



Gene W. Yeo, Ph.D., MBA

Professor

Dept 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

ewyeo@ucsd.edu

<https://www.yeolab.com>

twitter: @yeo_lab

Gene Yeo PhD MBA is a Professor of Cellular and Molecular Medicine at the University of California San Diego (UCSD), the founding Director for UCSD's Center for RNA Technologies and Therapeutics, the founding Chief Scientific Advisor for Sanford Laboratories for Innovative Medicine, a founding member of the Institute for Genomic Medicine and member of the UCSD Stem Cell Program and Moores Cancer Center. 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 from Massachusetts Institute of Technology, and an MBA from the UCSD Rady School of Management. Dr. Yeo serves as Co-Director of the Bioinformatics and Systems Biology Graduate Program, as Associate Director of a Genetics T32 training program at UCSD and as Chair of the Scientific Steering Committee of Sanford Consortium for Regenerative Medicine in La Jolla.

Dr. Yeo is a computational and experimental molecular and cell biologist who has contributed to genomics, RNA biology and therapeutics. His primary research interest is in understanding how RNA processing is regulated and the roles that RNA binding proteins (RBPs) play in development and disease. Gene has authored >200 peer-reviewed publications (**h-index 89 and i10-index 161**) 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. Gene's **mechanistic studies in RNA biology** tend to feature comprehensive, systematic and robust methodologies developed by his lab, such as enhanced CLIP for the purposes of large-scale mapping of protein-RNA interactions (Van Nostrand *et al*, *Nature Methods*, 2016; >1000 citations). His lab has also developed the STAMP technology (Brannan *et al*, *Nature Methods*, 2021) which is the first transcriptome-wide method for identifying RNA binding protein sites and measuring mRNA translation at single-cell resolution and with isoform-sensitivity. To facilitate biological interpretation of RBP interactomics data, Gene's lab also pioneers computational algorithms, such as CLIPper (Lovci *et al*, *NSMB*, 2013; >300 citations), SONAR (Brannan *et al*, *Molecular Cell*, 2016 and recently SKIPPER (Boyle *et al*, *Cell Genomics*, 2023). As a graduate student Dr. Yeo authored the MaxENT splice site algorithm (Yeo *et al*, *Journal Comp Biology*, 2003), which is arguably one of the most utilized and cited splice site scorers. Armed with these cutting-edge technologies, his lab is also a major contributor of resources to study RBPs that enable hundreds of labs across many areas of bioscience, such as the world's largest resource of RBP-specific antibodies that facilitated generation and interpretation of the most comprehensive maps of RBP-binding sites to date for hundreds of RBPs (Van Nostrand *et al*, *Nature*, 2020; >500 citations).

Dr. Yeo has also leveraged his understanding of how protein-RNA complexes control molecular and cellular pathways to develop **RNA-targeting therapeutics** and to identify **RBPs as candidate targets** for neurodevelopmental disorders, neurodegeneration and cancer. Gene's lab also develops stem cell-based models of human disorders such as myotonic dystrophy, Huntington's disease and ALS/FTD to study how defects in RNA processing leads to pathological hallmarks as well as evaluate therapeutic paradigms developed in his lab. To illustrate, Gene's lab has systematically studied normal and mutant RBPs in neurodegeneration, and uncovered RBPs that condense into RNA granules during stress and demonstrated strategies to leverage these for therapeutic use in neurodegeneration (Markmiller *et al*, *Cell*, 2018; >600 citations; Fang *et al*, *Neuron*, 2019; Wheeler *et al*, *Nature Methods*, 2020). His lab also demonstrated in vivo RNA targeting with CRISPR/Cas proteins (Nelles *et al*, *Cell*, 2016; >500 citations) with proof of concept in repeat expansion disorders in mice and 3D brain organoid models (Batra *et al*, *Cell*, 2017; Batra *et al*, *Nature Biomedical Engineering*, 2020; Morelli *et al*, *Science Translational Medicine*, 2022; Morelli *et al*, *Nature Neuroscience* 2022). Work from the Yeo lab has been highlighted in *Nature Methods* and *Nature Reviews Genetics* as "Method to Watch" and featured as a top story in *Discover* magazine. These efforts have led to clinical programs to develop medicines for RNA-related diseases.

Gene is on the **Editorial Boards** of the journals *Cell Reports*, *Cell Research* and *eLife*, and on the Advisory Board of *Review commons*. 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 inaugural Crick-Jacobs Fellow at the Salk Institute (2005-2008). Other awards include the Alfred P Sloan Fellowship in recognition of his work in computational molecular biology (2011), Alpha Chi Sigma-Zeta Chapter Krug Lecturer (2016), Singapore National Research Foundation Visiting Investigatorship Award (2017), the inaugural Early Career Award from the International RNA Society (2017), the Blavatnik National Award Finalist (2018 & 2019), San Diego Xconomy Awardee for 'Big Idea' (2019) and Highly Cited Researcher in Cross-Field category (2019, 2020, 2021, 2022), recognizing the world's most influential researchers of the past decade. Gene is also a **Paul Allen Distinguished Investigator (2020)** and received the **2021 Elisa Izaurralde Award for Innovation in Research, Teaching and Service from the RNA Society**. In 2023, Gene received the inaugural **Academia Europaea (AE) Sydney Brenner Medal (SBM)** given to honor the best in scholarship and personal achievements not more than 20 years after the PhD degree, given within the field of molecular biology and related disciplines. Gene is an elected member of AE. Gene is a **co-founder of biotech companies** which includes Locanabio, Eclipse Bioinnovations, Enzerna, Proteona (acquired by Singleron), Trotana and Orbital Therapeutics. Gene serves or had served on the scientific advisory boards of the Allen Institute of Immunology, Locanabio, Eclipse Bioinnovations, Proteona, CircBio, Aquinnah, Cell Applications, Tecan, LGC, Sardona Therapeutics, Insitro, Trotana, Nooma, Ribometrix, Automera, Atomic.AI, AmberBio and IntronX. Gene is among the top 50 life science academic entrepreneurs as released by BIOS Beaker List and recently received the inaugural Entrepreneurial Achievement Award by the Rady School of Management in 2023. Gene is a senior advisor to Accelerator Life Sciences Partners. Gene's lab has current or previous support from 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, Chan-Zuckerberg Initiative, Takeda, Genentech and Roche.

Gene is the faculty founder of DASL (Diversity and Science Lecture Series, 2020) providing a voice for scientists to discuss diversity, equity and inclusion challenges and celebrate their scientific achievements (now funded by CZI). Gene is the founder of the SCREEN (San Diego Covid-19 Research Enterprise Network, 2020) and founding member of the SEARCH (San Diego Epidemiology and Research for Covid Health, 2020) alliances in San Diego. SCREEN had ~1000 scientist members in San Diego focusing on grassroots research coordination and community outreach. SEARCH is focused on epidemiology studies of the prevalence of the virus completing a 12000-person study of viral spread. Gene helped found the EXCITE

(Expedited Covid Identification Environment) lab that performs Covid high-throughput testing at UCSD and served as a member of the Return-to-Learn steering committee at UCSD. 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 had completed 2 full Ironman-distance and multiple half-ironman-, olympic-, sprint-distance triathlons, full marathons and half-marathons, but now spends time rock climbing.

Contact information:
University of California San Diego
Sanford Consortium for Regenerative Medicine
2880 Torrey Pines Scenic Drive
La Jolla, CA 92037
858-534-9321 (office)
ewyeo@ucsd.edu

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. I have co-founded Eclipse Bioinnovations that leverages the enhanced CLIP technologies to provide RNA services and reagents to the broad community.
- ◆ **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. This has led to my co-founding Locana that is focused on bringing RNA-targeting gene therapy to the clinic for neuromuscular diseases. In my lab, 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	July 1 2016-current
	Department of Bioengineering, Affiliate Neuroscience Graduate Program	2018-current 2018-current
	Co-director, Bioinformatics and Systems Biology Graduate Program	
	Associate Professor, Department of Cellular and Molecular Medicine	July 1 2014-June 30 2016
University of California, San Diego, CA	Assistant Professor, Department of Cellular and Molecular Medicine	Oct 2008-June 30 2014
	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	

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

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, Director and Scientific Advisor, Locanabio (Incorporated May 3, 2016)	2016-current
Co-founder and Scientific Advisor, ProteoNA (Incorporated March 7, 2017, acquired by Singleron March 7, 2022)	2017-2022
Co-founder, Director and Scientific Advisor, Eclipse Bioinnovations (Incorporated June 23, 2017)	2017-current
Scientific Advisory Board member, Jumpcode	2017-current

Scientific Advisory Board member, Nugen now acquired by Tecan	2017-2018
Scientific Advisory Board member, Ribometrix	2018-2022
Scientific Advisory Board member, Allen Institute for Immunology	2018-current
Scientific Advisory Board member, LGC	2018-current
Scientific Advisory Board member, Sardona Therapeutics	2020-2021
Senior Advisor, Accelerator Life Sciences Partner	2020-current
Scientific Advisory Board member, Nooma	2021-current
Scientific Advisory Board member, Insitro	2021-current
Co-Founder, Scientific Advisory Board member, CircBio	2021-current
Advisor, Nucleate	2021-current
Board Member, n-Lorem	2021-current
Board Member, 1Strand	2021-current
Co-founder, Director and Scientific Advisor, Trotana (Incorporated August 27, 2019)	2021-current
Co-founder, Scientific Advisor, Orbital Therapeutics (March 8, 2022)	2022-current
Scientific Advisory Board member, Automera (June 1, 2022)	2022-current
Board member, ALSP Orchid (August 19, 2022)	2022-current
Scientific Advisory Board member, Atomic.AI (June 17, 2022)	2022-current
Scientific Advisory Board member, IntronX (August 1, 2022)	2022-current
Scientific Advisory Board member, LEXEO (October 1, 2022)	2022-current
Scientific Advisory Board member, Amber Bio (March 15, 2023)	2023-current
Chief Scientific Advisor (consultant), Sanford Laboratories for Innovative Medicine (June 9, 2023)	2023-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)
University of Illinois Alpha Chi Sigma-Zeta Chapter Krug Lecturer, 2016
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 Awardee for San Diego, Big Idea Award Winner, 2019
Finalist for Blavatnik National Awards for Young Scientists, 2019
Highly Cited Researcher 2019 by Clavirate Analytics ranked at the top 1% by citations for their field and year of publication (1 of 2500 for cross-field performance)
Editorial Board, eLife (Dec 2 2019-current)
Editorial Board, Review Commons (Dec 2019-current)
Paul Allen Distinguished Investigator (2020)
Highly Cited Researcher 2020 by Clavirate Analytics ranked at the top 1% by citations for their field and year of publication (1 of 2500 for cross-field performance)
RNA Society Elisa Izaurralde Award for Innovation in Research, Teaching and Service from the RNA Society in 2021. This award recognizes early career researchers who have not only enjoyed success in their research endeavors, but who have also employed innovative approaches to advancing RNA science in the classroom and within their greater communities.
On the Good Morning America Inspiration List's for Asian American Pacific Islander Heritage Month, nominated by Dr. Priscilla Chan (2021)
Editorial Board, RNA journal (2021-current)
Highly Cited Researcher 2021 by Clavirate Analytics ranked at the top 1% by citations for their field and year of publication (1 of 2500 for cross-field performance)
BIOS Beaker List, Top 50 Life Science Academic Entrepreneurs
Highly Cited Researcher 2022 by Clavirate Analytics ranked at the top 1% by citations for their field and year of publication (1 of 2500 for cross-field performance)
Rady School of Management Inaugural Entrepreneurial Achievement Award, May 8 2023
Inaugural Academia Europaea (AE) Sydney Brenner Medal (SBM) given to honor the best in scholarship and personal achievements not more than 20 years after the PhD degree, given within the field of molecular biology and related disciplines, 2023 (personally awarded by Carla Brenner)

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 Phi 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)
Single Cell Analysis Course, Cold Spring Harbor Laboratory, 2016 (Course Director and Speaker)
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, 2017 (Course Director 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)
Single Cell Analysis Course, Cold Spring Harbor Laboratory, 2018 (Course Director and Speaker)
5th annual RNA biology symposium by the Cancer science institute at NUS, Singapore (Co-organizer and chair)(2019)
Single Cell Analysis Course, Cold Spring Harbor Laboratory, 2019 (Course Director and Speaker)
Single Cell Analysis Course, Cold Spring Harbor Laboratory, 2020 (Course Director)
Biocom's Return to Work Task Force for Covid19, 2020 (Member and Contributor to Guide <https://www.biocom.org/coronavirus/return-to-work-resources/>)
26th Annual RNA Society 2021 Online Meeting, May 25-June 4, 2021 (Lead Organizer, Panel Chair)
RNA Society Awards Committee, 2021-current
RNA Society Annual Meeting Council Meeting, June 8, 2021
RNA Society Development Committee, 2021-current
RNA Society Nominating Committee (for Board and President), 2022-current
Keystone Symposia Conference: Protein-RNA Interactions, Vancouver, Canada, Jan 29- Feb 1, 2023 (Lead Organizer)
MDC Scientific Advisory Board Meeting (Virtual), July 26, 2023

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)
Co-Director, Bioinformatics and Systems Biology Graduate Program (2019-current)
Member, Bioinformatics and Systems Biology Graduate Program DEI committee (2020-current)
Initiated SCREEN (San Diego Covid Research and Enterprise Network) and member of SEARCH (2020)
UCSD Health Sciences Return To Learn Taskforce (2020)
Initiated Diversity and Science Lecture (DASL) series (2020)
Member of the search committee for the Chair of Pharmacology at UCSD, chaired by Susan Ackerman (2020)
Member of the search committee for Assistant/Associate faculty position at OB/GY at UCSD, chaired by Louise Laurent (2020)
Co-chair, Systems Biology and Data Science Research Area of Biomedical Sciences Graduate Program (2018,2019,2020)
SPAC advisor (since 2009)
Co-Director, EXCITE Laboratory (for Return-to-Learn program at UCSD) (2020)
Co-Organizer and Moderator, ASHG Session "Advances in Functional Transcriptomics: Linking Genetic Variation to RNA Processing" (Oct 30, 2020)
Organizing committee member, Institute for Genomic Medicine's annual ASHG Satellite Conference on "Spatial Omics" (2020)
Organizer, Nature Conference "RNA at the Bench and Bedside II" (2020)

UCSD Rady School of Management Industry Research Task Force (Feb, 2021)
Sanford Consortium for Regenerative Medicine Scientific Space Committee, Member (2017, 2018)
Sanford Consortium for Regenerative Medicine Scientific Space Committee, Chair (2019, 2020, 2021)
Sanford Consortium for Regenerative Medicine Scientific Steering Committee Member (2019, 2020, 2021)
Sanford Consortium for Regenerative Medicine Scientific Steering Committee Deputy Chair to Larry Goldstein (2021)
UCSD Big Idea Advisory Committee member. This is a new university-wide advisory committee focused on ideas with transformational societal impact and to bring significant private funding to the university, invited by Chancellor Khosla and Vice Chancellor Sandra Brown (2021).
UCSD School of Medicine Leadership Team to help strategic planning for research efforts, chaired by Susan Ackerman (2021).
Vice Chancellor for Health Sciences Search Committee Member (2022)
Advanced Cell Therapy Review Committee Member (2022-2023)
Led formation and organization of planning committee for CZ Biohub at San Diego (2022)
Structural Functional Genomics Retreat Speaker/Selection committee (2023)

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)
Grant reviewer for NINDS ZNS1 SRB-A(28) study section (2019, Oct 31)
Grant reviewer for NHGRI GNOM-G study section: CEGS (2019, Nov 7)
Grant reviewer for NIMH U19 review (2021, July 28)
Grant reviewer for ZRG1 BCMB-D, RM1 grants (2021, Oct 22)
External Advisory Board for FunGen-AD (2022, April 7)
Reviewer for NCI Laboratory of Receptor Biology and Gene Expression Site Visit (2022, Nov 14-16)
NIH Functional Genomics AD-2 Annual Meeting, External Advisory Board (2023, May 3)

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)
Editor, Elife (2019)

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) Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Bing Ren) (Spring 2010)	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	
Lecturer (Four 3-hour lectures) in BIOM 262 Quantitative Methods in Genetics organized by Bruce Hamilton (Winter 2014)	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	Spring 2014
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2014)	
University of California, San Diego	Fall 2014
Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen (Fall 2014)	
University of California, San Diego	Winter 2015
<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 Gene Yeo) (Winter 2015)	
University of California, San Diego	Spring 2015
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2015)	
University of California, San Diego	Fall 2015
Lecturer (4 hours) + Paper Discussion (2 hours) in BIOM 200 BMS Graduate Core Course organized by Kevin Corbett and Alysson Muotri (Fall 2015)	
University of California, San Diego	Winter 2016
<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>)	
University of California, San Diego	Spring 2016
Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Funari (Spring 2016)	
Cold Spring Harbor Laboratory, Single Cell Analysis Course	June 2016
June 7-17, 2016. Co-course director, assisted by Olga Botvinnik and Yan Song (https://github.com/YeoLab/single-cell-bioinformatics)	
University of California, San Diego	August 2016
Bioinformatics Bootcamp (Aug 1-5, 2016). Course director, assisted by Emily Wheeler.	
University of California, San Diego	Fall 2016
Lecturer (2 hours) + Paper Discussion (2 hours) in BIOM200 BMS Graduate Core Course organized by Kevin Corbett and Alysson Muotri (Fall 2015)	
University of California, San Diego	Fall 2016
Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen	

<p>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 <u>Course Director</u> and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo)</p>	Winter 2017
<p>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)</p>	July 2017
<p>University of California, San Diego Lecturer (1.5 hours) in BGGN 220 Graduate Molecular Biology organized by Jens Lykke-Andersen</p>	Fall 2017
<p>University of California, San Diego <u>Course Director</u> (10 weeks of 6-hour lectures a week) in CMM262 Quantitative Methods in Genetics <u>Course Director</u> and Lecturer (Four 3-hour lectures) in BIOM 254 Molecular and Cell Biology (directors: Arshad Desai and Gene Yeo)</p>	Winter 2018
<p>Cold Spring Harbor Laboratory, Single Cell Analysis Course June 29-July 14, 2018. Co-course director, teaching assistants Emily Wheeler, Alex Chaim, Brain Yee (https://github.com/ecwheele/CSHL_singlecellanalyses_2018)</p>	July 2018
<p>University of California, San Diego <u>Course Director</u> (with Alon Goren; 10 weeks of 6-hour lectures a week) in CMM262 Quantitative Methods in Genetics</p>	Winter 2019
<p>Cold Spring Harbor Laboratory, Single Cell Analysis Course June 28-July 13, 2019. Co-course director, teaching assistants Brian Yee, Shashank Sathe, Noorsher Ahmed, Yan Song (https://meetings.cshl.edu/courses.aspx?course=C-SINGLE&year=19)</p>	July 2019
<p>University of California, San Diego Lecturer (2 hours) in BIOM 200 BMS Graduate Core Course organized by Wendy Huang (Fall 2019)</p>	Fall 2019
<p>University of California, San Diego <u>Co-Course Director</u> with Alon Goren (10 weeks of 6-hour lectures a week) in CMM262 Quantitative Methods in Genetics (administrative role) <u>Co-Course Director</u> with Chris Benner (10 weeks of 6-hour lectures a week) in BIOM200C Introduction to Computational Biology</p>	Winter 2020
<p>University of California, San Diego Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Kelly Frazer and Radha Ayyagari</p>	Spring 2020
<p>University of California, San Diego Lecturer (2 hours) in BIOM 200 BMS Graduate Course organized by Wendy Huang</p>	Fall 2020

University of California, San Diego Panelist (2 hours) in PHAR234: Careers in Biomedical Sciences	Spring 2021
University of California, San Diego Lecturer (2 hours) in BIOM 200 BMS Graduate Course organized by Wendy Huang	Fall 2021
University of California, San Diego Lecturer (3 hours) in BIOM 252 Genetics and Genomics organized by Frank Furnari and Radha Ayyagari	Spring 2022
University of California, San Diego Lecturer (2 hours) in BIOM 200 BMS Graduate Course organized by Wendy Huang	Fall 2022
University of California, San Diego Lecturer (2 hours) in BIOM 200 BMS Graduate Course organized by Roger Sunahara and Phil Gordt	Fall 2023

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**).
20. Seila AC, Calabrese, JM, Levine SS, **Yeo, GW**, Rahl PB, Flynn RA, Young RA, Sharp PA, Divergent Transcription from Active Promoters. *Science*, 2008. Dec 19;322(5909):1849-51. Epub 2008 Dec 4. PMID: 19056940. (*Recommended by Faculty 1000*).
21. Li H, Lovci, MT, Kwon YS, Rosenfeld MG, Fu, XD, **Yeo GW**. Determination of tag density required for digital transcriptome analysis: Application to an androgen-sensitive prostate cancer model *Proceedings of the National Academy of Sciences, USA*. 2008. Dec 23;105(51):20179-84. Epub 2008 Dec 16. PMID: 19088194. ***Corresponding**.
22. **Yeo GW***, Coufal NG, Liang TY, Peng GE, Fu XD*, Gage FH* An RNA code for the FOX2 splicing regulator revealed by mapping RNA-protein interactions in stem cells. *Nature Structural & Molecular Biology*, 2009. Feb;16(2):130-7. Epub 2009 Jan 11. PMID: 19136955. ***Corresponding**.
23. Kuwabara T, Hsieh J, Muotri A, **Yeo GW**, Warashina M, Lie DC, Moore L, Nakashima K, Asashima M, Gage FH. Wnt-mediated activation of NeuroD1 and retroelements during adult neurogenesis, *Nature Neuroscience*, 2009. 12(9):1097-105. PMID: 19701198.
24. Lu Y-C, Smielewska M, Palakodeti D, Lovci MT, Aigner S, **Yeo GW***, Graveley BR* Deep sequencing identifies new and regulated microRNAs in *Schmidtea mediterranea*. *RNA*, 2009 Aug;15(8):1483-91. Epub 2009 Jun 24. PMID: 19553344. ***Corresponding**.
25. Thuret S, Toni N, Aigner S, **Yeo GW**, Gage FH. Hippocampus-dependent learning is associated with adult neurogenesis in MRL/MpJ mice. *Hippocampus*, 2009. Jul;19(7):658-69. PMID: 19140178.
26. Coufal NG., Garcia-Perez JL, Peng GE, **Yeo GW**, Mu Y, Lovci MT, Maria M, O'Shea KS, Moran JV, Gage FH. L1 Retrotransposition in Human Neural Progenitor Cells. *Nature*, 2009. 460(7259):1127-31. PMID: 19657334. (*Recommended by Faculty 1000*).
27. Marchetto MCN, **Yeo GW**, Kainohana O, Marsala M, Gage FH, Muotri AR. Transcriptional Signature and Memory Retention of Human-Induced Pluripotent Stem Cells. *PLoS ONE*, 2009. 4(9):e7076. PMID: 19763270.
28. Xue Y, Zhou Y, Wu T, Zhu T, Ji X, Kwon YS, Zhang C, **Yeo G**, Black DL, Sun H, Fu XD, Zhang Y. Genome-wide analysis of PTB-RNA interactions reveals a strategy used by the general splicing repressor to modulate exon inclusion or skipping. *Mol Cell*, 2009. Dec 25;36(6):996-1006. PMID: 20064465. (*Recommended by Faculty 1000*).
29. Zisoulis DG, Lovci MT, Wilbert ML, Hutt KR, Liang YL, Pasquinelli AE, **Yeo GW**. Comprehensive discovery of endogenous Argonaute binding sites in *C. elegans*. *Nature Structural & Molecular Biology*, 2010. Feb;17(2):173-9. Epub 2010 Jan 10. PMID: 20062054. **Corresponding**.

30. Hinton A, Afrikanova I, Wilson M, King CC, Maurer B, **Yeo GW**, Hayek A, Pasquinelli AE. A distinct microRNA signature for definitive endoderm derived from human embryonic stem cells. *Stem Cells Dev*, 2010; Feb; 17(2):173-9. PMID: 20062054.
31. Muotri AR, Marchetto MC, Coufal NG, Oefner R, **Yeo G**, Nakashima K, Gage FH. L1 retrotransposition in neurons modulated by MeCP2. *Nature*, 2010. 468(7322):443-6. PMID: 21085180.
32. Marchetto MC, Carromeu C, Acab A, Yu D, **Yeo GW**, Mu Y, Checn G, Gage FH, Muotri AR. A model for neural development and treatment of Rett syndrome using human induced pluripotent stem cells. *Cell*, 2010. 143(4):527-39. PMID: 21074045. (*Recommended by Faculty 1000*).
33. Van Wynsberghe PM, Kai ZS, Massirer KB, Burton VH, **Yeo GW**, Pasquinelli AE. LIN-28 co-transcriptionally binds primary let-7 to regulate miRNA maturation in *Caenorhabditis elegans*. *Nature Structural and Molecular Biology*, 2011. Mar;18(3):302-8. Epub 2011 Feb 6. PMID: 21297634.
34. Polymenidou M, Lagier-Tourenne C, Hutt KR, Huelga SC, Moran J, Liang TY, Ling S-C, Sun E, Wancewicz E, Mazur C, Kordasiewicz H, Sedaghat Y, Donohue JP, Shiue L, Bennett FC, **Yeo GW***, Cleveland DW*. Long pre-mRNA depletion and RNA missplicing contribute to neuronal vulnerability from loss of TDP-43. *Nature Neuroscience*, 2011. Apr;14(4):459-68. Epub 2011 Feb 27. PMID: 21358643. ***Corresponding**. (*Recommended by Faculty 1000*).
35. Stark TJ, Arnold JD, Spector DH, **Yeo GW**. High-resolution profiling and analysis of viral and host small RNAs during human cytomegalovirus infection. *Journal of Virology*, 2011. PMID: 22013051. **Corresponding**.
36. Huelga SC, Vu AQ, Arnold JD, Liang TY, Liu PP, Yan BY, Donohue JP, Shiue L, Hoon S, Brenner B, Ares M, **Yeo GW**. Integrative genome-wide analysis reveals cooperative regulation of alternative splicing by hnRNP proteins. *Cell Reports*, 2012. PMID: 22574288. **Corresponding**.
37. Andrade LN, Nathanson JL, **Yeo GW**, Menck CF, Muotri AR. Evidence for premature aging due to oxidative stress in iPSCs from Cockayne syndrome. *Hum Mol Genet*, 2012. PMID: 22661500
38. Zhu W, Kuo D, Nathanson J, Satoh A, Pao GM, **Yeo GW**, Bryant SV, Voss SR, Gardiner DM, Hunter T. Retrotransposon long interspersed nucleotide element-1 (LINE-1) is activated during salamander limb regeneration. *Dev Growth Differ*, 2012. PMID: 22913491
39. Dembowski J, Ping A, Scoulos-Hanson M, **Yeo G**, Han J, Fu XD, Grabowski PJ. Alternative splicing of a novel inducible exon diversifies the CASK guanylate kinase domain. *Journal of Nucleic Acids*, 2012. PMID: 23008758
40. Wilbert ML, Huelga SC, Kapeli K, Stark TJ, Liang TY, Chen SX, Yan BY, Nathanson JL, Hutt KR, Lovci MT, Kazan H, Vu AQ, Massirer KB, Morris Q, Hoon S, **Yeo GW**. LIN28 binds messenger RNAs at GGAGA motifs and regulates splicing factor abundance. *Molecular Cell*, 2012. PMID: 22959275. **Corresponding** (*Recommended by Faculty 1000*).
41. Lagier-Tourenne C, Polymenidou M, Hutt KR, Vu AQ, Baughn M, Huelga SC, Clutario KM, Ling S-C, Liang TY, Mazur C, Wancewicz E, Kim AS, Watt A, Freier S, Hicks GG, Donohue JP, Shiue L, Bennett CF, Ravits J, Cleveland DW, **Yeo GW**. Divergent roles of ALS-linked proteins FUS/TLS and TDP-43 intersect in processing long pre-mRNAs. *Nature Neuroscience*, 2012. PMID: 23023293. **Corresponding**. (*Recommended by Faculty 1000*).
42. Vollmers C, Schmitz RJ, Nathanson J, **Yeo GW**, Ecker JR, Panda S. Circadian Oscillations of Protein-coding and Regulatory RNAs in a Highly Dynamic Liver Epigenome. *Cell Metabolism*, 2012. PMID: 23217262
43. Arnold ES, Ling SC, Huelga SC, Lagier-Tourenne C, Polymenidou M, Ditsworth D, Kordasiewicz HB, McAlonis-Downes M, Platoshyn O, Parone PA, Da Cruz S, Clutario KM, Swing D, Tessarollo L, Marsala M, Shaw CE, **Yeo GW**, Cleveland DW. ALS-linked TDP-43 mutations produce aberrant RNA splicing and adult-onset motor neuron disease without aggregation or loss of nuclear TDP-43. *Proceedings of the National Academy of Sciences, USA*, 2013. PMID: 23382207
44. Hunter SE, Finnegan EF, Zisoulis DG, Lovci MT, Melnik-Martinez KV, **Yeo GW**, Pasquinelli AE. Functional genomic analysis of the let-7 regulatory network in *Caenorhabditis elegans*. *PLoS Genetics*, 2013. PMID: 23516374
45. Pandit S, Zhou Y, Shiue L, Coutinho-Mansfield G, Li H, Qiu J, Huang J, **Yeo GW**, Ares M Jr, Fu XD. Genome-wide analysis reveals SR protein cooperation and competition in regulated splicing. *Molecular Cell*, 2013. PMID: 23562324
46. Cai W, Albin S, Wei K, Willems E, Guzzo RM, Tsuda M, Giordani L, Spiering S, Kurian L, **Yeo GW**, Puri PL, Mercola M. Coordinate Nodal and BMP Inhibition Directs Baf60c-dependent Cardiomyocyte Commitment. *Genes & Development*, 2013. PMID: 24186978

47. Marchetto MCN, Narvaiza I, Denli AM, Benner C, Lazzarini TA, Nathanson JL, Paquola ACM, Desai KN, Herai RH, Weitzman MW, **Yeo GW**, Muotri AR, Gage FH. Differential L1 regulation in pluripotent stem cells of humans and other great apes. *Nature*, 2013. PMID: 24153179.
48. Verma SK, Deshmukj V, Liu P, Nutter CA, Espejo R, Hung M-L, Wang G-S, **Yeo GW**, Kuyumcu-Martinez MN. Reactivation of fetal splicing programs in diabetic hearts is mediated by protein kinase C signaling. *The Journal of Biological Chemistry*, 2013. PMID: 24151077
49. Lagier-Tourenne C, Baughn M, Rigo F, Sun S, Liu P, Li H-R, Jiang J, Watt AT, Chun S, Katz M, Qiu J, Sun Y, Ling S-C, Zhu Q, Polymenidou M, Drenner , Artates JW, McAlnois-Downes M, Markmiller S, Hutt KR, Pizzo DP, Cady J, Harms MB, Baloh RH, Vandenberg SR, **Yeo GW**, Fu X-D, Bennett CF, Cleveland DW, Ravits J. Targeted degradation of sense and antisense C9orf72 RNA foci as therapy for ALS and frontotemporal degeneration. *Proceedings of the National Academy of Sciences, USA*, 2013. PMID: 24170860.
50. Lovci MT, Ghanem D, Marr H, Arnold J, Gee S, Parra M, Liang TY, Stark T, Gehman LT, Hoon S, Massirer K, Pratt GA, Black DL, Gray J, Conboy JG, **Yeo GW**. Rbfox proteins regulate alternative mRNA splicing through evolutionarily conserved RNA bridges. *Nature Structural and Molecular Biology*, 2013. PMID: 24213538. **Corresponding**. (Highlighted in Editor's Choice in *Science*). (Recommended by Faculty 1000).
51. Washburn MC, Kakaradov B, Sundararaman B, Wheeler E, Hoon S, **Yeo GW***, Hundley HA*. The dsRBP and inactive editor, ADR-1, utilizes dsRNA binding to regulate A-to-I RNA editing across the *C. elegans* transcriptome. *Cell Reports*, 2014. PMID: 24508457. NIHMS 557942. ***Corresponding**.
52. Arsenio J, Kakaradov B, Metz PJ, Kim SH, **Yeo GW***, Chang JT*. Early specification of CD8+ T lymphocyte fates during adaptive immunity revealed by single-cell gene expression analyses. *Nature Immunology*, 2014. PMID: 24584088. ***Corresponding**.
53. Van Wynsberghe P, Finnegan EF, Stark T, Angelus E, Homan K, **Yeo GW**, Pasquinelli A. Period protein homolog LIN-42 negatively regulates microRNA biogenesis in *C. elegans*. *Developmental Biology*, 2014. PMID: 24699545.
54. Belzile JP, Stark TJ, **Yeo GW**, Spector DH. Human cytomegalovirus infection of human embryonic stem cell-derived primitive neural stem cells is restricted at several steps but leads to the persistence of viral DNA. *Journal of Virology*, 2014. PMID: 24453373.
55. Rush AM, Nelles DA, Blum AP, Barnhill S, Tatro ET, **Yeo GW**, Gianneschi NC. Intracellular mRNA regulation with self-assembled locked nucleic acid (LNA)-polymer nanoparticles. *Journal of the American Chemical Society*, 2014. PMID: 24827740.
56. Siddiqi S, Foo JN, Vu A, Azim S, Silver DL, Mansoor A, Tay SKH, Abbasi S, Hashmi AH, Janjua J, Khalid S, Tai ES, **Yeo GW**, Khor CC. A novel splice-site mutation in ALS2 establishes the diagnosis of juvenile amyotrophic lateral sclerosis in a family with early onset anarthria and generalized dystonias. *PLOS ONE*, 2014. PMID: 25474699.
57. Sun S, Ling S-C, Qiu J, Albuquerque CP, Zhou Y, Tokunaga S, Li H, Qiu H, Bui A, **Yeo GW**, Huang EJ, Eggan K, Zhou H, Fu X-D, Lagier-Tourenne C, Cleveland DW. ALS-causative mutations in FUS/TLS confer gain- and loss-of-function by altered association with SMN and U1-snRNP. *Nature Communications*, 2015. PMID: 25625564.
58. Metz PJ, Arsenio J, Kakaradov B, Kim SH, Remedios KA, Oakley K, Ohno S, **Yeo GW**, Chang JT. Regulation of asymmetric division and CD8+ T lymphocyte fate specification by protein kinase Ceta and protein kinase C lambda. *Journal of Immunology*, 2015. PMID: 25617472.
59. Kurian L, Aguirre A, Sancho-Martinez I, Benner C, Hishida T, Nguyen T, Reddy P, Nivet E, Krause MN, Nelles D, Esteban CR, Campistol J, **Yeo GW**, Belmonte JCI. Identification of novel long non-coding RNAs underlying vertebrate cardiovascular development. *Circulation*. 2015. PMID: 25739401.
60. Concepcion D, Ross KD, Hutt KR, **Yeo GW**, Hamilton BA. Nxf1 natural variant E610G is a semi-dominant suppressor of IAP-induced RNA processing defects. *PLoS genetics*, 2015. PMID: 25835743.
61. Shih HP, Seymour PA, Patel NA, Xie R, Wang A, Liu PL, **Yeo GW**, Magnuson MA, Sander M. A gene regulatory network cooperatively controlled by Pdx1 and Sox9 governs lineage allocation of foregut progenitor cells. *Cell Reports*, 2015. PMID: 26440894.
62. Lee SR, Pratt GA, Martinez FJ, **Yeo GW***, Lykke-Andersen J*. Target discrimination in nonsense-mediated mRNA decay requires Upf1 ATPase activity. *Molecular Cell*, 2015. PMID: 26253027. ***Corresponding**.

63. Hung T, Pratt G, Sundararaman B, Townsend MJ, Chaivorapol C, Bhangale T, Graham RR, Ortmann W, Criswell LA, **Yeo GW***, Behrens T. The Ro60 Autoantigen Binds Endogenous Retroelements and Regulates Inflammatory Gene Expression, **Science**, 2015. PMID: 26382853. ***Corresponding**.
64. Dickey AS, Pineda VV, Tsunemi T, Liu PP, Miranda HC, Gilmore-Hall SK, Lomas N, Sampat KR, Buttgereit A, Tores MM, Flores AL, Arreola M, Arbez N, Akimov SS, Gaasterland T, Lazarowski ER, Ross CA, **Yeo GW**, Sopher BL, Magnuson GK, Pinkerton AB, Masliah E, La Spada AR. PPAR-delta is repressed in Huntington's disease, is required for normal neuronal function and can be targeted therapeutically, **Nature Medicine**, 2015. PMID: 26642438. (*Recommended by Faculty 1000*).
65. Gerson-Gurwitz A, Wang S, Sathe S, Green R, **Yeo GW**, Oegema K, Desai A. A small RNA-catalytic Argonaute pathway tunes germline transcript levels to ensure embryonic divisions, **Cell**, 2016.
66. Sundararaman B, Zhan L, Blue S, Stanton R, Elkins K, Olson S, Wei X, Van Nostrand EL, Huelga SC, Smalec BM, Wang X, Hong EL, Davidson JM, Lecuyer E, Graveley BR, **Yeo GW**. Resources for the comprehensive discovery of functional RNA elements, **Molecular Cell**, 2016. **Corresponding**. PMID: 26990993. (*Recommended by Faculty 1000*).
67. Van Nostrand EL, Pratt GA, Shishkin AA, Gelboin-Burkhart C, Fang M, Sundararaman B, Blue SM, Nguyen TB, Surka C, Elkins K, Stanton R, Rigo F, Guttman M, **Yeo GW**. Enhanced CLIP (eCLIP) enables robust and scalable transcriptome-wide discovery and characterization of RNA binding protein binding sites, **Nature Methods**, 2016. **Corresponding**. PMID: 27018577. (*Recommended by Faculty 1000*).
68. Nelles DA, Fang M, O'Connell MR, Xu JL, Markmiller SJ, Doudna JA, **Yeo GW**. Programmable RNA tracking in Live Cells with CRISPR/Cas9, **Cell**, 2016. **Corresponding**. PMID: 26997482. (*Recommended by Faculty 1000, Top 100 stories in 2016 in Discover magazine, Dec 2016*).
69. Conway AE, Van Nostrand EL, Pratt GA, Aigner S, Wilbert ML, Sundararaman B, Freese P, Lambert NJ, Sathe S, Liang TY, Essex A, Landais S, Burge CB, Jones DL, **Yeo GW**. Enhanced CLIP uncovers IMP protein-RNA targets in human pluripotent stem cells important for cell adhesion and survival. **Cell Reports**, 2016. **Corresponding**. PMID: 27068461
70. Rentas S, Holzapfel N, Belew MS, Pratt G, Voisin V, Wilhelm BT, Bader GD, **Yeo GW***, Hope K*. Musashi-2 Posttranscriptionally Attenuates Aryl Hydrocarbon Receptor Signaling to Expand Human Hematopoietic Stem Cells, **Nature**, 2016. ***Corresponding**. PMID: 27121842
71. **Nutter** CA, Jaworski EA, Verma SK, Deshmukh V, Wang Q, Botvinnik OB, Lozano MJ, Abass IJ, Ijaz T, Brasier AR, Garg NJ, Wehrens XH, **Yeo GW**, Kuyumcu-Martinez MN. Dysregulation of RBFOX2 is an early event in cardiac pathogenesis of diabetes. **Cell Reports**, 2016. PMID: 27239029. (*Recommended by Faculty 1000*).
72. Kapeli K*, Pratt GA*, Vu AQ, Hutt KR, Martinez FJ, Sundararaman B, Freese P, Lambert NJ, Huelga SC, Chun S, Liang TY, Chang J, Donohue JP, Shiue L, Zhang J, Zhu H, Cambi F, Kasarskis E, Ares M, Burge CB, Rigo F, **Yeo GW**. Distinct and shared molecular targets and functions of ALS-associated TDP-43, FUS, and TAF15 revealed by comprehensive multi-system integrative analyses. **Nature Communications**, 2016. **Corresponding**. PMID: 27378374.
73. Bardy C, Hurk M, Kakaradov B, Erwin J, Jaeger B, Hernandez R, Eames T, Paucar A, Gorris M, Marchand C, Jappelli R, Barron J, Bryant A, Kellogg M, Lasken R, Rutten B, Steinbusch H, **Yeo GW***, Gage F. Predicting the functional states of human iPSC-derived neurons with single-cell RNA-seq and electrophysiology. **Molecular Psychiatry**, 2016. ***Corresponding**. PMID: 27698428.
74. Verma SK, Deshmukh V, Nutter CA, Jaworski E, Jin W, Wadhwa L, Abata J, Ricci M, Lincoln J, Martin JF, **Yeo GW**, Kuyumcu-Martinez MN. Rbfox2 function in RNA metabolism is impaired in hypoplastic left heart syndrome patient hearts. **Scientific Reports**. 2016. PMID: 27485310
75. Grabole N, Zhang JD, Aigner S, Ruderisch N, Costa V, Weber FC, Theron M, Berntenis N, Spleiss O, Ebeling M, **Yeo GW**, Jagasia R, Kialainen A. Genomic Analysis of the Molecular Neuropathology of Tuberous Sclerosis Using a Human Stem Cell Model. **Genome Medicine**. 2016. PMID: 27655340
76. Broughton JP, Lovci MT, Huang JL, **Yeo GW**, Pasquinelli AE. Pairing beyond the Seed Supports MicroRNA Targeting Specificity. **Molecular Cell**, 2016. PMID: 27720646
77. Brannan KW*, Jin W*, Huelga SC, Banks CAS, Gilmore JM, Florens L, Washburn MP, Van Nostrand EL, Pratt GA, Schwinn MK, Daniels DL, **Yeo GW**. SONAR discovers RNA binding proteins from analysis of large-scale protein-protein interactomes. **Molecular Cell**, 2016. PMID: 27720645
78. Martinez FJ, Pratt GA, Van Nostrand EL, Batra R, Huelga SC, Kapeli K, Freese P, Chun SJ, Ling K, Gelboin-Burkhart C, Fijany L, Wang H, Nussbacher JK, Broski, SM, Kim HJ, Lardelli R, Sundararaman B, Donohue JP, Javaherian A, Lykke-Andersen J,

- Finkbeiner S, Bennett F, Ares M, Burge CB, Taylor JP, Rigo F, **Yeo GW**. Protein-RNA networks regulated by normal and ALS-associated mutant HNRNPA2B1 in the nervous system. *Neuron*, 2016. PMID:27773581
79. Batra R, Stark TJ, Clark E, Belzile J-P, Wheeler EC, Yee BA, Huang H, Gelboin-Burkhart C, Huelga SC, Aigner S, Roberts BT, Bos TJ, Sathe S, Donohue JP, Rigo F, Ares M Jr, Spector DH, **Yeo GW**. RNA-binding protein CPEB1 remodels host and viral RNA landscapes. *Nature Structural and Molecular Biology*, 2016. PMID:27775709
80. Lippi G, Fernandes CC, Ewell LA, John D, Romoli B, Curia G, Taylor SR, Frady EP, Jensen AB, Liu JC, Chaabane MM, Belal Cc, Nathanson JL, Zoli M, Leutgeb JK, Biagini G, **Yeo GW**, Berg DK. MicroRNA-101 regulates multiple developmental programs to constrain excitation in adult network networks. *Neuron*. 2016. PMID:27939580
81. Van Nostrand EL, Gelboin-Burkhart C, Wang R, Pratt GA, Blue SM, **Yeo GW**. CRISPR/Cas9-mediated integration enables TAG-eCLIP of endogenously tagged RNA binding proteins. Special issue "Protein-RNA: Structure function and recognition" in *Methods*, 2016 (edited by Yael Mandel-Gutfreund). PMID:28003131.
82. Kakaradov B, Arsenio J, Widjaja CE, He Zhaoren, Aigner S, Metz PJ, Yu Bingfei, Wehrens E, Lopez J, Kim SH, Zuniga EI, Goldrath AW, Chang JT, **Yeo GW**. Early transcriptional and epigenetic regulation of CD8+ T cell differentiation revealed by single-cell RNA-seq. *Nature Immunology*, 2017. PMID:28218746. (*Recommended by Faculty 1000*).
83. Lardelli RM, Schaffer AE, Eggens VRC, Zaki MS, Grainger SL, Sathe S, Van Nostrand EL, Schlachetzki Z, Rosti B, Akizu N, Scott E, Heckman LD, Rosti RO, Dikoglu E, Gregor A, Guemez-Gamboa A, Musaev D, Mande R, Widjaja A, Shaw TL, Markmiller S, Marin-Valencia I, Davies JH, de Meirleir L, Kayserili H, Altunoglu U, Freckmann ML, Warwick L, Chitayat D, ÇağlayanAO, Bilguvar K, Per H, Fagerberg C, Kibaek M, Aldinger KA, Manchester D, Matsumoto N, Muramatsu K, Saitu H, Shiina M, Ogata K, Foulds N, Dobyns WB, Chi N, Traver D, Spaccini L, Bova SM, Gabriel SB, Gunel M, Valente EM, Nassogne M-C, Bennett EJ, **Yeo GW**, Baas F, Lykke-Andersen J, Gleeson JG. Biallelic mutations in the 3'exonuclease *TOE1* cause pontocerebellar hypoplasia and uncover a role in snRNA processing. *Nature Genetics*, 2017. PMID:28092684.
84. Carter H, Marty R, Hofree M, Gross A, Jensen J, Fisch KM, Wu Xingyu, DeBoever C, Van Nostrand EL, Song Y, Wheeler E, Kresiberg JF, Lippman SM, **Yeo GW**, Gutkind JS, Ideker T. Interaction landscape of inherited polymorphisms with somatic events in cancer. *Cancer Discovery*, 2017. PMID:28188128.
85. D'Antonio M, Woodruff G, Nathanson JL, D'Antonio-Chronowska A, Arias A, Matsui H, Williams R, Herrera C, Reyna SM, **Yeo GW**, Goldstein LSB, Panopoulos AD, Frazer KA. High-throughput and cost-effective characterization of induced pluripotent stem cells. *Stem Cell Reports*, 2017 PMID: 28410643
86. Panopoulos AD, D'Antonio M, Benaglio P, Williams R, Hashem SI, Schuldt BM, DeBoever C, Arias AD, Garcia M, Nelson B, Harismendy O, Grinstein JD, Drees F, Okubo J, Diffenderfer KE, Hishida Y, Modesto V, Dargitz CT, Feiring R, Zhao C, McGarry TJ, Matsui H, Reyna J, Aguirre A, Rao F, O'Connor DT, **Yeo GW**, Evans SM, Chi NC, Jepsen K, Nariai N, Müller F-J, Goldstein LSB, Izpisua Belmonte JC, Adler E, Loring JF, Berggren WT, D'Antonio-Chronowska A, Smith EN, Frazer KA. iPSCORE: A systemically derived resource of iPSC lines from 222 individuals for use in examining how genetic variation affects molecular and physiological traits across a variety of cell types. *Stem Cell Reports*, 2017. PMID:28410642
87. Zeng C, Mulas F, Sui Y, Guan T, Miller N, Tan Y, Liu F, Jin W, Carrano AC, Huising MO, Shirihai OS, **Yeo GW**, Sander M. Pseudotemporal ordering of single cells reveals metabolic control of postnatal beta-cell proliferation. *Cell Metabolism*, 2017. PMID:28467932
88. Song Y, Botvinnik OB, Lovci MT, Kakaradov B, Liu P, Xu JL, **Yeo GW**. Single-cell alternative splicing analysis with *Expedition* reveals splicing dynamics during neuron differentiation. *Molecular Cell*, 2017. PMID:28673540
89. Van Nostrand EL, Nguyen TB, Gelboin-Burkhart C, Wang R, Blue SM, Pratt GA, Louie AL, **Yeo GW**. Robust cost-effective profiling of RNA binding protein targets with single-end crosslinking and immunoprecipitation (seCLIP). *Methods in Molecular Biology*, 2017. PMID:28766298
90. Van Nostrand EL, Shishkin A, Pratt GA, Nguyen TB, **Yeo GW**. Variation in single-nucleotide sensitivity of eCLIP derived from reverse transcription conditions. *Methods in Molecular Biology*, 2017. PMID:28790018
91. Batra R, Nelles DA, Pirie E, Blue SM, Marina RJ, Wang H, Chaim IA, Thomas JD, Zhang N, Nguyen V, Aigner S, Markmiller S, Xia G, Corbett KD, Swanson MS, **Yeo GW**. Elimination of toxic microsatellite repeat expansion RNA by RNA-targeting Cas9. *Cell*, 2017. PMID:28803727. (*Recommended by Faculty 1000*).

92. Deffit SN, Yee BA, Manning AC, Rajendren S, Vadlamani P, Wheeler EC, Domissy A, Washburn MC, **Yeo GW***, Hundley HA*. The *C. elegans* neural editome reveals an ADAR target mRNA required for proper chemotaxis. *eLife*, 2017. ***Corresponding**. PMID:28925356
93. Lima SA, Chipman LB, Nicholson AL, Chen Y-H, Yee BA, **Yeo GW**, Collier J, Pasquinelli AE. Short Poly(A) Tails are a Conserved Feature of Highly Expressed Genes. *Nature Structural and Molecular Biology*, 2017.
94. Scott DD, Trahan C, Zindy PJ, Aguilar LC, Delubac MY, Van Nostrand EL, Adivarahan S, Wei KE, **Yeo GW**, Zenklusen D, Oeffinger M. Nol12 is a multifunctional RNA binding protein at the nexus of RNA and DNA metabolism. *Nucleic Acid Research*, 2017. PMID:29069457
95. Jiang L, Shao C, Wu QJ, Chen G, Zhou J, Yang B, Li H, Gou LT, Zhang Y, Wang Y, **Yeo GW**, Zhou Y, Fu XD. Neat1 scaffolds RNA-binding proteins and the microprocessor to globally enhance pri-miRNA processing. *Nature Structural and Molecular Biology*, 2017. PMID: 28846091
96. Markmiller S, Soltanieh S, Server KL, Mak R, Jin W, Fang MY, Luo E-C, Krach F, Yang D, Sen A, Fulzele A, Wozniak J, Gonzalez DJ, Kankel MW, Gao F-B, Bennet EJ, Lecuyer E, **Yeo GW**. Context-dependent and disease-specific diversity in protein interactions within Stress Granules. *Cell*, 2018. PMID:29373831
97. Nussbacher JK, **Yeo GW**. Systematic discovery of RNA binding proteins that regulate microRNA levels. *Molecular Cell*, 2018. PMID: 29547715
98. Huang H, Kapeli K, Jin W, Wong YP, Arumugam TV, Koh JH, Srimasorn S, Mallilankaraman K, Chua JJE, **Yeo GW**, Soong TW. Tissue-selective restriction of RNA editing of CaV1.3 by splicing factor SRSF9. *Nucleic Acids Res*, 2018. PMID: 29733375.
99. Krach F, Batra R, Wheeler EC, Vu AQ, Wang R, Rabin SJ, Baughn MW, Libby RT, Diaz-Garcia S, Stauffer J, Pirie E, Saberi S, Rodriguez M, Madrigal AA, Kohl Z, Winner B, **Yeo GW***, Ravits J. Transcriptome-pathology correlation identifies interplay between TDP-43 and the expression of its kinase CK1E in sporadic ALS. *Acta Neuropathologica*, 2018. (***Corresponding**). PMID: 29881994.
100. Dominguez D, Freese P, Alexis MS, Su A, Hochman M, Palden T, Bazile C, Lambert NJ, Van Nostrand EL, Pratt GA, **Yeo GW**, Graveley BR, Burge CB. Sequence, Structure and Context Preferences of Human RNA binding proteins. *Molecular Cell*, 2018. PMID: 29883606.
101. Van den Hurk M, Erwin JA, **Yeo GW**, Gage FH, Bardy C. Patch-seq Protocol for Multi-modal Single Cell Analysis of Human pluripotent stem cell-derived neurons. *Front Mol Neurosci*, 2018. PMID: 30147644.
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.
103. Parra M, Booth BW, Weiszmann, Yee B, **Yeo GW**, Brown JB, Celniker SE, Conboy JG. An important class of intron retention events in human erythroblasts is regulated by cryptic exons proposed to function as splicing decoys, *RNA*, 2018. PMID: 29959282.
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.
108. Ling S-C, Dastidar SG, Tokunaga S, Ho WY, Lim K, Ilieva H, Parone PA, Tyan S-H, Chang J-C, Platoshyn O, Bui NB, Bui A, Vetto A, Sun S, McAlonis-Downes M, Han JS, Swing D, Kapeli K, **Yeo GW**, Tessarollo L, Marsala M, Shaw CE, Tucker-Kellogg G, La Spada AR, Lagier-Tourenne C, Da Cruz S, Cleveland DW. Overriding FUS autoregulation triggers gain-of-toxic dysfunctions in autophagy-lysosome axis and RNA metabolism. *eLife*, 2019. PMID: 30747709.

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. PMID: 31018137.
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). PMID: 31042464.
113. Xiao R, Chen JY, Liang Z, Luo D, Chen G, Lu ZJ, Chen Y, Zhou B, Li H, Du X, Yang Y, San M, Wei X, Liu W, Lécuyer E, Graveley BR, **Yeo GW**, Burge CB, Zhang MQ, Zhou Y, Fu XD. Pervasive Chromatin-RNA binding protein interactions enable RNA-based Regulation of Transcription. **Cell**, 2019. PMID: 31251911.
114. 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. PMID: 31272829.
115. Trujillo CA, Gao R, Negraes PD, Gu J, Buchanan J, Preissl S, Wang A, Wu W, Haddard GG, Chaim IA, Domissy A, Vandenberghe M, Devor A, **Yeo GW**, Voytek B, Muotri AR. Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. **Cell Stem Cell**, 2019. PMID: 31474560.
116. Blum AP, Nelles DA, Hidalgo FJ, Touve MA, Sim DS, Madrigal AA, **Yeo GW***, Gianneschi NC*. Peptide Brush Polymers for Efficient Delivery of a Gene Editing Protein to Stem Cells. *Angew Chem Int Ed Engl*. 2019. (*Corresponding) PMID: 31404473.
117. Kaiser RWJ, Ignarski M, **Van Nostrand EL**, Frese CK, Jain M, Cukoski S, Heinen H, Schaechter M, Seufert L, Bunte K, Frommolt P, Keller P, Helm M, Bohl K, Höhne M, Schermer B, Benzinger T, Höpker K, Dieterich C, **Yeo GW**, Müller RU, Fabretti F. A protein-RNA interaction atlas of the ribosome biogenesis factor AATF. **Sci Rep**, 2019. PMID: 31363146
118. Di Stefano B, Luo EC, Haggerty C, Aigner S, Charlton J, Brumbaugh J, Ji F, Rabano Jiménez I, Clowers KJ, Huebner AJ, Clement K, Lipchina I, de Kort MAC, Anselmo A, Pulice J, Gerli MFM, Gu H, Gygi SP, Sadreyev RI, Meissner A, **Yeo GW***, Hochedlinger K*. The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. **Cell Stem Cell**, 2019. (*Corresponding). PMID: 31588046
119. Lorenz DA, Sathe S, Einstein JM, **Yeo GW**. Direct RNA sequencing enables m6a detection in endogenous transcript isoforms at base specific resolution. **RNA**, 2019. PMID: 31624092
120. Tang NH, Kim KW, Xu S, Blazie SM, Yee BA, **Yeo GW**, Jin Y, Chisholm AD. The mRNA decay factor CAR-1/LSM14 regulates axon regeneration via mitochondrial calcium dynamics. **Current Biology**, 2020. PMID: 31983639.
121. Koga T, Chaim IA, Benitez JA, Markmiller S, Parisian AD, Hevner RF, Turner KM, Hessenauer FM, D'Antonio M, Nguyen ND, Saberi S, Ma J, Miki S, Boyer AD, Ravits J, Frazer KA, Bafna V, Chen CC, Mischel PS, **Yeo GW***, Furnari FB. Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. **Nature Communications**, 2020. (*Corresponding). PMID: 34216543
122. Van Nostrand EL, Pratt GA, Yee BA, Wheeler E, Blue SM, Mueller J, Park SS, Garcia KE, Gelboin-Burkhart C, Nguyen TB, Rabano I, Stanton R, Sundararaman B, Wang R, Fu X-D, Graveley BR, **Yeo GW**. Principles of RNA processing from analysis of enhanced CLIP maps for 150 RNA binding proteins. **Genome Biology**, 2020. PMID: 32252787
123. Wheeler EC, Vu AQ, Einstein JM, DiSalvo M, Ahmed N, Van Nostrand EL, Shiskin AA, Jin W, Allbrighton NL, **Yeo GW**. Pooled CRISPR screens with image-based phenotyping on microRaft arrays reveals stress granule-regulatory factors. **Nature Methods**, 2020. PMID: 32393832
124. Tang X, Miao Y, Luo Y, Sriram K, Qi Z, Lin FM, Gu Y, Lai CH, Hsu CY, Peterson KL, Van Keuren-Jensen K, Fueger PT, **Yeo GW**, Natarajan R, Zhong S, Chen ZB. Suppression of Endothelial AGO1 promotes Adipose tissue browning and improves metabolic dysfunction. **Circulation**. 2020. PMID: 32393053.

125. Milner, J.J., Toma, C., He, Z., Kurd, N.S., Nguyen, Q.P., McDonald, B., Quezada, L.K., Widjaja, C.E., Witherden, D.A., Crowl, J.T., Shaw, L.A., **Yeo, G.W.**, Chang, J.T., Omilusik, K.D., Goldrath, A.W. Heterogeneous Populations of Tissue-Resident CD8+ T Cells Are Generated in Response to Infection and Malignancy. *Immunity* 2020. PMID: 32433949
126. Kurd, N.S., He, Z., Louis, T.L., Milner, J.J., Omilusik, K.D., Jin, W., Tsai, M.S., Widjaja, C.E., Kanbar, J.N., Olvera, J.G., Tysl, T., Quezada, L.K., Boland, B.S., Huang, W.J., Murre, C., Goldrath, A.W., **Yeo, G.W.***, Chang, J.T*. Early precursors and molecular determinants of tissue-resident memory CD8+ T lymphocytes revealed by single-cell RNA sequencing. *Science Immunology* 2020. (*Corresponding) PMID: 32414833
127. 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*, 2020. PMID: 32728249
128. ENCODE Project Consortium, Moore JE, Purcaro MJ, Pratt HE, Epstein CB, Shores N, Adrian J, Kawli T, Davis CA, Dobin A, Kaul R, Halow J, Van Nostrand EL, Freese P, Gorkin DU, Shen Y, He Y, Mackiewicz M, Pauli-Behn F, Williams BA, Mortazavi A, Keller CA, Zhang XO, Elhajjajy SI, Huey J, Dickel DE, Snetkova V, Wei X, Wang X, Rivera-Mulia JC, Rozowsky J, Zhang J, Chhetri SB, Zhang J, Victorsen A, White KP, Visel A, **Yeo GW**, Burge CB, Lécuyer E, Gilbert DM, Dekker J, Rinn J, Mendenhall EM, Ecker JR, Kellis M, Klein RJ, Noble WS, Kundaje A, Guigó R, Farnham PJ, Cherry JM, Myers RM, Ren B, Graveley BR, Gerstein MB, Pennacchio LA, Snyder MP, Bernstein BE, Wold B, Hardison RC, Gingeras TR, Stamatoyannopoulos JA, Weng Z. Expanded encyclopedias of DNA elements in the human and mouse genomes. *Nature*, 2020. PMID:32728249.
129. ENCODE Project Consortium, Snyder MP, Gingeras TR, Moore JE, Weng Z, Gerstein MB, Ren B, Hardison RC, Stamatoyannopoulos JA, Graveley BR, Feingold EA, Pazin MJ, Pagan M, Gilchrist DA, Hitz BC, Cherry JM, Bernstein BE, Mendenhall EM, Zerbino DR, Frankish A, Flicek P, Myers RM. Perspectives on ENCODE. *Nature*, 2020. PMID: 32728248
130. Donsbach P, Yee BA, Sanchez-Hevia D, Berenguer J, Aigner S, **Yeo GW**, Klostermeier D. The Thermus thermophilus DEAD-box protein Hera is a general RNA binding protein and plays a key role in tRNA metabolism. *RNA*, 2020. PMID: 32669294.
131. Coyne AN, Zaepfel BL, Hayes L, Fitchman B, Salzberg Y, Luo EC, Bowen K, Trost H, Aigner S, Rigo F, **Yeo GW**, Harel A, Svendsen CN, Sareen D, Rothstein JD. G4C2 repeat RNA initiates a POM121- mediated reduction in specific nucleoporins in C9orf72 ALS/FTD. *Neuron*, 2020. PMID:32673563
132. Begovich K, Vu AQ, **Yeo GW**, Wilhelm JE. Conserved metabolite regulation of stress granule assembly with AdoMet. *Journal of Cell Biology*, 2020. PMID:32609300.
133. Marcheva B, Perelis M, Weidemann BJ, Taguchi A, Lin H, Omura C, Kobayashi Y, Newman MV, Wyatt EJ, McNally EM, Fox JEM, Hong H, Shankar A, Wheeler EC, Ramsey KM, MacDonald PE, **Yeo GW**, Bass J. A role for alternative splicing in circadian control of exocytosis and glucose homeostasis. *Genes and Development*, 2020. PMID: 32616519
134. Luo E-C, Nathanson JL, Tan FE, Schwartz JL, Schmok JC, Shankar A, Markmiller S, Yee BA, Sathe S, Pratt GA, Scaletta DB, Ha Y, Hill DE, Aigner S, **Yeo GW**. Large-scale tethered function assays identify factors that regulate mRNA stability and translation. *Nature Structural & Molecular Biology*, 2020. PMID:32807991
135. Abbasi N, Long T, Li Y, Yee BA, Cho BS, Hernandez JE, Ma E, Patel PR, Sahoo D, Sayed IM, Varki N, Das S, Ghosh P, **Yeo GW**, Huang WJM. DDX5 promotes oncogene C3 and FABP1 expressions and drives intestinal inflammation and tumorigenesis. *Life Sci Alliance*, 2020. PMID: 32817623.
136. Boland BS, He Z, Tsai MS, Olvera JG, Omilusik KD, Duong HG, Kim ES, Limary AE, Jin W, Milner JJ, Yu B, Patel SA, Louis TL, Tysl T, Kurd NS, Bortnick A, Quezada LK, Kanbar JN, Miralles A, Huylebroeck D, Valasek MA, Dulai PS, Singh S, Lu LF, Bui JD, Murre C, Sandborn WJ, Goldrath AW, **Yeo GW***, Chang JT. Heterogeneity and clonal relationships of adaptive immune cells in ulcerative colitis revealed by single-cell analyses. *Sci Immunol*, 2020. PMID: 32826341. (*Corresponding)
137. Tavares CDJ, Aigner S, Sharabi K, Sathe S, Mutlu B, **Yeo GW**, Puigserver P. Transcriptome-wide analysis of PGC-1alpha-binding RNAs identifies genes linked to glucagon metabolic action. *PNAS*, 2020. PMID: 32848060.
138. Batra R, Nelles DA, Roth DM, Krach F, Nutter CA, Tadokoro T, Thomas JD, Sznajder L, Blue SM, Gutierrez H, Liu P, Aigner S, Platoshyn O, Miyanochara A, Marsala M, Swanson MS, **Yeo GW**. The sustained expression of Cas9 targeting toxic RNAs reverses disease phenotypes in mouse models of myotonic dystrophy type 1. *Nature Biomedical Engineering*, 2020. PMID:32929188
139. Van Nostrand JL, Hellberg K, Luo E-C, Van Nostrand EL, Dayn A, Yu J, Shokhirev MN, Dayn Y, **Yeo GW**, Shaw RJ. AMPK regulation of Raptor and TSC2 mediate metformin effects on transcriptional control of anabolism and inflammation. *Genes & Dev*, 2020. PMID: 32912901.

140. Lasman L, Krupalnik V, Viukov S, Mor N, Aguilera-Castrejon A, Schneir D, Bayerl J, Mizrahi O, Peles S, Tawil S, Sathe S, Nachshon A, Shani T, Zerbib M, Kilimnik I, Aigner S, Shankar A, Mueller JR, Schwartz S, Stern-Ginossar N, **Yeo GW**, Geula S, Novershtern N, Hanna JH. Context-dependent functional compensation between Ythdf m6a reader proteins. *Genes & Dev*, 2020. PMID: 32943573
141. Marina RJ, Brannan KW, Dong KD, Yee BA, **Yeo GW**. Evaluation of Engineered CRISPR-Cas-Mediated Systems for Site-Specific RNA Editing. *Cell Reports*, 2020. PMID:33147453
142. Biegging-Rolett KT, Kaiser AM, Morgens DW, Boutelle AM, Seoane JA, Van Nostrand EL, Zhu C, Houlihan SL, Mello SS, Yee BA, McClendon J, Pierce SE, Winters IP, Wang M, Connolly AJ, Lowe SW, Curtis C, **Yeo GW**, Winslow MM, Bassik MC, Attardi LD. Zmat3 is a Key Splicing Regulatory in the p53 Tumor Suppression Program. *Molecular Cell*, 2020. PMID: 33157015
143. Corley M, Flynn RA, Lee B, Blue SM, Chang HY, **Yeo GW**. Footprinting SHAPE-eCLIP Reveals Transcriptome-wide Hydrogen Bonds at RNA-protein Interfaces. *Molecular Cell*. 2020. PMID: 33287884.
144. Okholm TLH, Sathe S, Park SS, Kamstrup AB, Rasmussen AM, Shankar A, Chua ZM, Fristrup N, Nielsen MM, Vang S, Dyrskjor L, Aigner, Damgaard CK, **Yeo GW**, Pedersen JS. Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions review effects on circular RNA biogenesis and cancer pathway expression. *Genome Medicine*. 2020. PMID: 33287884.
145. Clark AE, Zhu Z, Krach F, Rich JN, **Yeo GW**, Spector DH. Zika virus is transmitted in neural progenitor cells via cell-to-cell spread and infection is inhibited by the autophagy inducer trehalose. *J Virol*. 2020. PMID: 33328307.
146. Bajaj J, Hamilton M, Shima Y, Chambers K, Spinler K, Van Nostrand EL, Yee BA, Blue SM, Chen M, Rizzeri D, Chuah C, Oehler VG, Broome E, Sasik R, Scott-Browne J, Rao A, **Yeo GW**, Reya T. An in vivo genome-wide CRISPR screen identifies the RNA-binding protein Staufen2 as a key regulator of myeloid leukemia. *Nature Cancer*, 2021. PMID: 34109316.
147. Trujillo CA, Rice ES, Schaefer NK, Chaim IA, Wheeler EC, Madrigal AA, Buchanan J, Preissl S, Wang A, Negraes PD, Szeto RA, Herai RH, Huseynov A, Ferraz MSA, Borges FS, Kihara AH, Byrne A, Marin M, Vollmers C, Brooks AN, Lautz JD, Semendeferi K, Shapiro B, **Yeo GW**, Smith SEP, Green RE, Muotri AR. Reintroduction of the archaic variant of Nova1 in cortical organoids alters neurodevelopment. *Science*, 2021. PMID: 33574182
148. Davis AG, Einstein JM, Zheng D, Jayne ND, Fu X-D, Tian B, **Yeo GW**, and Zhang D-E. A CRISPR RNA-binding protein screen reveals regulators of RUNX1 isoform generation. *Blood Advances*, 2021. PMID: 33656539.
149. Zeller M, Gangavarapu K, Anderson C, Smither AR, Vanchiere JA, Rose R, Dudas G, Snyder DJ, Watts A, Matteson NL, Robles-Sikisaka R, Marshall M, Feehan AK, Sabino-Santos G, Bell-Kareem A, Hughes LD, Alkuzweny M, Snarski P, Garcia-Diaz J, Scott RS, Melnik LI, Klitting R, McGraw M, Belda-Ferre P, DeHoff P, Sathe S, Marotz C, Grubaugh N, Nolan DJ, Drouin AC, Genemaras KJ, Chao K, Topol S, Spencer E, Nicholson L, Aigner S, **Yeo GW**, Farnaes L, Hobbs CA, Laurent LC, Knight R, Hodcroft EB, Khan K, Fusco DN, Cooper VS, Lemey P, Gardner L, Lamers SL, Kamil JP, Garry RF, Suchard MA, Andersen KG. Emergence of an early SARS-CoV-2 epidemic in the United States. *medRxiv*, 2021. PMID:33564781.
150. Washington NL, Gangavarapu K, Zeller M, Bolze A, Cirulli ET, Schiabor Barrett KM, Larsen BB, Anderson C, White S, Cassens T, Jacobs S, Levan G, Nguyen J, Ramirez JM, Rivera-Garcia C, Sandoval E, Wang X, Wong D, Spencer E, Robles-Sikisaka R, Kurzban E, Hughes LD, Deng X, Wang C, Servellita V, Valentine H, De Hoff P, Seaver P, Sathe S, Gietzen K, Sickler B, Antico J, Hoon K, Liu J, Harding A, Bakhtar O, Basler T, Austin B, Isaksson M, Febbo P, Becker D, Laurent M, McDonald E, **Yeo GW**, Knight R, Laurent LC, de Feo E, Worobey M, Chiu C, Suchard MA, Lu JT, Lee W, Andersen KG. Genetic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *medRxiv*, 2021. PMID: 33564780.
151. Washington NL, Gangavarapu K, Zeller M, Bolze A, Cirulli ET, Schiabor Barrett KM, Larsen BB, Anderson C, White S, Cassens T, Jacobs S, Levan G, Nguyen J, Ramirez JM, Rivera-Garcia C, Sandoval E, Wang X, Wong D, Spencer E, Robles-Sikisaka R, Kurzban E, Hughes LD, Deng X, Wang C, Servellita V, Valentine H, De Hoff P, Seaver P, Sathe S, Gietzen K, Sickler B, Antico J, Hoon K, Liu J, Harding A, Bakhtar O, Basler T, Austin B, Isaksson M, Febbo P, Becker D, Laurent M, McDonald E, **Yeo GW**, Knight R, Laurent LC, de Feo E, Worobey M, Chiu C, Suchard MA, Lu JT, Lee W, Andersen KG. Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *Cell*, 2021. PMID: 33861950.
152. Pirie E, Oh CK, Zhang X, Han X, Cieplak P, Scott HR, Deal AK, Ghatak S, Martinez FJ, **Yeo GW**, Yates JR 3rd, Nakamura T, Lipton SA. S-nitrosylated TDP-43 triggers aggregation, cell-to-cell spread, and neurotoxicity in hiPSCs and in vivo models of ALS/FTD. *Proc Natl Acad Sci*, 2021. PMID: 33692125.
153. Jourdain AA, Begg BE, Mick E, Shah H, Calvo SE, Skinner OS, Sharma R, Blue SM, **Yeo GW**, Burge CB, Mootha V. Loss of LUC7L2 and U1 snRNP subunits shifts energy metabolism from glycolysis to OXPHOS. *Molecular Cell*, 2021. PMID: 33852893.

154. Sanchez II, Nguyen TB, England WE, Lim RG, Vu AQ, Miramontes R, Byrne LM, Markmiller S, Lau AL, Orellana I, Curtis MA, Faul RLM, **Yeo GW**, Fowler CD, Reidling JC, Wild EJ, Spitale RC, Thompson LM. Huntington's disease mice and human brain tissue exhibit increased G3BP1 granules and TDP43 mislocalization. *J Clin Invest*. 2021. PMID: 33945510.
155. Brannan KW, Chaim IA, Marina RJ, Yee BA, Kofman ER, Lorenz DA, Jagannatha P, Dong KD, Madrigal AA, Underwood JG, **Yeo GW**. Robust single-cell discovery of RNA targets of RNA binding proteins and ribosomes. *Nature Methods*, 2021. PMID: 33963355
156. Einstein JM, Perelis M, Chaim IA, Meena JK, Nussbacher JK, Tankka AT, Yee BA, Li H, Madrigal AA, Neill NJ, Shankar A, Tyagi S, Westbrook TF, **Yeo GW**. Inhibition of YTDHF2 triggers proteotoxic cell death in MYC-driven breast cancer. *Molecular Cell*, 2021. PMID: 34216543
157. Fenix AM, Miyaoka Y, Bertero A, Blue S, Spindler MJ Tan KKB, Perez-Bermejo J, Chan AH, Mayer SJ, Nguyen T, Russell CR Lizarraga P, Truong An, Po-Lin So, Kulkarni A, Chetal K, Sathe S, Sniadecki NJ, **Yeo GW**, Murry CE, Conklin BR, Salomonis N. Gain-of-function cardiomyopathic mutations in RBM20 rewire splicing regulation and re-distribute ribonucleoprotein granules within processing bodies. *Nature Communications*, 2021. PMID: 34732726
158. Herzner A-M, Khan Z, Van Nostrand EL, Chan S, Cuellar T, Chen R, Pechuan-Jorge X, Komuves L, Solon M, Modrusan Z, Haley B, **Yeo GW**, Behrens TW, Albert ML. Adar and hnRNP C deficiency synergize in activating endogenous dsRNA-induced type I IFN responses. *J Exp Med*, 2021. PMID: 34297039
159. Tan FE, Sathe S, Wheeler EC, **Yeo GW**. Non-microRNA binding competitively inhibits LIN28 regulation. *Cell Reports*, 2021. PMID: 34380031
160. Markmiller S, Sathe S, Server KL, Nguyen TB, Fulzele A, Cody N, Javaherian A, Broski S, Finkbeiner S, Bennett EJ, Lecuyer E, **Yeo GW**. Persistent mRNA localization defects and cell death in ALS neurons caused by transient cellular stress. *Cell Reports*, 2021. PMID: 34496257. (*Recommended by Faculty Opinions as Exceptional*).
161. Wheeler EC, Vora S, Mayer D, Kotini AG, Olszewska M, Park S, Guccione E, Teruya-Feldstein J, Silverman L, Sunahara R, **Yeo GW***, Papapetrou EP*. Integrative RNA-omics discovers GNAS alternative splicing as a phenotypic driver of splicing factor-mutant neoplasms. *Cancer Discovery*, 2021. (*Corresponding) PMID: 34620690
162. Corley M, Flynn RA, Blue SM, Yee BA, Chang HY, **Yeo GW**. fSHAPE, fSHAPE-eCLIP and SHAPE-eCLIP probe transcript regions that interact with specific proteins. *STAR Protocols*, 2021. PMID:34485935.
163. Keehner J, Horton LE, Binkin NJ, Laurent LC on behalf of the SEARCH Alliance*, Pride D, Longhurst CA, Abeles SR, Torriani FJ. Resurgence of SARS-CoV-2 infection in a highly vaccinated health system workforce. *NEJM*, 2021. *I am a founder, and my lab members are part of the SEARCH Alliance. PMID: 34469645.
164. Salido RA, Cantú VJ, Clark AE, Leibel SL, Foroughshafiei A, Saha A, Hakim A, Nouri A, Lastrella AL, Castro-Martínez A, Plascencia A, Kapadia BK, Xia B, Ruiz CA, Marotz CA, Maunder D, Lawrence ES, Smoot EW, Eisner E, Crescini ES, Kohn L, Franco Vargas L, Chacón M, Betty M, Machnicki M, Wu MY, Baer NA, Belda-Ferre P, De Hoff P, Seaver P, Ostrander RT, Tsai R, Sathe S, Aigner S, Morgan SC, Ngo TT, Barber T, Cheung W, Carlin AF, **Yeo GW**, Laurent LC, Fielding-Miller R, Knight R. Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. *mSystems*, 2021. PMID: 34726486.
165. Qin Y, Huttlin EL, Winsnes CF, Gosztyla ML, Wacheul L, Kelly MR, Blue SM, Zheng F, Chen M, Schaffer LV, Licon K, Backstrom A, Vaites LP, Lee JJ, Ouyang W, Liu SN, Zhang T, Silva E, Park J, Pitea A, Kreisberg JF, Gygi Sp, Ma J, Harper JW, **Yeo GW**, Lafontaine DLJ, Lundberg E, Ideker T. A multi-scale map of cell structure fusing protein images and interactions. *Nature*. 2021
166. Long T, Abbasi N, Hernandez JE, Li Y, Sayed IM, Ma S, Iemolo A, Yee BA, **Yeo GW**, Telese F, Ghosh P, Das S, Huang WJM. *Gut*. 2021. PMID: 34853057.
167. Martinez NM, Su A, Burns MC, Nussbacher JK, Schaenin C, Sathe S, **Yeo GW***, Gilbert WV. Pseudouridine synthases modify human pre-mRNA co-transcriptionally and affect pre-mRNA processing. *Molecular Cell*. 2022 (*Corresponding)
168. Desi N, Tong QY, Teh V, Chan JJ, Zhang B, Tabatabaieian H, Tan HQ, Kapeli K, Jin W, Lim CY, Kwok ZH, Tan HT, Wang S, Siew BE, Lee KC, Chong CS, Tan KK, Yang H, Kappei D, **Yeo GW**, Chung MCM, Tay Y. Global analysis of RNA-binding proteins identifies a positive feedback loop between LARP1 and MYC that promotes tumorigenesis. *Cell Mol Life Science*. 2022. PMID: 35195778.
169. Smargon AA, Madrigal AA, Yee BA, Dong KD, Mueller JR, **Yeo GW**. Crosstalk between CRISPR-Cas9 and the human transcriptome. *Nature Communications*. 2022. PMID: 35236841.

170. Blue SM, Yee BA, Pratt GA, Mueller JR, Park SS, Shishkin AA, Starner AC, Van Nostrand EL, **Yeo GW**. Transcriptome-wide identification of RNA-binding protein binding sites using seCLIP-seq. *Nature Protocols*. 2022.
171. Nicholson-Shaw AI, Kofman ER, Yeo GW, Pasquinelli AE. Nuclear and cytoplasmic poly(A) binding proteins (PABPs) favor distinct transcripts and isoforms. *NAR*. 2022.
172. Krivdova G, Voisin V, Schoof EM, Marhon SA, Murison A, McLeod JL, Gabra MM, Zeng AGX, Aigner S, Yee BA, Shishkin AA, Van Nostrand EL, Hermans KG, Trotman-Grant AC, Mbong N, Kennedy JA, Gan OI, Wagenblast E, De Carvalho DD, Salmena L, Minden MD, Bader GD, **Yeo GW**, Dick JE, Lechman ER. Identification of the global miR-130 targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML. *Cell Reports*. 2022
173. Lee DP, Ray WJ, Mei TP, Hoon S, Scolnick J and **Yeo GW**. 2022. Antibody-Oligonucleotide Conjugation Using a SPAAC Copper-Free Method Compatible with 10x Genomics' Single-Cell RNA-Seq. *Methods Mol Biol*. 2022;2463:67-80. doi: 10.1007/978-1-0716-2160-8_6. PMID: 35344168.
174. Tang XE, Tan SX, Hoon S, **Yeo GW**. Pre-existing adaptive immunity to the RNA-editing enzyme Cas13d in humans. *Nature Medicine*. 2022
175. Cho H, Abshire ET, Popp MW, Proschel C, Schwartz JL, **Yeo GW**, Maquat LE. AKT constitutes a signal-promoted alternative exon junction complex that regulates nonsense-mediated decay. *Molecular Cell*. 2022
176. Hatch ST, Smargon AA, **Yeo GW**. Engineered U1 snRNAs to modulate alternatively spliced exons. *Methods*, 2022
177. Morelli KH, Jin W, Shathe S, Madrigal AA, Jones KL, Schwartz JL, Bridges T, Mueller JR, Shankar A, Chaim IA, Day JW, **Yeo GW**. MECP2-related pathways are dysregulated in a cortical model of myotonic dystrophy. *Sciences Translational Medicine*, 2022 (cover article).
178. Krach F, Wheeler EC, Regensburger M, Boerstler T, Holger W, Vu AQ, Wang R, Reischl S, Boldt K, Batra R, Aigner R, Ravits J, Winkler J, **Yeo GW***, Winner B*. *Acta Neuropathologica*, 2022 (*Corresponding)
179. Karthikeyan S, Levy JI, De Hoff P, Humphrey G, Birmingham A, Jepsen K, Farmer S, Tubb HM, Valles T, Tribelhorn CE, Tsai R, Aigner S, Sathe S, Moshiri N, Henson B, Mark AM, Hakim A, Baer NA, Barber T, Belda-Ferre P, Chacón M, Cheung W, Cresini ES, Eisner ER, Lastrella AL, Lawrence ES, Marotz CA, Ngo TT, Ostrander T, Plascencia A, Salido RA, Seaver P, Smoot EW, McDonald D, Neuhaard RM, Scioscia AL, Satterlund AM, Simmons EH, Abelman DB, Brenner D, Bruner JC, Buckley A, Ellison M, Gattas J, Gonias SL, Hale M, Hawkins F, Ikeda L, Jhaveri H, Johnson T, Kellen V, Kremer B, Matthews G, McLawhon RW, Ouillet P, Park D, Pradenas A, Reed S, Riggs L, Sanders A, Sollenberger B, Song A, White B, Winbush T, Aceves CM, Anderson C, Gangavarapu K, Hufbauer E, Kurzban E, Lee J, Matteson NL, Parker E, Perkins SA, Ramesh KS, Robles-Sikisaka R, Schwab MA, Spencer E, Wohl S, Nicholson L, Mchardy IH, Dimmock DP, Hobbs CA, Bakhtar O, Harding A, Mendoza A, Bolze A, Becker D, Cirulli ET, Isaksson M, Schiabor Barrett KM, Washington NL, Malone JD, Schafer AM, Gurfield N, Stous S, Fielding-Miller R, Garfein RS, Gaines T, Anderson C, Martin NK, Schooley R, Austin B, MacCannell DR, Kingsmore SF, Lee W, Shah S, McDonald E, Yu AT, Zeller M, Fisch KM, Longhurst C, Maysent P, Pride D, Khosla PK, Laurent LC, **Yeo GW**, Andersen KG, Knight R. Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. *Nature*. 2022.
180. Burnett CA, Wong AT, Vasquez CA, McHugh CA, **Yeo GW**, Komor AC. Examination of the Cell Cycle Dependence of Cytosine and Adenine Base Editors. *Frontiers in Genome Editing*. 2022
181. Liu L, Vujovic A, Deshpande NP, Sathe S, Anande G, Chen HTT, Xu J, Minden MD, **Yeo GW**, Unnikrishnan A, Hope KJ, Lu Y. The splicing factor RBM17 drives leukemic stem cell maintenance by evading nonsense-mediated decay of pro-leukemic factors. *Nature Communications*. 2022.
182. Ojeda-Juarez D, Lawrence JA, Soldau K, Pizzo DP, Wheeler E, Aguilar-Calvo P, Khoo H, Chen J, Malik A, Funk G, Nam P, Sanchez H, Geschwind MD, Wu C, **Yeo GW**, Chen X, Patrick GN, Sigurdson CJ. Prions induce an early Arc response and a subsequent reduction in mGluR5 in the hippocampus. *Neurobiology of disease*. 2022
183. Her H-L, Boyle E, **Yeo GW**. Metadensity: a background-aware python pipeline for summarizing CLIP signals on various transcriptomic sites. *Bioinformatics Advances*. 2022
184. Kameda-Smith MM, Zhu H, Luo E-C, Suk Y, Xella A, Yee B, Chokshi C, Xing S, Tan F, Fox RG, Adile AA, Bakhshiyhan D, Brown K, Gwynne WD, Subapanditha M, Miletic P, Picard D, Burns I, Moffat J, Paruch K, Fleming A, Hope K, Provias JP, Remke M, Lu Y, Reya T, Venugopal C, Reimand J, Wechsler-Reya RJ*, **Yeo GW***, Singh SK*. Characterization of an RNA binding protein interactome reveals a context-specific post-transcriptional landscape of MYC-amplified medulloblastoma. *Nature Communications*. 2022 (*Corresponding)

185. Morelli KH, Wu Q, Gosztyla ML, Liu H, Yao M, Zhang C, Chen J, Marina RJ, Lee K, Jones KL, Huang MY, Li A, Smith-Geater C, Thompson LM, Duan W*, **Yeo GW***. An RNA-targeting CRISPR-Cas13d system alleviates disease-related phenotypes in Huntington's disease models. *Nature Neuroscience* 2022 (*Corresponding)
186. Bouvrett LPB, Wang X, Boulais J, Kong J, Syed EU, Blue SM, Zhang L, Olson S, Stanton R, Wei X, Y B, Van Nostrand EL, Fu X-D, Burge CB, Graveley BR, **Yeo GW**, Lecuyer E. RBP Image Database: A resource for the systematic characterization of the subcellular distribution properties of human RNA binding proteins. *Nucleic Acids Research* 2022.
187. Lorenz DA, Her Hsuan-Lin, Shen KA, Rothamel K, Hutt KR, Nojadera AC, Bruns SC, Manakov SA, Yee BA, Chapman KB*, **Yeo GW***. Multiplexed transcriptome discovery of RNA-binding protein binding sites by antibody-barcode eCLIP. *Nature Methods* 2022. (*Corresponding)
188. Lin YH, Duong HG, Limary AE, Kim ES, Hsu P, Patel SA, Wong WH, Indralingam CS, Liu YC, Yao P, Chiang NR, Vandenberg SA, Anderson TR, Olvera JG, Ferry A, Takehara KK, Jin W, Tsai MS, **Yeo GW**, Goldrath AW, Chang JT. Small intestine and colon tissue-resident memory CD8+ T cells exhibit molecular heterogeneity and differential dependence on Eomes. *Immunity*. 2022. PMID: 36580919
189. Chen S, Roberts MA, Chen C-Y, Markmiller S, Wei H-G, **Yeo GW**, Granneman JG, Olzmann JA, Ferro-Novick S. VPS13A and VPS13C influence lipid droplet abundance. *Contact*. 2022
190. Kanbar JN, Ma S, Kim ES, Kurd NS, Tsai MS, Tysl T, Widjaja CE, Limary AE, Yee B, He Z, Hao Y, Fu XD, Yeo GW, Huang WJ, Chang JT. The long noncoding RNA Malat1 regulates CD8+ T cell differentiation by mediating epigenetic repression. *J Exp Med*. 2022.
191. Morelli KH, Smargon AA, **Yeo GW**. Programmable macromolecule-based RNA-targeting Therapies to Treat Human Neurological Disorders. *RNA*. 2023. PMID: 36693761
192. Quezada LK, Jin W, Liu YC, Kim ES, He Z, Indralingam CS, Tysl T, Labarta-Bajo L, Wehrens EJ, Jo Y, Kazane KR, Hattori C, Zuniga EI, **Yeo GW**, Chang JT. Early transcriptional and epigenetic divergence of CD8+ T cells responding to acute versus chronic infection. *PLoS Biol*. 2023. PMID: 36716323
193. Ma S, Yang Q, Chen N, Zheng A, Abbasi N, Wang G, Patel PR, Cho BS, Yee BA, Zhang L, Chu H, Evans SM, **Yeo GW**, Zheng Y, Huang WJM. RNA binding protein DDX5 restricts RORgammaT+ Treg suppressor function to promote intestine inflammation. *Science Advances* 2020. PMID: 36724232.
194. Arif W, Mathur B, Saikali MF, Chembazhi UV, Toohill K, Song YJ, Hao Q, Karimi S, Blue SM, Yee BA, Van Nostrand EL, Bangru S, Guzman G, **Yeo GW**, Prasanth KV, Anakk S, Cummins CL, Kalsotra A. Splicing factor SRSF1 deficiency in the liver triggers NASH-like pathology and cell death. *Nat Commun*. 2023. PMID: 36759613
195. Vujovic A, de Rooij L, Keyvani Chahi A, Chen HT, Yee BA, Loganathan SK, Liu L, Chan DCH, Tajik A, Tsao E, Moreira S, Joshi P, Xu J, Wong N, Balde Z, Jahangiri S, Zandi S, Aigner S, Dick JE, Minden MD, Schramek D, **Yeo GW**, Hope KJ. In vivo screening unveils pervasive RNA-binding protein dependencies in leukemic stem cells and identifies ELAVL1 as a therapeutic target. *Blood Cancer Discovery*, 2023. PMID: 36763002
196. Kathman SG, Koo SJ, Lindsey GL, Her H-L, Blue SM, Li H, Jaensch S, Remsberg JR, Ahn K*, **Yeo GW***, Ghosh B*, Cravatt BF*. Remodeling oncogenic transcriptomes by small molecules targeting NONO. *Nature Chemical Biology*. 2023 (*Corresponding)
197. Lazear MR, Remsberg JR, Jaeger MG, Rothamel K, Her H-L, DeMeester KE, Njomen E, Hogg SJ, Rahman J, Whitby LR, Won SJ, Schafroth MA, Ogasawara D, Yokoyama M, Lindsey GL, Li H, Germain J, Barbas S, Vaughan J, Hanigan TW, Vartabedian VF, Reinhardt CJ, Dix MM, Koo SJ, Heo I, Teijaro JR, Simon GM, Ghosh B, Abdel-Wahab O, Ahn K, Saghatelian A, Melillo B, Schreiber SL, **Yeo GW**, Cravatt BF. Proteomic discovery of chemical probes that perturb protein complexes in human cells. *Molecular Cell*, 2023
198. Boyle EA, Her H-L, Mueller JR, Naritomi JT, Nguyen GG and **Yeo GW**. Skipper analysis of eCLIP datasets enables sensitive detection of constrained translation factor binding sites. *Cell Genomics*. 2023.
199. Kejiou NS, Llan L, Aigner S, Luo E, Tonn T, Ozadam H, Lee M, Cole GB, Rabano I, Rajakulendran N, Yee BA, Najafabadi HS, Moraes TF, Angers S, **Yeo GW**, Cenik C, Palazzo. Pyruvate kinase M (PKM) binds ribosomes in a poly-ADP ribosylation dependent manner to induce translational stalling. *Nucleic Acids Research*. 2023.
200. Correia JC, Jannig PR, Gosztyla ML, Cervenka I, Ducommun S, Præsthholm SM, Dumont K, Liu Z, Liang Q, Edsgård D, Emanuelsson O, Gregorevic P, Westerblad H, Venckunas T, Brazaitis M, Kamandulis S, Lanner JT, **Yeo GW**, Ruas JL. ZFP697 is an RNA-binding protein that regulates skeletal muscle inflammation and regeneration. *bioRxiv* 2023.

201. Jin W, Brannan KW, Kapeli K, Park SS, Tan HQ, Gosztyla ML, Mujumdar M, Ahdout J, Henroid B, Rothamel K, Xiang JS, Wong L, **Yeo GW**. HyDRA: Deep-learning models for predicting RNA-binding capacity from protein interaction association context and protein sequence. *Molecular Cell*. 2023
202. Kofman E, Yee B, Medina-Munoz HC, **Yeo GW**. FLARE: a fast and flexible workflow for identifying RNA editing foci. *BMC Bioinformatics*. 2023
203. Lal NK, Le P, Aggarwal S, Zhang A, Wang K, Qi T, Pang Z, Yang D, Nudell V, **Yeo GW**, Banks AS, Ye L. Xiphoid nucleus of the midline thalamus controls cold-induced food seeking. *Nature*, 2023.
204. Song Y, Fothergill LJ, Lee KS, Liu BY, Koo A, Perelis M, Diwakarla S, Callaghan B, Huang J, Wykosky J, Furness JB, **Yeo GW**. Stratification of enterochromaffin cells by single-cell expression analysis. *bioRxiv*, 2023
205. Antal CE, Oh TG, Aigner S, Luo E-C, Yee BA, Campos T, Tiriac H, Rothamel K, Cheng Z, Jiao H, Wang A, Hah N, Lenkiewicz E, Lumibao JC, Truitt ML, Estepa G, Banyo E, Bashi S, Esparza E, Munoz R, Diedrich JK, Sodik NM, Mueller JR, Fraser CR, Borazanci E, Propper D, Von Hoff DV, Liddle C, Yu RT, Atkins AR, Han H, Lowy AM, Barrett MT, Engle DD, Evan GI, **Yeo GW**, Downes M, Evans RM. A super-enhancer regulated RNA-binding protein cascade drives pancreatic cancer. *Nature Communications*, 2023 PMID: 37673892

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. Smargon AS, Shi YJ, Yeo **GW**. RNA-targeting CRISPR systems from metagenomic discovery to transcriptomic engineering. *Nature Cell Biology*, 2020. PMID:32015437
25. Corley M, Burns MC, Yeo **GW**. How RNA binding proteins interact with RNA: molecules and mechanisms. *Molecular Cell*, 2020. PMID:32243832
26. Porto EM, Komor AC, Slaymaker IM, Yeo **GW**. Base editing: advances and therapeutic opportunities. *Nature Drug Discovery Reviews*, 2020. PMID:33077937
27. Schwartz JL, Jones KL, Yeo **GW**. Repeat RNA expansion disorders of the nervous system: post-transcriptional mechanisms and therapeutic strategies. *Critical Reviews in Biochemistry and Molecular Biology*, 2020. PMID: 33172304
28. Elmsauri S, Markmiller S, Yeo **GW**. APEX Proximity Labeling of Stress Granule Proteins. *Methods Mol Biol*. 2022. PMID: 35171492
29. Le P, Ahmed N, Yeo **GW**. Illuminating RNA biology through imaging. *Nature Cell Biology*. 2022
30. Rhine K, Al-Azzam N, Yu T, Yeo **GW**. Aging RNA granule dynamics in neurodegeneration. *Frontiers in Molecular Biosciences*, 2022.
31. Morelli KH, Smargon AA, Yeo **GW**. Programmable macromolecule-based RNA-targeting therapies to treat human neurological disorders. *RNA*. 2023. PMID: 36693761.

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 (SELECTED)

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 Society 2006. Highly conserved intronic elements proximal to mammalian exons predict tissue-specificity of alternatively spliced exons (POSTER).
9. RNA Society 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 Society 2008. CLIP-Seq reveals a network of FOX2 regulated alternatively spliced exons in human embryonic stem cells (SELECTED TALK).
22. RNA Society 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 Society 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, BIMS 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)
242. 24th Annual RNA Society Meeting, Krakow, June 11-16, 2019 (Co-Organizer and Workshop Chair)
243. Keystone Symposia "Neurodegenerative diseases: new insights and therapeutic opportunities", Keystone Colorado, June 16-20, 2019 (INVITED SPEAKER)
244. RNA therapeutics Meeting, U Mass Medical, June 27-29, 2019 (INVITED SPEAKER)
245. Cold Spring Harbor Laboratory Single Cell Analysis Course, July 7, 2019 (CO-COURSE ORGANIZER, INVITED SPEAKER)
246. Alzheimer's Association International Conference, Los Angeles Convention Center, July 15, 2019 (INVITED SPEAKER)
247. First Singaporean Researchers Global Summit, Singapore, Aug 6, 2019 (ORGANIZER, KEYNOTE SPEAKER)
248. Inception, La Jolla Aug 29, 2019 (INVITED SPEAKER)
249. Launchbio's Larger than Life Science Leading the Way, "UCSD Spinout success: Locana lighting the way", BioLabs, La Jolla, Aug 29, 2019 (INVITED PANELIST)
250. Science Alliance: Silencing Neurodegenerative diseases with Gene Editing, J Labs, La Jolla, Sept 4, 2019 (INVITED SPEAKER)
251. Myotonic Annual Conference, Professional Track, Philadelphia, Sept 13, 2019 (INVITED SPEAKER)
252. Hogg Seminar Series, MD Anderson, Austin, Sept 25, 2019 (INVITED SPEAKER)
253. 5th RNA Biology Symposium by Cancer Science Institute, NUS, Singapore, Oct 3-4, 2019 (CO-ORGANIZER)
254. Institute of Molecular Cell Biology, A*STAR, Singapore, Oct 9, 2019 (INVITED SPEAKER)
255. Genome editing in neurological disease symposium, Children's Hospital of Philadelphia, Oct 14, 2019 (INVITED SPEAKER)
256. National Cancer Institute RNA Initiative Seminar Series, Oct 21-22, 2019 (INVITED SPEAKER)

257. National Cooperative Reprogrammed Cell Research Groups and Convergent Neuroscience in studies of Mental Illness: Consortium Meeting, Chicago, Oct 23-23, 2019 (INVITED SPEAKER)
258. Keystone Conference on Non-coding RNAs: mechanism, function and therapies, Whistler, Canada, Jan 12-17, 2020 (INVITED SPEAKER)
259. 1st international conference on base editing – enzymes and applications (Deaminet 2020), Palm Springs, CA, Jan 26, 2020 (INVITED SPEAKER)
260. Single Cell Workshop, Sanford Burnham Conrad Prebys Research Institute, Feb 3, 2020 (INVITED SPEAKER)
261. UC Davis College of Biological Sciences Joint Seminar Series in Molecular Biology, UC Davis, Feb 11, 2020 (INVITED SPEAKER)
262. Dorris Neuroscience Center, Scripps Institute, La Jolla, Feb 18, 2020 (INVITED SPEAKER)
263. Regulus, La Jolla, March 3, 2020 (INVITED SPEAKER)
264. CHDI, April 3, 2020 (INVITED SPEAKER)
265. Biocom's Webinar on Return to Work: Testing Foundations for COVID, June 17, 2020 (INVITED PANELIST)
266. CZI Neurodegeneration Challenge Network: Diversity, Equity and Inclusion Keynote Panel, July 14, 2020 (INVITED SPEAKER)
267. Rady BioCom Career Panel, July 14, 2020 (INVITED PANELIST)
268. CZI Neurodegeneration Challenge Network: CRISPR Breakout Session Leader, July 15, 2020 (INVITED PANELIST)
269. Biocom Genomics Webinar to Congressional Staff, including Members of Congress' personal officers and committees of jurisdiction in the House and Senate, July 15, 2020 (INVITED SPEAKER)
270. Moores Cancer Center Structural and Functional Genomics Retreat, Virtual Meeting, Sept 17, 2020 (INVITED SPEAKER)
271. Columbia University Department of Systems Biology Distinguished Speaker Seminar Series Virtual Meeting, Sept 23, 2020 (INVITED SPEAKER)
272. Brandes/Rady Summit: Covid-19, Sept 2, 2020 (INVITED SPEAKER AND PANELIST)
273. Supporting Diversity, Inclusion and Equity in Neuroscience, Interview with Katja Brose at CZI, Sept 23, 2020 (INVITED PANELIST)
274. Virtual 6th Singapore RNA Biology Symposium, Oct 1, 2020 (INVITED SPEAKER AND PANELIST)
275. Center for RNA Biomedicine at University of Michigan, Oct 19, 2020 (INVITED SPEAKER)
276. Nature Conference "RNA at the Bench and Bedside II," Nov 11-13, 2020 (ORGANIZER, SESSION CHAIR, PANELIST AND KEYNOTE SPEAKER)
277. Molecular Medicine Program at SickKids Research Institute, Toronto (Virtual), Nov 30, 2020 (INVITED SPEAKER)
278. 3rd RNA-Targeted Drug Discovery Summit 2020, Dec 9, 2020 (INVITED SPEAKER AND PANELIST)
279. IMPRS-LM Distinguished Guests Seminar Series 2021 at the Max Planck Institute of Molecular Physiology, Feb 23-24, 2021 (INVITED SPEAKER)
280. 21st Packard Center Research Symposium, March 8, 2021 (INVITED SPEAKER)
281. MDA 2021 Virtual Clinical and Scientific Conference, March 15, 2021 (INVITED SPEAKER)
282. Targeting RNA Congress, March 16, 2021 (INVITED SPEAKER)
283. UCSD Health Sciences Research Council, April 14, 2021 (CO-MODERATOR OF PRECISION MEDICINE TALKS)
284. Spatial Biology Europe Online, April 16, 2021 (INVITED SPEAKER AND PANELIST)
285. Genomics of Brain Disorder, April 16, 2021 (INVITED SPEAKER AND PANELIST)
286. City of Hope Leading Edge Lecture Series The John Rossi Seminar Speaker, May 7, 2021 (INVITED SPEAKER)
287. Rady School of Management Innovation Panel Discussion on Passion, Drive & Innovation, May 13, 2021 (INVITED SPEAKER)
288. Harvard Medical School Initiative for RNA Medicine Seminar Speaker, May 25, 2021 (INVITED SPEAKER)
289. 26th RNA Society 2021 Online Meeting, May 25-June 4, 2021 (Lead Organizer, Award Recipient and Speaker, Panel Chair)
290. Vertex Pharmaceuticals Science and Medicine Series. 16 June, 2021 (INVITED SPEAKER)
291. CZI NDCN Annual Meeting, 23 June, 2021 (INVITED SPEAKER)
292. FASEB Protein aggregation Symposium, 23 June, 2021 (INVITED SPEAKER)
293. UCSD Department of Pathology Retreat, 21 August, 2021 (KEYNOTE SPEAKER)
294. ISSCR/ASGCT Symposium, 13 Sept, 2021 (INVITED SPEAKER/PANELIST)
295. James S McDonnell Department of Genetics Spring Seminar Series, Washington University in St. Louis (INVITED SPEAKER)
296. Denali Therapeutics Webinar to highlight ALS and FTD Development Programs, Oct 6, 2021 (INVITED SPEAKER/PANELIST)
297. Warren Alpert Award Symposium, 7 Oct, 2021 (INVITED SPEAKER, other invited speakers were Phil Sharp, Melissa Moore, honoring Lynne Maquat and Joan Steitz)
298. QB3 Seminar Series, 13 Oct 2021 (INVITED SPEAKER)
299. Inaugural Sanford Stem Cell Symposium, 15 Oct 2021 (INVITED SPEAKER)
300. UC Regents Special Committee on Innovation Transfer & Entrepreneurship. 21 Oct 2021 (INVITED SPEAKER)
301. X-Meeting XP Organization, Virtual. 27 Oct 2021 (KEYNOTE SPEAKER)
302. NIMH Joint Consortium Meeting for Convergent Neuroscience/NCRCRG/BICCN/PyschENCODE, 3-5 Nov, 2021 (PANEL MODERATOR)
303. A*STAR Scientific Conference celebrating A*STAR's 30th anniversary, 28 Nov, 2021 (INVITED SPEAKER)
304. UCLA Neurology Grand Rounds, Jan 12, 2022 (INVITED SPEAKER)
305. UCSD Cancer Genomics Meeting, Jan 26, 2022 (INVITED SPEAKER)
306. 2022 California ALS Research Summit, Jan 28, 2022 (INVITED SPEAKER)
307. EMBO course RNA binding proteins: From RNA binding to condensation and aggregation, India, 8-11 Feb, 2022 (INVITED SPEAKER)
308. CHDI's annual Huntington's disease therapeutic conference, Palm Springs, March 2, 2022 (INVITED SPEAKER)
309. National Center of Leadership in Academic Medicine (NCLAM), March 11, 2022 (INVITED SPEAKER)
310. Virtual workshop: Future use and expansion of the SFARI/NLMFF iPS Cell resource, March 18, 2022 (INVITED PANELIST)

311. Celebrating the Life and Science of Sydney Brenner (1927-2019), CSHL, March 24, 2022 (INVITED SPEAKER)
312. Allen Frontiers Symposium, March 29, 2022 (INVITED SPEAKER as Allen Distinguished Investigator)
313. Fireside Chat at UC Merced to talk about entrepreneurship, April 19, 2022
314. Drug Discovery Chemistry, San Diego, April 18-21, 2022 (INVITED SPEAKER)
315. Precision Genome Engineering, Keystone Conference, April 27-May 1, 2022 (INVITED SPEAKER)
316. REVOLUTION 22 (The symposium for CSOs focused on R&D Issues) (INVITED PANELIST)
317. USC School of Pharmacy, May 20, 2022 (INVITED SPEAKER)
318. Amgen Seminar Series, June 30, 2022 (INVITED SPEAKER)
319. CIRM Bridges Trainee Meeting, July 26, 2022 (INVITED SPEAKER)
320. Sixth Biennial Meeting of the LARP Society, York University, Toronto, Aug 7, 2022 (KEYNOTE SPEAKER)
321. John C. Lee Endowed Lecture UT Health San Antonio, San Antonio, Aug 26, 2022 (INVITED SPEAKER)
322. Riboclub Conference, Orford, Canada, 20 Sept 2022 (INVITED SPEAKER)
323. Discovery on Target, Oct 18, 2022 (INVITED SPEAKER)
324. UC Irvine School of Medicine Department of Microbiology & Molecular Genetics Seminar, Oct 19, 2022 (INVITED SPEAKER)
325. University of Texas, Dallas, Department of Biological Sciences, Seminar Series, Oct 27 2022 (INVITED SPEAKER)
326. University of California Riverside Center for RNA biology and medicine Inaugural Symposium, Nov 4, 2022 (INVITED SPEAKER)
327. Sacramento State University, Regenerative Medicine Lecture, Nov 9, 2022 (INVITED SPEAKER)
328. Nature Bench to Bedside III, Nov 8-10, 2022 (CO-ORGANIZER with Nature Editors and Stan Crooke, and SESSION CHAIR)
329. French-American Innovation Days, Clinical Trials In Gene Therapy, Nov 17-18, 2022 (INVITED SPEAKER)
330. Levine-Riggs Diabetes Research Symposium Program, Dec 1, 2022 (INVITED SPEAKER)
331. CHDI-hosted RNA Workshop, Dec 7-8, 2022 (INVITED SPEAKER AND CHAIR)
332. UCSD Board of Trustees, Dec 9, 2022 (INVITED SPEAKER)
333. Emerging Science & Innovation Seminar Series, Pfizer, Jan 26, 2023 (INVITED SPEAKER)
334. Keystone Symposia Conference: Protein-RNA Interactions, Vancouver, Canada, Jan 29- Feb 1, 2023 (Lead Organizer, Session Chair and INVITED SPEAKER)
335. Health Innovation and Translation Symposium, Design and Innovation Building, Feb 11, 2023 (INVITED SPEAKER)
336. Mount Sinai GGS Seminar Series, Feb 23, 2023 (INVITED SPEAKER, virtual visit)
337. Molecular and Precision Med Tricon by Cambridge Healthtech Institute, San Diego, March 6, 2023 (INVITED SPEAKER)
338. National Academies of Sciences, Engineering and Medicine, Toward Sequencing and Mapping for RNA modifications Workshop, Virtual, March 14, 2023 (INVITED SPEAKER AND PANELIST)
339. Cold Spring Harbor Laboratory Network Biology Meeting, March 17, 2023 (INVITED SPEAKER)
340. Gordon Research Conference on RNA Editing, March 21, 2023 (INVITED SPEAKER)
341. Spark Bio Panel for Company Build, March 26, 2023 (INVITED PANELIST)
342. UC Merced's 1st Innovation and Entrepreneurship Conference, April 7, 2023 (INVITED SPEAKER AND PANELIST)
343. UC Riverside CMDB/GGB/MCBL Seminar Series, April 26, 2023 (INVITED SPEAKER, VIRTUAL)
344. Sid Altman's Inaugural Memorial Symposium, May 2, 2023 (INVITED SPEAKER)
345. 4th Splicing factor mutations and RNA biology in Cancer, New York, May 11, 2023 (KEYNOTE SPEAKER)
346. STEP Ahead into an RNA World 2023, May 29-30, 2023 (ORGANIZER and CHAIR)
347. A*STARTCENTRAL Fireside Chat on Entrepreneurship, Singapore. May 31, 2023 (INVITED SPEAKER)
348. 28th Annual Meeting of the RNA Society 2023. Singapore, June 1, 2023 (INVITED SPEAKER AND CHAIR)
349. Advances in Genome Technology Development annual meeting, SCRUM, La Jolla, June 6, 2023 (INVITED SPEAKER AND CAREER WORKSHOP MODERATOR)
350. Dup15q Alliance 2023 Science Symposium, July 26, 2023 (INVITED SPEAKER, VIRTUAL)
351. Nucleate Summit 2023, San Diego, Aug 24, 2023 (INVITED TENT SPEAKER)
352. 16th Berlin Summer Meeting, MDC celebrates 15 years of BIMS, Sept 6, 2023 (INVITED SPEAKER, VIRTUAL)
353. BMS Computational Biology Track Orientation, UCSD, Sept 19, 2023 (INVITED SPEAKER)
354. Global Genes, Rare Disease Summit, San Diego, Sept 20, 2023 (INVITED PANELIST)
355. 22nd Annual Sanford-Burnham-Prebys Trainee Research Symposium, Sept 21, 2023 (KEYNOTE SPEAKER)
356. William Guy Forbeck Research Forum "Therapeutic Targeting of mRNA splicing in cancer", Asilomar, California, Sept 23, 2023 (INVITED SPEAKER)
357. Cambridge Innovation Conference on Small Molecules Targeting RNA, Boston, Sept 26, 2023 (INVITED SPEAKER, VIRTUAL)
358. Academia Europaea Annual Meeting, Gene presented the Sydney Brenner Medal for achievements in the Life Sciences, Munich, Oct 10, 2023 (Award Recipient and SPEAKER, Presented by Carla Brenner)
359. MDC Berlin, Oct 11, 2023 (SAB VISIT and SPEAKER)
360. 7th New England Biolabs Scientific Forum in China, Oct 31, 2023 (VIRTUAL INVITED SPEAKER)

COURSES/COURSEWORK ATTENDED

Senior Faculty Mentor Training 2021: Optimizing Health Sciences Faculty Mentoring Relationships at University of California, San Diego. Conducted by Dr. Angela Byars-Winston, CIMER Faculty Lead for Strategic Initiatives and Professor of Medicine, University of Wisconsin-Madison and Dr. Christine Pfund, CIMER Director, and Senior Scientist, Wisconsin Center for Education Research and Institute for Clinical and Translational Research, University of Wisconsin-Madison.

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

Domestic Active Grant Support

SFARI Pilot Award 668241	02/01/2020-01/31/2022	0.12 calendar
Simons Autism Foundation	Annual: \$125,000	Entire Period: \$250,000
Inhibition of UBAP2L as a treatment of fragile X syndrome		
We propose to use iPSC and mouse models of fragile X syndrome (FXS) to test if inhibition of UBAP2L, an RNA binding protein we identified as an FMRP-associated translation enhancer, can ameliorate FXS-associated molecular, cellular, functional and behavioral deficits.		
Role: PI		
5U01 HG009417-S1 (Xiao)	02/01/2021-01/31/2022	0.45 calendar
NIH/NHGRI	Annual: \$87,421 (Yeo)	Entire period: \$87,421 (Yeo)
<i>Analysis of functional genetic variants in RNA processing and expression</i>		
The major goal of this project is to develop computational tools to evaluate allele-specific binding for eCLIP data generated by the Yeo lab. Dr. Yeo is responsible for providing computational support and improving peak-calling on these eCLIP datasets.		
Role: Consortium PI		
Grant # 2020-217276	03/01/2020-02/28/2022	0.01 calendar
Chan Zuckerberg Initiative	Annual: \$87,500 (Yeo)	Entire Period: \$175,000
Deciphering the Microglial Inflammatory Response in 3D		
In this project, we develop and apply novel single-cell technologies to identify genetic determinants of microglial activation using iPSC-derived cells and mouse models. Dr. Yeo is responsible for single-cell experiments and analyses.		
Role: Co-Investigator		
R01 EY029166 (Yeo, Afshari, Gottesfeld)	04/01/2018-03/31/2022	0.30 calendar
NIH/NEI	Annual: \$156,073 (Yeo)	Entire Period: \$298,396 (Yeo)
Application of RNA-targeting Cas9 to Fuchs' dystrophy		
The major goal of this project is 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. Dr. Yeo is responsible for generating viral delivery vectors, and performing RNA-seq, single-cell RNA-seq, RNA-FISH, and eCLIP analyses in human corneal tissue and iPSC-derived corneal endothelial cells.		
Role: Contact MPI		
R01 NS103172 (Yeo, Swanson)	09/22/2017-05/31/2022	1.80 calendar
NIH/NINDS	Annual: \$385,942 (Yeo)	Entire Period: \$1,179,635
Therapeutic strategies for microsatellite expansion diseases using RNA-targeting CRISPR/Cas		
The major goal of this project is to develop AAV-based therapeutic strategies for microsatellite expansion diseases using RNA-targeting CRISPR/Cas (RCas9), perform in vivo safety studies and develop alternative RNA processing biomarkers reliable for measuring RCas9 treatment efficacy in myotonic dystrophy in muscle cells. Dr. Yeo is responsible for generating AAV-packaged RCas9 constructs, their validation in cell culture model of myotonic dystrophy, and for the generation and analysis of RNA-seq and TEMPO-seq data in the efficacy and safety studies.		
Role: Contact MPI		
U01 MH115747-03S1	07/01/2020-06/30/2022	0.46 calendar
NIH/NIMH	Annual: \$320,353 (Yeo)	Entire Period: \$640,706

The goal of the supplement and Dr. Yeo's responsibility are the addition of automated processing and analysis modules for proteomics and genomics data generated by the Psychiatric Cell Map Initiative and other consortia members, a standardized metadata framework for these domains, and an expansion of the current transcriptomic, imaging, and electrophysiological modules.

Role: Consortium Co-investigator

UCSD Proposal ID: 29011 (Andersen) 08/01/2020-07/31/2022 0.24 calendar

U.S. Centers for Disease Control Annual: \$133,333 (Yeo) Entire Period: \$266,667 (Yeo)

Genomic sequencing of SARS-CoV-2 to investigate local and cross-border emergence and spread

The goal of this contract is to develop and perform a COVID-19 genomic sequencing project to understand viral transmission dynamics.

Dr. Yeo is responsible for development and expansion of open-source software for sample tracking and data analysis.

Role: Subcontractor

NIH 3P42 ES010337-19S1 09/01/2020-08/31/2022 0.01 calendar

NIH/NIEHS Annual: \$6,284 (Yeo) Entire Period: \$12,568

Harnessing Technological Innovation and Community-Engaged Implementation Science to Optimize COVID-19 Testing for Women and Children in Underserved Communities

The goal of this supplement is to provide minorities and underserved communities in the San Diego area with facile, rapid and affordable access to COVID-19 testing.

Role: Co-investigator

U41 HG009889 (Graveley, Yeo) 02/05/2018-01/31/2022 1.62 calendar

NIH/NHGRI Annual: \$754,078 (Yeo) Entire Period: \$1,576,357 (Yeo)

A Comprehensive Functional Map of Human Protein-RNA Interactions

The major goal of this project is to continue generating functional protein-RNA interaction data for human RNA binding proteins. This community resource project will generate physical resources such as tagged cell lines, validated antibodies, and expression vectors as well as data resources such as eCLIP, RNA Bind-N-Seq, knockdown RNA-seq, and protein localization data. All data will be made available to the community as it is generated and prior to publication. Dr. Yeo is responsible for generating and analyzing eCLIP data.

Role: MPI

UCSD Proposal ID: 29557 (Yeo) 11/01/2020-10/31/2022 0.12 calendar

CHDI Foundation Annual: \$157,746 Entire period: \$315,100

Identification of HTT interaction partners

The goal of this project is to use state-of-the-art mass spectrometry and cross-linking immunoprecipitation assays in pluripotent stem cell-derived striatal neurons to identify protein and RNA interaction partners of mutant and normal huntingtin, and to validate these in postmortem brain tissue.

Role: PI

DoD AL29052 (Yeo) 01/01/2021-12/31/2022 0.12 calendar

U.S. Department of Defense Annual: \$140,000 (Yeo) Entire period: \$280,000 (Yeo)

RNA-Directed Therapy for C9ORF72-Linked ALS Using Engineered Zinc Finger Nucleases

The goal of this project is to develop adenoviral vector (AAV)-delivered RNA-targeting zinc finger protein effectors as therapeutic candidates for treatment of amyotrophic lateral sclerosis caused repeat expansion in *C9ORF72* (C9ALS). We will evaluate the ability of to eliminate repeat expansion RNA in patient cell lines and perform in vivo safety and efficacy studies in mice.

Role: PI

R01 HL137223 (Yeo, Hope) 05/01/2018-04/30/2023 0.75 calendar

NIH/NHLBI Annual: \$468,866 (Yeo) Entire Period: \$938,268 (Yeo)

Analysis of RNA binding proteins directing hematopoietic stem cell fate

The major goal of this project is to functionally characterize a novel MSI2-interactor and putative HSC-regulator. Dr. Yeo is responsible for performing eCLIP analyses, RCas9 and antisense oligonucleotide depletion experiments, and their computational integration of the data.

Role: Contact MPI

P01 AI132122 (Goldrath) 07/17/2018-06/30/2023 0.46 calendar

NIH/NIAID Annual: \$307,046 (Yeo) Entire Period: \$615,640 (Yeo)

Molecular Determinants of Tissue-resident Memory T Cell Fate in Acute and Chronic Infection

Dr. Yeo is the PI of the Single-Cell Transcriptomic and Epigenetics (SCTE) Core. The major goal of the SCTE Core is to provide a centralized resource for generating single-cell RNA-sequencing, histone modification ChIP-seq, transcription factor ChIP-seq, and ATAC-seq datasets and 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.

Role: Core PI

Allen Distinguished Investigator Award 08/05/2020-08/05/2023 2.40 calendar

Paul G. Allen Family Foundation Annual: \$500,000 Entire Period: \$1,500,000

Early Manifestations of Subcellular Defects in Neurodegenerative Diseases

In this project, we test the hypothesis that genetic mutations that cause late-onset neurodegenerative diseases lead to molecular and cellular defects in early development. We generate augmented stem cell models, to discover normal and aberrant changes in the protein and RNA components and identify the critical sub-cellular compartments and their components that protect the cell against degenerative disease.

Role: PI

R01 HG004659 (Yeo) 07/01/2017-06/30/2024 0.91 calendar
NIH/NHGRI Annual: \$348,728 (Yeo) Entire Period: \$1,785,909

Functional RNA elements in the human genome

The major goal of this project is to conduct systematic loss and gain-of-function studies to identify genes, networks and pathways involved in the regulation of RNA processing.

Role: PI

R01 HD101534-01A1 (Barrett, Yeo) 09/01/2020-05/31/2025 0.36 calendar
NIH/NICHD Annual: \$163,193 (Yeo) Entire Period: \$815,965 (Yeo)

Dissecting the role of FMRP in RNA processing using human stem cell models

The goal of this project is to elucidate fundamental molecular mechanisms of the RNA binding protein FMRP in relevant human cell types. Dr. Yeo is responsible for performing RNA-seq and eCLIP studies.

Role: Consortium Co-Investigator

Grant # 2021-235103 07/01/2022-06/30/2023
Chan Zuckerberg Initiative Annual: \$30,000 (Yeo) Entire Period: \$30,000

Subcellular RNA dynamics in HD

We aim to define global mRNA localization landscapes in normal and Huntington's disease iPSC-motor and striatal neurons to evaluate mRNA localization in nuclear, cytoplasmic, and insoluble fractions.

Role: Co-Investigator

R01 HG011864 (Yeo) 08/01/2021-07/31/2025 0.6 calendar
NIH/NHGRI Annual: \$348,728 (Yeo) Entire Period: \$1,785,909

STAMP technology to enable single-cell and isoform-sensitive detection of RBP sites

The goal of this project is to develop a novel scalable technology, reagent resource, experimental protocols and a computational framework for detecting RBP-RNA targets and translation at the single-cell and single-molecule levels.

Role: PI

Foreign Active Grant Support

UCSD Proposal ID: 20202249 02/25/2020-02/24/2022 0.01 calendar
Takeda Millennium Pharmaceuticals Annual: \$219,722 Entire Period: \$434,444

Targeting RNA binding proteins (RBPs) in Fragile X Syndrome: small molecule inhibitors of UBAP2L

The aim of this research project is to identify compounds that inhibit the functional interaction between UBAP2L and the ribosome and test efficacy of hit compounds in stem cell and mouse models of FXS.

Role: PI

Roche ROADS Innovation grant 01/01/2021-12/31/2022 0.01 calendar
F. Hoffmann – La Roche Switzerland Annual: \$110,000 (1st year) Entire Period: \$440,000

Modulation of RNA subcellular localization for the treatment of neurological diseases

The goal of this project is to generate comprehensive maps of RNA localization in cultured neurons and brain tissue at subcellular resolution and transcript isoform specificity, relevant to Parkinson's disease.

Role: PI

Visiting Investigatorship Award 04/01/2018-03/31/2023 0.012 calendar
Singapore National Research Foundation (NRF) & National University of Singapore (NUS)
Annual: \$200,000 Entire Period: \$400,000

Dr. Yeo received a competitive award for overseas senior Singaporean scientists to uplift and mentor young scientists in Singapore to help build their careers. The award provides for travel reimbursements to Singapore and honoraria for consulting to Dr. Yeo but no salary. The funding also helps initiate collaborations and visits from international scientists to visit Singapore and for young Singapore scientists to visit UCSD. This award also funds research at the National University of Singapore on the areas of technology development in immune- oncology in collaboration with other labs in Singapore. Funding from Singapore does not provide direct research support to NIH-funded projects (at UCSD). Similarly, NIH funding does not provide support to NUS/NRF projects in Singapore.

Role: PI (Position: Honorary Visiting Professor)

COMPLETED GRANTS

R56 AG069098 (Yeo)

09/30/2020-08/31/2021

NIH/NIA

Annual: \$419,995

Entire Period: \$419,995

Evaluating and Targeting RNA granules in neurodegenerative diseases

The goal of this project is to systematically interrogate the compositional landscape of pathological protein aggregates across a spectrum of cortical organoid models of neurodegenerative diseases, particularly dementia caused by tauopathies to identify convergent and divergent trajectories of SG dynamics and interactions in neurodegeneration.

Role: PI

R01 AI123202 (Chang, Yeo)

09/23/2016-08/31/2021

NIH/NIAID

Annual: \$173,949 (Yeo)

Entire Period \$723,464 (Yeo)

Using single-cell RNA-seq to interrogate host immunity to pathogens

The major goal of this project is to develop single-cell RNA sequencing and computational tools to understand the specification of the terminal effector and memory CD8+ T lymphocyte fates. Dr. Yeo is responsible for generating, analyzing and validating single-cell RNA data.

Role: MPI

UCSD Proposal ID: 28563 (Lo)

09/01/2020-08/31/2021

U.S. IARPA

Annual: \$150,000 (Yeo) Entire Period: \$150,000 (Yeo)

High throughput, sensitive, rapid detection of viral infection and spread with an innovative isothermal lateral flow assay

The goal of this project is to develop a viral lateral flow assay (LFA) based device for RNA/DNA (environmental DNA) detection, including COVID-19 detection, to achieve high throughput, short sample-to-result time, multiple viral targets, full automation, and high sensitivity and accuracy. Dr. Yeo is responsible for developing a web-based application for sample tracking and data visualization.

Role: Subcontractor

P01 AI132122 (Yeo)

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.

Role: PI

R01 HG004659 (Fu, Yeo)

6/1/2018-6/30/2020

NIH/NHGRI

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.

Role: PI

1U19 MH107367 (Yeo)

07/01/15-06/30/20

NIH/NIMH

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.

Role: PI

R01 HD085902-01 (Yeo, Chi)

03/01/2016-02/28/2021

NIH/NICHHD

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 (hiPSC)-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.

Role: PI

ALSA 17-IIP-352 (Yeo)

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

ALSA VC8370 (Yeo)

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.

Role: PI

3 U01HL107442-04S1 (Frazer and Yeo)

9/1/2014-6/30/15

NIH/NHLBI Supplement

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

Role: PI

R01 GM084317-01A1 (Ares, Yeo)

01/01/2009-12/31/2012

NIH/NIGMS (sub-award with UC Santa Cruz)

Genomic measurement of alternative splicing

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.

Role: PI

CIRM RB1-01413 Basic Biology I (Yeo)

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.

Role: PI

CIRM RB3-05219 Basic Biology III (Yeo, Spector)

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.

Role: Co-investigator

CIRM RB3-05009 Basic Biology III (Yeo)

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.

Role: PI

CIRM TR3-05676 Early Translation III (Yeo)

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.

Role: PI

CIRM RB4-06045 Basic Biology IV (Yeo)

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.

Role: PI

ALSA VC8K27 (Yeo)

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.

Role: PI

Roche EIN Grant (Yeo)

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.

Role: PI

CIRM RT2-01927 Tools and Technologies II (Yeo, Goldstein)

04/01/2011-03/31/2014

Developing a method for rapid identification of high-quality disease specific hiPSC lines

In this project with the Goldstein lab, we will focus on developing high-throughput assays and methods to generate and identify hiPSC lines.

Role: Co-investigator

Brain Research Foundation Grant BRFSG-2014-14 (Yeo)

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.

Role: PI

R01 NS075449-01A1 (Yeo)

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.

Role: PI

R01 HG004659-03 (Fu, Yeo)

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.

Role: PI

U54HG007005 (Graveley, Yeo)

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.

Role: co-PI

U01 HL107442-01 (Frazer, Yeo)

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.

Role: Co-PI

R01AI095277-03S1 (Chang, Yeo)

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.

Role: Co-PI

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 during their tenure in my lab
Past	Katlin Massirer	2010-2011	Katlin was appointed a Faculty (Professor) at the State University of Campinas, Sao Paulo, Brazil when she left my lab.
Past	Kasey Hutt	2010-2014	Kasey was recruited as a Bioinformatics Scientist, R&D, at Invivoscribe in San Diego.
Past	Jason Nathanson	2009-2014	Jason joined as a R&D Scientist at biotech Sequenom after leaving my lab. Jason is currently a Senior Translational Scientist at the Salk Institute.
Past	Leo Kurian	2013-2014	Leo was appointed as a Faculty (Group leader), Cologne University, Germany when he left my group.
Past	Suzanne Lee	2013-2014	Suzanne was appointed as Faculty, Dept of Biology, Western Washington University, Bellingham, WA when she left my lab.
Past	Katannya Kapeli	2012-2015	Katannya was recruited as a Senior Research Fellow at National University of Singapore when she left my lab. She is currently a Bioinformatics Data Scientist at Sengine Precision Medicine.
Past	Tomas Bos	2012-2017	Tomas was funded by the BAEF – Belgian American Education Foundation and my NIH Grants when he was in lab. He joined a biotech company in Belgium when he left the lab.
Past	Sebastian Markmiller	2011-2016	Sebastian was funded by the Larry L Hilblom Fellowship when he was in my lab. Sebastian is currently a Project Scientist in my lab and is a co-founder of a biotech startup company with me.

Past	Yan Song	2011-2015	Yan was funded by my NIH grants and was promoted to a Project Scientist funded on a Takeda-UCSD award. Yan is currently a scientist recruited by Takeda in San Diego.
Past	Ron Batra	2015-2017	Ron was funded by a Myotonic Dystrophy Association Fellowship. Upon leaving my lab Ron joined Verily Life Sciences. He was recruited to serve as VP R&D at Locanabio, a start-up company I co-founded based on his postdoctoral publications.
Past	Ashleigh Schaffer	2015-2017	Ashleigh Scaffer was funded by a NIH K99 Award in my lab. She was appointed as Faculty (Assistant Professor) at Case Western Reserve University when she left my lab.
Past	Sarah Barnhill	2017-2018	As a graduate student in my colleague Nathan Gianneschi's lab, Sarah collaborated with students in my lab. When Nathan left for Northwestern University, I adopted Sarah as a postdoctoral fellow to finish up her project. For personal reasons, Sarah moved to OHSU as a postdoctoral fellow. Sarah is currently working for Intel.
Past	Eric Van Nostrand	2012-2020	Eric was funded by a Damon Runyon Cancer Fellowship and then a NIH K99 Award in my lab. Eric was recruited as Faculty (Assistant Professor), Baylor College of Medicine after he left my lab.
Past	Meredith Corley	2017-2020	Meredith was funded as a Milton Safenowitz Postdoctoral Fellow in my lab. Meredith was recruited as a Senior Scientist at Ionis upon leaving my lab.
Past	Kristopher Brannan	2014-current	Kris was funded by a CIRM Post-doc Fellowship and then UC President's and Chancellor's Postdoc Fellowship. Kris is currently an Assistant Project Scientist in my lab and is applying to faculty positions.
Past	Frederick Tan	2015-current	Fred was funded by an American Cancer Society postdoc fellowship. Fred is currently an Assistant Project Scientist in my lab and has co-founded a biotech company. He is finishing up his manuscript and fund-raising for this company.
Current	Isaac Alexander Chaim	2016-current	Isaac is funded by a IRACDA Postdoctoral Fellowship; UC President's and Chancellor's Postdoc Fellowship.
Past	Mark Perelis	2017-2021	Mark is funded by a F32 NIH Postdoctoral Training Grant. Mark has obtained a Scientist position at Ionis Pharmaceuticals.
Current	Aaron Smargon	2018-current	Aaron is funded by my NIH Grant
Current	Joshua Schwartz	2018-current	Joshua is funded by my NIH Grant
Current	Kathryn Morelli	2018-current	Kathy was funded by an NIH Grant and is currently on a UC President's and Chancellor's Postdoc Fellowship
Current	Chun-Yuan (Elliot) Chen	2018-current	Elliot is funded by my NIH Grant
Current	Daniel Lorenz	2018-current	Dan is funded by my NIH Grant
Current	Shengnan Joy Xiang	2019-current	-
Current	Phuong Le	2020-current	Phuong is funded by my NIH Grant
Current	Wenhao Jin	2019-current	Wenhao is funded by my NIH Grant
Current	Hugo Medina	2020-current	Hugo is funded by a IRACDA Postdoctoral Fellowship
Current	Evan Boyle	2019-current	Evan is funded by Helen Hay Whitney Foundation Fellowship
Current	Katie Rothamel	2021-current	Katie is funded by my NIH Grant.
Current	Orel Mizrahi	2021-current	Orel is funded by my NIH Grant.

Graduate (PhD) students (2008-current)

Past / Current Trainee	Trainee Name	Graduate Program	Training Period	Position of Past Trainee upon leaving the lab	Source of Support for Trainee and Awards
Past	Melissa Wilbert	BMS	2008-2014	Computational Biologist, Bluebird, Boston	NIH Genetics Training Program and CIRM Predoc Fellowship. BMS Best Dissertation Award
Past	Stephanie Huelga	BISB	2009-2014	Bioinformatics Scientist at Nugen, currently employed by Eclipse Bioinnovations	ARCS Award (2012-2013), NSF Graduate Fellowship
Past	Michael Lovci	BMS	2009-2014	Driver Biotech and currently employed at Proteona	ARCS Award (2014-2015), NSF GK12 Fellowship, Gift from Genentech
Past	Thomas Stark	Biology	2008-2014	Informatics Health Scientist at CDC	Genetics Training Grant
Past	Anne Conway	BMS	2008-2014	Miltenyi Biotec	Genetics Training Grant
Past	Boyko Kakaradov	BISB	2012-2015	Bioinformatics Scientist, Human Longevity Institute; currently at Arrakis	NSF Graduate Fellowship
Past	David Nelles	Materials	2010-2016	Co-founder and Chief Technology Officer, Locanabio when he left the lab	ARCS Award (2015-2016), NSF Graduate Fellowship
Past	Fernando Martinez	BMS	2012-2016	Senior Scientist, Fountain Therapeutics	Genetics Training Grant
Past	Elaine Pirie	BMS	2012-2017	Scientist at Ionis	NIH grant (Yeo)
Past	Julia Nussbacher	BMS	2012-2018	Scientist at GNF/NIH T32 Cancer cell Training Grant, currently scientist at Locanabio	ARCS Award (2015-2016)
Past	Gabriel Pratt	BISB	2012-2018	Scientist at Twinstrand	NSF Graduate Fellowship
Past	Olga Botvinnik	BISB	2013-2017	Scientist at CZI Biohub/	ARCS Award (2016-2017), NDSEG Fellow, John Hunter Open Source Fellowship
Past	Leen Jamal	BISB	2013-2018	Data Scientist at Inova	NSF Graduate Fellowship
Past	Mark Fang	MSTP/ BMS	2015-2019	Medical School/Residency Program	MSTP program, NIH grant (Yeo)
Past	Zhaoren He	Biology	2015-2019	Bioinformatics scientist at Guardant Health	Joint student with Kees Murren
Past	Yilan Shi	BMS	2018-2020 (Terminal Masters)	Grant writer/Entrepreneur	NIH Genetics Training Grant
Past	Emily Wheeler	BMS	2015-2020	Postdoc Fellow (Harvard)	ARCS Award (2017-2018), NSF Graduate Fellowship
Past	En-ching Luo	Bioengineering	2015-2020	Scientist at Ionis	Taiwan government Fellowship
Past	Jaclyn Einstein	Bioengineering	2015-2020	Postdoc	ARCS Award (2018-2019), NIH F31 Fellowship, C BIO Training Grant

Current	Benjamin Lewis	Biology	2015-current (Joint student with Tony Hunter, Salk)	current student	NIH grant (Hunter)
Current	Anthony Vu	BMS	2016-current	current student	ARCS Award (2019-2020), NSF Graduate Fellowship
Current	Ryan Marina	BMS	2016-current	current student	ARCS Award (2018-2019), Genetics Training Grant, NIH F31 Fellowship
Current	Jonathan Schmok	Bioengineering	2018-current	current student	Canadian government Fellowship
Current	Noorsher Ahmed	BMS	2018-current	current student	Genetics Training Grant
Current	Margaret Burns	BMS	2018-current	current student	Endocrinology Training Grant
Current	Qishan Liang	Chemistry	2018-current (Joint Student with Kevin Corbett)	current student	NIH grant (Corbett)
Current	Danielle Schafer	BMS	2019-current (Joint Student with Nicole Coufal)	current student	Genetics Training Grant
Current	Clarence Mah	Bioinformatics	2019-current	current student	NSF Graduate Fellowship
Current	Sara Elmsaouri	BMS	2019-current	current student	NIH Genetics Training Grant
Current	Hsuan-lin Her	BISB	2020-current	current student	NIH Genetics Training Grant
Current	Pratibha Jagannatha	BISB	2020-current	current student	NIH Bioinformatics Training Grant
Current	Samantha Sison	Neuroscience	2020-current	current student	NSF Graduate Fellowship
Current	Maya Gosztyla	BMS	2020-current	current student	NSF Graduate Fellowship. Myotonic Dystrophy Graduate Fellowship
Current	Alexandra Tankka	BMS	2020-current	current student	CBIO Training Grant
Current	Eric Kofman	BISB	2020-current	current student	NSF Graduate Fellowship, NIH T32 Training Grant
Current	Alicia Van Enoo	Neuroscience	2020-current	current student	NIH Grant

Current	Sam Hatch	BMS	2021-current	current student	NIH Grant
Current	Norah Al-Azzam	Neuroscience	2021-current	current student	NIH Grant
Current	Hema Kopalle	Biology	2021-current	current student	NIH Grant

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 (Graduated, SPAC Advisor)
 Amy Michelle Chinn (Graduated, SPAC Advisor)
 Martha Flores, Biology (Graduated, 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 (Graduated, Nathan Gianneschi's Lab)
 Alexander Sinclair Hamil (Graduated, Steve Dowdy's Lab)
 Polly Pu Huang, BMS (Graduated, Pamela Mellon's Lab)
 Charles Bradford Larson (Graduated, 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, Maïke Sander's Lab)
 Soohwan Oh, Biology (Graduated, Michael Rosenfeld's Lab)
 Olubankole Adebayo (Graduated, John Ravits lab)
 Danielle Marie Garshott (Graduated, Eric Bennet's lab)
 Anna Guzikowski (Graduated, Brian Zid's lab)
 Angela Nicholson (Graduated, Amy Pasquinelli's lab)
 Delaney Pagliuso (Graduated, Amy Pasquinelli's lab)
 Alison Parisian (Graduated, Frank Furnari's lab)
 Sam Roth (Graduated, Chris Benner's lab)
 Jacob Wozniak (Graduated, David Gonzalez's lab)
 William Bradford (Graduated, Farah Sheikh's lab)
 Ember Tota (Graduated, Neal Deveraj's lab)
 Warren Chan (Graduated, Michael Burkart's lab)
 Wenyuan Wei (Graduated, Yeo lab), Masters
 Kayla Busby (Graduated, Neal Deveraj's lab)
 Jamison McCorrison (Graduated, Nicholas Shork's lab)

Kevin Ross (Graduated, Bruce Hamilton's lab)
William Schreiner (Graduated, Amy Pasquinelli's lab)
Brian Reilly (Graduated, Rafael Bejar's lab)
Daniel Jacobsen (Graduated, Kun Zhang's lab)
Anjali Gupta (Graduated, Rolf Bodmer's lab)
Ai Zhang (Graduated, Jeanne Loring's lab)
Kyle Begovich (Graduated, James Wilhelm's lab)
Jonathan Meritt (Graduated, Alysson Muotri's lab)
Tri Nguyen (Graduated, Sheng Zhong's lab)
Debha Amatya (Graduated, Rusty Gaeg's lab)
Kanishk Asthana (Current, Wei Wang's lab)
Hratch Baghdassarian (Current, Nathan Lewis' lab)
Raymond Berkeley (Current, Galia Debelouchina's lab)
Katherine Lee (Current, Heidi Cook-andersen's lab)
Carlos Medina (Current, Steve Dowdy's lab)
Andrew Ryan (Current, Matt Daugherty's lab)
Tyger Saltman (Current, Clodagh O'Shea's lab)
Erin Schiksnin (Current, Amy Pasquinelli's lab)
Lina Zheng (Current, Wei Wang's lab)
Joseph Herdy (Current, Fred Gage)
Juliet Nicodemus (Current, Jerold Chun's lab)
Melinda Beccari (Current, Don Cleveland's lab)
James Hocker (Current, Bing Ren's lab)
Jad Kanbar (Current, John Chang's lab)
Madison Edwards (Current, Simpson Joseph's lab)
Ashley Wong (Current, Alexis Komor's lab)
Amy Taylor (Current, John Ravit's lab)
Alanna Koehler (Current, Rob Hevner's lab)
Preston Dennett (Current, Clodagh O'Shea'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
Carlos Medina – Committee Member, 2017
Melinda Beccari – Chair, 2018
James Hocker – Committee Member, 2018
Alanna Koehler – Committee Member, 2018

UNDERGRADUATE RESEARCH ASSISTANTS IN YEO LAB

1. Lloyd Howard Wang, Biology (Graduated)
2. Yunhui Chang, Biology (Graduated)
3. Brett Roberts, Bioengineering (Graduated)
4. Bernice Yan, Biology (Graduated)
5. Stella Chen, Biology (Graduated)
6. Yiu Cheung Wong, Electrical Engineering (Graduated)
7. Jade Laguer, Biology (Graduated)
8. Ashley Wu, Biology (Graduated)
9. Jeremy Chang, Biology (Graduated)
10. Chau Ly, Biology (Graduated)
11. Clara Yuh, Biology (Graduated)
12. Duy Duong, Biology (Graduated)

13. Jasmine Kyung, Bioengineering (Graduated)
14. Thaomi Phuong, Bioengineering (Graduated)
15. Jake Gutkowski, Nanoengineering (Graduated)
16. Dylan Donn, Biology (Graduated)
17. Bianca Nguyen, Biology (Graduated)
18. Brandon Myszka, STARS Program, Canisius College (Graduated)
19. Ashley Louie, Psychology (Graduated)
20. Eyan Chee, Bioengineering (Graduated)
21. Kuunal Goel, Biology (Graduated)
22. Regina Woo, Biology (Graduated)
23. Samson Peter, Biology (Graduated)
24. Daniel Wen, Bioengineering (Graduated)
25. Kyle de Valle, Biology (Graduated)
26. Jessica Lettes, Computer Science (Graduated)
27. Grace Chen, Neuroscience (Graduated)
28. Chau Le, Biochemistry: Cell Biology
29. Yuanchi Ha, Computer Science
30. Ginny Wu, Bioinformatics
31. Rahul Nachnani, Biology (Graduated)
32. Lily Hahn, Biology (Graduated)
33. Eric Byeon, Biology (Graduated)
34. Vu Nguyen, Neuroscience and Physiology (Graduated)
35. Nigel Zhang, Neuroscience and Physiology (Graduated)
36. Tristan Bridges, SURF Program, San Diego City College (Graduated and joined the lab)
37. Harrison Wang, Bioengineering (Graduated)
38. Thai Bao Nguyen, Biology (Graduated)
39. Lucy Xu, Bioengineering (Graduated)
40. Megan Lo, Neuroscience (Graduated)
41. Enrique Amaya, STARS Program, University of Monterrey, Mexico (Graduated)
42. Colin Eckstein, SURF Program, Pomona College (Graduated)
43. Mayuresh Mujumdar, Human Biology (Graduated)
44. Annalisa Scafidi, Chemistry (Graduated)
45. Delia Jimenez, Natural Sciences Honor Program, University of Saint Katherine (Graduated)
46. Josephine Chu, CIRM Intern, SDSU (Graduated)
47. Minerva Contreras, STARS Program, Autonomous University of Querataro (Graduated)
48. Joshua Ahdout, Human Biology (Graduated)
49. Annalisa Scafidi, Chemistry (Graduated)
50. Steven Decker, CIRM Intern, SDSU (Graduated)
51. Jessica Octavio, CIRM Intern, SDSU (Graduated)
52. Krysten Leigh-Jones, CIRM Intern, Cal Poly, San Luis Obispo (Graduated)
53. Mehrnaz Siavoshi, STARS Program, Cal State University, Northridge (Graduated)
54. Samantha Oetjen, STARS Program, Chaminade University of Honolulu (Graduated)
55. Annalisa Scafidi, Chemistry (Graduated)
56. Delia Jimenez, Natural Sciences Honor Program, University of Saint Katherine (Graduated)
57. Ginny Wu, Biology (Graduated)
58. Esau Estrada, Cognitive Science
59. Sai Hosuru, Bioinformatics
60. Archishma Kavalipati, Bioinformatics
61. Juan Lerma Jr., Human Biology
62. Katherine Wong, Human Biology
63. Alex Sun, Biotechnology
64. Allison Li, Human Biology
65. Jocelyn Quiroz, Bioengineering
66. Bryce Henroid, Bioengineering
67. Seungmin Nam, Biology
68. Zoe Adelsheim, Neurobiology
69. Aryaman Agarwal, Cell and Molecular Biology
70. Brandon Liu, Cell and Molecular Biology
71. Vivian Pham, Molecular Biology
72. Gino Prasad, Bioinformatics
73. Je Seung An, Biology
74. Denhxiaoyu Shi, Bioinformatics
75. Nicholas Truong, Biochemistry (Santa Clara University)
76. Yueshan Liang, Biosystems and Biology