



PEQG22

Population, Evolutionary, and
Quantitative Genetics Conference
June 7–10, 2022



PROGRAM BOOK



GENETICS

 **GSA**

G3 
Genes | Genomes | Genetics

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Genetics Society of America



GSA is an international scientific society representing more than 5,000 researchers and educators around the world. As well as connecting researchers through conferences and career programs, we publish two peer-edited scholarly journals, GENETICS and G3: Genes|Genomes|Genetics. We encourage you to join GSA so you can make use of exclusive member benefits and get involved in the Society's many programs, including professional development training, awards, advocacy, and more. Join us as we work to advance the field and serve our community. Visit genetics-gsa.org for more information.

GENETICS

GENETICS has been innovating since 1916, publishing high quality original research across the breadth of the field.



G3: Genes|Genomes|Genetics is an open access journal that publishes high quality, useful results regardless of perceived impact.

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Sponsors

Conference Sponsors

Genetics Society of America and the organizers gratefully acknowledge the following sponsors:

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GENETICS



General Information

Registration Desk and Badges

You should have received your namebadge in advance via email. You should print and trim this prior to coming to the meeting. Badges will not be printed on-site. In the registration area in Merrill Hall, you will need to show your green check mark obtained from 42Chat (indicating you uploaded your vaccination verification and negative test results) and you will be given a badge holder and lanyard. For admission to the sessions, posters, exhibits, and receptions, you must have your official conference badge loaded into the badge holder and visible.

You can download the Program and Abstract Books on the conference website or access all the information in the Conference App. Certificates of Attendance and Participation can be picked up at the Registration Desk.

Registration Desk Schedule

Tuesday, June 7	12:00 p.m.–6:00 p.m.
Wednesday, June 8	7:00 a.m.–3:00 p.m.
Thursday, June 9	7:00 a.m.–1:00 p.m.

Conference App

In-person participants: Download the GSA Meetings app to your smartphone (available on both iOS and Android platforms) to have meeting information at your fingertips. Once you download the App, you will not need an internet connection to access previously downloaded information. You will only need an internet connection to download updates. Blackberry users and Windows Mobile Device users can access the App through the web desktop version available on the conference website.

Virtual participants: Virtual attendees will use the App to participate in the conference. Sign into the App using your registration badge ID number and last name. The App is available in two formats: Desktop App (for desktop and laptop computers), or Mobile App (for Apple iOS and Android mobile devices).

You can find your registration badge ID in your conference registration confirmation email, which was sent from the address NoReply@Convention-Mail.com.

Presenting Author Index

To search for specific oral and poster presenters, please use the search function in the Conference App.

Access the app at: genetics-gsa.org/peqg-2022/conference-app

Oral Presenters

All speakers must come to the Speaker Ready Room in Merrill Hall I **24 hours before the start of your session** to upload and review your presentation and become familiar with the equipment that will be used in the session room. You will NOT be able to use your own computer or upload your presentation in the session room. The day of your presentation, arrive 30 minutes before the start of your session (not your talk) and let the session chair know that you are there.

Poster Presentations

All poster authors have been invited to upload a pdf and audio overview of their poster. These electronic files will be available through the conference app June 3–30. Be sure to visit the app and leave your questions for the authors. Posters ending in V are only available online. Posters ending in W will be presented in person on Wednesday night (8:30–9:15 p.m. Even, 9:15–10:00 p.m. Odd) and those ending in T will be presented in person on Thursday night (8:30–9:15 p.m. Even, 9:15–10:00 p.m. Odd)

To view a poster online, look for the “Virtual Poster” link near the bottom of each poster’s entry in the App. If provided, the presenter’s personal calendar link is included so that you can set up individual meetings with them.

Posters for the in-person session should be no larger than 3’8” wide by 3’10” tall. Posters that are larger than 3’8” wide by 3’10” tall will be removed.

Please keep personal items with you at all times. GSA cannot be responsible for items left in the hall including but not limited to poster tubes, purses, backpacks, etc.

All in-person posters will be located in the Fireside Pavillion at Asilomar. You must be wearing your official meeting badge to enter the exhibits and posters. Poster presenters who are attending the conference in person have been assigned a presentation time according to the schedule on the following page.

In-person Poster Presentations

Wednesday, June 8	
9:00 a.m.	"W" posters can be mounted on poster board
9:00 a.m.–10:00 p.m.	"W" posters open poster viewing (authors do not have to be present)
8:30 p.m.– 9:15 p.m.	Even "W" poster presentations
9:15 p.m.–10:00 p.m.	Odd "W" poster presentations
10:15 p.m.	"W" posters must be removed
Thursday, June 9	
9:00 a.m.	"T" posters can be mounted on poster board
9:00 a.m.–10:00 p.m.	"T" posters open poster viewing (authors do not have to be present)
8:30 p.m.–9:15 p.m.	Even "T" poster presentations
9:15 p.m.–10:00 p.m.	Odd "T" poster presentations
10:15 p.m.	"T" posters must be removed

Viewing Sessions Online

All Keynote, and Platform sessions will be streamed live. Log in to the Online Planner on your laptop for the best viewing experience. You will also be able to access the live sessions through the App. Five minutes before a session starts, log in using your registration badge ID number and last name. Tap the "Join Webinar" button on the session. The Join Webinar button will be visible 10 minutes before the start of the session. A recording of each session will be available in the session listings on the App within 24 hours after the session ends. The recordings will be available until June 30.

Poster Sessions—To view a poster, look for the "Virtual Poster" link near the bottom of each poster's entry in the App.

Safety Protocols

In-person attendees are required to wear the most protective masks they can access, ideally N95s or KN95s, while attending the conference. If you do not have access to a high-quality mask, a limited supply of complementary masks are available at the Registration Desk in Merrill Hall.

Hand sanitizers will be available in all the meeting rooms and public space.

Coffee breaks will be available just outside of Merrill Hall. Please keep your mask on while in line and only remove to drink your coffee.

Daily self monitoring: If you experience any of the symptoms listed below, do not enter the meeting space. Those staying at the conference hotel should contact the front desk and gsaconferences@genetics-gsa.org to have a rapid test brought to you. Symptoms requiring a rapid test: fever or chills, cough, shortness of breath, fatigue, muscle or body aches, headache, new loss of taste or smell, sore throat, congestion or runny nose, nausea, vomiting or diarrhea.

COVID-19 Testing

[Onsite rapid antigen and PCR COVID tests](#) are available for a fee and by appointment for attendees who need or want to be tested (e.g. to comply with international travel regulations). The testing site will be in Dolphin and is open during the times listed below. Registrants are responsible for making an appointment and paying for any testing they require.



Tuesday, June 7	3:00 p.m.–5:00 p.m.
Wednesday, June 8	12:00 p.m.–2:00 p.m.
Thursday, June 9	12:00 p.m.–2:00 p.m.
Friday, June 10	12:00 p.m.–2:00 p.m.

Complimentary rapid antigen tests will be available to attendees who feel unwell or experience symptoms outside of the hours posted above.

Meals

Meals are not included in the conference registration fee but are included in your guest room rate if you are staying at Asilomar. Guests staying at Asilomar, and those who are staying off-grounds and purchased a meal plan, are invited to eat at Crocker Dining Hall. If you prefer not to eat inside the Dining Hall, you can pick up a to-go meal in Crocker Dining Hall and then sit at the picnic tables available in the Meadow outside or bring your meal back to your room. If you are staying off-property and purchased a meal plan, you can pick up your meal tickets at conference registration in Merrill.

Meals are offered at the following times:

Breakfast: 7:30 a.m.–9:00 a.m.

Lunch: 12:00 p.m.–1:00 p.m.

Dinner: 6:00 p.m.–7:00 p.m.

Due to COVID restrictions, Asilomar is not selling individual meal tickets.

Internet Access

Complimentary Wi-Fi is available in the meeting rooms and Fireside Pavillion.

Network: Asilomar Conference

Password: conference (all lower case).

Job and Meeting Postings

Individuals and institutions offering or seeking employment and organizers of meetings may post notices and resumes on the “Community Notices” bulletin board in the Poster Sessions. Employers are also welcome to post listings in the #jobs channel in the #PEQG22 Slack workspace.

Slack Chat Channels

The #PEQG22 Slack workspace is the place to meet other attendees online during the conference. You can join and create chat channels based on your interests. There are channels for getting technical help, discussing new papers and preprints, sharing job ads, and connecting with other attendees around shared interests.

Security/Lost and Found

For all emergencies and lost and found items, contact Asilomar security by dialing 0 from any house phone. The conference registration desk will be able to assist you as well.

Space

In addition to the many outdoor spaces, there are living rooms available in Lodge, Afterglow, Pirates Den, and Stuck Up Inn if you want to disconnect for a few minutes during a session. Space is available on a first come, first served basis. Please wear your mask.

Parking

Parking is complimentary on Asilomar grounds.

Conference Policies

Code of Conduct

The Genetics Society of America Conferences foster an international community of geneticists and provide an opportunity to discuss scientific advances and form new collaborations.

GSA values your attendance and wants to make your experience productive and inspiring by fostering an open exchange of ideas in a professional setting. Our Code of Conduct was established to communicate a transparent set of standards and guidelines for acceptable behavior at GSA Conferences and to provide a positive, safe, and welcoming environment for all attendees, vendors, volunteers, and staff.

All conference participants (regardless of their role) are expected to follow the Code of Conduct while attending any portion of the meeting, including but not limited to meeting rooms, the exhibit/poster hall, meeting areas in the official conference venue, and social events provided by the meeting or vendors.

Unacceptable Behaviors

Unacceptable behaviors include, but are not limited to:

- Intimidating, harassing, abusive, discriminatory, derogatory, or demeaning speech or actions by any participant and at all related events
- Harmful or prejudicial verbal or written comments or visual images related to gender, gender expression, gender identity, marital status, sexual orientation, race, religion, political orientation, socioeconomic, disability or ability status, or other personal characteristics, including those protected by law
- Inappropriate use of nudity and/or sexual images in public spaces (including presentation slides and posters)
- Deliberate intimidation, stalking, or following
- Violating the rules and regulations of the conference hotel
- Sustained disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Physical assault (including unwelcome touching or groping)
- Real or implied threat of physical harm
- Real or implied threat of professional or financial damage or harm
- Harassing or unwanted photography
- Photographing slides of oral presentations and posters without permission
- Recording of scientific and other sessions without permission

Taking Action or Making a Report

Need to file a complaint? For instructions on how to confidentially report a Code of Conduct violation, please visit genetics-gsa.ethicspoint.com. In addition, GSA staff is available to assist participants in contacting our Ethics Committee to make a report. Please email Tracey DePellegrin, GSA Executive Director, at tracey.depellegrin@genetics-gsa.org.

Consequences of Non-compliance

Anyone asked by GSA staff, a Session Chair, Workshop Leader, Moderator, Presenter, or Zoom representative to stop unacceptable behavior is expected to comply immediately. Retaliation toward GSA or toward someone reporting an incident or after experiencing any of the following consequences will not be tolerated and may result in additional sanctions.

The consequences of non-compliance with GSA's Code of Conduct may include:

- Immediate removal from accessing the online meeting and Slack channels without warning
- Restrictions from future GSA meeting attendance
- Termination of GSA membership or positions on GSA Boards or Committees
- Incidents may be reported to the proper authorities

Accessibility

GSA is committed to assisting attendees with special needs. If you have accessibility questions or requests, please email gsaconferences@genetics-gsa.org.

Diversity and Inclusion

GSA is committed to promoting equality, diversity, and inclusion to create greater opportunity for any individual to fulfill their scientific potential, irrespective of their background, gender, or circumstances. This diversity leads to innovation by attracting the widest possible talent to the community and fostering a greater diversity of ideas, approaches, and perspectives. The Organizing Committee aims to select speakers and session chairs that represent the breadth and diversity of the discipline and conference participants. GSA especially encourages the Committee to select excellent speakers from [groups traditionally underrepresented in science](#).

Social Media/Photo/Video Policy

Live tweeting of presentations is allowed unless the speaker explicitly opts out by stating so at the start of their talk. Taking or sharing photos or videos of posters is permitted only with the presenter's consent during the assigned poster session. Taking photos of posters while the presenter is not present is strictly prohibited. By attending a GSA conference, you grant GSA the right to use your photograph, name, and likeness for use in GSA educational, news, or promotional materials.

Schedule of Events

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Tuesday, June 07

1:00 p.m.–3:00 p.m.	Speaker Ready Room	Merrill
11:00 a.m.–3:00 p.m.	Virtual Posters Take time to view the posters that are available online through the app and leave a question for the author. Posters are available in the app from June 3 to June 30	Online
12:00 p.m.–6:00 p.m.	Registration Show your green validation check mark to pick up your conference materials	Merrill
1:00 p.m.–2:00 p.m.	Conference Success Tips and Welcome from the Early Career Leadership Program	Fred Farr
2:30 p.m.–3:00 p.m.	Getting Involved in GSA's Early Career Professional Development	Fred Farr
3:00 p.m.–5:00 p.m.	COVID-19 Testing by appointment	Dolphin
3:00 p.m.–4:00 p.m.	Multilingual Networking	Fred Farr
4:15 p.m.–5:45 p.m.	Welcome and Opening Keynote from Ryan Hernandez Session Chair: Jeffrey Ross-Ibarra University of California, Davis	Merrill
6:00 p.m.–7:00 p.m.	Dinner	Crocker Dining Hall
6:00 p.m.–7:00 p.m.	Virtual Networking	Online

Wednesday, June 08

7:00 a.m.–1:00 p.m.	Registration Show your green validation check mark to pick up your conference materials	Merrill
7:00 a.m.–1:00 p.m.	Speaker Ready Room	Merrill
7:30 a.m.–9:00 a.m.	Breakfast	Crocker Dining Hall
9:00 a.m.–10:00 p.m.	Open Poster Viewing "W"ednesday Posters	Fireside Pavillion
9:00 a.m.–11:50 a.m.	Platform Session 1 Complex Traits Session Chair: Lorin Crawford, Microsoft Research New England	Merrill

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Wednesday, June 08 (continued)

12:00 p.m.–2:00 p.m.	COVID-19 Testing by appointment	Dolphin
12:00 p.m.–1:00 p.m.	Lunch	Crocker Dining Hall
12:00 p.m.–1:00 p.m.	Virtual Networking	Online
1:30 p.m.–3:45 p.m.	James F. Crow Early Career Researcher Award Finalist Talks Session Chair: Bret Payseur, University of Wisconsin, Madison	Merrill
4:00 p.m.–5:15 p.m.	Platform Session #2 Genetics of Adaptation Session Chair: Daniel Runcie University of California, Davis	Merrill
6:00 p.m.–7:00 p.m.	Dinner	Crocker Dining Hall
7:30 p.m.–8:15 p.m.	Keynote #2 Magnus Nordborg Session Chair: Emilia Huerta-Sanchez, Brown University	Merrill
8:30 p.m.–10:00 p.m.	Poster Session "W"ednesday Poster Presentations 8:30–9:15 p.m. Even Poster Numbers 9:15–10:00 p.m. Odd Poster Numbers	Fireside Pavilion

Thursday, June 09

7:00 a.m.–1:00 p.m.	Registration Show your green validation check mark to pick up your conference materials	Merrill
7:00 a.m.–1:00 p.m.	Speaker Ready Room	Merrill
7:30 a.m.–9:00 a.m.	Breakfast	Crocker Dining Hall
7:30 a.m.–8:30 a.m.	Virtual Networking	Online
9:00 a.m.–10:00 p.m.	Open Poster Viewing "T"hursday Posters	Fireside Pavillion
9:00 a.m.–11:50 a.m.	Platform Session #3 Speciation, Hybridization, and Introgression Session Chair: Rafael Guerrero North Carolina State University	Merrill
12:00 p.m.–2:00 p.m.	COVID-19 Testing by appointment	Dolphin
12:00 p.m.–1:00 p.m.	Lunch	Crocker Dining Hall

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Thursday, June 09 (continued)

12:00 p.m.–1:30 p.m.	Publishing Q&A	Woodlands
1:30 p.m.–3:30 p.m.	Platform Session #4 Genome and Molecular Evolution Session Chair: Rori Rohlf, San Francisco State University	Merrill
3:45 p.m.–5:00 p.m.	Platform Session #5 Experimental Evolution Session Chair: Nancy Chen, University of Rochester	Merrill
5:00 p.m.–5:30 p.m.	Undergraduate Research Experience	Merrill
6:00 p.m.–7:00 p.m.	Dinner	Crocker Dining Hall
7:30 p.m.–8:15 p.m.	Keynote #3 Pleuni Pennings Session Chair: C. Brandon Ogbunu, Yale University <i>Sponsored by Ancestry</i>	Merrill
8:30 p.m.–10:00 p.m.	Poster Session "Thursday Poster Presentations 8:30–9:15 p.m. Even Poster Numbers 9:15–10:00 p.m. Odd Poster Numbers	Fireside Pavillion

Friday, June 10

7:00 a.m.–12:00 p.m.	Speaker Ready Room	Merrill
7:30 a.m.–9:00 a.m.	Breakfast	Crocker Dining Hall
9:00 a.m.–11:50 a.m.	Platform Session #6 Theory and Methods Session Chair: Priya Moorjani, University of California, Berkeley	Merrill
12:00 p.m.–2:00 p.m.	COVID-19 Testing by appointment	Dolphin
12:00 p.m.–1:00 p.m.	Lunch	Crocker Dining Hall
1:30 p.m.–4:50 p.m.	Keynote #4 (Session Chairs) Session Chair: Jeffrey Ross-Ibarra, University of California, Davis	Merrill
6:00 p.m.–7:00 p.m.	Dinner	Crocker Dining Hall
7:30 p.m.–9:30 p.m.	Closing Mixer and Awards	Merrill

Saturday, June 11

7:30 a.m.–9:00 a.m.	Breakfast	Crocker Dining Hall
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Oral Presentation and Workshop Session Listings

Oral Presentation and Workshop Session Listings

Tuesday, June 07

1:00 p.m.–2:00 p.m.

Fred Farr

Conference Success Tips and Welcome from the Early Career Leadership Program

The purpose of this event is to help first-time conference attendees and early career scientists make the most of the conference. Topics covered may include introductions to organizers of the meeting, advice on having meaningful interactions during the conference, a chance to meet other attendees in an informal setting, and an introduction to scientific events and other conference programming.

Tuesday, June 07

2:30 p.m.–3:00 p.m.

Fred Farr

Getting Involved in GSA's Early Career Professional Development

GSA Early Career Leadership Program (ECLP) members will join us in sharing how to get involved in GSA's professional development programming for early career scientists. GSA will walk through upcoming events and programs including how and when to apply to join the ECLP.

Oral Presentation and Workshop Session Listings

Tuesday, June 07

3:00 p.m.–4:00 p.m.

Fred Farr

Multilingual Networking

Join us for this exciting event to network in the language of your choice! At this multilingual networking event, #PEQG22 participants who speak languages other than English have a chance to network and talk about science in their native language or language of choice with other participants.

Tuesday, June 07

4:15 p.m.–5:45 p.m.

Merrill

Welcome and Opening Keynote from Ryan Hernandez

Session Chair

Jeffrey Ross-Ibarra, University of California, Davis

1 4:15 p.m. Welcome **Jeffrey Ross-Ibarra** University of California, Davis

2 4:25 p.m. GSA Welcome

Steve Munger The Jackson Laboratory, Bar Harbor, ME

3 4:40 p.m. Keynote Introduction **Jeffrey Ross-Ibarra** University of California, Davis

4 4:45 p.m. Evolutionary forces shape the genetic architecture of complex traits **Ryan Hernandez** UCSF

Oral Presentation and Workshop Session Listings

Wednesday, June 08

9:00 a.m.–11:50 a.m.

Merrill

Platform Session 1 Complex Traits

Session Chair

Lorin Crawford, Microsoft Research New England

5 9:00 a.m. High-Resolution Exploration of Collateral Sensitivity using Molecularly Barcoded *S. Cerevisiae* **Sam Apodaca** Arizona State University Biodesign Institute

6 9:15 a.m. Shared Features of Complex Trait Architecture Explained by Underlying Selection **Yuval B Simons** Stanford University

7 9:30 a.m. When should we expect adaptation via a highly polygenic response vs selective sweeps? **William Milligan** Columbia University

8 9:45 a.m. Guaranteeing unbiasedness in selection tests based on polygenic scores **Jennifer Blanc** University of Chicago

9 10:00 a.m. Improving Phenotype Prediction by Learning Patterns of Sharing across Multiple Phenotypes **Fabio Morgante** Clemson University

10:15 a.m. Break

10 10:35 a.m. Climate-driven natural selection across protein-coding and cis-regulatory genetic variation **Shannon Hateley** Carnegie Institution for Science

11 10:50 a.m. Genotype-by-Diet interactions unmask cryptic genetic variants that regulate lifespan in outbred *Drosophila* **Luisa F Pallares** Friedrich Miescher Laboratory of the Max Planck Society

12 11:05 a.m. Dominance genetic effects on complex traits in pigs, rats and mice are associated with trans-acting dominance gene expression effects **Leilei Cui** Dr UCL Genetics Institute

13 11:20 a.m. Evolutionary dynamics in simulated gene regulatory networks **Anastasia Teterina** University of Oregon

14 11:35 a.m. ARG-based Association Mapping **Vivian Link** University of Southern California

Oral Presentation and Workshop Session Listings

Wednesday, June 08

1:30 p.m.–3:45 p.m.

Merrill

James F. Crow Early Career Researcher Award Finalist Talks

Session Chair

Bret Payseur, University of Wisconsin, Madison

15 1:30 p.m. James F. Crow Early Career Researcher Finalist Talks **Bret Payseur** University of Wisconsin, Madison

16 1:40 p.m. Range expansion promotes introgression upon secondary contact **Ailene MacPherson** Simon Fraser University

17 2:05 p.m. An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function **Jacob L. Steenwyk** Vanderbilt University

18 2:30 p.m. The genetic basis of tail-loss evolution in humans and apes **Bo Xia** NYU Grossman School of Medicine

19 2:55 p.m. Agricultural adaptation of common waterhemp over the last two centuries **Julia M. Kreiner** University of British Columbia

20 3:20 p.m. Genetic basis of carotenoid coloration in birds. **Malgorzata A Gazda** Institut Pasteur

Wednesday, June 08

4:00 p.m.–5:15 p.m.

Merrill

Platform Session #2 Genetics of Adaptation

Session Chair

Daniel Runcie, University of California, Davis

21 4:00 p.m. Don't put all your eggs in one basket: what stochastic modeling tells us about bet hedger evolution **Maya Weissman** Brown University

22 4:15 p.m. Deciphering the mystery of sorghum tannin domestication in Africa: coevolution among sorghum, human, and bird **Xianran Li** USDA-ARS

23 4:30 p.m. The Population Genetics of Convergent Adaptation in Maize and Teosinte **Silas Tittes** UC Davis

24 4:45 p.m. Identifying the genetic basis of convergent local adaptation in conifers **Tom R Booker** University of British Columbia

25 5:00 p.m. Evolutionary consequences of domestication on the selective effect of new mutations in canids **Carlos Eduardo Guerra Amorim** California State University Northridge

Wednesday, June 08

7:30 p.m.–8:15 p.m.

Merrill

Keynote #2 Magnus Nordborg

Session Chair

Emilia Huerta-Sanchez, Brown University

26 7:30 p.m. The genetics of epigenetics **Magnus Nordborg** Gregor Mendel Institute

Thursday, June 09

9:00 a.m.–11:50 a.m.

Merrill

Platform Session #3 Speciation, Hybridization, and Introgression

Session Chair

Rafael Guerrero, North Carolina State University

27 9:00 a.m. Mating-related barriers to admixture shape ancestry patterns across the baboon genome **Arielle Fogel** Duke University

28 9:15 a.m. Hybrid fitness effects modify fixation probabilities of introgressed alleles **Aaron R Pfennig** Georgia Institute of Technology

29 9:30 a.m. Asymmetric introgression between selfer and outcrosser subspecies of *Clarkia xantiana* across a zone of secondary contact **Shelley Sianta** University of Minnesota

30 9:45 a.m. The spatiotemporal patterns of major human admixture events during the European Holocene **Manjusha Chintalapati** University of California Berkeley

31 10:00 a.m. Population genomics of an entire community of Galápagos finches **Erik Enbody** Santa Cruz

10:15 a.m. **Break**

32 10:35 a.m. Demographic History Inference and the Polyploid Continuum **Ryan N Gutenkunst** University of Arizona

33 10:50 a.m. Replicate hybrid populations reveal shared genome evolution across multiple species **Quinn Langdon** Stanford University

34 11:05 a.m. Molecular and morphological evolution across the most species-rich radiation in mammals **Gregg Thomas** Harvard University

35 11:20 a.m. Testing for a role of parent-offspring conflict in the emergence of postzygotic barriers in *Mimulus* using a combination of genetic mapping and RNA sequencing analysis **Elen Oneal** Duke University

36 11:35 a.m. When and how is introgression adaptive? A tale from two widely distributed sympatric oak species **Ruirui Fu** Zhejiang University

Thursday, June 09

1:30 p.m.–3:30 p.m.

Merrill

Platform Session #4 Genome and Molecular Evolution

Session Chair

Rori Rohlf, San Francisco State University

37 1:30 p.m. Predicting evolutionary divergence and parameters of relocated genes from their expression data **Antara Anika Piya** Florida Atlantic University

38 1:45 p.m. Critical role of insertion preference for the invasion trajectory of transposons **Manisha Munasinghe** University of Minnesota

39 2:00 p.m. Chromosomal inversions shape the genomic landscape of the deer mouse **Olivia S Harringmeyer** Harvard University

40 2:15 p.m. Recombination patterns in corn snakes suggest a tug of war between PRDM9 and promoter-like features **Carla Hoge** Columbia University

41 2:30 p.m. Genomic and Epigenomic Insights into Formation and Evolution of Polyploid Plants and Crops **Z. Jeffrey Chen** The University of Texas at Austin

42 2:45 p.m. Synergistic epistasis of the deleterious effects of transposable elements **Grace YC Lee** University of California, Irvine

43 3:00 p.m. Tracing the evolutionary dynamics of gene retrocopies in house mouse natural populations **Wenyu Zhang** Max Planck Institute for Evolutionary Biology

44 3:15 p.m. Epistatic drift causes gradual loss of predictability in molecular evolution **Yeonwoo Park** University of Chicago

Thursday, June 09

3:45 p.m.–5:00 p.m.

Merrill

Platform Session #5 Experimental Evolution

Session Chair

Nancy Chen, University of Rochester

45 3:45 p.m. Environmental adaptation in house mice: genetic and non-genetic effects on gene expression **Mallory A. Ballinger** University of California, Berkeley

46 4:00 p.m. Using an Evolve + Resequencing experiment to estimate the strength of selection on candidate genes underlying local serpentine adaptation in *Mimulus guttatus* **Amelia H Lawrence** Duke University

47 4:15 p.m. Fitness variation across subtle environmental perturbations reveals local modularity and global pleiotropy of adaptation **Grant Kinsler** Stanford University

48 4:30 p.m. Investigating the genetic determinants of *L. monocytogenes* stress tolerance to food-industry relevant stressors through adaptive laboratory evolution **Tyler Bechtel** University of Massachusetts Amherst

49 4:45 p.m. Pleiotropy is associated with the parallel gene expression evolution during adaptation to a novel environment **Wei-Yun Lai** Vienna Graduate School of Population Genetics

Oral Presentation and Workshop Session Listings

Thursday, June 09

5:00 p.m.–5:30 p.m.

Merrill

Undergraduate Research Experience

Session Chair

Nancy Chen, University of Rochester

50 5:00 p.m. Structure for a Functional Genomics CURE: Comparison of 26 RNAseq pipelines from mapping to functional pathway enrichment using *Daphnia*'s response to caloric restriction **Tonia S Schwartz** Auburn University

51 5:15 p.m. The Pond Team: An example of connecting interdisciplinary research and place-based learning for undergraduate research **Ashley Elias** Missouri Western State University

Thursday, June 09

7:30 p.m.–8:15 p.m.

Merrill

Keynote #3 Pleuni Pennings

Sponsored by Ancestry

Session Chair

C. Brandon Ogbunu, Yale University

52 7:30 p.m. Coding and data science programs for every biology student **Pleuni S Pennings** San Francisco State University

Friday, June 10

9:00 a.m.–11:50 a.m.
Merrill

Platform Session #6 Theory and Methods

Session Chair

Priya Moorjani, University of California, Berkeley

53 9:00 a.m. Improving the estimation of DFE using paired allele frequency and allele age information **Vivaswat Shastry** University of Chicago

54 9:15 a.m. To Scale or Not to Scale: The Influence of Scaling on Forward-in-time Population Genetics Simulations **Amjad Dabi** University of North Carolina at Chapel Hill

55 9:30 a.m. The fitness of an introgressing haplotype **Andrius Jonas Dagilis** University of North Carolina at Chapel Hill

56 9:45 a.m. Uncovering footprints of natural selection through time-frequency analysis of genomic summary statistics **Sandipan Paul Arnab** Florida Atlantic University

57 10:00 a.m. Heritable epigenetic variation facilitates maintenance of genetic variation **Amy Webster** University of Oregon

10:15 a.m. **Break**

58 10:35 a.m. The population genetics of collateral resistance and sensitivity **Sarah Ardell** University of California, San Diego

59 10:50 a.m. Examining polygenic adaptation in time-stratified genome samples with diffusion-based hidden-Markov models **Xiaoheng Cheng** University of Chicago

60 11:05 a.m. Interpretable machine learning improves performance in association, discovery, and prediction **Mariano Alvarez** Avalo

61 11:20 a.m. Response of Quantitative Traits to Directional Selection in Finite Populations **Hannah Götsch** University of Vienna

62 11:35 a.m. Phylogenomic comparative methods: accurate evolutionary inferences in the presence of gene tree discordance **Mark Hibbins** Indiana University

Friday, June 10

1:30 p.m.–4:50 p.m.

Merrill

Keynote #4 (Session Chairs)

Session Chair

Jeffrey Ross-Ibarra, University of California, Davis

63 1:30 p.m. Indirect genetic effects across life cycle stages in a cooperatively breeding bird **Nancy Chen** University of Rochester

64 2:00 p.m. Association and Fine-Mapping with Bayesian Machine Learning Methods **Lorin Crawford** Microsoft Research New England

65 2:30 p.m. How hybrid incompatibilities agglomerate on gene networks **Rafael F. Guerrero** North Carolina State University

3:00 p.m. **Break**

66 3:20 p.m. Timing and causes of evolution of human germline mutation spectrum **Priya Moorjani** University of California, Berkeley

67 3:50 p.m. Could medical privacy be compromised by associations between forensic loci and the expression levels of neighboring genes? **Rori V Rohlf** San Francisco State University

68 4:20 p.m. Uncovering the genetic basis of local adaptation in maize with large-scale multi-environment trials **Daniel Runcie** University of California Davis

Poster Session Listings

All poster authors have been invited to upload a pdf and audio overview of their poster. These electronic files will be available through the conference app June 3–30. Be sure to visit the app and leave your questions for the authors. Posters numbers followed by “V” are only available online. Poster numbers followed by “W” will be presented in person on Wednesday night (8:30–9:15 p.m. Even, 9:15–10:00 p.m. Odd) and those followed by “T” will be presented in person on Thursday night (8:30–9:15 p.m. Even, 9:15–10:00 p.m. Odd).

Evolutionary Genetics	72–193
Population Genetics.	196–331
Quantitative Genetics	336–413
Science & Society.	416–417

Evolutionary Genetics

72W Cross-species incompatibility between a DNA satellite and the *Drosophila* Spartan homolog poisons germline genome integrity **Cara Brand** University of Pennsylvania

73W Cracking Coevolution: Consequences of Space and Genetic Architecture **Victoria Caudill** University of Oregon

74T Coevolution between two essential telomere binding proteins preserves chromosome end-protection **Sung-Ya Lin** University of Pennsylvania

75T Distinct genetic mechanism underlining the trait evolution of male-specific wing spot in *Drosophila elegans* species sub-group **Atee-sha Negi** National Central University

76W The role of continuous geography in parasite local adaptation **Bob Week** Michigan State University

77W Predicting Antibiotic Resistance Through the Utilization and Comparison of Machine Learning Algorithms **Jameel Ali** San Francisco State University

78T Uncovering the mysteries of antibiotic resistance through phylogenetic analysis **MaryGracy Antony** San Francisco State University

79T Somatic Mutations in Mitochondrial DNA of *Drosophila* **Mara Baylis** University of California, Santa Cruz

80W Sex chromosome evolution in beetles **Ryan Bracewell** Indiana University Bloomington

81W Mapping the genomic basis of trophic level adaptation in Lake Malawi cichlid fishes **Aldo Carmona Baez** North Carolina State University

82T Using the *Eucalyptus polybractea* genome improved genetic variant identification compared to using a pseudo-reference **Swapan Chakrabarty** Michigan Technological University

83T Leveraging a de-novo long read assembly for comparative and functional genomics of the *Octopus bimaculoides* **Gabrielle Coffing** University of Oregon

84W Exploiting Natural Variation to Understand the Role of Mkt1p in Post-Transcriptional Gene Regulation **Crystal Crook** University of Arkansas

85W Gene regulation, environmental adaptation, and parallel expression divergence in *Mus musculus domesticus* **Sylvia Durkin** University of California, Berkeley

86T The genetic control of rapid genome content divergence in *Arabidopsis thaliana* **Christopher Fiscus** University of California, Riverside

87T Eukaryote-wide survey suggests unified proximate and ultimate models of *de novo* intron creation **Landen Gozashti** Harvard University

88W Island-specific evolution of a sex-primed autosome in the planarian *Schmidtea mediterranea* **Longhua Guo** UCLA

89W Evolution of the WRKY gene family in *Metrosideros* **Maryam Hadi** University of Nevada, Las Vegas

90T Evolutionary dynamics of stress-activated mobile elements in *Mimulus guttatus* **Lauren Hamm** University of California, Berkeley

91T The genome of shepard's purse (*Capsella bursa-pastoris*) and the genetic basis of extreme cosmopolitanism **Daniel Koenig** University of California Riverside

92W Rodents of Unusual Sperm: Molecular and Phenotypic Evolution of Male Reproduction in Murine Rodents **Emily Kopania** University of Montana

93W Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness **Amanda Kowalczyk** Carnegie Mellon University

94T Rice chromosome architecture at nucleosome-level resolution **Amina Kurbidaeva** New York University

95T Development across evolutionary time at a single cell resolution in the *Caenorhabditis* nematodes **Christopher Large** University of Pennsylvania

96W Investigation of convergent evolution with the southern marsupial mole and other subterranean mammals **Sarah Lucas** University of Utah

97W Ultra-accurate sequencing unveils early somatic lineage selection in *Drosophila melanogaster* **JAKOB MCBROOME** University of California, Santa Cruz

98T Hybridization underlies localized trait evolution in cavefish **Suzanne McGaugh** University of Minnesota

99T Identifying molecular evolutionary rate shifts accompanying dietary transitions in mammals **Wynn Meyer** Lehigh University

100W A *Drosophila* Reference Pangenome Graph **Cade Mirchandani** University of California Santa Cruz

101W Natural selection and correlated landscapes of diversity in the great apes **Murillo Rodrigues** University of Oregon

102T *Saccharomyces cerevisiae* on the rise: Characterizing domestication of *S. cerevisiae* for breadmaking **Margot Ruffieux** North Carolina State University

103T Evolved genetic variation due to epistatic mitochondrial-nuclear interactions **Samantha Sierra-Martinez** University of Miami

104W Gene expression and functional co-evolution in the *Drosophila* female reproductive tract **Rachel Thayer** University of California, Davis

105W Genomic signatures of desert adaptation at gene-rich regions in zebu cattle from the African drylands **Abdulfatai Tijjani** The Jackson Laboratory

106T Genetic structure and multiple paternity in invasive Red Swamp Crayfish in southeastern Michigan, USA **Nicole Adams** Michigan State University

107T Putative drought-adapted SNPs increase in frequency during severe drought **Daniel Anstett** Michigan State University

108W Rapid evolution of abdominal pigmentation in *Drosophila melanogaster* **Skyler Berardi** School of Arts and Sciences, University of Pennsylvania

109W Stability of the genetic structure and association with microhabitat of a wild wheat population over 36 years **Tal Dahan-Meir** The Weizmann Institute of Science

110T Genetic diversity loss in the Anthropocene **Moises Exposito-Alonso** Carnegie Institution for Science, Stanford University

111T Adaptive significance of flowering time plasticity: synthesising 10 years of *Arabidopsis* research in the field. **Alexandre Fournier-Level** The University of Melbourne

112W Genetic variation, covariation, and constraints in the evolution of sexual and clonal reproduction in a plant species **Jannice Friedman** Queens University

113W Genomics Facilitates Evaluation and Monitoring of McCloud River Redband Trout (*Oncorhynchus mykiss stoneri*) **Ensieh Habibi** UC Davis

114T Tracking adaptation to seasonal insecticide pressure in *Drosophila* **Marianthi Karageorgi** Stanford University

115T Runs of homozygosity reveal extensive inbreeding among K'gari Island dingoes **Ana Victoria Leon Apodaca** Pennsylvania State University

116W Effects of inbreeding, drift, and selection on mutation load in the Florida scrub-jay **Mitchell Lokey** Cornell University

117W The impact of climate change on parasite infection of bumblebees depends on mtDNA haplotypes of the host **Oliver Manlik** United Arab Emirates University

118T Genomic and population viability analyses predict extinction risk in the most endangered marine mammal, the vaquita (*Phocoena sinus*) **Jacqueline Robinson** University of California, San Francisco

119T Severe Inbreeding and Mutation Load in the Critically Endangered Devils Hole Pupfish **David Tian** UC Berkeley

120W Evolution of immunity to cestode parasites is a pyrrhic victory **Jesse Weber** University of Wisconsin-Madison

121W The Evolutionary Consequences of Host-Microbe Interactions: *Rapid seasonal evolution of multiple host phenotypes mediated by associated microbes* **Jack Beltz** University of Pennsylvania

122T Finding patterns of antibiotic-resistant infections through the diversity of pathogenic sequence types. **Lorena Benitez-Rivera** San Francisco State University

123T Barcoding the Lenski Long-Term Evolution Experiment for Massively Parallel Bulk Fitness Assays **Jack Edwards** Harvard University

124W Effect of inoculation dose on colonization success in gut-derived microbial communities **Doran Goldman** Stanford University

125W Experimental evolutionary genomics of herbivorous insects on multiple host plant species **Diler Haji** University of California, Berkeley

126T The role of sex in evolution: Sexual conflict and Sexual selection **Sheng-Kai Hsu** Vienna Graduate School of Population Genetics, Vetmeduni Vienna

127T Killer Yeast: Uncovering the evolutionary history and environmental/genetic underliers to the antimicrobial activity of three core metabolic enzymes in *Saccharomyces cerevisiae* **Hannah Kania** University of Michigan-Ann Arbor

128W Three range limit hypotheses tested in climate-manipulated common gardens **Laura Leventhal** Stanford University and Carnegie Institution

129W Diverse mating phenotypes impact the spread of *wtf* meiotic drivers in *Schizosaccharomyces pombe* **Jose Lopez Hernandez** Stowers Institute for Medical Research

130T The efficacy of QTL analysis to predict adaptive variation: a test using experimentally evolved populations of yeast **Helen Murphy** William and Mary

131T Coordinating nutrition and energy allocation in *Drosophila melanogaster*: Genetic mechanisms and evolution **Enoch Ng'oma** University of Missouri

132W Upper bound on the mutational burden imposed by a CRISPR-Cas9 gene drive element **Michael Overton** University of California San Diego

133W Experimental evolution reveals the synergistic genomic mechanisms of adaptation to ocean warming and acidification in a marine copepod **Melissa Pespeni** University of Vermont

134T A mitonuclear reality check on the evolutionary significance of Mother's Curse in *Drosophila*. **David Rand** Brown University

135T Interplay of structural and regulatory evolution in functional evolution of glycolytic enzymes **Mohammad Siddiq** University of Michigan

136W Colonization and evolution after antibiotic perturbation in the human gut microbiome **Katherine Xue** Stanford University

137W Detection of structural variants among inland annual and coastal perennial ecotypes of the yellow monkey flower, *Mimulus guttatus* **Leslie Kollar** Michigan State University

138T Evolution of gene expression patterns of paralogous hormones (IGF1 and IGF2) and paralogous receptors (IGF1R and INSR) across amniotes. **Tonia Schwartz** Auburn University

- 139T** Single-cell RNA sequencing identifies a unique set of cells that give rise to a diverse bone found in the mammalian penis **Caleb Ghione** University of Southern California
- 140W** Genetics of behavioral evolution in giant mice from a predator-free island. **Jered Stratton** University of Wisconsin–Madison
- 141W** Rapid evolution of microbial adherence by host protein domain shuffling. **EmilyClare Baker** University of Oregon
- 142T** The Genetics and Physiology of Switchgrass Local Adaptation Across North America **David Lowry** Michigan State University
- 143T** Sexually concordant and antagonistic genetic variation predicts the evolution of sexual dimorphism over millions of years **Jacqueline Sztepanacz** University of Toronto
- 144W** Viral load minimally affects the intra-host recombination rate of HIV **Elena Romero** University of Washington
- 145W** Understanding the spread of SARS-CoV-2 clusters through an integrated pipeline using UShER, Cluster Tracker and StrainHub **Adriano de Bernardi Schneider** University of California Santa Cruz
- 146T** State-Dependent Evolutionary Phylodynamic Model (SDevo) Infers Boundary-Driven Growth in Hepatocellular Carcinomas **Alison Feder** University of Washington
- 147T** Predicting Antibiotic Resistance Through the Utilization and Comparison of Machine Learning Algorithms **Meris Johnson-Hagler** San Francisco State University
- 148W** Extensive Trans-Species Polymorphism at the Major Histocompatibility Complex in Primates **Alyssa Lyn Fortier** Stanford University
- 149W** Treenome Browser: concurrent phylogeny-aware visualization of millions of genomes **Alexander Kramer** University of California, Santa Cruz
- 150T** The story behind the strains: Examining the phylogeography of wild yeast from woodlands **Jacqueline Pena** University of Georgia
- 151T** The repeated evolution of multiple traits between forest and prairie ecotypes of the deer mouse **Brock Wooldridge** Harvard
- 152W** A high-resolution map of *Drosophila* hybrid pairing connects BLACK heterochromatin to pairing loss, reproductive incompatibility, and DNA underreplication **James Baldwin-Brown** University of Utah
- 153W** Piecing Together the Periodical Cicada Puzzle **Robert Bush** Brigham Young University
- 154T** Identifying patterns of introgression in two species pairs of Texas *Phlox* **Samridhi Chaturvedi** University of California, Berkeley
- 155T** Patterns of population structure and polymorphic reproductive isolation in *Drosophila melanogaster* **Jenn Coughlan** University of North Carolina & Yale
- 156W** Hybrid seed inviability maintains species barriers in *Diplacus* (*Mimulus*) sect. *Eunanus* **Matthew Farnitano** University of Georgia
- 157W** Identification of reinforcement mutations with targeted long-read sequencing in *Phlox* **Austin Garner** Harvard University
- 158T** The temporal and genomic scale of selection against hybrids **Jefrey Groh** University of California, Davis
- 159T** Hotspots of disruption in placental regulatory gene networks reflect a common genetic architecture underlying hybrid placental dysplasia in rodents **Emily Moore** University of Montana
- 160W** Hybridization alters the shape of the genotypic fitness landscape, increasing access to novel fitness peaks during adaptive radiation **Austin Patton** University of California, Berkeley
- 161W** Color adaptation during the repeated domestication of grain amaranth **Markus Stetter** University of Cologne
- 162T** Recreating the mitochondrial endosymbiosis that gave rise to eukaryotes **Cara Hull** University of Southern California
- 163T** Genetic Analysis of Segregating Recessive Variation in the Nematode *Caenorhabditis becei* **Jose Salome-Correa** New York University
- 164V** Unique structure and positive selection promote the rapid divergence of *Drosophila* Y chromosomes **Ching-Ho Chang** Fred Hutchinson cancer research center
- 165V** STR mutation rates do not perfectly track cell divisions but covary with maternal age **Michael Goldberg** University of Washington
- 166V** Parallel Expansion and Divergence of the Hyr/Iff-like (Hil) Adhesin Family in Pathogenic *Candida* Yeasts **Bin He** University of Iowa
- 167V** The genetic basis of inherited DNA methylation variation in *Arabidopsis thaliana* **Eriko Sasaki** Kyushu University
- 168V** Transformation-mediated chromosome synthesis and replacement in eukaryotic cells **Alessandro Luis Venega Coradini** University of Southern California
- 169V** Mixing genome annotation methods in a comparative analysis inflates the apparent number of lineage-specific genes **Caroline Weisman** Princeton University
- 170V** Second time's the charm: adaptive evolution following a prior invasion increases the potential distribution of an invasive weed **Andhika Putra** University of Melbourne
- 171V** Characterizing Pareto fronts: Trade-offs in the yeast growth cycle constrain adaptation **Jason Tarkington** Stanford University
- 172V** Tissue-specific regulatory evolution involved in divergent migratory behavior **Matthew Louder** Texas A&M University
- 173V** Selection inference on epigenetic marks: Implications for the evolution of germline mutation rates **Kasper Hansen** Johns Hopkins University
- 174V** Coevolution is pervasive between unrelated glycosylation pathways and points to potential disease modifiers **Holly Thorpe** University of Utah
- 175V** Mutualism-enhancing mutations dominate early adaptation in a microbial community **Sandeep Venkataram** Stanford University
- 176V** Species-specific chromatin landscape determines how transposable elements shape genome evolution **Yuheng Huang** UC-Irvine
- 177V** Structural variation in the 6.5 Gb genome of the flowering plant *Phlox drummondii* **Danielle Khost** Harvard University
- 178V** Genome-wide Effects of the Y Chromosome on Gene Expression and Genome Architecture in *Drosophila melanogaster* **Matt Metzloff** Cornell University
- 179V** Cytonuclear stoichiometry in the wake of genome duplication **Joel Sharbrough** New Mexico Institute of Mining and Technology
- 180V** TMv01, an active mobile element in the genome of the fern, *Marsilea vestita* **Sruthi Srinivasan** University of Maryland College Park

181V The effect of crossbreeding on the transcriptome profiling of indigenous cattle populations: a case study **Mohammad Hossein Banabazi** Swedish University of Agricultural Sciences (SLU)

182V Detecting poaching hotspots, trade centers and sex-biased killing from tiger seizures: Implication in effective wildlife conservation **Sudhanshu Mishra** Uttaranchal University

183V Heat adaptation in cross-kingdom pathogenic fungus *Fusarium oxysporum* **Dilay Hazal Ayhan** University of Massachusetts Amherst

184V A multivariate approach to understanding the genetic basis of reproductive resource allocation **Joseph Gunn** Joseph Gunn

185V The response to selection across hundreds of traits in a century-long barley experiment **Jill Marzolino** University of California, Riverside

186V Can synergistic pleiotropy explain the low parallelism of temperature mediated gene expression evolution? **Dagny Asta Runarsdottir** Institute of population genetics, University of Veterinary Medicine Vienna

187V Effect of larval crowding on transcriptomic plasticity across populations **Tejashwini Hegde** University of Veterinary Medicine (Vetmeduni), Vienna

188V Genomic signature of sexual reproduction in a Bdelloid rotifer **Matthew Meselson** Harvard University

189V *In-silico* cross-contamination affects inference of genetic relationships in *Saccharomyces cerevisiae* **Audrey Ward** University of Georgia

190V Genetic Architecture and Temporal Analysis of Developmental Delay in Intra-species *Caenorhabditis briggsae* Hybrids **Joseph Ross** Cal. State Univ., Fresno

191V Genome-wide recombination rate plasticity in response to heat stress in *Drosophila pseudoobscura* **Laurie Stevison** Auburn University

192V Pervasive Under-Dominance in Gene Expression as Unifying Principle of Biomass Hybrid Vigor in *Arabidopsis thaliana* **Wei Yuan** Max Planck Institute for Biology

193V Early stages of butterfly speciation are associated with widespread gene expression divergence in sensory tissues **Wei Zhang** Peking University

Population Genetics

196W Revealing the dynamics of sunflower domestication with archaeological DNA **Benjamin Blackman** University of California, Berkeley

197W Genomic evidence for ancient migration routes along South America's Atlantic coast **Andre Luiz Campelo dos Santos** Florida Atlantic University

198T Genetic insights into the social organization of 13 Siberian Neanderthals **Laurits Skov** Dept of Molecular & Cell Biology

199T Hominin and faunal turnovers identified at Denisova Cave with sediment DNA **Elena Zavala** Max Planck Institute for Evolutionary Anthropology

200W The Genomics of Highly Variable Physiological Response to Temperature **Amanda DeLiberto** University of Miami

201W mRNA expression explains metabolic and thermal tolerance trait variation **Melissa Drown** University of Miami

202T Characterizing *Mimulus guttatus* adaptation to serpentine soil **Allison Gaudinier** UC Berkeley

203T Untangle the quantitative genetics of self and heterospecific pollen rejection during pollen-pistil interactions **Robin Hopkins** Harvard University

204W An agent-based model of signaling in *Bacillus subtilis* biofilms **Obadiah Mulder** University of Southern California

205W Refining Polygenic Score History Estimation from Reconstructed Ancestral Recombination Graphs **Dandan Peng** University of Southern California

206T Genome associations with soil phosphorus availability in sorghum and maize. **Fausto Rodriguez Zapata** North Carolina State University

207T Integrative pathway analysis of metabolites reveal genetic architecture of complex traits and disease **Courtney Smith** Stanford University

208W The influence of demographic history and genetic architecture on complex phenotypes via runs of homozygosity **Zachary Szpiech** Pennsylvania State University

209W Experimental Evolution of Hypoxia Tolerance in *Drosophila melanogaster* **Dan Zhou** Univ California, San Diego

210T Epistatic constraint on RNA secondary structure drives the evolution of SARS-CoV-2 **Mahsa Alemrajabi** Florida Atlantic University

211T The Evolutionary Patterns of Recombination in North American Gray Wolves (*Canis lupus*) and Domestic Dog (*C. familiaris*) **Christina Del Carpio** University of California, Los Angeles

212W Understanding the heterogeneity in gene regulatory responses to misfolded protein toxicity **Rachel Eder** Arizona State University

213W Assessing signatures of selection on transposable elements by accounting for non-uniform transposition rate **Mitra Menon** UC Davis

214T Human populations exhibit correlated abundances and variation of tandem repeat content. **Iskander Said** Cornell

215T Nematode genomes reveal a shift in mutation spectrum in the Chernobyl Exclusion Zone **Sophia Tintori** New York University

216W Allelic and array size variation at human centromeres **Carl Veller** University of California, Davis

217W Effects of mating system on the molecular evolution and expression of genes in the male reproductive tract of *Peromyscus* mice **Erin Voss** University of California Berkeley

218T Seasonal plasticity and adaptive fluctuations of gene expressions of *D. melanogaster* **Yang Yu** University of Virginia

219T Tracking the origins and rapid rise of two distinct insecticide resistance haplotypes **Jennifer Baltzegar** North Carolina State University

220W The genomic basis and repeatability of rapid seasonal evolution **Mark Bitter** Stanford University

221W When B is shaped like a U: is weak selection on deleterious alleles important? **Vincent Buffalo** University of Oregon

222T The battle of the sexes in humans is highly polygenic **Jared Cole** University of Texas at Austin

223T Estimation of selection components in a pedigreed population of Florida Scrub-Jays **Elissa Cosgrove** Cornell University

224W Does adaptation to past viral infections involve changes in protein stability in host virus-interacting proteins? **Chenlu Di** University of Arizona

225W Relentless Selection: Trait divergence under high gene flow **Moritz Ehrlich** University of Miami

226T Evolutionary dynamics in the human gut microbiome from infancy through adulthood **Nandita Garud** University of California, Los Angeles

227T Selection on gene expression under salinity stress in Rice **Sonal Gupta** New York University

228W Genomic basis of climatic adaptation and parallel evolution in house mice from North and South America **Yocelyn Gutierrez Guerrero** University of California, Berkeley

229W Using blood group serology and whole genome sequence data to identify malaria-protective variants introduced through admixture in Oman **Paige Haffener** University of Utah

230T A two-step adaptive walk rewires nutrient transport in a challenging edaphic environment **Angela Hancock** Max Planck Society

231T Contrasting the tempo and mode of adaptation on the X chromosome and the autosomes in *Drosophila melanogaster* **Mariana Harris** University of California, Los Angeles

232W Polygenic adaptation is not a major driver of disparities in disease mortality across global populations **Ujani Hazra** Georgia Institute of Technology

233W A fundamental constraint on adaptation of a biological module **Minkyu Kim** University of California, San Diego

234T Fitness effects for *Ace* insecticide resistance mutations are determined by ambient temperature **Anna Maria Langmüller** Cornell University

235T The impact of background selection on complex traits **Xinyi Li** University of Chicago

236W Genetic Basis of Lethal Alleles in Nature **Sarah Marion** Duke University

237W Balanced Inversions help maintain sexually antagonistic polymorphism **Christopher McAllester** UW Madsion

238T Plasticity in body size in response to diet among wild derived strains of house mice from the Americas **Megan Phifer-Rixey** Monmouth University

239T Allele ages reveal signature of balancing selection in human populations **Alyssa Pivirotto** Temple University

240W A heterogeneous landscape of selection and interactions in genes revealed by two-locus statistics **Aaron Ragsdale** University of Wisconsin-Madison

241W Strong, recent selective sweeps reshape genetic diversity in freshwater bivalve *Megalonias nervosa* **Rebekah Rogers** UNC Charlotte

242T Genetic constraint of complex traits for drought adaptation in Arabidopsis **Megan Ruffley** Carnegie Institution for Science

243T Large-scale comparative population genetics identifies repeated targets of natural selection in birds **Timothy Sackton** Harvard Univ

244W Allelic gene conversion frequently turns sweeps on single-origin *de novo* mutations into soft sweeps **Daniel Schrider** University of North Carolina

245W Ancestry-associated selection signatures in Pacific Islanders **Jan Sokol** Boston University School of Medicine

246T A new test of balancing selection and its application to data from humans **Vivak Soni** ASU

247T Signatures of positive and negative selection in the human gut microbiome **Richard Wolff** University of California, Los Angeles

248W Inferring polygenic selection from GWAS summary statistics for multiple traits and populations **Alexander Xue** Cold Spring Harbor Laboratory

249W Comparative genomics of *Aspergillus oryzae* genomes from different clades reveals signatures of artificial selection in primary and secondary metabolism in domesticated environments **katherine chacon-vargas** University of Massachusetts Amherst

250T Evolution of modifiers of conformity **Kaleda Denton** Stanford University

251T Do forensic genetic markers compromise medical privacy? **Jhony Zavaleta** San Francisco State University

252W Batch effects in population genomic studies with low-coverage whole genome sequencing data: Causes, detection, and mitigation **Runyang Lou** Cornell University

253W Genetic ancestors of an admixed population **Lily Agranat-Tamir** Stanford

254T The Polynesian Settlement of the Hawaiian Archipelago **Javier Blanco Portillo** Stanford University

255T Drivers of Diversity and Divergence in the Sea **Gideon Brad-burd** Michigan State University

256W The role of pollinators in shaping plant population genetic structure **Grace Burgin** Harvard University

257W Population structure and historical demography of a reptile species that has evolved insular dwarfism on the California Channel Islands. **Amanda Clark** Auburn University

258T Genomic diversity and invasion history of *Drosophila suzukii* **Siyuan Feng** University of Wisconsin Madison

259T The genomic status and evolutionary history of *Culex pipiens* mosquito ecotypes **Yuki Haba** Princeton University

260W Population genomics of large white-footed mice in the Boston Harbor archipelago **Emma Howell** University of Wisconsin-Madison

261W Uncovering natural histories of mutator alleles in budding yeast **Pengyao Jiang** University of Washington

262T Whole genome sequences of 3,000 individuals from India: Insights into South Asian Population History and Disease **Elise Ker-doncuff** University of California, Berkeley

263T Effects of isolation by distance on principal components **Lesly Lopez** University of California, Merced

264W Inference of the demographic history of commensal gut microbes **Jonathan Mah** University of California, Los Angeles

265W The evolutionary history and adaptive divergence of *Daphnia pulex* **Connor Murray** University of Virginia

266T Drivers of dispersal and genetic variation for bee species in a fragmented tropical habitat **Sevan Suni** University of San Francisco

267T Accumulation of hybrid incompatibilities on scale-free networks with purifying selection **Evgeny Brud** North Carolina State University

268W Human-Mediated Admixture in South American Neotropical Cats **Maximilian Genetti** University of California Santa Cruz

269W The genetic, organismal, and evolutionary origin of color pattern diversity in *Phylllobates* poison-dart frogs **Roberto Márquez** University of Michigan

270T Genomic islands of speciation have independent rates of molecular evolution across a butterfly hybrid zone **Tianzhu Xiong** Harvard University

271T Tensor decomposition-based feature extraction and classification to detect natural selection from genomic data. **Md Ruhul Amin** Florida Atlantic University

272W Expanding the Use of Generative Adversarial Networks in Population Genetics to Create Artificial Sequence Alignments **William Booker** University of North Carolina at Chapel Hill

273W Exploiting Genetic Variation to Model Localised Homing Gene Drives **Benjamin Camm** University of Melbourne

274T From pattern to function: eco-evolutionary representations of complex spatial structure for the new era of spatial biology **Oana Carja** Carnegie Mellon University

275T The effect of consanguinity on X-chromosomal and autosomal genomic sharing **Daniel Cotter** Stanford University

276W Efficient analysis of allele frequency variation from whole-genome pool-sequencing data **Lucas Czech** Carnegie Institution for Science

277W Neural ADMIXTURE: rapid population clustering with autoencoders **Albert Dominguez Mantes** Stanford University

278T Evolution of Evolvability In Rapidly Adapting Asexual Populations **James Ferrare** Stanford University

279T An EM algorithm for detecting general diploid selection in time series allele frequency data **Adam Fine** University of Chicago

280W Emergent evolutionary forces in spatial models of microbial growth in the human gut microbiota **Olivia Ghosh** Stanford University

281W SLiM 4: Multispecies eco-evolutionary modeling **Benjamin Haller** Cornell University

282T Digital image processing using alpha-molecules to detect selective sweeps **Mahmudul Hasan** Florida Atlantic University

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Week, Bob 76W
Weir, Bruce 331V
Weisman, Caroline 169V
Weissman, Maya 21
Weller, Cory 362T
Whitehouse, Logan S 300W
Widmayer, Samuel J 363T
Williams-Simon, Patricka 379T
Wolff, Richard 247T
Woods, Patrick 364W
Wooldridge, Brock 151T
Woolfolk, Maya L 365W
Wright, Kevin M 366T

X

Xia, Bo 18
Xiong, Tianzhu 270T
Xu, Frederick 380W
Xue, Alexander T 248W
Xue, Katherine S 136W

Y

Ye, Kaixiong 367T
Yu, Yang 218T
Yuan, Wei 192V
Yunusbayev, Bayazit 303V

Z

Zavala, Elena 199T
Zavaleta, Jhony A 251T
ZHANG, Gaotian 368W
Zhang, Wei 193V
Zhang, Wenyu 43
Zhou, Dan 209W
Zhu, Carrie 369W
Zhuang, Xuan 370T
Żukowska, Weronika B 328V

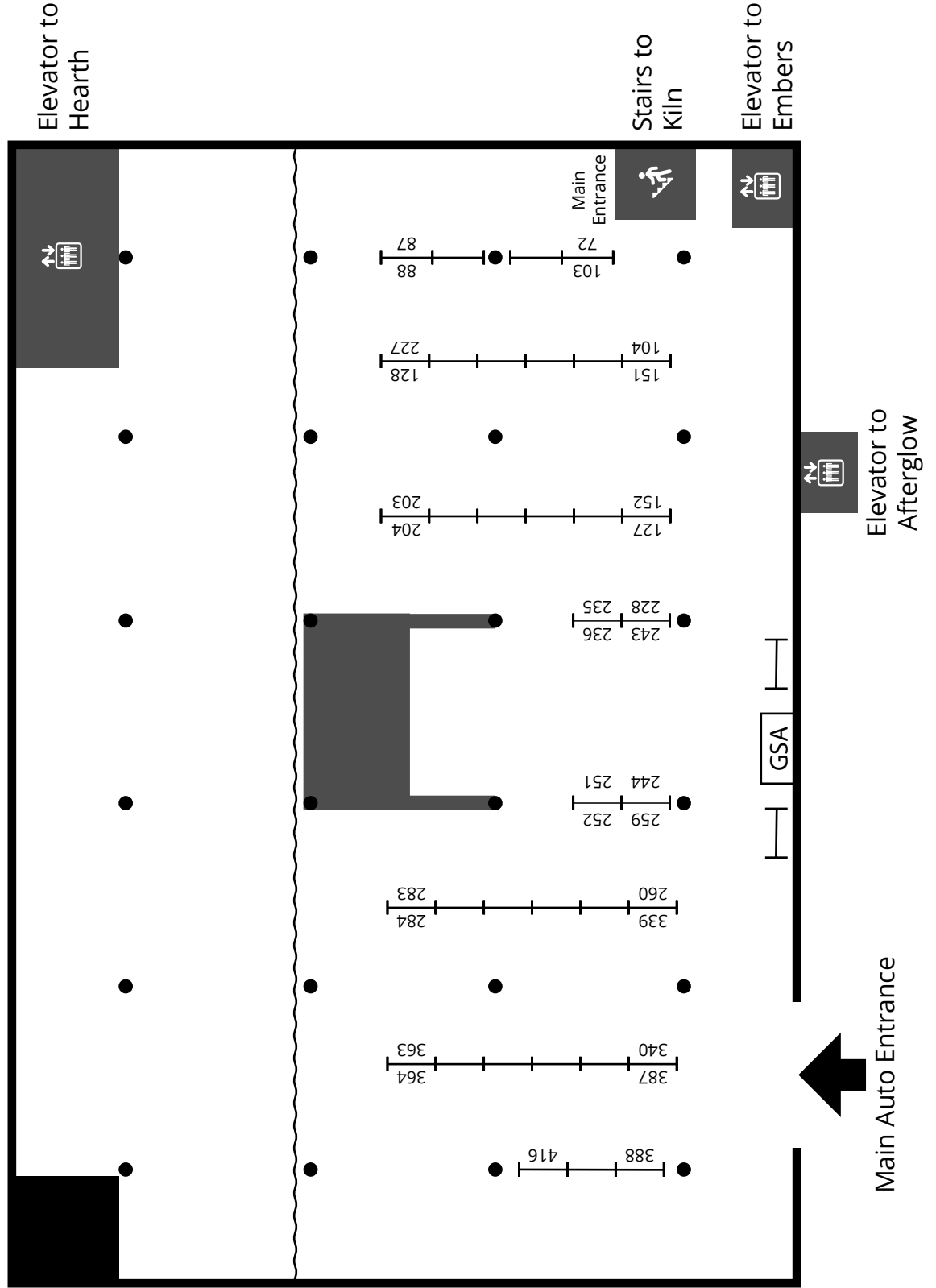
Poster and Exhibit Map



PEQG22

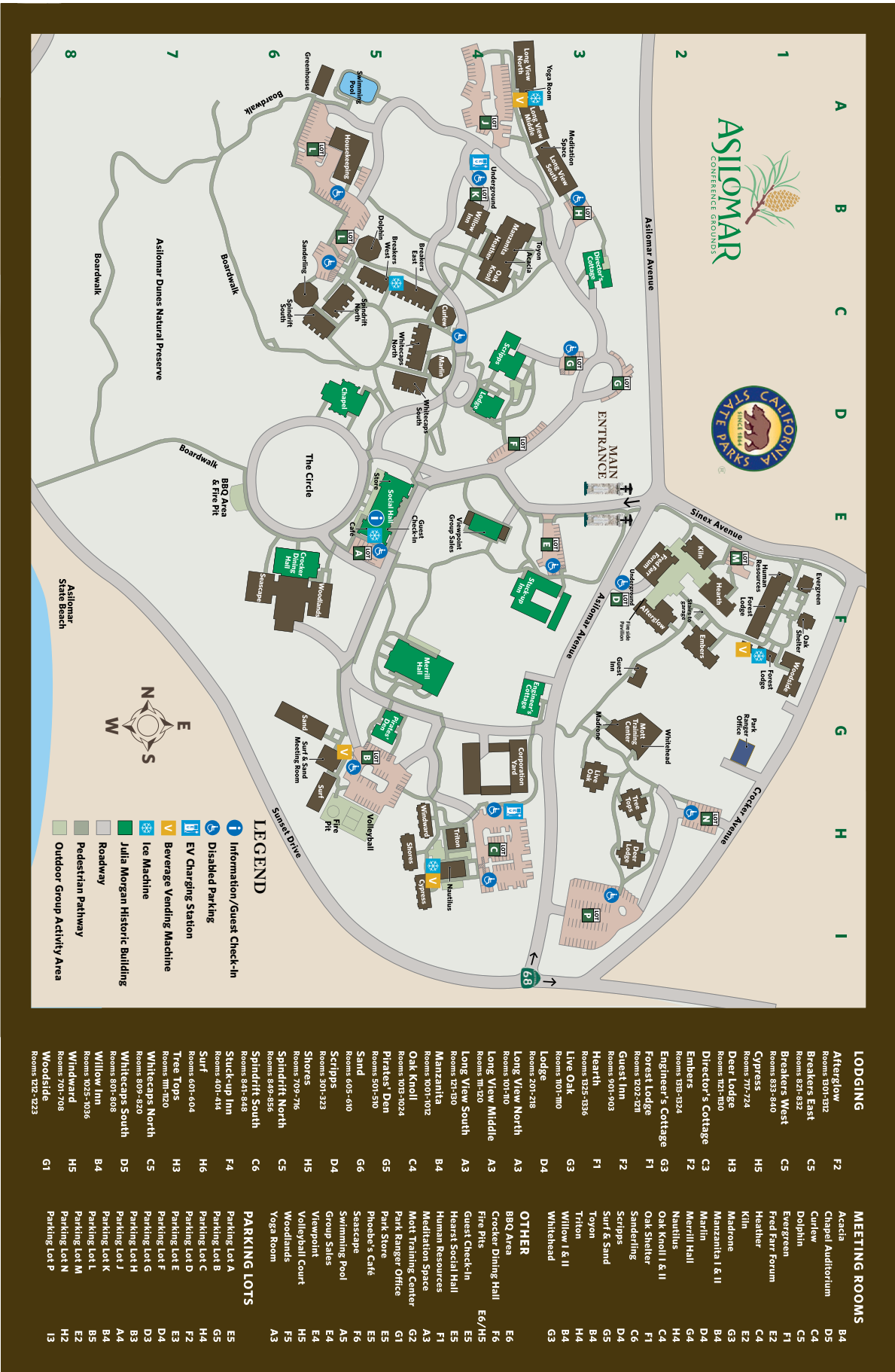
Population, Evolutionary, and
Quantitative Genetics Conference

POSTERS Fireside Pavillion



Floorplan

Property Map



USBiological Life Sciences

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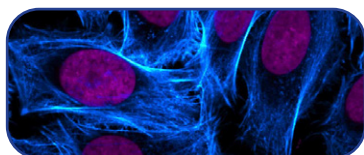
Since those early years, we have greatly expanded and now supply over 1 Million research reagents in the categories of: Antibodies, Biochemicals, Cell Culture Media, ELISA Kits and Proteins (Native and Recombinant).

Our prices are specially reduced for GSA Members and we encourage suggestions where lower cost reagents are needed for common or uncommon reagents.

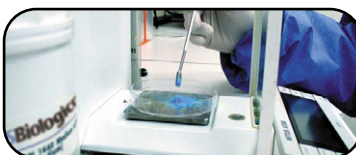
We look forward to continuing our partnership with GSA and their members.

Regards,

***Warren Shore
President
United States Biological***



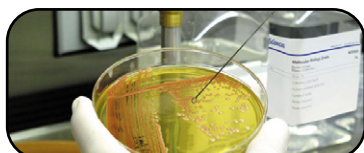
Antibodies



Biochemicals



Biologicals



Cell Culture Media



Molecular Biology



Kits & Assays

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 Genetics Society of America

TAGC 2024

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