The Non-Coding Genome,** EMBO/EMBL Symposium
2017 **Seminar**, Boston Children's Hospital
2017 **Seminar**, Massachusetts General Hospital
2016 **Epigenomics**, NIH Common Fund
2016 **Seminar**, Biotech Research and Innovation Centre (BRIC) Copenhagen
2016 **X Chromosome Inactivation: A Tribute to Mary Lyon**, The Royal Society,UK
2016 **American Society for Cell Biology** (ASCB) Annual Meeting
2016 **RNA: Structure meets function**, EMBO
2016 **Chromatin Structure and Function**, Gordon Research Conference
2016 **Systems Biology of ncRNAs**, EMBO
2015 **The Non-coding Genome**, EMBL
2015 **RNA Localization and localized translation**, EMBO
2015 **miRNAs and non-coding RNAs in cancer**, Keystone Symposium
2015 **Epigenomics**, Keystone Symposium
2015 **Developmental Biology Seminar**, University of California Irvine
2015 **Stem Cell Institute Seminar,** University of Southern California
2015 **Biochemistry Seminar**, University of Colorado Boulder
2014 **How Biology reinvents how we understand disease**, Forbes Under 30 Summit
2014 **Oligonucleotide Therapeutics Society Annual Meeting**
2014 **Illuminating Genomic Dark Matter: ncRNA in disease and cancer**, MD Anderson Cancer Center
2014 **Genetics Seminar**, Baylor College of Medicine
2014 **Long Regulatory RNA**, EMBO/ESF
2014 **Post transcriptional gene regulation,** Gordon Research Conference
2014 **Developmental Biology Symposium**, UCSF
2014 **Big data across disciplines**, Kavli foundation
2014 **Bioinformatics Seminar**, UCLA

2013 **Genomics Seminar**, Boston University
2013 **Chromosome Architecture in human cancer**, National Cancer Institute
2013 **Bioinformatics Seminar**, UCSD
2013 **Seminar**, Salk Institute for Biomedical Research
2013 **Meet the Experts: lncRNAs**, AACR annual meeting
2013 **Seminar**, Novartis Institute for Biomedical Research
2013 **Seminar**, University of Massachusetts Medical School
2013 **Stem cells and chromatin,** EMBO

## PROFESSIONAL EXPERIENCE/SERVICE

**2010-present Scientific Reviewer**, *Science, Nature, Cell, Cell Reports, Cell Stem Cell, Molecular Cell, EMBO, Genome Research, Genome Biology, Nature Structural and Molecular Biology, Nature Biotechnology, Nature Methods, Proceedings of the National Academies of Science, RNA*

***2018-present*** **Scientific Consultant,** Flagship Pioneering

***2018*** **Member, Imaging to OMICs working group**, NIH common fund 4DN program

***2015-2016*** **Scientific Consultant,** Fulcrum Therapeutics, Third Rock Ventures

***2014-2018*** **Co-chair, RNA working group**, Global Alliance for Genomics and Health (GA4GH)

***2015-present*** **Member, Analysis working group**, NIH common fund 4DN program

***2015-present*** **Member, OMICs working group**, NIH common fund 4DN program

***2017*** **Member, Therapeutic Approaches to Genetic Diseases Study Section**, NIH

***2016*** **Co-chair, Post Transcriptional Gene Regulation**, ASCB Annual Meeting

***2016*** **Program Committee, Applied Bioinformatics**, ISMB

***2015*** **Scientific Reviewer, National Science Foundation**

***2014*** **Member, Expert Panel 4D Nucleome Common Fund Initiative**, National Institutes of Health

***2013*** **Member, Expert Panel on Chromosome Architecture in Human Cancer**, National Cancer Institute

***2013*** **Member, Special Emphasis Panel on RNA Biosensors**, National Cancer Institute

### ***Service to Caltech***

| | |
|---|---|
| ***2014-present*** | Member, Biochemistry Graduate Admission committee |
| ***2013-2016*** | Co-organizer, Biology graduate recruitment |
| ***2017-2018*** | Chair, Quantitative Biology faculty search committee |
| ***2016-present*** | Member, Provost's committee on High Performance Computing |
| ***2015-2016*** | Member, Bioinformatics faculty search committee |
| ***2014*** | Member, Bioengineering faculty search committee |
| ***2013-2015*** | Co-organizer, Caltech BBE retreat |

## PATENTS

1) “Methods for Identifying Macromolecular Interactions” PCT 15/466,861 (Filed: March 22, 2017)
2) “HDAC Inhibitors for reactivation of the X chromosome” PCT 62/413,928 (Filed: 10/27/2016)
3) “Reactivation of X chromosome genes” PCT/US16/29265 (Filed: 4/25/2016)
4) “Targeting and Synthesizing Long Non-Coding RNA Regulatory Interactions” US Provisional application (Filed: 4/24/2015)
5) “Mapping high-dimensional macromolecular interactions in cells”, US Provisional application (filed January 8, 2014)
6) "Methods for the Detection of DNA-RNA Proximity in Vivo", WO 2014/144476 (filed March 15, 2013, issued September 18, 2014).
7) "Selective Purification of RNA and RNA-Bound Molecular Complexes", US Provisional application 61/784,069 (filed March 14, 2013).
8) "Massively Multiplexed RNA-SEQ Method", US Provisional application 61/786,103 (filed March 14, 2013).
9) "Method and Compositions for Obtaining 5’-and 3’-RNA-End Nucleic Acids", US Provisional application 61/843,241 (filed July 5, 2013).

## GRANTS

NIH/Office of the Director 09/24/12 – 08/31/17
DP5 OD012190
*Deciphering the mechanism of large ncRNA mediated regulation of cell state*
The goal of this proposal is to decipher the mechanism of lincRNA mediated regulation by understanding how lincRNA-Protein complexes form, localize to regulatory targets, and give rise to phenotypic states.
Role: PI

NIH/Human Genome Research Institute 09/29/14 – 04/30/19
U54 HG007990
*UCSC Center of Excellence for Big Data Computing in the Biomedical Sciences*
The Caltech portion of this project is aimed at developing an integrated computational framework for RNA-Seq analysis and advanced programmer interfaces (API) for analyzing cancer datasets.
Role: Barbara J. Wold, PI; Mitchell Guttman, PI, David H. Haussler, PI (UCSC)

Searle Scholars Program 07/01/14 – 06/30/17
*Deciphering the role of lncRNAs as scaffolds that coordinate cellular regulation*
The goal of this proposal is to develop methods to define the macromolecular complex assembled by the Xist lncRNA and decipher its role in orchestrating X-chromosome inactivation.
Role: PI

Sidney Kimmel Foundation 07/01/14 – 06/30/16
*Uncovering principles of large non-coding RNA regulatory specificity in cancer*

The goal of this proposal is to identify the direct genomic DNA targets of the IncRNAs and determine how IncRNAs physically interact with target sites, as well as search and identify target sites in cancer.
Role: PI

The Sontag Foundation 10/01/14 – 09/30/18
*Uncovering principles of large non-coding RNA regulatory specificity in cancer*
The goal of this project is to determine the principles governing IncRNA localization to genomic target sites in cancer.
Role: PI

Rose Hills Foundation 06/01/14 – 05/31/17
*Genomics, Gene Regulation, Stem Cell Biology, Chromosome Organization*
The goal of this project is to understand how lncRNAs regulate gene expression in embryonic stem cells.
Role: PI

Pew Scholars Program 08/01/15 – 07/31/20
Pew Scholars Award in Biomedical Sciences
*Uncovering mechanisms of IncRNA-mediated regulation of gene expression*
The goals of this project are to dissect the mechanism of the Xist lncRNA in controlling gene expression during the establishment of X chromosome inactivation.
Role: PI

NIH 09/01/15 – 08/31/20
U01 HL130007
*Novel tools to comprehensively map dynamic organization of RNA and DNA in higher-order nuclear structures within single cells*
The goal of this project is to develop a novel integrative sequencing and microfluidic approach to enable comprehensive single molecule mapping of the 3-dimensional DNA targets of all RNA molecules within thousands of single nuclei.
Role: PI

NIH 09/01/15 – 08/31/20
U01 DA040612
*Deciphering the function and mechanisms of lncRNA-mediated organization of nuclear compartments*
The goal of this project is to develop biochemical methods to purify specific lncRNA-mediated nuclear compartments and define their genomic DNA, RNA, protein, and histone modification properties.
Role: PI.

Sloan Foundation 09/15/15 – 09/14/17
*Alfred P. Sloan Research Fellowship in Computational & Evolutionary Molecular Biology*

A career development award to support computational molecular biology research in the Guttman lab.
Role: PI

New York Stem Cell Foundation 01/01/16 – 12/31/20
*How long non-coding RNAs control pluripotency and lineage differentiation in embryonic stem cells*
The goal of this project is to understand how lncRNAs control cellular identity – including pluripotency and lineage differentiation – in embryonic stem cells.
Role: PI

HMRI 09/01/15 – 08/31/18
Heritage Medical Research Institute
Heritage Principal Investigators in the Heritage Medical Research Institute for the Advancement of Medicine and Science
Role: PI

Chan Zuckerberg Initiative 12/01/18 – 5/31/24
*Deciphering the Role of RNA Aggregation in Neurodegeneration*
In this proposal, we will make use of our expertise and innovative new tools for studying RNA biology, RNA-protein interactions, and RNA-mediated bodies in the nucleus to decipher the molecular components of these mutant RNA foci, determine how these RNA-protein aggregates assemble upon disease progression, and how they impact global mRNA processing within neurons.
Role: PI

Mallinckrodt Scholar Award 10/01/19 – 09/30/23
Edward Mallinckrodt, Jr Foundation
*Quantitative, combinatorial, and 3-dimensional spatial models of gene regulation*
This proposal represents a fundamental transition towards understanding 3D spatial organization of molecules in the nucleus, phase transition properties of molecules, the molecular principles guiding these process, and the functional impact of these principles on gene regulation.
Role: PI