

Jesse R. Dixon
Salk Institute for Biological Studies
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EDUCATION

2015	M.D. School of Medicine	University of California, San Diego
2013	Ph.D. Biomedical Sciences Thesis advisor: Dr. Bing Ren	University of California, San Diego
2006	A.B. Molecular Biology	Princeton University

PROFESSIONAL APPOINTMENTS

2025-present	Associate Professor, Salk Institute for Biological Studies
2020-2025	Assistant Professor, Salk Institute for Biological Studies
2015-2020	Faculty Fellow, Salk Helmsley Fellows Program, Salk Institute for Biological Studies
2007-2015	Medical Scientist Training Program (MSTP), UC San Diego, Laboratory of Dr. Bing Ren
2006-2007	Research Technician, University of Michigan, Laboratory of Dr. Sean Morrison

SELECT HONORS, AWARDS, and FELLOWSHIPS

2024	Pew Biomedical Scholar Award
2023	Rita Allen Scholar Award
2022-2023	Clarivate Highly Cited Researchers
2016-2021	NIH Early Independence Award (DP5)
2014	UC San Diego Chancellor's Dissertation Medal for Biological Sciences
2013	UC San Diego Department of Biomedical Sciences Outstanding Dissertation Award
2012	James Kerr Award for the best paper of the year, Ludwig Institute for Cancer Research
2010-2012	California Institute for Regenerative Medicine Pre-Doctoral Fellowship
2006	Collegiate Golf All-American Scholar Award

CURRENT SUPPORT

2023-2028	Rita Allen Foundation Scholar Award (PI)
2024-2028	Pew Biomedical Scholar Award (PI)

COMPLETED SUPPORT

2020-2025	National Institutes of Health NCI U01 CA260700 (PI)
2019-2023	National Institutes of Health NHGRI R01 HG010634 (co-PI)
2016-2021	NIH Early Independence Award (DP5)
2018-2020	National Institutes of Health NHGRI R44 HG008118 (co-PI)
2018	Salk Innovation Grant (PI)
2018	Salk Cancer Center Pilot Grant (co-PI)
2017	Padres Pedal the Cause Cancer Research Award (co-PI)

PUBLICATIONS

1. Popay TM, Pant A, Munting F, Tastemel M, Black ME, Haghani N, Dixon JR. Genome-wide in vivo dynamics of cohesin-mediated loop extrusion and its role in transcription activation. *Nature Genetics* (accepted). First published as a bioRxiv preprint, doi: 10.1101/2024.10.02.616323
2. Ashkin EL, Tang YJ, Xu H, Hung KL, Belk J, Cai H, Lopez SS, Docen DN, Hebert JD, Li R, Ruiz PA, Keal T, Andrejka L, Chang HY, Petrov DA, **Dixon JR**, Xu Z, Winslow MM. A STAG2-PAXIP1/PAGR1 axis suppresses lung tumorigenesis. *The Journal of Experimental Medicine* 2024; 222 (1), e20240765
3. Heffel MG, Zhou J, Zhang Y, Lee DS, Hou K, Alonso OP, Abuhanna K, Galasso J, Kern C, Tai CY, Carcia-Padilla C, Nafisi M, Zhou Y, Schmitt AD, Li T, Haeussler M, Wick B, Zhang MJ, Xie F, Ziffra RS, Mukamel EA, Eskin E, Nowakowski TJ, **Dixon JR**, Pasaniuc B, Ecker JR, Zhu Q, Bintu B, Paredes MF#, Luo C#. Temporally distinct 3D multi-omic dynamics in the developing human brain. *Nature* 2024; 635, 481-489. First published as a *bioRxiv* preprint, doi: 10.1101/2022.10.07.511350

4. Liu H, Zeng Q, Zhou J, Bartlett A, Wang BA, Berube P, Tian W, Kenworth M, Althul J, Nery JR, Chen H, Castanon RG, Zu S, Li YE, Lucero J, Osteen JK, Pinto-Duarte A, Lee J, Rink J, Cho S, Emerson N, Nunn M, O'Connor C, Wu Z, Stoica I, Yao Z, Smith KA, Tasic B, Luo C, **Dixon JR**, Zeng H, Ren B, Behrens MM, Ecker JR. Single-cell DNA methylome and 3D multi-omic atlas of the adult mouse brain. *Nature* 2023; 624, 366-377. First published as a *bioRxiv* preprint, doi: 10.1101/2023.04.16.536509
5. Chapman, OS, Luebeck J, Sridhar S, Wong ITL, Dixit D, Wang S, Prasad G, Rajkumar U, Pagadala MS, Larson JD, He BJ, Hung KL, Lange JT, Dehkordi SR, Chandran , Adam M, Morgan L, Wani S, Tiwari A, Guccione C, Lin Y, Dutta A, Lo YY, Juarez E, Robinson JT, Korshunov A, Michaels JEA, Cho YJ, Malicki DM, Coufal NG, Levy ML, Hobbs C, Scheuermann RH, Crawford JR, Pomeroy SL, Rich JN, Zhang X, Chang HY, **Dixon JR**, Bagchi A, Deshpande AJ, Carter H, Fraenkel E, Mischel PS, Weschler-Reya RJ, Bafna V, Mesirov JP, Chaves L. Circular extrachromosomal DNA promotes tumor heterogeneity in high-risk medulloblastoma. *Nature Genetics* 2023; 55, 2189-2199. First published as a *bioRxiv* preprint, doi 10.1101/2021.10.18.464907
6. Liu Z*, Lee DS*, Liang Y, Zheng Y#, **Dixon JR#**. Foxp3 Orchestrates Reorganization of Chromatin Architecture to Establish T Cell Identity. *Nature Communications* 2023; 14 (6943). First published as a *bioRxiv* preprint, doi: 10.1101/2023.02.22.529589
7. Okonechnikov K, Camgoz A, Chapman O, Wani S, Park DE, Hubner JM, Chakraborty A, Pagadala M, Bump R, Chandran S, Kraft K, Acuna-Hidalgo R, Reid D, Sikkink K, Mauuermann M, Juarez EF, Jenseit A, Robinson JT, Pajtlar KW, Milde T, Jager N, Fiesel P, Morgan L, Sridhar S, Coufal NG, Levy M, Malicki D, Hobbs C, Kingsmore S, Nahas S, Snuderl M, Crawford J, Wechsler-Reya RJ, Davidson TBB, Cotter J, Michael G, Fleischhack G, Mundlos S, Schmitt A, Carter H, Michaelraj KA, Kumar SA, Taylor MD, Rich J, Buchholz F, Mesirov JP, Pfister SM, Ay F, **Dixon JR**, Kool M, Chavez L. 3D genome mapping identified subgroup-specific chromosome conformations and tumor-dependency genes in ependymoma. *Nature Communications* 2023; 14, 2300
8. Shah R, Gallardo CM, Jun YH, Clock B, **Dixon JR**, McFadden WM, Majumder K, Pintel DJ, Corces VG, Torbett BE, Tedbury PR, Sarafianos SG. Activation of HIV-1 provirus increases downstream chromatin accessibility. *iScience* 2022; 25 (12) 105490
9. Xu Z*, Lee DS*, Chandran S, Le VT, Bump R, Yasis J, Dallarda S, Marcotte S, Clock B, Haghani N, Cho CY, Akdemir K, Tyndale S, Futreal PA, McVicker G, Wahl GM, **Dixon JR#**. Structural variants drive context dependent oncogene activation in cancer. *Nature* 2022; 612, 564-572.
10. Popay TM, **Dixon JR#**. Coming full circle: on the origin and evolution of the looping model for enhancer-promoter communication. *Journal of Biological Chemistry* 2022; 298 (8) 102117
11. Luo C, Liu H, Xie F, Armand EJ, Siletti K, Bakken TE, Fang R, Doyle WI, Stuart T, Hodge RD, Hu L, Wang BA, Zhang Z, Preissl S, Lee DS, Zhou J, Niu SY, Castanon R, Bartlett A, Rivkin A, Wang X, Lucero J, Nery JR, Davis DA, Mash DC, Satija R, **Dixon JR**, Linnarsson S, Lein E, Behrens MM, Ren B, Mukamel EA, Ecker JR. Single nucleus multi-omics identifies human cortical regulatory genome diversity. *Cell Genomics* 2022; 2 (3) 100-110.
12. Song F, Xu J, Dixon JR, Yue F. Analysis of Hi-C Data for Discovery of Structural Variations in Cancer. *Methods in Molecular Biology* 2022; 2301:131-161.
13. Liu H, Zhou J, Tian W, Luo C, Bartlett A, Aldridge A, Lucero J, Osteen JK, Nery JR, Chen H, Rivkin A, Castanon RG, Clock B, Li YE, Hou X, Poirion OB, Preissl S, O'Connor C, Boggeman L, Fitzpatrick C, Nunn M, Mukamel EA, Zhang Z, Callaway EM, Ren B, **Dixon JR**, Behrens M, Ecker JR. DNA Methylation Atlas of the Mouse Brain at Single-Cell Resolution. *Nature* 2021; 598:120-128. First published as a *bioRxiv* preprint doi: 10.1101/2020.04.30.069377
14. Reid DA, Reed PJ, Schlachetzki JCM, Nitulescu II, Chou G, Tsui EC, Jones JR, Chandran S, Lu AT, McClain CA, Ooi JH, Wang TW, Lana AJ, Linker SB, Ricciardulli AS, Lau S, Schafer ST, Horvath S, **Dixon JR**, Hah N, Glass CK, Gage FH. Incorporation of a nucleoside analog maps genome repairs sites in postmitotic human neurons. *Science* 2021; 372 (6537) 91-94. First published as a *bioRxiv* preprint as doi: 10.1101/2020.03.25.008490
15. Kubo N, Ishii H, Xiong X, Bianco S, Meitinger F, Hu R, Hocker JD, Conte M, Gorkin D, Yu M, Li B, **Dixon JR**, Hu M, Nicodemi M, Zhao H, Ren B. Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. *Nature Structural & Molecular Biology* 2021; 28:152-161. First published as a *bioRxiv* preprint as doi: 10.1101/118737.
16. Akdemir KC, Le VT, Kim JM, Killcoyne S, King DA, Lin YP, Tian Y, Inoue A, Amin S, Robinson FS, Nimmakayalu M, Herrera RE, Lynn EJ, Chan K, Seth S, Klimczak LJ, Gerstung M, Gordenin DA, O'Brien J, Li L, Deribe YL, Verhaak RG, Campbell PJ, Fitzgerald R, Morrison AJ, **Dixon JR#**, Futreal PA#. Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. *Nature Genetics* 2020; 52 :178-1188. First published as a *bioRxiv* preprint as doi: 10.1101/426080
17. Kang H, Shokhirev MN, Xu Z, Chandran S, **Dixon JR**, Hetzer MW. Dynamic regulation of histone modifications and long-range chromosomal interactions during postmitotic transcriptional reactivation. *Genes and Development* 2020; 34:1-18

18. Akdemir KC, Le VT, Chandran S, Li Y, Verhaak RG, Beroukhim R, Campbell P, Chin L, PCAWG-Structural Variation Working Group, **Dixon JR**, Futreal PA, and PCAWG Consortium. Disruption of chromatin folding domains by somatic genomic rearrangements in human cancers. *Nature Genetics* 2020; 52 (3) 294-305
19. Xu Z, **Dixon JR**. Genome reconstruction and haplotype phasing using chromatin conformation capture methodologies. *Briefings in Functional Genomics* 2020; 19 (2), 139-150.
20. Lee DS*, Luo C*, Zhou J*, Chandran S, Rivkin A, Bartlett A, Nery JR, Fitzpatrick C, O'Connor C, **Dixon JR**, Ecker JR#. Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. *Nature Methods* 2019; 16 999-1006. First published as a *bioRxiv* preprint as doi: 10.1101/503235.
21. Song M, Yang X, Ren X, Maliskova L, Li B, Jones IR, Wang C, Jacob F, Wu K, Traglia M, Tam TW, Jamieson K, Lu SY, Ming GL, Li Y, Yao J, Weiss LA, **Dixon JR**, Judge LM, Conklin BR, Song H, Gan L, Shen Y. Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. *Nature Genetics* 2019; 51 (8) 1252-1262. First published as a *bioRxiv* preprint as doi: 10.1101/494450
22. Zhou J, Ma J, Chen Y, Cheng C, Bao B, Peng J, Sejnowski TJ, **Dixon JR**, Ecker JR. Robust single-cell Hi-C clustering by convolution-and random-walk-based imputation. *Proceedings of the National Academy of Sciences* 2019; 116 (28) 14011-14018. First published as a *bioRxiv* preprint as doi: 10.1101/506717.
23. Yang Y, Zhang Y, Ren B, **Dixon JR**, Ma J. Comparing 3D genome organization in multiple species using Phylo-HMRF. *Cell Systems* 2019; 8 494-505.
24. Barbosa K, Deshpande A, Chen BR, Ghosh A, Sun Y, Dutta S, Weetall M, **Dixon J**, Armstrong SA, Bohlander SK, Deshpande AJ. Acute myeloid leukemia driven by the CALM-AF10 fusion gene is dependent on BMI1. *Experimental Hematology* 2019; 74 42-51.
25. Gatchalian J, Malik S, Ho J, Lee DS, Kelso TWR, Shokhirev MN, **Dixon JR**, Hargreaves DC. A non-canonical BRD9-containing BAF chromatin remodeling complex regulates naïve pluripotency in mouse embryonic stem cells. *Nature Communications* 2018; 9:5139.
26. **Dixon JR***, Xu J*, Dileep V*, Zhan, Y, Song F, Le VT, Yardimci, GG, Chakraborty A, Bann DV, Wang Y, Clark R, Zhang L, Yang H, Liu T, Iyyanki S, An L, Pool C, Sasaki T, Rivera-Mulia JC, Ozadam H, Lajoie BR, Kaul R, Buckley M, Lee K, Diegel M, Pezic D, Ernst C, Hadjur S, Odom DT, Stamatoyannopoulos JA, Broach JR, Hardison R, Ay F#, Noble WS#, Dekker J#, Gilbert DM#, Yue F.# Integrative detection and analysis of structural variation in cancer genomes. *Nature Genetics* 2017; 50 (10) 1388-1398. First published as a *bioRxiv* preprint as doi: 10.1101/119651
27. Du Z, Zheng H, Huang B, Ma R, Zhang X, He J, Xiang Y, Wang Q, Li Y, Ma J, Zhang X, Zhang K, Wang Y, Zhang MQ, Gao J, **Dixon JR**, Wang Z, Zeng J, Xie W. Allelic reprogramming of 3D chromatin architecture during early mammalian development. *Nature* 2017; 547 (7662) 232-235.
28. **Dixon JR**#, Gorkin DU, Ren B#. Chromatin Domains: the unit of chromosome organization. *Molecular Cell* 2016; 62 (5) 668-680.
29. Diao Y, Li B, Meng Z, Jung I, Lee AY, **Dixon JR**, Maliskova L, Guan KL, Shen Y, Ren B. A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. *Genome Research* 2016; 26(3) 397-405.
30. Selvaraj, S, Schmitt AD, **Dixon JR**, Ren B. Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. *BMC Genomics* 2015; 16(1) 900.
31. **Dixon JR***, Jung I*, Selvaraj S*, Shen, Y, Antosiewicz-Bourget JE, Lee AY, Ye Z, Kim A, Rajagopal N, Xie W, Diao Y, Liang J, Zhao H, Lobanekov V, Ecker J, Thomson J, Ren B. Chromatin architecture reorganization during stem cell differentiation. *Nature* 2015; 518 331-336.
32. Roadmaps Epigenomics Consortium. Integrative analysis of 111 reference human epigenomes. *Nature* 2015; 518 317-330.
33. Li Y, Rivera CM, Ishii H, Jin F, Selvaraj S, Lee AY, **Dixon JR**, Ren, Bing. CRISPR Reveals a Distal Super-Enhancer Required for Sox2 Expression in Mouse Embryonic Stem Cells. *PLoS ONE* 2014; 9 (12): e114485.
34. Attanasio, C, Nord, AS, Zhu, Y, Blow, MJ, Biddie, SC, Mendenhall EM, **Dixon, JR**, Wright, C, Hosseini, R, Akiyama, JA, Holt, A, Plajzer-Frick, I, Shoukry, M, Afzal, V, Ren, B, Bernstein, BE, Rubin, EM, Visel, A, Pennachio, LA. Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. *Genome Research* 2014; 24 (6): 920-929.
35. Zuin J*, **Dixon JR***, van der Reijden M, Ye Z, Kolovos P, Brouwer R, van de Corput M, van de Werken H, Knoch T, van Ijcken W, Grosveld F, Ren B, Wendt K. Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. *Proceeding of the National Academy of Sciences* 2014; 111 (3), 996-1001.
36. Selvaraj S*, **Dixon JR***, Bansal V, Ren B. Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. *Nature Biotechnology* 2013; 31 (12), 1111-1118.
37. Jin F, Li Y, **Dixon JR**, Selvaraj S, Ye Z, Lee AY, Yen CA, Schmitt AD, Espinoza CA, Ren B. A high-resolution map of the three-dimensional chromatin interactome in human cells. *Nature* 2013; 503 (7475), 290-294.
38. Hu, M, Deng, K, Qin, Z, **Dixon, J**, Selvaraj, S, Fang, J, Ren, B, Liu, JS. Bayesian inference of spatial organizations of chromosomes. *PLoS Computational Biology* 2013; 9 (1), e1002893

39. Shen Y, Yue F, McCleary DF, Ye Z, Edsall L, Kuan S, Wagner U, **Dixon J**, Lee L, Lobanenkov VV, Ren B. A map of cis-regulatory sequences in the mouse genome. *Nature* 2012; 488 (7409):116-20.
40. **Dixon, JR**, Selvaraj S, Yue F, Kim A, Li Y, Shen Y, Hu M, Liu JS, Ren B. Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* 2012; 485 (7398) 376-80.
41. Barish, GD, Yu, RT, Karunasiri, M, Ocampo, CB, **Dixon, J**, Benner, C, Dent, AL, Tangirala, RK, Evans, RM. Bcl-6 and NF-kappaB cistromes mediate opposing regulation of the innate immune response. *Genes Dev.* 2010; 24 (24), 2760-2765
42. Pagliarini DJ, Wiley SE, Kimple ME, **Dixon JR**, Kelly P, Worby CA, Casey PJ, and Dixon JE. Involvement of a mitochondrial phosphatase in the regulation of ATP production and insulin secretion in pancreatic beta cells. *Mol. Cell* 2015; 19 (2), 197-207.

PRE-PRINTS

1. Chae J, Lee JS, Park J, Lee DS, Park WS, Clock B, **Dixon JR**, Jung YS, Hong D. Deciphering the Evolutionary History of Complex rearrangements in head and neck cancer patients using multi-omic approach. *bioRxiv* preprint 2022, doi: 10.1101/2022.08.19.504509.
2. Sen A, Xu Z, Tyndale S, Yasis J, Cho CY, Bump R, Chandran S, Luo L, Fu Y, Petersen LK, Shokhirev M, Kuo DJ, **McVicker GP#**, **Dixon JR#**. Heterogeneity in chromatin structure drives core regulator pathways in B-cell Acute Lymphoblastic Leukemia. *bioRxiv* preprint 2024, doi: 10.1101/2024.10.04.616668
3. Zhou J, Wu Y, Liu H, Tian W, Castanon RG, Bartlett A, Zhang Z, Yao G, Shi D, Clock B, Marcotte B, Nery JR, Liem M, Claffey N, Boggeman L, Barragan C, Arrojo e Drigo R, Weimer AK, Shi M, Cooper-Knock J, Zhang S, Snyder MP, Preissl S, Ren B, O'Connor C, Chen S, Luo C, **Dixon JR#**, Ecker JR#. Human Body Single-Cell Atlas of 3D Genome Organization and DNA Methylation. *bioRxiv* preprint 2025, doi: 10.1101/2025.03.23.644697
4. Zhao B, Cho CY, Ye L, Keal T, Mitchell T, Martin-Barrio I, Faraj CA, Unal M, Alsing J, Lawson NM, Kim ER, Chavez F, Rangel KM, Singh SK, McCarthy JH, Ashley DM, Yung WKA, Puduvalli V, Nir G, Weinberg JS, Wang L, Ligon KL, Genovese G, Van Loo P, Futreal PA, Huse JT#, **Dixon JR#**, Lang FF#, Akdemir KC#. Oncogenic drivers shape the tumor microenvironment in human gliomas. *bioRxiv* preprint 2025, doi: 10.1101/2025.05.16.654515.

*These authors contributed equally to this work

#Co-corresponding author

INVITED EDITORIALS/PERSPECTIVES

1. **Dixon JR** (2019). TADs for Life: Chromatin Domain Organization Regulated Lifespan in *C. elegans*. *Dev. Cell* 51 (2), 131-132.
2. Ren B, **Dixon JR** (2015). A CRISPR Connection between Chromatin Topology and Genetic Disorders. *Cell* 161(5) 955-957.

INTELLECTUAL PROPERTY

1. Ren B, Selvaraj S, **Dixon J**, Schmitt A. "Whole-genome haplotype reconstruction." U.S. Patent No. US18/942,959

SELECTED PROFESSIONAL SERVICE

2025	NIH Study Section, NCI F-series Fellowships F09A
2024	NIH Study Section, NCI P01 SEP-C
2023	NIH Study Section, Cancer Genetics (Ad Hoc)
2023	NIH Study Section, Small business: Cell and Molecular Biology (MCST 15)
2021	NIH Study Section, Maximizing Investigators' Research Award (MIRA) for Early Stage Investigators
2020	NIH Study Section, Genetic Variation and Evolution Study Section (Ad hoc)
2020	NIH Study Section, Special Emphasis Panel ZRG1 BST-T 50 – 4D Nucleome Data Integration, Modeling, Visualization, Coordination and Organizational Centers and Hubs
2020	Conference organizer, AACR Annual Meeting Educational Session "The Three Dimensional Cancer Genome"

SELECTED SALK/UCSD SERVICE

2022-2024	Salk Institute Seminar Committee (Co-chair)
2022-present	UC San Diego Biology Department Graduate Program Admission Committee
2019-present	UC San Diego Medical Scientist Training Program Admission Committee

2017-2024	Salk Institute Seminar Committee
2019-present	Salk Institute Internal Funding Committee

INVITED LECTURES

2025	Sanford, Burnham, Prebys Institute CCMD & CNS Center Faculty Retreat, <i>Invited Keynote Speaker</i>
2025	Dana Farber Cancer Center – Seminars in Oncology
2025	Sloan Kettering Institute Developmental Biology Program Seminar Series
2024	UCSD Genetics, Bioinformatics, and Systems Biology Colloquium
2023	MD Anderson Leading Edge of Cancer Symposium
2023	“A Single Cell View of 3D Genome Structure” CoB Workshop, Buxted Park, England
2023	MD Anderson Translational Molecular Pathology Department Distinguished Speaker Seminar Series
2023	OHSU Medical Scientist Training Program Retreat: <i>Invited Keynote Speaker</i>
2023	UCSF Pharmaceutical Sciences and Pharmacogenomics Seminar Series
2023	UT Southwestern Department of Molecular Biology Seminar Series
2022	UC San Diego Department of Pharmacology Seminar Series
2022	American Association for Cancer Research Annual Meeting, Workshop
2021	UT San Antonio Molecular Medicine Seminar Series
2020	American Association for Cancer Research Annual Meeting, Education Session
2019	University of Michigan Center for Computational Molecular Biology Seminar Series
2019	Purdue University Cancer Center Seminar Series
2019	American Association for Cancer Research Annual Meeting, Education Session
2016	Genentech Seminar Series
2016	f-TALES workshop, Ghent, Belgium
2015	TRR81 Symposium, Marburg Germany
2011	San Diego Center for Systems Biology NextGen Transcriptomics Workshop

TEACHING EXPERIENCE

2023	BIMM194 – Chromatin Structure & Dynamics (UCSD)
2022-2024	BICD194 – Epigenetics in Gene Regulation, Development, and Cancer (UCSD)
2016	Guest Lecturer, Salk Bioinformatics Core Workshop
2013	Teaching Assistant, Human Anatomy, UC San Diego School of Medicine

COMMUNITY OUTREACH

2018	Salk Annual High School Science Day Volunteer
2008-2009, 2014	UC San Diego Medical School Student Run Free Clinic Volunteer

RESEARCH TRAINING AND MENTORING

Postdoctoral Fellows

Yunwen Wu, Ph.D. (2025-present)
Tessa Popay, Ph.D (2021-present)
Zhichao Xu, Ph.D (2017-2025) Current position: Assistant Professor, UT Health Houston
Dong-sung Lee, Ph.D (2016-2020). Current position: Associate Professor, Seoul National University

Graduate Students

Tula Keal (2023-present) Ph.D student, UC San Diego Biomedical Sciences Graduate Program
Morgan Black, (2024-present) Ph.D student, UC San Diego Program in Biological Sciences
Ami Pant (2025-present) Ph.D student, UC San Diego Program in Biological Sciences
Juan Manuel Tzompantzi De Ita (2025-present) Ph.D student, UC San Diego Program in Biological Sciences
Meghana Hariprasad (2025-present) Masters Student, UC San Diego Biology Department

Research Assistants/Undergraduates

Meghana Hariprasad (2023-2025)
Ami Pant (2023-2025)
Femke Munting (2021-2023)
Morgan Black (2021-2024)
Nicholas Haghani (2021-2022)
Jean Yasis (2020-2021)

Samantha Marcotte (2020-2021)
Sofia Dallarda (2020-2021)
Benjamin Clock (2019-2020).
Kate Cho (2019-2020).
Sahaana Chandran (2017-2019).
Rosalind G. Bump (2017-2019).
Victoria T. Le (2015-2017).