

Gene W. Yeo, Ph.D., MBA

Professor of Cellular and Molecular Medicine, University of California San Diego
Founding member, UCSD Institute for Genomic Medicine
Member, UCSD Stem Cell Program
Member, UCSD Moores Cancer Center
National Research Foundation Visiting Investigatorship, Singapore
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Gene Yeo PhD MBA is a Professor of Cellular and Molecular Medicine at the University of California, San Diego (UCSD). Dr. Yeo has a BSc in Chemical Engineering and a BA in Economics from the University of Illinois, Urbana-Champaign, a Ph.D. in Computational Neuroscience (Machine Learning) from Massachusetts Institute of Technology and an MBA from the UCSD Rady School of Management. Gene's research interest is in understanding and manipulating RNA processing in development and disease using induced pluripotent stem cell and animal models. Gene's lab develops and utilizes multidisciplinary technologies ranging from machine learning, biochemistry, molecular biology, genomics, chemistry and materials research. Gene is widely collaborative and emphasizes on reproducibility and robustness in his data and results, and transparency and honesty in communicating with trainees and colleagues. Dr. Yeo has authored more than 160 peer-reviewed publications including invited book chapters and review articles in the areas of neurodegeneration, RNA processing, computational biology and stem cell models; and served as Editor on two books on the biology of RNA binding proteins. Recently, his lab developed enhanced CLIP for the purposes of large-scale mapping of protein-RNA interactions. His lab also demonstrated in vivo RNA targeting with CRISPR/Cas proteins with proof of concept in repeat expansion disorders. Gene is on the Editorial Boards of the journals *Cell Reports* and *Cell Research*. Gene joined

UCSD as an Assistant Professor in 2008, was promoted with tenure to Associate Professor in 2014 and to Professor in 2016. Gene was the first Crick-Jacobs Fellow at the Salk Institute (2005-2008) and is a recipient of the Alfred P Sloan Fellowship in recognition of his work in computational molecular biology (2011), Singapore National Research Foundation Visiting Investigatorship Award (2017), the inaugural Early Career Award from the International RNA Society (2017), a Blavatnik National Award Finalist (2018 & 2019) and San Diego Xconomy Award for 'Big Idea' (2019). Gene's research has been funded by the National Institute of Health, National Science Foundation, California Institute for Regenerative Medicine, TargetALS, ALS Foundation, Department of Defense, Myotonic Dystrophy Association, Myotonic Dystrophy Foundation and Chan-Zuckerberg Initiative. Gene has also been funded and collaborates with biotech and pharmaceutical companies such as Takeda, Genentech and Roche. Gene is a co-founder of biotech companies which includes Locana, Eclipse Bioinnovations, Enzerna and Proteona. Gene serves or had served on the scientific advisory boards of the Allen Institute of Immunology, Locana, Eclipse Bioinnovations, Proteona, Aquinnah, Cell Applications, Nugen and Ribometrix. Gene was a Sword of Honor recipient (the highest honor) in Officer Cadet School in 1999 and has served in the Singapore Navy as a Naval officer. Gene has completed 2 full Ironman-distance and multiple half-ironman-, olympic-, sprint-distance triathlons, full marathons and half-marathons.

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Gene W. Yeo

PhD MBA

Scientist/Entrepreneur

Professor
Dept. of Cellular and Molecular Medicine
UCSD Stem Cell Program
Institute for Genomic Medicine
Moores Cancer Center

RESEARCH INTERESTS

- ◆ **Understanding RNA processing:** My lab seeks to uncover mechanisms and pathways underlying post-transcriptional control, mediated by the interaction between RNA binding proteins and *cis*-regulatory elements. We utilize large-scale biochemical and genomics assays coupled with high-throughput sequencing to study the molecular mechanisms of and biological impact underlying alternative splicing, polyadenylation, transport, translation, RNA turnover and microRNA biology. We are the world's leader in developing the molecular and cellular resources and robust technologies required for truly large-scale studies of hundreds of RNA binding proteins and their RNA targets. We have published over a hundred papers in this space.
- ◆ **RNA Therapeutics:** My lab published the first demonstration of targeting RNA in live cells using the CRISPR/Cas9 technology in 2016 (Nelles et al, *Cell*, 2016) and we are pursuing multiple avenues of applications ranging from therapeutic intervention of neuromuscular diseases (Batra et al, *Cell*, 2017) to single cell RNA imaging. We are also developing new ways of using nucleic acids to manipulate RNA.
- ◆ **Neurological diseases:** My lab studies the molecular basis of mental disorders such as autism spectrum disorders and neuromuscular diseases (ALS) and myotonic dystrophy (DM) using *in vitro* stem cell models and *in vivo* mice models.
- ◆ **Virus-host** interactions: My lab reveals new insights into how DNA and RNA viruses affect the host transcriptome.
- ◆ **Single cell technologies and analysis:** My lab develops new molecular capture methods and machine-learning approaches to single cell RNA-seq/DNA analysis and visualization tools.

EDUCATION AND TRAINING

Salk Institute, La Jolla, CA	Junior Fellow, Crick-Jacobs Center for Computational and Theoretical Biology; Senior Fellow Mentors: Fred Gage and Sean Eddy	July 2005-Sept 2008
University of California, San Diego, CA	Masters of Business Administration at the Rady School of Management	Sept 2006- Aug 2008
Massachusetts Institute of Technology, Cambridge, MA	Ph.D. in Computational Neuroscience, Department of Brain and Cognitive Sciences; Advisors: Christopher Burge and Tomaso Poggio, Members: Phillip Sharp and Martha Constantine-Paton.	Sept 2000- Feb 2005
University of Illinois, Urbana-Champaign, IL	Bachelor of Science (B.S.) in Chemical Engineering, Highest Honors, Supervisor: Charles Zukoski. Bachelor of Arts (B.A.) in Economics, High Honors	1994-1998

PRIMARY FACULTY APPOINTMENTS

University of California, San Diego, CA	Professor, Department of Cellular and Molecular Medicine Department of Bioengineering, Affiliate Neuroscience Graduate Program Co-director, Bioinformatics and Systems Biology Graduate Program	July 1 2016-current 2018-current 2018-current
	Associate Professor, Department of	July 1 2014-June 30 2016

Cellular and Molecular Medicine

Assistant Professor, Department of Cellular
and Molecular Medicine
Institute for Genomic Medicine
UCSD Stem Cell Program
UCSD Moores Cancer Center
Bioinformatics Graduate Program
Biomedical Sciences Graduate Program
Material Science and Engineering
Graduate Program

Oct 2008-June 30 2014

OTHER APPOINTMENTS

National University of Singapore	Consultant (Visiting Professor), Department of Physiology	Aug 2013-present
	Adjunct Visiting Assistant Professor, Department of Biological Sciences	Aug 2009-Aug 2013
A*STAR	Visiting Fellow, Molecular Engineering Lab	Aug 2009-present

PROFESSIONAL EXPERIENCE

Beckman Institute of Advanced Science and Technology, University of Illinois, Urbana-Champaign Zukoski group: Conducted studies on Thin Film Drying stresses using an automated ellipsometer; Conducted studies on the effect of electric fields on 20 micro gold-coated glass spheres using an Atomic Force Microscope.	1996-1997
Affymetrix, Santa Clara, CA Research Technician	1997
Institute of Molecular and Cell Biology, Singapore Research Associate Mentors: Venkatesh Byrappa and Sydney Brenner: Regulatory elements conserved in non-coding regions.	2000
Chiron, Research and Development, Emeryville, CA Research Technician	2000
Millennium Pharmaceuticals, Millennium Predictive Medicine (MPMX), MA Bioinformatics Researcher Developed and critiqued millennium in-house web-tools for classification and feature selection for marker selection in large-scale microarray data. Integrated microarray data and clinical data using Bayesian networks.	2001
Neuron Systems, MA Bioinformatics Consulting	2004-2006
Co-founder, GeneBytes	2008-2010
Bioinformatics Consultant Clients include: ISIS Pharmaceuticals, Sequenom, Roche	2011-2012

Scientific Advisory Board Member, Aquinnah	2014-2017
Scientific Advisory Board Member, Interpreta	2014-2015
Co-founder, Enzerna	2014-current
Co-founder, acting CEO, CSO and Chair of the Scientific Advisory Board, Locana (Incorporated May 3, 2016)	2016-current
Co-founder and Scientific Advisory Board member, ProteoNA (Incorporated March 7, 2017)	2017-current
Co-founder and Scientific Advisory Board member, Eclipse Bioinnovations (Incorporated June 23, 2017)	2017-current
Scientific Advisory Board member, Jumpcode	2017-current
Scientific Advisory Board member, Nugen	2017-2018
Scientific Advisory Board member, Ribometrix	2018-current
Scientific Advisory Board member, Allen Institute for Immunology	2018-current
Scientific Advisory Board member, LGC	2018-current

HONORS, AWARDS AND FELLOWSHIPS

Dean's list, College of Engineering, 1994; College of Liberal Arts and Sciences, 1995-1997.
A.T. Widiger Chemical Engineering Scholarship, 1996.
Hauser Chemical Engineering Scholarship for research, 1996.
Chemical Engineering Alumni Award, 1997.
James Scholar, College of Liberal Arts and Sciences, 1996-1998.
Best in Company and Best in Physical Training Awards during Basic Military Training, 1998 (Singapore)
Sword of Honor, Officer Cadet School, Navy, 1999 (Singapore)
Brain-Cognitive Science Team Award for Outstanding Teaching, 2005
Lee Kuan Yew Graduate Scholarship, by the Lee Kuan Yew Foundation in Singapore, 2000-2005.
First Crick-Jacobs Junior Fellow, Crick-Jacobs Center for Computational and Theoretical Biology, Salk Institute, 2005-2008
Alfred P. Sloan Foundation Sloan Research Fellow, 2011 (2-year fellowships awarded yearly to researchers in recognition of distinguished performance and a unique potential to make substantial contributions on the field; announced in New York Times)
Editorial Board, Cell Reports (2011-current)
Editorial Board, Cell Research (2014-current)
Inaugural RNA Society's Early Career Award, 2017
National Research Foundation Visiting Investigatorship Award, Prime Minister's Office, Singapore, 2017
Finalist for Blavatnik National Awards for Young Scientists, 2018
Xconomy Awards for San Diego, Big Idea Award Winner, 2019
Finalist for Blavatnik National Awards for Young Scientists, 2019

PROFESSIONAL ASSOCIATIONS AND ACADEMIC SERVICE

MEMBERSHIPS AND EXTERNAL SERVICE AT PROFESSIONAL SOCIETIES AND CIVIC ORGANIZATIONS

The Honor Society of Phi Kappa Phi (1997-present)
The American Institute of Chemical Engineers (1997-present)
The Phil Lambdas Upsilon Honorary Chemical Society (1997-present)
The Tau Beta Pi National Engineering Honor Society (1997-present)
The Phi Beta Kappa Honor Society (1997-present)
The Golden Key Honor Society (1997-present)
The RNA Society (2005-present)
International Society of Computational Biology (2005-present)
Organizer for Alternative Splicing Special Interest Group, Satellite Conference of ISMB (2012)
Gordon Conference on Post-transcriptional gene regulation (2014, Poster Judge)
RNA society meeting (2015, May, Poster judge)
BIOCOM CRO Steering Committee (2015-current)
Advisory Board (for Oxford Global's 2016 Next Generation Sequencing and Single Cell Congress) (2015-current)
3rd annual RNA biology symposium by the Cancer science institute at NUS, Singapore (Co-organizer) (2017)
4th annual RNA biology symposium by the Cancer science institute at NUS, Singapore (Co-organizer and chair)(2018)

RNA Society, Kyoto, Japan, June 28- July 2, 2016 (Workshop chair: Computational analysis of RNA data)
SingaRNA Symposium, Singapore, July 5, 2016 (Conference organizer)
Keystone Symposia Conference: Protein-RNA Interactions: Scale, Mechanisms, Structure & Function of coding and noncoding RNPs, Banff, Canada, 6 Feb 2017 (Primary Organizer)
Systems biology: global regulation of gene expression, Cold Spring Harbor Laboratory, Feb 26-March 2, 2017 (Session Chair)
Single Cell Analysis Course, Cold Spring Harbor Laboratory, July 3, 2017 (Course instructor and Speaker)
Eukaryotic mRNA Processing Meeting, Cold Spring Harbor Laboratory, Aug 22-26, 2017 (Session chair)
American Society for Neurochemistry, RNA processing and regulation in brain development and disorders, Riverside, Mar 25, 2018 (Co-chair)

UNIVERSITY SERVICE

Stem Cell on the Mesa Planning Committee (2008, 2009, 2010)
UCSD Research Council chaired by Prof Susan Taylor (2008-present)
UCSD Institute for Genomic Medicine, Founding Member (2009-present)
Committee to restructure Biology Graduate Program by adding Bioinformatics, Chaired by Dr Gabriele Wienhausen, Assoc Dean for Education in Div Bio Sciences (2011)
Chair of Sanford Stem Cell Center Genomics and Bioinformatics Core Subcommittee (2011)
Organizing Committee, Institute for Genomic Medicine Annual Conference (2011)
UCSD Biomedical Sciences Graduate Program Admission Committee (2014)
Organizing Committee for IGM Symposium, Single Cell Genomics UCSD (2014)
UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2014)
UCSD Genomics Cores Steering Committee (2014-2015)
Center for Computational Biology and Bioinformatics Steering Committee (2013, 2014, 2015)
Institute for Genomic Medicine High-throughput sequencing Steering Committee (2013, 2014, 2015)
Sanford Consortium Stem Cell Genomics Core, Scientific Director and Chair of Steering Committee (2013, 2014, 2015)
Dept of CMM vice-representative For Academic Senate Assembly Meetings (2015)
Dept of CMM Faculty Search Committee (2015, 2016)
UCSD Biomedical Sciences Graduate Program Admission Committee (2015)
UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2015)
Chair, UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2016)
Chair, UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2017)
Chair, UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2018)
Co-Organizer (with Prashant Mali) for IGM Symposium, Genome and Transcriptome Engineering at UCSD (2018)
UCSD ORU 5-year review committee chair (2018)
Chair, UCSD Bioinformatics and Systems Biology Graduate Program Admission Committee (2019)
UCSD Bioinformatics and Systems Biology Graduate Program Bioinformatics Steering Committee (2019)

REVIEWER FOR GRANTS AND FELLOWSHIPS (NATIONAL AND INTERNATIONAL)

Ad Hoc Grant Reviewer, NIH/NSF, Collaborative Research in Computational Neuroscience (2008-09)
Ad Hoc Grant Reviewer, Israel Science Foundation (2008)
NIH reviewer for ZRG1 MOSS K(02) Special Emphasis Panel (2010)
Ad Hoc reviewer for GCAT (Genomics, Computational Biology and Technology) study section meeting (2010)
Invited reviewer for European Research Council (2010)
Ad Hoc reviewer for NIH/NHLBI SBIR (2012)
Ad Hoc reviewer for MNG study section (2012, June, Sept)
Grant reviewer for Pines Beatrix Fonds, The Netherlands
Grant reviewer for INSERM, France
Ad Hoc reviewer for GCAT study section (2012, Oct)
Grant reviewer for MNG study section (2013, Feb)
Grant reviewer for American Heart Association (2013, April)
Grant reviewer for Israel Science Foundation (2013)
Training Grant reviewer for CIRM predoc/clinical fellows (2013, May)
Grant reviewer for NIH K99 grants (2013, June)
Grant reviewer for MNG study section (2014, Feb)
Grant reviewer for GGG study section (2014, March)
Grant reviewer for MNG study section (2015, Feb, Co-chair)
Grant reviewer for MND association (2015, April)
Grant reviewer for MNG study section (2015, June, Co-chair)
Grant reviewer for MNG study section (2015, October, Co-chair)
Grant reviewer for Israel Science Foundation (2016)
Grant reviewer for MNG study section (2016, Feb, Co-chair)
Grant reviewer for MNG study section (2016, June, Co-chair)
Grant reviewer for MNG study section (2016, October, Chair)
Grant reviewer for National Research Foundation, Singapore, CRP (2016, July)

Grant reviewer for MNG study section (2017, Feb, Chair)
 Grant reviewer for MNG study section (2017, June, Chair)
 National Cancer Institute Genetics Branch Intramural Review (2017, November, Reviewer)
 Grant reviewer for MNG study section (2017, Sept, Chair)
 Grant reviewer for MNG study section (2018, Feb, Chair)
 Grant reviewer for Carver Trust Foundation (2018, April)
 Grant reviewer for Motor Neurone Disease Association (2018, April)
 Grant review for MRC (2018, April)
 Grant reviewer for GGG study section (Somatic Cell Genome Engineering) “Expanding the human genome editing repertoire” (2018, May 24)
 Grant reviewer for MNG study section (2018, June, Chair)
 Grant reviewer for ZRG1 GGG-P (70) study section: “Expanding the human genome editing repertoire” (2019, March 8)
 Grant reviewer for ZRG1 GGG-B (70) study section: “Human genome editing tools and platforms to evaluate adverse effects(2019, March 8)

PROFESSIONAL ROLES IN JOURNAL REVIEWS

Guest Editor, PLoS Genetics (2011)
 Editorial Board, Cell Reports (2011-current)
 Editorial Board, Cell Research (2014-current)
 Guest Editor, Elife (2015)

Active Reviewer (40-80 manuscripts reviewed a year) for *Nature, Science, Cell, ELife, Nature Structural & Molecular Biology, Nature Methods, Nature Cell Biology, Nature Biotechnology, Molecular Cell, Cell Stem Cell, Cancer Cell, Cell Reports, Neuron, Genes and Development, PLoS One, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PNAS, Nucleic Acids Research, Genome Research, RNA, Genome Biology, BMC Bioinformatics, Applied Bioinformatics, Bioinformatics, Molecular Biology and Evolution, Nature Review Genetics, Molecular Cell Biology, EMBO Molecular Medicine, Human Molecular Genetics, JoVE*

TEACHING

University of Illinois, Urbana-Champaign, Chemical Engineering Teaching Assistant Mass Transfer. Conducted discussion sections on diffusion, mass transfer coefficients, heat and mass transfer, distillation and absorption, membrane separations, and chemical reactions in mass transfer.	1997
Northeastern University, Bioinformatics Essentials Graduate Certification Course Lecturer Structured course syllabus and co-taught a 12 week course in microarray data analysis, including classification, feature selection, experimental design, Bayesian networks and microarray technology.	2001
Massachusetts Institute of Technology Teaching Assistant Course 9.02 (Brain Laboratory), 9.00 (Psychology), 9.35 (Vision)	2002-2004
University of California, San Diego Lecturer in BGGN220 (Graduate Molecular Biology) organized by Amy Pasquinelli.	2007, 2008
University of California, San Diego Lecturer in BGGN231. Current Concepts in Stem Cell Biology organized by Karl Willert (Winter 2009)	Winter 2009
University of California, San Diego Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Spring 2009) Lecturer in BIOM 252 (3 hours) Human Genetics and Genomics organized by Frank Funari (Spring 2009)	Spring 2009
University of California, San Diego Lecturer (Ten 1-hour group discussions) in BIOM 201 Seminars in Biomedical Research organized by Seth Field (Fall 2009) Lecturer in BGGN220 (Graduate Molecular Biology) organized by Amy Pasquinelli (Fall 2009)	Fall 2009
University of California, San Diego Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2010)	Winter 2010

University of California, San Diego	
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2010)	Spring 2010
Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Bing Ren) (Spring 2010)	
University of California, San Diego	Fall 2010
Lecturer (Two 2-hour lectures) in BIOM 200 BMS Graduate Core Course (directors: Karen Oegema and Dwayne Stupack) (Fall 2010)	
Lecturer (Ten 1-hour group discussions) in BIOM 201 Seminars in Biomedical Research organized by Seth Field (Fall 2010)	
Lecturer in BGGN220 (Graduate Molecular Biology) organized by Jens Lykke-Anderson (Fall 2010)	
University of California, San Diego	Winter 2011
Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2011)	
<u>Course Director</u> and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo) (Winter 2011)	
University of California, San Diego	Spring 2011
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2011)	
University of California, San Diego	Fall 2011
Lecturer (4.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Anderson (Fall 2011)	
Lecturer (Ten 1-hour group discussions) in BIOM 201 Seminars in Biomedical Research organized by Seth Field (Fall 2011)	
Lecturer (Two 2-hour lectures) in BIOM 200 BMS Graduate Core Course (directors: Karen Oegema and Dwayne Stupack) (Fall 2011)	
University of California, San Diego	Fall 2011
Lead (5 hours) Small Literature Group for Foundations of Human Biology organized by Connie Holm (Fall 2011)	
University of California, San Diego	Winter 2012
Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2012)	
<u>Course Director</u> and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo) (Winter 2012)	
Lecturer in BISP194 2.5 hours (director: Al La Spada) (Winter 2012)	
University of California, San Diego	Spring 2012
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2012)	
University of California, San Diego	Fall 2012
Lecturer (4.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Anderson (Fall 2012)	
University of California, San Diego	Winter 2013
Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2013)	
Course Director and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo) (Winter 2013)	
Lecturer in BISP194 2.5 hours (director: Al La Spada) (Winter 2013)	
University of California, San Diego	Spring 2013
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2013)	
University of California, San Diego	Fall 2013
Lecturer (4.5 hours) in BGGN 220 Graduate Molecular Biology organized by Emily Troemel (Fall 2013)	
University of California, San Diego	Winter 2014
Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2014)	
Course Director and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo) (Winter 2014)	

Lecturer in BISP194 2.5 hours (director: Al La Spada) (Winter 2014)	
University of California, San Diego Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2014)	Spring 2014
University of California, San Diego Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen (Fall 2014)	Fall 2014
University of California, San Diego <u>Course Director</u> (10 weeks of 6-hour lectures a week) and Lecturer (for 2 weeks) in BIOM 262 Quantitative Methods in Genetics (Winter 2015) Lecturer (1.5 hours) in NEU221 Advanced Topics in Neuroscience (Winter 2015) directed by Thomas Hnasko Course Director and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and <u>Gene Yeo</u>)	Winter 2015
University of California, San Diego Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2015)	Spring 2015
University of California, San Diego Lecturer (4 hours) + Paper Discussion (2 hours) in BIOM 200 BMS Graduate Core Course organized by Kevin Corbett and Alysson Muotri (Fall 2015)	Fall 2015
University of California, San Diego <u>Course Director</u> (10 weeks of 6-hour lectures a week) and Lecturer (for 3 weeks) in BIOM 262 Quantitative Methods in Genetics (Winter 2016) Course Director and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and <u>Gene Yeo</u>)	Winter 2016
University of California, San Diego Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2016)	Spring 2016
Cold Spring Harbor Laboratory, Single Cell Analysis Course June 7-17, 2016. Co-course director, assisted by Olga Botvinnik and Yan Song (https://github.com/YeoLab/single-cell-bioinformatics)	June 2016
University of California, San Diego Bioinformatics Bootcamp (Aug 1-5, 2016). Course director, assisted by Emily Wheeler.	August 2016
University of California, San Diego Lecturer (2 hours) + Paper Discussion (2 hours) in BIOM200 BMS Graduate Core Course organized by Kevin Corbett and Alysson Muotri (Fall 2015)	Fall 2016
University of California, San Diego Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen (Fall 2016)	Fall 2016
University of California, San Diego <u>Course Director</u> (10 weeks of 6-hour lectures a week) and Lecturer (for 2 weeks) in BIOM 262 Quantitative Methods in Genetics (Winter 2017) <u>Course Director</u> and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo)	Winter 2017
Cold Spring Harbor Laboratory, Single Cell Analysis Course June 30-July 13, 2017. Co-course director, assisted by Olga Botvinnik, Emily Wheeler, Alain Domissy (https://github.com/olgabot/cshl-singlecell-2017)	July 2017

Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen (Fall 2017)

Course Director (10 weeks of 6-hour lectures a week) in CMM262 Quantitative Methods in Genetics

Course Director and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo)

June 29-July 14, 2018. Co-course director, teaching assistants Emily Wheeler, Alex Chaim, Brain Yee (https://github.com/ecwheeel/CSHL_singlecellanalyses_2018)

REFEREED PUBLICATIONS (CHRONOLOGICAL ORDER)

1. Rifkin R, **Yeo, G** and Poggio T. Regularized Least-squares Classification. ***Advances in Learning Theory: Methods, Model and Applications, NATO Science Series III: Computer and System Sciences***, 2003; Vol. 190.
2. Eng L, Coutinho G, Nahas S, **Yeo G**, Tanouye R, Drk T, Burge CB and Gatti RA. Non-classical splicing mutations in the coding and non-coding regions of the ATM gene: a comparison of cDNA with maximum entropy estimates of splice junction strengths. ***Human Mutation***, 2004; 23(1), 67-76. PMID: 14695534.
3. **Yeo G**, and Burge, CB. Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. ***Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology***, 2003; April 10-13.
4. **Yeo G** and Burge C. Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. ***Journal of Computational Biology***, 2004; 11(2-3):377-94. PMID: 15285897.
5. Fairbrother WG, **Yeo, G**, Yeh, R, Goldstein, P, Mawson, M, Sharp PA, Burge CB. RESCUE-ESE identifies candidate exonic splicing enhancers in vertebrate exons. ***Nucleic Acids Res***, 2004. PMID: 15215377.
6. **Yeo G**, Hoon S, Venkatesh B, and Burge C.B. Variation in the splicing regulatory elements and their organization in vertebrate genomes. ***Proceedings of the National Academy of Sciences, USA***, 2004. PMID: 15505203.
7. **Yeo G**, Holste D, Kreiman G, Burge CB. Variation in alternative splicing across human tissues. ***Genome Biol.*** 2004; 5(10):R74. PMID: 15461793.
8. Wang Z, Rolish ME, **Yeo G**, Tung V, Mawson M, Burge CB. Systematic identification and analysis of exonic splicing silencers. ***Cell***. 2004. Dec 17; 119(6):831-45. PMID: 15607979.
9. **Yeo GW***, Van Nostrand E, Holste D, Poggio T, Burge CB*. Identification and analysis of alternative splicing events conserved in human and mouse. ***Proceedings of the National Academy of Sciences, USA***. 2005. Feb 22; 102(8):2850-5. PMID: 15708978. ***Corresponding**.
10. Han K*, **Yeo G***, An P, Burge CB, Grabowski PJ. A combinatorial code for splicing silencing: UAGG and GGGG motifs. ***PLoS Biology***. 2005. May; 3(5):e158. PMID: 15828859 (***equal contribution**).
11. Stadler MB, Shomron N, **Yeo GW**, Schneider A, Xiao X, Burge CB. Inference of splicing regulatory activities by sequence neighborhood analysis. ***PLoS Genetics***. 2006. Nov 24; 2(11):e191. PMID: 17121466. (*Recommended by Faculty 1000*).
12. Van Praag, H, Lucero, MJ, **Yeo G**, Stecker K, Heivand N, Zhao C, Yip E, Afanador M, Schroeter H, Hammerstone J, Gage FH. Plant-derived flavanol (-)epicatechin enhances angiogenesis and memory in mice. ***Journal of Neuroscience***, 2007. May 30;27(22):5869-78. PMID: 17537957.
13. Giorgi C, **Yeo G**, Stone ME, Katz DB, Burge C, Turrigiano C, Moore MJ. The EJC factor eIF4AIII modulates synaptic strength and neuronal protein expression. ***Cell***. 2007. Jul 13;130(1):179-91. PMID: 17632064.
14. **Yeo G***, Van Nostrand EL, Liang TY. Discovery and analysis of evolutionarily conserved intronic splicing regulatory elements in mammalian genomes. ***PLoS Genetics***. 2007. May 25;3(5):e85. PMID: 17530930. ***Corresponding**.

15. **Yeo G***, Xu X-D, Liang YT, Muotri AM, Carson C, Coufal N, Gage FH*. Alternative events Identified in Human embryonic stem cells and neural progenitors. *PLoS Computational Biology*, 2007. Oct;3(10):1951-67. Epub 2007 Aug 24. PMID: 17967047. ***Corresponding**.
16. Zimmerman, AM, **Yeo, G**, Howe K, Maddox, BJ, Steiner, LA. Immunoglobulin light chains in zebrafish: genomic configurations and inversional rearrangements between (V(L)-J(L)-C(L)) gene clusters. *Dev. Comp. Immunol.* 2008. 32(4):421-34. PMID: 18022691.
17. Olson S, Blanchette M, Park J, Savva Y, **Yeo G**, Yeakley J, Rio D, Graveley, B. A Regulator of Dscam Mutually Exclusive Splicing Fidelity. *Nature Structural and Molecular Biology*, 2007. Dec;14(2):1134-40. PMID: 21188797.
18. Calabrese JM, Seila AC, **Yeo GW**, Sharp PA. RNA sequence analysis defines Dicer's role in mouse embryonic stem cells. *Proceedings of the National Academy of Sciences, USA*, 2007. Nov 13;104(46):18097-102. PMID: 17989215
19. Palakodeti D, Smielewska M, Liu Y, **Yeo G,*** Graveley BR*. The PIWI proteins SMEDWI2 and SMEDWI3 are required for stem cell function and piRNA expression in planarians. *RNA*, 2008. Jun;14(6):1174-86. Epub 2008 May 2. PMID: 18456843 (***Corresponding**).
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102. Sommer A, Maxreiter F, Krach F, Fadler T, Grosch J, Maroni M, Graef D, Eberhardt E, Riemenschneider MJ, **Yeo GW**, Kohl Z, Xiang W, Gage FH, Winkler J, Prots I, Winner B. Th17 Lymphocytes induce neuronal cell death in a human iPSC-based model of parkinson's disease, *Cell Stem Cell*. 2018. PMID: 29979986.
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104. Tran SS, Jun K-I, Bahn JH, Azghadi A, Ramaswami G, Van Nostrand EL, Nguyen TB, Hsiao Y-HE, Lee C, Pratt GA, Martinez-Cerdeno V, Hagerman RJ, **Yeo GW**, Geschwind DH, Xiao X. Widespread RNA editing dysregulation in Autism Spectrum Disorders, *Nature Neuroscience*, 2018. PMID: 30559470.
105. Tan FE, Sathe S, Wheeler EC, Nussbacher JK, Peter S, **Yeo GW**. A transcriptome-wide translational program defined by LIN28B expression level, *Molecular Cell*, 2018. PMID: 30527666.
106. Yee BA, Pratt GA, Graveley BR, Van Nostrand EL, **Yeo GW**. RBP-Maps enables robust generation of splicing regulatory maps, *RNA*, 2018. PMID: 30413564.
107. Quinones-Valdez G, Tran SS, Jun HI, Bahn JH, Yang EW, Zhan L, Brümmer A, Wei X, Van Nostrand EL, Pratt GA, **Yeo GW**, Graveley BR, Xiao X. Regulation of RNA editing by RNA-binding proteins in human cells. *Commun Biol*, 2019. PMID: 30652130.
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109. Ganem NS, Ben-Asher N, Manning AC, Deffit SN, Washburn MC, Wheeler EC, **Yeo GW**, Zgayer OB, Mantsur E, Hundley HA, Lamm AT. Disruption in A-to-I Editing Levels Affects C. elegans Development More than A Complete Lack of Editing. *Cell Reports*, 2019.
110. Yang E-W, Bahn JH, Hsiao E, Tan BX, Sun Y, Fu T, Zhou B, Van Nostrand EL, Pratt GA, Freese P, Wei X, Quinones-Valdez G, Urban A, Graveley B, Burge CB, **Yeo GW**, Xiao X. Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. *Nature Communications*, 2019. PMID: 30902979.
111. Gould TW, Gould TW, Dominguez B, de Winter F, **Yeo GW**, Liu P, Sundararaman B, Stark T, Vu A, Degen JL, Lin W, Lee KF. Glial cells maintain synapses by inhibiting an activity-dependent retrograde protease signal. *PLoS Genet*, 2019. PMID: 30870413.
112. Markmiller S, Fulzele A, Higgins R, Leonard M, **Yeo GW***, Bennett EJ*. Active Protein Neddylaton or Ubiquitylation is Dispensable for Stress Granule Dynamics. *Cell Reports*, 2019 (*Corresponding)
113. Fang MY, Markmiller S, Vu AQ, Javaherian A, Dowdle WE, Jolivet P, Bushway PJ, Castello NA, Baral A, Chan M, Linsley JW, Linsley D, Mercola M, Finkbeiner S, Lecuyer E, Lewcock JW, **Yeo GW**. Small molecule modulation of TDP-43 recruitment to stress granules prevents persistent TDP-43 accumulation in ALS/FTD. *Neuron*, 2019.

114. Van Nostrand EL, Freese P, Pratt GA, Wang X, Wei X, Xiao R, Blue SM, Chen J-Y, Cody NAL, Dominguez D, Olson S, Sundararaman B, Zhan L, Bazile C, Bouvrette LPB, Bergalet J, Duff MO, Garcia KE, Gelboin-Burkhart C, Hochman M, Lambert NJ, Li H, Nguyen TB, Palden T, Rabano I, Sathe S, Stanton R, Su A, Wang R, Yee BA, Zhou B, Louie AL, Aigner S, Fu X-D, Lécuyer E, Burge CB, Graveley BR, **Yeo GW**. A Large-Scale Binding and Functional Map of Human RNA Binding Proteins. *Nature*, 2019 (in press).

INVITED REVIEWS AND BOOK CHAPTERS (CHRONOLOGICAL ORDER)

1. **Yeo G**. Splicing regulators: targets and drugs. *Genome Biology*, 2005. 6(12):240. PMID: 16356274.
2. Cao X, **Yeo G**, Muotri A, Kuwabara T and Gage FH. Noncoding RNAs in the Mammalian Central Nervous System. *Annual Review of Neuroscience*. 2006. 29:77-103. PMID: 16776580.
3. Van Nostrand E, **Yeo G**. Evolutionarily conserved intronic splicing elements in the human genome. *The Encyclopedia of Life Sciences*, 2008.
4. **Yeo GW**, Coufal N, Aigner S, Winner B, Scolnick JA, Marchetto MC, Muotri, AR, Carson C, Gage FH. Multiple layers of molecular controls modulate self-renewal and neuronal lineage specification of embryonic stem cells. *Hum Mol Genetic*. 2008. PMID: 18632700.
5. Aigner S, **Yeo G**. Terminal Differentiation: *REST*. *Developmental Neurobiology*, ed. Greg Lemke, Elsevier, Aug 2009.
6. Nelles DA, **Yeo GW**. Alternative splicing in stem cell self-renewal and differentiation. *Adv Exp Med Biol*. 2010; 695:92-104. PMID: 21222201.
7. Wilbert ML, **Yeo GW**. Genome-wide approaches in the study of microRNA biology. *Wiley Interdiscip Rev Syst Biol Med*. 2010. PMID: 21197653.
8. Zisoulis DG, **Yeo GW**, Pasquinelli AE. Comprehensive identification of miRNA target sites in live animals. *Methods Mol Biol*. 2011; 732:169-85. PMID: 21431713.
9. Lovci MT, Li H-R, Fu XD, **Yeo GW**. RNA-seq analysis of Gene expression and alternative splicing by double-random priming strategy. *Methods Mol Biol*. 2011; 729:247-55. PMID: 21365495.
10. Huelga, SC, **Yeo GW**. Genomics of Alternative Splicing in Stem Cells, "Computational Biology of Embryonic Stem Cells", edited by Zhan, Bentham Scientific, 2011.
11. Polymenidou M, Lagier-Tourenne C, Hutt KR, Bennett CF, Cleveland DW, **Yeo GW**. Misregulated RNA processing in amyotrophic lateral sclerosis. *Brain Res.*, 2012. PMID: 22444279
12. Kapeli K, **Yeo GW**. Genome-wide approaches to dissect the role of RNA binding proteins in translation control: implications of neurological diseases. *Frontiers in Neurogenomics*, 2012. PMID: 23060744
13. Nussbacher JK, Batra R, Lagier-Tourenne C, **Yeo GW**. RNA-binding proteins in neurodegeneration: Seq and you shall receive. *Trends in Neurosciences*, 2015. PMID: 25765321
14. Singh G, Pratt G, **Yeo GW**, Moore MJ, The Clothes make the mRNA: past and present trends in mRNP fashion. *Annu. Rev. Biochem*. 2015. 84:29.1–29.30. DOI: 10.1146/annurev-biochem-080111-092106. PMID: 25784054
15. Nelles DA, Fang MY, Aigner S, **Yeo GW**. Applications of Cas9 as an RNA-programmed RNA-binding protein. *Bioessays*. 2015 Jul;37(7):732-9. doi: 10.1002/bies.201500001. PMID:25880497
16. Tan FE, **Yeo GW**. Blurred Boundaries: The RNA binding protein Lin28A is also an epigenetic regulator. *Molecular Cell*. 2016. PMID:26748607
17. Van Nostrand EL, Huelga SC, **Yeo GW**. Experimental and computational considerations in the study of RNA binding protein-RNA interactions. *RNA processing, Disease and genome-wide probing*. Series Title: Adv Exp Med Biol, Vol. 907. doi:10.1007/978-3-319-29073-7_1. PMID:27256380
18. Bos TJ, Nussbacher JK, Aigner S, **Yeo GW**. Tethered function assays as tools to elucidate the molecular roles of RNA binding proteins. *RNA processing, Disease and genome-wide probing*. Series Title: Adv Exp Med Biol, Vol. 907. doi: 10.1007/978-3-319-29073-7_3. PMID:27256382
19. Brannan KW and **Yeo GW**. From Protein-RNA Predictions toward a Peptide-RNA Code. *Molecular Cell*. 2016. PMID:27814488

20. Einstein JM and **Yeo GW**. Making the cut in the dark genome: CRISPR screens will reveal important regulatory elements in the noncoding genome. *Science*. 2016. PMID:27846591
21. Wheeler EC, Van Nostrand EL, **Yeo GW**. Advances and challenges in the detection of transcriptome-wide protein-RNA interactions. *Wiley Interdisciplinary Reviews: RNA*. 2017. PMID: 28853213.
22. Kapeli K, Martinez FJ, **Yeo GW**. Genetic mutations in RNA-binding proteins and their roles in ALS. *Human Molecular Genetics*. 2017. PMID:28762175
23. Nussbacher JK, Tabet R, **Yeo GW***, Lagier-Tourenne C*. Disruption of RNA metabolism in neurological diseases and emerging therapeutic interventions. *Neuron*, 2019. (*Corresponding) PMID:30998900
- 24.

BOOKS PUBLISHED (CHRONOLOGICAL ORDER)

- i. **Yeo GW**, Editor, Systems Biology of RNA binding proteins. *Advances in Experimental Medicine and Biology*. Volume 825, Springer, 2014.
- ii. **Yeo GW**, Editor, RNA processing: Disease and genome-wide probing. *Advances in Experimental Medicine and Biology*. Volume 907, Springer, 2016.

INVENTIONS

MIRESQUE: Software for microRNA gene prediction from high-throughput sequencing, copyrighted (2008)
 Patent filed on "Regression-based methods for exon array analysis" invented by Gene Yeo, Fred Gage (2008)
 Patent filed on "GREPSEQ: An almost inexhaustible, cost-effective, high-throughput protocol for the generation of selector sequences" invented by Gene Yeo, Jonathan Scolnick, Fred Gage (2008)
 Patent disclosure for Programmable CRISPR/Cas for RNA applications at UCSD with Dave Nelles (2015)
 US Patent application "Tracking and manipulating cellular RNA via nuclear delivery of CRISPR/Cas9" 15/359567, Filed November 22, 2016

INVITED TALKS/ CONFERENCE PRESENTATIONS (CHRONOLOGICAL ORDER)

1. RECOMB 2003: Seventh annual international conference on research in computational molecular biology, April 10-13, Berlin, Germany, 2003. Yeo, G, and Burge, C.B. Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals (SELECTED TALK).
2. ISMB 2003: Intelligent systems for molecular biology conference, June 29-July 3, Brisbane, Australia, 2003. Yeo, G, Hoon, S and Burge C. Genomics of vertebrate splicing regulatory elements (BEST POSTER AWARD).
3. Eukaryotic mRNA processing meeting, Aug 20-24, Cold Spring Harbor Laboratory, 2003. Yeo, G, Hoon, S and Burge C. Variation in sequence and organization of splicing regulatory elements in vertebrate genes (POSTER).
4. RNA 2004: Ninth annual meeting of the RNA society, June 1-6, Madison, Wisconsin, 2004. Yeo, G, Holste D, Van Nostrand, E, Poggio, T and Burge, C.B. Predictive discrimination of conserved skipping events in human and mouse (SELECTED TALK).
5. SFN 2004: Society for Neuroscience, San Diego, 2004. Yeo, G, Van Nostrand, E, Holste D, Poggio, T and Burge, C.B. Predictive identification of alternative exons in mammals reveals neural-specific and RNA binding functions (POSTER).
6. Alternative Splicing Special Interest Group Meeting at Intelligent systems for molecular biology (ISMB), 2005. Identification and analysis of alternative splicing events conserved in human and mouse (INVITED TALK).
7. Regulatory RNAs, May 31-June 5, Cold Spring Harbor Laboratory, 2006. Rest-regulated MicroRNAs (POSTER).
8. RNA 2006. Highly conserved intronic elements proximal to mammalian exons predict tissue-specificity of alternatively spliced exons (POSTER).
9. RNA 2006. Identification of REST/NRSF regulated MicroRNAs (SELECTED TALK).
10. Alternative Splicing, Beyond Genome 2007. Intronic splicing regulatory elements in mammalian genomes and alternative splicing in stem cell differentiation (INVITED TALK).
11. 6th International Conference on Computational Systems Bioinformatics (CSB2007) sponsored by Life Sciences Society. Workshop on Alternative Splicing, 17th August, UCSD, 2007. Discovery of intronic regulatory elements in mammalian genomes (INVITED TALK).
12. Eukaryotic mRNA Processing Meeting, Aug 22-26, Cold Spring Harbor Laboratory, 2007 (SELECTED TALK).
13. The Stem Cell Meeting on the Mesa, Oct 19, Salk Institute, 2007. Small RNA analysis of neural differentiation from human ES cells (INVITED TALK).
14. Stower's Institute, Jan 28. Splicing bits and bytes (INVITED TALK).
15. Human Genetics Seminar, co-sponsored by CCMB and Human Genetics, University of Michigan, Ann Arbor, Feb 25, 2008. Uncovering the Splicing Code, and Alternative splicing in ES cells (INVITED TALK).
16. Genetics and Genomics Lecture Series, Department of Medicine, UCSD, March 6, 2008. Uncovering the Splicing Code, and Alternative splicing in ES cells (INVITED TALK).

17. Seminar in the Dept of Bioengineering and the Whitaker Institute of Biomedical Engineering, UCSD, March 7, 2008. Small RNA analysis in Stem Cells (INVITED TALK).
18. University of Massachusetts, Medical School Invited Talk, March 10, 2008. Uncovering the Splicing Code, and Alternative splicing in ES cells (INVITED TALK).
19. Keystone Conference on RNAi and non-coding RNAs, Whistler, Canada, March 25-30, 2008. Analysis of small RNAs in stem cells (INVITED TALK).
20. University of California, Los Angeles, Eli and Edythe Broad Center of Regenerative Medicine and Stem Cell Research. Uncovering the Splicing Code and Alternative splicing in stem cells (INVITED TALK).
21. RNA 2008. CLIP-Seq reveals a network of FOX2 regulated alternatively spliced exons in human embryonic stem cells (SELECTED TALK).
22. RNA 2008. Global analysis of small RNAs during neural specification of human embryonic stem cells (SELECTED TALK).
23. National University of Singapore, Department of Biological Sciences, hosted by Paul Matsudaira, April 15, 2009. Comprehensive identification of endogenous Argonaute binding sites in animals (INVITED TALK).
24. Institute of Genomic Medicine Symposium, June 3, 2009 Comprehensive identification of endogenous Argonaute binding sites in animals (INVITED TALK).
25. 16th Conversation, Albany, 2009. Alternative splicing and stem cells (INVITED TALK).
26. Alternative Splicing Special Interest Group Meeting at ISMB 2009 (Stockholm). Intelligent systems for molecular biology conference, 2009 Analysis of RNA binding networks (DISTINGUISHED SPEAKER).
27. Eukaryotic mRNA Processing Meeting, Aug18-Aug 22, Cold Spring Harbor Laboratory, 2009 (SELECTED TALK).
28. San Diego Consortium for Systems Biology (SDCSB) Next-Gen Sequencing Workshop, Aug 25, 2009 (INVITED TALK)
29. Keystone Conference on RNA Silencing: Mechanism, Biology and Application, Keystone, Colorado, Jan 14-19, 2010 (INVITED TALK)
30. Alternative Splicing in Neurodegenerative Diseases and Cancer, Tel Aviv, Israel, Feb 7-9, 2010 (INVITED TALK)
31. UCLA Bioinformatics Series Invited Speaker April 5, 2010 (INVITED TALK)
32. UCSD Physics of Evolution Series, August 21-Sept 2, 2010 (INVITED TALK)
33. From the RNA world to the Clinic, Janelia Farms, Sept 26-29, 2010 (INVITED TALK)
34. XVIII World Congress on Psychiatric Genetics, Athens, Greece, October 3-7, 2010 (1 INVITED TALK, 1 SELECTED TALK)
35. Institute for Genomic Medicine, October 11, 2010 (INVITED TALK)
36. First Workshop of the Postgraduate Program of the Genetics Department, Ribeirao Preto, Brazil, November 26-27, 2010 (KEYNOTE SPEAKER)
37. Integrated Biological Systems Seminar, Scripps Translational Science Institute, Feb 15, 2011 (INVITED TALK)
38. Cambridge HealthTech, XGEN Congress, San Diego, March 17, 2011 (INVITED TALK)
39. Genomics Institute of Novartis, La Jolla, March 18, 2011 (INVITED TALK)
40. 42nd Annual Meeting, American Society for Neurochemistry, March 19-23, 2011 (INVITED TALK)
41. Invited Seminar, Department of Human Genetics, University of Chicago, April 8, 2011 (INVITED TALK)
42. Workshop organized by the French National Research Agency (ANR) and California Institute for Regenerative Medicine (CIRM), July 12-13, 2011 (INVITED TALK)
43. Alternative Splicing Special Interest Group Meeting at ISMB July 15-16, 2011 (Vienna). Intelligent systems for molecular biology conference, 2011 (INVITED SPEAKER).
44. Merck-Serono, NeuroDegenerative Diseases, 19 July, 2011 (INVITED SPEAKER)
45. Roche, Basel, 22 July, 2011 (INVITED SPEAKER)
46. Eukaryotic mRNA processing meeting, Aug 23-27, Cold Spring Harbor Laboratory, 2011 (POSTER).
47. CONNECT's Frontiers in Science and Technology, Oct 11, 2011 (INVITED SPEAKER).
48. 6th Brain Research Conference, Nov 10-11, 2011 (INVITED SPEAKER).
49. Biochemistry and Molecular Biology Fall Seminar Series, University of Texas, Medical Branch, Dec 8, 2011 (INVITED SPEAKER)
50. Gladstone Institute for Cardiovascular Disease Seminar, Jan 9, 2012 (INVITED SPEAKER)
51. Social Stem Cell Symposium, Sanford-Burnham Institute, Jan 12, 2012 (INVITED SPEAKER)
52. John Hopkins Bloomberg School of Public Health BMB Seminar, April 30, 2012 (INVITED SPEAKER)
53. Robert Packard Center for ALS Research at John Hopkins, June 15, 2012 (INVITED SPEAKER)
54. Alternative Splicing Special Interest Group Meeting at ISMB July 13-14, 2012 (Long Beach, USA). Intelligent systems for molecular biology conference, 2012 (SELECTED TALK).
55. Gordon Research Conference in Post-transcriptional gene regulation meeting, July 15-20, 2012 (Rhode Island) (INVITED SPEAKER)
56. University of Nebraska Medical Center, Omaha, Department of Pharmacology and Experimental Neuroscience Seminar Series, July 27, 2012 (STUDENT INVITED SPEAKER)
57. University of Pennsylvania, Pittsburgh, Penn Bioinformatics Forum, 19 Sept, 2012 (STUDENT INVITED SPEAKER)
58. Achievement Rewards for College Scientists, Sanford Consortium for Regenerative Medicine, Sept 24, 2012 (INVITED SPEAKER)
59. University of North Carolina, Chapel Hill, Department of Pharmacology Seminar Series, Oct 16, 2012 (INVITED SPEAKER)
60. Congenital Cytomegalovirus Conference, Nov 1, 2012 (INVITED SPEAKER)
61. Yong Loo Lin School of Medicine Dept of Physiology, National University of Singapore, Jan 4, 2013 (INVITED SPEAKER)
62. University of Medicine and Dentistry of New Jersey, Jan 24, 2013 (INVITED SPEAKER)
63. Academic Leadership Symposium, Sanford Consortium for Regenerative Medicine, Feb 23, 2013 (INVITED SPEAKER)
64. Infectious Disease Journal Club, Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Mar 19, 2013 (INVITED SPEAKER)
65. Seminar, Genome Institute of Singapore, Biopolis, Singapore, Mar 21, 2013 (INVITED SPEAKER)

66. Seminar, Neuroscience Research Program, Biopolis, Singapore, Mar 22, 2013 (INVITED SPEAKER)
67. Seminar, School of Biological Sciences, Nanyang Technological University, Singapore, Mar 25, 2013 (INVITED SPEAKER)
68. Samuel Colella Lecture Series in Neurodegeneration, Pittsburgh Institute for Neurodegenerative Diseases, April 17, 2013 (INVITED SPEAKER)
69. Emory University, Department of Pharmacology Speaker Series, May 13, 2013 (INVITED SPEAKER)
70. University of Illinois, Urbana-Champaign, Neuroscience Program Seminar Series, Sept 3, 2013 (INVITED SPEAKER)
71. Oligonucleotide Therapeutics Society, Naples, Italy, Oct 8, 2013 (INVITED SPEAKER)
72. Genentech, Oct 29, 2013 (INVITED SPEAKER)
73. University of Southern California Keck School of Medicine Seminar Series, Nov 25, 2013 (INVITED SPEAKER)
74. World Stem Cell Summit, Single Cell Panel, Dec 4, 2013 (INVITED SPEAKER)
75. 8th biennial Chinese RNA society meeting, April 12, 2014 (INVITED SPEAKER)
76. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, April 14, 2014 (INVITED SPEAKER)
77. Quantitative Biology Seminar Series, Cold spring harbor laboratory, April 16, 2014 (INVITED SPEAKER)
78. Systems-to-synthesis Symposium hosted by the San Diego Center for Systems Biology, La Jolla, May 2, 2014 (INVITED SPEAKER)
79. 7th Annual Genetics Training Program Retreat, La Jolla, May 2, 2014 (INVITED SPEAKER)
80. Mini-RNA symposium, IRCM, Montreal, June 3, 2014 (INVITED SPEAKER)
81. RNA 2014, Quebec City, June 3-8, 2014 (SESSION CHAIR: Emerging and high-throughput techniques)
82. Nucleic Acid Research and Discovery Conference, San Diego, June 19-20, 2014 (INVITED SPEAKER)
83. Gordon Research Conference in Post-transcriptional gene regulation meeting, July 13-18, 2014 (Rhode Island) (INVITED SPEAKER)
84. Advanced Topics in Genomics and Cell Biology, Aug 4-6, 2014, UNICAMP, Campinas, Brazil (INVITED SPEAKER)
85. Inauguration ceremony of EPICENTER, Symposium "Biomedical science: a driver of health, wealth and knowledge generation", Aug 11, 2014, Pontificia Universidade Catolica do Parana (PUCPR), Curitiba, Brazil (KEYNOTE SPEAKER and PANELIST)
86. Center for RNA biology Seminar Series Speaker, Ohio State University, 9 Sept, 2014 (INVITED SPEAKER)
87. NUS-UCSD Inaugural symposium, Singapore, 2-3 Oct, 2014 (SPEAKER AND ORGANIZER)
88. 4th next generation sequencing and 2nd single cell genomics asia congress organized by Oxford Global, Singapore, 7 Oct, 2014 (KEYNOTE SPEAKER)
89. National Neuroscience Institute Research Seminar Series, Singapore, 9 Oct 2014 (INVITED SPEAKER)
90. ALS Association Investigator Research Workshop, PA 19-22 Oct 2014 (INVITED SPEAKER)
91. BaCaTec Wolfgang Summer School Lecture, San Diego, 12 Nov 2014 (INVITED SPEAKER)
92. BD Single Cell Genomics Symposium, San Jose, 13 Nov 2014 (INVITED SPEAKER)
93. RECOMB/ISCB Conference on Regulatory & Systems Genomics, 9-14 Nov 2014 (KEYNOTE SPEAKER)
94. Beckman Seminar Series, City of Hope, 18-19 Jan 2015 (INVITED SPEAKER)
95. The Buck Institute for Research on Aging Seminar Series, 23 Jan 2015 (INVITED SPEAKER)
96. Fluidigm's event: Beyond Biology's Next Frontier. La Jolla, 11 March 2015 (KEYNOTE SPEAKER)
97. Wayne State University School of Medicine Lecture Series, Detroit, 2 April 2015 (INVITED SPEAKER)
98. Protein-RNA Workshop hosted by McGill, Bellairs Research Institute, Barbados, 17-22 April 2015 (INVITED SPEAKER)
99. Stein Clinical Research Institute, University of California, San Diego, La Jolla, 1 May 2015 (INVITED SPEAKER)
100. Microbiology and Molecular Genetics Seminar Speaker, University of California, Irvine, 6 May 2015 (INVITED SPEAKER)
101. Advances and challenges in protein-RNA, Banff International Research Station, 7-12 June 2015 (INVITED SPEAKER)
102. Single Cell Analysis Course, Cold Spring Harbor Laboratory, 3-16 June 2015 (INVITED SPEAKER)
103. UC Santa Cruz - COAT RNA Informatics Summer School (LECTURER) and RNA SUMMIT CONFERENCE (INVITED SPEAKER)
104. Alnylam Pharmaceuticals, Cambridge, MA, 17 August 2015 (INVITED SPEAKER)
105. CECAD Noncode RNA symposium, Cologne, Germany, 24 August 2015 (INVITED SPEAKER)
106. University of London, Dept of Neurology, London, 26 August, 2015 (INVITED SPEAKER) hosted by Jernej Ule
107. University of London, RNA Club, London, 27 Aug 2015 (INVITED SPEAKER) hosted by Andres Ramos
108. Rady School of Management, UCSD, Biotech Demystified Lecture, 14 Sept 2015 (INVITED SPEAKER)
109. Bioinformatics Bootcamp, UCSD, 18 Sept 2015 (INVITED SPEAKER)
110. Riboclub Conference, Magog, Canada, 22 Sept 2015 (INVITED SPEAKER)
111. IRCM, Montreal, Canada, 24 Sept 2015 (INVITED SPEAKER)
112. Festival of Genomics, San Mateo, 5 Nov 2015 (INVITED SPEAKER)
113. Sixth Annual California ALS Research Summit, La Jolla, 9 Jan 2016 (INVITED SPEAKER)
114. Plant and Animal Genome XXIV, Post-transcriptional gene regulation. San Diego, 10 Jan 2016 (INVITED SPEAKER)
115. Invitae, San Francisco, 18 Feb, 2016 (INVITED SPEAKER)
116. Biomedical Sciences Graduate Program Recruitment, 26 Feb, 2016 (INVITED SPEAKER)
117. Lawrence Berkeley National Laboratory, Berkeley, CA, 1 March, 2016 (INVITED SPEAKER)
118. 10th St Jude-VIVA Forum in Pediatric Oncology, 6 March, 2016 (INVITED SPEAKER)
119. Institute of Molecular, Cellular Biology, A*STAR, Singapore, 9 March, 2016 (INVITED SPEAKER)
120. Physiology Lecture Series Speaker, Department of Physiology, Yong Loo Lin School of Medicine, 18 March, 2016 (INVITED SPEAKER)
121. IBS-CNRS Joint RNA Symposium, Hoam Faculty House, Seoul, Korea, 21-22 March, 2016 (INVITED SPEAKER)
122. Genetics Institute Series, University of Florida, Gainesville, Florida, 29 March, 2016 (INVITED SPEAKER)
123. Inception Sciences, La Jolla, 31 March, 2016 (INVITED SPEAKER)

124. Department of Human Genetics and Biochemistry, Tel Aviv University, 7 April, 2016 (INVITED SPEAKER)
125. BD Biosciences, La Jolla, 18 April, 2016 (INVITED SPEAKER)
126. University of Illinois Alpha Chi Sigma-Zeta Chapter Krug Lecture, 24 April, 2016 (KEYNOTE SPEAKER)
127. Biochemistry and Chemical & Biomolecular Engineering co-sponsored lecture, University of Illinois, Urbana-Champaign, 25 April, 2016 (INVITED SPEAKER)
128. Synapse to Circuits Club, University of California, Los Angeles, 29 April, 2016 (INVITED SPEAKER)
129. Genome Engineering 4.0 Workshop, Broad Institute, 6-7 May, 2016 (INVITED SPEAKER)
130. Biogen, Cambridge, MA, 9 May, 2016 (INVITED SPEAKER)
131. Novartis, Cambridge, MA, 9 May, 2016 (INVITED SPEAKER)
132. Cell Applications, San Diego, 17 May 2016 (SCIENTIFIC ADVISORY BOARD SPEAKER)
133. Single Cell Analysis Course, Cold Spring Harbor Laboratory 7 June, 2016 (INVITED SPEAKER)
134. RNA Society, Kyoto, Japan, June 28- July 2, 2016 (WORKSHOP CHAIR: Computational analysis of RNA data)
135. SingaRNA Symposium, Singapore, July 5, 2016 (CONFERENCE ORGANIZER)
136. California Institute for Regenerative Medicine Bridges Meeting, San Francisco, July 19, 2016 (INVITED SPEAKER)
137. Regulus, La Jolla, Aug 26, 2016 (INVITED SPEAKER)
138. Institute of Molecular Biology, Academia Sinica, Taipei, Sept 5, 2016 (INVITED SPEAKER)
139. RNA biology symposium, NUS, Singapore, 8-9 Sept, 2016 (INVITED SPEAKER)
140. Festival of Genomics, San Diego, 21 Sept 2016 (INVITED SPEAKER)
141. Genentech, South San Francisco, 22 Sept 2016 (INVITED SPEAKER)
142. Special Seminar, UC Berkeley, 23 Sept 2016 (INVITED SPEAKER)
143. Advances in Autism Research, MIT Alumni Association, 29 Sept 2016 (INTERVIEW)
144. Cell Applications, San Diego, 17 Oct 2016 (SCIENTIFIC ADVISORY BOARD SPEAKER)
145. SoCal Stem Cell Symposium, San Diego, 10 Nov 2016 (INVITED SPEAKER)
146. Gage Lab Symposium, San Diego, 10-11 Nov 2016 (INVITED SPEAKER)
147. Department of Biochemistry Seminar Series, University of Southern California, 14 Nov 2016 (INVITED SPEAKER)
148. NIMH Workshop: Using stem cell-based assays for biological and drug discovery, 17-18 Nov 2016 (INVITED SPEAKER)
149. CMDB/GGB/MCBL UC Riverside Seminar Program, 30 Nov 2016 (INVITED SPEAKER)
150. Denali Therapeutics, San Francisco, 1 Dec 2016 (INVITED SPEAKER)
151. American Society of Cell Biology Subgroup Session, 3 Dec 2016 (INVITED SPEAKER)
152. Cell Webinar on CRISPR and Imaging, 12 Dec 2016 (INVITED SPEAKER)
153. Nugen Technologies, San Carlos, 9 Jan 2017 (INVITED SPEAKER)
154. Genomics Institute of the Novartis Foundation, San Diego, 1 Feb 2017 (INVITED SPEAKER)
155. Biomedical Sciences Graduate Program Recruitment, UCSD, La Jolla, 3 Feb 2017 (INVITED SPEAKER)
156. Keystone Symposia Conference: Protein-RNA Interactions: Scale, Mechanisms, Structure & Function of coding and noncoding RNPs, Banff, Canada, 6 Feb 2017 (ORGANIZER and SPEAKER)
157. Academic Leadership Symposium, Sanford Consortium for Regenerative Medicine, Feb 24, 2017 (INVITED SPEAKER)
158. Phase Separation and RNA processing as drivers of cancer and neurodegenerative diseases, Sanford Consortium for Regenerative Medicine, Feb 24, 2017 (KEYNOTE SPEAKER)
159. Systems biology: global regulation of gene expression, Cold Spring Harbor Laboratory, Feb 26-March 2, 2017 (INVITED SPEAKER AND SESSION CHAIR)
160. Carnegie Mellon University Computational Biology Department Seminar Series, Pittsburgh, Mar 3, 2016 (INVITED SPEAKER)
161. Baylor College of Medicine, Department of Biochemistry Seminar Series, Houston, Mar 16, 2016 (INVITED SPEAKER)
162. Frontiers in Biology, Stanford University, Palo Alto, Mar 22, 2016 (INVITED SPEAKER)
163. Gladstone Institute of Neurological Disease Seminar Series, March 23, 2017 (INVITED SPEAKER)
164. Moderna Therapeutics, Cambridge, MA, March 27, 2017 (INVITED SPEAKER)
165. Neurology Seminar, University of Massachusetts Medical School, MA, March 28, 2017 (INVITED SPEAKER)
166. Wave Life Sciences, Belmont, MA, March 29, 2017 (INVITED SPEAKER)
167. Regeneron Pharmaceuticals, Tarrytown, NY, March 30, 2017 (INVITED SPEAKER)
168. Department of Biological Sciences, Columbia University, NY, April 3, 2017 (INVITED SPEAKER)
169. Rutgers New Jersey Medical, NY, April 4, 2017 (INVITED SPEAKER)
170. Mount Sinai, Icahn School of Medicine, NY, April 5, 2017 (INVITED SPEAKER)
171. Memorial Sloan Kettering, Departmental Biology Seminar Series, NY, April 6, 2017 (INVITED SPEAKER)
172. RNA symposium at University of California, Irvine, April 14, 2017 (INVITED SPEAKER)
173. Arcturus Pharmaceuticals, La Jolla, April 18, 2017 (INVITED SPEAKER)
174. Experimental Biology Meeting Post-transcriptional regulation of intestinal homeostasis: stem cells to cancer, Chicago, April 24, 2017 (INVITED SPEAKER)
175. Cleveland Clinic, Cleveland, Ohio, April 26, 2017 (INVITED SPEAKER)
176. Case Western Reserve University, RNA center distinguished lecture series, April 27, 2017 (INVITED SPEAKER)
177. Illumina User Group Meeting, Hilton Torrey Pines, La Jolla, 24 May, 2017 (INVITED SPEAKER)
178. 22nd Annual RNA Society Meeting, Prague, June 3, 2017 (EARLY CAREER AWARD RECIPIENT'S TALK)
179. Dagstuhl "Computational challenges in RNA-based gene regulation: protein-RNA recognition, regulation and prediction", Germany, June 18-21, 2017 (INVITED SPEAKER)
180. Max-Delbruck-Center for Molecular Medicine, BMSB Seminar Series, Germany, June 22, 2017 (INVITED SPEAKER)
181. Max-Delbruck-Center for Molecular Medicine, SysBio lecture series on "Reprogramming, development and genome editing", Germany, June 23, 2017 (INVITED SPEAKER)

182. 2nd International Symposium for Noncoding RNA Neo-Taxonomy, University of Tokyo, Japan, June 26, 2017 (INVITED SPEAKER)
183. Naito conference on Non-coding RNAs, Hokkaido, Japan, June 30, 2017 (INVITED SPEAKER)
184. Single Cell Analysis Course, Cold Spring Harbor Laboratory, July 3, 2017 (COURSE INSTRUCTOR AND SPEAKER)
185. Neuroscience and behavioral disorder seminar series at Duke-NUS Medical School, Aug 3, 2017 (INVITED SPEAKER)
186. Otto Warburg International Summer School and Research Symposium on RNA biology, Shanghai, China, Aug 14-18, 2017 (LECTURER AND INVITED SPEAKER)
187. Eukaryotic mRNA Processing Meeting, Cold Spring Harbor Laboratory, Aug 22-26, 2017 (SESSION CHAIR & GAVE 2 SELECTED TALKS & 1 POSTER).
188. International Myotonic Dystrophy Consortium, San Francisco, Sept 5-9, 2017 (KEYNOTE SPEAKER)
189. Science 1st: Designing Nucleic Medicines, JLABs, La Jolla, Sept 13, 2017 (INVITED SPEAKER)
190. UCSD Institute for Genomic Medicine Member Meeting, UCSD, La Jolla, Sept 14, 2017 (INVITED SPEAKER)
191. Cell Biology Virtual Event, Sept 21, 2017 (INVITED SPEAKER)
192. 13th Annual meeting of the Oligonucleotide Therapeutics Society, Bordeaux, France, Sept 24-27, 2017 (INVITED SPEAKER)
193. 3rd annual RNA biology symposium by the Cancer science institute at NUS, Singapore, 2017 (CO-ORGANIZER)
194. 5th annual Single Cell Analysis Asia Congress by Oxford Global, Singapore, October 10-11, 2017 (INVITED SPEAKER)
195. UT Southwestern Medical Center's Gene Regulation and Genomics Seminar Series, Dallas, October 16, 2017 (INVITED SPEAKER)
196. 4th Animal Models of Neurodegenerative Diseases, PIGMOD Center, Czech Republic, October 22-24, 2017 (INVITED SPEAKER, ONLINE)
197. CZI Science and NYSCF Workshop, New York, October 30-31, 2017 (INVITED SPEAKER)
198. American Association of Pharmaceutical Scientists, Challenges and Opportunities for Gene Editing and Delivery, San Diego, Nov 15, 2017 (INVITED SPEAKER)
199. UCSD Postdoc Appreciation Luncheon, UCSD, La Jolla, Nov 29, 2017 (KEYNOTE SPEAKER)
200. Center for Neurogenetics 3rd International BrainStorm Symposium, University of Florida, Gainesville, Florida, Jan 19, 2018 (INVITED SPEAKER)
201. IPSEN sponsored Bridging Biomedical Worlds "Genome Editing: the next Frontier", Biopolis, Singapore, Feb 5-7, 2018 (INVITED SPEAKER)
202. Rady School of Management Rady[X] conference on Disruptive Technologies, La Jolla, San Diego, Mar 2, 2018 (KEYNOTE SPEAKER)
203. Distinguished Speaker Seminar Series, Perelman School of Medicine, University of Pennsylvania, Mar 19, 2018 (DISTINGUISHED SPEAKER)
204. American Society for Neurochemistry, RNA processing and regulation in brain development and disorders, Riverside, Mar 25, 2018 (SPEAKER AND CO-CHAIR)
205. San Diego Public Library Lecture Series, La Jolla/Riford Library, April 3, 2018 (INVITED SPEAKER)
206. NCCR RNA & Disease Seminar Series, University of Bern, Bern, Switzerland, April 9, 2018 (INVITED SPEAKER)
207. Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland, April 10, 2018 (INVITED SPEAKER)
208. Biozentrum, University of Basel, Basel, Switzerland, April 11, 2018 (INVITED SPEAKER)
209. NCCR RNA & Disease Seminar Series, ETH, Zurich, Switzerland, April 12, 2018 (INVITED SPEAKER)
210. ASBMB Experimental Biology Symposium in "RNA in human disease," San Diego Convention Center, San Diego, April 23, 2018 (INVITED SPEAKER)
211. Taste of Science, Thorn Street Brewery, San Diego, April 24, 2018 (INVITED SPEAKER)
212. Biochemistry Seminar Series, Duke University, North Carolina, April 27, 2018 (INVITED SPEAKER)
213. Inaugural Stem Cell mini-symposium by Lee Kong Chian School of Medicine, Singapore, May 22, 2018 (INVITED SPEAKER)
214. NUS Physiology Department Science Pitch Day, Singapore, May 25, 2018 (INVITED JUDGE)
215. Precision CRISPR stem cell, Seattle, Allen Institute for Cell Science, June 13-14, 2018 (INVITED SPEAKER)
216. Takeda Autism Day, Takeda, La Jolla, June 26, 2018 (INVITED SPEAKER)
217. RNA Computational Biology Session at ISCB, Chicago, July 8, 2018 (KEYNOTE SPEAKER)
218. Blavatnik Science Symposium, 7 World Trade Center, New York, July 16, 17, 2018 (ATTENDED AS HONOREE)
219. Gordon Research Conference in Post-transcriptional gene regulation meeting, Sunday River, Portland, ME, July 15-20, 2018 (INVITED SPEAKER)
220. Angelman Syndrome/Dup15q Research Symposium, Chapel Hill, North Carolina, Aug 6-7, 2018 (INVITED SPEAKER)
221. Ribometrix Scientific Advisory Board Meeting, Durham, North Carolina, Aug 8, 2018 (INVITED SPEAKER)
222. Cell Signaling Technologies, Massachusetts, Aug 21, 2018 (INVITED SPEAKER)
223. Genome Engineering: The CRISPR-CAS Revolution, Cold Spring Harbor Laboratory, Aug 22-Aug 25, 2018 (INVITED SPEAKER).
224. Waisman Center Seminar Series, University of Wisconsin, Madison, Sept 7, 2018 (INVITED SPEAKER)
225. Genomics Institute of the Novartis Research Foundation Technology Showcase "Targeting RNA", La Jolla, Oct 4, 2018 (INVITED SPEAKER)
226. Cancer Cell Biology Training Grant, UCSD, Oct 5, 2018 (INVITED SPEAKER)
227. Nature/Ionis Symposium on RNA at the Bench and Bedside, Estancia Hotel, La Jolla, Oct 10, 2018 (INVITED SPEAKER)
228. UCSD Neuroscience Seminar Series, Oct 29, 2018 (INVITED SPEAKER)
229. 5th RNA Metabolism in Neurological Disease Conference, Nov 1, 2018 (INVITED SPEAKER)
230. Inside Innovation Seminar Series hosted by UCSD Office of Innovation and Commercialization, Nov 7, 2018 (INVITED SPEAKER)
231. Science webinar "Epitranscriptomics: the importance of RNA modifications and RNA binding proteins in disease," Nov 14, 2018 (INVITED SPEAKER)
232. CRG Student-invited Seminar Series, Barcelona, Nov 23, 2018 (INVITED SPEAKER)

233. Plant and Animal Genome XXVII, Equine Genome. San Diego, 13 Jan, 2019 (KEYNOTE SPEAKER)
 234. UCSD PRISM (Progress in the Science of Medicine) Lecture Series, UCSD, 11 Feb, 2019 (INVITED SPEAKER)
 235. Gordon Research Conference, Translation Machinery in Health and Disease, Galveston, 19 Feb 2019 (INVITED SPEAKER)
 236. University of Chicago, Biological Sciences Seminar Series, Chicago, 13 March 2019 (INVITED SPEAKER)
 237. Ribometrix Scientific Advisory Board Meeting, Durham, North Carolina, March 25, 2019 (INVITED CONSULTANT)
 238. MDA 2019 Clinical and Scientific Conference, Orlando, Florida, April 15, 2019 (INVITED SPEAKER AND SESSION CO-CHAIR)
 239. Nanyang Technology University MBA student Visit, UCSD Rady School of Management, April 25, 2019 (INVITED SPEAKER)
 240. Sanford Burnham Prebys Graduate Student Retreat, San Diego, May 16, 2019 (KEYNOTE SPEAKER)
 241. UCSD Neuroscience Graduate Program Spring Retreat, Lake Arrowhead, May 17, 2019 (INVITED SPEAKER)

COURSES/COURSEWORK ATTENDED

CSHL Single Cell Analysis Course. Course Directors: Gene Yeo, Mike McConnell, Amy Herr, June 7-17, 2016

Revolutionary Sequencing Technologies and Applications, Cold Spring Harbor Laboratory by Greg Hannon, Elaine Mardis, Gabor Marth, Richard McCombie, John McPherson and Michael Zody, November 2007

Brain development and function at Cold Spring Harbor Laboratory by Michael Posner and Ron McKay, June-July 2000.

Ph.D. coursework included Machine Learning (Jaakkola), Neural Networks (Seung), Statistical Learning Theory and Applications (Poggio), Computational Functional Genomics (Young, Gifford), Cognitive and Behavioral Genetics (Housman, Nedivi, Pinker), Neural Plasticity in Learning and Development (Tonegawa, Quinn, Wilson, Liu), Topics in Statistics (Hardy), Nucleic Acids (RajBhandary, Bartel) GPA: 5.0 / 5.0

GRANT SUPPORT

ACTIVE GRANTS

NIH GRANTS

Gene Yeo (contact PI)

P01 AI132122

7/1/2018-6/30/2019

NIH/NIAID

Single-cell transcriptomic and epigenetics core

The Single-Cell Transcriptomics and Epigenetics (SCTE) Core will support all three Projects and the Bioinformatics and Computational Biology (BCB) Core in generating robust single-cell transcriptomic and small-cell-number epigenetic datasets as well as performing DNA-sequencing for interpretation of in vivo shRNA-based functional screens. The SCTE Core will provide a centralized resource for generating single-cell RNA-sequencing, histone modification ChIP-seq, transcription factor ChIP-seq, and ATAC-seq datasets. Additionally, the SCTE Core will generate and analyze deep DNA-sequencing data to determine the distribution of shRNAs among transduced CD8+ T cells in the context of the functional screens. We envision that use of a single Core will increase rigor and reproducibility in experimental methodology, increase synergy among investigators and laboratories, and enable direct comparison of the resulting datasets. Generation of these datasets will enable the BCB Core and individual Projects to achieve the overall goal of elucidating the molecular heterogeneity, transcriptional and epigenetic regulation, and function of tissue-resident CD8+ T cells in the context of acute and chronic infection.

Gene Yeo (contact PI)

R01 EY029166

4/1/2018-3/31/2022

NIH/NEI

Analysis of RNA-targeting Cas9 to Fuchs' Dystrophy

Fuchs' endothelial corneal dystrophy is a degenerative disorder of the eye's corneal endothelium and the most common indication for corneal transplantation. The majority of patients carry a trinucleotide repeat expansion in the TCF4 gene, causing sequestration of the MBNL1 splicing factor and widespread mis-splicing of MBNL1- regulated transcripts. Here we propose to use patient-derived cells to provide a characterization of the molecular pathology of this disease and evaluate the potential of our newly developed RNA-targeting CRISPR/Cas9 system as a therapeutic modality to eliminate toxic repeat expansions in TCF4 RNA transcripts.

Brenton Graveley (contact PI), Gene Yeo (multi-PI)

U41 HG009889

2/5/2018-01/31/2022

NIH/NHGRI

A comprehensive functional map of human protein-RNA interactions.

The objective of the ENCORE (Encyclopedia of RNA Elements) Consortium is to develop a foundational, functional map of protein-RNA interactions of RNA binding proteins (RBPs) encoded in the human genome, and the RNA elements they bind to across the transcriptome. These RNA elements, when expressed, form the basis of co- and post-transcriptional regulation of human genes. Our strategy consists of developing and integrating a physical map of 300 RBPs in two different human cell lines with transcriptome-wide measurements of the effects of depleting these RBPs, their localization patterns and their binding preferences independent of co-factor

associations. Over the past 4 years, our consortium (Burge, Graveley, Lecuyer and Yeo) has established highly efficient data production workflows of experimental methods (RNA bind-n-seq, RNA-seq, Localization and enhanced CLIP) that will enable us to immediately expand these datasets, which form a crucial and missing link to decipher the mechanisms of post-transcriptional regulation and how these impact genetic variation and disease etiology. When combined with the data we generated over the past four years, these efforts will culminate in a comprehensive map of the functional RNA elements recognized by essentially all RBPs expressed in two human cell lines, representing approximately half of the known complement of human RBPs. ENCORE will (1) generate and validate a physical resource of cell lines expressing epitope-tagged RBPs, (2) develop transcriptomics and imaging databases of these RBPs to provide simple interfaces for the community to mine this resource, (3) develop and distribute workflows for integrative analyses and shareable results from these workflows and (4) provide training and outreach to establish ENCORE annotations as the standard reference for co- and post-transcriptional research and clinical genomics efforts in the long-term.

Xiang-dong Fu (contact PI), Gene Yeo (multi-PI)
R01 HG004659
NIH/NHGRI

6/1/2018-6/30/2020

Functional RNA elements in the human genome

This proposal seeks competitive renewal of a multi-PI project (Fu and Yeo), which aims to use global approaches to elucidate the regulatory principles of RNA binding proteins (RBPs) in mammalian genomes. Built upon our accomplishments in the past funding cycle, we propose to leverage the powerful experimental and computational tools we have developed to pursue four specific aims. In Aim 1, we will couple gain- and lost-of-function multi-target screens to deduce regulatory pathways at both splicing and polyadenylation levels. We will focus on determining the specific function of different RNA polymerase II (Pol II) subunits, rather than by the Pol II CTD alone, in the recruitment of RNA processing machineries for co-transcriptional RNA processing. In Aim 2, we will develop a general strategy for systematic identification of chromatin-associated RBPs to determine direct contribution of some RBPs to transcription and co-transcriptional RNA processing reactions. We will concentrate our efforts in dissecting a potential new pathway in epigenetic control of alternative splicing as well as broader roles of specific RBPs in direct transcriptional control. In Aim 3, we will use a novel strategy for identification and characterization of non-canonical RBPs. Focusing on a large number of newly identified finger zinc (Znf) proteins, we propose to determine their roles in binding to both DNA and RNA and deduce their transcriptome-wide interactions with RNA. We also propose to pursue a specific paradigm in this aim on a newly identified RBP known to associate with the nuclear pore to determine its role in selective mRNA nuclear export, which is pertinent to an ALS-regulated disease pathology. Combined, we believe that this comprehensive, interconnected, and hypothesis-driven research plan will greatly advance our understanding of regulated RNA processing and associated disease mechanisms.

Gene Yeo (contact PI)
R01NS103172
NIH/NINDS

9/22/17-05/31/22

Therapeutic strategies for microsatellite expansion diseases using RNA-targeting CRISPR/Cas

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas system has become widely adopted for DNA recognition, enabling applications such as genome editing and recruiting effector proteins to DNA to affect transcription or enable imaging. Recently in Nelles et al, Cell, 2016, we showed that with modifications, catalytically dead Cas9 with a modified oligonucleotide containing the PAM recognition sequence is able to bind specific mRNAs in living mammalian cells and is able to track their movement, opening up the potential for many RNA applications of Cas proteins. In this proposal, we aim at developing an adeno-associated virus (AAV)-based therapeutic strategy for myotonic dystrophy, a microsatellite expansion disease characterized by expanded CTG repeats, using RNA-targeting CRISPR/Cas9 (RCas9). We will perform in vivo safety and efficacy studies of our AAV-based therapy and evaluate the hypothesis that alternative RNA processing biomarkers are reliable for measuring treatment efficacy of RCas9 in myotonic dystrophy. If successful, we will have taken a significant step forward in developing a treatment for a class of microsatellite expansion diseases.

Gene Yeo (contact PI)
1U19 MH107367
NIH/NIMH

07/01/15-06/30/20

Collaboration on preclinical autism cellular assays, biosignatures, and network analyses (Copacabana)

This study aims to generate robust tools and workflows for creating human induced pluripotent stem cell (hiPSC)-based models of autism spectrum disorder (ASD), and to develop scalable assays for predictive molecular and cellular phenotypes relevant to autism. We have identified several key bottlenecks in the widespread adoption of hiPSCs as tools that allow the dissection of molecular mechanisms underlying neurological disease and enable preclinical drug screening. We have assembled a team of five leading experts in neuroscience, stem cell biology and computational biology, who will collaborate up with three innovation-driven biotech companies (Fluidigm, BD Biosciences and Synthetic Genomics) to overcome these roadblocks. Since autism is considered a disorder of synapse development and function that ultimately leads to circuit dysfunction in the brain, we will develop quantitative assays of synapse end network function that can be used in high-throughput drug screens. We also aim to uncover the upstream molecular events that precipitate synaptic and network dysregulation, and identify predictive RNA and protein signatures. Our strategy is to engineer models of genetic forms of autism by genomic manipulation using a well-characterized, neurotypical hiPSC line as the starting point. We will then differentiate these normal and mutant cells to cortical neurons and astrocytes, the two cell types that have been most strongly implicated in autism pathophysiology. Highly quantitative and sensitive assays at the single-cell level will be used to identify changes in protein and RNA expression that can distinguish ASD neurons and astrocytes from normal cells. Finally, we will develop assays measuring synapse density and strength using advanced technology that can be used in high-throughput format. We envision that our

tools, technologies and assays, all of which we will make publicly available as they are being generated, will both critically contribute to our understanding of ASD and accelerate preclinical research of neurological disease.

John Chang (contact PI), Gene Yeo (multi-PI)
R01 AI123202
NIH/NIAID

09/23/16-08/31/21

Using single-cell RNA-seq to interrogate host immunity to pathogens
Mortality from infectious diseases remains a leading cause of death worldwide, making the development of new vaccines an important priority of biomedical research. Immunologic memory is a cardinal feature of adaptive immunity and an important goal of vaccination strategies. Traditional vaccination strategies are very effective at generating neutralizing antibodies against bacteria and viruses. However, a vaccine capable of generating robust T lymphocyte memory is still beyond our research, due, in part, to an incomplete understanding of the molecular basis of lymphocyte fate specification. In this proposal, we will develop single-cell approaches to study specification of lymphocyte fates in response to microbial infection.

Gene Yeo (contact PI), Neil Chi (multi-PI)
R01 HD085902-01
NIH/NICHD

03/01/2016-02/28/2021

Reconstruction of cardiovascular regulatory networks from large-scale single-cell analyses of cardiovascular lineages.
The gene regulatory networks underlying early human cardiovascular (CV) development is poorly understood, in large part due to the dearth of molecular and genetic information specifying the diversity of cardiovascular progenitor cell-types (CVPCs). Human pluripotent stem cell (hPSC)-derived CV cells provide a model for human cardiogenesis and afford us the opportunity to reveal the various CV cell types generated during heart development and to also functionally discover and validate CV developmental gene regulatory networks. In this proposal, we will employ single cell transcriptome (RNA-seq) analysis to dissect the heterogeneity of early CV progenitor populations that give rise to the spectrum of distinct CV cell types and their intermediates. By identifying these potentially rare and novel progenitor cell types as well as studying their lineage choice decisions at the single cell level, the cellular and molecular networks underlying these progenitor cells and their differentiated CV cell types that control their differentiation can be revealed. To achieve our goal, a synergistic and complementary collaboration between the Yeo and Chi labs will aim to (1) investigate the diversity and organization of CV cellular subtypes during cardiogenesis in vitro, (2) develop novel algorithms that enable the extraction of gene regulatory programs that specify CV lineage sub-networks and (3) investigate the functional significance of identified CV cell subtypes. If successful, we will reveal pathways and cell-types that will advance our basic and translational framework for treating congenital heart disease.

ALSA 17-IIP-352

8/1/2016-7/31/2019

Discovery of stress granule components in models of ALS

The major goals of this project are to identify protein and RNA components in stress granules in motor neurons from ALS patient cells

COMPLETED GRANTS

Gene Yeo (PI)
ALSA VC8370

8/1/2015-7/31/2018

Comprehensive analysis of RNA localization and transport mechanisms in wildtype and ALS motor neurons

The major goals of this project are to use computational and molecular techniques to identify an RNA signature of TDP-43 dependent misregulation in human neurons derived from stem cells.

Gene Yeo (co-PI)
3 U01HL107442-04S1 (Frazer and Yeo)
NIH/NHLBI Supplement

9/1/2014-6/30/15

Regulatory Genomic Studies in a Cohort of IPS Cell Derived Cardiomyocytes

The goal of this grant is to perform single-cell sequencing to identify regulatory circuits during cardiomyocyte specification from induced pluripotent stem cells. My lab is responsible for all the single-cell RNA-seq library preparations and analyses

Gene Yeo (PI)
R01 GM084317-01A1 (Ares, M, Contact PI)
NIH/NIGMS (sub-award with UC Santa Cruz)
Genomic measurement of alternative splicing

01/01/2009-12/31/2012

In this multi-PI project, we will focus on the development and application of alternative splicing DNA microarrays that allow medium to high-throughput parallel detection and analysis of multiple alternative splicing patterns.

Gene Yeo (PI)
CIRM RB1-01413 Basic Biology I

10/01/2009-9/30/2012

RNA binding protein-mediated Post-transcriptional Networks Regulating HPSC Pluripotency

In this project, we will focus on comprehensively identify transcribed RNAs in human pluripotent stem cells that are directly targeted by RNA binding proteins important in pluripotency.

Gene Yeo (Co-investigator)
CIRM RB3-05219 Basic Biology III 10/01/2011-9/30/2014
Viral-host interactions affecting neural differentiation of human progenitors
In this project with the Spector lab, we focus on studying if HCMV infection of human neural progenitors affects differentiation using a battery of genomics and computational methods.

Gene Yeo (PI)
CIRM RB3-05009 Basic Biology III 10/01/2011-9/30/2014
Neural and general splicing factors control self-renewal, neural survival and differentiation
In this project, we focus on studying if splicing factors can control stem cell pluripotency and differentiation.

Gene Yeo (PI)
CIRM TR3-05676 Early Translation III 12/1/2012-11/30/2015
Molecules to correct aberrant RNA signature in human diseased neurons
In this project, we focus on using an RNA signature for ALS to screen for small molecules that reverse the signature to a healthy neuron.

Gene Yeo (PI)
CIRM RB4-06045 Basic Biology IV 3/01/2013-2/28/2016
Stem cell models to analyze the role of mutated C9ORF72 in neurodegeneration
In this project we will reprogram somatic cells from C9ORF72 mutant patients to generate human iPSC models for the disease. We will use genome-wide technologies to reveal molecular pathways that differ between motor neurons derived from C9ORF72 patients, isogenic controls and repeat-harboring ES cells.

Gene Yeo (PI)
ALSA VC8K27 8/1/2011-7/31/2013
Identification of an RNA Signature of TDP-43 Dependent Misregulation in Human Neurons
The major goals of this project are to use computational and molecular techniques to identify an RNA signature of TDP-43 dependent misregulation in human neurons derived from stem cells.

Gene Yeo (PI)
Roche EIN Grant 01/01/2012-01/01/2014
Reversing RNA processing defects, a common basis for neurodegenerative disorders
In this grant with Roche Pharmaceuticals, we will use robust, inexpensive and scalable genomic technologies to identify small molecules that can revert the RNA signature of an abnormal neuron to normality.

Gene Yeo (Co-investigator)
CIRM RT2-01927 Tools and Technologies II 04/01/2011-03/31/2014
Developing a method for rapid identification of high-quality disease specific hPSC lines
In this project with the Goldstein lab, we will focus on developing high-throughput assays and methods to generate and identify hPSC lines.

Gene Yeo (PI)
Brain Research Foundation Grant BRFSG-2014-14 06/01/2014-05/31/2015
Global analysis of transcriptome diversity at the single cell level in human neurons
This project funds single cell analysis in human neurons.

Gene Yeo (PI)
1 R01 NS075449-01A1 02/15/2012-01/31/2017
NIH/NINDS
Defining the messenger RNP code in the brain
This proposal seeks to establish the interactions among selected RNA binding proteins and their functional RNA elements in mammalian neurons. This will be a crucial first step in elucidating the RNA networks regulated by these RNA binding proteins in the brain. The goal is to identify the RNA maps and predictive models for RNA processing in the brain based on functional changes and binding of RNA binding proteins.

Fu, X-D, Gene Yeo (multi-PI)
R01 HG004659-03 06/01/2011-05/31/2014
NIH/NHGRI
Functional RNA elements in the human genome
In this multi-PI project, we will couple the CLIP (crosslinking immunoprecipitation) technology with high-throughput sequencing based on the Illumina/Solexa system to identify in vivo binding sites for RNA binding proteins in human 293 cells. We will focus on RNA binding proteins implicated in both constitutive and regulated pre-mRNA processing. We will perform profiling of alternative splicing in addition to physical mapping, which will enable the bioinformatics analysis necessary to decode the functional RNA elements in the human genome.

Gene Yeo (co-PI)

U54HG007005 (Graveley, B, Contact PI)

09/01/2012-8/31/2016

NIH/NHGRI

ENCODE Project: Comprehensive analysis of functional RNA elements in the human genome.

The goals of this project are to identify the functional RNA elements recognized by 250 RNA binding proteins in the human genome in HeLa-S3 and GM12878 cells.

Gene Yeo (PI)

U01 HL107442-01 (Frazer, K, Contact PI)

5/01/2011-4/30/2016

Regulatory Genomic Studies in a cohort of iPSC cell derived cardiomyocytes

In this multi-PI grant with the Frazer lab, we will use iPSC derived cardiomyocytes from genotyped individuals as cellular models to investigate how human genetic variation influences the gene regulatory networks involved in cardiac biology.

Gene Yeo (co-PI)

1 R01AI095277-03S1 (Chang, Contact PI)

09/1/2014-8/31/16

NIH/NIAID Supplement

Regulation and Function of Polarity and Asymmetric Cell Division in Immunity

The goal of this grant is to assess the regulation of asymmetric cell division of CD8+ T cells in immunity. My lab is responsible for all the single-cell RNA-seq library preparations and analyses.

MENTORING

Postdoctoral fellows (2008-current)

Past / Current Trainee	Trainee Name	Postdoc Research Training Period	Current Position of Past Trainees or Source of Support for Current Trainees
Past	Katlin Massirer	2010-2011	Faculty (Professor), State University of Campinas, Sao Paulo, Brazil
Past	Kasey Hutt	2010-2014	Bioinformatics Scientist, R&D, Invivoscribe, San Diego
Past	Jason Nathanson	2009-2014	Scientist II, R&D, Sequenom, San Diego
Past	Leo Kurian	2013-2014	Faculty (Group leader), Cologne University, Germany
Past	Suzanne Lee	2013-2014	Faculty , Western Washington University, Bellingham, WA
Past	Katannya Kapeli	2012-2015	Senior Research Fellow at National University of Singapore
Past	Tomas Bos	2012-2017	BAEF – Belgian American Education Foundation
Current	Sebastian Markmiller	2011-current	Larry L Hilblom Fellowship
Current	Eric Van Nostrand	2012-current	Damon Runyon Cancer Fellowship
Current	Kristopher Brannan	2014-current	CIRM Post-doc Fellowship; UC President's Fellowship
Current	Yan Song	2011-current	NIH Grant, Takeda-UCSD partnership
Current	Frederick Tan	2015-current	American Cancer Society fellowship
Past	Ron Batra	2015-2017	Myotonic Dystrophy Association Fellowship, VP R&D Locana
Past	Ashleigh Schaffer	2015-2016	Faculty (Assistant Professor) at Case Western Reserve University, previous NIH K99 Award
Current	Alex Chaim	2015-current	IRADCA postdoctoral fellow
Current	Mark Perelis	2017-current	NIH Grant

Current	Meredith Corley	2017-current	ALSA postdoctoral fellowship
Current	Joshua Schwartz	2018-current	NIH Grant

Graduate (PhD) students (2008-current)

Past / Current Trainee	Trainee Name	Training Period	Current Position of Past Trainee /Source of Support for Trainee
Past	Melissa Wilbert	2008-2014	Computational Biologist, Novartis, Boston/ Genetics Training Program and CIRM Predoc Fellowship
Past	Stephanie Huelga	2009-2014	Bioinformatics Scientist at Nugen /NSF Graduate Fellowship, ARCS scholarship
Past	Michael Lovci	2009-2014	Postdoc in Germany/NSF GK12 Fellowship, Gift from Genentech, ARCS scholarship
Past	Thomas Stark	2008-2014	Postdoc at CDC/ UCSD Genetics Training Program
Past	Anne Conway	2008-2014	Postdoc at UCSD/ Genetics Training Program
Past	Boyko Kakaradov	2012-2015	Bioinformatics Scientist, Human Longevity Institute/ NSF Graduate Fellowship
Past	David Nelles	2010-2016	NSF Graduate Fellowship, ARCS scholarship
Past	Julia Nussbacher	2012-2017	NIH T32 Cancer cell Training Grant, ARCS scholarship
Past	Fernando Martinez	2012-current	NIH Genetics Training Grant
Past	Gabriel Pratt	2012-2018	NSF Graduate Fellowship, ARCS scholarship
Past	Olga Botvinnik	2013-2017	NDSEG Fellow, John Hunter Open Source Fellow, ARCS scholarship
Past	Mark Fang	2015-2019	MSTP program, NIH grant (Yeo)
Past	Leen Jamal	2013-2018	NSF Graduate Fellowship
Current	Emily Wheeler	2015-current	NIH grant (Yeo); NSF fellowship, ARCS scholarship
Current	En-ching Luo	2015-current	Taiwan government Fellowship, NIH grant (Yeo)
Current	Jaclyn Einstein	2015-current	NIH grant (Yeo); F31 NIH NRSA pre-doc fellowship, ARCS scholarship
Current	Zhaoren He	2015-current	Joint student with Kees Murre
Current	Matthew Hunt	2015-current	Joint student with Mark Tuszynski
Current	Ben Lewis	2015-current	Joint student with Tony Hunter (Salk)
Current	Ryan Marina	2016-current	NIH grant (Yeo), ARCS scholarship
Current	Anthony Vu	2016-current	NSF fellowship
Current	Noorsher Ahmed	2018-current	NIH grant (Yeo)
Current	Margaret Burns	2018-current	NIH grant (Yeo)
Current	Jonathan Schmok	2018-current	NIH grant (Yeo)
Current	Yilan Shi	2018-current	NIH grant (Yeo)

PHD/MS THESIS COMMITTEE CHAIR/CO-CHAIR/(MEMBER by default)

Anthony Quoc Vu, Biology (Graduated, Fred Gage's Lab), MS, Summer 2008
 Beverly Chen, (Graduated, Michael Rosenfeld's Lab), MS, Fall 2010
 Mary Winn, BMS (Graduated, Nick Schork's Lab), PhD, Fall 2011, **Co-Chair**
 Benjamin O'Connor, Biology (Graduated, Jean Wang's Lab), PhD, Spring 2012
 Lorne Walker, BMS (Graduated, Doug Richman's Lab), PhD, Summer 2013
 Gloria Kuo Lefkowitz, BMS (Graduated, Ben Yu's Lab), PhD, Winter 2012
 Boris Reznik, Biology (Graduated, Jens Lykke-Andersen's Lab), PhD, Fall 2012
 Mark Kuei-Chun Wang, Bioengineering (Graduated, Shu Chien's Lab), PhD, Fall 2012
 Gregory Dane Clemenson, Biology (Graduated, Fred Gage's Lab), PhD, Winter 2012
 Yunghui Chang, Biology (Graduated), MS, Fall 2011
 Wesley Gifford, Group in Neurosciences (Graduated, Sam Pfaff's Lab), PhD, Spring 2013
 Nisha Rajagopal, Bioinformatics (Graduated, Bing Ren's Lab), PhD, Fall 2013
 Shannon Muir, BMS (Graduated, Karen Arden's Lab), PhD, Summer 2014
 Jeremy Coleman Davis-Turak, Bioinformatics (Graduated, Alex Hoffman's Lab), PhD, Summer 2014, **Co-chair**
 Charles Thomas, BMS (Graduated, Alysson Muotri's Lab), PhD, Summer 2014
 Qi Ma, Bioinformatics (Graduated, Michael Rosenfeld's Lab), Winter 2015, **Co-chair**
 Gary Johnston, Material Science (Graduated, Sung Ho Jin's Lab), PhD, Spring 2015
 Eleen Shum, BMS (Graduated, Miles Wilkinson's Lab), PhD, Spring 2015
 Allan Acab, BMS (Graduated, Alysson Muotri's Lab), PhD, Spring 2015
 Sol Reyna, BMS (Graduated, Larry Goldstein's Lab), PhD, Summer 2015
 Daria Merkurjev, Bioinformatics (Graduated, Michael Rosenfeld's Lab), PhD, Fall 2015
 Rui Fu, Biology (Graduated, Lykke-Andersen's Lab)
 Jennifer Higginbotham, BMS (Graduated, Clodagh O'Shea's Lab)
 Cory White, Bioinformatics (Graduated, Chris Woelk's Lab), PhD, Spring 2016
 Matthew Sternfeld, Biology (Graduated, Sam Pfaff's Lab)
 Lauren Fong, BMS (Graduated, Larry Goldstein's Lab), PhD,
 Steven Lee Ceto (Current, SPAC Advisor)
 Amy Michelle Chinn (Current, SPAC Advisor)
 Martha Flores, Biology (Current, Kees Murre's Lab)
 Elaine Pirie, BMS (Graduated, John Ravit's Lab), Co-chair, PhD
 Layla Fijany, Biology (Graduated, Yeo Lab), Advisor
 Jonathan Grinstein, BMS (Graduated, Neil Chi's Lab)
 Sarah Anne Barnhill, Materials Sciences (Current, Nathan Gianneschi's Lab)
 Alexander Sinclair Hamil (Graduated, Steve Dowdy's Lab)
 Polly Pu Huang, BMS (Current, Pamela Mellon's Lab)
 Charles Bradford Larson (Current, Bradley Moore/Victor Nizet's Lab)
 Naomi Ellen Searle, BMS (Graduated, Lorraine Pillus' Lab)
 Kristopher Standish, BMS (Graduated, Nicholas Schork's Lab), **Co-chair**
 Nicholas Vinckier, BMS (Graduated, Maik Sander's Lab)
 Soohwan Oh, Biology (Graduated, Michael Rosenfeld's Lab)

SERVED ON MINOR PROPOSITION COMMITTEE

Shannon Muir – Committee Member, 2009
 Jesse Dixon – Committee Member, 2009
 Sol Reyna - Committee Member, 2010
 Eleen Shum - Committee Member, 2010
 Brandon Sos - Committee Member, 2011
 Jacqueline Ward - Committee Member, 2011
 Babette Hammerling - Committee Member, 2012
 Elaine Pirie - Committee Member, 2012
 Charles Larson – Chair, 2013
 Kevin Ross - Committee Member, 2013
 Navarre Gutierrez-Reed - Committee Member, 2014
 Sarah Ur - Committee Member, 2014
 Vivian Fu - Committee Member, 2015
 David Jakubosky - Committee Member, 2015
 Jackson Jones - Committee Member, 2015