EKTA KHURANA
CURRICULUM VITAE

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Professional Experience

Weill Medical College of Cornell University, New York, NY

Professor of Systems and Computational Biomedicine	2026 to Present
Associate Professor of Systems and Computational Biomedicine	2025 to 2026
Associate Professor of Computational Genomics	2021 to 2025
Assistant Professor of Computational Genomics	2014 to 2021

Leader, Cancer Genetics and Epigenetics Program	2025 to Present
Co-Leader, Cancer Genetics and Epigenetics Program	2021 to 2025

Co-Director, Tri-Institutional PhD Program in Computational Biology & Medicine	2023 to 2024
Associate Director, Tri-Institutional PhD Program in Computational Biology & Medicine	2019 to 2023

Affiliations:
Meyer Cancer Center
Englander Institute for Precision Medicine
Department of Systems and Computational Biomedicine

New York Genome Center, New York, NY 2018 to Present
Affiliate Member

Yale University, New Haven, CT 2012 to 2014
Associate Research Scientist
Program in Computational Biology and Bioinformatics
Molecular Biophysics and Biochemistry Department

Yale University, New Haven, CT 2008 to 2012
Postdoctoral Research Associate
Program in Computational Biology and Bioinformatics
Molecular Biophysics and Biochemistry Department
Advisor: Prof. Mark B. Gerstein

Education

University of Pennsylvania, Philadelphia, PA 2002 to 2008
Ph. D. in Chemistry (Research area: Computational Biology)
Advisor: Prof. Michael L. Klein
Thesis title: Computational Studies of Natural and Synthetic Ion Channels

Indian Institute of Technology, Delhi, India 2000 to 2002
Masters of Science (Research area: Computational Biology)
Advisor: Prof. B. Jayaram
Thesis title: Chemical Model for Genome Analysis

St. Stephen's College, Delhi University, Delhi, India 1997 to 2000
Bachelors of Science

Peer-reviewed Journal Publications (Citations: 57,888; h-index: 48)

(* co-first authors, #corresponding author)

1. Purohit TA, Gawdzik J, Armstrong EA, Yang B, Schultz Z, Bahr K, Do TJ, Machhi R, Sardeson S, Rizvi M, Nakada SA, Singh A, Esbona K, Huang W, Roskes ML, **Khurana E**, Lewis PW, Denu JM, Jarrard DF.
   "Genetic loss of CHD1 regulates distinct histone post-translational modifications in the development of castration-resistant prostate cancer." Neoplasia 73 (01289) (2026)

2. Wong EWP, Sahin M, Yang R, Lee U, Li D, Zhan YA, Misra R, Tomas F, Alomran N, Polyzos A, Lee CJ, Trieu T, Martinez-Fundichely A, Wiesner T, Rosowicz A, Cheng S, Liu C, Lallo M, Shoushtari AN, Merghoub T, Hamard PJ, Koche R, **Khurana E**, Apostolou E, Zheng D, Chen Y, Leslie CS, Chi P.
   "Disruption of TAD hierarchy promotes LTR co-option in cancer." Nature Genetics 57(7):1754-1765 (2025)

3. Shukla S, Li D, Cho WH, Schoeps DM, Nguyen HM, Conner JL, Roskes ML, Tehim A, Bayshtok G, Pachai MR, Yan J, Teri NA, Campeau E, Attwell S, Trojer P, Ostrovnaya I, Gopalan A, **Khurana E**, Corey E, Chi P, Chen Y.
   "BET inhibitors reduce tumor growth in preclinical models of gastrointestinal gene signature-positive castration-resistant prostate cancer." J Clin Invest e180378 (2025)

4. Yost KE, Zhao Y, Hung KL, Zhu K, Xu D, Corces R, Shams S, Louie B, Sundaram L, Granja J, Luebeck J, Choudhry H, **Khurana E**, Bafna V, Felau I, Staudt L, Zenklusen JC, Laird P, Curtis C, Cancer Genome Atlas Analysis Network, Greenleaf W, Chang HY.
   "Three-dimensional genome landscape of primary human cancers." Nature Genetics 57(5):1189-200 (2025)

5. Breves SL, Di Giammartino DC, Cirigliano S, Nicholson J, Mahmood R, Martinez-Fundichely A, Jungverdorben J, Singhania R, Rajkumar S, Studer L, **Khurana E**, Polyzos A, Fine H, Apostolou E.
   "Three-dimensional regulatory hubs support oncogenic programs in glioblastoma." Molecular Cell 85, 1–19 (2025)

6. Sundaram L, Kumar A, Zatzman M, Salcedo A, Ravindra N, Shams S, Louie BH, Bagdatli ST, Myers MA, Sarmashghi S, Choi HY, Choi WY, Yost KE, Zhao Y, Granja JM, Hinoue T, Hayes DN, Cherniack A, Felau I, Choudhry H, Zenklusen JC, Farh KK, McPherson A, Curtis C, Laird PW; Cancer Genome Atlas Analysis Network‡; Demchok JA, Yang L, Tarnuzzer R, Caesar-Johnson SJ, Wang Z, Doane AS, **Khurana E**, Castro MAA, Lazar AJ, Broom BM, Weinstein JN, Akbani R, Kumar SV, Raphael BJ, Wong CK, Stuart JM, Safavi R, Benz CC, Johnson BK, Kyi C, Shen H, Corces MR, Chang HY, Greenleaf WJ.
   "Single-cell chromatin accessibility reveals malignant regulatory programs in primary human cancers." Science 385 (6713) (2024)

7. Forbes AN*, Xu D*, Cohen S, Pancholi P, **Khurana E#**.
   "Discovery of novel therapeutic targets in cancer using patient-specific gene regulatory networks." Cell Systems 15 (9) (2024)

8. Xu D*, Forbes AN*, Cohen S, Palladino A, Karadimitriou T, **Khurana E#**.
   "Recapitulation of patient-specific 3D chromatin conformation using machine learning." Cell Reports Methods 100578 (2023)
   Featured with Perspective Article in Cell Reports Methods.

9. Li D, Zhan Y, Wang N, Tang F, Lee CJ, Bayshtok G, Moore AR, Wong EWP, Pachai MR, Xie Y, Sher J, Zhao JL, Khudoynazarova M, Gopalan A, Chan J, **Khurana E**, Shepherd P, Navone NM, Chi P, Chen Y.
   "ETV4 mediates dosage-dependent prostate tumor initiation and cooperates with p53 loss to generate prostate cancer." Science Advances 9(14) (2023)

10. Martinez-Fundichely A#, Dixon A, **Khurana E#**.
    "Modeling tissue-specific breakpoint proximity of structural variations from whole-genomes to identify cancer drivers." Nature Communications 13, 5640 (2022)

11. Tang F*, Xu D*, Wang S*, Wong CK*, Martinez-Fundichely A, Lee CJ, Cohen S, Park J, Hill CE, Eng K, Bareja R, Han T, Liu EM, Palladino A, Di W, Gao D, Abida W, Beg S, Puca L, Meneses M, Stanchina ED, Berger MF, Gopalan A, Dow LE, Mosquera JM, Beltran H, Sternberg CN, Chi P, Scher HI, Sboner A, Chen Y#, **Khurana E**#.
    "Chromatin profiles classify castration-resistant prostate cancers suggesting therapeutic targets." Science, 376(6596) (2022)
    Noted as one of the top six papers in prostate cancer research in 2022 by Prostate Cancer Foundation.

12. Yan J, Chen Y, Patel AJ, Warda S, Lee CJ, Nixon BG, Wong EW, Miranda-Román MA, Yang N, Wang Y, Pachai MR, Sher J, Giff E, Tang F, **Khurana E**, Singer S, Liu Y, Galbo PM Jr, Maag JL, Koche RP, Zheng D, Antonescu C, Deng L, Li M, Chen Y, Chi P.
    "Tumor-intrinsic PRC2 inactivation drives a context-dependent immune-desert microenvironment and is sensitized by immunogenic therapeutic viruses." J Clin Invest, e153437 (2022)

13. Aguiar-Pulido V, Wolujewicz P, Martinez-Fundichely A, Elhaik E, Thareja G, AbdelAleem A, Chalhoub N, Cuykendall T, Al-Zamer J, Lei Y, El-Bashir H, Musser J, Al-Kaabi A, Shaw G, **Khurana E**, Suhre K, Mason E, Elemento O, Finnell H, Ross E.
    "Systems biology analysis of human genomes points to key pathways conferring spina bifida risk." Proc Natl Acad Sci U S A, **118**(51), e2106844118 (2021)

14. Baggiolini A, Callahan S, Montal E, Weiss J, Trieu T, Tagore M, Tischfield S, Walsh R, Suresh S, Fan Y, Campbell N, Perlee S, Saurat N, Hunter M, Simon-Vermot T, Huang T, Ma Y, Hollmann T, Tickoo S, Taylor B, **Khurana E**, Koche R, Studer L, White R.
    "Developmental chromatin programs determine oncogenic competence in melanoma." Science, 373(6559) (2021)

15. Carrot-Zhang J, Yao X, Devarakonda S, Deshpande A, Damrauer JS, Silva TC, Wong CK, Choi HY, Felau I, Robertson AG, Castro MAA, Bao L, Rheinbay E, Liu EM, Trieu T, Haan D, Yau C, Hinoue T, Liu Y, Shapira O, Kumar K, Mungall KL, Zhang H, Lee JJ, Berger A, Gao GF, Zhitomirsky B, Liang WW, Zhou M, Moorthi S, Berger AH, Collisson EA, Zody MC, Ding L, Cherniack AD, Getz G, Elemento O, Benz CC, Stuart J, Zenklusen JC, Beroukhim R, Chang JC, Campbell JD, Hayes DN, Yang L, Laird PW, Weinstein JN, Kwiatkowski DJ, Tsao MS, Travis WD, **Khurana E**, Berman BP, Hoadley KA, Robine N; TCGA Research Network, Meyerson M, Govindan R, Imielinski M.
    "Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway." Cell Rep, 108707 (2021)

16. Liu EM, Martinez-Fundichely A, Bollapragada R, Spiewack M, **Khurana E**#.
    "CNCDatabase: a database of non-coding cancer drivers", Nucleic Acids Research, gkaa915, (2020)

17. Han T, Goswami S, Hu Y, Tang F, Zafra MP, Murphy C, Cao Z, Poirier JT, **Khurana E**, Elemento O, Hechtman JF, Ganesh K, Yaeger R, Dow LE.
    "Lineage reversion drives WNT independence in intestinal cancer." Cancer Discov, CD-19-1536 (2020)

18. Xu D, Gokcumen G, **Khurana E**#.
    "Loss-of-function tolerance of enhancers in the human genome", PLoS Genetics, 16(4), e1008663 (2020)

19. Trieu T, Martinez-Fundichely A, **Khurana E**#.
    "DeepMILO: a deep learning approach to predict the impact of non-coding sequence variants on 3D chromatin structure", Genome Biol, Mar 26;21(1):79 (2020)

20. Kumar S, Warrell J, Li S, McGillivray PD, Meyerson W, Salichos L, Harmanci A, Martinez-Fundichely A, Chan CWY, Nielsen MM, Lochovsky L, Zhang Y, Li X, Lou S, Pedersen JS, Herrmann C, Getz G, **Khurana E**, Gerstein MB.
    "Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences", Cell, Mar 5;180(5):915-927 (2020)

21. **PCAWG Transcriptome Core Group**, … **PCAWG Transcriptome Working Group**, Brazma A, Brooks AN, G.ke J, Ratsch G, Schwarz RF, Stegle O, Zhang Z; **PCAWG Consortium**.
“Genomic basis for RNA alterations in cancer”, Nature, Feb;578(7793):129-136 (2020)

22. Rheinbay E, … **Khurana E**, Campbell PJ, Lopez-Bigas N; PCAWG Drivers and Functional Interpretation Working Group; PCAWG Structural Variation Working Group, Weischenfeldt J, Beroukhim R, Martincorena I, Pedersen JS, Getz G; PCAWG Consortium.
“Analyses of non-coding somatic drivers in 2,658 cancer whole genomes”, Nature, Feb;578(7793):102-111 (2020)

23. Li Y, Roberts ND, Wala JA, Shapira O, Schumacher SE, Kumar K, **Khurana E**, Waszak S, Korbel JO, Haber JE, Imielinski M; PCAWG Structural Variation Working Group, Weischenfeldt J, Beroukhim R, Campbell PJ; PCAWG Consortium.
“Patterns of somatic structural variation in human cancer genomes”, Nature, Feb;578(7793):112-121 (2020)

24. Reyna MA, Haan D, Paczkowska M, Verbeke LPC, Vazquez M, Kahraman A, Pulido-Tamayo S, Barenboim J, Wadi L, Dhingra P, Shrestha R, Getz G, Lawrence MS, Pedersen JS, Rubin MA, Wheeler DA, Brunak S, Izarzugaza JMG, **Khurana E**, Marchal K, von Mering C, Sahinalp SC, Valencia A; PCAWG Drivers and Functional Interpretation Working Group, Reimand J, Stuart JM, Raphael BJ; PCAWG Consortium.
“Pathway and network analysis of more than 2500 whole cancer genomes”, Nat Commun, Feb 5;11(1):729 (2020)

25. Zhang Y, …Brazma A; **PCAWG Transcriptome Working Group**; **PCAWG Structural Variation Working Group**; **PCAWG Consortium**.
“High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations”, Nat Commun, Feb 5;11(1):736 (2020)

26. **ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium**.
“Pan-cancer analysis of whole genomes”, Nature, Feb;578(7793):82-93 (2020)
I led one of the working groups, the PCAWG Reference Annotations Working Group, in this large consortium study.

27. EM Liu, A Fundichely, BJ Diaz, B Aronson, T Cuykendall, M MacKay, P Dhingra, E Wong, P Chi, E Apostolou, NE Sanjana, **E Khurana**[#],
“Identification of cancer drivers at CTCF insulators in 1,962 whole-genomes”, Cell Systems, 8, 446 (2019)

28. D Backenroth, Z He, K Kiryluk, V Boeva, L Pethukova, **E Khurana**, A Christiano, J Buxbaum, I Ionita-Laza,
“FUN-LDA: A latent Dirichlet allocation model for predicting tissue-specific functional effects of noncoding variation”, American Journal of Human Genetics, 102, 920 (2018)

29. M Bailey ….. **E Khurana** ….. The Cancer Genome Atlas Research Network…..L Ding,
“Comprehensive Characterization of Cancer Driver Genes and Mutations”, Cell, 173, 371 (2018)

30. J Kim, FC Geyer, LG Martelotto, CKY Ng, RS Lim, P Selenica, A Li, F Pareja, N Fusco, M Edelweiss, R Kumar, R Gularte-Merida, AN Forbes, **E Khurana**, O Mariani, S Badve, A Vincent-Salomon, L Norton, JS Reis-Filho, B Weigelt,
“MYBL1 rearrangements and MYB amplification in breast adenoid cystic carcinomas lacking the MYB-NFIB fusion gene”, The Journal of Pathology, 244, 143 (2018)

31. P Dhingra, A Fundichely, A Berger, F Huang, A Forbes, EM Liu, D Liu, A Sboner, P Tamayo, D Rickman[#], M Rubin, **E Khurana**[#],
“Identification of novel prostate cancer drivers using RegNetDriver: A framework for integration of genetic and epigenetic alterations with tissue-specific regulatory network”, Genome Biology, 18, 141 (2017)
Selected for ‘Top 10 Papers Reading List’ in Regulatory & Systems Genomics by RECOMB/ISCB

32. A Romanel, S Garritano, B Stringa, M Blattner, D Dalfovo, D Chakravarty, D Soong, K Cotter, G Petris, P Dhingra, P Gasperini, A Cereseto, O Elemento, A Sboner, **E Khurana**, A Inga, M Rubin, F Demichelis,

"Inherited determinants of early recurrent somatic mutations in prostate cancer", Nature Communications, 8, 48 (2017)

33. M Feigin, T Garvin, P Bailey, N Waddell, D Chang, D Kelley, S Shuai, S Gallinger, J McPherson, S Grimmond, **E Khurana**, L Stein, A Biankin, M Schatz, D Tuveson,
"Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma", Nature Genetics, 49, 825 (2017)

34. T Cuykendall, M Rubin, **E Khurana**#,
"Non-coding genetic variation in cancer", Current Opinion in Systems Biology, 1, 9 (2017)

35. P Dhingra, Y Fu, M Gerstein#, **E Khurana**#,
"Using FunSeq2 for coding and noncoding variant annotation and prioritization", Current Protocols in Bioinformatics, 57, 15.11.1 (2017)

36. **E Khurana**#,
"Cancer Genomics: Hard-to-reach repairs", Nature, 532, 181 (2016)
Invited News & Views article

37. **E Khurana**#, Y Fu, D Chakravarty, F Demichelis, M Rubin#, M Gerstein#,
"Role of non-coding sequence variants in cancer", Nature Reviews Genetics, 17, 93 (2016)

38. The **Cancer Genome Atlas Research Network**
"The molecular taxonomy of primary prostate cancer", Cell, 163(4), 1011 (2015)

39. The **1000 Genomes Project Consortium**
"A global reference for human genetic variation", Nature, 526, 68 (2015)

40. L Lochovsky, J Zhang, Y Fu, **E Khurana**, M Gerstein,
"LARVA: An integrative framework for large-scale analysis of recurrent variants in noncoding annotations", Nucleic Acids Research, 43(17), 8123 (2015)

41. Y Fu, Z Liu, S Lu, J Bedford, X Mu, K Yip, **E Khurana**#, Gerstein M#,
"FunSeq2: A framework for prioritizing noncoding regulatory variants in cancer", Genome Biology 15, 480 (2014) (co-senior author).

42. K Talbert-Slagle, KE Atkins, KK Yan, **E Khurana**, M Gerstein, EH Bradley, D Berg, AP Galvani, J Townsend,
"Cellular Superspreaders: An Epidemiological Perspective on HIV Infection inside the Body", PLoS Pathogens 10, e1004092 (2014)

43. **E Khurana***, Y Fu*, V Colonna*, X Mu*, HM Kang, …..1000 Genomes Project Consortium….. M Rubin, C Tyler-Smith, M Gerstein,
"Integrative annotation of variants from 1092 humans: application to cancer genomics", Science, 342, 84 (2013)
Research Highlight in Nature, 502, 144 (2013) and Nature Genetics, 45, 1273 (2013)

44. **E Khurana***, Y Fu*, J Chen, M Gerstein,
"Interpretation of genomic variants using a unified biological network approach", PLoS Computational Biology, 9, e1002886 (2013)

45. **E Khurana**#,
"Learning to swim in a sea of genomic data", Genome Biology, 14, 315 (2013)
Invited report on the American Society of Human Genetics meeting, 2013

46. The **1000 Genomes Project Consortium**
"An integrated map of genetic variation from 1,092 human genomes", Nature, 491, 56 (2012)

47. The **ENCODE Project Consortium**
    “An integrated encyclopedia of DNA elements in the human genome”, Nature, 489, 57 (2012)

48. L Habegger, S Balasubramanian, D Chen, **E Khurana**, A Sboner, A Harmanci, J Rozowsky, D Clarke, M Snyder, M Gerstein,
    “VAT: A computational framework to functionally annotate variants in personal genomes within a cloud-computing environment”, Bioinformatics, 28, 2269 (2012)

49. M Gerstein*, A Kundaje*, M Hariharan*, S Landt*, K Yan*, C Cheng*, X Mu*, **E Khurana***, J Rozowsky*, R Alexander*, R Min*, P Alves*, A Abyzov, N Addleman, N Bhardwaj…40 authors…M Snyder,
    “Architecture of the human regulatory network derived from ENCODE data”, Nature, 489, 91 (2012)

50. D MacArthur…...**E Khurana**…..M Gerstein, C Tyler-Smith,
    “A systematic survey of loss-of-function variants in human protein-coding genes”, Science, 335, 823 (2012)

51. The **ENCODE Project Consortium**
    “A User’s Guide to the Encyclopedia of DNA elements”, PLoS Biology, 9, e1001046 (2011)

52. R Mills…..**E Khurana**….. J Korbel, 1000 Genomes Project,
    “Mapping copy number variation by population-scale genome sequencing”, Nature, 470, 59 (2011)

53. Z Lu, K Yip, G Wang, C Shou, L Hillier, **E Khurana**, A Agarwal, R Auerbach, J Rozowsky, C Cheng, M Kato, D Miller, F Slack, M Snyder, R Waterston, V Reinke, M Gerstein,
    “Prediction and characterization of non-coding RNAs in C. elegans by integrating conservation, secondary structure and high throughput sequencing and array data”, Genome Research, 21, 276 (2011)

54. **E Khurana[#],** R DeVane, MD Peraro, ML Klein[#],
    “Computational study of drug binding to the membrane-bound tetrameric M2 peptide bundle from influenza A virus”, Biochimica et Biophysica Acta- Biomembranes, 1808, 530 (2011)

55. M Gerstein….. **E Khurana**….. modENCODE Consortium… R Waterston,
    “Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project”, Science, 330, 1775 (2010)

56. The **1000 Genomes Project Consortium**,
    “A map of human genome variation from population scale sequencing”, Nature, 467, 1061 (2010)

57. **E Khurana,** H Lam, C Cheng, N Carriero, P Cayting, M Gerstein,
    “Segmental duplications in the human genome reveal details of pseudogene formation”, Nucleic Acids Research, 38, 6997 (2010)

58. M Holford, **E Khurana**, K Cheung, M Gerstein,
    “Using semantic web rules to reason on an ontology of pseudogenes”, Bioinformatics, 26, i71 (2010)

59. Y Arinaminpathy*, **E Khurana**[*,#], D Engelman, M Gerstein[#],
    “Computational analysis of membrane proteins: the largest class of drug targets”, Drug Discovery Today, 14, 1130 (2009)

60. Y Liu, D Zheng, S Balasubramanian, N Carriero, **E Khurana**, R Robilotto, M Gerstein,
    “Comprehensive analysis of the pseudogenes of glycolytic enzymes in vertebrates: the anomalously high number of GAPDH pseudogenes highlight a recent burst of retrotranspositional activity”, BMC Genomics, 10, 480 (2009)

61. H Lam, **E Khurana**, G Fang, P Cayting, N Carriero, K Cheung, M Gerstein,
    “Pseudofam: the pseudogene families database”, Nucleic Acids Research, 37, D738 (2009)

62. K Talbert-Slagle, S Marlatt, F Barrera, **E Khurana**, J Oates, M Gerstein, D Engelman, A Dixon, D Dimaio, "Artificial transmembrane oncoproteins smaller than the bovine papillomavirus E5 protein redefine sequence requirements for activation of the platelet derived growth factor β receptor", Journal of Virology, 83, 9773 (2009)

63. **E Khurana**[#], MD Peraro[#], R DeVane, S Vemparala, WF DeGrado[#], ML Klein, "Molecular dynamics calculations suggest a conduction mechanism for the M2 proton channel from influenza A virus", Proceedings of the National Academy of Sciences USA, 106, 1069 (2009)

64. **E Khurana**[#], R DeVane, A Kohlmeyer, ML Klein, "Probing peptide nanotube self-assembly at a liquid-liquid interface with coarse-grained molecular dynamics", Nano Letters, 8, 3626 (2008)

65. **E Khurana**[#], S Nielsen, B Ensing, ML Klein, "Self-assembling cyclic peptides: molecular dynamics studies of dimers in polar and nonpolar solvents", Journal of Physical Chemistry B, 110, 18965 (2006)

66. **E Khurana**[#], S Nielsen, ML Klein, "Gemini surfactants at the air/water interface: a fully atomistic molecular dynamics study", Journal of Physical Chemistry B, 110, 22136 (2006)

67. S Dutta, P Singhal, P Agrawal, R Tomer, Kritee, **E Khurana**, B Jayaram, "A physicochemical model for analyzing DNA sequences", Journal of Chemical Information and Modeling, 46, 78 (2006)

Honors and Awards

1. Prostate Cancer Foundation Challenge Award (2026)
2. Presidential Early Career Award for Scientists and Engineers, PECASE, awarded by the White House (President Joe Biden) (2024)
3. Finalist for Johnson & Johnson Women in STEM Award (37 finalists across 6 disciplines out of >500 applications) (2023)
4. WorldQuant Foundation Research Scholar (2021 to 2026)
5. Irma T. Hirschl Career Scientist Award (2019 to 2024)
6. Invited Faculty Member of F1000 'Bioinformatics, Biomedical Informatics & Computational Biology: Systems & Network Biology' section (2019 to Present)
7. Invited Keynote Speaker at High Throughput Sequencing Algorithms track at the ISMB 'Intelligent Systems for Molecular Biology' conference (2018)
8. Chosen for 'Emerging Leaders in Systems-Level Biology symposium' at Cincinnati Children's Hospital Medical Center (2014)
9. Featured as 'Promising Young Investigator in Genomics' by GenomeWeb (2013)
10. Chair's fund for Gordon Conference on Computer Aided Drug Design (2007)
11. Marie Curie fellowship awarded by International School of Solid State Physics to attend the course 'Computer Simulations in Condensed Matter' at Erice, Italy (2005)
12. Science Meritorious Award awarded by Delhi University for academic excellence (1997-1998)

Invited Conference/Symposia/Workshop/Roundtable Lectures

1. Coffey-Holden Prostate Cancer Academy Meeting (2026)
2. Society for Basic Urological Research Meeting at the American Urological Association Annual Meeting in Washington, DC (2026)
3. Cancer Epigenetics Symposium, Institut Curie & Gustave Roussy Cancer Center, Paris, France (2025)
4. Annual Genitourinary Retreat, Memorial Sloan Kettering Cancer Center (2024)
5. Coffey-Holden Prostate Cancer Academy Meeting (2024)
6. Keynote Speaker & Oncology Thought Leader at the DAVA Oncology Global Summit on Genitourinary Malignancies (2023)

7. Prostate Cancer Foundation Annual Retreat (2023)
8. The Biology of Genomes (Invited session-co-chair), Cold Spring Harbor Laboratory, NY (2023)
9. Symposium on 'Stromal and epithelial plasticity in cancer progression and therapy resistance' at Weill Cornell Medicine (2023)
10. Meyer Cancer Center Director's Seminar Series (2022)
11. Roundtable by CIFAR (Canadian Institute for Advanced Research) on 'Cancer and the Dark Genome' (2021, 2022)
12. Artificial Intelligence in Genomics workshop, New York Genome Center (2021)
13. STEM Panel on Faculty Job Search, University of Pennsylvania, Philadelphia, PA, USA (2021)
14. Cancer Genomics Research Network Meetings, New York Genome Center, New York, NY, USA (2021)
15. Probabilistic Modeling in Genomics (Invited session-co-chair), Cold Spring Harbor Laboratory, NY (2021)
16. American Association for Cancer Research Annual Meeting: Invited talk in the session '3D Cancer Genome' (2020)
17. Genomic Basis of Cancer Symposium, University of Helsinki, Finland (2020)
18. The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods, Banff International Research Station, Banff, Canada (2019)
19. Keynote Speaker at HiTSeq18 (High Throughput Sequencing Algorithms track of the ISMB meeting), Chicago, Illinois, USA (2018)
20. Advanced Sequencing Technologies & Applications, Cold Spring Harbor Laboratory, NY (2018)
21. Gordon Research Conference on Human Genetic Variation and Disease, Maine, USA (2018)
22. Systems Genetics of Cancer, The Francis Crick Institute, London, UK (2017)
23. Cancer Genomics Research Network Meetings, New York Genome Center, New York, NY, USA (2017)
24. NGS Tech & Applications Congress, Philadelphia, PA, USA (2017)
25. Systems Genetics of Cancer, Cambridge, UK (2016)
26. Workshop on Models for Oncogenesis, Clonality and Tumor Progression, Mathematical Biosciences Institute, Ohio State University, Columbus, OH (2016)
27. ENCODE User's Meeting, Stanford University, Palo Alto, CA (2016)
28. Early Career Investigators Meeting on Quantitative Problems in Human Health and Genetics, Banff International Research Station, Banff, Canada (2016)
29. Human Genome Variation Society Meeting, Vancouver, Canada (2016)
30. Talk: "Integrating large-scale genomics data to understand the role of non-protein-coding regions in cancer" & Panel discussion on "Unleashing the potential of next generation sequencing data for therapeutic development", Festival of Genomics, San Francisco, CA (2015)
31. Next Generation Sequencing Congress, Harvard Medical School, Boston, MA (2015)
32. Pint of Science festival, New York, NY (2015)
33. American Association for Cancer Research Annual Meeting, San Diego, CA (2014)
34. Emerging Leaders in Systems-Level Biology Symposium, Cincinnati Children's Hospital Medical Center, Ohio (2014)

Invited Institute/University Talks

1. Cornell University, Ithaca (2026)
2. University of Toronto, Toronto, Canada (2025)
3. MacMillan Center for the Study of the Non-coding Cancer Genome, New York Genome Center (2025)
4. Affiliate Member Lecture Series, New York Genome Center (2025)
5. Dana Farber Cancer Institute, Boston, MA (2024)
6. Johns Hopkins School of Medicine, Baltimore, MD (2024)
7. University of California San Francisco (2023)
8. Northwestern University, Chicago, IL, USA (2023)
9. MD Anderson Cancer Center, Houston, Texas, USA (2023, 2018)
10. Icahn School of Medicine at Mount Sinai, New York, NY, USA (2022, 2016)
11. Jackson Laboratory for Genomic Medicine, Farmington, CT, USA (2022, 2013)
12. Yale University, New Haven, CT, USA (2022)
13. University of California, San Diego, CA, USA (2021)
14. Duke University (2021)
15. New York Genome Center (2019)
16. Cornell University, Ithaca (2018)

17. IBM Thomas J. Watson Research Center, Yorktown Heights, NY, USA (2018)
18. Aarhus University, Aarhus, Denmark (2017)
19. Columbia University, New York, NY, USA (2017)
20. Rutgers University, Camden, NJ, USA (2017)
21. Five Points Lecture, New York Genome Center, New York, NY, USA (2015)
22. University of Massachusetts Medical School, Worcester, MA, USA (2015)
23. Wellcome Trust Sanger Institute, Cambridge, UK (2014)
24. London Research Institute, London, UK (2014)
25. Memorial Sloan Kettering Cancer Center, New York, USA (2014)
26. Institute for Systems Genetics, New York University, New York, USA (2014)
27. Cornell University, Ithaca, USA (2014)
28. University of Toronto, Toronto, Canada (2014)
29. University of Montreal, Montreal, Canada (2014)
30. Cincinnati Children's Hospital Medical Center, Cincinnati, USA (2014)
31. Weill Cornell Medical College, New York, USA (2013)
32. University of Calgary, Calgary, Canada (2013)
33. McGill University and Genome Quebec Innovation Center, Montreal, Canada, (2012)
34. Ste Justine University Hospital Research Center, University of Montreal, Montreal, Canada (2011)
35. National Center for Biological Sciences, Bangalore, India (2009)
36. Yale Center for Genomics and Proteomics, New Haven, CT, USA (2009)
37. Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India (2007)

Other Professional Contributions

Editorial Board

Science Advances (2023 to 2024)
Current Protocols in Bioinformatics (2016 to 2018)

Invited referee

Nature, Science, Cell, Nature Genetics, Nature Methods, Nature Communications, Cancer Cell, Cell Systems, Cancer Research, Genome Biology, Genome Medicine, PLoS Genetics, PLoS Computational Biology, eLife, Bioinformatics, Nucleic Acids Research, Scientific Reports, Modern Pathology, Molecular Cancer Research, BMC Systems Biology, BMC Genomics, BMC Cancer, Oncotarget, Biophysical Journal, Journal of Physical Chemistry, Soft Matter, Proteins

Grant Reviewer

NIH Cancer Genetics Study Section (Standing member 2025 to 2029)
Prostate Cancer Foundation (2023, 2026)
NIH Fellowship Review Panel (2025)
Department of Defense Lung Cancer Research Program (2024)
NIH Genomic, Computation & Technology Study Section (2019, 2022, 2024)
NIH Cancer Genetics Study Section (2020, 2024)
European Research Council (2023)
NIH K99 Mosaic (2023)
Genome Canada (2022)
NIH Special Emphasis Panel for 'Genes, Genomes and Genetics' (2021)
Wellcome Trust UK and Department of Biotechnology India (2020)
NSF BIO Advisory Panel (2016, 2017, 2021)
Prostate Cancer UK (2019)
The Royal Society and Wellcome Trust UK (2018)
European Research Council, Medical Research Council UK, Worldwide Cancer Research (2016)

Program Committee Member

Intelligent Systems for Molecular Biology, ISMB Annual Meeting (2022, 2023, 2024, 2025, 2026)
American Association for Cancer Research, AACR Annual Meeting (Bioinformatics, Convergence Science, and System Biology Subcommittee) (2021)

RECOMB-Seq/CCB (Workshops on Massively Parallel Sequencing and Computational Cancer Biology) (2015, 2017, 2018, 2019)
GLBIO/CCBC (Great Lakes Bioinformatics Conference/Canadian Computational Biology Conference) (2016)

Conference Abstract Reviewer/Session Chair
The Biology of Genomes, Cold Spring Harbor Laboratory, NY (2023)
Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory, NY (2021)
American Society of Human Genetics Meeting (2016, 2017, 2018)

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