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University of California, San Francisco

CURRICULUM VITAE

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Position: Professor, Step 2
Laboratory Medicine
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EDUCATION

1988 - 1992	Stanford University, Stanford, CA	B.S.	with Honors, Biological Sciences	
1988 - 1992	Stanford University, Stanford, CA	A.B.	Classical Studies	
1992 - 1998	Harvard University, Cambridge, MA	Ph.D.	Biology	R.C. Lewontin & L. L. Cavalli-Sforza
1998 - 2000	Harvard School of Public Health, Boston, MA	postdoc	Population Genetics	

LICENSES, CERTIFICATION

2020 UCSF Diversity Equity and Inclusion Champion Training

PRINCIPAL POSITIONS HELD

2000 - 2001	Harvard School of Public Health	Research Associate	Population Genetics
2002 - 2009	Harvard School of Public Health	Assistant Professor	(tenure track)
2002 - 2004	Genome Institute of Singapore	Group Leader	Population Genetics
2004 - 2009	Genome Institute of Singapore	Associate Director & Senior Group Leader	Human Genetics

2010 - 2015	University of California, San Francisco	Associate Professor	Laboratory Medicine
2011 - 2015	University of California, San Francisco	Associate Professor	Epidemiology and Biostatistics
2015 - present	University of California, San Francisco	Professor	Laboratory Medicine
2015 - present	University of California, San Francisco	Professor	Epidemiology and Biostatistics

OTHER POSITIONS HELD CONCURRENTLY

1994 - 1996	Stanford University	Visiting Scholar	Genetics
1995 - 1995	Addis Ababa University, Ethiopia	Visiting Scholar	Biology
2000 - 2002	University of Khartoum, Sudan	Visiting Assistant Professor	(Third World Academy of Sciences, Trieste, Italy)
2004 - 2010	National University of Singapore	Adjunct Associate Professor	Centre for Molecular Epidemiology
2005 - 2008	Harvard School of Public Health	Adjunct Assistant Professor	Genetics and Complex Diseases
2009 - 2010	Harvard School of Public Health	Adjunct Assistant Professor	Epidemiology
2010 - 2012	Genome Institute of Singapore	Adjunct Investigator	Human Genetics
2012 - 2012	Monash University Malaysia Campus	Visiting Professor	Human Genetics
2010 - 2018	Blood Systems Research Institute	Associate Investigator	Epidemiology
2012 - present	University of California San Francisco	Faculty Affiliate	Institute for Global Health Sciences
2010 - present	University of California San Francisco	Faculty Affiliate	Institute for Human Genetics
2010 - present	University of California San Francisco	Investigator	Quantitative Biosciences Institute (QBI)

HONORS AND AWARDS

1985	French Government -- Société Honoraire de Français Scholarship for study in France	
1990	Classics Undergraduate Prizes (1990, 1991, and 1992)	Stanford University
1990	Lionel Pearson Award for study at the Intercollegiate Center for Classical Studies (Rome) and for archeological study in Tunisia and Turkey.	Stanford University
1991	Travel Award for excavation work in Panakton, Greece and for archeological study in Jordan and Egypt.	Stanford University
1991	Howard Hughes Medical Institute Major Grant for thesis research on the molecular systematics of the butterfly genus, Colias.	Stanford University
1992	National Institutes of Health Genetics Trainee	Harvard University
1993	National Science Foundation Predoctoral Fellow	Harvard University
1994	U.S. National Science Foundation -- Graduate University for Advanced Studies,Yokohoma; Summer Research Fellowship at the Japanese National Institute of Genetics, Mishima	
1994	Arthur Green Fund (Harvard University) Grants for field research in Sudan (1994 and 1998); Ethiopia (1995); and Thailand and Vietnam (1997-1998)	Harvard University
1996	L.S.B. Leakey Society Award for field research in Mali (1996); Thailand and Vietnam (1997-8)	Harvard University
2000	National Research Service Award, National Institute of General Medical Sciences (F32 GM20425-01) (declined)	Harvard University
2000	Principal Investigator, Research Career Award, U.S. National Human Genome Research Institute (K22 HG00053-01; US$1,047,678) (2000-2002).	Harvard University
2002	The Keville-DePalma Founders Lecture.	Salem State University

2002	The Horning Lecture in the Humanities	Oregon State University
2016	The Sir John Monash Lecture	Monash University
2019	Fulbright Senior Scholar	Academia Sinica, Taiwan
2021	Elected Member	Sigma Xi
2021	Fellow (Biological Sciences)	American Association for the Advancement of Science (AAAS)

KEYWORDS/AREAS OF INTEREST

human genetics, population genetics, genomics, genetic epidemiology, immunogenetics, autoimmunity, infectious diseases, immunology, type 2 diabetes, metabolism, evolution, anthropology.

PROFESSIONAL ACTIVITIES

MEMBERSHIPS

1998 - present	American Society of Human Genetics
1998 - 2013	Genetics Society of America
2002 - present	American Association for the Advancement of Science
2003 - present	Human Genome Organization (HUGO)
2007 - present	International Genetic Epidemiology Society
2011 - 2012	International Society of Computational Biology
2021 - present	European Society of Human Genetics

SERVICE TO PROFESSIONAL ORGANIZATIONS

2009 - 2010	Illumina Genotyping Advisory Panel (unpaid)	
2014 - present	American Society of Human Genetics	DNA Day Judge (annually)
2015 - 2018	International Genetic Epidemiology Society	Education Committee
2015 - present	American Association for the Advancement of Science (AAAS)	Student Poster Judge

SERVICE TO PROFESSIONAL PUBLICATIONS

2007 - 2014	Editorial Board, The HUGO Journal (formerly titled Genomic Medicine)
2008 - present	Senior Editor, Annals of Human Genetics
2009 - present	Associate Editor, BMC Medical Genomics
2011 - 2019	Review Editor, Frontiers in Evolutionary and Population Genetics

2010 - present Frequent ad hoc referee for Science; Nature Genetics; The American Journal of Human Genetics; Genome Research; Human Molecular Genetics; Vaccine; DNA and Cell Biology; Tissue Antigens; PLoSONE; Scientific Reports; JAMA; Current Biology; Immunological Investigations; and Journal of Human Genetics. Grant reviewer for the National Science Foundation Physical Anthropology Section. Grant Reviewer for the LSB Leakey Foundation.

INVITED PRESENTATIONS - INTERNATIONAL

1997 Trinational Workshop on Molecular Evolution, University of Munich (June 5-7, 1997).

1997 Department of Biological Anthropology Colloquium, University of Cambridge, UK (June 19, 1997).

1997 Department of Biology Seminar, Chiang Mai University, Thailand (November, 1997).

1999 Department of Epidemiology Seminar, Beijing Medical University (November 8, 1999).

2000 Department of Bio. Anthropology Seminar, University of Oxford (March 17, 2000).

2001 Eijkman Institute for Molecular Biology, Jakarta, Indonesia (July 9, 2001).

2001 Genome Institute of Singapore, Singapore (September 25, 2001).

2002 Institute of Mathematical Sciences, Workshop on Population and Statistical Genetics; National University of Singapore (March 26, 2002).

2002 6th Annual NUS-NUH Annual Scientific Meeting, Singapore (August 16, 2002).

2003 Biomedical Research Council Symposium, Singapore (July 31, 2003).

2004 3rd International Eijkman Symposium, Yogyakarta (Oct. 1, 2004).

2004 5th HUGO Pacific Meeting, Pattaya, Thailand (November 18, 2004).

2005 Royal Dutch Academy of Sciences Open Science Meeting, Yogyakarta (Sept. 28, 2005).

2005 Institute of Mathematical Sciences, Workshop on Genomics, Singapore (Nov. 15, 2005).

2006 Affymetrix User Group Meeting, Singapore (Nov. 12, 2006).

2006	8th International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Bangkok (Nov. 30, 2006).
2006	7th International Symposium on Host Genetic Epidemiology, Seoul National University (Dec. 8, 2006).
2007	Symposium & Workshop on Forensic DNA, Jakarta (5th February 2007).
2007	Illumina User Group Meeting, Siena, Italy (26th April 2007).
2007	Center for Molecular Medicine, Karolinska Institutet, Stockholm (9th May 2007).
2007	International Medical & Health Conference, Kota Bahru, Malaysia (25th May 2007).
2007	Instituto Nacional de Medicina Genomica, Mexico City (4th September 2007).
2007	Clinician Scientist Unit, National University Hospital, Singapore (29th October 2007).
2007	Singapore Eye Research Institute, Singapore (31st October 2007).
2007	Eijkman International Symposium, Bali (16th November 2007).
2008	Indian Society of Human Genetics, Annual Meetings, Vishakhapatnam (12th February 2008).
2008	Centre for Cellular and Molecular Biology, Hyderabad (14th February 2008).
2008	1st Asia Pacific Inflammatory Bowel Disease Scientific Meeting & Postgraduate Course, Singapore (24th February 2008).
2008	Illumina User Group Meeting, Cebu, the Philippines (31st March 2008).
2008	Combined Analysis of Three Genome-Wide Scans Reveals Novel Loci Associated with Rheumatoid Arthritis. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (5th April 2008).
2008	The Population Genetics of SNPs and CNVs in Southeast Asian Populations. Affymetrix Integrated Genomics Solution Seminar. Singapore. (22nd September 2008).
2008	Genome-Wide Studies for Chronic Diseases. The Singapore Epidemiology of Eye Diseases Symposium. (13th October 2008).

2009 Korean National Institutes of Health, Seoul, Korea (April 27, 2009).

2009 Global Diabetes Consortium Meeting, Hong Kong (March 15, 2009).

2010 Genetics of Nasopharyngeal Carcinoma Workshop, National Cancer Centre, Singapore (February 20th, 2010)

2016 University of the Philippines Manila and Diliman.

2019 Institute for Biomedical Sciences, Academia Sinica, Taipei Taiwan

2019 Tzu Chee University School of Medicine, Hualien, Taiwan

2020 Monash University Malaysia

KEYNOTE

2001 The 2nd Annual Conference on Sex and Gene Expression of the Society for Women's Health Research. (March 8-11, 2001).

2006 The Malaysian Society of Molecular Biology and Biochemistry. Bangi, Malaysia (August 17, 2006).

2007 The Genes That Cause Autoimmune Disease. Federation of Clinical Immunology Societies Annual Meeting, San Diego (11th June 2007).

2008 Mapping Human Genetic History in Asia. Opening Plenary. HUGO-Asia-Pacific meetings 2008, Cebu, the Philippines (2nd April 2008).

2008 Mapping Human Genetic History in Asia. Special Plenary. Human Genome Meetings 2008 (HUGO), Hyderabad, India (28th September 2008).

2009 Japan College of Rheumatology International Symposium, Tokyo, Japan (April 24th, 2009).

2011 University of Sao Paulo, Brazil. (April 4th, 2011)

2011 Hemocentro Sao Paulo, Brazil. (April 5th, 2011)

2011 The inaugural Affymetrix Pan-Asian GWAS Meeting, Shanghai, China (May 16, 2011).

2011 The European Society of Human Genetics Annual Meeting, Amsterdam, the Netherlands (May 30, 2011)

2011 The Wellcome Trust Sanger Centre, Hinxton, the United Kingdom (June 13, 2011)

2012	Monash University Malaysia Campus, Seminar (April 26, 2012)
2012	University Malaya, Seminar (April 26, 2012)
2013	Joint Human Genome Meeting and 21st International Congress of Genetics, Singapore (April 15, 2013)
2016	Sir John Monash Lecture, Monash University
2019	Asia Society of Human Genetics Meetings, Manila, Philippines (November 7, 2019)

INVITED PRESENTATIONS - NATIONAL

2000	Division of Human Genetics Seminar, Washington University (March 22, 2000).
2005	Seminar, Center for Human Genetics, University of California, San Francisco (Sept. 9, 2005).
2006	Illumina User Group Meeting, San Diego (March 14, 2006).
2009	Program for Quantitative Genetics, Harvard School of Public Health, Boston, MA (October 27, 2009).
2009	Session Chair, Program for Quantitative Genetics Annual Conference, Harvard University, Boston, MA (November 12, 2009).
2011	Third biennial Affymetrix Best Practices in Genotyping Meeting, Chicago, IL (July 13, 2011).

INVITED PRESENTATIONS - REGIONAL AND OTHER INVITED PRESENTATIONS

2011	Blood Systems Research Institute Epidemiology Site Visit (February 25, 2011)	Program Presenter
2011	Biomedical Sciences (BMS) Ph.D. Program Retreat (October 8, 2011)	speaker
2012	Blood Systems Research Institute, Scientific Retreat (September 24, 2012).	speaker
2016	SF General Hospital, Endocrinology Department	speaker

GOVERNMENT AND OTHER PROFESSIONAL SERVICE

2009 - 2015	U01 supported Type 2 Diabetes GENES (T2D-GENES) Steering Committee (10 members comprised of representatives from the Broad Institute, Oxford University, University of Chicago, Southwest Foundation Medical Research Institute, and University of Michigan	Member

2010 -	GenomeBC (British Columbia), Genomics and Health: Personalized Medicine Program	Review Panel Member
2011 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2012 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2012 -	Grant Review Committee for the Wellcome Trust, UK.	Member
2012 -	Malaria Genomics Grant Review Committee for Gates Foundation	Member
2013 -	NIH National Eye Institute Special Emphasis Study Section on Integrative Data Analysis for Vision Research	Member
2013 -	NIH Genotype and Tissue Expression (GTEx) Special Emphasis Study Section	Member
2013 -	NIDDK Special Emphasis study section to evaluate Inflammatory Bowel Disease Program Project application	Member
2014 -	NIH Special Emphasis study section to evaluate Genetics of Zoster, Zoster Pain and Immune Responses to Zoster Vaccine Program Project Application	Member
2015 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (J3)	Member
2015 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (M3)	Member
2016 -	NIH (NIDDK) Special Emphasis study section ZDK1 GRB-8 (M3)	Member
2017 -	NIH (NIDDK) Study Section Digestive Diseases and Nutrition C Subcommittee (DDK-C)	Member
2017 -	Health Research Board (Ireland)	Proposal Reviewer
2018 -	National Eye Institute (NEI) Special Emphasis Panel (ZEY VSN (01))	Member
2018 -	NIH Special Emphasis Panel: Chronic Disease and Epidemiology	Member
2019 -	NEI Special Emphasis Panel R13/R21/R01 Review	Member

UNIVERSITY AND PUBLIC SERVICE

SERVICE ACTIVITIES SUMMARY

I serve actively on multiple mostly Senate Committees and have advanced to the Leadership of the Rules and Jurisdiction Committee. In addition, I have actively and continuously served on the Basic Research in HIV Study Section for RAP/CFAR and have reviewed multiple grants

in twice annual meetings since 2010. I assist actively in the admissions and recruitment for 2 Ph.D. programs, Biomedical Sciences (BMS) and Biological and Medical Informatics (BMI).

UNIVERSITY SERVICE

UC SYSTEM AND MULTI-CAMPUS SERVICE

2016 - 2017	UC Systemwide Committee Representative	Member
2017 - 2020	UC Systemwide Library and Scholarly Information Advisory Committee (SLASIAC)	Member
2018 - 2020	SLASIAC□s Standing Subcommittee on Copyright Policy (SSCP)	Member
2021 -	President's Postdoctoral Fellowship Program (PPFP)	Review Panel

UCSF CAMPUSWIDE

2010 - present	Basic Research in HIV Study Section for RAP/CFAR	member
2010 - present	application screener for BMI PhD student applications	
2011 - present	application screener for BMS PhD student applications	
2011 - 2014	Graduate Council	member
2011 - 2011	San Diego State University outreach visit and talk to minority/disadvantaged students interested in UCSF's undergraduate summer programs and graduate study at UCSF (September 23, 2011).	speaker/discussion leader
2014 - 2017	OSR Service Partnership Agreement Committee	member
2015 - 2018	APB Campus Finance Subcommittee	member
2015 - 2018	Committee on Library and Scholarly Communication (COLASC)	member
2015 - 2019	Rules and Jurisdiction Committee	member
2016 - 2019	Standing Panel for Faculty Code of Conduct Investigations	member
2016 - 2017	Rules and Jurisdiction Committee	Vice-Chair
2017 - 2019	Rules and Jurisdiction Committee	Chair
2017 - 2019	UCSF Senate Executive Council	member
2017 - 2021	Biomedical Sciences (BMS) Ph.D. Program Admissions Committee	member
2020 - present	Biological and Medical Informatics (BMI) Ph.D. Program Admissions Committee	member
2020 - present	Biological and Medical Information (BMI) Ph.D. Program Diversity, Equity and Inclusion Committee	member

DEPARTMENTAL SERVICE

2012 - 2012	Organized BSRI Scientific Retreat	
2013 - 2016	Laboratory Medicine Committee on Advancements and Promotions	Member

CONTRIBUTIONS TO DIVERSITY

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I have actively mentored several Filipino (considered by UCSF to be under-represented) students in the context of a collaboration with the University of the Philippines in Diliman and Manila. Two of these students (Maria Elizabeth Mercado and Alvin Lirio) were enrolled in the Clinical and Translational Science Program in the Department of Epidemiology and Biostatistics. Currently, one (Maria Elizabeth Mercado) is a faculty member at the University of the Philippines, and another (Alvin Lirio) is employed by the Philippine Genome Center in addition to practicing medicine at the University of the Philippines in Manila.

Another (Dominic Albao) is entering (Fall 2020) a Ph.D. program at Scripps in Florida. The other, Margarette Mariano, who I employed and mentored for several years as a research assistant is soon to enter her 3rd year in the Albert Einstein College of Medicine Ph.D. Program.

As a Hispanic myself, I have been sought out by several Latinx students at UCSF, and have mentored three here at UCSF: including Roxana Ordonez in the BMI Ph.D. Program; Carlos Rojo (currently a faculty member at San Jose City College) in the BMS Ph.D. Program; and have co-mentored and served on the thesis committee of Raul Torres in the BMS Ph.D. Program.

My research has largely been conducted in non-European populations, especially East Asian populations. This has brought much needed diversity to the study and understanding of complex disease genetics. Whether East Asian populations are under-represented in the ranks of an Institution like ours, unquestionably these populations have not been well represented until recently (partly on account of my own work) in genetic studies.

TEACHING AND MENTORING

TEACHING SUMMARY

I participate actively in three Ph.D. programs: Biomedical Sciences (BMS), Biological and Medical Informatics (BMI), and Epidemiology & Translational Science. I have lectured in courses for BMI and BMS; participated actively in annual retreats; journal clubs; pizza talks; and student coaching. I have also led weekly student discussion sessions for core BMS courses.

I have also supervised one student□s rotation project in the Epidemiology and Translational Science Program; and have supervised what became a one-year terminal Master□s project by an NSF-funded Ph.D. student in the BMI program, Roxana Ordonez. Currently, I am the advisor for Carlos Rojo, a student in the BMS program.

I have been and expect to continue to be fully engaged in these programs by participating in annual retreats, admissions activities for applicants, as well as informal and formal seminars, classroom teaching etc.

I have also was sole supervisor, over two and a half years, of a Clinical and Translational Research (CTR) Fellow (formerly known as the PACTRR program). This highly talented UCSF M.D. student (Dustin Long) was a remarkable addition to my lab, and has performed from day-one at the level of an advanced Ph.D. student. I also supervised and examined his thesis for the M.D. with Distinction degree, through the Pathways to Discovery in Molecular Medicine. After finishing a one year internship with Kaiser after graduating from UCSF in 2013, he recently began a residency in Anesthesiology at the Massachusetts General Hospital.

Finally, I am active in teaching at the Blood Systems Research Institute and participate in their summer student program.

FORMAL TEACHING

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	1992 - 1992	Teaching Assistant, Biological Sciences 2, Harvard University, Cambridge, MA	Graduate TA		300
	1996 - 1996	Teaching Assistant, Molecular Biology Core (Science B-46), Harvard College, Cambridge, MA	Graduate TA		30
	2000 - 2000	Lecturer, Course on Human Genome Diversity, ICGEB, Islamabad, Pakistan	Lecturer		50
	2004 - 2004	Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet - National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology	Course Director and Lecturer		25

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	2006 - 2006	Course Director and Lecturer (2 lecturers, organized a graduate course of 20 lectures), Introduction to Genomics, Karolinska Institutet - National University of Singapore joint Ph.D. Program in Genetic and Molecular Epidemiology	Course Director and Lecturer		25
	2006 - 2006	Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).	Lecturer		100
	2008 - 2008	Lectured for graduate Molecular Biology Course at the Institute for Molecular and Cell Biology, Singapore (Byrappa Venkatesh, Course Director).	Lecturer		30
	2010 - 2010	BMI 206; Bioinformatics & Computational Biology	1 lecture + 1 student-led paper discussion	Grad	7
	2011 - 2011	Controversies in IBD: 2011; Office of Continuing Medical Education	Delivered a half hour lecture summarizing genetic advances and potential in IBD research.	Medicine	200
	2012 - 2012	BMS 255B; Tissue and Organ Biology (Genetics)	2 lectures	Grad	28
	2013 - 2013	BMS 255B; Tissue and Organ Biology (Genetics)	2 lectures	Grad	22

	Academic Yr	Course No. & Title	Teaching Contribution	School	Class Size
	2013 - 2013	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	9
	2014 - 2014	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	12
	2015 - 2015	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2016 - 2016	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2017 - 2017	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader (4 sessions)	Grad	10
	2016 - 2017	IDS121A-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	9
	2016 - 2017	IDS121B-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2016 - 2017	IDS121C-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2016 - 2017	IDS121E-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2020 -	IDS121E-CIC Core Inquiry Curriculum	Small Group Leader	Medicine	8
	2017 - 2017	BMS 260	Student Proposal & Presentation Evaluator	Grad	30
	2019 -	Wu Ta You Foundation Summer School on Biomedical Sciences	Lecturer and small group facilitator	Grad	110
	2020 - 2021	IDS121A-CIC Core Inquiry Curriculum	Small Group Facilitator	Medicine	11
	2021 -	BMS 255B; Tissue and Organ Biology (Genetics)	Discussion Leader	Grad	11

INFORMAL TEACHING

2010 - present Frequent participation and speaking at BMI and BMS student retreats

2010 - present Annually coach 2-5 BMI and BMS students in their journal club presentations

2010 - present Present 1-3 times each year at student journal clubs

2010 - present Give informal research "pizza talks" to first and second year students, 1-2 times per year

MENTORING SUMMARY

Since Summer 2017, I am the primary advisor for Elizabeth "Aprille" Mercado, M.D., who is pursuing an M.Sc. in the Master's Degree Program in Clinical Research in the Department of Epidemiology and Biostatistics at UCSF.

Since mid-2016 I have mentored an Assistant Clinical Research Coordinator, hired on my diabetes grant, Ms. Margarette Mariano. This has involved intensive co-mentoring with Drs. Sarah Kim and Lisa Murphy of the Department of Endocrinology; and is centered on the enrollment of research subjects in the CRS and at outside sites. In addition, I am mentoring to Student volunteers who assist on this project, Ms. Irah Rubio and Matthew Roces.

From 2010-2013, I have mentored Assistant Adjunct Professor Adam Lauring, M.D., Ph.D., an infectious disease physician and expert in viral evolution and diversity, as he sought exposure to and training in human genetics. The two of us collaborated closely and published on 2 or 3 projects centered on identifying human genetic variation that determines varying susceptibilities and outcomes to infections. He has since begun his first tenure track Assistant Professor position at the University of Michigan.

Beginning in October 2011, BSRI hired a new senior scientist in Bioinformatics, Dr. Xutao Deng, whom I have co-mentored on projects in human genetics and genomics -- subjects with which he had had some, but not the deepest exposure previously. The collaborative work has been both enjoyable and incredibly productive.

PREDOCTORAL STUDENTS SUPERVISED OR MENTORED

Dates	Name	Program or School	Mentor Type	Role	Current Position
2002 - 2006	Methawee Srikummool	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Lecturer, Narasuen University, Phitsanulok, Thailand
2003 - 2007	Jatupol Kampuansai	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Assistant Professor, Chiang Mai University, Chiang Mai, Thailand

Dates	Name	Program or School	Mentor Type	Role	Current Position
2008 - 2012	Wibhu Kutanan	Chiang Mai University Ph.D.	Project Mentor,Career Mentor,Co-Mentor/Clinical Mentor	co-advisor	Assistant Professor, Khon Kaen University, Thailand.
2006 - 2012	Eileen Png	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	postdoc at Genome Institute of Singapore
2007 - 2012	Chee Seng Ku	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc at National University of Singapore, Cancer Centre
2008 - 2011	Rajkumar Dorajoo	ASTAR-Imperial University, London, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc in Singapore
2009 - 2012	Rick T.H. Ong	National University of Singapore, Ph.D.	Research/Scholarly Mentor,Project Mentor,Career Mentor	co-advisor	postdoc at National University of Singapore
2010 - 2011	Roxanna Ordonez	BMI, UCSF	Research/Scholarly Mentor,Project Mentor	advisor	pursued a Master's thesis in my lab
2011 - 2011	Shenhaochen Zhu	BSRI summer student (from SFSU)	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	industry
2011 - 2013	Dustin Long	M.D. w/ Distinction, UCSF; Clinical and Translational Fellow	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	Anesthesia Resident, Massachusetts General Hospital

Dates	Name	Program or School	Mentor Type	Role	Current Position
2012 - 2012	Evan McCartney-Melstad	BSRI summer student	Project Mentor	advisor	Ph.D. student, UCLA
2012 - 2012	Katherine Nishimura	Epidemiology and Translational Science Ph.D., UCSF	Project Mentor,Career Mentor	rotation advisor	Ph.D. candidate
2014 - 2014	Carlos Rojo	BMS, UCSF	Research/Scholarly Mentor,Project Mentor,Career Mentor	advisor	faculty, City College of San José
2014 - present	Raul Torres	BMS, UCSF	Project Mentor,Career Mentor	thesis committee chair	employed in industry
2016 - 2018	Matthew Roces	UC Berkeley	Research/Scholarly Mentor,Project Mentor	advisor	M.D. student at UCSF
2016 - 2018	Irah Rubio	UC Berkeley	Research/Scholarly Mentor,Project Mentor	advisor	pursuing Physician's Assistant
2017 - 2019	Elizabeth "Aprille" Mercado	Master's Degree Program in Clinical Research	Research/Scholarly Mentor,Project Mentor,Career Mentor	primary mentor/advisor	Faculty, University of the Philippines
2018 - present	Wesley Marin	BMI, UCSF	Co-Mentor/Clinical Mentor	thesis committee member	Ph.D. candidate

POSTDOCTORAL FELLOWS AND RESIDENTS MENTORED

Dates	Name	Fellow	Mentor Role	Faculty Role	Current Position

Dates	Name	Fellow	Mentor Role	Faculty Role	Current Position
2004 - 2008	Terry KL Toh	postdoc		Research Supervision	Clinical Scientist, National University Hospital, Singapore
2005 - 2007	Jenny Hui Hui Tan	postdoc		Research Supervision	Instructor, Ministry of Education, Singapore
2006 - 2010	Vikrant Kumar	postdoc		Research Supervision	Research Associate, Genome Institute of Singapore
2009 - 2010	Devindri Perera	postdoc		Research Supervision	Lecturer, Murdoch University (Australia)
2013 - 2013	Jonathan Esensten	resident		Research Supervision	Assistant Professor, UCSF

FACULTY MENTORING

Dates	Name	Position while Mentored	Mentor Type	Mentoring Role	Current Position
2010 - 2012	Adam Lauring, M.D., Ph.D.	Assistant Adjunct Professor		supervised his K project as he moved from viral evolution into human genetics.	Assistant Professor University of Michigan

VISITING FACULTY MENTORED

2013 - 2013 Prof. Maude Phipps Monash University Malaysia

2015 - 2015 Prof. Maude Phipps Monash University Malaysia

RESEARCH AND CREATIVE ACTIVITIES

RESEARCH AND CREATIVE ACTIVITIES SUMMARY

RESEARCH INTERESTS

My research centers on the identification of inherited variation that influences disease risk in humans. The hope is that this will lead to tangible improvements in public and individual

health, via the identification of novel genes and pathways involved in the physiology of a particular disease process or non-disease phenotype. Neither of these rather lofty aims - the identification of disease related variation, nor the translation into clinical utility - has been realistic for complex diseases until recently. But with the completion of the human genome project and rapid developments in SNP genotyping and DNA sequencing technology, progress has been accelerated greatly. Results from genome-wide association studies (GWAS) have demonstrated both their feasibility, and their potential for identifying unexpected pathways of disease physiology - pathways that seem likely, in many cases, to be the targets of successful new therapies and predictive risk assessments.

I have been fortunate to have designed, executed, and led numerous such studies, each of which has led directly to years of productive follow-up research. I have chosen to concentrate particularly on disorders of immunity and metabolism for several reasons. First is my belief that deaths from epidemics or famine are likely to have been among the two greatest selective forces in our evolutionary past. This leads to the expectation that the magnitude of genetic effects contributing to susceptibility to infection, autoimmunity, and metabolic disease is significant, and probably larger than for many other complex diseases that have so far proved refractory to genetic analysis. This should increase the likelihood of identifying relevant genes via population-based association studies, and should serve as a better testing ground for methodology that might then be more successfully applied to diseases with more subtle genetic etiologies. It also leads to the attractive hypothesis (which my research program aims to test) that our adaptations to survive infections and periods of food scarcity have left us maladapted to modern life in which infectious mortality has been sharply reduced by improvements in hygiene, antibiotics/antivirals, and vaccines; and in which an overabundance of food poses a greater threat to the health of a growing fraction of the global population, than does its scarcity. In addition to susceptibility to infections and overt autoimmune conditions; immune genes are now known to play key roles in many cancers, allergic and hyper-responsive disorders of rapidly increasing incidence such as asthma, metabolic disease/diabetes, as well cardiac and vascular disease. By using pathogens, vaccines, and autoimmune diseases as probes of functionally relevant immunogenetic variation, I believe we can gain a broader understanding of numerous other diseases that all converge in one way or another on the nexus of immune genes - and my research program at UCSF seeks to uncover the genetic underpinnings of both immune-related and metabolic diseases of humans.

Among the most productive recent projects, with funding from a U01 grant from the NIDDK, has been my participation and leadership within the T2D-GENES consortium. In this consortium, working with leading researchers from the University of Chicago, University of Michigan, the Broad Institute (of Harvard and MIT) and, the University of Oxford; we are performing whole genome sequencing of 1,000 Latino pedigree members with a high diabetes prevalence, and exome sequencing of 20,000 case and control individuals from diverse global populations, including Asians and African-Americans. As a program for the follow-up of GWAS studies of diabetes, the scale and comprehensiveness are unprecedented and world-leading. For the first time, we are also able to examine the role of low-frequency genetic variation in the etiology of complex human disease on a genome-wide level. I will increasingly be applying genome-scale sequencing to a variety of infectious, autoimmune and metabolic diseases.

RESEARCH AWARDS - CURRENT

1. A127149	PI	20 % effort	Seielstad (PI)
Philippine Commission on Higher Education		01/01/2016	01/31/2021

Metagenomic Contributions to Type 2 Diabetes Among Filipino Populations $ 384,324 direct/yr 1 $ 980,000 total

Our goal is to characterize the gene-environment interactions that drive T2D susceptibility in Filipinos, leading to interventions that may begin to reduce the incidence and cost curves of this rapidly increasing disease.

Designed study, convened co-investigators, wrote proposal. Will oversee all aspects of the research study, beginning from the enrollment of case and control subjects in both the Bay Area and the Philippines; will supervise all aspects of the genomic data collection (in the Philippines); and will design and oversee the data analysis. There will also be a substantial teaching and training component.

RESEARCH AWARDS - SUBMITTED

1. 1 R01 AG052869-01 PI 25 % effort Seielstad (PI)

   NIAID 09/01/2018 07/31/2023

   Genetic Susceptibility to Herpes Zoster: a Model for Immunosenescence $ 292,613.00 direct/yr 1 $ 874,704.00 total

   Herpes zoster (HZ), caused by the reemergence of the chicken pox virus, occurs most often in the elderly and is characterized by a painful and often debilitating skin rash. Using HZ as a model, the goal of the proposed research study is to identify genes and other biological factors that cause the immune system to weaken with age. Results may help focus HZ prevention efforts, including use of the vaccine, and may inform the epidemiology of other infections in the elderly.

   PI, responsible for overseeing all aspects of design, research conduct, analysis and publication.

2. 1 R01 AI153529-01 PI 25 % effort Seielstad (PI)

   NIH 2020 2024

   Identifying determinants of hepatitis b viral immunity via genomic and focused HLA-KIR gene studies $ 250,000 direct/yr 1 $ 1,000,000 total

   We intend to identify host genetic variation impacting both HBV vaccine response, AND the ability to spontaneously clear an HBV infection, by analyzing a large, extant cohort of serologically and genetically characterized Chinese individuals living in Taiwan.

   PI. Conceived and wrote the proposal.

RESEARCH AWARDS - PAST

1. 5R01CA104021-02 co-investigator

   NIH/NCI 2005-09-01 2010-06-30

   Genetic determinants of postmenopausal breast cancer. $ 1,264,708 direct/yr 1

2. N01 HB-57181 co-investigator Busch (PI)

   NHLBI 01/01/2011 06/30/2011

	Retrovirus Epidemiology Donor Study-II (REDS-II) - Central Laboratory. Central laboratory for all REDS specimen testing, including specific project		$ 139,015 direct/yr 1	$ 139,015 total
3.	GIS/05-PB2101	PI		
	Genome Institute of Singapore (GIS) intramural		2005-04-01	2009-03-31
	High-Throughput SNP Genotyping Facility		$ 2,983,900 direct/yr 1	
4.	GIS/09-BR2102	PI		
	Genome Institute of Singapore Intramural Funding		2005-04-01	2010-03-31
			$ 5,979,847 direct/yr 1	
5.	N66001-08-C-2014	PI		
	DARPA (USA)		2008-05-01	2009-08-31
	Genetic Biomarkers for Prediction of Vaccine Response		$ 830,829 direct/yr 1	
6.	W911QY-06-C-0085	PI		
	DARPA		2006	2007
	Genetic Biomarkers for Prediction of Vaccine Response		$ 325,000 direct/yr 1	
7.	Susan G. Komen Breast Cancer Foundation	co-investigator		
	Genetic and environmental determinants of postmenopausal breast cancer		2004	2006
			$ 952,057 direct/yr 1	
8.	05/1/36/19/413	co-investigator		
	Biomedical Research Council, Singapore		2006	2009

The Genetics of High Density Lipoprotein Cholesterol Metabolism — $ 886,250 direct/yr 1

9. National Medical Research Council, Singapore — collaborator
   Genome-wide case-control studies to identify genetic variants and gene-environment interactions involved in the pathogenesis of type 2 diabetes mellitus in Chinese, Malays and Asian Indians living in Singapore — 2008 — 2011
   $ 500,000 direct/yr 1

10. NMRC/1111/2007 — co-investigator
    National Medical Research Council, Singapore — 2007 — 2010
    Environmental and genetic determinants of adiponectin in Chinese, Malays and Asian Indians, National Medical Research Council, Singapore — $ 150,000 total

11. National Medical Research Council, Singapore — collaborator
    Translational Research Innovations in Ocular Surgery
    $ 3,600,000 direct/yr 1

12. 1U01DK085545-01 — principal investigator — Seielstad (PI)
    NIH/NIDDK — 09/20/2009 — 07/31/2015
    Identifying Variants Causal for Type 2 Diabetes in Major Human Populations — $ 547,230 direct/yr 1 — $ 2,500,000 total

13. 1R01DK080720-01A1 — co-investigator — Pereira (PI)
    NIH/NIDDK — 03/01/2009 — 02/28/2015
    Genetic and Environmental Determinants of Type 2 Diabetes in Chinese Singaporeans. — $ 681,811 direct/yr 1

14. HHSF223201210412A — co-investigator — Klein (PI)

FDA	09/17/2012	03/31/2015
A Genome-Wide Association Study to Examine Genes Associated with an Increased Risk of Febrile Seizure in Children Following Measles Containing Vaccines	$ 306,377 direct/yr 1	$ 306,377 total

15. 5R01AR065174-02	co-investigator	3.54 % effort	Liao (PI)
NIAMS		07/19/2013	05/31/2018
Identification of causal variants in Psoriasis		$ 465,839 direct/yr 1	$ 1,848,109 total

Genome-wide association studies (GWAS) have successfully identified approximately 36 psoriasis susceptibility loci. However, the causal variants at these loci remain largely unknown, and it is very likely that a large number of additional loci remain to be identified. In this proposal, we pursue a comprehensive strategy to identify both common and rare causal variants in psoriasis, and then perform targeted functional studies of these variants.

Genetics expertise.

16. NHLBI-HB-11-01	co-investigator	10 % effort	Busch (PI)
NHLBI		01/14/2013	09/30/2018
Recipient Epidemiology and Donor Evaluation Study-III (REDS-III) □ Central Laboratory. Genome-wide search for genetic variation increasing risk of HLA-alloimmunization following pregnancy or blood transfusion.		$ 1,212,889 direct/yr 1	$ ~$7,000,000 total

Improving blood component safety and availability in the U.S. and internationally through the conduct of epidemiologic, survey, and laboratory studies is the cornerstone of the REDS program.

Genetics and genotyping expertise for multiple genetics related sub-projects.

17. NHLBI-HB-11-04	co-investigator	5 % effort	Busch (PI)
NHLBI		03/01/2014	09/30/2018
Recipient Epidemiology and Donor Evaluation Study-III (REDS-III) □ International Sites. Compilation of extensive blood donor/donation data/specimens; 4 projects on critical TM issues in Latin America.		$ 1,074,774 direct/yr 1	$ ~$6,000,000 total

Improving blood component safety and availability in the U.S. and internationally through the conduct of epidemiologic, survey, and laboratory studies is the cornerstone of the REDS program.

Genetics and genotyping expertise.

PEER REVIEWED PUBLICATIONS

1. **Seielstad** MT, Hebert JM, Lin AA, Underhill PA, Ibrahim M, Vollrath D, Cavalli-Sforza LL (1994) Construction of human Y-chromosomal haplotypes using a new polymorphic A to G transition. Human Molecular Genetics, 3:2159-61.

2. Ruiz-Linares A, Nayar K, Goldstein DB, Hebert JM, **Seielstad** MT, Underhill PA, Lin AA, Feldman MW, and Cavalli-Sforza LL (1996) Geographic clustering of human Y chromosome haplotypes. Annals of Human Genetics , 60:401-408.

3. Wells RS, **Seielstad** M, Bunce M, Tyan DB, Bekele E, and Parham P (1997) Cw*1701 defines a divergent African HLA-C allelic lineage. Immunogenetics, 46:173-180.

4. Perez-Lezaun A, Calafell F, Seielstad M, Mateu E, Comas D, Bosch E, and Bertranpetit J (1997) Population genetics of Y-chromosome short tandem repeats in humans. Journal of Molecular Evolution, 45:265-270.

5. Seielstad M, Minch E, and Cavalli-Sforza LL (1998) Genetic evidence for a higher female migration rate in humans. Nature Genetics, 20:278-280.

6. Seielstad M, Bekele E, Ibrahim M, Touré A, and Traoré M (1999) A view of modern human origins from Y chromosome microsatellite variation. Genome Research, 9:558-567.

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10. Su B, Xiao C, Deka R, Seielstad M, Kangwanpong D, Xiao J, Lu D, Underhill P, Cavalli-Sforza L, Chakraborty R and Jin L (2000) Y chromosome haplotypes reveal prehistorical migrations to the Himalayas. Human Genetics, 107:582-90.

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12. Niu T, Seielstad M, Zeng X, Apffel A, Li G, Hahnenberger K, Xu X. (2001) Detection of novel ALAD gene polymorphisms using denaturing high-performance liquid chromatography. Human Biology, 73:429-42.

13. Ardlie K, Lunetta K and Seielstad M (2002) Testing for population subdivision and association in four case-control studies. American Journal of Human Genetics, 71:304-311.

14. Bereir RE, Mohamed HS, Seielstad M, El Hassani AM, Khalil EA, Peacock CS, Blackwell JM, Ibrahim ME. (2003) Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. Genetica, 119:57-63.

15. Seielstad M, Yuldasheva N, Singh N, Underhill P, Oefner P, Shen P, Wells RS (2003) A novel Y-chromosome variant puts an upper limit on the timing of first entry into the Americas. American Journal of Human Genetics, 73:700-705.

16. Chia KS, Lee JJM, Cheung P, Cheung KH, Seielstad M, Liu E (2004) Twin births in Singapore: a population-based study using the national birth registry. Annals Academy of Medicine Singapore, 33:195-199.

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18. Teo YY, Fry AE, Clark TG, Tai ES, & Seielstad M. (2007) On the Usage of HWE for Identifying Genotyping Errors. Ann Hum Genet. 71:701-3.

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   ****corresponding author**

   I was PI of and led, designed and funded the GWAS of Chinese psoriasis patients that comprised a major component of this multi-ethnic study. This included developing the study design, enrolling patients and controls from the National Skin Centre in Singapore, directing the genome-wide SNP genotyping and primary association analysis. Also, I was instrumental in bringing together and leading the collaborating groups, directing the meta-analysis, as well as the publication describing results.

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   I was PI of and one of ten members of the Steering Committee that planned, directed, and conducted this landmark study appearing in Nature. As Steering Committee member I made several seminars contributions to the design of the study, chiefly in adopting a whole exome (vs. more limited target region) sequencing approach. The paper results from the fusion of two jointly submitted papers with partially overlapping authors that the editors directed us to combine into a single publication. As a result, there was considerable jostling of co-authorsips. My ultimate position amongst the senior authors ultimately is not commensurate with the numerous substantive contributions I made to the design, conduct, and analysis of the study data.

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   I designed, funded, and led this study of whole exome sequencing applied to the outcomes to an infectious disease (West Nile Virus Infection). This is the first and most comprehensive application published to date, and the study highlights the potential and the pitfalls for whole exome and whole genome sequencing studies.

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   I was PI of and one of ten members of the Steering Committee that planned, directed, and conducted this landmark study appearing in Nature. As Steering Committee member I made several seminars contributions to the design of the study, chiefly in adopting a whole exome (vs. more limited target region) sequencing approach. The paper results from the fusion of two jointly submitted papers with partially overlapping authors that the editors directed us to combine into a single publication. As a result, there was considerable jostling of co-authorsips. My ultimate position amongst the senior authors ultimately is not commensurate with the numerous substantive contributions I made to the design, conduct, and analysis of the study data.

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   I was PI for this project. I wrote the proposal that funded the research, and I designed and oversaw every aspect of the work, through and including publication. This move into epigenetic also marks a significant new innovation for my lab, and highlights a significant and fruitful new avenue for future research.

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20. Identification of genes influencing serum levels of brain-derived neurotrophic factor in large Mexican American pedigrees. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
21. Whole-exome sequencing of 10,000 type 2 diabetes cases and controls from five major ancestry groups. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
22. Deep whole genome sequencing in pedigrees illuminates the contribution of low frequency and private mutations to the genetic architecture of metabolic quantitative traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
23. Analyzing Deep Whole Genome Sequence and Genotype Data of >1,000 Individuals from Large Mexican-American Pedigrees in the T2D-GENES Study. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.
24. The impact of genetic variation on diabetes-related quantitative traits from whole exome sequences: The T2D-GENES Consortium. T2D-GENES, American Society of Human Genetics Annual Meetings 2012.

25. Large-scale exome chip association analysis identifies rare and low-frequency coding variants associated with glycemic traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
26. Fine-mapping of Type 2 Diabetes susceptibility loci via trans-ethnic meta-analysis. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
27. Gene-set test for rare variants. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
28. Meiotic gene conversion in humans: rate, sex ratio and GC bias. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
29. Statistical dissection of genetic factors influencing antibodies against Epstein-Barr virus nuclear antigen 1 (EBNA-1) using whole-genome sequence data.T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
30. Gene pathway burden test application to cardiovascular disease using whole genome sequencing data. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
31. Deep Sequencing in Extended Pedigrees Reveals a Major Rare Non-Synonymous Variant Influencing the De Novo Ceramide Synthesis Pathway. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
32. A test of association of genome-wide coding variation with type 2 diabetes in 13,000 individuals from five ancestry groups. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
33. Loss of function mutations in SLC30A8 protect against type 2 diabetes. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
34. Deep whole-genome sequencing in pedigrees to quantify the contribution of private variants to type 2 diabetes and related metabolic traits. T2D-GENES, American Society of Human Genetics Annual Meetings 2013.
35. Esensten JH, Cheng MH, Anderson MS, Chehab F.F, Gundling K, **Seielstad** M. A Case of Good Syndrome with a Full Genome Analysis of the Patient and Family. Academy of Clinical Laboratory Physicians and Scientists (ACLPS) Annual Meeting, 2014.
36. Genome wide association and exome sequence data analysis for more than 100 traits in Mexican Americans. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
37. A low frequency AKT2 coding variant enriched in the Finnish population is associated with fasting insulin levels. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
38. Gene-centric association tests applied to cardiovascular disease using whole genome sequencing. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
39. An exome-wide sequencing study for type 2 diabetes-associated kidney disease in African Americans. T2D-GENES, American Society of Human Genetics Annual Meetings 2014.
40. Yin, X ; Low, H; Seielstad, M ; Liao, W ; Stahle, M ; Franke, A; Zhang, X ; Liu, J. Trans-ethnic genome-wide meta-analysis identifies multiple novel associations and reveals

ethnic heterogeneity of psoriasis susceptibility. Annual Meeting of the Society-for-Investigative-Dermatology. 2015

41. Nititham, J; Taylor, KE ; Gupta, R ; Ahn, R ; Lee, KM ; Chen, H ; Liu, J ; Seielstad, M ; Ma, A ; Bowcock, AM ; Criswell, LA ; Stahle, M ; Liao, W. Meta-analysis of the TNIP1 region in psoriasis identifies two independent association signals. Annual Meeting of the Society-for-Investigative-Dermatology. 2015
42. Page, GP ; Guo, Y ; Seielstad, M ; Keating, B ; Westhoff, CM; Hoppe, C ; Bordbar, A ; Custer, B ; Lu, Y; Busch, M ; Lu, Y ; Busch, M. Development and Evaluation of a Transfusion Medicine Genome-wide SNP Array. AABB Annual Meeting. 2016
43. Rajan, J ; Deng, X ; Seielstad, M ; Semitala, F ; Kamya, M ; Yoon, C; Cattamanchi, A. Performance Of Gene Expression Signatures In The Context Of Intensified Tuberculosis Case Finding Among People Living With Hiv (plhiv). International Conference of the American-Thoracic-Society (ATS) 2017
44. MARIA ELIZABETH P. MERCADO, SARAH KIM, EVA MARIA C. CUTIONGCO DE LA PAZ, MARK SEIELSTAD, ELIZABETH PAZ-PACHECO, ELIZABETH MURPHY. Discordance between A1C and Glucose for the Diagnosis of Prediabetes in a Filipino-American Population. American Diabetes Association Annual Meeting. 2019

OTHER CREATIVE ACTIVITIES

1. Led and managed an effort to describe haplotype variation in three ethnic populations inhabiting Singapore (Chinese, Malays and Indians) and helped develop a website to distribute the data: http://www.nus-cme.org.sg/SGVP username: Reviewer; password: sgvp

ADDITIONAL RELEVANT INFORMATION

LANGUAGES

French, Italian (primarily reading), Latin (reading only, limited), and Attic Greek (reading only, very limited).